SEIR MODEL WITH A VACCINATION PARAMETER USING COVID-19 AS A CASE STUDY

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Abstract

The SEIR mathematical model with a vaccination parameter is formulated to study the spread of COVID-19. The equilibrium points of the system of differential equations are obtained. The local and global stabilities of the disease-free and endemic equilibria are presented. The basic reproduction number of the model is obtained. The parameters used in the model are estimated. The system of differential equations representing the model is solved numerically using the scilab software application. The result of the simulation shows that in the long term, the presence of a vaccination parameter causes the disease to converge to the disease-free equilibrium for any value of the basic reproduction number.

Keywords: Stability, SEIR Model, Vaccination parameter, COVID-19, Scilab

1. Introduction

A COVID-19 vaccine is a vaccine intended to provide acquired immunity against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus that causes coronavirus disease 2019 (COVID-19).The COVID-19 vaccines are widely credited for their role in reducing the severity and death caused by COVID-19 [1]. Many countries have implemented phased distribution plans that prioritize those at highest risk of complications, such as the elderly, and those at high risk of exposure and transmission, such as healthcare workers [2].

As of 1 February 2022, 10.1 billion doses of COVID-19 vaccines have been administered worldwide based on official reports from national public health agencies [3]. By December 2020, more than 10 billion vaccine doses had been preordered by countries, [4] with about half of the doses purchased by high income countries comprising 14% of the world's population [5].

There are several authors [6-11] who have recently developed mathematical models to study the effect of vaccination strategies in the control of the dynamics of COVID-19. In this article, we have formulated a simple mathematical model to study the effect of vaccination on the spread of COVID-19 in a population. We present results for the stability analysis of the steady states of the model and we carry out a numerical simulation on the model.

2. Materials and Methods
SEIR Model Assumptions:
1. 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, recovery or vaccination), denoted by (R).
2. The population under consideration has a constant size P and is sufficiently large, so that the sizes of each class can be considered as continuous variables
3. The population is homogeneously mixing. Individuals make contact at random and do not mix mostly in a smaller subgroup.
4. We assume that there is no immigration or emigration

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5.   The model includes vital dynamics (births and deaths). We assume that the births and deaths occur at equal rates and all newborns are susceptible.

6.   Individuals are removed by death from each class at a rate proportional to the class size with proportionality constant γ (the birth or death rate).

7.   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 $\frac{\tau}{P}$. The contact rate τ (rate of infection) is the average number of adequate contacts per infective per unit time.

8.   From the exposed class (E), an individual becomes infective and moves into the infective class at a rate proportional to the class size E with proportionality constant δ.

9.   Individuals recover and leave the infective class (I) at rates proportional to the class size I, with proportionality constants α_1 and α_2. Individuals that don't survive the disease die and leave the class (I) with proportionality constant μ.

10.   Individuals from the susceptible class (S) who are vaccinated, move into the removed class (R) at a rate proportional to the class size S, with proportionality constant θ.

Parameters of the Model:

1. γ: 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 [12]. $\mu = \frac{1}{26280} = 0.000038 day^{-1}$.

2. τ: The rate of infection τ = (number of new cases over a time period)/ (total population at risk during the same time period).

3. δ: Transition rate from Exposed class to Infective class (We assume it is inversely proportional to the latent period of the disease). In [13], 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; $\delta = \frac{1}{3} = 0.33 day^{-1}$.

4. α_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 [14], we get;
$$\alpha_1 = \frac{1}{14} = 0.07143 day^{-1} \ .$$

5. α_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 [14], we get:
$$\alpha_2 = \frac{1}{31.5} = 0.031746$$

6. μ: Disease-related death rate μ = (number of deaths over a defined period of time) / (confirmed cases diagnosed within that time period).

