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A Mathematical Model on the Spread of COVID-19

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Abstract

In this paper, a nonlinear mathematical model of COVID-19 was formulated. We proposed a SEIQR model using a system of ordinary differential equations. COVID-19 free equilibrium and endemic equilibrium points of the model are obtained. A basic reproduction number of the model is investigated by the next-generation matrix. The stability analysis of the model equilibrium points was investigated using basic reproduction numbers. The results show that the disease-free equilibrium of the COVID-19 model is stable if the basic reproduction number is less than unity and unstable if the basic reproduction number is greater than unity. Sensitivity analysis was rigorously analyzed. Finally, numerical simulations are presented to illustrate the results.

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

1. Introduction

Coronaviruses are a massive own circle of relatives of viruses which could purpose contamination in human beings that acknowledged to purpose respiration infections ranging from the now not unusual place bloodless to extra excessive illnesses together with Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS).A novel

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coronavirus, formerly precise 2019-nCoV, turned into recognized because the purpose of a cluster of Pneumonia instances in Wuhan, a town with inside the Hubei Province of China, on the cease of 2019.It eventually unfold at some stage in China and elsewhere, turning into a international fitness emergency. In February 2020, the World Health Organization (WHO) distinct the ailment COVID-19, which stands for coronavirus ailment 2019 a international pandemic [13].

According to the WHO report (WHO, 2020), all over the world, as of December 29th, 2020, there have been 79,931,215 confirmed cases of COVID-19, including 1,765,265 deaths, reported to WHO [14]. Investigations are still ongoing to assess the source of the disease, the mode or modes of transmission and the extent of infection. Currently, available evidence of the emerging Corona virus and past experiences with other Corona viruses (Middle East Respiratory Syndrome (MERS) and SARS virus) and other respiratory symptoms viruses (such as bird flu) indicate the possibility of the new virus transmission from an animal source [6,7,2,1].

The main transmission routes of the coronavirus are through coughing, sneezing, contacting infected people, or touching items or surfaces that are contaminated with fecal traces [4]. In order to combat this pandemic, different preventive measures are recommended, such as avoiding close contact with sick people, avoiding touching the eyes, nose, and mouth with unwashed hands, washing hands often with soap and water for at least 20 seconds, using an alcohol-based hand sanitizer containing at least 60% alcohol when soap and water are not available.

Developing a mathematical model for the coronavirus (COVID-19) is of great importance as it helps to explain the extent of the disease taking into consideration that it is an invisible and infectious virus. Based on this mathematical model, we can judge whether approved measures such as quarantine are sufficient to limit the spread of the virus.

Many studies and research of mathematical models can be used to analyze the spread of Corona Virus [12, 3, 8, 5, 7, 10]. In [8], the SEIR version concerning the susceptible, the exposed, the infected, and the recovered people become considered. Results after simulating diverse eventualities imply that dismissing social distancing and hygiene measures could have devastating consequences for the human population. In [12], a mathematical model was developed to integrate asymptomatic people and the isolation of infected persons, the quarantine of contacting people, and the home containment of all population, strategies. It is established by theoretical investigation and illustrated by simulations that the level of containment is very important to prevent the disease from spreading in the absence of a vaccine. In [10], the SEIRU version concerning the susceptible, the exposed, the infected, the quarantined, and the recovered people changed into consideration. It turned into expected that there's a hazard of a decline in secondary infections while all precautionary measures are determined globally.

We will propose a mathematical model that defines and describes the spread of the new Coronavirus (COVID-19). During the development of epidemiology modeling in the

population; compartmental models played a central role. Majority of cases of (the COVID-19) virus spread from human-to-human connection. In this work we by adopting the basic SEIR (Susceptible-Exposed-Infected-Recovered) model and we extend it into SEIQR where the quarantined Q class is added.

2. Model Description and Analysis

We propose a continuous model SEIQR to describe the interaction within a population where the disease COVID-19 exists. We consider the cases of (the COVID-19) virus spread from a human-to-human connection. The model subdivides the entire human population period at time t denoted as $N(t)$ into susceptible $S(t)$, exposed $E(t)$, Infected people with symptoms and carriers of the virus $I(t)$, Quarantined Infected (Hospitalized cases) $Q(t)$ and the recovered as R(t). The total number of the human population at time t is given by $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$. Individuals are recruited at π is the new birth rate in the susceptible human population, β_1 represents the transmission coefficient from susceptible individuals to exposure due to the movement and contact that occur among them, β_2 represents the transmission coefficient from susceptible individuals infected individuals with symptoms and carriers of the virus due to the movement and contact that occur among them, μ represents the natural death rate in all compartments, σ represents the progression rate from E to either I or R. The exposed individuals become infectious and join the infected compartment at $\delta\sigma$ and the remaining proportion of these exposed individuals develop natural immunity and recovered from the disease at $(1-\delta)\sigma$ and ω is the transmission coefficient of the infected people with symptoms and carriers of the virus to the quarantined infected (hospitalized cases) γ is the transmission coefficient of the quarantined infected (hospitalized cases) to the recovered cases. The recovered individuals become again susceptible to the disease at a rate of θ, α_1 and α_2 respectively representing the death rate of the infected population and the death rate of the quarantined infected (hospitalized cases) population due to Covid-19 infection. Based on the above state variables and model assumptions we consider the following system of five non-linear differential equations:

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

$$\frac{dE}{dt} = \frac{\beta_1 SE + \beta_2 SI}{N} - (\mu + \sigma)E \quad (2)$$

$$\frac{dI}{dt} = \delta\sigma E - (\mu + \alpha_1 + \omega)I \quad (3)$$

$$\frac{dQ}{dt} = \omega I - (\mu + \alpha_2 + \gamma)Q \quad (4)$$

$$\frac{dR}{dt} = (1-\delta)\sigma E + \gamma Q - (\mu + \theta)R \quad (5)$$

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With the initial condition $S(0) > 0, E(0) \geq 0, I(0) \geq 0, Q(0) \geq 0$ and $R(0) \geq 0$.

