

Research article

Population Dynamics of a COVID-19 Model with Isolation and Non-Linear Recovery Rate

Timothy Terfa Ashezua^{1*}, Ninuola Ifeoluwa Akinwande², Philip Aondofa Wayo³

¹Department of Mathematics, Joseph Sarwuan Tarka University, Makurdi, Nigeria

²Department of Mathematics, Federal University of Technology, Minna, Nigeria

³Department of Mathematics, National Open University of Nigeria, Jabi, Abuja, Nigeria

*Correspondence to: Timothy Terfa Ashezua; ttashezua@gmail.com or timothy.asheszua@uam.edu.ng

Citation: Ashezua TT, Akinwande NI, Wayo PA (2024) Population Dynamics of a COVID-19 Model with Isolation and Non-Linear Recovery Rate. Sci Academique 5(2): 89-101

Received: 3 October, 2024; **Accepted:** 29 October, 2024; **Published:** 6 November, 2024

Abstract

COVID-19 has in recent times created a major health concern in both developed and developing parts of the world. In this wise, there is every need to theoretically explore ways that will provide some insights into curtailing the spread of the disease in the population. In this paper, we present a population model for COVID-19 pandemic incorporating isolation and non-linear recovery rate. The reproduction number was obtained using the next generation method. The disease-free equilibrium (DFE) of the model (1) was found to be locally and globally asymptotically stable whenever the associated reproduction number is less than unity. Results from the sensitivity analysis of the model, using the reproduction number, R_c show that the top parameters that largely drive the dynamics of COVID-19 in the population are COVID-19 transmission rate and the proportion of individuals progressing to the class of reported symptomatic infectious individuals. Numerical simulations of the model shows that increasing the recovery rate of infected patients in the population will lead to an initial decrease in the number of hospitalized patients before subsequent increase. The reason for this could be attributed to the number of unreported symptomatic infectious individuals who are progressing to reported symptomatic infectious stage of infection for immediate isolation.

Keywords: COVID-19, Reproduction number, Isolation, Stability, Nonlinear recovery rate

Introduction

Coronavirus disease 2019 (COVID-19) is a highly contagious infectious disease caused by

severe acute respiratory syndrome coronavirus 2 (SARS-COV-2) Coronavirus are a family of viruses that can cause respiratory illness in human from both developed and developing countries of the world [5]. The disease, accounts for about 6 million deaths globally [9]. Coronaviruses are often found in bats, cats and camels. SARS-COV-2, the virus that causes COVID-19, enters the body through the mouth, nose or eyes (that is, directly from the airborne droplets or from the transfer of the virus from the hand to the face) [5].

The virus can be contracted due to the respiratory droplets released into the air when an infected person coughs, sneezes, talks, sings or breathes near an individual. An individual may be infected if these droplets are inhaled [5]. As stated in Khan et al. [7], isolation of infected individuals play a vital role in managing the spread of an infectious diseases.

Mathematical modelling has been a veritable tool over the years utilized to provide useful insights into the transmission dynamics, prevention and control of infectious diseases [2,14]. Many authors have conducted research works on COVID-19, for example, Samui et al. [12] designed and analyzed a mathematical model to study the reported and unreported cases of COVID-19 in India. In their work, they predicted the possibility of the disease reaching its peak after 60 days and will continue to subsequently persist for a long time. Tang et al. [13] proposed a model for COVID-19 by considering symptomatic individuals to get the patient's epidemiological status and obtained the reproduction number of the model as 6.47. Rai, et al. [10] explored the impact of social media advertisements with quarantine on the spread of COVID-19 pandemic in the presence of asymptomatic, symptomatic and aware individuals. Their research findings emphasized continuous awareness (through social media and internet platforms) and quarantine of asymptomatic individuals as better strategies for reducing COVID-19 burdens in India.

Recently, Akinwande et al. [2] modelled the impacts of media campaign and double dose vaccination in controlling COVID-19 in Nigeria. In their work, a deterministic model with an optimal control problem for assessing the community level impact of media campaign and double dose vaccination on the transmission and control of COVID-19 was studied. Qualitative analysis of the model shows that, the dynamics of the model was completely determined by the reproduction number (R_{mv}). Further, the model was shown to undergo the phenomenon of forward bifurcation in the absence of double dose vaccination effects. Numerical simulation of the model using data relevant to the transmission dynamics of the disease in Nigeria, show that certain values of the basic reproduction number ($R_0 \geq 7$) may not prevent the spread of the pandemic even if 100 percent media compliance is achieved. In all the aforementioned works, non-incorporated non- linear recovery rates in their work. As stated in Khan et al. [7], the nonlinear recovery rate can display rich dynamics such as saddle-node, backward, Hopf, and Bogdanov-Takens bifurcations (BT).

