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Modeling Covid-19 Virus after Lifting Preventive Measures: A Case Study of Kisii County

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Abstract

Purpose: This research is about a new COVID-19 SIR model containing three classes; susceptible S(t), infected I(t), and recovered R(t) with the convex incident rate.

Methodology: The NCOVID-19 model was formulated in the following system, the whole population N(t) was divided into three classes S(t), I(t), and R(t), which represented Susceptible, Infected, and Recovered compartments in the form of differential equations. Lyapunov functions were used to validate the stability of the equilibrium of the ordinary differential equations, linearization of the system was also done using Jacobian matrices by finding the derivatives of f(x) for x.

Findings: Covid-19 is an infectious disease caused by the novel coronavirus identified as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). The people infected by COVID-19 experience mild respiratory problems such as; Fever, dry cough, throat infection, and fatigue. People may also have symptoms such as nasal infection, aches, and sore throat. The pandemic has led to a dramatic loss of human life in Kenya, Africa, and the whole world as it presents an unprecedented challenge to public health, food systems, and the world of work. This case study seeks to model covid-19 virus after lifting preventive measures with a major focus on Kisii County, the subject model was presented in the form of differential equations and the disease-free and endemic equilibrium was calculated for the model. Also, the basic reproduction number $R_0 = 0.7831$ was calculated and the disease-free equilibrium was found to be asymptotically stable meaning that the virus could be eliminated from the population, this showed that the county government of Kisii was in good control of the COVID-19 situation., in addition, The global stability of the model was calculated using the Lyapunov function construction while the Local stability was calculated using the Jacobian matrices. The numerical solutions were calculated using the non-standard finite difference scheme (NFDS) and MATLAB software.

Unique Contribution to Theory, Practice and Policy: This study has laid a foundation for future research in the area. In the future, a study that can include the rate of COVID-19 virus mutation and its impacts is recommended.

Keywords: *Covid-19 SIR Model, Basic Reproduction Number R_0, Global Stability, Local Stability, Non-Standard Finite Difference Scheme, Citations*

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INTRODUCTION

The covid-19 pandemic unfolded as a cluster of patients being admitted to the hospital in late December 2019, these patients were diagnosed with pneumonia. At first, the cause of the disease was linked to a seafood and wet animal market in Wuhan, Hubei Province China. It is now known that the etiological agent of the disease is a novel coronavirus identified as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). WHO declared COVID-19 a pandemic in March 2020 and as of mid-July 2020 the virus had spread to 213 countries causing about 15,969,465 infections and 643,390 deaths. So far, the virus has devastated almost everything around the world. Social life, health, economy, education- all segments of human life have been severely affected. Health researchers, governmental policymakers, and healthcare authorities are puzzled about combating the deadly outbreak (*Khan et al., 2020*). They all have their point of view on the situation. They are trying hard to, at least, minimize the number of deaths caused by the outbreak. The people infected by the coronavirus pandemic experience mild respiratory problems such as; Fever, dry cough, throat infection, and fatigue. People may also have the symptoms as follows; nasal infection, aches, and sore throat.

According to the WHO dashboard and the Ministry of Health, the first case of COVID-19 in Kenya was reported on 13th March 2020 with the capital Nairobi being the epicenter, this prompted the government to lock the country down which saw schools shut down, all places of social gatherings i.e., churches, mosques, and temples were also shut. Non-pharmaceutical containment measures such as wearing face masks, social distancing, quarantining of suspected cases, and contact tracing were imposed by the government. In this model data from the Kisii teaching and referral hospital WHO Coronavirus Disease Dashboard was fitted and used to project and predict the cumulative number of reported cases as well as to give insights on the likely peak time for COVID-19 based on the SIR mathematical model.

MODEL FORMULATION

The NCOVID-19 model was formulated in the following system, the whole population N(t) was divided into three classes S(t), I(t), and R(t), which represent Susceptible, Infected, and Recovered compartments in the form of differential equations given below

$$\left.\begin{aligned} \frac{dS(t)}{dt} &= b - k(1-AS(t)I(t)) - \alpha k\beta S(t)I(t) - \mu S(t) \\ \frac{dI(t)}{dt} &= k\,(1-\alpha S(t)I(t)) + \alpha k\beta S(t)I(t) - (d_0 + \gamma + \mu)\, I(t) \\ \frac{dR(t)}{dt} &= \gamma I(t) - \mu R(t) \end{aligned}\right\} \quad (1)$$

