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A mathematical model for transmission dynamics of COVID-19 in Nigeria and its post effects

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Abstract

This study presents a mathematical model formulated through a system of differential equations to analyze the dynamics of COVID-19 in Nigeria and its post effects. The total population (N), is divided into six compartments: susceptible (S), vaccinated (V), exposed (E), infected (I), deceased (D), and recovered (R). Our primary objective is to conduct a comprehensive mathematical analysis of the disease and elucidate its post-effects. Qualitative analyses such as identification of invariant regions, positivity of solutions, and stability analyses are performed. The basic reproduction number is obtained using the next-generation matrix, and its epidemiological significance such as threshold for epidemic spread, intervention decision and estimation of herd immunity are discussed. Sensitivity analysis is conducted to determine the most influential parameters and numerical simulation is carryout using MATLAB which revealed the model behavior in real-life. Post-effects of COVID-19 in Nigeria which include increased in poverty levels, reduced income, job losses, strain in healthcare system, educational disruption are identified. Our findings underscore the importance of implementing targeted public health interventions to mitigate the socio-economic impact of the pandemic, strengthen the healthcare system's resilience, and address the educational disruptions. Recommendations include prioritizing vaccination efforts to achieve herd immunity, enhancing healthcare infrastructure and capacity, implementing social protection measures to support vulnerable populations, and adopting innovative approaches to facilitate remote learning and educational recovery.

Keywords and phrases: COVID-19, Post effects of COVID-19, Epidemiology, Basic reproduction number, Sensitivity analysis.

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1 Introduction

The COVID-19 pandemic, caused by the novel Coronavirus SARS-CoV-2, has emerged as one of the most significant global health crises in recent history. The virus belongs to the family Coronaviridae and is characterized by its high transmissibility and ability to cause severe respiratory illness, ranging from mild symptoms to acute respiratory distress syndrome and death [1, 2]. The primary mode of transmission is through respiratory droplets produced when an infected individual coughs, sneezes, or talks, although airborne and surface transmission also contribute to its spread [1].

In Nigeria, COVID-19 was first reported on February 27, 2020, when an Italian citizen tested positive for the virus in Lagos, the country's largest city [1, 3]. Since then, the virus has spread to various states within the country, prompting significant public health interventions and mitigation measures by the Nigerian government and health authorities [3]. The transmission dynamics of COVID-19 in Nigeria are influenced by factors such as population density, mobility patterns, healthcare infrastructure, and socio-economic disparities. Preventing the spread of COVID-19 relies on a combination of public health measures, including hand hygiene, respiratory etiquette, physical distancing, wearing face masks, and vaccination [2]. These interventions aim to reduce the likelihood of viral transmission and mitigate the burden on healthcare systems. Vaccination campaigns have been initiated globally and in Nigeria to immunize populations against COVID-19 and achieve herd immunity [1, 2, 4]. While several treatments and vaccines have been developed to combat COVID-19, management primarily focuses on supportive care to alleviate symptoms and prevent complications [2, 4]. Severe cases may require hospitalization, oxygen therapy, and in some instances, mechanical ventilation in intensive care units. Additionally, antiviral medications, corticosteroids, and monoclonal antibodies have been used to treat hospitalized patients with COVID-19 [1, 2]. Diagnosing COVID-19 involves various methods, including molecular tests (such as reverse transcription-polymerase chain reaction or RT-PCR) to detect viral RNA, antigen tests to identify viral proteins, and serological tests to detect antibodies produced in response to infection [1, 2]. Prompt and accurate diagnosis is crucial for initiating appropriate management and implementing public health measures to prevent further transmission.

Adekunle *et al* [5], developed a compartmental mathematical model to simulate the dynamics of COVID-19 transmission in Nigeria. Their model incorporated parameters such as population size, contact rates, and intervention measures. The main findings revealed that early implementation of non-pharmaceutical interventions (NPIs) significantly reduced the spread of the virus and mitigated the burden on the healthcare system. The study concluded that a combination of NPIs, including social distancing and mask-wearing, was essential for controlling the pandemic in Nigeria. Ogunnaiké *et al* [6], developed a susceptible-exposed-infectious-recovered (SEIR) compartmental model to assess the impact of intervention strategies on COVID-19 transmission dynamics in Nigeria. The model considered factors such as population density, mobility, and healthcare capacity. Their findings suggested that early implementation of stringent control measures, coupled with widespread testing

and contact tracing, could effectively suppress the spread of the virus and reduce the number of cases and deaths. Adekunle *et al* [7], developed a dynamic compartmental model to predict the spread of COVID-19 in Nigeria under different scenarios. Their model incorporated parameters such as transmission rates, contact patterns, and the effectiveness of control measures. The study found that without intervention, the virus would overwhelm the healthcare system. However, early implementation of interventions such as lockdowns and mass testing could mitigate the impact of the pandemic and reduce the number of cases and deaths. Teslya *et al* [8], developed a mathematical model to investigate COVID-19 transmission dynamics in various population density settings globally. Their model considered factors such as population density, mobility, and the effectiveness of intervention measures. The study found that population density significantly influenced the transmission rate of COVID-19, with higher-density areas experiencing faster spread. The findings underscored the importance of tailored intervention strategies based on population density to control the pandemic. Flaxman *et al* [9], employed a Bayesian approach to model COVID-19 transmission dynamics in different regions of the United States. Their model incorporated data on reported cases, testing rates, and intervention measures. The study identified regional variations in transmission rates and the effectiveness of control measures. The findings highlighted the importance of targeted interventions and surveillance strategies tailored to regional dynamics to effectively control the spread of the virus. This study aims to contribute to the understanding of COVID-19 transmission dynamics in Nigeria through mathematical modeling, with the goal of informing evidence-based policy decisions and interventions to control the spread of the virus and minimize its socio-economic consequences.

