03.31.2025 JOURNAL OF

Systematic and Modern Science Research (JSMSR) Vol. 7 No.9

USING NONLINEAR MATHEMATICAL MODEL TO STUDY THE IMPACT OF INFECTIOUS DISEASE ON CORONAVIRUS DISEASE IN A FUZZY ENVIRONMENT

ALHASSAN CHARITY JUMAI[1] AND AKPAGHER, AONDOTSEA CALEB[2]

Department of Mathematics, Edo University, Iyamho

Corresponding Author: charity.alhassan@edouniversity.edu.ng

DOI Link: https://doi.org/10.70382/bejsmsr.v7i9.004

ABSTRACT

Coronavirus disease 2019 (COVID-19, also known as SARS-2) is a contagious disease caused by the coronavirus disease caused by coronavirus SARS-CoV-2. A Mathematical Model for quantitative analysis of COVID-19 in fuzzy environment is formulated and computed the model disease free equilibrium state and analyzed its local stability in a well – defined positively invariant and attracting set Ω for human populations using the next generation matrix. The disease-free equilibrium was proven to be locally asymptotically stable if $\mathcal{R}_t < 1$ and unstable when the $\mathcal{R}_t > 1$. Sensitivity analysis was carried out on the fuzzy reproduction number $\mathcal{R}_t$ in order to

Introduction

Coronavirus disease 2019 (COVID-19) is an illness caused by virus. The virus is called severe acute respiratory syndrome of coronavirus 2 (SARS-CoV-2). It started spreading at the end of 2019 and became pandemic disease in 2020. Coronavirus is termed as zoonotic disease meaning it is transmitted among animals and human and it first started in Wuhan city of Hubei Province. Coronavirus was officially reported to World Health Organization

E-ISSN 3027-2939 P-ISSN 3026-8397

determine the parameters of the model that are most sensitive and be targeted by way of intervention strategy.

Keywords: Nonlinear Mathematical Model, Impact, Infectious Disease, Coronavirus Disease, Fuzzy Environment.

(WHO) on December 31st 2019. A novel coronavirus was identified as the cause by Chinese authorities on 7 January 2020 and was temporarily named 2019 –nCoV (WHO, 2020a). In December 19 2020, confirmed cases of COVID – 19 are 74.299.042, death 1.669.982.

Shortly on January 30th coronavirus was declared as an outbreak of global health emergency by World Health Organization .As of January 21, 2020 World Health Organization (WHO) published the first situation report about the novel coronavirus (2019-ncov),on which the origin of COVID-19,report cases (WHO, 2020a).

Coronavirus primary transmission mode is person-to-person contact through large respiratory droplets containing the SARS-coV-2 virus generated when an infected person exhaled, coughing, sneezing, singing, speaking the droplet falls on the floor or surfaces due to the heaviness to hang on the air and research have shown the survival of this virus on different surfaces that it is viable for up to 72 hours on plastic and stainless, up to 4 hours on copper, up to 24hours on cardboard (WHO, 2020b).

The incubation period of the disease for symptom is 5-6 days and been estimated for those who develop symptoms will do so within 1-14 days of infection. Coronavirus have three stages: early infection marked by viral response, a pulmonary phase, hyper- inflammation sign by host inflammatory response. The early infected stage is associated with fever, dry cough, mild constitutional symptom. The pulmonary phase is associated with shortness of breath with or without hypoxia, hyper-inflammation phase is associated with acute respiratory distress syndrome, shock, cardiac failure (WHO, 2020b).

Anyone can get coronavirus. Most cases of people at risk are those age 60 years and above, and those with underlying medical problem like high blood pressure, heart and lung problem, cancer or obesity, diabetes. However, stay safe by taking some simple precaution such as physical distancing, wearing a mask, keeping rooms well ventilated, avoiding over crowds and close contact, regularly cleaning your hands and coughing into bent elbow or tissue (WHO, 2020c).

World Health Organization recommends that all cases of suspected coronavirus be confirmed using anti body test, which tells whether someone has had an infection in the past, even if they hand not had symptom. Also known as serological tests and usually done on a blood sample (WHO, 2020c).

In Africa, Nigeria in particular record it first case of coronavirus on 27th February 2020 when an Italian citizen who work in Nigeria and returned from Milan, Italy to Lagos. As of 20 July 2021 confirmed cases 179,908 and recovered 166,203 and deaths 2,195 (CDC, 2021a).

Coronavirus is a life threating disease that has claimed millions of lives around the world. The global record of coronavirus case 198964259 and 4232713 deaths as of 5th August 2021. In Africa coronavirus case 6755397 and 171239 deaths (CDC, 2021a).

Vaccination is the administration of a vaccine to help the immune system develop protection from a disease, the vaccine for coronavirus is called Oxford-AstraZeneca COVID-19. Globally, 11 august 2021, there have been 203,944,144 confirmed cases and 4,312,902 deaths of COVID-19. A total of 4,394,596,684 vaccine doses have been administered (WHO, 2021a)

Statement of the Problem

Coronavirus is the disease caused by a new coronavirus called COVID - 19 and it is a zoonotic disease, transmitted by contact from an infected person through respiratory droplet. It is known as an outbreak of global health emergency that has claimed millions of lives and the world population is at risk .As of 22nd of November 2021, the world recorded about 256,966,237

confirmed cases and 5,151,643 deaths, and 7,408,870,760 vaccine doses have also administered globally (WHO,2021b). In Nigeria, the case is not different, 213589 confirmed cases and 2974 deaths (NCDC, 2021a), with this health burden many effort been put in place by epidemiologist and other scientist in finding the dynamics of coronavirus and to control its transmission. Thus, this study aims at modeling the quantitative analysis of COVID – 19 in fuzzy environment.

LITERATURE REVIEW

Epidemiology of COVID - 19

Coronavirus is one of the deadliest infection disease that have claimed millions of lives around the globe. The disease is caused by novel coronavirus called severe acute respiratory syndrome coronavirus (SARS-CoV-2) and transmitted from person to person through a contact from an infected person respiratory droplet containing SARS-CoV-2 virus on the surface or on the floor. The symptoms such as fever, dry cough, shortness of breath, shock, cardiac failure with an incubation period of 5 – 6 days with an estimated 1 – 14 days of infection (WHO, 2020b).