For the above system (1) is presented in the form of a flow chart. Table 1, describes the parameters used in system (1). adding all equations implies

$$\frac{dN(t)}{dt} = -\,(\mu N(t) + d_0 I(t) - b) \quad (2)$$

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Model Diagram

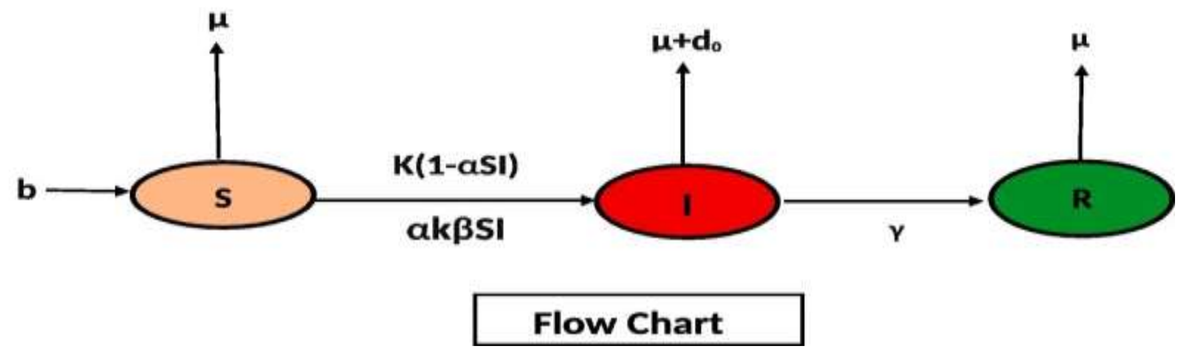

Figure 1

EQUILIBRIA

For system 1 above an assumption is made that the Disease-Free Equilibrium exists for some values of the variables used, and they are denoted by $E_0 = (S^0, 0,0)$

$$E_0 = (S^0, 0, 0) = \left(\frac{b}{\mu}, 0, 0\right)$$

Endemic Equilibria

$$\mathbf{S^*(t)} = \frac{(\mu + d_0 + \gamma)I(t) - b}{\mu}$$

$$\mathbf{I^*(t)} = \frac{k\mu}{k\alpha(1-\beta)(\mu + d_0 + \gamma - b)I^*(t) + \mu(\mu + d_0 + \gamma)}$$

$$\mathbf{R^*(t)} = \frac{\gamma}{\mu}\mathbf{I^*(t)}$$

THE BASIC REPRODUCTION NUMBER R_0

In epidemiology the R_0 is the most important parameter because it gives the researcher an idea of the disease flows in the entire population, it also dictates what needs to be done to control the rate of spread. In this research, the R_0 is obtained as follows.

$$\frac{dX}{dt} = G - H \qquad G = \begin{pmatrix} k(1 - \alpha I(t)S(t)) + \alpha k\beta I(t)S(t) \\ 0 \end{pmatrix} \qquad H = \begin{pmatrix} b - S(t) \\ (d_0 + \gamma + \mu) \end{pmatrix}$$

I(t)

The Jacobian of G is $G = \begin{pmatrix} -k\alpha S^0 + k\alpha\beta S^0 & 0 \\ 0 & 0 \end{pmatrix}$ and Jacobian of H is $H = \begin{pmatrix} -\mu & 0 \\ 0 & d_0 + \gamma + \mu \end{pmatrix}$

0

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$H^{-1} = \frac{1}{-\mu(\gamma+d0+\mu)}\begin{pmatrix} \mu + d_0 + \gamma & 0 \\ 0 & -\mu \end{pmatrix}$ $GH^{-1} = \begin{pmatrix} k\alpha\,(\beta - 1)\,S^0 & 0 \\ 0 & 0 \end{pmatrix}$ which gives the R_0

$$R_0 = \frac{k\alpha(1-\beta)b}{\mu.\mu} \quad (3)$$

The R_0 was computed using the parameters in Table 2 below and the value obtained was R_0= 0.7831, this showed that the county government of Kisii was in good control of the COVID-19 situation.

Theorem 1

(i) If $R_0 \leq 1$there is no positive equilibrium of the system.

(ii) If $R_0 > 1$there is a unique positive equilibrium $E^*= (S^*(t), I^*(t), R^*(t))$ of the model(1), called the endemic equilibrium.

Table 2: Description of Parameters and Their Values

Parameters	Physical description	Numerical value
S(t)	Susceptible compartment	220 in millions
I(t)	Infected compartment	0 in million
R(t)	Recovered compartment	0 in million
d0	Death due to corona	0.02
M	Natural death	0.0062
B	Birth rate	10.7
Β	Protection rate	0.009, 0.0009
K	Constant rate	0.00761
Α	Isolation rate	0.009, 0.0009
Γ	Recovery rate	0.0003

LOCAL STABILITY

To get the local stability, the model was reduced to a set of two differential equations subject to the initial conditions given below.

$$\frac{dS(t)}{dt} = b - k\,(1 - \alpha S(t)I(t)) - \alpha k\beta S(t)I(t) - \mu S(t)$$

$$\frac{dI(t)}{dt} = k\,(1 - \alpha S(t)I(t)) + \alpha k\beta S(t)I(t) - (\mu + d_0 + \gamma)\,I(t) \quad (4)$$

Subject to the following initial conditions $S(0) = S0 \geqslant 0, I(0) = I0 \geqslant 0$.Which is explained by the following

Theorem 2

If $R_0 < 1$, then the system(4)is locally asymptotically stable at the disease-free equilibrium E_0.