2.1. Basic Properties of the Model

2.1.1. Invariant Region

In this subsection, we determine a region in which the solution of model (1-5) is bounded. For this model the total population is $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$. Then, differentiating $N(t)$ with respect to time we obtain:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt} + \frac{dR}{dt} = \pi - \alpha_1 I - \alpha_2 Q - \mu N$$

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

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

After evaluating, we obtain

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

As $t \to \infty$, we obtain $\Omega = \left\{(S, E, I, Q, R) \in R_+^5 : 0 < N \leq \frac{\pi}{\mu}\right\}$.

Therefore, the model equation is wellposed epidemiologically and mathematically. Hence, it is sufficient to study the dynamics of the basic model in the region Ω.

2.1.2. Positivity of Solutions

Theorem 1: If $S(0) > 0, E(0) \geq 0, I(0) \geq 0, Q(0) \geq 0, R(0) \geq 0$ are positive in the feasible set Ω, then the solution set $(S(t), E(t), I(t), Q(t), R(t))$ of system (1-5) is positive for all $t \geq 0$.

Proof: From the first equation of the system

$$\frac{dS}{dt} = \pi + \theta R - \mu S - \frac{\beta_1 SE + \beta_2 SI}{N}$$

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

This equation is a first order linear ordinary differential equation. Whose integrating factor

$$IF = e^{\int_0^t \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) d\tau}.$$

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Now multiplying the differential equation by its integrating factor, we obtain:

$$e^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}\frac{dS}{dt}+e^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)S=e^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}(\pi+\theta R)$$

$$d\left(Se^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}\right)=e^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}(\pi+\theta R)dt$$

Integrate both sides in the interval $[0,t]$

$$\int_0^t d\left(Se^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}\right)=\int_0^t e^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}(\pi+\theta R)\,d\tau$$

$$S(t)e^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}-S(0)=\int_0^t e^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}(\pi+\theta R)\,d\tau$$

$$S(t)=e^{-\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}\left[S(0)+\int_0^t e^{\int_0^t\left(\mu+\frac{\beta_1E+\beta_2I}{N}\right)d\tau}(\pi+\theta R)\,d\tau\right]>0$$

Similarly, it can be shown that $E(t)>0, I(t)>0, Q(t)>0\ and\ R(t)>0$. Thus, the solutions $S(t), E(t), I(t), Q(t), R(t)$ of system (1-5) remain positive for all $t>0$. If $S(t), E(t), I(t), Q(t)$ and $R(t)$ are non-negative, then $N(t)=S(t)+E(t)+I(t)+Q(t)+R(t)>0$.

2.1.3. Equilibrium Points of the Model

The equilibrium points of the model system are obtained by setting the right hand side of the differential equations equal to zero and solving each to get a constant solution. Epidemiological models usually have two equilibrium points, namely disease free equilibrium point and endemic equilibrium point.

2.1.4. Disease Free Equilibrium Point (DFEP)

The disease free equilibrium of the model, (1) to (5), is obtained by making $\frac{dS}{dt}=\frac{dE}{dt}=\frac{dI}{dt}=\frac{dQ}{dt}=\frac{dR}{dt}=0$. Further at the disease free equilibrium point there is no infectious person of the disease in the population, i.e. $E=I=Q=0$.Therefore, the disease free equilibrium point is given by:

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$$X_0 = \left(\frac{\pi}{\mu}, 0,0,0,0\right).$$

The point $X_0$is non-negative equilibrium, which exists without any condition. This equilibrium implies that in the absence of any infection, the total population size remains at its equilibrium value $\frac{\pi}{\mu}$.

2.1.5. Endemic Equilibrium Point (EEP)

The endemic equilibrium point of the model, (1) to (5), is obtained by making $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = 0$. From the model we have;

$$\frac{dS}{dt} = \pi + \theta R - \mu S - \frac{\beta_1 SE + \beta_2 SI}{N} = 0 \quad 6$$

$$\frac{dE}{dt} = \frac{\beta_1 SE + \beta_2 SI}{N} - (\mu + \sigma)E = 0 \quad 7$$

$$\frac{dI}{dt} = \delta\sigma E - (\mu + \alpha_1 + \omega)I = 0 \quad 8$$

$$\frac{dQ}{dt} = \omega I - (\mu + \alpha_2 + \gamma)Q = 0 \quad 9$$

$$\frac{dR}{dt} = (1 - \delta)\sigma E + \gamma Q - (\mu + \theta)R = 0 \quad 10$$

From equation (8), $\delta\sigma E - (\mu + \alpha_1 + \omega)I = 0$ we get:

$$E = \frac{(\mu + \alpha_1 + \omega)I}{\delta\sigma} \quad 11$$

From equation (9), $\omega I - (\mu + \alpha_2 + \gamma)Q = 0$ we get:

$$Q = \frac{\omega I}{\mu + \alpha_2 + \gamma} \quad 12$$

From equation (10),$(1 - \delta)\sigma E + \gamma Q - (\mu + \theta)R = 0$ we get:

$$R = \frac{(1-\delta)\sigma E + \gamma Q}{\mu + \theta}.$$

Substituting the value of $E = \frac{(\mu + \alpha_1 + \omega)I}{\delta\sigma}$ and $Q = \frac{\omega I}{\mu + \alpha_2 + \gamma}$into the equation$R = \frac{(1-\delta)\sigma E + \gamma Q}{\mu + \theta}$ implies;

$$R = \left[\frac{(1-\delta)(\mu + \alpha_1 + \omega)}{\delta(\mu + \theta)} + \frac{\gamma\omega}{(\mu + \alpha_2 + \gamma)(\mu + \theta)}\right] I, \quad 13$$