The goal of this paper is to propose a mathematical model for the dynamics of COVID-19 pandemic incorporating isolation and non-linear recovery rate. This model is an extension of the model by Samui et al. [12], by introducing isolation and nonlinear recovery rate. The model is based on the following assumptions:

- The present study incorporates the class of isolated individuals. This assumption is in line with the information obtained from [5].
- This study incorporates the use of nonlinear recovery rate as used in the work of [7].
- This study adopts the use of standard incidence function since it is more appropriate for large population [2].
- This study assumes that the reported symptomatic infectious individuals will no longer contribute to the infection as they are isolated and moved to the Intensive Care Unit (ICU) for treatment [12]. Consequently, the rate at which individuals undergoing treatment will transmit the disease is negligible.

The rest of the paper is organized as follows. The model is developed in Section 2 and analyzed in Section 3. Sensitivity analysis and numerical simulations of the model are presented in Sections 4 and 5, respectively while the concluding remarks in Section 6.

Model Formulation

The total population at time t , denoted by $N(t)$, is divided into the mutually exclusive compartments of the susceptible individuals ($S(t)$), asymptomatic individuals ($A(t)$), reported symptomatic infectious individual ($I(t)$), unreported symptomatic infectious individuals ($U(t)$), hospitalized individuals ($H(t)$) and recovered individuals ($R(t)$).

Infectious interactions in the population are modelled using a standard incidence function and nonlinear recovery rate.

Let Λ represent the recruitment rate of individuals (assumed susceptible) into the population while β is the COVID-19 transmission rate. The terms $\rho\theta$ and $(1-\rho)\theta$ represents the proportion of individuals progressing from class A to I and U , respectively. The parameter η_1 accounts for the reduced rate of transmission of COVID-19 associated with the asymptomatic individuals while η_2 accounts for the rapid rate of transmission of COVID-19 associated with the unreported symptomatic infectious individuals.

Further, individuals who are identified to have COVID-19 in the U class will progress to the I at a rate σ and subsequently moved to the isolation center for treatment at a rate τ . Individuals in the H class who are successfully treated recover at a rate κ . Furthermore, natural death rate occurs in all the classes at a rate μ , while individuals in I and H classes suffer an additional COVID-19 induced death rate δ . Putting together these definitions and assumptions, it follows that the model for the transmission dynamics of COVID-19 in the population is given by the followingsystem of non-linear ordinary differential equations (a flow diagram of the model is shown in Figure 1, and the state variables and parameters of the model are presented in Table 1):

$$\begin{aligned}
 \frac{dS(t)}{dt} &= \Lambda - \lambda S - \mu S, \\
 \frac{dA(t)}{dt} &= \lambda S - [\theta\rho + (1 - \rho)\theta + \mu]A, \\
 \frac{dI(t)}{dt} &= \rho\theta A + \sigma U - (\mu + \delta + \tau)I, \\
 \frac{dU(t)}{dt} &= (1 - \rho)\theta A - (\sigma + \mu)U, \\
 \frac{dH(t)}{dt} &= \tau I - \left[\gamma_0 + (\gamma_1 - \gamma_0) \frac{\phi}{\phi + H} \right] - (\mu + \delta)H, \\
 \frac{dR(t)}{dt} &= \left[\gamma_0 + (\gamma_1 - \gamma_0) \frac{\phi}{\phi + H} \right] - \mu R
 \end{aligned} \tag{1}$$

