Mathematical Epidemiology Model Analysis on the Dynamics of COVID-19 Pandemic

Abayneh Fentie Bezabih, Geremew Kenassa Edessa, Purnachandra Rao Koya

Department of Mathematics, Wollega University, Nekemte, Ethiopia

Email address:
abaynehf@hu.edu.et (A. F. Bezabih), gbonsa.kena@gmail.com (G. K. Edessa), drkpraophd@gmail.com (P. R. Koya)

Abstract: In the present work, Susceptible-Exposed-Infected-Recovered-Susceptible (SEIRS) mathematical model for COVID-19 Pandemic is formulated and analyzed. The positivity, boundedness, and existence of the solutions of the model are proved. The Disease-free equilibrium point and endemic equilibrium points are identified. Local Stability of disease-free Equilibrium point is checked with the help of Next generation matrix. Global stability of endemic equilibrium point is proved using the Concept of Liapunove function. The basic reproduction number for Novel Corona virus pandemic is computed as $R_0 = (\alpha\beta\Lambda) / [(\delta + \mu) (\beta + \delta + \mu) (\gamma + \delta + \mu)]$ which depend on six different parameters. It is observed that if basic reproduction number is less than one, then number of cases decrease over time and eventually the disease dies out, and if the basic reproduction number is equals to one, then number of cases are stable. On the other hand, if the basic reproduction number is greater than one, then the number of cases increase over time gets worth. Sensitivity analysis of the basic reproduction number is done with respect to each parameter. It is observed that only some parameters Λ, α, β have high impact on the basic reproduction number. Consequently, with real data on the parameter it is helpful to predict the disease persistence or decline in the present situation. Lastly, numerical simulations are given using DEDiscover software to illustrate analytical results.

Keywords: COVID-19 Pandemic, Stability Analysis, Next Generation Matrix, Basic Reproduction Number, Simulation

1. Introduction

Corona virus disease 2019 (COVID-19) is an infectious disease that can cause illnesses range from the common cold to much more severe illnesses like SARS, MERS, and COVID-19 [1-3].

Severe acute respiratory syndrome corona virus 2 (SARS-Cov-2), commonly known as Novel Corona virus (nCoV), is a single, positive-stranded, RNA virus that belongs to Nidoviral type, which are responsible for the Current covid-19 Pandemic [4]. A species that host corona virus is known to be bat. Recent research shows that SARS-CoV-2 virus and bat corona virus have 96% identical genetic sequences [1, 2].

The novel corona virus (nCoV) or COVID-19 may show signs of fever, cough, breathing difficulties, organ failures or even death of whole society. [1, 5]. It can be transmitted from person to person even before any actual signs appeared, which is difficult to prevent and control [5]. Researchers all round the world have been trying to know how the virus spreads and find out effective ways control the outbreak. Compared the reproduction number R_0 of severe acute respiratory syndrome of H1N1 virus (1.25), SARS (2.2-3.6), the R_0 of COVID-19 indicates awful potential transmission as 2.2, 3.8 and 2.68 by different researcher in the world. WHO published an estimated R_0 of COVIDh-19 is (1.4-2.5). The larger basic reproduction number R_0 the greater power of transmission rate of disease and the smaller the basic reproduction number R_0 the lower the transmission rate of the disease [1, 4, 6]

According to WHO report, the virus that causes COVID-19 is mainly transmitted through droplets generated when an infected person coughs, sneezes, or speaks. These droplets are too heavy to hang in the air. They quickly fall on floors or surfaces. You can be infected by breathing in the virus if you are within 1 meter of a person who has COVID-19, or by touching a contaminated surface and then touching your

eyes, nose or mouth before washing your hands. There is no specific medicine to prevent or treat corona virus disease (COVID-19). People may need supportive care to help them breathe. If you have mild symptoms, stay at home until you have recovered. You can relieve your symptoms if you:(i) rest and sleep, (ii) keep warm, (iii) drink plenty of liquids, and (iv) use a room humidifier or take a hot shower to help ease a sore throat and cough. People with COVID-19 develop signs and symptoms, including mild respiratory symptoms and fever, on an average of 5-6 days after infection (mean incubation period 5-6 days, range 1-14 days).

According to WHO report, most people infected with the COVID-19 virus will experience mild to moderate respiratory illness and recover without requiring special treatment. Older people, and those with underlying medical problems like cardiovascular disease, diabetes, chronic respiratory disease, and cancer are more likely to develop serious illness.

Novel Corona virus (2019-nCoV), Situation Report-1, Initially the Disease spread in china, republic of Korea, and Thailand and It was 282 number of confirmed cases reported globally up to 21 January 2020. Coronavirus disease 2019 (COVID-19) Situation Report-94, shows that there are 2, 695, 418 peoples are infected and 188, 804 peoples are died and 739, 871 peoples are recovered from Corona virus disease (Covid-19) pandemic up to 23 April 2020. Therefore it is urgent to study and provide more scientific information for a better understanding of the novel corona virus (nCoV) or Covid-19. Thus susceptible-Exposed-infectious-recovered-susceptible (SEIRS) model is adopted to estimate the dynamics and the potential spread based on the current data of cases, to calculate the basic reproduction number R_0 under different scenarios of the epidemics and to draw preliminary conclusions about the effectiveness of public health measures like hygiene, Masks.

The main purpose of this article is to formulate and to made Mathematical model analysis that describes the disease transmission dynamics of COVID-19 based on different literature reviews. The paper will create better understanding of the current corona virus pandemic. In [2, 4] SEIR epidemic model of a data-driven analysis is done, and some parametric estimation is computed based on curve fitting and numerical methods. In [2] SIRS model of COVID-19 is constructed in the case of Indian country.

This paper is organized as follows: In section 2, Mathematical model formulation Model assumptions, description of variables and parameters, Model diagram and Model equations are presented. In section 3, Mathematical Analysis of Model: positivity, Boundedness, and existence of solution, Equilibrium points are Discussed. In section 4, Stability Analysis of Equilibrium points; Next Generation matrix, Local Stability of disease free equilibrium point (LSDFEP), Global Stability of endemic equilibrium point (GSEEP), Basic Reproduction number will be presented. In Section 5, Simulation Study of our model equations are performed with initial conditions given for the variables and some values are assigned for the parameters. The results and discussion are given in section 6. In Section 7, Conclusions and Recommendations are drawn depend on the stability analysis and simulation study.

