



# **Deterministic Mathematical Model on the Transmission Dynamics of Corona Virus COVID-19 In a Heterogeneous Nigeria Population**

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## **ABSTRACT**

The disease covid-19 pandemic has imposed lot of challenges to the world at large and Nigeria is no exception. Understanding the transmission dynamics of coronavirus (COVID-19) is very important for positive change. This study present a suitable way of determining the spread and control of Covid-19. Themodel high-lighted some various parameters such as Susceptible, Exposed, Infectious, Isolation and Recovered ( $S_1 S_2 E_1 E_2 I R$ ) underlying health conditions that influence the transmission dynamics of the virus. A primary data was employed which was gotten from Enugu State University Teaching Hospital Parklane, a flow chat was constructed and the analysis was carried out using matlab, the disease was discussed in detailed at the methodology. Some epidemiological parameters such as reproduction number, contact rates and population movement were used to project the potential spread of covid-19 in different regions in Nigeria. The basic reproduction number was calculated and the stability analysis of the equilibrium points was determined. the model also provides insights into the effectiveness of the public health measures on the spread and control outbreak, the model analysis showed that susceptible vaccinated individuals can become susceptible and also be exposed once the vaccination expires which will lead to spread of the disease.

**Keywords:** Coronavirus, Transmission dynamics, SEIR-model, infectious rate, heterogeneous population, deterministic model.

## **INTRODUCTION**

The novel corona virus pandemic is a global disease that has caused a lot of damages to all strata of the society with the global infected cases. The pandemic has tentatively placed over 3 million people with confirmed death in excess of 171,152. For instance, the number of infected in the United States of America (USA) stands at 787960 with 42361 death and many more are still dyeing. Economy of some many countries has being affected since the discovery of the coronavirus (Covid-19) in December 2019 at Wuhan china. Coronavirus (COVID -19-Z) is one of the thirty-six coronavirus in the family of Coronavindae within the order Nichovirales. Members of the Corovindae are known to cause respiratory or intestinal infections in humans and other animals. In human, several coronavirus are known to cause respiratory infections ranging from common cold, cough, sneezing to more severe disease such as Middle East respiratory syndrome (MERS) and severe Acute respiratory syndrome (SARS). The most recently discovered coronavirus causes coronavirus disease (covid-19). According to WHO, NCDC and MOHFW guidelines, COVID-19 is an infectious condition an can be spread directly or indirectly from one person to another.

Despite a degree of phylogenetic divergence from other corona virus SARS-COV together with bat SARS-COV are now considered group 2L Coronavirus [see for instance 1, 2]. Transmission dynamic models owe a necessary first step in understanding the pandemic potential of an emergency infectious disease, including estimating the reproduction number- the number of new cases arising from typically infected cases. [3, 4]. The first published dynamic study of COVID-19 was rapid and uncomplicated, estimating the basic reproduction number as time invariant without explaining some of the major underlying assumptions, such as lack of infectiousness. Many estimate for the reproduction rates having appeared ranging from around 2 to more than 6. In [5], the major assumptions of the earlier works were addressed and contributed, that a time varying reproduction number showed the effect of massive public interventions. There are two strains of the virus, the infectious rate of the first is put on the average of 20-65% while the other strains has a very high infectious rate and the carriers are called Super-spreaders [6]. According to [7], modelling studies have aided understanding of COVID-19 dynamics from the first announcement of the epidemic and the publication of the genetic sequence. Initial phylogenetic analysis of the closely related viruses suggested highly linked person-to-person spread of SARS-COV-2 [8,9]. Modelers provided simple calculation that identified a mismatch between reported cases from china and reported importation of cases from travelers. Based on travel volumes, modelers inferred that the cases in Wuhan china were underestimated.

