STABILITY ANALYSIS OF THE EQUILIBRIA OFA SIMPLE COMPARTMENTAL MODEL FOR COVID-19 TRANSMISSION

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ABSTRACT

The SEIQR mathematical model is formulated to study the spread of COVID-19. The equilibrium points of the system of differential equations are obtained. The local stability of the disease-free and endemic equilibria is studied. The global stability of the disease-free and endemic equilibria is also studied. 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 the disease will eventually die out of the population for any value of the basic reproduction number.

INTRODUCTION

The COVID-19 outbreak is an ongoing global pandemic of viral pneumonia caused by the severe acute respiratory syndrome coronavirus 2 (SARS- CoV-2) virus [Zhu *et al,* 2020]. The outbreak was first identified in Wuhan, China, in December 2019 [(WHO) Novel Coronavirus-China, 2020], [Huang *et al*, 2020]. According to the World Health Organization (WHO), most people infected with the COVID-19 virus experience mild to moderate respiratory illness and recover without requiring special treatment [Bryner, 2020]. 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 [European Centre for Disease Prevention and Control, 2020]. Typical symptoms of COVID-19 infection include dry cough, fever, fatigue, breathing difficulty, and bilateral lung infiltration in severe cases, similar to those caused by SARS-CoV and MERS-CoV infections [Gralinsky & Menachery, 2020].Adults and people with medical conditions, such as cardiovascular disease, diabetes, chronic respiratory disease and cancer are more likely to develop serious complications after contracting the disease[Bryner, 2020]. The average incubation period of the disease is estimated to be 6.4 days [Backer *et al*, 2020], although typically ranges from one to fourteen days [(WHO) Report of the WHO-China joint mission on coronavirus disease 2019 (COVID-19), 2020]. In [Yang *et al*, 2020], it is reported that the median time prior to symptom onset is 3 days, the shortest 1 day, and the longest 24 days. According to [(WHO) Report of the WHO-China joint mission on coronavirus disease 2019 (COVID-19), 2020], for people with mild disease, the average recovery time is about 2 weeks. For people with severe symptoms, recovery is between 3 to 6 weeks. Several authors; [Li *et al*, 2020], [Cakir & Savas, 2020], [Ivorra *et al,* 2020], [Liang, 2020], [Liu *et al*], [Annas *et al*, 2020], [Wiah *et al*, 2020], [Yang, *et al*, 2020], [Nave *et al*], [Din *et al*], 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 study the stability analysis for the model and obtain conditions for the stability of the steady states.

MATERIALS AND METHODS

SEIQR Model Assumptions

The population under consideration is divided into five 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), the Quarantined class, denoted by (Q) 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 μ (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$\frac{\gamma}{N}$. The contact rate γ (rate of infection) is the average number of adequate contacts per infective per unit time. 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 β. Individuals from the exposed class (E), move into the quarantined class at a rate proportional to the class size E with a constant of proportionalityα.

Individuals recover and leave the infective class (I) at rates proportional to the class size I, with proportionality constants $r_1\ and\ r_2$. Individuals that don't survive the disease die and leave the class (I) with proportionality constant δ. Individuals from the quarantined class who are treated, recover and leave the class at rates proportional to the class size Q, with constants of proportionality: r_1 and r_2. Individuals from the quarantined class who are treated but don't recover, die and move into the deceased class at a rate proportional to the class size Q, with the proportionality constant δ.

Parameters of the Model

μ: 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 [Roser *et al,* 2013].

$$\mu = \frac{1}{26280} = 0.000038day^{-1}.$$

γ: The rate of infection γ = (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 assume it is inversely proportional to the latent period of the disease). In [Liu *et al*, 2020], 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; $\beta = \frac{1}{3} = 0.33day^{-1}$.