7. θ: The rate at which individuals from the susceptible class are removed by vaccination. We assume that it is inversely proportional to the average duration of the immunity conferred by the COVID-19 vaccine. If we take the average duration of immunity to be six months [15], we get: $\theta = \frac{1}{180} \approx 0.0056 day^{-1}$

The dynamics of the disease is represented by the following system of differential equations:

$$\frac{dS}{dt} = \gamma P - \frac{\tau}{P} SI - \gamma S - \theta S$$
$$\frac{dE}{dt} = \frac{\tau}{P} SI - (\delta + \gamma)E \qquad\qquad\qquad (1)$$
$$\frac{dI}{dt} = \delta E - (\alpha_1 + \alpha_2 + \mu + \gamma)I$$
$$\frac{dR}{dt} = (\alpha_1 + \alpha_2 + \mu + \gamma)I + \theta S - \gamma R$$

$\gamma, \delta, \tau, \mu, \alpha_1, \alpha_2, \theta > 0 \qquad\qquad S, E, I, R > 0$

Equilibria of the Model: From Eq. (1) we get the following;

$$\gamma P - \frac{\tau}{P} \bar{S}\bar{I} - (\gamma + \theta)\bar{S} = 0 \qquad\qquad\qquad (2)$$
$$\frac{\tau}{P} \bar{S}\bar{I} - (\delta + \gamma)\bar{E} = 0 \qquad\qquad\qquad (3)$$

$$\delta \bar{E} - (\alpha_1 + \alpha_2 + \mu + \gamma)\bar{I} \tag{4}$$
$$(\alpha_1 + \alpha_2 + \mu + \gamma)\bar{I} + \theta \bar{S} - \gamma \bar{R} = 0 \tag{5}$$

From Eq. (3), we get;
$$\bar{E} = \frac{(\alpha_1 + \alpha_2 + \mu + \gamma)}{\delta}\bar{I} \tag{6}$$
Putting Eq. (6) into Eq. (3), we get;
$$\left[\frac{\tau}{P}\bar{S} - \frac{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\delta}\right]\bar{I} = 0 \tag{7}$$
$\bar{I} = 0$ gives; $\bar{S} = \frac{\gamma P}{\gamma + \theta}$, $\bar{E} = 0$, and $\bar{R} = \frac{\theta P}{\gamma + \theta}$

One steady state is:
$$[S_1, 0, 0, R_1] = \left[\frac{\gamma P}{\gamma + \theta},\ 0,\ 0,\ \frac{\theta P}{\gamma + \theta}\right]$$
From Eq. (7), we get: $\bar{S} = \frac{P(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\tau \delta} \tag{8}$

Putting Eq. (8) into Eq. (2), we get $\bar{I} = \frac{\delta \gamma P}{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)} - \frac{P(\gamma + \theta)}{\tau}$

From Eq. (4), $E = \frac{\gamma P}{\delta + \gamma} - \frac{P(\gamma + \theta)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\tau \delta}$

From Eq. (5), we get $\bar{R} = \frac{\delta P}{\delta + \gamma} - \frac{P(\gamma + \theta)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\gamma \tau} + \frac{\theta P(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\tau \delta \gamma}$

This gives us another steady state: $[S_2, E_2, I_2, R_2] = \left[\frac{P(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\tau \delta},\ \frac{\gamma P}{\delta + \gamma} - \frac{P(\gamma + \theta)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\tau \delta},\right.$

$\left. \frac{\delta \gamma P}{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)} - \frac{P(\gamma + \theta)}{\tau},\ \frac{\delta P}{\delta + \gamma} - \frac{P(\gamma + \theta)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\gamma \tau} + \frac{\theta P(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)}{\tau \delta \gamma}\right]$

Basic Reproduction Number
Lemma 2.1 The basic reproduction number for the model Eq. (1) is:

$$R_0 = \sqrt{\frac{\tau \delta}{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)}}$$

Proof From the linearized infection subsystem of Eq. (1), we get;
$$\frac{dE}{dt} = \tau I - (\delta + \gamma)E$$
$$\frac{dI}{dt} = \delta E - (\alpha_1 + \alpha_2 + \mu + \gamma)$$
This gives rise to the transmission matrix;
$Q = \begin{bmatrix} 0 & \tau \\ \delta & 0 \end{bmatrix}$ and the transmission matrix: $T = \begin{bmatrix} -(\delta + \gamma) & 0 \\ 0 & -(\alpha_1 + \alpha_2 + \mu + \gamma) \end{bmatrix}$

