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Mathematical Analysis of the Transmission Dynamics of Covid-19

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ABSTRACT

This work presents a nonlinear deterministic model, referred to as GESAVRDP, intended to examine the transmission dynamics of COVID-19 within a population. The model is formulated as a system of ordinary differential equations that represents interactions among primary population groupings following the onset of the initial case in a disease-free community. We provide a solid foundation for understanding how the infection changes over time by computing the basic reproduction number (R0) and confirming several basic mathematical features, like positivity, existence, and uniqueness of solutions.

KEYWORDS: GESAVRDP, COVID-19, Mathematical Modeling, Vaccination, Reinfection, Infectious Deaths, Surface Virus, Non-Pharmaceutical Interventions.

I. INTRODUCTION

Coronaviruses, classified in the Coronavirinae subfamily of the Coronaviridae family, exemplify the application of these theories. Viruses in the Nidovirales order and the Orthocoronavirus genus can infect people in several ways. Alpha-coronaviruses, particularly SARS-CoV and MERS-CoV, have instigated substantial outbreaks of human disease, whereas gamma- and delta-coronaviruses predominantly circulate within animal populations, including bats and mice [6–14]. The global coronavirus outbreak emerged in December 2019, after a novel respiratory virus was first detected in Wuhan, China. It was the sixth global pandemic since the flu epidemic in 1918. As of April 24, 2025, the virus has infected more than 778 million people around the world. The US, China, and India have reported 108 million, 99.5 million, and 45 million cases, respectively.

. Mathematical models, especially the SIR framework, have been very important for figuring out how COVID-19 will spread and how well interventions like isolation, lockdowns, and vaccine will function [17]. Numerous models have neglected the potential for reinfection, which current research substantiates as a critical element in disease dynamics [18]. A commonly overlooked factor is the transmission of viruses during funerary and traditional burial rites. In many African groups, these ceremonies possess traditional value and generally entail physical interaction with the corpse, frequently disregarding health protocols such as social distance [19].

II MODEL FORMULATION

2.1 Description of the Variable

Table2.1 State Variables

S/N	State Variable	Description of the Variable
1	N	Total Population
2	G	Susceptible Population
3	E	Exposed Population
4	S	Symptomatic Population
5	A	Asymptomatic Population
6	V	Vaccinated Population
7	R	Recovered yet Susceptible Population
8	D	Infected and Diseased population
9	P	Surfaces Virus
10	t	time

With $N = G + E + S + A + V + D + R$ 2.1

$$\frac{dG}{dt} = \lambda_1 N + \rho_1 R + \eta_2 V - \left(\theta_1 \frac{S}{N} + \theta_2 \frac{A}{N} + \varphi_1 P + \delta_1 \frac{D}{N} + \eta_1(1-m) + \mu_1\right) G - \theta_3 N^2 \quad 2.2$$

$$\frac{dE}{dt} = \left(\theta_1 \frac{S}{N} + \theta_2 \frac{A}{N} + \varphi_1 P + \delta_1 \frac{D}{N}\right) G - (\omega_1 + \mu_1) E \quad 2.3$$

$$\frac{dS}{dt} = (1-k)\omega_1 E + \tau_1 A - (\beta_1 + \sigma_1 + \mu_1)S \quad 2.4$$

$$\frac{dA}{dt} = k\omega_1 E - (\beta_2 + \tau_1 + \mu_1)A \quad 2.5$$

$$\frac{dV}{dt} = \eta_1(1-m)G + \theta_4 R - (\eta_2 + \mu_1)V \quad 2.6$$

Symbol	Paraphrased Description	Value	Units	Source
λ_1	Average rate of births per individual in the population	0.0000433	Day^{-1}	[1, 2]
θ_1	Transmission rate between susceptible individuals and those showing symptoms	0.05	Day^{-1}	[1, 2]
θ_2	Transmission rate between susceptible individuals and asymptomatic carriers	0.124	Day^{-1}	[1]
φ_1	Rate at which surface pathogens infect susceptible humans	0.00000123	Virus^{-1} Day^{-1}	[2]
β_1	Rate of recovery among symptomatic individuals	0.0987	Day^{-1}	[2]
β_2	Rate of recovery among asymptomatic individuals	0.854	Day^{-1}	[2]
θ_3	Per capita amount of available resources for humans	0.00024	Human^{-1} Day^{-1}	[2]
μ_1	Average natural mortality rate of humans	0.000035	Day^{-1}	[2]
τ_1	Rate at which asymptomatic individuals lose their status	0.035	Day^{-1}	[2]
k	Fraction of exposed individuals who progress to infection	0.005	Non-dimensional	[2]
α_1	Amount of virus shed onto surfaces by symptomatic individuals	0.0398	Viruses Human^{-1} Day^{-1}	[2]
α_2	Amount of virus released onto surfaces by asymptomatic individuals	0.001	Viruses Human^{-1}	[2]
φ_2	Transmission rate from surface pathogens to susceptible individuals	0.00000123	Virus^{-1} Day^{-1}	[2]
ω_1	Rate of progression from the exposed stage to the infectious stage	0.000479	Day^{-1}	[2]
γ_1	Rate of decay or death of the virus on surfaces	0.01	Day^{-1}	[20]
σ_1	Mortality rate caused directly by the infection	0.043	Day^{-1}	[21]
η_1	Rate at which susceptible individuals receive vaccination	0.0196	Human^{-1} Day^{-1}	[1]

