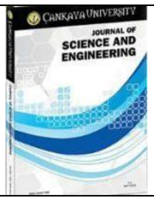
e-ISSN: 2564-7954 CUSJE 19(2): 078-094 (2022) Research Article



Çankaya University

Journal of Science and Engineering

CUJSE

https://dergipark.org.tr/cankujse

Mathematical Modeling and Simulation of Coronavirus (COVID-19) in Lagos State, Nigeria

Sefiu Adekunle Onitilo[1], Deborah Oluwatobi Daniel[2*]

[1]Department of Mathematical Sciences, Olabisi Onabanjo University, Nigeria
[2]Department of Mathematics and Computer Science, Southwestern University, Nigeria

Keywords

COVID-19, Transmission Dynamics, Coronavirus Disease, SEAIQR Model, Mathematical Model, Control Measures.

Abstract

Coronavirus Disease (COVID-19) is regarded as one of the biggest respiratory illness outbursts influencing different nations concurrently including Nigeria and a novel strain of Coronavirus (SARS-CoV 2) has been distinguished as the causative agent. To study the transmission dynamics of COVID-19, SEAIQR model is presented. The existence and stability of Disease Free Equilibrium (DFE) are established. Numerical evaluation of observed data and model data is fitted using a nonlinear least square method, implemented in Python. Simulations were conducted to further monitor the effect of complaisance with control strategies. It is found that the optimal control shows the effectiveness of control measures (reducing contact rate and usage of mask) when being applied. It is noticed that the best option is to observe social distancing against the use of a mask. Nonetheless, the effective approach is the compliance with both control measures, that is, complaisance with social distancing as well as the utilization of a mask. Hence, it is recommended that there should be educational campaigns on the impact of embracing social distancing, wearing a mask, need to be vaccinated; enforcement and sanctions for non-complaisance with the aforementioned control measures.

1. Introduction

The world keeps combating Coronavirus diseases 2019 (COVID-19) triggered by severe acute syndrome coronavirus 2 which is considered an exceptionally dangerous infection that interrupts the human respiratory system. It has resulted in globally basic health as well as economic situations stemming directly from the infection and the likely damaging side effects of the control measures applied to control its spread out. Its burden has exceeded those of its associated coronaviruses.

The pandemic began towards the end of December 2019 with patients on admission to health centres with a preliminary diagnosis of pneumonia. The patients' health issues were connected to the seafood and damp animal marketplace in Wuhan, Hubei District, China [1]. On January 2, 2020, an overall lot of 41 patients on admission were confirmed to be infected with COVID-19 [2]. Several inexplicable cases of coughing, pneumonia, dyspnea, fatigue as well fever in Wuhan, China, for a brief time. The inception of COVID-19 led to the shutdown of organisations, businesses, colleges, marketplace, travelling within and outdoors, intermingling, curfew, and reducing the number of people attending social gatherings to a few numbers of people, to mention but a few. On January 22, 2020, China had around 7734 confirmed COVID-19 cases, while 90 cases were mentioned in around thirteen nations [1,3]. Since the inception, a total amount of 495,685,661 COVID-19 cases with the following breakdown: Africa – 11,787,400; Europe - 182,315,949; Asia - 142,494,852; North America – 96,859,714; South America – 56,294,934; Oceania – 5,932,091 has been disclosed around 226 countries as at April 7, 2022 including 6,192,935 fatalities with the following breakdown: Africa- 253,098; Europe - 1,795,474; Asia – 1,408,365; North America - 1,446,731; South America – 1,289,718; Oceania – 9,534The united states: 640,513 fatalities, Europe:

* Corresponding Author: oludeborahdaniel@gmail.com
Received: 8. April. 2022, Accepted: 26. August. 2022

265,565 fatalities, Oceania: 1,051 fatalities, as well as others: 7 fatalities) [4]. Nigeria has fallen under countries influenced by the COVID-19 pandemic. February 27, 2020, capped in the first case of COVID-19 in Lagos state, southwestern, Nigeria when an Italian person came into the country on the 24th of February and was isolated at a health centre on the 26th of February, 2020 [5].

COVID-19 is transmitted from individual to individual through route exposure to contaminated surface areas as well as via respiratory drops' internal breadth coming from infected people. Initially, there was no vaccine to fight the widespread COVID-19. However, currently, there is a development of a vaccine or even antiviral therapy authorized for the avoidance or monitoring of COVID-19 [6]. Before the influx of COVID_19 into Nigeria, the Federal authorities ensured states in Nigeria put together medical centres having isolation facilities with the focus to curb the widespread of the disease. To appropriately lessen the widespread of COVID-19, federal authorities via Nigeria Center for Disease Control (NCDC) have been executing numerous control measures including enforcing stringent, necessary lockdown as well as encouraging (and in many cases stringently imposing) other measures including people sustaining a minimum required range between themselves (social distancing), steering clear of congested celebrations, enforcing an optimum number of people in any sort of gathering (religious as well as social) and also making use of nose masks in public. To aid minimization of the widespread of COVID-19, contact tracing of suspected individuals was tipped up in many nations as well as confirmed cases (asymptomatic individuals and symptomatic individuals) are promptly separated in isolation for immediate treatment.

Mathematical modelling is a beneficial tool used successfully to control widespread infectious diseases. It is a summary of the operations of real-life using mathematical symbols, equations, as well as formulas, and is generally utilized in a lot of areas, including physical sciences, biology, medicine [7], farming, administration, and social sciences [8] etc. The compartmental models and actual cases are more efficient in offering beneficial details about a certain disease outbreak. Such models can either be linear or nonlinear, stochastic or deterministic. In the health sector, a mathematical model is being applied to forecast the outburst of diseases, and prevent or treat these health problems. Presently, a lot of mathematical models are utilized to describe the transmission of diseases and are published in journals related to biomathematics [9]. Since the inception of COVID-19, researchers across many countries have been formulating different mathematical models utilizing ordinary differential equations [11, 12, 13, 14, 15], delay differential equations [16] etc., as a procedure for getting expertise in the transmission mechanism of the widespread of the disease, effect of the disease, prevention and control of the disease, precautionary measure to curb the spread of the disease varying from cleaning of hands along with a disinfectant, 2-5 meters distance in social gathering and the use of nose mask [10, 11].

