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Mathematical modelling and vaccination acceptability analysis of COVID-19 in Nigeria

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Abstract: Some The novel coronavirus 2019 known as (COVID-19) pandemic caused by SARS-CoV-2 occurred in Wuhan town of China in 2019. The virus has rapidly spread all over the world and has continued to affect the public well-being. This paper focuses on a mathematical model with vaccination acceptability of COVID-19 with which to examine to what extent the vaccine would be accepted in Nigeria. Specifically, the paper introduces a compartmental model to measure the potential impact of the COVID-19 vaccine. The vaccination acceptability model results show that up to 80% of the Nigerian populace accepted the vaccination campaign, despite the gabs on the COVID-19 vaccine by some health workers and the communities in Nigeria. It also shows that 90% vaccinated susceptible plus 50% effectiveness of face-mask use has brought about a decrease of the pandemic while mortality rate has decreased drastically which shows that the vaccine is effective. The result also reveals that the recovered individuals from COVID-19 have increased in alignment and, the vaccine has a significant impact on the populace. Finally, possible extensions of the model as well as open challenges associated with the formulation and analysis of COVID-19 dynamics will be addressed.

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1 Introduction

The novel coronavirus 2019 (COVID-19) pandemic caused by SARS-CoV-2 occurred in Wuhan town of China in 2019. The virus has rapidly spread over the world, including Nigeria and, has continued to impact negatively on public health. The symptomatology of the patients with symptoms such as fever, malaria, dry cough, and dyspnea are often diagnosed as viral pneumonia [7, 8, 9, 27]. The pandemic started as an outbreak of pneumonia as an unknown cause. It rapidly became a devastating pandemic, spreading to every country and affecting public health and causing socio-economic difficulties globally [2]. According to the weekly epidemiological update on COVID-19, the number of death cases have decreased in June 2021 with 2.5 million

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weekly new cases and 64000 deaths, 6% and 12% decrease respectively when compared with the previous cases. While the cases reported globally now exceeded 177 million, the lowest weekly incidence was in February 2021. Globally, the mortality rate remains high with more than 9000 deaths on a daily basis over the past weeks. However, the number of deaths reported had decreased in all regions except for the Eastern Mediterranean and the African regions. Also, there was a special focus update provided on SARS-CoV-2 Variants of Interest (VOIs) and Variants of Concern (VOCs) Alpha (B.1.1.7), Beta (B.1.351), Gamma (P.1), and Delta (B.1.617.2). It also included an update on emerging evidence surrounding the phenotypic features of VOCs (transmissibility, infection severity, risk of re-infection and impacts on diagnostics and vaccine performance) as well as updates on the environmental spreading of VOCs. The report included a summary of a Global Consultation on SARS-CoV-2 Variants of concern and their impact on public health interventions [23].
Similarly, as at Sept 2021, 2,997,060 was sampled and tested, 377 cases and two deaths were recorded in Nigeria out of which 203,081 cases were confirmed, 191,609 of the infected were discharged and 2,666 deaths were recorded in 36 states and the Nigerian capital, Abuja. A multi-sectorial National Emergency Operations Centre (NEOC), initiated at Level two has continued to manage the national response events [16]. However, proof of human-to-human transmission developed powerfully after a visit by the World Health Organization (WHO) delegation to the town of Wuhan [24]. [3] and there was a mathematical model for the COVID-19 pandemic in Iran to simulate the progression of the pandemic with modified mathematical modelling. Result showed that the most active precautions are by paying maximal attention to hygiene, having a natural and healthy diet, an increase in mobility, exercise and social isolation.

In addition to the preventive measures is by staying at least one meter away from others, covering cough or sneeze with the elbow, frequent cleaning of hands, wearing a mask and avoiding poorly ventilated rooms. There and then, the WHO assessed the vaccines against COVID-19 and concluded that the vaccines met the necessary criteria for safety and efficacy. The following vaccine companies are AstraZeneca/Oxford vaccine, Johnson and Johnson, Moderna, Pfizer/BioNTech, Sinopharm, and Sinovac [25]. In addition, some national regulators have also assessed other COVID-19 vaccine products for use in their countries such as Russia and Iran. These conditions include hypertension, diabetes, asthma, pulmonary, liver and kidney disease as well as chronic infections that are stable and controlled. Also, taking painkillers such as paracetamol before receiving the COVID-19 vaccine to prevent side effects was not recommended because it is not known how pain killers may affect the workings of the vaccine. The more health workers allow the virus to spread, the more opportunity the virus has to change. In June 2021, the WHO's Strategic Advisory Group of Experts (SAGE) concluded that the Pfizer/BioNTech vaccine was suitable for people aged 12 years and above. Children aged between 12 and 15 who are at high risk may be offered this vaccine alongside other priority groups for vaccination [22, 23].
Vaccination is the process through which kill or weaken viruses in the body. The immune system recognizes vaccine agents as external and triggers an immune response through antibodies. As a result, if the same types of viruses get into the body again, they will be damaged much faster by the antibodies. Thus, an individual that is immunized is safe against the disease. If a large majority of people are vaccinated, it is much more difficult for an epidemic disease to occur [12]. According to [12,13], vaccination is applied only to healthy individuals and so only susceptible individuals get vaccinated. Vaccination is one of the greatest achievements of public health. For instance, vaccination has led to the complete eradication of small-pox worldwide, and near eradication of Poliomyelitis. The difference is that some classes of models assume that individuals enter the system at a point in their life when they either get vaccinated or miss vaccination and are made susceptible [12, 13].

According to [4], 98% are aware of what a vaccine is, 51.1% are willing to take COVID-19 vaccine, 30.5% are not willing to take it and 18.4% are uncertain. However, 52% of the respondents of different ideas rejected a compulsory vaccination of COVID-19 vaccine in Nigeria. [11] developed Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen to handle the virus. Their results supported the progenitor of SARS-CoV-2 being capable of efficient human to human transmission as a consequence of its adaptive evolutionary history in bats, which created a relatively generalist virus. [8. 9] developed a mathematical model for understanding the transmission dynamics and control of COVID-19 in Nigeria with control measures such as social distancing, community lockdown, quarantine of suspected cases, isolation of confirmed cases, and the use of face masks in public places. Similarly, [6] built a mathematical model for understanding the dynamics of the COVID-19 vaccine with a primer for analyzing and simulating. They illustrated how some basic non-pharmaceutical interventions against COVID-19 could be merged into the epidemic model. Moreso, [5] developed a Model with Transmission and Dynamics of COVID-19 Via Self-protection and Isolation as control measures. It is observed from their work that increasing the Self-protection coefficient and isolation rate on humans has a significant impact on the rate of spread of COVID-19 transmission. [10] Presented a mathematical model with an optimal control strategy of transmission of the COVID-19 pandemic virus. Their model measure was to reduce the spread of the virus, diagnosis, surveillance at airports and the quarantine of infected people. [18] Presented an analysis of a mathematical model for COVID-19 population dynamics in Lagos, Nigeria. It showed the effects of control measures, most specifically social distancing, use of face mask and case detection on the dynamics of COVID-19.

