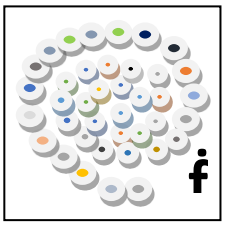

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Mathematical model for COVID-19 transmission with impact of vaccination

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Abstract

The novel coronavirus disease (COVID-19) caused by SARS-CoV-2 remains a major public health concerned globally. In this article, we developed and analyzed an epidemic model of COVID-19 with impact of vaccination governed by a five system of ordinary differential equations. The developed model is analyzed and the threshold quantity known as the effective reproduction number R_V is obtained by using the next generation matrix. We investigate the equilibrium stability of the system, and the disease-free equilibrium is said to be locally asymptotically stable when the effective reproduction number is less than unity, and unstable otherwise. It is observed that the system undergoes the phenomenon of backward bifurcation. Numerical simulations of the overall system are implemented in MATLAB for demonstration of the theoretical results.

Keywords: Covid-19; vaccination; effective reproduction number; backward bifurcation

1 Introduction

Coronavirus disease (COVID-19) is a contagious disease caused by the virus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). It has caused a worldwide crisis due to its effects on society and global economy. The World health organization (WHO) declared COVID-19 as a worldwide health hazard at beginning of 2020. The first scenario was observed in China (Wuhan) (Wang et al., 2020).

As a result of the absence of specific anti-COVID-19 medical treatments, some countries had been relying on non-pharmaceutical interventions, such as wearing of face masks, social/physical distancing, partial/total lockdown, travel restrictions, and closure of schools and work centers, in order to curtail the spread of the disease before December 2020 However, these measures have been insufficient to control the pandemic globally as medical facilities were overstretched and death

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toll heightened (Pérez & Oluyori, 2021). In order to defeat COVID-19 like a pandemic, suitable vaccination strategies are essential to be implemented with non-pharmaceutical interventions (Das et al., 2021). The best way to prevent and slow down transmission is to be well informed about the disease and how the virus spreads. Protect yourself and others from infection by staying at least 1 metre apart from others, wearing a properly fitted mask, and washing your hands or using an alcohol-based rub frequently. Get vaccinated when it's your turn and follow local guidance (WHO,2022)

Covid-19 vaccines remain extensive measures that carried a significant socioeconomic impact to defeating pandemic. There are 13 types of COVID-19 vaccines that have been administered, 132 vaccines are in clinical development, and 194 more vaccines are in pre-clinical development. On 16 November 2021, there are 4,132,325,886 people who have taken at least one dose of vaccine inoculation, and 3,251,575,096 people have received two-shot vaccination, making up 52.47% and 41.29% of the world's total population, respectively (Guo et al., 2022). However, the administered vaccines have various efficacy's levels. COVID-19 vaccines authorized by WHO are mostly effective at reducing the risk of developing serious illness and death but does not provide 100% full protection WHO. In this situation depending on vaccination only for the controlling or eliminating the disease cannot give a full protection for the population against the disease. Various mathematical models have been developed to quantitatively investigate and predict the trends in the transmission of COVID-19 under several vaccination setting. See (Iboi et al., 2020; Pérez & Oluyori, 2021),(Benahmadi et al., 2022; Zhao et al., 2021). These studies suggest that, even with a large-scale vaccination program, non-pharmaceutical interventions are still needed to effectively curb the spread of the disease.

The subsequent part of the paper are as follows: In Section 2, the model of interest is formulated. In Section 3, basic qualitative properties, including positivity and boundedness of model solutions, stability of equilibrium points of the model, are discussed. In Section 4, the model is numerically simulated to illustrate the analytical results obtained and to study the impact of model parameters on model result behavior. Finally, in Section 5, we present our conclusion from our study.