The next generation matrix is given by:
$$X = -QT^{-1} = \begin{bmatrix} 0 & \tau \\ \delta & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\delta + \gamma} & 0 \\ 0 & \frac{1}{\alpha_1 + \alpha_2 + \mu + \gamma} \end{bmatrix}, \text{ from which we compute } R_0:$$

$$R_0 = \rho(X) = \frac{1}{2}\left(trace\ X + \sqrt{(trace\ X)^2 - 4\det(X)} = \sqrt{\frac{\tau \delta}{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)}}\right., \text{ where } \rho \text{ is}$$

the spectral radius.

3. **Results and Discussion**
Local Stability Analysis. Theorem 2.2 The disease-free equilibrium of the SEIR model is locally asymptotically stable when $R_0 < 1$

Proof From the system in Eq. (1), we get the Jacobian matrix:
$$J = \begin{bmatrix} -(\gamma + \frac{\tau \bar{I}}{P}) & 0 & \frac{-\tau \bar{S}}{P} & 0 \\ \frac{\tau \bar{I}}{P} & -(\delta + \gamma) & \frac{\tau \bar{S}}{P} & 0 \\ 0 & \delta & -(\alpha_1 + \alpha_2 + \mu + \gamma) & 0 \\ \theta & 0 & \alpha_1 + \alpha_2 + \mu + \gamma & -\gamma \end{bmatrix}$$

At the steady state: $[S_1, 0, 0, R_1]$:

$$J = \begin{bmatrix} -u & 0 & -\frac{\tau\gamma}{u} & 0 \\ 0 & -w & \frac{\tau\gamma}{u} & 0 \\ 0 & \delta & -v & 0 \\ \theta & 0 & v & -\gamma \end{bmatrix}$$

Where, $u = \gamma + \theta$, $v = \alpha_1 + \alpha_2 + \mu + \gamma$ and $w = \delta + \gamma$

$$J - \lambda I = \begin{bmatrix} -u - \lambda & 0 & -\frac{\tau\gamma}{u} & 0 \\ 0 & -w & \frac{\tau\gamma}{u} & 0 \\ 0 & \delta & -v & 0 \\ \theta & 0 & v & -\gamma \end{bmatrix}$$

$$|J - \lambda I| = 0 \Rightarrow \begin{vmatrix} -u - \lambda & 0 & -\frac{\tau\gamma}{u} & 0 \\ 0 & -w - \lambda & \frac{\tau\gamma}{u} & 0 \\ 0 & \delta & -v - \lambda & 0 \\ \theta & 0 & v & -\gamma - \lambda \end{vmatrix} = 0$$

$$(-u - \lambda)\begin{vmatrix} -w - \lambda & \frac{\tau\gamma}{u} & 0 \\ \delta & -v - \lambda & 0 \\ 0 & v & -\gamma - \lambda \end{vmatrix} - \frac{\tau\gamma}{u}\begin{vmatrix} 0 & -w - \lambda & 0 \\ 0 & \delta & 0 \\ \theta & 0 & -\gamma - \lambda \end{vmatrix} = 0$$

This gives us: $(-u - \lambda)(-\gamma - \lambda)\left[(-w - \lambda)(-v - \lambda) - \frac{\delta\tau\gamma}{u}\right] = 0$

$(-u - \lambda)(-\gamma - \lambda) = 0 \Rightarrow \lambda_1 = -u, \lambda_2 = -\gamma$

$(-w - \lambda)(-v - \lambda) - \dfrac{\delta\tau\gamma}{u} = 0 \Rightarrow \lambda^2 + \lambda(v + w) + vw - \dfrac{\delta\tau\gamma}{u} = 0$

Let $f(\lambda) = \lambda^2 + \lambda(v + w) + vw - \dfrac{\delta\tau\gamma}{u}$ and

