



MODELING THE EFFECT OF POPULATION DENSITY AND SOME RELATED FACTORS ON COVID-19 PANDEMIC IN NIGERIA: AN APPLICATION OF COUNT DATA REGRESSION

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ABSTRACT: *Aim:* Nigeria's population density and other factors like confirmed, admitted, and discharged cases have adversely impacted health behaviors and the management of the COVID-19 pandemic. This study aims to investigate how population, population density, confirmed, admitted, and discharged cases affect the prevalence of the COVID-19 pandemic in the 36 states of Nigeria, including the FCT. **Method:** The number of COVID-19-related deaths, confirmed, admitted, and discharged individuals, from June 20, 2021, to December 31, 2022, were extracted from the Nigeria Centre for Disease Control (NCDC) online database, while data set on the Nigeria population and density were collected from Nigeria's National Population Commission (NPC) website. Three count data regression techniques; Poisson, Negative Binomial, and Generalized Poisson Regression models were employed to analyze these count data. **Result:** It was found that the number of admitted patients has a significant negative impact on COVID-19, whereas the number of confirmed laboratory COVID-19 cases has a significant positive effect on the number of deaths related to COVID-19. Additionally, the result showed that Nigeria's COVID-19 death rate is negatively impacted by discharged cases, population, and population density. **Conclusion:** It is inferred that the Generalized Poisson Regression model is the most suitable count data regression model for over-dispersion and is the best model for predicting the number of COVID-19-related deaths in Nigeria between June 20, 2021, and December 31, 2022.

KEYWORDS: COVID-19 pandemic, Poisson regression, Negative binomial regression, Generalized Poisson regression, Population density, Confirmed cases.



INTRODUCTION

The COVID-19 pandemic has had a significant impact on global economics and public health. The measures to restrict people's mobility and redirect health services to combat the virus's spread have also had an impact on the control of several other diseases, including cancer, dementia, and high blood pressure. [1-2] observed that COVID-19 has a direct impact on patients with any comorbidity, particularly chronic diseases; and indirectly, through behavioral changes in the population, such as a decrease in demand for health services and a fear of disease spread [3-4]. COVID-19 has mostly spread to Zimbabwe through imported cases and, to a lesser extent, local transmissions. Children and non-traveling women are among the high-risk groups for the disease's spread. Therefore, these social groups should be carefully considered by authorities when developing effective prevention strategies [5]. Because no drugs or vaccines have yet demonstrated their efficacy, it is necessary to act on its two components to reduce the effective contact rate, which is necessary to control the epidemic; the contact recurrence and the contact viability. The preventive technique in Algeria has mostly reached recurrence decrease by control and quarantine, this has uncovered new territorial flare-ups and has distinguished and detach contaminated individuals and their environmental factors with screening tests if accessible, on the opposite side, it is feasible to follow up on contact viability by adding to great cleanliness propensities, a guidance to wear the clinical veil by customary populace outside [6]. China is the only country that has approved the CoronaVac vaccine at this time. Twenty countries, including Turkey, have approved the vaccine for use in emergency situations. It began on January 14, 2021, in Türkiye, and all health professionals who wanted to be vaccinated quickly have been added [7]. Additionally, CoronaVac vaccine offers a positive confidence interval in antibody responses after some doses [8].

Importantly, the implementation of collective measures of social distance to combat COVID-19 altered the service routine. In a variety of clinical contexts, the switch from face-to-face hospital care to distance care (Telehealth) encouraged the rescheduling of elective procedures and the redistribution of hospital flow. Clinically, there is a critical association between instances of Coronavirus that have been conceded and released, which is an important arrangement of seriousness and mortality indicators. Examples include delaying treatment for episodes of these chronic conditions that are getting worse, making it difficult to make an early diagnosis, reducing the virus's spread through non-pharmacological means like avoiding the hospital, and so on.

