



## A Mathematical Model for Analyzing the Spread of Coronavirus in Nigeria, Including Population Migration Factors

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### Keywords

COVID-19,  
SEIR model,  
Population,  
Migration,  
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### Abstract

This study presents a mathematical model analyzing COVID-19 spread in Nigeria, incorporating population migration and asymptomatic cases. Expanding on the traditional SEIR (Susceptible-Exposed-Infectious-Recovered) model, it uses nonlinear ordinary differential equations to track the dynamics of different population groups. Key parameters, including transmission, immigration, emigration, and death rates, were estimated using data from the Nigeria Centre for Disease Control (NCDC) and fitted with the Nelder-Mead method. Simulations reveal a basic reproduction number ( $R_0$ ) of -0.0095, indicating a high risk of secondary infections. The model shows that symptomatic infections peaked around 20 days before declining, while recovery rates continued to rise. The study emphasizes the importance of adhering to COVID-19 precautions and controlling population migration to mitigate the pandemic's impact. The findings offer valuable insights for effective disease control strategies in Nigeria.

### 1. Introduction

All around the world, infectious illnesses plague communities and cultures. Whenever an infectious illness begins to spread over a population, individuals search for the best ways to stop the outbreak or at the very least reduce the number of infections, this is because the outbreak of any disease cause a massive reduction in the economic growth and development of any nation as several measures will be taken to curb its spread. Researchers have come a long way in the fight against illness. However, infectious infections continue to be a leading cause of death. In epidemiology, the goal is to examine the development of health and illness within a particular community in order to manage associated health issues. The commonly known infectious disease are common cold, influenza, stomach, hepatitis, and coronavirus among others.

Human coronaviruses were first identified in the 1960s and were mostly responsible for gastrointestinal or respiratory illnesses in humans [1]. The coronavirus, also known as SARS-CoV-2 or COVID-19, can be fatal and produces a severe acute respiratory illness. On December 27, 2019, in Wuhan, China, it was initially detected. This illness is very infectious and has already given rise to several strains. Over 187 million cases have been confirmed since the middle of July 2021, and over 4 million deaths have been documented worldwide [2].

Since the outbreak of coronavirus till November 2022, there has been over 634million reported cases worldwide with over 66.1million of this figure on the death toll. Meanwhile, Nigeria has reported over 266000 cases including over 3,155 deaths due to the disease. The Nigerian outbreak, the first confirmed cases of which were reported on February 27, 2020, is unquestionably a real challenge that has posed a serious threat, resulting in lockdowns and business closures. The outbreak's negative effects included widespread employee layoffs and retrenchments throughout the country's various economic sectors, which were caused by a decline in demand for

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goods and services, disruptions in the supply chain, and restrictions on movement, among other things. The Covid-19 epidemic generally affects Nigeria's economy in social, religious, political, and economic domains. The epidemic has caused many individuals to lose their employment, and some people who rely only on one firm for their survival are now regretting it. Meanwhile, relying only on one source of income is like putting all your eggs in one basket, and it might be terrible if that source of money disappears. This is one of the important lessons learned from the epidemic [3].

Along with the Nigerian agriculture and aquaculture industries, it had an impact on other significant industries as well. It raised input and raw material costs, made markets more inaccessible, and decreased the number of walk-in clients visiting farms. This is a result of certain actions made by the government, such as border closures and restrictions on migration [4]. When the cost of food procurement is high in any country, it poses a huge threat of survival for humans and animals in such society. Therefore, there is a need to curb the spread of diseases worldwide.

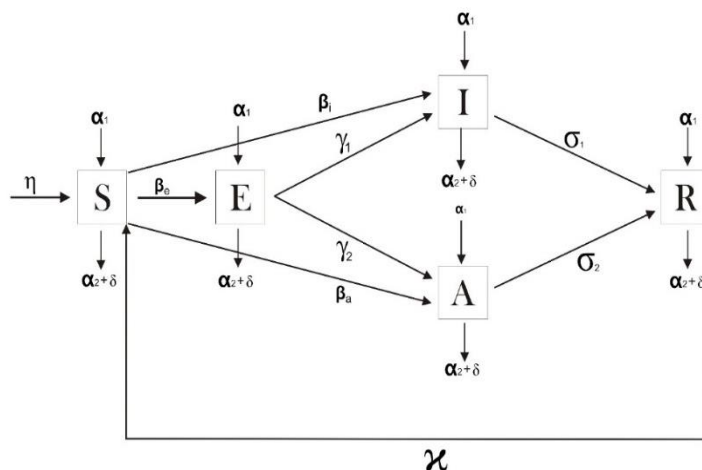
An essential tool for deconstructing and examining the transmission of infectious illnesses is the mathematical model. They aid in comprehension and make forecasting easier. The plausibility of epidemiological explanations is also tested using models. Another use is predicting structural changes through early warning signals and anticipating the potential repercussions of changes in system dynamics, which enables the containment of an emergent disease epidemic.

