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Modeling in Mathematics in Estimation and Prediction of the Coronavirus Infections in Kitui County. A Case with Isolation of the Vulnerable

Grace Mumbanu Maithya[1,*], Winnie Kaluki[1], Virginia Kitetu[1]

[1]Department of Mathematics and Actuarial Science, Catholic University of Eastern Africa, Nairobi, Kenya.

[*]Correspondent author: Grace Mumbanu Maithya

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Abstract: **People's lives have been affected socially by the coronavirus around the globe. Because of its social and economic impact, some measures for the prevention of the disease have been placed so that the spread can reduce. Quarantine, social distancing, and social distancing are some of the control measures. One that is considered to be very effective is for the vulnerable population to be isolated. A Model including six compartments was developed so that the number of people recovering may increase, so to achieve this vulnerable population was isolated. These six compartments are namely below; Susceptible, Exposed, Infected, Quarantined, Isolation of Vulnerable, and Recovered. Formulation of endemic equilibrium points, disease-free equilibrium, and local stability of disease-free equilibrium were theoretically proved. By use of the next generation matrix, derivation of basic reproductive number which is abbreviated as R_o was done. There is THE stability of disease-free equilibrium which is also abbreviated as a disease-free equilibrium when the basic reproductive number is less than one, which is $R_0 < 1$. There is the stability of endemic equilibrium, the endemic equilibrium point when the basic reproductive number is greater than one, which is $R_0 > 1$. There is instability in disease-free equilibrium when $R_0 > 1$. Susceptible, Exposed, Infected, Isolated Vulnerable and Recovered population model was solved numerically by Runge Kutta 4th order; the drawn graphs also showed that when the vulnerable population is isolated there is an increment in the number of people who recover and a reduction in deaths. More isolation Centers so as to isolate vulnerable populations to recover more is recommended whereby the world health organization and ministry of health in Kenya need to put it in place.**

Keywords: **Isolation Infected, Coronavirus, Vulnerable, Pandemic, Quarantine, Susceptible, Exposed; and Recovery.**

1. INTRODUCTION

Coronavirus disease triggers infection in tract respiratory system which leads to symptoms in the human body like high temperatures, difficulties in breathing, coughing, and sneezing by Ranjith Kumar [1]. It started in a province called Wuhan in Chinese Country. Immediately, the World Health Organization declared it a pandemic globally and by then there were no vaccines, so isolation was the control measure that was put in place to stop the spreading of the disease. Different countries reported cases of infection and the Indian government reported all visas belonging to its travelers. Curfew was put across which was taking 14 hours [2]. The disease was endemic in Indian urban Centers, its seventy-five locations had infections so the lockdown days were more than twenty-one and the lockdown rules and regulations were strictly followed

up [3]. In India, there were five lockdown periods and when the infections were low, these lockdowns were loosened up [5]. A model in this paper is very useful and important for analyzing the infections so that predictions of the future can be done. To explain coronavirus elements of transmission, a model with differential equations is the best. To control infections Okhu –ese [6] did a Susceptible, Infectious and Recovered model. A model in logistic growth regression to estimate the coronavirus spread was done by Batista [7]. Anwar et al came up with a coronavirus model which contained class isolation. They realized that coronavirus is transmitted from one person to another through droplets from sneezing or coughing when people are in close contact. Soyoung et al. did a model of coronavirus on SIER model with quarantined people in the hospital. Qiuhui et al did a model on the effects of hospital isolations for patients with few signs and symptoms of coronavirus like coughing and sneezing. A model for creating awareness of coronavirus disease was developed in India by Nagaraj [8]. A model was developed in India by Ghosh [9] to show how the country had inadequately dealt with infections that were increasing in number. This was done in India when the lockdown was there and the economy was highly affected because the country was inadequately prepared for the outbreak. A model was done by Wu [11] that did a clarification in the dynamics in transmission of coronavirus globally and nationally. A model by Chen [12] on stage based transmission of the virus was done. A model on clinical development and the requisite extent of intervention of patients' status was done by Tang [13]. A current treatment protocol for coronavirus in the Indian model was done by Surbhi Sharma [14]. A model on vaccination, dietary habits, and climate conditions that spread coronavirus in developed countries and in India were developed by Kundu [15]. To predict disease outbreaks, an estimation of values of reproductive number by authors is calculated by Poisson Assumption [16] which states that human to human contact is the major spread of the coronavirus. When the vulnerable population is isolated, the future spread of the coronavirus is stopped, which is discussed in this paper. The rest of our work is organized as shown below whereby, in the second section; the model is formulated, in the third section; analysis and numerical results are done, and in the fourth section; the study is concluded, recommended and applications are done. The current study focuses on developing a mathematical model that incorporates the isolation of vulnerable compartment, studying the dynamics of the developed model, developing a numerical solution, and determining the contribution of δ isolation of the vulnerable in order to recover.

2. MODEL DESCRIPTION AND FORMULATION

In our work, the total population is considered and it's represented by N, given by the equation below;

