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Qualitative Analysis of the Transmission Dynamics and Optimal Control of Covid-19

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Abstract

Globally, the COVID-19 presents a serious concern to the wellbeing of people. COVID-19 was first detected in Wuhan, China. The disease became a source of concern for Nigerians after the country registered its first case in February 2020. Currently, the country has recorded 255,103 confirmed cases, 249,246 recovered cases, and 3,142 deaths as of March 21, 2022.

We proposed a SEQIHRV model to investigate the spread of coronavirus disease in Nigeria. This model defines the infection dynamics' transmission routes as well as effect of contaminated surfaces on the human population. Unfortunately, the virus's propagation and mortality from COVID-19 is increasing daily. Therefore, it is required to manage and control the flow of the infection. The impact of control measures as time-dependent interventions was investigated in this study utilizing optimization technique to determine their effects on the spread of Corona virus. The basic reproduction was calculated and used to calcite the sensitive parameters affecting the system, which revealed the key parameters leading to COVID-19 propagation. The control optimization of the sytem was performed using Pontryagin's maximum principle to determine the best approach for controlling the spread. The discoveries from the simulation showed that the combination of all four control approaches will help to reduce infection to zero in the population.

Keywords: Reproduction Number; Stability Analysis; SEQIHRV model; Control measures; Sensitivity Analysis

INTRODUCTION

According to [1], Coronaviruses (CoVs) are the most numerous groups of viruses in the Nidovirales. Coronavirus virion is round and has a diameter of about 125 nm. The most noticeable characteristics of the virus is the club-shaped spiky projections on the virion's surface. The virion called Coronaviridaeis found in a broad range of hosts& carriers, infecting many avian species/subspecies and even mammalian, this virion most times affect the upper respiratory, hepatic, gastrointestinal, and central nervous system through several of infection [2, 3, 4].

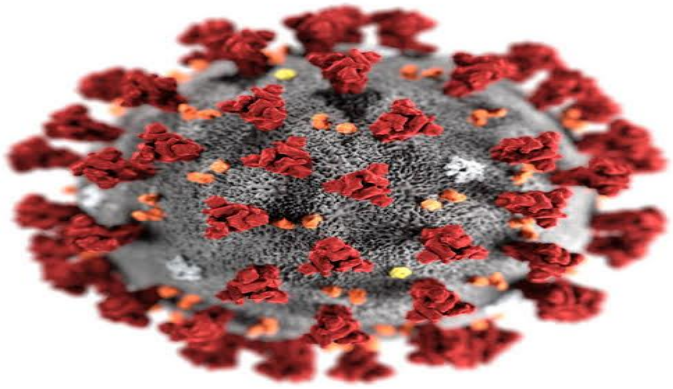

Figure 1 Diagram showing the shape of COVID-19

According to the [13], the virus has spread to all over the country, resulting in a total of 255190 reported cases as of March 21, 2022.

Due to the rapid rate of spread of corona virus in Nigeria, It is important to formulate a model to examine the disease flow and dissemination, including quarantined persons, hospitalized/confirmed patients, and pathogen concentrations in the environment. However, presently, COVID-19 has no cure and it is very dangerous to human health [5, 6, 3,]. COVID-19 has caused 3,142 deaths across the country as of March 21, 2022 [7]. Nevertheless, the spread of the infection can be controlled.

Several models has been developed to investigate the flow of infectious diseases and the effect of control interventions on such disease [8, 3] Erinle-Ibrahim, Idowu and Sulola, 2021) and some studies are particular about COVID-19 [9, 10, 11, 12]. In [12], the SEIQCRW model were presented. The result of the findings predicts that the confirmed cases in Nigeria will increase to about 55,000 individuals towards the end of 2020. However, the study did not consider spraying the personal protection and environment as a control measure for COVID-19.

However, the model with the quarantined individual, hospitalized individuals, and control interventions (personal protection, effort used to hospitalize/Isolate the infectious not hospitalized, and effort used in spraying of the environment) has not been considered [8]. Therefore, we presented a dynamical system for corona virus and also a control model for the disease.

Model Formulation

A non-linear model for coronavirus disease is formulated. The following symbols are used to describe the variable in the system. *N(t)* represents the summative number of the human individuals at the time (t), *S(t)* denotes susceptible individuals, E(t) is the Exposed individuals, and *Q(t)* is the Quarantined. *I(t)* is the Infectious state not hospitalized, *H(t)* is the Isolated/Hospitalized state, *R(t)* represents Recovered individuals and *V(t)* denotes viruses' infections in the environmental reservoir. We further extend the model by considering the probability of humans in the quarantine population who tested negative returning to the disease free state. *Q(t)* consists of individuals from regions with high COVID-19 cases and contact with infected humans in the population. The quarantined population is kept for the incubation period (14 days). *I(t)* consists of those that escaped quarantined but later contracted the infection. However, they are eventually moved to the Isolated/ Hospitalized class. The force of infection is

$$\lambda = \beta\left(I + \varepsilon_1 E + \varepsilon_2 Q + \varepsilon_3 H + \varepsilon_4 V\right) \tag{1}$$

Where β denotes the probability of humans getting infected, ε_1, ε_2, ε_3 and ε_4 denote the adjustment rate infectious states. The parameters ε_2, ε_3 are related with the quarantine and hospitalized individuals' hygiene consciousness.

