



# International Journal of Pure and Applied Mathematics Research

Publisher's Home Page: <https://www.svedbergopen.com/>



Research Paper

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## Estimating the Basic Reproduction Number for the Second Wave of Covid-19 Pandemic in Nigeria

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### Article Info

Volume 2, Issue 2, October 2022

Received : 09 April 2022

Accepted : 12 September 2022

Published : 05 October 2022

doi: [10.51483/IJPAMR.2.2.2022.1-9](https://doi.org/10.51483/IJPAMR.2.2.2022.1-9)

### Abstract

It is no news that the Covid-19 pandemic has affected many persons in different ways. As the number of reported cases rises across the globe, efforts are geared towards production and administration of effective vaccines for the disease. However, many developing countries are faced with the dilemma of how to slow the spread and flatten the curves of the disease as the available vaccines are not enough. Interestingly, the dynamics of the disease can be analyzed to get useful insights to enhance the making of suitable preventive policies that will slow the spread, ultimately flatten the curves of the disease and also help in managing any future occurrence. In this work, the aim is to analyze the dynamics, and estimate the basic reproduction number of the second wave of the pandemic in Nigeria using a Susceptible-Infected-Recovered-Deceased (SIRD) compartmental-based model. The dynamics of the disease is described by a system of nonlinear ordinary differential equations. The model takes into consideration the current control policies in place-social distancing, mask usage, personal hygiene and quarantine. Available data provided by Nigeria Centre for Disease Control (NCDC), World Health Organization (WHO) and Wolfram Data Repository were used for the computations. The Quasi-Newton algorithm was implemented in fitting the proposed model to the available data and a sensitivity analysis was presented. Major parameters—effective contact rate, average recovery time, average mortality rate, and overall effectiveness of the control policies-influencing the dynamics of the disease, and the basic reproduction numbers were estimated. The turning points of the disease during the second wave were also obtained. The proposed model gave estimated values for the parameters influencing the spread of the disease. Also, the measure of the overall effectiveness of the current control policies gave insight into how effective the measures are.

**Keywords:** *Coronavirus, Covid-19, Pandemic, Compartmental model, Nigeria*

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### 1. Introduction

CoronaVirus Disease 2019 (Covid-19) has since been a global menace which affects different people in different ways (Le et al., 2020; Yuki et al., 2020). With its symptoms ranging from mild symptoms to severe illness, Covid-19 has, since

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its discovery, infected 491 million people and killed 6 million people globally. It is more fatal to aged population as well as others with underlying medical conditions, such as cardiovascular diseases, diabetes, chronic respiratory disease or cancer (Sohrabi et al., 2020; Jebriil, 2020). The virus is known to spread from an infected person's mouth or nose in small liquid particles when they sneeze, cough, speak, sing or breathe. Measures such as lockdown, restriction of public meetings, mandatory use of nose masks, vaccination and booster vaccinations etc. are implemented by the government to curb the spread and fatal effects of the deadly virus (Struyf et al., 2021; Elibol, 2021; Chen et al., 2021).

The pandemic, which has been with us since about three years, has attracted a massive scholarly attention. Since Covid-19 datasets became publicly available, many computational and mathematical models have been proposed in understanding the dynamics of the virus. Machine learning models have been developed to predict the spread and severity of the virus using known symptoms of the virus (De Felice and Polimeni, 2020; Kushwaha et al., 2020; Syeda et al., 2021). Deep learning models have also been proposed by authors in detecting the virus using medical images (Liu et al., 2022; Gaur et al., 2021; Shorten et al., 2021; Kaur and Kaur, 2021). Epidemiological models have been discovered to be relatively more effective in the overall understanding of the dynamics of the virus. These models provide a comprehensive pathway into the understanding of the behavior of the epidemic outbreak. Compartmental models are systems of Ordinary Differential Equations (ODE) used for predicting, determining, validating and analyzing the rate of susceptibility, exposure, infection, recovery and mortality (Wusu et al., 2022; Wusu et al., 2021; Wusu and Olabanjo, 2020; Annas et al., 2020; Loli and Zama, 2020).

The classical Susceptible-Infected-Recovered (SIR) model is considered as one of the simplest compartmental model in epidemiology (Kermack and McKendrick, 1927). For years, it has been adapted and modified in various ways to study several diseases with different dynamics and also used as the basis for several other complex models (Gautam et al., 2011; Gautam et al., 2014; Wang et al., 2018; Gai et al., 2020). In recent times, several authors have proposed different models which are modifications and adaptation of the SIR model to describe Covid-19 pandemic dynamics (AlQadi and Bani-Yaghoub, 2022; De la Sen and Ibeas, 2020; Cooper et al., 2020; Al-Abdulla et al., 2022, Ram and Schaposnik, 2021). The authors in AlQadi and Bani-Yaghoub (2022) extended the SIR model by incorporating the global dynamics of the COVID-19 pandemic. In De la Sen and Ibeas (2020), a logistic equation was used to describe and interpret a SIR model which in turn was applied to the Covid-19 pandemic data.