α: Transition rate from Exposed class to the Quarantined class. We assume it is inversely proportional to the average incubation period of the disease. If we take the average incubation period to be 6.4 days [Backer et al, 2020], we get; $\alpha = \frac{1}{6.4} = 0.15625day^{-1}$.

r_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 [(WHO) Report of the WHO-China joint mission on coronavirus disease 2019 (COVID-19), 2020], we get; $v_1 = \frac{1}{14} = 0.07143day^{-1}$.

r_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 [(WHO) Report of the WHO-China joint mission on coronavirus disease 2019 (COVID-19), 2020], we get: $v_2 = \frac{1}{31.5} = 0.03175day^{-1}$

δ: Disease-related death rate δ = (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 SEIQR model):

$$\frac{dS}{dt} = \mu N - \frac{\gamma}{N} SI - \mu S$$

$$\frac{dE}{dt} = \frac{\gamma}{N} SI - (\alpha + \beta + \mu)E \quad (2.1)$$

$$\frac{dI}{dt} = \beta E - (r_1 + r_2 + \delta + \mu)I$$

$$\frac{dQ}{dt} = \alpha E - (r_1 + r_2 + \delta + \mu)Q$$

$$\frac{dR}{dt} = (r_1 + r_2 + \delta)I + (r_1 + r_2 + \delta)Q - \mu R$$

$$\gamma, \delta, \alpha, \beta, \mu, r_1, r_2 > 0,$$

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

Equilibria of the Model

From (2.1), we have;

$$\mu(N - \bar{S}) - \frac{\gamma}{N}\bar{S}\bar{I} = 0 \quad (2.2)$$

$$\frac{\gamma}{N}\bar{S}\bar{I} - (\alpha + \beta + \mu)\bar{E} = 0 \quad (2.3)$$

$$\beta\bar{E} - (r_1 + r_2 + \delta + \mu)\bar{I} = 0 \quad (2.4)$$

$$\alpha\bar{E} - (r_1 + r_2 + \delta + \mu)\bar{Q} = 0 \quad (2.5)$$

$$(r_1 + r_2 + \delta)\bar{I} + (r_1 + r_2 + \delta)\bar{Q} - \mu\bar{R} = 0 \quad (2.6)$$

From (2.4) we get;

$$\bar{E} = \frac{r_1 + r_2 + \delta + \mu}{\beta}\bar{I}$$

Putting $\bar{E}$ into (2.3), we have:

$$\left[\frac{\gamma}{N}\bar{S} - (\alpha + \beta + \mu)\frac{r_1 + r_2 + \delta + \mu}{\beta}\right]\bar{I} = 0$$

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

$$\left[\frac{\gamma}{N}\bar{S} - (\alpha + \beta + \delta)\frac{r_1 + r_2 + \delta + \mu}{\beta}\right]\bar{I} = 0 \quad (2.7)$$

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

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

The other solution is:

$$\bar{S} = \frac{N(\alpha + \beta + \mu)(r_1 + r_2 + \delta + \mu)}{\gamma\beta} \quad (2.8)$$

Substituting (2.8) into (2.2), we get;

$$\bar{I} = \frac{\beta\mu N}{(\alpha + \beta + \delta)(r_1 + r_2 + \delta + \mu)} - \frac{\mu N}{\gamma} \quad (2,9)$$

Putting (2.9) into (2.4), we get;

$$\bar{E} = \frac{\mu N}{\alpha + \beta + \mu} - \frac{\mu N(r_1 + r_2 + \delta + \mu)}{\gamma\beta} \quad (3.0)$$

Putting (3.0) into (2.5), we get;

$$\bar{Q} = \frac{\alpha\mu N}{(r_1 + r_2 + \delta + \mu)(\alpha + \beta + \mu)} - \frac{\alpha\mu N}{\gamma\beta}$$

And from (2.6) we get;

$$\bar{R} = \frac{\beta(r_1 + r_2 + \delta)}{(\alpha + \beta + \mu)(r_1 + r_2 + \delta + \mu)} + \frac{\alpha(r_1 + r_2 + \delta)N}{(\alpha + \beta + \mu)(r_1 + r_2 + \delta + \mu)} - \frac{N(r_1 + r_2 + \delta)}{\gamma} - \frac{\beta N(r_1 + r_2 + \delta)}{\beta\gamma}$$