Furthermore, [9] developed a mathematical model for assessing the impact of a hypothetical imperfect COVID-19 vaccine on the control of COVID-19 in the United States. An analytical expression for the minimum percentage of unvaccinated susceptible individuals needed to be vaccinated to achieve vaccine-induced community group immunity is derived. Their results showed that 82% of the susceptible US population needed to be vaccinated in other to achieve the group immunity threshold. Also, the infection decreases to 72%, that is, if half of the US population regularly wears face masks in the public but decreases to 46% if everyone wears face masks. Moreover, [13, 17] developed a new mathematical assessment of the impact of non-pharmaceutical interventions on curtailing the COVID-19 in the US. From their results, the use of effective face-masks such as surgical masks, with estimated efficacy of 70% in public could lead to the elimination of the pandemic. Using face masks in public including the low efficacy cloth masks is very good in reducing community transmission.

[19] Used linear regression analyses to investigate the association between intention to be vaccinated or not in the UK. Their result showed that 64% of participants reported of being expected to be vaccinated against COVID-19 while 27% were uncertain and 9% were doubtful. [28] built a mathematical model to examine the combined effects of nanoparticles of Copper and Alumina in unsteady channel flow of water (river) based nanofluids was established.

This paper focuses on a mathematical model to measure the vaccination acceptability and the way forward at reducing the transmission dynamics of the COVID-19 pandemic among Nigerians. This study aims at extending the existing models [6, 8, 9, 17] by incorporating COVID-19 induced mortality rate from isolation/hospitalized, proportional rate of vaccinated individuals and effectiveness of using face masks. Therefore, the affirmation gabs above are to be addressed in this paper.

2. Method and materials

To formulate a COVID-19 pandemic model, it should be noted that infection happens when a susceptible individual has contact with an infectious individual. Therefore, according to [15] the number of vaccinated individuals with the first dose as at Sept, 2021 in 36 States with the Nigerian capital, Abuja was 4,532,725 with the proportional rate of 4.1% while individuals vaccinated with the first and second dose fully was 1,796,255.

The model vaccination and transmission dynamics of COVID-19 in a community with the flow diagram is given;

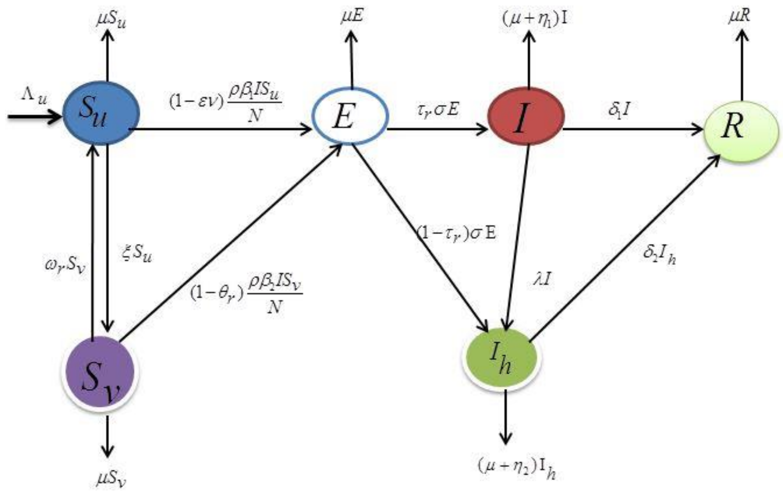


Figure 1: showing the diagram for the transmission dynamics of Covid-19 pandemic

Table 1: Description of variables and parameters of the COVID-19 model (1)

Variables and Parameters	Description
$S_u(t)$	Unvaccinated susceptible individuals at a given time (t)
$S_v(t)$	Vaccinated susceptible individuals at a given time (t)
$E(t)$	exposed individuals at a given time (t)
$I(t)$	Infectious individuals at a time (t)
$I_h(t)$	Isolation/hospitalization individuals at a given time (t)
$R(t)$	Recovered individuals at a given time (t)
β_1	Effective contact rate (a measure of social distancing)
β_2	Contact rate at which isolation/hospitalization individuals transmit covid-19 to susceptible class
ε	Is the proportion of individuals who wear the mask in public
η_1	Covid-19 induced mortality rate for infectious individuals
η_2	Covid-19 induced mortality rate from isolation/hospitalization
θ_r	Is the proportion rate of vaccinated susceptible individuals
Λ_u	Recruitment rate (immigration/birth)
ω_r	Is the rate of loss of vaccine-induced immunity

ν	Is the effectiveness of face masks to prevent the acquisition of infection by susceptible individuals
ξ	Accepted and vaccinated individual rates
τ_r	The rate at which new infectious progressed from the exposed individuals move to the infectious class
ρ	Is a terrorist transmission probability per contact
σ	Is the rate of progression from the exposed class to the infectious class ($1/\sigma$ is the incubation period)
μ	Is the natural death rate of all individuals in the class
$(1-\tau_r)$	Fraction of exposed individuals who show clinical symptoms at the end of the incubation period
δ_1	The recovery rate from individuals in the infectious class
δ_2	The recovery rate from isolation/hospitalization individuals to $R(\mathrm{t})$
λ	Is the isolation/hospitalization rate for infectious individuals
$(1-\theta_r)$	Is the fraction of vaccine efficiency

