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A MATHEMATICAL MODEL OF COVID-19 TRANSMISSION DYNAMICS WITH EFFECTS OF AWARENESS AND VACCINATION PROGRAM

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Abstract
This study introduces a deterministic mathematical model for understanding the transmission dynamics of COVID-19, considering the influence of vaccination and awareness program, which target susceptible individuals. The model is based on a system of differential equations, resulting in an SVEIR model. Through qualitative analysis, various aspects of the model, such as disease-free equilibrium, endemic equilibrium, basic reproduction number, and local and global stability, were thoroughly explored. The disease-free equilibrium is proven to be both locally and globally stable when $R_0 < 1$, while it ∼becomes unstable when $R_0 > 1$. Simulation results demonstrate that the combination of vaccination and awareness programs emerges as the most effective approach to mitigate the spread of COVID-19 within the population.

Keywords
mathematical model, basic reproduction number, vaccination, COVID-19, computer simulation

Introduction

The Covid-19 pandemic is a global pandemic caused by severe acute respiratory syndrome coronavirus (SAR-Covid-2). The new virus was named by International committee on Taxonomy of Viruses (ICTV) as "SARS-Covid-2" because the virus is genetically related to the coronavirus responsible for the SARS outbreak of 2003 (World Health Orgnaization, 2020). The recent pandemic was first identified in December 31st 2019 in Wuhan, the capital of Hubei, and has spread globally to become the the fifth documented pandemic since in the 1918 flu pandemic (Agbata et al., 2020; Nigeria Centre for Disease control, 2020). As of 19 September 2020, the disease was confirmed in more than 30.3 million cases reported globally in 188 countries and territories with over 949,000 deaths and over 206 million have fully recovered globally (Maclean and Dahir, 2020). The pandemic was first confirmed and announced in Nigeria on 27 February, 2020, when an Italian citizen in Lagos tested positive for the virus and the second case was reported on 9 March, 2020 in Ewekoro, Ogun State when a Nigerian citizen had contact with the Italian citizen (Maclean and Dahir, 2020; Nigeria Centre for Disease control, 2020). COVID-19 is spread from human to human through direct or indirect close proximity with contaminated surface, objects or with secretion droplets, saliva or respiratory secretions expelled from mouth or nose of an infected individual, it can also spread when an infected person coughs, sings, sneezes or speaks. The sign and symptoms of COVID-19 usually start two to 14 days after contact with infected person or contaminated surface, this period of time after exposure and before having symptoms is known as incubation period. Common sign and symptoms of Covid-19 include, cough, fever, tiredness, shortness of breath, sore throat etc. Older people with underlying medical challenges like serious heart diseases (heart failure, coronary arterial disease or cardionry-opatty), cancer, type 2 diabetes, sickle cell disease, high blood pressure easily contract the disease (John Hopkins University, 2020). According to WHO 2022 (World Health Organization, 2020), the number of new COVID-19 cases and deaths has continued to decline globally since end of March 2022. As at April 2022 through May first 2022, over 3.8 million cases and over 15000 deaths were reported, decreases of 17% and 3% respectively noted. Several authors have proposed mathematical model on COVID-19. Eikenberry et al. (2020) developed a mechanistic model to study the potential impact of the use of face-masks by the public to curtail the spread of the COVID-19 pandemic. Their results suggest that the use of face masks by public is potentially of high significance in curtailing the burden of the pandemic. The community-wide benefits are likely to be greatest when face masks are used in conjunction with other non-pharmaceutical practices (such as social or physical distancing), and high universal adoption and compliance. Salihu et al. (2012) formulated a mechanistic model which incorporates different hospitalization measures for mild and severe cases to assess the effect of awareness programs on the dynamics of COVID-19 infection. They fit the epidemic curve using Nigeria COVID-19 cases report published by Nigeria Center for Disease and Control (NCDC2020), accessed via https://covid19.ncdc.gov.ng/, and estimate some control parameters for COVID-19 epidemic in Nigeria and beyond. Their simulation results offer insights into the trends of COVID-19 epidemic in Nigeria, and as-

sess or evaluate the effect of awareness programs, as well as draw useful guidelines for the design of control and prevention strategies, their model framework can be applied to other countries, or be built into one multiple-patch model for modeling multiple countries context. They performed Sensitivity analysis of their model. Eikenberry et al. (2020) developed and analyzed a deterministic model which incorporates quarantine and hospitalization to estimate the transmission risk of the COVID-19 and its implication for public health interventions. Other relevant works on mathematical modelling include Agbata et al. (2019); Derrick and Groosman (1976); Diekmann et al. (1990); Lin et al. (2020); Ojih et al. (2019).