The underlying premise of mathematical models of epidemics is the ability to partition the observed population into many subgroups, or compartments. In 1927, Kermack and McKendrick provided a description of the most basic compartmental model. The Kermack-McKendrick Model, sometimes known as the KM, is based on very straightforward assumptions about the rates of flow between the various compartments in its current iteration. It uses a latency time and a generic form of transmission to simulate the spread of a contagious disease. The SIR and SEIR models describe non-linear transmission. The impact of immunity against reinfection is taken into account in these models. This suggests that people are moving from the vulnerable class "S" to the exposed class "E" and finally to the infected class "I." Following an infection, people are classified as "R," meaning they have been eliminated from the population of interest, either by immunity or death. This model has a lot of underlying hypotheses. For example, a big and closed population is considered. Additionally, during the epidemics, normal births and deaths are ignored. Other simplifications include homogenous mixing, lifetime immunity upon recovery, and the absence of a latency phase (individuals become infectious as soon as they become infected). Despite being straightforward, the SIR model illustrates the fundamental principles that underlie the transmission of disease in a community: following a potential first epidemic, the infected population either tapers to zero or reaches a stable endemic level [5].

Because of the peculiarities of COVID-19, well-known models like the Susceptible–Exposed–Infectious–Recovered (SEIR) model cannot be applied. And perhaps most crucially, COVID-19 is not just spreading among sick people; it is also spreading among asymptomatic people. More precisely, a new model has to account for, in contrast to earlier SEIR models. There are two categories of COVID-19 exposure characteristics: symptomatic and asymptomatic. It would then be feasible to examine the pathophysiology and dynamic transmission of infectious illnesses and discover the best way to stop the virus from spreading by combining the two kinds into a new model.

With the aim of studying the impact of population migration to SEIR model, this paper introduces a model by incorporating asymptomatic infections, population migration into SEIR, investigates the basic reproduction number of the model, and identifies the curve of the number of infections.

## 2. Model Formation and Analysis



**Figure 1.** Schematic diagram of the population migration SEIAR model showing the interaction of people within the classes of the model

The COVID-19 pandemic is simulated by expanding the SEIR model to include five compartments. Within a population, five state variables are taken into account:  $S(t)$ ,  $E(t)$ ,  $I(t)$ ,  $A(t)$ , and  $R(t)$ , which stand for susceptible, exposed, symptomatic, asymptomatic, and recovered, respectively. The following nonlinear ordinary differential equations then regulate the SEIAR population migration model:

$$\frac{dS}{dt} = \eta + \alpha_1 S - \frac{\beta_i SI}{N} - \frac{\beta_e SE}{N} - \frac{\beta_a SA}{N} + \kappa R - (\alpha_2 + \delta)S \tag{1}$$

$$\frac{dE}{dt} = \frac{\beta_e SE}{N} + \frac{\beta_i SI}{N} + \frac{\beta_a SA}{N} + \alpha_1 E - (\alpha_2 + \delta)E - \gamma_1 E - \gamma_2 E \tag{2}$$

$$\frac{dI}{dt} = \gamma_1 E + \alpha_1 I - (\alpha_2 + \delta)I - \sigma_1 I \tag{3}$$

$$\frac{dA}{dt} = \gamma_2 E + \alpha_1 A - (\alpha_2 + \delta)A - \sigma_2 A \tag{4}$$

$$\frac{dR}{dt} = \sigma_1 I + \sigma_2 A + \alpha_1 R - (\alpha_2 + \delta)R - \kappa R \tag{5}$$

The SEIAR model took population movement and the presence of asymptomatic infected individuals into account. People who are sick but do not exhibit symptoms may nonetheless die from the virus. At time  $t$ , the population density of these groups is represented, respectively, by  $S(t)$ ,  $E(t)$ ,  $I(t)$ ,  $A(t)$ , and  $R(t)$ . Let  $N(t)$  be the entire population at time  $t$ .

