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Stability Analysis of Hyperbolic Equilibria of the SEIR Model for COVID-19 Transmission

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Abstract: ***We formulate the SEIR mathematical model for the transmission dynamics of COVID-19. We study the stability of the equilibrium points for the system of differential equations modeling the disease. We obtain conditions for the local and global stabilities of the disease-free and endemic equilibria of the SEIR model. The basic reproduction number for the model is also derived. Values of the parameters used in the model are estimated and numerical simulation is conducted using the Scilab software application. The result of the simulation shows that the whole population becomes susceptible and the disease dies out very rapidly within a very short time, when the basic reproduction number is less than one. On the other hand, when the basic reproduction number is greater than one, a large proportion of the population gets infected while a much larger proportion die or recover from the disease.***

Keywords: COVID-19, Stability Analysis, SEIR Model, Basic reproduction number

Mathematics Subject Classification 2010: 92-10, 92B05, 92D30, 34D20, 34D23, 34C60

1. Introduction

The COVID-19 (Coronavirus disease, 2019) pandemic, is an ongoing global pandemic, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [18]. The outbreak was first identified in Wuhan, China, in December2019 [19], [2]. The World Health Organization declared the outbreak a Public Health Emergency of International Concern on 30 January 2020 and a pandemic on 11 March 2020 [21]. The virus is mostly spread between people during close contact. The mode of transmission is often via small droplets produced by coughing, sneezing and talking [5]. Symptoms commonly include fever, fatigue, cough, loss of sense of smell, and shortness of breath [20]. Complications often include acute respiratory distress syndrome and pneumonia [17]. The average incubation period of the disease is estimated to be 6.4 days [6], although typically ranges from one to fourteen days [15]. According to [15], for people with mild disease, the average recovery time is about 2 weeks. For people with severe symptoms, recovery is between 3 to6 weeks.

Several authors: [22], [23], [1], [8], [24], [16], [4], [25], [10], [14], have recently developed mathematical models for the transmission dynamics of COVID-19.

In this study, we formulate a simple compartmental model to represent the dynamics of COVID-19. We investigate the stability analysis for the mode lands obtain conditions for the stability of the steady states.

2. Seir Model of COVID-19

2.1 Model Assumptions

- The population under consideration is divided into four disjoint classes which change with time (t).These classes are: The Susceptible class, denoted by (S), the Exposed class, denoted by (E), the Infective class, denoted by (I) and the Removed class (which comprises of individuals removed from the population by either death or recovery), denoted by (R).
- The population under consideration has a constant size N and is sufficiently large, so that the sizes of each class can be considered as continuous variables.
- The population is homogeneously mixing. Individuals make contact at random and do not mix mostly in a smaller subgroup.
- We assume that there is no immigration or emigration.
- The model includes vital dynamics (births and deaths). We assume that the births and deaths occur at equal rates and all newborns are susceptible. Individuals are removed by death from each class at a rate proportional to the class size with proportionality constant δ (the death or birth rate)
- In the susceptible class S, a susceptible person becomes infected and moves into the Exposed class at a rate proportional to the product SI with proportionality constant $\frac{\alpha}{N}$. The contact rate α (rate of infection) is the average number of adequate contacts per infective per unit time. An adequate contact of an infective is an interaction which results in infection of the other individual if he is susceptible.
- From the exposed class (E), an individual becomes infective and moves into the infective class at a rate proportional to the class size with proportionality constant λ.
- Individuals recover and leave the infective class (I) at rates proportional to the class size I, with proportionality constants ν_1 and ν_2. Individuals that don't survive the disease die and leave the class (I) with proportionality constant δ_1.

2.2 Parameters of the Model

- δ: Natural mortality rate (Birth or Death rate). The time unit is set at day. The constant natural mortality rate is assumed to be inversely proportional to the global average life expectancy of birth. This is taken to be

approximately 72 years [11]. $\delta = \frac{1}{26280} = 0.000038 day^{-1}$.