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From equation (7), $\frac{\beta_1 SE+\beta_2 SI}{N} - (\mu+\sigma)E = 0$ we get:

$$S = \frac{(\mu+\sigma)EN}{\beta_1 E+\beta_2 I},$$

Substituting the value of $E = \frac{(\mu+\alpha_1+\omega)I}{\delta\sigma}$ into the equation $S = \frac{(\mu+\sigma)EN}{\beta_1 E+\beta_2 I}$ implies;

$$S = \frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}, \qquad 14$$

From equation (6), $\pi + \theta R - \mu S - \frac{\beta_1 SE+\beta_2 SI}{N} = 0$ we get:

Substituting the value of $E, R \text{ and } S$ into the equation $\pi + \theta R - \mu S - \frac{\beta_1 SE+\beta_2 SI}{N} = 0$ implies

$$\pi + \theta\left[\frac{(1-\delta)(\mu+\alpha_1+\omega)}{\delta(\mu+\theta)} + \frac{\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right]I - \frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2} - \frac{\beta_1\left(\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}\right)\left(\frac{(\mu+\alpha_1+\omega)I}{\delta\sigma}\right) + \beta_2\left(\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}\right)I}{N} = 0$$

$$\pi + \left[\frac{(1-\delta)\theta(\mu+\alpha_1+\omega)}{\delta(\mu+\theta)} + \frac{\theta\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right]I - \frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2} - \beta_1\left(\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}\right)\left(\frac{(\mu+\alpha_1+\omega)}{\delta\sigma}\right)I - \beta_2\left(\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}\right)I = 0$$

$$\left[\frac{(1-\delta)\theta(\mu+\alpha_1+\omega)}{\delta(\mu+\theta)} + \frac{\theta\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right]I - \frac{\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)}I - \frac{\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}I = \frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2} - \pi$$

$$\left[\frac{(1-\delta)\theta(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)+\delta\theta\gamma\omega}{\delta(\mu+\theta)(\mu+\alpha_2+\gamma)}\right]I - \frac{\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N+\delta\sigma\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)}I = \frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2} - \pi$$

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$$\left[\frac{\begin{matrix}[(1-\delta)\theta(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)+\delta\theta\gamma\omega]\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)- \\ \left[\begin{matrix}\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N \\ +\delta\sigma\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N\end{matrix}\right](\mu+\theta)(\mu+\alpha_2+\gamma)\end{matrix}}{\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)(\mu+\theta)(\mu+\alpha_2+\gamma)}\right]I$$

$$=\frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}-\pi$$

$$I=\frac{A[\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N-\pi(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)]}{[\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2][K-M(\mu+\theta)(\mu+\alpha_2+\gamma)]} \qquad 15$$

Where $A=\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)(\mu+\theta)(\mu+\alpha_2+\gamma)$,

$K=[(1-\delta)\theta(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)+\delta\theta\gamma\omega]\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)$ and
$M=\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N+\delta\sigma\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N.$

Therefore, the Endemic Equilibrium Point (EEP) denoted by $X^*$of the model in Equation (1) to (5) is given by:

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

Where $S^*=\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}$, $E^*=\frac{(\mu+\alpha_1+\omega)I^*}{\delta\sigma}$

$$I^*=\frac{\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)(\mu+\theta)(\mu+\alpha_2+\gamma)}{[\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N-\pi(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)]}{[\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2][K-M(\mu+\theta)(\mu+\alpha_2+\gamma)]}$$

$Q^*=\frac{\omega I^*}{\mu+\alpha_2+\gamma}$ and $R^*=\left[\frac{(1-\delta)\sigma(\mu+\alpha_1+\omega)}{\delta\sigma(\mu+\theta)}+\frac{\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right]I^*$

$K=[(1-\delta)\theta(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)+\delta\theta\gamma\omega]\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)$ and
$M=\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N+\delta\sigma\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N$

2.1.6. The Basic Reproduction Number

The basic reproduction number, usually denoted as R_0defines the average number of secondary infections caused by an individual in an entirely susceptible population. The value of R_0will 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 reproduction number, we will use

the method of next generation matrix [11] and is defined as the spectral radius (or dominant eigenvalue) of the model. The first step is rewriting the model equations, starting with newly infective classes:

$$\frac{dE}{dt} = \frac{\beta_1 SE + \beta_2 SI}{N} - (\mu + \sigma)E$$

$$\frac{dI}{dt} = \delta\sigma E - (\mu + \alpha_1 + \omega)I$$

$$\frac{dQ}{dt} = \omega I - (\mu + \alpha_2 + \gamma)Q$$

Setting $x = (E, I, Q, R, S)^T$, then system (1) can be written as

$$\frac{dx}{dt} = f(x) - v(x)$$

Here the new infection matrix $f(x)$and the transition matrix $v(x)$are defined by

$$f(x) = \begin{pmatrix} \frac{\beta_1 SE + \beta_2 SI}{N} \\ 0 \\ 0 \end{pmatrix} \text{ and } v(x) = \begin{pmatrix} (\mu + \sigma)E \\ (\mu + \alpha_1 + \omega)I - \delta\sigma E \\ (\mu + \alpha_2 + \gamma)Q - \omega I \end{pmatrix}$$

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

$$F = \begin{pmatrix} \beta_1 & \beta_2 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad \text{and} \quad V = \begin{pmatrix} \mu + \sigma & 0 & 0 \\ -\delta\sigma & \mu + \alpha_1 + \omega & 0 \\ 0 & -\omega & \mu + \alpha_2 + \gamma \end{pmatrix} \quad \text{then;}$$

$$V^{-1} = \begin{pmatrix} \frac{1}{\mu + \sigma} & 0 & 0 \\ \frac{\delta\sigma}{(\mu + \sigma)(\mu + \alpha_1 + \omega)} & \frac{1}{\mu + \alpha_1 + \omega} & 0 \\ \frac{\delta\sigma\omega}{(\mu + \sigma)(\mu + \alpha_1 + \omega)(\mu + \alpha_2 + \gamma)} & \frac{\omega}{(\mu + \alpha_1 + \omega)(\mu + \alpha_2 + \gamma)} & \frac{1}{\mu + \alpha_2 + \gamma} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} \frac{\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma}{(\mu + \sigma)(\mu + \alpha_1 + \omega)} & \frac{\beta_2}{(\mu + \alpha_1 + \omega)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