Aim and Objectives of the Study

The aim of this research work is to develop and analyze a mathematical model of COVID-19 transmission dynamics with effects of awareness and vaccination program while the objectives include: (1) to determine the effects of awareness and vaccination through numerical simulation. (2) to investigate disease free equilibrium and local stability of the model. (3) to compute the basic reproduction number (R_0) of the model and make useful recommendations.

Significance of the Study

The significance of the study include: (1) the study will educate the general public on prevention of COVID-19 through awareness and vaccination program.(2) the study will create awareness on COVID-19 which in return helps people to adhere to the preventive measures.(3) the study will form basis for further study in the field of epidemiology.

Materials and Methods

Model Formulation

In this work we formulate a simple modified (SVEIR) model for COVID-19 pandemic which Incorporates awareness and vaccination programs. The total population N(t) is divided into five epidemiological compartment including awareness and unaware susceptible individuals (S_{au}), vaccination individuals (v) exposed individuals (E) infected individuals (I) and Recovered individuals (R). π is the constant recruitment rate where the susceptible are recruited by birth and immigration. Furthermore, we assume that the susceptible individuals can be vaccinated at the rate θ_1 and vaccinated individuals can be susceptible again due to vaccine failure at the rate θ_2, the natural death rate μ is equal in all compartment. The susceptible individual can be exposed to the disease with rate ω_1 and exposed individual can be infected or recovered due to treatment with rates ϕ_1 and α_1 respectively. The infected individuals recovered with rate ϕ_2 and the recovered individuals can be susceptible to the disease again after recovered with rate α_2.

Model Assume Potions

The model is formulated under the following assumptions:

1. Sex, age, face and social status do not affect the probability of individuals being infected
2. The aware and unaware individuals can be vaccinated and the vaccinated individuals can be susceptible due to vaccine failure
3. The recruitment rate is through both birth and immigration
4. The recovered individuals can be susceptible to the disease again after recovered

Variables and Parameters Description

Table 1. Interpretation of the state variables and parameters used in the model

Variables	Description
$N(t)$	Total human population
$S_{au}(t)$	Aware and unaware susceptible individuals
$E(t)$	Exposed individuals
$I(t)$	Infected individuals
$R(t)$	Recovered humans
Parameters	
$\beta(t)$	Susceptible contact rare
σ	Modification parameter for decrease on infectiousness in S_a
$\mu(t)$	Natural death rate
$\omega(t)$	Rate at which susceptible individuals become exposed
$\phi_1(t)$	Rate at which exposed individuals become infected
$\phi_2(t)$	Recovery rate
$\phi_3(t)$	COVID-19 induced death rate
$\theta_1(t)$	Vaccination rate
$\theta_2(t)$	Rate at which vaccinated individuals become susceptible
$\pi(t)$	Recruitment rate
$\alpha_1(t)$	Rate at which exposed individuals recovered
$\alpha_2(t)$	Rate at which recovered individuals becomes susceptible

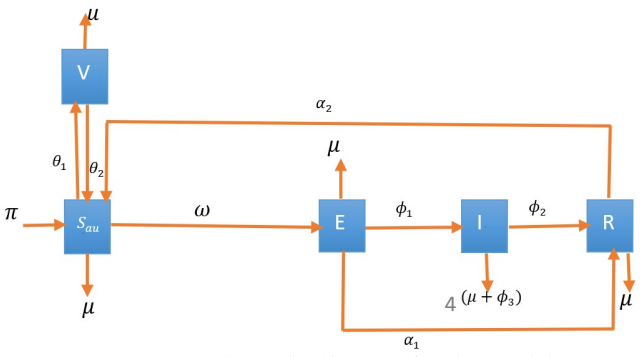

Figure 1. Schematic diagram for the model

$$\omega = \frac{\sigma\beta I}{N} S_{au} = S_a + S_u = S$$

Model Equations

From the mathematical assumptions and the schematic diagram above, have the following differential equations.

