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A Global Post Effects of COVID-19: A Mathematical Modelling Study

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Abstract This study presents the global post-effects of COVID-19 through a mathematical modeling approach. A compartmental model, dividing the total population into six epidemiological compartments, is developed to simulate the dynamics of the disease. These compartments include susceptible humans (S), exposed humans (E), infected humans (I), deceased humans (D), individuals in treatment class (T), and recovered humans (R). The study extensively discusses the post-effects of COVID-19 in Africa and the sensitivity analysis reveals that the contact rate of infection exhibits a positive sensitivity index, indicating that interventions aimed at reducing contact rate ϕ would significantly diminish the spread of the virus within the population. Conversely, the treatment rate ω shows a negative sensitivity index, suggesting that promoting higher treatment rates would lead to an increased recovery rate, thereby effectively controlling the spread of the disease. Numerical simulations carried out using MATLAB further confirms that a high treatment rate, avoidance of contact rate with any infected person or infectious surface, coupled with adherence to COVID-19 control measures, could help prevent the spread and outbreaks of COVID-19 in the future. The implications of these findings extend to healthcare workers, policymakers, and the general public, offering valuable insights into disease transmission dynamics and informing preparedness for future pandemics. Overall, this study considers the importance of proactive measures and effective healthcare interventions in mitigating the impact of COVID-19 and preventing the resurgence of infectious diseases in Africa.

Keywords Global stability, sensitivity analysis, COVID-19, endemic equilibrium, numerical simulations

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1. Introduction

The emergence of the novel coronavirus disease 2019 (COVID-19) has posed unprecedented challenges to global public health, economic stability, and social well-being. Belonging to the family Coronaviridae, the causative agent of COVID-19, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was first identified in December 2019 in Wuhan, Hubei Province, China [1, 10]. Since then, it has rapidly spread across continents, leading to a pandemic declared by the World Health Organization (WHO) on March 11, 2020 [8]. COVID-19 primarily manifests as a respiratory illness ranging from mild symptoms to severe respiratory distress, multi-organ failure, and death, particularly among older adults and those with underlying health conditions [8]. The virus spreads primarily through respiratory droplets when an infected person coughs, sneezes, or talks, with close contact being the main mode of transmission [8]. Understanding the genetic makeup and evolutionary pathways of SARS-CoV-2 has been instrumental in elucidating its pathogenesis and in aiding the development of diagnostic tools and potential therapeutics [2]. The transmission dynamics of COVID-19 are multifaceted, influenced by factors such as population density, social behaviors, healthcare infrastructure, and public health interventions [7]. Asymptomatic and pre-symptomatic individuals can unknowingly spread the virus, complicating containment efforts [6]. Although transmission primarily occurs through respiratory droplets, emerging evidence suggests the possibility of airborne transmission in certain settings, necessitating continuous monitoring and adaptation of preventive measures [9]. Prompt and accurate diagnosis of COVID-19 is crucial for controlling its spread and mitigating its impact on individuals and communities [4]. Various diagnostic approaches, including reverse transcription-polymerase chain reaction (RT-PCR) testing, antigen testing, and serological assays, play pivotal roles in identifying infected individuals, tracing contacts, and guiding clinical management [3, 4]. Additionally, non-pharmaceutical interventions such as wearing masks, practicing hand hygiene, maintaining physical distancing, and vaccination have proven effective in reducing transmission rates and preventing severe illness [4]. The origin of COVID-19 has been a subject of intense scientific investigation. The virus responsible for COVID-19, SARS-CoV-2, is a betacoronavirus closely related to other coronaviruses known to infect bats and other animals [10]. While the exact origins of SARS-CoV-2 are still being investigated, the prevailing theory suggests zoonotic transmission, meaning the virus likely jumped from animals to humans. Several early cases of COVID-19 were linked to a seafood market in Wuhan, China, leading to initial speculation that the virus originated from there. However, subsequent research has indicated that while the market likely played a role in amplifying the outbreak, the virus may have been circulating in humans before its detection [2]. Genomic analysis suggests that SARS-CoV-2 shares a high degree of similarity with bat coronaviruses, particularly those found in horseshoe bats. It is believed that the virus may have undergone genetic changes through recombination events or mutations, potentially in an intermediate host species, before spilling over into humans. The identification of such an intermediate host remains a key focus of ongoing investigations [2, 10].

1.1. Transmission dynamics of COVID-19

Understanding the origin and transmission dynamics of COVID-19 is essential for developing effective public health interventions, guiding clinical management, and mitigating the impact of the pandemic on individuals and communities. Ongoing research and surveillance efforts are critical for further elucidating these aspects and informing strategies for controlling the spread of the virus. The transmission dynamics of COVID-19 are complex, influenced by various factors, including viral characteristics, host factors, environmental conditions, and human behavior.

1.1.1. Modes of transmission

- Respiratory Droplets: The primary mode of transmission is through respiratory droplets expelled when an infected person coughs, sneezes, talks, or exhales. These droplets can be inhaled by nearby individuals or deposited on surfaces, where the virus can remain infectious for varying periods [9].
- Aerosol Transmission: In addition to respiratory droplets, growing evidence to indicates that SARS-CoV-2 can also spread through aerosols, particularly in enclosed indoor settings with poor ventilation [9].
- Contact Transmission: The virus can also be transmitted through direct contact with infected individuals or indirect contact with contaminated surfaces or objects, followed by touching the face, particularly the mouth, nose, or eyes [9].

1.1.2. Factors influencing transmission

- Asymptomatic and Pre-symptomatic Spread: Individuals infected with SARS-CoV-2 can transmit the virus to others even if they do not show symptoms (asymptomatic) or before they develop symptoms (pre-symptomatic), making it challenging to identify and isolate cases [6].
- Close Contact: Transmission is most likely to occur in close proximity to an infected individual, particularly in enclosed spaces with poor ventilation and prolonged exposure [7].
- Super-spreading Events: Certain events or settings, such as crowded gatherings, healthcare facilities, and congregate settings, have been associated with large outbreaks or super-spreading events, where one individual infects a disproportionately high number of others [7].
- Behavioral Factors: Adherence to preventive measures such as wearing masks, practicing hand hygiene, maintaining physical distancing, and avoiding large gatherings can significantly reduce the risk of transmission [6].

1.2. COVID-19 in Africa

The COVID-19 pandemic has significantly impacted Africa, presenting unique challenges to the continent's public health systems, socio-economic structures, and communities. Despite initial concerns about the potential devastation COVID-19 could wreak in Africa due to its fragile healthcare infrastructure and high burden of infectious diseases, the continent has demonstrated resilience in its response to the pandemic [1]. Early interventions, including travel restrictions, lockdowns, and public health awareness campaigns, contributed to slowing the spread of the virus in many African countries. However, Africa's diverse socio-economic landscape and healthcare disparities have resulted in varying experiences with COVID-19 across the continent. While some countries successfully contained outbreaks through proactive measures and effective public health responses, others faced significant challenges in controlling transmission, particularly in densely populated urban areas and informal settlements [5]. Limited access to testing, personal protective equipment (PPE), and healthcare services posed additional barriers to pandemic control efforts, exacerbating existing health inequities. The impact of COVID-19 extends beyond the realm of public health, with far-reaching consequences for Africa's economy, education, and social well-being. The pandemic has disrupted livelihoods, strained healthcare systems, and widened socio-economic disparities, disproportionately affecting vulnerable populations such as women, children, and refugees [1]. School closures, disruptions to essential services, and restrictions on movement have further exacerbated pre-existing challenges, including food insecurity, poverty, and unemployment. Amidst these challenges, African countries have demonstrated resilience and innovation in their response to COVID-19. Governments, healthcare workers, researchers, and communities have collaborated to enhance surveillance, testing, treatment, and vaccination efforts across the continent [5]. Investments in healthcare infrastructure, capacity building, and research have been pivotal in strengthening pandemic preparedness and response, while local innovations and community engagement initiatives have contributed to tailored, context-specific interventions.

1.3. Post-effects of COVID-19

1. Economic Impact
    - Job Losses and Unemployment: The economic fallout from COVID-19 has led to widespread job losses and increased unemployment rates across Africa. Lockdown measures, business closures, and disruptions to industries such as tourism and hospitality have left many individuals without sources of income [11].
    - Disruptions to Supply Chains: The pandemic has disrupted global supply chains, affecting trade and commerce in Africa. Restrictions on movement, border closures, and logistical challenges have impeded the flow of goods and services, leading to shortages of essential commodities and hindering economic recovery efforts [12].
2. Health Impact
    - Overburdened Healthcare Systems: COVID-19 has placed immense strain on healthcare systems in Africa, overwhelming facilities and healthcare workers. Limited resources, including hospital beds, medical supplies, and personnel, have hindered the ability to effectively respond to the pandemic and provide adequate care to patients [13].
    - Delayed or Disrupted Healthcare Services: The focus on COVID-19 response has led to the postponement or cancellation of routine healthcare services, including immunizations, maternal and child health services, and treatment for chronic diseases. This has resulted in increased morbidity and mortality from preventable and treatable conditions [14].
3. Social Impact

  - Increased Poverty and Food Insecurity: The economic downturn triggered by COVID-19 has pushed many households into poverty and exacerbated food insecurity in Africa. Lost income, rising food prices, and disrupted agricultural activities have left millions of people vulnerable to hunger and malnutrition [15].
  - Disruption of Education: School closures and learning disruptions have had profound consequences for children and young people in Africa. Limited access to online learning resources, lack of technology infrastructure, and socio-economic disparities have widened educational inequalities and threatened long-term prospects for millions of students [16].

