MATHEMATICAL MODELING OF COVID-19 TRANSMISSION DYNAMICS IN NIGERIA

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ABSTRACT

The coronavirus disease (COVID-19) pandemic caused by Severe Acute Respiratory Syndrome Corona virus-2 SARS-CoV-2, has posed significant health and socio-economic challenges worldwide, including Nigeria. Understanding the disease's dynamics is essential for effective public health interventions. This study develops a mathematical model to analyze COVID-19 transmission in Nigeria, considering vaccination, isolation/hospitalization, and recovery processes. A compartmental SVEIHR (Susceptible, Vaccinated, Exposed, Infected asymptomatic, Infected symptomatic, Hospitalized, and Recovered model was formulated, dividing the population into susceptible, vaccinated, exposed, asymptomatic, symptomatic, hospitalized, and recovered groups. The model's equilibrium points were analyzed mathematically for stability. Key epidemiological parameters including the basic reproduction number $R_{0,}$ were derived to assess disease progression. Numerical simulations were conducted using MAPLE 18.0 software to evaluate vaccination and hospitalization impacts. The model demonstrated that solutions remained non-negative and bounded under epidemiologically realistic conditions. A disease-free equilibrium was stable when $R_0 < 1$, indicating the potential for eradication under controlled conditions. Simulations showed that increased vaccination rates reduced susceptible and infectious populations, while hospitalization effectively curtailed symptomatic and asymptomatic cases. The SVEIHR model underscores the critical role of vaccination and hospitalization in controlling COVID-19. These findings provide valuable insights for policymakers to optimize intervention strategies and mitigate the pandemic's impact in Nigeria.

Keywords: Epidemiological Model, COVID-19, Equilibrium Point, Basic Reproduction Number

1.0. INTRODUCTION

Coronavirus Disease (COVID-19) is an infectious respiratory illness characterized by symptoms such as fever, dry cough, fatigue, shortness of breath or difficulty breathing, and occasional gastrointestinal issues, severe acute respiratory syndrome (SARS), caused by the coronavirus SARS-CoV, is affected by temperature (Owolabi *et al.,* 2022*;* Tan *et al.*,2005).

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On December 31, 2019, an outbreak of respiratory illness, later confirmed as COVID-19, began in Wuhan, Hubei, China (Owolabi *et al.*,2022; Shao *et al.,* 2020). Many early cases were linked to a seafood market in Wuhan, which also sold live wild animals, raising concerns about animal-to-human transmission (Adhikari *et al.,* 2020; Giordano *et al.,* 2021). On March 11, 2020, the WHO declared COVID-19 a global pandemic, marking its first such declaration since the H1N1 influenza pandemic in 2009 due to the virus's alarming levels of spread and severity worldwide (Bedford *et al.,* 2020).

Nigeria reported its first case of COVID-19 through a 44-year-old Italian citizen diagnosed in Lagos State. The Italian consultant arrived in Nigeria on February 27, 2020, and the case was confirmed by the Nigerian Center for Disease Control (NCDC) on February 28, 2020, marking the first reported case of COVID-19 in sub-Saharan Africa (Bassey and Akaninyene, 2020). This case came after the initial outbreak in China in January 2020. The index case arrived at the Murtala Muhammad International Airport in Lagos at 10 p.m. on February 24, 2020, aboard a Turkish Airlines flight from Milan, Italy (Nigeria Center for Disease Control (NCDC)**;**Ojo, and Akinola2020). NCDC has been monitoring and reporting the cumulative and new number of confirmed cases, number of critical cases, and recorded deaths since the first occurrence of COVID-19 in Nigeria (Adejumo *et al*., 2020). To curb the spread of the virus, the Nigerian government implemented various measures (NCDC, 2020), the virulence power of SARS COV-2 remained formidable and has spread exponentially worldwide, with negative effects on the healthcare system, economic, financial, commercial, and social development across the globe (Owolabi *et al.*,2023; Odekina *et al*.,2022). These included travel restrictions, quarantine protocols, and public health awareness campaigns. Lockdowns and restrictions were enforced in major cities, leading to the closure of schools and businesses. The government also mandated the use of face masks, regular hand washing, and restrictions on movement. Additionally, testing and monitoring efforts were intensified to quickly identify and isolate cases, with testing centers established nationwide.

The Nigerian government collaborated closely with international organizations such as the World Health Organization (WHO) to receive support in the form of expertise, medical supplies, and equipment. As COVID-19 vaccines became available, Nigeria launched vaccination campaigns to immunize the population. These efforts aimed to achieve widespread coverage and mitigate the impact of the virus.

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Mathematical Modeling and simulation are important means of making useful decisions on transmission dynamics and control of both infectious and non-infectious diseases (Anderson, 1979; Akinsola and Oluyo, 2019). Modelling infectious diseases mathematically has proven essential in understanding disease transmission dynamics and evaluating control measures (Castillo-Chavez and Song, 2004; Adeyemi *et al*, 2020; Oladejo *et al*, 2020; Akinsola *et al*, 2023). The present work studies the impact of vaccination and hospitalization on COVID-19 transmission dynamics in Nigeria, considering an SVEIHR epidemic model.