Enahoro and Oluwaseun (2020). Conducted a research on transmission dynamics COVID-19 pandemic in Nigeria. Using the public media with the following key word: COVID-19, SARS-CoV-2, social-distancing, lockdown, non-pharmaceutical interventions (NPIs). The model, which was rigorously analysed and parametrized using COVID-19 data published by the Nigeria Centre for Disease Control (NCDC), was used to assess the community-wide impact of various control and mitigation strategies in some jurisdictions within Nigeria (notably the states of Kano and Lagos, and the Federal Capital Territory, Abuja). Numerical simulations of the model showed that COVID-19 can be effectively controlled in Nigeria using moderate levels of social-distancing strategy in the jurisdictions and in the entire nation. Although the use of face masks in public can significantly reduce COVID-19 in Nigeria, its use, as a sole intervention strategy, may fail to lead to a substantial reduction in disease burden. Such substantial reduction is feasible in the jurisdictions (and the entire Nigerian nation) if the public face mask use strategy is complemented with a social-distancing strategy. The community lockdown measures implemented in Nigeria on March 30, 2020 need to be maintained for at least three to four months to lead to the effective containment of COVID-19 outbreaks in the country. Relaxing, or fully lifting, the lockdown measures sooner, in an effort to re-open the economy or the country, may trigger a deadly second wave of the pandemic.

Ebraheem (2020): Mathematical Model for Corona virus Disease 2019 (COVID-19) Containing Isolation Class. The research was carried by developing a mathematical model to present the dynamical behavior of COVID-19 infection by incorporating isolation class. First, the formulation of model is proposed; then, positivity of the model is discussed. The local stability and global stability of proposed model are presented, which depended on the basic reproductive. For the numerical solution of the proposed model, the nonstandard finite difference (NSFD) scheme and Runge-Kutta fourth order method are used. Finally, some graphical results are presented. Their findings show that human to human contact is the potential cause of outbreaks

of COVID-19. Therefore, isolation of the infected human overall can reduce the risk of future COVID-19 spread.

Salihu, Sania et al (2021): Mathematical modeling of COVID-19 epidemic with effect of awareness programs. In this paper, we propose a mathematical model to study the transmission dynamics of COVID-19 in Nigeria. Our model incorporates awareness programs and different hospitalization strategies for mild and severe cases, to assess the effect of public awareness on the dynamics of COVID-19 infection. We fit the model to the cumulative number of confirmed COVID-19 cases in Nigeria from 29 March to 12 June 2020. We find that the epidemic could increase if awareness programs are not properly adopted. We presumed that the effect of awareness programs could be estimated. Further, our results suggest that the awareness programs and timely hospitalization of active cases are essential tools for effective control and mitigation of COVID-19 pandemic in Nigeria and beyond. Finally, we perform sensitive analysis to point out the key parameters that should be considered to effectively control the epidemic.

Juliane (2021). Carried out a research on Mathematical modeling of COVID-19 in 14.8 million individuals in Bahia, Brazil. Mathematical modeling was used to study the dynamics of COVID-19 in Bahia, a state in northeastern Brazil, considering the influences of asymptomatic/non-detected cases, hospitalizations, and mortality. The impacts of policies on the transmission rate were also examined. Their results underscore the difficulties in maintaining a fully operational health infrastructure amidst the pandemic. Lowering the transmission rate is paramount to this objective, but current local efforts, leading to a 36% decrease, remain insufficient to prevent systemic collapse at peak demand, which could be accomplished using periodic interventions. Non-detected cases contribute to a ~55% increase in  $R_0$ . Finally, they discuss their results in light of epidemiological data that became available after the initial analyses.

Yusuf, Aliyu et al (2020). Mathematical Modeling of Covid19 Transmission and Control Strategies in the Population of Bauchi State, Nigeria. This research work extends the epidemic SEIR model by introducing new parameters based on the transmission dynamics of the novel COVID-19 pandemic and preventive measures. The total population of Bauchi State at the time of the study, given by is compartmentalized into five (5) different compartments as follows: Susceptible (S), Exposed (E), Infectious (I), Quarantined (Q) and Recovered (R). The new model is SEIQR.  $N = S \rightarrow E \rightarrow I \rightarrow Q \rightarrow R$  Data was collected by accessing Bauchi state electronic database of COVID-19 project to derive all the model parameters, while analysis and model building was done using Maple software. At the time of this study, it was found that the reproduction number  $R$ , for COVID-19 in Bauchi state, is  $2.6 \times 10^{-5}$ . The reproduction number  $R$  decreased due to the application of control measures. The compartmental SEIRQ model in this study, which is a deterministic system of linear differential equations, has a continuum of disease-free equilibria, which is rigorously shown to be locally asymptotically stable as the epidemiological threshold, known as the control reproduction number  $R = 0.0000026$  is less than unity. The implication of this study is that the COVID-19 pandemic can be effectively controlled in Bauchi, since  $R < 1$ . Contact tracing and isolation must be increased as the model shows, the rise in infected class is a sign of high vulnerability of the population. Unless control measures are stepped up, despite high rate of recovery as shown by this study, infection rate will keep increasing as currently there is a no vaccine for COVID-19.