2.1. Description of the model

The total population $N(\mathrm{t})$ is divided into six classes. The six classes are **unvaccinated susceptible individuals** $S_u(\mathrm{t})$: These are at risk of contact with the COVID-19 infectious through interaction. It is assumed that unvaccinated susceptible individuals are recruited by increasing the population with Λ (birth and immigration) while ω_r increase the population at the rate of loss of vaccine-induced immunity from $S_v(\mathrm{t})$ to $S_u(\mathrm{t})$ and decrease the population by $\frac{(1-\varepsilon\nu)\rho\beta_1 IS_u}{N}$ (proportion of individuals who wear the mask in public together with the effectiveness of face masks, with Covid-19 transmission probability per contact and effective contact rate (a measure of social-distancing) from unvaccinated susceptible individuals with Covid-19 infectious interaction), then decreased by $\mu+\delta$ (natural death rate of unvaccinated susceptible individuals, with the vaccination individuals rate).

$$\frac{dS_u}{dt} = \Lambda_u + \omega_r S_v - \left(\frac{(1-\varepsilon\nu)\rho\beta_1 IS_u}{N}\right) - (\mu+\xi)\mathrm{S}_u \tag{2.1}$$

The Vaccinated susceptible individuals $\mathrm{S}_v(\mathrm{t})$: This class of susceptible reduces the rate of infection compared to the infection of unvaccinated susceptible individuals. It is also assumed that vaccine-induced immunity may not last a lifetime. This group is increasing by ξ (the vaccination individuals rate) and decreasing by $\frac{(1-\theta_r)\rho\beta_2 IS_v}{N}$ (proportion or fraction of vaccine efficiency, with COVID-19 transmission probability per contact and contact rate at which isolation/hospitalization individuals transmit COVID-19 to susceptible class) also, the population decreasing by $\mu+\omega_r$ (natural death rate with the rate of loss of vaccine-induced immunity).

$$\frac{dS_v}{dt} = \xi S_u - \frac{(1-\theta_r)\rho\beta_2 IS_v}{N} - (\mu+\omega_r)\mathrm{S}_v \tag{2.2}$$

The exposed individuals $\mathrm{E(t)}$: Is representing the individuals who are vulnerable to contracting the covid-19 disease makes a potentially disease-transmitting contact, that individuals become exposed. This class of Covid-19 infectious is increasing by $\frac{(1-\theta_r)\rho\beta_2 IS_v}{N}$ (proportion or fraction of vaccine efficiency, with COVID-19 transmission probability per contact and contact rate at which infectious individuals transmit covid-19 to susceptible individuals), decreasing by $\frac{(1-\varepsilon\nu)\rho\beta_1 IS_u}{N}$ (proportion of individuals who wear the mask in public together with the effectiveness of face masks, with covid-19 transmission probability per contact and effective contact rate (a measure of social-distancing) from unvaccinated susceptible individuals with covid-19 infectious interaction) and decreasing with $\mu+\sigma$ (natural death with the rate of progression from the exposed class to the infectious class ($1/\sigma$ is the incubation period).

$$\frac{dE}{dt} = \frac{(1-\varepsilon\nu)\rho\beta_1 IS_u}{N} + \frac{(1-\theta_r)\rho\beta_2 IS_v}{N} - (\mu+\sigma)\mathrm{E} \tag{2.3}$$

The infected individuals $\mathrm{I(t)}$: Is representing the number of individuals who have developed the symptom of the COVID-19. These individuals are increasing in population by $\tau_r\sigma$ (the rate at which new infection progressed from the exposed individuals move to the infectious class with the rate of exposed class), and decreasing by $\mu+\eta_1+\delta_1+\lambda$ (natural death, covid-19 induced mortality rate for infectious individuals and isolation/hospitalization rate for infectious individuals).

$$\frac{dI}{dt} = \tau_r\sigma E - (\mu+\eta_1+\delta_1+\lambda)I \tag{2.4}$$

The isolation/hospitalization of individuals $\mathrm{I}_h\mathrm{(t)}$ **:** Is signifying the number of suspected individuals in a self-isolation/hospitalization. This class of individual can be increasing by $(1-\tau_r)\sigma$ (Fraction of exposed individuals who show clinical symptoms at the end of the incubation period with the rate of progression from the exposed class to the infectious class), λ (is the isolation/hospitalization rate for infectious individuals) and decreasing by $\mu+\eta_2+\delta_2$ (natural death rate, covid-19 induced mortality rate from isolation/hospitalization recovery rate from isolation/hospitalization individuals to $R\mathrm{(t)}$).

$$\frac{dI_h}{dt} = (1-\tau_r)\sigma E + \lambda I + (\mu+\eta_2+\delta_2)I_h \tag{2.5}$$

The recovered individuals $\mathrm{R(t)}$: Is representing the number of recovered individuals. This class of individuals are increasing by $\delta_1+\delta_2$ (the recovery rate from individuals in the infectious class and recovery rate from isolation/hospitalization individuals to $R\mathrm{(t)}$) and decreasing by μ (natural death rate).

$$\frac{dR}{dt} = \delta_1 I + \delta_2 \mathrm{I}_h - \mu R \tag{2.6}$$

The total population in this paperwork is given by;

$$\frac{dN}{dt} = S_u(\mathrm{t}) + S_v(\mathrm{t}) + E(\mathrm{t}) + I(\mathrm{t}) + I_h(\mathrm{t}) + \mathrm{R(t)} \tag{2.7}$$

The equations corresponding to the model vaccination acceptability are given by non-linear differential equations;

$$\left.\begin{aligned}
\frac{dS_u}{dt} &= \Lambda_u + \omega_r S_v - \left(\frac{(1-\varepsilon\nu)\rho\beta_1 I S_u}{N}\right) - (\mu+\xi)\mathrm{S}_u \\
\frac{dS_v}{dt} &= \xi S_u - \frac{(1-\theta_r)\rho\beta_2 I S_v}{N} - (\mu+\omega_r)\mathrm{S}_v \\
\frac{dE}{dt} &= \frac{(1-\varepsilon\nu)\rho\beta_1 I S_u}{N} + \frac{(1-\theta_r)\rho\beta_2 I S_v}{N} - (\mu+\sigma)\mathrm{E} \\
\frac{dI}{dt} &= \tau_r \sigma E - (\mu+\eta_1+\delta_1+\lambda) I \\
\frac{dI_h}{dt} &= (1-\tau_r)\sigma E + \lambda I + (\mu+\eta_2+\delta_2) I_h \\
\frac{dR}{dt} &= \delta_1 I + \delta_2 \mathrm{I}_h - \mu R \\
\frac{dN}{dt} &= S_u(\mathrm{t}) + S_v(\mathrm{t}) + E(\mathrm{t}) + I(\mathrm{t}) + I_h(\mathrm{t}) + \mathrm{R(t)}
\end{aligned}\right\} \tag{2.8}$$

with the initial condition;

$$S_u(0) = \mathrm{S}_{u(0)} \geq 0, \mathrm{S}_v(0) = \mathrm{S}_{v(0)} \geq 0, \mathrm{E}(0) = \mathrm{E}_0 \geq 0, \mathrm{I}(0) = I_0 \geq 0, \mathrm{I}_h(0) = I_{h(0)} \geq 0, R(0) = \mathrm{R}_0 \geq 0.$$