2. Mathematical Model Formulation

In the present study SEIRS model of COVID-19 is Constructed as follows. The total populations are divided into four classes: (i) Susceptible class denoted by S Contains population which are capable of becoming infected (ii) Exposed class denoted by E consists of populations being infected but not infectious and waiting for a short period time is called latency period.(iii) Infected class denoted by I consists of population which are infected with COVID-19 and are also infectious and (iv) Recovered class denoted by R consists of recovered class from infectious disease COVID-19. Mathematical SEIRS model of COVID-19 is formulated based on the following hypotheses so as to predict the past or future dynamics of COVID-19 progression and transmission Dynamics in the world.

(i)   The size of total population is assumed to be constant, $N = S(t) + E(t) + I(t) + R(t)$

(ii) Both the number of births and death are may not be equal and populations are well mixed.

(iii) Susceptible class are recruited into the compartment $S(t)$ at a constant rate Λ

(iv) The Exposed class has short incubation period and not yet infective but moved to infective class at rate β

(v)   Susceptible class are infected when they come into contact with COVID-19 patient and the disease transmitted according to bilinear interaction rate $\alpha\lambda(t)S$ where, $\lambda(t) = I(t)$ which is force of infection.

(vi) Recovered class revert to the susceptible class after losing their immunity at a rate ρ

(vii) All types of population suffer natural mortality at a rate μ.

(viii) All types of population suffer die due to Covid-19 Pandemic at a rate δ

(ix) All parameters in the model are positive.

Table 1. Notations and description of model variables.

Variable	Description
S(t)	Number of susceptible individuals at time t
$E(t)$	Number of Exposed individuals at time t (infected but not infectious)
I(t)	Number of infective individuals at time t (infectious class)
R(t)	Number of recovered individuals at time t (removed, or immune)

Parameter	Description
Λ	*Constant influx of new susceptible*. With this rate new susceptible class will Recruited and will enter into susceptible class
α	*Infection rate or Contact rate or effective contact rate*. With this rate covid-19 transfer from compartment S to E
β	*Latency transfer rate*. With this rate exposed class moves from compartment E to compartment I.
γ	*Recovery rate or removal rate*. With this rate infected class moves from compartment I to R
ρ	*Loss immunity (re-infection rate)*. With this rate recovered class moves from compartment R to S
δ	*Death rate due to infection of COVID-19*. With this rate all class of compartment suffer due to the diseases.
μ	*Natural death rate*. With this rate all class of Compartment suffer natural death rate.

Having the above assumptions, variables, and parameters the model diagram can be given as in Figure 1
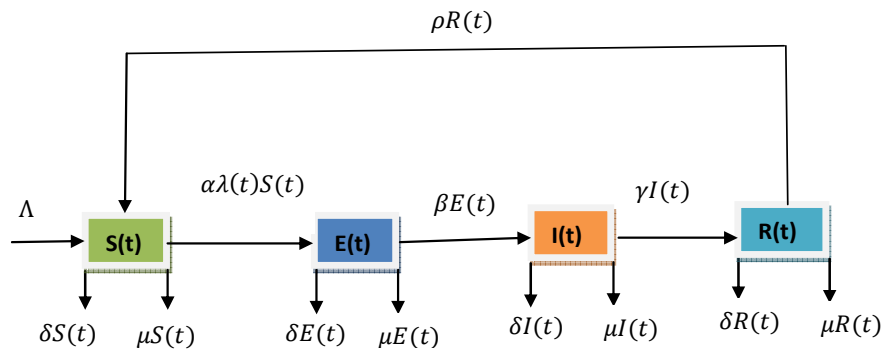

Figure 1. *Model diagram.*

Based on the assumptions, the notations of variables, parameters, and Model diagram, system of ordinary differential equations are formulated as follows:

$$dS/dt = \Lambda + \rho R(t) - \alpha S(t)I(t) - \delta S(t) - \mu S(t) \quad (1)$$

$$dE/dt = \alpha S(t)I(t) - \beta E(t) - \delta E(t) - \mu E(t) \quad (2)$$

$$dI/dt = \beta E(t) - \gamma I(t) - \delta I(t) - \mu I(t) \quad (3)$$

$$dR/dt = \gamma I(t) - \rho R(t) - \delta R(t) - \mu R(t) \quad (4)$$

with initial conditions,
$S(0) > 0, E(0) \geq 0, I(0) \geq 0, R(0) \geq 0$, $\lambda(t) = I(t)$ which is force of infection

3. Mathematical Model Analysis

In this section mathematical model analysis part is Presented. The analysis consists of the following features:(i) positivity of solutions the model, (ii) Boundedness of solutions of the model, (iii) Existence of solutions of the model, (iv) equilibrium points of the model: Disease free equilibrium points, endemic equilibrium points (v) Basic reproduction number (vi) Stability analysis of equilibrium points: Local stability of disease free equilibrium point and (vii) Global stability of endemic equilibrium point

3.1. Positivity, Boundedness, and Existence of Solution

In order to show that the model is biologically valid, it is required to prove that the solutions of the system of ordinary differential equations (1)-(4) are positive and bounded for all time [7].

Theorem 1 (Positivity) Solutions of the model equations (1)–(4) together with the initial conditions ,

$S(0) > 0, E(0) \geq 0, I(0) \geq 0, R(0) \geq 0$ are   always positive That is, the model variables $S(t), E(t), I(t)$, and $R(t)$ are positive for all t and will remain in $\mathbb{R}_+^4$.

Proof: Positivity of the model variables is shown separately for each of the model variables, $S(t), E(t), I(t)$, and $R(t)$.

Positivity of $S(t)$: The model equation (1) given by $dS/dt = \Lambda + \rho R - \alpha SI - \delta S - \mu S$ can be expressed without loss of generality, after eliminating the positive terms ($\Lambda + \rho R$) which are appearing on the right hand side, as an inequality as $dS/dt \geq -(\alpha I + \delta + \mu)S$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $S(t) \geq e^{-(\alpha I + \delta + \mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent, Hence, it can be concluded that $S(t) \geq 0$.

Positivity $E(t)$: *The* model equation (2) arranged as $dI/dt = \alpha SI - \beta E - \delta E - \mu E$ can be expressed without loss of generality, after eliminating the positive term (αSI) which are appearing on the right hand side, as an inequality as $dE/dt \geq -(\beta + \delta + \mu)E$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $E(t) \geq e^{-(\beta + \delta + \mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent. Hence, it can be concluded that $E(t) \geq 0$.

Positivity of $I(t)$: The model equation (3) arranged $dI/dt = \beta E - \gamma I - \delta I - \mu I$ can be expressed without loss of generality, after eliminating the positive term (βE) which are appearing on the right hand side, as an inequality as $dI/dt \geq -(\gamma + \delta + \mu)I$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $I(t) \geq e^{-(\gamma + \delta + \mu)t}$. Recall that an exponential function is always

non–negative irrespective of the sign of the exponent. Hence, it can be concluded that $I(t) \geq 0$.