ρ_1	Rate at which recovered individuals lose immunity and become susceptible again	0.084	Day^{-1}	[1, 2]
m	Fraction of individuals avoiding vaccination due to misinformation or conspiracy beliefs	0.98	Day^{-1}	[1]
η_2	Rate at which vaccine-induced protection diminishes over time	0.08	Day^{-1}	[1]
θ_4	Rate of administering vaccines to recovered individuals	0.89	Day^{-1}	[1]
δ_1	Frequency of contact between susceptible individuals and infectious corpses during burial	0.5	Day^{-1}	Assumed
δ_2	Average rate at which deceased individuals are buried	0.07	Day^{-1}	Assumed

Let's look at the different parts of the population as parts of the whole population:

G=GN^{-1}, E=EN^{-1} ,S=S N^{-1},A=A N^{-1},V=V N^{-1},R=R N^{-1}.

So,

$$\hat{G} + \hat{E} + \hat{S} + \hat{A} + \hat{V} + \hat{R} = 1$$

Let $\hat{P}$=PP$_0$ $^{-1}$, $\widehat{N}$=NN$_0$ $^{-1}$, $\widehat{D}$=DD$_0$ $^{-1}$, $\hat{t}$=tt$_0$ $^{-1}$. 2.20

S0,

$$\frac{d\hat{G}}{d\hat{t}} = t_0\lambda_1 + t_0\rho_1\hat{R} + t_0\eta_2\hat{V} - t_0[\theta_1\hat{S} + \theta_2\hat{A} + \delta_1\widehat{D} + \varphi_1 P_0\hat{P} + \eta_1(1-m)]\hat{G} - t_0\theta_3 N_0(1-\hat{G})\widehat{N} + t_0\sigma_1\hat{S}\hat{G}$$

$$\frac{d\hat{E}}{d\hat{t}} = t_0(\theta_1\hat{S} + \theta_2\hat{A} + \delta_1\widehat{D} + \varphi_1 P_0\hat{P})\hat{G} - t_0(\omega_1 + \lambda_1)\hat{E} + t_0\theta_3 N_0\hat{G}\widehat{\hat{N}} + t_0\sigma_1\hat{S}\hat{E}$$

$$\frac{d\hat{S}}{d\hat{t}} = t_0(1-k)\omega_1\hat{E} + t_0\tau_1\hat{A} - t_0(\beta_1 + \sigma_1 + \lambda_1)\hat{S} + t_0\theta_3 N_0\hat{S}\widehat{N} + t_0\sigma_1\hat{S}^2$$

$$\frac{d\hat{A}}{d\hat{t}} = t_0 k\omega_1\hat{E} - t_0(\beta_2 + \tau_1 + \lambda_1)\hat{A} + t_0\theta_3 N_0\widehat{N}\hat{A} + t_0\sigma_1\hat{A}\hat{S}$$

$$\frac{d\hat{V}}{d\hat{t}} = t_0\eta_1(1-m)\hat{G} + t_0\theta_4\hat{R} - t_0\eta_2\hat{V} - t_0\lambda_1\hat{V} + t_0\theta_3 N_0\widehat{N}\hat{V} + t_0\sigma_1\hat{V}\hat{S}$$

$$\frac{d\hat{R}}{d\hat{t}} = t_0\beta_1\hat{S} + t_0\beta_2\hat{A} - t_0(\rho_1 + \lambda_1 + \theta_4)\hat{R} + t_0\theta_3 N_0\hat{R}\widehat{N} + t_0\sigma_1\hat{R}\hat{S}$$

$$\frac{d\widehat{D}}{d\hat{t}} = \{t_0 N_0(\sigma_1 + \mu_1)\,\hat{S}\widehat{N} + \widehat{\mu_1 A}\widehat{N}\}/D_0 - t_0\delta_2\widehat{D}.$$

$$\frac{d\hat{P}}{d\hat{t}} = \{t_0 N_0\alpha_1\hat{S}\widehat{N} + t_0 N_0\alpha_2\hat{A}\widehat{N} + t_0 D_0\alpha_3\widehat{D} - P_0 t_0 N_0\varphi_2\widehat{N}\hat{P}\hat{G} - P_0 t_0\gamma_2\hat{P}\}/P_0$$

$$\frac{d\widehat{N}}{d\hat{t}} = t_0(\lambda_1 - \mu_1)\widehat{N} - t_0\sigma_1\hat{S}\widehat{N} - t_0\theta_3 N_0 N^2$$

2.11

We modified the duration based on the proportion of the vaccinated human population, resulting in the succeeding dimensionless parameters.