Jayatilaka, Patel et al (2020). Conducted A Mathematical Model of COVID-19 Transmission. Disease transmission is studied through disciplines like epidemiology, applied mathematics, and statistics. Mathematical simulation models for transmission have implications in solving public

and personal health challenges. The SIR model uses a compartmental approach including dynamic and nonlinear behavior of transmission through three factors: susceptible, infected, and removed (recovered and deceased) individuals. Using the Lambert W Function, they propose a framework to study solutions of the SIR model. This demonstrates the applications of COVID-19 transmission data to model the spread of a real-world disease. Different models of disease including the SIR, SIR mp and SEIR model are compared with respect to their ability to predict disease spread. Physical distancing impacts and personal protection equipment use will be discussed in relevance to the COVID-19 spread.

Masaki, Mitsuo et al (2020). A mathematical model for COVID-19 pandemic-SIIR model: Effects of asymptomatic individuals. A new mathematical model called SIIR model is constructed to describe the spread of infection by taking account of the characteristics of COVID-19 and is verified by the data from Japan. The following features of COVID-19: (a) there exist presymptomatic individuals who have infectivity even during the incubation period, (b) there exist asymptomatic individuals who can freely move around and play crucial roles in the spread of infection, and (c) the duration of immunity may be finite, are incorporated into the SIIR model. The SIIR model has the advantage of being able to explicitly handle asymptomatic individuals who are delayed in discovery or are extremely difficult to be discovered in the real world. It is shown that the conditions for herd immunity in the SIIR model become more severe than those in the SIR model; that is, the presence of asymptomatic individuals increases herd immunity threshold (HIT).

Daniel Deborah O (2020): Mathematical Model for the Transmission of Covid-19 with Nonlinear Forces of Infection and the Need for Prevention Measure in Nigeria. This paper proposes a mathematical model SEIQRW which adopts the SEIR model to study the current outbreak of COVID-19 in Nigeria with nonlinear forces of infection. This model defines the transmission channels in the infection dynamics and the impact of the environmental reservoir in the transmission and spread of this disease to humans. The existence of the region where the model is epidemiologically feasible is established. A detailed numerical simulation of this model was conducted using the Nigeria Centre for Disease Control (NCDC) reported data. Our analytical and simulation results between February 29, 2020 and May 14, 2020 are in good agreement. Further simulation indicates that Nigeria's cumulative number of confirmed cases will reach 55,000 individuals in December 25, 2020. Mitigation strategies and its effectiveness in reducing the spread of COVID-19 across Nigeria are considered. After a lot of citation on a lot of authors, the study aims to formulate a mathematical model for the transmission dynamics of covid-19 pandemic and the main objective of this study is to Formulation of mathematical model on covid-19, Establishing existence of Equilibrium State, Disease free Equilibrium and Endemic Equilibrium, Carry out stability analysis for the disease free equilibrium state, Draw conclusion on the nature of the disease to help international institutions and policy makers.

## Methodology

Corona virus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus according to Wikipedia. They are a family of viruses that cause respiratory and intestinal illnesses in humans and animals according to World Health Organization (WHO). They usually cause mild colds in people but the emergence of the severe acute respiratory syndrome (SARS) epidemic in China in 2002–2003 and the Middle East respiratory syndrome (MERS) on the Arabian Peninsula in 2012 show they can also cause severe disease. Seven human corona viruses (HCoVs) have been identified. Four of them are common; less high risk and typically cause only

mild respiratory illnesses in healthy human adults. However, they contribute to a third uncommon cold infections and, high risk people with weak immune systems; they can cause long term, life-threatening illnesses. The other three (those causing MERS, SARS and COVID- 19 cases) are known to cause more severe illness such as shortness of breath and even death according to WHO. There are various methods for solving the transmission dynamics of covid- 19 which includes: SIR, SIRS, SEIR.

