



## An SEIQR Mathematical Model for The Spread of COVID-19

Samuel B. Apima<sup>1\*</sup> and Jacinta M. Mutwiwa<sup>2</sup>

<sup>1</sup> Department of Mathematics and Statistics, Kaimosi Friends University College, Kenya.

<sup>2</sup> Department of Mathematics, Kibabii University, Kenya.

### Authors contributions

This work was carried out in collaboration between both authors. SBA designed the study, performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. JMM managed the analyses of the study. Both authors read and approved the final manuscript.

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## Abstract

COVID-19, a novel coronavirus, is a respiratory infection which is spread between humans through small droplets expelled when a person with COVID-19 sneezes, coughs, or speaks. An SEIQR model to investigate the spread of COVID-19 was formulated and analysed. The disease free equilibrium point for formulated model was shown to be globally asymptotically stable. The endemic states were shown to exist provided that the basic reproduction number is greater than unity. By use of Routh-Hurwitz criterion and suitable Lyapunov functions, the endemic states are shown to be locally and globally asymptotically stable respectively. This means that any perturbation of the model by the introduction of infectives the model solutions will converge to the endemic states whenever reproduction number is greater than one, thus the disease transmission levels can be kept quite low or manageable with minimal deaths at the peak times of the re-occurrence.

\*Corresponding author: E-mail: [sapima@kafuco.ac.ke](mailto:sapima@kafuco.ac.ke);

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## 1 Introduction

Coronaviruses consist of a family of viruses that affect humans as well as some mammals like bats and pigs [1, 2]. COVID-19, a novel coronavirus, is a respiratory infection which is spread between humans through small droplets expelled when a person with COVID-19 sneezes, coughs, or speaks [3]. The virus was first reported in Wuhan city, Hebei Province, China in December, 2019. It has since spread to many countries and has been declared as a global pandemic by the World Health Organization (WHO). According to WHO, the symptoms for COVID-19 virus include fever, dry cough, fatigue, sore throat, aches, diarrhea, nasal congestion and loss of taste or smell among others [3, 4].

The total confirmed cases globally and the confirmed deaths as at 5<sup>th</sup> July, 2020 is over 11.4 million people and over 534,000 deaths respectively, more of this information can be obtained in [3, 5]. The virus has also affected many economies: some countries have gone into total or partial lockdown, many people have lost their jobs, some people have been forced to work from home and learning institutions as well as some businesses being closed during this pandemic. Other countries have also imposed curfews to curb the spread of the virus.

In Kenya, the first case was reported on 12<sup>th</sup> March, 2020, this led to learning institutions, worship places and businesses like eateries and bars, being closed so as to contain this virus. Since then, a further 7885 cases have been confirmed with 160 (2.03%) deaths and 2287 (29%) recoveries [6].

Adam *et. al.* [7] and Mwalili *et. al.* [8] mathematically modeled the transmission of COVID-19 using an SEIR (Susceptible-Exposed-Infected-Recovered) model. Without considering the people who are quarantined cannot infect others at the same rate as those who have not been quarantined. Jumpen *et. al.* [9] modeled the transmission of pandemic influenza using an SEIQR (Susceptible-Exposed-Infected-Quarantined-Recovered) model but assumed that once a person is cured from the virus, then that person gains permanent immunity. COVID-19 remains a major challenge to many countries, many countries have chosen to quarantine or advice those who have been exposed to the virus to self isolate, thus in this paper, we introduce the quarantined class and that class will not infect other classes. Those exposed and infected can infect the susceptible class. A fraction of those who have recovered from the virus can become susceptible again. In this article, an SEIQR (Susceptible-Exposed-Infected-Quarantined-Recovered) model is developed and analyzed.

## 2 The Model

We formulate a model in which the total human population at any time  $t$  denoted by  $N$  is subdivided into classes,  $S(t)$  the class of individuals susceptible to COVID-19 infection. Recruitment into susceptible class is done at a rate  $\Lambda$ . The parameter  $E(t)$  denotes the number of individuals who are exposed to the virus or infected with the virus but without the typical symptoms of the infection, this progression from  $S(t)$  to  $E(t)$  is done at a rate  $\lambda$ . Individuals develop symptoms of COVID-19 and progress from the class  $E(t)$  to the class  $I(t)$  at the rate  $\delta$ . In the  $I(t)$  class, Some individuals are put on quarantine at a rate  $\rho$  and progress to  $Q(t)$  class, while others die due to the infection at  $\kappa$ . Some people recover from the virus without being quarantined at a rate  $\omega$  and progress from class  $I(t)$  to the class  $R(t)$ . Mortality occurs among COVID-19 patients who are quarantined at the rate  $\sigma$ , while those who recover progress to  $R(t)$  at a rate  $\tau$ . Individuals in the  $R(t)$  class become susceptible again at an average rate  $\nu$ . Natural death is assumed to occur in all classes at the rate  $\mu$ . It is assumed that those people who are quarantined cannot help in transmitting the virus as they are in isolation.

