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Modelling the transmission dynamics of Omicron variant of COVID-19 in densely populated city of Lagos in Nigeria

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Abstract

The kernel of the work in this article is the proposition of a model to examine the effect of control measures on the transmission dynamics of Omicron variant of coronavirus disease in the densely populated metropolis of Lagos. Data as relate to the pandemic was gathered as officially released by the Nigerian authority. We make use of this available data of the disease from 1st of December, 2021 to 20th of January, 2022 when omicron variant was first discovered in Nigeria. We computed the basic reproduction number, an epidemiological threshold useful for bringing the disease under check in the aforementioned geographical region of the country. Furthermore, a forecasting tool was derived, for making forecasts for the cumulative number of cases of infection as reported and the number of individuals where the Omicron variant of COVID-19 infection is active for the deadly disease. We carried out numerical simulations of the model using the available data so gathered to show the effects of non-pharmaceutical control measures such as adherence to common social distancing among individuals while in public space, regular use of face masks, personal hygiene using hand sanitizers and periodic washing of hands with soap and pharmaceutical control measures, case detecting via contact tracing occasioning clinical testing of exposed individuals, on the spread of Omicron variant of COVID-19 in the city. The results from the numerical simulations revealed that if detection rate for the infected people can be increased, with majority of the population adequately complying with the safety protocols strictly, then there will be a remarkable reduction in the number of people being afflicted by the scourge of the highly communicable disease in the city.

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1. Introduction

Most humans inhabiting the planet earth are currently under the yoke of COVID-19 pandemic; mankind is being tormented once again as it was on planet earth in 1918 when a worldwide pandemic occurred. Though the origin of the current pandemic is shrouded in mystery, the pandemic was reported to have first broken out in the city of Wuhan in China, in the year 2019, where a number of individuals who fell ill after having patronised a market where sea foods are sold in Wuhan. They were admitted to hospitals in December 2019, they were first diag-

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nosed with pneumonia [1]. As of 22nd of January 2020, 571 cases of individuals infected with the coronavirus disease were confirmed as having contacted the disease in several parts of China [1, 2]. As of 30th January, 2020, there was confirmation of 7734 cases in China while 90 individuals infected with the disease were reported across Europe involving 13 countries; America and some parts of Asia [3, 1]. It was reported that through-out the world, a case of about 5,656,615 of COVID-19 has occurred with 355,355 deaths as at May 27, 2020 [4].

The disease was first reported in Nigeria on February 27, 2020 [5], with 8,733 cases resulting in 254 deaths and 5,978 active cases of infection requiring treatment, whereas 2,501 cases of discharged patients were reported by May 27, 2020. As of 23rd July, 2020, a total number of 38,948 cases, with 833 deaths, and 22,887 active number of cases of individuals undergoing treatment in different isolation centres were announced by the Nigerian authority as a nationwide situation of the disease while as of the same date, particularly for Abuja, one of the epicentres of the disease, 2,957 total number of cumulative cases and 78 new cases, 39 deaths, and 2,042 active cases of COVID-19 were announced. However, it is worth mentioning that for a country of over 200 hundred million people, only less than half a million people were tested for the virus, unlike the United States, China, Canada and other advanced countries of the world have tested millions of their people for the virus. Obviously, hundreds of thousands of cases might have been detected in Nigeria if adequate tests were carried out. The expectation is that it will become very clear the correct situation of the disease in Nigeria as there is improvement in contact tracing and the rate of testing [6].

When a healthy individual makes contact with an infected person, then there will be human-to-human transmission of the disease by way of inhaling droplets from the atmosphere or making contact with contaminated surfaces [7]. It is revealed through clinical evidence that the range of incubation period of the disease is between 2 to 14 days, in which case, infected people not showing any symptoms of the disease and may not be conscious of having being infected of the deadly disease during this period are capable of transmitting the disease to those around them. Coughing, breathing difficulties, and fever, are the symptoms of the disease [8]. It should be noted that there are no antiviral drugs or vaccines that have been discovered for the prevention or management of deadly disease for now [9]. Consequently, heavy reliance is on detecting in time and the quarantine of symptomatic individuals as measures for guiding against the spread of the disease. Among other strategies to combat the spread of the disease are impositions of lockdown, strict enforcement of safety protocols, avoidance of crowded events, wearing of highly efficacious face masks by individuals while in public spaces, maintenance of a specific distance between individuals [10].

Mathematical models are a great way to study the transmission and control of contagious illnesses (see the models in [6,11-17]). A number of researchers have developed mathematical models to examine the transmission and control of coronavirus disease in a number of nations. This include deterministic model without demographic parameters but incorporating non-pharmaceutical control measures through which a study of the transmission dynamics of the deadly disease in Nigeria was made [6]. In their findings, they discovered that when the inhabitants of the sub-Saharan country can adhere strictly to the COVID-19 safety protocol, the affliction associated with the scourge of the highly contagious disease will be adequately mitigated and the curve of the transmission of the disease will be ultimately flattened in no time. In their work, Khan and Atagana proposed a deterministic model with fractional order derivatives, through which they obtained approximate solution to the system of fractional order differential equations so formulated [18]. Likewise, Muhammed and Atangana formulated a system of fractional order differential equations to gain insights into the dynamics of the transmission of the disease. Using real life data obtained from the city of Wuhan, they did simulation of their model through which some thresholds as regards the control of the disease in the community were obtained. Major recommendation from their work was that scientists must expedite action at obtaining cure for the disease so that humanity can be saved from the scourge of the deadly disease [8]. Sowole et al studied the early stage of the disease using regression model to make forecast and projections that will help in the control of the spread of the disease [19]. Waku et al proposed an approach on how to estimate the highest number of reproduction numbers of COVID-19. They made recommendations has to measures that can be put in place to bring the values of the reproduction numbers down towards effectively controlling the spread of the highly communicable disease in a community [20].

As a result, the primary goal of this research is to develop a system of nonlinear equations that can be used to investigate the extent to which non-pharmaceutical strategies can be used to combat the scourge of coronavirus disease in Nigeria. The major aim of this work is the provision of the detailed assessment of the spread of the disease in the city. We shall do this by parameterizing our model, applying the number of cases of infection reported and the number of actively infected individuals in Lagos as obtained from the statutory authority officially saddled with such a responsibility. Consequently, we will do the quantitative study of the model by using relevant data gathered carefully towards assessing the impact of the afore-mentioned non-pharmaceutical measures such as adherence to safety protocols for COVID-19 on the spread of the disease in Lagos. The sole purpose of doing this is to be able to make forecasts and projections towards ascertaining the time the curve of the spread of the disease will be flattened.

Consequently, the scope of this work is formulation of deterministic epidemiological model without demographic parameters in form of system of non-linear differential equations by incorporating the safety strategies to adequately capture the dynamics of the transmission of coronavirus vis-à-vis the safety protocols being enforced by the Nigerian health policy makers that are needed to put under control the spread of the disease. While the specific objectives of the study are:

(i) To rigorously analyse the model for its basic properties: local and global asymptotic stability with a view to obtaining thresholds needed as necessary and sufficient con-

ditions for the effective control of the spread of the disease.

(ii) To compute the final size of the epidemic in Lagos city, Nigeria.

(iii) To carry out uncertainty and sensitivity analysis that will help determining the top rank parameters that play dominant role in the dynamics of the spread of the deadly disease with a view to making them available for the health care policy makers to target towards effectively controlling the spread of the disease in Nigerian community.

(iv) To do data fitting to our model using real life data that were obtained from the relevant Nigeria authority for the disease control towards estimating adequate parameter values that will be needed to carry out numerical simulations of the model so formulated.

(v) Using some parameters values so obtained from data fitting to model initially carried out in addition to other parameters values so obtained from literature, we shall conduct numerical simulation of the model with a view to obtain imitation of current real life realities as it pertains to COVID-19 disease.

(vi) To develop a predictive tool that will be of help to make forecasts and projections about the dynamics of the disease.