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

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$$R_0 = \frac{\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma}{(\mu+\sigma)(\mu+\alpha_1+\omega)}$$ 16

3. Stability Analysis of Diseases-Free Equilibrium

Theorem 2: The disease free equilibrium point $X_0$of the dynamical system (1) - (5) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof: The Jacobian matrix at any equilibrium point $X = (S, E, I, Q, R)$is given by

$$J(X) = \begin{bmatrix} \frac{-\beta_1 E - \beta_2 I}{N} - \mu & \frac{-\beta_1 S}{N} & \frac{-\beta_2 S}{N} & 0 & \theta \\ \frac{\beta_1 E + \beta_2 I}{N} & \frac{\beta_1 S}{N} - (\mu+\sigma) & \frac{\beta_2 S}{N} & 0 & 0 \\ 0 & \delta\sigma & -(\mu+\alpha_1+\omega) & -(\mu+\alpha_2+\gamma) & \sigma \\ 0 & 0 & \omega & \gamma & -(\mu+\theta) \\ 0 & (1-\delta)\sigma & 0 & & \end{bmatrix}$$

The Jacobian matrix at the disease-free equilibrium point $X_0 = \left(\frac{\pi}{\mu}, 0,0,0,0\right)$ is given by

$$J(X_0) = \begin{bmatrix} -\mu & -\beta_1 & -\beta_2 & 0 & \theta \\ 0 & \beta_1 - (\mu+\sigma) & \beta_2 & 0 & 0 \\ 0 & \delta\sigma & -(\mu+\alpha_1+\omega) & 0 & 0 \\ 0 & 0 & \omega & -(\mu+\alpha_2+\gamma) & \sigma \\ 0 & (1-\delta)\sigma & 0 & \gamma & -(\mu+\theta) \end{bmatrix}$$

The characteristic equation of this matrix is given by$\det(J(X_0) - \lambda I_5) = 0$, where $I_5$is a square identity matrix of order 5 and λ is eigenvalues of the Jacobian matrix. Therefore, the characteristic equation is $(\mu+\lambda)\big[\lambda^4 + (4\mu + \alpha_1 + \omega + \sigma + \theta + \alpha_2 + \gamma - \beta_1)\lambda^3 + \big[(2\mu + \alpha_1 + \omega + \sigma - \beta_1)(2\mu + \theta + \alpha_2 + \gamma) + (\mu + \alpha_2 + \gamma)(\mu + \theta) - \big[(\beta_1 - (\mu+\sigma))(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] + \sigma\gamma\big]\lambda^2 + \big[(\mu + \alpha_2 + \gamma)(\mu + \theta)(2\mu + \alpha_1 + \omega + \sigma - \beta_1) - (2\mu + \theta + \alpha_2 + \gamma)\big[(\beta_1 - (\mu+\sigma))(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] + \sigma\gamma(\mu + \alpha_1 + \omega + \mu + \sigma - \beta_1)\big]\lambda - \sigma\gamma\big[(\beta_1 - (\mu+\sigma))(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] - (\mu + \alpha_2 + \gamma)(\mu + \theta)\big[(\beta_1 - (\mu+\sigma))(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big]\big] = 0$.

The Jacobian evaluated at the DFE has five eigenvalues, one of which is $\lambda_1 = -\mu$ which is negative.

The remaining four are eigenvalues of the roots of the equation given by:

$$a_4\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0$$

Where

$$a_4 = 1,\ a_3 = 4\mu + \alpha_1 + \omega + \sigma + \theta + \alpha_2 + \gamma - \beta_1$$

$$a_2 = \big[(2\mu + \alpha_1 + \omega + \sigma - \beta_1)(2\mu + \theta + \alpha_2 + \gamma) + (\mu + \alpha_2 + \gamma)(\mu + \theta) - \big[(\beta_1 - (\mu + \sigma))(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] + \sigma\gamma\big],$$

$$a_1 = \big[(\mu + \alpha_2 + \gamma)(\mu + \theta)(2\mu + \alpha_1 + \omega + \sigma - \beta_1) - (2\mu + \theta + \alpha_2 + \gamma)\big[(\beta_1 - (\mu + \sigma))(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] + \sigma\gamma(2\mu + \alpha_1 + \omega + \sigma - \beta_1)\big],$$

$$a_0 = -\sigma\gamma\big[(\beta_1 - (\mu + \sigma))(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] - (\mu + \alpha_2 + \gamma)(\mu + \theta)\big[(\beta_1 - (\mu + \sigma))(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big].$$

By Routh-Hurwitz criteria the DFE equilibrium X_0 is local asymptotically stable if

$a_0 > 0, a_1 > 0, a_2 > 0, a_3 > 0, a_3a_2 - a_1 > 0$ and $a_3a_2a_1 - {a_1}^2 - a_0{a_3}^2 > 0$.

4. Stability Analysis of Endemic Equilibrium Point

Theorem 3: The endemic equilibrium point $X^*$of the dynamical system (1) - (5) is locally asymptotically stable if $R_0 > 1$ and unstable if $R_0 < 1$.

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

$$J(X^*) = \begin{bmatrix} k_1 & k_2 & k_3 & 0 & \theta \\ k_4 & k_5 & k_6 & 0 & 0 \\ 0 & \delta\sigma & -(\mu + \alpha_1 + \omega) & 0 & 0 \\ 0 & 0 & \omega & -(\mu + \alpha_2 + \gamma) & \sigma \\ 0 & (1-\delta)\sigma & 0 & \gamma & -(\mu + \theta) \end{bmatrix}$$

$k_1 = \frac{-\beta_1E^* - \beta_2I^*}{N} - \mu, k_2 = \frac{-\beta_1S^*}{N},\ k_3 = \frac{-\beta_2S^*}{N},\ k_4 = \frac{\beta_1E^* + \beta_2I^*}{N},\ k_5 = \frac{\beta_1S^*}{N} - (\mu + \sigma)$ and $k_6 = \frac{\beta_2S^*}{N}$.