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

$$(\bar{S}, \bar{E}, \bar{I}, \bar{Q}, \bar{R}) = \left(\frac{N(\alpha + \beta + \mu)(r_1 + r_2 + \delta + \mu)}{\gamma\beta}, \frac{\mu N}{\alpha + \beta + \mu} - \frac{\mu N(r_1 + r_2 + \delta + \mu)}{\gamma\beta}, \frac{\beta\mu N}{(\alpha + \beta + \delta)(r_1 + r_2 + \delta + \mu)} - \frac{\mu N}{\gamma}, \frac{\alpha\mu N}{(r_1 + r_2 + \delta + \mu)(\alpha + \beta + \mu)} - \frac{\alpha\mu N}{\gamma\beta}, \frac{\beta(r_1 + r_2 + \delta)}{(\alpha + \beta + \mu)(r_1 + r_2 + \delta + \mu)} + \frac{\alpha(r_1 + r_2 + \delta)N}{(\alpha + \beta + \mu)(r_1 + r_2 + \delta + \mu)} - \frac{N(r_1 + r_2 + \delta)}{\gamma} - \frac{\beta N(r_1 + r_2 + \delta)}{\beta\gamma}\right)$$

Basic Reproduction Number

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

$$R_0 = \sqrt{\frac{\gamma\beta}{(\alpha + \beta + \delta)(r_1 + r_2 + \delta + \mu)}}$$

Proof

Using the next-generation matrix(NGM) method [Diekmann *et al,* 2010], from (2.1), we get the linearized infection subsystem:

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

$$\frac{dI}{dt} = \beta E - (r_1 + r_2 + \delta + \mu)I$$

From which we get the transmission matrix;

$K = \begin{bmatrix} 0 & \gamma \\ \beta & 0 \end{bmatrix}$ and the transition matrix$L = \begin{bmatrix} -(\alpha + \beta + \mu) & 0 \\ 0 & -(r_1 + r_2 + \delta + \mu) \end{bmatrix}$

We get the next-generation matrix:

$$G = -KL^{-1} = \begin{bmatrix} 0 & \gamma \\ \beta & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\alpha + \beta + \mu} & 0 \\ 0 & \frac{1}{r_1 + r_2 + \delta + \mu} \end{bmatrix} = \begin{bmatrix} 0 & \frac{\gamma}{r_1 + r_2 + \delta + \mu} \\ \frac{\beta}{\alpha + \beta + \mu} & 0 \end{bmatrix}$$

From which we compute R_0:

$$R_0 = \rho(F) = \frac{1}{2}(trace\ F + \sqrt{(trace\ F)^2 - 4\det(F)} = \sqrt{\frac{\gamma\beta}{(\alpha + \beta + \mu)(r_1 + r_2 + \delta + \mu)}}$$

where ρ is the spectral radius.

RESULTS AND DISCUSSION

Local Stability Analysis

Theorem 2.2 The disease-free equilibrium of the SEIQR model is unstable for any value of R_0

Proof

The system (2.1) is gives rise to the Jacobian matrix;

$$J=\begin{bmatrix} \frac{-\gamma I}{N}-\mu & 0 & \frac{-\gamma S}{N} & 0 & 0 \\ \frac{\gamma}{N} & -(\alpha+\beta+\mu) & \frac{\gamma S}{N} & 0 & 0 \\ 0 & \alpha & 0 & -(r_1+r_2+\delta+\mu) & 0 \\ 0 & \beta & -(r_1+r_2+\delta+\mu) & 0 & 0 \\ 0 & 0 & r_1+r_2+\delta & r_1+r_2+\delta & -\mu \end{bmatrix}$$

At $(S,E,I,Q,R)=(N,0,0,0,0)$;

$$J-\lambda I=\begin{bmatrix} -\mu-\lambda & 0 & -\gamma & 0 & 0 \\ 0 & -c-\lambda & \gamma & 0 & 0 \\ 0 & \alpha & -\lambda & -b & 0 \\ 0 & \beta & -b & -\lambda & 0 \\ 0 & 0 & b-\mu & b-\mu & -\mu-\lambda \end{bmatrix}$$

where $c=\alpha+\beta+\delta$, and $b=r_1+r_2+\delta+\mu$

$\det(J-\lambda I)=0$ gives; $(\mu-\lambda)^2=0$ or

$$(-\lambda)^3+c\lambda^2-(\alpha\gamma+b^2)\lambda+\beta\gamma b-b^2c=0$$

Let $f(\lambda)=(-\lambda)^3+c\lambda^2-(\alpha\gamma+b^2)\lambda+\beta\gamma b-b^2c=0$ (3.1)

By Descartes rule, [Haukkanen, 2011], we have at least one positive root. Let (3.1) be in the form of:

$$K_1=M_1\lambda^3+M_2\lambda^2-M_3\lambda+M_4$$

where $M_1=1,\ M_2=c,\ M_3=\alpha\gamma+b^2,\ M_4=\beta\gamma b-b^2c$, with $M_1,M_2,M_3>0$.