$$\begin{aligned}\frac{dS}{dt} &= \pi + \theta_2 V + \alpha_2 R - (\omega + \theta + \mu)S \\ \frac{dV}{dt} &= \theta_1 S - (\theta_2 + \mu)V \\ \frac{dE}{dt} &= \omega S - (\phi_1 + \alpha_1 + \mu)E \\ \frac{dI}{dt} &= \phi_1 E - (\phi_2 + \phi_3 + \mu)I \\ \frac{dR}{dt} &= \phi_2 I + \alpha_1 E - (\alpha_2 + \mu)R\end{aligned} \tag{1}$$

Invariant Region

The total population at times t is

$$\begin{aligned}N(t) &= S + V + E + R \\ \frac{dN}{dt} &= \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE}{dt} + \frac{dR}{dt}\end{aligned} \tag{2}$$

At steady state when there is no infection in the system and summing equation 1, then equation 2 becomes

$$\begin{aligned}\frac{dN}{dt} &= \pi - \mu S \\ \frac{dN}{dt} &= \pi - \mu N \text{ where } N = S \\ \pi - \mu N &= 0 \\ N &= \frac{\pi}{\mu}\end{aligned}$$

Theorem 1. *Solutions of the model system (1) are feasible for all $t > o$, if they enter the invariant region Ω_c.*

Proof Let $\Omega_c = (S,V,E,I,R) \in R_+^5$ be any solution of the model system (1) with non-negative initial conditions. From equation (2)

$$\begin{aligned}\frac{dN}{dt} &= \pi - \mu N \\ \frac{dN}{dt} + \mu N &= \pi\end{aligned}$$

Multiply both sides by ℓ^{ut} the integrating factor we have

$$\begin{aligned}\frac{dN}{dt}\left(e^{ut}\right) + \mu N\left(e^{ut}\right) &= \pi\left(e^{ut}\right) \\ d\left(Ne^{ut}\right) &\leq \pi e^{ut} dt \\ Ne^{ut} &\leq \frac{\pi e^{ut} dt}{\mu} + K_o \\ N(t) &\leq \frac{\pi}{\mu} + K_o e^{-ut}\end{aligned}$$

Applying the initial conditions

$$\begin{aligned}t(0) \leq N(0) \text{ we have} \\ N(0) &\leq \frac{\pi}{\mu} + K_o \\ N(0) - \frac{\pi}{\mu} &\leq K_o\end{aligned}$$

Therefore

$$N(t) \leq \frac{\pi}{\mu} + \left(N(0) - \frac{\pi}{\mu}\right)e^{-ut} \tag{3}$$

Hence the human population approaches the carrying capacity as $\frac{\pi}{\mu}$ as $t \longrightarrow \infty$ and the feasible solution set of model system (1) enter the invariant region

$$\left\{\Omega_c = (S,V,E,I,R) \in R_+^5 : N < \frac{\pi}{\mu}\right\}$$

Therefore, the model system is well posed and we have investigate dynamics of the disease.

Positivity of Solution

Theorem 2. *Let the initial condition under consideration be given as $\{S(t),V(t),E(t),I(t),R(t) \geq 0\} \in \Omega_c$*

Then the solution of system (1) are positive for all $t > 0$

Proof

$$\begin{aligned}\frac{dS}{dt} &= \pi + \theta_2 V + \alpha_2 R - (\omega + \theta_1 + \mu)S \\ \frac{dS}{dt} &\geq -(\omega + \theta_1 + \mu)S \\ \frac{dS}{S} &\geq -(\omega + \theta_1 + \mu)dt \\ \ln S &\geq -(\omega + \theta_1 + \mu)t + K \\ S(t) &\geq e^{-(\omega+\theta_1+\mu)t+K} \\ S(t) &\geq e^{-(\omega+\theta_1+\mu)t}\end{aligned}$$