The characteristic equation of this matrix is given by $\det(J(X^*) - \lambda I_5) = 0$, where $I_5$is a square identity matrix of order 5 and λ is eigenvalues of the Jacobian matrix. Therefore, the characteristic equation is;

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

Where

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$$a_5 = 1$$

$$a_4 = 3\mu + \alpha_1 + \alpha_2 + \gamma + \theta + \omega - k_5 - k_1$$

$$\begin{aligned} a_3 = {} & (2\mu + \alpha_2 + \gamma + \theta)(\mu + \alpha_1 + \omega - k_5) + (\mu + \alpha_2 + \gamma)(\mu + \theta) + k_4 k_2 \\ & - [(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] - \sigma\gamma - k_1(3\mu + \alpha_1 + \alpha_2 + \gamma + \theta + \omega - k_5) \end{aligned}$$

$$\begin{aligned} a_2 = {} & (\mu + \alpha_2 + \gamma)(\mu + \theta)(\mu + \alpha_1 + \omega - k_5) \\ & + k_4[(\mu + \alpha_1 + \omega + k_3\delta\sigma)k_2 + (\mu + \theta)k_2 + \theta(1 - \delta)\sigma \\ & + (\mu + \alpha_2 + \gamma)k_2] - (2\mu + \alpha_2 + \gamma + \theta)[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] \\ & - \sigma\gamma(\mu + \alpha_1 + \omega - k_5) \\ & - k_1[(2\mu + \alpha_2 + \gamma + \theta)(\mu + \alpha_1 + \omega - k_5) + (\mu + \alpha_2 + \gamma)(\mu + \theta) \\ & - [(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] - \delta\gamma] \end{aligned}$$

$$\begin{aligned} a_1 = {} & k_4[(\mu + \theta)(\mu + \alpha_1 + \omega + k_3\delta\sigma)k_2 + \theta(1 - \delta)\sigma(\mu + \alpha_1 + \omega) \\ & + (\mu + \alpha_2 + \gamma)[(\mu + \alpha_1 + \omega + k_3\delta\sigma)k_2) + (\mu + \theta)k_2 + \theta(1 - \delta)\sigma] \\ & - \gamma k_2\sigma] + (\mu + \alpha_1 + \omega)\gamma k_5\sigma + \gamma k_6\delta\sigma^2 \\ & - k_1[(\mu + \alpha_2 + \gamma)(\mu + \theta)(\mu + \alpha_1 + \omega - k_5) \\ & - (2\mu + \alpha_2 + \gamma + \theta)[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] - \sigma\gamma(\mu + \alpha_1 + \omega - k_5)] \\ & - (\mu + \alpha_2 + \gamma)(\mu + \theta)[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] \end{aligned}$$

$$\begin{aligned} a_0 = {} & k_1(\mu + \alpha_2 + \gamma)(\mu + \theta)[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] - (\mu + \alpha_1 + \omega)\gamma k_5 k_1\sigma \\ & + \gamma k_1 k_6\delta\sigma^2 - k_4\gamma k_2\sigma(\mu + \alpha_1 + \omega) - k_4\gamma\delta\sigma(k_3\sigma - \theta\omega) \\ & + k_4(\mu + \alpha_2 + \gamma)[(\mu + \theta)(\mu + \alpha_1 + \omega + k_3\delta\sigma)k_2 \\ & + \theta(1 - \delta)\sigma(\mu + \alpha_1 + \omega)] \end{aligned}$$

By Routh-Hurwitz criteria the endemic equilibrium$X^*$is locally asymptotically stable if

$a_4 > 0, \frac{a_3 a_4 - a_2}{a_4} > 0, a_2 - \frac{a_1 a_4^2 - a_0 a_4}{a_3 a_4 - a_2} > 0, \frac{a_1 a_4 - a_0}{a_4} - \frac{(a_0 a_3 a_4 - a_0 a_2)(a_3 a_4 - a_2)}{a_4(a_2 a_3 a_4 - a_2^2 - a_1 a_4^2 + a_0 a_4)} > 0$ and $a_0 > 0$.

5. Parameter Estimation for Numerical Simulation

To perform numerical simulation, we collect the following parameter values obtained from different sources.

Table 1. Parameter Estimation.

Parameter symbol	Value	Source
N	2000	Assumed
π	100	[6]
β_1	0.045	Assumed
β_2	0.04	Assumed
μ	0.016	[3]
θ	0.15	[3]
σ	0.07	[3]
δ	0.7	[3]
ω	0.024	[6]
α_1	0.001	[6]
α_2	0.004	[6]
γ	0.015	[6]

Therefore basic reproduction number($\boldsymbol{R_0}$) of the model is equal to

$$R_0 = \frac{\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma}{(\mu + \sigma)(\mu + \alpha_1 + \omega)} = 1.07912$$

6. Numerical Analysis

The numerical analysis is obtained from the graphs of basic reproduction number with respect to the parameters obtained and given in the above Table1.

Let Us Take Our Control Parameter to be $\boldsymbol{\beta_1}$

The basic control parameters that can decrease the spread of the disease is $\beta_1$which is the transmission coefficient from susceptible individuals to expose individuals due to the movement and contact that occur among them. The graphical representation of the control parameter $\beta_1 vs$ the basic reproduction number R_0 is given below;

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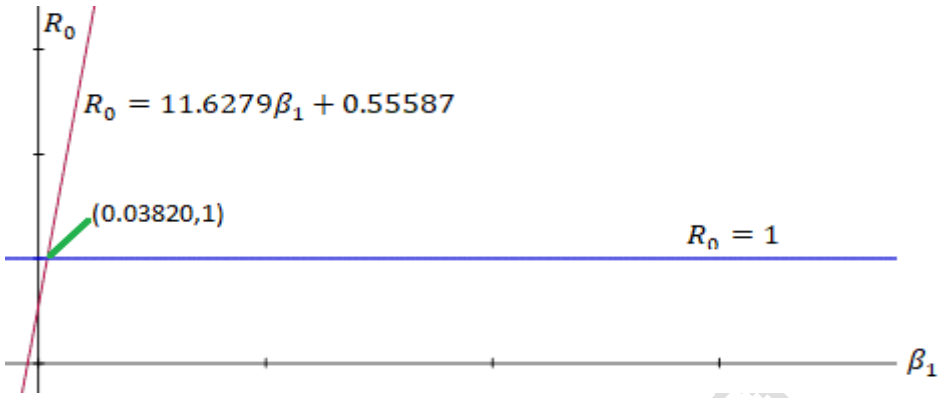

Fig.1 This figure shows the impact of the control parameter β_1 on the basic reproduction number R_0.