$$t_0 = \frac{1}{\eta_1}, \lambda = \frac{\lambda_1}{\eta_1}, \rho = \frac{\rho_1}{\eta_1}\ a = \frac{\theta_1}{\eta_1}, b = \frac{\theta_2}{\eta_1}, \mu = \frac{\mu_1}{\eta_1}, d = \frac{\varphi_1 V_0}{\eta_1}, e = \frac{\beta_2}{\eta_1}, \sigma = \frac{\sigma_1}{\eta_1},$$

$$f = \frac{\theta_3 H_0}{\eta_1}, \tau = \frac{\tau_1}{\eta_1}, \omega = \frac{\omega_1}{\eta_1}, g = \frac{\alpha_1 N_0}{\eta_1 V_0}, h = \frac{\alpha_2 N_0}{\eta_1 V_0}, \theta = \frac{\theta_4}{\eta_1}, \gamma = \frac{\gamma_1}{\eta_1}, \eta = \frac{\eta_2}{\eta_1}, \varphi = \frac{\varphi_2 N_0}{\eta_1}$$

$$\beta = \frac{\beta_1}{\eta_1}, \delta = \frac{\delta_1}{\eta_1}, \ r = \frac{\alpha_3 D_0}{\eta_1 P_0}, \varepsilon = \frac{\alpha_3 D_0}{\eta_1 P_0}, q = \frac{\delta_2}{\eta_1}$$

2.12

By inserting equation (2.12) into equation (2.11) and omitting the notational accents for simplicity, the resulting expression becomes

$$\frac{dG}{dt} = \lambda/1(1-G) + R\rho + V\eta - [aS + bA + D\delta + Pd + (1-m)]G + f(G-1)N + \sigma G \quad 2.13$$

$$\frac{dE}{dt} = (aS + bA + \delta D + dP)G - (\omega + \lambda)E + fEN + \sigma ES \quad 2.14$$

$$\frac{dS}{dt} = (1-k)\omega E + \tau A - (\beta + \sigma + \lambda)S + fSN + \sigma S^2 \quad 2.15$$

$$\frac{dA}{dt} = k\omega E - (e + \tau + \lambda)A + fAN + \sigma AS \quad 2.16$$

$$\frac{dV}{dt} = (1-m)G + \theta R - (\eta + \lambda)V + fVN + \sigma VS \quad 2.17$$

$$\frac{dR}{dt} = \beta S + eA - (\theta + \rho + \lambda)R + fRN + \sigma RS \quad 2.18$$

$$\frac{dD}{dt} = (\sigma + \varepsilon)SN + \varepsilon A - qD. \quad 2.19$$

$$\frac{dP}{dt} = gSN + hAN + rD - \varphi NPG - \gamma P. \quad 2.20$$

$$\frac{dN}{dt} = (\lambda - \mu)N - \sigma SN - fN^2. \quad 2.21$$

3. ANALYSIS

3.1 Basic Reproduction Number, R_0

The next-generation matrix methodology, as explained in references [2,20,21], is used to get it.

$W' = \frac{dW}{dt}$, where,

$W' = FW - MW$

$$F = \begin{bmatrix} 0 & aG_0 & bG_0 & \delta G_0 & dG_0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix},$$

$$M = \begin{bmatrix} h_1 & 0 & 0 & 0 & 0 \\ -h_6 & h_2 & -\tau & 0 & 0 \\ -h_7 & 0 & h_3 & 0 & 0 \\ 0 & -h_4 & -\varepsilon & q & 0 \\ 0 & -h_5 & -h_9 & -r & h_8 \end{bmatrix}, \quad W = \begin{bmatrix} E \\ S \\ A \\ D \\ P \end{bmatrix}$$

In this formulation, FW indicates the generation of new infection cases, MW represents the transfer or progression of infections across compartments, and W refers to the infection pool or source, while "where" identifies the specific site of infection.

The relationships among the parameters can be expressed as:

$\lambda = \mu + r_1, k = 1 - r_2, m = 1 - r_3, \sigma + \varepsilon = r_4,$

with the conditions

$\lambda > \mu, k < 1, m < 1.$

$G_0 = \frac{\eta+\mu}{\eta+\mu+r_3}$,

$h_1 = \omega + \mu,\ h_2 = \beta + \sigma + \mu,\ h_3 = e + \tau + \mu,$

h4=r4r1f^{-1}, h5=gr1f^{-1}, h6=r2ω, h7=kω, h8=ϕr1G0f^{-1}+γ, h9 =hr1f^{-1}.

The largest eigenvalue of $G^* = FM^{-1} = R_0$.

$R_0 = \frac{aG_0K_1 + bG_0K_2 + \delta G_0K_3 + dG_0K_4}{h_1h_2h_3qh_8}$ ***

Where

K1=qh8(h3h7+h6τ),
K2=qh8(h7h2),
K3=h8(h2h6ε+h3h4h7+h4h6τ),
K4=h1h3h8.