4. Mental Health Impact
    - Increased Rates of Anxiety and Depression: The stress and uncertainty caused by COVID-19 have contributed to a rise in mental health disorders, including anxiety and depression, across Africa. Fear of infection, social isolation, and economic hardship have taken a toll on the psychological well-being of individuals and communities [17].
    - Trauma and Grief: COVID-19-related deaths have resulted in widespread grief and trauma in African communities. Restrictions on funeral rites and traditional mourning practices have compounded the emotional distress experienced by bereaved families, further straining mental health resources [18].
5. Gender Impact
    - Gender-Based Violence: The lockdown measures implemented in response to COVID-19 have heightened the risk of gender-based violence (GBV) in Africa. Stay-at-home orders, economic stress, and social isolation have worsened existing vulnerabilities and inequalities, leading to an increase in cases of domestic violence and abuse [19].
    - Disproportionate Impact on Women in the Workforce: Women have been disproportionately affected by the economic fallout from COVID-19, facing job losses, reduced incomes, and increased caregiving responsibilities. Pre-existing gender inequalities in the workforce have been exacerbated, further widening the gender gap in employment and economic opportunities [20].
6. Disruption of HIV/AIDS and Tuberculosis Services
    - Interruption of Treatment and Care: COVID-19 has disrupted essential healthcare services for diseases such as HIV/AIDS and tuberculosis (TB) in Africa. Lockdown measures, travel restrictions, and diversion of resources to COVID-19 response efforts have led to interruptions in the delivery of antiretroviral therapy (ART) and TB treatment, compromising the health and well-being of affected individuals [21].
    - Increased Mortality and Morbidity Rates: The disruption of HIV/AIDS and TB services has resulted in increased mortality and morbidity rates among affected populations in Africa. Interruptions in treatment adherence, delayed diagnosis, and missed healthcare appointments have led to poor health outcomes and exacerbation of existing health disparities [22].
7. Impact on Small and Informal Businesses

- Closure of Small Enterprises: COVID-19-related restrictions and economic downturns have resulted in the closure of many small businesses across Africa. Limited access to financial resources, market disruptions, and reduced consumer demand have forced small enterprises to shut down, leading to loss of livelihoods and economic instability [23].
- Loss of Livelihoods for Informal Workers: Informal workers, who constitute a significant portion of Africa's workforce, have been disproportionately affected by the economic fallout from COVID-19. Lockdown measures, reduced economic activity, and restrictions on informal trading have resulted in loss of income and livelihoods for millions of informal workers, exacerbating poverty and socio-economic inequalities [24].

8. Political and Governance Challenges
    - Diversion of Resources and Attention from Other Priorities: The COVID-19 pandemic has diverted resources, attention, and political capital from other pressing issues and priorities in Africa. Governments have had to allocate significant resources to pandemic response efforts, leaving fewer resources available for other critical sectors such as education, infrastructure, and social welfare [25].
    - Increased Risk of Political Instability: The socio-economic impacts of COVID-19, combined with existing political tensions and governance challenges in Africa, have increased the risk of political instability and unrest. Economic hardship, social inequalities, and perceptions of government mismanagement of the pandemic have fueled public discontent and protests in some countries, threatening political stability and democratic governance [26].
9. Environmental Impact
    - Changes in Air Quality and Pollution Levels: The COVID-19 pandemic has resulted in changes in air quality and pollution levels in Africa. Lockdown measures and reduced industrial activities have led to temporary improvements in air quality in some urban areas, offering a glimpse of the potential benefits of reduced pollution on public health and the environment [8].
    - Disruption of Conservation Efforts and Biodiversity Conservation: COVID-19-related disruptions to tourism, conservation efforts, and environmental protection initiatives have posed challenges for biodiversity conservation in Africa. Reduced funding, staffing shortages, and increased pressure on natural resources have threatened conservation gains and biodiversity conservation efforts across the continent [27].
10. Digital Divide and Access to Information
    - Limited Access to Digital Technologies and Internet Connectivity: The COVID-19 pandemic has highlighted existing disparities in access to digital technologies and internet connectivity in Africa. Limited infrastructure, high costs, and low digital literacy rates have hindered access to online education, remote work opportunities, and telehealth services, exacerbating socio-economic inequalities [28].
    - Challenges in Disseminating Accurate Health Information and Education: The digital divide in Africa has posed challenges in disseminat-

> ing accurate health information and education about COVID-19. Misinformation, rumors, and lack of access to reliable sources of information have hindered efforts to promote public awareness, preventive measures, and vaccination campaigns, undermining pandemic response efforts (UNICEF, 2020).

Mathematical modeling is a powerful tool used in various fields to understand complex systems, make predictions, and inform decision-making processes. It involves the creation of mathematical representations or simulations of real-world phenomena, allowing researchers to explore the dynamics of systems and evaluate different scenarios. In the context of epidemiology, mathematical modeling plays a crucial role in studying the transmission dynamics of infectious diseases, assessing intervention strategies, and predicting disease outcomes [29]. Mathematical models of infectious diseases typically incorporate parameters such as population demographics, disease characteristics, and transmission dynamics to simulate how infections spread within a population over time. These models can range from simple compartmental models, such as the susceptible-infected-recovered (SIR) model, to more complex agent-based models that simulate individual interactions within a population. By calibrating models to available data and validating their predictions against observed outcomes, researchers can gain insights into the underlying mechanisms driving disease transmission and evaluate the potential impact of interventions [30]. Nkengasong & Mankoula, studied Modeling COVID-19 Epidemic in Africa in 2020 [31], they developed a compartmental SEIR (susceptible-exposed-infected-recovered) model tailored to the demographics and healthcare infrastructure of African countries. The model projected a wide range of potential outcomes, highlighting the importance of early intervention and healthcare capacity in mitigating the spread of COVID-19 in Africa. Haider et al., studied modeling the COVID-19 epidemic in Africa 2020 [32]: Transmission Dynamics and Impact of Public Health Interventions. This study used a mathematical model to assess the transmission dynamics of COVID-19 in Africa and to evaluate the potential impact of public health interventions such as social distancing and travel restrictions. The model suggested that early implementation of stringent control measures could significantly reduce the burden of COVID-19 in Africa, but sustained efforts would be needed to prevent resurgence. Ogwang et al., investigated mathematical modeling of COVID-19 transmission dynamics in Africa in 2020 [33]: Implications for Control Measures. This study employed a mathematical model to investigate the impact of various control measures, including testing, contact tracing, and isolation, on COVID-19 transmission in African settings. The model highlighted the importance of rapid and targeted interventions in containing outbreaks and emphasized the need for enhanced surveillance and healthcare infrastructure. Acheneje et al. 2024 [56] developed a continuous-time mathematical model to analyze the co-infection dynamics of COVID-19 and monkeypox. They applied the discrete-time Pontryagin maximum principle and the MATLAB optimization toolbox to determine optimal control strategies, minimizing both infections and costs. Their results highlighted that intensified use of face masks, rodenticides, PPEs, immunization, and social distancing effectively reduces disease prevalence. Odiba et al. formulated a compartmental deterministic model with non-linear differential equations to analyze the co-infection dynamics of COVID-19 and HIV. They established the local and global stability of the disease-free equilibrium and estimated key model parameters using real-life data. Their numerical simulations in MATLAB provided insights into disease interactions, informing policy recommendations for effective co-infection control.