The emergence of coronavirus disease in Wuhan city of Hubei province China has done nothing good than harm by placing the world population at risk. In December 19, 2020 confirmed cases was 74,299,042 and 1,669,982 deaths (WHO, 2020a). Coronavirus accounts for high level of effect or contact rate in people aged 60 years and over, and those with underlying medical problems like high blood pressure, lungs and heart problems, cancer or obesity, diabetes. However, some preventive practices according to world health organization include physical distancing, wearing a face mask, keeping rooms well ventilated, avoiding over crowds and close contact, regularly cleaning your hands, and coughing into bent elbow or tissue (WHO, 2020c).

SARS-CoV-2 infection in children rarely causes severe illness or deaths. When children do exhibit symptom, they are usually mild and may be noon-specific, gastrointestinal disturbance been reported alongside respiratory features

and fever .About 2 month into the pandemic, cases of hyper-inflammatory and or toxic shock-like syndrome began to be reported and this multisystem inflammatory syndrome in children (MIS-C) is now thought to be a rare late manifestation of SARS CoV-2 infection perhaps in individuals who are susceptible either generally or because of comorbidities or both .For this reason, careful monitoring for any such rare disease manifestation remains important in the evaluation of safety of candidate vaccine against COVID-19. Coronavirus is a disease caused by novel called SARS-CoV-2 (severe acute respiratory syndrome), it reduces both B-cell (antibody) and T-cell specific immune response (WHO, 2020c)

A serological focused on the spike (s) and nucleoprotein (NP) although responses to other viral antigens are also reported. There is also interest in antibodies to the receptor (ACE2) binding domain (RBD) of the trimetric protein as these are predicted to interfere with viral entry into the host cell and thus to be neutralizing and protective. Although the relative importance of B and T-cell response in clearance of the virus and in the maintenance of protein remains unclear at this time, there is some evidence that the magnitude of responses is positively associated with the severity of disease, perhaps relating to the size of viral load experienced by the patient (WHO, 2020c).

There is limited risk that SARS-CoV-2 can be transmitted via human milk. WHO recommend that mothers continue to breastfeed their infant. Indeed the main concern in this the ability of the mothers to follow the strict precaution to avoid spreading the virus via the recognized horizontal routes. And no specific antiviral treatment to date has shown significant reduction in mortality. WHO recommends the use of corticosteroids in severe and critically COVID-19 patients and not to be use in other patients for those with mild/moderate illness (WHO, 2020b).

Mathematical Models of Coronavirus Transmission

Tomochi and Kono (2020), proposed a mathematical model for covid-19 pandemic-SIIR model with effects of asymptomatic individuals. They obtained

that presymptomatic individuals have infectivity even during incubation period, asymptomatic individuals can freely move and interact and play a vital role in the spread of infection and that the duration of immunity can be counted, and fixed into the SIIR model which is able to explicitly handle asymptomatic individuals who are delayed or are extremely difficult to be identified in the real world. It is shown that the herd immunity threshold (HIT) increases as the result of asymptomatic individuals compares to the SIR (susceptible- infected-recovered).

Daniel (2020) developed a mathematical model SEIQCRIN which incorporate the SEIR model to study current outbreak of COVID-19 in Nigeria with non-linear forces of infection which is based on the transmission channels in the infection dynamics and impact of the environmental reservoir in the transmission and spread of the disease to humans. In his work the existence of the region where the model is epidemiologically feasible is established, the model comprises of six compartment at a given time respectively which are: the susceptible individuals E(t), asymptomatic infected individuals I(t), infected individuals yet to be isolated Q(t), quarantine individuals Q(t), recovered individuals R(t). The basic reproduction number was obtained using the next generation method and the disease free equilibrium state, the stability of the disease free state which read that is asymptomatically stable if is less than one and unstable if is greater than one been carried out.

Zeb *et al*. (2020) present a mathematical model of COVID-19 containing isolation class, their finding shows that the local stability and global stability depends on the basic reproduction number and the numerical solution is done by non-standard finite difference (NSFD) scheme and Rung-kutta method. Finally they shows that human to human contacts is the potential cause of outbreak of COVID-19. Hence, isolation of the infected human overall can reduce the risk of future COVID-19 spread.

Baek *et al.* (2020) developed a mathematical model for COVID-19 transmission within a 2500-bed tertiary hospital of South Korea SEIR (susceptible-exposed-infected-recovered) model. The model comprises of

four compartment: doctor, nurse, patients, and caregiver and with the following strategies such as front door screening, quarantine unit for newly admitted patients, early testing of suspected infected people and personal protective equipment for both medical staff and visitors were considered. they infer that the early testing (within eight hour) of infected cases and monitoring the quarantine ward for newly patients admitted are effective measure for decreasing incidence of COVID-19 within hospital (81.3 percent and 70 percent clearance of number of cases respectively, during 60day), the front door screening 42 percent effective for detecting suspected cases and the protective measure could reduce the size of hospital outbreaks.

Ahmed *et al*. (2020) developed a mathematical model to investigate the transmission and control of the COVID-19 from human to human. Their finding shows that the calculated basic reproduction number is approximately 1.7031. However two equilibrium points were established; the disease free equilibrium point (DFE) that is locally asymptotically stable whenever the basic reproduction number is less than one, and the endemic equilibrium point which shows that is globally asymptotically stable whenever the basic reproduction number is greater than one. Existence and uniqueness of the solution was established via the technique of fixed-point theorem. Also using the least square curve fitting method in MATLAB optimization toolbox and solved fractional model numerically using the atangana-Toufik numerical scheme with the mathematical analysis is done using ordinary differential equations and fractional differential equations.

Madubueze *et al* (2020) developed a mathematical model for controlling the spread of COVID-19. In their work they obtained the effect of these different control strategies such as time- dependent intervention using optimal control approach. The model is divided into subpopulation namely: susceptible, S(t); Exposed E(t); Quarantined Q(t); Infectious not hospitalized I(t); Hospitalized, isolated infectious J(t); and Recovered R(t). The basic reproduction number and the effective basic reproduction number were computed with and without intervention respectively and the optimal control been carryout using

the pontryagins maximum principle to figure out the optimal strategy to curtail the disease which resulted that the time-dependent intervention reduced the number of exposed and infected individuals compared to time-independent intervention, done, within the first 100 days of the outbreak. Hence, that the multi-intervention need to be deployed early in order to reduce the virus to the barest minimum.