2 Model development and fundamental properties

In this section, we develop a COVID-19 infection model to investigate the vaccination. The total host population has been categorized into five compartments representing a sub-population: susceptible (S), vaccinated (V) exposed (E), infected (I) and recovered(R). In this study, the total population is assumed to be constant (N), μ is the natural death rate. The recruitment rate is Λ and β is the effective contact rate. The rate at which the latently infected population progresses to active COVID-19 compartment is κ and γ is the rate of recovery and death rate caused by COVID-19 is δ, It is possible that recovered individuals acquire certain level of immunological memory for a certain duration (Wangari, 2022; Wangari et al., 2021) and we assume that recovered individuals are losing immunological memory at a rate of $(1-\alpha)\beta$ where $0<\alpha<1$. The vaccine coverage rate is ν and vaccinated individuals can get infected with force of infection $(1-\eta)\beta I$ where η is the vaccine efficacy. The value of η is between 0 and 1 with $\eta=1$ means perfect vaccine and $\eta=0$ means that the vaccine is not effective. Here we assume that the vaccine is imperfect, that is a vaccinated individual is not completely protected and can still become infected when they come in

contact with an infected person. We also assume that the vaccination can fail, i.e., vaccinated individual goes back to become susceptible at the rate ρ.

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \beta IS + \rho V - (\nu + \mu)S, \\
\frac{dV}{dt} &= \nu S - (1-\eta)\beta IV - (\rho + \mu)V, \\
\frac{dE}{dt} &= \beta IS + (1-\eta)\beta VI + (1-\alpha)\beta IR - (\kappa + \mu)E, \\
\frac{dI}{dt} &= \kappa E - (\mu + \gamma + \delta)I, \\
\frac{dR}{dt} &= \gamma I - (1-\alpha)\beta IR - \mu R.
\end{aligned} \tag{1}$$

$N = S + V + E + I + R,$
with the initial conditions

$$S(0) = S_0 \geq 0, V_0 \geq 0, E(0) = E_0 \geq 0, I(0) = I_0 \geq 0, R(0) = R_0 \geq 0. \tag{2}$$

We assumed that all the parameters of system (1) are positive when time t > 0. In the following subsections, we discussed the clinical assumptions of the proposed model.

1. There is a constant recruitment rate to the susceptible population and natural cause death affects individuals in all compartments, with an extra COVID-19-induced death rate in the infected class.
2. Some susceptible individuals who have been successfully vaccinated lose their vaccine induced immunity (i.e., vaccine failed), and these previously vaccinated individuals join the susceptible compartment again at the rate ρ.
3. Those in the vaccination class are not at a completely protective level, due to the imperfect vaccine. The vaccinated individuals become infected and move into the exposed class. We assume that this occurs at a lower transmission rate $\eta\beta$, where $\eta \in [0,1]$ is the decrease coefficient.
4. The individuals in the susceptible class move to the exposed class with the transmission rate β.
5. The individuals in the exposed class become infectious and move to the infected class. After recovery, they move to the recovered compartment at the rate α, where $0 < \alpha \leq 1$.

2.1 Basic properties

The following theorem guarantees the non-negativity of the solutions to system (2).
Theorem 1 Given the initial conditions
conditions $S(0) = S_0 \geq 0, V(0) = V_0 \geq 0, E(0) = E_0 \geq 0, I(0) = I_0 \geq 0, R(0) = R_0 \geq 0,$ the solution of system (1), namely $S(t), V(t) E(t), I(t)$ and $R(t)$ remains in the non-negative region for all t > 0.

Proof :The method described in (Ullah et al., 2023), is applied. We use the first equation to consider the non-linear system of (1), which clearly shows that

$$\frac{dS}{dt} + (\lambda(t) + \mu)S > 0 \tag{3}$$

by utilizing integrating factor gives

$$\frac{d}{dt}\left[S \exp\left(\int \left(\lambda(\varepsilon) + \mu \right) d\varepsilon \right] > 0. \right. \tag{4}$$

Using the initial conditions and integrating (4) results in

$$S(t) > S_0 \exp\left[-\left(\int_0^t \lambda(\varepsilon) + \mu \right) d\varepsilon \right] > 0.$$

In a similar way one can easily deduce that the other state variables are also non-negative for $t > 0$. Hence the required result is obtained.

Next, we establish the boundness the solutions of system (1) via the following theorem.