Then,

$$S(t) + E(t) + I(t) + A(t) + R(t) = N(t) \tag{6}$$

### 2.1. Definition of Parameters

S = Susceptible group

E = Exposed group

I = Infected group (symptomatic infected)

A = Asymptomatic infected

R = Recovery group

$\eta$  = Birth rate

$\alpha_1$  = Immigration rate

$\alpha_2$  = Emigration rate

$\beta_i$  = Transmission rate of symptomatically infected

$\beta_a$  = Transmission rate of asymptotically infected

$\beta_e$  = Transmission rate of exposed

$\delta$  = Death rate

$Y_1$  = Proportion of exposed entering into symptomatic infected

$Y_2$  = Proportion of exposed entering into asymptomatic infected

Note:  $Y_1 + Y_2 = 1$

$\sigma_1$  = Proportion of symptomatic infected entering into recovered

$\sigma_2$  = Proportion of asymptomatic infected entering into recovered

$\kappa$  = Proportion of recovered going back into susceptible

### 2.1.2. The Basic Reproduction Number

The next generation matrix is used to derive the Basic Reproduction Number  $R_0$ . It was invented by Dickman and Hesterbeck in 1990 and its given by  $R_0 = e(FV^{-1})$

Thus  $R_0$  is the dominant eigen value of  $FV^{-1}$

Where:

$F$  is terms which contains only secondary

$V$  do not contain secondary infection  $F$  and  $V$  are matrix of partial derivatives of the disease class

The disease class is:

$$\frac{de}{dt} = \beta_i si + \beta_e se + \beta_a sa + \alpha_1 e - (\alpha_2 + \delta)e - Y_1 e - Y_2 e$$

$$\frac{di}{dt} = Y_1 e + \alpha_1 i - (\alpha_2 + \delta)i - \sigma_1 i$$

$$\frac{da}{dt} = Y_2 e + \alpha_1 a - (\alpha_2 + \delta)a - \sigma_2 a$$

$$F = \begin{bmatrix} \beta_i si + \beta_e se + \beta_a sa \\ 0 \\ 0 \end{bmatrix} \tag{7}$$

$$V = \begin{bmatrix} \alpha_1 e - (\alpha_2 + \delta)e - Y_1 e - Y_2 e \\ Y_1 e + \alpha_1 i - (\alpha_2 + \delta)i - \sigma_1 i \\ Y_2 e + \alpha_1 a - (\alpha_2 + \delta)a - \sigma_2 a \end{bmatrix} \tag{8}$$

Hence,

$$R_0 = \left[ -\frac{\beta_e}{-\alpha_1 + \alpha_2 + \delta + Y_1 + Y_2} - \frac{\beta_i Y_1}{(-\alpha_1 + \alpha_2 + \delta + Y_1 + Y_2)(-\alpha_1 + \alpha_2 + \delta + \sigma_1)} - \frac{\beta_a Y_2}{(-\alpha_1 + \alpha_2 + \delta + Y_1 + Y_2)(-\alpha_1 + \alpha_2 + \delta + \sigma_2)} \right] \tag{9}$$

The Basic Reproduction Number ( $R_0$ ) in epidemiology indicates how many people one infected person can spread the disease to. If  $R_0$  is less than 1, the disease will fade out. If  $R_0$  is greater than 1, it can spread widely but usually slows as fewer people remain susceptible. At  $R_0$  equals 1, the disease may become endemic in the population.

