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Research Article

EFFECT OF VACCINATION ON MATHEMATICAL MODELING OF COVID-19

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Abstract

Corona virus 2019 (Covid-19) have been endemic both in Africa and the whole world. In this paper we have formulated and analyze mathematical model of covid-19 that monitors the temporal dynamics of the disease in the presence of preventive vaccine since the most effective ways of controlling the transmission of infection disease is through vaccination and treatment. Due to transmission characteristics of covid-19, we have divided the population into six classes. That is; susceptible(S), vaccinated (V), infective (I), hospitalized (H), home based care (H_B) and recovery(R). We have formulated non-linear system of differentials equation governing the model to compute and solve using quantitative analysis. Feasibility region, positivity of model variable, disease free equilibrium and local stability of the model are discussed. The solution has been computed using numerical classical fourth order Runge Kutta integration method to gauge its effectiveness. The model monitor reproduction number $R_O$which describe the dynamics of the Covid-19.The disease fee equilibrium is local asymptotically stable when $R_o < 1$ and unstable when $R_o > 1$. MAPLE will be used to carry out the simulation and graphical results, then presented and discussed to explain the solution of the problem.

Keywords: Covid-19 model, Basic reproduction number,qualitative analysis.

INTRODUCTION

Coronavirus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus. The global spread of SARS-CoV-2 and thousands of deaths caused by coronavirus disease led World Health Organization to declare a pandemic on 12 march 2020[2].In Kenya ,we got over 250K confirmed cases of Covid-19 and more than 5150 deaths while in the whole world it's 219M total cases and 4.55m deaths case reported to WHO.As of 27 September 2021[3]. Covid-19 is mainly transmitted from person-to-person via respiratory droplets from infectious person .The best way to prevent and slow down transmission is to be well informed about the disease and how the virus spreads most people infected with the virus will experience mild to moderate respiratory illness and recover without requiring special treatment. However, some will become seriously ill and require medical attention. Older people and those with underlying medical conditions like cardiovascular disease, diabetes, chronic respiratory disease, or cancer are more likely to develop serious illness. Anyone can get sick with COVID-19 and become seriously ill or die at any age. To prevent infection and to slow transmission of COVID-19, the following can be done: Get vaccinated, Stay at least 1 meter apart from others, even if they don't appear to be sick, wear a properly fitted mask when physical distancing is not possible or when in poorly ventilated settings, Choose open, well-ventilated spaces over closed ones. Open a window if indoors, Wash your hands regularly with soap and water or clean them with alcohol-based hand rub, Cover your mouth and nose when coughing or sneezing and If you feel unwell, stay home and self-isolate until you recover. Vaccination is a simple, safe, and effective way of protecting you against harmful diseases, before you come into contact with them. It uses your body's natural defenses to build resistance to specific infections and makes your immune system stronger. Vaccines train your immune system to create antibodies, just as it does when it's exposed to a disease. However, because vaccines contain only killed or weakened forms of germs like viruses or bacteria, they do not cause the disease or put you at risk of its complications. The first mass vaccination programmer started in early December 2020 and the number of vaccination doses administered is updated on a daily basis website of world health organization provided by department of the Ministry of Health in each country. At least 13 different vaccines (across 4 platforms) have been administered. A total of 3712030 vaccine doses has been administered. Since the vaccination was introduces in Kenya daily cases reduced. Upton date over 1M have receive the first dose and over 450k have been vaccinated fully. This study as allow us to examined and analyzed the Covid-19 model to monitor disease in presence of consistent preventive vaccination. Those with covid-19 can take medication in home-based care or in the hospital. We have monitor recovery rate for those getting treatments after being vaccinated.The rest of the paper is organized as follows; the Covid -19 model formulated in section 2 and model properties analyzed in section 3,Qualitative analysis at section 4 where numerical simulation is performed to support theoretical results. The conclusion is provided in section 6.