The parameter  $\lambda$  represents contact between susceptible people with those who have the virus, i.e. those exposed and those infected but are not in quarantine facilities. It is given by  $\lambda = \alpha I + \beta E$ .

At a given time the total population is given by:

$N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$  From the above definitions, the resulting diagram for the model is given below.

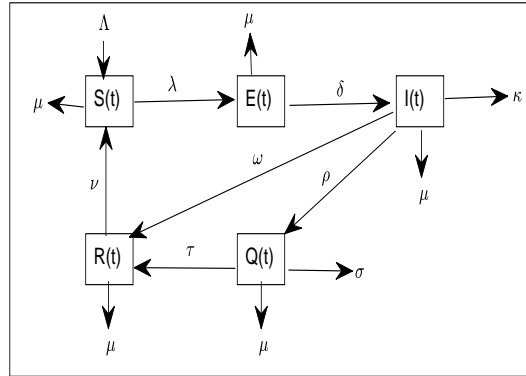


Fig. 1. Flow chat of the model

The dynamics described can be represented mathematically as;

$$\begin{aligned}
 \dot{S}(t) &= \Lambda + \nu R - \mu S - \alpha IS - \beta ES, \\
 \dot{E}(t) &= \alpha IS + \beta ES - (\delta + \mu)E \\
 \dot{I}(t) &= \delta E - (\mu + \kappa + \omega + \rho)I \\
 \dot{Q}(t) &= \rho I - (\tau + \mu + \sigma)Q \\
 \dot{R}(t) &= \tau Q + \omega I - (\nu + \mu)R
 \end{aligned} \tag{1}$$

### 3 Model Analysis

Based on the fact that the model deals with human population, all the state variables and parameters are assumed to be non-negative  $\forall t \geq 0$ . This model is studied in the feasible region  $\mathbb{R}$  where  $\{S(t), E(t), I(t), Q(t), R(t)\} \in \Omega \in \mathbb{R}_+^5$  and it can be shown that as  $t$  tends to infinity;

$$0 \leq N(t) \leq \frac{\Lambda}{\mu} \tag{2}$$

Which shows that the set of solutions is bounded. Thus, the model Equation (1) is epidemiologically well posed in the region  $\Omega$ . The basic reproduction number  $R_0$ , computed using the next generation matrix method approach for Equation (1) is given by

$$R_0 = \frac{\delta \alpha S + \beta S(\mu + \kappa + \omega + \rho)}{(\mu + \delta)(\mu + \kappa + \omega + \rho)} \tag{3}$$

## 4 Disease-free Equilibrium Point

The disease-free equilibrium point is a steady-state solution for which there is no disease or infection in the population [10]. To obtain the disease-free equilibrium point we set the normalised model system (1) equal to zero as shown below,  $E^0 = \{S(t), E(t), I(t), Q(t), R(t)\} = (\frac{\Lambda}{\mu}, 0, 0, 0, 0)$

## 5 Local Stability of the Disease-free Equilibrium

The Jacobian matrix of Equation (1) is given by

$$J_1 = \begin{pmatrix} -\mu & -\beta S & -\alpha S & 0 & \nu \\ 0 & \beta S - (\delta + \mu) & \alpha S & 0 & 0 \\ 0 & \delta & -(\mu + \kappa + \omega + \rho) & 0 & 0 \\ 0 & 0 & \rho & -(\tau + \mu + \sigma) & 0 \\ 0 & 0 & \omega & \tau & -(\nu + \mu) \end{pmatrix} \quad (4)$$

The trace of the matrix (4) is negative for  $(\delta + \mu) + \mu + (\mu + \kappa + \omega + \rho) + (\tau + \mu + \sigma) + (\nu + \mu) > \beta S$  and the determinant is given by

$$\det J_1 = -\mu(-\mu - \nu)(-\mu - \sigma - \tau)(-\alpha\delta S + (\beta S - \delta - \mu)(-\kappa - \mu - \rho - \omega))$$

Thus the  $\det J_1 > 0$ , provided  $(\beta S - \delta - \mu)(-\kappa - \mu - \rho - \omega) \leq 0$

Therefore, the disease-free equilibrium is locally asymptotically stable.