If $M_4>0$, then we will have only one positive root. Hence, the disease-free equilibrium of the SEIQR model is unstable.

Theorem 2.3 *The endemic equilibrium of the SEIQR model is unstable for any value of* R_0

Proof

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

$$J=\begin{bmatrix} \frac{-\gamma\beta\mu}{bc} & 0 & \frac{-bc}{\lambda} & 0 & 0 \\ \frac{\gamma\beta\mu}{bc}-\mu & -c & \frac{bc}{\beta} & 0 & 0 \\ 0 & \alpha & 0 & -b & 0 \\ 0 & \beta & -b & 0 & 0 \\ 0 & 0 & b-\mu & b-\mu & -\mu \end{bmatrix}$$

$$\det(J-\lambda I)=\begin{vmatrix} \frac{-\gamma\beta\mu}{bc}-\lambda & 0 & \frac{-bc}{\lambda} & 0 & 0 \\ \frac{\gamma\beta\mu}{bc}-\mu & -c-\lambda & \frac{bc}{\beta} & 0 & 0 \\ 0 & \alpha & -\lambda & -b & 0 \\ 0 & \beta & b & -\lambda & 0 \\ 0 & 0 & b-\mu & b-\mu & -\mu-\lambda \end{vmatrix}$$

$\det(J-\lambda I)=0$ gives $(-\mu-\lambda)=0$ or

$$\lambda^4-\left(\frac{\mu\gamma\beta}{bc}+c\right)\lambda^3+\left(\frac{\mu\gamma\beta}{b}-b^2-\frac{\alpha bc}{\beta}\right)\lambda^2+\left(\frac{\alpha c^2+\gamma\beta^2}{\beta c}\right)\lambda+\mu b^2c-\beta b\gamma\mu=0$$

Let

$$f(\lambda)=\lambda^4-\left(\frac{\mu\gamma\beta}{bc}+c\right)\lambda^3+\left(\frac{\mu\gamma\beta}{b}-b^2-\frac{\alpha bc}{\beta}\right)\lambda^2+\left(\frac{\alpha c^2+\gamma\beta^2}{\beta c}\right)\lambda+\mu b^2c-\beta b\gamma\mu=0 \quad (3.2)$$

Based on Descartes' rule [Haukkanen, 2011], we can only have a maximum of three positive roots. Let (3.2) be in the form of:

$K_2=N_1\lambda^4-N_2\lambda^3+N_3\lambda^2+N_4\lambda+N_5$

where$N_1 = 1, \quad N_2 = \frac{\beta\gamma\mu}{bc} + c,\ N_3 = \frac{\beta\gamma\mu}{b} - b^2 - \frac{\alpha bc}{\beta},\ N_4 = \frac{\alpha c^2 + \gamma\beta^2}{\beta c},\ N_5 = \mu b^2 c - \beta b\gamma\mu,$ with $N_1, N_2, N_4 > 0$.
If $N_3, N_5 > 0,$ then we will have two positive roots.
If $N_3 > 0,\ N_5 < 0$, then we will have three positive roots.
If $N_3 < 0,\ N_5 > 0$, then we will have two positive roots.
If $N_3,\ N_5 < 0,$ then we will have three positive roots. Hence, by Descartes' rule, the endemic equilibrium of the SEIQR model is unstable.

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

$$D_1 = \left\{(S, E, I, Q, R) \in \mathbb{R}_+^5 : S < \frac{N(\alpha + \beta + \mu)}{\gamma}\right\}$$

