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Stability Analysis of a Mathematical Modeling of Spread and Control of Corona Virus Disease (Covid-19) Incorporating Vaccination Class

Japheth CHEMBE[1*], Samuel Abu SOMMA[1]

[1] *Department of Mathematics, Federal University of Technology Minna, Nigeria.*

Research Article

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ABSTRACT

In this paper some mathematical models of COVID 19 were extended by incorporating vaccination, social distancing, and proper use of face mask and hand sanitizers for the spread and control of Corona virus (COVID-19). The analysis of the Disease-Free Equilibrium (DFE) and Endemic Equilibrium (EE) points were carried out. The trace -determinant approaches for local stability and Castilo-chaves for global stability were used in the stability and sensitivity analyses. At the stability of the equilibrium points, we find out that the basic reproduction number which implies the (DFE) is locally asymptotically stable, but global asymptotic stability of (EE) exists at . Sensitivity analysis identifies the model's most sensitive parameters; which are responsible for disease transmission and control. Visualization of the effect of the key parameters on the basic reproduction number was carried out. The data visualization demonstrates that vaccination and recovery rate are crucial parameters for eradicating COVID-19 from the population, while contact rate, lack of social distancing, and improper use of facemasks and hand sanitizers are crucial for COVID-19 persistence. The risks of close proximity to infected people should indeed be made known to the general public. The government needs to step up its vaccination efforts.

1. Introduction

An unusual Coronavirus Disease 2019 (COVID-19) which is linked to Acute Respiratory Distress Syndrome was declared pandemic on March 11th, 2020, by World Health Organization (WHO). COVID-19 belongs to a new strain of novel coronaviruses known as SARS-CoV-2 [1]. The virus was discovered late December 2019 with patients admitted to hospitals with an initial diagnosis of pneumonia. Patients' illnesses were traced back to a market in Wuhan, Hubei Province, China that sells seafood and wet animals [2]. Because there were so many infected people in the "Huanan Seafood Market," the situation became increasingly dire [3].

A virus with symptoms including pneumonia was reported to the Chinese government, but its exact nature was unknown. Cases from the reported virus rose from 0 to over 40 cases in just 30 days. The virus had a history of killing approximately 770 people in China. They died from what was then called the SARS disease in 2002 and 2003.

Incubation for this virus, which causes respiratory issues, is between two and fourteen days [4]. Its symptoms include ; dry cough, flu, short breath, a runny nose, a sore throat, problems with musculoskeletal joints, diarrhea, and, in rare cases, a loss of sense of smell or taste. The two most common ways for COVID-19 to be transmitted from one individual to another are through respiratory droplet inhalation and skin-to-skin contact. Many people who contract the COVID-19 viral infection will experience moderate to severe respiratory illness, but will eventually get better without any special treatment. In Africa, Nigeria recorded her first case on February 27, 2020, but as of 13th Nov, 2021 the figure had risen to 213,127 infections with 2960 deaths so far [5]. It is sad to note that most of the mortalities of COVID-19 especially in developing countries are attributed to poor medical facilities and medical personnel.

To effectively reduce the spread of COVID-19, governments have been implementing various control measures such as imposing strict, mandatory lockdowns and encouraging (and in some cases strictly enforcing) other measures such as individuals maintaining a minimum distance between themselves (social distancing), avoiding crowded events, imposing a maximum number of individuals in any gathering (religious and social), and the use of face masks in public [5]. To further help mitigate the spread of COVID-19, contact tracing of suspected infected cases has been stepped up in several countries and detected cases (asymptomatic and symptomatic) are quickly placed in isolation for prompt treatment [8].

As COVID-19 vaccines are being deployed worldwide, we formulate and qualitatively analyze a COVID-19 mathematical model, taking into consideration available therapeutic measures, vaccination of susceptible and treatment of hospitalized/infected individuals. Our proposed model

[*] *Department of Mathematics, Federal University of Technology Minna, Main Campus, Gidan Kwano, P.M.B 65, Minna, Nigeria.*
E-mail address: japhet.chembe@st.futminna.edu.ng

incorporates some key epidemiological and biological features of COVID-19, including demographic parameters (recruitment/birth and death). The minimum population of Nigeria that must be vaccinated to curb the transmission of COVID 19 was estimated by the herd immunity thresh hold at 36.638%.

2. Materials and Methods

2.1 The Model Description and Formulation

In this model, we focus solely on Nigeria human population. The model partitioned the population into six (6) compartments namely "susceptible," "exposed," "quarantine/isolated," "infected," "recovered," and vaccinated. Recruitment into the susceptible class is by birth at the rate Λ. Susceptible individuals who have enough contact with the infected individuals are moved to the exposed class with the infection force. Susceptible individuals can also be vaccinated into the vaccination class at the rate. If the vaccine is ineffective (denotes the vaccine inefficacy), those individuals who are vaccinated with the vaccine and have made contact with infected individuals are also moved into the exposed class *E(t)* with the force of infection. The exposed individuals are moved into the infected class *I(t)* at the rate ω or just moved into the quarantine class *Q(t)* at rate τ. Individuals who are in the quarantine class without showing symptoms after 14 days of incubation are moved to the recovered class *R(t)* at the rate while those that showed symptoms are moved into the infected class *I(t)* at the rate. The infected individuals who after treatment recovered are moved into the recovered class *R(t)* at the rate γ. We assume that recovery from Covid-19 does not confer permanent immunity. Thus, the recovered individuals who were not vaccinated can return to the susceptible class at the rate ρ.

Individuals in each class can die a natural death at the rate μ. Those individuals in the infected class have an additional death burden as a result of the infection.

The transition rates from susceptible and vaccinated to exposed is given by the following force of infection.

$$\alpha = \frac{\varepsilon(1-\eta)(1-\xi)}{N(t)}(E+I+Q) \tag{1}$$

Where η is the population that maintains social distancing to prevent the spread of Covid-19 and is denoted by $0< \eta \leq 1$ while represents the proportion of the population that makes proper use of face masks and hand sanitizers denoted by $0< \xi \leq 1$. All parameters are positive. Table 2 defines all the variables and parameters used for the formulation of the model (fig 1).