The novelty of this study lies in its comprehensive integration of mathematical modeling, epidemiological analysis, and socio-economic impact assessment to provide a holistic understanding of COVID-19 dynamics in Nigeria. Unlike previous studies that focus solely on disease transmission or economic consequences, this research uniquely formulates a system of differential equations incorporating vaccination as a distinct compartment, allowing for a nuanced exploration of its role in controlling the epidemic. The study not only derives the basic reproduction number and conducts stability and sensitivity analyses but also bridges the gap between mathematical epidemiology and real-world policy implications by linking the model outcomes to critical socio-economic effects such as poverty, healthcare strain, job losses, and educational disruptions. The use of MATLAB for numerical simulations enhances the study's practical relevance by demonstrating real-life disease progression and intervention impacts. Furthermore, its emphasis on post-pandemic recovery strategies, including healthcare resilience, targeted social protections, and innovative educational solutions, underscores its originality in addressing both immediate and long-term consequences of the pandemic. This multi-faceted approach provides a novel framework that can guide policymakers in developing data-driven interventions tailored to Nigeria's unique demographic and economic landscape.

2 Post effects of COVID-19 in Nigeria

The COVID-19 pandemic has left a lasting impact on Nigeria, extending beyond its initial health crisis to profoundly affect various facets of society, economy, and governance. One significant post-effect is the strain on the country's healthcare system, which has been overwhelmed by the surge in cases and strained resources. This strain has exposed underlying weaknesses in Nigeria's healthcare infrastructure, including shortages of medical supplies, inadequate facilities, and challenges in healthcare workforce management [10]. Moreover, the diversion of attention and resources towards managing the pandemic has disrupted routine healthcare services, leading to delays in accessing essential medical care for non-COVID-19 conditions. These disruptions have the potential to exacerbate existing health disparities and contribute to worsened health outcomes in the long term, particularly among vulnerable populations.

The economic repercussions of COVID-19 in Nigeria have been profound, with widespread disruptions to livelihoods, businesses, and economic activities. The implementation of lockdowns and containment measures to curb the spread of the virus resulted in mass unemployment, income losses, and economic instability [11]. Small and medium-sized enterprises (SMEs), which are the backbone of Nigeria's economy, were particularly hard-hit, facing challenges such as reduced demand, supply chain disruptions, and financial constraints. The socio-economic fallout from the pandemic has exacerbated poverty, inequality, and social tensions, posing significant challenges to Nigeria's development aspirations and efforts to achieve sustainable growth and prosperity [12].

3 Model formulation

The total population $N(t)$ is divided into six epidemiological compartments. The susceptible humans $S(t)$, exposed humans $E(t)$, the infected humans $I(t)$, the deceased $D(t)$, treatment class $T(t)$, recovered humans $R(t)$. Individuals are recruited into the susceptible population at rate Λ , the susceptible population reduces at the rate α_1 , that is, the rate at which a susceptible individuals became exposed to the disease. ω_1 is the vaccination rate of susceptible individual and ω_2 , ω_3 are the rates at which vaccinated individuals became exposed and infected respectively due to vaccine failure. The exposed population is further reduced by α_2 which is the rate at which exposed human interacted with COVID-19 infected individuals, γ represents disease induced death rate whereas ρ is the burial rate of deceased population and α_3 denotes recovery rate of infected individuals. Population of every compartment is reduced at the rate μ which represents natural death rate.

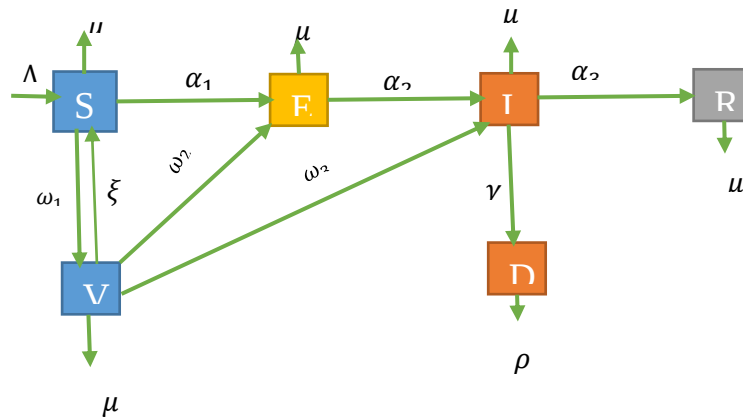


Fig. 1. Schematic Diagram for the model.

Figure 1, gives the schematic diagram for the model, Schematic diagram is essential tools in modeling as it visually illustrates the structure, relationships, and interactions within a mathematical or conceptual framework [2, 13]. This diagram provides a clear representation of system components and their connections, making complex models more accessible to modelers and stakeholders alike [14]. In mathematical modeling, they typically depict how variables, parameters, and equations interact, showing causal relationships and dependencies that govern system behavior [13]. Schematic diagrams aid in conceptualizing model architecture, defining initial conditions and constraints, and outlining system dynamics under different scenarios.

The model Equations

$$\left. \begin{aligned}
 \frac{dS}{dt} &= \Lambda + \xi V - (\alpha_1 + \omega_1 + \mu)S \\
 \frac{dV}{dt} &= \omega_1 S - (\xi + \omega_2 + \omega_3 + \mu)V \\
 \frac{dE}{dt} &= \alpha_1 S + \omega_2 V - (\alpha_2 + \mu)E \\
 \frac{dI}{dt} &= \alpha_2 E + (\alpha_3 + \gamma + \mu)I \\
 \frac{dD}{dt} &= \gamma I - \rho D \\
 \frac{dR}{dt} &= \alpha_3 I - \mu R
 \end{aligned} \right\} \quad (1)$$

$$\alpha_1 = \frac{\beta(I + D)}{N}$$

3.1 Model Variables and Descriptions

Table 1. Description of parameters and variables

Variable	Description
S	Susceptible humans
V	Vaccinated individuals
E	Exposed individuals
I	Infected individuals
D	Diseased compartment
R	Recovered individuals
Parameter	Description
Λ	Constant recruitment level
ω_1	Vaccination rate