One of the popular epidemiological models is the Susceptible-Infectious-Recovered-Deceased (SIRD) model (Matadi, 2014; Sen and Sen, 2021; Nisar et al., 2021). These models offer a precious tool to public health and government authorities for the control of the pandemic vis-a-vis prevention and control. They also offer long and short term predictions which can assist stakeholders optimize control strategies, minimize constraints and make the most effective and efficient decisions (Shringi et al., 2021; Ferrari et al., 2020). These models are typically constructed in the form of ODE and are characterized by a set of parameters whose values are not known a-priori and have to be experimentally determined from the data (Li and Muldowney, 1995).

In this work, we constructed a parameter-varying modification of the SIRD model in order to understand the possible structural changes of the pandemic's characteristics in Nigeria. This helped us to estimate the basic reproduction number of the virus in the second wave of the infection in Nigeria. The Basic Reproduction Number (BRN),  $R_0$ , is the number of secondary cases which a single case can likely produce in a susceptible population. This model is dependent on the period of infection, likelihood of infecting a susceptible individual during a contact and the number of new susceptible individual contacted in a given time (Dietz, 1993). The simplest interpretation to the significance of reproduction number is that if  $R_0 > 1$ , then the pandemic is spreading, else it is contracting.  $R_0$  is a threshold parameter for invasion of a virus into a completely susceptible population (Alimohamadi et al., 2020; Delamater et al., 2019; Heesterbeek and Roberts, 2007; You et al., 2020).

## 2. Related Works

For a given disease, the SIR model (Kermack and McKendrick, 1927) assumes that the population at any given time can be categorise into three (3) main compartments—Susceptible (fraction of the population that are not yet infected but are susceptible to the disease), Infected (fraction of the population already infected) and those who have been Removed (fraction of the population who recovered or died of the disease). However, many diseases usually have some latency period during which an infected person is not yet infectious, i.e., the person has been exposed to the disease.

To properly model such situation, a modification of the SIR model referred to as the SEIR-Susceptible-Exposed-Infected-Removed is often used. Unlike the SIR and SEIR models, the SIRD-Susceptible-Infected-Recovered-Deceased model differentiates between Recovered (fraction of the population that recovered from the disease) and Deceased (fraction of the population that died of the disease). Some works have been done in the construction of mathematical models and estimation of basic reproduction number for Covid-19.

Authors have used to determine the effectiveness of public health interventions (passenger air travel, driving, walking and transit mobility) in curbing the spread of Covid-19 in some selected European countries ((Alimohamadi et al., 2020; Linka et al., 2020). Certain study in China used Poisson likelihood-based method (ML), Exponential Growth Rate (EGR)-based method and stochastic Susceptible-Infected-Removed (SIR)dynamic model-based method to estimate the basic and controlled reproduction numbers. It concluded that strong measures taken by the China government was effective in the containment of the spread of the pandemic (You et al., 2020; Wang et al., 2020). Same study was conducted and similar conclusions were reached by researchers in Saudi Arabia (Alkahtani et al., 2021). Republic of Korea and Italy (Zhuang et al., 2020).

These and several other studies (Sahafizadeh and Sartoli, 2020; Karnakov et al., 2020; Alimohamadi and Sepandi, 2020) have shown that the SEIR model and the basic reproduction number can aid in the understanding of the dynamics of Covid-19 and in the measurement of the effectiveness of the control measures and enforced policies in a given geographical region. While much efforts have gone into the development of epidemiological models and estimation, it is noteworthy that much of this study has not been prevalent in Africa, and more precisely, Nigeria. In a country of about 200 million people which specific screening and testing measures, different threshold of control policies and a peculiar robustness in health care services, the importance of this study cannot be overemphasized. This will help in the determination of the effectiveness of the measures taken by the Nigeria government in flattening the curve of Covid-19 spread in Nigeria. Reports in research studies have shown that is context-based and must be understood on a country-by-country basis (Najafimehr et al., 2020; Kong et al., 2021; Maruotti et al., 2021).

### 3. Model Formulation

We proposed a compartmental-based model with the basic assumption that each member of the population is either Susceptible (S), Infectious (I), Recovered (R) from the disease or Died (D) of the disease. The model shall be referred to as Susceptible-Infectious-Recovered-Deceased (SIRD) model throughout this work. We choose this form of model based on the available Covid-19 data for Nigeria since it consists of the number of susceptible, infected, recovered, and deceased persons.