2.2. Assumptions of the model: In this paper, the vaccine does not guarantee complete protection from a COVID-19 infection, some of the vaccinated individuals can become infected. Also, it assumed that the potential COVID-19 vaccine is imperfect, infection of vaccinated susceptible individuals can occur, but at a reduced rate, compared to the infection of unvaccinated susceptible individuals in a population. It is also assumed that vaccine-induced immunity may not last a lifetime. Similarly, β_2 represent the rate at which isolation/hospitalized individuals transmit COVID-19 to susceptible individuals, ξ is the vaccination rate, $0 < \varepsilon\nu \leq 1$ is the vaccine efficacy to protect against development infection in vaccinated susceptible individuals, and ω_r is the rate of loss of vaccine-induced immunity. It is also assumed that vaccine-induced safety can decrease at a constant rate since it may not last for a lifetime. Finally, the natural death rate μ is for all humans and $1/\sigma$ is the incubation period for the rate of progression from the exposed class to the infectious class.

2.3. Model Analysis

2.3.1. Properties of the Model

The basic properties of the SEIR model are feasible solution or sometimes called invariant region and positivity of the solution. The feasible solution of the model equations shows the region in which the solution of the equations are biologically expressive and the positivity of the solutions tells the non-negative of the solutions. The feasible solution set which is invariant region is obtained by;

$\Omega = \left\{ (\mathrm{S}_u, \mathrm{S}_v, \mathrm{E}, \mathrm{I}, \mathrm{I}_h, \mathrm{R}) \in \Re_+^6 \mid \mathrm{N(t)} = \mathrm{S}_u(\mathrm{t}) + \mathrm{S}_v(\mathrm{t}) + \mathrm{E(t)} + I(\mathrm{t}) + I_h(\mathrm{t}) + \mathrm{R(t)} \right\}$, which is the feasible solution set for the model system (2.8) and all the solution set is bounded in Ω .

Where;

$N(\mathrm{t})$ is the initial time of the total population. The linear asymptotic stability of the DFE can be resolve using the next generation method [21]. To apply this method, it is convenient to consider the collecting $(\mathrm{E(t)}, \mathrm{I(t)}, \mathrm{I}_h(\mathrm{t}))$ of the infected classes of the system (8). The method involves calculating two matrices, the non-negative matrix (F) of new infection that is the force of infection near the DFE, and matrix (V) infected class associated with the model system (2.8). Using the collation $(\mathrm{E(t)}, \mathrm{I(t)}, \mathrm{I}_h(\mathrm{t}))$ it can be deduced that ($N(\mathrm{t}) = \mathrm{S}_u(\mathrm{t}) + S_v(\mathrm{t}) + E(\mathrm{t}) + I(\mathrm{t}) + I_h(\mathrm{t}) + R(\mathrm{t})$).

2.3.2. Stability of Disea1.se-Free Equilibrium (DFE)

The vaccination model system (2.8) has a unique disease-free equilibrium. In a situation, where there is no COVID-19 pandemic the points are at steady-state solutions, means $E_{0v} = 0$.

The COVIV-19 is occurred and obtained by taking the right side of the system (2.8) to zero using Maple16 software to solved the equations and obtained;

$$E_{0v}(\mathrm{S}_u, \mathrm{S}_v, \mathrm{E}, \mathrm{I}, \mathrm{I}_h, \mathrm{R}) = \left(\frac{\Lambda_u(\mu + \omega_r)}{\mu(\mu + \omega_r + \xi)}, \frac{\Lambda_u \xi}{\mu(\mu + \omega_r + \xi)}, 0, 0, 0, 0 \right) \tag{2.9}$$

Where;

$$\frac{S_v^*}{N^*} = \frac{\xi}{(\mu + \xi + \omega_r)} .$$

2.3.3. Calculation of Basic reproduction number (R_0)

The threshold quantity in studying disease is the time-varying effective reproduction number, denoted by $R_c(t)$. For the system (2.8), $R_c(t) = R_0 = \dfrac{S(t)}{N(t)}$. The number of disease increases when $R_c(t) > 1$ reaches a highest when $R_c(t) = 1$, and decays when $R_c(t) < 1$ [17].

Following the idea of [6] the result of the basic reproduction control number is generated by the next-generation matrix method. The basic control reproduction number of the system (2.8) is the average number of new potential cases of COVID-19 individuals coming into the infectious individual in a population, where a certain proportion is protected. Therefore, the control reproduction number becomes the basic reproduction number. [20] employed the next generation to solve the basic reproduction number. Therefore, the model equations can be rewritten by starting with newly COVID-19 individuals in the compartment.

The basic reproduction number R_0 , denoted by $\Gamma(\mathrm{FV}^{-1})$, where Γ is a spectral radius and at disease-free equilibrium gives;

$$F=\begin{bmatrix} 0 & (1-\varepsilon\nu)\rho\beta_1\left(\frac{S_u^*}{N^*}\right)+(1-\theta_r)\rho\beta_2\left(\frac{S_v^*}{N^*}\right) & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$ and

$$V=\begin{bmatrix} \mu+\sigma & 0 & 0 \\ -\tau_r\sigma & (\mu+\eta_1+\delta_1+\lambda) & 0 \\ -(1-\tau_r)\sigma & -\lambda & -(\mu+\eta_2+\delta_2) \end{bmatrix}$$

Thus;

$\Re_0=\Gamma(\mathrm{FV}^{-1})$ and the result is given as

$$\Re_0=\Re_c=\sigma\tau_r\left[\frac{(1-\varepsilon\nu)\rho\beta_1\left(\frac{S_u^*}{N^*}\right)+\rho\beta_2\left(\frac{S_v^*}{N^*}\right)(-1+\theta_r)}{(\mu+\sigma)(\mu+\eta_1+\delta_1+\lambda)}\right] \tag{2.10}$$

2.3.4. Local Stability Analysis of Disease-Free Equilibrium

The local stability is determined by the eigenvalues of the Jacobian calculated at that disease-free equilibrium and the vaccination model (2.8) has a unique disease-free equilibrium point. Using the basic reproduction number obtained from the system (2.8), the result of the local stability analysis of the equilibrium follows.