Theorem 2 The solution of system (2) is strictly contained in the bounded region

$$\Omega = \left\{ (S, V, E, I, R) \in \Re^5 : S + V + E + I + R \le \frac{\Lambda}{\mu} \right\}.$$

Proof: Summing both sides of system (2) give

$$\frac{d(S + V + E + I + R)}{dt} = \frac{dN}{dt} \le \Lambda - N - \delta I. \tag{5}$$

If there is no death from COVID-19, then the equation (5) above becomes

$\frac{dN}{dt} \le \Lambda - \mu N$, which is solves

$$0 \le N \le \frac{\Lambda}{\mu} + N(0)e^{-\mu t},$$

where $N(0)$ is the initial value of the total population, assumed to be non-negative. Therefore, if $S(t), E(t), I(t)$ and $R(t)$ are inside of Ω, then $S(t), E(t), I(t)$ and $R(t)$ will stay within Ω as $t \to \infty$. Likewise, if the initial condition starts outside of Ω, then the solution will approach Ω as $t \to \infty$. That completes the prove of the theorem 2.

2.3. Equilibrium and the basic reproduction number

With a straightforward calculation, system (2) has a unique disease-free equilibrium as follows.

$$T_0 = (S_0, V_0, E_0, I_0, R_0) = \left(\frac{\Lambda(\mu+\rho)}{\mu(\mu+\rho+\nu)}, \frac{\Lambda\nu}{\mu(\mu+\rho+\nu)} 0, 0, 0 \right). \quad (6)$$

Employing the next-generation matrix (Van den Driessche & Watmough, 2002; Wangari et al., 2021), the basic reproduction number (R_0) of system (2) is given by

$$R_V = \frac{\beta\kappa\Lambda(\mu+\rho+\nu-\eta\nu)}{(\kappa+\mu)(\mu+\gamma+\delta)(\mu+\rho+\nu)}. \quad (7)$$

2.4 Local Stability of the disease-free equilibrium

To establish the local stability of the DFE, the Jacobian of the model is considered. The characteristic equation is then derived from the Jacobian and thus the result of the eigenvalue is obtained.

Theorem 3. The DFE of COVID-19 model (2) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

To establish the local stability of the system, the Jacobian of the COVID-19 model (1) is evaluated at DFE which is given by:

Proof: The prove of the local stability of disease-free equilibrium is obtained by first computing the Jacobian matrix of the system (1) at the DFE T^0. The first three eigenvalues of the Jacobian matrix at the DFE are $\lambda_1 = -(\mu+\nu), \lambda_2 = -\mu, \lambda_3 = -(\mu+\nu+\rho),$ while the other two eigenvalues 4 and 5 are the solutions of the quadratic equation $F_0\lambda^2 + F_1\lambda + F_2 = 0,$ where $F_0 = 1, F_1 = 2\mu+\kappa+\delta$ = 1, and $F_2 = (\kappa+\mu)(\mu+\gamma+\delta)(1-R_V)$. Applying Routh-Hurwitz criteria (Patil, 2021) on this quadratic equation shows that 4 and 5 have negative real parts. Since all the eigenvalues are either negative or they have negative real parts, it shows that the DFE point is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$.

3 Endemic equilibrium point and bifurcation analysis

The endemic equilibrium of the model system (1) is denoted by $T^* = \left(S^*, V^*, E^*, I^*, R^*\right)$ and is determined by setting the right-hand side of model system one to zero:

$$\begin{aligned}
&\Lambda - \beta IS + \rho V - (\nu + \mu) S = 0,\\
&\nu S - (1-\eta)\beta IV - (\rho + \mu)V = 0,\\
&\beta IS + (1-\eta)\beta VI + (1-\alpha)\beta IR - (\kappa + \mu)E = 0,\\
&\kappa E - (\mu + \gamma + \delta)I = 0,\\
&\gamma I - (1-\alpha)\beta IR - \mu R = 0.
\end{aligned}$$

Thus, the endemic equilibrium of equation above is given as

$$T^* = \left(S^* = \frac{\Lambda\left[(1-\eta)\beta I^* + (\mu+\rho)\right]}{C_1 I^{*2} + C_2 I^* + C_3}, V^* = \frac{\nu\Lambda}{C_1 I^{*2} + C_2 I^* + C_3}, I^* = I^*, E^* = \frac{(\gamma+\mu+\delta)I^*}{\kappa}, R^* = \frac{\gamma I^*}{\mu + (1-\alpha)\beta I^*} \right),$$

where

$$C_1 = (1-\eta)\beta^2, C_2 = \left(\beta(\mu+\rho) + (\mu+\nu)(1-\eta)\beta\right), C_3 = \mu(\mu+\rho+\nu).$$