β	Contact rate of susceptible individuals with infected individuals
α_2	Infectious rate of exposed individuals
γ	Disease induced rate
ω_2	Rate at which the vaccinated individuals becomes exposed due to vaccine failure
ω_3	Rate at which the vaccinated individuals became infected due to vaccine failure
μ	Natural death rate
ρ	Burial rate of diseased humans
α_3	Recovering rate
ξ	Rate at which vaccinated individuals become Susceptible

Table 1, gives the parameters and variables used for the study, Parameters and variables are essential elements in mathematical modeling, each playing distinct yet complementary roles in defining and simulating complex systems [13]. Parameters are constants that characterize the system's properties and initial conditions, setting the framework within which the model operates. They control the model's behavior and are crucial for sensitivity analysis, identifying which parameters significantly impact model outcomes. Variables, on the other hand, represent the changing quantities within the system, such as outputs of interest or dynamic states over time [14, 15]. They depend on parameters and other variables, providing insights into system behavior and enabling predictions and scenario analyses. Together, parameters and variables form the foundation of mathematical models, translating real-world complexities into structured frameworks for analysis, prediction, and understanding of diverse phenomena across scientific and engineering disciplines [13].

3.2 Invariant Region of the Model

The model solutions are feasible for all $t > 0$, if they enter the invariant region D , which is given by:

$$D = \left\{ (S, V, E, I, D, R) : S > 0, V > 0, E > 0, I > 0, D > 0, R > 0, N < \frac{\Lambda}{\mu} \right\}$$

Proof

The total population of the model is given as

$$N(t) = S + V + E + I + D + R$$

Adding the differential equations is

$$N'(t) = S' + V' + E' + I' + D' + R'$$

On evaluating the algebraic terms, we obtain

$$N'(t) = \Lambda - (S + V + E + I + D + R)\mu - \rho D$$

$$N'(t) = \Lambda - \mu N - \rho D$$

$$\frac{dN}{dt} \leq \Lambda - \mu N$$

$$\frac{dN}{dt} + \mu N = \Lambda$$

Multiplying through by the integrating factor $e^{\mu t}$, gives

$$d(Ne^{\mu t}) \leq \Lambda e^{\mu t} dt$$

Integrating both sides

$$\int d(Ne^{\mu t}) \leq \int \Lambda e^{\mu t} dt$$

$$N(t) \leq \frac{\Lambda}{\mu} + K_0 e^{-\mu t}$$

Therefore, D remains a positively invariant set within the trajectory outlined by model (1), ensuring that no solution trajectory exits through the boundary of region D . Consequently, within this domain, the model can be deemed both epidemiologically and mathematically well-defined [16].

3.3 Epidemiological meaning of the fraction $\frac{\Lambda}{\mu}$

In the model, the ratio $\frac{\Lambda}{\mu}$ holds significance in understanding the demographic dynamics of the population concerning the spread of COVID-19. The constant recruitment rate (Λ) signifies the pace at which new individuals join the population, either through birth or migration. In the case of COVID-19, this influx of susceptible individuals into the population could contribute to the pool of

people at risk of contracting the disease. Conversely, the natural death rate (μ) represents the rate at which individuals in the population perish due to causes unrelated to COVID-19 infection. This encompasses deaths from old age, diseases other than COVID-19, accidents, and other non-COVID-19-related factors [16, 17].

Thus, the ratio $\frac{\Lambda}{\mu}$ indicates the equilibrium between the addition of new susceptible individuals to the population and the removal of individuals through natural mortality. Concerning COVID-19, a higher ratio $\frac{\Lambda}{\mu}$ implies a population with a greater influx of susceptible individuals, potentially heightening the likelihood of COVID-19 transmission and outbreaks. Conversely, a lower ratio indicates a population where natural deaths are more prevalent, possibly diminishing the pool of susceptible individuals and thus the potential for COVID-19 transmission [18, 19].

Comprehending the $\frac{\Lambda}{\mu}$ ratio within the COVID-19 disease model aids in assessing the population's vulnerability to COVID-19 outbreaks and assists in devising effective vaccination strategies and public health interventions.

3.4 Positivity of solution of the model

It is necessary to show that all state variable of the model in are non-negative for all time (t), for the model to be epidemiologically and mathematically feasible in the region D given by [16, 20]:

$$D = \{(S, V, E, I, D, R) \in R_+^6 : (S + V + E + I + D + R) \leq N\}$$

This can be done by considering,

$$\{(S, V, E, I, D, R) \geq 0 \in R_+^6\}$$

Lemma 1:

Supposed the initial data for the given model (1) be $(S, V, E, I, D, R) > 0$. Then the solutions (S, V, E, I, D, R) of the model (1) are positive for all time $t > 0$

Proof

Let $t_1 = \sup \{t > 0 : S > 0, V > 0, E > 0, I > 0, D > 0, R > 0 \in [0, t]\}$. Thus $t > 0$.