#### SIR Model

This basic model is divided into three subsets: Susceptible, Infectious, Recovered (SIR). There are transitions between three parts. Susceptible person are derived by subtracting persons who are confirmed to be virus carriers via testing in hospitals from the total population. In details, the transition from Susceptible (S) state to Infectious (I) state is not deterministic, but is always stochastic Rahim (2021). The number infected person's decreases with recoveries and deaths. And recovered individual can no more change to susceptible stage. This model offers two possible outcomes, first possibility is that the disease might, if new infections are not controlled, end up being an epidemic. The second possibility is that the virus dies up, if the necessary measures are taken. It is a basically tools used for analyzing infectious disease outbreak according to Rahim (2021).

#### SIRS Model

SIRS model is a model made up of the subset Susceptible, Infectious, Recover, and Susceptible. The model allows underlying clustering patterns for transmission rate, recovery rate, and loss of immunity rate for the latest corona virus (covid19) among different regions. This method provides simultaneously inference on parameter estimation and clustering information which contains both number of clusters and cluster configuration Hu and Geng (2021)

#### SEIRS Model

SEIRS model is made up of the susceptible, exposed, infectious, recovered, and susceptible. The model predicts the covid19 epidemic dynamics incorporating pathogen in the environment and interventions according to Samuel et al (2020).

#### Assumptions of model

We assume that people with travel experience (S1), people without travel experience (S2), exposed due to quarantine (E1), exposed due to interaction (E2), infected people (I), recovered people (R) die at the same natural rate  $\mu$ .

We assume that the treated individual recovers.

Also, we assume that vaccinated individuals do not acquire permanent immunity because the efficacy of the vaccine wanes.

We assume that the individuals with travel experience can be infected.

The quarantine individual undergo special treatment

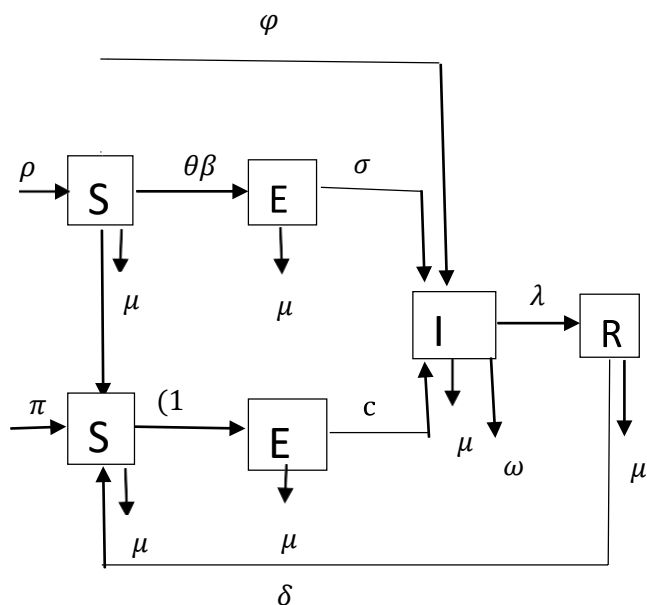
Disease induced death rate  $\omega$

**Table 1.** Variables used for the transmission dynamic of COVID-19 model.

Variables	Description
$S_1(t)$	People with travel experience
$S_2(t)$	No travel experience
$E_1(t)$	Exposed due to quarantine at the entry port
$E_2(t)$	Exposed due to interaction/human to human contact
$I(t)$	Infected people
$R(t)$	Recovery people