Proof

At E_0 the Jacobian matrix is given by $J^0 = \begin{pmatrix} -\mu & \frac{k\alpha(1-\beta)b}{\mu} \\ 0 & Ro-1 \end{pmatrix}$ and the auxiliary equation J^0 is given by $w^3 + w^2a_1 + wa_2 + a_3 = 0$ where

$a_1 = (\mu+\beta)(\mu + \alpha) + (\mu + d_0 + \gamma)(1-R_0) > 0$

$a_2 = (\mu+\beta)(\mu+\beta)[1 + (\mu + \gamma + d_0)(1-R_0) > 0$

$a_3 = (\mu+\beta)(\mu + \alpha)(\mu + \gamma + d_0)(1-R_0) > 0$

$a_1a_2 - a_3 = (\mu+\beta)(\mu + \alpha)((\mu + \gamma + d_0)^2+(\mu+\beta)(\mu + \alpha)[(d_0 + \gamma + \mu) + 1])(1-R_0) > 0$ (5)

The Routh-Hurwitz stability criteria are satisfied as $a_1 > 0$, $a_2 > 0$, $a_3 > 0$, and $a_1r_2 - r_3 > 0$ if $R_0 < 1$. which shows the system (1) is locally asymptotically stable at E^0. Furthermore, at E* the system (4) is locally asymptomatically stable analogous to $R_0 > 1$ which is proved in Theorem 3 below.

5.2 Theorem 3

At E*, if $R_0 > 1$ then system(4) is locally asymptotically stable.

Proof

For system (4) Jacobian matrix is $J_1 = \begin{pmatrix} \alpha kI^*(t) - \mu - \alpha k\beta I^*(t) & \alpha kS^*(t) - \alpha k\beta S^*(t) \\ -\alpha kI^*(t) + \alpha k\beta I^*(t) & -k\alpha S^*(t) + \alpha k\beta S^*(t) - (\mu+d_0+\gamma) \end{pmatrix}$

The matrix J_1 was operated on to give matrix M_1 as

$$M_1 = \begin{pmatrix} -\mu & -(\mu+d_0+\gamma) \\ -\alpha k(1-\beta)I^*(t) & -k\alpha(1+\beta)S^*(t) - (\mu+d_0+\gamma) \end{pmatrix}$$

The trace and determinant of M_1 is given by tra $(M_1) = -2\mu - k\alpha(\beta+1)S^*(t) - d0 - \gamma < 0$, (6)

And det $(M_1) = \mu[\alpha\beta(1+\beta) + d0 + \mu + \gamma] + \alpha k(\mu + d_0 + \gamma)(\beta+1) > 0$.
(7) The determinant of $J_1 > 0$. The real part at E*(t) "endemic equilibrium" of the model (4) has a negative value. Thus, with condition $R_0 > 1$, the endemic equilibrium E*of system (4) is locally asymptotically stable.

GLOBAL STABILITY

The global stability for the disease-free and endemic equilibrium is presented using Lyapunov functions as shown in theorems 4 and 5

Theorem 4

If $R_0 < 1$ then the disease-free equilibrium of the system(4)is globally asymptotically stable. Otherwise, unstable. To prove this theorem a Lyapunov function was constructed as follows.
$P = c_1(S(t)-S0) + c_3I(t)$, (8)

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such that c_1, c_2 and $c_3 > 0$ are constants. For time (t) *t*aking the derivative of (8), the PDE obtained is

$\frac{pd}{dt}$ = $c_1(b- k(1-\alpha S(t)I(t))b - \alpha k\beta S(t)I(t) - \mu S(t)) + c_2(k(1 -\alpha S(t)I(t)) +\alpha k\beta S(t)I(t) - (\mu+d_0+\gamma)I(t))$.

$\frac{pd}{dt}$ = $c_1b+k(1-\alpha S(t)I(t)) (c_2 - c_1) +\alpha k\beta S(t)I(t) (c_2 - c_1) + c_1\mu S(t) - c_2\mu I(t) - c_1d_0I(t) - c_2\gamma I(t)$

Assuming that $c_1 = c_2 = c_3 = 1$, then $\frac{dp}{dt} = - (\mu N(t) - b) - (d_0 + \gamma) I(t) < 0$ hence globally asymptotically stable for system (1) with $R_0 < 1$.