We have from the first equation that

$$\frac{dS}{dt} = \Lambda + \xi V - \alpha_1 S - (\omega_1 + \mu) S$$

$$\frac{dS}{dt} \geq -(\omega_1 + \mu) S$$

$$\int \frac{dS}{dt} \geq -\int (\omega_1 + \mu) dt$$

$$\ln S \geq -(\omega_1 + \mu)t + c$$

$$S(t) \geq Ce^{-(\omega_1 + \mu)t}$$

Applying the given initial, $t = 0$, $S(0) = C$

Therefore, $S(t) \geq S(0)e^{-(\omega_1 + \mu)t}$ and $(\omega_1 + \mu) > 0$

Similarly, it can be demonstrated that $V, E, I, D, R > 0$

4 Asymptotic stability of the disease-free equilibrium of the model

The equilibrium state where there is no infection (or absence of the disease), a point where $E = I = D = R = 0$ is called the disease-free equilibrium point (DFE) which is given

$$\eta_0 = \{S^*, V^*, E^*, I^*, D^*, R^* > 0\} = \left\{ \frac{\Lambda(\xi + \mu)}{\xi\omega_1 - (\omega_1 + \mu)(\xi + \mu)}, \frac{\omega_1 \Lambda}{\mu^2 + \xi\alpha_1 + \omega_1 + (\xi + \omega_1)\mu}, 0, 0, 0, 0 \right\}$$

4.1 Basic reproduction number (R_0) of the model

The basic reproduction number R_0 is a fundamental concept in epidemiology that measures the average number of secondary infections generated by a single infected individual in a population where everyone is susceptible to the disease. In simpler terms, it represents the potential for a disease to spread within a population [18]. R_0 is defined as the expected number of secondary cases produced by a single infected individual in a population where everyone is susceptible to the disease and no control measures are in place [16]. It serves as a crucial epidemiological parameter for understanding the transmission dynamics of infectious disease. An R_0 greater than 1 indicates that, on average, each infected individual is spreading the disease to more than one other person, leading to sustained transmission and potential outbreaks. Conversely, an R_0 less than 1 suggests that the disease is unlikely to cause an epidemic as each infected individual infects fewer than one other person, leading to the disease eventually dying out. [18, 21]. Hence, it follows that

$R_0 = \rho(FV^{-1})$ ρ is given by dominant eigenvalue of FV^{-1}

$$F = \begin{bmatrix} 0 & \frac{\beta(\xi + \mu)}{\mu + \xi + \omega_1} & \frac{\beta(\xi + \mu)}{\mu + \xi + \omega_1} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \quad V = \begin{bmatrix} K_2 & 0 & 0 \\ -\alpha_2 & K_3 & 0 \\ 0 & -\gamma & \rho \end{bmatrix}$$

$$F.V^{-1} = \begin{bmatrix} \frac{\beta(\xi + \mu)\alpha_2}{(\mu + \xi + \omega_1)K_2K_3} + \frac{\beta(\xi + \mu)\alpha_2\gamma}{(\mu + \xi + \omega_1)K_2K_3\rho} & \frac{\beta(\xi + \mu)}{(\mu + \xi + \omega_1)K_3} + \frac{\beta(\xi + \mu)\gamma}{(\mu + \xi + \omega_1)K_3\rho} & \frac{\beta(\xi + \mu)}{(\mu + \xi + \omega_1)\rho} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

Therefore, the basic reproduction number of the model is

$$R_0 = \frac{\beta\alpha_2(\beta + \gamma)(\xi + \mu)}{(\mu + \xi + \omega_1)K_2K_3\rho}$$

$$R_0 = \frac{\beta\alpha_2(\gamma\mu + \gamma\xi + \mu\rho + \rho\xi)}{(\mu + \xi + \omega_1)K_2K_3\rho}$$

4.2 Local asymptotic stability of the DFE of the model

Theorem 1

The disease-free equilibrium points of the is locally asymptotically stable (LAS) if $R_0 < 1$, and unstable if $R_0 > 1$.

Proof

Using Jacobian matrix to prove the local stability of the disease-free equilibrium point

$$J(\varepsilon_0) = \begin{bmatrix} -(\omega_1 + \mu) & \xi & 0 & \frac{-\beta(\xi + \mu)}{\mu + \xi + \omega_1} & \frac{-\beta(\xi + \mu)}{\mu + \xi + \omega_1} & 0 \\ \omega_1 & -K_1 & 0 & 0 & 0 & 0 \\ 0 & \omega_2 & -K_2 & \frac{\beta(\xi + \mu)}{\mu + \xi + \omega_1} & \frac{\beta(\xi + \mu)}{\mu + \xi + \omega_1} & 0 \\ 0 & 0 & \alpha_2 & -K_3 & 0 & 0 \\ 0 & 0 & 0 & \gamma & -\rho & 0 \\ 0 & 0 & 0 & \alpha_3 & 0 & -\mu \end{bmatrix}$$

Since the diagonal of the first and last column consist of only the diagonal element, we can reduce $J(\varepsilon_0)$ to

$$J_1(\varepsilon_0) = \begin{bmatrix} \xi & 0 & -\frac{\beta(\xi + \mu)}{\mu + \xi + \omega_1} & \frac{-\beta(\xi + \mu)}{\mu + \xi + \omega_1} \\ -K_1 & 0 & 0 & 0 \\ \omega_2 & -K_2 & \frac{\beta(\xi + \mu)}{\mu + \xi + \omega_1} & \frac{\beta(\xi + \mu)}{\mu + \xi + \omega_1} \\ 0 & \alpha_2 & -K_3 & 0 \end{bmatrix}$$

The characteristics polynomial of $J_1(\varepsilon_0)$ is

Applying Routh-Hurwitz criterion to the Characteristics polynomial, we have that

$$\Rightarrow R_0 < 1$$

Where $K_1 = (\xi + \omega_2 + \omega_3 + \mu)$, $K_2 = (\alpha_2 + \mu)$, $K_3 = (\alpha_3 + \gamma + \mu)$,

When the basic reproduction number (R_0) is less than 1, it indicates that, on average, each infected individual will transmit the COVID-19 virus to fewer than one other individual during their infectious period. This finding holds significant epidemiological implications for the dynamics of COVID-19

transmission and control efforts. A basic reproduction number below 1 suggests that the disease is not self-sustaining within the population. In other words, the chain of transmission is not perpetuated, and the number of new infections generated by each existing case is insufficient to maintain the disease at endemic levels. Instead, the infection tends to die out over time as the number of susceptible individuals decreases due to immunity acquired through vaccination or recovery from previous infection [16–18]. From an epidemiological perspective, a basic reproduction number below 1 is a promising sign for disease control and elimination efforts. It signifies that the spread of COVID-19 is inherently limited within the population, making it more feasible to implement interventions aimed at reducing transmission and preventing outbreaks. With an R_0 less than 1, there's a reduced risk of widespread COVID-19 transmission within the community. Control measures such as vaccination campaigns, contact tracing, isolation of cases, and public health education can be more effective in containing the disease and preventing its resurgence. Vaccination strategies, in particular, play a crucial role in boosting population immunity and reducing the pool of susceptible individuals, further lowering the likelihood of COVID-19 transmission [19, 22].