Table 1 Definitions of Variable Used in the Model

Variables	**Description**
$S(t)$	Susceptible individuals
$E(t)$	Exposed individuals
$Q(t)$	Quarantine individuals
$I_1(t)$	Infected not hospitalized individuals
$H(t)$	Hospitalized individuals
$R(t)$	Recovered individuals
$V(t)$	Viral spread n the environment

Table 2 Definitions of Parameters Used in the Model

Parameters	**Description**
Λ	Immigration rate into the population
π	Probability that an immigrant coming from a high-risk region for COVID-19
q	Probability that a quarantined individual will return to the susceptible class
σ_1	Movement rate from the quarantine class to susceptible class
μ	Natural death rate
ϕ	Probability that an exposed individual will miss quarantine
ω_1	Movement rate from exposed population into the infected not hospitalized class
ω_2	Movement rate from the exposed population into the quarantined class
σ_2	Rate of movement of quarantined individuals into the hospitalized class
γ_1	Movement rate from infected not hospitalized class into the hospitalized class
d	Death caused by the diseased
m	Rate of recovery
f_1	Virus in the exposed class moving to the environment
f_2	Virus in the infectious not hospitalized class moving to the environment
d_v	The decay rate of the virus in the environment
β	Probability of infection

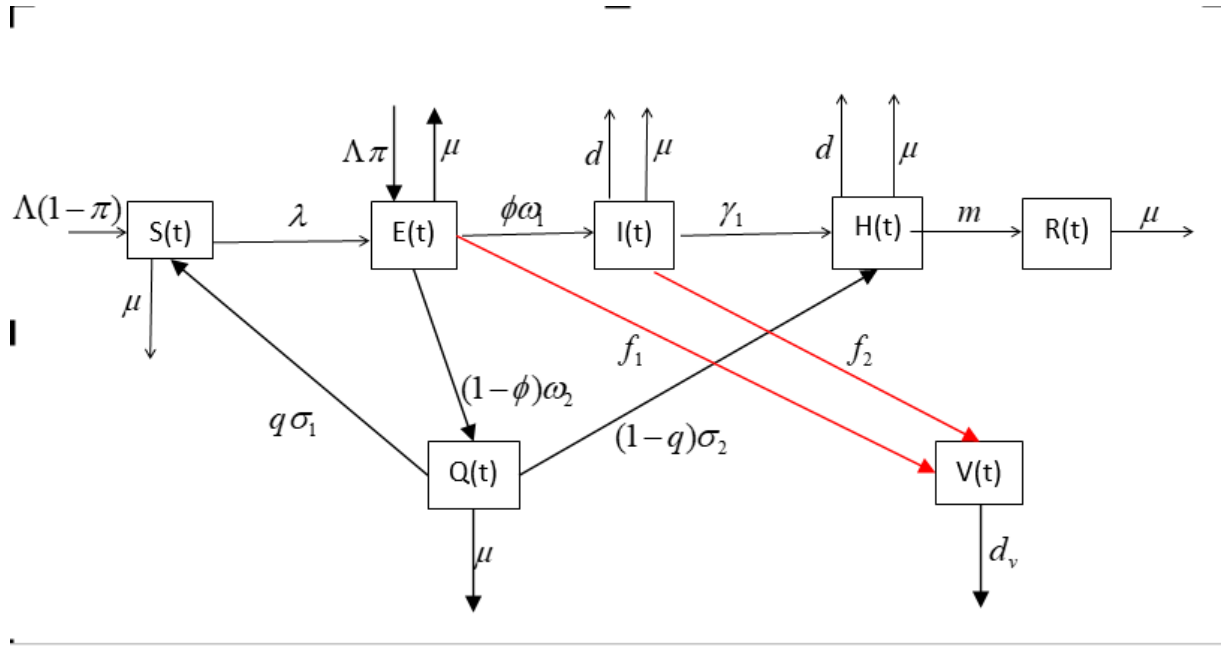

Figure 2 Transmission dynamics for COVID 19 Model (SEQIHRV)

$$
\begin{aligned}
\frac{dS}{dt} &= \Lambda(1-\pi) + q\sigma_1 Q - \lambda S - \mu S \\
\frac{dE}{dt} &= \Lambda\pi + \lambda S - \phi\omega_1 E - (1-\phi)\omega_2 E - \mu E \\
\frac{dQ}{dt} &= (1-\phi)\omega_2 E - q\sigma_1 Q - (1-q)\sigma_2 Q - \mu Q \\
\frac{dI}{dt} &= \phi\omega_1 E - \gamma_1 I - \mu I - dI \\
\frac{dH}{dt} &= (1-q)\sigma_2 Q + \gamma_1 I - mH - \mu H - dH \\
\frac{dR}{dt} &= mH - \mu R \\
\frac{dV}{dt} &= f_1 E + f_2 I - d_v V
\end{aligned}
\qquad (2)
$$

Model Analysis

Positive Invariant and Boundedness

Theorem I: The result of the model of the human population are bounded consistently in a positive fixed domain $\Omega_1 = \{S(t), E(t), Q(t), I(t),, H(t), R(t) \in R_+^6, N \le \frac{\Lambda}{\mu}\}$.

At each period t, the overall population is defined by (1) and

$$\frac{dN}{dt} = \Lambda - \mu N - dI - dH \le \Lambda - \mu N \tag{3}$$

So $\frac{dN}{dt} + \mu N \le \Lambda$

The integrating factor here is $e^{\int \mu dt} = e^{\mu t}$, Therefore, $N(t) \le Ce^{-\mu t} + \frac{\Lambda}{\mu}$

At t = 0, we get $N(0) - \frac{\Lambda}{\mu} \le C$

By substituting C into the equation, we have.

This denotes that as $t \to \infty$, $N(t) \le Max\left(N(0), \frac{\Lambda}{\mu}\right)$

Positivity of The Solution: According to the theorem 1 below, the solution of the model is nonnegative for $t \ge 0$

Theorem II: Given the initial solution satisfying all initial values of each state greater than zero. Then the solutions are positive or equal to zero and fall within the region, $\Omega = \left(S(t), E(t), Q(t), I(t), H(t), R(t), V(t)\right) \in R_+^7$

Proof:

Using equation (2)

$$\frac{dS}{dt} = \Lambda(1-\pi) + q\sigma_1 Q - \lambda S - \mu S \tag{4}$$

$$\frac{dS}{dt} \ge -(\lambda + \mu)S$$

Solving (7) gives

$$S(t) \ge S(0)e^{-(\lambda+\mu)t} \ge 0 \tag{5}$$

In the same way,

$$E(t) \ge E(0)e^{-(\phi\omega_1 + (1-\phi)\omega_2 + \mu)t} \ge 0 \tag{6}$$

$$Q(t) \ge Q(0)e^{-(q\sigma_1 + (1-q)\sigma_2 + \mu)t} \ge 0 \tag{7}$$

$$I(t) \ge I(0)e^{-(\gamma_1 + \mu + d)t} \ge 0 \tag{8}$$

$$H(t) \ge H(0)e^{-(m+\mu+d)t} \ge 0 \tag{9}$$

$$R(t) \ge R(0)e^{-\mu t} \ge 0 \tag{10}$$

$$V(t) \ge V(0)e^{-d_v t} \ge 0 \tag{11}$$

This satisfy that the solutions of the system is not less than zero for each $t \ge 0$

Existence of Disease Free Equilibrium (DFE)

The DFE (E_0) point is attained when we have no highly infectious recruitments (i.e. $\pi = 0$) and no infected individuals in the population.

The equilibrium state exists when all the states in the system (2) are equal to zero.
Solving (2) simultaneously, we have

$$E_0 = \left(\frac{\Lambda}{\mu}, 0,0,0,0,0,0 \right)$$

Basic Reproduction Number R_0

The basic reproduction number R_0 is the number of persons that an infected person will transfer the infection to in susceptible population. If $R_0 < 1$, the infection will no longer exist in the population. If $R_0 > 1$, the spread of the infection will continue in the population. We compute R_0 by applying the Next-generation method. The infection rate and transfer rate is given by

$$F = \begin{bmatrix} (\varepsilon_1 E + \varepsilon_2 Q + I + \varepsilon_3 H + \varepsilon_4 V)\beta S \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} (\phi\omega + (1-\phi)\omega_2 + \mu)E \\ -(1-\phi)\omega_2 E + (q\sigma_1 + (1-q)\sigma_2 + \mu)Q \\ -\phi\omega_1 E + (\gamma + \mu + d)I \\ -(1-q)\sigma_2 Q - \gamma I + (m + \mu + d)H \\ -f_1 E - f_2 I + d_v V \end{bmatrix}$$

The partial derivatives of F and V at E_0, gives

$$G = \begin{bmatrix} \frac{\varepsilon_1\beta\Lambda}{\mu} & \frac{\varepsilon_2\beta\Lambda}{\mu} & \frac{\beta\Lambda}{\mu} & \frac{\varepsilon_3\beta\Lambda}{\mu} & \frac{\varepsilon_4\beta\Lambda}{\mu} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \text{ and } U = \begin{bmatrix} m_1 & 0 & 0 & 0 & 0 \\ -a_1 & m_2 & 0 & 0 & 0 \\ -a_2 & 0 & m_3 & 0 & 0 \\ 0 & -a_3 & -\gamma & m_4 & 0 \\ -f_1 & 0 & -f_2 & 0 & d_v \end{bmatrix}, \text{ respectively}$$

where $m_1 = \phi\omega_1 + (1-\phi)\omega_2 + \mu, m_2 = q\sigma_1 + (1-q)\sigma_2 + \mu, m_3 = \gamma_1 + \mu + d, m_4 = m + \mu + d$ and $a_1 = (1-\phi)\omega_2, a_2 = \phi\omega_1, a_3 = (1-q)\sigma_2$

The spectral radius of the matrix gives R_0, and is given as

$$R_0 = r\left(GU^{-1}\right) = \frac{\Lambda\beta\varepsilon_1}{\mu m_1} + \frac{\Lambda\beta\varepsilon_2 a_1}{\mu m_1 m_2} + \frac{\Lambda\beta a_2}{\mu m_1 m_3} + \frac{\Lambda\beta\varepsilon_3 a_3 a_1}{\mu m_1 m_2 m_4} + \frac{\Lambda\beta\varepsilon_3\gamma a_2}{\mu m_1 m_3 m_4} + \frac{\Lambda\beta\varepsilon_4\left(f_1 m_3 + f_2 a_2\right)}{\mu m_1 m_3 d_v} \quad (12)$$

The first five parts of R_0 in (12) estimate the role that human-to-human flows (exposed to susceptible, quarantined to susceptible, early infectious to susceptible, hospitalized to susceptible respectively) and The sixth will analyze the environmental impact to the human transmission channel. These pathways represent the total risk of complications for the COVID-19 epidemic.

If $\phi = 0$, then $I = 0$. Then

$$R_{0q} = \frac{\Lambda\beta\varepsilon_1}{\mu m_1^*} + \frac{\Lambda\beta\varepsilon_2\omega_2}{\mu m_1^* m_2} + \frac{\Lambda\beta\varepsilon_3 a_3\omega_2}{\mu m_1^* m_2 m_4} + \frac{\Lambda\beta\varepsilon_4 f_1 m_3}{\mu m_1^* m_3 d_v} \tag{13}$$

where $m_1^* = \omega_2 + \mu$

If $\phi = 1$, then the basic reproduction number with no quarantine is then given as

$$R_{0nq} = r\left(GU^{-1}\right) = \frac{\Lambda\beta\varepsilon_1}{\mu m_1^+} + \frac{\Lambda\beta\omega_1}{\mu m_1^+ m_3} + \frac{\Lambda\beta\varepsilon_3\gamma\omega_1}{\mu m_1^+ m_3 m_4} + \frac{\Lambda\beta\varepsilon_4\left(f_1 m_3 + f_2\omega_1\right)}{\mu m_1^+ m_3 d_v} \tag{14}$$

where $m_1^+ = \omega_1 + \mu$

Stability of DFE Point

Theorem III: E_0 is asymptotically stable if $J(E_0) < 1$ and unstable if $J(E_0) > 1$