Applying the initial conditions $t = 0,\ S(t) = K$

$$S(t) \geq S(0)e^{-(\omega+\theta_1+\mu)t} \geq 0$$

Similarly

$$\begin{aligned}\frac{dV}{dt} &\geq -(\theta_2 + \mu)V \\ \frac{dV}{V} &\geq -(\theta_2 + \mu)dt \\ \ln V &\geq -(\theta_2 + \mu)t + K_2 \\ V(t) &\geq e^{-(\theta_2+\mu)t+K_2} \\ V(t) &\geq K_2 e^{-(\theta_2+\mu)t}\end{aligned}$$

Applying the initial condition $t = 0,\ V(0) = K_2$ we have

$$V(t) \geq V(0)e^{-(\theta_2+\mu)t} \geq 0$$

By repeating the same process for other variable in model system (1) respectively we have

$$\begin{aligned}E(t) &\geq K_3 e^{-(\phi_1+\alpha_1+\mu)t} \geq 0 \\ I(t) &\geq K_4 e^{-(\phi_2+\phi_3+\mu)t} \geq 0 \\ R(t) &\geq K_5 e^{-(\alpha_2+\mu)t} \geq 0\end{aligned}$$

Existence and Uniqueness of Solution

For all mathematical model to be well posed it depends on whether there exist a solution for the model and uniqueness of this solution Lipchitz conditions can be used to verify the existence and uniqueness of solution of model system (1).

Let

$$\begin{aligned} f_1 &= \pi + \theta_2 V + \alpha_2 R - (\omega + \theta_1 + \mu)S \\ f_2 &= \theta_1 S - (\theta_2 + \mu)V \\ f_3 &= \omega S - (\varphi_1 + \alpha_1 + \mu)E \\ f_4 &= \varphi_1 E - (\varphi_2 + \varphi_3 + \mu)I \\ f_5 &= \varphi_2 E + \alpha_1 E - (\alpha_2 + \mu)R \end{aligned}$$

Theorem 3. *(Derrrick and Groosman, 1976)*
Let Ω *denoted the region* $|t-t_0| \leq a, ||x-x_0|| \leq 1,\ x = (x_1, x_2 .... x_n)\ x_0 = x_i$ *where* $i = 10, 20, ..., no.$

If $f(t,0)$ satisfied the Lipchitz conditions

$$x||f(t,x_1) - f(t,x_2)|| \leq K||x_1 - x_2||$$

And $(t,x_1),(t,x_2) \in \Omega$ where K is a positive constant. Then there exist a constant $\sigma \geq 0$ such that there exist a unique continuous vector solution of $x(t)$ for the model system in the interval.

$$t - t_0 \leq \delta and \frac{\partial f_i}{\partial xj} = i,\ j = 1,2,3...,n,$$

In other to establish the uniqueness of solution of model system (4). We show that $\frac{\partial f_i}{\partial xj} = i, j = 1,2,...,n$, are continuous and bonded in Ω. Since, we have five system of differential equations, $n = 5$.

Theorem 4. *Let* Ω *denotes the region* $0 \leq a \leq R$*, then the model system (4) have a unique solution* Ω*.*

Proof

$$\begin{aligned} \frac{\partial f1}{\partial s} &= -(\omega + \theta_1 + \mu) \\ \left|\frac{\partial f_1}{\partial s}\right| &= |-(\omega + \theta_1 + \mu)| < \infty \\ \frac{\partial f_2}{\partial s} &= \theta_1 \\ \left|\frac{\partial f_2}{\partial s}\right| &= |\theta_1| < \infty \\ \left|\frac{\partial f_2}{\partial V}\right| &= -(\theta_1 + \mu) \\ \left|\frac{\partial f_2}{\partial s}\right| &= |-(\theta_1 + \mu)| < \infty \\ \frac{\partial f_1}{\partial R} &= \alpha_1 \\ \left|\frac{\partial f_1}{\partial s}\right| &= |a_2| < \infty \\ \frac{\partial f_1}{\partial V} &= \theta_2 \\ \left|\frac{\partial f_1}{\partial V}\right| &= |\theta_2| < \infty \\ \frac{\partial f_3}{\partial S} &= \omega \\ \left|\frac{\partial f_3}{\partial S}\right| &= |\omega| < \infty \\ \frac{\partial f_3}{\partial E} &= -(\phi_1 + \alpha_1 + \mu) \\ \left|\frac{\partial f_3}{\partial E}\right| &= |-(\phi_1 + \alpha_1 + \mu)| < \infty \\ \frac{\partial f_5}{\partial R} &= -(a_2 + \mu) \\ \left|\frac{\partial f_5}{\partial R}\right| &= |-(\phi_1 + \alpha_1 + \mu)| < \infty \end{aligned}$$