Positivity of $R(t)$: The model equation (4) arranged $dR/dt = \gamma I - \rho R - \delta R - \mu R$ can be expressed without loss of generality, after eliminating the positive term (γI) which are appearing on the right hand side, as an inequality as $dR/dt \geq -(\rho + \delta + \mu)R$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $R(t) \geq e^{-(\rho+\delta+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent. Hence, it can be concluded that $R(t) \geq 0$. Thus, the model variable $S(t), E(t), I(t),$ and $R(t)$ representing population size of different class are positive quantities and will remain in $\mathbb{R}_+^4$ for all t.

Theorem 2 (Boundedness) The positive solutions of the system of model equations (1)-(4) are bounded. That is, the model variables $S(t), E(t), I(t),$ and $R(t)$ are bounded for all t.

Proof: Recall that each population size is bounded if and only if the total population size is bounded. Hence, in the present case it is sufficient to prove that the total population size $N = S(t) + E(t) + I(t) + R(t)$ is bounded for all t. It can be shown that all feasible solutions are uniformly bounded in a proper subset $\Omega \in \mathbb{R}_+^4$ where the feasible region Ω is given by

$\Omega = \{(S, E, I, R) \in \mathbb{R}_+^4; \, N \leq (\Lambda/(\delta + \mu))\}$ It is clear that the derivative of total population with respect to time t is given by

$dN/dt = [dS/dt] + [dE/dt] + [dI/dt] + [dR/dt]$. Then summation of all the four model equations (1)-(4) as follows:

$$dN/dt = [\Lambda + \rho R - \alpha SI - \delta S - \mu S] + [\alpha SI - \beta E - \delta E - \mu E] + [\beta E - \gamma I - \delta I - \mu I] + [\gamma I - \rho R - \delta R - \mu R]$$

which simplified $N(t)/dt = \Lambda - (\delta + \mu)(S + E + I + R)$. This can be written as $dN(t)/dt = \Lambda - (\delta + \mu)N(t)$ Now, $\Lambda - (\delta + \mu)N(t) \geq 0$ if $\Lambda \geq (\delta + \mu)N(t)$ which is $\Lambda/(\delta + \mu) \geq N(t) = S + E + I + R \geq 0$. Thus it can be concluded that $N(t)$ is bounded as it is shown that $0 \leq N(t) \leq (\Lambda/(\delta + \mu))$. Therefore, $(\Lambda/(\delta + \mu))$ is an upper bound of $N(t)$. Hence, feasible solution of the system of model equations (1)-(4) remains in the region Ω which is positively invariant set. Thus, the system is biologically meaningful and mathematically well posed in the domain Ω. it is sufficient to consider the dynamics of the populations represented by the model system (1)-(4) in that domain. Therefore, it can be summarized the result of theorem 2 as the model variables $S(t), E(t), I(t),$ and $R(t)$ are bounded for all t.

Theorem 3 (Existence) Solutions of the model equations (1)–(4) together with the initial conditions,

$S(0) > 0, E(0) \geq 0, I(0) \geq 0, R(0) \geq 0$ exist in $\mathbb{R}_+^4$ i.e. the model variables $S(t), E(t), I(t),$ and $R(t)$ exist for all

t and will remain in $\mathbb{R}_+^4$.

Proof: Let the system of equation (1)-(4) arranged as follows: $f_1 = \Lambda + \rho R - \alpha SI - (\delta + \mu)S$

$$f_2 = \alpha SI - (\beta + \delta + \mu)E$$

$$f_3 = \beta E - (\gamma + \delta + \mu)I$$

$$f_4 = \gamma I - (\rho + \delta + \mu)R$$

According to Derrick and Grossman theorem, let us now define the feasible region Ω that has been discussed under primarily results boundedness of the solutions,

$\Omega = \{(S, E, I, R) \in \mathbb{R}_+^4; \, N \leq (\Lambda/(\delta + \mu))\}$

Then equations (1)–(4) have a unique solution if $(\partial f_i)/(\partial x_j), i, j = 1, 2, 3, 4$ are continuous and bounded in Ω [7]. Here, $x_1 = S, x_2 = E, x_3 = I, x_4 = R$, The continuity and the boundedness are shown in Table 3 as follows:

***Table 3.** Partial derivatives of functions with respect of model variables.*

For f_1:	For f_3:
$\|(\partial f_1)/(\partial S)\| = \|-\alpha I - (\delta + \mu)\| < \infty$	$\|(\partial f_3)/(\partial S)\| = 0 < \infty$
$\|(\partial f_1)/(\partial E)\| = 0 < \infty$	$\|(\partial f_3)/(\partial E)\| = \|\beta\| < \infty$
$\|(\partial f_1)/(\partial I)\| = \|-\alpha S\| < \infty$	$\|(\partial f_3)/(\partial I)\| = \|-(\gamma + \delta + \mu)\| < \infty$
$\|(\partial f_1)/(\partial R)\| = \|\rho\| < \infty.$	$\|(\partial f_3)/(\partial R)\| = 0 < \infty$
For f_2:	For f_4:
$\|(\partial f_2)/(\partial S)\| = \|\alpha I\| < \infty$	$\|(\partial f_4)/(\partial S)\| = 0 < \infty$
$\|(\partial f_2)/(\partial E)\| = \|-(\beta + \delta + \mu)\| < \infty$	$\|(\partial f_4)/(\partial E)\| = 0 < \infty$
$\|(\partial f_2)/(\partial I)\| = \|\alpha S\| < \infty$	$\|(\partial f_4)/(\partial I)\| = \|\gamma\| < \infty$
$\|(\partial f_2)/(\partial R)\| = 0 < \infty$	$\|(\partial f_4)/(\partial R)\| = \|-(\rho + \delta + \mu)\| < \infty$

Thus, all the partial derivatives , $(\partial f_i)/(\partial x_j), i, j = 1, 2, 3, 4$ exist, continuous and bounded in Ω. Hence, by Derrick and Groosman theorem, a solution for the model (1)-(4) exists and is unique.

To understand the dynamics of the system, it is necessary to identify equilibrium points of the model Equation. An equilibrium solution is a steady state solution of the model equations (1)-(4) in the sense that if the system begins at such a state, it will remain there for all times. In other words, the population sizes remain unchanged and thus the rate of change

for each population vanishes. Equilibrium points of the model are found, categorized, stability analysis is done and the results have been presented in the following sub-sections.