1.4. Aim and objectives of the study

The aim of this study is to assess the post-effects of COVID-19 in Africa using a mathematical modeling approach. Specifically, we aim to analyze the long-term impacts of the pandemic on key epidemiological parameters, healthcare systems, socio-economic factors, and public health interventions in African countries while the objectives include:

1. Develop a Mathematical Model: Formulate a compartmental mathematical model that incorporates the dynamics of COVID-19 transmission, including susceptible (S), exposed (E), infected (I), treated (T), deceased (D), and recovered (R) compartments. This model will be tailored to capture the unique demographic, healthcare, and socio-economic characteristics of African populations.
2. Assess Post-Effects of COVID-19: Evaluate the post-effects of COVID-19 in Africa by simulating the dynamics of the epidemic over an extended time horizon. Analyze the long-term trends in key epidemiological parameters, including infection rates, mortality rates, and healthcare demand, to understand the enduring impact of the pandemic on public health outcomes.
3. Propose Solutions for COVID-19 Control: Proffer solutions or suggest better ways to control COVID-19 in countries where it exists and future preparation for countries like Africa where its spread has stopped or been reduced. This objective will involve identifying effective public health interventions, such as vaccination campaigns, testing and contact tracing strategies, and community engagement initiatives, to mitigate the spread of COVID-19 and prevent future outbreaks.
4. Evaluate Socio-Economic Consequences: Examine the socio-economic consequences of COVID-19 on African communities, including the effects on livelihoods, poverty levels, food security, and access to essential services. Explore the differential impacts of the pandemic on vulnerable populations, such as women, children, and marginalized groups.
5. Qualitative Analysis of the Model: Conduct a qualitative analysis of the developed mathematical model to assess its validity, robustness, and applicability to real-world scenarios. Evaluate the model's assumptions, limitations, and sensitivity to parameter variations to ensure its reliability in informing policy decisions and public health interventions.

2. Model formulation

2.1. Model assumptions

The underlying assumptions used in formulating the mathematical model of COVID-19 includes:

1. The COVID-19 dead bodies are very infectious in spreading the disease.

2. Individuals with weakened immune systems in the treatment class can die and progress into the deceased class.
3. Individuals are assumed to get full recovery from the disease in the treatment class.

The mathematical model developed in this study is a compartmental model that captures the dynamics of COVID-19 transmission within a population. It consists of several compartments representing different stages of disease progression and population groups. The model is based on differential equations that describe the flow of individuals between compartments over time, allowing for the simulation of epidemic spread and the evaluation of intervention strategies. The total population $N(t)$ is divided into six epidemiological compartment. The susceptible humans $S(t)$ exposed humans $E(t)$, the infected humans $I(t)$, the disclosed humans $D(t)$, individuals in treatment class $T(t)$ and recovered humans $R(t)$.

Let Λ be the constant recruitment rate that recruited individuals into the susceptible population. The susceptible population is reduced at the rate λ which denotes the force of infection of COVID-19 which is a function of the contact rate of the susceptible and the infected humans, and the exposed individuals become infected at the rate ε_1 where ω and α_1 are the treatment and disease induced death rate respectively, γ is the recovery rate of infected individuals rate of diseased humans is α_2 and population of every compartment except $D(t)$ reduced by μ which is the natural death rate.

2.2. Compartment explanation:

- Susceptible (S): This compartment represents individuals who are susceptible to COVID-19 infection. Susceptible individuals can become infected upon exposure to the virus.
- Exposed (E): The exposed compartment represents individuals who have been exposed to the virus but are not yet infectious. During the latent period, exposed individuals are infected but do not exhibit symptoms and cannot transmit the virus to others.
- Infected (I): The infected compartment represents individuals who are infectious and capable of transmitting the virus to others. Infected individuals may exhibit symptoms of COVID-19, such as fever, cough, and fatigue.
- Treated (T): The treated compartment represents individuals who have been diagnosed with COVID-19 and are receiving medical treatment. Treatment may include hospitalization, supportive care, and antiviral medications to alleviate symptoms and reduce disease severity.
- Deceased (D): The deceased compartment represents individuals who have died from COVID-19 infection. Mortality rates may vary depending on factors such as age, underlying health conditions, and access to healthcare.
- Recovered (R): The recovered compartment represents individuals who have recovered from COVID-19 infection and have developed immunity to the virus. Recovered individuals may have acquired immunity through natural infection or vaccination.

Each compartment interacts with the others through transitions, which are governed by parameters such as transmission rates, recovery rates, and mortality rates.

By simulating the flow of individuals between compartments over time, the model can predict the trajectory of the epidemic, evaluate the impact of interventions, and inform public health decision-making. This compartmental model provides a simplified yet insightful representation of COVID-19 transmission dynamics, allowing for the exploration of various scenarios and the assessment of intervention strategies to control the spread of the virus in African populations.

Variables	**Description**
$S(t)$	Susceptible individuals
$E(t)$	Exposed individuals
$I(t)$	Infected individuals
$D(t)$	Deceased class
$T(t)$	Treatment compartment
$R(t)$	Recovered class
Parameters	**Description**
Λ	Constant recruitment rate
λ	Force of infection
μ	Natural death rate
ε_1	Rate at which exposed humans become infected
α_1	Disease-induced death rate
ω	Treatment rate
γ	Recovery rate
α_2	Burial rate of deceased body
ϕ	Contact rate of susceptible and infected humans

Table 1. Description of model variables and parameters

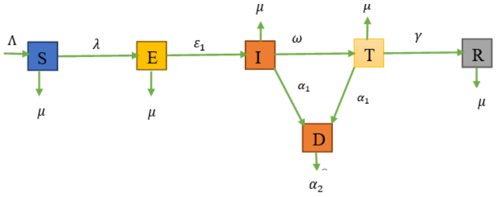


Figure 1. Schematic diagram for the model

3. Model equations

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (\lambda + \mu)S,\\
\frac{dE}{dt} &= \lambda S - (\varepsilon_1 + \mu)E,\\
\frac{dI}{dt} &= \varepsilon_1 E - (\alpha_1 + \omega + \mu)I,\\
\frac{dT}{dt} &= \omega I - (\alpha_1 + \mu)T,\\
\frac{dD}{dt} &= \alpha_1 I + \alpha_1 T - \alpha_2 D,\\
\frac{dR}{dtS} &= \gamma T - \mu R,
\end{aligned} \tag{3.1}$$

where $\lambda = \frac{\phi(I+D+T)}{N}$ denotes the force of infection of the COVID-19 model.

4. Analysis of the model

4.1. Invariant region of the model

In mathematical modeling, the invariant region denotes a collection of conditions or states within the model that remain unchanged over time, irrespective of initial conditions or variations in parameters [37]. In epidemiology, this concept translates to a stable set of conditions that characterize the behavior of a disease within a population. The identification of the invariant region is pivotal as it offers insights into the enduring behavior of the disease and aids in comprehending the fundamental mechanisms dictating its transmission. By delineating the boundaries of this region, researchers can enhance their ability to forecast the dynamics of the disease, evaluate the efficacy of control measures, and devise strategies for disease management and prevention [37, 38]. Ultimately, the invariant region serves as a fundamental element in shaping public health policies and interventions aimed at mitigating the impact of infectious diseases like COVID-19.

Theorem 4.1. *The solutions set of the proposed model are feasible whenever* $t > 0$, *if they enter the invariant region D, which is given by* $\Omega \in \mathcal{R}^6_+$.

Proof.

The total population of the model is given as

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

The sum of the differential equations is

$$N^{'}(t) = S^{'} + E^{'} + I^{'} + T^{'} + D^{'} + R^{'}.$$

On evaluating the algebraic terms, we obtain

$$N^{'}(t) = \Lambda - (S + E + I + T + D + R)\,\mu - (\omega I + \alpha_1 T + \alpha_2 D)\,,$$

$$N^{'}(t) = \Lambda - \mu N - (\omega I + \alpha_1 T + \alpha_2 D)\,,$$

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

Solving the differential equation using the integrating factor method, we obtain

$$N(t) \leq \frac{\Lambda}{\mu} + \left(N(0) - \frac{\Lambda}{\mu}\right) e^{-\mu t}.$$

Applying Birkhoff and Rota's theorem on the inequality, we obtain

$$0 \leq N \leq \frac{\Lambda}{\mu} \text{ as } t \to \infty.$$

Thus, D is a positively invariant set with respect to the schemaatic described by the model so that no solution path leaves through the boundary of region D. Thus, in this region, the model is said to be epidemiologically and mathematically well posed [6,7]. □

5. Positivity of solution of the model

It is necessary to show that all state variables of the model are non-negative for all time t, for the model to be epidemiologically and mathematically feasible in the region D given by [7,8]:

$$\Omega = \left\{(S, E, I, T, D, R) \in \mathbb{R}^6_+ : (S + E + I + T + D + R) \leq N\right\}.$$

This can be done by considering

$$\left\{(S, E, I, T, D, R) \geq 0 \in \mathbb{R}^6_+\right\}.$$

Lemma 5.1. *Suppose the initial data for the given model (3.1) is* $(S, E, I, T, D, R) > 0$. *Then the solutions* (S, E, I, T, D, R) *of the model (3.1) are positive for all time* $t > 0$.