2.2 Model Equation

$$\frac{dS(t)}{dt} = \Lambda - \alpha S + \rho R - (\mu + \upsilon)S \tag{2}$$

$$\frac{dE(t)}{dt} = \alpha S + \kappa\alpha V - (\omega + \mu + \tau)E \tag{3}$$

$$\frac{dQ(t)}{dt} = \tau E - (\sigma_1 + \sigma_2 + \mu)Q \tag{4}$$

$$\frac{dI(t)}{dt} = \omega E + \sigma_2 Q - (\mu + \delta + \gamma)I \tag{5}$$

$$\frac{dR(t)}{dt} = \gamma I + \sigma_1 Q - (\rho + \mu)R \tag{6}$$

$$\frac{dV(t)}{dt} = \upsilon S - \kappa\alpha V - \mu V \tag{7}$$

Table 1. Notations and Definition of Variables and Parameters.

Symbol	Description
S(t)	Susceptible class at time t
E(t)	Exposed class at time t
I(t)	Infected class at time t
Q(t)	Quarantine class at time t
R(t)	Recovered class at time t
V(t)	Vaccinated class at time t
Λ	Recruitment rate into the susceptible class
α	Transmission rate of infection
σ_1	Transition rate to the recovered class after incubation period
σ_2	Progression rate to the infected class
μ	Per capita natural death rate
ρ	Rate of loss of immunity after treatment as time passes by
υ	Vaccination rate
η	Rate of social distancing
ξ	Rate of use of facemask and hand sanitizers
ω	Progression rate from exposed to infected class
τ	Rate at which exposed individuals are taken into isolation
κ	Vaccination ineffectiveness (inefficacy)
δ	Death rate due to infection
γ	Rate of recovery from the infection

2.3 Existence of Equilibrium Point

At equilibrium

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = \frac{dV}{dt} = 0 \tag{8}$$

Let

$$E^* = \left(S^*, E^*, Q^*, I^*, R^*, V^*\right) = \left(S, E, Q, I, R, V\right) \tag{9}$$

Therefore, the system (2) to (7) become

$$\Lambda + \rho R^* - \left(\alpha + B_1\right) S^* = 0 \tag{10}$$

$$\alpha S^* + \kappa\alpha V^* - B_2 E^* = 0 \tag{11}$$

$$\tau E^* - B_3 Q^* = 0 \tag{12}$$

$$\omega E^* + \sigma_2 Q^* - B_4 I^* = 0 \tag{13}$$

$$\gamma I^* + \sigma_1 Q^* - (\rho + \mu) R^* \tag{14}$$

$$\upsilon S^* - (\kappa\alpha + \mu) V^* = 0 \tag{15}$$

Where,

$$\left.\begin{aligned} B_1 &= \left(\mu + \upsilon\right), B_2 = \left(\omega + \mu + \tau\right), B_3 = \left(\sigma_1 + \sigma_2 + \mu\right) \\ B_4 &= \left(\mu + \delta + \gamma\right), B_5 = \left(\rho + \mu\right) \end{aligned}\right\} \tag{16}$$

2.4 Disease Free Equilibrium (DFE) State

Let $X^0 = \left(S, E, I, Q, R, V\right) = \left(S^0, E^0, I^0, Q^0, R^0, V^0\right)$ be the DFE point with $I = 0$

Then, equation (10)-(15) becomes

$$X^0 = \left(S^0, E^0, I^0, Q^0, R^0, V^0\right) = \left(\frac{\Lambda}{B_1}, 0, 0, 0, \frac{\upsilon\Lambda}{\mu B_1}\right) \tag{17}$$

At DFE

$$\left.\begin{aligned} N^0 &= S^0 + E^0 + Q^0 + I^0 + R^0 + V^0 \\ N^0 &= \frac{\Lambda}{\mu} \end{aligned}\right\} \tag{18}$$

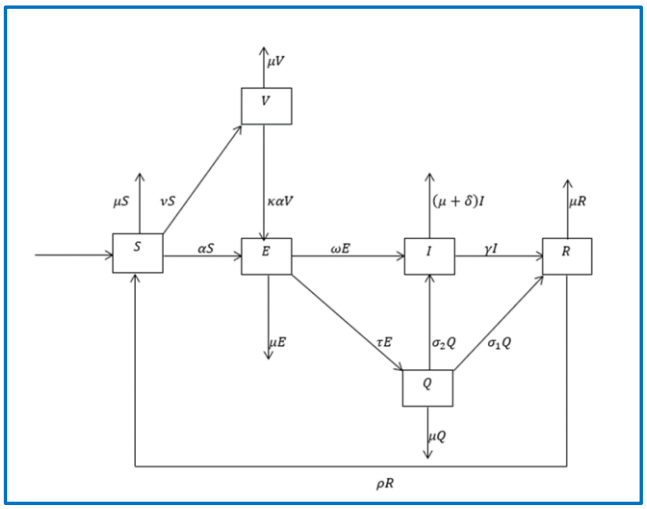

Fig. 1 Schematic Diagram of the model.

2.5 Basic Reproduction Number R_0

The potential for the spread of a disease can be estimated using the basic reproduction number R_0. The basic reproduction number (R_0) of an infectious agent, such as the corona virus, is defined as the average amount of secondary infections actually generated by an infectious person in a susceptible host population [9].

Using the basic reproduction number, one can predict how quickly a disease might spread. Reproduction number (R_0) is the average number of new infections caused by a single infectious person in a susceptible host population [9]. The corona virus, like many other infectious agents, has a relatively high reproduction number.

A model's basic reproductive number is equal to the largest eigenvalue of FV^{-1} or the spectral radius of the model. The basic reproduction number $R_o = \rho\left(FV^{-1}\right)$ will be computed using the method of [10], where $f_i(\mathrm{x})$ is the rate at which infected people emerge in compartment i, $V_i^+(\mathrm{x})$ is the rate at which people move into compartment via all mechanisms

Table 2. Description of Variables with their Values.

Variables	Description	Values	Source
S(0)	Susceptible class	199,950,894	A9
E(0)	Exposed class	3,550,457	A7
Q(0)	Quarantined class	3,392,457	A5
I(0)	Infected class	212,127	A3
R(0)	Recovered class	205,491	A4
V(0)	Vaccinated class	5,776,679	A8
N(0)	Total Human Population	213,089,105	A1

other than epidemic spread, and $V_i^-(\mathrm{x})$ is the rate at which people move out of compartment i.