It is also assumed that the population size is constant and the rate of infection is proportional to the contact. Like all compartmental-based model, each compartment in the proposed model represents a group of individuals in the same medical history. Rate and direction of movement from one compartment to another is given in Figure 1. These movements are mathematically described by the system of ordinary differential equations in Equation (1).

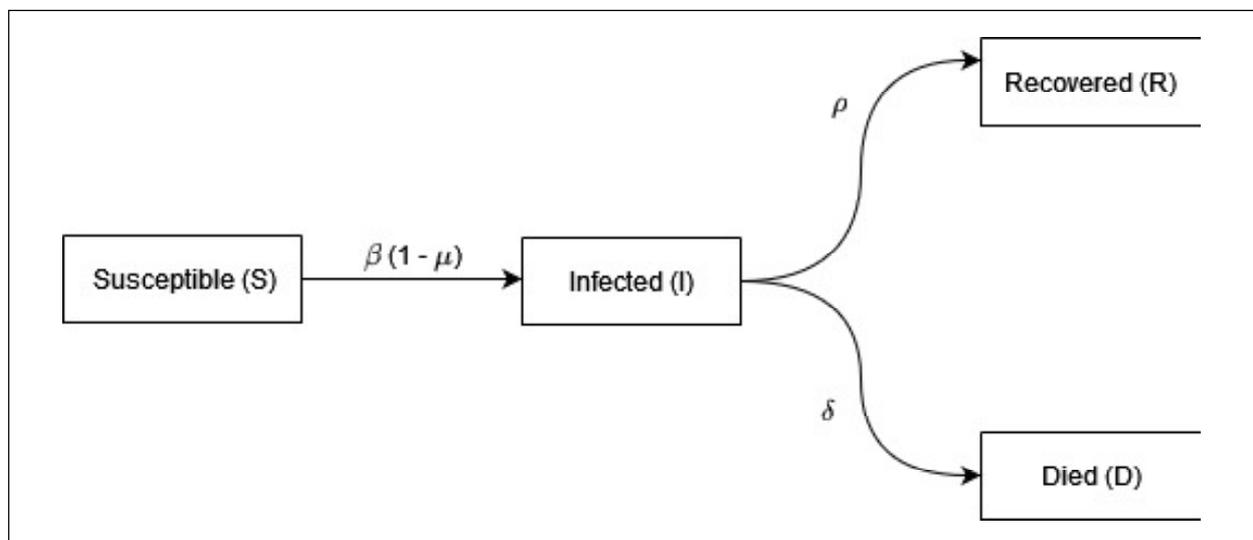


Figure 1: Rate and Direction of Movement from One Compartment to Another

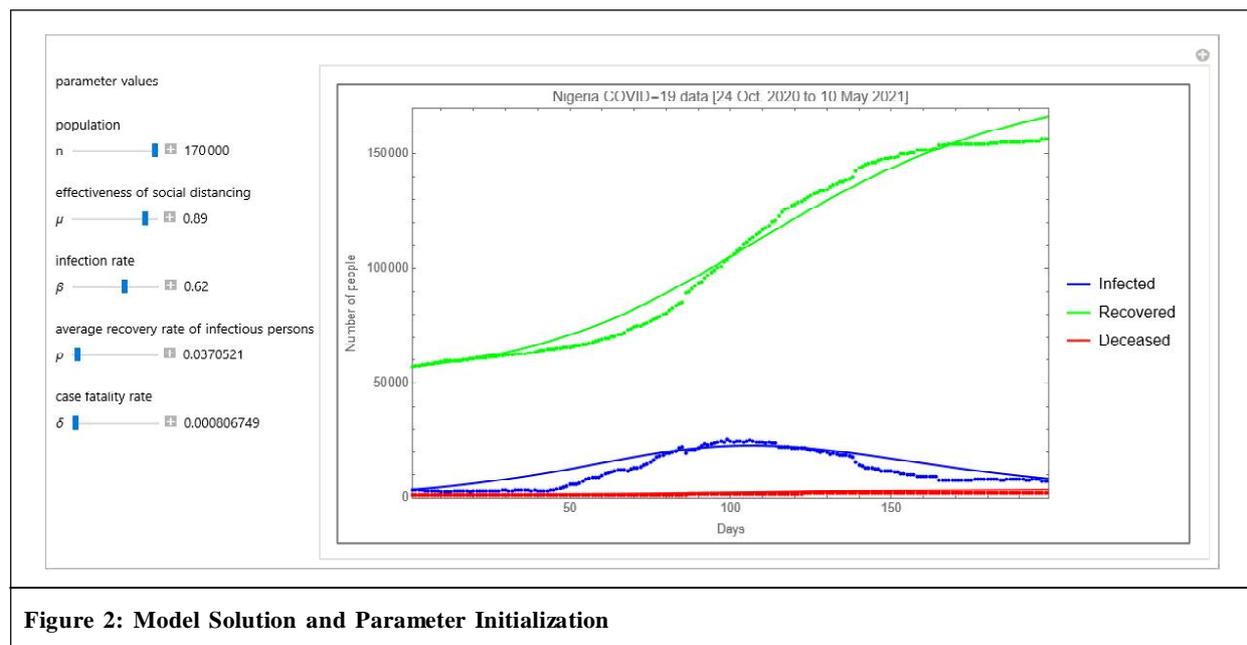
$$\left. \begin{aligned} \frac{dS}{dt} &= -\beta(1 - \mu)S(t)I(t) \\ \frac{dI}{dt} &= \beta(1 - \mu)S(t)I(t) - \rho I(t) - \delta I(t) \\ \frac{dR}{dt} &= \rho I(t) \\ \frac{dD}{dt} &= \delta I(t) \end{aligned} \right\} \dots(1)$$