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

We have from the first equation that

$$\frac{dS}{dt} = \Lambda - (\lambda + \mu)S,$$
$$\frac{dS}{dt} \geq -(\lambda + \mu)S,$$

This can also be written as

$$\int \frac{dS}{S} \geq -\int (\lambda + \mu)\, dt.$$

We obtain:

$$\ln S \geq -(\lambda + \mu)t + C,$$
$$S(t) \geq Ce^{-(\lambda+\mu)t}.$$

Applying the initial condition: when $t = 0$, $S(0) = C$.
Hence, $S(t) \geq S(0)e^{-(\lambda+\mu)t} \geq 0$ since $(\lambda + \mu) > 0$.
In the same way, it can be shown that $E(t), I(t), T(t), D(t), R(t) > 0$. □

5.1. Asymptotic stability of the disease-free equilibrium of the model

In mathematical modeling of infectious diseases, achieving disease-free equilibrium (DFE) represents a crucial milestone denoting a stable state within the model where the population remains devoid of the disease. Mathematically, DFE is attained when the rate of new infections reaches zero, effectively halting disease transmission. This equilibrium point serves as a pivotal reference for assessing the effectiveness of control measures and interventions. By comparing the model's behavior around the DFE with and without interventions, researchers can quantitatively evaluate the impact of various strategies on disease spread, aiding in the formulation of evidence-based public health policies [44].

Furthermore, stability analysis of the DFE provides valuable insights into the long-term behavior of the disease within the population. Stability refers to the system's tendency to return to the equilibrium state following perturbations or parameter changes. A stable DFE indicates that the population will persist in a disease-free state under typical conditions, while an unstable DFE indicates the potential for outbreaks or epidemics. Incorporating DFE analysis into mathematical models enables researchers to anticipate disease dynamics, assess intervention efficacy, and inform proactive measures for disease management and prevention [45].

Thus, disease-free equilibrium serves as a cornerstone in understanding infectious disease dynamics and guiding public health responses to mitigate disease spread. The steady state where infection does not exist (or absence of the disease), a point where $E = I = T = D = R = 0$, is called the disease-free equilibrium point (DFE), which is given by

Theorem 5.1. *The disease-free equilibrium point (DFE) of the system is given by* $\varepsilon_0 = \{S^*, E^*, I^*, T^*, D^*, R^*\} = \left\{\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0\right\}$.

5.2. The basic reproduction number R_0

The basic reproduction number, also called the fundamental reproductive rate of infected persons, R_0, refers to the average number of new infections caused by one COVID-19 infected individual in a completely susceptible population throughout their infectious period. This value is determined by employing the next generation operator method on the dynamical system [8]. We calculate the basic reproduction number by using the next generation matrix approach on the dynamical system. Hence, it follows that

$R_0 = \rho(FV^{-1})$ where ρ is the spectral radius (dominant eigenvalue) of FV^{-1}.

$$F = \begin{bmatrix} 0 & \phi & \phi & \phi \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} K_1 & 0 & 0 & 0 \\ -\varepsilon_1 & K_2 & 0 & 0 \\ 0 & -\alpha_1 & \alpha_2 & -\alpha_1 \\ 0 & -\omega & 0 & K_3 \end{bmatrix},$$

FV^{-1}

$$= \begin{bmatrix} \frac{\phi\varepsilon_1}{K_1K_2} + \frac{\phi\alpha_1\varepsilon_1(\omega+K_3)}{K_1K_2\alpha_2K_3} + \frac{\phi\omega\varepsilon_1}{K_1K_2K_3} & \frac{\phi}{K_2} + \frac{\phi\alpha_1(\omega+K_3)}{K_2\alpha_2K_3} + \frac{\phi\omega}{K_1K_2} & \frac{\phi}{\alpha_2} & \frac{\phi\alpha_1}{\alpha_2K_3} + \frac{\phi}{K_3} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}.$$

Therefore, the basic reproduction number is expressed as:

$$R_0 = \frac{\phi\varepsilon_1\left(\omega\alpha_1 + \omega\alpha_2 + K_3\alpha_1 + K_3\alpha_2\right)}{K_1K_2\alpha_2K_3}$$

with the constants defined as:

$$K_1 = \varepsilon_1 + \mu, \quad K_2 = \alpha_1 + \omega + \mu, \quad K_3 = \alpha_1 + \mu.$$

5.3. Effects of reproduction number (R_0) of COVID-19 on public health measures

The Basic Reproduction Number (R_0) of COVID-19, which represents the average number of secondary infections caused by one infected individual in a susceptible population, greatly influences public health measures.

- Impact on Transmissibility: A higher R_0 of COVID-19 signifies increased transmissibility, necessitating more stringent public health measures to curb transmission rates. These measures may include widespread testing, contact tracing, mandatory quarantine, and enforced social distancing to limit the spread of the virus [38].
- Severity of Outbreak Control Measures: The magnitude of the R_0 directly influences the severity of outbreak control measures implemented by public health authorities. Higher R_0 values often require more aggressive interventions, such as lockdowns, travel restrictions, and mass vaccination campaigns, to mitigate the risk of widespread transmission and protect public health [39].
- Resource Allocation: Higher R_0 values strain healthcare resources and infrastructure, leading to challenges in providing adequate medical care for COVID-19 patients. Healthcare systems may face shortages of hospital beds, ventilators, and medical personnel, necessitating resource allocation strategies to address surges in demand and ensure equitable access to care for all patients [40].
- Vaccination Prioritization: The R_0 of COVID-19 guides prioritization strategies for vaccination efforts. Populations with higher R_0 values may be prioritized for vaccination to interrupt transmission chains and reduce overall community spread. Additionally, vaccination campaigns may focus on vulnerable populations and high-risk settings to minimize the impact of the virus on public health [42].
- Behavioral Interventions: Understanding the R_0 of COVID-19 informs the design and implementation of behavioral interventions aimed at reducing transmission rates. Public health messaging, education campaigns, and community engagement initiatives may target behaviors that contribute to the spread of the virus, such as non-compliance with mask-wearing, inadequate hand hygiene, and participation in large gatherings [41].

- Surveillance and Monitoring: Continuous surveillance and monitoring of COVID-19 transmission dynamics are essential for assessing the effectiveness of public health measures and adapting strategies as needed. Monitoring changes in the R_0 over time provides valuable insights into the trajectory of the epidemic, the impact of interventions, and the emergence of new variants or strains that may alter transmission dynamics [43].

5.4. Local asymptotic stability of the DFE of the model

The concept of local stability in modeling, particularly in the context of dynamical systems, refers to the behavior of a system around a particular equilibrium point or steady state. Local stability analysis is crucial for understanding the behavior of dynamical systems near equilibrium points and is often used in various fields such as physics, biology, economics, and engineering [23, 51].

- Equilibrium Point: An equilibrium point of a dynamical system is a state where the system does not change over time. Mathematically, it is represented as a point where the derivatives of all variables with respect to time are zero. In other words, it is where the system “settles down” and stays put unless disturbed [49, 51].
- Local Stability: Local stability refers to the behavior of the system in the vicinity of an equilibrium point. It addresses the question of what happens to the system if it is perturbed slightly away from the equilibrium point. A system is locally stable if, after a small disturbance, it returns to its equilibrium point over time [39].
- Linearization: One common method to analyze local stability is linearization. This involves approximating the behavior of a nonlinear system near its equilibrium point by a linear system. This approximation is valid as long as the perturbations from the equilibrium point are small. Linearization simplifies the analysis because linear systems are generally easier to study [31, 51].
- Eigenvalues: In linear systems, the stability of an equilibrium point is determined by the eigenvalues of the system’s Jacobian matrix evaluated at that point. If all eigenvalues have negative real parts, the equilibrium point is stable (locally). If any eigenvalue has a positive real part, the equilibrium point is unstable [51].
- Phase Space Analysis: Another approach to analyze local stability involves examining the phase space behavior of the system. This involves plotting the trajectories of the system’s state variables to understand how they evolve over time. In the vicinity of a stable equilibrium point, trajectories tend to converge towards it, while in the vicinity of an unstable equilibrium point, trajectories diverge away from it [49, 51].

Theorem 5.2. *The disease-free equilibrium point of the model is locally asymptotically stable (LAS) if $R_0 < 1$, and unstable if $R_0 > 1$.*

Proof. Applying Jacobian matrix to show the local stability of the disease free equilibrium point

$$J\left(\varepsilon_0\right)=\begin{bmatrix} -\mu & 0 & -\phi & -\phi & -\phi & 0 \\ 0 & -K_1 & \phi & \phi & \phi & 0 \\ 0 & \varepsilon_1 & -K_2 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & -\alpha_2 & \alpha_1 & 0 \\ 0 & 0 & \omega & 0 & -K_3 & 0 \\ 0 & 0 & 0 & 0 & \gamma & -\mu \end{bmatrix}.$$

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

$$J_1\left(\varepsilon_0\right)=\begin{bmatrix} -K_1 & \phi & \phi & \phi \\ \varepsilon_1 & -K_2 & 0 & 0 \\ 0 & \alpha_1 & -\alpha_2 & \alpha_1 \\ 0 & \omega & 0 & -K_3 \end{bmatrix}.$$