- α: The rate of infection α =(number of new cases over a time period)/ (total population at risk during the same time period).
- β: Transition rate from Exposed class to Infective class (We assumeit is inversely proportional to the latent period of the disease). In [25], it is reported that the median time prior to symptom onset (latent period), is 3 days. If we take the latent period to be 3 days, (range 1-24 days), we get; $\beta = \frac{1}{3} = 0.33 day^{-1}$.
- v_1: Recovery rate for patients with mild symptoms. We assume it is inversely proportional to the average period of infectivity (the time between COVID-19 infection and recovery for people with mild symptoms). If we take the average recovery time for people with mild symptoms to be 2 weeks [15], we get; $v_1 = \frac{1}{14} = 0.07143 day^{-1}$.
- v_2: Recovery rate for patients with more severe symptoms. We assume it is inversely proportional to the average period of infectivity(the time between COVID-19 infection and recovery for people with severe symptoms). If we take the average recovery time for people with severe symptoms to be 4.5 weeks [15], we get: $v_2 = \frac{1}{31.5} = 0.03175 day^{-1}$
- δ_1:Disease-related death rate δ_1=(number of deaths over a defined period of time)/ (confirmed cases diagnosed within that time period).

The transmission dynamics of the disease is represented by the following system of ordinary differential equations (The SEIR model):

$$\begin{aligned}
\frac{dS}{dt} &= \delta N - \frac{\alpha}{N} SI - \delta S \\
\frac{dE}{dt} &= \frac{\alpha}{N} SI - (\beta + \delta)E \\
\frac{dI}{dt} &= \beta E - (v_1 + v_2 + \delta_1 + \delta)I \\
\frac{dR}{dt} &= (v_1 + v_2 + \delta_1)I - \delta R
\end{aligned} \qquad (2.1)$$

$$\delta, \alpha, \beta, \delta_1, v_1, v_2 > 0,$$

$$S, E, I, R > 0$$

2.3 Steady States

From (2.1), we have;

$$\delta(N - S) - \frac{\alpha}{N}\bar{S}\bar{I} = 0 \qquad (2.2)$$

$$\frac{\alpha}{N}\bar{S}\bar{I} - (\beta + \delta)\bar{E} = 0 \qquad (2.3)$$

$$\beta\bar{E} - (v_1 + v_2 + \delta_1 + \delta)\bar{I} = 0 \qquad (2.4)$$

$$(v_1 + v_2 + \delta_1)\bar{I} - \delta\bar{R} = 0 \qquad (2.5)$$

where $(\bar{S}, \bar{E}, \bar{I}, \bar{R})$ is the steady state or equilibrium point of the system (2.1)

From (2.4) and (2.5), we get;

$$\bar{E} = \frac{v_1 + v_2 + \delta_1 + \delta}{\beta}\bar{I} \quad and \quad \bar{R} = \frac{v_1 + v_2 + \delta_1}{\delta}\bar{I}$$

From (2.3), we have:

$$\left[\frac{\alpha}{N}\bar{S} - (\beta + \delta)\frac{v_1 + v_2 + \delta_1 + \delta}{\beta}\right]\bar{I} = 0$$

This gives us two possible solutions: $\bar{I} = 0$ and

$$\left[\frac{\alpha}{N}\bar{S} - (\beta + \delta)\frac{v_1 + v_2 + \delta_1 + \delta}{\beta}\right]\bar{I} = 0 \qquad (2.6)$$

Substituting $\bar{I} = 0$ into (2.4) and (2.5), we get: $\bar{E} = 0 \ and \ \bar{R} = 0$. From (2.2), we get $\bar{S} = N$.

Hence the disease-free steady state of the system (2.1) is $(N, 0, 0, 0)$.

From (2.6), we have,

$$\bar{S} = \frac{N(\beta + \delta)(v_1 + v_2 + \delta_1 + \delta)}{\alpha\beta} \qquad (2.7)$$

Substituting (2.7) into (2.2), we get;

$$\bar{I} = \frac{\beta\delta N}{(\beta + \delta)(v_1 + v_2 + \delta_1 + \delta)} - \frac{\delta N}{\alpha} \qquad (2,8)$$

Putting (2.8) into (2.4), we get;

$$\bar{E} = \frac{\delta N}{\beta + \delta} - \frac{\delta N(v_1 + v_2 + \delta_1 + \delta)}{\alpha\beta} \qquad (2.9)$$

Putting (2.8) into (2.5), we get;

$$\bar{R} = \frac{\beta N}{\beta + \delta} - \frac{(v_1 + v_2 + \delta_1)N}{\alpha}$$