Proof
Consider the Lyapunov function $V = E$, we have;
$\frac{dV}{dt} = \left\{\frac{\gamma}{N}S - (\alpha + \beta + \mu)\right\}E \leq 0 \ \ if \ \ S < \frac{N(\alpha + \beta + \mu)}{\gamma}$
That is; $\frac{dL}{dt} \leq 0$ in the domain $D_1 = \left\{(S, E, I, Q, R) \in \mathbb{R}_+^5 : S < \frac{N(\alpha+\beta+\mu)}{\gamma}\right\}$.
So, for the positive definite function V, the derivative $\frac{dV}{dt}$ is negative semi-definite in D_1. Now, we consider the set where $\frac{dV}{dt} = 0$.
Let $\Delta_1 = \left\{(S, E, I, Q, R) \in D_1 : \frac{dV}{dt} = 0\right\} = \{(S, E, I, Q, R) \in D_1 : E = 0\}$.
Let U be the largest invariant set in Δ_1. Then in Δ_1, we get;
$\frac{dS}{dt} = \mu(N - S)(3.3)$
$\frac{dI}{dt} = -(r_1 + r_2 + \delta + \mu)I \qquad (3.4)$
$\frac{dQ}{dt} = -(r_1 + r_2 + \delta + \mu)Q \qquad (3.5)$
$\frac{dR}{dt} = -\mu R \qquad (3.6)$
From (3.6), we have $R \to 0$ as $t \to \infty$. From (3.5), we have $Q \to 0$ as $t \to \infty$. From (3.4), we have $I \to 0$ as $t \to \infty$. From (3.3), we have $S \to N \ as \ t \to \infty$. Hence,$U$ is $\{(N,\ 0,\ 0,\ 0,\ 0)\}$. Hence by the LaSalle-Lyapunov theory [Hale, 1980], the disease-free equilibrium $(N,\ 0,\ 0,\ 0,\ 0)$ is globally asymptotically stable in D_1.
Now, from $D_1,\ S < \frac{N(\alpha+\beta+\mu)}{\gamma}$ gives; $\frac{\gamma}{\alpha+\beta+\mu} < 1,$ and we have that;
$\frac{\gamma\beta}{(\alpha+\beta+\mu)(r_1+r_2+\delta+\mu)} < \frac{\gamma}{\alpha+\beta+\mu} < 1$ implies that $R_0 < 1$.
Theorem 2.5*The endemic equilibrium point* $(S_1,\ E_1,\ I_1,\ R_1)$ *is globally asymptotically stable in the region:* $D_2 = \left\{(S,\ E,\ I,\ Q,\ R) \in \mathbb{R}_+^5 : 1 < \frac{E_1}{E} < \frac{I_1}{I} < \frac{Q_1}{Q} < \frac{R_1}{R} < \frac{S_1}{S}\right\}$.

Proof
Consider a Lyapunov function W defined as follows:

$$V = \int_{S_1}^{S} \frac{S - S_1}{S} dS + \int_{E_1}^{E} \frac{E - E_1}{E} dE + \int_{I_1}^{I} \frac{I - I_1}{I} dI + \int_{Q_1}^{Q} \frac{Q - Q_2}{Q} dQ + \int_{R_1}^{R} \frac{R - R_1}{R} dR$$

We have; $\frac{dW}{dt} = \left(\frac{S-S_1}{S}\right)\frac{dS}{dt} + \left(\frac{E-E_1}{E}\right)\frac{dE}{dt} + \left(\frac{I-I_1}{I}\right)\frac{dI}{dt} + \left(\frac{Q-Q_1}{Q}\right)\frac{dQ}{dt} + \left(\frac{R-R_1}{R}\right)\frac{dR}{dt} = (S - S_1)\left(\frac{\mu N}{S} - \frac{\mu N}{S_1} - \frac{\gamma I}{N} + \frac{\gamma I_1}{N}\right) + (E - E_1)\left(\frac{\gamma}{N}\frac{SI}{E} - \frac{\gamma}{N}\frac{S_1 I_1}{E_1}\right) + (I - I_1)\left(\frac{\beta E}{I} - \frac{\beta E_1}{I_1}\right) + (Q - Q_1)\left(\frac{\alpha E}{Q} - \frac{\alpha E_1}{Q_1}\right) + (R - R_1)\{(r_1 + r_2 + \delta)\frac{I}{R} - (r_1 + r_2 + \delta)\frac{I_1}{R_1} + (r_1 + r_2 + \delta)\frac{Q}{R} - (r_1 + r_2 + \delta)\frac{Q_1}{R_1}\} =$

