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Mathematical Modeling and Estimation of the Regional Variations in COVID-19 Infections Transmission in Nigeria: A Retrospective Data Analysis

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Abstract

This study estimated the reproduction number, which was used to determine the rate of spread of a communicable disease at sub-national levels in Nigeria and thereby provides state specific information needed to plan public health interventions. A Susceptible-Infectious-Recovered (SIR) model was first formulated from the compartmentalization of the whole disease population, and the SIR parameters for rate of spread of coronavirus (COVID)-19 computed and the reproduction numbers of infection were estimated across states in Nigeria. A log-linear model was also formulated from an exponential growth curve of COVID-19 infection, and thereafter the basic reproduction numbers were as well determined. The SIR analysis yielded the median reproduction number of COVID-19 transmission rate across states in Nigeria of 0.04473, range between 0.00082 and 1.2870, while the log-linear model yielded the median reproduction number of 2.003 ranges between 1.9759 and 2.0262 The results further reveals that there were significant disparities emerged when applying these models to the Nigerian context with notable under-estimation in some states perhaps due to under-reported cases at the early stage. The second approach, log-linear model with time-dependent transmission and removal rates to account for possible random errors across Nigeria states and estimates of reproduction numbers across states are greater than one ($R_t > 1$), may be due to the specified formula. The predictive ability of the log-linear model may be more suitable for modeling the incidence of COVID-19 and other infectious diseases in both the growth and decay phases, as well as for short-term predictions of the growth (or decay) of the number of new cases when no intervention measures had been recently implemented before the advent of vaccines. The general findings may reflect the effectiveness of virus control strategies and non-pharmaceutical interventions.

1. Introduction

The novel coronavirus disease 2019, COVID-19, caused by the severe acute respiratory syndrome virus 2 (SARS-CoV-2), has had profound impacts on social and economic life worldwide. The virus outbreak was first reported in Wuhan, China, in late December 2019 by the World Health Organization[1]. Subsequently, WHO later declared it as a global pandemic on March 11, 2020 [2]. As the pandemic unfolded, governments at sub-national, national, and regional levels implemented a range of measures aimed at mitigating the severity of the disease and reducing its fatality rate as highlighted in [3]. These measures included household-based prevention models such as hand hygiene, respiratory hygiene, remote work, self-isolation, and adherence to standard public health safety recommendations in WHO guidelines[1] such as reducing exposure, maintaining hand hygiene, using face masks, and following good food safety practices. The COVID-19 pandemic has displayed apparent regional variations in its case-fatality rate, as reported by WHO [1], and variations in the basic reproduction number as

observed by[4,5, 6]. These variations are indicative of the spatial heterogeneity of preventive measures and their effects across different regions. The timeliness in the individual country response and its effectiveness of mitigation measures have been emphasized in [7], and highlighted the importance of their timely implementation. Other factors, such as the proportion of individuals who were unable to work remotely, especially socio-economically disadvantaged individuals relying on informal activities, may also influence the effectiveness of these measures.

Traditionally, epidemiological models such as the Susceptible-Infectious-Recovered (SIR) models have been extensively employed to explain COVID-19 transmission dynamics. Recent research has extended the use of mathematical modelling to understand and estimate the complex regional variations in disease propagation. For instance, Jaya *et al.*[8] explored a Bayesian spatiotemporal method and estimated risk prediction for joint assessment of COVID-19 patients at intensive care unit (ICU) admissions and deaths in Sweden. The approach offered a wide disparity estimated in COVID-19 incidence in the sub-national context in Sweden. Similarly, Ferrández *et al.* [9] employ a multi-objective optimization approach to estimate parameters of compartmental epidemiological models on Ebola Virus Disease epidemics, thereby demonstrating the sophistication ability of a Bayesian method to understand and predict outbreaks of a highly contagious disease . Chu [10]investigated COVID-19 infections in Italy and Spain using two epidemiological growth models, revealing that the log-linear model is more suitable for short-term predictions of new case growth compared to the traditional SIR model, while Al-Ani [11], on the other hand, employed nonlinear growth models such as Gompertz, Richards and Weibull Probability Distributions to study the daily cumulative number of COVID-19 cases in Iraq. The Weibull model was adjudged to be the most effective model in describing the epidemic curve of COVID-19 and estimating crucial epidemiological parameters of the peak of daily cumulative cases, which could facilitate efficient monitoring of the epidemic's evolution in Iraq.

The early dynamics of COVID-19 transmission and its control strategies were investigated by [12], who offer insights into the potential impact of interventions during the emerging stages of the pandemic, while [13]unravel the patterns that underpin its initial spread, while [14] estimated the extreme COVID-19 mortality risks at sub-national levels having given consideration to geographic disparities in mortality rates. In [15], a comprehensive mathematical modelling was undertaken to analyse and evaluate the COVID-19 pandemic in Nigeria. Their research emphasizes the importance of timely intervention measures in shaping disease outcomes.[16]focuses on mathematical modelling of COVID-19 spread in China while estimating the number of undetected cases and analysing the impact of different intervention measures. Furthering the understanding of COVID-19 transmission dynamics, [17]provide real-time forecasts of COVID-19 epidemic progression in China, providing invaluable insights into its potential trajectory, while in [18] a time-varying transmission dynamic method was exploited to study the COVID-induced Pneumonia disease in China, and the approach provides an in-depth understanding of its evolving spread patterns in the country.

Other studies have justified the incorporation of spatially structured models in COVID-19 transmission dynamics. For instance, Roelofs *et al.*,[19] investigated the intricate interplay between spatial mobility patterns and COVID-19 incidence during the pandemic's second wave in the Netherlands, and they found that the spatial determinants are significant confounders of COVID-19 transmission. Additionally, studies such as[20]highlight the significance of undocumented infections in facilitating the rapid dissemination of SARS-CoV-2, calling attention to the role of asymptomatic carriers in fuelling the pandemic's spread. Also in [21] , the basic reproduction number of COVID-19 was estimated for countries across Africa and the study provided insights into the disease's transmissibility at the earlier stage of the COVID-19 pandemic in the African continent.

Despite these valuable studies at national and continental levels, there is a need to further investigate the regional variations of COVID-19 transmission, particularly in countries like Nigeria. Understanding these variations at sub-national levels is essential for tailoring targeted interventions and optimizing the allocation of resources for disease control and prevention efforts. This research aims to estimate the growth models of COVID-19 transmission rates at sub-national levels in Nigeria. This study provides valuable insights in shaping policies and strategic actions needed to be taken to effectively mitigate pandemic in different regions of Nigeria. The optimal applicability of infection disease modeling and model adequacy would be measured by its model ability in determining the transmission rates and lowering the trajectory curves.

This paper is organized as follows: The study design and data section use detailed COVID-19 incidence data from Nigeria for the main analysis and provides a brief summary of the findings. This section also offers insights into the emergence and spread of COVID-19 in Nigeria, including geographical maps that place Nigeria in the context of its neighboring states. The method section outlines the Susceptible-Infectious-Recovered model and the log-linear model used to estimate basic reproduction number and effective reproduction number as measures of the infectiousness of diseases an. Section 4 presents the findings and discussions of the results. The final section presents the concluding remarks of the study.