where

$$\lambda = \frac{\beta(\eta_1 A + \eta_2 U)}{N}, \tag{2}$$

and

$$N = S + E + I + U + H + R. \tag{3}$$

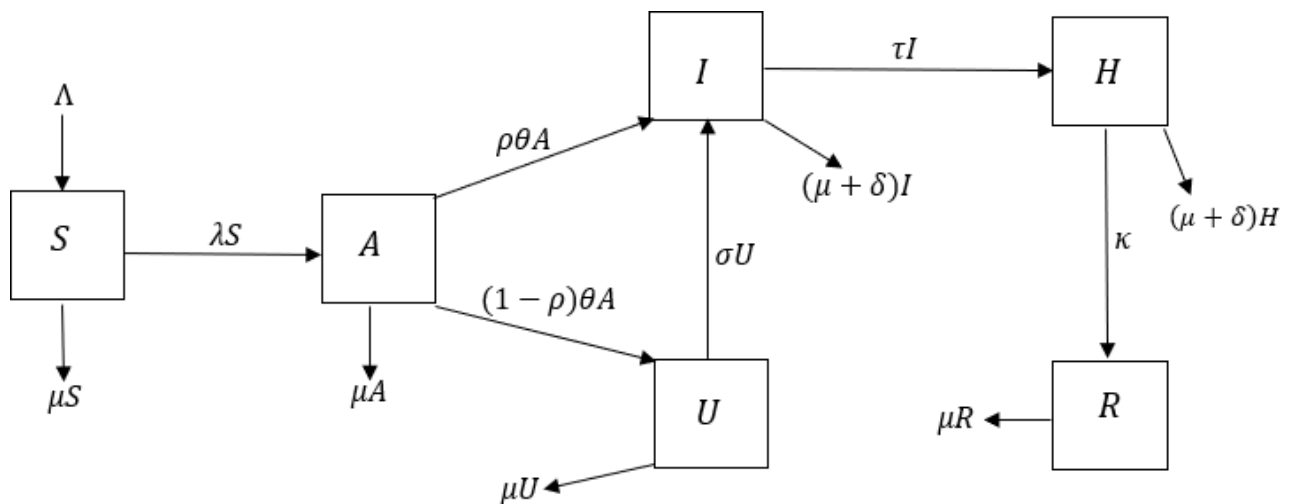


Figure 1: Schematic diagram for model (1)

Variables/parameters	Interpretation
S	Susceptible individuals
A	Asymptomatic individuals
I	Reported symptomatic infectious individuals
U	Unreported symptomatic infectious individuals
H	Hospitalized individuals
R	Recovered individuals
Λ	Recruitment rate
μ	Natural death rate
β	COVID-19 transmission rate
θ	Progression rate
δ	COVID-19 induced death rate
ρ	Proportion of individuals progressing to I
$(1 - \rho)$	Proportion of individuals progressing to U
τ	Isolation rate
σ	Progression rate from U to I
γ_0	Minimum recovery rate
γ_1	Maximum recovery rate
ϕ	Impact of the quantity of clinic beds
η_1	Modification parameter for the asymptomatic individuals
η_2	Modification parameter for the symptomatic individuals
λ	Force of infection

Table 1: Description of state variables/parameters in the COVID-19 model (1).

Basic properties

For model (1) to be epidemiologically meaningful, it is vital to show that all its state variables are non-negative for all time, t . In other words, the solutions of model (1) with positive initial data will remain positive for all $t \geq 0$.

Positivity and boundedness of solution.

Since the model (1) monitors the human population, the state variables and parameters of the model are non-negative. Consider the biologically feasible region.

$$\Gamma = \{(S, A, I, U, H, R) \in \mathbb{R}_+^6 : N \leq \frac{\Lambda}{\mu}\}. \quad (4)$$

It can be shown that the set Γ is a positively invariant set and a global attractor of this system. This implies that, any phase trajectory initiated anywhere in the non-negative region \mathbb{R}_+^6 of the phase space will eventually enter the region Γ and remains in Γ thereafter.

Lemma 2.1. The region Γ is positively invariant for model (1).

Proof. The rate of change of the total population with time is given by

$$\frac{dN}{dt} = \Lambda - \mu N. \quad (5)$$

Since the right-hand side of (5) is bounded by $\Lambda - \mu N$, we can show using a standard comparison theorem [8] that

$$N(t) \leq N(0)exp^{-\mu t} + \frac{\Lambda}{\mu}(1 - exp^{-\mu t}). \quad (6)$$

In particular, if $N(0) \leq \frac{\Lambda}{\mu}$, then $N(t) \leq \frac{\Lambda}{\mu}$. Therefore, Γ is positively invariant.

Hence, no solution path leaves through any boundary of Γ and it is sufficient to consider the dynamics of model (1) in Γ . Hence, in this region, the model can be thus considered as being mathematically and epidemiologically well posed [6].