Substituting the values of $S^*, V^* E^*$ and R^* into equation(1), put the values of C_1, C_2 and C_3 and simplify, then I^* is gotten from the positive roots of the cubic polynomial:

$$f(I) = B_1 I^3 + B_2 I^2 + B_3 I + B_4, \tag{8}$$

where

$$\begin{aligned}
B_1 &= (1-\eta)\beta^3(1-\alpha)\left((\kappa+\mu)(\kappa+\mu+\delta)\kappa\gamma\right),\\
B_2 &= -\kappa\beta^3\Lambda(1-\alpha)(1-\eta) - \gamma(1-\alpha)\kappa\beta^2\left((\mu+\rho) - (\mu+\nu)(1-\eta)\right)\\
&+ (\kappa+\mu)(\gamma+\mu+\delta)\left(\mu(1-\eta)\beta^2 + (\mu+\nu)(1-\eta) + (1-\alpha)\beta^2(\mu+\rho)\right),\\
B_3 &= -\kappa\beta^2\Lambda(1-\eta)\mu - (1-\alpha)\kappa\beta^2\Lambda(\mu+\rho) - \gamma(1-\alpha)\kappa\beta\mu(\mu+\rho+\nu) - (1-\eta)\kappa\beta^2\nu\Lambda(1-\alpha)\\
&+ \left(\beta\mu(\mu+\rho) + \mu(1-\eta)\beta(\mu+\nu)\right)(\kappa+\mu)(\gamma+\mu+\delta)\\
&+ (1-\alpha)\beta\mu(\kappa+\mu)(\gamma+\mu+\delta)(\mu+\rho+\nu),\\
B_4 &= \mu^2 = (\mu+\rho+\nu)(\kappa+\mu)(\gamma+\mu+\delta)(1-R_V).
\end{aligned}$$

Here, R_V is the effective basic reproduction number given in (7). It is clear that I is given by the positive real roots of the polynomial (8). The number of possible positive real roots of the cubic polynomial (8) depends on the signs of B_2, B_1 and B_0 and B_0. This will be investigated by

employing Descarte's rule of sign. A number of possibilities are illustrated in Table 1. Therefore, the outcomes can be established by the following theorem.

Table 1: Number of Possible Positive Roots According to Descarte's Rule

Cases	B_1	B_2	B_3	B_4	R_V	Sign Changes	Total Possibility of Positive Roots
1	+	-	-	-	$R_V > 1$	1	1
2	+	+	-	-	$R_V > 1$	1	1
3	+	+	+	-	$R_V > 1$	1	1
4	+	-	+	-	$R_V > 1$	3	3,1
5	+	-	-	+	$R_V < 1$	2	2,0
6	+	+	-	+	$R_V < 1$	2	2,0
7	+	-	+	+	$R_V < 1$	2	2,0
8	+	+	+	+	$R_V < 1$	0	0

From Table 1, we can conclude the following:

1. A unique endemic equilibrium when $R_V > 1$ which satisfies case 1–3.
2. One or three endemics equilibrium when $R_V > 1$ and case 4 is satisfied.
3. Two endemic equilibria when $R_V < 1$ and this satisfies cases 5–7.
4. There is no endemic equilibrium when $R_V < 1$ which satisfies case 8.

Therefore, the results above indicate the possibility of backward bifurcation when either B_2 or B_3 is negative.