2. Study Design and Methods

2.1 Data Source

The data source for this study comprises official statistics provided by the Nigeria Center for Disease Control (NCDC), located in Abuja, Nigeria. The first documented COVID-19 case was on February 27th, 2020 and reported by the Ministry of Health (MoH). Since that date, the NCDC has been delivering daily updates on the COVID-19 situation, encompassing total cases, tests conducted, recoveries, fatalities, and active cases. This dataset is available for download at the website of the Nigeria Centre for Disease Control (NCDC, 2021). The study uses daily COVID-19 case reports in Nigeria from February 27th, 2020 to January 2nd, 2022. Weekly case aggregates were formed, excluding weeks 35-37 of 2020 and weeks 21-24, 30, and 31 of 2021. The study covers 232,157 reported cases sourced from the Nigeria Centre for Disease Control (NCDC, 2021) as collected from all 36 states and FCT, Abuja with emphasis on contiguous states (37 districts) is shown in Figure 1.

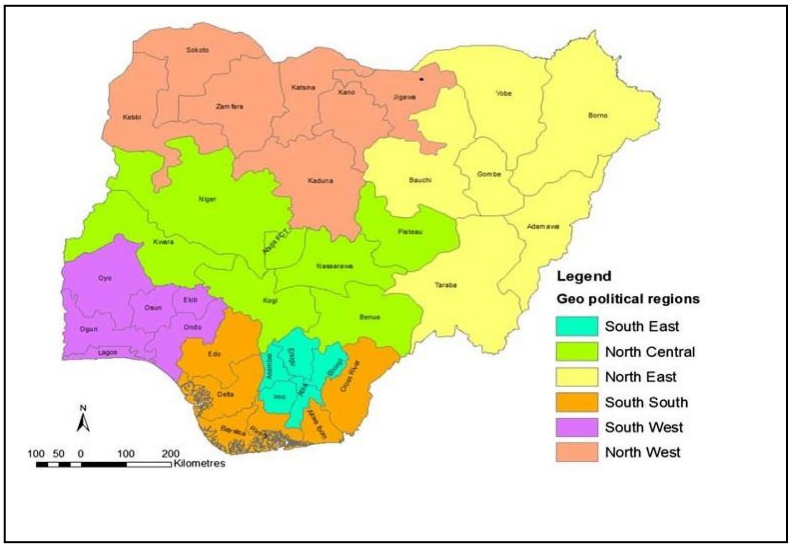


Figure 1: Map of Nigeria showing 37 districts (36 states and Federal Capital Territory, Abuja) and states grouped into six geo-political zones.

2.2. Formulation of Susceptible-Infectious-Recovered (SIR) Model

The compartmental models used to mathematically describe the spread of infectious diseases within populations serve as a valuable tool as described in [23]. The study adopts the susceptible-infectious-recovered (SIR) model initially proposed by[24] and a modified version by [25]. Other applications were recently employed in several infectious disease studies COVID-19 in Spain and Italy [10], reproduction number of COVID-19 in different African countries [21]and spatial mobility patterns in the Netherlands [19]. In the traditional SIR model, the entire population was categorized into three segments which comprised those susceptible (S) to the disease but not yet infected, those who are infectious (I), and those who have recovered (R) and are immune to the disease or have passed away.

The SIR model operates under the assumption of a fixed population size N. According to the World Health Organization (WHO) [2], the entire population is considered susceptible to COVID-19 infection, intensive care (IC) admission, and the potential outcome of death due to COVID-19 infection. For this study, the projected populations of each state (sub-nationals) for the year 2020 serve as the susceptible population.

Designating the variables S(t), I(t), and R(t) as the counts of individuals within the respective compartments mentioned earlier, as functions of time t, we adopt a SIR model as described by [22]. This SIR model was formulated as a set of three ordinary differential equations and associated initial values conditions given as equations (1)-(3) by

$$\frac{dS}{dt} = -\frac{\beta IS}{N}, \qquad S(0) = S_0 \geq 0 \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I, \qquad I(0) = I_0 \geq 0 \tag{2}$$

$$\frac{dR}{dt} = \gamma I, \qquad R(0) = R_0 \geq 0, \tag{3}$$

where $r = \frac{\gamma}{\beta}$ is the relative removal rate. In equation (1), it indicates that $\frac{dS(t)}{dt} < 0$, i.e., in the elapse of time, the susceptible population $S(t)$ in the compartment will be decreased. The infected population, $I(t)$ initially increases exponentially, and then moves to a plateau, and finally shrinks to zero if the disease is abolished completely after a finite time interval as described in [26, 27].

At $t = 0$ the initial conditions of the model are described in [28] as

$$S(0) = S_0 > 0, I(0) = I_0 > 0, R(0) = 0 \quad \text{associated with} \quad I << S. \tag{4}$$

According to [27], these initial conditions stated in equations (4) and it would also ensure that the condition $I << S$ holds. Furthermore, assuming $N(t)$ to be constant for a closed population, implies that the analyst needs to focus on S and I. By adding up equations (1), (2), and (3), we obtain:

$$\frac{dS(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0 \tag{5}$$

And integrating we get we get the total population size in the SIR model as

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

The set of equations (1)-(3) encapsulate the dynamics of an infectious disease outbreak and elucidate the rates of change in the compartments within the population. The model assumes standard incidence, a recovery (removal) rate of γ as defined in equation (3), and a short enough time span for analysis where $N(t)$ remains constant (i.e., no births or deaths altering the susceptible population). Additionally, the COVI-19 transmission processes of the SIR model are guided by the parameters, infection rate (β) and recovery rate (γ), representing the transition rates from S to I (Susceptibility to Infection) and from I to R (Infection to Recovery or Death).

From equation (2) above, SIR model can be formulated in terms of reproduction number R_0 as

$$\left.\begin{aligned} \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I \\ &= \gamma\left[\frac{\beta}{\gamma}\frac{S}{N} - \mathbf{1}\right]I \\ &= \gamma\left[\mathbf{R}_0\frac{S}{N} - \mathbf{1}\right]I \end{aligned}\right\} \tag{7}$$

Per-capita transmission is maximized when $S \approx N$

$$\frac{dI}{dt} = \gamma(R_0 - 1)I \tag{8}$$

The disease infection (*I*) increases if $R_0 > 1$, decreases if $R_0 < 1$. R_0 is the basic reproductive number = β x 1/γ = β x (average duration of infection), which indicates that the average number of secondary infections caused by an infectious individual when the population is almost entirely susceptible. For further readings SIR model see [22] and [29].

Recently, other studies have employed multivariate Analyses of COVID-19 pandemic by investigating the socio-demographic factors of the population such as COVID-19-related mortality in USA [30], and spatial modeling of COVID-19 fatality in [31]. Other works have studies have employed different versions of mathematical models in the literature that try to describe the dynamics of the evolution of COVID-19. A non-linear graphical modeling of preventive actions and healthcare factors is detailed in [32]. Three phenomenological models are proposed by [33] for early COVID-19 pandemic in China, which were validated with outbreaks of other diseases different from COVID-19, which have been used to generate and assess short-term forecasts of the cumulative number of reported cases. Other works such as in [34] propose SEIR-type models with little variations and some of them incorporate stochastic components. COVID-19 is a disease caused by a novel virus with account of its known specific characteristics.