2.0. METHODOLOGY

Model Formulation of the COVID-19 Model

At time *t*, the total human population denoted by $N(t)$, is divided into seven distinct groups: the Susceptible, $S(t)$, (individuals vulnerable to COVID-19), Vaccinated $V(t)$, (those who received the vaccine dose), Exposed $E(t)$, (individuals who contacted infected persons), $I_A(t)$ (represent those showing no symptoms of COVID-19), $I_s(t)$ (represent individuals showing symptoms), $H(t)$ (individuals that are to be the isolated/hospitalized), and $R(t)$,(the recovered individuals). The total human population is therefore given by

$$N(t) = S(t) + V(t) + E(t) + I_A(t) + I_s(t) + H(t) + R(t) \tag{1}$$

2.1. Population Dynamics

Individuals in the subpopulation $S(t)$ are recruited into the population by birth or immigration at a rate Λ, out of which some individuals are vaccinated at a rate θ and these individuals move to $V(t)$.The vaccine wanes at a rate ω, and so $V(t)$, reduces by ωV while $S(t)$ increases by ωV. The class $S(t)$ is further reduced by natural mortality at a rate μ, (which occur in all the subpopulations) as well as by contact with individuals who are either asymptomatic/ symptomatic infectious $\beta(\alpha I_A + I_S)$ and then moves to the exposed subpopulation, $E(t)$, where β is the effective contact rate and α is a modification parameter.

The subpopulation $E(t)$ is decreased by the progression rate ρ, $(1-\varepsilon)\rho$ fraction of which populate $I_A(t)$ and the other fraction, $\varepsilon\rho$ populates $I_s(t)$. $I_A(t)$ is decreased by natural recovery at a rate γ, while $I_s(t)$ is decreased by COVID-19 individual death rate δ and hospitalization/ isolation rate ϕ. $H(t)$ is populated by ϕ, the isolation rate and decreased by

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δ and symptoms treatment at a rate τ. The recovered population is increased when there are recoveries in the $I_A(t)$ and $H(t)$ at the rate γ and τ respectively. $R(t)$ is decreased by natural mortality at a rate μ as applied to other subpopulations.

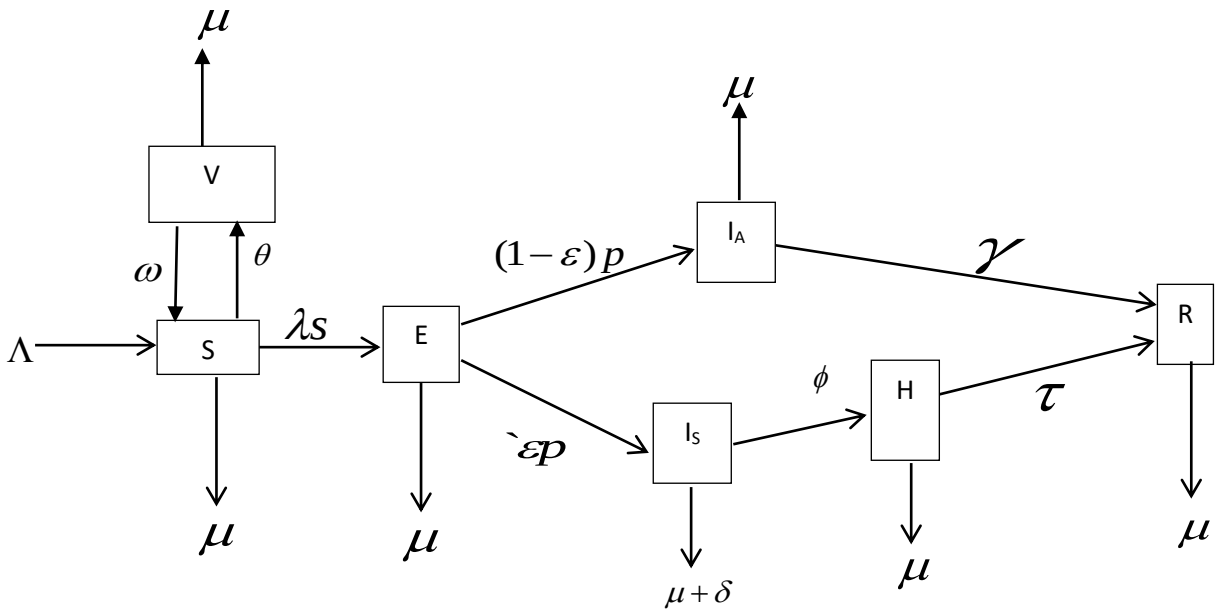

Figure 1: Schematic Flow of the SVEIHR Model

Using the flow diagram, Figure 1 and the dynamics of the disease as described above, the proposed model is mathematically expressed through a system of ordinary differential equations, incorporating the conventional incidence rate structure as given in Equation (2).