3.2. Disease Free Equilibrium Point

Disease free equilibrium points are steady state solutions where there is no disease in the population. In the absence of the disease this implies that $I(t) = R(t) = 0$ and the right hand side of the model is equal to zero.

Thus $\Lambda - (\delta + \mu)S = 0$ which implies $S = \Lambda/(\delta + \mu)$.

Thus, the disease-free equilibrium point of the model equation in (1)–(4) above is given by,

$$E(S, \ E, \ I, \ R) = (\Lambda/(\delta + \mu), \ 0, \ 0, \ 0)$$

3.3. Endemic Equilibrium Point

The endemic equilibrium point $E^*\{S^*, E^*, I^*, R^*\}$ in the feasible region is a steady state solution where the disease persists in the population. The endemic equilibrium point is obtained by setting rates of changes of variables with respect to time in model equations (1)-(4) to zero. That is, setting

$dS/dt = dE/dt = dE/dt = dR/dt = 0$ the model equations can be written as the system of non linear equations

$$\Lambda + \rho R - \alpha SI - aS = 0 \tag{5}$$

$$\alpha SI - bE = 0 \tag{6}$$

$$\beta E - cI = 0 \tag{7}$$

$$\gamma I - dR = 0 \tag{8}$$

Where, $a = \delta + \mu, b = \beta + \delta + \mu, c = \gamma + \delta + \mu, d = \rho + \delta + \mu$ solving equations (7) and (8) will give expression for I and R in terms of variable E as follows:

$$I = (\beta/c)E \tag{9}$$

$R = (\gamma/d)I = (\gamma/d)(\beta/c)E$, This expression could be re-written as

$$R = (\beta\gamma/dc)E \tag{10}$$

Now substitute (9) and (10) into (6) so as to solve E which results $\alpha S(\beta/c)E - bE = 0$

This can be arranged $[\alpha S(\beta/c) - b]E = 0$ However, E does not vanish, since the disease is assumed endemic and it is a computation of non zero equilibrium point of the system. Thus the only meaningful solution $\alpha S(\beta/c) - b = 0$, then solution is given by the expression

$$S^* = [bc]/[\alpha\beta] \tag{11}$$

Then substituting equations (9), (10) and (11) into (5) give $\Lambda + \rho[(\beta\gamma/dc)E] - \alpha(bc/\alpha\beta) - a(bc/\alpha\beta) = 0$. after some algebraic simplifications an expression for I^* can be obtained as

$$E^* = [dc\{bc(\alpha + a) - \alpha\beta\Lambda\}]/[\alpha\beta^2\gamma\rho] \tag{12}$$

Finally, substitution of I^* in (10) and (11) will give expressions for I^* and R^* in terms of parameters

$$I^* = [d\{bc(\alpha + a) - \alpha\beta\Lambda\}]/[\alpha\beta\gamma\rho] \tag{13}$$

$$R^* = [\{bc(\alpha + a) - \alpha\beta\Lambda\}]/[\alpha\beta\rho] \tag{14}$$

Therefore the endemic equilibrium points computed above is given by

$$E^*(S^*, \ E^*, \ I^*, \ R^*)$$
$$= ([bc]/[\alpha\beta], \ [dc\{bc(\alpha + a) - \alpha\beta\Lambda\}]/[\alpha\beta^2\gamma\rho], \ [d\{bc(\alpha + a) - \alpha\beta\Lambda\}]/[\alpha\beta\gamma\rho], \ [\{bc(\alpha + a) - \alpha\beta\Lambda\}]/[\alpha\beta\rho])$$

3.4. Basic Reproductive Number

The basic reproduction number represent the average number of new infections generated by each infected person [7-9]. The higher value of R_o the speedy the disease transmission rate and the Smaller values of R_o the slower the disease transmission rate [12]. There are three options for the values of R_o (i) $R_o < 1$ means the number of new cases will decrease over time and eventually the outbreak will end on its own.(ii) $R_o = 1$ means the cases are stable. (iii) $R_o > 1$ means the outbreak is self-sustaining unless effective control measures are implemented. According to WHO Determining factors of basic reproduction number R_o: (i) *infectious period*- how long the infection is contagious, for instance flu typically up to 8 days and in children up to 2 weeks. The longer an infection is contagious for the higher the reproduction number.(ii) *Contact rate*-how many people an infected person comes into contact with R_o will be lower if a person stays at home, higher if they are out and about. (iii) *Mode of transmission* (shedding potential): *rapid speed transmission*, if the disease transmitted by airborne, flu or measles, no physical contact or fomite necessary, and *Slower transmission,* the disease transmitted by body fluids, Ebola, Hepatitis B, C, or HIV. [1, 5, 9] In the discussion of disease transmission if 20% of infected individuals are responsible for 80% of transmissions those spreaders is called *Super-*

spreaders and if 80% of infected individuals are responsible for 20% of transmissions are called *mini-spreaders.* [1, 5]

To drive the general reproduction number for the formulated model of Covid-19 under the discussion of primary results. $S^* \geq \Lambda/a$, if and only if $[bc]/[\alpha\beta] \geq \Lambda/a$.

Without losing original generality dividing both sides of the inequality by $[bc]/[\alpha\beta]$ yields $1 \geq (\alpha\beta\Lambda)/(abc) = R_0$, where the letters notation a, b, c and d are given by $a = \delta + \mu, b = \beta + \delta + \mu, c = \gamma + \delta + \mu, d = \rho + \delta + \mu$ and hence the basic reproduction number of the model (1)-(4) would be $R_0 = (\alpha\beta\Lambda)/[(\delta + \mu)(\beta + \delta + \mu)(\gamma + \delta + \mu)]$.

4. Stability Analysis

4.1. Stability Analysis of the Disease Free Equilibrium

In absence of the infectious disease, the model equations have a unique disease free steady state E_0.

It is shown that DFEP of model (1)-(4) is given by $E_0 = \{[\Lambda/(\delta + \mu)], \ 0, \ 0, \ 0\}$. Now local stability analysis of DFEP is presented in the following theorem and proved with the help of next generation matrix.