$$N(t) = S(t) + E(t) + I(t) + Q(t) + I_V(t) + R(t) \quad (1)$$

The total number of people is subdivided into six compartments which include the people who are susceptible S (t), which shows the individuals with the capability of becoming infected. The population which is exposed E (t), are the people who are incubating infection and have been in contact with the infected people. The people who are infected I (t), represent the people who have been diagnosed with the disease and have tested positive. The quarantine population Q (t), restricts and separates the exposed to a movement of people with a contagious disease and are exposed to see if they become infected. They represent both vulnerable and non-vulnerable who are sick. The isolated vulnerable $I_V(t)$, refers to the separation of coronavirus populations which is infected from the susceptible population in the progression of clinical signs and symptoms. It separates people who have not been infected with coronavirus from people who have been infected with the coronavirus. Most vulnerable people in isolation wards, receive treatment in those isolation centers. The recovered people R (t), are those that are healed and test negative for coronavirus. This model has an assumption of the population which is completely susceptible with uniform mixing, a represents the rate of natural birth, while μ represents the natural rates of death. There is an incubation period of the disease and after that, the individuals who are exposed become infected at the rate β. The individuals who are exposed are removed then they are added to the infectious at the rate α and also added to the quarantine at rate K. The infectious individuals are separated and taken to the quarantine at a rate q, others recover at a rate γ. Those who recover from infectious individuals are only some of the non-vulnerable individuals. The quarantined individuals including both vulnerable and non-vulnerable are removed and added to the isolation of the most vulnerable at a rate θ. The isolation of the most vulnerable $I_V(t)$ is for the population who are most vulnerable who undergo treatment here. The individuals who have recovered from I, Q, and I_V go to R at rates of $\gamma, \psi,$ and δ respectively. An assumption is put in place that shows that once a person recovers, they gain strong immunity meaning that they do not become susceptible nor exposed.

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Mathematical Model Equations

$$\frac{dS}{dt} = a - (\mu + \beta E)S \quad (2)$$

$$\frac{dE}{dt} = \beta SE - (\mu + \alpha + k)E \quad (3)$$

$$\frac{dI}{dt} = \alpha E - (\mu + \gamma + q)I \quad (4)$$

$$\frac{dQ}{dt} = KE + qI - (\mu + \psi + \theta)Q \quad (5)$$

$$\frac{dI_V}{dt} = \theta Q - (\mu + \delta)I_V \quad (6)$$

$$\frac{dR}{dt} = \gamma I + \psi Q + \delta I_V - \mu Q \quad (7)$$

Mathematical Model

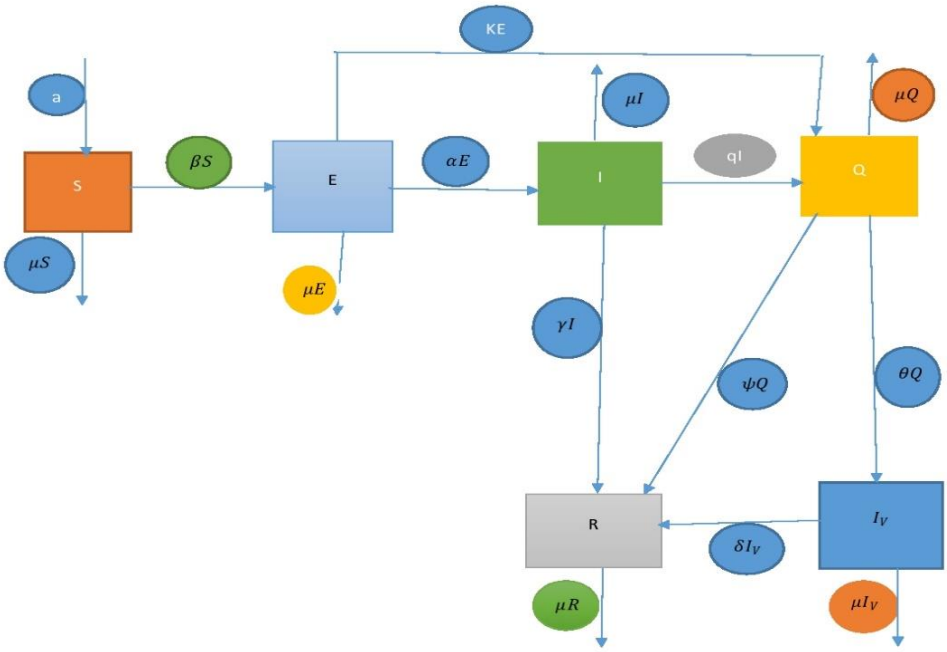

Figure 1

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Nomenclature and abbreviations

θ: Rate at which quarantined population move to the isolated of the most vulnerable.

α: Rate at which exposed move to infectious.

β: Rate at which susceptible move to exposed.

δ: Rate at which isolated of the most vulnerable recover.

K: Rate at which exposed move to quarantine.

E: Exposed.

I: Infectious population.

γ: Rate at which infected recover.

a: Natural birth rate.

Q: Quarantine population.

I_V: Isolated population for the most vulnerable.

ψ: Rate at which the quarantined recover.

R: Recovered population.

μ: Natural death rate.

q: Rate at which infectious move to quarantine.

P: Rate at which recovered become exposed.

PHEIC: Public Health Emergency of International Concern.

ODEs: Ordinary Differential EquationsODEs

SARS − COV − 2: Severe Acute Respiratory Syndrome Corona Virus.

WHO: World Health Organization.

MHA: Ministry of Home Affairs.

MATLAB: Matrix Laboratory.

DFE: Disease Free Equilibrium.

EE: Endemic Equilibrium.

Basic reproductive number R_0

According to Kalyan R_0 measures the spread of infections in the population. They defined this basic reproductive number by the next-generation matrix [27]. The basic reproductive number is abbreviated asR_0. Its purpose is to determine whether the infection will remain constant, die out or spread. The disease will spread and each person infects more than one person on average if the basic reproductive number is greater than one. If the infection is less than one person, then the disease will die out and the basic reproductive number is less than one. If a person infects one other person exactly, it becomes endemic, whereby it moves throughout the total number of people without decreasing nor increasing and the basic reproductive number is equal to one.