Theorem 5

The endemic equilibrium E* of the model (1) is asymptotically globally stable if $R_0 > 1$ this was proved by constructing Lyapunov functions as shown below

$\omega = (\mu + \beta) (S(t) - S^*(t)) + (\mu + \beta) I(t)$. (9), differentiating equation (9) for time (t) given. $\frac{d\omega}{dt} = (\mu+\beta) (S^*(t)) + (\mu + \beta) I^*(t)$

substituting the values from equation (1) in the derivative above, yielded

$\frac{d\omega}{dt} = (\mu+\beta) (b-k(1-\alpha S(t)I(t)) - \alpha k\beta S(t)I(t) - \mu S(t)) +(\mu+\beta) (k (1- \alpha S(t)I(t)) + \alpha k\beta S(t)I(t) - (\mu+d_0+\gamma) I^*(t))$.

$\frac{d\omega}{dt} = -(\mu+\beta) (\mu S(t) + (\mu +d_0 +\gamma) I^*(t)) < 0$. Thus $\frac{d\omega}{dt} < 0$ the endemic equilibrium E* of the model (1) is globally asymptotically stable, showing that $R_0 > 1$.

NUMERICAL RESULTS AND DISCUSSION

The numerical solution for model (1) was calculated using values in table (2), COVID-19 scientific data from Kisii County subjected to different compartments involved in the system was plugged into the Non-Standard Finite Difference scheme hence rewriting the system as

$$\frac{dS(t)}{dt} = b -k(1 -\alpha S(t)I(t)) - \alpha k\beta S(t)I(t) - \mu S(t) \quad (10)$$

Which was decomposed using the Non-Standard Finite Difference scheme as follows

$$\frac{Sj+1 - Sj}{h} = b - k(1 - \alpha S_j(t)I_j(t)) - \alpha k\beta S_j(t)I_j(t) - \mu S_j(t) \quad (11)$$

Equation (1) was also written in Non-Standard Finite Difference scheme as

$$\left.\begin{aligned} S_{J+1} &= S_j + h(b - k(1-\alpha S_j(t)I_j(t)) - \alpha k\beta S_j(t)I_j(t) - \mu S_j(t) \\ I_{j+1} &= I_j + h(k(1 - \alpha S_j(t)I_j(t)) + \alpha k\beta S_j(t)I_j(t) - (d_0 + \gamma + \mu)I_j(t)) \\ R_{j+1} &= R_j + h(\gamma I_j(t) - \mu R_j(t)) \end{aligned}\right\} \quad (12)$$

