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Analyzing Covid-19 Infection Patterns in Nigeria's Geopolitical Zones: A Comparative Study Using Count Distribution Models

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ABSTRACT

Count data regression is a commonly employed technique in various fields, particularly within the health sector, where precise model selection depends on the characteristics of the response variable. While continuous response variables are typical in regression analyses, significant attention has been devoted to modeling discrete variables. Notably, existing literature has underscored the potential spatial variance in COVID-19 incidence counts within Nigeria. Numerous scholars have explored alternative estimation methods for COVID-19 cases, motivating this study to investigate frequency disparities among different regions in Nigeria. The primary aim of this study is to compare the prevalence of COVID-19 infection cases and identify the optimal model for characterizing infection case prevalence across geographical zones in Nigeria. To achieve this, five statistical models were assessed: Poisson, Negative Binomial, Generalized Poisson, Zero-Inflated Poisson, and Zero-Inflated Negative Binomial (ZINB) distributions. Model selection criteria, including AIC, P-values, and Chi-square values, were employed for each infection case in every zone. Both ZINB and Negative Binomial models consistently address over-dispersion. However, ZINB, by accounting for excessive zeros, emerges as the optimal choice, providing accurate insights into pandemic dynamics across diverse regions in Nigeria. These findings offer actionable guidance for combating COVID-19, with ZINB models consistently demonstrating effectiveness in representing infection data across Nigeria's various regions, effectively managing over-dispersion and excess zeros.

Keywords: COVID-19, Comparison, Infections, Count Models, Over-dispersion, Excess Zeros.

INTRODUCTION

The rapid and alarming surge in COVID-19 cases, the challenges in controlling its spread, and the evolving nature of the outbreak across global cities have transformed it from an epidemic into a pandemic, affecting every corner of the world. The emergence of the novel coronavirus disease 2019 (COVID-19) in late 2019 presented an unprecedented global health crisis. Nigeria, Africa's most populous nation, confirmed its first case in February 2020. Since then, the virus has spread throughout the country, with varying infection patterns observed across its six geopolitical zones. Understanding these variations is crucial for informing targeted public health interventions. Several studies have investigated COVID-19 transmission dynamics in Nigeria. Adeniyi et al. (2020) employed a susceptible-exposed-infected-recovered (SEIR) model to assess the early stages of the outbreak, while Ihekweazu et al. (2020) explored the role of travel restrictions in curbing the spread. However, a gap exists in our understanding of how COVID-19 infection patterns differ across Nigeria's geopolitical zones.

This comparative analysis will provide valuable insights into the factors driving geographical disparities in COVID-19 transmission within Nigeria. The findings can inform the development of regionally tailored public health strategies to mitigate the spread of the virus and protect vulnerable populations. The COVID-19 pandemic has emerged as one of the most significant global health crises of the 21st century, challenging nations worldwide to implement effective strategies for containment and mitigation. In Nigeria, the impact of the pandemic has been particularly pronounced, with the country experiencing multiple waves of infection and varying degrees of transmission across its diverse geopolitical zones (NCDC, 2020). As policymakers and public health officials grapple with the complexities of managing the pandemic, understanding the epidemiological dynamics of COVID-19 at the subnational level is essential for implementing targeted interventions and resource allocation strategies tailored to the unique characteristics of different regions.

While previous studies have provided valuable insights into national-level trends and risk factors associated with COVID-19 transmission in Nigeria (Oladipo et al., 2021; Olawale et al., 2020), there remains a notable gap in the literature regarding regional disparities and their implications for public health interventions. Nigeria's geopolitical landscape, comprising six distinct zones with varying population densities, socio-economic indicators, and healthcare infrastructure, presents a complex mosaic of factors that may influence the spread and severity of COVID-19 within each region (Oduwole et al., 2018). This study aims to address this gap by employing count distribution models to analyze COVID-19 case data for each of Nigeria's six geopolitical zones. Count distribution models, such as the Poisson or Negative Binomial models, are well-suited for analyzing discrete count data like daily COVID-19 cases (Sani, et al, 2023). By comparing the model fits across zones, we can identify statistically significant differences in infection patterns. By leveraging data collected from reputable sources such as the Nigeria Centre for Disease Control (NCDC) and other relevant databases, we aim to assess the performance of five count distribution models: Poisson, Negative Binomial, Generalized Poisson, Zero-Inflated Poisson, and Zero-Inflated Negative Binomial (ZINB) distributions. These models offer distinct advantages in capturing the heterogeneity and complexity of COVID-19 transmission patterns, including over-dispersion and excess zeros commonly observed in infectious disease data (Hilbe, 2014; Cameron & Trivedi, 2013).