3.2 Existence, Positivity and Uniqueness of Solution

The region over which the model is valid is expressed as:

Ω

$\in \mathbb{R}^9 = \{G,\ E, S, A, R, V, D, P, N: G \geq 0, E \geq 0, S \geq 0, A \geq 0, R \geq 0, V \geq 0\ P \geq 0, N > 0, G + E + S + A + V + R = 1\}$

2.5

Assuming that at $t = 0$, when all assumed or stated inclusive variables are non-negative, we have $G(0) + E(0) + S(0) + A(0) + V(0) + R(0) = 1$, while $D(0) = 0$and $P(0) = 0$. If $E = 0$ and all other variables belong to Ω, then $(\partial E/\partial t) \geq 0$. This same condition applies to the remaining variables defined in equations (3.15) – (3.19). For $N = 0$, it follows that $(\partial N/\partial t) = 0$. However, when $N > 0$and assuming $\lambda > \mu$, then with suitable initial conditions, $(1/N)(\partial N/\partial t) > 0$for every $t > 0$. Therefore, the right-hand sides of equations (3.13)–(3.21) remain continuous and possess continuous first partial derivatives. Thus, a unique and well-defined solution exists for the system.

Hence, the model admits both mathematically consistent and biologically feasible solutions in the domain Ωfor all $t \in [0, \infty)$.

3.3 Solution for Equilibrium Point E_0

The coordinates (G,E,S,A,V,R,D,P) = $((G_0, 0,0,0, V_0, 0,0,0)$. define the equilibrium point E_0. S and A are both equal to 0 when there is no covid-19. When you put these values into the right side of equations (3.15), (3.18), and (3.19), you get $R = 0, E = D = 0$. If you put $S = A = R = E = D = P = 0$ into equations (3.17) and (3.13), you get $V_0 = \frac{r_3}{\eta+\mu+r_3}$ and $G_0 = \frac{\eta+\mu}{\eta+\mu+r_3}$ respectively. Solving the logistic equation of (2.21), we get, $N(t) = \frac{KN_0}{N_0 + (K - N_0)e^{-r_1 t}}$, With $K = \frac{r_1}{f}$. As t approaches infinity, N(t) approaches K, which is the ecosystem's carrying capacity.

3.4 Linear stability assessment for the disease-free point E_0

Next, the Jacobian matrix of the system is determined at the disease-free equilibrium point, expressed as: $(G, E, S, A, R, V, D, P) = (G_0, 0,0,0,0, V_0, 0,0)$

$$\begin{bmatrix} -h_{10} & 0 & -aG_0 & -bG_0 & \rho & \eta & -\delta G_0 & -dG_0 \\ 0 & -h_1 & aG_0 & bG_0 & 0 & 0 & \delta G_0 & dG_0 \\ 0 & h_6 & -h_2 & \tau & 0 & 0 & 0 & 0 \\ 0 & h_7 & 0 & -h_3 & 0 & 0 & 0 & 0 \\ 0 & 0 & \beta & e & -h_{11} & 0 & 0 & 0 \\ r_3 & 0 & h_{13} & 0 & \theta & -h_{12} & 0 & 0 \\ 0 & 0 & h_4 & \varepsilon & 0 & 0 & -q & 0 \\ 0 & 0 & h_5 & h_9 & 0 & 0 & r & -h_8 \end{bmatrix}$$

The **characteristic polynomial** corresponding to (**) can be written in terms of the eigenvalue $\sigma^{(**)}$as:

$$(\sigma^{**} + h_{11})(\sigma^{**} + M_1)(\sigma^{**} + M_2)(\sigma^{**5} + \sigma^{**4}D_1 + \sigma^{**3}D_2 + \sigma^{**2}D_3 + \sigma^{**}D_4 + D_5)=0 \quad 3.9$$

Where

$$M_1 = -\frac{1}{2}h_{10} - \frac{1}{2}h_{12} + \frac{1}{2}\sqrt{4\eta r_3 + h_{10}^2 - 2h_{10}h_{12} + h_{12}^2}$$

$$M_2 = -\frac{1}{2}h_{10} - \frac{1}{2}h_{12} - \frac{1}{2}\sqrt{4\eta r_3 + h_{10}^2 - 2h_{10}h_{12} + h_{12}^2}$$

$$D_1 = h_1 + h_2 + h_3 + h_8 + q$$

$$D_2 = G_0ah_6 + G_0bh_7 + h_1h_2 + h_1h_3 + h_1h_8 + h_1q + h_2h_3 + h_2h_8 + h_2q + h_3h_8 + h_3q + h_8q$$

$$D_3 = G_0dh_5h_6 + G_0dh_7h_9 + G_0ah_3h_6 + G_0ah_6h_8 + G_0ah_6q + G_0ah_7\tau + G_0bh_2h_7 + G_0bh_7h_8 + G_0bh_7q + G_0\delta h_4h_6 + G_0\delta h_7\varepsilon + h_1h_2h_3 + h_1h_3h_8 + h_1h_3q + h_1h_8q + h_2h_3h_8 + h_2h_3q + h_2h_8q + h_3h_8q$$

$$D_4 = G_0dh_2h_7h_9 + G_0dh_3h_5h_6 + G_0dh_4h_6r + G_0dh_5h_6q + G_0ah_6q + G_0dh_5h_7\tau + G_0dh_7h_9q + G_0dh_7r\varepsilon + G_0ah_3h_6h_8 + G_0ah_3h_6q + G_0ah_6h_8q + G_0ah_3h_8\tau + G_0ah_3q\tau + G_0bh_2h_7h_8 + G_0bh_2h_7q + G_0bh_7h_8q + G_0\delta h_2h_7\varepsilon + G_0\delta h_3h_4h_6 + G_0\delta h_4h_6h_8 + G_0\delta h_4h_7\tau + G_0\delta h_7h_8\varepsilon + h_1h_2h_3h_8 + h_1h_2h_3q + h_1h_3h_8q + h_2h_3h_8q$$