where  $\beta$  is the effective contact rate,  $\rho^{-1}$  is the average recovery time (days) of infectious persons,  $\delta$  is the mortality rate,  $\mu \in [0,1]$  is the overall measure of the effectiveness of the current control policies.

#### 4. Parameter Estimation

Data on the Covid-19 pandemic for Nigeria between October 26, 2020 and May 10, 2021 used in this work was obtained from the Wolfram Data Repository (Research, 2022). It consists of estimated cases of Covid-19 infection in Nigeria between October 26, 2020 and May 10, 2021 and grouped into confirmed, infected, recovered, and deceased categories. It is also available as a comma-separate-file attached with this manuscript. The URL to the source is also available in Research (2022). In order to understand the dynamics of the pandemic, the parameters of the model are estimated in this section.

This is necessary as they significantly influence the behavior of the model under consideration. The dynamics of the disease can be visualized by varying the parameters as seen in Figure 2.



**Figure 2: Model Solution and Parameter Initialization**

Here, the first step in obtaining estimates of the parameter is that Equation (1) be solved in terms of the parameters. Since the curve fitting also requires that the parameter be initialized, the parameters were manually tuned to get the needed initial values. After the initialization of parameters, the Quasi-Newton algorithm was used to fit the resulting curves obtained from the solution of Equation (1) to get the best-fit parameter values as presented in Table 1. Quasi-Newton methods are good optimization techniques for finding local maxima and minima of functions.

They are based on Newton’s method to find the stationary point of a function, where the gradient is zero. The choice of using a Quasi-Newton algorithm in this work is based on the fact that they are typically quite fast and do not require computation of the Hessian matrix.

#### 5. Interpretation of Model Solution

This work describes the dynamics of the pandemic for the period under consideration by a four-compartmental based model Equation (1). Optimal values of the parameters that show the rates of movements from one compartment to

**Table 1: Asymptotic Parameter Correlation Matrix**

	Estimate	Standard Error	t-Statistic	p-Value
$N$	163963	3231.35	50.7415	9.72773 x 10-278
$\mu$	0.433618	923.121	0.00046973	0.999625
$\beta$	0.123347	201.037	0.000613551	0.999511
$\rho$	0.0388827	0.000661253	58.8015	2.30379 x10-249
$\delta$	0.000455552	0.00016139	2.82268	0.00492253

another and fit the model to the available data were obtained. The model solution showed that the second wave of the pandemic has a turning point around early February, 2021. Also, it indicated that the recovery curve is still rising and the mortality curve began flattening around early March 2021.

The effectiveness of the control measures was estimated to be 43.36%, which is below average. Similarly, the rate of infection was estimated as  $\beta = 0.123347$ . The average recovery time was also measured to be  $\rho^1 \approx 26$  days, while the mortality rate was estimated as  $\delta = 0.000455552$ .

**6. Estimation of the Basic Reproduction Number**

The basic reproduction number ( $R_0$ ) is essential in measuring the transmission potential of a disease. It is the average number of secondary infections produced by a single case of an infection in a susceptible population. In this section, we estimate its value for the second wave of the pandemic by the next generation method. Using the proposed model-Equation (1), we have

$$\left. \begin{aligned} \mathcal{F}_1 &= \beta(1 - \mu)SI \\ \mathcal{V}_1 &= (\rho + \delta)I \\ \mathcal{G}_1 &= -\beta(1 - \mu)SI \\ \mathcal{G}_2 &= \rho I \\ \mathcal{G}_3 &= \delta I \end{aligned} \right\} \dots(2)$$

From Equation (2), we obtain

$$\left. \begin{aligned} F &= \frac{\partial \mathcal{F}_1}{\partial I} \Big|_{S=1} = \beta(1 - \mu) \\ V &= \frac{\partial \mathcal{V}_1}{\partial I} = \rho + \delta. \end{aligned} \right\} \dots(3)$$