Gweryina *et al.* (2021) developed a mathematical model describing the dynamics of coronavirus disease .Their model is to assess the role of denial on the spread of the pandemic called COVID-19 with non-linear incidence and treatment approach. SEIR model was use for the COVID-19 transmission dynamics using the Beddington-De angelis functional response and Holling type2 treatment on the infectious model. The total population is divided into five class: susceptible people S(t),(who are under risk of contacting the COVID-19); Exposed people E(t), (who are in close contact with infected people but not yet infected); Asymptomatic people A(t),(who harbor the coronavirus without clinical symptom but capable of transmitting the disease); Symptomatic people I(t), (who are infected with coronavirus with clinical symptom and are capable of transmitting the disease); Hospitalized people H(t), (infectious people who are isolated for treatment); and Recovered people R(t), (who survived the COVID-19 infection). In their model the disease free equilibrium and the endemic equilibrium point are globally asymptotically stable whenever the basic reproduction number is less than unity and greater than unity respectively, when this happened the rate of denial of COVID-19 is above its upper bound there by applying optimal control strategies for controlling the spread of disease by pr0tective measure such as hospitalization and maximum treatment efforts using the pontryagin maximum principle.

Lobato *et al.*(2021) developed a deterministic and stochastic SIDR model of the second wave of COVID-19 infection .Their finding shows that an effective methodology for estimating parameters of compartmental models in multiples wave scenarios by means of a dynamics data segmentation

approach and time-dependent function to described the probability of transmission by contact for each wave, a stochastic strategy used for uncertainties of the parameters for a better and realistic result on basic reproduction number , and a constraint is stated into the problem .All data collected from the first of the two countries to experience the second wave of the infection (Germany and Italy), with 166 and 187 days from the beginning of the epidemic respectively. The estimated effective reproduction number for the first wave is close to that obtained by other approaches, for both countries. The results demonstrate that the proposed methodology which is able to find good estimates for all parameters.

All the works reviewed in this study and to the best of our knowledge, none of the author's modelled COVID – 19 in fuzzy environment. Thus, this study aims at modeling the quantitative analysis of COVID – 19 in fuzzy environment

METHODS

Review of the model

We develop a mathematical model for quantitative analysis of COVID-19 in fuzzy environment. The model is classified into five epidemiological classes of human population denoted by $N(t)$ in the mutually exclusive sub-populations: Susceptible human population $S(t)$, Exposed human population $E(t)$, Asymptomatic infected population $I_A(t)$, Symptomatic infected population $I_S(t)$ and Recovered population $R(t)$ all at time t. The model also comprises of the Environmental pathogens compartment denoted by $P(t)$ at time t. The assumptions and parameters of the governing model are considered as follows;

Assumptions of the Model

The following are the assumption considered in this work:

i. The population is compartmentalized into Susceptible human population $S(t)$, Exposed human population $E(t)$, Asymptomatic infected population $I_A(t)$, Symptomatic infected population $I_S(t)$

Recovered population $R(t)$ and Environmental pathogens compartment denoted by $P(t)$ all at time t.

ii. The disease is transferred from one person to another through mass action transmission mode of transmission.

Table 1: State Variables of the Governing Model

Variable	Description
$\overline{S}(t)$	Susceptible human population at time t
$\overline{E}(t)$	Exposed human population at time t
$\overline{I_A}(t)$	Asymptomatic human population at time t
$\overline{I_S}(t)$	Symptomatic human population at time t
$\overline{R}(t)$	Recovered human population at time t
$\overline{P}(t)$	Environmental pathogens compartment denoted by all at time t.

Table 2: Parameters of the Governing Model

Parameters	Description
Λ	Recruitment rate of the susceptible humans
β_1	Transmission rate between susceptible humans and the environmental pathogens
β_2	Transmission rate between susceptible humans and the asymptomatic infectious humans
β_3	Transmission rate between susceptible humans and the symptomatic infectious humans
ψ	Recovery rate of exposed human without immunity
ω	The rate at which the exposed humans become infected
α	Disease induced death rate
θ_A, θ_S	Recovery rate of the asymptomatic and the symptomatic population respectively
η_A, η_S	Rate of virus spread to the environment by the asymptomatic and the symptomatic population respectively

μ_p	Natural removal rate of the environmental pathogens
μ	Natural death rate of humans