The disease transmission model consists of the system of equations

$$x_i = f_i(\mathrm{x}) = \mathrm{F}_i(\mathrm{x}) - \mathrm{V}_i(\mathrm{x}) \tag{19}$$

Where,

$$V_i = V_i^-(\mathrm{x}) - \mathrm{V}_i^+(\mathrm{x}) \tag{20}$$

$$V = \left[\frac{\partial f_i(\mathrm{X}^0)}{\partial x_j}\right] \tag{21}$$

Where $\mathrm{x}_j = E, I, Q$ or j=1,2,3 and X^0 is the Disease Free Equilibrium Point.

Secondary infections are predicted to occur within E,I,Q, and this is modeled in equations (10) through (15). The occurrence of new infections in each section is detailed in the matrix.

$$f = \begin{pmatrix} \frac{\varepsilon(1-\eta)(1-\xi)(\mathrm{E}+\mathrm{I}+\mathrm{Q})\mathrm{S}}{N} + \frac{\kappa\varepsilon(1-\eta)(1-\xi)(\mathrm{E}+\mathrm{I}+\mathrm{Q})\mathrm{V}}{N} \\ 0 \\ 0 \end{pmatrix} \tag{22}$$

Let $l_1 = \varepsilon(1-\eta)(1-\xi)$

Equation (22) becomes

$$f = \begin{pmatrix} \frac{l_1}{N}(S+\kappa V)(E+I+Q) \\ 0 \\ 0 \end{pmatrix} \quad (23)$$

At the point where disease-free equilibrium is achieved, the Jacobian matrix F equals;

$F = \left[\frac{\partial f_i(\mathrm{X}^0)}{\partial x_j}\right]$, where $x_j = E, I, Q$ for j=1,2,3 and X^0 is the Disease Free Equilibrium Point.

Jacobian matrix of (233) at the equilibrium point where there is no disease;

$$F = \begin{pmatrix} l_1\left(\frac{\mu+\upsilon\kappa}{B_1}\right) & l_1\left(\frac{\mu+\upsilon\kappa}{B_1}\right) & l_1\left(\frac{\mu+\upsilon\kappa}{B_1}\right) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad (24)$$

The following matrix describes the rate at which individuals leave and enter the infective compartment.

$$V_i = V_i^- - \mathrm{V}_i^+ = \begin{pmatrix} B_2E \\ B_4I - \omega E - \sigma_2 Q \\ B_3Q - \tau E \end{pmatrix} \quad (25)$$

Where

$$V_i^- = \begin{pmatrix} B_2E \\ B_4I \\ \mathrm{B_3Q} \end{pmatrix} \quad (26)$$

And

$$V^+ = \begin{pmatrix} 0 \\ \omega E + \sigma_2 Q \\ \tau E \end{pmatrix} \quad (27)$$

The matrix (25) evaluated at the disease-free equilibrium point is given as;

$$V = \left[\frac{\partial f_i(\mathrm{X}^0)}{\partial x_j}\right] = \begin{pmatrix} B_2 & 0 & 0 \\ -\omega & B_4 & -\sigma_2 \\ -\tau & 0 & B_3 \end{pmatrix} \quad (28)$$

Where $x_j = E, I, Q$ for j=1,2,3 and X^0 is the Disease Free Equilibrium Point.

The inverse of V is computed using Gauss Jordan method, After carefully solving, we obtain V^{-1} to be

$$V^{-1} = \begin{pmatrix} \frac{1}{B_2} & 0 & 0 \\ \frac{\omega B_3 + \tau\sigma_2}{B_2B_3B_4} & \frac{\sigma_2}{B_3B_4} & \frac{1}{B_4} \\ \frac{1}{B_2B_3} & 0 & \frac{1}{B_3} \end{pmatrix} \quad (29)$$

The next generation matrix FV^{-1} is given by (30)

$$FV^{-1} = \begin{pmatrix} l_1(\mu+\upsilon\kappa)\left[\frac{B_3B_4 + \omega B_3 + \tau\sigma_2 + B_4}{B_1B_2B_3B_4}\right] & l_1(\mu+\upsilon\kappa)\left[\frac{\sigma_2}{B_1B_3B_4}\right] & l_1(\mu+\upsilon\kappa)\left[\frac{B_3+B_4}{B_1B_3B_4}\right] \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad (31)$$

$\rho(\mathrm{FV}^{-1})$ is the dominating eigenvalue of the (FV^{-1}) matrix.

The eigenvalue is gotten using $\left|Fv^{-1} - \lambda I\right| = 0$

Where;

$$\left.\begin{aligned} &\left(l_1(\mu+\upsilon\kappa)\left[\frac{B_3B_4 + \omega B_3 + \tau\sigma_2 + B_4}{B_1B_2B_3B_4}\right] - \lambda_1\right)\begin{vmatrix} -\lambda_2 & 0 \\ 0 & -\lambda_3 \end{vmatrix} - \left(l_1(\mu+\upsilon\kappa)\left[\frac{\sigma_2}{B_1B_3B_4}\right]\right)\begin{vmatrix} 0 & 0 \\ 0 & -\lambda_3 \end{vmatrix} \\ &+l_1\left(l_1(\mu+\upsilon\kappa)\left[\frac{B_3+B_4}{B_1B_4}\right]\right)\begin{vmatrix} 0 & -\lambda_2 \\ 0 & 0 \end{vmatrix} = 0 \end{aligned}\right\} \quad (32)$$

$$\lambda_1 = l_1(\mu + \upsilon\kappa)\left[\frac{B_3B_4 + \omega B_3 + \tau\sigma_2 + B_4}{B_1B_2B_3B_4}\right] \quad (33)$$

$$\lambda_1 = l_1(\mu + \upsilon\kappa)\left[\frac{B_3B_4 + \omega B_3 + \tau\sigma_2 + B_4}{B_1B_2B_3B_4}\right] \quad (34)$$

Then

$$R_0(\upsilon) = l_1(\mu + \upsilon\kappa)\left[\frac{B_3B_4 + \omega B_3 + \tau\sigma_2 + B_4}{B_1B_2B_3B_4}\right] \quad (35)$$

Where $B_1 = (\mu + \upsilon)$

Equation (35) gives the effective reproduction number, $R_0(v)$ when there was vaccine in circulation. In the absence of vaccinations (that is $v = 0$) then, the basic reproductive number $\Re_0$ is given as;

$$\Re_0 = R_0(0) = l_1\left[\frac{B_3B_4 + \omega B_3 + \tau\sigma_2 + B_4}{B_2B_3B_4}\right] \quad (36)$$

$\Re_0$ is the basic reproduction number which is the average number of secondary cases arising from one infectious individual in a completely susceptible population.