Covid -19 model formation

The model is divided into six sub-classes according to their disease status and the movement between them from the human population(N); that is, susceptible(S),vaccinated(V), infectived (I), hospitalized(H), home base care(H_B) and recovered(R) compartment. The model assumes that a fraction of the population has been recruited to susceptible individuals which are those likely to be affected by Covid-19.

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The infective individual is those who have been infected with covid-19.The home based care individuals are contracted the covid-19 disease and they are taking medication at home prescribed by qualified medical personnel. The hospitalized individuals are those infected by the covid-19 disease and admitted in medical facility and attended by qualified health facilities. The recovered individuals are those who get well after a corona infection and tested negative. Vaccinated individuals are recruited into the population at the rate of $\boldsymbol{\varphi}$ and the supceptibe individual can be recruited at the rate of$(1-\boldsymbol{\varphi})$**.** The susceptible individual can be vaccinated at the rate of $\boldsymbol{q}$ and those vaccinated can be infective at the rate of $\boldsymbol{p}$ or recover at contact rate of Θ. The infected individual can be recruited at the rate of β from susceptible class. The rate at which the infected can either get treatment over covid-19 and be home based care and being attend by qualified doctors at the rate of $\boldsymbol{\omega}$or received treatment in hospital at the rate$\boldsymbol{\kappa}$.The rate at which the hospitalizes recover is $\boldsymbol{\varepsilon}$ while the rate at which those on home –based care recover is χ.The recovered individual can attained permanent immunity of which when they carry the covid-19 test negative at the rate δ.The infected individual can recover at contact rate $\boldsymbol{\delta}$ .The model takes In account both death cause by nature μ and caused by corona virus at the rate of α_1, α_2 *and* $\alpha_3$under the assumption that all the parameters are constant. The total population **N= S+V+I+H+**H_B**+R** and all rates are between zero to one.

From the Covid-19 model flow diagram of the disease transmission mechanisms Figure 1, we derive the following are non-linear system of ordinary differential equations:

$$\begin{cases} \frac{dS}{dt} = (\mathbf{1}-\boldsymbol{\varphi})\Lambda + \pi R - (\beta SI + qS + \mu S) \\ \frac{dV}{dt} = \boldsymbol{\varphi}\Lambda + qS - (p + \Theta + \mu)\mathrm{V} \\ \frac{dI}{dt} = \beta SI + \mathrm{pV} - (k + \omega + \delta + \mu + \alpha_1)I \\ \frac{dH_B}{dt} = \omega\mathrm{I} - (\chi + \mu + \alpha_2)H_B \\ \frac{dH}{dt} = \mathrm{kI} - (\varepsilon + \mu + \alpha_3)\mathrm{H} \\ \frac{dR}{dt} = \varepsilon H + \chi H_B + \Theta\mathrm{V} + \delta\mathrm{I} - (\pi + \mu)\mathrm{R} \end{cases} \quad (1)$$

with initial condition S (0) =S_0 ,V(0)=V_0 $I = 0$ H = 0 H_B = 0 R=0≥0 and N=S+V+I+H+H_B+R

A sum of the model in equation (1) gives,

$$\frac{dN}{dt} = \Lambda - \mu N + (H + H_B)\alpha \quad (2)$$

All the model parameters and their description, values and the source are presented in Table 1 below;