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \beta(\alpha I_A + I_S)S - (\mu + \theta)S + \omega V \\
\frac{dV}{dt} &= \theta S - (\mu + \omega)V \\
\frac{dE}{dt} &= \beta(\alpha I_A + I_S)S - (\mu + \rho)E \\
\frac{dI_A}{dt} &= (1-\varepsilon)\rho E - (\mu + \gamma)I_A \\
\frac{dI_S}{dt} &= \varepsilon\rho E - (\mu + \delta + \phi)I_S \\
\frac{dH}{dt} &= \phi I_S - (\mu + \delta + \tau)H \\
\frac{dR}{dt} &= \gamma I_A + \tau H - \mu R
\end{aligned} \tag{2}$$

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For simplicity, we let

$$k_1 = \beta(\alpha I_A + I_S),\ k_2 = (\mu+\theta),\ k_3 = (\mu+\omega),\ k_4 = (\mu+\rho),\ k_5 = (\mu+\gamma),\ k_6 = (\mu+\delta+\phi)$$

$$k_7 = (\mu+\delta+\tau)$$

Table 1: The Description of Parameters

Parameters	Reference value	Source
Λ	3 594 368	Calculated from demographic data
β	0.0109	Acheneje (2024)
ω	0.084	NCDC (2022)
θ	0.038	NCDC (2022)
α	0.5	Chen *et al* (2020)
δ	0.00001384480	Calculated from demographic data
ϕ	0.0135	Okuoghae (2020)
γ	0.13978	Acheneje (2024)
τ	0.067	Okuoghae (2020)
ε	0.5	Okuoghae (2020)
ρ	0.04775	Calculated from demographic data
μ	0.0158	Worldometers (2023)

3.0. ANALYSIS OF THE COVID-19 MODEL

3.1. Positivity and boundedness of solutions of the model

Theorem 1: Let the initial conditions of the model (2.2)be such that

$$\{S(0)\geq 0,\ V(0)\geq 0,\ E(0)\geq 0,\ I_A(0)\geq 0,\ I_s(0)\geq 0,\ H(0)\geq 0,\ R(0)\geq 0\}\in\Omega. \tag{3}$$

Then the solution set $\{S(t),\ V(t),\ E(t),\ I_A(t),\ I_s(t),\ H(t),\ R(t)\}\in\Omega$ is non-negative in Ω for all time $t\geq 0$.

Proof: By examining the first equation of the model (2), we observe that

$$\frac{dS}{dt} \geq -[\mu+\theta+\beta(\alpha I_A + I_S)]S \tag{4}$$

Separating the variables gives

$$\Rightarrow \frac{dS}{S(t)} \geq -[\mu+\theta+\beta(\alpha I_A + I_S)]d(t) \tag{5}$$

Integrating both sides gives

$$\ln S(t) \geq -\left[(\mu+\theta)t + \int \beta(\alpha I_A + I_S)dt\right] + C_1 \tag{6}$$

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$$\therefore\ S(t) = S_0 e^{-\left[(\mu+\theta)t+\int \beta(\alpha I_A + I_S)dt\right]} \tag{7}$$

It follows that $S(t) \geq 0$ holds true only when $S(0) \geq 0$. Analogous reasoning applies to the remaining state variables, ensuring their non-negativity. Consequently, nonnegative initial conditions guarantee non-negative state variables for all $t \geq 0$.

Theorem 2: Every solution in the feasible region

$$\Omega = \left\{ S(t), V(t), E(t), I_A(t), I_s(t), H(t), R(t) \in \Re_+^7 : S(t) + V(t) + E(t) + I_A(t) + I_s(t) + H(t) + R(t) \leq \frac{\Lambda}{\mu} \right\} \tag{8}$$

is positivity invariant with respect to the COVID-19 model (2) in human population.

Proof: Recall from (1) that $N(t) = S(t) + V(t) + E(t) + I_A(t) + I_s(t) + H(t) + R(t)$.

Differentiating this with respect to *t* gives

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dV(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI_A(t)}{dt} + \frac{dI_s(t)}{dt} + \frac{dH(t)}{dt} + \frac{dR(t)}{dt} \tag{9}$$

Putting the derivatives from (2) reduces (9) to

$$\frac{dN(t)}{dt} = \Lambda - \mu N - \delta\left(I_S + H\right) \tag{10}$$

$$\frac{dN(t)}{dt} \leq \Lambda - \mu N \tag{11}$$

Using the integrating factor, I.F= $e^{\int \mu dt} = e^{\mu t}$

$$\mathrm{N(t)} \leq e^{-\mu t}\left[\int \Lambda e^{\mu t} dt\right] \tag{12}$$

$$\mathrm{N(t)} \leq e^{-\mu t}\left[\frac{\Lambda}{\mu} e^{\mu t} + C\right] \tag{13}$$

$$\mathrm{N(t)} \leq \left[\frac{\Lambda}{\mu} e^{\mu t} + C\right]\ e^{-\mu t} \tag{14}$$

Therefore, $0 \leq N(t) \leq \frac{\Lambda}{\mu}$ (15)

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Analyzing limits as t approaches 0 and infinity reveals $N(t)$ approaches $N(0)$ and $\frac{\Lambda}{\mu}$ respectively. Hence, $0 \le N(t) \le \frac{\Lambda}{\mu}$. This demonstrates model (2) solutions are non-negative and bounded within Ω for all $t \ge 0$, ensuring epidemiological realism and mathematical coherence.