2.6 The Model Stability Analysis

Theorem 1: The DFE point E^0 of the model is Locally Stable if $R_0 < 1$

Proof: The disease free equilibrium point is said to be locally asymptotically stable, if all the eigenvalues of the Jacobian matrix at DFE are negative or unstable if otherwise.

At DFE, the Jacobian matrix of the underlying equation system is

$$J(\mathrm{E}^0) = \begin{pmatrix} -B_1 & 0 & 0 & 0 & \rho & 0 \\ 0 & -B_2 & 0 & 0 & 0 & 0 \\ 0 & \tau & -B_3 & 0 & 0 & 0 \\ 0 & \omega & \sigma_2 & -B_4 & 0 & 0 \\ 0 & 0 & \sigma_1 & \gamma & -B_5 & 0 \\ \upsilon & 0 & 0 & 0 & 0 & -\mu \end{pmatrix} \quad (37)$$

Reducing equation (37) to upper triangular matrix gives equation whose characteristics equation is;

$$\left|J(\mathrm{E}^0) - \lambda \mathrm{I}\right| = 0 \quad (38)$$

$$J(\mathrm{E}^0) = \begin{vmatrix} -B_1 - \lambda & 0 & 0 & 0 & \rho & 0 \\ 0 & -B_2 - \lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & -B_3 - \lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & -B_4 - \lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & -B_5 - \lambda & 0 \\ 0 & 0 & 0 & 0 & 0 & -\mu - \lambda \end{vmatrix} = 0 \quad (39)$$

$$(-B_1 - \lambda)(-B_2 - \lambda)(-B_3 - \lambda)(-B_4 - \lambda)(-B_5 - \lambda)(-\mu - \lambda) = 0 \quad (40)$$

Either

$$-(B_1 + \lambda_1) = 0 \text{ or } -(B_2 + \lambda_2) = 0 \text{ or } -(B_3 + \lambda_3) = 0 \text{ or } -(B_4 + \lambda_4) = 0 \quad (41)$$

$$-(B_5 + \lambda_5) = 0 \text{ or } -\mu - \lambda_6 = 0 \quad (42)$$

From equation (42)

$$\lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_5, \lambda_6 < 0 \quad (43)$$

Hence, the disease free equilibrium point is locally asymptotically stable.

3.7 The Disease-Free Equilibrium Analysis

Theorem 2 Equations (10) to (15) describe a disease free equilibrium that is globally asymptotically stable under the condition that $R_0 < 1$ holds, but unstable under the state that $R_0 > 1$.

Proof: Referring to [11], the system of equations (10) to (15) can be written as;

$$\left.\begin{aligned} \frac{dx(\mathrm{t})}{dt} &= F(x, y) \\ \frac{dy(\mathrm{t})}{dt} &= G(x, y) \end{aligned}\right\} \quad (44)$$

Whereas $x = (\mathrm{S}, \mathrm{R}, \mathrm{V}) \in \Re^3$ represents the various compartments of healthy human beings, $y = (E, Q, I) \in \Re^3$ represents the various compartments of infected human beings.

Therefore, DFE = (x^0, 0), where

$$x^0 = \begin{pmatrix} \frac{\Lambda}{B_1} & 0 & \frac{\upsilon\Lambda}{\mu B_1} \end{pmatrix} \quad (45)$$

It is paramount to show that,

$\frac{dx(\mathrm{t})}{dt} = F(\mathrm{x},0), x^0$ is Globally Asymptotically Stable (G.A.S.), and

$G(\mathrm{x},\mathrm{y}) = \mathrm{Cy} - G(\mathrm{x},\mathrm{y}), G(\mathrm{x},\mathrm{y}) \geq 0$ for $(\mathrm{x},\mathrm{y}) \in \Omega$

H1: consider the uninfected subsystem,

$$\frac{dx(\mathrm{t})}{dt} = F(\mathrm{x},\mathrm{y}) = \begin{pmatrix} \Lambda + \rho R - (\alpha + \mathrm{B}_1)\mathrm{S} \\ \gamma I + \sigma_1 Q - B_5 R \\ \upsilon S - (\kappa\alpha + \mu)\mathrm{V} \end{pmatrix} \quad (46)$$

When $y = 0$ that is $E = Q = I = 0$

Then, equation (46) becomes,

$$F(\mathrm{x},0) = \begin{pmatrix} \Lambda + \rho R - \mathrm{B}_1\mathrm{S} \\ -B_5 R \\ \upsilon S - \mu\,\mathrm{V} \end{pmatrix} \quad (47)$$

By so doing we obtained

$$\mathrm{S(t)} = \frac{(\Lambda + \rho R)}{B_1} + \left(\mathrm{S}(0) - \frac{(\Lambda + \rho R)}{B_1}\right)\ell^{-B_1 t} \quad (48)$$

$$R = R(0)\ell^{-B_5 t} \quad (49)$$

$$V = \frac{(\upsilon S)}{\mu} + \left(V(0) - \frac{(\upsilon S)}{\mu}\right)\ell^{-\mu t} \quad (50)$$

As $t \to \infty, S \to \frac{\Lambda + \rho R}{B_1}, R \to 0, V \to \frac{\upsilon S}{\mu}$ regardless of the value of S(0), R(0) and V(0)

Therefore,

$x_0 = \begin{pmatrix} \frac{\Lambda}{B_1} & 0 & \frac{\upsilon\Lambda}{\mu B_1} \end{pmatrix}$ satisfies global asymptotical stability