Hence the endemic equilibrium of the system (2.1) is at;

$$\begin{aligned}
&(\bar{S}, \bar{E}, \bar{I}, \bar{R}) \\
&= \left(\frac{N(\beta + \delta)(v_1 + v_2 + \delta_1 + \delta)}{\alpha\beta}, \frac{\delta N}{\beta + \delta}\right. \\
&- \frac{\delta N(v_1 + v_2 + \delta_1 + \delta)}{\alpha\beta}, \frac{\beta\delta N}{(\beta + \delta)(v_1 + v_2 + \delta_1 + \delta)} \\
&\left. - \frac{\delta N}{\alpha}, \frac{\beta N}{\beta + \delta} - \frac{N(v_1 + v_2 + \delta_1)}{\alpha}\right)
\end{aligned}$$

2.4 Basic Reproduction Number

Lemma 2.1 The basic reproduction number for the model (2.1) is:

$$R_0 = \sqrt{\frac{\alpha\beta}{(\beta + \delta)(v_1 + v_2 + \delta_1 + \delta)}}$$

Proof

Using the next-generation matrix (NGM) method [9], from (2.1), we get the linearized infection subsystem:

$$\frac{dE}{dt} = \alpha I - (\beta + \delta)E$$

$$\frac{dI}{dt} = \beta E - (v_1 + v_2 + \delta_1 + \delta)I$$

From which we get;

$$A = \begin{bmatrix} 0 & \alpha \\ \beta & 0 \end{bmatrix} \quad \text{and}$$

$$B = \begin{bmatrix} -(\beta + \delta) & 0 \\ 0 & -(v_1 + v_2 + \delta_1 + \delta) \end{bmatrix}$$

Where A is the transmission matrix and B is the transition matrix. We have;

$$F = -AB^{-1} = \begin{bmatrix} 0 & \alpha \\ \beta & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\beta+\delta} & 0 \\ 0 & \frac{1}{\nu_1+\nu_2+\delta_1+\delta} \end{bmatrix}$$

$$= \begin{bmatrix} 0 & \frac{\alpha}{\nu_1+\nu_2+\delta_1+\delta} \\ \frac{\beta}{\beta+\delta} & 0 \end{bmatrix}$$

From which we compute R_0:

$$R_0 = \rho(F) = \frac{1}{2}(trace\ F + \sqrt{(trace\ F)^2 - 4\det(F)}$$

$$= \sqrt{\frac{\alpha\beta}{(\beta+\delta)(\nu_1+\nu_2+\delta_1+\delta)}}$$

where ρ is the spectral radius.

2.5 Stability Analysis.

Theorem 2.2 The disease-free equilibrium of the SEIR model is locally asymptotically stable if the basic reproduction number: $R_0 < 1$, and is unstable otherwise.

Proof

The Jacobian matrix of the system (2.1) is given by;

$$J = \begin{bmatrix} -\delta & 0 & \frac{-\alpha}{N}S & 0 \\ 0 & -(\beta+\delta) & \frac{\alpha}{N}S & 0 \\ 0 & \beta & -(\nu_1+\nu_2+\delta_1+\delta) & 0 \\ 0 & 0 & \nu_1+\nu_2+\delta_1 & -\delta \end{bmatrix}$$

At $(N, 0, 0, 0)$;

$$J = \begin{bmatrix} -\delta & 0 & -\alpha & 0 \\ 0 & -(\beta+\delta) & \alpha & 0 \\ 0 & \beta & -(\nu_1+\nu_2+\delta_1+\delta) & 0 \\ 0 & 0 & \nu_1+\nu_2+\delta_1 & -\delta \end{bmatrix}$$

$$J - \lambda I = \begin{bmatrix} -\delta-\lambda & 0 & -\alpha & 0 \\ 0 & -(\beta+\delta)-\lambda & \alpha & 0 \\ 0 & \beta & -(\nu_1+\nu_2+\delta_1+\delta)-\lambda & 0 \\ 0 & 0 & \nu_1+\nu_2+\delta_1 & -\delta-\lambda \end{bmatrix}$$

where $a = \beta + \delta$, and $b = \nu_1 + \nu_2 + \delta_1 + \delta$

$$\det(J - \lambda I) = (-\delta-\lambda)^2[(-a-\lambda)(-b-\lambda) - \alpha\beta]$$