3.2. COVID-19 free equilibrium point, ε_0

Model (2) equilibrium points are characterized by constant solutions that fulfil

$$\frac{dS(t)}{dt} = \frac{dV(t)}{dt} = \frac{dE(t)}{dt} = \frac{dI_A(t)}{dt} = \frac{dI_s(t)}{dt} = \frac{dH(t)}{dt} = \frac{dR(t)}{dt} = 0 \tag{16}$$

$$E = I_A = I_S = H = 0. \tag{17}$$

The disease-free equilibrium ε_0, obtained by solving system (2) subject to (17) as

$$\varepsilon_0 = \left(\frac{(\mu+\omega)\Lambda}{\mu(\mu+\theta+\omega)}, \frac{\theta\Lambda}{\mu(\mu+\theta+\omega)}, 0,0,0,0,0 \right) \tag{18}$$

3.3. Basic Reproduction Number, R_0

The basic reproduction number $R_{0,}$, is the average number of secondary cases of the disease made by a typical infectious person during his infectious period in a complete susceptible population. Using the next generation operator approach described by Diekmann *et al.* (1990); Van den Driessche and Watmough (2002),

$$R_0 = \rho\left(FV^{-1}\right) \tag{19}$$

At equilibrium ε_0, F signifies the transmission Jacobian given by

$$f = \begin{pmatrix} \beta(\alpha I_A + I_S)S \\ 0 \\ 0 \\ 0 \end{pmatrix} \quad \text{and} \quad \upsilon = \begin{pmatrix} (\mu+\rho)E \\ -(1-\varepsilon)\rho E + (\mu+\gamma)I_A \\ -\varepsilon\rho E + (\mu+\delta+\phi)I_S \\ -\phi I_S + (\mu+\delta+\tau)H \end{pmatrix} \tag{20}$$

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$$F = DF\,|_{E0} = \begin{pmatrix} 0 & \alpha\beta & \beta & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V = D\upsilon\,|_{E0} = \begin{pmatrix} \mu+\rho & 0 & 0 & 0 \\ -(1-\varepsilon)\rho & \mu+\gamma & 0 & 0 \\ -\varepsilon\rho & 0 & \mu+\delta+\phi & 0 \\ 0 & 0 & -\phi & \mu+\delta+\tau \end{pmatrix} \tag{21}$$

And V denotes the transition Jacobian of υ evaluated at ε_0

Hence, $R_0 = \dfrac{\beta S^0}{\mu+\rho}\left[\dfrac{(1-\varepsilon)\rho\alpha}{\mu+\gamma} + \dfrac{\varepsilon\rho}{\mu+\delta+\varphi}\right]$ (22)

3.4. COVID-19 endemic equilibrium, ε^*

The human population is said to be in a state of COVID-19-endemic equilibrium, ε^*, when

$$E \neq I_A \neq I_S \neq H \neq 0. \tag{23}$$

Solving (2.2) subject to (3.17) gives

$$\varepsilon^* = \left(S^*, V^*, E^*, I_A{}^*, I_S{}^*, H^*, R^*\right), \tag{24}$$

where,

$$S^* = \frac{\mu+\omega}{\mu(\mu+\theta+\omega)}\left[\Lambda - (\mu+\rho)E^*\right]$$

$$V^* = \frac{\theta(\mu+\omega)}{\mu(\mu+\omega)(\mu+\theta+\omega)}\left[\Lambda - (\mu+\rho)E^*\right]$$

$$I_A{}^* = \frac{(1-\varepsilon)\rho E^*}{\mu+\gamma}$$

$$I_S{}^* = \frac{\varepsilon\rho E^*}{\mu+\delta+\phi}$$

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$$H^* = \frac{\varepsilon\rho\phi E^*}{(\mu+\delta+\phi)(\mu+\delta+\tau)}$$

$$R^* = \frac{1}{\mu}\left[\frac{(1-\varepsilon)\rho\gamma}{\mu+\gamma} + \frac{\varepsilon\rho\tau}{\mu+\delta+\phi}\right]E^*,$$

with $E^* = \frac{\Lambda(R_0-1)}{R_0(\mu+\rho)}$,

where $R_0 = \frac{\beta}{\mu+\rho}\left[\frac{(1-\varepsilon)\rho\alpha}{\mu+\gamma} + \frac{\varepsilon\rho}{\mu+\delta+\phi}\right]S^0$.

Hence, a unique endemic equilibrium exists for the COVID-19 model if $R_0 > 1$.