Furthermore, a basic reproduction number below 1 indicates the potential for achieving COVID-19 elimination in a given population. Elimination occurs when the disease is no longer continuously transmitted within a defined geographic area or population group. By maintaining high vaccination coverage and implementing robust surveillance systems to detect and respond to sporadic cases, it becomes possible to interrupt the chain of transmission and achieve sustained COVID-19 control [17].

A basic reproduction number less than 1 provides valuable information to epidemiologists, health workers, and policymakers, assisting them in several key ways:

1. **Guiding Control Strategies:** Epidemiologists rely on the R_0 value to assess disease transmission potential and devise appropriate control measures. An R_0 below 1 indicates that the disease is not self-sustaining, guiding decisions on the intensity and duration of interventions such as vaccination campaigns and case isolation [23].
2. **Optimizing Resource Allocation:** Health workers and policymakers can allocate resources more effectively based on the R_0 value. With R_0 below 1, resources can be prioritized for interventions in areas with the highest risk of transmission, ensuring maximum impact [22].
3. **Informing Vaccination Strategies:** For vaccine-preventable diseases like COVID-19, knowledge of R_0 below 1 underscores the importance of achieving high vaccination coverage. This information guides vaccination strategies and coverage targets to interrupt transmission [19].
4. **Supporting Policy Decisions:** Policymakers use epidemiological data, including R_0 , to make informed decisions about public health policies. An R_0 below 1 provides evidence of effective control measures, supporting continued investment in disease prevention programs [17].

5. Monitoring Progress towards Goals: Epidemiologists monitor progress towards disease control and elimination goals using R_0 as a metric. Regular surveillance of disease dynamics helps detect changes in R_0 and ensures ongoing progress towards elimination targets [24] .

4.4 Global asymptotic stability of the disease-free equilibrium point

To investigate the global stability of the disease-free equilibrium, we apply the method implemented by Castillo-Chavez and Song.

We write the equation in the uninfected class as

$$\frac{dX}{dt} = F(X, Z)$$

And we re-write the equation in the infected class as

$$\frac{dZ}{dt} = G(X, Z)$$

where $X = S \in R_+^1$ represents the uninfected compartment and

$Z = (E, I, D, R) \in R_+^4$ represents the infected compartment

$\varepsilon_0 = (X^*, 0)$ denotes the disease-free equilibrium of the system, and it globally asymptotically stable if it satisfies the following conditions:

$$H_1 : \frac{dX}{dt} = F(X^*, 0), X^* \text{ is globally asymptotically stable}$$

$$H_2 : \frac{dZ}{dt} = D_Z G(X^*, 0)Z - \hat{G}(X, Z)$$

$\hat{G}(X, Z) \geq 0$ for all $(X, Z) \in D$ and where $D_Z G(X^*, 0)$ is an M- matrix (i.e the diagonal elements are no-negative and it is also the Jacobian of $\hat{G}(X, Z) \geq 0$ evaluated at $(X^*, 0)$.

If the system satisfies the above condition, then the theorem below holds [18, 21].

Theorem 2

The equilibrium point $\varepsilon_0 = (X^*, 0)$. is globally asymptotically stable if $R_0 \leq 1$ and H_1, H_2 are satisfied.

$$F(X, Z) = \begin{bmatrix} \Lambda + \xi V - (\alpha_1 + \omega_1 + \mu)S \\ \omega_1 S - (\xi + \omega_2 + \omega_2 + \mu)V \\ \alpha_3 I - \mu R \end{bmatrix}$$

$$G(X, Z) = \begin{bmatrix} \alpha_1 S + \omega_2 V - (\alpha_2 + \mu)E \\ \alpha_2 E - (\alpha_3 + \gamma + \mu)I \\ \gamma I - \rho D \end{bmatrix}$$

At disease free equilibrium,

$H_1 :$

$$\frac{dS}{dt} = \Lambda + \xi V - (\omega_1 + \mu)S$$

$$\frac{dR}{dt} = 0$$

$H_2 :$

$$D_Z G(X^*, 0)Z = \begin{bmatrix} \alpha_1 S + \omega_2 V - (\alpha_2 + \mu)E \\ \alpha_2 E - (\alpha_3 + \gamma + \mu)I \\ \gamma I - \rho D \end{bmatrix}$$

$$\hat{G}(X, Z) = D_Z G(X^*, 0)Z - G(X, Z)$$

$$\hat{G}(X, Z) = \begin{pmatrix} \beta(I + D)\left(1 - \frac{S}{N}\right) \\ 0 \\ 0 \end{pmatrix}$$

Clearly, $1 \geq \frac{S}{N}$ this implies that $\hat{G}(X, Z) \geq 0$

Clearly, $1 \geq S$ this means that $\hat{G}(X, Z) \geq 0$.

Hence, the disease free equilibrium of the given model is globally asymptotically stable [16].

5 Endemic equilibrium point of the model

The endemic equilibrium point is the steady state where there is persistence or prevalence of a disease in the population.

To obtain the endemic equilibrium we set the RHS of the differential equations in (1) to zero and solve for the state variables.