Disease free equilibrium

DFE point, is determined when the people who are infected are zero equated to zero the right-hand side of the equation as follows

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dI_V}{dt} = \frac{dR}{dt} = 0 \qquad (8)$$

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When the disease is not there, then $E = 0, I = 0, Q = 0, I_V = 0, R = 0$

In consideration of equation (2) to each equation of the model,

$S = \frac{a}{(\mu+\beta E)}$ But $E = 0\ S = \frac{a}{\mu}$

Again, when the second model equation is considered,

$\beta SE - (\mu + \alpha + k)E = 0$ Then $E = 0$

In addition to the third model equation

$\alpha E - (\mu + \gamma + q)I = 0$ Therefore $I = 0$

By considering the same procedure, equation (5)

$KE + qI - (\psi + \theta + \mu)Q = 0$ Then $Q = 0$

$\theta Q - (\delta + \mu)I_V = 0$ Then $I_V = 0$

$\gamma I + \psi Q + \delta I_V - \mu R$ Hence $R = 0$

Therefore, $E_0 = \left(S^0, E^0, I^0, Q^0, {I_V}^0, R^0\right) = \left(\frac{a}{\mu}, 0,0,0,0,0\right)$ (9)

The equation (9) stands for the state in which there is the absence of infection which is referred to as DFE.

Basic reproduction number

It's used to determine if the infection will remain constant, spread, or die out. When a person infects more than one other person then, the $R_0 > 1$ and the disease will continue in society. Again, if an individual infects less than one individual, then $R_0 < 1$, meaning there is a decrease in disease spread and it dies out. In addition to that, when an individual infects on average exactly one other person then$R_0 = 1$, so the disease will become endemic, therefore the disease will move throughout in the total number of people.

It is defined as the number of secondary infections that a person would create over the period of infection provided that everyone else is capable of contracting the disease [18]. The R_0 also depends on the following parameters namely, the contact rate, the possibility that contact between the susceptible people and an infected person leads to an infection, and the duration of the infectious period [20].

The next generation matrix is used in the derivation of R_0.

The compartments with infected individuals of the most vulnerable (E and Q compartments) are considered to calculate the next generation matrix.

By obtaining the Jacobian matrix of F and V with respect to E and Q at disease free equilibrium.

The Jacobian matrix of F and V at disease free equilibrium is given by

$\frac{dE}{dt} = \beta SE - (\mu + \alpha + k)E$ (10)

$\frac{dQ}{dt} = KE + qI - (\mu + \psi + \theta)Q$ (11)

Let $x = [S, E, I, Q, I_V, R]^T$,$F(x)$ be the number of incoming new infections into the system and $V(x)$ to be the number incoming new infections out of the system, then the model can be written as,

$F(x) = \begin{bmatrix} \beta SE \\ KE + QI \end{bmatrix}$ And $V(x) = \begin{bmatrix} (\mu + \alpha + k)E \\ (\mu + \psi + \theta)Q \end{bmatrix}$

By obtaining the Jacobian matrix of F and V with respect to E and Q at disease free equilibrium

$F(x) = \begin{bmatrix} \beta S & 0 \\ K & 0 \end{bmatrix}$ And $V(x) = \begin{bmatrix} (\mu + \alpha + k) & 0 \\ 0 & (\psi + \mu + \theta) \end{bmatrix}$

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The Jacobian matrix of F and V at disease free equilibrium is given by

$$F(x) = \begin{bmatrix} \frac{(\mu+\alpha+k)\beta^2 a}{2\mu(\mu+\alpha+k)-\beta a} & 0 \\ K & 0 \end{bmatrix} \text{ And } V(x) = \begin{bmatrix} (\mu+\alpha+k) & 0 \\ 0 & (\psi+\mu+\theta) \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} \frac{(\mu+\alpha+k)\beta^2 a}{2\mu(\mu+\alpha+k)-\beta a} & 0 \\ K & 0 \end{bmatrix} \begin{bmatrix} (\mu+\alpha+k) & 0 \\ 0 & (\psi+\mu+\theta) \end{bmatrix} = \begin{bmatrix} \frac{\beta^2 a}{2\mu(\mu+\alpha+k)-\beta a} & 0 \\ \frac{k}{\mu+\alpha+k} & 0 \end{bmatrix}$$

The eigenvalues of FV^{-1} are given by

$$\begin{vmatrix} \frac{\beta^2 a}{2\mu(\mu+\alpha+k)-\beta a} - A & 0 \\ \frac{k}{\mu+\alpha+k} & -A \end{vmatrix} = 0$$

Where A is the eigenvalues of FV^{-1}

$$A^2 - A\left[\frac{\beta^2 a}{2\mu(\mu+\alpha+k)-\beta a}\right] = 0$$

The eigenvalues are

$$A_1 = 0\ ,\ A_2 = \frac{\beta^2 a}{2\mu(\mu+\alpha+k)-\beta a}$$

The reproductive number is the most dominant eigenvalue

$$R_0 = \frac{\beta^2 a}{2\mu(\mu+\alpha+k)-\beta a}$$

3. STABILITY OF DISEASE FREE EQUILIBRIUM

Local stability of Disease free equilibrium

The eigenvalues are obtained by getting the PDE of the functions. They help in obtaining the local stability of the DFE. The equilibrium point is stable if the Jacobian matrix evaluated at the point has Eigenvalues that are negative. Routh-Hurwitz criterion was utilized so as to get the local stability [26].

Theorem: DFE is locally unstable when $R_0 > 1$ and it's stable if $R_0 < 1$.