3.5. Local stability of COVID-19 free equilibrium point

Theorem 3: The disease-free equilibrium ε_0 is locally asymptotically stable, if the reproduction numbers are such that (i) $R_1 < 1$ (ii) $R_2 < 1$

Proof: The local asymptotic stability is investigated using the Jacobian matrix approach as follows:

First, the Jacobian of the system (2) is obtain at ε_0, thus

$$J(\varepsilon_0) = \begin{pmatrix} -(\mu+\theta) & \omega & 0 & -\alpha\beta S^0 & -\beta S^0 & 0 & 0 \\ \theta & -(\mu+\omega) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\mu+\rho) & \alpha\beta S^0 & \beta S^0 & 0 & 0 \\ 0 & 0 & (1-\varepsilon)\rho & -(\mu+\gamma) & 0 & 0 & 0 \\ 0 & 0 & \varepsilon\rho & 0 & -(\mu+\delta+\phi) & 0 & 0 \\ 0 & 0 & 0 & 0 & \phi & -(\mu+\delta+\tau) & 0 \\ 0 & 0 & 0 & \gamma & 0 & \tau & -\mu \end{pmatrix} \tag{25}$$

The eigenvalues of the Jacobian matrix $J(\varepsilon_0)$ are

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$$\lambda_1 = -(\mu+\theta);\ \lambda_2 = \frac{-\mu(\mu+\theta+\omega)}{\mu+\theta};\ \lambda_3 = -(\mu+\rho);\ \lambda_4 = -(\mu+\gamma)(1-R_1);$$

$$\lambda_5 = -(\mu+\delta+\phi)\left[1+\frac{R_1R_2}{1-R_1}\right];\ \lambda_6 = -(\mu+\delta+\tau);\quad \text{and} \qquad \lambda_7 = -\mu,$$

which are all negative provided that: $(i)\ R_1<1;\ (ii)\ 1+\frac{R_1\ R_2}{1-R_1}>0;\ (iii)\ R_2<1.$

Hence, the disease-free equilibrium ε_0 is locally asymptotically stable if conditions (i) – (iii) hold.

3.6. Global stability of COVID-19 free equilibrium point

THEOREM 4: The diseases-free equilibrium, ε_0, is globally asymptotically stable if $R_0 \le 1$ and unstable if $R_0 > 1$.

Proof: Let L be a candidate Lyapunov function such that

$$L(S,E,I_A,I_S) = \left(S - S^0 - S^0 \ln\frac{S}{S^0}\right) + \frac{(1-\varepsilon)\rho\alpha E}{(\mu+\rho)(\mu+\gamma)} + \frac{\varepsilon\rho E}{(\mu+\rho)(\mu+\delta+\phi)} + \frac{\alpha I_A}{\mu+\gamma} + \frac{I_S}{\mu+\delta+\phi} \tag{26}$$

where $S^0 = \frac{(\mu+\omega)\Lambda}{\mu(\mu+\theta+\omega)}$ is the equilibrium point if $S(t)$at DFE clearly from (26), L is positive definite since $S^0 \le S$.

$$\frac{dL}{dt} = \left(1-\frac{S^0}{S}\right)\frac{dS}{dt} + \frac{(1-\varepsilon)\rho\alpha}{(\mu+\rho)(\mu+\gamma)}\frac{dE}{dt} + \frac{\varepsilon\rho}{(\mu+\rho)(\mu+\delta+\phi)}\frac{dE}{dt} + \frac{\alpha}{\mu+\gamma}\frac{dI_A}{dt} + \frac{1}{\mu+\delta+\phi}\frac{dI_s}{dt}$$

$$\frac{dL}{dt} = \left(\frac{S-S^0}{S}\right)\left[\Lambda - \beta(\alpha I_A + I_S)S - (\mu+\theta)S + \omega V\right] + \frac{(1-\varepsilon)\rho\alpha}{(\mu+\rho)(\mu+\gamma)}\left[\beta(\alpha I_A + I_S)S - (\mu+\rho)E\right]$$
$$+ \frac{\varepsilon\rho}{(\mu+\rho)(\mu+\delta+\phi)}\left[\beta(\alpha I_A + I_S)S - (\mu+\rho)E\right] + \frac{\alpha}{\mu+\delta}\left[(1-\varepsilon)\rho E - (\mu+\gamma)I_A\right] + \frac{1}{\mu+\delta+\phi}\left[\varepsilon PE - (\mu+\delta+\phi)I_S\right]$$

(27)

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Thus, $(S,V,E,I_A,I_S,H,R) \to \left(\frac{(\mu+\omega)\Lambda}{\mu(\mu+\theta+\omega)}, \frac{\theta\Lambda}{\mu(\mu+\theta+\omega)}, 0,0,0,0,0 \right)$ as $t \to \infty$, and the largest compact invariant set is the singleton $\{\varepsilon_0\}$, and so by LaSalle's invariance principle (LaSalle, 1976), every solution of the model equation (2) approaches ε_0 as $t \to \infty$ whenever $R_0 < 1$. Hence, the model's disease-free equilibrium is globally asymptotically stable if $R_0 \leq 1$, and unstable if $R_0 > 1$.