The characteristic equation: $\det(J - \lambda I) = 0$ gives;

$(-\delta-\lambda)^2 = 0, \quad or\ (-a-\lambda)(-b-\lambda) - \alpha\beta = 0$

We have;

$\lambda_{1,2} = -\delta, \quad \lambda_3 = \frac{-(a+b)-\sqrt{(a-b)^2+4\alpha\beta}}{2}, \quad and\ \lambda_4 = \frac{-(a+b)+\sqrt{(a-b)^2+4\alpha\beta}}{2}$

$\lambda_3 < 0, \quad \lambda_4 < 0 \quad iff \quad \sqrt{(a-b)^2+4\alpha\beta} < a+b$

This gives: $\frac{\alpha\beta}{(\beta+\delta)(\nu_1+\nu_2+\delta_1+\delta)} < 1 \quad or \quad R_0 < 1$

Theorem 2.3 *The endemic equilibrium of the SEIR model is locally asymptotically stable for $R_0 > 1$ and is unstable otherwise.*

Proof

At the endemic equilibrium, the Jacobian matrix is given by;

$$J = \begin{bmatrix} \frac{-\alpha\beta\delta}{ab} & 0 & \frac{-ab}{\beta} & 0 \\ \frac{\alpha\beta\delta}{ab} - \delta & -a & \frac{ab}{\beta} & 0 \\ 0 & \beta & -b & 0 \\ 0 & 0 & b-\delta & -\delta \end{bmatrix}$$

$$\det(J - \lambda I) = \begin{vmatrix} \frac{-\alpha\beta\delta}{ab} - \lambda & 0 & \frac{-ab}{\beta} & 0 \\ \frac{\alpha\beta\delta}{ab} - \delta & -a-\lambda & \frac{ab}{\beta} & 0 \\ 0 & \beta & -b-\lambda & 0 \\ 0 & 0 & b-\delta & -\delta-\lambda \end{vmatrix}$$

Solving $\det(J - \lambda I) = 0$, we get:

$$(-\delta-\lambda)[(-\nu-\lambda)(-a-\lambda)(-b-\lambda) - ab(-\nu-\lambda) - ab(\nu-\delta)] = 0, \quad where\ \nu = \frac{\alpha\beta\delta}{ab}$$

$(-\delta-\lambda) = 0$ gives $\lambda_1 = -\delta$

$(-\nu-\lambda)(-a-\lambda)(-b-\lambda) - ab(-\nu-\lambda) - ab(\nu-\delta) = 0$ gives:

$-\lambda^3 - (a+b+\nu)\lambda^2 - \nu(a+b)\lambda - ab(\nu-\delta) = 0$

Let $f(\lambda) = -\lambda^3 - (a+b+\nu)\lambda^2 - \nu(a+b)\lambda - ab(\nu-\delta)$, then

$$f(-\lambda) = \lambda^3 - (a+b+\nu)\lambda^2 + \nu(a+b)\lambda - ab(\nu-\delta) = 0 \qquad (2.9)$$

Based on Descartes' rule [12], the number of negative roots of the characteristic equation (2.9) is equal to the maximum number of coefficient sign changes. Hence, (2.9) has three negative roots. If (2.9) is in the form of:

$K = L_1\lambda^3 - L_2\lambda^2 + L_3\lambda - L_4$

where;

$$L_1 = 1$$
$$L_2 = (a+b) + \nu$$
$$L_3 = \nu(a+b)$$
$$L_4 = ab(\nu-\delta)$$

with the condition; $L_1,\ L_2,\ L_3,\ L_4 > 0$

Hence we have; if $\nu > \delta$ *and* $L_1,\ L_2,\ L_3,\ L_4 > 0$, *then* $\lambda_2,\ \lambda_3,\ \lambda_4 < 0$

Therefore, the SEIR endemic equilibrium $(S_1,\ E_1,\ I_1,\ R_1)$ is locally asymptotically stable if:

$$\nu > \delta \quad or \quad \alpha\beta > ab \quad or \quad \frac{\alpha\beta}{(\beta+\delta)(\nu_1+\nu_2+\delta_1+\delta)} > 1$$