The transmission dynamics of COVID-19 in Lagos, Nigeria are examined in [17], while the outbreak cases of COVID-19 were studied in [11, 15, 18, 19, 20]. In [11], SEIQCRW was adopted to examine the outbreak of COVID-19 in Nigeria. The model considered the human-human and environment-human mode of transmission with nonlinear forces of infection. Different mitigation strategies to curb the spread of the disease were also examined. It was suggested in addition to the already known mitigation strategies, that there should be fumigation of the environment to reduce the transmission mode between humans and the environment. [15] adopted SEIAHQRS model which considers hospitalized, asymptomatic and quarantined individuals. The model also considered the re-infection of recovered individuals and reported that there are 94% chances for secondary reinfection of disease when recovered individuals have interaction with hospitalized and exposed individuals through contact. On the contrary, it is reported in [19], that there are 99.9% chances of reinfection and infection when there is contact between the infected individuals and exposed individuals in the susceptible compartment. This deviation might have resulted from the SEIR model considered unlike in [15] which considered a broader class of the population. Furthermore, It is suggested in [18] that there need for reliable involvement of community health personnel for a proper response to COVID-19 was explained. It was figured out that the feasible proof of ongoing and increasing community transmission of COVID-19 infections, insufficient screening ability and overwhelming health resources. It disclosed the infection of many health personnel despite the existence of a shortage of experienced health personnel. It was suggested that the federal authorities should immediately bring community health workers aboard, release quick epidemic intelligence and scale up making use of mobile applications for contact tracing. It was also recommended that reducing the transmission rate of infection alone is not enough to eliminate the disease due to the visibility of backward bifurcation but the need for Nigerians to additionally adhere stringently to COVID-19 protocols in alleviating the widespread and demise of coronavirus [20]. The community-wide effect of numerous control and minimization approaches in some territories within Nigeria (especially the conditions of Kano, Lagos and Federal Capital Territory, Abuja) were analysed in [10]. Numerical simulations of the model revealed that COVID-19 might successfully be managed in Nigeria making use of modest degrees of social-distancing approach in the territories and the whole country. Although, making use of nose masks in public places can substantially lower COVID-19 in Nigeria, its use as an exclusive intervention tactic, might fail to result in a considerable decrease in the burden caused by the disease. Such a decrease is viable in the territories (and the whole of Nigeria country) if everyone can adhere to the use of a masking strategy complemented with the social-distancing strategy.

Scientists in various regions have presented excellent exposition on precautionary and curative measures to contain the pandemic and have mentioned better results. Nonetheless, a more review of the current form of models along with a justified and sufficient evaluation is needed. It is observed, that many of the models proposed in the literature considered the vital dynamics but the report showed that the rate of transmission of this virus is more than the birthrate and death rate in many countries [1], hence the need to examine the non-vital dynamics of COVID-19. Therefore, in this paper, SEAIQR model combining the effect from the exposed, asymptomatic, symptomatic, and quarantined individuals, is developed with the focus on the non-vital dynamics of the model of COVID-19 due to the rapid spreading of the virus. Also, numerical simulations of the model were fitted with COVID-19 confirmed cases in Lagos State, Nigeria and some mitigation strategies were applied to observe the rate of transmission of COVID-19.

2. Model Formulation

SEAIQR model is developed to examine the transmission mechanism of COVID-19 among humans. The total number of people at time t is symbolized as $N(t)$ which is distributed within six compartments. The susceptible humans are symbolized as S, the exposed humans are symbolized as E, the asymptomatic infected humans are symbolized as A, the symptomatically infected humans are symbolized as I, the quarantined humans are symbolized as Q and the recovered humans symbolized as R.

The susceptible humans S are persons are those likely to be infected, the exposed humans E are those persons vulnerable to the virus. The asymptomatic infected humans A are persons at the incubation period of the virus, as a result, they are infected but without symptoms. The symptomatic infected humans I are persons at the latent period of the virus, which implies, they are infected and fully showing the symptoms of the disease. The quarantined humans Q are persons whose infection is confirmed and isolated for treatment. After a period of treatment, these persons recovered R.

To mathematically formulate the model, it is assumed there are no migration, birth rate and death rate are neglected. The susceptible persons can be infected by getting in contact with asymptomatic, symptomatic and quarantined persons, with β accounting for the transmission rate. Exposed persons progress into the Infected class I at a rate of σ. η_A and η_Q measures the reduction in disease transmission for asymptomatic persons and quarantined persons respectively. a is the fraction of the exposed persons without traces of the disease at the end of the incubation period. q_E, q_A and q_I respectively represent the rate at which Exposed persons, Asymptomatic persons, and symptomatic persons become quarantined. After a period of treatment, these persons are either discharged from the hospital at a rate of ρ_I and ρ_A respectively or face death. Consequently, δ_I and δ_A respectively represents the disease-induced death rate. κ is the proportion of patients with incomplete treatments, thus becoming asymptomatic infected. The general transmission dynamics are displayed in Figure 1.

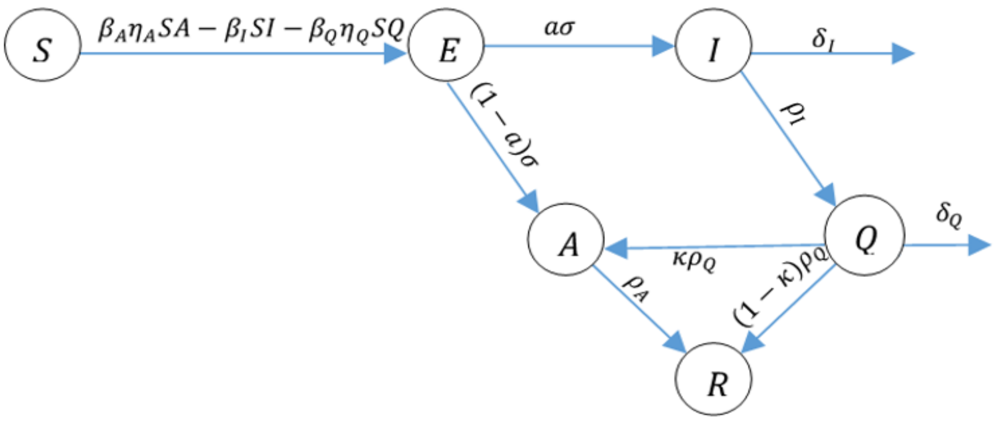


Figure 1. Transmission Dynamics of COVID-19 using SEAIQR model

A system of time evolution of the population state describing the transmission mechanism of COVID-19 is expressed from Figure 1 in the following systems of nonlinear ODEs:

$$\begin{cases} \frac{dS}{dt} = -\beta_A\eta_ASA - \beta_ISI - \beta_Q\eta_QSQ \\ \frac{dE}{dt} = \beta_A\eta_ASA + \beta_ISI + \beta_Q\eta_QSQ - (q_E+\sigma)E \\ \frac{dA}{dt} = \sigma aE + \kappa\rho_QQ - (\rho_A + q_A)A \\ \frac{dI}{dt} = \sigma(1-a)E - (\rho_I + q_I + \delta_I)I \\ \frac{dQ}{dt} = q_EE + q_AA + q_II - (\rho_Q + \delta_Q)Q \\ \frac{dR}{dt} = (1-\kappa)\rho_QQ + \rho_AA + \rho_II \end{cases} \tag{1}$$

$N(t) = S(t) + E(t) + A(t) + I(t) + Q(t) + R(t)$

The state variables and parameters describing the transmission dynamics of COVID-19 in (1) are defined in the table below:

Table 1. Description of state variable of COVID-19 model (1)

State variable	Description
S	Total number of the susceptible persons
E	Total number of the exposed persons
A	Total number of the asymptomatic infectious persons
I	Total number of the symptomatic infectious persons
Q	Total number of the quarantined persons
R	Total number of the recovered persons

Table 2. Description of the parameters of the model (1)

Parameters	Description
β	Contact rate from the infected persons to the susceptible persons
$1/q_E$	Incubation period of the virus
q_I	Quarantined rate for symptomatic infected persons
q_A	Quarantined rate for asymptomatic infected persons
δ_I	Disease induced death rate for the infectious compartment
δ_Q	Disease induced death rate for the quarantined compartment
ρ_I	Rate at which symptomatic infectious persons recovers
ρ_A	Rate at which asymptomatic infectious persons recovers
ρ_Q	Rate at which a quarantined person recovers
κ	Fraction of hospitalized persons with incomplete recovery
a	Fraction of exposed persons showing no symptoms at the end of the incubation period
η_A	reduction in the widespread of disease for asymptomatic persons
η_Q	reduction in the widespread of disease for symptomatic persons
$1-a$	Fraction of exposed persons that are highly infectious at the end of the incubation period

3. Steady State of Model 1

3.1. The Disease-Free Equilibrium Point

For the Disease-Free Equilibrium of model 1, let

$$\mathcal{E}_0 = (S_0, E_0, A_0, I_0, Q_0, R_0)$$

Thus, at the DFE point $\mathcal{E}_0$, $E_0, A_0, I_0, Q_0, R_0 = 0$ that is, in the absence of COVID-19, by resolving system (1), the resulting DFE point is

$$\mathcal{E}_0 = (S(0),0,0,0,0,0)$$

where $S(0)$ is the initial size of the susceptible persons ($N(0) = S(0)$) [15].

3.2. Basic Reproduction Number

Reproduction Number denoted by $\mathcal{R}_0$ plays a major role in the epidemiological model. It forecasts if an infection will widespread throughout the human population or not. It is defined as the number of secondary infections produced from primary infection in a susceptible host population. When $\mathcal{R}_0 > 1$, then the disease is epidemic and there will continually be an increase in the number of cases among susceptible populations if no environmental changes or external influences intervene. When $\mathcal{R}_0 = 1$, the disease is endemic and when $\mathcal{R}_0 < 1$, there will be a decrease in the number of cases.

To complete the basic reproduction number of the model (1), the next-generation matrix technique is adopted.

The infection matrix is

$$F = \begin{pmatrix} 0 & \beta_I & \beta_A\eta_A & \beta_Q\eta_Q \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{2}$$

The transition matrix

$$V = \begin{pmatrix} (q_E+\sigma) & 0 & 0 & 0 \\ -\sigma a & \rho_A + q_A & 0 & -\kappa\rho_Q \\ -\sigma(1-a) & 0 & (\rho_I + q_I + \delta_I) & 0 \\ -q_E & -q_A & -q_I & \rho_Q + \delta_Q \end{pmatrix} \tag{3}$$

The reproduction number for model (1) is

$$\begin{aligned} \mathcal{R}_0 = \rho(FV^{-1}) \quad &= \frac{\beta_A\eta_A\kappa\rho_A(\sigma a q_A(\rho_I+q_I+\delta_I)+(\rho_A+q_A)(q_I\sigma(1-a)+q_E(\rho_I+q_I+\delta_I))}{(\rho_I+q_I+\delta_I)(q_E+\sigma)\big((q_A+\rho_A)(\delta_Q+\rho_Q)-\kappa q_A\rho_Q\big)} \\ &+ \frac{\beta_I\sigma(1-a)}{(\rho_I+q_I+\delta_I)(q_E+\sigma)} \\ &+ \frac{\beta_Q\eta_Q(\sigma a q_A(\rho_I+q_I+\delta_I)+(\rho_A+q_A)\big(q_I\sigma(1-a)+q_E(\rho_I+q_I+\delta_I)\big))}{(\rho_I+q_I+\delta_I)(q_E+\sigma)\big((q_A+\rho_A)(\delta_Q+\rho_Q)-\kappa q_A\rho_Q\big)} \end{aligned} \tag{4}$$

where $\rho(.)$ is the spectral radius such that

$$\mathcal{R}_0 = \mathcal{R}_A + \mathcal{R}_I + \mathcal{R}_Q$$

$\mathcal{R}_I, \mathcal{R}_A$ and $\mathcal{R}_Q$ measures the contribution from highly infected persons, asymptomatically infectious persons and quarantined persons respectively. these three communication routes of the disease cover the whole infection threat for the outburst of COVID-19.

The constituent reproduction number $\mathcal{R}_A$ measures the product of the contact rate of susceptible persons from asymptomatic persons near the DFE β_A, the proportion of quarantined persons and symptomatic persons move to asymptomatic or mildly infected compartment due to hospitalized persons with incomplete recovery at a rate κ that is, $\frac{\beta_A\eta_A\kappa\rho_A(\sigma a q_A(\rho_I+q_I+\delta_I)+(\rho_A+q_A)(q_I\sigma(1-a)+q_E(\rho_I+q_I+\delta_I))}{\big((q_A+\rho_A)(\delta_Q+\rho_Q)-\kappa q_A\rho_Q\big)}$ over the average duration in the symptomatic infected and exposed compartment $\frac{1}{(\rho_I+q_I+\delta_I)(q_E+\sigma)}$

Similarly, the contribution of the reproduction number $\mathcal{R}_I$ measures the contact rate of susceptible persons from infected persons near the β_I, the portion of those highly infectious after the incubation period that is $\beta_I\sigma(1-a)$ over the average duration of $\frac{1}{(\rho_I+q_I+\delta_I)(q_E+\sigma)}$

Lastly, the constituent number $\mathcal{R}_Q$ measures the product of the contact rate of susceptible persons from quarantined persons near the DFE β_Q, the proportion of asymptomatic infected persons near the DFE β_Q, the proportion of asymptomatic infected persons and symptomatic persons who are quarantined that is $\frac{\beta_Q\eta_Q(\sigma a q_A(\rho_I+q_I+\delta_I)+(\rho_A+q_A)\big(q_I\sigma(1-a)+q_E(\rho_I+q_I+\delta_I)\big))}{\big((q_A+\rho_A)(\delta_Q+\rho_Q)-\kappa q_A\rho_Q\big)}$ over the average duration in the symptomatic infected and exposed compartment $\frac{1}{(\rho_I+q_I+\delta_I)(q_E+\sigma)}$.