2.3 Reproduction Number (R_0) Estimation

The basic reproduction number plays an important role to explain the outbreak of the epidemic disease. This number indicates the likelihood of recovery from the infectious disease in society. The basic reproduction number, denoted as R_0, which was developed to study demographers in the early 20th century, R_0 found its way into the realm of infectious disease research in the 1950s as stated in [35]. From the SIR model presented earlier, the basic reproduction number is computed as

$$R_0 = \frac{the\ transmission\ rate}{the\ recovery\ rate} = \frac{\beta}{\gamma} \tag{9}$$

At the equilibrium condition stated in equation (5) holds and using the first two terms, then the basic reproduction number can be derived at time, $t = 0$. The expected number of secondary infections arising from a single individual during their entire infectious period in a population of susceptible individuals as described by[22], R_0 has cemented its status as a traditional concept in epidemiological studies. In simpler terms, it quantifies the projected number of people an infected individual will go on to infect.

The R_0 value serves as a vital indicator of the severity of an infectious disease outbreak as highlighted in previous studies[35; 36]and summarized as follows: If $R_0 < 1$, each infected individual is expected to transmit the disease to less than one individual on a weekly average, leading to the disease dying out. However, if $R_0 = 1$, each infected individual will infect exactly one person on weekly average (equivalent 7 daily rate) maintaining a stable level of spread. If $R_0 > 1$, the infected individual would be expected to transmit the disease to more than one person on a daily average (7 days per week equivalent), which indicates that the disease will continue to spread exponentially in a pandemic. This value can be estimated by substituting the (estimated) optimal values of β and γ as outlined in[22,37]. In general, the reproduction number, R_0 holds in a scenario where no individual was already infected or immune to the disease. This assumption might hold more validity at the initial stages of an outbreak. However, in a real-world outbreak, an infectious disease transmission is seldom captured at the precise moment when the infected individual had contact with a susceptible one. Additionally, it is important to note that R_0 values computations under different models may varying under different environments, see Heffernan *et al.* [35]. As such, the specific model and its associated parameters play a significant role in determining the R_0 value.

2.4 Log-linear model

The state count data of infections constitute the response, y_{it} assumes to be exponentially distributed over time $i = 1,....,37$ (36 states and FCT-Abuja), $t = 1,.....,83$ (time), for the cases of the COVID-19 pandemic time-dependent model. The log-linear relationship of COVID-19 infection cases over time as a transformation of exponential distribution of growth curve rate presents a straightforward approach for capturing the incidence of infectious diseases as shown in growth curves presented in Figure 2. Generally, the course of infectious disease outbreaks can be divided into two phases: the growth phase and the decay phase.

In this study, the initial growth rate is studied at sub-national levels (states) as presented in Figure 1. It could be observed that for most affected states in Nigeria, the weekly incremental incidence exhibits an approximate exponential trend at the early stage. The daily COVID-19 incidences were aggregated to weekly approximately follows a sigmoid curve as indicated in the plot. The log transform of the curves can be expressed in the form of a log linear of exponential distribution given by

$$\text{Log}\,(\lambda) = \alpha_i + \beta_0 \text{X} + \beta_1 \text{t} \tag{10}$$

By ignoring the state-effect covariates (e.g. socio-demographic factors, X), equation (10) can be simply re-written as separate time- dependent log linear models for confined cases, recovered and death respectively as given by

$$\log(\lambda_{\text{i,C}}) = \alpha_i^C + \beta_{it}^C \text{t}_{\text{ij}} \tag{11a}$$

$$\log(\lambda_{\text{i,R}}) = \alpha_i^R + r_{it}^R \text{t}_{\text{ij}} \tag{11b}$$

$$\log(\lambda_{\text{,iD}}) = \alpha_i^D + \text{d}_{it}^D \text{t}_{\text{ij}} \tag{11c}$$

Where $\alpha_{i\,i}$ denotes the overall of state-specific -risk (intercept) COVID-19 incidence in i^{thh}, state as indicated in the set of equations (11a) - (11 c) for confirmed(C), recovered (R) and death (D) respectively and indicated in superscript , here r_i denoted the growth rate of the invectives at state, i and d denoted the death rate and t the duration of infected population (in number of days or weeks) since the first confirmed cases, and α_i are the intercepts respectively of i^{th} state. The linear relationship is frequently used in infectious disease epidemiology, with the term 1/b interpreted as mean generation interval in Ferguson *et al*.[38] or as duration of the infectious period as detailed in [39].

The log-linear model was fitted to obtain the optimal values of the parameters the incidence package[40] in R programming (R Development Core Team, 2020). The estimated parameters of the fitted models were then used to compute the trajectory of the incidence up until the peak incidence in the growth phase. Finally, R_0 may be determined from the intrinsic growth rate of the infected population The basic reproduction number R_0 value was later computed using the model parameters of the log-linear models, which are derived from the exponentially distribution of the infections as a time –dependent transmissions. the linear relationship and the growth(slope) rate r_i as defined in[41] and R_0 is computed as

$$R_0 = 1 + \frac{r}{d} \tag{12}$$

where r_i is the estimated exponential growth rate for infected cases and d is the death rate as indicated in equations (11 a, b, c) and d denotes the same rate as γ in equation (3). A good review of basic compartmental disease transmission models is provided by Hethcote [22] and a recent wider review of R_0 *a*s given by Heffernan *et al.* [35]. A number of recent studies have used this approach, including Pybus et al. [39] and Mills *et al.* [42].

3. Application to COVID-19 infection Data and Data Analysis Results

3.1. *Exploratory Data Analysis*

Table 1 presents an overview of the COVID-19 transmission dynamics across different states within Nigeria. Notably, during the initial surge of the virus within the country, Taraba State emerged as the epicenter, registering the highest incidence with six confirmed cases. Similarly, states such as Akwa-bom, Gombe, and Rivers demonstrated a notable presence in the early stages of the outbreak, each reporting five confirmed cases. Moreso, Abia, Kogi, Kwara, and Zamfara exhibited an initial surge characterized by two confirmed cases. Conversely, certain states, including Anambra, Lagos, Oyo, Osun, and Yobe, along with the remaining states, confronted a more contained initiation, each reporting a solitary confirmed case during the preliminary surge of COVID-19 transmission. As the pandemic progressed, a notable pattern emerged, with Lagos becoming the epicenter of the outbreak, recording the highest number of cases at 3,393. Following Lagos, the Federal Capital Territory, Abuja, ranked second with 734 confirmed cases. Interestingly, Kogi State was a unique case, consistently maintaining its initial count of only two cases throughout the pandemic. This indicates that most states in Nigeria experienced a steady increase in reported COVID-19 cases, with Kogi State being the notable exception.