Mathematical Analysis

Asymptotic Stability of Disease-free Equilibrium (DFE)

The DFE of the model (1) is given by $E_0 = (S(t), A(t), I(t), U(t), H(t), R(t), R^*) = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0\right)$

The local stability of E_0 will be obtained using the next generation operator method [15]. The notations as used in [15] is adopted, the non-negative matrix, F , of new infection terms and the M -matrix, V , of transition terms associated with the model (1) are

$$F = \begin{pmatrix} \eta_1 & 0 & \eta_1 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} k_1 & 0 & 0 \\ -\rho\theta & k_2 & -\sigma \\ -k_3 & 0 & k_4 \end{pmatrix}$$

Where;

$$k_1 = [\theta\rho + (1 - \rho) + \mu], k_2 = (\mu + \delta + \tau), k_3 = (1 - \rho)\theta, k_4 = (\sigma + \mu), k_5 = (\mu + \delta). \quad (7)$$

It follows that the effective reproduction number of the model (1), denoted by R_c , is given by

$$R_c = \rho(FV^{-1}) = \frac{\eta_1}{k_1} + \frac{\eta_2 k_3}{k_1 k_4} \quad (8)$$

where $\rho(FV^{-1})$ is the spectral radius of the matrix (FV^{-1}) .

The result below follows from Theorem 2 in [15].

Lemma 3.1. The DFE (E_0) of the model (1) is locally asymptotically stable if $R_c < 1$ and unstable if $R_c > 1$.

The threshold quantity, R_c is the effective reproduction number of COVID-19 [15]. By definition, it represents the average number of secondary COVID-19 infections generated by a typical infected person in a completely susceptible population [15]. The implication of Lemma 3.1 epidemiologically is that when $R_c < 1$ is less than one, COVID-19 can be eliminated from the population if the initial sizes of the subpopulation of the model are in the basin of attraction of the DFE (E_0) . Hence, a small inflow of COVID-19 infected persons into the community will not generate large COVID-19 outbreaks, and the disease will die out time.

Theorem 3.2. The DFE for the special case of the model (1) with $\theta = \gamma = 0$ is globally asymptotically stable in Γ whenever $\widehat{R}_c \leq 1$.

Proof. Note here that the equations for the infected classes of the model (1) can be written in the matrix-vector form as follows:

$$\frac{dG(t)}{dt} = \left[(F - V) - \left(1 - \frac{S}{N}\right)M \right] G(t), \quad (9)$$

where $G(t) = (E(t), I_a(t), I_s(t), Q(t), R(t))^T$ and the matrices F and V are given in Section 3. Furthermore,

$$M = \begin{pmatrix} \eta_1 & 0 & \eta_2 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

Since M is a nonnegative matrix and $S \leq N$ in Γ , it follows that

$$\frac{dG(t)}{dt} \leq [(F - V)]G(t). \quad (10)$$

Using the fact that the eigenvalues of the matrix $F - V$ all have negative real parts (that is, $\rho(FV^{-1}) < 1$ if $R_c < 1$), it follows that the linearized differential inequality system (10) is stable whenever $R_c < 1$. Thus, by comparison Theorem [8],

$$\lim_{t \rightarrow \infty} (A(t), I(t), U(t), H(t), R(t)) = (0, 0, 0, 0, 0). \quad (11)$$

It can be shown by substituting (11) into (1) that, $S(t) \rightarrow \frac{\Lambda}{\mu}$, as $t \rightarrow \infty$. Hence,

$$\lim_{t \rightarrow \infty} (S(t), A(t), I(t), U(t), H(t), R(t)) = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0 \right) = E_0. \quad (12)$$

Thus, every solution to the equation of the model (1) and initial conditions in Γ , approaches the DFE (E_0) as $t \rightarrow \infty$ whenever $R_c < 1$.