Table 1. Summary of parameter descriptions

Parameter interpretation	Values per day	Source
$\boldsymbol{\Lambda}$ Recruitment rate	10	Estimated
$\boldsymbol{\beta}$ Rate of recruitment to infective class from susceptible	0.5787	Estimated
q Rate of recruitment to vaccination from susceptible	0.4213	Calculated
k Rate of recruitment to hospital treatment from infective class	0.5493	calculated
$\boldsymbol{\omega}$ Rate of recruitment to home based care from infective class	0.9506	Estimated
$\boldsymbol{\alpha_1}$Death rate at infective as a results of covid-19	0.009	Estimated
$\boldsymbol{\alpha_2}$Death rate at home based care as a results of covid-19	0.007	Estimated
$\boldsymbol{\alpha_3}$Death rate at hospitalization as a results of covid-19	0.00961	(parra, 2021)
$\boldsymbol{\mu}$ Death rate as a results of natural calamities	0.00411	(Deressa, 2020)
$\boldsymbol{\varepsilon}$Recovery rate of hospitalized covid-19 patients	0.15	Calculated
X Recovery rate of home based care individual	0.1612	Calculated
$\boldsymbol{\pi}$ Rate at which recovery individual can be susceptible	0.1	Estimated
$\boldsymbol{\delta}$ Rate at which infective individual can recover	0.189	Calculated
$\boldsymbol{\rho}$ Rate at which vaccinated individual can be infective	0.2	Estimated

BASIC MODEL PROPERTIES

Feasible region

We seek a region in which the model system solutions are non-negative and uniformly bounded. The feasible region of model variables in (1) in$\mathbb{R}^{\mathbf{6}}$ are confined in the region

$$\Omega = (\mathrm{S}, \mathrm{V}, \mathrm{I}, \mathrm{H}, H_B, \mathrm{R}) \in \mathbb{R}^6 : 0 \leq \mathrm{S} + \mathrm{V} + \mathrm{I} + \mathrm{H} + H_B + \mathrm{R} \leq \aleph e^{(1-\mu)t} \quad (3)$$

So that the covid-19 model that is uniformly bounded for all time and biologically feasible.

Positivity of the model

Theorem 1. Let the $\Omega=\{S_0, V_0, I_0, H_0, H_{B0}, R_0 \geq 0\} \in \mathbb{R}^6$ then the solution set $\{ S_t, V_t, I_t, H_t, H_{Bt}, R_t \}$ of a model is positive for all t >0.

The Disease Free Equilibrium point

In absence of corona infection, the system gives the existence of disease fee equilibrium.We assume that the susceptible individual receives constant vaccination against the Covid-19 disease for us to get DFE. Which is obtained by setting the equation(1) to zero i.e.

$$\frac{dS}{dt} \; and \; \frac{dV}{dt} \neq 0, \qquad \frac{dI}{dt} = \frac{dH}{dt} = \frac{dH_B}{dt} = \frac{dR}{dt} = 0$$

Hence disease free equilibrium solution becomes $=(S_0 V_0 I_0 H_{B\,0} H_0 R_0)$

$\frac{(\mathbf{1}-\boldsymbol{\varphi})\Lambda}{q+\mu} = S_0$,

$\frac{\boldsymbol{\varphi}\Lambda}{\mu} = V_0$.

Thus $(\frac{(\mathbf{1}-\boldsymbol{\varphi})\Lambda}{q+\mu}, \frac{\boldsymbol{\varphi}\Lambda}{\mu}, 0, 0, 0, 0)$.

The reproduction number

The Jacobian of model equation in (1) at DFE; (4)

The basic reproduction number of the model is established using Next generation matrix [4, 9, 28].We find a matrix FV^{-1}which defines the rate of appearance of new infections and the rate of transfer of individuals.

$$F=\begin{bmatrix} \beta SI \\ 0 \\ 0 \end{bmatrix},$$

$$V=\begin{bmatrix} \mathrm{pV} - (k+\omega+\delta+\mu+\alpha_1)I \\ \omega \mathrm{I} - (\chi+\mu+\alpha_2)H_B \\ \mathrm{kI} - (\varepsilon+\mu+\alpha_3)\mathrm{H} \end{bmatrix} \text{ thus } FV^{-1} = \begin{bmatrix} \frac{\beta S_0}{k+\omega+\delta+\mu+\alpha_1} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

thus the effective reproduction number is given by

$$R_O = \frac{\beta(\mathbf{1}-\boldsymbol{\varphi})\Lambda}{(k+\omega+\delta+\mu+\alpha_1)(q+\mu)} \qquad (5)$$

The effective reproduction number is defined as the mean number of new covid-19 infectionsin which a covid-19 infected individual gets introduced to fully susceptible population or vaccinated population.