(vii) To interprete the plots gotten from the numerical simulations of the model with a view to ascertaining measures that will help in the control of the spread of the disease.

(viii) To make adequate recommendations that will be of great help to healthcare policy makers in formulation of policies that will help curtail the spread of the disease and ultimately help put it under control.

The following, therefore, is how we organized this article. The formulation of the mathematical modeling of the disease was given in section 2. In section 3, we established the model's basic features and their stability. Following that, in section 4, we ran numerical simulations of the model, fitted pertinent data to the model for the time period under consideration, and presented the numerical results.

2. Description of how the model was formulated

The total inhabitants of the city at time (t), represented by $N(t)$ has its components being susceptible individuals $S(t)$, exposed latently-infected individuals $E(t)$, exposed individuals that are latently-infected and quarantined $E_Q(t)$, infected individuals that are asymptomatic $I_A(t)$, infected individuals that are symptomatic $I_S(t)$, infected individuals who are asymptomatic and symptomatic and who are diagnosed via contact tracing occasioned by testing $I_D(t)$, infected individuals who are treated after case detection $I_T(t)$ and those people who recovered from the disease $R(t)$. It is presumed that those in the $I_D(t)$ class are people in isolation centres and are segregated from the general population. Thus,

$$N(t) = S(t) + E(t) + E_Q(t) + I_A(t) + I_S(t) + I_D(t) + I_T(t) + R(t)$$

The susceptible population class $S_U(t)$ are made up of all living individuals in the geographical region under consideration, people progressed out of this class at the rate $\lambda = \frac{\beta_c(\alpha I_A + I_S + \eta_T I_T)}{N-(E_Q+I_D+I_T)}$, where λ is the force of infection, α being the tuning parameter which accounts for the decreased infectiousness in the infected asymptomatic class $I_A(t)$ as compared to individuals in the $I_S(t)$ class; η_T (for $\eta_T \geq 1$) is the risk associated with infectiousness of individuals in the treated class $I_T(t)$ in comparison with individuals in the classes $I_A(t)$ and $I_S(t)$; and β_c is the effective rate of contact with infected person, with the fraction, f, where $0 < f < 1$ is for individuals that progressed to latently-infected class $E(t)$ and the remaining fraction $(1-f)$ are for the individuals who are latently-infected and progressed to $E_Q(t)$ class. The progression rate for individuals moving from $E(t)$ to latently-infected quarantined class $E_Q(t)$ is given by δ while those that progressed from $E_Q(t)$, do so at the rate $q\sigma$ and $(1-q)\sigma$ to actively infected classes $I_A(t)$ and $I_S(t)$ respectively for $0 < q < 1$ while the individuals that progressed from these actively-infected classes to the class of those that are diagnosed of the disease via contact tracing and testing in the class $I_D(t)$ do so at the rate θ and Ψ respectively. Individuals that moved from detected infected class progress at the rate γ_j while individuals that recovered from actively infected classes $I_A(t), I_S(t), I_D(t)$ and treated class $I_T(t)$ do so at the rate γ_a,γ_i, γ_0, and γ_b respectively.

The proposed nonlinear system of differential equations are as follows (see Figure 1 for a schematic diagram and table 1 for a summary of the model's variables and parameters):

$$\begin{aligned}
\frac{dS}{dt} &= \frac{-\beta_c(\alpha I_A + I_S + \eta_T I_T)}{N-(E_Q+I_D+I_T)}S \\
\frac{dE}{dt} &= \frac{f\beta_c(\alpha I_A + I_S + \eta_T I_T)}{N-(E_Q+I_D+I_T)}S - \delta E \\
\frac{dE_Q}{dt} &= \frac{(1-f)\beta_c(\alpha I_A + I_S + \eta_T I_T)}{N-(E_Q+I_D+I_T)}S + \delta E - \sigma E_Q \\
\frac{dI_A}{dt} &= q\sigma E_Q - (\theta+\gamma_a) I_A \\
\frac{dI_S}{dt} &= (1-q)\sigma E_Q - (\Psi+\gamma_0+d_0) I_S \\
\frac{dI_D}{dt} &= \theta I_A + \Psi I_S - \left(\gamma_i + d_D + \gamma_j\right) I_S \\
\frac{dI_T}{dt} &= \gamma_j I_D - (\gamma_b + d_T) I_T \\
\frac{dR}{dt} &= \gamma_i I_D + \gamma_a I_A + \gamma_0 I_S + \gamma_b I_T
\end{aligned} \tag{1}$$

The model's assumptions are listed as follows:

(i) Since we are dealing with a pandemic in this work, then demographic parameters, natural birth rate, and death rate are excluded from our model in line with similar previous works [6,9,21-14].

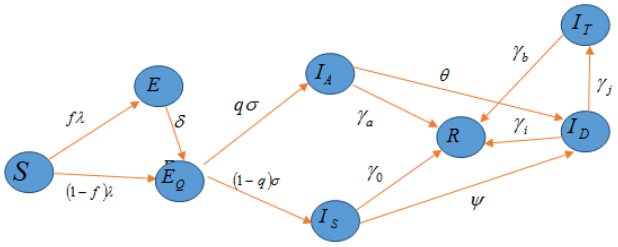

Figure 1. Schematic diagram of model (1) with $\lambda = \frac{\beta_c(\alpha I_A + I_S + \eta_T I_T)}{N-(E_Q+I_D+I_T)}$.

(ii) Susceptible individuals who made contact with infected individuals diagnosed of COVID-19 after testing are quarantined and are in class $E_Q(t)$ of the model.

(iii) In line with clinical evidence, people undergoing treatment are open to being infected with the disease. Due to strong antibodies that often kill the virus in healthy individuals before it starts wreaking havoc in the system, there is natural recovery from the infection with the disease.

(iv) Death rates due to the disease are the same in all infected compartments of the model.

Our model (1) is an extension of models that have been formulated towards gaining insights into how the novel coronavirus disease is transmitted from one person to another, such as those in [6,18,25-33], by inter alia:

(i) Introducing a compartment for exposed individuals who come in contact with confirmed infected individuals diagnosed of the disease after contact tracing occasioned by testing; note that works on COVID-19 existing in literature such as those in [6,18,31-33] do not include this compartment in their model.

(ii) Introducing a compartment for infected individuals undergoing treatment of one form or the other in isolation centres. Note that this is not obtainable in the models in [6,25,26,33,34].

(iii) Introducing parameters to represent COVID-19 common safety protocols such as the use of efficacious face masks, maintenance of minimum social distance among individuals while in public, in the force of infections of the model as to adequately capture reality circumstances as it relates to the control of the disease, and these are missing in the models in [18,25,31,33,34].

We reformulated our model (1) by introducing the safety strategies to adequately capture the dynamics of the transmission of coronavirus vis-à-vis the safety protocols being enforced by the Nigerian health policy makers to put under control its spread represented by parameters, where ρ stands for the fraction of the inhabitants of the city that maintain the minimum distance, at least one metre apart, required to prevent an infection, so that $0 \leq \rho \leq 1$, parameter ε represents the proportion of the inhabitants of the city that effectively wear highly