4.0 NUMERICAL SIMULATIONS AND DISCUSSION

The numerical simulations of the model were carried out with the aid of MAPLE 18.0 software to validate the results of the qualitative analysis and to visualize the behaviour of the populations in the presence of COVID-19. Parameter values used in simulations were sourced from available literature, with estimates made for unavailable data, as presented in Table 1.

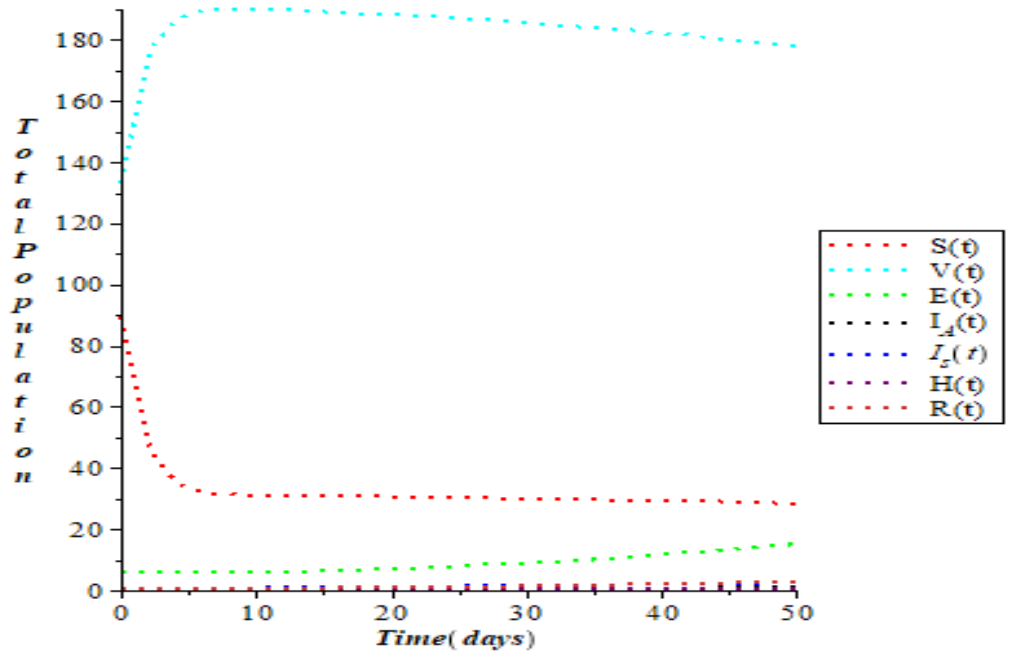

Figure 2: Solution plots of the model equations showing the behavior of the population in the presence of COVID-19

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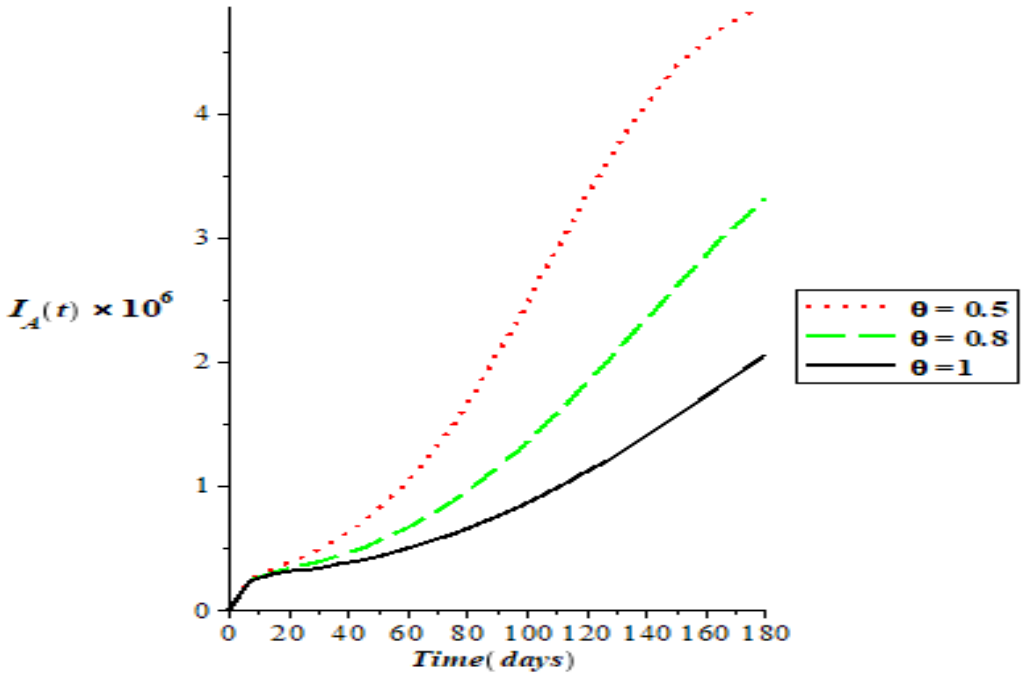