$$D_5 = -G_0dh_2h_7h_9q - G_0dh_2h_7r\varepsilon - G_0dh_3h_4h_6r - G_0dh_3h_5h_6q - G_0dh_4h_7r\tau - G_0dh_5h_7q\tau - G_0ah_3h_6h_8q - G_0ah_3h_8q\tau - G_0bh_2h_7h_8q - G_0bh_2h_7h_8\varepsilon - G_0\delta h_3h_4h_6h_8 - G_0\delta h_4h_7h_8\tau + h_1h_2h_3h_8$$

There are three negative real roots for equation (4.9). But, from the quintic equation

$$M_1 = -\frac{1}{2}h_{10} - \frac{1}{2}h_{12} + \frac{1}{2}\sqrt{4\eta r_3 + h_{10}^2 - 2h_{10}h_{12} + h_{12}^2}$$

$$M_2 = -\frac{1}{2}h_{10} - \frac{1}{2}h_{12} - \frac{1}{2}\sqrt{4\eta r_3 + h_{10}^2 - 2h_{10}h_{12} + h_{12}^2}$$

$$D_1 = h_1 + h_2 + h_3 + h_8 + q$$

$$D_2 = G_0ah_6 + G_0bh_7 + h_1h_2 + h_1h_3 + h_1h_8 + h_1q + h_2h_3 + h_2h_8 + h_2q + h_3h_8 + h_3q + h_8q$$

$$D_3 = G_0dh_5h_6 + G_0dh_7h_9 + G_0ah_3h_6 + G_0ah_6h_8 + G_0ah_6q + G_0ah_7\tau + G_0bh_2h_7 + G_0bh_7h_8 + G_0bh_7q + G_0\delta h_4h_6 + G_0\delta h_7\varepsilon + h_1h_2h_3 + h_1h_3h_8 + h_1h_3q + h_1h_8q + h_2h_3h_8 + h_2h_3q + h_2h_8q + h_3h_8q$$

$$D_4 = G_0dh_2h_7h_9 + G_0dh_3h_5h_6 + G_0dh_4h_6r + G_0dh_5h_6q + G_0ah_6q + G_0dh_5h_7\tau + G_0dh_7h_9q + G_0dh_7r\varepsilon + G_0ah_3h_6h_8 + G_0ah_3h_6q + G_0ah_6h_8q + G_0ah_3h_8\tau + G_0ah_3q\tau + G_0bh_2h_7h_8 + G_0bh_2h_7q + G_0bh_7h_8q + G_0\delta h_2h_7\varepsilon + G_0\delta h_3h_4h_6 + G_0\delta h_4h_6h_8 + G_0\delta h_4h_7\tau + G_0\delta h_7h_8\varepsilon + h_1h_2h_3h_8 + h_1h_2h_3q + h_1h_3h_8q + h_2h_3h_8q$$

$$D_5 = -G_0dh_2h_7h_9q - G_0dh_2h_7r\varepsilon - G_0dh_3h_4h_6r - G_0dh_3h_5h_6q - G_0dh_4h_7r\tau - G_0dh_5h_7q\tau - G_0ah_3h_6h_8q - G_0ah_3h_8q\tau - G_0bh_2h_7h_8q - G_0bh_2h_7h_8\varepsilon - G_0\delta h_3h_4h_6h_8 - G_0\delta h_4h_7h_8\tau + h_1h_2h_3h_8$$

Proposition 4.4.1. When R_0<1, the disease-free equilibrium condition is asymptotically locally stable and unstable when R_0>1,

Proof.

According to *** $R_0 = \frac{aG_0K_1 + bG_0K_2 + \delta G_0K_3 + dG_0K_4}{h_1h_2h_3qh_8}$. If Ro is smaller than 1, then $h_1h_2h_3qh_8$ is greater than $aG_0K_1 + bG_0K_2 + \delta G_0K_3 + dG_0K_4$. Since every coefficient in the fifth-degree polynomial (4.10) is positive, **Descartes' Rule of Signs** implies that all the corresponding eigenvalues are negative occurring in one, three, or five instances while any complex eigenvalues appear as conjugate pairs. To further assess stability, the **Routh–Hurwitz stability criterion** is applied to this fifth-order polynomial.

$$D_1D_2D_3 > D_3^2 + D_1^2D_4,$$

$$(D_1D_4 - D_5)(D_1D_2D_3 - D_3^2 - D_1^2D_4) > D_5(D_1D_2 - D_3)^2 + D_1D_5^2$$

are both satisfied. By letting $F = D_1D_2D_3 - D_3^2 - D_1^2D_4$, We express the stability condition as **F > 0**, which consequently implies that **Q > 0**, where:

$$Q = (D_1D_4 - D_5)F - D_5(D_1D_2 - D_3)^2 + D_1D_5^2$$

It is important to represent **Q** as a finite sum of computable expressions involving the model's dependent parameters. Using the symbolic computation software **Maple**, it was confirmed that both **F** and $\mathbf{Q_1}$ consist solely of positive terms, ensuring their overall positivity.