Through a rigorous statistical framework and comparative analysis of infection counts, we seek to identify regions with disproportionately high infection rates or unique transmission dynamics, thereby providing actionable insights for policymakers and public health officials involved in pandemic response efforts. By tailoring interventions to the specific needs and challenges of each geopolitical zone, we aim to mitigate the spread of COVID-19 and minimize its impact on vulnerable populations, ultimately contributing to the broader global effort to control the pandemic.

Yildirim, Kaciranlar & Yildirim (2022) states that the choice of an appropriate regression model is crucial in analyzing the dynamics of the pandemic. While continuous response variables are typically used in regression models, there has been a significant focus on developing models for discrete variables. Count data regression models have emerged as effective tools when the response variable represents the count of occurrences and is non-negative. These models have found extensive application across various fields, with particular interest in the healthcare sector.

Poisson and Negative Binomial regression models have gained significant attention in a wide range of disciplines, including medicine, biostatistics, biology, finance, demography, astronomy, business management, earth sciences, communication, and insurance. However, clinical studies often face the issue of 'over-dispersion,' where the variance of case counts exceeds the mean. The Poisson distribution assumes that the variance equals the mean, which can be too restrictive for clinical data that tend to exhibit greater variation than the mean suggests (Dobson & Barnett, 2008).

Literature Review

The COVID-19 pandemic has prompted a surge of research aimed at understanding its transmission dynamics, risk factors, and the effectiveness of interventions across various contexts. In the context of Nigeria, studies exploring COVID-19 infection patterns have contributed valuable insights into the epidemiological landscape of the virus within the country's geopolitical zones. This literature review synthesizes recent research focusing on COVID-19 infection patterns in Nigeria, highlighting key findings and gaps in knowledge.

Oladipo et al. (2021) conducted a comprehensive epidemiological analysis of COVID-19 cases in Nigeria, exploring spatiotemporal trends and identifying factors associated with increased transmission rates. Their study revealed significant regional disparities in infection rates, with certain geopolitical zones experiencing higher case burdens than others. Factors such as population density, socio-economic status, and healthcare infrastructure were identified as influential determinants of COVID-19 transmission dynamics within Nigeria.

In a similar vein, Olawale et al. (2020) examined the socio-economic and demographic determinants of COVID-19 infection in Nigeria using data from the Nigeria National Household Survey. Their findings underscored the disproportionate impact of the pandemic on vulnerable populations, particularly those residing in densely populated urban areas with limited access to healthcare services. Socio-economic factors such as poverty, overcrowding, and lack of access to clean water and sanitation facilities were identified as significant risk factors for COVID-19 transmission.

While these studies provide valuable insights into the broader epidemiological trends of COVID-19 in Nigeria, there remains a notable gap in the literature regarding regional disparities and the effectiveness of targeted interventions within specific geopolitical zones. This gap is particularly pronounced given Nigeria's diverse geopolitical landscape, characterized by varying population densities, socio-economic indicators, and healthcare infrastructure across its six geopolitical zones.

To address this gap, the current study employs advanced count distribution models to analyze COVID-19 infection patterns within Nigeria's geopolitical zones. By comparing the performance of different statistical models, including Poisson, Negative Binomial, and Zero-Inflated Negative Binomial distributions, we aim to identify the optimal approach for characterizing infection prevalence and transmission dynamics within each zone. This comparative analysis will provide actionable insights for policymakers and public health officials, enabling the development of targeted interventions tailored to the specific needs and challenges of each region.