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

$$\begin{aligned} &\lambda^4+(K_3+\alpha_2+K_2+K_1)\lambda^3 \\ &+\big(-\varepsilon_1\phi+K_2K_1+K_3K_1+\alpha_2K_1+K_3K_2+\alpha_2K_2+K_3\alpha_2\big)\lambda^2 \\ &+\big(-\omega\varepsilon_1\phi-\phi K_3\varepsilon_1-\alpha_1\varepsilon_1\phi-\phi\alpha_2\varepsilon_1 \\ &\qquad+K_1K_2K_3+K_1K_2\alpha_2+K_1K_3\alpha_2+K_2K_3\alpha_2\big)\lambda \\ &-\omega\varepsilon_1\phi\alpha_1-\omega\varepsilon_1\phi\alpha_2-\phi K_3\alpha_1\varepsilon_1-\phi K_3\alpha_2\varepsilon_1+K_1K_2\alpha_2K_3, \end{aligned}$$

$$\begin{aligned} &\lambda^4+(K_3+\alpha_2+K_2+K_1)\lambda^3 \\ &+\big(-\varepsilon_1\phi+K_2K_1+K_3K_1+\alpha_2K_1+K_3K_2+\alpha_2K_2+K_3\alpha_2\big)\lambda^2 \\ &+\big(-\omega\varepsilon_1\phi-\phi K_3\varepsilon_1-\alpha_1\varepsilon_1\phi-\phi\alpha_2\varepsilon_1 \\ &\qquad+K_1K_2K_3+K_1K_2\alpha_2+K_1K_3\alpha_2+K_2K_3\alpha_2\big)\lambda \\ &+K_1K_2\alpha_2K_3\left(1-\frac{\phi\varepsilon_1(\omega\alpha_1+\omega\alpha_2+K_3\alpha_1+K_3\alpha_2)}{\alpha_2K_1K_2K_3}\right), \end{aligned} \tag{5.1}$$

$$\begin{aligned} &\lambda^4+(K_3+\alpha_2+K_2+K_1)\lambda^3 \\ &+\big(-\epsilon_1\phi+K_2K_1+K_3K_1+\alpha_2K_1+K_3K_2+\alpha_2K_2+K_3\alpha_2\big)\lambda^2 \\ &+\big(-\omega\varepsilon_1\phi-\phi K_3\varepsilon_1-\alpha_1\varepsilon_1\phi-\phi\alpha_2\varepsilon_1 \\ &\qquad+K_1K_2K_3+K_1K_2\alpha_2+K_1K_3\alpha_2+K_2K_3\alpha_2\big)\lambda \\ &+K_1K_2\alpha_2K_3(1-R_0). \end{aligned}$$

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

$$(1-R_0)>0$$

$$R_0<1$$

Thus, the DFE point of the given model is locally asymptotically stable.

Remark 5.1. Epidemiologically,

$(i)\ \ if\ \ R_0 < 1,$

- Epidemiological Meaning: When R_0 is less than 1, it indicates that each infected individual, on average, transmits the disease to fewer than one other person. This suggests that the infection is not self-sustaining in the population.
- Implication: With R_0 less than 1, the number of new infections is decreasing over time, leading to the eventual extinction of the disease within the population.
- Public Health Response: In the context of public health, an R_0 value less than 1 implies that the disease is not capable of causing sustained transmission. Public health efforts should focus on maintaining surveillance and monitoring for any potential resurgence of the disease, while resources may be redirected to address other health priorities [34].

$(ii)\ \ if\ \ R_0 = 1,$

- Epidemiological Meaning: When R_0 is equal to 1, it indicates that each infected individual, on average, transmits the disease to exactly one other person. This suggests that the infection is endemic but not growing exponentially.
- Implication: With R_0 equal to 1, the number of new infections remains stable over time, with no net increase or decrease in the number of cases.
- Public Health Response: An R_0 value equal to 1 implies that the disease is endemic within the population but is not causing an epidemic. Public health efforts should focus on maintaining control measures and surveillance to prevent any increase in transmission and to ensure the disease remains at manageable levels [36].

$(iii)\ \ if\ \ R_0 > 1,$

- Epidemiological Meaning: When R_0 is greater than 1, it indicates that each infected individual, on average, transmits the disease to more than one other person. This suggests that the infection is capable of sustained transmission and may lead to an epidemic.
- Implication: With R_0 greater than 1, the number of new infections is increasing over time, leading to exponential growth in the number of cases.
- Public Health Response: An R_0 value greater than 1 signifies the potential for an epidemic. Public health measures should be implemented promptly to reduce transmission rates and prevent widespread outbreaks. Strategies may include vaccination campaigns, social distancing measures, and enhanced surveillance to identify and isolate cases [34].

□

5.5. Global asymptotic stability of the disease free equilibrium point of the model

In mathematical modeling, global stability is a crucial concept used to analyze the long-term behavior of dynamical systems, including those representing infectious disease transmission dynamics. Global stability refers to the property of a system whereby it converges to a single equilibrium state regardless of the initial conditions [43, 49]. In the context of infectious disease modeling, global stability analysis helps determine whether the disease-free equilibrium (DFE) or endemic equilibrium (EE) is stable over time. A system is globally stable if trajectories starting from any initial condition converge to the desired equilibrium point. This property is essential for understanding the overall behavior of the system and assessing the effectiveness of control measures in containing disease spread [46].The global stability of equilibrium points in infectious disease models is typically analyzed using mathematical techniques such as Lyapunov functions, linear stability analysis, and the theory of dynamical systems. Lyapunov functions are particularly useful for proving global stability by demonstrating that the function decreases along trajectories and attains its minimum at the equilibrium point. Linear stability analysis, on the other hand, involves evaluating the eigenvalues of the Jacobian matrix of the model at the equilibrium points to determine their stability properties. By analyzing the stability of equilibrium points, researchers can predict the long-term behavior of infectious diseases within populations and assess the impact of interventions on disease control [47, 49]. Global stability analysis plays a critical role in informing public health policies and interventions aimed at controlling infectious diseases on a global scale. By establishing the global stability of equilibrium points in mathematical models, researchers can identify effective strategies for disease management and prevention. Understanding the conditions under which the disease-free equilibrium or endemic equilibrium is stable provides valuable insights into the dynamics of disease transmission and guides decision-making processes to mitigate the impact of infectious diseases on public health [48, 49]. To investigate the global stability of the disease free equilibrium, we use the technique implemented by Castillo-Chavez and song [15, 66].

To do this, we write the equation in the uninfected class as

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

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

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

where $X = S \in R^1_+$denotes the uninfected population and $Z = (E, I, H, D) \in R^4{}_+$ denotes the infected population.

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

$$H_1: \quad \frac{dX}{dt} = F\left(X^*, 0\right), \ X^*$$

is globally asymptotically stable.

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

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

If the system satisfies the above condition, then the theorem below holds.

Theorem 5.3. *The equilibrium point* $\varepsilon_0 = (X^*, 0)$. *is globally asymptotically stable if* $R_0 \leq 1$.

Proof.

$$F(X, Z) = \left[\Lambda - (\lambda + \mu)S\right], \ G(X, Z) = \begin{bmatrix} \lambda S - (\varepsilon_1 + \mu)E \\ \varepsilon_1 E - (\alpha_1 + \omega + \mu)I \\ \omega I - (\alpha_1 + \mu)T \\ \alpha_1 I + \alpha_1 T - \alpha_2 D \end{bmatrix}.$$

At disease free equilibrium,

H_1 :

$$\frac{dS}{dt} = \left[\Lambda - (\lambda + \mu)S\right],$$

H_2 :

$$D_Z G\left(X^*, 0\right) Z = \begin{bmatrix} \lambda S - (\varepsilon_1 + \mu)E \\ \varepsilon_1 E - (\alpha_1 + \omega + \mu)I \\ \omega I - (\alpha_1 + \mu)T \\ \alpha_1 I + \alpha_1 T - \alpha_2 D \end{bmatrix},$$

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

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

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

□

Hence, the disease free equilibrium of the model is globally asymptotically stable.

The global asymptotic stability of the disease free equilibrium (DFE) of the COVID-19 model in (3.1) has significant implication for health care providers. Mathematically, it implies that regardless of the initial number of infections, the disease will eventually be eradicated if control measures ensure that the basic reproduction number remains below one. From a health care perspective, it suggests that consistent implementation of preventive measures - such as vaccination, social distancing and improved hygiene – can lead to the eventual elimination of COVID-19 from the population. Also, the stability means that temporary fluctuations in infection rates will not lead to recurrent outbreaks if control strategies remain effective.

5.6. Endemic equilibrium point of the model

In mathematical modeling of infectious diseases, the endemic equilibrium point represents a stable state within the model where the disease persists at a constant level within the population over an extended period. This equilibrium point occurs when the rates of infection, recovery, and other disease-related processes balance out, resulting in a stable prevalence of the disease [47, 49]. The endemic equilibrium is characterized by a non-zero level of infected individuals in the population, indicating ongoing transmission of the disease. This concept is essential for understanding the long-term dynamics of infectious diseases and evaluating the effectiveness of control measures in reducing disease prevalence [48].