Following the results in Peter et al. (2017) the above partial derivatives exist continuous and bonded, and the model system (4) has a unique solution (Derrrick and Groosman, 1976).

Results and Discussion

Model Analysis

In this session, we carry out analysis of the model in order to understand transmission dynamics of the disease.

Existence of Equilibrium Point

At equilibrium point

$$\begin{aligned} \frac{dS}{dt} = \frac{dV}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} &= 0 \\ \pi + \theta_2 V + a_2 R - (\omega + \theta_1 + \mu)S &= 0 \\ \theta_1 S - (\theta_2 + \mu)V &= 0 \\ \omega S - (\phi_1 + \alpha_1 + \mu)E &= 0 \\ \phi_1 E - (\phi_2 + \phi_3 + \mu)I &= 0 \\ \theta_2 I + \alpha_1 E + (a_2 + \mu)R &= 0 \end{aligned}$$

Existence of Disease-Free Equilibrium Point (DFE)

The equilibrium state where there is no infection is called disease free equilibrium state. The disease-free equilibrium state of our model is given below

$$\begin{aligned} \varepsilon_0 &= (S^0, V^0, E^0, I^0, R^0) \\ &= \left[\frac{\pi A}{[BA - C]}, \frac{\pi\theta_2 A}{A[BA - C]}, 0, 0, 0\right] \end{aligned}$$

here $A = (\theta_2 + \mu), B = (\omega + \theta_1 + \mu)$ *and* $C = \theta_1\theta_2$

Estimation of Basic Reproduction Number (R_0)

The basic reproduction number (R_0) is the average number of secondary infections caused by an infectious individual during his or her entire period of infectiousness (Diekmann et al.,

1990). We used the basic reproduction number to analyze disease free equilibrium, endemic equilibrium and stabilities of a model.
If $R_0 < 1$, means that every infectious individuals will cause less than one secondary infection and hence the disease can be eradicated from the population and when $R_0 > 1$ every infectious individual will cause more than one secondary infection and hence the disease persists in the population.
The basic reproduction number of our model is given by the next generation matrix

$$F = \begin{bmatrix} \frac{\sigma\beta S^0}{0} & 0 \\ \phi_1 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} (\phi_1 + \alpha_1 + \mu) & 0 \\ 0 & (\phi_2 + \phi_3 + \mu) \end{bmatrix}$$

R_0 is the spectral radius of FV^{-1}

$$|V| = (\phi_1 + \alpha_1 + \mu)(\phi_2 + \phi_3 + \mu)$$

$$V^{-1} = \begin{bmatrix} \frac{1}{(\phi_1 + \alpha_1 + \mu)} & 0 \\ 0 & \frac{1}{(\phi_2 + \phi_3 + \mu)} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} \frac{1}{(\phi_1 + \alpha_1 + \mu)} & 0 \\ 0 & \frac{1}{(\phi_2 + \phi_3 + \mu)} \end{bmatrix} \begin{bmatrix} \frac{\sigma\beta S}{N} & 0 \\ \phi_1 & 0 \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} \frac{\sigma\beta S}{N(\phi_1 + \alpha_1 + \mu)} & 0 \\ \frac{\phi_1}{(\phi_2 + \phi_3 + \mu)} & 0 \end{bmatrix}$$

$$R_0 = \frac{\sigma\beta k}{N(\phi_1 + \alpha_1 + \mu)}$$

where $k = \frac{\pi(\theta_2+\mu)}{[(\omega+\theta_1+\mu)(\theta_2+\mu)-\theta_1\theta_2]}$.