To control the spread of the COVID-19, the numerical value of the control parameter β_1 never greater than 0.03820.

Let Us Take Our Control Parameter to be β_2

The basic control parameters that can decrease the spread of the disease is $\beta_2$which is the transmission coefficient from susceptible individuals to infected individuals with symptoms and carriers of the virus due to the movement and contact that occur among them. The graphical representation of the control parameter $\beta_2 vs$ the basic reproduction number R_0 is given below;

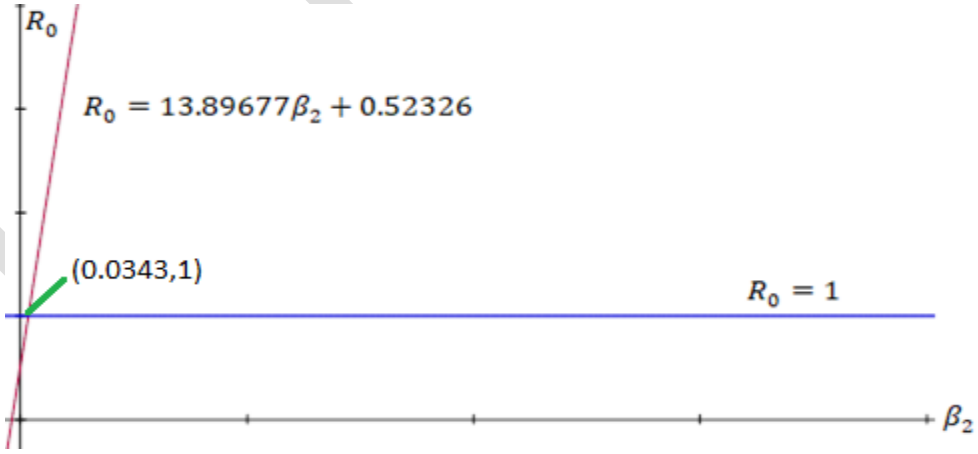

Fig.2. This figure shows the impact of the control parameter β_2 on the basic reproduction number R_0.

To control the spread of the COVID-19, the numerical value of the control parameter β_2 never greater than 0.0343.

Let Us Take Our Control Parameter to be σ

The basic control parameters that can decrease the spread of the disease is σ which is the progression rate from E to either I or R. The graphical representation of the control parameter σ vs the basic reproduction number R_0 is given below;

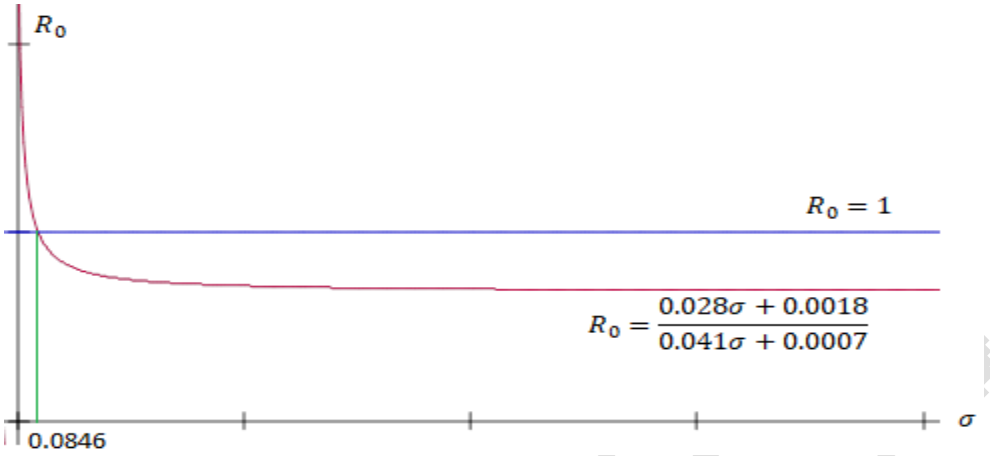

Fig.3. This figure shows the impact of the control parameter σ on the basic reproduction number R_0.

To control the spread of the COVID-19, the numerical value of the control parameter σ never less than 0.0846.

Let Us Take Our Control Parameter to be ω

The basic control parameters that can decrease the spread of the disease is ω which is the transmission coefficient of the infected people with symptoms and carriers of the virus to the quarantined infected (hospitalized cases).The graphical representation of the control parameter ω vs the basic reproduction number R_0 is given below;

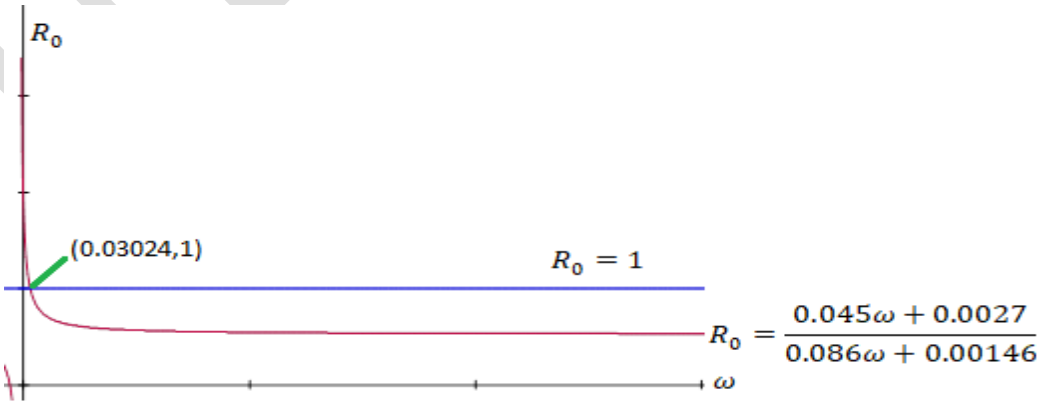

Fig. 4. This figure shows the impact of the control parameter ω on the basic reproduction number R_0.