Mathematically, the endemic equilibrium point is defined as the solution to the system of differential equations governing the dynamics of the disease transmission model. At this equilibrium point, the rates of change of the different compartments (such as susceptible, infected, and recovered individuals) are equal to zero, indicating a stable state where the disease prevalence remains constant over time. The stability of the endemic equilibrium can be analyzed using mathematical techniques such as linear stability analysis and Lyapunov functions, which assess the behavior of the system around the equilibrium point and determine whether it is stable or unstable [47, 49, 50]. Understanding the endemic equilibrium point is crucial for informing public health policies and interventions aimed at controlling infectious diseases [64, 65]. By identifying the conditions under which the disease persists within the population, researchers can assess the impact of interventions on disease transmission and develop targeted strategies for disease management and prevention. The endemic equilibrium provides valuable insights into the long-term dynamics of infectious diseases and guides decision-making processes to mitigate the impact of diseases on public health.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 to zero and solve for the state variables.

Thus, at the endemic equilibrium point,

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

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

We have that,

$$S^{**} = \frac{\Lambda}{(\lambda^{**} + \mu)},$$

$$E^{**} = \frac{\lambda^{**}\Lambda}{(\lambda^{**} + \mu)(\varepsilon_1 + \mu)},$$

$$I^{**} = \frac{\lambda^{**}\Lambda\varepsilon_1}{(\lambda^{**} + \mu)(\varepsilon_1 + \mu)(\alpha_1 + \omega + \mu)},$$

$$T^{**} = \frac{\lambda^{**}\Lambda\varepsilon_1\omega}{(\lambda^{**} + \mu)(\varepsilon_1 + \mu)(\alpha_1 + \omega + \mu)(\alpha_1 + \mu)},$$

$$D^{**} = \frac{\lambda^{**}\Lambda\alpha_1\varepsilon_1\omega + \lambda^{**}\Lambda\alpha_1\varepsilon_1}{\alpha_2(\lambda^{**} + \mu)(\varepsilon_1 + \mu)(\alpha_1 + \omega + \mu)(\alpha_1 + \mu)},$$

$$R^{**} = \frac{\lambda^{**}\Lambda\gamma\varepsilon_1\omega}{\mu(\lambda^{**}+\mu)(\varepsilon_1+\mu)(\alpha_1+\omega+\mu)(\alpha_1+\mu)}.$$

Substituting into the force of infection of the COVID-19 model, we obtained the endemic polynomial as

$$\lambda\left(a_0\lambda^2+a_1\lambda+a_2\right)=0,$$
$$\left(a_0\lambda^2+a_1\lambda+a_2\right)=0,$$

where

$$\begin{aligned} a_0 =& \left(\alpha_1+\mu\right)\left(\varepsilon_1+\mu\right)\alpha_2\left(\alpha_1+\omega+\mu\right) \\ & \times\Lambda\left(\mu^3\alpha_2+\alpha_2\left(\omega+2\alpha_1+\varepsilon_1\right)\mu^2+\left(\left(\alpha_1+\varepsilon_1\right)\alpha_2+\varepsilon_1\right)\left(\alpha_1+\omega\right)\mu+\gamma\omega\alpha_2\varepsilon_1\right) \\ & >0, \end{aligned}$$

$$\begin{aligned} a_1 =& 2\mu\left(\begin{array}{c} \left(\begin{array}{c} \mu^3+(\omega+2\alpha_1+\varepsilon_1)\mu^2+((-\phi/2+\omega+3/2\alpha_1)\varepsilon_1+\alpha_1(\alpha_1+\omega))\mu \\ -1/2\left(-{\alpha_1}^2+(\phi-\omega)\alpha_1+\omega(\phi-\gamma)\right)\varepsilon_1 \end{array}\right)\alpha_2 \\ +1/2\varepsilon_1(\alpha_1+\omega)(\mu-\phi) \end{array}\right) \\ & \times\alpha_2\left(\varepsilon_1+\mu\right)\left(\alpha_1+\omega+\mu\right)\left(\alpha_1+\mu\right)\Lambda, \end{aligned}$$

$$\begin{aligned} a_2 =& \Lambda\left(\alpha_1+\mu\right)\mu^2\left(\varepsilon_1+\mu\right)\left(\left(\alpha_1+\omega+\mu\right)\left(\mu^2+\left(\alpha_1+\varepsilon_1\right)\mu-\varepsilon_1\left(\phi-\alpha_1\right)\right)\alpha_2\right. \\ & \left.-\phi\varepsilon_1\left(\alpha_1+\omega\right)\right)\times\alpha_2\left(\alpha_1+\omega+\mu\right)\left(1-R_0\right)>0 \end{aligned}$$

whenever $R_0 < 1$.

At the endemic equilibrium, $\lambda \neq 0$.

The endemic equilibria of the model (3.1) can be obtained by solving for λ in the polynomial and substituting the positive values of λ into the endemic equilibrium points. The quadratic equation can be analyzed for the possibility of multiple equilibria when $R_0 < 1$. Hence, the following result is obtained.

Theorem 5.4. *The model (3.1) has*

1. *a unique endemic equilibrium if* $a_2 < 0 \Rightarrow R_0 > 1$*;*
2. *a unique endemic equilibrium if* $(a_1 < 0$ *and* $a_2 = 0)$ *or* $a_1^2 - 4a_0a_2 = 0$*;*
3. *two endemic equilibria if* $a_2 > 0, a_1 < 0$ *and* $a_1^2 - 4a_0a_2 > 0$*;*
4. *no endemic equilibrium otherwise.*

Thus, Case 2 of Theorem (5.4) suggests the possibility of backward bifurcation, where a LAS DFE co-exist with a LAS endemic equilibrium when the associated basic reproduction number is less than unity [62,63]. The epidemiological implication of backward bifurcation is that the classical requirement of the basic reproduction number being less than unity, though necessary is no longer sufficient for eradicating the disease from the population.

5.7. Sensitivity analysis of the model

Sensitivity analysis is a critical component of mathematical modeling that assesses the impact of parameter variations on model outcomes, providing insights into the robustness and reliability of the model's predictions. In the context of infectious disease modeling, sensitivity analysis helps identify the key parameters that drive the dynamics of disease transmission and quantifies their influence on model outcomes, such as disease prevalence, epidemic peak, and intervention effectiveness [50, 51]. One common approach to sensitivity analysis is to vary each model parameter individually while keeping other parameters fixed and observe the resulting changes in model outputs. Sensitivity measures, such as the partial derivative of the output with respect to the parameter (i.e., sensitivity coefficients), are calculated to quantify the sensitivity of model outcomes to parameter variations. Parameters with higher sensitivity coefficients have a greater impact on model outcomes and are considered more influential in shaping the dynamics of the disease [51,61]. It is carried out to determine the parameters that enhances the spread as well as control of an infection in a population.

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

$$\Im_x^{R_0} = \frac{\partial R_0}{\partial x} \times \frac{x}{R_0}.$$

Given that

$$R_0 = \frac{\phi\varepsilon_1(\omega\alpha_1+\omega\alpha_2+K_3\alpha_1+K_3\alpha_2)}{K_1K_2\alpha_2K_3},$$

$$\Im_\phi^{R_0} = 1.0000,$$

$$\Im_\omega^{R_0} = -\frac{\mu\omega}{(\alpha_1+\omega)(\alpha_1+\omega+\mu)} = -0.2507,$$

$$\Im_{\alpha_1}^{R_0} = -\frac{\alpha_1(\alpha_1{}^2\alpha_2+((2\mu-2\alpha_2)\omega-2\alpha_2\mu)\alpha_1+(\mu-\alpha_2)\omega^2+\mu(\mu-\alpha_2)\omega-\mu^2\alpha_2)}{(\alpha_1+\omega)(\alpha_1+\mu)(\alpha_1+\alpha_2)(\alpha_1+\omega+\mu)}$$
$$= 0.2848,$$

$$\Im_{\varepsilon_1}^{R_0} = -\frac{\mu}{\varepsilon_1+\mu} = 0.7334,$$

$$\Im_\mu^{R_0} = -\frac{(\alpha_1{}^2+(2\mu+\omega)\alpha_1+\mu^2+2\omega\mu+\omega\varepsilon_1)\mu}{(\varepsilon_1+\mu)(\alpha_1+\mu)(\alpha_1+\omega+\mu)} = -0.7805,$$

$$\Im_{\alpha_2}^{R_0} = -\frac{\alpha_1}{\alpha_1+\alpha_2} = 0.9869.$$

From the sensitivity analysis, it is observed that parameters with positive sensitivity index like $\phi, \epsilon_1, \alpha_1$ enhance the spread of COVID-19 in the population. Conversely, parameters with negative sensitivity indices like ω, μ, α_2 reduce the prevalence of the disease within the human population.