The prevalence of COVID-19 had also been cited as a factor in these states' high population densities, which may have contributed to the disease's expansion. These findings are supported by the literature, which includes significant correlations between population densities and COVID-19 cases in England, the United States, and Turkey [9–12] and a higher distribution of cases in areas with higher densities [13]. A significant number of COVID-19 infections were also observed in states with lower densities during the third wave in Malaysia, including Sarawak (9.3%) and Sabah (8.8%) [14]. This is on the ground that despite the fact that these states are bigger and have a lower in general populace thickness at the state level, they are composed of various locales that are profoundly crowded and have high populace densities. Consequently, determining the effect of population and population density on COVID-19 cases at higher levels (such as the state) may be inaccurate and misleading. Findings would be more meaningful and accurate if they were based on the incidence and distribution of COVID-19 cases in Malaysia at the district level, as well as their correlation with absolute population and population density before and after the Delta variant dominated Malaysia [15]. Cases of



COVID-19 were found to be strongly correlated with population density and absolute population size ($r = 0.87$ and 0.78 , respectively) During the Delta dominant period, the majority of districts saw an increase in the number of COVID-19 cases compared to the pre-Delta period.

Numerous COVID-19 studies have utilized count data regression models to date. For instance, selected counts data models were used in a study [16] to model the daily COVID-19 deaths in Nigeria. The results show that Generalized Poisson Regression was the best model for fitting daily cumulative confirmed, active, and critical COVID-19 cases in Nigeria when overdispersion was present in the predictors because it had the lowest $-2\log$ -Likelihood, AIC, and BIC. Additionally, it was discovered that active and critical cases have a positive impact on the number of COVID-19-related deaths in Nigeria. [17] compare the zero inflated negative binomial, generalized Poisson, and zero inflated Poisson models' estimated mean predictions. It was shown through simulation that the zero inflated negative binomial model and the zero inflated Poisson model are superior to the generalized Poisson model when the data contain a lot of zeros.

We are aware of no studies that have modeled the impact of confirmed laboratory cases, admissions, discharges, population density, or other factors on the number of covid-19 deaths in Nigeria. This paper's main contributions are as follows: i) to provide a statistical and descriptive analysis of COVID-19 for Nigeria's thirty-seven states; ii) to use count regression models to figure out how population density and other factors like confirmed, admitted, and discharged cases affects COVID-19 prevalence in Nigeria. iii) utilize additional extended Poisson Regression (PR), such as the Negative Binomial Regression (NBR) and Generalized Poisson Regression (GPR) models, to account for overdispersion in the counts' data. There are four sections to this paper. The modeling method is described in detail in section 2. The study's results and discussion are presented in section 3, while the conclusions are presented in section 4