Theorem 4 [Local Stability of Disease-free equilibrium points (LSDFEP)] The model equations (1)-(4) is locally asymptotically stable at disease free equilibrium point (DFEP) E_0

Proof: Consider the right hand side expressions of the equations (1)-(4) as functions to compute Jacobian matrix

$$dS/dt = \Lambda + \rho R - \alpha SI - aS \equiv f(S, \quad E, \quad I, \quad R)$$

$$dE/dt = \alpha SI - bE \equiv g(S, \quad E, \quad I, \quad R)$$

$$dI/dt = \beta E - cI \equiv h(S, \quad E, \quad I, \quad R)$$

$$dR/dt = \gamma I - dR \equiv k(S, \quad E, \quad I, \quad R)$$

Where, $a = \delta + \mu, b = \beta + \delta + \mu, c = \gamma + \delta + \mu, d = \rho + \delta + \mu$ Now the Next generation matrix of functions (f, g, h, k) with respect to $(S, \quad E, \quad I, \quad R)$ is given by

$$J(S \quad E \quad I \quad R) = \begin{bmatrix} -\alpha I - a & 0 & -\alpha I & \rho \\ \alpha I & -b & 0 & 0 \\ 0 & \beta & -c & 0 \\ 0 & 0 & \gamma & -d \end{bmatrix}$$

Therefore the Next generation matrix J of model at the disease free equilibrium E_0 reduces to

$$J[(\Lambda/a) \quad 0, \quad 0, \quad 0] = \begin{bmatrix} -a & 0 & (-\alpha \Lambda)/a & \rho \\ 0 & -b & (-\alpha \Lambda)/a & 0 \\ 0 & \beta & -c & 0 \\ 0 & 0 & \gamma & -d \end{bmatrix}$$

Then the eigen values of $J(E_0)$ are computed from characteristic equation $det[J(E_0) - \lambda I] = 0$.

$$\begin{vmatrix} -a - \lambda & 0 & (-\alpha \Lambda)/a & \rho \\ 0 & -b - \lambda & (-\alpha \Lambda)/a & 0 \\ 0 & \beta & -c - \lambda & 0 \\ 0 & 0 & \gamma & -d - \lambda \end{vmatrix} = 0$$

$$(-a - \lambda) \begin{vmatrix} -b - \lambda & (-\alpha \Lambda)/a & 0 \\ \beta & -c - \lambda & 0 \\ 0 & \gamma & -d - \lambda \end{vmatrix} = 0$$

$$(-a - \lambda)(-d - \lambda) \begin{vmatrix} -b - \lambda & (-\alpha \Lambda)/a \\ 0 & -c - \lambda \end{vmatrix} = 0$$

$$(-a - \lambda)(-d - \lambda)(-b - \lambda)(-c - \lambda) = 0$$

Thus the four eigen values of the matrix are found as $\lambda_1 = -a \lambda_2 = -d \lambda_3 = -b \lambda_4 = -c$

$$\lambda_1 = -(\delta + \mu) \, \lambda_2 = -(\rho + \delta + \mu) \, \lambda_3 = -(\beta + \delta + \mu) \, \lambda_4 = -(\gamma + \delta + \mu)$$

Therefore, it is concluded that the LSDFEP E_0 of the system of differential equations (1)-(4) is locally asymptotically stable due to all eigen value is negative.

4.2. Global Stability Analysis of Endemic Equilibrium Point

The Global stability Analysis of endemic equilibrium point $E^*(S^*, \quad E^*, \quad I^*, \quad R^*)$ is stated in Theorem 5 and proved by taking appropriate liapunove function. [7, 8]

Theorem 5 [Global Stability of endemic equilibrium point (GSEEP)] The endemic equilibrium point $E^*(S^*, \quad E^*, \quad I^*, \quad R^*)$ is globally asymptotically stable.

Proof:

Let

$$L(S, \quad E, \quad I, \quad R) = m_1 (s - s^*)^2/2 + m_2 (E - E^*)^2/2 + m_3 (I - I^*)^2/2 + m_4 (R - R^*)^2/2 \text{ [7, 8]}$$

$$dL/dt = m_1(s - s^*)\{ds/dt\} + m_2(E - E^*)\{dE/dt\} + m_3(I - I^*)\{dI/dt\} + m_4(R - R^*)\{dR/dt\} \tag{15}$$

Now substitute the model equation (1)-(4) into (15)

$$dL/dt = m_1(s - s^*)\{\Lambda + \rho R - \alpha SI - aS\} + m_2(E - E^*)\{\alpha SI - bE\}$$

$$+ m_3(I - I^*)\{\beta E - cI\}$$

$$+ m_4(R - R^*)\{\gamma I - dR\}$$

Take out S, E, I, Rand put as change

$$dL/dt = m_1(s - s^*)(s - s^*)\{[(\Lambda + \rho R)/S] - \alpha I - a\} + m_2(E - E^*)((E - E^*))\{(\alpha SI/E) - b\}$$

$$+ m_3(I - I^*)(I - I^*)\{(\beta E/I) - c\}$$

$$+ m_4(R - R^*)(R - R^*)\{(\gamma I/R) - d\}$$

By rearranging and take out negative sign from the bracket it could be obtained as

$$dL/dt = -m_1(s - s^*)^2\{-[(\Lambda + \rho R)/S] + \alpha I + a\} - m_2(E - E^*)^2\{-(\alpha SI/E) + b\}$$

$$- m_3(I - I^*)^2\{-(\beta E/I) + c\}$$

$$- m_4(R - R^*)^2\{-(\gamma I/R) + d\}$$

Thus it is possible to set m_1, m_2, m_3, m_3 are non negative   integers such that $dL/dt \leq 0$ and endemic equilibrium point

is globally stable.

5. Numerical Simulation

In this section, the numerical simulation of model equations (1)-(4) is carried out using the software DE Discover 2.6.4. For Simulation purpose, a set of meaningful values are assigned to the model parameters. A set of initial conditions are given to the model variables. These sets of parametric values are given in Tables 4 and Model equations and parameter is arranged for DEDiscover software in this way for simulation purpose:

dS/dt=Lambda+Rho*R-Alpha*S*I-(Delta+Mu)*S // the number of Susceptible class

dE/dt=Alpha*S*I-(Beta+Delta+Mu)*E // the number of Exposed class

dI/dt=Beta*E-(Gamma+Delta+Mu)*I // the number of infective class

dR/dt=Gamma*I-(Rho+Delta+Mu)*R // the number of Recovered class

***Table 4.** Parameter values used for Simulation.*

Parameter	Value	Reference
Λ	271.230	[3]
α	2.50000	[2]
β	0.14280	[1]
γ	0.06600	[3]
ρ	0.000095	[5]
δ	0.13100	estimated
μ	0.000001	[5]

Using the parameter values given in Table 2 with different initial conditions in model equations (1)-(4) a simulation is done and the results are given in Figure 2-5.