5.8. Data fitting of the COVID-19 model

In this section, we estimate the values of some of the key parameters used in the formulation of our COVID-19. Using the MATLAB fmincon algorithm, we fit our COVID-19 model to the cumulative cases of the disease in Nigeria obtained from

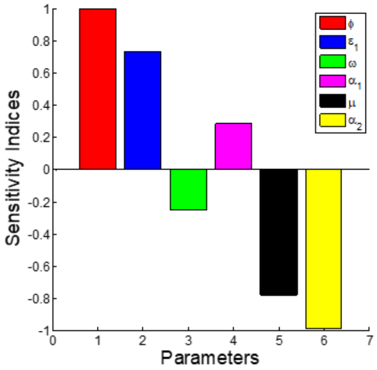


Figure 2. Sensitivity barchart

NCDC `https://ncdc.gov.ng/diseases/sitreps/?cat=14&name=An%20update%20of%20COVID-19%20outbreak%20in%20Nigeria` as presented in Table (2). The results of our estimates are presented in the parameter table of values in Table (3)

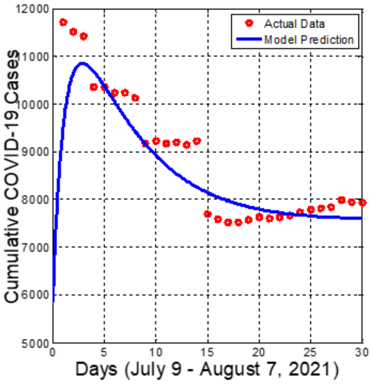


Figure 3. Data fitting for the COVID-19 model

6. Numerical simulations

Numerical simulations in mathematical modeling involve using computational techniques to approximate the behavior of complex systems described by mathematical equations. In the context of infectious disease modeling, numerical simulations are employed to predict the spread of diseases like COVID-19 within populations and assess the effectiveness of various intervention strategies [52, 53]. Numerical simulations play a crucial role in infectious disease modeling by providing insights into the potential trajectory of outbreaks, identifying key factors driving disease transmission, and informing public health decision-making [52]. They enable researchers and policymakers to assess the effectiveness of interventions, optimize resource allocation, and develop strategies for disease control and prevention. Numerical simulation of mathematical models for COVID-19 can have profound implications for

Table 2. Nigeria COVID-19 Daily reported cases from Jul. 9 - Aug. 7, 2021. **Source:** `https://ncdc.gov.ng/diseases/sitreps/?cat=14&name=An%20update%20of%20COVID-19%20outbreak%20in%20Nigeria`

Date	**Cases**
Jul. 9	11713
Jul. 10	11515
Jul. 11	11421
Jul. 12	10357
Jul. 13	10363
Jul. 14	10243
Jul. 15	10237
Jul. 16	10126
Jul. 17	9174
Jul. 18	9231
Jul. 19	9170
Jul. 20	9202
Jul. 21	9139
Jul. 22	9227
Jul. 23	7700
Jul. 24	7594
Jul. 25	7518
Jul. 26	7520
Jul. 27	7578
Jul. 28	7626
Jul. 29	7599
Jul. 30	7625
Jul. 31	7669
Aug. 1	7734
Aug. 2	7782
Aug. 3	7821
Aug. 4	7840
Aug. 5	7986
Aug. 6	7949
Aug. 7	7929

public health responses and the comprehension of the outbreak dynamics. In mathematical epidemiology, numerical simulation is useful in the following ways.

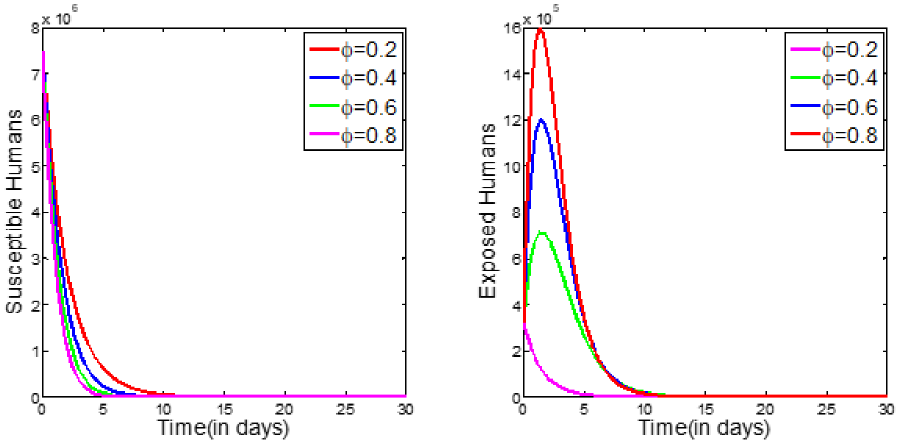
- Prediction and Forecasting: Through numerical simulations, mathematical models offer predictions and forecasts regarding the spread of COVID-19. These simulations empower public health officials to anticipate the course of the outbreak, identify regions at heightened risk, and deploy resources more efficiently [53].
- Evaluation of Control Measures: Simulation of mathematical models facilitates the assessment of diverse control measures and interventions in a virtual environment prior to real-world implementation. Policymakers can gauge the potential impact of interventions like vaccination campaigns, quarantine protocols, and treatment strategies [52].
- Optimization of Resource Allocation: By simulating various scenarios, mathematical models aid in optimizing the distribution of scarce resources such as healthcare staff, medical equipment, and treatment centers. This ensures the efficient allocation of resources to curb the outbreak [54].
- Understanding Transmission Dynamics: Numerical simulations provide insights into the transmission dynamics of COVID-19, encompassing elements such as asymptomatic transmission, contact tracing efficacy, and the influence of population mobility. This comprehension is pivotal for crafting tailored interventions [52].
- Scenario Planning: Simulation facilitates scenario planning, enabling health authorities to explore hypothetical situations and evaluate potential outcomes. This aids in crafting contingency plans and preparedness strategies for various scenarios, including worst-case scenarios [53].
- Communication and Education: Visualizations derived from numerical simulations serve as valuable tools for communicating intricate epidemiological concepts to the public, policymakers, and other stakeholders. They enhance public understanding of the outbreak dynamics and the rationale behind public health measures [52].

To perform numerical simulations of the model, appropriate initial conditions were estimated using COVID-19 data from Nigeria. These values were derived from publicly available sources such as the Nigeria Centre for Disease Control (NCDC), the World Health Organization (WHO), and other relevant epidemiological studies. The initial conditions for the state variables are as follows: Susceptible (S_0) was estimated as the total population of Nigeria minus the cumulative number of infected, exposed, treated, deceased, and recovered individuals at the start of the study. Based on the National Population Commission of Nigeria, the total population in 2020 was approximately 206 million [58]. Given the infection prevalence, we used $S_0 \approx 205,000,000$. Exposed (E_0) represents individuals in the latent period who are infected but not yet symptomatic or infectious. Using available data on the incubation period (approximately 5–6 days) and the rate of new infections at the time, we estimated $E_0 \approx 10,000$ [59]. Infected (I_0) corresponds to the number of confirmed active cases in Nigeria at the onset of the study period, approximately $I_0 \approx 3,500$ [59]. Treated (T_0) denotes the number of individuals receiving medical care, including those hospitalized or in isolation centers, estimated at $T_0 \approx 1,200$

(NCDC, 2020). Deceased (D_0) is the total number of recorded COVID-19-related deaths at the start of the study period, approximately $D_0 \approx 120$ [60]. Recovered (R_0) represents individuals who had recovered from COVID-19 at the beginning of the study, estimated at $R_0 \approx 750$ (NCDC, 2020).

Table 3. Parameter table of values

Parameter	Value	Source
Λ	$\frac{10000}{59 \times 365}$	Estimated
μ	$\frac{1}{59 \times 365}$	Estimated
ϕ	0.6000	[55]
γ	0.216555	Fitted
α_1	0.1	Fitted
ε_1	0.5000	[55]
α_2	0.483231	Fitted
ω	0.024011	Fitted

