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Estimating the Basic Reproduction Number for the Second Wave of COVID–19 Pandemic in Nigeria

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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 analysed 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 analyse 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

1. Introduction

CoronaVirus Disease 2019 (COVID-19) has since been a global menace which affects different people in different ways [1,2]. With its symptoms ranging from mild symptoms to severe illness, COVID-19 has, since 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 [3,4]. 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 [5–7].

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 [8–10]. Deep learning models have also been proposed by authors in detecting the virus using medical images [11–14]. 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 behaviour 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 [15–19].

The classical Susceptible-Infected-Recovered (SIR) model is considered as one of the simplest compartmental model in epidemiology [20]. 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 [21–24]. In recent times, several authors have proposed different models which are modifications and adaptation of the SIR model to describe Covid-19 pandemic dynamics [25–29]. The authors in [25] extended the SIR model by incorporating the global dynamics of the COVID-19 pandemic. In [26], 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 [30–32]. 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 [33,34]. 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 [35].

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 [36]. 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 [37–40].

2. Related Works

For a given disease, the SIR model [20] 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.

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Authors have used R_0 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. [37,41]. Certain study in China used Poisson likelihood-based method (ML), exponential growth rate-based method (EGR) and stochastic Susceptible-Infected-Removed dynamic model-based method (SIR) 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 [40,42]. Same study was conducted and similar conclusions were reached by researchers in Saudi Arabia [43], Republic of Korea and Italy [44].

These and several other studies [45–47] 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 R_0 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 R_0 is context-based and must be understood on a country-by-country basis [48–50].

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 Eq (1).

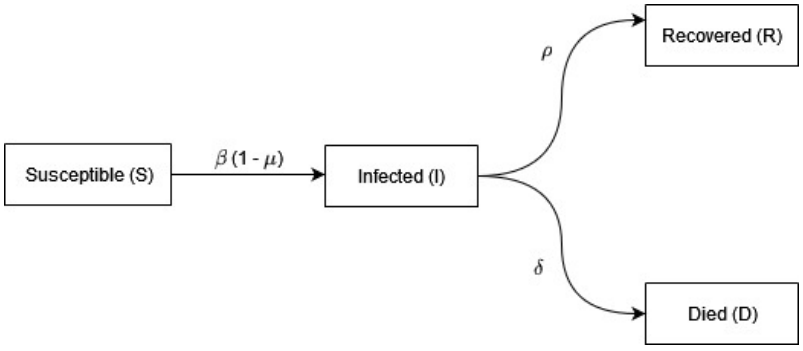

Figure 1. Rate and direction of movement from one compartment to another

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

where β is the effective contact rate, ρ^{-1} is the average recovery time (days) of infectious persons, δ 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 [51]. 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 [51]. 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 behaviour of the model under consideration. The dynamics of the disease can be visualized by varying the parameters as seen in Figure 2.

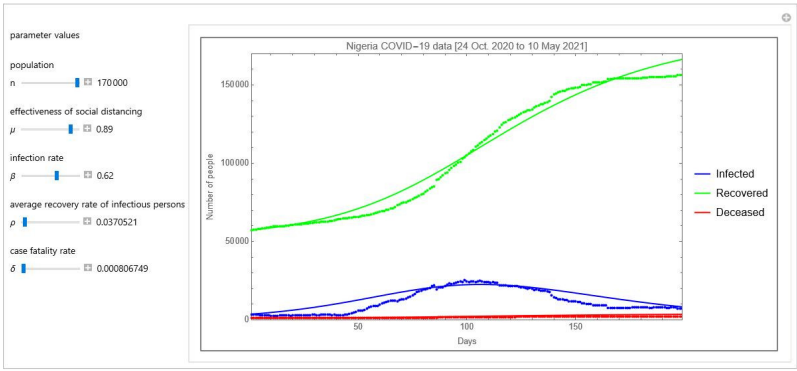

Figure 2. Model solution and parameter initialisation

Here, the first step in obtaining estimates of the parameter is that Eq (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 Eq (1) to get the best-fit parameter values as presented in Table **??**. 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.

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Table 1. Asymptotic parameter correlation matrix

	Estimate	Standard Error	t-Statistic	p-Value
N	163963	3231.35	50.7415	9.72773×10^{-218}
μ	0.433618	923.121	0.00046973	0.999625
β	0.123347	201.037	0.000613551	0.999511
ρ	0.0388827	0.000661253	58.8015	2.30379×10^{-249}
δ	0.000455552	0.00016139	2.82268	0.00492253

5. Interpretation of model solution

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

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

From Eq (2), we obtain

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

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

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

Substituting the estimated values of the parameters β, μ, ρ and δ from Table **??** in Eq (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 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.

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Table 2. Asymptotic parameter correlation matrix

	N	μ	β	ρ	δ
N	1	0.0491035	0.049104	0.756856	0.250101
μ	0.0491035	1	1	-0.0461756	0.0196529
β	0.049104	1	1	-0.0461732	0.0196544
ρ	0.756856	-0.0461756	-0.0461732	1	0.0631494
δ	0.250101	0.0196529	0.0196544	0.0631494	1

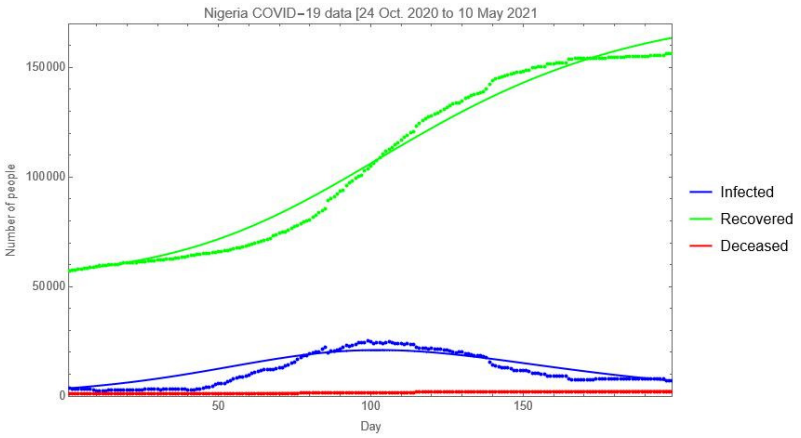

Figure 3. Plot of Fitted Model to Available Data

8. Conclusions

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 behaviour 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.

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