H2: consider an infected subsystem

$$y^1 = G(\mathrm{x},\mathrm{y}) = \begin{bmatrix} \frac{l_1}{N}(\mathrm{E}+\mathrm{I}+\mathrm{Q})\mathrm{S} + \frac{l_1}{N}\kappa(\mathrm{E}+\mathrm{I}+\mathrm{Q})\mathrm{V} - \mathrm{B}_2 E \\ \omega E + \sigma_2 Q - B_4 I \\ \tau E - B_3 Q \end{bmatrix} \quad (51)$$

Such that,

$$G(\mathrm{x},\mathrm{y}) = \mathrm{Cy} - \hat{\mathrm{G}}(\mathrm{x},\mathrm{y}) \quad (52)$$

Then,

$$\hat{\mathrm{G}}(\mathrm{x},\mathrm{y}) = \mathrm{Cy} - G(\mathrm{x},\mathrm{y}) \quad (53)$$

Where $C = \frac{\partial G(\mathrm{x},0)}{dt}$ (54)

$$C = \begin{pmatrix} \frac{l_1}{N}\mathrm{S} + \frac{l_1}{N}\kappa\,\mathrm{V} - \mathrm{B}_2 & \frac{l_1}{N}\mathrm{S} + \frac{l_1}{N}\kappa\,\mathrm{V} & \frac{l_1}{N}\mathrm{S} + \frac{l_1}{N}\kappa\,\mathrm{V} \\ \omega & \sigma_2 & -B_4 \\ \tau & -B_3 & 0 \end{pmatrix} \quad (55)$$

$$Cy = \begin{pmatrix} \frac{l_1}{N}\mathrm{S} + \frac{l_1}{N}\kappa\,\mathrm{V} - \mathrm{B}_2 & \frac{l_1}{N}\mathrm{S} + \frac{l_1}{N}\kappa\,\mathrm{V} & \frac{l_1}{N}\mathrm{S} + \frac{l_1}{N}\kappa\,\mathrm{V} \\ \omega & \sigma_2 & -B_4 \\ \tau & -B_3 & 0 \end{pmatrix} \begin{pmatrix} E \\ Q \\ I \end{pmatrix} \quad (56)$$

$$Cy = \begin{bmatrix} \frac{l_1}{N}(\mathrm{E}+\mathrm{I}+\mathrm{Q})\mathrm{S} + \frac{l_1}{N}\kappa(\mathrm{E}+\mathrm{I}+\mathrm{Q})\mathrm{V} - \mathrm{B}_2 E \\ \omega E + \sigma_2 Q - B_4 I \\ \tau E - B_3 Q \end{bmatrix} \quad (57)$$

$$\hat{G}(x,y)=\begin{pmatrix}\frac{l_1}{N}(\mathrm{E+I+Q})\mathrm{S}+\frac{l_1}{N}\kappa(\mathrm{E+I+Q})\mathrm{V}-\mathrm{B}_2E\\ \omega E+\sigma_2 Q-B_4 I\\ \tau E-B_3 Q\end{pmatrix}-\begin{pmatrix}\frac{l_1}{N}(\mathrm{E+I+Q})\mathrm{S}+\frac{l_1}{N}\kappa(\mathrm{E+I+Q})\mathrm{V}-\mathrm{B}_2E\\ \omega E+\sigma_2 Q-B_4 I\\ \tau E-B_3 Q\end{pmatrix} \tag{58}$$

$$\hat{G}(x,y)=\begin{pmatrix}\hat{G}_1(x,y)\\ \hat{G}_2(x,y)\\ \hat{G}_3(x,y)\end{pmatrix}=\begin{pmatrix}0\\0\\0\end{pmatrix} \tag{59}$$

Which implies that $\hat{G}(x,y)=0$ for all $(\mathrm{x},\mathrm{y})\in\Omega$. Therefore, the conditions (H1) and (H2) are satisfied. Thus, the global stability of the DFE is obtained. This completes the proof.

Hence, the disease free equilibrium point is globally asymptotically stable when $R_0 < 1$

2.8 The Endemic Equilibrium State

Let $X^1=(S,E,Q,I,R,V)=(S^1,E^1,Q^1,I^1,R^1,V^1)$ (60)

Suppose $I\neq 0$

Then,

$$\left.\begin{aligned}&\Lambda+\rho R-(\alpha+B_1)S=0\\ &\alpha S+\kappa\alpha V-B_2E=0\\ &\tau E-B_3Q=0\\ &\omega E+\sigma_2 Q-B_4 I=0\\ &\gamma I+\sigma_1 Q-B_5 R=0\\ &\upsilon S-(\kappa\alpha+\mu)V=0\end{aligned}\right\} \tag{61}$$

Becomes

$$\begin{pmatrix}S^{**}\\E^{**}\\Q^{**}\\I^{**}\\R^{**}\\V^{**}\end{pmatrix}=\begin{pmatrix}\frac{K_6B_2-K_1K_6(K_3+K_4)+K_1K_2K_7}{[B_2-K_1(K_3+K_4)]}\\ \frac{K_2}{[\mathrm{B}_2-K_1(K_3+K_4)]}\\ \frac{\tau K_2}{[\mathrm{B}_2B_3-B_3K_1(K_3+K_4)]}\\ \frac{K_2K_5}{[\mathrm{B}_2-K_1(K_3+K_4)]}\\ \frac{K_1K_2}{[\mathrm{B}_2-K_1(K_3+K_4)]}\\ \frac{K_8\mathrm{B}_2-K_1K_8(K_3+K_4)+K_1K_2K_9}{[\mathrm{B}_2-K_1(K_3+K_4)]}\end{pmatrix} \tag{62}$$

Where

$$K_1=\frac{\omega\gamma B_3+\tau\sigma_2\gamma-\sigma_1\tau B_4}{B_3B_4B_5}$$

$$K_2=\frac{\alpha\Lambda(\kappa\alpha+\mu)+\alpha\Lambda\kappa\upsilon}{(\alpha+B_1)(\kappa\alpha+\mu)},K_3=$$

$$:\frac{\alpha\rho}{(\alpha+B_1)},K_4=\frac{\alpha\rho\upsilon\kappa}{(\alpha+B_1)(\kappa\alpha+\mu)}$$

$$K_5=\left(\frac{\omega B_3+\sigma_2\tau}{B_3B_4}\right)$$

$$K_6=\frac{\Lambda}{(\alpha+B_1)},K_7=\frac{\rho}{(\alpha+B_1)}$$

$$K_8=\frac{\Lambda\upsilon}{(\alpha+B_1)(\kappa\alpha+\mu)},$$

$$K_9=\frac{\rho\upsilon}{(\alpha+B_1)(\kappa\alpha+\mu)}$$

respectively

Equation (62) is the Endemic Equilibrium Point (EEP).