3.3. Stability of the Disease-Free Equilibrium

Theorem 1. The DFE of the coronavirus disease is globally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable otherwise

Proof. Let $\pi(E, E, I, Q)$ be a Lyapunov function with some nonnegative parameters $\omega_1, \omega_2, \omega_3$ and ω_4 such that

$$\Pi(E, A, I, Q) = \omega_1 E + \omega_2 A + \omega_3 I + \omega_4 Q$$

Differentiating the Lyapunov function

$$\frac{d\pi}{dt} = \omega_1 \frac{dE}{dt} + \omega_2 \frac{dA}{dt} + \omega_3 \frac{dI}{dt} + \omega_4 \frac{dQ}{dt} \tag{5}$$

Substituting for $\frac{dE}{dt}, \frac{dA}{dt}, \frac{dI}{dt}, \frac{dQ}{dt}$ in equation (5) yields

$$\begin{aligned}\frac{d\pi}{dt} &\leq \omega_1\big(\beta_A \eta_A SA + \beta_I SI + \beta_Q \eta_Q SQ - (q_E + \sigma)E\big) \\ &+\omega_2\big(\sigma a E - (\rho_A + q_A)A + \kappa \rho_Q Q\big) + \omega_3(\sigma(1-a)E - (\rho_I + q_I + \delta_I)I) \\ &\omega_4\big(q_E E + q_A A + q_I I - (\rho_Q + \delta_Q)Q\big)\end{aligned}$$

Grouping like terms yields

$$\begin{aligned}\frac{d\pi}{dt} &\leq \omega_1\big(\beta_A \eta_A SA + \beta_I SI + \beta_Q \eta_Q SQ\big) - (\omega_1(q_E + \sigma) + \omega_2 \sigma a + \omega_3 \sigma(1-a))E \\ &-((\rho_A + q_A) - \omega_4 q_A)A - \big(\omega_4(\rho_Q + \delta_Q) - \kappa \rho_Q \omega_2\big)Q \\ &-(\omega_3(\rho_I + q_I + \delta_I) - \omega_4 q_I)I\end{aligned}$$

At DFE $\mathcal{E}_0, E_0, A_0, I_0, Q_0 = 0$.

Hence substituting the values of $E_0 = 0, A_0 = 0, I_0 = 0, Q_0 = 0$

$$\begin{aligned}\frac{d\pi}{dt} &\leq -(\omega_1(q_E + \sigma) + \omega_2 \sigma a + \omega_3 \sigma(1-a))E - (\omega_2(\rho_A + q_A) - \omega_4 q_A)A \\ &-\big(\omega_4(\rho_Q + \delta_Q) - \kappa \rho_Q \omega_2\big)Q - (\omega_3(\rho_I + q_I + \delta_I) - \omega_4 q_I)I\end{aligned} \tag{6}$$

Equating the coefficient of A in (6) to zero and applying the multiplication property of equality which states that if $p = q$ as well as if $r = s$ then and there $pr = qs$ yields

$$\omega_2(\rho_A + q_A) = q_A \omega_4$$

Choosing $\omega_4 = (\rho_A + q_A), \omega_2 = q_A$ Also equation the coefficient of I in equation 6 to zero and substituting for ω_4 and solving for ω_3 yields

$$\omega_3 = \frac{q_I(\rho_A + q_A)}{(\rho_I + q_I + \delta_I)}$$

Lastly, equating the coefficient of E in equation (6), substituting for ω_2, ω_3 and solving for ω_1 yields

$$\omega_1 = -\frac{q_1(\rho_A + q_A)\sigma(1-a)}{(\rho_I + q_I + \delta_I)(q_E + \sigma)} - \frac{\sigma q_A}{(q_E + \sigma)}$$

Substituting for $\omega_1, \omega_2, \omega_3$, and ω_4 in equation (5) gives

$$\begin{aligned}\frac{d\pi}{dt} \leq & -\left(-\frac{q_1(\rho_A+q_A)\sigma(1-a)}{(\rho_I+q_I+\delta_I)} - \sigma q_A + \sigma a q_A + \frac{q_I(\rho_A+q_A)}{(\rho_I+q_I+\delta_I)}\sigma(1-a)\right)E \\ & -(q_A(\rho_A+q_A)-(\rho_A+q_A)q_A)A - \left((\rho_A+q_A)(\rho_Q+\delta_Q)-q_A\kappa\rho_Q\right)Q \\ & -\left(\frac{q_I(\rho_A+q_A)}{(\rho_I+q_I+\delta_I)} - q_I(\rho_A+q_A)\right)I\end{aligned} \quad (7)$$

$$\frac{d\pi}{dt} \leq \ -\left((\rho_A+q_A)(\rho_Q+\delta_Q)-q_A\kappa\rho_Q\right)Q \quad (8)$$

$$\begin{aligned}\frac{d\pi}{dt} \leq & \left[-\begin{pmatrix}\frac{\beta_A\eta_A\kappa\rho_A(\sigma a q_A(\rho_I+q_I+\delta_I)+(\rho_A+q_A)(q_I\sigma(1-a)+q_E(\rho_I+q_I+\delta_I))}{(\rho_I+q_I+\delta_I)(q_E+\sigma)} \\ +\frac{\beta_I\sigma(1-a)\left((\rho_A+q_A)(\rho_Q+\delta_Q)-q_A\kappa\rho_Q\right)}{(\rho_I+q_I+\delta_I)(q_E+\sigma)} \\ +\frac{\beta_Q\eta_Q(\sigma a q_A(\rho_I+q_I+\delta_I)+(\rho_A+q_A)(q_I\sigma(1-a)+q_E(\rho_I+q_I+\delta_I)))}{(\rho_I+q_I+\delta_I)(q_E+\sigma)}\end{pmatrix}\right. \\ & \left. +\left((\rho_A+q_A)(\rho_Q+\delta_Q)-q_A\kappa\rho_Q\right)[\mathcal{R}_0-1]\right]Q\end{aligned} \quad (9)$$

Therefore, $\frac{d\pi}{dt} = 0$ iff $Q = 0$ and $\frac{d\pi}{dt} < 0$ if $\mathcal{R}_0 < 1$. Hence, the largest compact invariant set in $\Omega = \{SEAIQR \in \mathbb{R}^6 : \frac{d\pi}{dt} = 0\}$ is the singleton set $\{\mathcal{E}_0\}$. From La Salle's invariant principle, it can be concluded that $\mathcal{R}_0 < 1$ implies $\{\mathcal{E}_0\}$ is globally asymptotically stable in Ω.