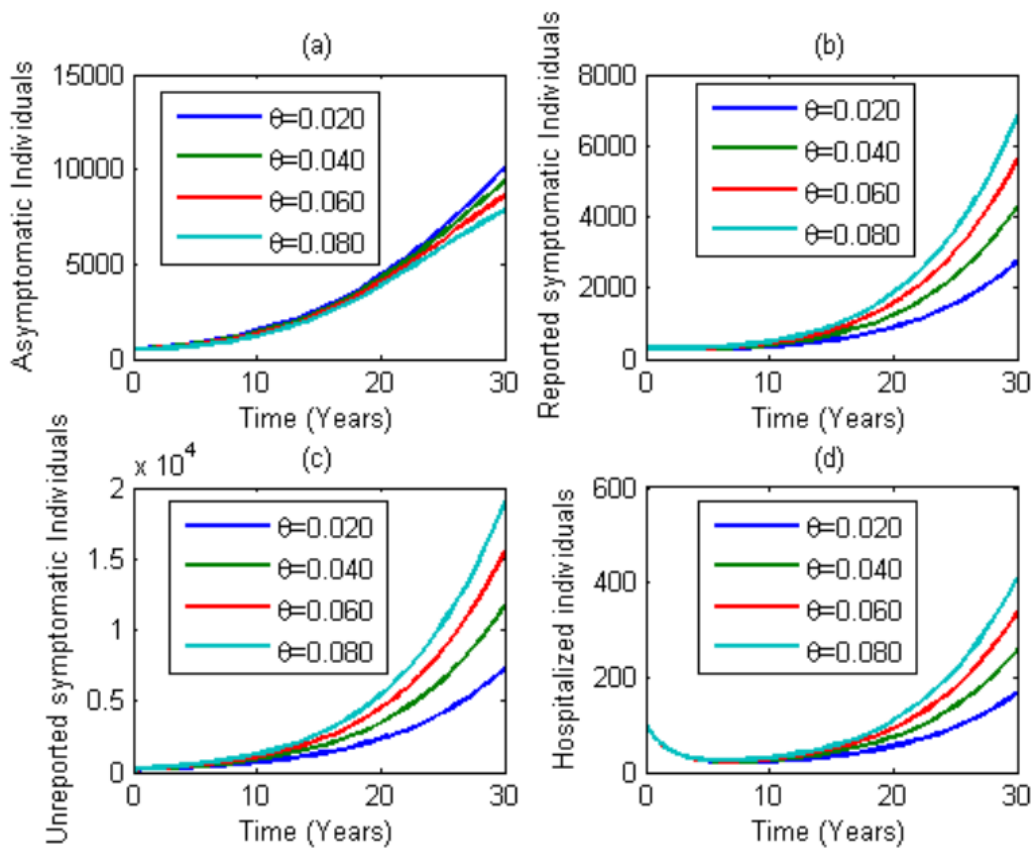


Figure 2: Simulation of model (1) showing the number of infected individuals in the asymptomatic, reported symptomatic, unreported symptomatic and hospitalized individuals. Here, the progression rate (θ) from the asymptomatic to classes I and U is varied from 0.020 to 0.080. Parameter values used are as in Table 2.