$f(-\lambda) = \lambda^2 - \lambda(v + w) + vw - \dfrac{\delta\tau\gamma}{u}$,

Since $\lambda > 0$, then by Descartes' rule [16], there are two negative real

eigenvalues if $vw - \dfrac{\delta\tau\gamma}{u} > 0$

$$vw - \frac{\delta\tau\gamma}{u} > 0 \Rightarrow \frac{\delta\tau\gamma}{(\gamma + \theta)(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)} < 1$$

$$\frac{\delta\tau\gamma}{(\gamma + \theta)(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)} < \frac{\delta\tau}{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)} < 1 \Rightarrow R_0 < 1$$

Theorem 2.3 The endemic equilibrium of the SEIR model is locally asymptotically stable if $R_0 > 1$

Proof At the equilibrium point $[S_2, E_2, I_2, R_2]$, the Jacobian matrix is given by:

$$J = \begin{bmatrix} -\frac{\tau\delta\gamma}{vw} & 0 & -\frac{vw}{\delta} & 0 \\ \frac{\tau\delta\gamma}{vw} - u & -w & \frac{vw}{\delta} & 0 \\ 0 & \delta & -v & 0 \\ \theta & 0 & v & -\gamma \end{bmatrix}$$

$$J - \lambda I = \begin{bmatrix} -\frac{\tau\delta\gamma}{vw} - \lambda & 0 & -\frac{vw}{\delta} & 0 \\ \frac{\tau\delta\gamma}{vw} - u & -w - \lambda & \frac{vw}{\delta} & 0 \\ 0 & \delta & -v - \lambda & 0 \\ \theta & 0 & v & -\gamma - \lambda \end{bmatrix}$$

From $|J - \lambda I| = \begin{vmatrix} -\frac{\tau\delta\gamma}{vw} - \lambda & 0 & -\frac{vw}{\delta} & 0 \\ \frac{\tau\delta\gamma}{vw} - u & -w - \lambda & \frac{vw}{\delta} & 0 \\ 0 & \delta & -v - \lambda & 0 \\ \theta & 0 & v & -\gamma - \lambda \end{vmatrix} = 0$, we get:

$(-\gamma - \lambda)\left\{(-w - \lambda)(-v - \lambda)\left(-\dfrac{\tau\delta\gamma}{vw} - \lambda\right) + vw(\lambda + u)\right\} = 0$

We have: $(-\gamma - \lambda) = 0 \Rightarrow \gamma = -\lambda$

$(-w - \lambda)(-v - \lambda)\left(-\frac{\tau\delta\gamma}{vw} - \lambda\right) + vw(\lambda + u) = 0 \Rightarrow -\lambda^3 - \lambda^2\left(v + w + \frac{\tau\delta\gamma}{vw}\right) - \lambda\left(vw + \frac{\tau\delta\gamma}{w} + \frac{\tau\delta\gamma}{v}\right) + vw(\lambda + u) - \tau\delta\gamma = 0$

Let $f(\lambda) = -\lambda^3 - \lambda^2\left(v + w + \frac{\tau\delta\gamma}{vw}\right) - \lambda\left(vw + \frac{\tau\delta\gamma}{w} + \frac{\tau\delta\gamma}{v}\right) + vw(\lambda + u) - \tau\delta\gamma = 0$, also, let

$f(-\lambda) = \lambda^3 - \lambda^2\left(v + w + \frac{\tau\delta\gamma}{vw}\right) + \lambda\left(vw + \frac{\tau\delta\gamma}{w} + \frac{\tau\delta\gamma}{v}\right) + vw(\lambda + u) - \tau\delta\gamma = 0$,

By Descartes' rule, the eigenvalues will be negative if $vw(\lambda + u) - \tau\delta\gamma < 0$

$vw(\lambda + u) - \tau\delta\gamma < 0 \Rightarrow vw(\lambda + u) < \tau\delta\gamma \Rightarrow 1 < \dfrac{\tau\delta\gamma}{vw(\lambda + u)}$

$1 < \dfrac{\tau\delta\gamma}{(\delta + \gamma)(\lambda + \gamma + \theta)(\alpha_1 + \alpha_2 + \mu + \gamma)} < \dfrac{\tau\delta}{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)} \Rightarrow 1 < \dfrac{\tau\delta}{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)}$