## 6 Global Stability of the Disease-free Equilibrium

For global stability of the DFE, the technique by Castillo [11] is used. There are two conditions that if met, guarantee the global asymptotic stability of the disease free state. Equation (1) may be written in the form

$$\begin{aligned} \frac{dX}{dt} &= H(X, Z), \\ \frac{dZ}{dt} &= G(X, Z), G(X, 0) = 0 \end{aligned} \quad (5)$$

Where  $X \in \mathbb{R}^2$  and  $X = \{S(t), R(t)\}$  denotes the number of uninfected individuals and  $Z \in \mathbb{R}^3$  where  $Z = \{E(t), I(t), Q(t)\}$  denotes the number of infected individuals.  $E^0 = (\frac{\Lambda}{\mu}, 0, 0, 0, 0)$  denotes the disease free equilibrium point of this system where

$$X^* = \frac{\Lambda}{\mu}$$

Conditions in (6) must be met to guarantee a local asymptotic stability:

$$\frac{dX}{dt} = H(X, 0), X^* \text{ is globally asymptotically stable (GAS)}$$

$$G(X, Z) = PZ - \hat{G}(X, Z), \hat{G}(X, Z) \geq 0 \text{ for } (X, Z) \in \Omega \quad (6)$$

Where,  $P = D_z G(X^*, 0)$  is an M-matrix (the off-diagonal elements of  $P$  are non-negative) and  $\Omega$  is the region where the model makes biological sense.

**Theorem 1.** *If system (5) satisfies conditions (6), then the fixed point  $E^0 = (X^*, 0, 0, 0, 0)$  is a globally asymptotically stable equilibrium of system (5) provided that  $R_0 < 1$  and the assumptions in (6) are satisfied*

*Proof.* Consider

$$H(X, O) = \Lambda + \nu R - \mu S, -(\nu + \mu)R \text{ and } G(X, Z) = PZ - \hat{G}(X, Z)$$

Where  $P = (-(\delta + \mu)00\delta - (\mu + \kappa + \omega + \rho)00\rho - (\tau + \mu + \sigma)$

And

$$G(X, Z) = \left( \hat{G}_1(X, Z)\hat{G}_2(X, Z)\hat{G}_3(X, Z) = (-(\alpha I + \beta E + \gamma D)00 \right)$$

Considering the Jacobian matrix, and replacing  $S(t) = \frac{\Lambda}{\mu}, E(t) = 0, I(t) = 0, Q(t) = 0$  and  $R(t) = 0$  we obtain  $\hat{G}_1(X, Z) = 0$  and so the conditions in (6) are met so  $E^0$  is globally asymptotically stable when  $R_0 < 1$ . Global asymptotic stability shows that regardless of any starting solution, the solutions of the model will converge to DFE whenever  $R_0 < 1$ . This implies that we do not expect the disease outbreak for life. Thus, the epidemic will die out or will not develop in the population.  $\square$

## 7 Local Stability of the Endemic Equilibrium

The total population  $N$  from Equation (3) is  $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$ . Thus we study the equations at the endemic state  $E^* \{S^*(t), E^*(t), I^*(t), Q^*(t), R^*(t)\}$ . The Jacobian of Equation (1) at endemic state  $E^*$  is given by

$$J_2 = \begin{pmatrix} -(\mu + \alpha I^* + \beta E^*) & \beta S^* & \alpha S^* & 0 & \nu \\ \alpha I^* + \beta E^* & -(\delta + \mu) & 0 & 0 & 0 \\ 0 & \delta & -(\mu + \kappa + \omega + \rho) & 0 & 0 \\ 0 & 0 & \rho & -(\tau + \mu + \sigma) & 0 \\ 0 & 0 & \omega & \tau & -(\nu + \mu) \end{pmatrix} \quad (7)$$

An important criterion by Routh-Hurwitz gives the necessary and sufficient conditions for all the roots of the characteristic polynomial (with real coefficients) to lie in the left half of the complex plane. In other words, all the roots of the polynomial are negative or have negative real roots if the determinants of all Hurwitz matrices are positive [12].

The trace of matrix (7) is negative and the determinant is given by

$$\det J_2 = (-\nu - \mu)(-\tau - \mu - \sigma)(-\alpha\alpha S^* I^* - \alpha\beta S^* E^*)\delta + (-\alpha\beta S^* I^* - \beta\beta S^* E + \alpha\mu I^* + \mu\mu + \alpha\delta I^* + \beta\delta E^* + \mu\delta)(-\mu - \kappa - \omega - \rho) + (\alpha I^* + \beta E^*)\nu(\rho\delta\tau + \mu\delta\omega + \delta\sigma\omega + \delta\tau\omega)$$

Thus the  $\det J_2 > 0$ , provided  $(-\nu - \mu)(-\tau - \mu - \sigma)(-\alpha\alpha S^* I^* - \alpha\beta S^* E^*)\delta + (-\alpha\beta S^* I^* - \beta\beta S^* E + \alpha\mu I^* + \mu\mu + \alpha\delta I^* + \beta\delta E^* + \mu\delta)(-\mu - \kappa - \omega - \rho) \geq 0$

Since the trace is negative and the determinant is positive, then the eigenvalues of Equation (7) will have negative real parts. Therefore, the endemic equilibrium is locally asymptotically stable.