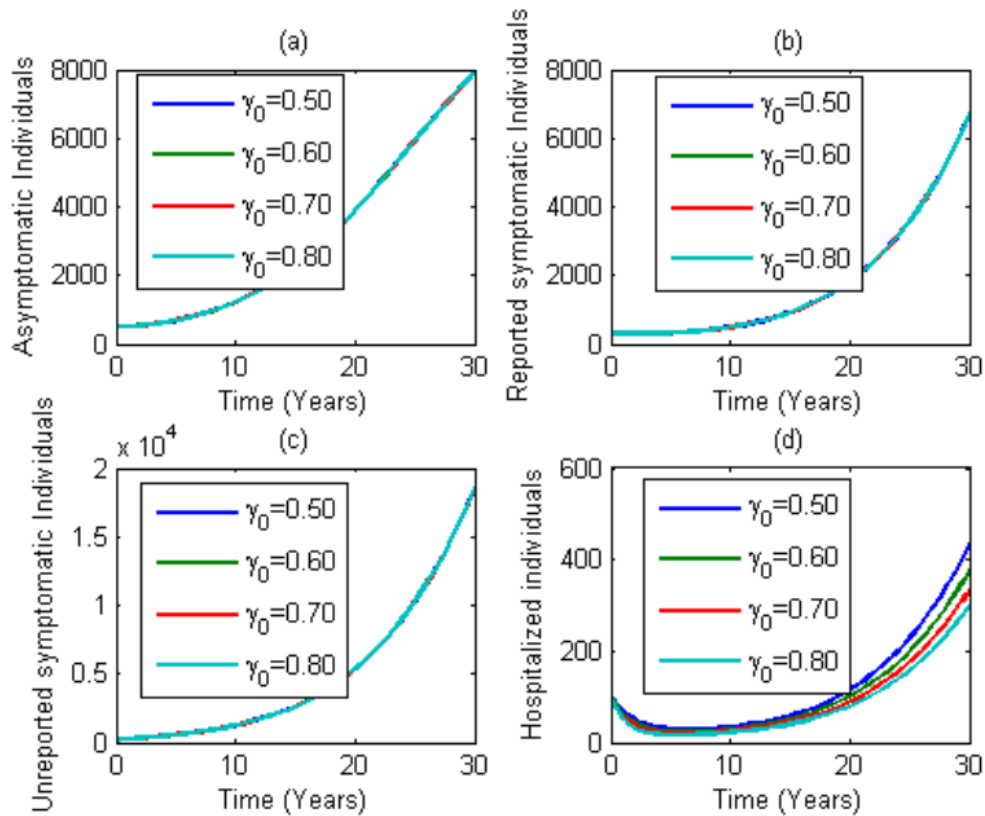


Figure 3: Simulation of model (1) showing the number of infected individuals in the asymptomatic, reported symptomatic, unreported symptomatic and hospitalized individuals. Here, the minimum recovery rate (γ_0) is varied from 0.50 to 0.80. Parameter values used are as in Table 2.

Sensitivity Analysis

In this section, we conduct sensitivity analysis on the parameters of the model connected with the reproduction number, R_c using the parameter values in Table 2. The essence of this analysis is to determine the relative importance of each parameter in the model that depicts COVID-19 transmission. A method similar to the ones outlined in the works of [3,4,11] were utilized to obtain the sensitivity index of all the parameters connected to the reproduction number using the formula in (13).

$$\Pi_p^{R_c} = \frac{\partial R_c}{\partial \xi} \times \frac{\xi}{R_c}, \quad (13)$$

where ξ denotes model parameters contained in R_c . We obtained from (13) the sensitivity indices of the parameters associated with the reproduction number as presented in Table 3. The

parameters with positive sensitivity indices signify a high impact burden of COVID-19 in the population if their values keep increasing. Further, parameters in which their sensitivity indices are negative have a great effect in reducing COVID-19 burden in the population as their values increase while the others remain constant. Hence, as their values increase, the reproduction number decreases thus reducing the endemicity of COVID-19 in the population.

From the results of the sensitivity analysis presented in Table 3, some of the key parameters with high positive and negative indices are the COVID-19 transmission rate (β) and the proportion of individuals progressing to the class of reported symptomatic infectious individuals (ρ), respectively. These are the top parameters that significantly drive the dynamics of COVID-19 in the population. Consequently, to control the spread of the disease in the population, COVID-19 transmission rate (β) must be sufficiently reduced. This implies that as soon as individuals are suspected of having COVID-19 symptoms, they should be quickly isolated for possible treatment if the disease must be curtailed in the population.

Numerical Simulations

In this section, numerical simulations are carried out on model (1) using the parameter values in Table 2. The model (1) is solved numerically using MATLAB ODE45 solver. Figure 4 shows the effect of the progression rate from the asymptomatic class to the reported symptomatic infectious and unreported symptomatic infectious classes. An increase in the progression rate (θ) leads to an increase in the number of asymptomatic, reported symptomatic, unreported symptomatic and hospitalized individuals.

In Figure 3, we observe that, increasing the minimum recovery rate of COVID-19 infected patients leads to an initial decrease in the number of hospitalized patients before subsequent increase. The reason for this could be attributed to the number of unreported symptomatic infectious individuals who are progressing to reported symptomatic infectious class for immediate isolation. It is therefore not surprising that, this parameter had no significant effect on the number of infected individuals in the asymptomatic, reported symptomatic and unreported symptomatic stages of infection. Consequently, concerted effort must be put in place by health experts to identify all unreported cases of COVID-19 for prompt isolation.

Parameter	Nominal value (day^{-1})	Reference
Λ	1000	Assumed
μ	0.01138	[1]
β	0.274	[12]
θ	0.078	[12]
δ	0.031	[1]
ρ	0.072	[1]
τ	0.043	[1]
σ	0.072	[1]
γ_0	0.55	Assumed
γ_1	0.94	[1]
ϕ	0.65	Assumed
η_1	0.40	Assumed
η_1	0.65	Assumed

Table 2: The parameter values of model (1)

Parameter	Sensitivity indices
β	+1.0000
θ	-0.2875
ρ	-0.0454
σ	-0.5053
η_1	+0.4148
η_2	+0.5852

Table 3: Sensitivity indices of some parameters values.