Theorem 2.4 *If $R_0 < 1$, then the disease-free equilibrium point $(N,\ 0,\ 0,\ 0)$ is globally asymptotically stable in the domain:*

$$D_1 = \left\{(S, E, I, R) \in \mathbb{R}_+^4 : S < \frac{N(\beta+\delta)}{\alpha}\right\}$$

Proof

Define a Lyapunov function $L = E$, then:

$\frac{dL}{dt} = \left\{\frac{\alpha}{N}S - (\beta+\delta)\right\}E \leq 0 \ \ if \ \ S < \frac{N(\beta+\delta)}{\alpha}$

That is; $\frac{dL}{dt} \leq 0$ in the domain $D_1 = \left\{(S,E,I,R) \in \mathbb{R}_+^4 : S < N\beta+\delta\alpha.\right.$

So, for the positive definite function L, the derivative $\frac{dL}{dt}$ is negative semi-definite in D_1. Now, we consider the set where $\frac{dL}{dt} = 0$.

Let $\triangle = \left\{(S,\ E,\ I,\ R) \in D_1 : \frac{dL}{dt} = 0\right\} = \{(S,\ E,\ I,\ R) \in D1 : E=0.$

Let T be the largest invariant set in $\triangle$. Then in $\triangle$, we get;

$$\frac{dS}{dt} = \delta(N-S) \qquad (2.10)$$

$$\frac{dI}{dt} = -(\nu_1+\nu_2+\delta_1+\delta)I \qquad (2.11)$$

$$\frac{dR}{dt} = -\delta \qquad (2.12)$$

From (2.12), we have $R \to 0$ as $\to \infty$. From (2.11), we have $I \to 0$ as $t \to \infty$. From (2.10), we have $S \to N$ as $t \to \infty$. Hence T is $\{(N,\ 0,\ 0,\ 0)\}$. Hence by the LaSalle-Lyapunov theory [7], the disease-free equilibrium $(N,\ 0,\ 0,\ 0)$ is globally asymptotically stable in D_1.

Now, from D_1, $S < \frac{N(\beta+\delta)}{\alpha}$ gives; $\frac{\alpha}{\beta+\delta} < 1$, and we have that;

$\frac{\alpha\beta}{(\beta+\delta)(\nu_1+\nu_2+\delta_1+\delta)} < \frac{\alpha}{\beta+\delta} < 1$ implies that $R_0 < 1$.

□

Theorem 2.5 *The endemic equilibrium point $(S_1,\ E_1,\ I_1,$ R1 is globally asymptotically stable in the region: D2=S, E, I, R∈ℝ+4 :1<E1E<I1I<R1R<S1S.*

Proof

Consider a Lyapunov function V defined as follows:

$$V = \int_{S_1}^{S}\frac{S-S_1}{S}dS + \int_{E_1}^{E}\frac{E-E_1}{E}dE + \int_{I_1}^{I}\frac{I-I_1}{I}dI + \int_{R_1}^{R}\frac{R-R_1}{R}dR$$

We have; $\frac{dV}{dt} = \left(\frac{S-S_1}{S}\right)\frac{dS}{dt} + \left(\frac{E-E_1}{E}\right)\frac{dE}{dt} + \left(\frac{I-I_1}{I}\right)\frac{dI}{dt} + \left(\frac{R-R_1}{R}\right)\frac{dR}{dt} = (S-S_1)\left(\frac{\delta N}{S} - \frac{\delta N}{S_1} - \frac{\alpha I}{N} + \frac{\alpha I_1}{N}\right) + (E-$ E1αNSIE−αNS1I1E1+I−I1βEI−βE1I1+R−R1ν1+ν2+δ1IR−I1R1=