Theorem 1: The disease-free state, E_{0v}, is locally asymptotically stable if $\Re_0<1$ and unstable if $\Re_0>1$.

Proof: Let the Jacobian matrix of system (2.8) be evaluated at the disease-free equilibrium point E_{0v} and obtain;

$$\mathrm{J}(E_{0v})=\begin{bmatrix} -(\mu+\xi) & -\omega_r & 0 & (1-\varepsilon\nu)\rho\beta_1\left(\frac{S_u^*}{N^*}\right) & 0 & 0 \\ \xi & (\mu+\omega_r) & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\mu+\sigma) & 0 & 0 & 0 \\ 0 & 0 & 0 & (\mu+\eta_1+\delta_1+\lambda) & 0 & 0 \\ 0 & 0 & 0 & 0 & (\mu+\eta_2+\delta_2) & 0 \\ 0 & 0 & 0 & -\delta_1 & \delta_2 & -\mu \end{bmatrix}$$

The given values of the matrix $J(\mathrm{E}_{0v})$ are the roots of the characteristic equation and are given by;

$$\left(\lambda_1^2+(\omega_r+\xi)\lambda_1+\mu(\mu+\omega_r+\xi)\right)(\lambda_1+\sigma+\mu)(\mu+\eta_1+\delta_1+\lambda+\lambda_1)(\mu+\eta_2+\delta_2+\lambda_1)(\mu+\lambda_1)=0 \quad (2.11)$$

From (2.11) the expression can be rewriting as;

$$(\mu+\lambda_1)(\lambda_1+\sigma+\mu)(\mu+\eta_1+\delta_1+\lambda+\lambda_1)(\mu+\eta_2+\delta_2+\lambda_1)\left[\lambda_1^2+a\lambda_1+b\right]=0 \quad (2.12)$$

Thus;
The last expression resolved to quadratic equation as;

$$\left[\lambda_1^2+a\lambda_1+b\right]=0 \quad (2.13)$$

Therefore, the values for λ_1 in (2.12) give;

$(\mu+\lambda_1)=0 \Rightarrow \lambda_{11}=-\mu<0,$

$(\mu+\sigma+\lambda_1)=0 \Rightarrow \lambda_{12}=-\mu-\sigma<0,$

$(\mu+\eta_1+\delta_1+\lambda+\lambda_1)=0 \Rightarrow \lambda_{13}=-\mu-\eta_1-\delta_1-\lambda<0,$

$(\mu+\eta_2+\delta_2+\lambda_1)=0 \Rightarrow \lambda_{14}=-\mu-\eta_2-\delta_2.$

This result shows that the disease-free equilibrium of the COVID-19 pandemic is locally asymptotically stable iff $\Re_c<1$ or otherwise unstable if $\Re_c>1$. Going by Routh-Hurwitz criteria using the idea of [14], the criteria was employed on (2.13) and it has strictly negative real root iff $a>0, b>0$. The Ruth-Hurwitz criterion stated that all root of determinants polynomial must have negative real parts iff $a_1>0, a_2>0, a_3>0, a_4>0, a_5>0, a_1a_2a_3>a_3^2+a_1^2a_4$ and $(a_1a_4-a_5)(a_1a_2a_3-a_3^2+a_1^2a_4)>a_5(a_1a_2-a_3)^2+a_1a_5^2$ for $\Re_0>1$, which E_e^* is locally asymptotically stable if satisfied the above assertion and endemic equilibrium exists.

Where; $a=\omega_r+\xi$ and $b=\mu(\mu+\omega_r+\xi)$.

This result shows that COVID-19 can be eliminated if the initial size of the disease is in the basin of attraction of the disease-free equilibrium point. Separately, to ensure the pandemic threats reduce, it is essential to show that the disease-free equilibrium (DFE) is globally stable.

2.3.5. Globally Stability Analysis of DFE

Theorem 2: The COVID-19 pandemic at DFE of the vaccination model (2.8) is globally asymptotically stable in Ω if $\Re_c \le 1$.

Proof: The proof is based on using the Lyapunov function by considering the vaccination model (2.8) $\Re_c<1$. Using the idea of [6], the Lyapunov function needs to satisfy the vaccination model system of the infected class $E=I=0$ to be asymptotically stable.

Let $L=m_1E+m_2I$ (2.14)

The Lyapunov derivative to time is given by;

$$\frac{dL}{dt}=m_1\frac{dE}{dt}+m_2\frac{dI}{dt} \quad (2.15)$$

Substituting for m_1 and m_2 , then simplifying obtain;

$$\frac{dL}{dt}=\left[(k_1+k_2)-(\mu+\sigma)\mathrm{E}\right]+m_2\left[\tau_r\sigma\,\mathrm{E}-(\mu+\eta_1+\delta_1+\lambda)\,\mathrm{I}\right] \tag{2.16}$$

By rearranging (2.16) obtain;

$$\frac{dL}{dt}=m_1(\mathrm{k}_1+\mathrm{k}_2)-m_2(\mu+\eta_1+\delta_1+\lambda)\,\mathrm{I}-m_1(\mu+\sigma)\,\mathrm{E}+\mathrm{m}_2(\tau_r\sigma\,\mathrm{E}) \tag{2.17}$$

Taking $m_1=\left(\dfrac{\tau_r\sigma}{\mu+\sigma}\right)m_2$ and substitute the value of m_1 in (2.17) obtain;

$$\frac{dL}{dt}=\left[\left(\frac{\tau_r\sigma}{\mu+\sigma}(\mathrm{k}_1+\mathrm{k}_2)m_2\right)-\left(m_2(\mu+\eta_1+\delta_1+\lambda)\,\mathrm{I}\right)\right] \tag{2.18}$$