3.4. Section Numbering

3.4.1. Existence of the Endemic State

The final size of the COVID-19 pandemic using model (1) is obtained here. Using the notation $x \in \mathbb{R}_+^4, y \in \mathbb{R}_+$ and $z \in \mathbb{R}_+$ to represent the sets of asymptotically infected, exposed, asymptotically infected, quarantined, susceptible, and the recovered class of the model. Consequently,

$$x(t) = (E(t), A(t), I(t), Q(t))^T,\ y(t) = S(t)\ and\ z(t) = R(t)$$

Let F be the $m \times n$ diagonal matrix whose diagonal entries are denoted by $\epsilon_i(i = 1,2,3,\cdots,m)$ are the comparative susceptibilities of the equivalent susceptible compartment. Define Γ as the $m \times n$ with the property (i,j) representing the proportion of the $j^{\ th}$ susceptible persons that go into the infected component when infected with the infectious disease. Let f be an n-dimensional row of a vector of relative horizontal widespread of the disease. Let Γ be the infection rate $(\beta_A, \beta_I, \beta_Q)$ of the model (1) such that $\Gamma = \beta_A(x,y,z) + \beta_I(x,y,z) + \beta_Q(x,y,z)$. Define the m −dimensional vector

$$\Pi = [\Pi_1, \Pi_2, \Pi_3, \dots, \Pi_m] = \Gamma f V^{-1} \Lambda F$$

From model (1) it follows that

$$f = [0,1,1,0], \Pi = \mathcal{R}_0, F = 1, \Lambda = \begin{bmatrix}1\\0\\0\\0\end{bmatrix}$$

With regards to the above change, variables and definition of the model reduces to

$$\begin{aligned}\frac{dx}{dt} &= \Lambda F y \Gamma(x,y,z)dx - Vx \\ \frac{dy}{dt} &= -fy\Gamma(x,y,z)dx \\ \frac{dz}{dt} &= Wx\end{aligned} \quad (10)$$

Where V is the transition matrix (3), W is a $k \times n$ matrix with the property that the (i, j) entry signifies the degree of transition from the j th infected class into the recovered (i th) class upon recovery.

Theorem 2. The endemic size of the epidemic model (1) or (equivalently (10)) is given by

$$\ln\left(\frac{S(0)}{S(\infty)}\right) \geq \mathcal{R}_0\left(1 - \frac{S(\infty)}{S(0)}\right) \tag{11}$$

Proof:

$$\frac{dS}{dt} + \frac{dE}{dt} + \frac{dA}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = -\delta_A A - \delta_I I \tag{12}$$

Since all the solutions in the system (1) are non-negative and bounded from (12), it can be deduced that as $t \to \infty, E \to 0, A \to 0, I \to 0, Q \to 0, S \to S(\infty) \geq 0$. Assume that the total population N is constant for $t \geq T$ and

$$\mathcal{R}_\mathrm{e} = \mathcal{R}_0 \frac{S(T)}{N(T)} \tag{13}$$

as an effective reproduction number. Define the function

$$M(t) = \ln S(t) + \frac{E(t)}{N(T)} + \frac{A(t)}{N(T)} + \frac{I(t)}{N(T)} + \frac{Q(t)}{N(T)} + \frac{R(t)}{N(T)} \tag{14}$$

$M(t)$ is invariant for $t \geq T$, estimating the derivatives along with the solution of the system (1) which is $M'(T) = 0$. Hence, $M(T) = M(\infty)$. Also, when there is no more infection the population $E(\infty) = A(\infty), I(\infty), Q(\infty) = 0$, and $N(T) = S(T) + E(T) + A(T) + I(T) + Q(T) + R(T) = S(\infty) + R(\infty) = N(\infty)$, implying that $R(\infty) = N(\infty) - S(\infty)$, From (14)

$$\ln S(T) + \frac{E(T)}{N(T)} + \frac{A(T)}{N(T)} + \frac{I(T)}{N(T)} + \frac{Q(T)}{N(T)} + \frac{R(T)}{N(T)} = \ln S(\infty) + \frac{N(\infty) - S(\infty)}{N(T)} \tag{15}$$

Using (13)

$$\ln \frac{S(T)}{S(\infty)} = -\frac{E(T)}{N(T)} - \frac{A(T)}{N(T)} - \frac{I(T)}{N(T)} - \frac{Q(T)}{N(T)} + \frac{R_e(N(\infty) - S(\infty) - R(T))}{S(T)} \tag{14}$$

When $T = 0$ with the initial condition $E(0) = A(0) = Q(0) = R(0) = 0$ and with $S(0) = \mathrm{N}(0) > 0$, the endemic state given by the inequality (14) reduces to

$$\ln\left(\frac{S(0)}{S(\infty)}\right) = \mathcal{R}_0\left(1 - \frac{S(\infty)}{S(0)}\right) \tag{15}$$

4. Numerical Simulation

4.1. Parameter Estimation and Model Fitting

Estimates of some parameters of the model (1) are sourced from the literature as indicated in Table 3. While other unknown parameters are estimated by fitting the cumulative number of confirmed cases reported NCDC website to those generated by the model (1) and are presented in Table 4.

For simulation convenience and computational flexibility, the population of Lagos State is re-scaled to 5 million i.e. S(0)=5,000,000 with a pandemic starting with one index case which was confirmed and isolated in Lagos State on March 16, 2020. Other initial state variables are set as follows

$$E(0) = 2, A(0) = 5, R(0) = 0, I(0) = 0$$

The data fitting technique involves using a mathematical technique called the Nelder-Mead method which is used to estimate the unknown values of the parameter used in the model (1). To implement the nonlinear least square method, the model (1) is written in vector form consisting of the parameters to be estimated for the initial values of the state variables. The nonlinear least square method permits the solution of the set of parameters that minimizes the sum of the squares of the difference between the observed cumulative confirmed cases reported by NCDC and the cumulative confirmed cases predicted by the model which is implemented using a computer program called Python.

Figures 2 and 4 show the daily incidence of confirmed cases and the cumulative number of confirmed cases in Lagos State.

The numerical simulation is done and plotted against time using Python and the results are shown in Figures 4 – 6 to illustrate the effect of assessment control i.e complaisance with either social distancing or usage of mask and both.

To assess control strategies in combating the pandemic. The following control strategies are considered namely:

1. Effect of social distancing
2. Effect of mask usage
3. Effect of compliance with both control strategies

4.2. Effect of Compliance with Social Distancing

The effect of compliance with social distancing is observed using the parameters in Tables 3 and 4 for the simulation of the model (1) at different levels of measures of compliance with social distancing as follows:

1. No compliance with social distancing: This involves simulating the model (1) using the baseline values for $\beta_A, \beta_I, \beta_Q$ in Table 4.

2. Slight compliance with social distancing: This involves simulating model (1) by reducing the contact rate $(\beta_A, \beta_I, \beta_Q)$ in Table 4 by 8%.

3. Moderate compliance with social distancing: This involves simulating model (1) by reducing the contact rate $(\beta_A, \beta_I, \beta_Q)$ in Table 4 by 10%.

4. Strict compliance with social distancing: This involves simulating the model (1) by reducing the contact rate $(\beta_A, \beta_I, \beta_Q)$ in Table 4 by 15%.

The effect of compliance with social distancing is presented in Figure 4.