The Jacobian of the model calculated at DFE*(E_0)* was used to establish the local stability of the DFE. The stability depends on the eigenvalue of the corresponding Jacobian. The Jacobian of the system (2) at DFE is obtained as

$$J(E_0) = \begin{bmatrix} -\mu & -\frac{\Lambda\beta\varepsilon_1}{\mu} & q\sigma_1 - \frac{\Lambda\beta\varepsilon_2}{\mu} & -\frac{\Lambda\beta}{\mu} & -\frac{\Lambda\beta\varepsilon_3}{\mu} & 0 & -\frac{\Lambda\beta\varepsilon_4}{\mu} \\ 0 & -m_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & a_1 & -m_2 & 0 & 0 & 0 & 0 \\ 0 & a_2 & 0 & -m_3 & 0 & 0 & 0 \\ 0 & 0 & a_3 & \gamma & -m_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & m & -\mu & 0 \\ 0 & f_1 & 0 & f_2 & 0 & 0 & -d_v \end{bmatrix} \tag{15}$$

where $m_1 = \phi\omega_1 + (1-\phi)\omega_2 + \mu, m_2 = q\sigma_1 + (1-q)\sigma_2 + \mu, m_3 = \gamma_1 + \mu + d, m_4 = m + \mu + d$ and $a_1 = (1-\phi)\omega_2, a_2 = \phi\omega_1, a_3 = (1-q)\sigma_2$

We need to show that the eigenvalues of $J(E_0)$ are all negative. Clearly, we see that the eigenvalues of $J(E_0)$ are the diagonals $-\mu$, $-m_1$, $-m_2$, $-m_3$, $-m_4$, $-\mu$, and $-d_v$. Hence, all the eigenvalues of $J(E_0)$ are all negative which implies the disease-free equilibrium are asymptotically stable and there is no condition for which the DFE will be unstable.

Existence of the Endemic Equilibrium

We shall show that the model formulated has an endemic equilibrium point E_*. Define $E_* = (S_*, E_*, Q_*, I_*, H_*, R_*, V_*)$ to be the nontrivial equilibrium of the model. The equilibrium state of model (2) is $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dQ}{dt} = \frac{dI}{dt} = \frac{dH}{dt} = \frac{dR}{dt} = \frac{dV}{dt} = 0$

Solving these simultaneously, these equations give

$$S_* = \frac{\Lambda a_2 m_2 + \left(q \sigma_1 a_1 - m_1 \ m_2\right) m_3 I_*}{\mu a_2 m_2},\ E_* = \frac{m_3 I_*}{a_2},\ Q_* = \frac{a_1 m_3 I_*}{a_2 m_2},\ H_* = \frac{\left(\gamma a_2 m_2 + a_3 a_1 m_3\right) I_*}{a_2 m_2 m_4}$$

$$R_* = \frac{\left(\gamma a_2 m_2 + a_3 a_1 m_3\right) m I_*}{a_2 m_2 m_4 \mu} \text{ and } V_* = \frac{\left(f_1 m_3 + f_2 a_2\right) I_*}{a_2 d_v}$$

Substituting $S_*, E_*, Q_*, I_*, H_*, R_*, V_*$ and simplifying gives the quadratic,

$$XI_*^2 + YI_* + Z = 0$$

Where,

$$X = \beta m_1 m_3^2 m_4 d_v R_0 (q\sigma_1 a_1 - m_1 m_2)$$
$$Y = \beta a_2^2 m_1 m_2^2 m_3 m_4 d_v (R_0 - 1)$$
$$Z = \mu m_2^2 m_4 d_v a_2^2 \Lambda \pi$$

If $\pi = 0$, $Z = 0$
So equation () becomes $XI_*^2 - YI_* = 0$
When $\pi = 0$

$$I_* = 0 \text{ or } I_* = \frac{Y}{X}$$

Also, at $\pi > 0$ we have from equation () that

$$I_{**} = \frac{Y + \sqrt{Y^2 + 4}}{X}$$

Sensitivity Analysis

To determine where to focus efforts to reduce disease death and morbidity, we need to understand the impact of various model parameters in the system on the flow of infection. Therefore, we carry out a sensitivity analysis on R_0 to find the essential parameter that will help control the flow of the infectious disease. This is done using the partial derivative of R_0.

$$\chi_{\mathrm{A}}^{R_0} = \frac{\partial R_0}{\partial A} \tag{16}$$

Where $\chi_{\mathrm{A}}^{R_0}$ denotes sensitivity index of R_0 with respect to A.

As a result, we calculate the sensitivity ratings for each component in R_0. For example, the sensitivity rating of R_0 with respect to the parameter β is given as

$$\chi_{\beta}^{R_0} = \frac{\partial R_0}{\partial \beta} = +1 \tag{17}$$

Table 3 Sensitivity indices for other parameters in reproduction number

Parameters	**Values**	**Source**	**Index sign**	**Sensitivity index Value**
β	0.25 person^{-1}day^{-1}	Madubueze, Sambo, & Isaac, (2020)	+	1
ω_1	0.1429 day^{-1}	Madubueze, Sambo, & Isaac, (2020)	+	0.1953059387
ω_2	0.1259 day^{-1}	Madubueze, Sambo, & Isaac, (2020)	-	0.4838230838
σ_1	0.07143 day^{-1}	Madubueze, Sambo, & Isaac, (2020)	-	0.02011845172
σ_2	0.13333 day^{-1}	Madubueze, Sambo, & Isaac, (2020)	-	0.0198557003
m	0.06667 day^{-1}	Madubueze, Sambo, & Isaac, (2020)	-	0.04360841951
γ_1	0.03521 day^{-1}	Madubueze, Sambo, & Isaac, (2020)	-	0.3472328578
f_1	2.010 day^{-1}	(Daniel, (2021)	+	0.1211804256
f_2	0.235 day^{-1}	(Daniel, (2021)	+	0.01371903977
d_v	1	(Daniel, (2021)	-	0.1348994653
ε_1	0.3	Madubueze, Sambo, & Isaac, (2020)	+	0.1808663068
ε_2	0.1	Madubueze, Sambo, & Isaac, (2020)	+	0.041255667174
ε_3	0.1	Madubueze, Sambo, & Isaac, (2020)	+	0.0591896299
ε_4	0.1	Assumed	+	0.1348994653