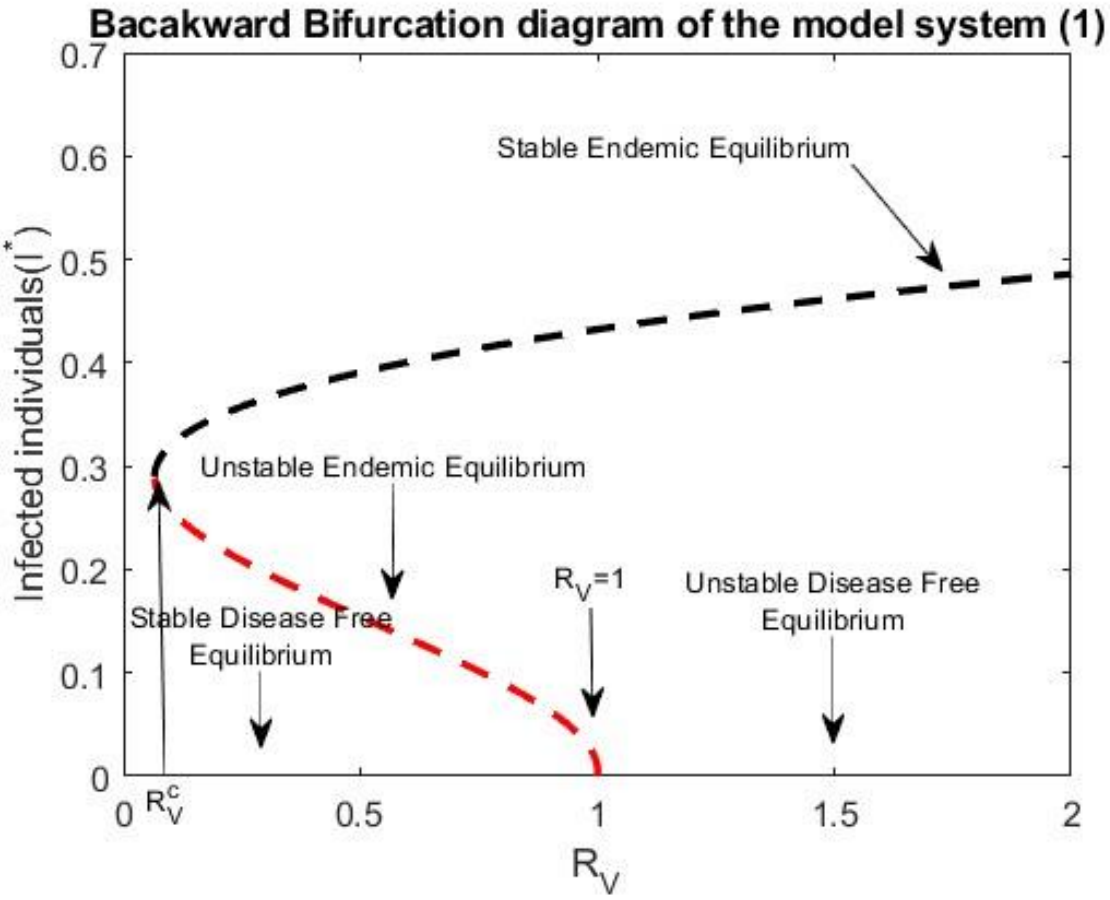

Figure 1: Graph of the value I^* in equilibrium versus R_V that shows a backward bifurcation diagram for the model (1) with parameters stated in Table (1)

Figure 1 illustrates the backward bifurcation diagram of the system (1) as the effective basic reproduction number R_V varies against the infected population (I). In this state, endemic equilibrium can exist when $R_V < 1$. More specifically, a bistability region exists for $0 < R_V^c < R_V < 1$. This occurred when a stable endemic equilibrium exists simultaneously with a stable DFE (see Figure 1). As R_V increases slightly above 1, a big jump in the number of infectives is observed, creating a hysteresis loop. From epidemiological perspective, once R_V crosses unity, it is no longer sufficient to reduce R_V to below unity to eradicate the disease. A disease-free state can only be achieved if the value of R_V is reduced further to below some critical value R_V^c.

5 Numerical simulations and discussion

The numerical results of the model system (1), is performed with the values of the parameters described in Table 2. We used ode45 solver in MATLAB which depends on the Runge-Kutta technique to stimulate model system (1) with the parameter values presented in Table 2, as well as the following initial conditions:

$S(0)=0.7, V(0)=0.2, E(0)=0.1, I(0)=0, R(0)=0.$

Table 2: Description and values of the parameters.