Thus, at the endemic equilibrium point,

$$\frac{dS}{dt} = \frac{dV}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dD}{dt} = \frac{dR}{dt} = 0.$$

Let $\varepsilon^{**} = (S^{**}, V^{**}, E^{**}, I^{**}, D^{**}, R^{**})$ be the endemic equilibrium point.

We have that,

$$S^{**} = \frac{\Lambda(\xi + \omega_2 + \omega_3 + \mu)}{\xi\omega_1 - (\alpha_1 + \omega_1 + \mu)(\xi + \omega_2 + \omega_3 + \mu)}$$

$$V^{**} = \frac{\omega_1 \Lambda}{\mu^2 + (\xi + \alpha_1 + \omega_1 + \omega_3 + \omega_2)\mu + (\xi + \omega_3 + \omega_2)\alpha_1 + \omega_1(\omega_3 + \omega_2)}$$

$$E^{**} = \frac{\Lambda\alpha_1}{(\alpha_1 + \omega_1 + \mu)(\alpha_2 + \mu)}$$

$$I^{**} = \frac{\Lambda\alpha_1\alpha_{2-}}{(\alpha_1 + \omega_1 + \mu)(\alpha_2 + \mu)(\alpha_3 + \gamma + \mu)}$$

$$D^{**} = \frac{\Lambda\gamma\alpha_1\alpha_{2-}}{\rho(\alpha_1 + \omega_1 + \mu)(\alpha_2 + \mu)(\alpha_3 + \gamma + \mu)}$$

$$R^{**} = \frac{\Lambda\alpha_1\alpha_2\alpha_3}{\mu(\alpha_1 + \omega_1 + \mu)(\alpha_2 + \mu)(\alpha_3 + \gamma + \mu)}$$

5.1 Sensitivity analysis of the model

Sensitivity analysis is a crucial tool in assessing the robustness and reliability of models, especially complex ones like those used to simulate the spread of diseases such as COVID-19. In the context of COVID-19 modeling, sensitivity analysis involves examining how changes in model parameters impact the model outputs, such as infection rates, mortality rates, and other epidemiological indicators. Sensitivity analysis helps researchers understand which parameters have the most significant influence on model outcomes and how uncertainties in those parameters might affect model predictions [15, 25]. Regarding the effects of R_0 with negative and positive values, it's essential to note that R_0 represents the average number of secondary infections in a completely susceptible population. Therefore, in realistic scenarios, R_0 is typically a positive value greater than zero. However, in theoretical contexts or models, negative values of R_0 might be used to represent scenarios where the disease is dying out or when interventions are so effective that transmission rates become negative.

(i.e., cases decrease over time). In practice, negative values of R_0 are not observed because they imply disease extinction [14, 26].

The sensitivity index of the reproduction number of the model with respect to any parameter say x is given by:

$$\mathfrak{S}_x^{R_0} = \frac{\partial R_0}{\partial x} \times \frac{x}{R_0}$$

Given that

$$\mathfrak{S}_\beta^{R_0} = 1$$

$$\mathfrak{S}_{\alpha_2}^{R_0} = \frac{\mu}{\alpha_2 + \mu} = 0.2307$$

$$\mathfrak{S}_\rho^{R_0} = -\frac{\gamma}{\rho + \gamma} = -0.1071$$

$$\mathfrak{S}_\gamma^{R_0} = \frac{(\alpha_3 + \mu - \rho)\gamma}{(\alpha_3 + \gamma + \mu)(\rho + \gamma)} = -0.1431$$

$$\mathfrak{S}_\xi^{R_0} = \frac{\omega_1 \xi}{(\mu + \xi + \omega_1)(\xi + \mu)} = 0.1531$$

$$\mathfrak{S}_\mu^{R_0} = -2 \frac{\left(\mu^3 + (2\xi + \alpha_2/2 + \alpha_3/2 + \gamma_c/2 + \omega_1/2)\mu^2 + \xi(\xi + \alpha_2 + \alpha_3 + \gamma_c + \omega_1)\mu + (\alpha_2/2 + \alpha_3/2 + \gamma/2)\xi^2 + 1/2\omega_1(\alpha_2 + \alpha_3 + \gamma)\xi - 1/2\alpha_2\omega_1(\alpha_3 + \gamma) \right)}{(\mu + \xi + \omega_1)(\alpha_2 + \mu)(\alpha_3 + \gamma_c + \mu)(\xi + \mu)} = -0.2334$$

$$\mathfrak{S}_{\alpha_3}^{R_0} = -\frac{\alpha_3}{\alpha_3 + \gamma_c + \mu} = -0.7467$$

$$\mathfrak{S}_{\omega_1}^{R_0} = -\frac{\omega_1}{\mu + \xi + \omega_1} = -0.1534$$

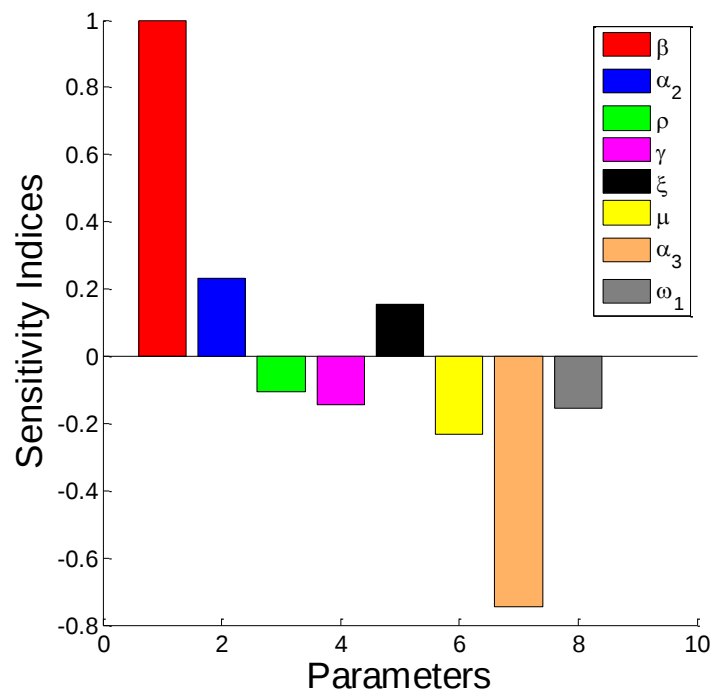


Fig. 2. Sensitivity bar chat

Figure 2, gives a sensitivity bar chart, the Sensitivity bar chart is a crucial visual tool in modeling that illustrates how alterations in input parameters impact model outputs [13]. They pinpoint pivotal parameters by emphasizing those that significantly influence predictions, directing efforts toward refining parameter estimation and management to improve model precision [15].