Taking $m_2=1$

Where; $\mathrm{k}_1=(1-\varepsilon\nu)\rho\beta_1\left(\dfrac{S_u^*}{N^*}\right)$ and $\mathrm{k}_2=(1-\theta_r)\rho\beta_2\left(\dfrac{S_v^*}{N^*}\right)$

$$\leq\left[\frac{\tau_r\sigma}{\mu+\sigma}\left((1-\varepsilon\nu)\rho\beta_1\left(\frac{S_u^*}{N^*}\right)+(1-\theta_r)\rho\beta_2\left(\frac{S_v^*}{N^*}\right)\right)-(\mu+\eta_1+\delta_1+\lambda)\right]I \tag{2.19}$$

Substituting $\Re_0$ in (2.19) and simplifying the expression further obtain;

$$\frac{dL}{dt}\leq\left[(\mu+\eta_1+\delta_1+\lambda)(\Re_0-1)\right]I \tag{2.20}$$

Hence, $\dfrac{dL}{dt}\leq 0$ iff $\Re_0\leq 1$ and $\dfrac{dL}{dt}=0$, iff $I(\mathrm{t})=0$.

Following the idea of [1] the result shows that $S_u(\mathrm{t}),\mathrm{S}_v(\mathrm{t}),\mathrm{E}(\mathrm{t}),\mathrm{I}(\mathrm{t}),\mathrm{I}_h(\mathrm{t}),\mathrm{R}(\mathrm{t})\to\mathrm{N}(0)$ as $t\to\infty$. Therefore, by Lasalle's invariance principle, the DFE point of vaccination model system (2.8) is globally asymptotically stable Ω whenever $\Re_0\leq 1$.

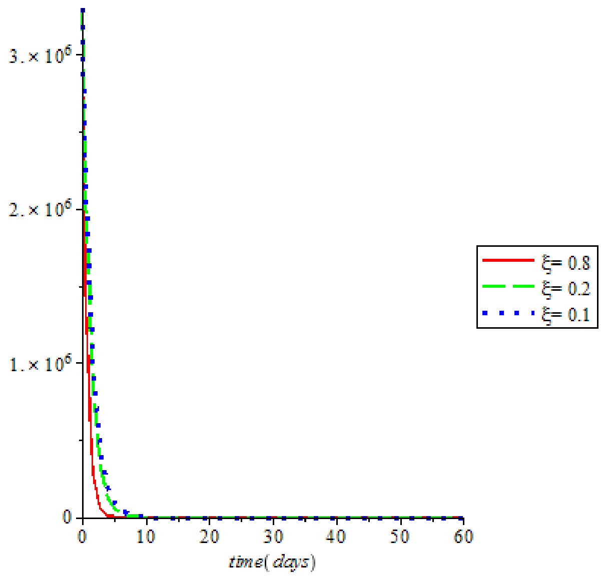
3. Numerical Simulation

In this sub-division, the results were acquired by numerically solving the non-linear differential equation system. Different simulations were carried out using various values of state variables and parameters in MAPLE16 software to present a numerical approach to the model of COVID-19 with vaccination acceptability among Nigerians.

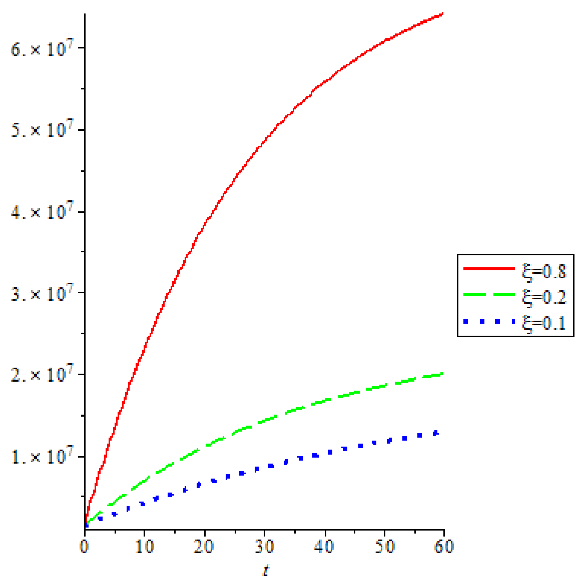
Table 2: Values and Source for Variables/Parameter of COVID-19 model (1)

Variables and Parameters	Values	Source

S_u(t)	2.9	[15]
S_v(t)	1.6	[15]
E(t)	2	[15]
I(t)	0.8	[15]
I_h(t)	1	[10]
R(t)	1.9	[15]
β_1	0.6597	[6]
β_2	0.3665	Assumed
ε	0.1704	[8]
η_1	0.01264	[16]
η_2	0.01264	[16]
θ_r	0.9	Varies
Λ_u	0.000301	[26]
ω_r	0.00011	[6]
ν	0.5	[6]
ξ	0.8	Varies
τ_r	0.35	[8]
ρ	0.5925	[22]
σ	0.25	[9]
μ	0.000301	[26]
δ_1	0.1428	[6]
δ_2	0.07143	[6]
λ	0.0514	[6]