4.3. Effect of the Usage of Mask

The effect of compliance with the usage of a mask is observed using the parameters in Tables 3 and 4 for the simulation of the model (1) at different levels of measures of compliance with the usage of a mask as follows:

1. No Usage of Mask: This involves simulating the model (1) using the baseline values for η_A, η_Q in Table 4.

2. Low Usage of Mask: This involves simulating the model (1) by reducing the values of the reduction rate of the disease transmission (η_A, η_Q) in Table ref4.2 by 10%.

3. Moderate Usage of Mask: This involves simulating the model (1) by reducing the values of the reduction rate of the disease transmission (η_A, η_Q) by 40%.

4. Strict Usage of Mask: This involves simulating the model (1) by reducing the values of the reduction rate of the disease transmission (η_A, η_Q) by 80%.

The effect of compliance with the usage of a mask is presented in Figure 5.

4.4. Effect of the Compliance with Control Strategies

The effect of compliance with control strategies is observed using the parameters in Tables 3 and 4 for the simulation of the model (1) at different levels of measures of compliance with control strategies as follows:

1. No Compliance: This involves simulating the model (1) using the initial values for $\beta_A, \beta_I, \beta_Q, \eta_A, \eta_Q$ in Table 4.

2. Low rate of compliance: This involves simulating the model (1) by reducing the values of $\beta_A, \beta_I, \beta_Q, \eta_A$ and η_A, η_Q in Table 4 by 0.08% and 10% respectively.

3. Average rate of compliance: This involves simulating the model (1) by reducing the values of $\beta_A, \beta_I, \beta_Q, \eta_A$ and η_A, η_Q in Table 4 by 0.1% and 40% respectively.

4. Strict/High rate of compliance: This involves simulating the model (1) by reducing the values of $\beta_A, \beta_I, \beta_Q, \eta_A$ and η_A, η_Q in Table 4 by 0.15% and 80% respectively.

The effect of compliance with the control strategies is presented in Figure 6.

Table 3. Initial value of the parameters used for the model (1)

Parameters	**Values**	**Reference**
σ	1/5.1 per day	[21]
a	0.025 per day	[5]
ρ_I	1/7 per day	[5,11]
ρ_Q	1/14 per day	[5,11]
δ_I	0.043 per day	Estimated from [10]
δ_Q	0.186 per day	Estimated from [10]

Table 4. Fitted parameter of the model (1) with the cumulative number of confirmed cases for Lagos State

Fitted Parameters	**Values**
η_Q	0.151 per day
η_A	4.935 per day
ρ_A	0.00408 per day
β_A	0.00457 per day
β_I	5.04 per day
β_Q	0.1169 per day
κ	0.4588 per day
q_A	0.223 per day

q_I	1.238 per day
q_E	0.4687 per day

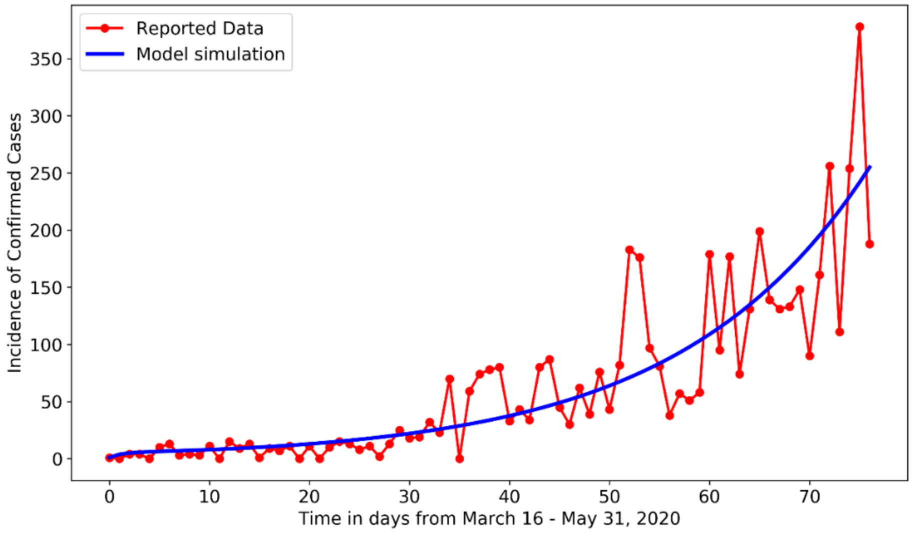


Figure 2. Model Fitting of daily incidence of confirmed cases of COVID-19 in Lagos State provided by NCDC

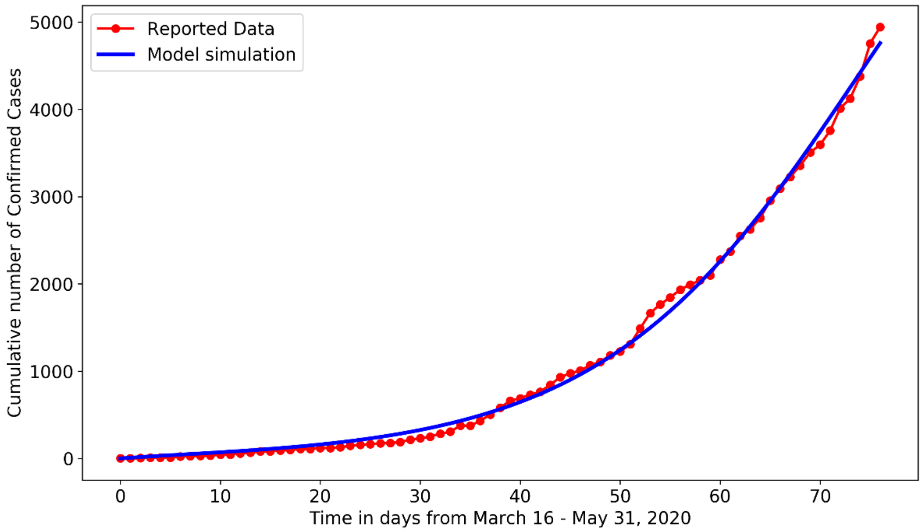


Figure 3. Model Fitting with cumulative confirmed cases of COVID-19 in Lagos State

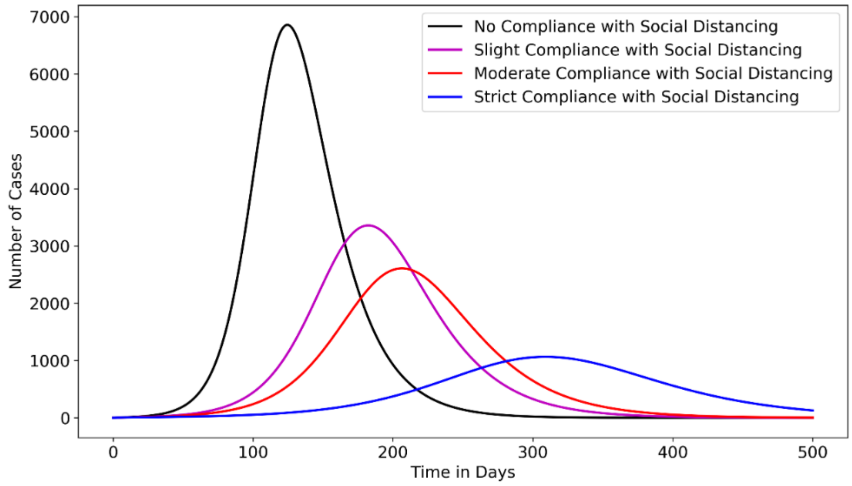


Figure 4. Model simulation for different levels of compliance with social distancing in a void of mask usage.