$$(S-S_1)\left(\mu N\frac{(S_1-S)}{SS_1}+\frac{\gamma}{N}(I_1-I)\right)+(E-E_1)\left(\frac{\gamma}{N}\frac{SIE_1-S_1I_1E}{EE_1}\right)+\beta(I-I_1)\frac{(EI_1-IE_1)}{II_1}$$
$$+\alpha(Q-Q_1)\left(\frac{EQ_1-QE_1}{QQ_1}\right)$$
$$+(r_1+r_2+\delta)(R-R_1)\left(\frac{(IR_1-I_1R)}{RR_1}+\frac{QR_1-RQ_1}{RR_1}\right)$$
$$<(S-S_1)\left(\mu N\frac{S_1-S}{SS_1}+\frac{\gamma}{N}(I_1-I)\right)+(E-E_1)\frac{\gamma}{N}\left(\frac{(SIE_1-S_1I_1E)}{EE_1}\right)$$
$$+\beta(I-I_1)\frac{(EI_1-IE_1)}{II_1}+\alpha(Q-Q_1)\frac{EQ_1-QE_1}{QQ_1}$$
$$+(r_1+r_2+\delta)(R-R_1)\left(\frac{IR_1-RI_1}{RR_1}+\frac{QR_1-RQ_1}{RR_1}\right)$$

Since $1<\frac{E_1}{E}<\frac{I_1}{I}<\frac{Q_1}{Q}<\frac{R_1}{R}<\frac{S_1}{S}$, we have; $1<\frac{S_1}{S}$ and $1<\frac{I_1}{I}$, which gives; $SI<S_1I_1$.

Hence, we get;

$$\frac{dW}{dt}<-\frac{\mu N}{SS_1}(S_1-S)^2-\frac{\square}{\square}(\square_1-\square)(\square_1-\square)-\frac{\square}{\square}\square_1\square_1(\square_1-\square)^2$$
$$-\square\frac{(\square_1-\square)(\square\square_1-\square\square_1)}{\square\square_1}-\square(\square_1-\square)\frac{\square\square_1-\square\square_1}{\square\square_1}$$
$$-(\square_1+\square_2+\square)(\square_1-\square)\left(\frac{\square\square_1-\square\square_2}{\square\square_1}+\frac{\square\square_1-\square\square_1}{\square\square_2}\right)<0$$

This implies, $\frac{\square\square}{\square\square}<0$ in the region $\square_2$

Numerical Simulation

Scilab plot of the SEIQR model for $\square_{\square}<1$.

Define a solution to the system (2.1) for the parameter values; $\square=0.000038$, $\square=0.37$, $\square=0.33$, $\square=0.15625$, $\square_1=0.07143$, $\square_2=0.03175$, $\square=2.08$, subject to the initial conditions: $\square(0)=0.7$, $\square(0)=0.15$, $\square(0)=0.1$, $\square(0)=0.03$ $\square(0)=0.02$, where $\square=\frac{\square}{\square}$, $\square=\frac{\square}{\square}$, $\square=\frac{\square}{\square}$, $\square=\frac{\square}{\square}$, $\square=\frac{\square}{\square}$.The population N is taken to be 1000.

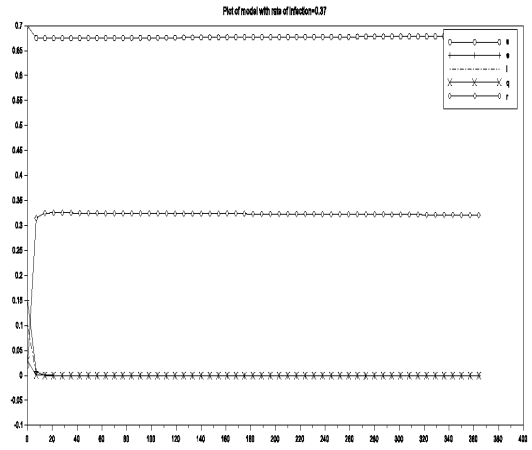

Figure 1. Numerical Plot of Model for $R_0<1$

Scilab Code

function y dot=SEIQR model (t, y)

ydot=[da*y(1)*y(3)d*y(1);a*y(1)*y(3)(b+n+d)*y(2);n*y(2)(v1+v2+d1+d)*y(3);b*y(2)(v1+v