Table 1: Descriptive summary of COVID-19 transmission across states in Nigeria (first case and peak case)

State	Date of First Case	$t = 0$	Date of Peak Case	Peak Case	Date Diff. (days)
Abia	20th April, 2020	2	2nd February, 2021	103	288
Adamawa	22nd April, 2020	1	4th March, 2021	180	316
Akwa-Ibom	1st April, 2020	5	12th August, 2021	141	498
Anambra	10th April, 2020	1	16th February, 2021	344	312
Bauchi	1st April, 2020	1	10th March, 2021	75	343
Bayelsa	26th April, 2020	1	16th June, 2020	54	51
Benue	4th May, 2020	1	2nd January, 2022	202	608
Borno	19th April, 2020	1	26th December, 2021	166	616
Cross River	6th July, 2020	5	26th February, 2021	57	235
Delta	7th April, 2020	1	25th October, 2021	508	566

Ebonyi	26th April, 2020	1	12th July, 2020	108	77
Edo	23rd March, 2020	1	21st December, 2021	155	638
Ekiti	18th March, 2020	1	21st August, 2021	49	521
Enugu	28th April, 2020	1	2nd February, 2021	81	280
FCT	22nd March, 2020	1	23rd December, 2021	734	641
Gombe	20th April, 2020	5	3rd November, 2021	109	562
Imo	25th April, 2020	1	26th September, 2021	124	519
Jigawa	19th April, 2020	1	7th May, 2020	44	18
Kaduna	28th March, 2020	1	22nd January,2021	545	300
Kano	11th April, 2020	1	6th February, 2021	124	301
Katsina	7th April, 2020	1	17th December, 2020	70	254
Kebbi	26th April, 2020	1	9th December, 2020	45	227
Kogi	27th May, 2020	2	27th May, 2020	2	NA
Kwara	6th April, 2020	2	23rd December, 2020	397	261
Lagos	16th March, 2020	1	22nd December, 2021	3,393	646
Nasarawa	28th April, 2020	1	29th December, 2021	92	610
Niger	10th April, 2020	1	1st February, 2021	69	297
Ogun	27th February, 2020	1	9th June, 2020	108	103
Ondo	3rd April, 2020	1	4th September, 2021	180	519
Osun	25th March, 2020	1	9th February, 2021	120	321
Oyo	22nd March, 2020	1	25th December, 2021	234	643
Plateau	23rd April, 2020	1	15th January, 2021	273	267
Rivers	25th March, 2020	1	30th December, 2021	420	645
Sokoto	20th April, 2020	1	9th January, 2021	58	264
Taraba	26th April, 2020	6	20th October, 2021	109	542
Yobe	29th April, 2020	1	7th April, 2021	24	343
Zamfara	24th April, 2020	2	10th January, 2021	45	261

Figure 1 lots of the weekly incremental growth trend in COVID-19 transmission across states with Lagos, FCT-Abuja, Ogun, Oyo, Rivers and Jos, Plateau state having the lead in the trend across states in Nigeria. In Figure 2, the graph presents the plots of all cumulative incidences appears to show an exponential trend, increasing slowly for the first few weeks after the first confirmed cases before growing rapidly.

Figure 2plots the weekly cumulative incidence for Nigeria and its 36 states and FUT- Abuja (37 districts) over the study period. The cumulative incidences appear to describe an exponential growth, which rose slowly for the first 3-5 weeks after the first cases were confirmed before growing rapidly. Checking through the curve plots on a log-linear scale as shown in Figure 2, it was found that the logarithm of COVID-19 confirmed cases for most states exhibited an approximate non-linear trend suggesting that cumulative incidence truly represent exponential curve. However, the majority of states (sub-nationals) and overall cases for the country did not demonstrate exactly linear thread, but resemble slightly exponential (or sigmoid) growth curves.

3.2 Estimation SIR Model parameters of COVID-19 infections at state levels in Nigeria

Table2 presents the results of parameter estimates of the incidence of COVID-19 infections for each state, the projected population size, the cumulative number of cases at 52 weeks after the first confirmed cases, and estimates for R_0. The estimates of the parameters β and γ do not show any particular trends and this is reflected in the estimated R_0 values.

From Table 2, it can be seen that the estimated reproduction number R_0 values for all states in Nigeria fall between 0 and 1, except FCT-Abuja and Lagos, which are epicenters and the entry points to many airlines. This suggests that the COVID-19 disease infection would likely fade out in a short in Nigeria. The summary of the overall prevalence rate of COVID-19 across the states in Nigeria using the SIR model is presented in Figure 3.

The information presented in Figure 3 demonstrates that as time passes, the infection rate tends toward zero. This suggests that the COVID-19 will likely fade out over time.

3.3. Log-Linear Model Analysis Across States in Nigeria

Table 3 presents the estimates summary of the log-linear model for confirmed, recovery and fatalities of COVID-19 across states in Nigeria. From Table 3, the alpha (α) values indicate the approximate (integer) weekly averages of infection, recovery, and death cases. On the other hand, the slope β values represent the corresponding incidence rates. Notably, for the majority of states, the infection rates (confirmed cases) are below 1, which suggests that the growth curves would ultimately reach a saddle point in the long run.In Figure 4, the confirmed case data from Table 3 are synthesized to ascertain the statistically significant levels of the model parameters. The visual representation in Figure 4 displays the 95% confidence intervals (CI) of the model parameters concerning confirmed cases across 36 states and the Federal Capital Territory, Abuja.