### 2.1.3. Disease Free Equilibrium Point

A disease model's steady-state solutions in the absence of infection or sickness are known as the disease-free equilibrium (DFE) points. There isn't any sickness in the population right now. Setting all of the derivatives to zero yields the disease-free equilibrium point of the SEAIR model, as illustrated below:

$$e = i = a = r = 0 \tag{10}$$

Substituting equation (9) into the governing equation

Recall that the governing equation is

Then

$$\frac{ds}{dt} = \eta - \beta_i si - \beta_e se - \beta_a sa + \alpha_1 s + \kappa r - (\alpha_2 + \delta)s$$

$$\frac{ds}{dt} = \eta - \beta_i s(0) - \beta_e s(0) - \beta_a s(0) + \alpha_1 s + \kappa r - (\alpha_2 + \delta)s$$

$$\frac{ds}{dt} = \eta + \alpha_1 s + \kappa r - (\alpha_2 + \delta)s \tag{11}$$

Recall equation (11)

$$\begin{aligned} \eta + \alpha_1 s - (\alpha_2 + \delta)s &= 0 \\ \eta + \alpha_1 s - \alpha_2 s - \delta s &= 0 \\ s(\alpha_1 - \alpha_2 - \delta) &= -\eta \end{aligned}$$

$$s = \frac{-\eta}{\alpha_1 - \alpha_2 - \delta} \tag{12}$$

The solution of equation (11) is

$$s^* = \left\{ 0, \frac{-\eta}{\alpha_1 - \alpha_2 - \delta} \right\} \tag{13}$$

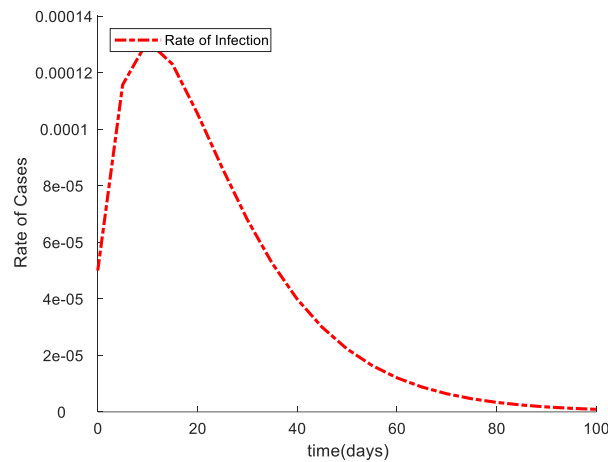
### 3. Results and Discussion

The result from the numerical simulation showed that  $R_0$  is  $-0.0095$  which is less than 1, and it implies that there is 99.99% chances of secondary infection when asymptomatic and symptomatic individuals interact with susceptible individuals through contact.

The value of parameters used in the numerical simulation for the Non-Deterministic Model of are presented in Table 1.

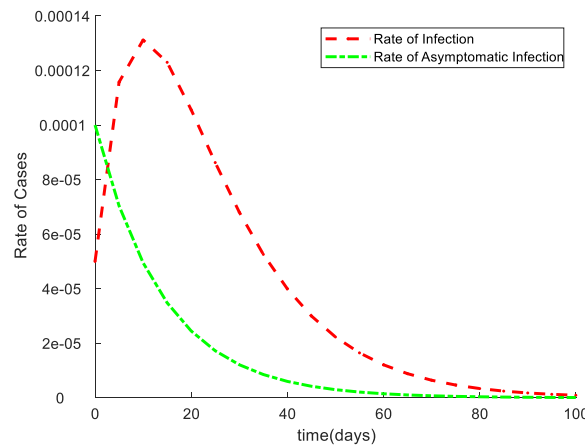
**Table 1.** Parameters values used in the numerical simulation

Fitted Parameters	Values	Source
$\gamma_1$	0.027	Assumed
$\gamma_2$	0.073	Assumed
$\alpha_1$	0.00000095	Assumed
$\alpha_2$	0.0004	Assumed
$\beta_e$	0.0009	Assumed
$\beta_i$	0.0000005	Assumed
$\beta_a$	0.0000095	Assumed
$\kappa$	0.0000006	Assumed
$\sigma_1$	1/15	[2]
$\sigma_2$	0.14286	[2]
$\delta$	0.0001	Assumed
$\eta$	22655	[1]
$N$	200e6	[1]
$E(0)$	0.009	Assumed
$I(0)$	0.0005	Estimated
$R(0)$	0.0001	Estimated
$A(0)$	0.0001	Assumed