Now, the basic reproduction number ( $R_0$ ) is calculated as  $R_0 = FV^{-1}$ . Hence,

$$R_0 = \frac{\beta(1-\mu)}{\rho+\delta} \dots(4)$$

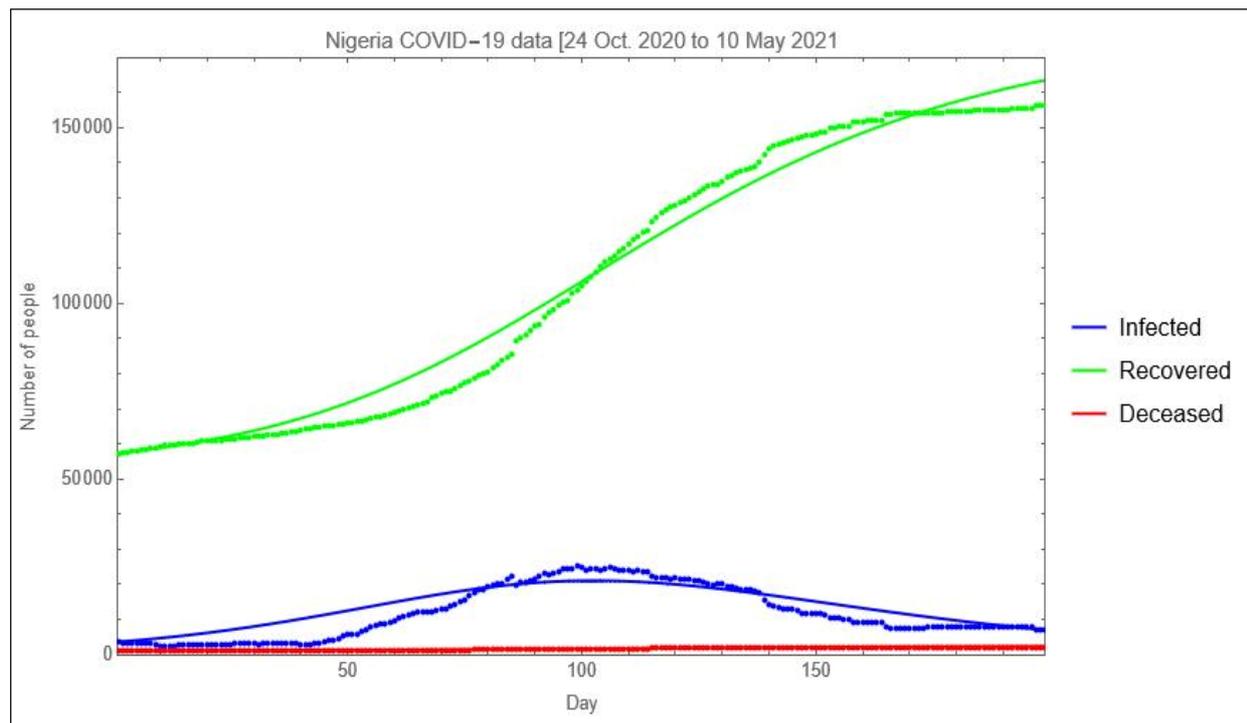
Substituting the estimated values of the parameters  $\beta, \mu, \rho$  and  $\delta$  from Table 1 in Equation (4), the estimated value of the basic reproduction number for the pandemic in the second wave is obtained as  $R_0 = 1.77591 > 1$ .

**7. Sensitivity Analysis**

To understand the dynamics of the model over time with respect to the parameters, a sensitivity analysis was carried out

**Table 2: Asymptotic Parameter Correlation Matrix**

	$N$	$\mu$	$\beta$	$\rho$	$\delta$
$N$	1	0.0491035	0.049104	0.756856	0.250101
$\mu$	0.04911035	1	1	-0.0461756	0.0196529
$\beta$	0.049104	1	1	-0.0461732	0.0196544
$\rho$	0.756856	-0.0461756	-0.0461732	1	0.0631494
$\delta$	0.250101	0.0196529	0.0196544	0.0631494	1



**Figure 3: Plot of Fitted Model to Available Data**

on the data by a systematic varying of the parameters values. Table 2 shows the asymptotic parameter correlation matrix while Figure 3 shows the fitted curve based on the optimal parameter estimates.

## 8. Conclusion

In this work, we used a SIRD model (1) to describe the dynamics of the second wave of the Covid-19 pandemic in Nigeria. Major parameters influencing the behavior of the model were estimated. An estimate of the basic reproduction number was obtained. The model fits the deceased compartment well, it also revealed that the recovered compartment recovers almost as fast as the data. The overall effectiveness of the control policies was obtained as 43.36%. This is an indication that control policies are not really that effective.