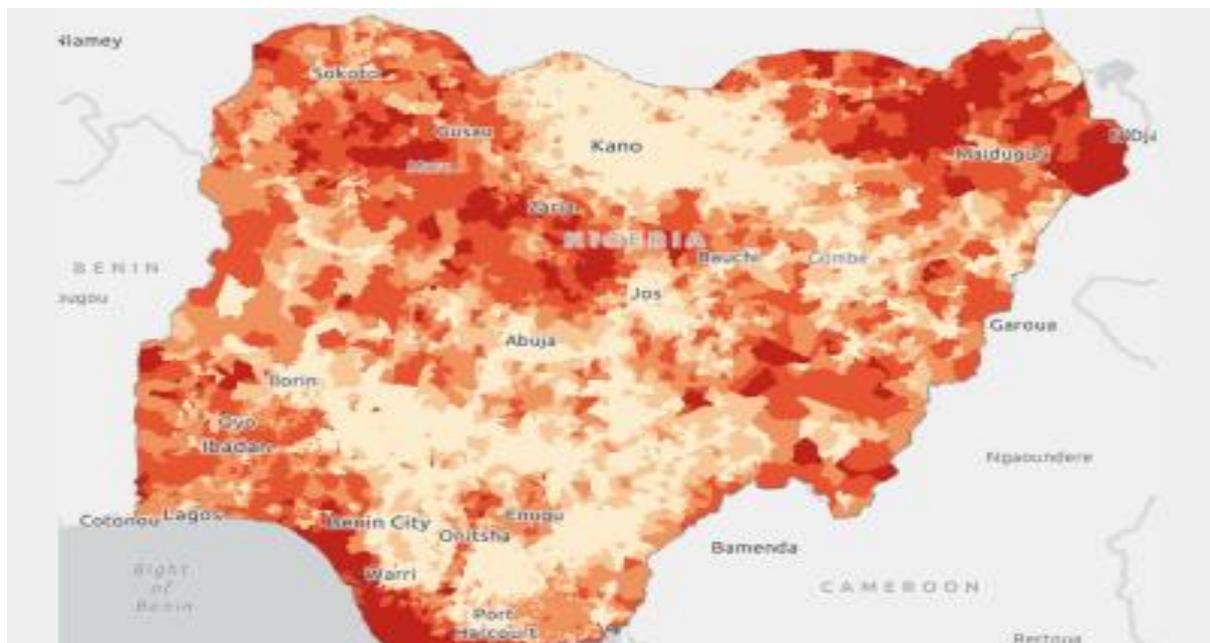
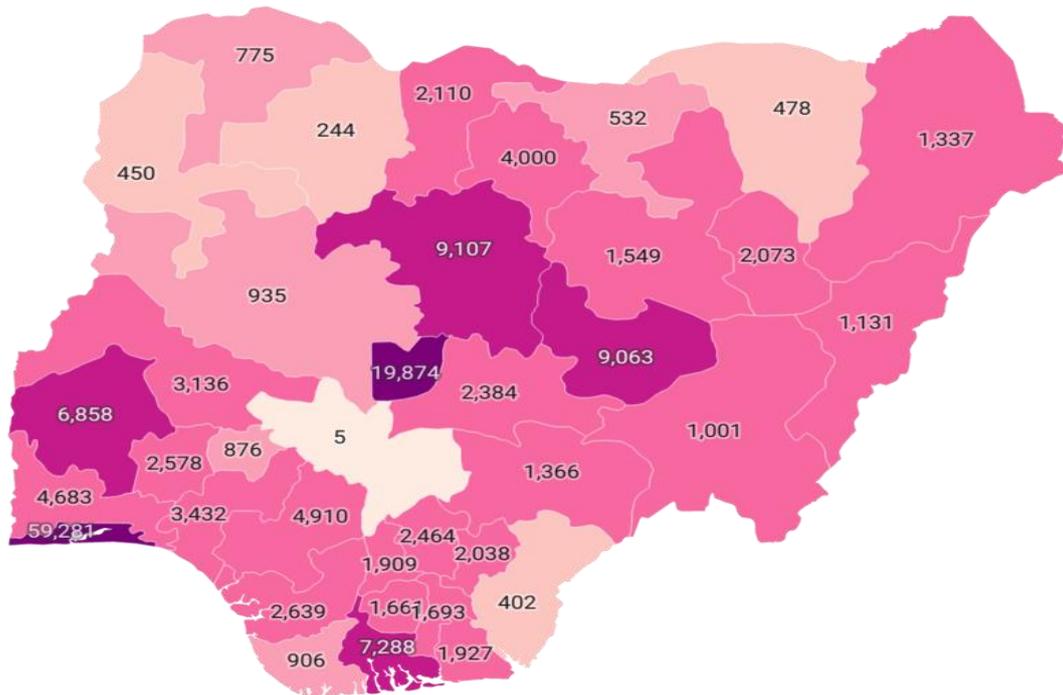


Fig. 3. Confirmed COVID-19 cases in Nigeria by state, as of 15 June 2021. | <100 | 100-500 | 500-1,000 | 1,000-5,000 | 5,000-10,000 | ≥10,000.

(Source: Nigeria Centre for Disease Control <https://covid19.ncdc.gov.ng/>)



MATERIALS AND METHODS

Source of Data

This is a study of secondary data from a past time using daily COVID-19 cases from June 20, 2021 to December 31, 2022 from the online database of the Nigeria Centre for Disease Control (NCDC). From a total of 139,532,063 people and a population density of 10,564, 251,341 laboratory cases were confirmed, 23,286 people were admitted, 224,939 people were discharged after treatment, and 3,116 people died from COVID-19 infection in Nigeria's thirty-seven states. Additionally, information and socio-demographic data for each state were retrieved online from state gazettes. Count regression models written in STATA version 14 were used to model the extracted data.