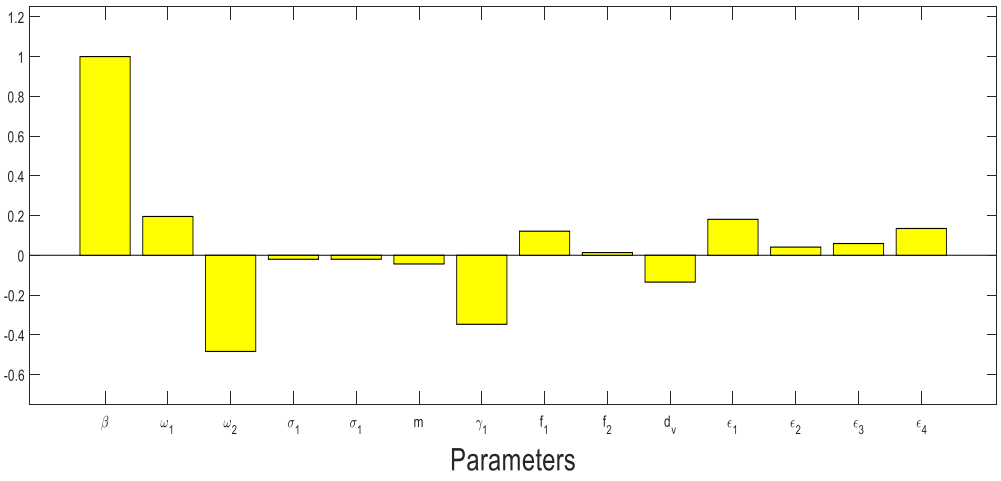

Figure 3 Graphical representation of sensitivity parameters

From Table 3, the most critical parameters are in the order of importance $\beta, \omega_2, \gamma_1, \omega_1, \varepsilon_1, \varepsilon_4, d_v$ etc. These parameters will stop the flow of infection by lowering the values of $\beta, \omega_1, \varepsilon_1, \varepsilon_4$ and increasing ω_2, γ_1, d_v.

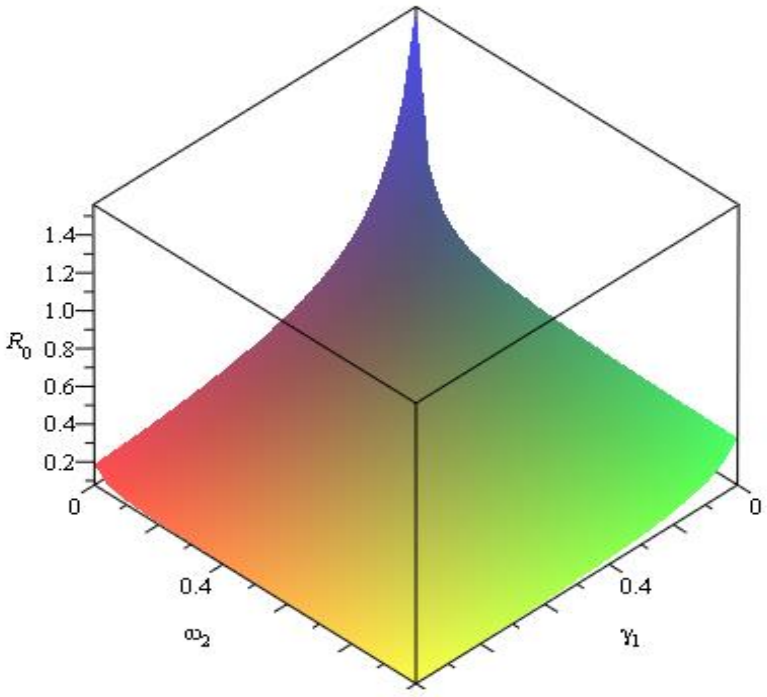

Figure 4 Effect of ω_2, γ on the R_0

Control Analysis

Following the system (2) above, this section presents a new model problem with control measures; We adjust the transfer rate by lowering the ratio by $(1-u_1)$, where u_1 denotes personal protections. The control variable u_2 denotes the effort on exposed-quarantined transition, u_3 represent the effort on infected-isolated transitions. The fourth control variable u_4 measures the rate of virus elimination from the environment. With regards to these assumptions, we have the new system of equations below:

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Lambda(1-\pi) + q\sigma_1 Q - (1-u_1)\lambda S - \mu S \\
\frac{dE}{dt} &= \Lambda\pi + (1-u_1)\lambda S - \phi\omega_1 E - (1-\phi)u_2 E - \mu E \\
\frac{dQ}{dt} &= (1-\phi)u_2 E - q\sigma_1 Q - (1-q)u_2 Q - \mu Q \\
\frac{dI}{dt} &= \phi\omega_1 E - u_3 I - \mu I - dI \\
\frac{dH}{dt} &= (1-q)u_2 Q + u_3 I - (m+\mu+d)H \\
\frac{dR}{dt} &= mH - \mu R \\
\frac{dV}{dt} &= f_1 E + f_2 I - (d_v + u_4)V
\end{aligned}\right\} \quad (18)$$

Analysis of the Model with control Measures

We developed an objective functional model and demonstrated the possibility of control using Pontryagin's Maximum Principle. Considering the optimal system (18), we showed the existence of the following control issue before describing it for global optimization. The optimization challenge of choosing the most efficient methods is described by the objective functional J. The overall predetermined goal is to minimize the number of confined, exposed, and infected persons as well as viral propagation in the environment within a defined time span [0, T].

$$U = \{(u_1, u_2, u_3, u_4) \in U\} \text{is Lebesgue measurable on } [0,1],\ 0 \le u_i(t) \le 1 \in [0,T], i = 1,2,3,4$$

We define the objective functional J, as follows:

$$J(u_1, u_2, u_3, u_4) = \int_0^T \left(A_1 V + A_2 I + A_3 Q + A_4 E + \frac{1}{2}\left(B_1 {u_1}^2 + B_2 {u_2}^2 + B_3 {u_3}^2 + B_4 {u_4}^2\right)\right) dt \quad (19)$$