Our total population using the endemic equilibrium points is given as;

2.9 Stability of the Endemic Equilibrium State

$\Re_0=R_0(0)=1.578177354>1$, then the system has an endemic infection because of the introduction of those with secondary infection. Here, we consider the case where $I\neq 0$. The Jacobian matrix of the system of equation (10) to (15) at Disease Endemic Equilibrium Point is evaluated. The stability will be determined based on the sign of the eigenvalues of the Jacobian matrix.

$$N^{**} = \frac{B_2(\mathrm{K}_6+\mathrm{K}_8) - \mathrm{K}_1(\mathrm{K}_3+\mathrm{K}_4)(\mathrm{K}_6+\mathrm{K}_8) + \mathrm{K}_1\mathrm{K}_2(\mathrm{K}_7+\mathrm{K}_9) + \mathrm{K}_2(1+\tau B_3+\mathrm{K}_5+\mathrm{K}_1)}{B_2 - \mathrm{K}_1(\mathrm{K}_3+\mathrm{K}_4)} \quad (63)$$

The equation for the endemic equilibrium with the force of infection α_0^{**} (infection force) is as follows:

$$\alpha_0^{**} = \frac{\varepsilon(1-\eta)(1-\xi)\left(\mathrm{K}_2+\tau\,\mathrm{K}_2\,B_3+\mathrm{K}_2\mathrm{K}_5\right)}{B_2(\mathrm{K}_6+\mathrm{K}_8) - \mathrm{K}_1(\mathrm{K}_3+\mathrm{K}_4)(\mathrm{K}_6+\mathrm{K}_8) + \mathrm{K}_1\mathrm{K}_2(\mathrm{K}_7+\mathrm{K}_9) + \mathrm{K}_2(1+\tau B_3+\mathrm{K}_5) + \mathrm{K}_1\mathrm{K}_5} \quad (64)$$

$$J = \begin{pmatrix} -\alpha - B_1 & 0 & 0 & 0 & \rho & 0 \\ \alpha & -B_2 & 0 & 0 & 0 & \kappa\alpha \\ 0 & \tau & -B_3 & 0 & 0 & 0 \\ 0 & \omega & \sigma_2 & -B_4 & 0 & 0 \\ 0 & 0 & \sigma_1 & \gamma & -B_5 & 0 \\ \upsilon & 0 & 0 & 0 & 0 & -\kappa\alpha - \mu \end{pmatrix} \quad (65)$$

Reducing equation (65) to upper triangular matrix gives equation whose characteristics equation is;

$$\left|J(\mathrm{X}^1) - \lambda \mathrm{I}\right| = 0 \quad (66)$$

$$J = \begin{pmatrix} -\alpha_0^{**} - B_1 - \lambda & 0 & 0 & 0 & \rho & 0 \\ 0 & -B_2 - \lambda & 0 & 0 & 0 & \kappa\alpha_0^{**} \\ 0 & 0 & -B_3 - \lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & -B_4 - \lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & -B_5 - \lambda & 0 \\ 0 & 0 & 0 & 0 & 0 & -\kappa\alpha_0^{**} - \mu - \lambda \end{pmatrix} = 0 \quad (67)$$

The determinant gives;

$$\left(-\alpha_0^{**} - B_1 - \lambda\right)(-B_2 - \lambda)(-B_3 - \lambda)(-B_4 - \lambda)(-B_5 - \lambda)(-\kappa\alpha_0^{**} - \mu - \lambda) = 0 \quad (68)$$

Equation (68) implies;

$$-\alpha_0^{**} - B_1 - \lambda_1 = 0 \quad \text{or} \quad -B_2 - \lambda_2 = 0 \quad \text{or} \quad -B_3 - \lambda_3 = 0 \quad \text{or} \quad -B_4 - \lambda_4 = 0 \quad (69)$$

$$-B_5 - \lambda_5 = 0 \text{ or } -\kappa\alpha_0^{**} - \mu - \lambda_6 = 0$$

Therefore

$$\lambda_1 = -(\alpha_0^{**} + B_1) \text{ or } \lambda_2 = -B_2 \text{ or } \lambda_3 = -B_3 \text{ or } \lambda_4 = -B_4 \text{ or } \lambda_5 = -B_5 \text{ or } \lambda_6 = -(\kappa\alpha_0^{**} + \mu) \quad (70)$$

From equation

$$\lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_5, \lambda_6 < 0 \quad (71)$$

Hence, the disease endemic equilibrium point is asymptotically stable. This means that the disease is prevalent.

2.10 Covid-19 Vaccine Effectiveness Analysis: Herd Immunity Ratio

For the disease to be prevented, this is the minimum percentage of the population that must be vaccinated [12]. provides an equation for the Herd Immunity Threshold indicated by H_1.

$$H_1 = 1 - \frac{1}{\Re_0} \quad (72)$$

$$H_1 = 1 - \frac{B_2B_3B_4}{l_1(B_3B_4 + \omega B_3 + \tau\sigma_2 + B_4)} \quad (73)$$

3. Results

The coefficient estimates of model variables and parameters used to conduct the sensitivity analysis and generate the graph display of sensitive constraints against R_0 are provided in Table 3 and 3 respectively.

3.1 Detailed explanation of all of the parameters and their current values

Table 3. Description of Variables with their Values.

Variables	Description	Values	Source
S(0)	Susceptible class	199,950,894	A9
E(0)	Exposed class	3,550,457	A7
Q(0)	Quarantined class	3,392,457	A5
I(0)	Infected class	212,127	A3
R(0)	Recovered class	205,491	A4
V(0)	Vaccinated class	5,776,679	A8
N(0)	Total Human Population	213,089,105	A1

Table 4. Description of Parameters with their Value.