Conceptualization, A.W. and O.O.; methodology, A.W. and O.O.; software, A.W. and M.M.; validation, A.W. and O.O.; formal analysis, A.W. and O.O.; investigation, A.W. and O.O.; resources, A.W. and O.O.; data curation, A.W. and O.O.; writing—original draft preparation, A.W. and O.O.; writing—review and editing, M.M. and A.W.; visualization, A.W. and O.O.; supervision, M.M. and A.W. All authors have read and agreed to the published version of the manuscript.

## Funding

This research received no external funding

## Data Available in a Publicly Accessible Repository

The data presented in this study are openly available in Wolfram Data Repository at <https://doi.org/10.24097/wolfram.04123.data>.

## Acknowledgment

The authors acknowledge the effort of the Wolfram community in providing an excellent, curated and structured dataset on the Covid-19 pandemic.

## Conflicts of Interest

The authors declare no conflict of interest.

## References

- Al-Abdulla, O., Kallstrom, A., Valderrama, C. and Kauhanen, J. (2022). Simulation of the Progression of the COVID-19 Outbreak in Northwest Syria Using a Basic and Adjusted SIR Model. *Zoonotic Disease*, 2, 44-58. <https://doi.org/https://doi.org/10.3390/zoonoticdis2020006>.
- Alimohamadi, Y. and Sepandi, M. (2020). Basic Reproduction Number: An Important Indicator for the Future of the COVID-19 Epidemic in Iran. *Journal of Military Medicine*, 22, 96-97.
- Alimohamadi, Y., Taghdir, M. and Sepandi, M. (2020). Estimate of the Basic Reproduction Number for COVID-19: A Systematic Review and Meta-analysis. *Journal of Preventive Medicine and Public Health*, 53, 151.
- Alkahtani, T.A., Alakeel, A., Alakeel, R.A., Khorshid, F.A., Alshammari, H.H., Alguwaihes, A.M., Almohideb, M., Ali, E.M., Bin-Jumah, M., Abdel-Daim, M.M. et al. (2021). The Current Reproduction Number of COVID-19 in Saudi Arabia: Is the Disease Controlled? *Environmental Science and Pollution Research*, 28, 44812-44817.
- AlQadi, H. and Bani-Yaghoub, M. (2022). Incorporating Global Dynamics to Improve the Accuracy Of Disease Models: Example of a COVID-19 SIR Model. *PLoS ONE*, 17. <https://doi.org/https://doi.org/10.1371/journal.pone.0265815>.
- Annas, S., Pratama, M. I., Rifandi, M., Sanusi, W. and Side, S. (2020). Stability Analysis And Numerical Simulation of Seir Model for Pandemic COVID-19 Spread in Indonesia. *Chaos, Solitons & Fractals*, 139, 110072.
- Chen Laurent, Chen, X., Laurent S., Onur O.A., Kleineberg, N.N., Fink, G.R. and Warnke, C. (2021). A Systematic Review of Neurological Symptoms and Complications of COVID-19. *Journal of Neurology*, 268, 392-402.
- Cooper, I. Mondal, A. and Antonopoulos, C.G. (2020). A SIR Model Assumption for the Spread of COVID-19 in Different Communities. *Chaos, Solitons, and Fractals*, 139:110057. <https://doi.org/https://doi.org/10.1016/j.chaos.2020.110057>.
- De Felice, F. and Polimeni, A. (2020). Coronavirus Disease (COVID-19): A Machine Learning Bibliometric Analysis. *in vivo*, 34, 1613-1617.
- De la Sen, M. and Ibeas, A. (2020). On an Sir Epidemic Model for the COVID-19 Pandemic and the Logistic Equation. *Discrete Dynamics in Nature and Society*, <https://doi.org/https://doi.org/10.1155/2020/1382870>.
- Delamater, P.L., Street E.J., Leslie, T.F., Yang, Y.T. and Jacobsen, K.H. (2019). Complexity of the Basic Reproduction Number (R0). *Emerging Infectious Diseases*, 25, 1.
- Dietz, K. (1993). The Estimation of The Basic Reproduction Number for Infectious Diseases. *Statistical Methods in Medical Research*, 2, 23-41.
- Elibol, E. (2021). Otolaryngological Symptoms in COVID-19. *European Archives of Oto-Rhino-Laryngology*, 278, 1233-1236.
- Ferrari, L., Gerardi, G., Manzi, G., Micheletti, A., Nicolussi, F., Biganzoli, E. and Salini, S. (2020). Modelling Provincial Covid-19 Epidemic Data in Italy Using an Adjusted Time-dependent SIRD Model. *arXiv preprint arXiv:2005.12170*.
- Gai, C., Iron, D. and Kolokolnikov, T. (2020). Localized Outbreaks in an SIR Model with Diffusion. *Journal of Mathematical Biology*, 80, 1389-1411.
- Gaur, L., Bhatia, U., Jhanjhi, N., Muhammad, G. and Masud, M. (2021). Medical Image-based Detection of COVID-19 Using Deep Convolution Neural Networks. *Multimedia Systems*, 1-10.
- Gautam, R., Bani-Yaghoub, M., Neill, W. H., Döpfer, D., Kaspar, C. and Ivanek, R. (2011). Modeling the Effect of Seasonal Variation in Ambient Temperature on the Transmission Dynamics of a Pathogen With A Free-living Stage: Example of *Escherichia coli* O157: H7 in a Dairy Herd. *Preventive Veterinary Medicine*, 102, 10-21.
- Gautam, R., Lahodny, G., Bani-Yaghoub, M., Morley, P. and Ivanek, R. (2014). Understanding the Role of Cleaning in The Control of *Salmonella typhimurium* in Grower-finisher Pigs: A Modelling Approach. *Epidemiology & Infection*, 142, 1034-1049.
- Heesterbeek, J. and Roberts, M. (2007). The Type-reproduction Number T in Models for Infectious Disease Control. *Mathematical Biosciences*, 206, 3-10.