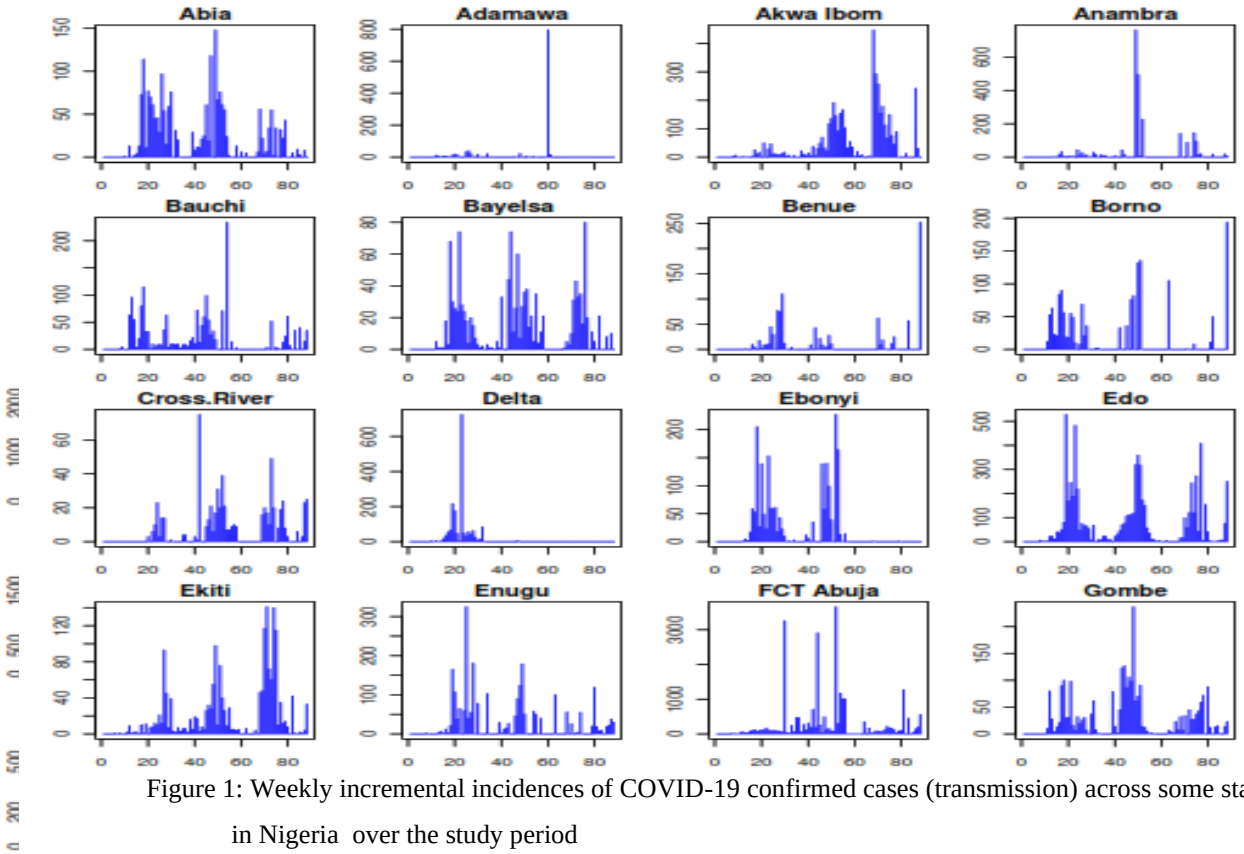
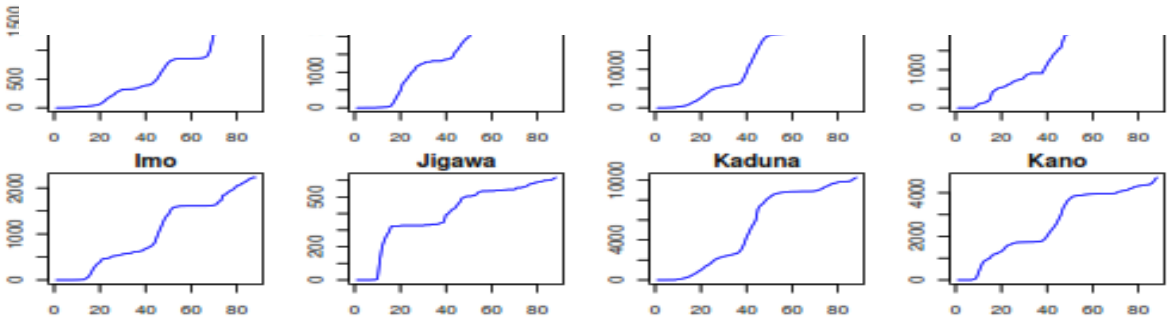


Figure 1: Weekly incremental incidences of COVID-19 confirmed cases (transmission) across some states in Nigeria over the study period



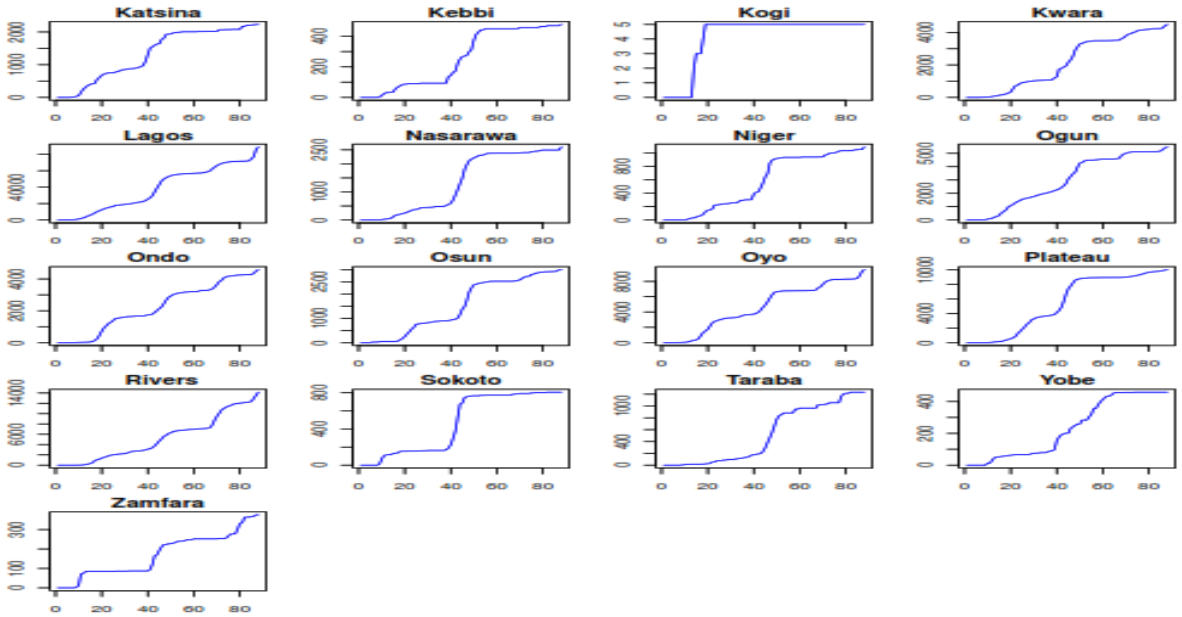


Figure 2: Plots the weekly cumulative incidence for Nigeria and its 36 states and FCT- Abuja (37 districts) over the study period.

Table 2 Estimated SIR model parameters and R_0 of COVID-19 cases at state levels in Nigeria

State	Population* (2020)	Cumulative Case	β	γ	R_0
Abia	3,841,943	103	1.34047E-05	0.003	0.0270
Adamawa	4,536,948	180	3.96743E-05	0.003	0.0878
Akwa-Ibom	4,780,581	141	5.89887E-06	0.002	0.0206
Anambra	5,599,910	344	6.14296E-05	0.003	0.1342
Bauchi	7,540,663	75	9.94608E-06	0.003	0.0239
Bayelsa	2,394,725	54	2.25496E-05	0.020	0.0081
Benue	5,787,706	202	3.49016E-05	0.002	0.1485
Borno	5,751,590	166	2.88616E-05	0.002	0.1245
Cross River	4,175,020	57	2.73053E-06	0.004	0.0045
Delta	5,307,543	508	9.57129E-05	0.002	0.3792
Ebonyi	3,007,155	108	3.59144E-05	0.013	0.0194
Edo	4,461,137	155	3.47445E-05	0.002	0.1552
Ekiti	3,350,401	49	1.46251E-05	0.002	0.0533
Enugu	4,396,098	81	1.84254E-05	0.004	0.0361
FCT-Abuja	2,702,443	734	0.000271606	0.002	1.2187
Gombe	3,623,462	109	6.01635E-06	0.002	0.0237
Imo	5,167,722	124	2.39951E-05	0.002	0.0872
Jigawa	6,779,080	44	6.49056E-06	0.056	0.0008
Kaduna	8,324,285	545	6.54711E-05	0.003	0.1375
Kano	14,253,549	124	8.69959E-06	0.003	0.0183
Katsina	9,300,382	70	7.52657E-06	0.004	0.0134
Kebbi	5,001,610	45	8.9971E-06	0.004	0.0143
Kogi	4,153,734	2	2.40747E-07	0.000	NA
Kwara	3,259,613	397	6.08968E-05	0.004	0.1113