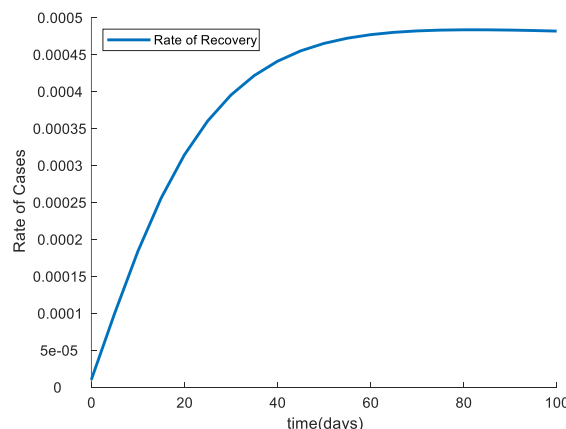
**Figure 2.** Simulation showing rate of symptomatic infection

Figure 2 shows the rate of symptomatic infection in 100 days from 17th of March 2020. It is observed that the rate keeps increasing till after 20 days and started declining.



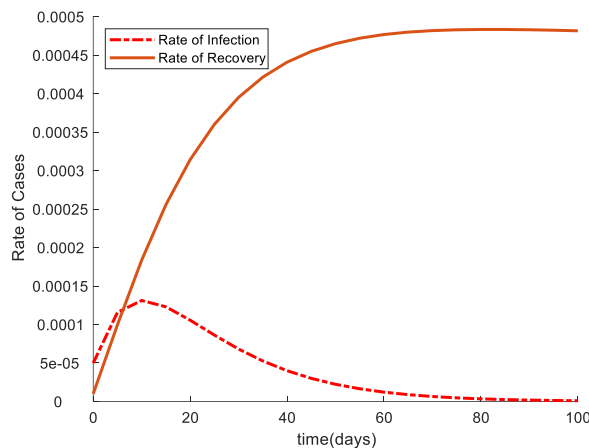
**Figure 3.** Simulation showing rate of asymptomatic infection and symptomatic infection

Figure 3 shows the rate of asymptomatic and symptomatic infections in 100 days from 17th of March 2020. It is observed that the rate of symptomatic infection keeps increasing till after 20 days and started declining, while the rate of asymptomatic infection declines probably because of the awareness of COVID-19 and individuals taking to precautionary measures to fight the disease.



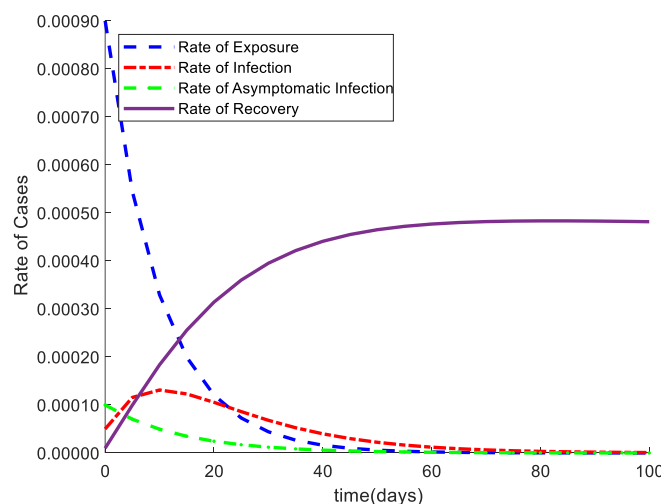
**Figure 4.** Simulation showing rate of recovery

Figure 4 shows the rate of recovery in 100 days from 17th of March 2020. It is observed that the rate of recovery will continue to increase over time.



**Figure 5.** Simulation showing rate of infection and recovery

Figure 5 shows the rate asymptomatic and symptomatic infections in 100 days from 17th of March 2020. It is observed that the rate of symptomatic infection keeps increasing till after 20 days and started declining but the rate of recovery will continually be on the increase as a result of awareness and adherence to COVID-19 precautionary measures.



**Figure 6.** Simulation showing rate of exposure, asymptomatic infection, symptomatic infection and recovery

Figure 6 shows the rate at which individuals are exposed, asymptomatic and symptomatic infections and recovery rate in 100 days from 17th of March 2020. It is observed that the rate at which people are exposed and asymptomatic infected to COVID-19 reduces drastically. Also, the rate of symptomatic infection keeps increasing till after 20 days and started declining but the rate of recovery will continually be on the increase as a result of awareness and adherence to COVID-19 precautionary measures.