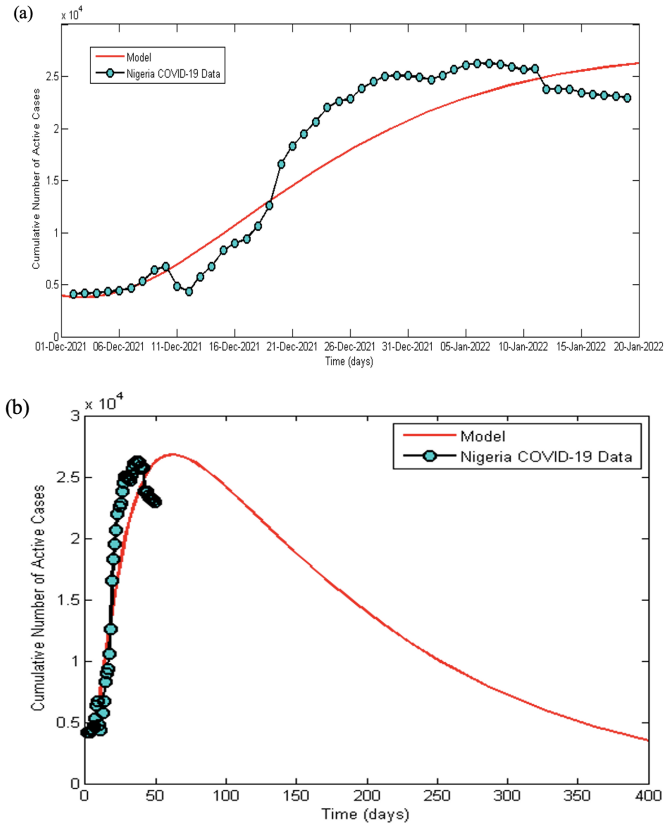

Figure 2. Plot on cumulative number of active cases showing (a) Data fitting of the cumulative number of active cases (b) Projection on the cumulative number of active cases.

efficacious face masks at any time they are in public, so that $0 \leq \varepsilon \leq 1$. Another parameter ω stands for the proportion of the inhabitants of the city that effectively indulge frequently in personal hygiene involving periodic use of hand sanitizers and washing of hands with soaps when they interact with surfaces that may be contaminated, so that $0 \leq \omega \leq 1$. When these are incorporated into model (1), we have:

$$
\begin{aligned}
\frac{dS}{dt} &= \frac{-\beta_c(1-\rho)(1-\varepsilon)(1-\omega)(\alpha I_A + I_S + \eta_T I_T)}{N-(E_Q+I_D+I_T)}S \\
\frac{dE}{dt} &= \frac{f\beta_c(1-\rho)(1-\varepsilon)(1-\omega)(\alpha I_A + I_S + \eta_T I_T)}{N-(E_Q+I_D+I_T)}S - \delta E \\
\frac{dE_Q}{dt} &= (1-f)(1-\rho)(1-\varepsilon)(1-\omega)\lambda S + \delta E - \sigma E_Q \\
\frac{dI_A}{dt} &= q\sigma E_Q - (\theta+\gamma_a) I_a \\
\frac{dI_S}{dt} &= (1-q)\sigma E_Q - (\Psi+\gamma_0+d_0) I_S \\
\frac{dI_D}{dt} &= \theta I_A + \Psi I_S - \left(\gamma_i + d_D + \gamma_j\right) I_D \\
\frac{dI_T}{dt} &= \gamma_j I_D - (\gamma_b + d_T) I_T \\
\frac{dR}{dt} &= \gamma_i I_D + \gamma_a I_A + \gamma_0 I_S + \gamma_b I_T
\end{aligned} \tag{2}
$$

Note that in this work, the circumstance under consideration is the Nigerian government's strict adherence to COVID-19

Table 1. Parameters and their interpretation for model (1)

Parameter	Interpretation
β_c	Effective transmission rate
δ	Rate of progression from exposed latently-infected compartment to exposed quarantine compartment
σ	Progression rate from exposed latently-infected quarantine compartment to infectious state
q	Fraction of new infectious individuals that progressed to infectious asymptomatic and symptomatic infected class.
f	Fraction of infectious individuals that progressed from susceptible class to
f	exposed classes.
η_T	The risk of infectiousness of individuals in the treated class $I_T(t)$ in comparison with individuals in other infectious classes.
α	Modification parameter to account for reduction in infectiousness of individuals in the $I_A(t)$ compartment when compared to individuals in the $I_S(t)$ compartment.
$\gamma_a, \gamma_0, \gamma_i, \gamma_j$	Rate of recovery for individuals in infected compartments $I_A(t)$,$I_S(t)$, $I_D(t)$ and $I_T(t)$ respectively.
Ψ	Rate of detection obtained through contact-tracing and testing for the individuals in infected symptomatic class $I_S(t)$.
θ	Rate of detection obtained through contact-tracing and testing for the individuals in infected asymptomatic class$I_A(t)$
ε	Proportion of the inhabitants of the city that effectively wear highly efficacious face masks at any time they are in public.
ρ	Fraction of the inhabitants of the city that maintain the minimum social distance
ω	Proportion of the inhabitants of the city that effectively indulge frequently in personal hygiene.
d_0, d_D, d_T	Death rates due to the disease for those in the infected class $I_S(t)$, $I_D(t)$ and $I_T(t)$ classes respectively.

safety protocols, which includes proper wearing of face masks and maintaining a minimum distance between members of the society, which were vigorously promoted and enforced, particularly in Lagos, Nigeria's commercial nerve centre and the epicentre of the pandemic, since the pandemic have been wreaking havoc in the city.

Towards gaining insights into the dynamical features of the disease so as to combat its spread, we now rigorously analyse our model (2).

3. Dynamical Features of model (2)

The norm in mathematical epidemiology is that when a new mathematical model is formulated to study the transmission dynamics of contagious diseases, such model will be analysed for its dynamical features. Consequently, in this section, we now do the qualitative study of the dynamical features of the transmission dynamics of model (2).

3.1. Analysis of the model

3.1.1. Positivity and boundedness of the model

In order for our model to make sense epidemiologically, there is compelling need to prove that for all time(t), all the state variables contained in the model are non-negative and are greater than zero, and there is the need to show that each of the equations in the model is bounded. This is what we do in this section. The following is claimed:

Theorem 3.1. *Let us assume that the inceptive data for the model* (2) *be* $S(0) \geq 0, E(0) \geq 0, E_Q(0) \geq 0, I_A(0) \geq 0, I_S(0) \geq 0, I_D(0) \geq 0, I_T(0) \geq 0, R(0) \geq 0$. *Consequently, solutions* $(S(t), E(t), E_Q(t), I_A(t), I_s(t), I_D(t), I_T(t), R(t))$ *of the model* (2) *are positive for all time* $t > 0$.

Proof: let $t_1 = sup\{t > 0 : S(t) > 0, E(t) > 0, E_Q(t) > 0, I_A(t) > 0, I_S(t) > 0, I_D(t) > 0, I_T(t), R(t) \in [0, t]\}$. Hence, $t_1 > 0$. By considering the first of the equations in model (2), we have: $\frac{ds}{dt} = -\lambda S$ where $\lambda = \frac{f\beta_c(1-\rho)(1-\varepsilon)(1-\omega)(\alpha I_A + I_S + \eta_T I_T)}{N-(E_Q+I_D+I_T)}$

Which can be rewritten as: $\int \frac{ds}{dt} = -\int \lambda S$, so that $S(t_1) = S(0)\left[-\int_0^{t_1} \lambda(u)\, du\right] > 0$. By following the same procedure, it can be shown that $E(0) \geq 0$, $E_Q(0) \geq 0$, $I_A(0) \geq 0$, $I_S(0) \geq 0$, $I_D(0) \geq 0$, $I_T(0) \geq 0$, $R(0) \geq 0$.

Lemma 1. *Given that region*

$$D = \left\{(S(t), E(t), E_Q(t), I_A(t), I_s(t), I_D(t), I_T(t), R(t)) \in \mathbb{R}_+^8 : N(t) \leq N(0)\right\}.$$

Then D *is positively-invariant, and it attracts all positive solutions of the model* (2).

Proof. Taking the summation of all the equations of the model (2), we have:

$$\frac{dN}{dt} = -(d_0 I_S + d_D I_D + d_T I_T)$$

, which when rewritten gives:

$\frac{dN}{dt} \leq \delta N$, with $\delta = min\,(d_0, d_D, d_T)$.

Thus, $\int \frac{dN}{dt} \leq -\int \delta dt$

So that $N(t) \leq N(0)e^{-\delta t}$

$N(t) \to N(0)$,as $t \to \infty$. Hence, the domain D is positively-invariant. Consequently, all the solutions in $\mathbb{R}^7_+$ is attracted to region D.

Since the domain D is positively-invariant, it is sufficient to investigate the dynamics of the flow generated by the Omicron variant of COVID-19 model (2) in D. Consequently, the model (2) is both mathematically and epidemiologically well posed.