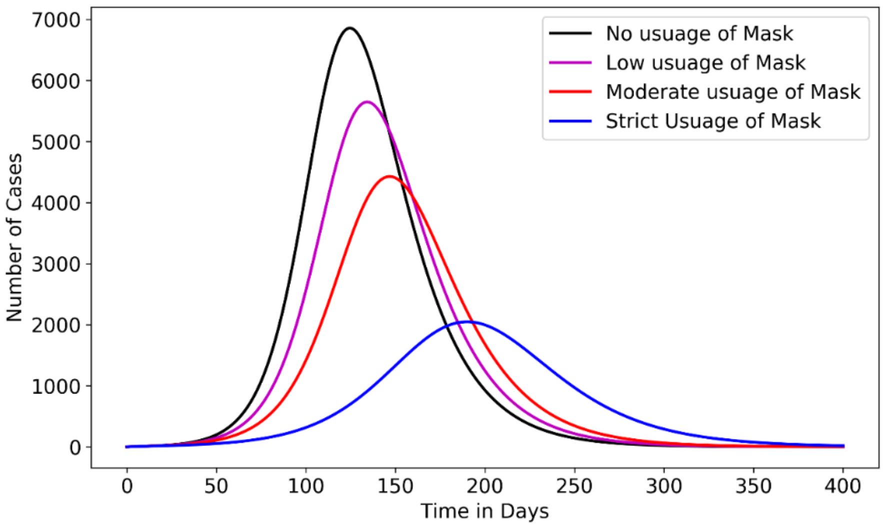


Figure 5. Model simulation for different levels of usage of mask usage in a void of social distancing

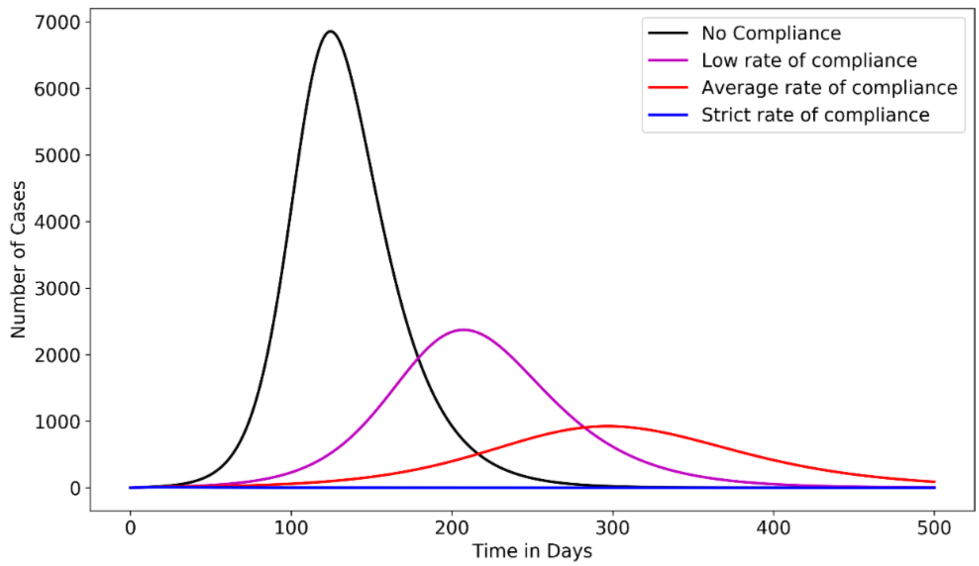


Figure 6. Model simulation for different efficiency of both control measures (social-distancing and mask usage)

Figures 2 and 3 respectively show the fitting of the model (1) with data of daily incidence and number of cumulative confirmed cases of COVID-19 in Lagos State provided by NCDC. It is observed that it is well fitted and the parameter estimation is presented in Table 4.

Figure 4 shows the model simulation for different efficiency resulting from compliance with social distancing in a void of mask usage. The result shows that the peak for non-compliance with the social distancing of daily incidence of confirmed cases of about 6900 is attained around 120 days from the inception of the disease. Slight compliance with social distancing reduces the peak of daily incidence of confirmed cases from 6900 to 3100 which is attained 180 days from inception. Moderate compliance with social distancing reduces the peak of daily incidence of confirmed cases from 6900 to 2500 which is attained 200 days from inception. Strict compliance with social distancing reduces the daily incidence peak of confirmed cases from 6900 to 900 which is attained 310 days from inception.

Figure 5 presents the model simulation for different efficiency of mask usage in the absence of social distancing. It is observed that the peak for no compliance with the usage of a mask of daily incidence of confirmed cases of about 6900 is attained around 120 days from the inception of the disease. A low rate of compliance with the usage of masks reduces the peak of daily incidence of confirmed cases from 6900 to 5500 which is attained 135 days from inception. A moderate rate of compliance with mask usage reduces the peak of daily incidence of confirmed cases from 6900 to 4200 which is attained 150 days from inception. A strict/high rate of compliance with mask usage drastically reduces the peak daily incidence of confirmed cases from 6900 to about 1800 which is attained 180 days from inception.

Figure 6 displays the model simulation for different efficiency of both control measures (social-distancing and mask usage). It is observed that the peak for no compliance with control measures (usage of mask and social distancing) of daily incidence of confirmed cases of about 6900 is attained around 120 days from the inception of the disease. A low rate of compliance with control measures reduces the peak of daily incidence of confirmed cases from 6900 to 2100 which is attained 210 days from inception. A moderate rate of compliance with control measures reduces the peak of daily incidence of confirmed cases from 6900 to 900 which is attained 300 days from inception. A strict/high rate of compliance with control measures drastically reduces the peak of daily incidence of confirmed cases from 6900 to about 0 i.e the peak is flattening.