The SEIAR model was formulated with population migration and presented and analyzed in this thesis and the summary, conclusion and recommendations are presented in this chapter.

### 3.1. Parameter Estimation and Model Fitting

As shown in Table 2, estimates of a few model parameters are taken from the literature. Other unknown parameters, which are displayed in Table 2, are approximated by fitting the total number of confirmed cases reported on the NCDC website to those produced by the model.

To enhance computational flexibility and ease of simulation, the population of Nigeria has been rescaled to 5 million, or  $S(0)=5,000,000$ . The first piece of data used in this research is dated March 17, 2020. The NCDC data is appropriate for Nigeria and covers the period from March 17 to May 5, 2020. The following other initial state variables are set:

$$E(0) = 500, A(0) = 200, R(0) = 351, I(0) = 0$$

To estimate the unknown values of the parameter employed in the model, the Nelder-Mead approach is a mathematical methodology used in the data fitting procedure. The model is represented in vector form with the parameters to be estimated with regard to the starting values of the state variables in order to use the nonlinear least squares approach. With the use of the least squares approach, the set of parameters that minimizes the discrepancy between the total of cumulative confirmed cases that the model predicts and the total of the product of cumulative confirmed cases that are observed and reported by the NCDC and the logarithms of cumulative confirmed cases that the model predicts can be solved.

$$LS = \sum Y - \sum(OB * \log(Y))$$

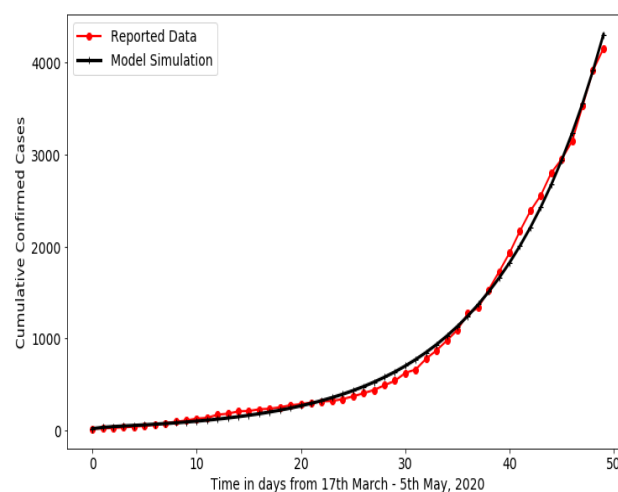
Where  $Y$  is the cumulative cases predicted by the model

$OB$  is Observed data reported by the NCDC

Python is the name of the computer software used to accomplish this procedure. The total number of confirmed cases in Nigeria is displayed in Figure 7.

**Table 2.** Shows the cumulative number of confirmed cases.

Fitted Parameters	Values	Source
$\gamma_1$	0.03241	Estimated
$\gamma_2$	0.96759	Estimated
$\alpha_1$	0.39884	Estimated
$\alpha_2$	0.21504	Estimated
$\beta_e$	0.16676	Estimated
$\beta_i$	0.09486	Estimated
$\beta_a$	0.65099	Estimated
$\kappa$	0.4037	Estimated
$\sigma_1$	1/15	[2]
$\sigma_2$	0.14286	[2]
$\delta$	0.0182	[3]
$\eta$	22655	[1]



**Figure 7.** Model Fitting with cumulative confirmed cases of COVID-19 in Nigeria

The NCDC's data on the daily incidence and total number of confirmed cases of COVID-19 in Nigeria are used to fit the model, as shown in Figure 4.6. It is seen to be well fitted, and Table 1 displays the parameter estimation.



#### 4. Conclusion

The traditional SIR model has been increased to a five compartment SEAIR model which shows a good characteristic of COVID-19 as the asymptomatic infected was put into consideration. The population migration into the country was incorporated to the model. The model was normalized, and constant population was justified to be sure that the model was well formulated. The basic reproduction number  $R_0$  was calculated with the aid of a mathematical software, Maple 2021 and the result was shown in equation (9), also the disease-free equilibrium of the model is calculated which is presented in equation (12).