To control the spread of the COVID-19, the numerical value of the control parameter ω never less than 0.03024.

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Let Us Take Our Control Parameter to be α_1

The basic control parameters that can decrease the spread of the disease is $\boldsymbol{\alpha_1}$which is the death rate of Infected population due to Covid-19 infection. The graphical representation of the control parameter $\boldsymbol{\alpha_1}$ vs the basic reproduction number R_0 is given below;

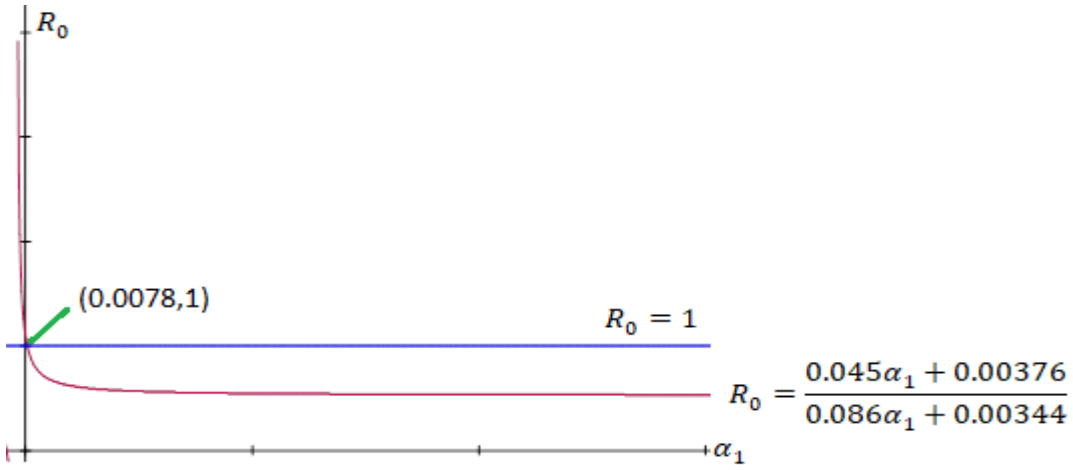

Fig. 5. This figure shows the impact of the control parameter α_1 on the basic reproduction number R_0.

To control the spread of the COVID-19, the numerical value of the control parameter $\boldsymbol{\alpha_1}$ never less than 0.0078.

Let Us Take Our Control Parameter to be μ

The basic control parameters that can decrease the spread of the disease is $\boldsymbol{\mu}$ which is the natural death rate. The graphical representation of the control parameter $\boldsymbol{\mu}$ vs the basic reproduction number R_0 is given below;

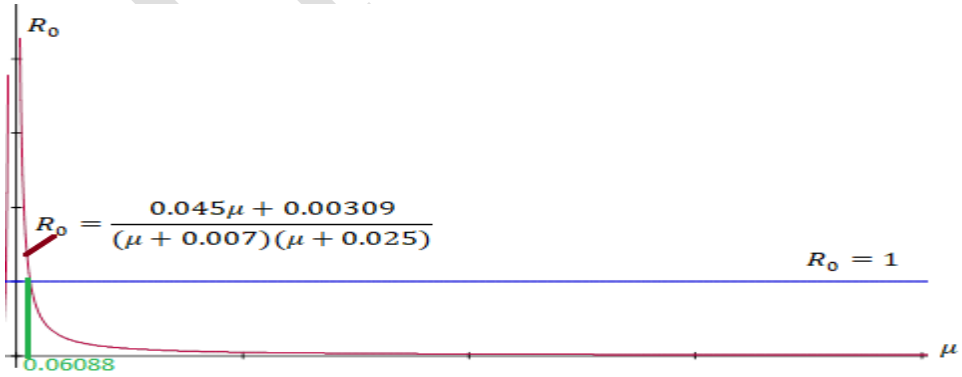

Fig. 6. This figure shows the impact of the control parameter μ on the basic reproduction number R_0.

If the natural death rate μ between 0 and 0.06088, then the reproduction number is decreases, with $R_0 > 1$and this tells us the disease still persists. If the natural death rate is greater than

0.06088, then the reproduction number is decreases, with $R_0 < 1$ and this tell us the disease dies out.

7. 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 numberR_0 (because there are usually errors in data collection and presumed parameter values).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 $m = \beta_1, \beta_2, \sigma, \alpha_1, \omega$ and μ.The sensitivity indices of $R_0$with respect to m is given as:

$$H_{\beta_1}^{R_0} = \frac{\beta_1(\mu + \alpha_1 + \omega)}{\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma}$$

$$H_{\beta_2}^{R_0} = \frac{\beta_2\delta\sigma}{\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma}$$

$$H_{\sigma}^{R_0} = \frac{-\beta_1\sigma(\mu + \alpha_1 + \omega) + \beta_2\sigma\delta(\mu + \sigma) - \beta_2\delta\sigma^2}{(\mu + \sigma)[\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma]}$$

$$H_{\alpha_1}^{R_0} = \frac{-\alpha_1\beta_2\delta\sigma}{(\mu + \alpha_1 + \omega)[\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma]}$$

$$H_{\omega}^{R_0} = \frac{-\omega\beta_2\delta\sigma}{(\mu + \alpha_1 + \omega)[\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma]}$$

$$H_{\mu}^{R_0} = \frac{\beta_1\mu(\mu + \sigma)(\mu + \alpha_1 + \omega) - \mu[\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma](2\mu + \alpha_1 + \omega + \sigma)}{(\mu + \sigma)(\mu + \alpha_1 + \omega)[\beta_1(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma]}$$