$$\begin{aligned}
&(S-S_1)\left(\delta N\frac{(S_1-S)}{SS_1} + \frac{\alpha}{N}(I-I_1)\right)\\
&\quad + (E-E_1)\left(\frac{\alpha}{N}(S-S_1)\right)\\
&\quad + \beta(I-I_1)\frac{(EI_1-IE_1)}{II_1}\\
&\quad + (\nu_1+\nu_2+\delta)(R-R_1)\frac{(IR_1-I_1R)}{RR_1}\\
&= \delta N(S-S_1)\frac{S_1-S}{SS_1}\\
&\quad + \frac{\alpha}{N}(S-S_1)(I_1-I)\\
&\quad + \frac{\alpha}{N}(E-E_1)\frac{(SIE_1-S_1I_1E)}{EE_1}\\
&\quad + \beta(I-I_1)\frac{(EI_1-IE_1)}{II_1}\\
&\quad + (\nu_1+\nu_2+\delta_1)(R-R_1)\frac{(IR_1-I_1R)}{RR_1}\\
&= -\frac{\delta N}{SS_1}(S_1-S)^2 - \frac{\alpha}{N}(S_1-S)(I_1-I)\\
&\quad + \frac{\alpha}{N}(E-E_1)\frac{(SIE_1-S_1I_1E)}{EE_1}\\
&\quad - \beta(I_1-I)\frac{(EI_1-IE_1)}{II_1}\\
&\quad - (\nu_1+\nu_2+\delta_1)(R_1-R)\frac{(IR_1-I_1R)}{RR_1}\\
&< -\frac{\delta N}{SS_1}(S_1-S)^2 - \frac{\alpha}{N}(S_1-S)(I_1-I)\\
&\quad + \frac{\alpha}{N}(E-E_1)(S_1I_1E_1-S_1I_1E)\\
&\quad - \beta(I_1-I)\frac{(EI_1-IE_1)}{II_1}\\
&\quad - (\nu_1+\nu_2+\delta_1)(R_1-R)\frac{(IR_1-I_1R)}{RR_1}
\end{aligned}$$

Since $1 < \frac{E_1}{E} < \frac{I_1}{I} < \frac{R_1}{R} < \frac{S_1}{S}$, we have; $1 < \frac{S_1}{S}$ and $1 < \frac{I_1}{I}$, which gives; $SI < S_1I_1$. From

which we get:

$$\begin{aligned}
\frac{dV}{dt} &= -\frac{\delta N}{SS_1}(S_1-S)^2 - \frac{\alpha}{N}(S_1-S)(I_1-I)\\
&\quad - \frac{\alpha}{N}S_1I_1(E_1-E)^2\\
&\quad - \beta\frac{(I_1-I)(EI_1-IE_1)}{II_1}\\
&\quad - (\nu_1+\nu_2+\delta_1)(R_1-R)\frac{(IR_1-I_1R)}{RR_1}\\
&< 0
\end{aligned}$$

Hence, $\frac{dV}{dt} < 0$ in the region: $\left\{(S,\ E,\ I,\ R) \in \mathbb{R}_4^+ : 1 < E1E<I1I<R1R<S1S\right.$

3. Numerical Simulation

3.1 Numerical plot of the SEIR model of COVID-19 for $R_0 < 1$.

Define a solution to the system (2.1) for the parameter values; $\delta = 0.000038,\ \alpha = 0.37,\ \beta = 0.33,\ \nu_1 =$

0.07143, $\nu_2 = 0.03175$, $\delta_1 = 2.03$, subject to the initial conditions: $s(0) = 0.7$, $e(0) = 0.15$, $i(0) = 0.1$, $r(0) = 0.05$, where $s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, $r = \frac{R}{N}$, the population N is taken to be 1000.