Subject to

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Lambda(1-\pi) + q\sigma_1 Q - (1-u_1)\lambda S - \mu S \\
\frac{dE}{dt} &= \Lambda\pi + (1-u_1)\lambda S - \phi\omega_1 E - (1-\phi)u_2 E - \mu E \\
\frac{dQ}{dt} &= (1-\phi)u_2 E - q\sigma_1 Q - (1-q)\sigma_2 Q - \mu Q \\
\frac{dI}{dt} &= \phi\omega_1 E - u_3 I - \mu I - dI \\
\frac{dH}{dt} &= (1-q)\sigma_2 Q + u_3 I - (m+\mu+d)H \\
\frac{dR}{dt} &= mH - \mu R \\
\frac{dV}{dt} &= f_1 E + f_2 I - (d_v + u_4)V
\end{aligned}\right\}$$

T is the final time and quantities A_1 *to* A_4 are weights constants of the virus in the environment, infectious not quarantined individuals, exposed individuals and quarantined respectively.

The aim of this The aim of this section is to reduce the operating cost (19). Also we look into the social cost $(B_1{u_1}^2)$, $(B_2{u_2}^2, B_3{u_3}^2)$, and $B_4{u_4}^2$.

In other to achieve the objective of the control problem, we seek the functions

$\left(u_1^*(t), u_2^*(t), u_3^*(t), u_4^*(t)\right)$ such that

$$J\left(u_1^*(t), u_2^*(t), u_3^*(t), u_4^*(t)\right) = \min\left\{J(u_1,u_2,u_3,u_4), (u_1,u_2,u_3,u_4) \in U\right\} \tag{20}$$

Existence of an Optimal Control

Theorem 1V. Considering $J(u_1,u_2,u_3,u_4)$as in (20), subject to (18) with initial conditions given at t = 0, then we have the optimal control $u^* = \left(u_1^*(t), u_2^*(t), u_3^*(t), u_4^*(t)\right)$ such that

$$J\left(u_1^*(t), u_2^*(t), u_3^*(t), u_4^*(t)\right) = \min\left\{J(u_1,u_2,u_3,u_4), (u_1,u_2,u_3,u_4) \in U\right\}$$

Proof: Due to the convexity of the integrand of J with respect to the control measures u_1, u_2, u_3, u_4, then the optimal control exists.

Now we need to show the optimal solution. The Lagrangian is given as

$$L = A_1V + A_2I + A_3Q + A_4E + \frac{1}{2}\left(B_1{u_1}^2 + B_2{u_2}^2 + B_3{u_3}^2 + B_4{u_4}^2\right) \tag{21}$$

The Hamiltonian function for the system is

$$\begin{aligned} H_A &= A_1V + A_2I + A_3Q + A_4E + \frac{1}{2}\left(B_1{u_1}^2 + B_2{u_2}^2 + B_3{u_3}^2 + B_4{u_4}^2\right) \\ &+ \psi_S\left[\Lambda(1-\pi) + q\sigma_1Q(t) - (1-u_1)\lambda S(t) - \mu S(t)\right] \\ &+ \psi_E\left[\Lambda\pi + (1-u_1)\lambda S - \phi\omega_1E - (1-\phi)u_2E - \mu E\right] \\ &+ \psi_Q\left[(1-\phi)u_2E - q\sigma_1Q - (1-q)\sigma_2Q - \mu Q\right] \\ &+ \psi_I\left[\phi\omega_1E - u_3I - \mu I - dI\right] + \psi_H\left[(1-q)\sigma_2Q + u_3I - (m+\mu+d)H\right] \\ &+ \psi_R\left[mH - \mu R\right] + \psi_V\left[f_1E + f_2I - (d_v + u_4)V\right] \end{aligned} \tag{22}$$

Where $\psi_j, j \in \{S,E,Q,I,H,R,V\}$ are the disjoint variables.

Now we can apply the necessary conditions to the Hamiltonian (H).

In order to determine the adjoint equation and the transversality condition, we make use of the Hamiltonian H. we differentiate the Hamiltonian with respect to S, Q, E, I, R, V. Then we have the adjoins equation to be

$$\begin{aligned}
\frac{d\psi_S}{dt} &= -\frac{\partial H}{dS} = [(1-u_1)\lambda + \mu]\psi_S - [(1-u_1)\lambda]\psi_Q \\
\frac{d\psi_Q}{dt} &= -\frac{\partial H}{dQ} = -A_4 - \alpha_4\psi_S + (\alpha_4 + \mu + \alpha_1)\psi_Q - \alpha_1\psi_E \\
\frac{d\psi_E}{dt} &= -\frac{\partial H}{dE} = -A_3 + (\alpha_4 + \sigma + \mu)\psi_E - \alpha_2\psi_I - f_1\psi_V \\
\frac{d\psi_I}{dt} &= -\frac{\partial H}{dI} = -A_2 + [(1-u_1)aS]\psi_S - [(1-u_1)aS]\psi_Q + \\
&\qquad u_2\psi_I - (u_2 + \alpha_3)\psi_R - f_2\psi_V \\
\frac{d\psi_R}{dt} &= -\frac{\partial H}{dR} = -\delta\psi_S + (\delta + \mu)\psi_R \\
\frac{d\psi_V}{dt} &= -\frac{\partial H}{dV} = -A_1 + [(1-u_1)bS]\psi_S - [(1-u_1)bS]\psi_Q + (m + u_3)\psi_V
\end{aligned} \tag{26}$$

Where $a = \beta_1\varepsilon_1\phi$ and $b = \beta_2\varepsilon_2\phi$

With transversality conditions

$$\psi_j(T) = 0,\ j \in \{S, Q, E, I, R, V\}$$

To minimize the Halmitonian, H, with respect to the optimal controls, we differentiate H with respect to u_1, u_2, u_3. We then obtain the solution by equating the results to zero. This gives the optimal control required.