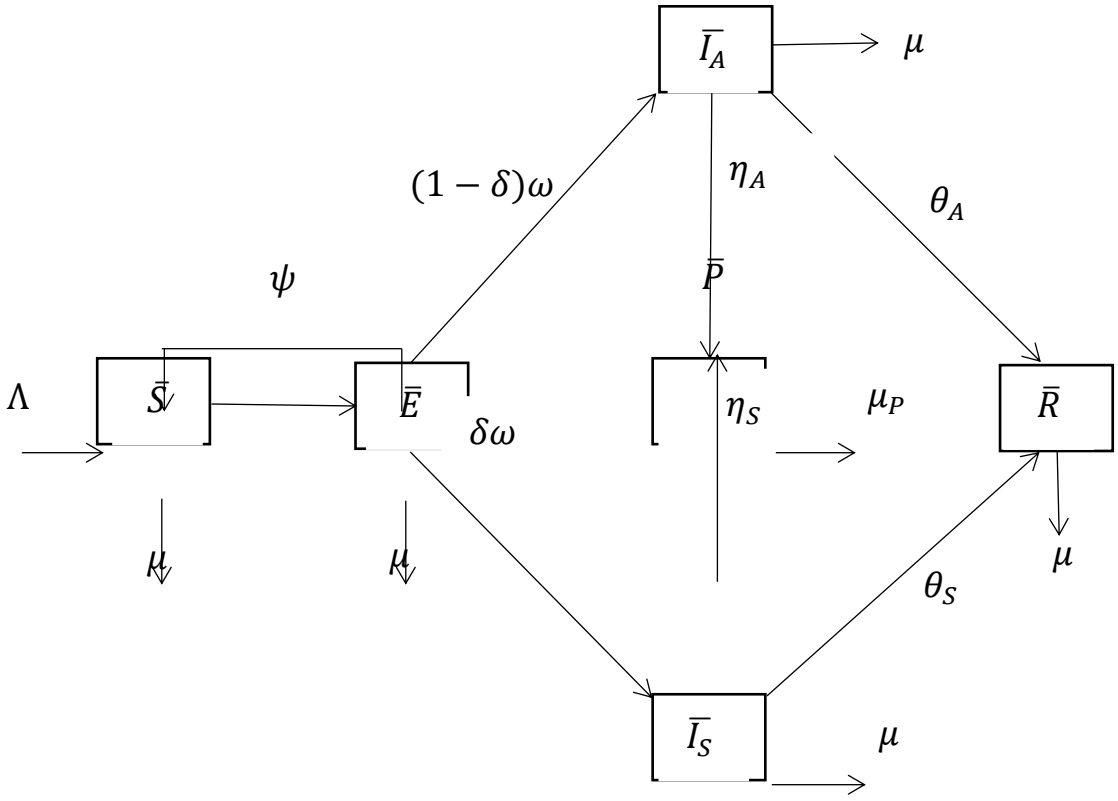

Figure 1: The schematic diagram of the governing model

Equation of the model

The formulated model is based on the assumptions made in section (3.1.1), state variables in Table 1, parameter in Table 2 and the description in figure 1

$$\frac{d\bar{S}}{dt} = \Lambda + \psi E - \lambda S - \mu S \quad (1)$$

$$\frac{d\bar{E}}{dt} = \lambda S - (\mu + \psi + \omega)E \quad (2)$$

$$\frac{d\bar{I_A}}{dt} = (1-\delta)\omega E - (\mu + \alpha + \theta_A + \eta_A)I_A \quad (3)$$

$$\frac{d\bar{I_S}}{dt} = \delta\omega E - (\mu + \alpha + \theta_S + \eta_S)I_A \quad (4)$$

$$\frac{d\bar{R}}{dt} = \theta_S I_S + \theta_A I_A - \mu R \quad (5)$$

$$\frac{d\bar{P}}{dt} = \eta_S I_S + \eta_A I_A - \mu_P P \quad (6)$$

where

$$\lambda = \beta_1 P + \beta_2 I_A + \beta_3 I_S \quad (7)$$

and

$$\eta_S(\Omega) = \begin{cases} 0 & if\ \Omega < \Omega_m \\ \dfrac{\Omega - \Omega_{min}}{\Omega_m - \Omega_{min}} & if\ \Omega_{min} \le \Omega \le \Omega_m \\ 1 & if\ \Omega_m < \Omega \end{cases} \quad (8)$$

With the total human population defined as;

$$N = S + E + I_A + I_S + R \quad (9)$$

Taking the derivative of (9) we obtained;

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI_A}{dt} + \frac{dI_S}{dt} + \frac{dR}{dt} \quad (10)$$

Substituting the respective values of (1) – (5) into (10) and evaluating accordingly we get;

$$\frac{dN}{dt} = \Lambda - (S + E + I_A + I_S + R)\mu - \alpha I_A - \alpha I_S \quad (11)$$

$$\frac{dN}{dt} = \Lambda - \mu N - \alpha(I_A + I_S) \quad (12)$$

Invariant region

This region will be obtained by considering the following proposition.

Proposition 1: The solution of the system (1) – (5) is feasible for all $t > 0$ if they enter the invariant region

$$\Pi = \left\{(S, E, I_A, I_S, R) \in \mathbb{R}^6 : S \ge 0, E \ge 0, I_A \ge 0, I_S \ge 0, N \le \frac{\Lambda}{\mu}\right\}$$

Proof 1:

Let $\Pi = (S, E, I_A, I_S, R)$ be any solution of the system (1) – (5) with non-negative initial conditions.

From (12), we see that in the absence of COVID-19 induced death rate $\alpha = 0$, equation (12) becomes

$$\frac{dN}{dt} \leq \Lambda - \mu N \tag{13}$$

Rearranging (13) we have

$$\frac{dN}{dt} + \mu N \leq \Lambda \tag{14}$$

Solving the differential equation in (14), we have

$$N(t) \leq \frac{\Lambda}{\mu} + Ce^{-\mu t} \tag{15}$$

Applying the initial conditions

$N(0) = N_0$ into (15) gives

$$N_0 - \frac{\Lambda}{\mu} \leq C$$

Such that (3.17) becomes

$$N(0) \leq \frac{\Lambda}{\mu} + \left(\mu_0 - \frac{\Lambda}{\mu}\right) e^{-\mu t} \tag{16}$$

Applying Birkhoff and Rota's theorem on differential inequality (Birkhoff and Rota's, 1989), we get

$0 \leq N \leq \frac{\Lambda}{\mu}, as\ t \to \infty$

Thus, the total population tends to $P = \frac{\Lambda}{\mu}, as\ t \to \infty$

Hence, the feasible solution set of the model (1) – (5) enters the region.

So, $\prod = \left\{(S, E, I_A, I_S, R) \in \mathbb{R}^5 : S + E + I_A + I_S + R \leq \frac{\Lambda}{\mu}, S \geq 0, E \geq 0, I_A \geq 0, I_S \geq 0, E \geq 0, N \leq \frac{\Lambda}{\mu}\right\}$ is positively invariant.