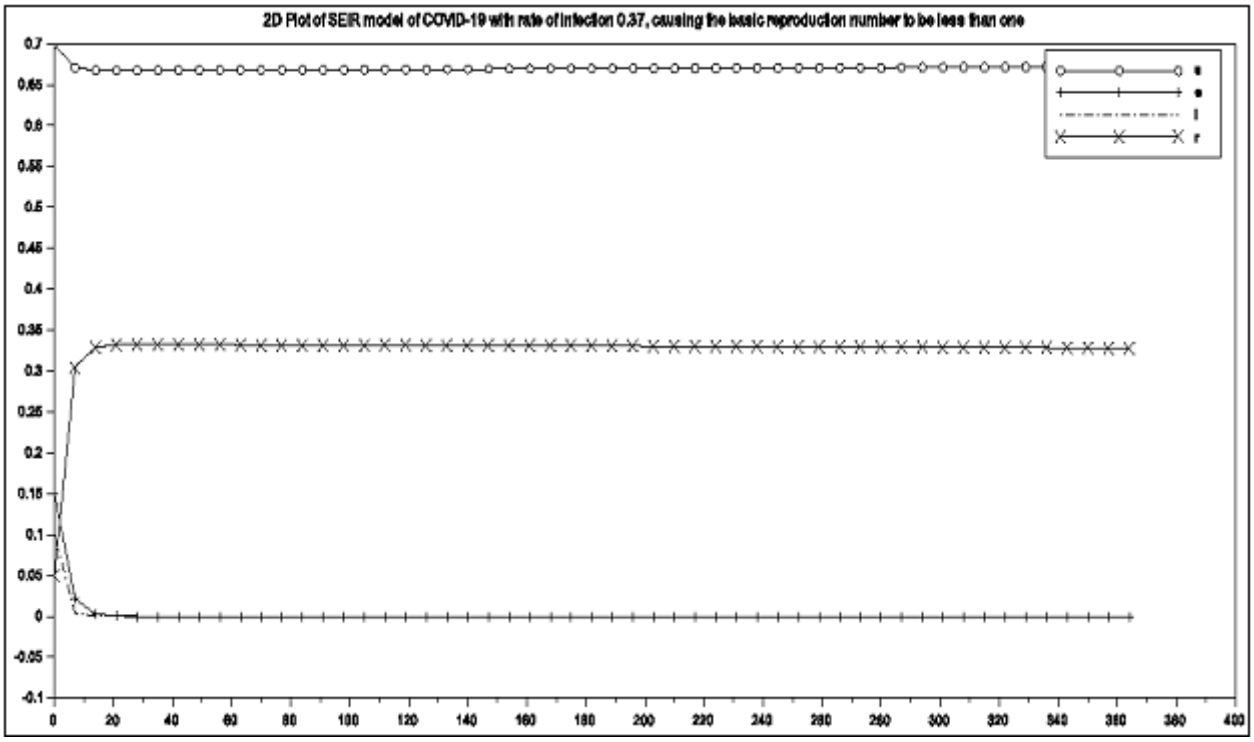

Figure 1: Numerical plot of model for $R_0 < 1$

3.2 Scilab Code:

```
function ydot=SEIRdmodel(t, y)
ydot= [d-a*y(1)*y(3)-d*y(1);a*y(1)*y(3)-
(n+d)*y(2);n*y(2)(v1+v2+d1+d)*y(3);(v1+v2+d1)*y(3)-
d*y(4)]
endfunction
d=0.000038;
a=0.37;
n=0.33;
v1=0.07143;
v2=0.03175;
d1=2.08;
y0= [0.7;0.15;0.1;0.05];
t0=0;
t=0:7:365;
sol=ode(y0, t0, t, SEIRdmodel);
plot(t, sol(1, :), 'k-o-', t, sol(2, :), 'k-+-', t, sol(3, :), 'k-.', t, sol(4, :), 'k-x-')
title("2D Plot of SEIR model of COVID-19 with rate of infection 0.37, causing the basic
reproduction number to be less than one", "fontsize", 2)
hl=legend( ['s';'e';'i';'r']);
```

3.3 Numerical plot of the SEIR model of COVID-19 for $R_0 > 1$

Define a solution to the system (2.1) for the parameter values; $\delta = 0.000038$, $\alpha = 12$, $\beta = 0.33$, $\nu_1 = 0.07143$, $\nu_2 = 0.03175$, $\delta_1 = 3.11$, subject to the initial conditions: $s(0) = 0.7$, $e(0) = 0.15$, $i(0) = 0.1$, $r(0) = 0.05$, where $= \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, $r = \frac{R}{N}$.