## 8 Global Stability of the Endemic Equilibrium

The global stability of the equilibria is obtained by means of the Lyapunov's direct method and LaSalle's invariance principle [13]. Consider the non-linear Lyapunov function  $V : (S, E, I, Q, R) \in$

$\Omega \subset \mathbb{R}_+^5 : S, E, I, Q, R > 0$  defined as

$$V = S - S^* \ln S + E - E^* \ln E + I - I^* \ln I + Q - Q^* \ln Q + R - R^* \ln R \quad (8)$$

Where  $V$  is in the interior of the region  $\Omega$ .  $E^*$  is the global minimum of  $V$  on  $\Omega$  and  $V : (S, E, I, Q, R) = 0$ . The time derivative of Equation (8) is given by

$$\frac{dV}{dt} = \dot{V} = \dot{S}(1 - \frac{S^*}{S}) + \dot{E}(1 - \frac{E^*}{E}) + \dot{I}(1 - \frac{I^*}{I}) + \dot{Q}(1 - \frac{Q^*}{Q}) + \dot{R}(1 - \frac{R^*}{R})$$

$$\dot{V} = (\Lambda + \nu R - (\mu + \alpha I + \beta E)S)(1 - \frac{S^*}{S}) + (\alpha IS + \beta ES - (\delta + \mu)E)(1 - \frac{E^*}{E}) + (\delta E - (\mu + \kappa + \omega + \rho)I)(1 - \frac{I^*}{I}) + (\rho I - (\tau + \mu + \sigma)Q)(Q - \frac{Q^*}{Q}) + (\omega I + \tau Q - (\nu + \mu)R)(1 - \frac{R^*}{R})$$

$$\dot{V} = (\Lambda - \Lambda \frac{S^*}{S} + \nu R - \nu R \frac{S^*}{S} - (\mu + \alpha I + \beta E)S + (\mu + \alpha I + \beta E)S^*) + (\alpha IS - \alpha IS \frac{E^*}{E} + \beta ES - \beta ES \frac{E^*}{E} - (\delta + \mu)E + (\delta + \mu)E^*) + (\delta E - \delta E \frac{I^*}{I} - (\mu + \kappa + \omega + \rho)I + (\mu + \kappa + \omega + \rho)I^*) + \rho I - \rho I \frac{Q^*}{Q} - (\tau + \mu + \sigma)Q + (\tau + \mu + \sigma)Q^* + \omega I - \omega I \frac{R^*}{R} + \tau Q - \tau Q \frac{R^*}{R} - (\nu + \mu)R + (\nu + \mu)R^*$$

At endemic states:  $\dot{V} = (\Lambda + \nu R^*)(1 - \frac{S^*}{S}) + (\alpha S^* I^* + \beta E^* S^*)(1 - \frac{E^*}{E}) + \delta E^*(1 - \frac{I^*}{I}) + \rho I^*(1 - \frac{Q^*}{Q}) + (\omega I^* + \tau Q^*)(1 - \frac{R^*}{R}) \leq 0$

Hence  $V < 0$ . We see that  $V = 0$  iff  $S = S^*, E = E^*, I = I^*, Q = Q^*$  and  $R = R^*$ . Thus the largest compact invariant set in  $\{S, E, I, Q, R\} \in \Omega : V = 0$  is the Singleton  $E^*$ , where  $E^*$  is the endemic equilibrium. Thus  $E^*$  is globally asymptotically stable in the interior of the region  $\Omega$ . Epidemiologically, any perturbation of the model by the introduction of infectives shows that the model solutions will converge to the  $E^*$  whenever  $R_0 > 1$ . This implies that the disease transmission levels can be kept quite low or manageable with minimal deaths at the peak times of the re-occurrence.

## 9 Conclusion

A model to investigate the spread of COVID-19 was formulated and shown to be positively invariant as well as bounded. The disease free equilibrium point for Equation (1) is shown to be globally asymptotically stable. This implies that we do not expect the disease outbreak for life. Thus, the disease will die out of the population. The endemic states are shown to exist provided that the reproduction number is greater than unity. By use of Routh-Hurwitz criterion and suitable Lyapunov functions, the endemic states are shown to be locally and globally asymptotically stable respectively. This means that any perturbation of the model by the introduction of infectives the model solutions will converge to the  $E^*$  whenever  $R_0 > 1$  thus the disease transmission levels can be kept quite low or manageable with minimal deaths at the peak times of the re-occurrence. For future works, one can incorporate some measures taken to stop the virus like use of face masks, social distancing and the role of governments and media in enlightening the general public concerning the virus.

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## Competing Interests

Authors have declared that no competing interests exist.

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