- Jebri, N. (2020). World Health Organization dEclared A Pandemic Public Health Menace: A Systematic Review of the Coronavirus Disease 2019 “COVID-19”. Available at SSRN 3566298.
- Karnakov, P., Arampatzis, G., Kièiæ, I., Wermelinger, F., Wälchli, D., Papadimitriou, C. and Koumoutsakos, P. (2020). Data-driven inference of the Reproduction Number for COVID-19 Before and After Interventions for 51 European Countries. *Swiss Medical Weekly*, 150, w20313.
- Kaur, J. and Kaur, P. (2021). Outbreak COVID-19 in Medical Image Processing Using Deep Learning: A State-of-the-Art Review. *Archives of Computational Methods in Engineering*, 1-32.
- Kermack, W.O. and McKendrick A.G. (1927). A Contribution to The Mathematical Theory of Epidemics. *Proceedings of The Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character*, 115, 700-721.
- Kong, J.D., Tekwa, E.W. and Gignoux-Wolfsohn, S.A. (2021). Social, Economic, and Environmental Factors Influencing The Basic Reproduction Number of COVID-19 Across Countries. *PloS One*, 16, e0252373.
- Kushwaha, Bahl, Kushwaha, S., Bahl S., Bagha, A.K., Parmar, K.S., Javaid, M., Haleem, A. and Singh, R.P. (2020). Significant Applications of Machine Learning for COVID-19 Pandemic. *Journal of Industrial Integration and Management*, 5, 453-479.
- Le Andreadakis, Le, T.T., Andreadakis, Z., Kumar, A., Román, R.G., Tollefsen, S., Saville, M., Mayhew, S. et al. (2020). The COVID-19 Vaccine Development Landscape. *Nat Rev Drug Discov*, 19, 305-306.
- Li, M.Y. and Muldowney J.S. (1995). Global Stability for the SEIR Model in Epidemiology. *Mathematical Biosciences*, 125, 155-164.
- Linka, K., Peirlinck, M. and Kuhl, E. (2020). The Reproduction Number of COVID-19 and its Correlation with Public Health Interventions. *Computational Mechanics*, 66, 1035-1050.
- Liu, Siegel, Liu T., Siegel, E. and Shen, D. (2022). Deep Learning and Medical Image Analysis for COVID-19 Diagnosis and Prediction. *Annual Review of Biomedical Engineering*, 24.
- Loli Piccolomini, E. and Zama, F. (2020). Monitoring Italian COVID-19 Spread by a Forced SEIRD Model. *PloS One*, 15, e0237417.
- Maruotti, A., Ciccozzi, M. and Divino, F. (2021). On the Misuse of the Reproduction Number in the COVID-19 Surveillance System in Italy. *Journal of Medical Virology*.
- Matadi M. B. (2014). The SIRD Epidemial Model. *Far East Journal of Applied Mathematics*, 89, 1-14.
- Najafimehr, H., Mohamed Ali, K., Safari, S., Yousefifard, M. and Hosseini, M. (2020). Estimation of Basic Reproduction Number For Covid-19 and the Reasons for Its Differences. *International journal of clinical practice*, 74.
- Nisar, K.S., Ahmad, S., Ullah, A., Shah, K., Alrabaiah, H. and Arfan, M. (2021). Mathematical Analysis of SIRD Model of COVID-19 with Caputo Fractional Derivative Based on Real Data. *Results in Physics*, 21, 103772.
- Ram, V. and Schaposnik, L.P. (2021). A Modified Age-structured SIR Model for COVID-19 Type Viruses. *Scientific Reports*, 11. <https://doi.org/https://doi.org/10.1038/s41598-021-94609-3>.
- Research, W. (2022). Epidemic Data for Novel Coronavirus COVID-19. *Wolfram Data Repository*. <https://doi.org/https://doi.org/10.24097/wolfram.04123.data>
- Sahafizadeh, E. and Sartoli, S. (2020). Estimating the Reproduction Number of COVID-19 in Iran using Epidemic Modeling. *MedRxiv*.
- Sen, D. and Sen, D. (2021). Use of a Modified SIRD Model to Analyze COVID-19 Data. *Industrial & Engineering Chemistry Research*, 60, 4251-4260.
- Shorten, C., Khoshgoftaar, T. M. and Furht, B. (2021). Deep Learning Applications for COVID-19. *Journal of Big Data*, 8, 1-54.