The numerical simulation of the non-deterministic model shows the basic reproduction number  $R_0 = -0.0095$  which suggests there is a very big chance of secondary infection when asymptomatic and symptomatic individuals interact with susceptible individuals through contact probably within the population or through migration of people carrying the infection into Nigeria. It is observed that the rate of symptomatic infection keeps increasing till after 20 days and started declining. Figure 2 shows clearly the rise and decline of the rate of symptomatic infection in 100 days from 17th of March 2020. Within this period, the rate of asymptomatic infection keeps declining probably because a lot of measures were been put in place which includes the Nigerian government announcing a total lockdown in Abuja and Lagos which is the epicenter of the disease in Nigeria and the lockdown was also extended to Ogun because of its proximity to Lagos. Figure 3 shows a clear relationship between the rate of symptomatic infection and the rate of asymptomatic infection. The rate of recovery within this period increases and still continue to increase over time as shown in Figure 4. The relationship between the rate of infection and that of recovery is presented in Figure 4 and Figure 6 shows the relationship between the rate of exposure, asymptomatic infection, symptomatic infection and recovery which shows that the rate of recovery will continually rise as people adhere to the COVID-19 precautionary measures and immigration of the people carrying the infections into the population is controlled.

From the numerical simulation, the basic reproduction number  $R_0$  is 2.61. In particular, the contribution of the exposed individuals in the prevalence of COVID-19 is  $-0.199 < 1$ , which implies that there is 99.80% chances of secondary infection when exposed individuals interact with susceptible through contact. The asymptomatic infected individuals contribute much to the prevalence of COVID-19 due to the fact that they are infected but without symptoms and can move around and can easily infect others very fast when in crowded places e.g. bank, social gatherings, marketplaces etc.

In order to achieve stability, the rate of transmission for exposed, asymptomatic infected and symptomatic infected have to reduced. These could be reduced by strictly adhering to the COVID-19 precautionary measures which includes washing of hands frequently and carefully, avoid touching of face, stop shaking hands and hugging people, clean and disinfect surfaces, covering of mouth and nose when you cough and sneeze, take physical (social) distancing seriously, wear of (homemade) mask etc.

This study emphasizes migration and asymptomatic cases to manage COVID-19 in Nigeria. In contrast against other studies, Wang et al.'s model incorporates socio-psychological factors to refine predictions based on public behavior, while Zhang et al. examine periodic trends in epidemic models, influencing adjustments for cyclical patterns. Each approach offers unique insights into epidemic dynamics, with this model focusing on local factors and the other studies addressing broader and cyclical influences.

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#### Declaration of Competing Interest

No conflict of interest was declared by the authors.

## Authorship Contribution Statement

**Moyosola Ayodele:** Writing, Data Preparation

**Sefiu Onitilode:** Methodology and Editing

**Olutunde Odetunde:** Supervision, Reviewing

## References

- [1] J. O. Bamidele, and O. J. Daniel, "Epidemiology of Coronavirus Disease (COVID-19) in Nigeria," *Ann Health Res*, vol. 6, no. 2, pp. 125-132, May 2020, doi: 10.30442/ahr.0602-01-74.
- [2] S. G. Georgiev, and L. G. Vulkov, "Identification of COVID-19 dynamics and economic impact for a fractional SEIR," *AIP Conference Proceedings*, vol. 2505, no. 1, 080025, pp.1-9, Sep. 2022, doi: 10.1063/5.0101044.
- [3] J. O. Owoyemi, and Y. Edime, "Covid-19 and job loss in Nigeria: A sociological analysis," *CRR*, vol. 1, no. 1, pp. 1-10, Nov. 2022, doi: 10.57219/crrj.2022.1.1.0002.
- [4] S. Omega, A. T. Nuer, and E. Ametepey, "Effect of Coronavirus on Aquaculture in Oyo state, Nigeria," *J Agricultural Sci*, vol. 13, no. 11, pp. 153-166, Oct. 2021, doi: 10.5539/jas.v13n11p153.
- [5] S. Chauhan, P. O. Misra, and J. Dhar, "Stability Analysis of SIR Model with Vaccination," *Amer J Computational App Math*, vol. 4, no. 1, pp. 17-23, Jan. 2014, doi: 10.5923/j.ajcam.20140401.03.