Existence of Endemic Equilibrium

The equilibrium state with presence of infection is known as endemic equilibrium state.
The endemic equilibrium of our model is given below:

$$\varepsilon_* = (S*, V*, E*, I*, R*)$$

where

$$S* = \frac{N(\phi_2 + \phi_3 + \mu)}{\phi_1\sigma\beta}$$

$$V* = \frac{N\phi_1(\phi_2 + \phi_3 + \mu)}{\phi_1\sigma\beta(\theta_2 + \mu)}$$

$$E* = \frac{\eta_1\eta_2(\phi_2 + \mu) - \eta_3[\pi\phi_1\sigma\beta(\phi_2 + \mu) + \eta_2]}{\alpha_1\phi_1\sigma\beta(\phi_2 + \mu)[\phi_1\phi_2 + \alpha_1(\phi_2 + \phi_3 + \mu)]}$$

$$I* = \frac{\eta_1\eta_2\phi_1(\phi_2 + \mu) - \eta_3\phi_1[\pi\phi_1\sigma\beta(\phi_2 + \mu) + \eta_2]}{\eta_4\alpha_1\phi_1[\phi_1\phi_2 + \alpha_1(\phi_2 + \phi_3 + \mu)]}$$

$$R* = \frac{\eta_1(\phi_2 + \mu) - [\pi\phi_1\sigma\beta(\phi_2 + \mu) + \eta_2]}{\alpha_1\phi_1\sigma\beta(\phi_2 + \mu)}$$

$$\eta_1 = N(\omega+\theta_1+\mu)(\phi_2 + \phi_3 + \mu)$$

$$\eta_2 = N\theta_1\theta_2(\phi_2 + \phi_3 + \mu)$$

$$\eta_3 = (\phi_2 + \phi_3 + \mu)(a_2 + \mu)$$

$$\eta_4 = (\phi_2 + \phi_3 + \mu)(\phi_2 + \mu)$$

Local Stability of Disease Free Equilibrium

The disease free equilibrium is locally asymptotically if $R_0 <$ 1 otherwise unstable.

Proof The Jacobian matrix to the model system is

$$J(\varepsilon_0) = \begin{bmatrix} -A & \theta_2 & 0 & \frac{\sigma\beta k}{N} & a_2 \\ \theta_1 & -B & 0 & 0 & 0 \\ 0 & 0 & -C & \frac{\sigma\beta k}{N} & 0 \\ 0 & 0 & \phi_1 & -D & 0 \\ 0 & 0 & a_2 & \phi_2 & -E \end{bmatrix}$$

where A = $(\omega+\phi)$, B = $(\theta_2+\mu)$ C = $(\phi_1+\alpha_1+\mu)$, D = $(\phi_2+\phi_3+\mu)$, E = $(a_2+\mu)$.
The characteristic polynomial of the above matrix is

$$det|J(\varepsilon_*) - \lambda I| = 0$$

$$J(\varepsilon_0) = \begin{bmatrix} -A-\lambda & \theta_2 & 0 & \frac{\sigma\beta k}{N} & a_2 \\ \theta_1 & -B-\lambda & 0 & 0 & 0 \\ 0 & 0 & -C-\lambda & \frac{\sigma\beta k}{N} & 0 \\ 0 & 0 & \phi_1 & -D-\lambda & 0 \\ 0 & 0 & a_2 & \phi_2 & -E-\lambda \end{bmatrix}$$

where A = $(\omega+\phi)$, B = $(\theta_2+\mu)$, C = $(\phi_1+\alpha_1+\mu)$, D = $(\phi_2+\phi_3+\mu)$, E = $(a_2+\mu)$.
The eigen values are $\lambda_1 = -(\omega+\phi), \lambda_2 = -(\theta_2+\mu), \lambda_3 = -(\phi_1+\alpha_1+\mu), \lambda_4 = -(\phi_2+\phi_3+\mu), \lambda_5 = -(a_2+\mu)$.
Since $\lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_5 < 0$, then the disease can be controlled.