Local stability of disease free equilibrium

Theorem 2. The disease free equilibrium is locally asymptotically stable if R_O<1 and unstable ifR_O>1. Local stability of an equilibrium point of Covid -19 means that if you put the system somewhere nearby the point then it will move itself to the equilibrium point in some time hence infection may not grow.

$$J_{DFE} = \begin{bmatrix} -(q+\mu) & 0 & -B(\frac{(\mathbf{1}-\boldsymbol{\varphi})\Lambda}{q+\mu}) & 0 & 0 & \pi \\ q & -(q+\rho+\mu) & 0 & 0 & 0 & 0 \\ 0 & \rho & B(\frac{(\mathbf{1}-\boldsymbol{\varphi})\Lambda}{q+\mu}) - (k+\omega+\delta+\mu+\alpha_1) & 0 & 0 & 0 \\ 0 & 0 & \omega & -(x+\mu+\alpha_2) & 0 & 0 \\ 0 & 0 & k & x & -(x+\mu+\alpha_3) & \delta \\ 0 & \phi & \delta & 0 & \varepsilon & -(\pi+\mu) \end{bmatrix}$$

Which yields the following eigenvalues ; $\begin{pmatrix} -(q+\mu) \\ -(x+\mu+\alpha_2) \\ -(x+\mu+\alpha_3) \\ -(\pi+\mu) \\ -(q+\rho+\mu) \\ B\frac{(1-\varphi)\Lambda}{q+\mu} - (k+\omega+\delta+\mu+\alpha_1) \end{pmatrix}$

The five eigenvalues are negative hence to make the system stable we need to have $B\frac{(1-\varphi)\Lambda}{q+\mu} - (k+\omega+\delta+\mu+\alpha_1) > 0$ .In conclusion , if $B\frac{(1-\varphi)\Lambda}{q+\mu} > (k+\omega+\delta+\mu+\alpha_1)$,this means the disease free equilibrium is asymptotically locally stable.

Global stability of disease free equilibrium

Theorem 3. Global stability means that the system will come to the equilibrium point from any possible starting point. The stability at the equilibrium points is analyzed based on the Lyapunov invariance principal, the uninfected equilibrium point is proven to be globally asymptotically stable when the reproduction number is less than one and unstable otherwise.

L=$\frac{1}{k+\omega+\delta+\mu+\alpha_1} l_c$

Then

$\frac{dL}{dt} = \frac{1}{(k+\omega+\delta+\mu+\alpha_1)(q+\mu)}\frac{dc}{dt} = \frac{1}{k+\omega+\delta+\mu+\alpha_1}(Bsl_c - (k+\omega+\delta+\mu+\alpha_1)(q+\mu)l_c) = \frac{Bsl_c}{(k+\omega+\delta+\mu+\alpha_1)(q+\mu)} - l_c \leq 0$
(6)

Thus ,the system globally asymptotic stability.

Endemic equilibrium

Let denote **t**he endemic equilibrium by $E*$and defined as a steady state solution for the Model. This can occur when there is a persistence of the disease. It can be obtained by equating the system of equation to zero.

Hence $E* = (S*; V*; H_B*; H*; I*; R*)$ is the endemic equilibrium of the model

Local stability of endemic equilibrium (EE)

Theorem If R_o>1 then the endemic equilibrium $Eu=(S^*, V^*, I^*, H_B{}^*, H^*, R^*)$of the governing model differential equation (1) will be asymptotically stable. Using the Jacobian approach method.

$$J_{E^u} = \begin{bmatrix} -BI^* - q - \mu & 0 & -BS^*I^* & 0 & 0 & \pi \\ q & -(q+\rho+\mu) & 0 & 0 & 0 & 0 \\ BI^* & \rho & BS^*I^* - (k+\omega+\delta+\mu+\alpha_1) & 0 & 0 & 0 \\ 0 & 0 & \omega & -(x+\mu+\alpha_2) & 0 & 0 \\ 0 & 0 & k & 0 & -(x+\mu+\alpha_3) & \delta \\ 0 & \phi & \delta & x & \varepsilon & -(\pi+\mu) \end{bmatrix}$$