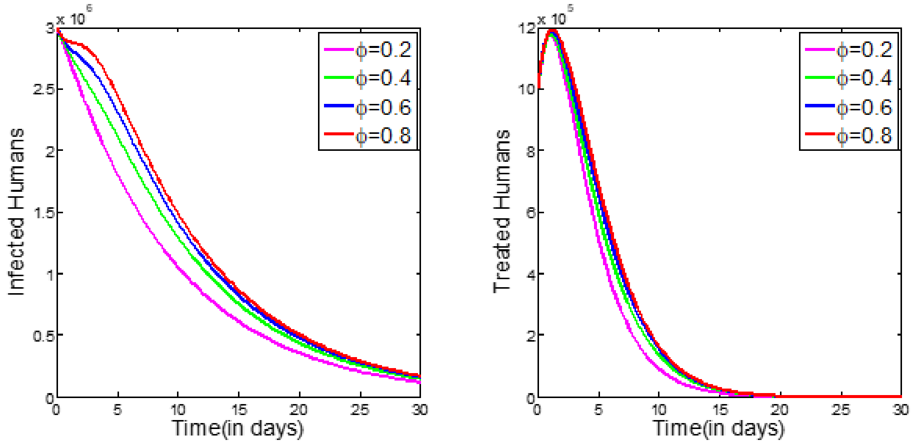


(a) Graph of susceptible humans against time

(b) Graph of exposed humans against time

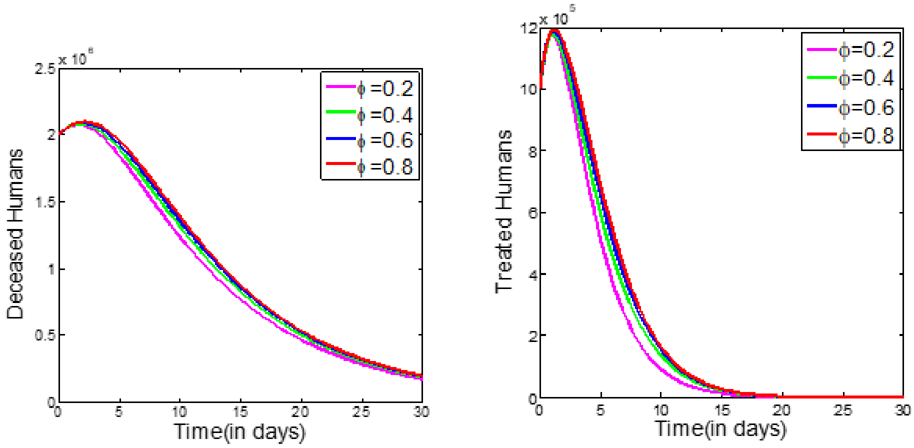
Figure 4. Human Population

As seen in Figure (4(a)), an increase in the contact rate between susceptible and infected humans (ϕ) results in a decrease in the population of susceptible humans over time. This indicates the highly infectious nature of the disease in the human population; hence, adequate measures to substantially reduce the contact rate between susceptible and infected individuals should be implemented to curb the prevalence of the disease. The initial increase in the population of exposed humans, as seen in Figure (4(b)), is due to the influx from the susceptible class



(a) Graph of infected humans against time (b) Graph of treated humans against time

Figure 5. Human Population



(a) Graph of deceased population against time (b) Graph of recovered humans against time

Figure 6. Human Population

resulting from their contact rate (ϕ) with infectious individuals. However, at a certain point, exposed individuals progress into the infected class, which explains the subsequent decline observed in the exposed population. The infected population, as seen in Figure (5(a)), declines over time due to the presence of adequate and enhanced treatment centers. Consequently, the treatment class experiences an increase as infected individuals transition into this category. The adequate medical attention and care provided to these infected individuals lead to their rapid recovery, resulting in a steady increase in the population of recovered humans over time, as shown in Figure (6(b)). This suggests that enhancing the treatment of individuals infected with COVID-19 can significantly reduce the burden of the disease in the human population. Moreover, infected individuals who refuse to seek treatment may progress into the deceased class, as indicated by the initial increase in this category in Figure (6(a)). To mitigate the spread of the disease from infectious COVID-19-related deaths, the proper disposal of infected bodies contributes to the decline in the deceased population over time.

6.1. Findings from the work

- Positive Sensitivity index of Contact Rate (ϕ) : Our study revealed a positive sensitivity index associated with the contact rate of infection (ϕ). This indicates that any interventions aimed at reducing the contact rate would significantly diminish the spread of the virus within the population.
- Negative Sensitivity index of Treatment Rate (ω): Conversely, we observed a negative sensitivity index concerning the treatment rate (ω). This suggests that promoting higher treatment rate would lead to an increased recovery rate, thereby effectively controlling the spread of the disease.
- Implications for Health Workers: These findings hold significant implications for healthcare workers involved in the control of COVID-19. Understanding the dynamics of transmission, particularly the sensitivity of contact and treatment rates, can aid in the development of more effective strategies for disease containment.
- Insights into Post-Effects: Our research provides valuable insights into the post-effects of COVID-19 in Africa. By elucidating the sensitivity of key parameters such as contact and treatment rates, we contribute to a deeper understanding of how the disease manifests and spreads within the region.
- Preparation for future Pandemics: The transmission dynamics uncovered in our study not only inform current control measures but also serve as a blueprint for preparing for future pandemics. By comprehending the factors that influence disease transmission, individuals and healthcare systems can better equip themselves to respond effectively to similar challenges in the future.
- Reduction in Disease Spread: As a result of our findings, it is evident that targeted interventions aimed at reducing contact rates can lead to a significant reduction in the spread of COVID-19. This highlights the importance of proactive measures in mitigating the impact of the disease on African populations.
- Contributions to Public Health: Ultimately, our research contributes to the broader field of public health by offering actionable insights into the dynam-

ics of infectious disease transmission. By identifying the sensitivity of key parameters, we empower policymakers, healthcare professionals, and the general public to make informed decisions that safeguard public health and mitigate the impact of future pandemics.

6.2. Conclusion

From the sensitivity analysis and the resulting bar chart depicted in Figure 2, it is evident that parameters exhibiting positive sensitivity indices contribute to the transmission of COVID-19 within the human population. Therefore, parameters such as $\phi,\ \varepsilon_1\ and\ \alpha_1$ facilitate the endemicity of the disease within the population. Conversely, parameters like $\omega,\ \mu,\ \alpha_2$ with negative sensitivity indices are anticipated to mitigate the prevalence of COVID-19 within the human population. The contact rate ϕ has a negative sensitivity index which implies that any effort taken to avoid contact rate between susceptible humans and infected humans would reduce the spread of COVID-19 within the population. In Figure (4(a)), the number of susceptible individuals diminishes to zero over time, while Figure (4(b)) illustrates a rapid increase in the number of exposed individuals which subsequently declines swiftly toward zero, due to a decrease in contact rate between susceptible and infected humans. Figure (5(a)) demonstrates a monotonic decrease in the number of infected individuals due to effective treatment (see Figure (5(b))), indicating that the disease can be eradicated from the population. In Figure (6(a)), the number of deceased decreases the zero over time as a result of effective control measures such isolation of infected individual to reduce contact rate and improved treatment. A high recovery rate, is observed in Figure (6(b)) which signifies effective control measure. In conclusion, our mathematical modeling study on the assessment of post-COVID-19 effects in Africa has unveiled crucial insights into the dynamics of disease transmission and control measures. Through rigorous qualitative analysis, we have demonstrated the pivotal role of contact and treatment rates in influencing the spread and containment of the virus. Our findings underscore the importance of targeted interventions aimed at reducing contact rates to mitigate disease transmission, while also emphasizing the significance of promoting higher treatment rates to enhance recovery and limit further spread. These insights hold profound implications for healthcare workers, policymakers, and the general public, providing a road map for more effective strategies in combating not only COVID-19 but also future pandemics. By fostering a deeper understanding of transmission dynamics, our study contributes to the collective effort in safeguarding public health and preparing for the challenges that lie ahead in a post-pandemic world.

6.3. Recommendations

Based on the findings of this study, we have the following recommendations

- Implement Targeted Intervention Strategies: It is necessary to develop and implement targeted intervention strategies aimed at reducing contact rates within communities. This may include measures such as social distancing protocols, mask mandates, and restrictions on large gatherings to minimize opportunities for virus transmission.
- Enhance Healthcare Infrastructure: Government should invest in and enhance healthcare infrastructure to ensure sufficient capacity for treating COVID-19

patients. This includes increasing the availability of hospital beds, medical supplies, and trained healthcare personnel to effectively manage and treat cases, thereby improving treatment rates and recovery outcomes.

- Promote Access to Testing and Treatment: Effort should be taken to promote widespread access to COVID-19 testing and treatment facilities to facilitate early detection, isolation, and treatment of infected individuals. This includes expanding testing capacities, providing affordable or free testing and treatment options, and implementing outreach programs to vulnerable communities.
- Strengthen Public Health Education: Effort should be made to launch comprehensive public health education campaigns to raise awareness about the importance of adhering to preventive measures, such as hand hygiene, wearing masks, and getting vaccinated. Emphasize the role of individual responsibility in reducing contact rates and preventing the spread of the virus within communities.
- Invest in Pandemic Preparedness: Effort should be taken to invest in long-term pandemic preparedness efforts to better equip healthcare systems and communities to respond effectively to future outbreaks. This includes establishing robust surveillance systems for early detection of emerging infectious diseases, stockpiling essential medical supplies, and conducting regular training exercises to ensure readiness to deploy response measures promptly.

Direction for future research: There exist several avenues in extending the research endeavors of this work. These include:

1. The incorporation of time dependent optimal control measures to adequately reduce the burden of the disease in the human population.
2. The use of age structured modeling approach to understand the transmission dynamics of COVID-19 across different age groups.
3. The use of Laplace Adomian Decomposition method to obtain the series solutions of the COVID-19 model.

Conflict of interest

The authors declare that they have no competing interest.

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Availability of data

The data used in this study are referenced and presented in Table (3) above.

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