Parameters	Description	Values	Source
Λ	Recruitment rate into the susceptible class	0.036855	A2
μ	Per capita natural death rate	0.011382	A10
δ	Death rate due to infection	0.013888	A6
γ	Recovery rate from infection	0.96417	A11
υ	Vaccination rate	0.0456	A15
ρ	Rate of loss of immunity after treatment as time passes by	0.00103	A16
ω	Progression rate from exposed to infected class	0.06002	A14
τ	Rate at which exposed individuals are taken into quarantine/isolation	0.9554	A13
κ	Vaccination ineffectiveness (inefficacy)	0.087	A12
η	Rate at which people maintain social distancing	0.2	Assumed
ε	Contact rate	1.2	Assumed
ξ	Rate at which people make proper use of face masks and hand sanitizers	0.2	Assumed
σ_1	Progression rate to the recovered class after incubation period	0.937	A18
σ_2	Progression rate from quarantine to the infected class	0.0628	A17

3.2 Sensitivity Analysis

Sensitivity analysis is the study of how the uncertainty in the output of a model can be apportioned to different sources of uncertainty in the model input [12]. The sensitivity analysis in this study follows the procedure outlined in [13]. The normalized forward sensitivity indices with respect to a parameter value Q is defined as

$$\alpha_Q^{R_0} = \frac{\partial R_0}{\partial Q} \times \frac{Q}{R_0} \tag{74}$$

Where

$$Q = \{\varepsilon, \upsilon, \gamma, \eta, \xi\} \tag{75}$$

Calculating the sensitivity index requires the use of the Maple 16 software as well as the variables found in Table 5.

The results presented in Table 5 demonstrate that the parameters can have either a positive or negative impact on R_0. R_0 will increase when the parameters are positive, but it will decrease when the parameters are negative. The sensitivity index is highest for the contact rate, followed by the other parameters in descending order.

3.3 Estimation of the Basic Reproductive Ratio R_0 of COVID-19 Transmission without Vaccination

From the model equations, we had the basic reproductive ratio of COVID-19 transmission without vaccination as

$$\Re_0 = R_0(0) = l_1\left[\frac{B_3B_4 + \omega B_3 + \tau\sigma_2 + B_4}{B_2B_3B_4}\right] \tag{76}$$

Putting the value of the parameters in Table 3.2 into equation (76) we have;

$$\Re_0 = R_0(0) = 1.578177354 > 1 \tag{77}$$

Since $R_0 > 1$, the prevalence of Corona Virus is considered an epidemic.

Table 5. Parameter sensitivity analysis.

Parameters	Sensitivity index
ε	1.0000000
η	-0.8002527
υ	-0.2500000
γ	-0.974460
ξ	-0.2500000

3.4 Estimation of the Basic Reproductive Ratio R_0 of COVID-19 Transmission with Vaccination

From the model equations, we had the basic reproductive ratio of COVID-19 transmission with vaccination as

$$R_0(\upsilon) = l_1(\mu + \upsilon\kappa)\left[\frac{B_3B_4 + \omega B_2B_3 + \tau\sigma_2B_2 + B_4}{B_1B_2B_3B_4}\right] \quad (78)$$

Putting the value of the parameters in Table 3.2 into equation (78) we have;

$$R_0(\upsilon) = 0.42568 < 1 \quad (79)$$

Since the $R_0(\upsilon) < 1$, it implies that with the proper use of vaccine, the virus can die out naturally if given a clean health bill.

3.5 The Herd Immunity Threshold (H1) Estimation

According to the herd immunity hypothesis, infectious diseases that are managed to pass from one individual to another are more likely to have their chains of transmission broken when there are a lot of people in a community who are immune to the disease or have a reduced risk of contracting it. For the purpose of determining the Herd Immunity Threshold H1, this research makes use of the method described in [12].

$$H1 = 1 - \frac{1}{\Re_0}$$

Where $\Re_0$ is the Basic Reproduction Number in

$= 0.36638$

the absence of vaccination.

Therefore, at least 36.638% of the population is going to be vaccinated to control the epidemic.

3.7 Graphical Presentation of R_0 and Some Parameters of the Model

Some of the parameters that can significantly affect R_0 are shown graphically in Fig 2 through 5.

4. Discussions

In this paper, we analysed the sensitivity of the model and studied the existence and stability of both the disease-free and disease-endemic equilibria. Herd immunity was also considered as the sole method of vaccination in our analysis. We compared our stability with that of the existing works and discovered that the local and the global stability of both our work and that of the existing works were locally and globally asymptotically stable at Disease Free Equilibrium point (DFE). All efforts to compare our estimated held immunity threshold

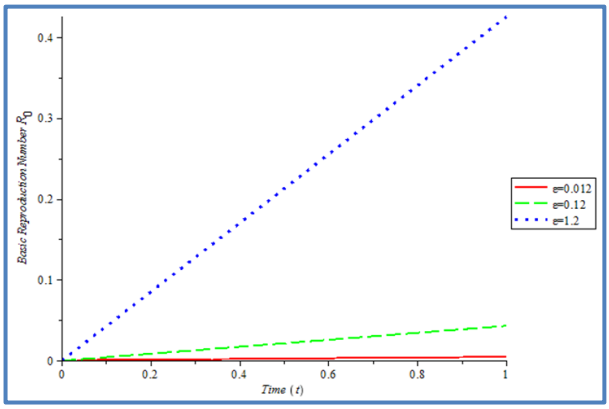

Fig. 2 The Effect of Contact Rates on R_0.

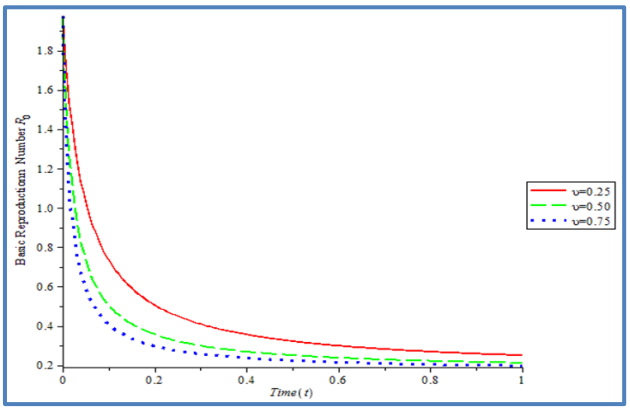

Fig. 3 The Effect of Vaccination Rates on R_0.