3.2. *The disease-free equilibrium (DFE) of the model* (2)*: its local asymptotic stability*

By setting each of the expressions on the right-hand-sides of the equations in eqn. (2) to zero, the DFE for coronavirus disease model (2) is obtained, which is given by:

$$\xi_0 = \left(S^*(t), E^*(t), E^*_Q(t), I^*_A(t), I^*_S(t), I^*_D(t), I^*_T(t), R^*(t)\right) = (N(0), 0, 0, 0, 0, 0, 0, 0)$$

We investigate the linear stability of the DFE using the next generational operator technique on equation (2). The matrix of new infection terms denoted by F and that of transfer terms denoted by V, using the notations in [35] are stated as follows respectively and setting:

$$F = \begin{pmatrix} 0 & 0 & fB_0\alpha & fB_0 & 0 & fB_0\eta_T \\ 0 & 0 & (1-f)B_0\alpha & (1-f)B_0 & 0 & (1-f)B_0\eta_T \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \delta & 0 & 0 & 0 & 0 & 0 \\ -\delta & \sigma & 0 & 0 & 0 & 0 \\ 0 & -q\sigma & \theta+\gamma_a & 0 & 0 & 0 \\ 0 & -(1-q)\sigma & 0 & k_1 & 0 & 0 \\ 0 & 0 & -\theta & -\Psi & k_2 & 0 \\ 0 & 0 & 0 & 0 & -\gamma_j & \gamma_b + d_T \end{pmatrix}$$

, where $B_0 = \beta_c(1-\rho)(1-\varepsilon)(1-\omega)$, $k_1 = \Psi + \gamma_0 + d_0$ $k_2 = \gamma_i + d_D + \gamma_j$. The controlled reproduction number, represented as $R_0 = \rho\left(FV^{-1}\right)$ is given by:

$$R_0 = \frac{B_0\left(\alpha q\sigma B_3B_4B_5 + B_1B_2B_4B_5 + \eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2)\right)}{\sigma B_1B_3B_4B_5} \quad (3)$$

Where $B_1 = \theta + \gamma_a, B_2 = (1-q)\sigma, B_3 = \Psi + \gamma_0 + d_0$, $B_4 = \gamma_i + d_D + \gamma_j, B_5 = \gamma_b + d_T$.

Consequently, from [35] the basic reproduction number of the model (2),R_0, is rewritten as:

$$R_0 = \frac{B_0\alpha q}{B_1} + \frac{B_0B_2}{\sigma B_3} + \frac{B_0\eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2)}{\sigma B_1B_3B_4B_5}$$

Therefore,

$$R_0 = B_0\left[\frac{\alpha q}{B_1} + \frac{B_2}{\sigma B_3} + \frac{\eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2)}{\sigma B_1B_3B_4B_5}\right] \quad (4)$$

That is, $R_0 = R_A + R_S + R_{I_T}$. The quantity R_0 is the addition of the sub-reproduction numbers associated with the number of new coronavirus disease brought about by asymptomatically-infected individuals (R_A), symptomatically infectious humans (R_S), and detected infectious humans receiving one form of treatment or the other in health care centres (R_{I_T}).

Theorem 2: *The DFE, ξ_0, of the model* (2) *is locally asymptotically stable (LAS) if $R_0 < 1$, and unstable if $R_0 > 1$.*

Proof: We analyse the LAS of the coronavirus model (2) at DFE, ξ_0, by evaluating the Jacobian matrix which is given by:

$$J(\xi_0) = \begin{pmatrix} 0 & 0 & 0 & -B_0\alpha & -B_0 & 0 & -B_0\eta_T & 0 \\ 0 & -\delta & 0 & fB_0\alpha & fB_0 & 0 & fB_0\eta_T & 0 \\ 0 & \delta & -\sigma & M\alpha & M & 0 & M\eta_T & 0 \\ 0 & 0 & q\sigma & -B_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & B_2 & 0 & -B_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & \Psi & -B_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma_j & -B_5 & 0 \\ 0 & 0 & 0 & \gamma_a & \gamma_0 & \gamma_i & \gamma_b & 0 \end{pmatrix}$$

With $M = (1-f)B_0, B_1 = \theta + \gamma_a, B_2 = (1-q)\sigma, B_3 = \Psi + \gamma_0 + d_0, B_4 = \gamma_i + d_D + \gamma_j$, and $B_5 = \gamma_b + d_T$.

The eigenvalues of the Jacobian matrix, $J(\xi_0)$, are the solutions of its characteristic polynomial given below:

$$\lambda^6 + A_0\lambda^5 + A_1\lambda^4 + A_2\lambda^3 + A_3\lambda^2 + A_4\lambda + A_5 = 0, \quad (5)$$

where

$$\begin{aligned}
A_0 &= \delta + \sigma + B_1 + B_3 + B_4 + B_5, \\
A_1 &= \delta\sigma + (\delta+\sigma)(B_1 + B_3 + B_4 + B_5) \\
&+ B_1(B_3 + B_4 + B_5) + B_3B_4 + B_3B_5 + B_4B_5 \\
&- (1-f)B_0(\alpha q\sigma + B_2) \\
A_2 &= \delta\sigma B_1 + B_1B_3(B_4 + B_5) \\
&+ B_4B_5(B_1 + B_3) + (B_3 + B_4 + B_5) \\
&\times (B_1(\delta+\sigma) + \delta\sigma) + \\
&(B_3B_4 + B_3B_5 + B_4B_5)(\delta+\sigma) \\
&\times B_0(\alpha q\sigma(1-f)(B_3 + B_4 + B_5) \\
&+ B_2(1-f)(B_1 + B_4 + B_5) + \delta(\alpha q\sigma + B_2)) \\
A_3 &= B_3B_4B_5(\delta + \sigma + B_1) + (B_1 + \delta\sigma)(B_3B_4 + B_3B_5 + B_4B_5) \\
&+ \delta\sigma B_1(B_3 + B_4 + B_5) + B_0fB_2(B_1(B_4 + B_5) + B_4B_5) \\
&- B_0(\alpha q\sigma(1-f)(B_3B_4 + B_3B_5 + B_4B_5) \\
&+ \eta_T\gamma_j(1-f)(\theta q\sigma + \Psi B_2) + B_2(B_1B_4 + B_1B_5 + B_4B_5) \\
&+ \alpha q\sigma\delta(B_3 + B_4 + B_5) + \delta B_2(B_1 + B_4 + B_5)) \\
A_4 &= B_1B_3B_4B_5(\delta + \sigma) + \delta\sigma B_1B_3(B_4 + B_5) \\
&+ \delta\sigma B_4B_5(B_1 + B_3) + B_0fq\sigma\left(\alpha B_4B_5 + \theta\eta_T\gamma_j\right) \\
&+ B_0fB_1B_2\left(B_4B_5 + \eta_T\Psi\gamma_j\right) - B_0(\alpha q\sigma\delta(B_3B_4 + B_3B_5 + B_4B_5) \\
&+ q\sigma\left(\alpha B_3B_4B_5 + \delta\theta\eta_T\gamma_j\right) + \eta_T\gamma_j(q\sigma\theta B_3 + \delta\Psi B_2) \\
&+ B_1B_2\left(\eta_T\Psi\gamma_j + \delta(B_4 + B_5)\right) + B_2B_4B_5(\delta + B_1)\Big), \\
A_5 &= \delta\sigma B_1B_3B_4B_5(1 - R_0).
\end{aligned}$$

Applying the Routh-Hurwitz criterion which asserts that all roots of the polynomial (5) have negative real parts if the coefficients of A_i are positive, for $i = 0, 1, 2, 3, 4, 5$. Clearly, for $A_5 > 0$ in equation (5); then $R_0 < 1$. Therefore, the DFE ξ_0 is Locally Asymptotically Stable (LAS) if $R_0 < 1$.