$\Rightarrow \dfrac{\tau\delta}{(\delta + \gamma)(\alpha_1 + \alpha_2 + \mu + \gamma)} > 1 \text{ or } R_0 > 1$

Global Stability Analysis

Theorem 2.5 If $R_0 > 1$ and $\tau < (\gamma + \delta)$, then the disease-free equilibrium point is globally asymptotically stable in the domain:

$\mho_0 = \left\{(S,\ E,\ I,\ R) \in \mathbb{R}_+^4 : S < \frac{P}{\tau}(\gamma + \delta)\right\}$

Proof Define a Lyapunov function $W = E$. We have that:

$\frac{dW}{dt} = \left[\frac{\tau}{P}S - (\delta + \gamma)\right]E \le 0$ if $S < \frac{P}{\tau}(\delta + \gamma)$, that is, $\frac{dL}{dt} \le 0$ in the domain $\mho_0$.

For the positive definite function W, the derivative $\frac{dW}{dt}$ is negative semi-definite in

$\mho_0$. Now we consider the set where $\frac{dW}{dt} = 0$.

Let $\Psi = \left\{(S,\ E,\ I,\ R) \in \mho_0 : \frac{dW}{dt} = 0\right\} = \{(S,\ E,\ I,\ R) \in \mho_0 : E = 0\}$

Let M be the largest invariant set in $\mho_0$. Then in $\mho_0$, we have:

$\frac{dS}{dt} = \gamma(P - S) - \theta S$ (9)

$\frac{dI}{dt} = \delta I - vI$ (10)

$\frac{dR}{dt} = vI + \theta S - \gamma R$ (11)

From Eq. (1), we have $R \longrightarrow \frac{\theta P}{\gamma + \theta}$ as $t \longrightarrow \infty$. From Eq. (10),

if $\delta < v$, we have $I \longrightarrow 0$ as $t \longrightarrow \infty$. From Eq. (9), we have $S \longrightarrow \frac{\gamma P}{\gamma + \theta}$ as

$t \longrightarrow \infty$. The steady state is globally asymptotically stable if

$\delta < v \Longleftrightarrow \frac{\delta}{\alpha_1 + \alpha_2 + \mu + \gamma} < 1 \Longrightarrow \frac{\tau\delta}{(\gamma + \delta)(\alpha_1 + \alpha_2 + \mu + \gamma)} < \frac{\delta}{\alpha_1 + \alpha_2 + \mu + \gamma} < 1$ if $\tau < \gamma + \delta$.

Theorem 2.6 The endemic steady state is globally asymptotically stable in the

domain: $\mho_1 = \left\{(S,\ E,\ I,\ Q,\ R) \in \mathbb{R}_+^4 : 1 < \frac{E_2}{E} < \frac{I_2}{I} < \frac{R_2}{R} < \frac{S_2}{S}\right\}$

Proof Consider a Lyapunov function M defined as follows:

$M = \int_{S_2}^{S} \frac{S - S_2}{S}dS + \int_{E_2}^{E} \frac{E - E_2}{E}dE + \int_{I_2}^{I} \frac{I - I_2}{I}dI + \int_{R_2}^{R} \frac{R - R_2}{R}dR$

We have;