$$(C_1 - E_2) + \{h_3^2E_2 + C_2(g_0 + E_1)\}(g_0 - E_1)$$

Where,

Q_1 represents the aggregation of multiple positive expressions that depend on the parameter space.

$$C_1 = h_1h_2qh_8,$$

$$C_2 = h_1 + h_2 + h_3 + q + h_8,$$

$$C_3 = h_1h_8^2\{h_8(4h_2^2 + 5h_1q) + 4h_2^3 + 8h_2^2q + 8h_2q^2$$

$$C_4 = h_1\{5h_2^3q + 8h_2^2q^2 + 5h_2q^3) + 4h_2^3q^2 + 4h_2^2q^3 + h_2q^3 + h_2q^4\}$$

,

$$C_5 = h_1h_8\{h_8^3(h_2 + q) + 4q^2 + 4q^3h_8 + q^4 + 2h_2^3h_8^2 + 4h_2^3q^2 + 4h_8(h_2^4 + 5h_2^2h_8^3)\}$$

,

$$C_6 = h_2q(h_2^2q + h_2^2h_8 + 2h_2q^2 + 5h_2qh_8 + q^3 + 5q^2h_8$$

$$C_7 = h_1 h_8^3\{h_8(h_2^2 + h_2 q + q^2) + 5h_2^2 h_8 + 5h_2 q^2 + 2h_2 q h_8 + 2q^3\}$$

$$C_8 = h_1 h_8^2(8h_2^2 q^2 + 5h_2 q^3 + q^4) + h_1 h_2 q^4 h_8 + h_2^4 q^2 h_8$$

$$E_1 = aG_0K_2 + bG_0K_3$$

$$E_2 = \delta G_0 K_4 + dG_0 K_5$$

$$Z_1 = h_3 + 2(h_1 + h_2 + q + h_8)$$

$$Z_2 = h_1(h_1 + 3h_2 + 2h_3 + 3q + 3h_8 + 3h_2^2 + 4 + h_{2h_8})$$

$$Z_3 = h_1(6h_2 q + 6h_2 h_8 + 4h_8 q + 4h_3 h_8 + 3q^2)$$

$$Z_4 = 6h_1 q h_8 + 3h_1 h_8^2 + h_2^3 + 2h_2^2 h_3 + 3h_2^2 q$$

$$Z_5 = q(q^2 + 3h_2 q + 3q h_8 + 2h_3 q + 3h_8^2 + 4h_3 h_8 + 6h_2 h_8$$

$$Z_6 = 4h_2 h_3 q + h_8^3 + 2h_3 h_8^2 + 3h_2^2 h_8 + 4h_2 h_3 h_8$$

$$Z_7 = C_1^2(h_2 h_4 + h_8^4)(h_2 + q) + C_1^2 h_8(h_2^2 + h_2 q + q^4) + C_8$$

$$Z_8 = 2C_1 h_2 q h_8^4(h_2 + q) + (h_2 h_4 + h_8^4)(h_2 + q) + 2C_1 h_2 q h_8^3(5h_2 q + 4h_2^2 + 4q^2 + C_3$$

$$Z_9 = h_2^2 q^2(h_2 + q)^2 + h_1 h_8 q^2(8h_2^2 + 5h_2 q + q^2) + C_4 + C_5$$

$$Z_{10} = h_2^2(C_1 + C_6 C_7)$$

3.6 Simulation of Computation

This research employs **numerical simulations** implemented in **MATLAB** using the **ODE45s solver**, which is based on a variable-order **Runge–Kutta integration scheme.** The computation is executed with a **relative tolerance of 10^{-8}** and an **absolute tolerance of 10^{-9}** to ensure precision. All simulations are conducted using **non-dimensional parameters,** defined alongside their corresponding numerical values as follows: $\lambda = 8.8\times10^{-3}$, a = 8.02×10^{-1}, b = 1.55×10^{0}, d = 1.15×10^{0}, q = 8.0×10^{-1}, $\beta = 5.04\times10^{0}$, e = 1.74×10^{0}, f = 4.89×10^{-3}, $\mu = 3.88\times10^{-3}$, $\eta = 5.53\times10^{-1}$, $\tau = 1.79\times10^{0}$, g = 8.1×10^{-3}, $\delta = 2.31\times10^{-5}$, h = 5.10×10^{-2}, $\omega = 2.44\times10^{-2}$, $\sigma = 8.70\times10^{-3}$, $\rho = 1.88\times10^{-1}$, $\theta = 9.00\times10^{-2}$, $\varphi = 3.90\times10^{-2}$, r = 9.90×10^{-1}, z = 2.03×10^{-1}, $\gamma = 2.00\times10^{-2}$. The **initial conditions** were set as follows: G = 9.9×10^{-1}, E = 1.0×10^{-2}, S = 0, A = 0, V = 0, R = 0, D = 0, P = 0, and N = 1.0×10^{0}.