5. Conclusions

The transmission and the widespread of COVID-19 using SEAIQR model are being examined. The SEAIQR model consists of systems of the ordinary differential equation describing the transmission dynamics of COVID-19 among susceptible persons, exposed persons, asymptomatic persons, symptomatic persons, quarantined persons and recovered persons. The existence and stability of DFE are established. The existence of the endemic state and the endemic size of the population is discussed. Numerical evaluation of observed data and model data is fitted using a nonlinear least square method, implemented using Python. Simulations were conducted to further monitor the effect of complaisance with control strategies. Although, the issue of the dependability, correctness and standard of the disclosed data is complex and out of the content of the research as the research centred more on the part of mathematical modelling. Besides, the model is not age-structured and does not take into consideration the birth rate, natural death rate and migration. Furthermore, there may be under-reporting of the confirmed cases and fatalities disclosed during and after lock-down because of inadequate health facilities experienced in Nigeria in regards to monitoring and the degree of screening.

From the numerical results, the optimal control shows the effectiveness of control measures (reducing contact rate and usage of mask) when being applied. It is noticed that the best option is to observe social distancing against the use of a mask. Nonetheless, the effective approach is the use of both control measures, that is, complaisance with social distancing as well as the utilization of a mask.

The following recommendation is needed to curb the epidemic in Lagos and Nigeria as a whole: Educational campaigns on the impact of embracing social distancing, wearing a mask and the need to be vaccinated; Enforcement and sanctions for non-complaisance with the aforementioned control measures.

Acknowledgements

Declaration of Competing Interest

No conflict of interest was declared by the authors.

Authorship Contribution Statement

Sefiu Onitilo: Writing, Reviewing and Editing

Deborah Daniel: Methodology, Data Preparation and Analysis

References

[1] H. A. Rothan, and S. N. Byrareddy, "The epidemiology and pathogenesis of coronavirus disease (COVID-19) outbreak," *Journal of Autoimmunity*, vol. 109, no. 102433, 2020. doi: 10.1016/j.jaut.2020.102433.

[2] H. Lu, "Drug treatment options for the 2019-new coronavirus (2019-nCoV)," *Bioscience Trends*, vol. 14, no. 1, pp. 69-71, 2020. doi: 10.5582/bst.2020.01020.

[3] M. Bassetti, A. Vena, and D. R. Giacobbe, "The novel Chinese coronavirus (2019-nCoV) infections: challenges for fighting the storm," *European Journal of Clinical Investigation*, vol. 50, no. 3, article e13209, 2020. doi: 10.1111/eci.13209.

[4] Worldometer. "COVID live – Coronavirus statistics" https://www.worldometers.info/coronavirus/ (accessed: 07.04.2022).

[5] NCDC. "Nigeria centre for disease control. covid-19 outbreak in Nigeria: situation report" https://ncdc.gov.ng/diseases/sitreps/?cat=14&name=An%20update%20of%20COVID-19%20outbreak%20 in%20 Nigeria (accessed: 14.10.2021) .

[6] B. Tang, X. Wang, Q. Li, N. L. Bragazzi, S. Tang, Y. Xiao and J. Wu, "Estimation of the transmission risk of the 2019-nCoV and its implication for public health interventions," *Journal of Clinical Medicine*, vol. 9, no. 2, pp. 462, 2020.

[7] A. Pack and D. Murray-Smith, "Mathematical models and their applications in medicine," *Scott Medical Journal*, vol. 17, no. 12, pp. 401-409, 1972.

[8] G. Pokhariyal, and A. Rodrigues, "An accurate epidemiological model," *Applied Mathematics and Computation*, vol. 53, no. 1, pp. 1-12, 1993.

[9] R. M. Anderson, and R. M. May, "Helminth infections of humans: mathematical models, population dynamics, and control,*" Advances in parasitology*, Elsevier, vol. 24: pp. 1-101, 1985.

[10] A. O. Egonmwan, and D. Okuonghae, "Mathematical analysis of a tuberculosis model with imperfect vaccine," *International Journal of Biomathematics*, vol. 12, no. 7, 2019. doi: 10.1142/S1793524519500736.

[11] D. O. Daniel, "Mathematical Model for the Transmission of Covid-19 with Nonlinear Forces of Infection and the Need for Prevention Measure in Nigeria," *Journal of Infectious Diseases and Epidemiology*, vol. 6, no. 5, pp. 158, 2020. doi: 10.23937/2474-3658/1510158.

[12] E. A. Iboi, O. O. Sharomi, C. N. Ngonghala, and A. B. Gumel, "Mathematical Modeling and Analysis of COVID-19 Pandemic in Nigeria," *Mathematical Biosciences and Engineering*, vol. 17, pp. 7192-7220, 2020. doi: 10.3934/mbe.2020369

[13] İ. H. Aslan, M. Demir, M. M. Wise, and S. Lenhart, "Modeling COVID-19: Forecasting and Analyzing the Dynamics of the Outbreak in Hubei and Turkey", *Mathematical Methods in the Apllied Sciences*, vol. 45, no. 10, pp. 6481-6494, 2022.

[14] M. S. Alqarni, M. Alghamdi, T. Muhammad, A. S. Alshomrani, and M. A. Khan, "Mathematical modeling for novel coronavirus (COVID-19) and control," *Numerical Methods for Partial Differential Equations*, vol. 38, no. 4, pp. 760-776, 2020. doi: 10.1002/num.22695.

[15] S. A. Onitilo, M. A. Usman, O. S. Odetunde, F. A. Hammed, Z. O. Ogunwobi, H. A. Haruna, and D. O. Daniel, "Mathematical modeling of 2019 novel Coronavirus (2019 – NCOV) Pandemic in Nigeria," *Chemistry: Bulgarian Journal of Science Education*, vol. 29, no. 3, pp. 398-413, 2020.

[16] S. Zhao and H. Chen, "Modeling the epidemic dynamics and control of COVID-19 outbreak in China," *Quantitative Biology*, vol. 8, no. 1, pp. 11-19, 2020. doi: 10.1007/s40484-020-0199-0.

[17] D. Okuonghae, and A. Omame, "Analysis of a mathematical model for covid-19 population dynamics in Lagos, Nigeria," *Chaos Solitons and Fractals*, vol. 139, 2020.

[18] W. Ajisegiri, O. Odusanya, and R. Joshi, "Covid-19 outbreak situation in Nigeria and the need for effective engagement of community health workers for epidemic response," *Global Biosecurity*, vol. 1, no. 4, 2020.

[19] S. A. Onitilo, D. O. Daniel and H. A. Haruna. "Modeling analysis of coronavirus epidemic in Nigeria using Lyapunov functions," *FUW Trends in Science & Technology Journal*, vol. 6, no. 2, pp. 627-632, 2021.

[20] I. I. Oke, Y. T. Oyebo, O. F. Fakoya, V. S. Benson, and Y. T. Tunde, "A Mathematical Model for Covid-19 Disease Transmission Dynamics with Impact of Saturated Treatment: Modeling, Analysis and Simulation," *Open Access Library Journal*, vol. 8, no. 5, pp. 1- 20, 2021.

[21] R. Li, S. Pei, B. Chen, Y. Song, T. Zhang, W. Yang and J. Shaman, “Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV2),” *Science*, vol. 368, no. 6490, pp. 489-493, 2020.