$\frac{dM}{dt} = \left(\frac{S - S_2}{S}\right)\frac{dS}{dt} + \left(\frac{E - E_2}{E}\right)\frac{dE}{dt} + \left(\frac{I - I_2}{I}\right)\frac{dI}{dt} + \left(\frac{R - R_2}{R}\right)\frac{dR}{dt} = (S - S_2)\left(\frac{\gamma P}{S} - \frac{\gamma P}{S_2} + \frac{\tau I_2}{P} - \frac{\tau I}{P}\right) + (E - E_2)\left(\frac{\tau}{P}\frac{SI}{E} - \frac{\tau}{P}\frac{S_2 I_2}{E_2}\right) + (I - I_2)\left(\frac{\delta E}{I} - \frac{\delta E_2}{I_2}\right) + (R - R_2)\left(\frac{wI}{R} - \frac{wI_2}{R_2} + \frac{\theta S}{R} - \frac{\theta S_2}{R_2}\right) = (S - S_2)\left(\frac{\gamma P(S_2 - S)}{SS_2} + \frac{\tau(I_2 - I)}{P}\right) + (E - E_2)\left(\frac{\tau}{P}\frac{(E_2 SI - S_2 I_2 E)}{EE_2}\right) + (I - I_2)\left(\frac{\delta(I_2 E - IE_2)}{II_2}\right) + (R - R_2)\left(\frac{w(IR_2 - I_2 R)}{RR_2} + \frac{\theta(SR_2 - S_2 R)}{RR_2}\right) = -\frac{\gamma P(S_2 - S)^2}{SS_2} - \frac{\tau(S_2 - S)(I_2 - I)}{P} - \frac{\tau}{P}\frac{(E_2 - E)(SIE_2 - S_2 I_2 E)}{EE_2} - \frac{\delta(I_2 - I)(I_2 E - IE_2)}{II_2} - \frac{w(R_2 - R)(IR_2 - I_2 R)}{RR_2} - \frac{\theta(R_2 - R)(SR_2 - S_2 R)}{RR_2}$

From the region: $1 < \frac{E_2}{E} < \frac{I_2}{I} < \frac{R_2}{R} < \frac{S_2}{S}$, we have; $IS_2 - SI_2 < I(S_2 - S)$, $ES_2 - SE_2 < E(S_2 - S)$, $EI_2 - IE_2 < E(I_2 - I)$, $IR_2 - RI_2 < I(R_2 - R)$, $SR_2 - RS_2 < S(R_2 - R)$, and $SI < S_2 I_2$.

Hence, we get;

$$\frac{dM}{dt} < \frac{\gamma P(S_2-S)^2}{SS_2} - \frac{\tau(S_2-S)(I_2-I)}{P} - \frac{\tau}{P}\frac{S_2I_2(E_2-E)^2}{EE_2} - \frac{\delta E(I_2-I)^2}{II_2} - \frac{wI(R_2-R)^2}{RR_2} - \frac{\theta S(R_2-R)^2}{RR_2} < 0$$

Numerical Simulation.

Scilab plot of the SEIR model for $R_0 < 1$ [Fig. 1] Define a solution to the system in Eq. (1) for the parameter values;

$\gamma = 0.000038, \quad \tau = 0.2, \quad \delta = 0.33, \quad \alpha_1 = 0.07143, \quad \alpha_2 = 0.03175, \quad \delta = 2.08, \quad \theta = 0.00556$ subject to the initial conditions: $s(0) = 0.7, \quad e(0) = 0.15, \quad i(0) = 0.1, \quad r(0) = 0.05,$

where $s = \frac{S}{N}, \quad e = \frac{E}{N}, \quad i = \frac{I}{N}, \quad q = \frac{Q}{N}, \quad r = \frac{R}{N}$. The population N is taken to be 1000.

Scilab Code: function **ydot**=SEIRdmodel(**t, y**)

```
ydot=[p-t*y(1)*y(3)-p*y(1)-s*y(1);t*y(1)*y(3)-(d+p)*y(2);d*y(2)-
(a1+a2+u+p)*y(3);(a1+a2+u+p)*y(3)+s*y(1)-
p*y(4)]
endfunction
p=0.000038;
t=0.3;
d=0.33;
a1=0.07143;
a2=0.03175;
u=2.08;
s=0.0056;
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 rate of infection =0.3", "fontsize",3)
hl=legend(['s';'e';'i';'r']);
```
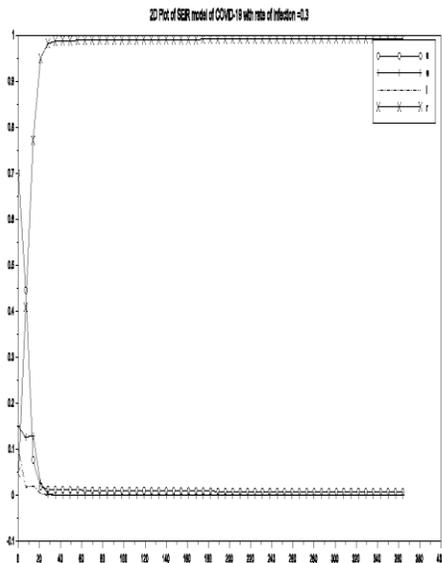