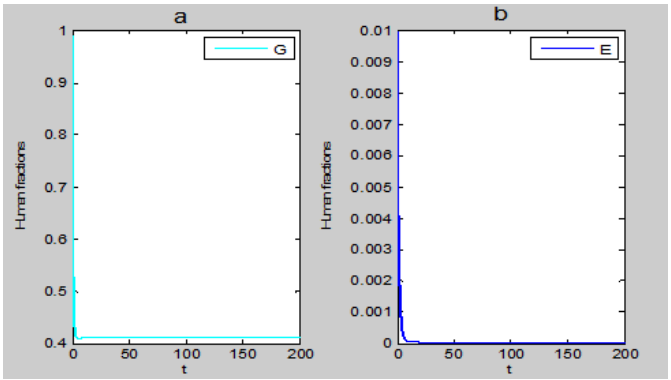

Fig. 3.1: Simulation results illustrating the impact of vaccination on the susceptible and latent population groups. Here, t = 1 corresponds to approximately five days in real time. The simulation was conducted using the following initial conditions: G = 0.99, E = 0.01, S = 0, A = 0, V = 0, R = 0, D = 0, P = 0, and N = 1. The parameter values employed are as specified in Section 3.2.

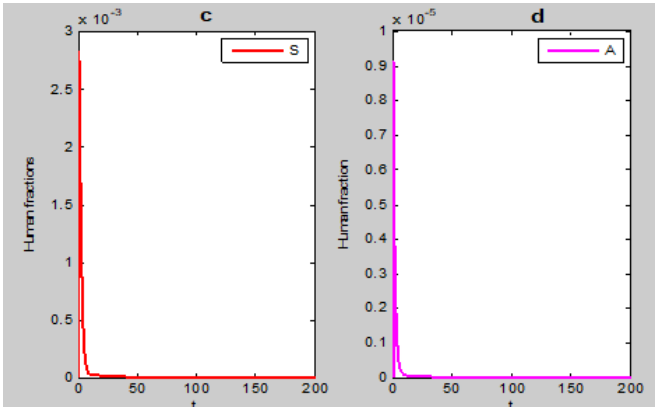

Fig. 3.2: Simulation output depicting the influence of vaccination on the symptomatic and asymptomatic human populations. In this model, t = 1 corresponds to roughly five days in real time. The simulation begins with the initial conditions: G = 0.99, E = 0.01, S = 0, A = 0, V = 0, R = 0, D = 0, P = 0, and N = 1. The parameter values applied are consistent with those specified earlier

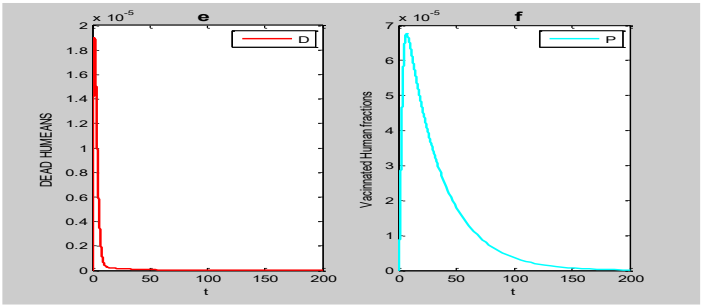

Fig. 3.3: Simulation results illustrating the **impact of vaccination** on the **deceased human population** and the **surface viral load.** In this simulation, *t = 1* represents approximately **five days in real time**. The initial conditions applied are G = 0.99, E = 0.01, S = 0, A = 0, V = 0, R = 0, D = 0, P = 0, and N = 1, with **parameter values** identical to those specified above.

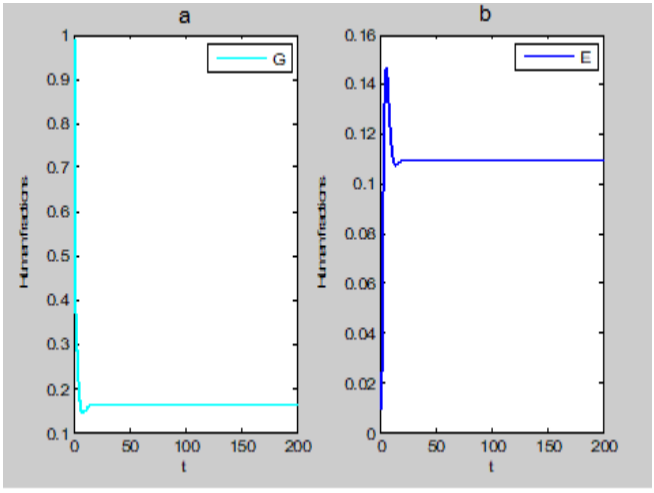

Fig. 3.4: Simulation outcome illustrating how an increased contact rate between susceptible individuals and infectious corpses during burial rituals influences the disease dynamics under the condition $R_0 > 1$. The simulation parameters are identical to those used previously, except for the following modified values: a = 10.9018, b = 16.553, δ = 10.31, and ω = 0.96.