Proof: DFE of the model is done by computation of its Jacobian matrix in order to prove this theorem the DFE of the model is done by computing it in the Jacobian matrix. At the DFE, the PDE of each equation in the system for state variables S, E, I, Q, I_V, R which are used in the generation of the Jacobian matrix.

$$J(S^*, E^*, I^*, Q^*, {I_V}^*, R^*) = \begin{bmatrix} \frac{\partial S}{\partial S} & \frac{\partial S}{\partial E} & \frac{\partial S}{\partial I} & \frac{\partial S}{\partial Q} & \frac{\partial S}{\partial I_V} & \frac{\partial S}{\partial R} \\ \frac{\partial E}{\partial S} & \frac{\partial E}{\partial E} & \frac{\partial E}{\partial I} & \frac{\partial E}{\partial Q} & \frac{\partial E}{\partial I_V} & \frac{\partial E}{\partial R} \\ \frac{\partial I}{\partial S} & \frac{\partial I}{\partial E} & \frac{\partial I}{\partial I} & \frac{\partial I}{\partial Q} & \frac{\partial I}{\partial I_V} & \frac{\partial I}{\partial R} \\ \frac{\partial Q}{\partial S} & \frac{\partial Q}{\partial E} & \frac{\partial Q}{\partial I} & \frac{\partial Q}{\partial Q} & \frac{\partial Q}{\partial I_V} & \frac{\partial Q}{\partial R} \\ \frac{\partial I_V}{\partial S} & \frac{\partial I_V}{\partial E} & \frac{\partial I_V}{\partial I} & \frac{\partial I_V}{\partial Q} & \frac{\partial I_V}{\partial I_V} & \frac{\partial I_V}{\partial R} \\ \frac{\partial R}{\partial S} & \frac{\partial R}{\partial E} & \frac{\partial R}{\partial I} & \frac{\partial R}{\partial Q} & \frac{\partial R}{\partial I_V} & \frac{\partial R}{\partial R} \end{bmatrix}$$

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$$J_{E_0} = \begin{pmatrix} -\mu & -\frac{\beta a}{\mu} & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta a}{\mu} - (\mu+\alpha+k) & 0 & 0 & 0 & 0 \\ 0 & \alpha & -(\mu+\gamma+q) & 0 & 0 & 0 \\ 0 & k & q & -(\mu+\psi+\theta) & 0 & 0 \\ 0 & 0 & 0 & \theta & -(\mu+\delta) & 0 \\ 0 & 0 & \gamma & \psi & \delta & -\mu \end{pmatrix}$$

Finding the determinant of the Jacobian matrix of DFE

Since all the eigenvalues are negative, DFE is locally asymptotically stable.

Endemic equilibrium

At endemic equilibrium state, all the variables in the dynamic system that is Exposed, Infection, Quarantine, Isolation of most vulnerable and Recovery are taken into consideration. The EE is given by

$EE = S^*, E^*, I^*, Q^*, {I_V}^*, R^*$

From the dynamic system, we get

$\frac{dS}{dt} = a - (\mu + \beta E)S$

$a - (\mu + \beta E)S = 0\ ,\ S = \frac{a}{(\mu+\beta E)}$ (12)

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

$\beta SE - (\mu + \alpha + k)E = 0$

$S = \frac{(\mu+\alpha+k)}{\beta}$ (13)

Using equations (12) and (13) yields

$\frac{a}{(\mu+\beta E)} = \frac{(\mu+\alpha+k)}{\beta}$

$E^* = \frac{\mu(\mu+\alpha+k)-\beta a}{\beta(\mu+\alpha+k)}$ (14)

$S^* = \frac{(\mu+\alpha+k)a}{2\mu(\mu+\alpha+k)-\beta a}$ (15)

Again from the dynamic system, we have

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

$\alpha E - (\mu + \gamma + q)I = 0$

Using equation (14), we get

$I^* = \frac{\alpha[\mu(\mu+\alpha+k)-\beta a]}{\beta(\gamma+q+\mu)(\mu+\alpha+k)}$ (16)

$\frac{dQ}{dt} = KE + qI - (\mu + \psi + \theta)Q$

$KE + qI - (\mu + \psi + \theta)Q = 0$

Using equation (14) and (16), we get

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$$Q^* = \frac{(k+kq\alpha)[\mu(\mu+\alpha+k)-\beta a]}{\beta(\psi+\mu+\theta)(\gamma+q+\mu)(\mu+\alpha+k)} \quad (17)$$

$$\frac{dI_V}{dt} = \theta Q - (\delta+\mu)Q$$

$$\theta Q - (\delta+\mu)Q = 0$$

Using equation (17), we get

$$I_V{}^* = \frac{(k\theta+kq\alpha\theta)[\mu(\mu+\alpha+k)-\beta a]}{\beta(\delta+\mu)(\psi+\mu+\theta)(\gamma+q+\mu)(\mu+\alpha+k)} \quad (18)$$

$$\frac{dR}{dt} = \gamma I + \psi Q + \delta I_V - \mu R$$

$$\gamma I + \psi Q + \delta I_V - \mu R = 0$$

Using equations (16),(17) and (18) we get

$$R^* = \frac{\{[\mu(\mu+\alpha+K)-\beta a][\alpha\gamma(\delta+\mu)(\psi+\theta+\mu)+\psi(\delta+\mu)(k+kq\alpha)+(k\theta+kq\alpha\theta)]\}}{\beta(\delta+\mu)(\psi+\mu+\theta)(\gamma+q+\mu)(\mu+\alpha+k)} \quad (19)$$

Therefore, the endemic equilibrium $EE = S^*, E^*, I^*, Q^*, I_V{}^*, R^*$

$$(S^*, E^*, I^*, Q^*, I_V{}^*, R^*) = \left[\begin{array}{c} \frac{(\mu+\alpha+k)a}{2\mu(\mu+\alpha+k)-\beta a}, \frac{\mu(\mu+\alpha+k)-\beta a}{\beta(\mu+\alpha+k)}, \frac{\alpha[\mu(\mu+\alpha+k)-\beta a]}{\beta(\gamma+q+\mu)(\mu+\alpha+k)}, \\ \frac{(k+kq\alpha)[\mu(\mu+\alpha+k)-\beta a]}{\beta(\psi+\mu+\theta)(\gamma+q+\mu)(\mu+\alpha+k)}, \frac{(k\theta+kq\alpha\theta)[\mu(\mu+\alpha+k)-\beta a]}{\beta(\delta+\mu)(\psi+\mu+\theta)(\gamma+q+\mu)(\mu+\alpha+k)}, \\ \frac{\{[\mu(\mu+\alpha+K)-\beta a][\alpha\gamma(\delta+\mu)(\psi+\theta+\mu)+\psi(\delta+\mu)(k+kq\alpha)+(k\theta+kq\alpha\theta)]\}}{\beta(\delta+\mu)(\psi+\mu+\theta)(\gamma+q+\mu)(\mu+\alpha+k)} \end{array}\right]$$

Endemic equilibrium and stability

The analysis of stability shows the behavior of epidemic near the equilibrium points. Korobeinikov and Wake [29] proposed the logarithmic Lyapunov function to prove the global stability of EE for SIS, SIR, SIRS models.