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After some simplifications and numerical calculation, we get values of sensitivity index for the important parameters mentioned by the table below:

Table 1: Numerical values of sensitivity indices of R_0

Parameter symbol	Sensitivity Index
β_2	0.5151
β_1	0.4849
μ	-0.3871
ω	-0.3015
σ	-0.2345
α_1	-0.0013

The parameters given in Table 2 are ordered from most sensitive to the least sensitive. The parameter values $\beta_1 = 0.045, \beta_2 = 0.04, \mu = 0.016, \delta = 0.7, \sigma = 0.07\,, \alpha_1 = 0.001$ and $\omega = 0.024$ are used to determine the sensitivity indices.

From the sensitivity indices of R_0above, generally it shows that when the parameter values β_1 and $\beta_2$increase while the other parameters remain constant the value of R_0 increase implying that they increase the endemicity of the disease as they have positive indices. When the parameters ω, μ, α_1, and σ increase the other parameters remain constant the value of R_0 decrease implying that they decrease the endemicity of the disease as they have negative indices.

The most sensitive parameter are β_2(the transmission coefficient from susceptible individuals to infected individuals with symptoms and carriers of the virus due to the movement and contact that occur among them)and β_1(the transmission coefficient from susceptible individuals to exposed individuals with symptoms and carriers of the virus due to the movement and contact that occur among them) and the least sensitive parameter is the death rate of the infected population due to Covid-19 infection α_1.

8. Conclusions

In this study, a deterministic model for the dynamics of COVID-19 is presented and analyzed. The diseases free equilibrium and endemic equilibrium were obtained and their stabilities investigated. The basic reproduction number (R_0) was computed using the next generation matrix method. The model showed that the diseases free equilibrium is unstable when $R_0 > 1$ that means that the disease will be persist. We also studied the sensitivity analysis of model parameters to know the parameters that have a high impact on the reproduction number R_0.

From the above numerical simulation we would like to recommend the following to control the spread of COVID-19:To control the spread of the COVID-19 we investigate five most influential control parameters to make the basic reproduction number R_0 to be less than one. The numerical value of the control parameter β_1(the transmission coefficient from susceptible individuals to expose individuals due to the movement and contact that occur among them) never exceed 0.0382, the numerical value of the control parameter β_2(the transmission coefficient from susceptible individuals to infected individuals with symptoms and carriers of the virus due to the movement and contact that occur among them) never exceed 0.0343, the numerical value of the control parameter σ (the progression rate from E to either I or R) never less than 0.0846, the numerical value of the control parameter ω (the transmission coefficient of the infected people with symptoms and carriers of the virus to the quarantined infected) never less than 0.3024, the numerical value of

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the control parameterα_1(the death rate of Infected population due to Covid-19 infection) never less than 0.0078.

References

[1] Assiri, J.A. Al-Tawfiq, A.A. Al-Rabeeah, F.A. Al-Rabiah, S. Al-Hajjar, A. Al-Barrak, H.Flemban,W.N.Al Nassir, H.H. Balkhy, R.F. Al-Hakeem, H.Q. Makhdoom, A.I. Zumla, Z.A. Memish (2013). Epidemiological, demographic, and clinical characteristics of 47 cases of middle east respiratory syndrome coronavirus disease from Saudi Arabia: a descriptive study, *Lancet Infect. Dis.* 13, 752–761.

[2] Zaki A.M., van Boheemen S., Bestebroer T.M., Osterhaus A.D.M.E., Fouchier R.A.M. (2012). Isolation of a Novel Coronavirus from a man with pneumonia in Saudi Arabia. *N. Engl. J. Med.* 367, 1814–1820.

[3] Alemneh, H. T., &Telahun, G. T. (2020). Mathematical modeling and optimal control analysis of covid-19 in ethiopia. medRxiv.

[4] Coronavirus: Common symptoms, preventive measures, & How to diagnose it; https: //www. caringlyyours.com/coronavirus/, caringly yours. Retrieved January 28, 2020.

[5] Khoshnaw, S. H., Salih, R. H., &Sulaimany, S. (2020). Mathematical modelling for coronavirus disease (COVID-19) in predicting future behaviours and sensitivity analysis. *Mathematical Modelling of Natural Phenomena*, *15*, 33.

[6] Labzai, A., Kouidere, A., Balatif, O., &Rachik, M. (2020). Stability analysis of mathematical model new corona virus (COVID-19) disease spread in population. *Commun. Math. Biol. Neurosci., 2020*, Article-ID.

[7] Tahir M., IS. Ali Shah, G. Zaman, T. Khan (2018). Prevention strategies for mathematical model MERS-corona virus with stability analysis and optimal control. *J Nanosci. Nanotechnol. Appl*. 3, 101.

[8] Mwalili, S., Kimanthi, M., Ojiambo, V., Gathungu, D., &Mbogo, R. W. (2020). SEIR model for COVID-19 dynamics incorporating the environment and social distancing. 5

[9] Chintis N., Hyman J. M., and Cushing J. M. (2008). Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model. *Bulletin of Mathematical Biology*. 70(5), 1272 - 1296.

[10] Okhuese VA (2020). Mathematical predictions for COVID-19 as a global pandemic. medRxiv.

[11] P. Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math. Biosci.* 180 (1), 29–48.

[12] Serhani, M., &Labbardi, H. (2020). Mathematical modeling of COVID-19 spreading with asymptomatic infected and interacting peoples.

[13] WHO: Coronavirus disease 2019 (COVID-19): situation report, 51.

[14] World Health Organization. (2020). Coronavirus disease 2019 (COVID-19): situation report, 29. World Health Organization. https://apps.who.int/iris/handle/10665/331118.

https://doi.org/10.22105/jarie.2023.385542.1531