From Figure 2, it is observed that when the number of exposed individual increases then the number of infected people will increase that leads to the decrease on the susceptible and recovered populations. Figure 3, shows all those class of population changing for some time and eventually the populations will be constant. Thus in any situations there will exist those class of populations and continue in stable state after some time in future.

From Figure 4, recovered and infected populations are inversely proportional. That is if the population gets greater the number of infection, then will be less the number of recovery may be due to lack of resources or management, and Similarly, from Figure 5, exposed and infected populations are directly proportional. If there is more infection in the community, there will be more exposed individual and the less infected community, the less the exposed community.
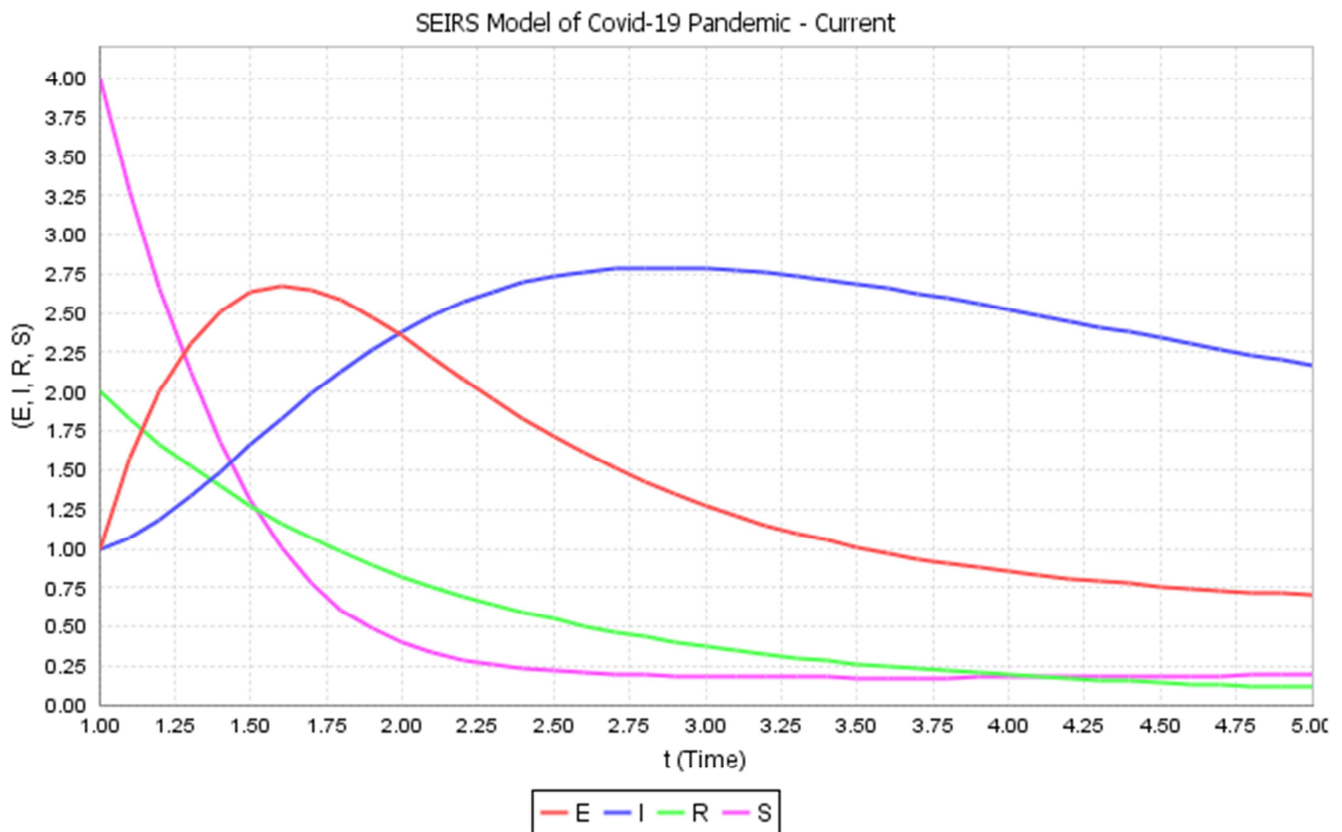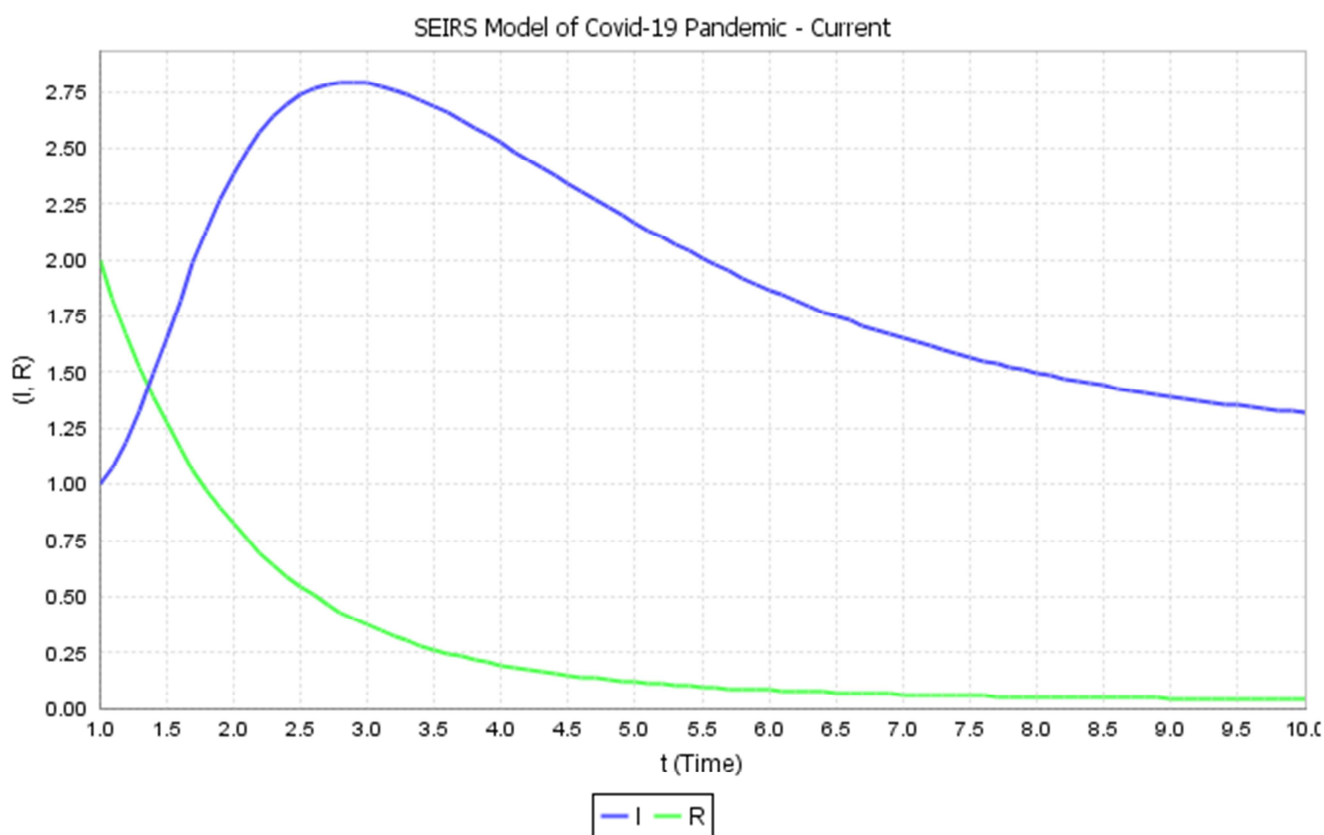