We show the stability of the matrix J_{E^u} by verifying the Rourth-Hurwitz conditions, that is, all the roots of the resulting characteristic equations must have negative real part. The charectaristic polynomial of Jacobian matrix at E^u is given by det$J_{E^u} - \lambda \mathrm{I} = 0$. Where λ is the eigenvalue and I is 6× 6 identity matrix .Thus,

$$[J_{E^u} - \lambda \mathrm{I}] = \begin{bmatrix} -BI^* - q - \mu & 0 & -Bs^*I^* & 0 & 0 & \pi \\ q & -(q+\rho+\mu) & 0 & 0 & 0 & 0 \\ -BI^* & \rho & -Bs^*I^* - (k+\omega+\delta+\mu+\alpha_1) & 0 & 0 & 0 \\ 0 & 0 & \omega & -(x+\mu+\alpha_2) & 0 & 0 \\ 0 & 0 & k & 0 & -(x+\mu+\alpha_3) & \delta \\ 0 & \phi & \delta & x & \varepsilon & -(\pi+\mu) \end{bmatrix}$$

$= -Bs^*I^* - (k+\omega+\delta+\mu+\alpha_1) - \lambda 1[(x+\mu+\alpha_2) - \lambda 2[-(x+\mu+\alpha_3) - \lambda 3][-(\pi+\mu) - \lambda 4]]$
$\lambda 1 = -(k+\omega+\delta+\mu+\alpha_1) < 0$
$\lambda 2 = -(x+\mu+\alpha_2) < 0$
$\lambda 3 = -(x+\mu+\alpha_2) < 0$
Meaning $\lambda 4,5,6 < 0$ (all roots are negative).
Hence by Routh-Hurwitz criteria as in Boyce et-al. (2001), we have that the eigenvalues of J_{E^u} has negative real part when vaccination reproduction number $R_0 > 1$. This shows that the endemic equilibrium E^u is locally asymptotically stable.

Global stability of endemic equilibrium

We determine the global stability of the endemic equilibrium E^u by defining the following Lyapunov function:

$V(S^*V^*I^*H_B{}^*H^*R^*)=(S-S^*-S^*log\frac{S^*}{s})+(V-V^*-V^*log\frac{V^*}{V})+(I-I^*-I^*log\frac{I^*}{I})+(H_B-H_B{}^*-H_B{}^*log\frac{H_B{}^*}{H_B})+(H-H^*-H^*log\frac{H^*}{H})+(R-R^*-R^*log\frac{R^*}{R})$...V is positive definite since V=0 when$(S, V, I, H, H_B, R) = (S^*, V^*, I^*, H_B{}^*, H^*, R^*)$ and V>0 otherwise;We also note that V is radically unbounded. Hence, V is a Lyapunov function.

We also prove that, the derivative of V with respect to t is negative.

The derivate of V, $V' =(\frac{S-S^*}{S})S'+(\frac{V-V^*}{V})V'+(\frac{I-I^*}{I})I'+(\frac{H_B-H_B{}^*}{H_B})H_B{}'+(\frac{H-H^*}{H})H'+(\frac{R-R^*}{R})R'$

Hence $V' =(\frac{S-S^*}{S})[\ (\mathbf{1}-\boldsymbol{\varphi}\ )\Lambda+\pi R-(\beta I+q+\mu)]\ +(\frac{V-V^*}{V})\ [(\boldsymbol{\varphi}\Lambda+qS-(p+\Theta+\mu)]\ +(\frac{I-I^*}{I})\ [\beta SI+\mathrm{pV}-(k+\omega+\delta+\mu+\alpha_1)]+(\frac{H_B-H_B{}^*}{H_B})\ [\omega\mathrm{I}-(\chi+\mu+\alpha_2)]\ +(\frac{H-H^*}{H})\ [\mathrm{kI}-(\varepsilon+\mu+\alpha_3)]\ +(\frac{R-R^*}{R})\ [\varepsilon H+\chi H_B+\Theta\mathrm{V}+\delta\mathrm{I}-(\pi+\mu)]$ Or $V'=F-G$