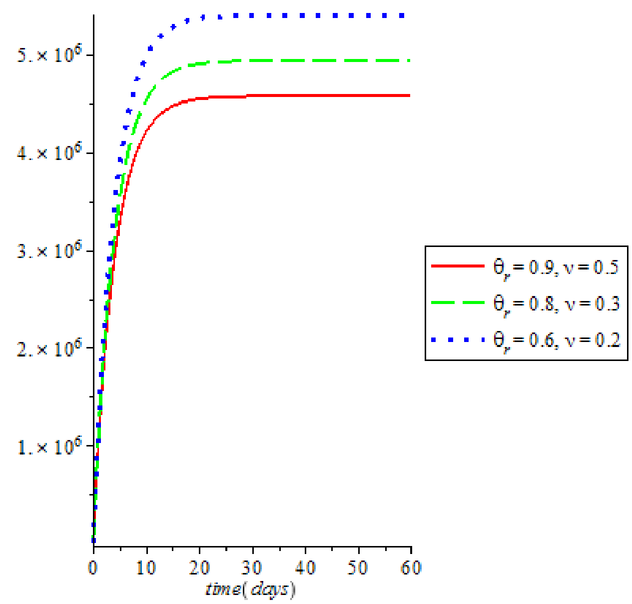


Graph of unvaccinated susceptible individuals against time

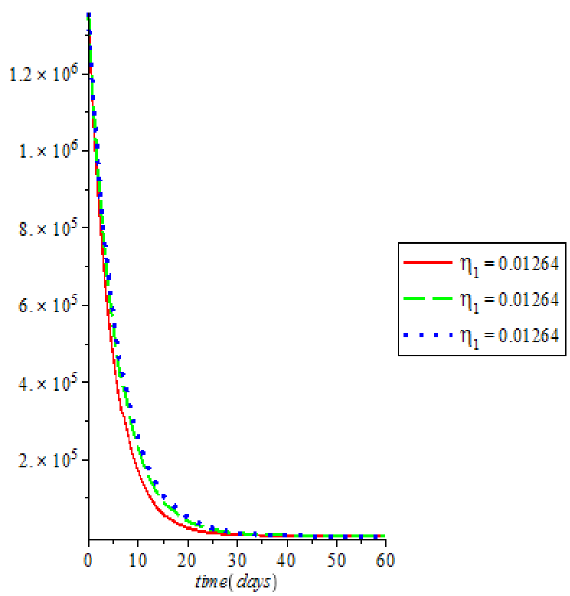


Graph of vaccinated susceptible individuals against time

Figure 2 and 3: Both show the graphs of unvaccinated susceptible and vaccinated susceptible individuals against time respectively.



Graph of exposed individuals against time



Graph of infectious individuals against time

Figure 4 and 5: Show the graphs of both the exposed and the infected individuals against time respectively.

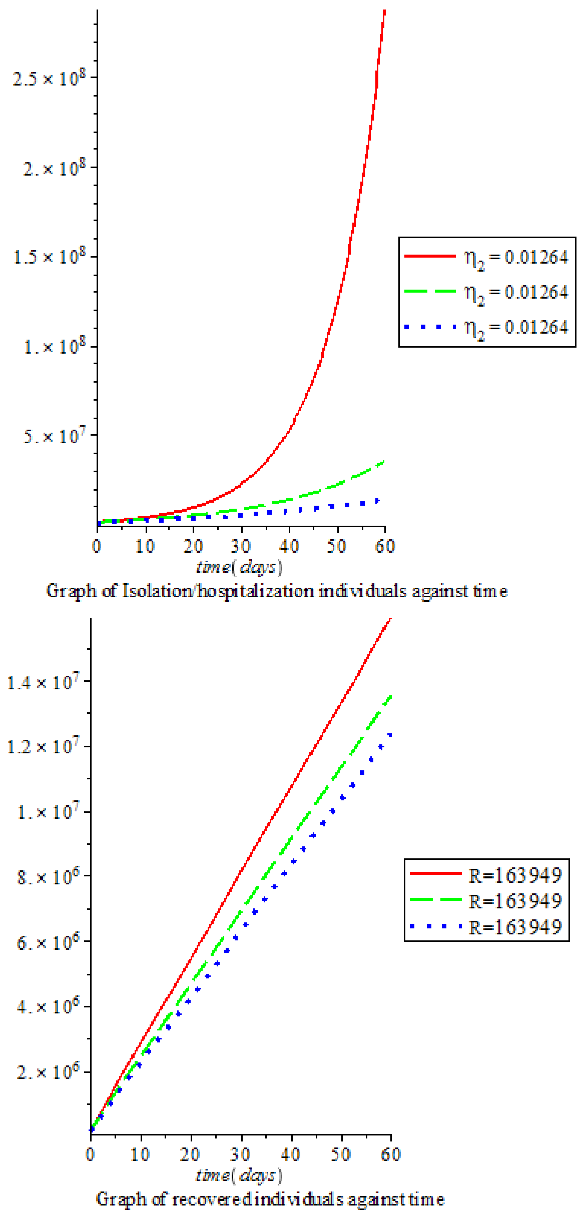


Figure 6 and 7: Show the graphs of both isolation/hospitalized and recovered individuals against time respectively.

4. Discussion of Result

The model vaccination was constructed to measure the vaccination acceptability of COVID-19 dynamics in Nigeria. The simulations result shows that since the vaccine is not completely protected, the COVID-19 protocol must be observed. This can be deduced from Fig. 1 where the unvaccinated susceptible individuals against time decrease the population to zero with the accepted and vaccinated individuals rate. ξ Also, from the graph of unvaccinated

Individuals in Fig. 2, the nationwide eradication of COVID-19 can be done if at least 85.4% of the Nigerian population is vaccinated. This can be achieved if health workers apply media campaign strategies for enlightenment. Similarly, Fig. 3 shows that up to 80% of the Nigerian populace accepted the vaccination campaign, despite the gabs on the COVID-19 vaccine by both some health workers and the community respectively in Nigeria.

Furthermore, the simulation results obtained depicted in Fig. 4 shows that the exposed individuals to COVID-19 increases at an initial time, but when the COVID-19 protocol strategies applied with vaccinated susceptible individuals together with the effectiveness of face-mask at rates θ_r, ν decreases the exposed individuals. From the graph of exposed individuals, 90% vaccinated susceptible and 50% effectiveness of face-mask use decreases the pandemic. Fig. 5 shows a graph of infected individuals against time with different rate of COVID-19 induced mortality η_1. The disease death mortality decreased drastically to zero which shows that the vaccine is effective and the community needs to accept it. Fig. 6 shows a graph of isolation/hospitalized individuals with different rate of disease-induced death mortality η_2. The scenario behaviour is similar to Fig. 5 where the disease death mortality decreased and approached zero with time. This shows that the vaccine has a significant impact on COVID-19. Fig. 7 shows a graph of recovered individuals from COVID-19 where the number of recovered patients increases in alignment with 191,609 [16]. This result shows that the vaccine has a significant impact on the populace.

5. Conclusion

A deterministic mathematical model with vaccine acceptability and transmission dynamics of COVID-19 in Nigeria was developed. The model was solved and analysed which was shown to be locally and globally asymptotically. This provides a necessary condition for the eradication of COVID-19 pandemic in Nigeria. The epidemic model with dynamics structure was designed to assess the potential impact of imperfect anti-COVID-19 vaccination acceptability in Nigeria. Simulations were carried out at various settings based on face-mask use and vaccination acceptability among the Nigerian community. Furthermore, the model was offered and appeared to be quite suitable for addressing COVID-19 vaccine in Nigeria. Acceptability of COVID-19 vaccine in Nigeria is based on the collaborative effort of the governments, health workers, policymakers, media sources and social media companies. In this study, the efficacy of current available COVID-19 vaccines reduced the rate of spreading the pandemic in a population. Finally, a plan to incorporate other issues would be addressed in future study.