Count Data Models

The models used in this study are poisson regression, generalized poisson regression, and negative binomial regression. These models are in line with the specific goal of this study. The daily confirmed laboratory cases serve as the dependent variable in the count data, while the socio-demographic factors; whose independent variables are the cumulative number of active, critical, and confirmed cases of COVID-19. Continuous count data cover every variable under consideration.

Poisson Regression

Considering the limit of the probability mass function (PMF) of the Binomial distribution, as n tends to infinity and p tends to zero with $np = \lambda$, where $\lambda > 0$, then the resultant distribution has the density

$$P(Y = y) = \frac{e^{-\lambda} \lambda^y}{y!} y = 0,1 \quad (1)$$

This distribution is called the Poisson distribution with parameter λ . The Poisson density has mean and variance,

$$E(Y_i) = Var(Y_i) = \lambda_i \quad (2)$$

To incorporate covariates and to ensure non-negativity, the mean or the fitted value is assumed to be multiplicative, that is, $E(Y_i|x_i) = \lambda_i = e_i \exp(x_i^T \beta)$, where e_i denote a measure of exposure, x_i a $p \times 1$ vector of explanatory variables, and β a $p \times 1$ vector of regression parameters.

The Negative Binomial Regression

One approach to address the problem of over dispersion is to assume alternatively, that y_i has a negative binomial distribution, also known as the Poisson-Gamma distribution which has become the most commonly used probabilistic distribution for modeling overdispersion in count data, with an additional parameter called the dispersion parameter which permits the variance to exceed the mean [14 – 17]. The probability mass function of a negative binomial regression model for independent count data observations $Y_i, i = 1, \dots, n$ with parameters $d > 0$ and $\mu_i > 0$, represented by $Y_i \sim NB(d, \mu_i)$, is defined as



$$P(Y_i = y_i | d, \mu_i) = \frac{\Gamma(y_i + d)}{\Gamma(d)\Gamma(y_i + 1)} \cdot \left(\frac{d}{\mu_i + d}\right)^d \cdot \left(\frac{\mu_i}{\mu_i + d}\right)^{y_i}, \mu > 0, d > 0, y = 0, 1, \dots \quad (3)$$

This distribution also arises from a Poisson distribution where the dispersion parameter d is assumed to be constant and follows a Gamma distribution with mean and variance given as;

$$E\left(\frac{Y_i}{d}, \mu_i\right) = u \text{ and } Var\left(\frac{Y_i}{d}, \mu_i\right) = \mu_i \left(1 + \frac{\mu_i}{d}\right) \quad (4)$$

The parameter d with a fixed assumption over time for each region μ_i , depends on covariates through the transformation:

$$\ln \ln(\mu_i) = \beta X_i \quad (5)$$

As $d \rightarrow \infty$ in the limit, the negative binomial distribution converges to the Poisson distribution with parameter μ [18] and the logarithmic series distribution is obtained as $d \rightarrow 0$ [19 – 20]. Consequently, the unobserved heterogeneity among observations can be used to interpret the overdispersion in the negative binomial model.

The Generalized Poisson Regression

The Generalized Poisson Distribution (GPD) was introduced in [21] and studied extensively by [22]. The generalized Poisson (GP) distribution, when defined using the maximum likelihood estimation methods for its parameters, has the probability density function [23].

$$P(Y_i = y_i) = \left(\frac{\mu_i}{1 + a\mu_i}\right)^{y_i} \frac{(1 + ay_i)^{y_i - 1}}{y_i!} \exp\left(-\frac{\mu_i(1 + ay_i)}{1 + a\mu_i}\right), y_i = 0, 1, \dots \quad (6)$$

$$\text{with mean } E(Y_i) = \mu_i \text{ and variance } Var(Y_i) = \mu_i(1 + a\mu_i)^2 \quad (7)$$