Disease Free Equilibrium

$$\mathcal{E}_0 = (S^0, 0,0,0,0,0) = \left(\frac{\Lambda}{\mu}, 0,0,0,0,0\right) \tag{21}$$

Fuzzy basic reproduction number, $\mathcal{R}_t$

The fuzzy basic reproduction number denoted as $\mathcal{R}_t$ is defined as the expected number of secondary cases produced by a single infection in a completely susceptible population. It is the important parameters that tell us whether an infection will spread through the population or not. The

Therefore, the following definitions are made for fuzzy reproduction number;

$$\begin{aligned}
\mathcal{R}_t^1 &= \frac{\phi_4\beta_2 S^0}{\phi_1\phi_2} \\
\mathcal{R}_t^2 &= \frac{\phi_5\beta_3 S^0}{\phi_1\phi_3} \\
\mathcal{R}_t^3 &= \frac{\phi_4\eta_A\beta_1 S^0}{\phi_1\phi_2\mu_P} \\
\mathcal{R}_t^4 &= \frac{\phi_5\eta_A\beta_1 S^0}{\phi_1\phi_3\mu_P}
\end{aligned} \tag{38}$$

$$\mathcal{R}_t = \begin{cases} \dfrac{\Lambda\omega(1-\delta)(\beta_2\mu_P+\beta_1\eta_A)}{\mu\mu_P(\mu+\psi+\omega)(\mu+\alpha+\theta_A+\eta_A)} \\ + \\ \dfrac{\Lambda\delta\omega(\beta_3\mu_P+\beta_1\eta_s)}{\mu\mu_P(\mu+\psi+\omega)(\mu+\alpha+\theta_S+\eta_S)} \end{cases} \tag{41}$$

Numerical Simulation

In this section, we will carry out numerical simulation of governing model (1) – (5). This is done by using some of the parameters and initial values of the variables whose sources are mainly from the works of Daniel (2020) and Gweryina *et al*. (2021). Tables 3 present the values and their respective sources.

Parameter values

The following tables contain the values of the state variables and parameters to be used in the simulations in the MATLAB programming language.

Table 3: Parameter values for numerical simulations

Parameters	Value	Source
Λ	22655	Gweryina *et al,* (2021)
β_1	0.5	Gweryina *et al,* (2021)
β_2	0.3	Gweryina *et al,* (2021)
β_3	0.1	Gweryina *et al,* (2021)
ω	0.192	Okuonghae (2020)
α	0.031	Okuonghae (2020)
ψ	0.1	Okuonghae (2020)
θ_A	0.143	Gweryina *et al,* (2021)
θ_S	0.072	Gweryina *et al,* (2021)
η_A	0.93	Gweryina *et al,* (2021)
η_S	0.067	Gweryina *et al,* (2021)
δ	0.56	Gweryina *et al,* (2021)
μ_P	0.02	Gweryina *et al,* (2021)
μ	0.00182	Gweryina *et al,* (2021)

Sensitivity analysis of the basic reproduction number with respect to the model's parameters

To determine how best we can do in order to reduce human mortality and morbidity due to Diphtheria Disease, it is necessary to know the relative importance of different factors responsible for its transmission and prevalence. We know that, initial disease transmission is directly related to $\mathcal{R}_e$. We calculate the sensitivity indices of the basic reproduction number, $\mathcal{R}_e$ to the parameters in the model. These indices tell us how vital each parameter is to disease transmission and prevalence. Sensitivity analysis is commonly used to determine the robustness of model predictions to parameter values (since there are usually errors in data collection presumed parameter values). Thus, we use it to discover parameter that have a high impact on $\mathcal{R}_e$ and should be targeted by intervention strategies. The explicit expression for $\mathcal{R}_e$

is given by (41) since $\mathcal{R}_e$ depends only on twelve parameters, we derive an analytical expression using its sensitivity index, see for example (Chitnis *et al.,* 2005) as follows;

A small perturbation δ_ρ of parameter ρ and the corresponding change in $\mathcal{R}_e$ as $\delta\mathcal{R}_e$ is given by

$$\delta\mathcal{R}_e = \delta\mathcal{R}_e(\rho+\delta\rho) - \mathcal{R}_e(\rho) = \frac{\delta\mathcal{R}_e(\rho+\delta\rho)-\mathcal{R}_e(\rho)}{\delta\rho} \approx \delta\rho.\frac{\partial\mathcal{R}_e}{\partial_\rho} \quad (50)$$

The normalized sensitivity index $X_\rho^{\mathcal{R}_e}$ is defined as

$$X_\rho^{\mathcal{R}_e} = \frac{\partial\mathcal{R}_e}{\partial_\rho} \times \frac{\rho}{\mathcal{R}_e} \quad (51)$$

Thus, the normalized sensitivity indices for the twelve parameters are obtained using the values in Table 3 as shown below.

$$S_\beta^{\mathcal{R}_t} = \frac{\partial\mathcal{R}_t}{\Lambda} \times \frac{\Lambda}{\mathcal{R}_C} = +1.0000$$

$$S_\rho^{\mathcal{R}_t} = \frac{\partial\mathcal{R}_t}{\psi} \times \frac{\psi}{\mathcal{R}_t} = \frac{-\psi}{\mu+\omega+\psi} = -0.3358$$

In a similar fashion, we compute the rest of the sensitivity indices for all the parameters used in equation (1) – (6). Table 4 shows the sensitivity indices of $\mathcal{R}_o$ with respect to the fourteen parameters.

RESULTS AND DISCUSSIONS

In this chapter, we present the main findings from the study classified under the following sub-headings:

Sensitivity analysis results

In section, we present our findings from sensitivity analysis results with respect to each parameter that occur in the effective reproduction number

Table 4: Sensitivity indices of $\mathcal{R}_t$ with respect to each parameter

S/No	Parameter	Sensitivity index	Sign
1.	Λ	1.0000	+
2.	β_1	0.9706	+
3.	ω	0.3419	+
4.	η_S	0.2024	+
5.	μ_P	0.0294	+
6.	β_3	0.0215	+
7.	η_A	0.0904	+
8.	β_2	0.0079	+
9.	θ_A	0.0799	−
10.	α	0.0862	−
11.	θ_S	0.1599	−
12.	ψ	0.3358	−
13.	δ	0.4052	−
14.	μ	1.0112	−

Analytical Results of the Governing Model

In this section, we present some results based on the basic properties and stability analysis of the model (1) − (5)

The basic properties of the model

Proposition 1: The solution of the system (1) – (5) is feasible for all $t > 0$ if they enter the invariant region

$$\Pi = \left\{(S, E, I_A, I_S, R,) \in \mathbb{R}^6 : S \geq 0, E \geq 0, I_A \geq 0, I_S \geq 0, R \geq 0, N \leq \frac{\Lambda}{\mu}\right\}$$