Fig 1. Scilab plot of the SEIR Model for $R_0 < 1$ Fig 2. Scilab plot of the SEIR Model for $R_0 > 1$
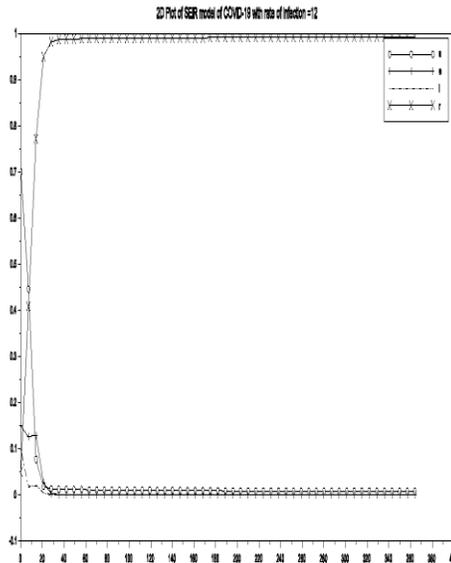
Scilab plot of the SEIR model for $R_0 > 1$. [Fig. 2] Define a solution to the system in Eq. (1) for the parameter values; $\gamma = 0.000038$, $\tau = 12$ $\delta = 0.33$, $\alpha_1 = 0.07143$, $\alpha_2 = 0.03175$, $\delta = 2.08$, $\theta = 0.00556$ subject to the initial conditions: $s(0) = 0.7$, $e(0) = 0.15$, $i(0) = 0.1$, $r(0) = 0.05$, where $s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, $q = \frac{Q}{N}$, $r = \frac{R}{N}$. The population N is taken to be 1000.

Scilab Code: function **ydot**=SEIRdmodel(**t**, **y**)
ydot=[p-**t*****y**(1)***y**(3)-p***y**(1)-s***y**(1);**t*****y**(1)***y**(3)-(d+p)***y**(2);d***y**(2)-
(a1+a2+u+p)***y**(3);(a1+a2+u+p)***y**(3)+s***y**(1)-p***y**(4)]
endfunction
p=0.000038;
t=12;
d=0.33;
a1=0.07143;
a2=0.03175;
u=2.08;
s=0.0056;
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 rate of infection =12", "fontsize",3)
hl=legend(['s';'e';'i';'r']);

Discussion of Results
We have formulated an SEIR model with a vaccination parameter for the transmission dynamics of COVID-19. We studied the stability of the equilibrium points of the system in Eq. (1). The local stability of the disease-free equilibrium implies that if a small number of infected individuals are introduced into the population, after a short time the system will converge to the disease-free equilibrium point (that is, the disease will die out of the population). For the endemic equilibrium, the local stability implies that if a small number of infected individuals are introduced into the population, then after a short time, the system will converge back to the endemic equilibrium point (that is, the disease will die out). The global stability of the disease-free equilibrium point implies that whatever the number of the infected individuals introduced into the population, in the long run, the disease will eventually die out of the population. On the other hand, the global stability of the endemic equilibrium implies that in the long run, the disease will become endemic or will continue to prevail in the population, irrespective of the number of infected individuals introduced into 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, in a very short time individuals in the population are removed by death, recovery or vaccination and the disease eventually dies out of the population. The same trend is observed when the basic reproduction number is greater than one. This happens because of the vaccination parameter θ.

4. Conclusion
Based on the results of the study, it was concluded that the SEIR model with a vaccination parameter could be used as a reference model for the spread of COVID-19 in a population. Analyses of the model provides an overview of global and local stability in the spread of COVID-19 depending upon the value of the basic reproduction number.
The simulation results provide a predictive picture of the short-term and long-term behavior of
the disease outbreak, and also shows that the presence of the vaccination parameter causes the disease to die out of the population regardless of the value of the basic reproduction number.

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