Lagos	12,772,884	3,393	0.000265641	0.002	1.2012
Nasarawa	2,632,239	92	3.49512E-05	0.002	0.1492
Niger	6,220,617	69	1.10921E-05	0.003	0.0231
Ogun	5,945,275	108	1.81657E-05	0.010	0.0131
Ondo	4,969,707	180	3.62194E-05	0.002	0.1316
Osun	4,237,396	120	2.83193E-05	0.003	0.0636
Oyo	7,512,855	234	3.11466E-05	0.002	0.1402
Plateau	4,400,974	273	6.20317E-05	0.004	0.1159
Rivers	7,034,973	420	5.97017E-05	0.002	0.2696
Sokoto	5,863,187	58	9.89223E-06	0.004	0.0183
Taraba	3,331,885	109	5.45237E-06	0.002	0.0207
Yobe	3,398,177	24	7.06261E-06	0.003	0.0170
Zamfara	5,317,793	45	4.23108E-06	0.004	0.0077
Nigeria	201,135,262				

* Country Meters, C. (2020). Nigeria Population

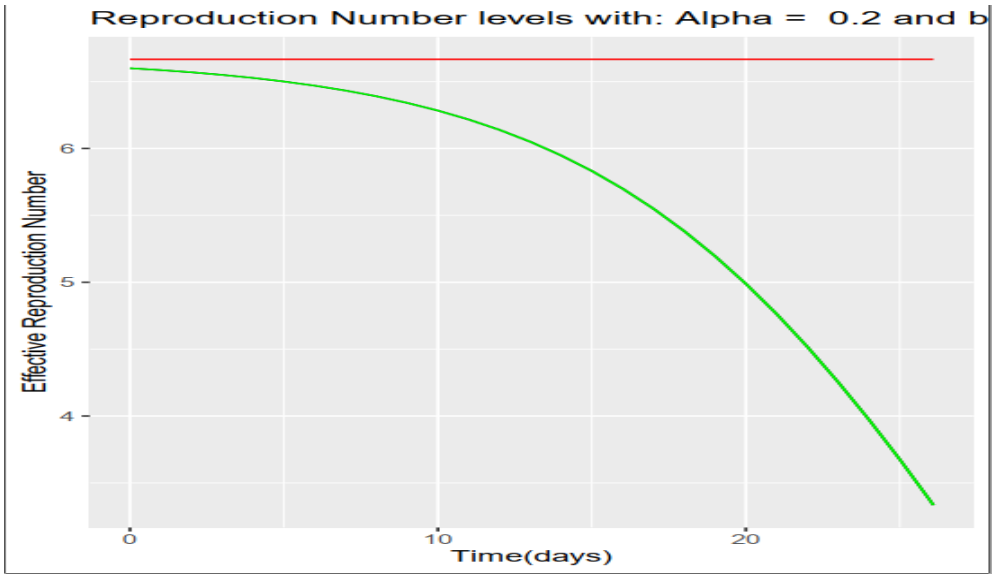


Figure 3: SIR Model Trend

Table 3: Estimates summary of log-linear models on confirmed, recovery and Fatalities of COVID-19 across states in Nigeria

States	Confirmed		Recovered		Fatality		R_0
	α	r	α	β	α	d	$R_0 = 1 + \frac{r}{d}$
Abia	17	0.989	17	0.984	2	1.0582	1.9940
Adamawa	9	0.989	5	0.978	2	1.1099	1.9940
Akwa-Ibom	9	1.008	9	1.010	1	1.1120	2.0120
Anambra	7	1.000	7	0.987	1	1.1429	2.0050
Bauchi	17	0.989	16	0.982	1	1.0582	1.9940
Bayelsa	9	0.996	11	0.989	1	1.1107	2.0010
Benue	8	0.995	5	0.986	1	1.1244	2.0000
Borno	2	1.007	12	0.972	2	1.5035	2.0121
Cross River	4	1.006	5	0.999	1	1.2515	2.0111
Delta	17	1.000	13	0.961	2	1.0588	2.0060

Ebonyi	22	0.974	20	0.961	1	1.0443	1.9789
Edo	35	0.995	36	0.991	3	1.0284	2.0030
Ekiti	6	1.009	6	1.007	1	1.1682	2.0131
Enugu	14	0.997	9	0.994	1	1.0712	2.0020
FCT	123	1.002	84	0.998	4	1.0081	2.0091
Gombe	23	0.990	19	0.988	2	1.0430	1.9960
Imo	12	1.000	14	0.989	2	1.0833	2.0050
Jigawa	4	0.994	5	0.987	1	1.2485	1.9990
Kaduna	63	0.994	79	0.988	2	1.0158	2.0000
Kano	35	0.990	49	0.983	2	1.0283	1.9960
Katsina	30	0.971	12	0.983	2	1.0324	1.9759
Kebbi	4	1.011	4	0.983	1	1.2528	2.0161
Kogi	NA	NA	NA	NA	NA	NA	NA
Kwara	26	0.994	20	0.975	2	1.0382	2.0000
Lagos	456	1.002	126	0.976	5	1.0022	2.0111
Nasarawa	25	0.976	4	0.976	1	1.0390	1.9809
Niger	8	0.988	6	0.980	1	1.1235	1.9920
Ogun	33	0.992	37	0.987	2	1.0301	1.9980
Ondo	20	1.002	11	0.991	2	1.0501	2.0080
Osun	13	0.997	17	0.992	2	1.0767	2.0030
Oyo	37	0.993	34	0.996	3	1.0268	2.0000
Plateau	72	0.987	76	0.980	2	1.0137	1.9930
Rivers	36	1.019	42	1.014	3	1.0283	2.0262
Sokoto	5	1.007	6	0.982	1	1.2014	2.0121
Taraba	5	1.003	4	0.998	1	1.2006	2.0080
Yobe	3	1.010	5	0.984	1	1.3367	2.0141
Zamfara	2	1.004	3	0.993	1	1.5020	2.0080

The model parameters and their associated 95% CIs are depicted as horizontal lines. When these lines are positioned above the zero vertical line, it indicates a significantly higher incidence rate for the corresponding state. Conversely, if the lines fall below the vertical zero line, it suggests significantly lower incidence rates (lower than zero bar). By exponentiating the coefficient greater than zero as indicated in Figure 4. The result showed that ten 10 states (Lagos, FCT, Plateau, Kaduna, Oyo, Rivers, Kano, Edo, Ogun, and Katsina) exhibit significantly higher infection (transmission) rates. In contrast, approximately eleven (11) states (Kogi, Anambra, Ekiti, Taraba, Sokoto, Jigawa, Cross-River, Kebbi, Yobe, Zamfara, and Borno) showcase notably lower infection rates.