Fuzzy basic reproduction number

The following definitions are made for fuzzy basic reproduction number as already explained in equations (38) and (41) respectively;

$$\mathcal{R}_t^1 = \frac{\phi_4 \beta_2 S^0}{\phi_1 \phi_2}$$

$$\mathcal{R}_t^2 = \frac{\phi_5 \beta_3 S^0}{\phi_1 \phi_3}$$

$$\mathcal{R}_t^3 = \frac{\phi_4 \eta_A \beta_1 S^0}{\phi_1 \phi_2 \mu_P}$$

$$\mathcal{R}_t^4 = \frac{\phi_5 \eta_A \beta_1 S^0}{\phi_1 \phi_3 \mu_P}$$

and

$$\mathcal{R}_t = \begin{cases} \dfrac{\Lambda\omega(1-\delta)(\beta_2\mu_P + \beta_1\eta_A)}{\mu\mu_P(\mu+\psi+\omega)(\mu+\alpha+\theta_A+\eta_A)} \\ + \\ \dfrac{\Lambda\delta\omega(\beta_3\mu_P + \beta_1\eta_S)}{\mu\mu_P(\mu+\psi+\omega)(\mu+\alpha+\theta_S+\eta_S)} \end{cases}$$

Local Stability

Theorem 3.1: The disease-free equilibrium of the models is locally asymptotically stable (**LAS**) if $\mathcal{R}_t < 1$ otherwise $\mathcal{R}_t > 1$.

Numerical Results

In this sub – section, we presents the results of our numerical simulations as follows;

Numerical results on the simulation of the model reproduction numbers

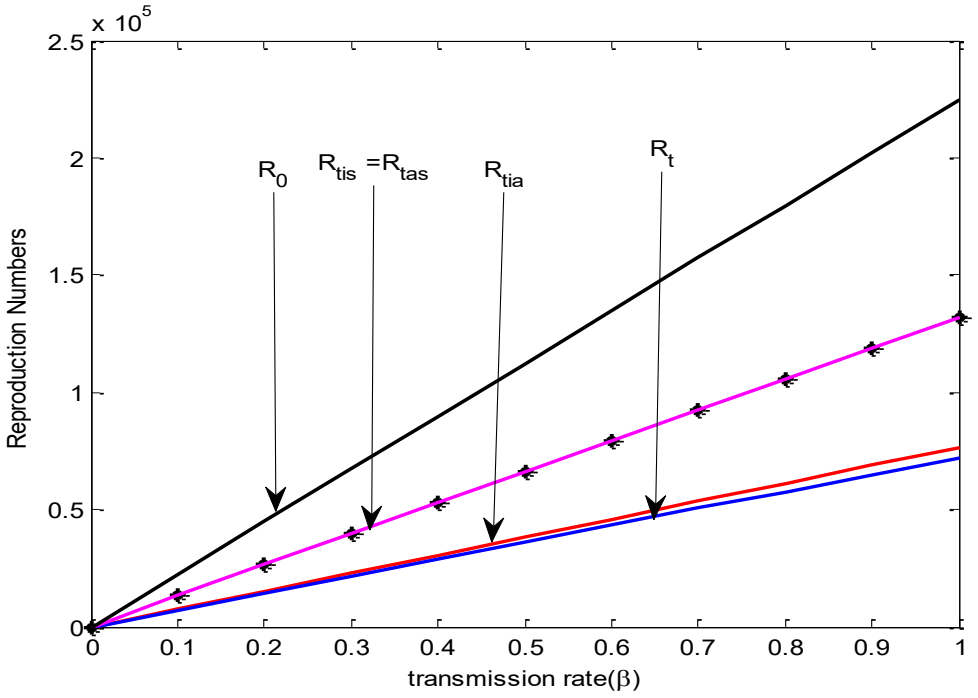

Figure 2: The relationship between reproduction numbers and β changes

Impact of recovery rates θ_A and θ_S on the asymptomatic, symptomatic and the recovered populations