The Generalized Poisson (GP) is a natural extension of the Poisson distribution. If a equals zero, the Generalized Poisson reduces to the Poisson distribution, resulting into $E(Y_i) = Var(Y_i)$. If $a > 0$, the variance is larger than the mean, $Var(Y_i) > E(Y_i)$, and the distribution represents count data with overdispersion. If $a < 0$, the variance is smaller than the mean, $Var(Y_i) < E(Y_i)$, so that now the distribution represents count data with underdispersion. The main advantage of using the Generalized Poisson distribution is that it can be fitted for both overdispersion, $Var(Y_i) > E(Y_i)$ as well as underdispersion, $Var(Y_i) < E(Y_i)$, which serves as an advantage over the negative binomial distribution.

Fitting the Multilevel Models

For the analysis of the socio-demographic risk factors to determine the effects of these covariates and the various mass densities Poisson (P), Negative Binomial (NB) and generalized Poisson (GP) model would give produce three (3) multilevel models in the following order;

$$\log \lambda_i = \beta_0 + \sum_{i=1}^3 X_i \beta_i + \epsilon_i \text{ with } O_i \sim P(a, \lambda_i) \quad (8)$$



$$\log \lambda_i = \beta_0 + \sum_{i=1}^3 X_i \beta_i + \epsilon_i \text{ with } O_i \sim NB(b, \lambda_i) \quad (9)$$

$$\log \lambda_i = \beta_0 + \sum_{i=1}^3 X_i \beta_i + \epsilon_i \text{ with } O_i \sim GP(c, \lambda_i) \quad (10)$$

Where; λ_i is the number of death from COVID-19 (response variable), which is expressed in terms of five predictor variables namely; confirmed laboratory cases (x_1), number admitted (x_2), number discharged (x_3), target population (x_4), and population density (x_5).

Model Comparison

When taking into account the bound of the probability mass function (PMF) of the binomial distribution, the density of the resultant distribution is determined by applying the Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), and Chi-Square $-2\log$ likelihood model selection criteria to the three count data models in order to select the most suitable model for Nigerian COVID-19 cases.

RESULTS AND DISCUSSIONS

The results of the summary statistics, such as maximum, minimum, standard deviation, and mean. This section also provided the correlation matrix results for the response and explanatory variables. In this section, the results of the count data selection criteria as well as the Poisson, Negative Binomial, and Generalized Poisson regression models were displayed for Nigerian COVID-19 cases. This is done by taking into account the bound of the probability mass function (PMF) of the Binomial distribution.

Results

The maximum, minimum, standard deviation, and mean of the summary statistics. The correlation matrix results for the response and explanation variables were also provided in this section. In this segment, the aftereffects of the consider information choice measures well as the Poisson, Negative Binomial, and Summed up Poisson relapse models were shown

Summary Statistics

Table 1 displays the descriptive statistics for the confirmed COVID-19 death rate and other associated factors. Because the standard deviations were higher than the mean values, this result indicates that there is over-dispersion. The standard error and significance of the regression parameters may be understated by the Poisson regression model's overdispersion. It is incorrect to draw conclusions about the regression parameters based on this condition.

Correlation Matrix

Table 2 displays the Pearson correlation coefficient matrix of their confirmed COVID-19 cases and demographic variables. The results show that the majority of the variables have a strong, positive, and statistically significant relationship with the variables that explain the results. At levels of 1% and 5%, this relationship correlation is statistically significant. It is evident that there was a positive and significant correlation between confirmed cases and the number of



admissions, discharges, deaths, population, and population density. Their respective correlation coefficients of $r_{xy} = 0.98, 0.99, 0.94, 0.52,$ and 0.89 demonstrated that this was the case.