2+d1+d)*y(4);(v1+v2+d1)*y(3)+(v1+v2+d1)*y(4)-d*y(5)]

end function

```
d=0.000038;
a=0.37;
n=0.33;
v1=0.07143;
v2=0.03175;
d1=2.08;
b=0.15625
y0=[0.7;0.15;0.1;0.03;0.02];
t0=0;
t=0:7:365;
sol=ode([0.7;0.15;0.1;0.03;0.02],t0,t,SEIQRmodel);
plot(t,sol(1,:),'k-o-',t,sol(2,:),'k-+-',t,sol(3,:),'k-.',t,sol(4,:),'k-x-',t,sol(5,:),'k-d-')
title(" Plot of model with rate of infection=0.37", "fontsize",2)
hl=legend(['s';'e';'i';'q';'r']);
```

Scilabplot of the SEIQR model for $\boldsymbol{R_0 > 1}$

Define a solution to the system (2.1) for the parameter values; $\Lambda = 0.000038,\ \beta = 10,\ \mu = 0.33,\ \alpha = 0.15625,\ \gamma_1 = 0.07143,\ \gamma_2 = 0.03175,\ \delta = 2.08,$ subject to the initial conditions: $S(0) = 0.7,\ E(0) = 0.15,\ I(0) = 0.1,\ Q(0) = 0.03,\ R(0) = 0.02,$ where $\Lambda = \frac{\Lambda}{N},\ \beta = \frac{\beta}{N},\ \mu = \frac{\mu}{N},\ \alpha = \frac{\alpha}{N},\ \gamma = \frac{\gamma}{N},\ \delta = \frac{\delta}{N}.$ and the population N is taken to be 1000.

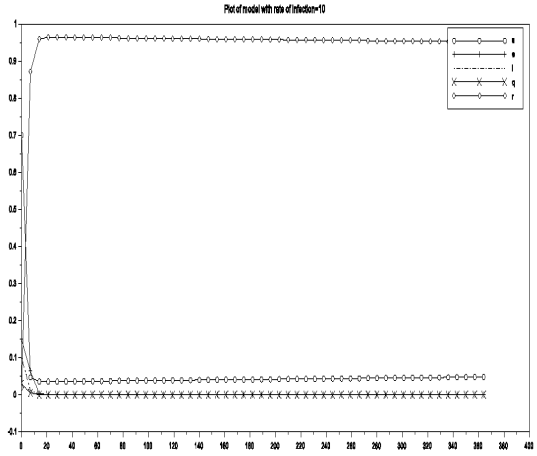

Figure 2. Numerical Plot of Model for $\mathcal{R}_0 > 1$

***Scilab Code*:**

```
function y dot=SEIQR model(t, y)
ydot=[da*y(1)*y(3)d*y(1);a*y(1)*y(3)(b+n+d)*y(2);n*y(2)(v1+v2+d1+d)*y(3);b*y(2)(v1+v
2+d1+d)*y(4);(v1+v2+d1)*y(3)+(v1+v2+d1)*y(4)-d*y(5)]
end function
d=0.000038;
a=10;
n=0.33;
v1=0.07143;
v2=0.03175;
d1=2.08;
b=0.15625
y0=[0.7;0.15;0.1;0.03;0.02];
t0=0;
t=0:7:365;
sol=ode([0.7;0.15;0.1;0.03;0.02],t0,t,SEIQRmodel);
plot(t,sol(1,:),'k-o-',t,sol(2,:),'k-+-',t,sol(3,:),'k-.',t,sol(4,:),'k-x-',t,sol(5,:),'k-d-')
```

```
title("Plot of model with rate of infection=10", "fontsize",2)
hl=legend(['s';'e';'i';'q';'r']);
```

Discussion of Results

We have formulated an SEIQR model for the transmission dynamics of COVID-19. We studied the stability of the equilibrium points of the system (2.1). The local instability 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 endemic equilibrium (that is, the disease will continue to spread in the population). For the endemic equilibrium, the local instability 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 disease-free 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, a very small number of individuals from the susceptible class gets infected. Individuals from the infected and quarantined classes are removed by death or recovery and the disease quickly dies out of the population. On the other hand, if the basic reproduction number is greater than one, a very large number of individuals from the susceptible class gets infected. Individuals from the infected and quarantined classes are removed by death or recovery very quickly and the disease dies out from the population.

CONCLUSION

Based on the results of the study, it was concluded that the SEIQR model could be used as a reference model for the spread of COVID-19 in a population. Analysis 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, and provides information on the endemic state of the disease. The simulation results provide a predictive picture of the short-term and long-term behavior of the disease outbreak, and also show that the isolation period can slow down the spread of the disease outbreak.

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