Theorem: The EE point W^* is asymptotically stable when $R_0 > 1$ and unstable when $R_0 < 1$.

Proof: To analyze stability of the EE the logarithmic Lyapunov function is used then given in the form written below.

$W = \sum_{i=1}^{6}[x_i - x_i{}^* \ln(x_i)]$

Where a positive constant is represented by a_i, $x_i$represents some free virus in compartment i, $x_i{}^*$denotes the number of free viruses in compartment i at an equilibrium point. Then, the model system is now written as follows;

$$W(SEIQI_VR) = [A_1(S - S^*\ln(S)) + A_2(E - E^*\ln(E)) + A_3(I - I^*\ln(I)) + A_4(Q - Q^*\ln(Q)) + A_5(I_V - I_V{}^*\ln(I_V)) + A_6(R - R^*\ln(R))]$$

The constant $A_1, A_2, A_3, A_4, A_5, A_6$ are non-negative constants and the functions W which is said to be continuous and also said to be differentiable. Consider the derivative with respect to each compartment:

$$\frac{dW}{dt} = \left[A_1\left(1-\frac{S^*}{S}\right)\frac{dS}{dt} + A_2\left(1-\frac{E^*}{E}\right)\frac{dE}{dt} + A_3\left(1-\frac{I^*}{I}\right)\frac{dI}{dt} + A_4\left(1-\frac{Q^*}{Q}\right)\frac{dQ}{dt} + A_5\left(1-\frac{I_V{}^*}{I_V}\right)\frac{dI_V}{dt} + A_6\left(1-\frac{R^*}{R}\right)\frac{dR}{dt}\right]$$

At the endemic equilibrium point,

$$a = (\mu+\beta E)S^*$$

$$\beta SE = (\mu+\alpha+k)E^*$$

$$\alpha E = (\mu+\gamma+q)I^*$$

$$KE + qI = (\mu+\psi+\theta)Q^*$$

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$$\theta Q = (\delta + \mu){I_V}^*$$

$$\gamma I + \psi Q + \delta I_V = \mu R^*$$

$$\frac{dW}{dt} = A_1\left(\frac{S-S^*}{S}\right)[(\mu+\beta E)(S-S^*)] + A_2\left(\frac{E-E^*}{E}\right)[(\mu+\alpha+k)(E-E^*)] + A_3\left(\frac{I-I^*}{I}\right)[(\mu+\gamma+q)(I-I^*)]$$
$$+ A_4\left(\frac{Q-Q^*}{Q}\right)[(\mu+\psi+\theta)(Q-Q^*)] + A_5\left(\frac{I_V-{I_V}^*}{I_V}\right)[(\mu+\delta)(I_V-{I_V}^*)]$$
$$+ A_6\left(\frac{R-R^*}{R}\right)[(\mu)(R-R^*)]$$

$$\frac{dW}{dt} = -A_1\left[(\mu+\beta E)\left(\frac{S-S^*}{S}\right)^2\right] - A_2\left[(\mu+\alpha+k)\left(\frac{E-E^*}{E}\right)^2\right] - A_3\left[(\mu+\gamma+q)\left(\frac{I-I^*}{I}\right)^2\right]$$
$$- A_4\left[(\mu+\psi+\theta)\left(\frac{Q-Q^*}{Q}\right)^2\right] - A_5\left[(\mu+\delta)\left(\frac{I_V-{I_V}^*}{I_V}\right)^2\right] - A_6\left[(\mu)\left(\frac{R-R^*}{R}\right)^2\right]$$

$$S \to S^*, E \to E^*, I \to I^*, Q \to Q^*, I_V \to {I_V}^*, R \to R^*$$

Therefore $\frac{dW}{dt} \leq 0$, and the function W is negative when

$W(S,E,I.Q,I_V,R) \geq 0$, by following the approach of [29],the largest invariant set D is a singleton set W which is the endemic equilibrium point, and using La Salle [30]. Invariant principle, W is globally stable asymptotically when $R_0 \geq 1$ in D.

Sensitivity of parameters values

By validation of the analytical findings, we fit the values of the parameters values of the $SEIQI_VR$ model. Quantitative analysis of the system in this session is performed of model differential equations by use Runge-Kutta 4th order scheme. We consider December 31st, 2020 to December 31st, 2021 for model curve fitting. We take daily cases of Covid-19 in Kenya (From MOH) for this purpose. We enlist the model parameters in a table from the data that is estimated from MOH in Kitui County, Kenya. By fitting the model to the basis of daily report, seven parameters of the $SIEQI_VR$ model $\beta, \alpha, q, k, \mu, \theta, \delta, \psi$ have been used to generate the results.