**Table 2.** Parameters used for the transmission dynamic of COVID -19 model.

Parameters	Descriptions
$\pi$	Rate at which people become non experienced
$\rho$	Rate at which people become experienced
$\theta\beta$	Rate at which experience people become exposed
$(1 - \theta)\beta$	Rate at which non experience people become exposed with interaction
$r$	Rate at which experience people become not experienced
$\mu$	Natural death
$\varphi$	Rate at experienced individuals becomes infected
$\delta$	Rate at which recover people become not experienced
$C$	Rate at which exposed due to interaction become infected
$\lambda$	Rate at which infectious individuals become recovers
$\sigma$	Rate at which exposed become infectious
$\omega$	Disease induce death rate



**Figure 1.** Flow chart on the transmission dynamic of Covid-19  
 Equation derived from the flow chart

$$\frac{dS_1}{dt} = \rho - \theta\beta(t)S_1(t) - \varphi S_1(t) - \mu S_1(t) - rS_1(t) \quad (1)$$

$$\frac{dS_2}{dt} = \pi - (1 - \theta)I(t)S_2(t) + \delta R(t) - \mu S_2(t) + rS_1(t) \quad (2)$$

$$\frac{dE_1}{dt} = \theta\beta(t)S_1(t) - \mu E_1(t) - \sigma E_1(t) \quad (3)$$

$$\frac{dE_2}{dt} = (1 - \theta)I(t)S_2(t) - \mu E_2(t) - cE_2(t) \quad (4)$$

$$\frac{dI}{dt} = \varphi S_1(t) + \sigma E_1(t) + cE_2(t) - \mu I(t) - \omega I(t) - \lambda I(t) \quad (5)$$

$$\frac{dR}{dt} = \lambda I(t) - \delta R(t) - \mu R(t) \quad (6)$$

## Result and Discussion

At Endemic Equilibrium State

To obtain the endemic equilibrium points for the systems of differential equation above by equating each of the equations (1) to (6) to zero.

$$\rho - \mu S_1 - \varphi S_1 - \theta \beta I S_1 - r S_1 = 0 \quad (7)$$

$$\pi - (1 - \theta) I S_2 + r S_1 - \mu S_2 - \delta R = 0 \quad (8)$$

$$\theta \beta I S_1 + \alpha I S_2 - \mu E_1 - \sigma E_1 = 0 \quad (9)$$

$$(1 - \theta) \beta I S_2 - \mu E_2 - c E_2 = 0 \quad (10)$$

$$\varphi S_1 + \sigma E_1 - c E_2 - \mu I - \omega I - \lambda I = 0 \quad (11)$$

$$\lambda I + r R_H - \mu R = 0 \quad (12)$$

The calculating results will be in two equilibrium points, one being the Disease free equilibrium (DFE), while the other being the Endemic equilibrium.

1. Endemic equilibrium: the endemic equilibrium of the model is give as

$D^* = (S_1^*, S_2^*, E_1^*, E_2^*, I^*, R^*)$ . From equation (7) to (12) then

Let  $a = \beta I, b = \alpha I, k_1 = (\mu + \omega + a), k_2 = (\mu + b), k_3 = (\mu + \sigma), k_4 = (\mu + c + \delta + \gamma)$

$k_5 = (\mu + \theta + r)$ , The equation (7) to 12 becomes

$$k_1 S_1 = \pi \rho \quad (14)$$

$$\omega S_1 - k_2 = (-1) \rho \quad (15)$$

$$a S_1 + b S_2 - k_3 E = 0 \quad (16)$$

$$\sigma E - k_4 = 0 \quad (17)$$

$$\delta I - k_5 R_H = 0 \quad (18)$$

$$\gamma I + r R_H - \mu R = 0 \quad (19)$$



Then,

$$S_1^* = \frac{\pi}{k_1},$$

$$S_2^* = \frac{\omega\pi\rho - k_1(1 - \pi)\rho}{k_2},$$

$$E^* = \frac{ak_2\pi\rho + bk_1(\omega\pi\rho - k_1(1 - \pi)\rho)}{k_1k_2k_3},$$

$$I^* = \frac{[ak_2\pi\rho + bk_1(\omega\pi\rho - k_1(1 - \pi)\rho)]}{k_1k_2k_3k_4},$$

$$R_H^* = \frac{\sigma[ak_2\pi\rho + bk_1(\omega\pi\rho - k_1(1 - \pi)\rho)]}{k_1k_2k_3k_4k_5},$$