Global Stability of Disease Free Equilibrium

Theorem 5. *The disease free equilibrium of the model system is global asymptotically stable (GAS) in the region* Ω *whenever* $R_0 \leq 1$.

Table 2. Parameter values of the total population of Nigeria as of 16th July 2023 estimated at 224,021,818 and 266,675 confirmed cases of COVID-19 with 3,155 deaths, according to Worldometer (2023) and World Health Organization (2023)

Parameter	Values	Description	Source
1. ω	0.1818	Rate at which susceptible individuals become exposed	Worldometer (2023)
2. ϕ_1	0.1000	Rate at which exposed individuals become infected	Ojih et al. (2019)
3. ϕ_3	0.0752	Disease induced death rate	World Health Organization (2023)
4. μ	0.5000	Natural mortality rate	World Health Organization (2023)
5. θ_1	0.200	Vaccination rate	Estimated
6. α_1	0.1500	Rate at which exposed people get recovered	Estimated
7. α_2	0.0780	Rate at which recovered individuals become susceptible	Estimated
8. π	2.6000	Recruitment rate	Agbata et al. (2020)
9. ϕ_2	0.2000	Recovering rate of infected individuals	Estimated
10. θ_2	1.5000	Rate of vaccine failure	Estimated
11. β	0.1000	Probability of getting COVID-19	Estimated
12. σ	0.9700	Modification parameter	Estimated

Proof The Lyapunor function H is given below
$\dot{H} = b_1\dot{E} + b_2\dot{I}$

Substituting the value of $\dot{E}$ and $\dot{I}$ we have

$$\dot{H} = b_1\left[\frac{\sigma\beta IS}{N} - AE\right] - b_2[\phi_1 E - A]$$

$$\dot{H} = \frac{b_1\sigma\beta IS}{N} - b_1AE - b_2\phi_1 E - b_2(\phi_2+\phi_3+\mu)I$$

here A = $(\phi_1+\alpha_1+\mu), b_2 = (\phi_1+\alpha_1+\mu)$ & $b_1 = \phi_1$

$$\dot{H} = \frac{\phi_1\sigma\beta IS}{N} - b_1AE(\phi_2+\phi_3+\mu)I$$

$$\dot{H} = \frac{\phi_1\sigma\beta IS}{NA(\phi_2+\phi_3+\mu)I} - 1$$

$$\dot{H} = [MR_0 - 1]$$

$$\dot{H} = \frac{\phi_1 I}{(\phi_2+\phi_3+\mu)I}R_0 - 1$$

$\dot{H} = (GR_0 - 1) \leq 0$ for $R_0 \leq 1$ where $G = \frac{\phi_1 I}{(\phi_2+\phi_3+\mu)I}$
for $S \leq S^0 = \frac{\pi}{\mu}$ and $\dot{H} \leq 0$ for $R_0 < 1$ and only if $I = 0$. This This implies that the only trajectory of the system (1) on which $\dot{H} = 0$ $DFE(\varepsilon_0)$. Therefore by Lasalles invariant principle ε_0 is globally asymptotically stable in Ω.

Numerical Simulation

In this session, we carry out numerical simulation of the model in order to determine effects of the control measure. The numerical simulation of our model is performed using MATLAB and set of parameter values as presented in Table 2:

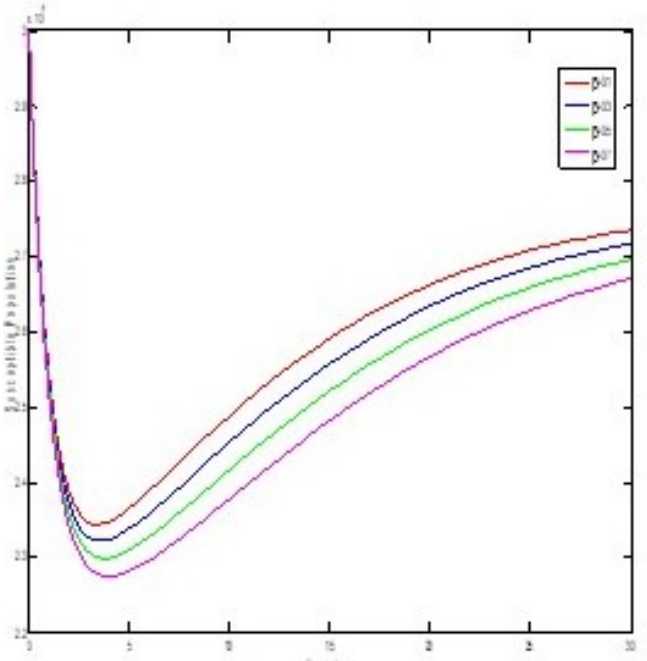

Figure 2. Graph of susceptible population with time

Conclusion

In the article, a mathematical model of COVID-19 transmission dynamics considering the impact of awareness and vaccination program was presented. The existence and uniqueness of the solution were investigated to ensure that the validity of the model is mathematical and biological. The basic reproduction number R_0 was determined using the next generation matrix method. Local and global stability of the model was assessed, revealing that the disease can be eliminated from the population through vaccination and awareness program. Numerical simulation results demonstrated that the most effective approach to curbing the spread of COVID-19 is the implementation of vaccination and awareness program. Figure 4 illustrates an exponential increase in vaccination rate over time due to the awareness program, resulting in a rapid decrease in the infected population (as seen in Figure 3). Although the number of infected individuals initially rises

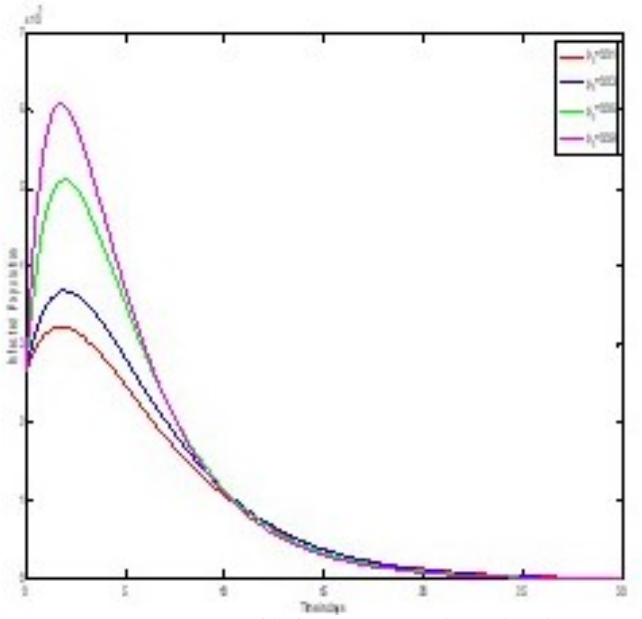

Figure 3. Graph of infected population with time

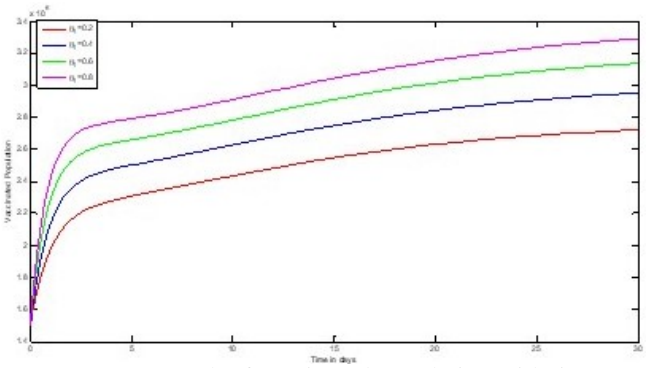

Figure 4. Graph of vaccinated population with time

quickly, it eventually declines to zero, indicating successful disease control through therapeutic measures, vaccination, and awareness. Despite the implementation of effective vaccination and awareness program, it is strongly advised that the general public strictly adheres to government policies on COVID-19 prevention, including social distancing, mask usage, and regular sanitation.

Data Availability

The data used to support the findings of this study are those used in related research works on COVID-19 and are fully referenced for accessibility and those obtained through Data Repository for Nigeria 2023 available from `https://covid19.who.int/region/afro/country/ng`

Conflicts of Interest

The authors declare there is no conflicts of interest.

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