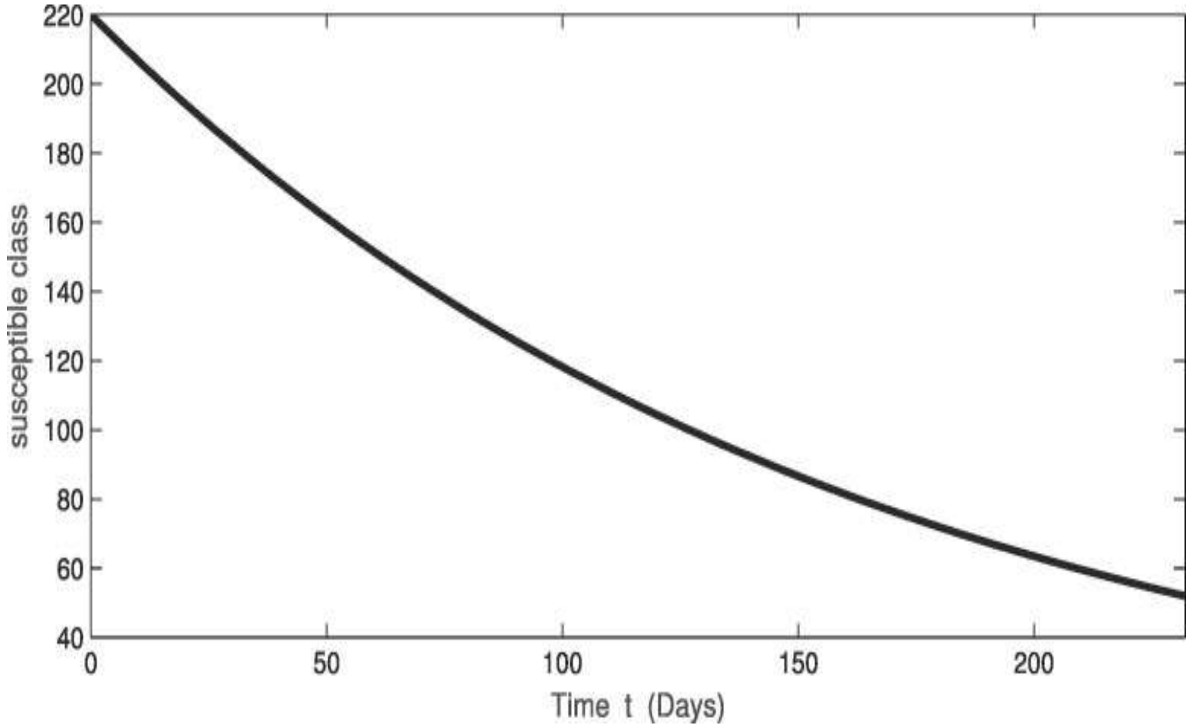

Figure 1: The Dynamical Behavior of Susceptible Population of the Considered Model