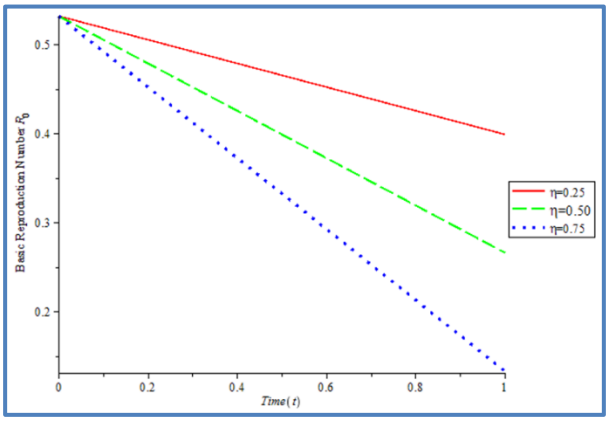

Fig. 4 The Effect of Social Distancing on R_0.

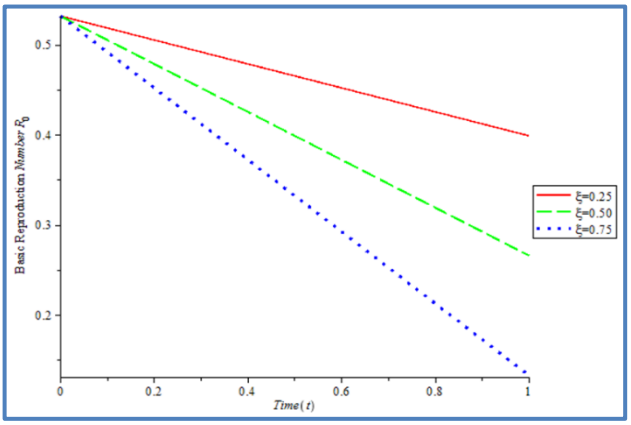

Fig. 5 The Effect of Proper Use of Face Mask on R_0.

Data in Table 4 allowed us to determine that the basic reproductive number for COVID-19 transmitting without vaccination is R_0 = 1.578177354>1. This suggests an outbreak. This suggestion is in agreement with the work of Pakwan et al. (2021) whose R_0 =1.40995>1 and other literature are considered in this work. COVID-19 transmission with vaccination has a basic reproductive number of R_0 =0.42568. The introduction of vaccination into the model has resulted in a drop in the value of R_0. As a result, increased vaccination will help to prevent the spread of coronavirus.

That is to say, if stakeholders in the country take adequate measures to prevent the disease but if vaccination programs are bolstered generally, the disease will be eradicated for good.

In order to prevent the spread of disease, it is necessary for at least 36.638% of the population to be vaccinated, as determined by the Herd Immunity Threshold that was calculated in this research.

People who have not received vaccinations have a significantly higher risk of contracting diseases from both other people and, more dangerously, from surfaces they come into contact with. If a sufficient number of people are vaccinated through mass vaccination, the disease will be eliminated if it reaches and then transcends the Herd Immunity Threshold level. As a result, 36.638% of the population will have to be vaccinated in order to successfully eradicate the pathogen from the population. If the vaccine used is insufficiently effective or the required coverage cannot be reached, the programme may not be able to exceed the herd immunity threshold; it can, however, disturb the balance of the infection without eliminating it. This change occurs simply because there are now fewer susceptible individuals in the population who can be infected. On the other hand, if the vaccination exercise causes the proportion of immune persons in a population to exceed the Herd Immunity Threshold for a significant length of time, transmission of the COVID-19 disease in that population will gradually come to a halt.

Also, from our simulations, it was found that when the numbers of vaccinated humans are increased, the number of humans that will have attained a level of immunity also increase. If vaccination is done properly, then we are sure to have a lot of COVID-19 immune persons in our system, thereby decreasing the spread of Corona Virus amongst humans.

As shown in Fig. 2, the Basic Reproduction Number R_0 rises as the rate of contact increases over time. This means that those who are susceptible should stay away from infected people to prevent the virus from spreading.

As shown in Fig. 3, as the vaccination rate rises, the Basic Reproduction Number R_0 falls. In other words, if enough people get the vaccinated, the disease could be contained.

As can be seen in Fig. 4, social distance has a negative impact on the R_0. R_0 decreases as the speed of social distancing increased. This means that susceptible people who abstain from social gatherings have a lower risk of contracting the virus; so, we should practice good social distancing to limit the spread of the disease.

Proper use of face mask has a noticeable impact on the basic reproduction number R_0, as shown in Fig. 5. R_0 decreases as more people start using face masks correctly. This means that those who are susceptible but who keep using a face mask while around infected people have a better chance of avoiding infection; consequently, we need to keep using face masks correctly to prevent the disease from spreading further.

5. Conclusion

In this study, we analysed the Local and Global stabilities of the DFE and calculated the DFE and EE in terms of the infectious force. Since the DFE is consistent everywhere, this implies that the Corona Virus can be contained when R_0 is less than 1. Based on the sensitivity analysis results, it is clear that the contact rate R_0 is the most important factor in raising the R_0, while the vaccination rate v is the most important factor in lowering the R_0. The data visualization shows that eradicating the Corona Virus requires not only a higher vaccination rate, but also a higher recovery rate. Additionally, as shown in Figure 1, the basic reproduction number increases as the amount of contact with infected patients of the Corona Virus grow. Therefore, to lessen the spread of epidemics, infected people should be kept apart from healthy ones. It has also been suggested that the government should invest more in the Corona virus vaccines as well as the distribution of face masks and hand sanitizers to help slow the spread of the disease.

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Orcid-ID

Chembe JAPHETH https://orcid.org/0000-0002-0897-5860
Somma Abu SAMUEL https://orcid.org/0000-0002-8354-2010

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