Figure 3: Effect of vaccination rate on asymptomatic infective population

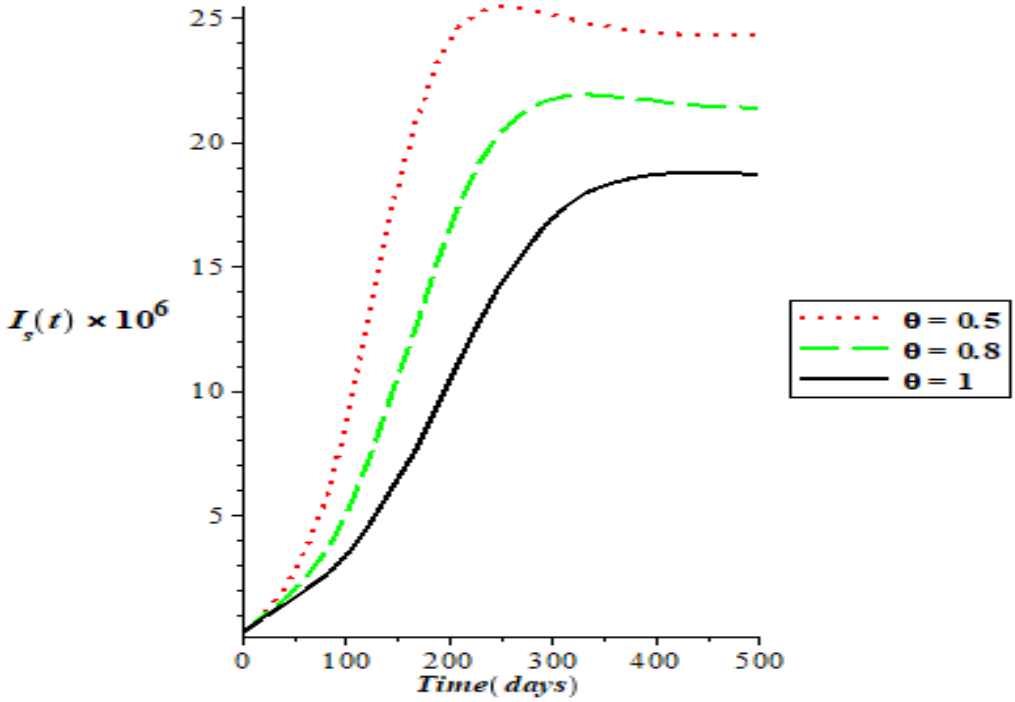

Figure 4: Effect of vaccination rate on symptomatic infective population

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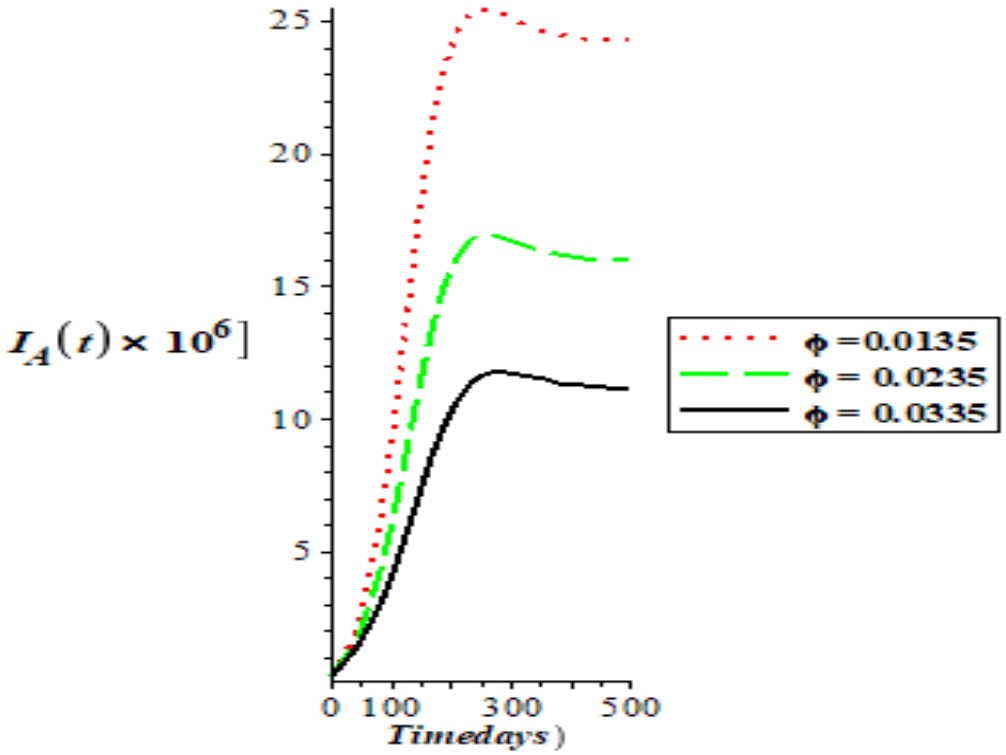