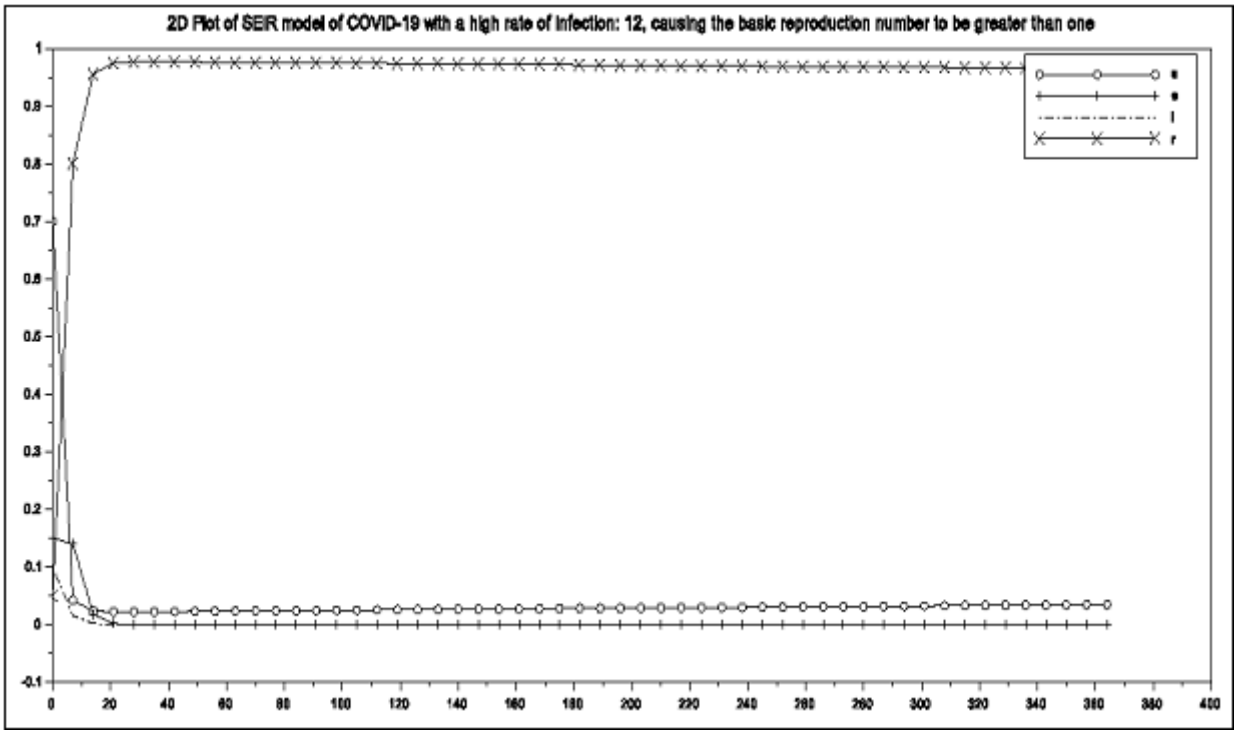

Figure 2: Numerical plot of model for $R_0 > 1$

3.4 Scilab Code

```
function ydot=SEIRdmodel(t, y)
ydot= [d-a*y(1)*y(3)-d*y(1);a*y(1)*y(3)-(n+d)*y(2);n*y(2)-(v1+v2+d1+d)*y(3);(v1+v2+d1)*y(3)-d*y(4)]
endfunction
d=0.000038;
a=12;
n=0.33;
v1=0.07143;
v2=0.03175;
d1=3.11;
y0= [0.7;0.15;0.1;0.05]';
t0=0;
t=0:7:365;
sol=ode( [0.7;0.15;0.1;0.05], t0, t, SEIRdmodel);
plot(t, sol(1, :), 'k-o-', t, sol(2, :), 'k-+-', t, sol(3, :), 'k-.', t, sol(4, :), 'k-x-')
title("2D Plot of SEIR model of COVID-19 with a high rate of infection: 12, causing the
basic reproduction number to be greater than one", "fontsize", 3)
hl=legend( ['s';'e';'i';'r']);
```

4. Discussion of Results and Conclusion

We have formulated an SEIR model for the transmission dynamics ofCOVID-19. Upon studying the stability of the steady states, we have found that, at the disease-free equilibrium point, if the basic reproduction number is less than one, the population remains disease-free. At the endemic equilibrium point, if the disease continues to spread and the basic reproduction number is greater than one, the disease persists in the population.

The parameters of the model were estimated and the model was solved numerically using the scilab software. The result of the simulation shows that, if the basic reproduction number is less than one, the disease dies out very rapidly within a very short time. Also, a very small proportion of the population that get infected are rapidly removed by death and recovery, and we still have a very large proportion of the population remaining in the susceptible class. On the other hand, if the basic reproduction number is greater than one, a large proportion of the population gets infected within a short time. Also, a large proportion of the population gets removed by death or recovery.

4.1 Recommendations

If the basic reproduction number can be reduced by applying various preventive strategies like the use of face masks, social distancing, staying at home, avoiding crowded places, etc., the spread of the disease can at least be effectively controlled, and a lot of deaths can be prevented in the parts of the world where vaccines are yet to be administered.

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