Where F is positive terms and G is negative terms of the equation. Hence F<G in the equation above, then we have that $V'=0$. We also note that $V'=0$ if and only if $S=S^*, V=V^*, I=I^*, H_B=H_B{}^*, H=H^*, R=R^*$.

Thus E^u is the endemic equilibrium of the model. Boyce et-al.(2001) and is globally asymptotically stable if F<G.

QUALITATIVE ANALYSIS OF THE MODEL

We perform the qualitative analysis on the mathematical differential equation (1) .we make use of the parameters given in table 2 for simulation. We investigate the impact of vaccination on mitigating the spread of covid-19 using the classical fourth order Runge-Kutta method .The method yields rapidly convergent solutions, reliable, effective and yields higher accuracy if a small step-size, h is employed for both linear and non-linear deterministic equations [20].

Table 1. Table showing initial value

Parameters	Values
S(0)	1400
V(0)	300
I(0)	150
$\boldsymbol{H_B}(0)$	200
H(0)	250
R(0)	100

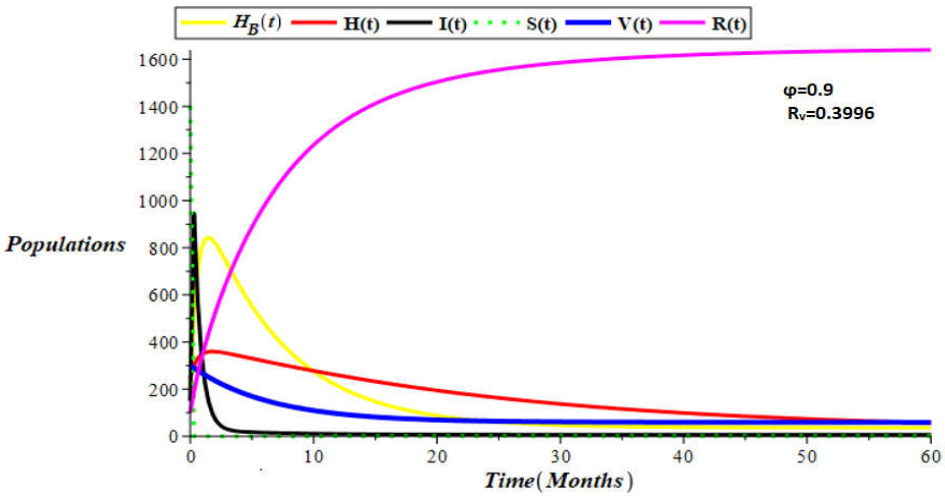

Figure 1. simulation for population dynamics with low vaccination coverage

Fig 1 demonstrates the impact of high vaccination coverage on the disease free initial population dynamics. The total population is assumed that at the initial year all the human population is susceptible to the covid-19 disease; this implies that all individuals are likely to be affected by the disease. We note that the population of the susceptible individuals decreases with time while that of the Recovered group gradually increases due to recruitment of vaccinated susceptible individuals. The population of individuals under treatment both in hospital and those under home based care decrease gradually due to high vaccination rate. It is very interesting to note that with an initial low number of infective populations the covid-19 disease gradually grows until it attains a peak value

then decreases gradually to disease Free State. The exponential rise of infections initially is due to recruitment of susceptible as a result of high force of infection witnessed in covid-19 disease. The sharp decrease from peak to disease free state is due to treatment and high vaccination coverage (φ= 0.9). The Population eventually attains disease free with all the time.