6. Declaration of competing interest

The authors acknowledged no financial provision for this study and there is no conflict of interest.

Reference

[1] A. Bernoussi and K. Hattaf, Global Dynamics of an SIRSI Epidemic Model with Discrete Delay and General Incidence Rate, Journal of Applied Nonlinear Dynamics, 10(3) 2021, 547-562.

[2] H. Branswell and A. Joseph, WHO declares the coronavirus outbreak –a pandemic. Stat, 2020.

[3] Z. Cakir and H. B. Savaş, A mathematical modelling for the COVID-19 pandemic in Iran, Ortadoğu Tıp Dergisi, 12(2) 2020, 206-210.

[4] A.P. Chiedozie, O.J. Chukwuebuka, C.F. Chidimma, O.V. Onyinyechi, A.K. Chijioke, O.S. Chibuzor and U.B. Chioma, Willingness to Accept a Potential COVID-19 Vaccine in Nigeria, American Journal of Medical Sciences, 9(1) 2021, 1-5.

[5] D. Dejene, T. Worku and P.R. Koya, Modelling the Transmission and Dynamics of COVID-19 Using Self-protection and Isolation as Control Measures. Mathematical Modelling and Applications, 5(3) 2020, 191.
[6] A.B. Gumel, E.A. Iboi, C.N. Ngonghala, E.H. Elbasha, A primer on using mathematics to understand COVID-19 dynamics: Modeling, analysis and simulations. Infectious Disease Modelling, (6) 2021, 148-168.
[7] C. Huang, Y. Wang, X. Li, L. Ren, J. ZhaoY. Hu and B.Cao, Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China, The lancet, 395(10223) 2020, 497-506.
[8] E.A. Iboi, O.O. Sharomi, C.N. Ngonghala, A.B. Gumel, Mathematical Modeling and Analysis of COVID-19 pandemic in Nigeria, medRxiv, 2020.
[9] E.A. Iboi, C.N. Ngonghala, A.B. Gumel, Will an imperfect vaccine curtail the COVID-19 pandemic in the US?, Infectious Disease Modelling, (5) 2020, 510-524.
[10] A. Kouidere, B. Khajji, A. El-Bhih, O. Balatif, R. Rachik, Mathematical modelling with optimal control strategy of transmission of COVID-19 pandemic virus. Commun. Math. Biol. Neurosci, 2020.
[11] O.A. MacLean, S. Lytras, S. Weaver, J.B. Singer, M.F. Boni, P. Lemey, D.L. Robertson, Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen, PLoS Biology, 19(3) 2021, e3001115.
[12] M. Martcheva, An introduction to mathematical epidemiology 61 2015, New York: Springer.
[13] A. McDonnell, R. Van Exan, S. Lloyd, L. Subramanian, K. Chalkidou, A. La Porta, D. Reader, COVID-19 Vaccine predictions: using mathematical modelling and expert opinions to estimate timelines and probabilities of success of COVID-19 vaccines, Center for Global Development Washington, 2020.
[14] D.R. Merkin, Introduction to the Theory of Stability 24 2012, Springer Science & Business Media.
[15] National Primary Health Care Development Agency, COVID-19 vaccinated update 2021, Retrieved from https://www.nphcda.gov.ng (accessed 5th July 2021).
[16] Nigerian Centre for Disease Control, 2021, Retrieved from https://covid19.ncdc.gov.ng (accessed 1st of July 2021).
[17] C.N. Ngonghala, E. Iboi, S. Eikenberry, M. Scotch, C.R. MacIntyre, M.H. Bonds, A.B. Gumel, Mathematical assessment of the impact of non-pharmaceutical interventions on curtailing the 2019 novel Coronavirus. Mathematical biosciences, (325) 2020, 108364.
[18] D. Okuonghae and A. Omame, Analysis of a mathematical model for COVID-19 population dynamics in Lagos, Nigeria. Chaos, Solitons & Fractals, (139) 2020, 110032.
[19] S.M. Sherman, L.E. Smith, J. Sim, R. Amlôt, M. Cutts, H. Dasch, N. Sevdalis, COVID-19 vaccination intention in the UK: results from the COVID-19 vaccination acceptability study (CoVAccS), a nationally representative cross-sectional survey. Human vaccines & immunotherapeutics, 17(6) 2021, 1612-1621.
[20] P. Van den Driessche, Reproduction numbers of infectious disease models. Infectious Disease Modelling, *2*(3) 2017, 288-303.
[21] P. Van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical biosciences, 180(1-2) 2002, 29-48.
[22] World Health Organization, COVID-19 weekly epidemiological update, 2020.
[23] World Health Organization, Interim recommendations for use of the Pfizer–BioNTech COVID-19 vaccine, BNT162b2, under emergency use listing: interim guidance, first issued 8 January 2021, updated 15 June 2021 (No. WHO/2019-nCoV/vaccines/SAGE_recommendation//BNT162b2/2021.2), 2021, World Health Organization.
[24] World Health Organization, Mission summary: WHO Field Visit to Wuhan, China 20-21 January 2020. Online information available at https://www. who. int/china/news/detail/22-01-2020-field-visit-wuhan-china-jan-2020 (accessed 19th April 2020*)*.
[25] World Health Organization, Overview of public health and social measures in the context of COVID-19: interim guidance, *18 May 2020* (No. WHO/2019-nCoV/PHSM_Overview 2020, World Health Organization.
[26] Z.Q. Xia, J. Zhang Y.K. Xue, G.Q. Sun, Z. Jin, Modeling the transmission of Middle East respirator syndrome Corona virus in the Republic of Korea. PloS one, 10(12) 2015, 0144778.
[27] N. Zhu, D. Zhang, W. Wang, X. Li, B. Yang, J. Song, W. Tan, A novel Coronavirus from patients with pneumonia in China, New England journal of medicine, 2020.
[28] H.A. Lyeme, Mathematical modeling of the impacts of the nanoparticle in River-Aquatic system with convective cooling, Mathematics and Computational Sciences, 1(4) 2021, 1-3.