***Figure 2.** Time series plot for all variables with different initial condition.*
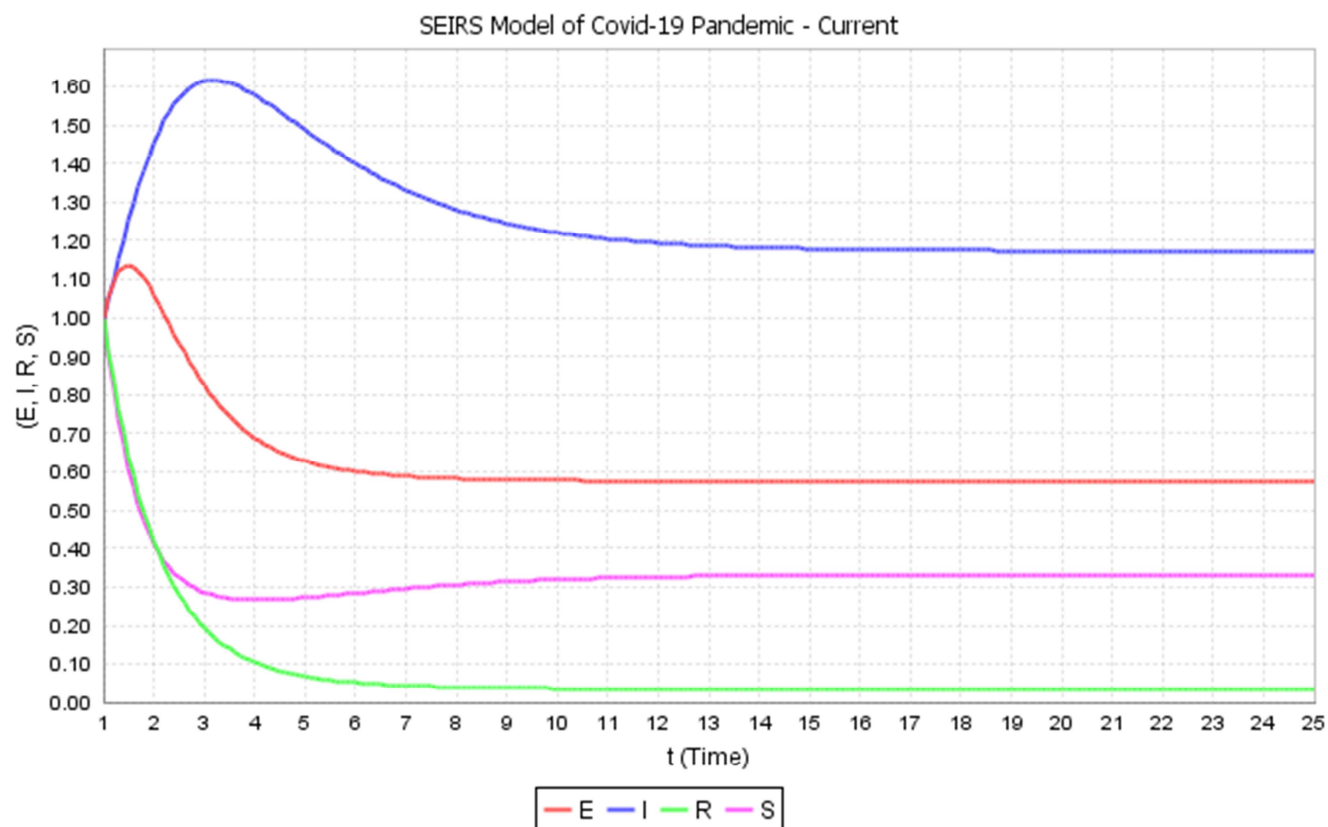
Figure 3. *Time series plot for all variables with same initial condition.*