Conclusion

This paper presents a population model for COVID-19 pandemic incorporating isolation and nonlinear recovery rate. The disease-free equilibrium (DFE) of the model (1) is locally asymptotically stable whenever the associated reproduction number is less than unity. The disease-free equilibrium of the model (1) is shown to be globally asymptotically stable whenever the associated reproduction number is less than unity. Results from the sensitivity analysis of the model, using the reproduction number, R_c show that the top parameters that largely drive the dynamics of COVID-19 in the population are COVID-19 transmission rate and the proportion of individuals progressing to the class of reported symptomatic infectious individuals. Numerical simulations of the model suggest increasing the minimum recovery rate of COVID-19 infected patients in the population leads to an initial decrease in the number of hospitalized patients before subsequent increase. The reason for this could be attributed to the number of unreported symptomatic infectious individuals who are progressing to reported symptomatic infectious stage of infection for immediate isolation.

The study is preliminary and can be extended in the following ways:

- By establishing the type of bifurcation model (1) can undergo.
- Theoretical results such as the global asymptotic stability of the unique
- endemic equilibrium can be obtained

Disclosure

Acknowledgements: The authors sincerely appreciate their various institutions for providing a conducive research environment.

Funding: This work did not enjoy funding from any institution or agency.

Competing interests: The authors declare that they have no financial or competing interests

References

1. Akinwande NI, Ashezua TT, Gweryina RI (2022) Mathematical model of covid-19 transmission dynamics incorporating booster vaccine program and environmental contamination. *Heliyon* 8(11): e11513.
2. Akinwande NI, Somma SA, Olayiwola RO, Ashezua TT, Gweryina RI, et al. (2023) Modelling the impacts of media campaign and double dose vaccination in controlling COVID-19 in Nigeria. *Alexandria Engineering Journal* 80: 167–190.
3. Annas S, Pratama MI, Rifandi M, Sanusi W, Side S (2020) Stability Analysis and Numerical Simulation of SEIR Model for pandemic COVID-19 Spread in Indonesia. *Chaos, Solitons and Fractals* 139(110072).
4. Ashezua TT, Gweryina RI, Kaduna FS (2023) Population dynamics of a mathematical model for monkeypox. *International Journal of Mathematical Analysis and Modelling* 6: 40–63.

5. Cleveland Clinic. Coronavirus, covid-19. retrieved on May 20, 2024.
6. Hethcote HW (2000) The mathematics of infectious diseases. *SIAM Rev* 42(4): 599–653.
7. Khan IU, Qasim M, Koufi AM, Ullah H (2022) The stability analysis and transmission dynamics of the sir model with nonlinear recovery and incidence rates. *Hindawi Mathematical Problems in Engineering*.
8. Lakshmikantham S, Leela S, Martynuk AA (1989) Stability Analysis of Nonlinear Systems, Marcel Dekker, New York.
9. National Library of Medicine. Covid-19. retrieved on May 20, 2023.
10. Rai RK, Khajanchi S, Tiwari PK, Venturino E, Misra AK (2020) Impact of social media advertisements on the transmission dynamics of covid-19 pandemic in india. *J. Appl. Math. Comput* 68: 19–44.
11. Rangkuti YM, Firmansyah, Landong A (2022) Sensitivity analysis of seir epidemic model of covid-19 spread in Indonesia. *Journal of Physics: Conference Series*, 2193.
12. Samui P, Mondal J, Khajanchi S (2020) A mathematical model for covid-19 transmission dynamics with a case study of India. *Chaos, Solitons and Fractals* 140: 110173.
13. Tang B, Wang X, Li Q, Bragazzi NL, Tang S, Xiao Y, et al. (2020). Estimation of the transmission risk of the 2019-ncov and its implication for public health interventions. *J. Chin. Med* 9(2): 462.
14. Turkyilmazoglu M (2022) An extended epidemic model with vaccination: weak immune. *Physics A*, 598: 127429.
15. van den Driessche P, Watmough J (2002) Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences* 180: 29–48.