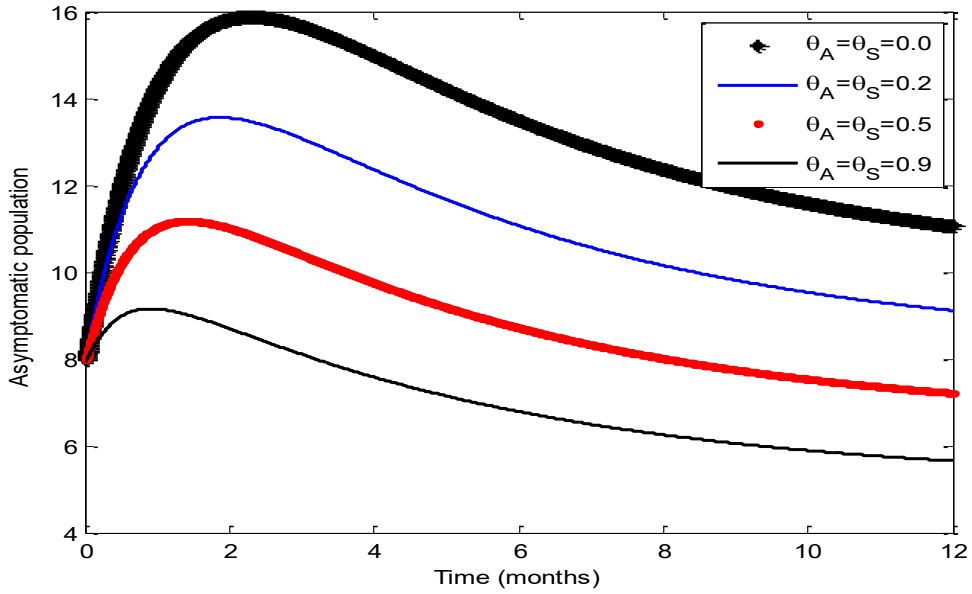

Figure 3: Impact of recovery rates θ_A and θ_S on the asymptomatic populations

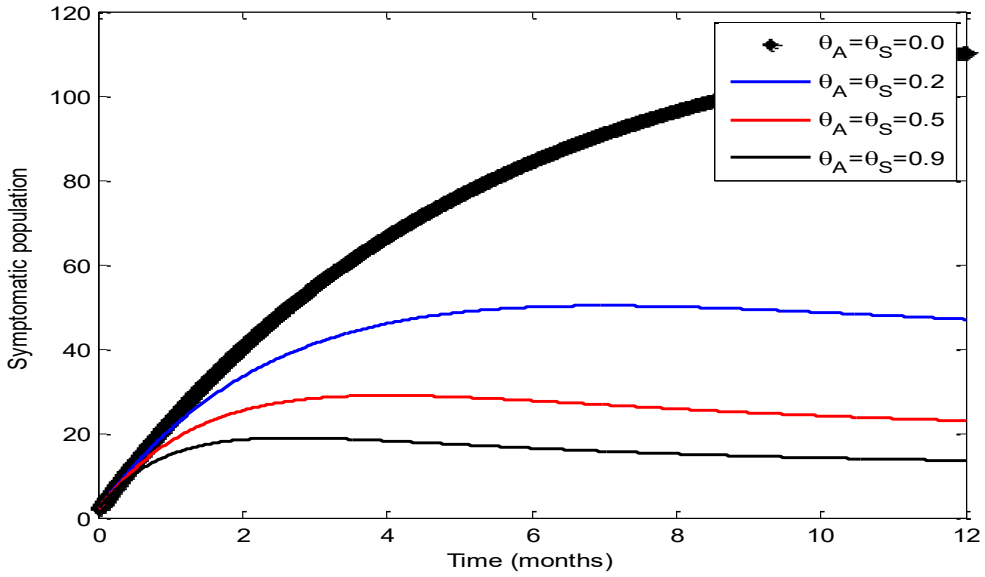

Figure 4: Impact of recovery rates θ_A and θ_S on the symptomatic populations

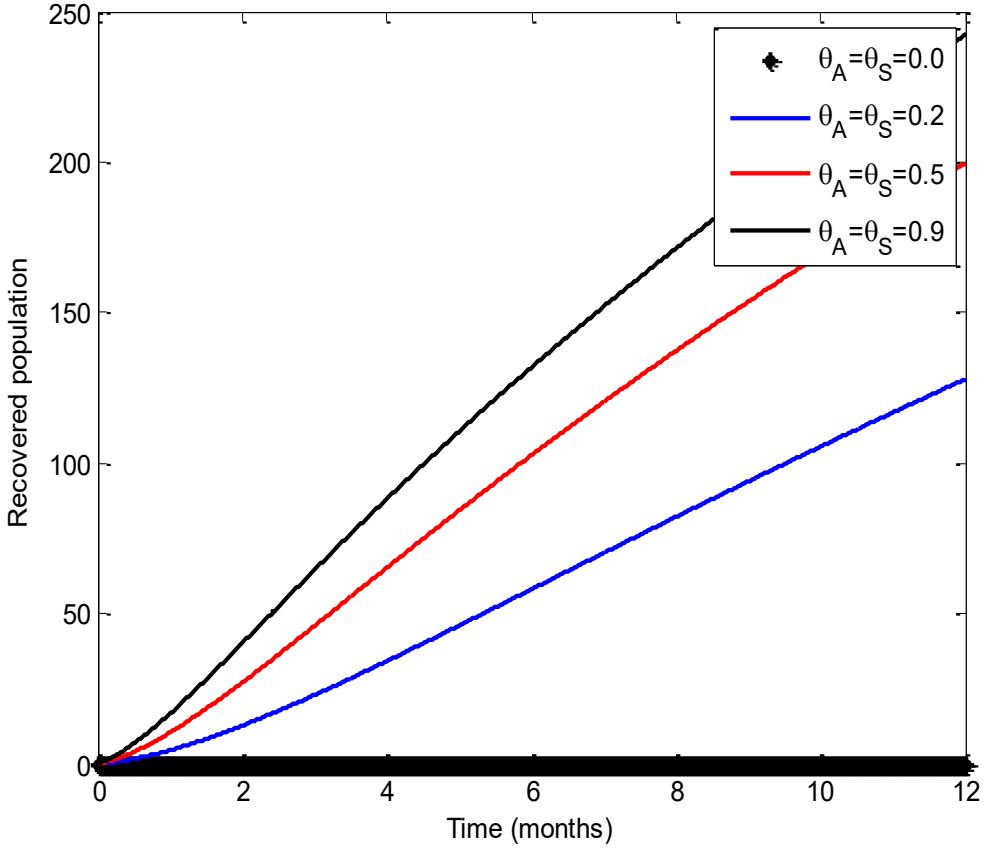

Figure 5: Impact of recovery rates θ_A and θ_S on the recovered populations

Discussion

Interpretation of sensitivity indices

Table 3 shows that, parameters $\Lambda, \beta_1, \beta_2, \beta_3, \eta_A, \eta_S, \mu_P, \psi$ and ω have positive indices, implying that the fuzzy reproduction number increases whenever the values of these parameters increases and they have to be targeted as a way of intervention otherwise a major outbreak may occur. Similarly, parameters $\theta_A, \theta_S, \alpha, \mu, \delta$ and ψ do have negative indices indicating that the fuzzy reproduction number decreases even when the values of these parameters increase. Therefore, in order to control the spread of COVID – 19, recruitment rate and contact between the susceptible and the contaminated environment should be minimized. On the other hand, boosting immune system will go a long way in controlling the spread of COVID – 19 in the population.

Numerical results interpretation

From figure 2, we observed that $\mathcal{R}_0 > \mathcal{R}_{tis} = \mathcal{R}_{tas}$ that is, the fuzzy basic reproduction number $\mathcal{R}_0$ is greater than the fuzzy reproduction number with immunity and recovery rate of the symptomatic individuals $\mathcal{R}_{tis}$ because of the strong immune system and treatment.

Again, we observed that $\mathcal{R}_{tis} = \mathcal{R}_{tas} > \mathcal{R}_{tia}$ that is, the fuzzy reproduction number with immunity and recovery rate of the symptomatic individuals $\mathcal{R}_{tis}$ is greater than the fuzzy reproduction number with immunity and recovery rate of the asymptomatic individuals $\mathcal{R}_{tia}$ because the recovery of the symptomatic individuals will be obvious and that will help in controlling the spread of the disease.

Finally, we also observed that $\mathcal{R}_{tia} > \mathcal{R}_t$ that is, the fuzzy reproduction number with immunity and recovery rate of the asymptomatic individuals $\mathcal{R}_{tia}$ is greater than the fuzzy reproduction number $\mathcal{R}_t$ because boosting immune system and administering effective treatment will go a long way in controlling the spread of COVID – 19 disease in a population.