Let $S = S^*, Q = Q^*, E = E^*, I = I^*, R = R^*, V = V^*$

Then

$$\begin{aligned}
\frac{dH}{du_1} &= B_1 u_1^* + \lambda S\psi_S - \lambda S\psi_E = 0 \\
\frac{dH}{du_2} &= B_2 u_2^* - (1-\phi)E\psi_E + (1-\phi)E\psi_Q = 0 \\
\frac{dH}{du_3} &= B_3 u_3^* - I\psi_I + I\psi_H = 0 \\
\frac{dH}{du_4} &= B_3 u_3^* - \psi_V V = 0
\end{aligned} \tag{27}$$

$$u_1^* = \frac{(\psi_E - \psi_S)\lambda S}{B_1}$$

$$u_2^* = \frac{(\psi_E - \psi_Q)(1-\phi)E}{B_2}$$

$$u_3^* = \frac{(\psi_I - \psi_H)I}{B_3}$$

$$u_4^* = \frac{\psi_V V}{B_4}$$

Using the boundary condition of these controls, the solution (74) becomes

$$u_1^* = \min\{1, \max\{0, \Lambda_1\}\},$$
$$u_2^* = \min\{1, \max\{0, \Lambda_2\}\},$$
$$u_3^* = \min\{1, \max\{0, \Lambda_3\}\},$$
$$u_4^* = \min\{1, \max\{0, \Lambda_4\}\}$$

Where

$$\Lambda_1 = \frac{(\psi_E - \psi_S)\lambda S}{B_1}, \Lambda_2 = \frac{(\psi_E - \psi_Q)(1-\phi)E}{B_2}, \Lambda_3 = \frac{(\psi_T - \psi_H)I}{B_3} \text{ and } \Lambda_4 = \frac{\psi_V V}{B_4}$$

Proved

Numerical Simulation

This portion of the paper focuses on computational methods for the built-in optimization framework using a fourth-order Runge-Kutta with a forward-backward sweep approach that is exceedingly effective, helpful, and dependable. Many writers concerned with efficient simulation and dynamic systems have used this adaptive approach [8, 11]. The initial conditions for the state variables are as follows: *S(0) =216746934, E(0) = 1000011, Q(0) = 2554, I(0) = 2494, H(0) = 2715, R(0) = 249246, and V(0) = 0*. Also Λ = 22655 persons^{-1}day^{-1}, and μ = 0.0182 day^{-1} and fixing π = 0.3. Parameter values required for simulation are presented in Table 3. The details of the scheme are presented can be found in []