Table 1: Summary Statistics of COVID-19 Confirmed Death and Other Factors

Variable	Observation	Mean	Std. Dev.	Minimum	Maximum
Death	537	84.216	134.09	2	769
Confirmed	537	6793	16279	5	97839
Admitted	537	629.4	2789.2	0	17004
Discharged	537	325.9	14258	28	17654
Population	537	377113	172278	130452	940129
Population density	537	285.5	445.4	41	2724.5

Table 2: Correlation Matrix

	Confirmed	Admission	Discharged	Deaths	Population	Population Den.
Confirmed	1					
Admission	0.97066**	1				
Discharged	0.99879**	0.95770**	1			
Deaths	0.93923**	0.89211**	0.9409*	1		
Population	0.52493*	0.50673*	0.524419*	0.539*	1	
Population Den.	0.89501**	0.91966**	0.883476**	0.8318**	0.5698*	1

*Correlation is significant at 0.05 level of significance **Correlation is significant at 0.01 level of significance

Poisson, Negative Binomial, and Generalized Poisson Regression Model

According to the parameter estimation of the Poisson Regression model, confirmed laboratory cases, admitted cases, discharged cases, population, and density were significant at the 5% level, whereas population density was not significant. This suggests that the number of COVID-19 deaths increases or decreases in tandem with the other variables admission, discharge, population, and population density. This indicates that, except for population density, all of the explanatory variables have a significant impact on the number of deaths caused by COVID-19. Additionally, the outcome showed that; the death rate is positively impacted by confirmed laboratory cases, the target population, and population density, while the number of COVID-19 deaths is significantly impacted by admitted and discharged cases.

Confirmed laboratory, admitted, and discharged cases were found to be significant at the 5% level in the Negative Binomial regression model in Table 4, whereas target population and density were not. Additionally, the outcome showed that; the death rate is influenced positively by confirmed laboratory cases, target population, and density, while the number of COVID-19 deaths is influenced negatively but significantly by admitted and discharged cases. The Generalized Poisson regression parameter estimation resulted in the following, as shown in Table 5, discharged cases, target population, and density were not significant at the 0.05 level because $p\text{-value} > 0.05$, whereas confirmed laboratory cases and admitted cases were



significant at the 5% level. Additionally, the outcome revealed that while admitted and discharged cases had negative but significant impact on the number of COVID-19 deaths, confirmed laboratory cases, the target population, and density have a positive impact on the death rate. This indicates that the number of COVID-19-related deaths will increase by 0.01986, 0.000133, and 0.000326 per unit increase in confirmed laboratory cases, while the number of deaths will decrease by 0.01125 and 0.01855 per unit increase in admitted and discharged cases, respectively.

The results of the model performance evaluation for the three count data regression models, Negative Binomial Regression, Generalized Poisson Regression, and Poisson Regression, are presented in Table 6. The Generalized Poisson Regression had the lowest AIC (309.2), BIC (346.9), and $-2 \log$ likelihood (-204.0945), according to the outcome. According to this finding, the count data regression model of choice for estimating the number of COVID-19-related deaths in Nigeria's thirty-six states and Federal Capital Territory (FCT), target population, and admitted and discharged cases is GPR.

Table 3: Poisson Regression Model

Coefficient	Estimate	Std. Error	t-value	$P_r(> t)$	LogL	AIC	BIC
Intercept	3.04146	0.058883	51.65	0.000	-578.884	645.6	664.8
Confirmed Cases	0.00741	0.000244	30.88	0.000			
Admitted	-0.00782	0.000242	-32.34	0.000			
Discharged	-0.00736	0.000242	-30.39	0.000			
Population	0.00058	0.0000013	4.53	0.000			
Population density	0.000068	0.0001382	0.49	0.623			

Table 4: Negative Binomial Regression Model

Coefficient	Estimate	Std. Error	t-value	$P_r(> t)$	LogL	AIC	BIC
Intercept	2.94774	0.161877	18.21	0.000	-202.2114	335.7	386.4
Confirmed Cases	0.01044	0.001667	6.27	0.000			
Admitted	-0.010947	0.001671	-6.55	0.000			
Discharged	-0.010408	0.001682	-6.19	0.000			
Population	0.000158	0.000043	0.43	0.670			
Population density	0.000326	0.000369	0.88	0.378			