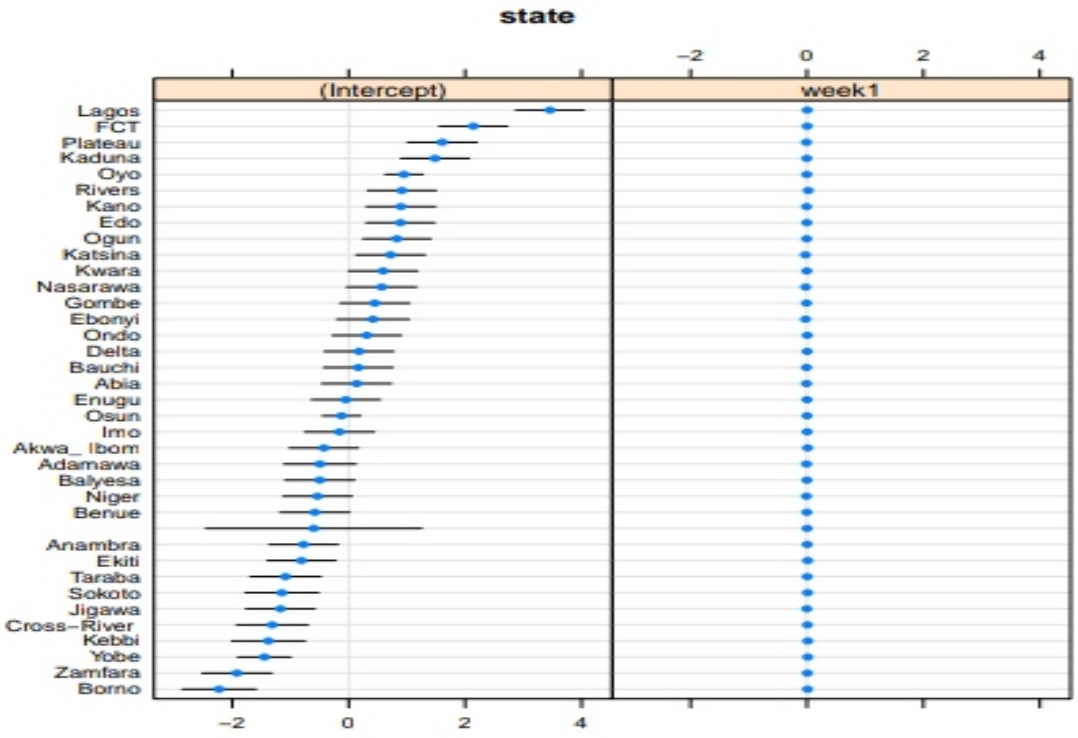


Figure 4: Plot of estimated weekly confirmed cases and 95% confidence intervals

Figure 5 presents the 95% confidence interval (CI) of model parameters for recovery cases across 36 states and FCT- Abuja. Figure 5 reveals that ten (10) states (Lagos, FCT, Plateau, Kaduna, Oyo, Rivers, Kano, Edo, Ogun and Katsina) have significantly higher recovery rate while 11 states (Kogi, Anambra, Ekiti, Taraba, Sokoto, Jigawa, Cross-River, Kebbi, Yobe, Zamfara and Borno) have significantly lower rate of recovery. Interestingly, the number of states with significantly higher infection (transmission) rates also demonstrates significantly higher recovery rates and vice versa.

Figure 6 presents the 95% confidence interval (CI) of model parameters for fatality cases across 36 states and FCT- Abuja. Figure 6 shows that only eight states (Lagos, the Federal Capital Territory (FCT), Edo, Oyo, Rivers, Ondo, Kano, and Delta) experienced significantly higher fatality rates from COVID-19. In contrast, sixteen states had significantly lower fatality rates, while the remaining states did not show any statistically significant differences in COVID-19 fatality rates during the study period.

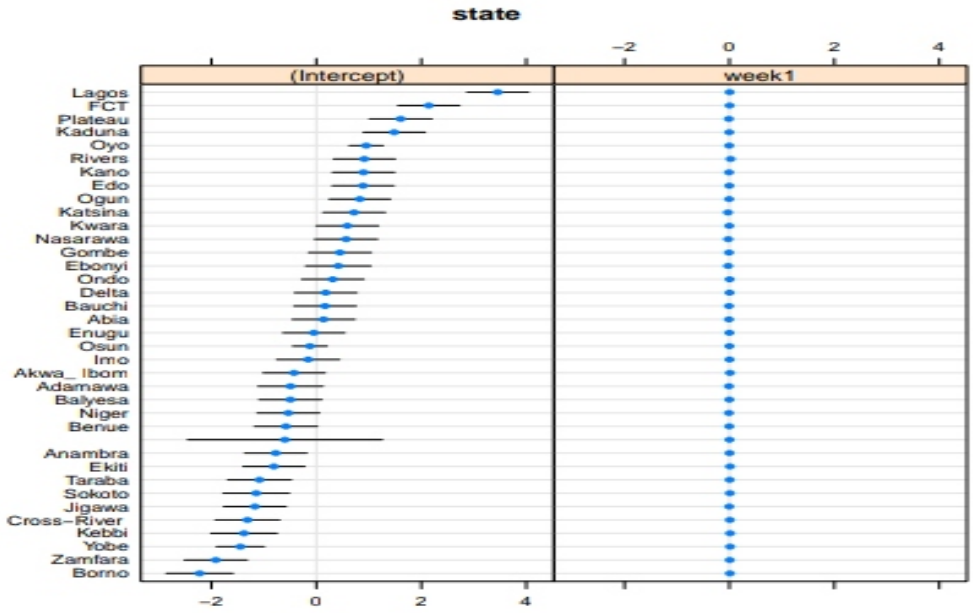


Figure 5: Plot of estimated weekly recovery rates and 95% Confidence Intervals.

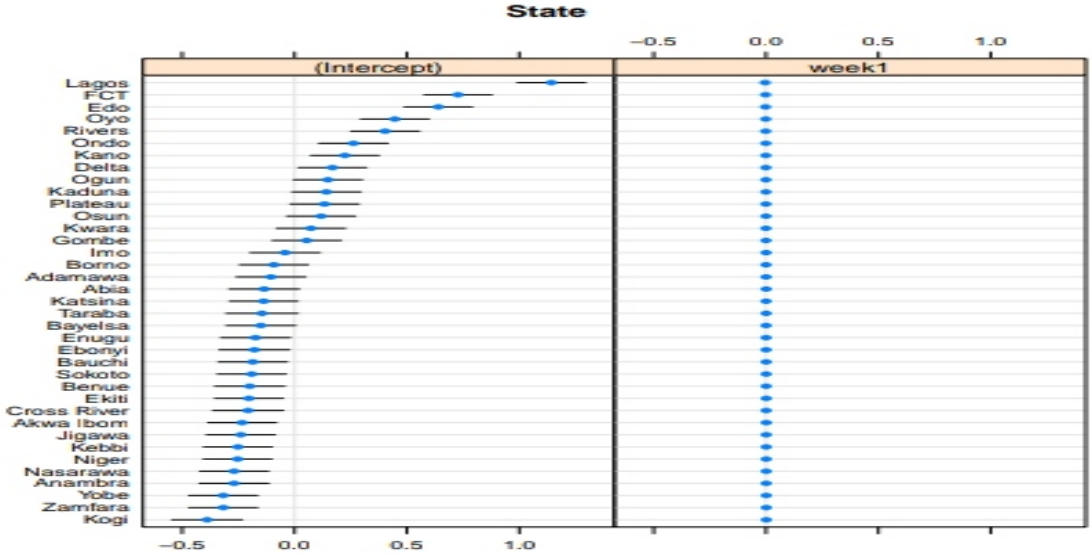


Figure 6: Plot of estimated weekly fatality rate and 95% C.I.