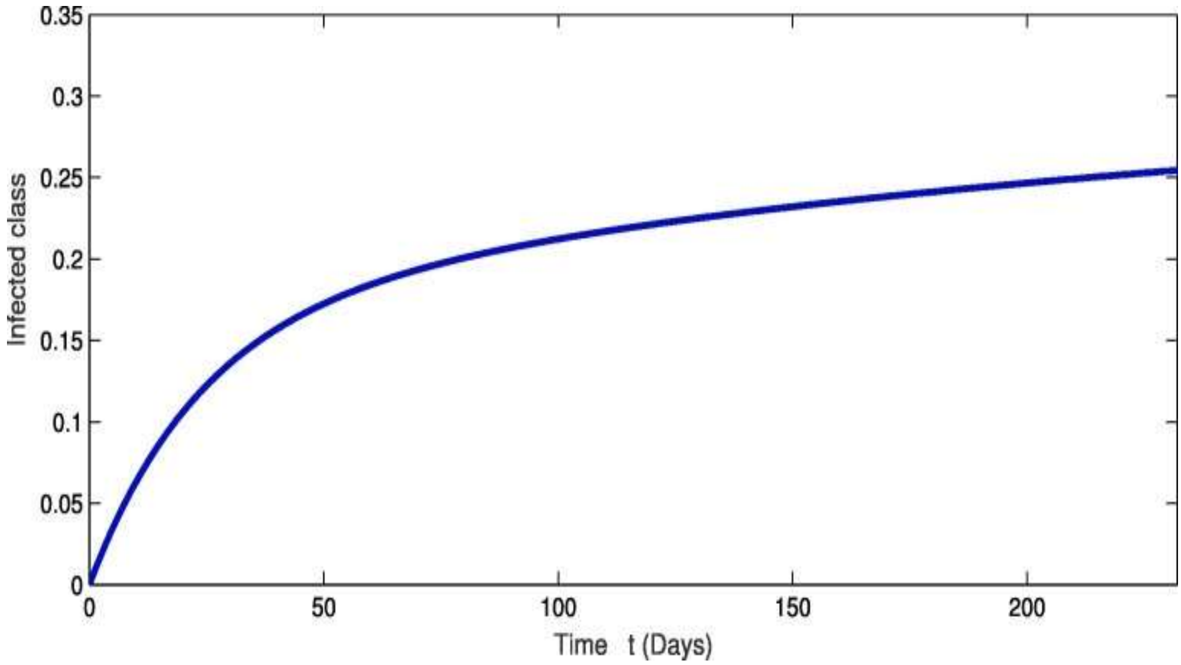

Figure 2: The Dynamical Behavior of Infected Population of the Considered Model

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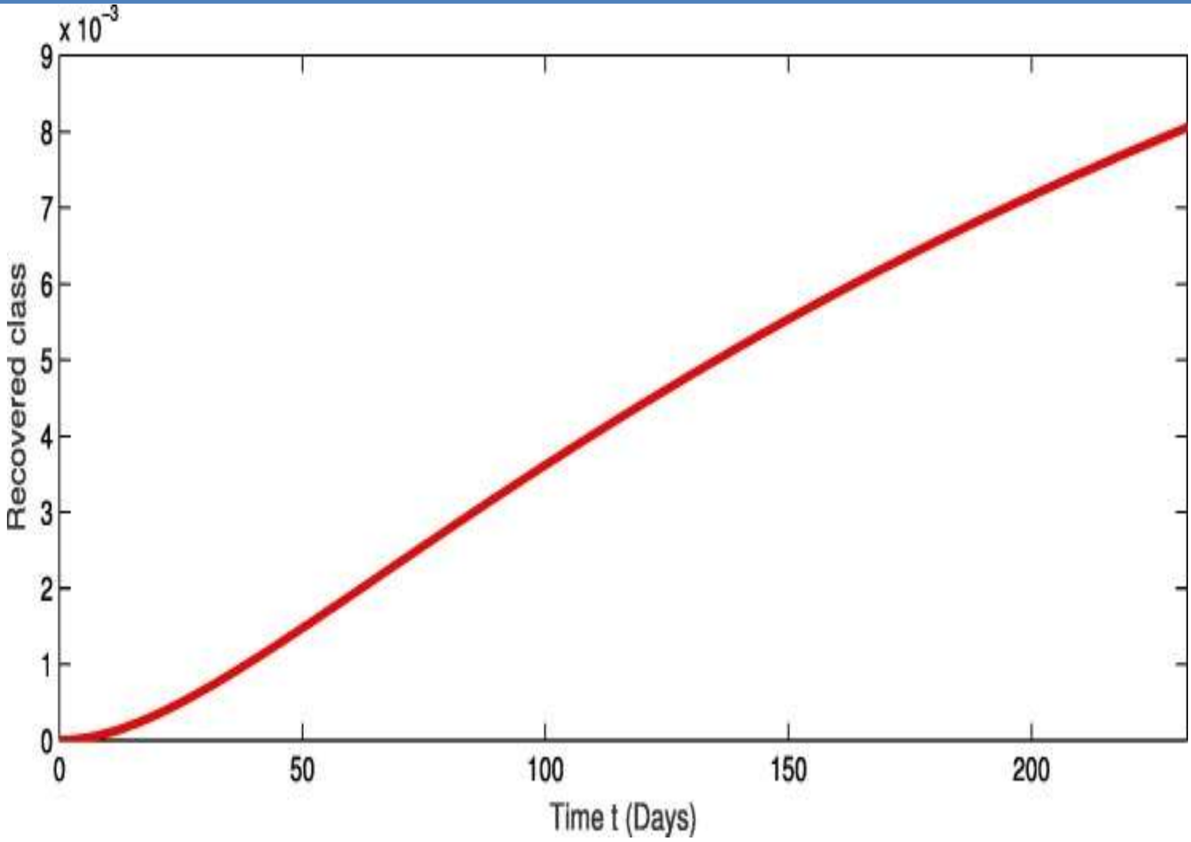

Figure 3: The Dynamical Behavior of the Recovered Population of the Considered Model

In this research model (1) was tested by taking the values of the parameter from Table 2 from the first of February 2023 to the 20th of September 2023, from the figure 1and 3 it is clearly seen that as the susceptibility was decreasing the level of infection was increasing in the first four months but in the month of July and August the infection rate slowed and finally in the last month it was nearly stable. From Figure 3 the rate of recovery from infection was rapid, the simulation was performed by taking the protection parameters α and β to be 0.009 and further decreasing the protection and isolation rate up to α=0.0009 and β=0.0009.Finally the results were plotted in graphs Fig. 4, Fig. 5, and Fig. 6 for scientific interpretation. We see that the infection rate slowed down reducing the protection and isolation rate. The recovery rate was also slow. From this simulation, we observed that protection and isolation rates played significant roles in controlling the infection from further spreading in the community. see Fig. 2,.