6 Numerical simulations of the model

Numerical simulation is a critical tool in mathematical modeling of infectious diseases like COVID-19, enabling researchers to understand the dynamics of disease transmission, evaluate intervention strategies, and forecast the course of epidemics. It offers a powerful tool for understanding disease

dynamics, assessing intervention strategies, and guiding public health decision-making. By combining mathematical models with computational techniques, researchers can generate valuable insights into the spread of infectious diseases and inform effective responses to epidemics.

Table 2. Parameter values and their source

Parameter	Value	Source
Λ_{ss}	0.02755	[2]
μ	2.500	[4]
ω_1	0.020	[4]
β	0.1000	[27]
α_1	0.40	Assumed
α_2	0.7	[28]
γ	0.167	Assumed
ω_2	0.002	Assumed
ω_3	0.09091	Assumed

Table 2, gives parameter values used for numerical simulation, Parameter values in numerical simulation are fundamental to modeling, serving multiple critical roles to ensure model accuracy and applicability. They define essential system characteristics such as physical constants, material properties, initial conditions, and boundary constraints [13, 15]. These parameters are calibrated against empirical data to align model predictions with observed behavior, thereby enhancing the model's reliability and predictive power. Sensitivity analysis systematically evaluates the impact of parameter variations on model outputs, identifying influential parameters that significantly affect outcomes and guiding model refinement efforts [13].

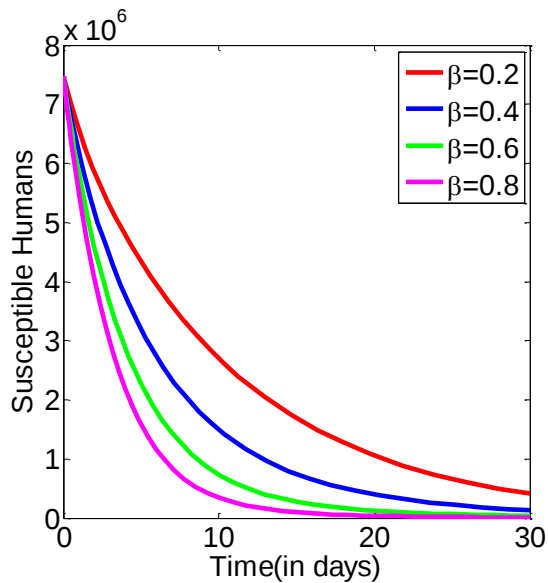


Fig. 3a. Graph of susceptible human against time.

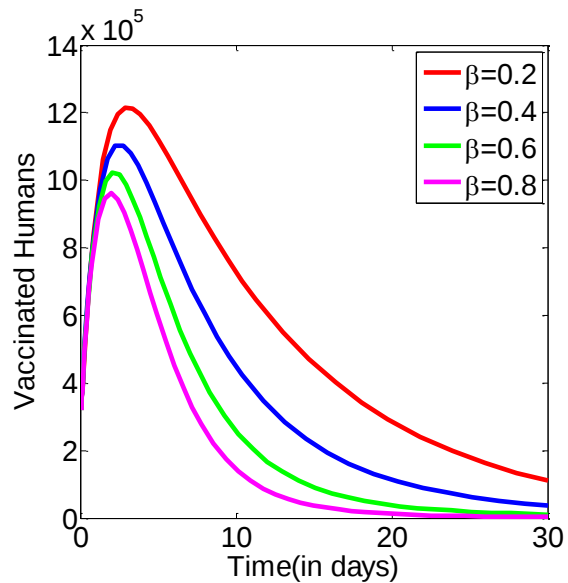


Fig. 3b..Graph of vaccinated humans against time

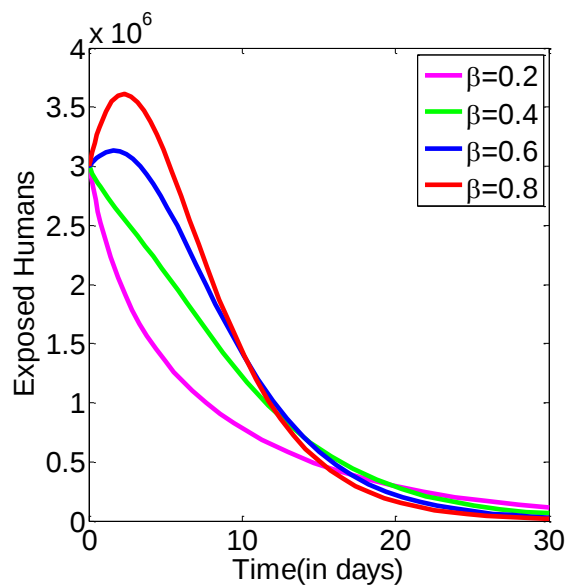


Fig. 3c. Graph of exposed humans against time.