Note that the quantity R_0 represent the average number of secondary infections brought about by a typical actively infected individual introduced into a totally susceptible population where COVID-19 safety protocols (control measures) are being implemented [35]. The implication of theorem 2 epidemiologically is that coronavirus disease will be made to die out from the population when $R_0 < 1$, if the model's initial population sizes are within DFE's attraction region. To ensure that covid-19 elimination is independent of the initial sizes of the infected individuals in the population, it is necessary to show that the DFE is globally asymptotically stable.

3.3. Global asymptotic stability (GAS) of the DFE of the model (2)

In view of the fact that the linear Lyapunov function has found wide application to prove the GAS of the DFE [11, 36]. We apply the method as follows via the Lyapunov function:

$$\begin{aligned}\mathcal{L} &= (B_4B_5(\alpha q\sigma B_3 + B_1B_2)\\ &+\eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2))E\\ &+(B_4B_5(\alpha q\sigma B_3 + B_1B_2)\\ &+\eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2))E_Q\\ &+\sigma B_3(\theta\eta_T\gamma_j + \alpha B_4B_5)I_A\\ &+\sigma B_1(\Psi\eta_T\gamma_j + B_4B_5)I_S\\ &+\sigma B_1B_3\eta_T\gamma_jI_D + \sigma B_1B_3B_4\eta_TI_T,\end{aligned} \tag{6}$$

where $B_1 = \theta + \gamma_a, B_2 = (1-q)\sigma, B_3 = \Psi + \gamma_0 + d_0, B_4 = \gamma_i + d_D + \gamma_j, B_5 = \gamma_b + d_T$. With Lyapunov derivatives (where a dot represents differentiation with respect to time).

$$\begin{aligned}\dot{\mathcal{L}} &= (B_4B_5(\alpha q\sigma B_3 + B_1B_2) + \eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2))\dot{E}\\ &+(B_4B_5(\alpha q\sigma B_3 + B_1B_2) + \eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2))\dot{E_Q}\\ &+\sigma B_3(\theta\eta_T\gamma_j + \alpha B_4B_5)\dot{I_A} + \sigma B_1(\Psi\eta_T\gamma_j + B_4B_5)\dot{I_S}\\ &+\sigma B_1B_3\eta_T\gamma_j\dot{I_D} + \sigma B_1B_3B_4\eta_T\dot{I_T}\end{aligned} \tag{7}$$

$$\begin{aligned}\dot{\mathcal{L}} &= (B_4B_5(\alpha q\sigma B_3 + B_1B_2) + \eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2))\\ &\times\left(\frac{f\beta_c(1-\rho)(1-\varepsilon)(1-\omega)(\alpha I_A + I_S + \eta_TI_T)S}{N-(E_Q+I_D+I_T)} - \delta E\right) +\\ &(B_4B_5(\alpha q\sigma B_3 + B_1B_2) + \eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2))\\ &\times\left(\frac{(1-f)\beta_c(1-\rho)(1-\varepsilon)(1-\omega)(\alpha I_A + I_S + \eta_TI_T)S}{N-(E_Q+I_D+I_T)}\right.\\ &\left.+\delta E - \sigma E_Q\right) + \sigma B_3(\theta\eta_T\gamma_j + \alpha B_4B_5)(q\sigma E_Q - B_1I_A)\\ &+\sigma B_1(\Psi\eta_T\gamma_j + B_4B_5)(B_2E_Q - B_3I_S)\\ &+\sigma B_1B_3\eta_T\gamma_j(\theta I_A + \Psi I_S + B_4I_D) +\\ &\sigma B_1B_3B_4\eta_T(\gamma_jI_D - B_5I_A).\end{aligned} \tag{8}$$

Simplifying the above equation, we have:

$$\begin{aligned}\dot{\mathcal{L}} &= (B_4B_5(\alpha q\sigma B_3 + B_1B_2)\\ &+\eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2))\\ &\times\left(\frac{\beta_c(1-rho)(1-\varepsilon)(1-\omega)(\alpha I_A + I_S + \eta_TI_T)S}{N-(E_Q+I_D+I_T)}\right) -\\ &\alpha\sigma B_1B_3B_4B_5I_A - \sigma B_1B_3B_4B_5I_S - \eta_T\sigma B_1B_3B_4B_5I_T\end{aligned} \tag{9}$$

Note: $S(t) \le N(t) - (E_Q(t) + I_D(t) + I_T(t))$ for all time t, so

$$\begin{aligned}\dot{\mathcal{L}} &\le (B_4B_5(\alpha q\sigma B_3 + B_1B_2)\\ &+\eta_T\gamma_j(q\sigma\theta B_3 + \Psi B_1B_2))\\ &\beta_c(1-\rho)(1-\varepsilon)(1-\omega)(\alpha I_A + I_S + \eta_TI_T) -\\ &\sigma B_1B_3B_4B_5(\alpha I_A + I_S + \eta_TI_T)\end{aligned} \tag{10}$$

$$\begin{aligned}\dot{\mathcal{L}} &\le (\alpha I_A + I_S + \eta_TI_T)\\ &\times(\beta_c(1-rho)(1-\varepsilon)(1-\omega)\\ &\times\left(B_4B_5(\alpha q\sigma B_3 + B_1B_2) + \eta_T\gamma_j(q\eta_T\theta B_3 + \Psi B_1B_2)\right)\\ &-\sigma B_1B_3B_4B_5)\end{aligned} \tag{11}$$

$$\begin{aligned}\dot{\mathcal{L}} &\le (\alpha I_A + I_S + \eta_TI_T)\\ &\times\sigma B_1B_3B_4B_5(B_4B_5(\alpha q\sigma B_3 + B_1B_2)\\ &+\eta_T\gamma_j(q\sigma\eta_T B_3 + \Psi B_1B_2))\\ &\times\left(\frac{\beta_c(1-\rho)(1-\varepsilon)(1-\omega)}{\sigma B_1B_3B_4B_5} - 1\right)\end{aligned} \tag{12}$$

$$\dot{\mathcal{L}} \le (\alpha I_A + I_S + \eta_TI_T)\sigma B_1B_3B_4B_5(R_0 - 1) \tag{13}$$

Since all the model parameters are non-negative, it follows that from equation (13), $\dot{\mathcal{L}} \le 0$ for $R_0 \le 1$ with $\dot{\mathcal{L}} = 0$ if and only if $E = 0, E_Q = 0, I_A = 0, I_S = 0, I_D = 0$ *and* $I_T = 0$. Hence, L in equation (13) is a Lyapunov function for the model (2). Therefore, by the LaSalle's invariance principle [37], the DFE of the Omicron variant of COVID-19 model (2) is globally asymptotically stable whenever $R_0 \le 1$.

3.4. Final Size of the epidemic

In this section, we derive a relation between the basic reproduction number corresponding to the model (2) and the size of the epidemic. The final size of an epidemic can be defined as the total number of people experiencing infection during an outbreak. It is typically called the *attack rate* by applied epidemiologist [38]. The final size relation is a relation involving the basic reproduction number and the number of the members of the population that remain in each disease-free compartment over the course of the epidemic [39]. To derive the final size relation, it is necessary to carry out some change of variables of model (2) so as to reduce model (2) into a three dimensional system as observed in [38, 40]. Consequently, we say let $x \in \mathbb{R}_+^6$ represents the set of infected compartments, $y \in \mathbb{R}_+$ represents the susceptible compartment, and $z \in \mathbb{R}_+$ represents the recovered compartment of model (2). That is, variable y is defined as $y(t) = S(t)$, variable x is defined as:

$$\begin{aligned}&x(t) = (E(t), E_Q(t), I_A(t), I_S(t), I_D(t), I_T(t))^T,\\ &\text{and } z(t) = R(t).\end{aligned} \tag{14}$$