The model initial values are assumed as shown below;

$S_0, E_0, I_0, Q_0, I_{V_0}, R_0 = [3000,2500,1500,900,150,200]$

4. NUMERICAL RESULTS

Parameters values used in the simulation

Parameters	Values	Sources	Sensitivity index
A	8.94	Assumed	−79.44
B	0.015	Assumed	−2043
α	0.85	Assumed	01591
Θ	0.2435	Assumed	0
Δ	0.039	[39]	0
K	0.2439	[33]	0.0456
M	0.0104	[31]	−0.2085
Ψ	14 days	MOD data	0
Γ	0.07	[32]	0
Q	0.099	Assumed	0

Susceptible and infected population

From figure 2.1 below, shows the susceptible corona virus population with time, a period of 10 months and infected with given time. The susceptible individuals in the population decreases exponentially with given time.

When infected individuals are compared, in the first month, the number is 1500 individuals, the same month the infection rate increases but after the first month to the tenth month the infection rate decreases exponentially with time. This may be due to the impact of isolation of the most vulnerable population given in isolation centers. Towards the tenth month, the graphs tend to decrease showing that people may stop being infected with Covid 19 in Kitui County, Kenya.

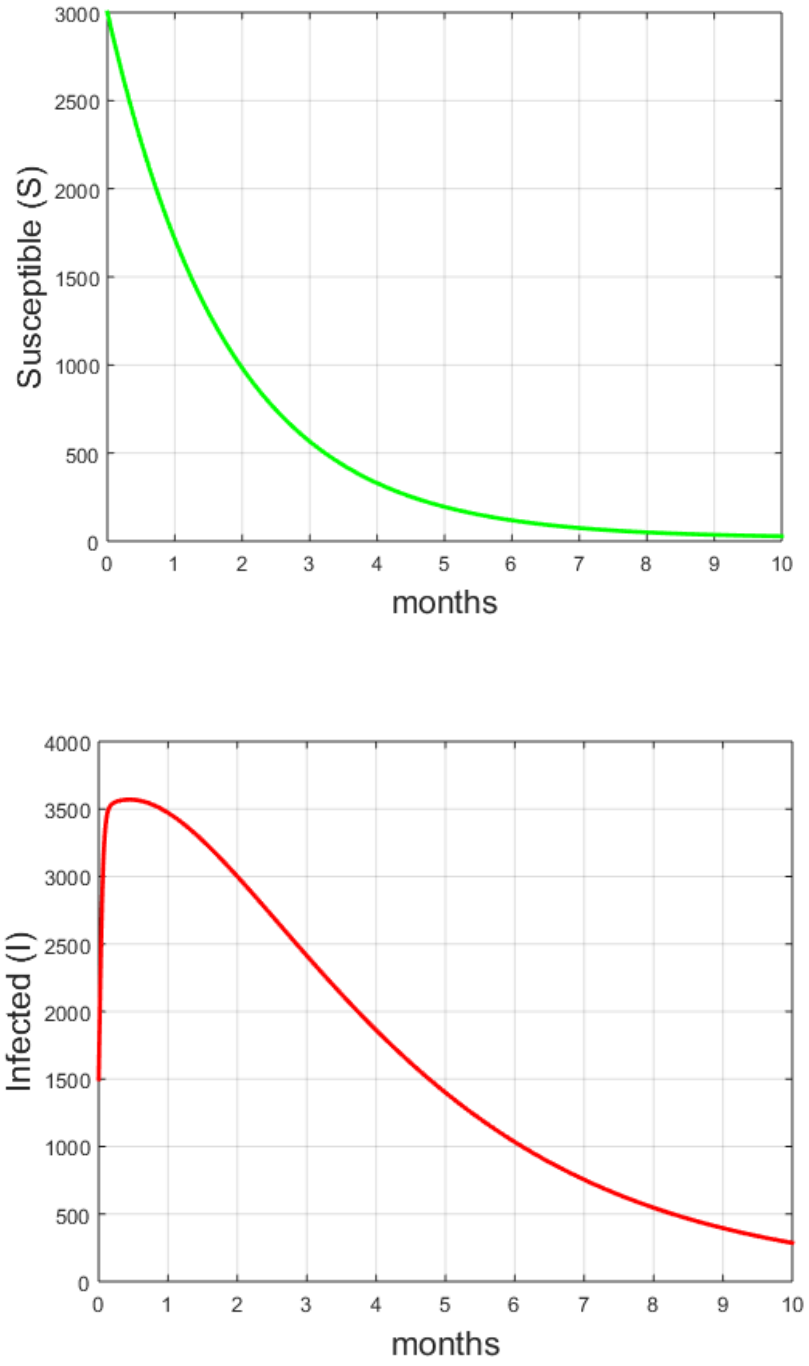

Figure 2

Exposed and infected population

In figure 2 shows the graphs of exposed population with time in months and also infected with time in months. The individuals who are exposed to corona virus decrease with time also the infected population decreases with time. This implies that isolation of the vulnerable population helps reduce the number of infection with time.