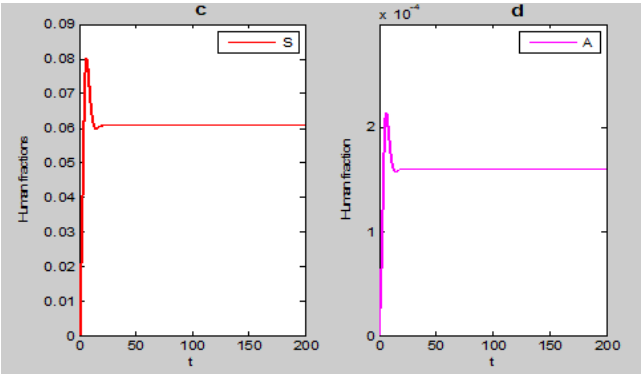

Fig. 4.5: Simulation output illustrating the impact of an elevated contact rate between susceptible individuals and infectious deceased persons during burial events on disease progression dynamics, under the condition $R_0 > 1$. The simulation parameters remain as previously specified, except for the modified values: a =10.9018, b =16.553, and

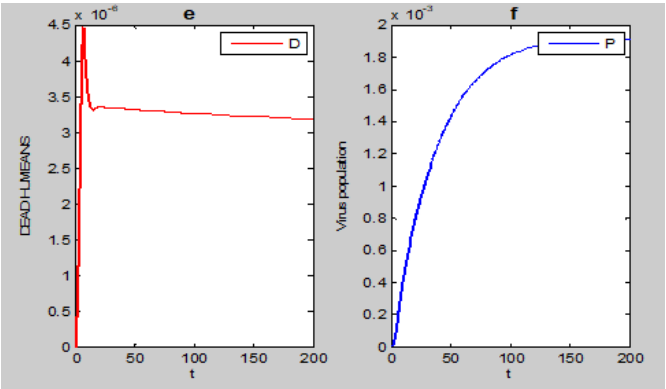

Fig.4.6: The simulation illustrates how an elevated rate of contact between susceptible individuals and infectious corpses during burial practices influences the disease transmission dynamics under the condition $R_0 > 1$. The parameter values used are identical to those applied earlier, except for the following adjustments: a = 10.9018, b = 16.553, δ = 10.31, and ω = 0.96.

4.DISCUSSION AND CONCLUSION

4.1 Discussion

The suggested model clarifies the mechanics of COVID-19 transmission, emphasizing the interaction of vaccination, reinfection, and cultural behaviours, such as burial ceremonies, in perpetuating the disease's prevalence. The simulation results show that higher vaccination rates and continuous preventive measures greatly lower infection rates, which might lead to the virus's complete disappearance. This confirms the prevailing consensus that immunization is among the most effective strategies for controlling COVID-19.

However, the results show that vaccination alone is not enough to completely stop the disease from becoming endemic. The stopping of important preventive steps, like wearing masks, keeping a distance from others, and washing hands, makes it more likely that the disease will spread, especially when people are together, as at funerals or other community events. These situations often involve direct contact with infected individuals or contaminated environments, facilitating the virus's transmission, even among those who are partially vaccinated.

The model emphasizes the importance of characteristics such as the frequency of interactions between susceptible individuals and infectious corpses, together with the duration of viral viability on surfaces. Higher transmission rates or a slow drop in the virus may keep the infection running in a group of people, even when vaccination attempts are still going on. The findings align with prior studies emphasizing the necessity of continuous behavioural evaluations for effective long-term illness management.

The stability study shows that when $R_0 < 1$ indicates that the **disease dies out over time**, which means that the infection will eventually go away provided control measures are put in place correctly. On the other hand, when R0 is greater than 1, the infection lasts, which makes it an endemic condition. This underscores the imperative for comprehensive programs that amalgamate immunisation efforts with ongoing compliance to preventive strategies, particularly in regions where conventional burial customs are predominant.

The model underscores the complex interactions of human behaviour, biological factors, and environmental settings that affect the efficacy of COVID-19 management measures. This sets out a basic framework for decision-makers to understand the risks associated with relaxing preventive measures during vaccination attempts and stresses the importance of getting the community involved and improving public health education.

4.2 CONCLUSION

This study presented a nonlinear deterministic model, designated GESAVRDP, aimed at evaluating the dynamics of COVID-19 transmission. It looks at things like vaccination, reinfection, and the dangers of being around sick remains and dirty surfaces. The study confirms the model's mathematical soundness by making sure that all of its variables are positive and fall inside certain ranges. The actual RO, which is the basic reproduction number is an important figure for figuring out whether an infection is likely to last or go away.

Simulation results show that large vaccination campaigns can greatly lower infection rates, and when used with other preventive measures, they may even get rid of the disease

completely. If you don't follow these safety rules at social events, including funerals and other cultural celebrations, the vaccine won't work as well, and the virus will keep spreading.

The effective treatment of COVID-19 requires the integration of pharmacological and behavioural strategies. To stop habits that spread disease, public health programs need to focus on educating the population and running campaigns that are sympathetic to different cultures. The results of this model can help policymakers come up with flexible solutions that take into account both local cultural norms and epidemiological statistics.

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