- Shringi, S., Sharma, H., Rathie, P.N., Bansal, J. C. and Nagar, A. (2021). [Modified SIRD Model for COVID-19 Spread Prediction for Northern and Southern States of India.](#) *Chaos, Solitons & Fractals*, 148, 111039.
- Sohrabi, Alsafi, Sohrabi C., Alsafi, Z., O'neill N., Khan, M., Kerwan A., Al-Jabir, A., Iosifidis, C. and Agha R. (2020). [World Health Organization Declares Global Emergency: A Review of the 2019 Novel Coronavirus \(COVID-19\).](#) *International Journal of Surgery*, 76, 71-76.
- Struyf Deeks, Struyf T., Deeks J.J., Dinnes J., Takwoingi Y., Davenport C., Leeflang M.M., Spijker R., Hooft, L., Emperador D., Domen, J. et al. (2021). [Signs and Symptoms to Determine if a Patient Presenting In Primary Care or Hospital Outpatient Settings has COVID-19.](#) *Cochrane Database of Systematic Reviews*, 17.
- Syeda, Syed, Syeda, H.B., Syed, M., Sexton, K.W., Syed, F., Prior, F. and Yu Jr F. (2021). [Role of Machine Learning Techniques to Tackle the COVID-19 Crisis: Systematic Review.](#) *JMIR Medical Informatics*, 9, e23811.
- Wang, Y., You, X., Wang, Y., Peng, L., Du, Z., Gilmour, S., Yoneoka, D., Gu, J., Hao, C., Hao, Y. et al. (2020). [Estimating the Basic Reproduction Number of COVID-19 in Wuhan, China.](#) *Zhonghua liu xing bing xue za zhi= Zhonghua liuxingbingxue zazhi*, 41, 476-479.
- Wang, Z.C., Zhang, L. and Zhao X.Q. (2018). [Time Periodic Traveling Waves for a Periodic and Diffusive SIR Epidemic Model.](#) *Journal of Dynamics and Differential Equations*, 30, 379-403.
- Wusu, A.S. and Olabanjo, O.A. (2020). [SEIRD Model for Analyzing Coronavirus \(COVID-19\) Pandemic.](#) *Wolfram Demonstrations Project*, 1.
- Wusu, A.S., Olabanjo, O.A. and Aribisala, B.S. (2021). [A SEIRD Model for Analysing the Dynamics of Coronavirus \(COVID-19\) Pandemic in Nigeria.](#) *Universal Journal of Applied Mathematics*, 9, 10-15. <https://doi.org/10.13189/ujam.2021.090102>.
- Wusu, A.S., Olabanjo, O.A. and Akanbi, M.A. (2022). [A Model For Analysing The Dynamics of The Second Wave of Corona Virus \(COVID-19\) in Nigeria.](#) *J. Math. Comput. Sci.-JMCS* 2022, 16-21.
- You, C., Deng, Y., Hu, W., Sun, J., Lin, Q., Zhou, F., Pang, C.H., Zhang, Y., Chen, Z. and Zhou, X.H. (2020). [Estimation of the Time-varying Reproduction Number of COVID-19 Outbreak in China.](#) *International Journal of Hygiene and Environmental Health*, 228, 113555.
- Yuki, Fujiogi, Yuki, K., Fujiogi, M. and Koutsogiannaki, S. (2020). [COVID-19 Pathophysiology: A Review.](#) *Clinical Immunology*, 215, 108427.
- Zhuang, Z., Zhao S., Lin, Q., Cao, P., Lou, Y., Yang, L., Yang, S., He, D. and Xiao, L. (2020). [Preliminary Estimates of the Reproduction Number of the Coronavirus Disease \(COVID-19\) Outbreak in Republic of Korea and Italy by 5 March 2020.](#) *International Journal of Infectious Diseases*, 95, 308-310.

**Cite this article as:** Ashiribo Senapon Wusu, Olusola Aanu Olabanjo and Manuel Mazzara (2022). [Estimating the Basic Reproduction Number for the Second Wave of Covid-19 Pandemic in Nigeria.](#) *International Journal of Pure and Applied Mathematics Research*, 2(2), 1-9. doi: 10.51483/IJPAMR.2.2.2022.1-9.