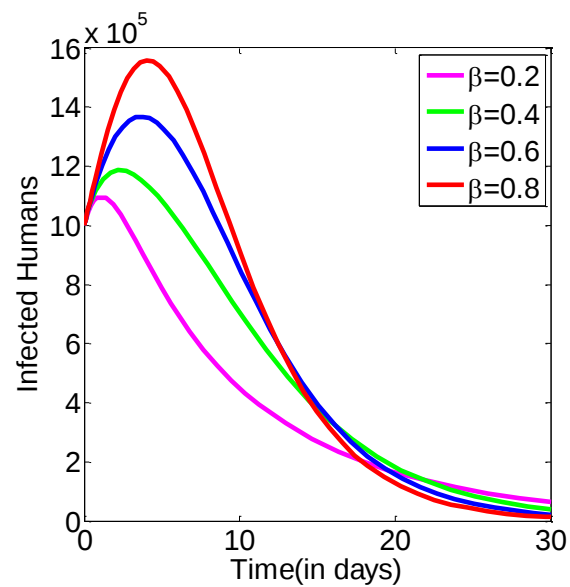


Fig. 3d. Graph of infected humans against time

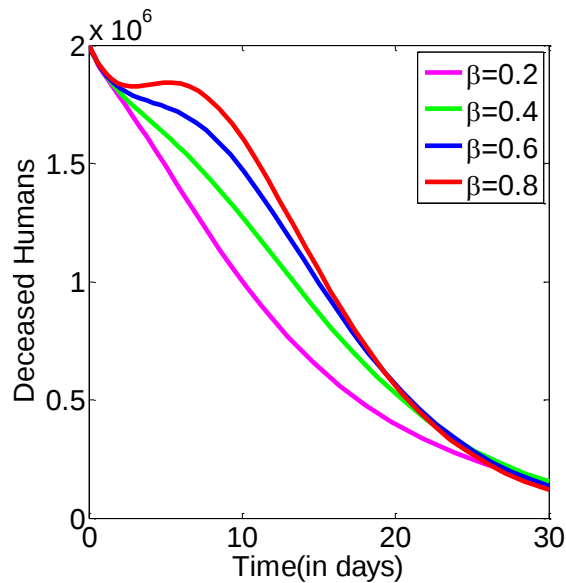


Fig. 3e. Graph of deceased humans against time.

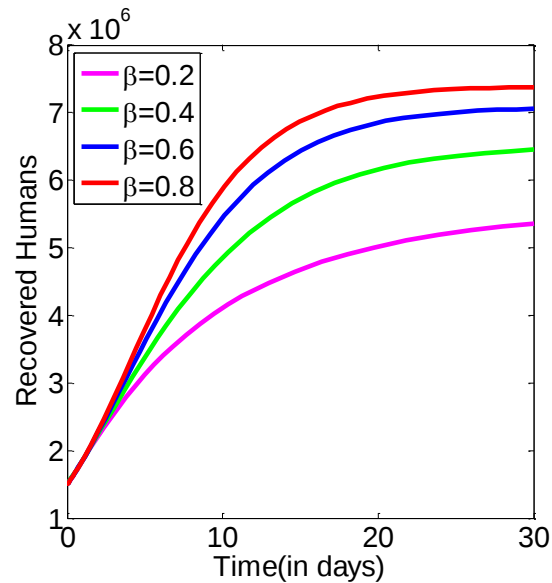


Fig. 3f. Graph of recovered humans against time

7 Conclusion

From the sensitivity analysis and the resulting bar chart in Figure 2, it is evident that parameters with positive sensitivity indices contribute to the transmission of COVID-19 within the human population. For instance, the contact rate β exhibits a positive sensitivity index, indicating that reducing the contact rate between uninfected and infected individuals could effectively halt the spread of COVID-19. Conversely, parameters such as the vaccination rate ω_1 , which has a negative sensitivity index, are crucial in mitigating the prevalence of COVID-19. This highlights the importance of increasing vaccination rates to control the disease effectively.

In Figure 3a, the number of susceptible individuals decreases to zero over time, while Figure 3b illustrates a rapid increase in vaccinated individuals followed by a decline due to increased contact rates between susceptible and infected humans. Figure 3c shows an initial increase and subsequent rapid decrease in the number of exposed individuals, indicating effective disease control. In Figure 3d, the number of infected individuals decreases markedly over time, leading to fewer deaths in Figure 3e and a high recovery rate as depicted in Figure 3f. These simulations emphasized that high vaccination rates and reduced contact rates are crucial factors in achieving control over COVID-19.

In conclusion, even though the spread of COVID-19 in Nigeria has declined, our study remains significant in its potential for future preparedness and response efforts. Despite the absence of active transmission, understanding the dynamics of COVID-19 transmission and its post-effects remains

crucial for preemptive measures and contingency planning. By developing a mathematical model and conducting qualitative analysis including sensitivity analysis, and numerical simulations, our study provides a framework for evaluating the potential impact of COVID-19 reintroduction or future outbreaks in Nigeria. The significance of this study lies in its capacity to inform proactive strategies for maintaining public health vigilance, optimizing healthcare resources, and mitigating the socio-economic consequences of any future resurgence of COVID-19. Through evidence-based insights into transmission dynamics and post-effects, policymakers, public health authorities, and stakeholders can develop targeted response plans, refine surveillance systems, and strengthen healthcare infrastructure to ensure swift and effective responses to emerging threats.

Furthermore, the results from this study can be extrapolated to other infectious disease outbreaks and public health emergencies, enhancing Nigeria's overall preparedness and resilience. By leveraging mathematical modeling and data-driven analysis, we can foster a culture of proactive risk management and evidence-based decision-making, ultimately safeguarding the health and well-being of the Nigerian population in the face of future health challenges.

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Declaration of competing interests

The authors declare that they have no competing interests

Ethics Approval

Not Applicable

Availability of data.

The data used in this study are referenced and presented in Table 2 above.

Consent for Publication

The Authors hereby declare that the manuscript has neither been published previously nor is under consideration for publication elsewhere; that is publication is approved by all authors.

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