We let D be an $m \times m$ diagonal matrix whose diagonal entries $\sigma_i > 0$ are the relative susceptibilities of the corresponding susceptible class: Note that if $m = 1$ then$D$ is a scalar. We let Π be an $n \times m$ matrix with the property that the(i, j)entry represents the fraction of the jth susceptible compartment that goes into the ith infective compartment on becoming infected [40]. We also let b be an n-dimensional row vector of relative horizontal transmissions, this vector is multiplied by the scalar factor representing infectivity [40]. We use β as the infection rate of the coronavirus model (2), for the general incidence this factor is a function of the total population size and / or infective population size and we write it as $\beta(x, y, z)$ [40]. By applying the above transformation to the model (2) we have:
$m = 1, n = 6, b = \begin{bmatrix} 0 & 0 & \alpha & 1 & 0 & \eta_T \end{bmatrix}$, D is the scalar $(1-\rho)(1-\varepsilon)(1-\omega)$ and $\Pi = \begin{bmatrix} f \\ 1-f \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$,

$$\begin{aligned} \dot{x} &= \Pi D y \beta(x, y, z) bx - Vx, \\ \dot{y} &= -D y \beta(x, y, z) bx, \\ \dot{z} &= Wx, \end{aligned} \tag{15}$$

Here, the $n \times n$ matrix V describes the transitions between infected compartments as previously define in section **3.2**. The $k \times n$ matrix W has the property that the (i, j) entry represents the rate at which members of the jth disease compartment go into the ith recovered compartment. The disease-free set $\{(x, y, z) | x = 0, y \geq 0, z \geq 0\}$ is invariant. Suppose that the point $(0, y_0, z_0)$ is referred to as the disease-free equilibrium, then the reproduction number is given as:

$$R_0 = \beta(0, y_0, z_0) bV^{-1} \Pi D y_0 \tag{16}$$

Theorem 3.2: Consider the Omicron variant of COVID-19 model (2), and let $S(\infty) = lim_{t \to \infty} S(t)$. The final size relation of the covid-19 pandemic is given by:

$$\begin{aligned} & ln\left(\frac{S(0)}{S(\infty)}\right) \\ & \geq R_0 \left(\frac{S(0) - S(\infty)}{S(0)}\right) \\ & + \beta \left(\frac{\alpha q}{B_1} + \frac{B_2}{\sigma B_3} + \frac{\eta_T \gamma_j (q\sigma\theta B_3 + \Psi B_1 B_2)}{\sigma B_1 B_3 B_4 B_5}\right)(E(0) + E_Q(0)) \\ & + \beta \left(\frac{\alpha}{B_1} + \frac{\eta_T \gamma_j \theta}{B_1 B_4 B_5}\right) I_A(0) + \beta \left(\frac{1}{B_3} + \frac{\eta_T \gamma_j \Psi}{B_3 B_4 B_5}\right) I_S(0) \\ & + \frac{\beta \eta_T \gamma_j}{B_4 B_5} I_D(0) + \frac{\beta \eta_T}{B_5} I_T(0). \end{aligned} \tag{17}$$

4. Numerical Simulations and Results

In a work of this nature, uncertainties do occur in the estimation of some parameters in the mathematical model representing the transmission dynamics of the novel Coronavirus disease COVID-19, there is a need to carry out an analysis of this, together with sensitivity analysis to determine how sensitive some of the parameters in the model are. These is what we do in this section. Also, to assess the impact of various control strategies necessary to reduce the transmission burden of the disease, we carry out the numerical simulations of the model. The mode of doing this is by solving numerically the equations in model (2) using MATLAB ODE 45 solver which is based on the famous Runge-Kutta method of the fourth order. Note that the stability of our method is well established in [32].

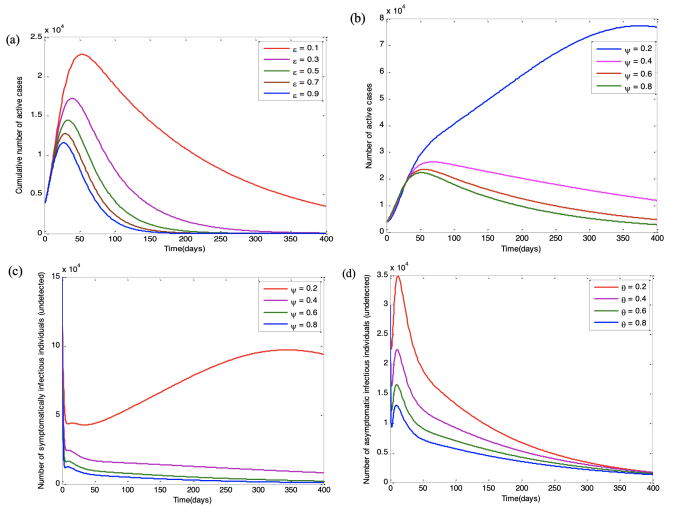

Figure 3. (a) Effects of varying ε on the number of active cases. (b) Effects of varying ψ on the number of active cases. (c) Effects of ψ on the number of symptomatic infectious individuals (undetected). (d) Effects of θ on the number of asymptomatic infectious individuals (undetected).

4.1. Uncertainty and sensitivity Analysis

We implemented Latin Hyper-cube Sampling (LHS) [41] on the parameters of the model in order to do the estimates of parameters involved in the numerical simulations of the model; while we carry out a Partial Correlation Coefficient (PRCC) between values of the parameters in the response function and that derived from the sensitivity analysis for the required (sensitivity) analysis. Tens of Hundred simulations of the model (2) were run in all, where it was observed as shown in table 2, using the reproduction number R_j as the response function that transmission rate β_c, the case detection rates for asymptomatic and symptomatic infectious humans, θ and Ψ, respectively, the modification parameter accounting for infectiousness of asymptomatic infectious humans, α are the top-ranked parameters that drive the dynamics of model (2). From the PRCC results, whereas, β_c and α are positively correlated, on the other hand, θ and Ψ are negatively correlated. It is pertinent to note that the public health implication of this, is that, a reduction in the transmission rate of Omicron variant of COVID-19, achieved through strict adherence to safety protocols involving non-pharmaceutical control measures, such as use of face masks, regular washing of hands and keeping of social distancing and effective treatment of symptomatic infectious individu-