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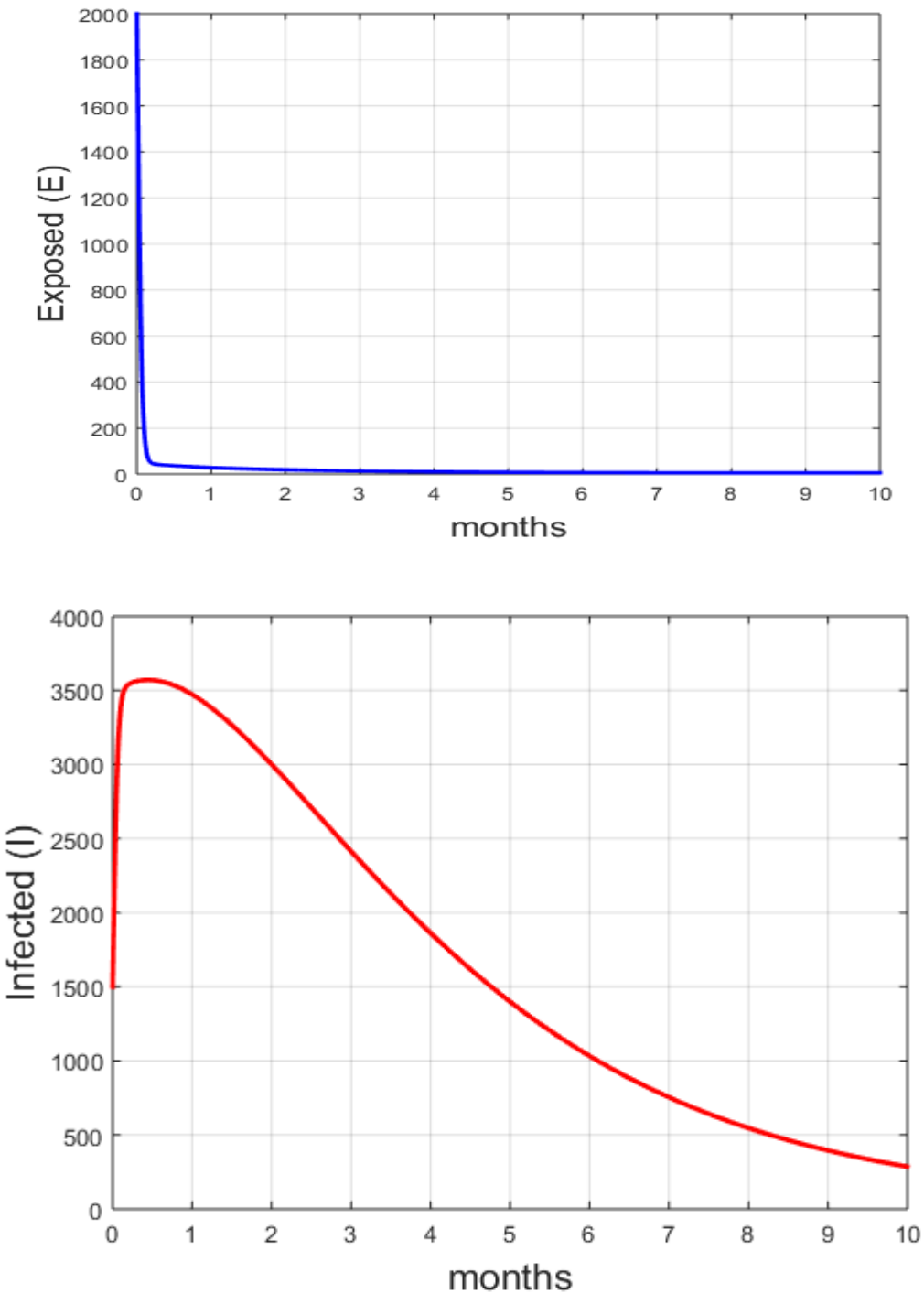

Figure 3

Quarantined and vulnerable population.

In figure 3, shows the quarantined population against time in ten months and vulnerable population against time in months. The quarantined population and the vulnerable population, the number has reduced over time. This may be due to taking medication, being taken care of by eating balanced diet in isolation Centers. That is why the number is decreasing. Taking medicine can help population reduce the death of the most vulnerable.

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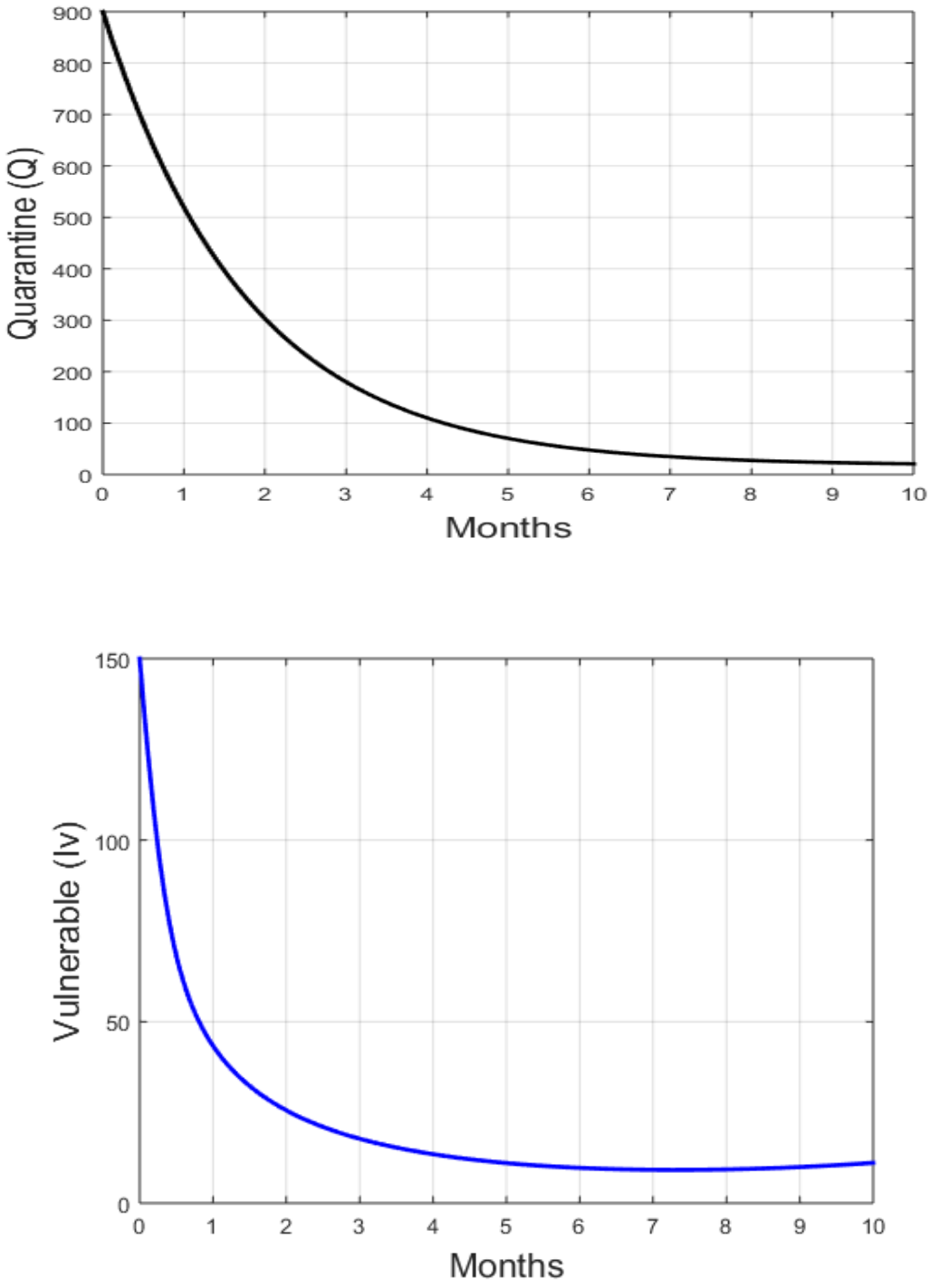