Figure 5: Effect of hospitalization rate on asymptomatic infective population

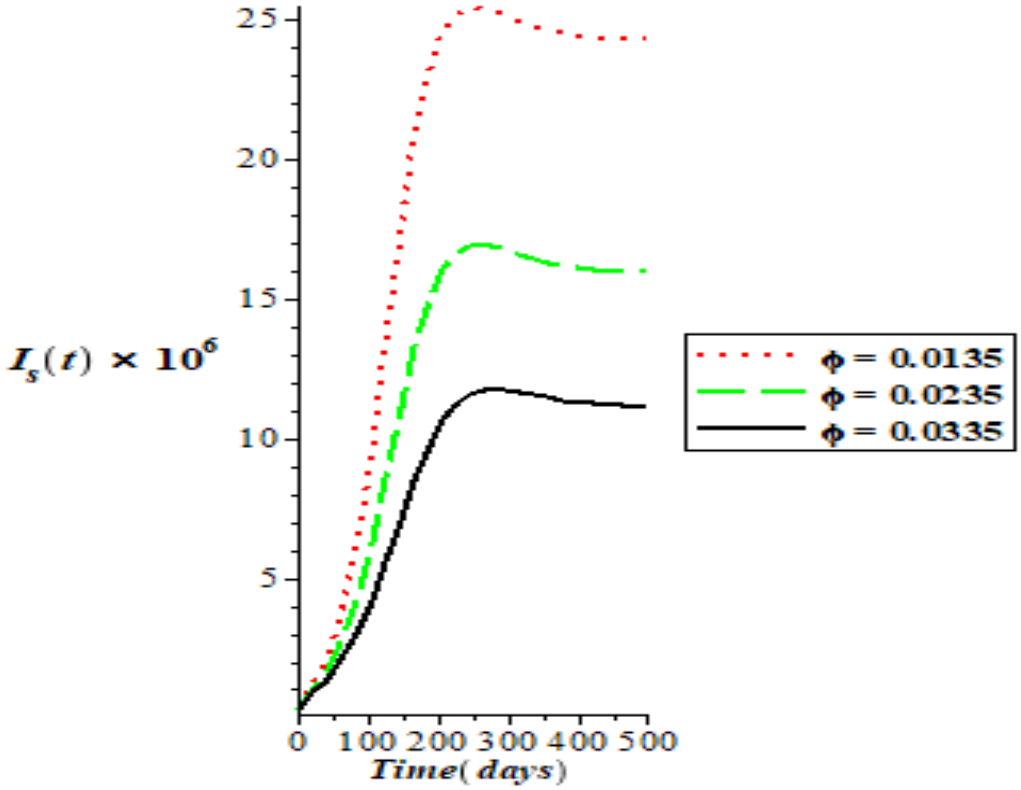

Figure 6: Effect of hospitalization rate on symptomatic infective population

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Figure 2 shows that the model captures the decline in the susceptible population over time, reflecting the natural progression of the epidemic as individuals either become exposed, vaccinated, or recover from the disease. The increase in recovered individuals demonstrates the positive impact of recovery rates, but it also highlights the need for sustained control measures to mitigate further transmission.

From Figures 3 and 4, increased vaccination rates (θ) lead to a significant reduction in both asymptomatic and symptomatic infectious populations. This underscores the role of widespread immunization in breaking transmission chains. The simulations highlight the importance of targeting high-contact populations and maintaining consistent vaccine distribution to achieve herd immunity.

From Figures 5 and 6, hospitalization rates (ϕ) are shown to reduce the infectious population effectively. By isolating symptomatic individuals, the model demonstrates a corresponding decrease in disease transmission. This finding emphasizes the importance of expanding healthcare infrastructure, including hospital capacity and isolation facilities, as a critical component of epidemic control.

5.0. CONCLUSION

This study introduces an innovative mathematical framework to investigate COVID-19 transmission dynamics in human populations. Our proposed model undergoes rigorous mathematical analysis, demonstrating epidemiological viability and well-posedness through non-negativity and boundedness of solutions inside a permissible region. Analysis in this work shows that both the disease-free equilibrium is globally asymptotically stable if $R_0 \leq 1$ and a unique endemic equilibrium exists whenever $R_0 > 1$. The basic reproduction number R_0 serves as a critical threshold, determining the disease's fate. Specifically: for $R_0 < 1$, COVID-

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19 disease is controllable and will be eradicated, while forR_0> 1, COVID-19 persists in the population. Strategically administering vaccine does significantly reduces this rate.

The findings of this research provided valuable insights for policymakers and healthcare professionals, highlighting the importance of vaccination programs targeting high-contact populations, maternal vaccination initiatives, effective recovery and management strategies. The findings from this research also reinforce the need for a multi-pronged approach to COVID-19 control, combining vaccination campaigns, effective isolation protocols, and public awareness initiatives. Policymakers should prioritize resource allocation to maintain high vaccination rates and support healthcare systems in managing severe cases. Investments in data-driven modelling and surveillance systems will enable adaptive responses to emerging variants or future pandemics. By understanding the dynamics of COVID-19 transmission and the impact of key parameters, this research informs evidence-based interventions to control and potentially eliminate this disease.

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