3.4. Discussion

This study approach employed both the traditional Susceptible-Infectious-Recovered (SIR) model and a log-linear regression model. These models are well-established in the field of epidemiology and are utilized to elucidate trends, the incidence trajectory and estimate the critical basic reproduction number. A key parameter in epidemiology is that represents the initial rate of spread of the disease. It is a threshold parameter for the SIR model as stated in [43]. If $R_0 < 1$, disease-free equilibrium of COVID-19 will be locally asymptotically stable, which is in agreement with the analysis of this study. The SIR model exhibited a commendable fit during the initial stages of the outbreak, aligning well with cumulative incidence patterns observed in Spain and its heavily affected regions[44;45].

However, it is worth noting that significant disparities emerged when applying the model to the Nigerian context. Specifically, notable underestimations were detected for states such as Abia, Lagos, Enugu, Bayelsa, Kano, Ogun, Oyo, and Abuja. This disparity in fit could be attributed to several factors, including varying population sizes, unique contact rates, and potentially diverse healthcare infrastructure across these regions. Of particular interest were the basic reproduction number estimates obtained from the SIR model during the early outbreak phase. These estimates were comparatively lower than those reported in similar studies conducted in regions like Italy and Spain, as documented by [10]. The regional inequalities in the COVID-19 spread could be attributed to the complex interplay between population dynamics and initial contact rates, underscoring the necessity of considering local context in epidemic modeling. Our findings indicate that the transmission dynamics of COVID-19 across Nigerian states can be effectively controlled if strong non-pharmaceutical interventions are put in place. The implications of the SIR model suggest that coordinated efforts to implement these measures could successfully reduce the spread of the disease within the Nigerian population.

Furthermore, the introduction of log-linear regression models in this study delves deeper into incidence trends and time-dependent structure. Notably, the models indicated that the outbreak in most Nigerian states was characterized by a phase of relatively moderate growth, suggesting that current interventions were having a stabilizing effect. However, certain states, including Abia, Lagos, Enugu, Bayelsa, Kano, Ogun, Oyo, and the Federal Capital Territory (FCT) of Abuja, exhibited higher growth rates, which could potentially be managed through appropriate intervention strategies.

To address the rarity of detailed clinical data at the state level, our approach has incorporated the random effect intercept and random slope terms to capture state-specific variation in the application of the log-linear regression models. This could enhance the linear mixed models by including spatial variations in a logarithmic scale[45]. Our study benefitted from leveraging established serial interval distributions of COVID-19, enhancing the predictive capabilities of the models.

However, despite the valuable insights from the study and its reliance on historical data, it may not fully account for temporary short-term changes in COVID-19 infections. Therefore, the predictions should be viewed as indicative of future preparedness and should be adapted to evolving circumstances, including new health interventions and public policies. Further research could be designed to address the temporal limitations identified in this study. Given the dynamic nature of the COVID-19 pandemic

and the continuously changing interventions and policies, it is essential to develop methodologies that can accommodate real-time adjustments. To overcome the reliance on historical data, other studies on COVID-19 could have incorporated advanced predictive modeling techniques such as dynamic Bayesian models [8, 30], temporal joint disease mapping of Covid-19 cases and deaths in England [46] and machine learning algorithms [47, 48].

In epidemiology, the quantities considered to be most important are the numbers of invectives to be produced by a primary infective in a fully susceptible population [49,50]. It is also worth noting that other factors such as environmental conditions and the behavior of the infected population play vital roles in how fast an infection spreads in the population as defined in [51], but it is necessarily not a biological pathogen itself. There is no general method to calculate the basic reproduction number. The computational approach is widely varied from region to region depending on the country, culture, calculation, and stage of the outbreak. In this study, two different methods were adopted to compute R_0, while the SIR method seemed to have captured the transmission dynamics of the epidemics, the log linear model can be effective for predicting the temporal trends. It has been reported that different authors take different methods to determine R_0 for controlling the disease as reported in [52]. If $R_0 < 1$, the infection fades out in a population. If the infected individuals are present in the population, there will be an epidemic if and only if $\frac{dI}{dt} > 0$ as prescribed in [53].

4. Conclusion

This study has discussed aspects of SIR model for the pandemic outbreak of COVID-19 and it was apparently demonstrated that the models were as powerful and flexible tools to understand the spread of disease and performing public health interventions. The SIR model provided a basic framework for computing the reproductive number of a measure of disease spread of the COVID-19 pandemic and structured the whole infection population in three compartments. In other hands, the log-linear models were formulated from exponential distribution and later computed the reproduction number which outperformed better than the SIR model. Perhaps, the SIR underestimation of R_0 may be due to under-reported cases of the covid-19 due to lack of awareness and limited testing facilities or laboratories at sub-national or local levels at the earlier stage of the pandemic.

The proper guidance and awareness can help individuals to prevent and control of global pandemic in timely. The findings underscore its significance in shedding light on the complicated epidemiological dynamics of COVID-19 across the most severely impacted states of Nigeria. The findings of study may appear straight forward and contribute invaluable insights into the disease's progression and potential containment strategies using retrospective data on COVID-19 dynamics in Nigeria. The log-linear regression model emerges as a promising tool for capturing both the growth and decay phases of COVID-19 and analogous infectious diseases. Its predictive capabilities, especially for short-term forecasting under the assumption of limited recent interventions, hold promise for informing policy decisions aimed at curtailing subsequent waves of the pandemic.

In conclusion, this study contributes to the understanding of COVID-19's regional variations in Nigeria and offers actionable insights for policymakers. The log-linear regression model could be employed to provide valuable short-term predictions, which could serve a complementary role to more SIR complex models.

Conflict of interest

The authors declared that there is no conflict of interest.

Author's contributions

RAA, RA, and JSO designed and conceptualized the study. RAA proposed the models and wrote the R code and carried out the statistical analyses. RA worked on the data cleaning and wrote the original draft of the manuscript, while JSO and SMO advised on the proposed models and commented on the first draft. RAA and JSO edited the draft and implemented the final corrections of the manuscript. RAA worked on a comprehensive model the final revisions. All authors read and approved the final manuscript.

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