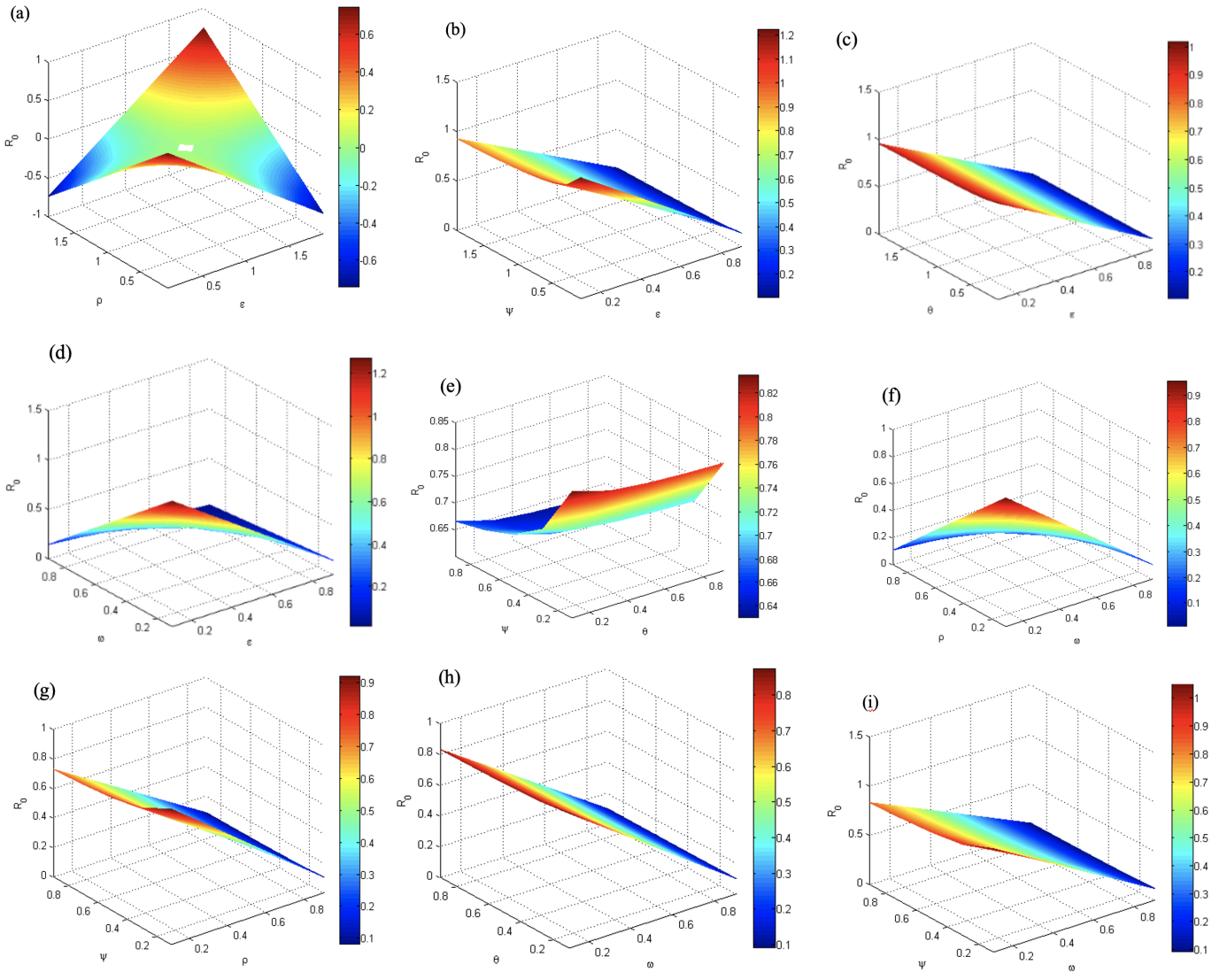

Figure 4. Surface plots showing impacts of various COVID-19 parameters on R_0. (a) Surface plot of R_0 against ε and ρ. (b) Surface plot of R_0 against ε and Ψ. (c) Surface plot of R_0 against ε and θ. (d) Surface plot of R_0 against ε and ω. (e) Surface plot of R_0 against θ and Ψ. (f) Surface plot of R_0 against ω and ρ. (g) Surface plot of R_0 against ρ and Ψ. (h) Surface plot of R_0 against ω and θ. (i) Surface plot of R_0 against ω and Ψ.

als can be a panacea to effective control of the dreaded disease via reduction in transmission rate. Furthermore, when efforts are geared up to increase the detection rates for the asymptomatic and symptomatic infectious individuals towards isolating them for adequate treatment, this will ultimately lead to significant reduction in disease burden of COVID-19 in the population under reference.

By using the number of individuals in the class of those individuals who are symptomatically infected, I_A as the response function, it is the transmission rate, β_c , the fraction of exposed individuals who progress to the class of those asymptomatically infected, q, the transition rate out of the class of those exposed quarantined, σ and the detection rate for asymptomatic infectious humans, θ that play dominant role on the dynamics of the dreaded disease. On the other hand, by using as response function, the number of individuals in the class of those individuals who are symptomatically infected, I_S , we have as driving force in the transmission dynamics of the disease, top-ranked parameters, the transmission rate, β_c, the transition rate out of the class of exposed quarantined individuals, σ, case detection rate for symptomatic infected individuals, Ψ and the fraction of exposed individuals who progress to the class of those asymptomatically infected, q. Furthermore, when we used as response function, the population of those infected individuals that are detected, I_D, the top-ranked parameters that are dominant in the dynamics of the disease are: the transmission rate, β_c, the detection rates symptomatic and asymptomatic infectious individuals Ψ and θ, respectively, the transition rate out of the class of exposed quarantined individuals, σ, and the recovery rate for detected infectious humans, γ_i. Finally, by using the total number of people receiving one form of treatment or the other, in class I_T as the response function, we have effective contact rate

β_c, case detection rate for symptomatic and asymptomatic infected individuals, Ψ and θ, respectively, and the transition rate out of the class of exposed quarantined individuals, σ and the recovery rate for detected infectious humans, γ_b , are the five top-ranked parameters that has strong influence on the dynamics of the disease.

In the table 2, are the values of ePRCC for model (2) parameters where we used the total number of infected individuals and the reproduction number, R_j associated with COVID-19 as response functions. Written in bold fonts are the parameters which has strong influence on the transmission dynamics of the model with respect to each of the response functions.

Table 2. Parameters and the partial correlation coefficient values for model (2). Par represent parameters.

Par	I_A	I_S	I_D	I_T	R_j
β_c	**0.1736**	**0.2784**	**0.2617**	**0.3199**	**1**
δ	−0.0436	−0.0592	−0.0661	−0.0065	−0.0342
σ	0.7541	**0.7459**	0.7849	**0.7483**	0.0730
q	**0.0975**	**0.0664**	−0.0791	0.0551	0.0560
f	0.2553	0.4031	0.3049	0.2674	−0.4443
η_T	−0.0758	0.0014	0.0325	−0.0637	−0.0634
α	−0.0092	0.0408	−0.0705	−0.0868	−0.0141
γ_a	−0.6450	−0.1000	0.0830	−0.0162	0.0503
γ_0	−0.0519	−0.2414	−0.2751	−0.2270	−0.1868
γ_i	0.1369	−0.0229	**−0.1702**	−0.1451	0.0223
γ_j	0.1361	−0.0281	−0.0566	0.3476	0.0018
γ_b	0.1420	0.0179	0.1141	**−0.1971**	0.0242
Ψ	0.1526	**−0.1121**	**0.4083**	**0.3808**	−0.1180
θ	**−0.6935**	0.0070	**−0.0719**	**−0.0551**	−0.0854
d_0	0.0591	−0.2092	−0.2305	−0.0945	0.0732
d_D	0.0718	−0.3151	−0.3295	−0.1352	0.1605
d_T	0.0710	0.0136	−0.2005	−0.0777	0.1634
ω	−0.3589	0.5442	−0.5205	−0.5025	−0.7047
ρ	0.0676	−0.2624	−0.2916	−0.1204	0.1093
ε	−0.4225	−0.5466	−0.4913	−0.4080	−0.7483

4.2. Starting values of the model's parameters

We now implement our model (2) to examine the disease's dynamics in Nigeria using data from the COVID-19 outbreak as reported day-to-day by the Nigeria Centre for Disease Control (NCDC). To perform numerical simulations on the model, we extracted data from 1st of December, 2021 to 20th of January, 2022 when omicron variant was first discovered in Nigeria. We estimate the parameters in the model by fitting the model with the daily cumulative number of active cases in Nigeria obtained from NCDC. The model fitting was performed using the *fmincon* algorithm in MATLAB.

By following the reasoning of Okuonghae and Omame [6] on modelling the dynamics of the pandemic in the city of Lagos, we estimated some of our parameters to be $\sigma = 1/5.2$ per day, $\alpha = 0.5$ per day, $d_0 = d_D = 0.015$ per day and $\gamma_0 = \gamma_a = 0.013978$ per day. On the other hand, we estimated other parameters β_c, θ and Ψ, by fitting the model (2) with the daily "cumulative number of reported cases and number of active cases". Furthermore, we will estimate the starting number of latently infected and infectious persons who were detected in the city in the period the index case for Omicron variant of COVID-19 was reported on the 1st December, 2021, that is, $E(0)$, $E_Q(0)$ and $I_D(0)$; by taking note that the population of Lagos is $14,368,332$ so that we take this value as the starting point, our initial condition for our simulation, thus setting $S(0) = 14,368,332$, while we set $I_D(0) = 1$ and $R(0) = 0$, we do this by considering the reported date of the index case. Logically, there exists some undetected infected individuals among the city's population, owing to the fact that extensive spread screening and testing of the population for the disease had not yet begun. Similarly, for the remaining state variables, it is necessary to estimate the potential values of other beginning conditions, namely: , $E(0)$, $E_Q(0)$, $I_A(0)$, $I_S(0)$, and $I_T(0)$. Table 3 shows the values of the other parameters that we used in our simulations.