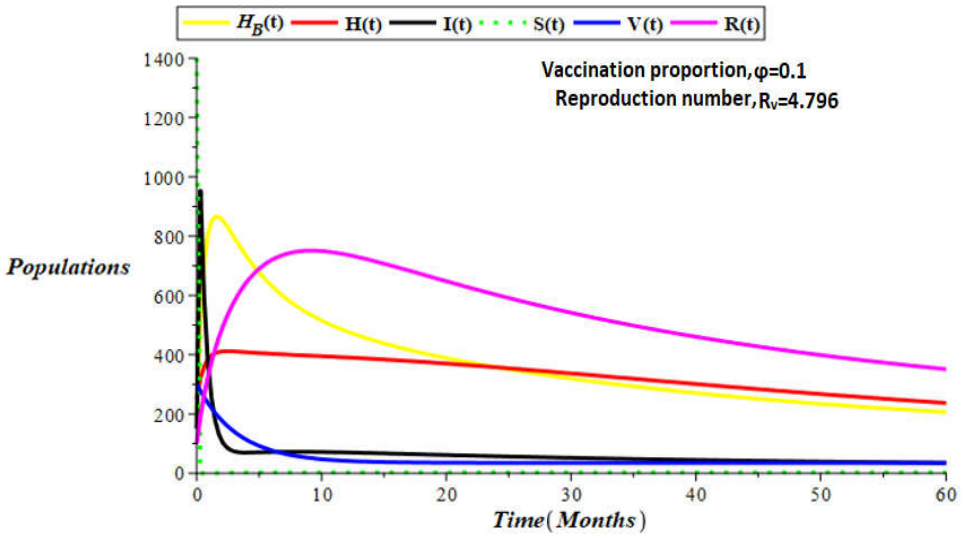

Figure 2. Simulation for population dynamics with low vaccination coverage

Fig 2 shows the effect of low vaccination proportion on the dynamics of population with low number of infective present in the community. The population of the susceptible group reduces gradually with time as well as small increase in the population of recovered group is noted. There will be high reproduction number. However, it is important to observe that the population of infective may never disappear with time and the endemic state will not be achieved. This demonstrates that a disease free equilibrium only occurs when "R> 0". Hence, low vaccination coverage level, " R<0 " leads to persistence of the covid-19 disease in the Community with the endemic state beings stable asymptotically.

Conclusion

A $SVIHH_BR$ deterministic model formulated that monitors the temporal dynamics of covid-19 disease in the presence of preventive vaccination. The mathematical analysis was done using ordinary differential equation(ODE).The data used in simulation is based on the disease spread in kenya early 2022.The model incorporates the fact that susceptible are infectious to the community. We prove the existence of the feasible region that is mathematically is non-negative and uniformly bounded. The model has positive parameters and variables since we are dealing with human population. The existences of diseases free and endemic equilibrium were also determined. The model is theoretically analyzed; its effective and basic reproduction numbers are derived. The model fits quite well the observed daily data of covid-19 from Kenya early this year disease eradication. It is observed that, when $R_O < 1$ the disease free equilibrium is locally asymptotically stable and the disease could be eradicated otherwise is unstable. The behavior of the system further confirms the situation in Kenya. The equations indicate that the covid-19 disease is declining with a very high number of individuals recovery. The critical vaccination threshold is derived, and it is noted that if the vaccine efficiency is low and the disease reproduction number is high, the disease may not be eradicated even if a large proportion of the population is vaccinated. The global stability of endemic equilibrium is attain if vaccination reproduction number is greater than unity. Fourth order Runge-Kutta method are employed to solve numerical simulation of the model. The computation indicates that covid-19 can be controlled in the community with the implementation of vaccination and treatment while our results suggest that vaccination will reduce the spread of disease.

Conflict of Interests: The authors declare no conflicts of interests.

Data Availability: The covid-19 model data were obtained from published articles, reported studies and Kenya covid-19 data between January to march 2022. Some of the parameter values are estimated.

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