Parameter	Description	Value	**Reference**
β	**Effective contact rate**	**0.86 (0-1)**	**Varying**
Λ	Recruitment rate	**270**	**(Ahmad et al., 2022)**
κ	**Progression rate**	**0.19230**	**(Okuonghae & Omame, 2020)**
δ	**Disease induced death rate**	**0.0034**	**(Peter et al., 2023)**
μ	**Natural death rate**	$\frac{1}{65\times 365}$	**(Saha et al., 2022)**
γ	**Recovery rate**	**0.20**	**(Wangari, 2022)**
ρ	**Vaccine failure**	**0-1**	**Varying**
η	**Vaccine efficacy**	**0-1**	**Varying**
ν	**Vaccine coverage**	**0-1**	**Varying**
α	Rate of immunological memory loss	**0.533**	**(Wangari et al., 2021)**

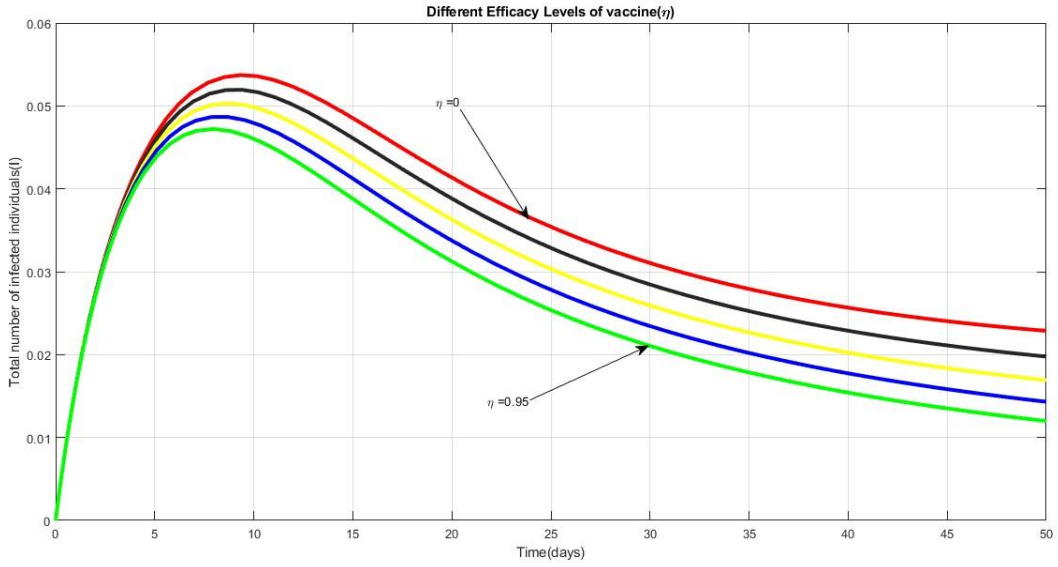

Figure 2: Impact of different efficacy levels of vaccine (η)

Figure 2 show the simulations of model system (1) using different values for the vaccine efficacy (η) on the infected individuals ranging from 0 to 0.95. From Figure 2, the highest value of (η) significantly reduced the spread of infection in a population, but did not completely lead to the elimination of COVID-19 infections.

6 Conclusion

In this article, we presented, a mathematical model of COVID-19 infection with impact of vaccination using deterministic approach. We showed that our proposed model has multiple disease-free equilibria and investigated the effective reproduction number, R_V employing the next-generation matrix approach. We showed that the set of disease-free equilibria is locally asymptotically stable when $R_V < 1$ and unstable when $R_V > 1$ Moreover, we demonstrated that the model system (1) underwent backward bifurcation, where the disease may persist in the population, even if the classical epidemiological criterion of $R_V < 1$ is fulfilled; although it was still necessary to effectively control the spread of COVID-19 in a population.

A backward bifurcation will make it a hatful difficult to control COVID-19 because a critical value of the R_V which is much less than 1 is needed to achieve disease-free state. The mathematical simulation of the model shows that the highest value of vaccine efficacy (η) significantly reduced the spread of infection in a population, but did not completely lead to the elimination of COVID-19 transmission. Thus, results suggested that vaccination alone is not sufficient for the elimination of COVID-19 infection.

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