Table 3. Parameters and their baseline values for model (2)

Parameter	Baseline value (/day)	Range (/day)	Reference
β_c	Fitted	–	Estimated
α	0.5	$[0, 1]$	[42, 6]
δ	$\frac{1}{5.2}$	$\left[\frac{1}{14}, \frac{1}{3}\right]$	Estimated
σ	$\frac{1}{5.2}$	$\left[\frac{1}{14}, \frac{1}{3}\right]$	[1, 6]
q	0.5	$[0, 1]$	[42, 6]
η_T	0.5	$[0, 1]$	[42, 6]
γ_i	$\frac{1}{15}$	$\left[\frac{1}{3}, \frac{1}{30}\right]$	[42, 6]
$\gamma_a = \gamma_0 = \gamma_b$	0.13978	$\left[\frac{1}{3}, \frac{1}{30}\right]$	[43, 6]]
θ	Fitted	–	Estimated
$d_0 = d_D$	0.015	$[0.001, 0.11]$	[28, 6]
d_T	0.017	$[0.002, 0.12]$	Estimated
Ψ	Fitted	–	Estimated
γ_j	Fitted	–	Estimated

4.3. Model fitting

For our MATLAB-based function optimizer, we use the Genetic Algorithm (GA) for model fitting [44]. The GA approach used in the coding helped us locate the accurate basin of attraction, which provided the starting values of the estimated parameters used in the "*fmincon*" function in the MATLAB optimization toolbox.

To obtain a more accurate estimate, we adopt a combination of two optimization methods for data fitting, the GA method and the *fmincon* method in MATLAB. The implementation of our model fitting is for the period, 1st December 2021 the time that the first case of Omicron variant of COVID-19 was reported in Lagos to 20*th* January. Our choice of the days that the Omicron variant of COVID-19 was afflicting people of Lagos as chosen here is such that we shall be able to capture the disease's dynamics in Lagos and the disease's rate of transmission. We seek to estimate effective transmission rate, rate of detection through testing and contact tracing and the initial conditions $E(0), A(0)$ and $I(0)$. It is pertinent to note that there could be

under reporting in the city caused by little tests performed during the period under consideration. Furthermore, it should be noted that during this period in the city of Lagos, the enforcement of "*social distancing*" and "*use of face masks*" while in public were no longer being adequately and strictly observed too. See table 3 for specific values used for simulations.

4.3.1. Results of simulations when data and model fitting was done using the cumulative number of reported cases of COVID-19 infections

We simulate the model using the data pertaining to daily cumulative number of reported cases of infections within the period under review, noting that except otherwise stated all model fitting was done with settings $\varepsilon = \delta = 0$ as previously explained.

From the plot in Figure 2(a), it was observed that model (2) fitted on cumulative number of active cases. The Cumulative number of active cases of the disease reaches its pick within fifty days, meaning that starting from 1st December 2021 when the Omicron variant of COVID-19 was first discovered in Nigeria, it reaches its peak by end of January 2022 and start declining from first week of February 2022 till date through to in four hundred days' time. (Here we got the peak of the pandemic in Lagos, the epicentre of the disease in Nigeria). From figures 3(c) and 3(d), the effect of increase in detection rate for infected individuals was shown revealing an increase in the number of active undetected symptomatic cases with peak period varying between 35 to 42 days from the start of the discovery of the variant of COVID-19 in Lagos. The number of active cases is expected to reduce after some period as projected in Figure 2(b).

The effects of ε on the number of active cases over some days is shown in Figure 3(a). When ε is small (i.e., $\varepsilon = 0.1$), the cumulative activate cases attained its peak around the first 50 days after which is started showing a monotonic behaviour. As ε increases, the cumulative number of active cases was reducing, attaining peak level within the first 50 days then reducing. This implies that as the proportion of the inhabitants of the city that effectively wear highly efficacious face masks at any time they are in public increases, the cumulative active cases is reducing and after some period of time, the virus is eradicated. We study the effects of Ψ on number of activate cases in figure 3(b) and number of infected symptomatic class. Increasing the rate of detection through contact-tracing and testing for individuals can reduce the number of active cases as shown in figure 3(b), ensuring that COVID-19 (active) cases is eradicated after some days. In a similar reasoning, increasing the rate of detection Ψ help in reducing the number of infected symptomatic class (I_s) as in Figure 3(c). This declining number will take some days before the class I_s can be eradicated. In Figure 3(d), the effects of rate of detection, θ in infected asymptomatic class at varying θ. As θ increases the class I_A is reducing after some days. The peak is attached within the first 20 days after which the number of class I_A shows monotonic behaviour.

The basic reproduction number, R_0 is a threshold parameter for the stability of the disease and is closely related to an epidemic's peak and final size, together with the important parameter can help us to gain insights into the dynamics of the disease. We study R_0 with other parameters as shown in Figure 4. From Figure 4(a), as fraction of the inhabitants of the city of Lagos that maintain the minimum distance increases, this leads to decrease in the proportion of the individuals that effectively use face masks at any time when they are in public, leading to increase in diseases transmission. In Figure 4(b), as the rate of detection of COVID-19 in infected symptomatic class increases, the proportion of the individuals that effectively use face masks reduces, resulting to decrease in disease transmission. In Fig. 4(c), when there is reduction in transmission as a result of increasing rate of detection of infected asymptomatic class even though the proportion of the individuals that effectively wear face masks reduces. The parameters such as minimum distancing, indulging personal hygiene and increasing rate of detection of class I_A can have impact on R_0 as shown in Figures 4(d) – 4(f). The disease transmission can be reduced when there is either increase in rate of detection of class I_S, maintaining social distances or individuals indulging frequently in personal hygiene while in public, the pandemic will be gotten rid of as shown in figures 4(g) – 4(i). Revelation from Figure 4(i) is that if policy makers in Lagos city can increase their case detection rate for infected symptomatic class, then the reproduction number of the pandemic can be flattened below unity such that a great decrease in the disease's burden will be certain.

To effectively manage the transmission of the Omicron in the city of Lagos, we show how different parameters can help to reduce the burden. Wearing of face mask in the public can help to reduce the active cases as people have lesser chance of transmitting disease or getting infected. Increasing the detection rate in both symptomatic and asymptomatic classes is another way of reducing the number of active cases. Then, the surface plots in Figs. 4 shows how combination of some model parameters can help to reduce the spread of the virus.

5. Conclusion

This research study the dynamics of the Omicron variant of COVID-19 in Lagos, the epicentre of the pandemic in Nigeria. We assessed the impact of COVID-19 safety protocols such as keeping of minimum *social distancing* among individuals, regular *hands washing* and *use of sanitizers*, wearing of face masks among the inhabitants of the city while in public spaces. We calculated the pandemic's reproduction number using the available data, and we established a forecast tool for the "*cumulative number of active cases*" using the model developed to capture the disease's dynamics. From model fitting to data and numerical simulations, the effects of COVID-19 safety measures (safety protocols) on the disease's transmission dynamics in the city was assessed. Furthermore, the revelation from this work is that disease transmission can be effectively controlled if detection rate of infected and infectious individuals can be increased, more individuals practice personal hygiene, maintain minimum social distances, as strict observance of these mea-

sures have huge impacts on the transmission dynamics of Omicron variant of COVID-19 (see Fig. 4).

As contribution to knowledge, in future work on the subject matter, optimal control measures can be incorporated into the model towards procuring more adequate measures to effectively combat the scourge of the deadly disease. Consequently, our recommendations towards curtailing the spread of the disease at the community level is that policy makers implement strict measures in order to discover new cases of infection through general screening and testing, in combination with strict observance and compliance with COVID-19 safety protocols, namely: usage of face masks for individuals while in public spaces, regular washing of hands with soap, keeping of minimum social distances so as to be able to obtain considerable reduction of the disease's burden and effectively control it.

Declaration of Competing Interest

The authors declare that there are no known competing interests.

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