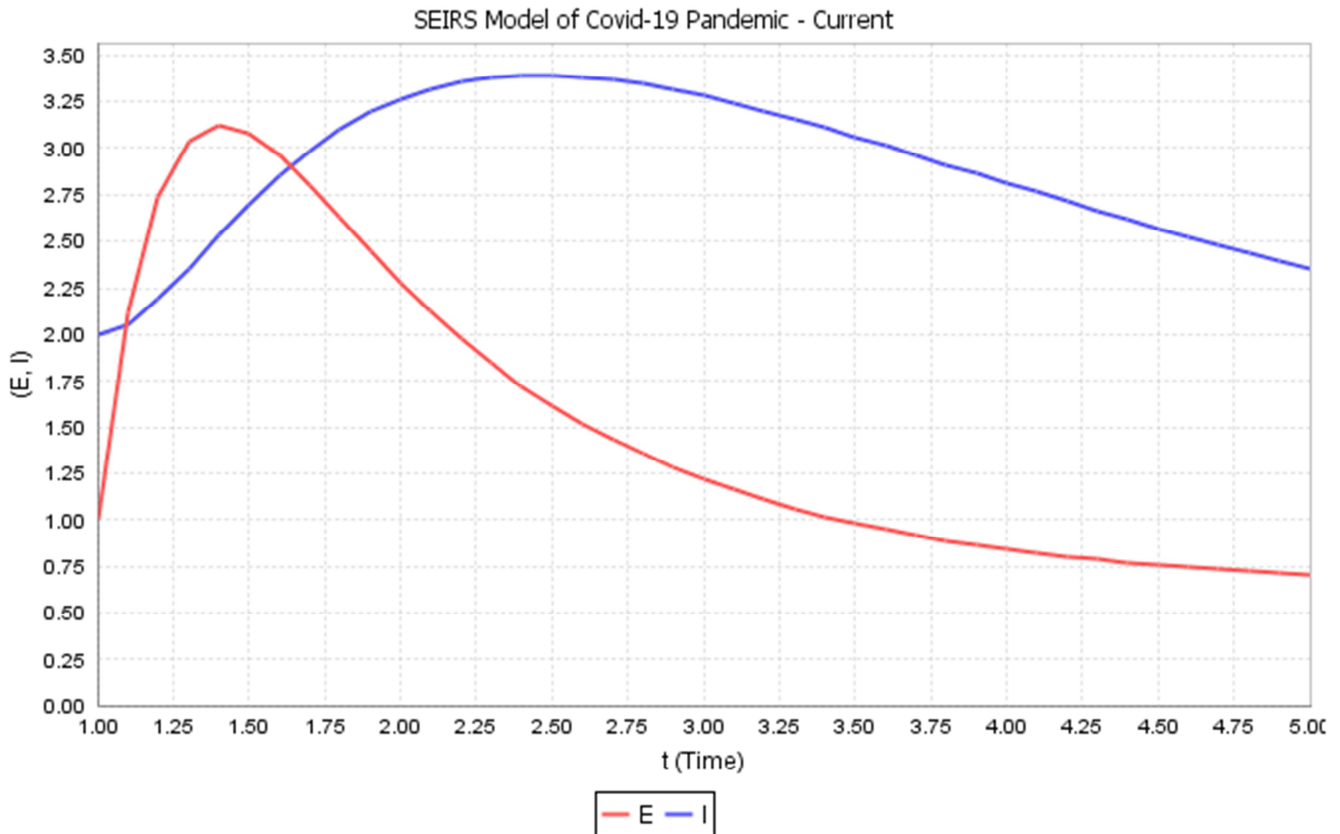**Figure 4.** *Time series plot for infected and recovered population.*

Figure 5. *Time series plot for exposed and infected population.*

6. Sensitivity Analysis

Sensitivity analysis tells us how important each parameter is to disease transmission. It is used to discover parameters that have a high impact on R_0 and should be targeted by intervention strategies. Sensitivity indices allow us to measure the relative change in a variable when a parameter changes. The normalized forward sensitivity index of a variable with respect to a parameter is the ratio of the relative change in the variable to the relative change in the parameter. If the result is negative, then the relationship between the parameters and R_0 is inversely proportional. In this case, we will take the modulus of the sensitivity index so that we can deduce the size of the effect of changing that parameter. On the other hand, a positive sensitivity index means an increase in the value of a parameter.

A highly sensitive parameter should be carefully estimated, because a small variation in that parameter will lead to large quantitative changes. An insensitive parameter, on the other hand, does not require as much effort to estimate, since a small variation in that parameter will not produce large changes to the quantity of interest [9, 11, 13]

The explicit expression of R_0 is given by

$R_0 = [\alpha\beta\Lambda]/[(\delta + \mu)(\beta + \delta + \mu)(\gamma + \delta + \mu)]$. Since R_0 depends only on six parameters, we derive an analytical expression for its sensitivity to each parameter using the normalized forward sensitivity index as follows:

Table 5. *Sensitivity of R_0 for the Parameter values.*

Parameter	Sensitivity index of R_0	Sign
Λ	$Y_\Lambda^{R_0} = \dfrac{\partial R_0}{\partial \Lambda} \times \dfrac{\Lambda}{R_0} = 1$	+ve
α	$Y_\alpha^{R_0} = \dfrac{\partial R_0}{\partial \alpha} \times \dfrac{\alpha}{R_0} = 1$	+ve
β	$Y_\beta^{R_0} = \dfrac{\partial R_0}{\partial \beta} \times \dfrac{\beta}{R_0} = \dfrac{\delta\mu}{(\beta + \delta\mu)^2}$	+ve
γ	$Y_\gamma^{R_0} = \dfrac{\partial R_0}{\partial \gamma} \times \dfrac{\gamma}{R_0} = \dfrac{-\gamma}{\gamma + \delta + \mu}$	-ve
δ	$Y_\delta^{R_0} = \dfrac{\partial R_0}{\partial \alpha} \times \dfrac{\delta}{R_0} = \dfrac{-\delta[(a + b)c + ab]}{abc}$	-ve
μ	$Y_\mu^{R_0} = \dfrac{\partial R_0}{\partial \alpha} \times \dfrac{\mu}{R_0} = \dfrac{-\mu[(a + b)c + ab]}{abc}$	-ve

where, $a = \delta + \mu, b = \beta + \delta + \mu, c = \gamma + \delta + \mu, d = \rho + \delta + \mu$, and From the Table 5, It is to be noted that the parameters Λ, α, β are positive and hence play a vital role in controlling the stability aspects of the system, and the remaining parameters are negative and hence have not big influence on the system.

7. Result and Discussion

A mathematical SEIRS model of COVID-19 was Conducted and the sensitivity indices of the basic reproduction number R_0 is Computed to determine the relative importance of the model parameters in the disease transmission. This information leads us to identify the influence of each model parameter in the basic reproduction number. Consequently, it is helpful to know

and predict the disease progress, persistent or decline in the past, present and future.

This mathematical model analysis may provide critical information for decision makers and public health officials, who may have to deal with infectious disease of COVID-19 pandemic. I hope that the paper will have a great impact on citizens of the whole world to concentrate on prevention and control of COVID-19 pandemic. Such contribution is interesting regarding to COVID-19, which causes a large disruption in the lives of sufferers and has enormous socio-economic costs occurred in the world.

Almost all latest research recommend the following protective measures: hygiene, masks, physical distancing, staying indoors, boosting immune system, raising awareness through networking (like face book, and twitter), boosting moral of front-line workers such as (medical practitioners, nursing staff, cleaning staff, health care centers) who are interacting directly with the patients.

8. Conclusion

In this Paper, SEIRS mathematical model describing the dynamics of COVID-19 is formulated and analyzed. The model is developed based on biologically reasonable assumptions. The mathematical analysis has shown that if basic reproduction number is less than one, then number of cases decrease over time and eventually the disease die out, and if the basic reproduction number is equals to one, then cases are stable. On the other hand, if the basic reproduction number is greater than one then the number of cases increase over time gets worth, and the disease continue to spread more rapidly.

Moreover, existence, positivity and boundedness of the solution of the model is shown to clarify the model is biologically meaningful and mathematically well posed. Stability analysis of the model is checked with help of next generation matrix and global stability are proved by taking appropriate liapunove function.

Acknowledgements

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