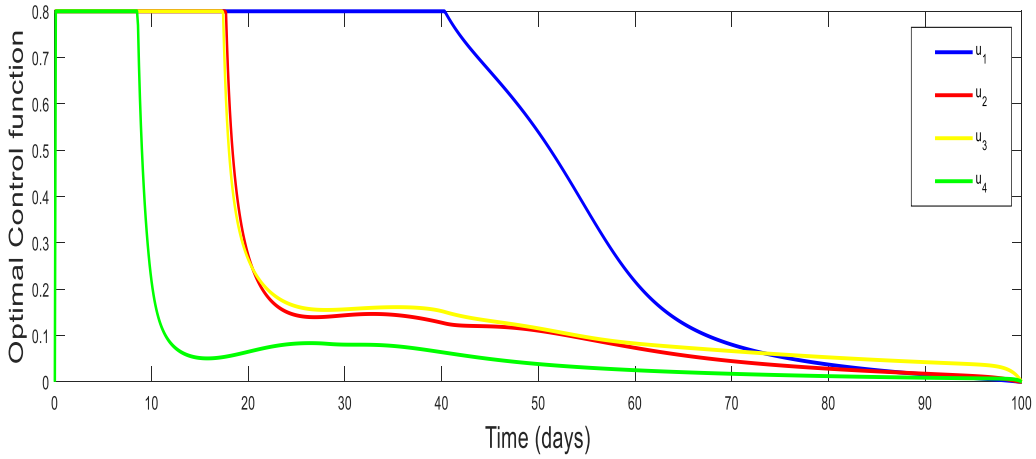

Figure 5 Optimal control functions

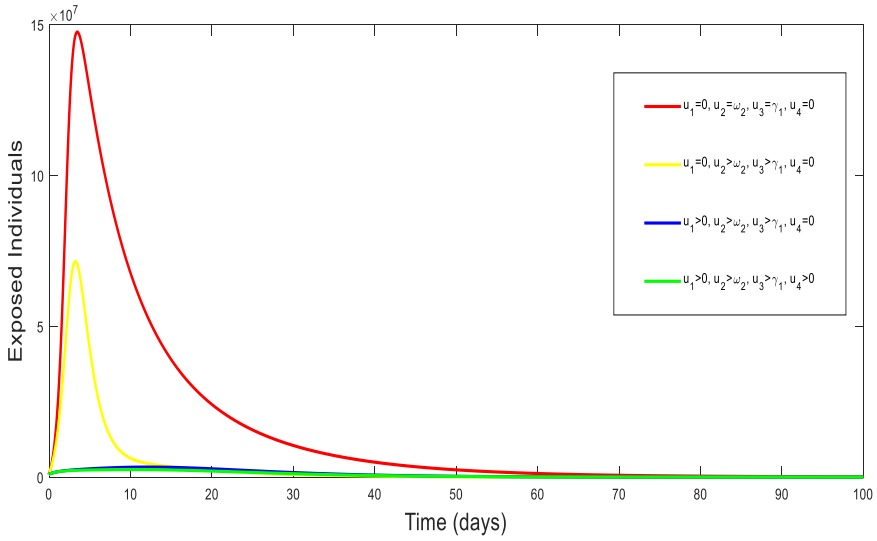

Figure 6 Solution trajectories for the exposed individuals

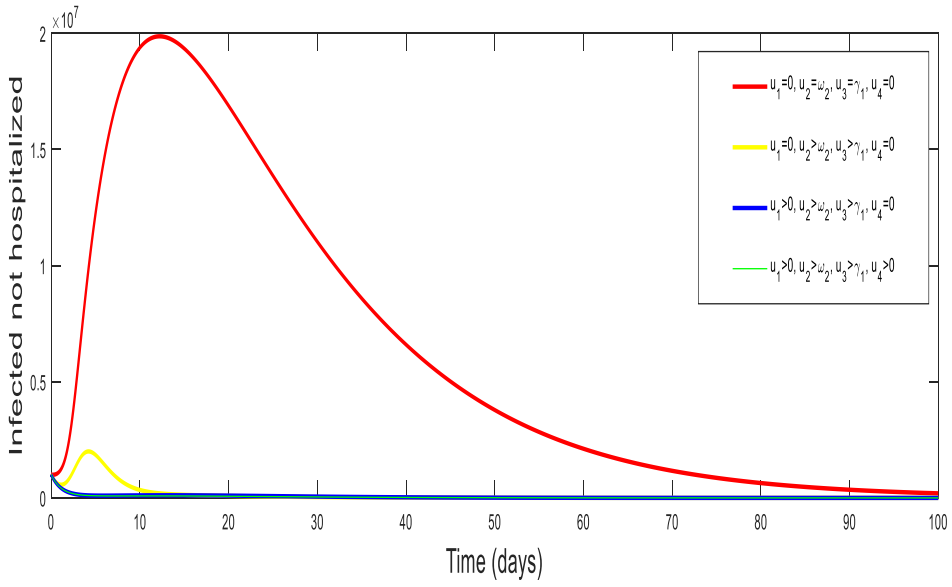

Figure 7 Solution trajectories for the infected individuals

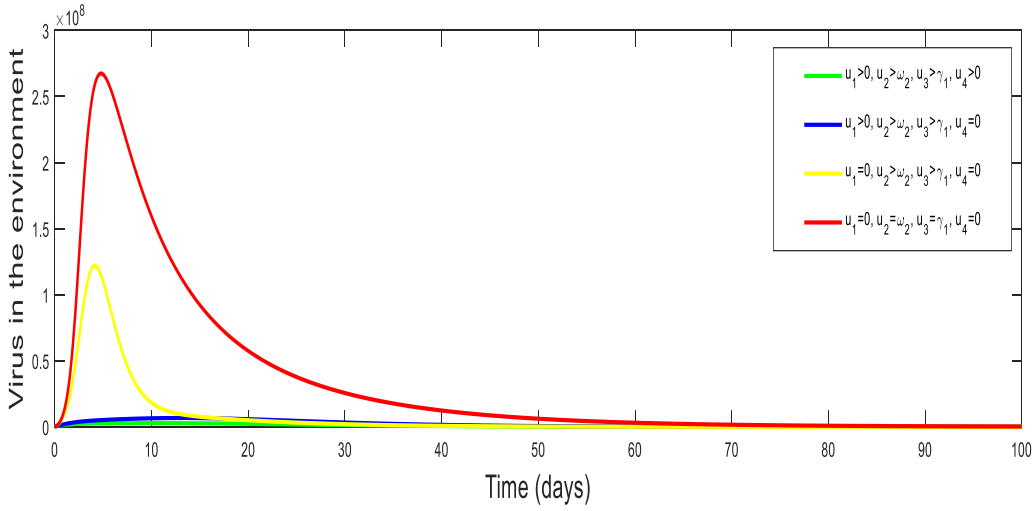

Figure 8 Solution trajectories for the concentration of virus in the environment

DISCUSSION

A seven compartmental system for corona virus 19 transmissions was developed. The model has an invariant region, which has been demonstrated. The basic reproduction number $R_{0q} = 6.61$ when there is no quarantine compared to $R_{0nq} = 1.74$ when there is quarantine. This indicates that without quarantine, a single infected person may spread the virus to about seven other people, whereas quarantine allows an infected person to spread the infection to two additional people.

However, it is important to note that quarantine alone is not enough to stop the transmission of COVID-19. Therefore, the need to investigate the effect of control interventions on the transmission dynamics of the COVID-19 model formulated. We proposed three control interventions to investigate COVID-19 dynamics, a lethal viral illness. In the nonlinear dynamical optimal control issue, we added four optimal time-dependent control functions. Personal protection, quarantine of exposed persons, isolation of sick individuals, and spraying of the environment were among the control functions. The numerical simulation

results show that optimal control measures can result in a large drop in the population's number of COVID-19 cases. We discovered that the number of period necessary for the virus to be removed is dramatically decreased. The numerical result also show that by improving the rate of movement from the exposed state into the quarantined state and improving the rate of movement of persons from infected not hospitalized class to hospitalized class, we can significantly control the number of new confirmed cases. Also, we confirm that improving the personal protection of individuals further helps in reducing the spread of the infection. Finally, we combined the effect of spraying the environment on the human population alongside all other control measures. We then discovered that the combination of all these control measures can help in eradicating the spread of the infection among the human population.

CONCLUSION

We have proposed a mathematical model to consider the transmission flow of COVID-19. The positivity and boundedness, local and global stability analysis, reproduction number, and sensitivity were all analytically solved. It was found that Disease-free equilibrium point is stable if $R_0 < 1$ and that the endemic equilibrium state exists only if $R_0 > 1$. Also, the sensitivity analysis carried out on the basic reproduction number showed that the parameters ω_2, γ_1, d_v will reduce the spread of the infection if they are increased. This means that to reduce the rate of infection, movement of individuals from the exposed class to the quarantined class should be increased, movement of individuals from the infected not hospitalized to the hospitalized class should also be increased and finally, the removal rate of the virus in the environment should be increased. It is in this that we then considered the optimal control strategies i.e. personal protection, the effort used to quarantine the exposed individuals, effort used to isolate infected individuals, and spraying of the environment. Simulation of results was carried out using MATLAB software. The result showed that all the control interventions must be combined in order to eradicate the disease in the environment.

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