Figure 4

Human population dynamics

In figure 5 below, the dynamics of the corona virus in total population comprising of Susceptible, Infected, Exposed and Recovered is analyzed. The number of susceptible, exposed and infected populations decreases with time in months. The recovered population increases with time hence by the end of 10 months; there are more recoveries than the susceptible, exposed and infected. This also means that the death rates decreases because of the impact of isolation of the most vulnerable who are most likely to infect the disease and die with time.

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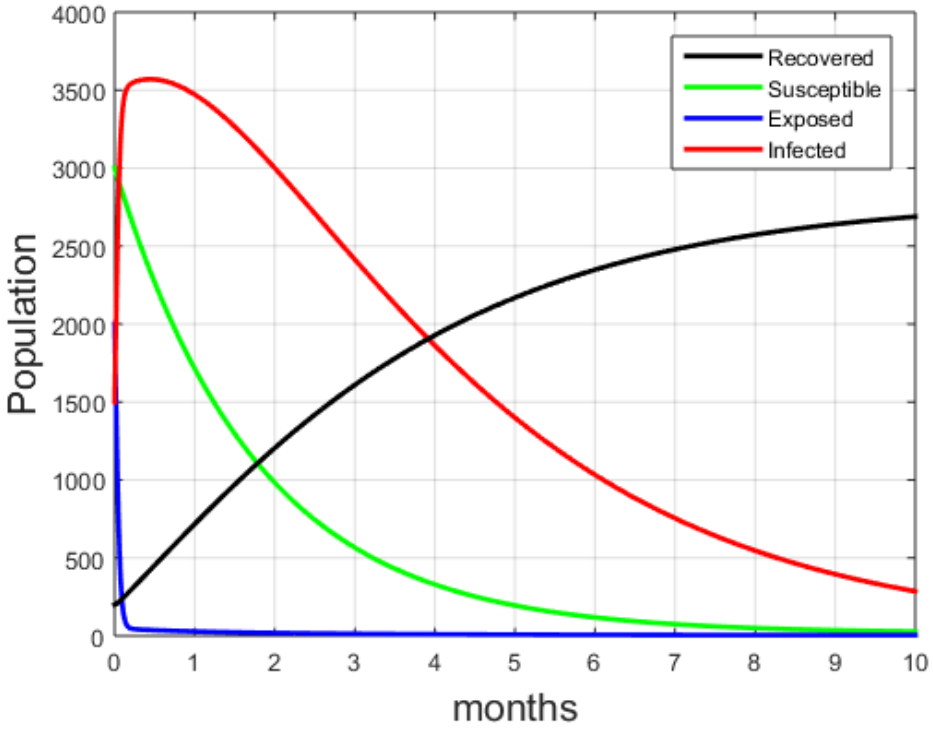

Figure 5

5. CONCLUSION

By taking into account SEIQIvR model in this study that contains isolation of the vulnerable population has been constructed. We have pointed out isolation of the vulnerable compartment as the one that will increase the recovery. We have obtained solution boundedness, positivity of the solution. Again, we have provided both the endemic equilibrium and disease free equilibrium points. We have evaluated basic reproductive number using the next generation matrix. We have also investigated local stability of DFE, where when $R_O \geq 1$the DFE is unstable and when$R_0 \leq 1$, the DFE is stable asymptotically. We have also investigated EE point W* is stable asymptotically when $R_O \geq 1$and unstable when$R_0 \leq 1$.

According to the results in the figures that have been represented, figure 2, the total number of population which is susceptible decreases exponentially with given time. The infected population also decreases with given time.

In figure 3, the exposed and infected individual decreases with time. In figure 4, quarantined population and vulnerable population decreases with time.

In figure 5, the number of susceptible, exposed and infected population decreases with time in months. The recovered population increases with time; hence by the end of 10 months, more recoveries are seen. According to these figures, there are more recoveries because of the impact of the isolation of the vulnerable.

6. RECOMMENDATIONS

Further research can be done considering isolation of the non-vulnerable population. WE therefore recommend that ministry of health and world health organization to get more isolation Centres so as to isolate the vulnerable so that recovery rate increases in Kitui County Kenya.

As we have demonstrated in this study, isolation of the vulnerable population can reduce the death rates and increase recovery rates. Ministry of health, world health organization and non-profit organizations can build more isolation Centres to isolate vulnerable so as to increase recovery rates in Kitui county Kenya. This can be done by building isolation Centres in hospitals and dispensaries and providing proper treatment with special balanced diet once someone is isolation.

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