$$R^* = \frac{(\tau\sigma\delta + \gamma\sigma k_5)(ak_2\pi\rho + bk_1(\omega\pi\rho - k_1(1 - \pi)\rho))}{\mu k_1k_2k_3k_4k_5}$$

$$F = \begin{bmatrix} 0 & 0 & \theta\beta \\ 0 & 0 & (1 - \theta)\beta \\ 0 & 0 & 0 \end{bmatrix} \quad V = \begin{bmatrix} \mu + \sigma & 0 & 0 \\ 0 & \mu + \epsilon & 0 \\ -\sigma & -\epsilon & \mu + \omega + \lambda \end{bmatrix}$$

$$V^{-1} = \begin{bmatrix} \frac{1}{\mu + \sigma} & 0 & 0 \\ 0 & \frac{1}{\mu + \epsilon} & 0 \\ \frac{\sigma}{(\mu + \sigma)(\mu + \omega + \lambda)} & \frac{\epsilon}{(\mu + \epsilon)(\mu + \omega + \lambda)} & \frac{1}{\mu + \omega + \lambda} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} \frac{\sigma\theta\beta}{(\mu + \sigma)(\mu + \omega + \lambda)} & \frac{\theta\beta\epsilon}{(\mu + \epsilon)(\mu + \omega + \lambda)} & \frac{\theta\beta}{\mu + \omega + \lambda} \\ \frac{(1 - \theta)\beta\sigma}{(\mu + \sigma)(\mu + \omega + \lambda)} & \frac{\epsilon(1 - \theta)\beta}{(\mu + \epsilon)(\mu + \omega + \lambda)} & \frac{(1 - \theta)\beta}{\mu + \omega + \lambda} \\ 0 & 0 & 0 \end{bmatrix}$$

Reproduction number ( $R_0$ ) is the number of the dominant eigenvalues of the matrix

$$R_0 = \frac{\sigma\theta\beta}{(\mu+\sigma)(\mu+\omega+)} + \frac{(1-\theta)\beta}{(\mu+\sigma)(\mu+\omega+)}$$

$$R_0 = \left( \frac{\sigma\theta}{(\mu+\sigma)} + \frac{\beta(1-\theta)}{(\mu+\sigma)} \right) \frac{\beta}{(\mu+\omega+)}$$

A compartmental mathematical model on the study of corona virus disease was formulated. This study focus on the transmission dynamics of covid19 in the community using the Susceptible, Exposed, Infectious, Isolated and Recovered ( $S_1 S_2 E_1 E_2 I R$ ). From the analysis carried out we discovered that Covid19 can be prevented. This study shows that susceptible vaccinated individual can be exposed once the vaccination expires which will lead to the spread of the disease, This is reflected to the fact that many healthcare workers became infected from the infectious patients and some died from the disease, in several other countries due to the high contact rate with infectious individuals at different place of gathering like worship centers, clubs, markets and town hall meeting, Regardless of wearing the face mask and surgical mask, it has reported number of infections and death from COVID-19 among individuals in several environments in Italy, china, US, South Africa ,UK and several other countries. It is generally believed that social distancing of 2 m is a safe distance and many country including Nigeria have implemented such social distancing, however since COVID-19 is an airborne infectious disease as declared by WHO, it can be transmitted up to a distance of 6 m through coughing and 8 m through sneezing, which makes the disease more complex for implemented preventive measures, Many countries has implemented some interventions to combat COVID-19 transmission, such as social distancing ,national lockdown, contact tracing and mass testing. However, regardless of these preventive measure,COVID-19 remains a public health and economic threat worldwide.

## Conclusion

In conclusion, the study shows that susceptible vaccinated individuals can become susceptible and also can be exposed once the vaccination expires and it will lead to spread of the disease, the study also emphasizes adherence to standard operating procedures, early detection and treatment of covid-19 patients especially those that do not have underlying health conditions, so as to lessen community transmission of the disease, the study also show that COVID-19 transmission was increased by high contact rate between infectious and susceptible individuals ,and asymptomatic individuals might be super spreaders of the disease.

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