**Table 5: Generalized Poisson Regression Model**

Coefficient	Estimate	Std. Error	Z-value	$P_r(> t)$	LogL	AIC	BIC
Intercept	2.76549	0.157438	17.94	0.000	-204.0945	309.2	346.9
Confirmed Cases	0.01986	0.001589	6.16	0.000			
Admitted	-0.01855	0.001675	-6.66	0.000			
Discharged	-0.01125	0.001578	-6.77	0.613			
Population	0.000133	0.000052	0.56	0.432			
Population density	0.000326	0.000334	0.94	0.378			

Table 6: Model Performance Evaluation Results

Model	Log	AIC	BIC
Negative Binomial	-202.2114	335.7	386.4
Generalized Poisson	-204.0945*	309.2*	346.9*

DISCUSSION OF FINDINGS

Findings in this study indicated that the target population and density have a positive but insignificant effect on the number of COVID-19-related deaths. The finding suggests that the incidence of COVID-19 in Nigeria's 36 states and federal capital territory will increase by 0.013 percent and 0.033 percent, respectively, for every one-unit increase in the target population and density. This finding is consistent with the findings of the study by [15], which looked at the incidence and distribution of COVID-19 cases in Malaysia at the district level and found that they were correlated with absolute population and population density both before and after the Delta variant took over. Cases of COVID-19 were strongly correlated with population density and absolute population size. When compared to the pre-Delta period, the majority of districts experienced an increase in the number of COVID-19 cases during the Delta dominant period.

This study demonstrates that a unit increase in confirmed laboratory cases will result in a 1.98 percent increase in COVID-19-related deaths and a 1.8% and 1.1% decrease in admissions and discharges from isolation, respectively. Similar to [28-32], this evidence on the negative impact of admitted and discharged cases on COVID-19 prevalence in their investigation into how admission affected the pandemic in populations other than COVID-19. To avoid negative outcomes, certain medical conditions like stroke and acute ST-elevation myocardial infarction necessitate prompt treatment in the hospital; As a result, fewer patient harms are almost certainly associated with fewer hospitalizations for such medical conditions. During the pandemic, leaders of the health system and authorities in public health should concentrate on the most effective methods for ensuring that patients with conditions requiring hospitalization receive it.



CONCLUSION AND RECOMMENDATIONS

The three-count data regression method was used in this study; the Poisson, Negative Binomial, and Generalized Negative Binomial Regression to model the effects of confirmed COVID-19 laboratory cases, admitted, discharged cases, population, and population density on COVID-19 prevalence-related deaths in Nigeria's 36 states and Federal Capital Territory. Secondary data for the period from June 20, 2021, to December 31, 2022, from the online database of the Nigeria Centre for Disease Control (NCDC) were used in the study. The response variable was the number of COVID-19-related deaths in Nigeria, while the explanatory variables were the confirmed, admitted, discharged, and target population and population density. The three-count data regression method, specifically the Poisson, Negative Binomial, and Generalized Negative Binomial Regressions was utilized to model the effects of confirmed COVID-19 laboratory, admitted, discharged cases, population, and population density on the number of deaths caused by COVID-19 prevalence in Nigeria's 36 states and Federal Capital Territory. The study's findings indicated that; to model count data with overdispersion, Poisson regression was ineffective, so other count data regression techniques like; the count data were analyzed using Generalized Poisson Regression (GPR) and Negative Binomial Regression (NBR). The finding indicates that the Generalized Poisson Regression model is the most suitable count data regression model for over-dispersion and is the best model for predicting the number of COVID-19-related deaths in Nigeria between June 20, 2021, and December 31, 2022. The following model selection criteria were used to infer this result: $BIC = 346.9$, $AIC = 309.2$, and $-2\log L = -204.0945$. Because it had the lowest value of all three selection criteria, the Generalized Poisson Regression was determined to be the best model by the three measures. The analysis produced the following findings: The number of admitted patients was found to have a significant negative impact on COVID-19, whereas the number of confirmed laboratory COVID-19 cases has a significant positive effect on the number of deaths related to COVID-19. Additionally, the result showed that; Nigeria's COVID-19 death rate is negatively impacted by discharged cases, population, and population density.

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