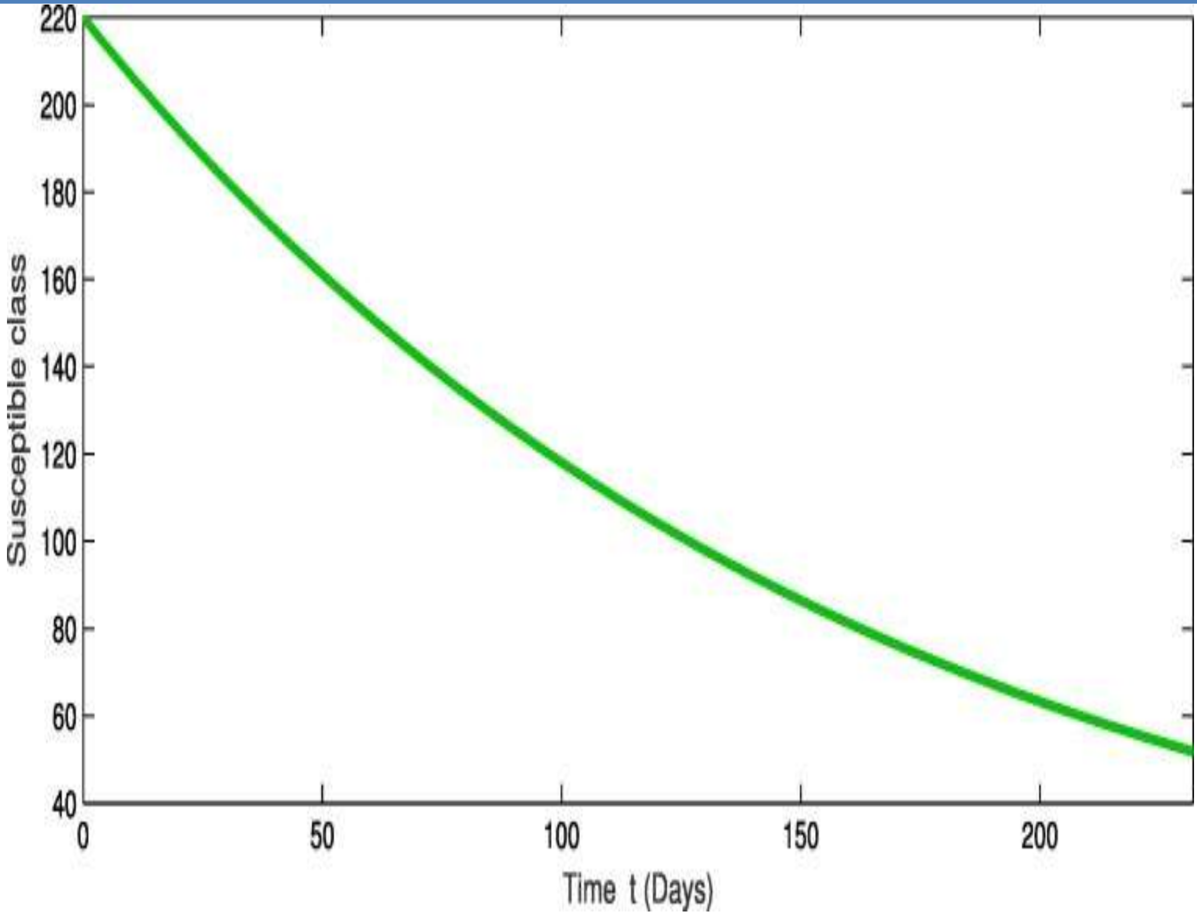

Figure 4: Dynamical Behavior of Susceptible Population of the Considered Model

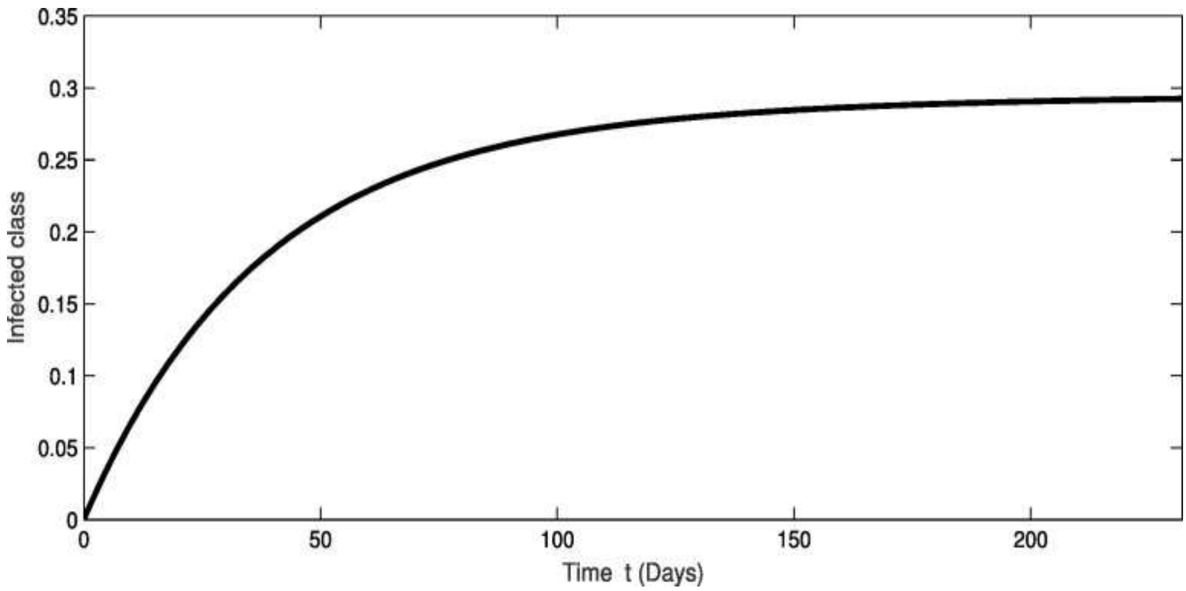

Figure 5: Dynamical Behavior of Infected Population of the Considered Model

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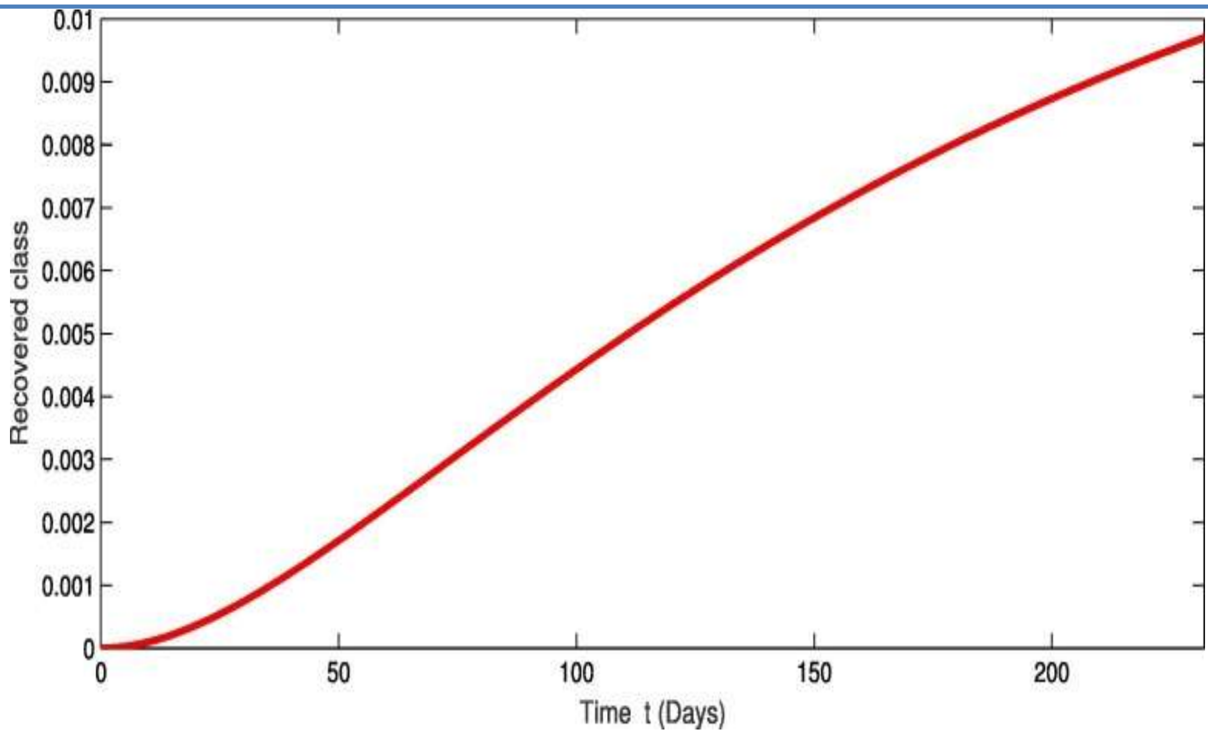

Figure 6: Dynamical Behavior of Recovered Population of the Considered Model

CONCLUSION AND RECOMMENDATION

Conclusion

The objective of this study was to model the transmission of COVID-19 in Kisii county, and to come up with a way of lowering the disease transmission rate, the model showed great success in projecting and predicting the transmission of the virus among individuals. Further the stability analysis was done using a series of partial differential equations which turned out to be asymptotically stable.

The R_0 was computed and found to be 0.7831 which is less than 1 (locally asymptotically stable) this meant that as the susceptibility was decreasing the level of infection was increasing in the first four months but in July and August the infection rate slowed and finally in the last month it was nearly stable. This research declared the high contagious rate from the infected population to the susceptible population. To overcome the pandemic the movement of people from one sub-county to the other should strictly be reduced for the sake of saving humanity. Also, the immigration of the exposed population to the infected community increased the infection. Isolation of infected individuals alongside observing safety protocols is the best option to secure a healthy community. It is necessary to judge the spread of the virus and model it with various parameters for proper supervision. The proper treatment of this pandemic is for Kenyan citizens to get fully vaccinated, observe the government safety protocols, and keep infected individuals away from healthy people.

A healthy diet is also a key factor in the fight against this disease as it helps to build a strong immunity, the model also showed that if early detection of this deadly disease was made, then immediate action would be taken, leading to complete eradication. Hence the disease would not be endemic.

Recommendations for Future Research

The study has been a success in projecting and predicting the COVID-19 outbreak in Kisii County, early mitigation of the disease can help in eradicating the virus in case of an outbreak to prevent a surge.

Since the disease is highly transmissible among individuals the county government should increase COVID-19 screening processes as well as encourage the natives to adhere to the safety protocols.

This study has laid a foundation for future research in the area. In the future, a study that can include the rate of COVID-19 virus mutation and its impacts is recommended.

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