Based on the analysis above the following relationships holds:

$$\mathcal{R}_t < \mathcal{R}_{tia} < \mathcal{R}_{tis} = \mathcal{R}_{tas} < \mathcal{R}_0$$

From the above inequality, we can conclude that, boosting immune system and administering effective treatment in a sterile environment is a sure way of eradicating COVID – 19 disease in a population as illustrated in figure 2.

Figures 3 – 5 illustrates the impact of recovery rates on the asymptomatic, symptomatic and the recovered populations. Here, we observed that the asymptomatic and the symptomatic individuals decline with increase in the recovery rates meaning, at high recovery rates as a result of maintaining COVID – 19 protocol such as education campaign, social distancing, wearing of face mask to mention a few, the disease will the disease in the population with time. On the other hand, increase in the recovery rates increases the recovered population. The sharp growth in the recovered population clearly shows the effect of the control measures on the disease

CONCLUSION AND RECOMMENDATIONS

Conclusion

In this research work, we formulate a mathematical model for quantitative analysis of COVID-19 in fuzzy environment and computed the model disease free equilibrium state and analyzed its local stability in a well – defined positively invariant and attracting set Ω for human populations using the next generation matrix. The disease-free equilibrium was proven to be locally asymptotically stable if $\mathcal{R}_t < 1$ and unstable when the $\mathcal{R}_t > 1$. Sensitivity analysis was carried out on the fuzzy reproduction number $\mathcal{R}_t$ in order to determine the parameters of the model that are most sensitive and be targeted by way of intervention strategy. The results from the sensitivity analysis shows that; to control the spread of COVID – 19 disease in a population, contact between the susceptible and the infected individuals should be minimized and maintaining strong immune system will go a long way in reducing the spread of COVID – 19 disease in a population. Numerical simulation was also carried out and the results indicate that; boosting immune system and maintaining COVID – 19 protocols will help in eradicating the disease in a population.

Recommendations

i. For total eradication of COVID – 19 disease in a population, we recommend boosting immune system for healthy body system.
ii. We also recommend adherence to COVID – 19 protocols as a sure way for eradicating the disease in a population.
iii. Further research should be carried out on the analysis of the local and global stability of the endemic equilibrium state of the model.

REFERENCES

Ahmed, I., Modu, G.U, Yusuf A. ,Kumam P. , and Yusuf, I. (2020).A mathematical model of COVID-19 containing asymptomatic and symptomatic class .*Result in physics*.21(2021)103776. DOI:https://doi.org/10.1016/j.rinp.2020.103776

Baek, Y.J, Lee, T, Cho, Y., Hyun, J.H, Kim M.H., and Sohn, Y. (2020). A mathematical model of COVID-19 transmission in a tertiary hospital and assessment of the effects of different intervention strategies. *PLoS ONE* 15(10):e0241169. https;//doi.org/10.1371/*journal.pone*.0241169.

Birkhoff, G. and Rota, G.C. (1989). Ordinary Differential Equations.4th Editions New York, John Willey and Sons. NY, USA.

CDC (2021a).Centre for Disease Control and Protection: situation report Available at; https://www.cdc.eroupe Retrieved on 11 August, 2024

Chitnis, N., Hyman, J. M. and Cushing, J. M. (2005). Determining the important parameters in the spread of Malaria through the Sensitivity Analysis of a Mathematical Model. Bulletin of Mathematical Biology, 70:1272 – 1296.

Daniel, D.O. (2020). Mathematical Model for the Transmission of COVID-19 with Non-linear forces of Infection and the need for Prevention Measure in Nigeria. *Journal of Infectious Disease and Epidemiology. 6(5):1-12*.

Diekmann, O., Heesterbeek, J.A.J, and Metz, J.A.J. (1990). On the definition and the computation of the basic reproduction ratio in models for infectious diseases in heterogeneous populations. *Mathematical Bioscience* 28(2):365-382.

Gweryina R.I., Madubueze, C.E, and Kaduna F.S. (2021). Mathematical Assessing of the role of denial on COVID-19 transmission with non-linear incidence and treatment function. *Scientific Africa*. 12(2021):e00811.

Kimbir, A.R., Aboiyar, T., Abu, O. and Onah, E.S. (2014). Modeling Hepatitis B virus transmission dynamics in the presence of vaccination and treatment. *Mathematical theory and modeling,* 4(12):29-43.

Lobato, F.S., Libotte B.G., and Platt M.G., (2021).Mathematical modelling of the second waves of COVID-19 infections using deterministic and stochastic SIDR models. *Non-linear Dynamics*. doi:https://doi.org/10.1007//s11071-021-06680-0.

Madubueze, C.E., Dachollon, S. and Onwubuya O.I. (2020) Controlling the spread of COVID-19; Optimal control analysis .*Computational and mathematical methods in medicine.* doi:https/doi.org/10.1155/2020/6862516.

NCDC (2021a).Nigeria Centre For Disease Control: Coronavirus update in Nigeria. Sourced from: www. https://covid19.ncdc.gov.ng/.com

Tomochi, M. and Kono, M. (2020) Mathematical model of COVID-19 pandemic-SIIR model: Effects of Asymptomatic Individuals. *Journals of General and Family Medicine.* doi:10.1002/jgf2.382.

WHO (2020a). World Health Organisation Report on covid-19 Available at: https:// www.covid-19.who.int/table. Retrieved on 27 October, 2024.

WHO (2020b). World Health Organisation Report on covid-19 Sourced from:https://www.who.int/publication/i/item/who-sage-values-framework-for-the-allocation-and-prioritization-of-covid-19-vaccination.

WHO (2020c). World Health Organisation report on covid-19 Available at:https://www.who.int/docs/default/source/coronavirus-2019/situation/report.

E-ISSN 3027-2939 P-ISSN 3026-8397

WHO (2021a).World Health Organisation report on covid-19 Available at: www.who.int/countries/nga.

WHO (2021b). World Health Organization report on covid-19 Sourced from: https://who.covid19.int/factsheeet.

Zeb, A. Alzahrani, E. Erturk, V.S. and Zman, G. (2020). Mathematical model for the coronavirus disease 2019 COVID-19 containing isolation class. *Biomedical research international.* doi:https://doi.org/10.1155/2020/3452402.