In summary, while existing research has shed light on the broader epidemiological trends of COVID-19 in Nigeria, there is a pressing need for studies that delve into regional disparities and their implications for public health interventions. By conducting a comparative analysis of infection patterns across Nigeria's geopolitical zones, this study seeks to fill this gap in the literature and inform evidence-based decision-making in the ongoing fight against the COVID-19 pandemic.

COVID-19 and its Impact on Nigeria

The emergence of COVID-19 in late 2019 has had a devastating impact on global health, with Nigeria being no exception. As the most populous country in Africa, Nigeria confirmed its first COVID-19 case in February 2020. The virus has since spread nationwide, posing significant challenges to the country's healthcare system (Salako et al., 2020).

Several studies have explored different aspects of the COVID-19 pandemic in Nigeria. Adeniyi et al. (2020) utilized a mathematical modeling approach, specifically a SEIR model, to analyze the initial stages of the outbreak and predict its trajectory. Their study provided valuable insights into the early transmission dynamics of COVID-19 in Nigeria. Similarly, Ihekweazu et al. (2020) investigated the effectiveness of travel restrictions implemented by the Nigerian government in curbing the spread of the virus. Their findings highlighted the importance of non-pharmaceutical interventions in mitigating the initial spread of COVID-19.

Heterogeneity in COVID-19 Transmission Across Nigeria

While the aforementioned studies provide valuable insights into the national picture of COVID-19 in Nigeria, it is crucial to acknowledge the potential for geographical variations in transmission patterns. Nigeria is a vast country with diverse demographics, socioeconomic conditions, and healthcare infrastructure across its six geopolitical zones (North-central, Northeast, Northwest, Southeast, South-south, and Southwest). These factors can significantly influence the spread of infectious diseases, including COVID-19 (Adebayo & Oyerinde, 2020).

A study by Ogunbodede et al. (2021) explored these disparities using spatial analysis techniques. Their findings suggest a significant spatial heterogeneity in COVID-19 cases across Nigeria, with the Northwest zone exhibiting the highest burden. This highlights the need for more granular analyses that consider geographical variations in transmission patterns.

Application of Count Distribution Models in Infectious Disease Epidemiology

Count distribution models are statistical tools widely employed in analyzing infectious disease data, particularly when dealing with discrete count outcomes like daily COVID-19 cases (Farrington, 1996). These models allow researchers to characterize the underlying distribution of case counts and identify factors associated with variations in these counts. Commonly used count distribution models in infectious disease epidemiology include the Poisson and Negative Binomial models (Lloyd, 2007).

Previous research has demonstrated the effectiveness of count distribution models in analyzing COVID-19 case data. A study by Ali et al. (2020) employed a Negative Binomial model to analyze daily COVID-19 cases in Pakistan and identify factors associated with increased transmission risk. Similarly, a study by Meyer et al. (2020) utilized a zero-inflated Poisson model to analyze COVID-19 cases in Germany, accounting for days with zero reported cases.

Gaps in Knowledge and the Current Study

While existing research has shed light on various aspects of the COVID-19 pandemic in Nigeria, a gap remains in our understanding of how infection patterns differ across the country's geopolitical zones. This study aims to address this gap by employing count distribution models to analyze and compare COVID-19 case data for each of Nigeria's six geopolitical zones. By identifying statistically significant differences in the model fits across zones, this study can provide valuable insights into the factors driving geographical disparities in COVID-19 transmission within Nigeria.

In summary, this study aims to contribute to the growing body of literature on COVID-19 epidemiology by examining subnational variability in infection patterns within Nigeria. By employing advanced statistical techniques and regional-level data analysis, we seek to inform evidence-based decision-making and support the development of targeted interventions to combat the ongoing pandemic in Nigeria and beyond.

MATERIALS AND METHODS

Scope of the Study

This study encompasses all six geopolitical zones in Nigeria, each serving as an administrative division comprising a specific number of states. These zones, officially designated as North-Central, North-East, North-West, South-East, South-South, and South-West, were included to capture the geographic and administrative diversity of the country.

Method of Data Collection

The data utilized in this study consisted of COVID-19 infection records recorded between February 2020 and February 2022 within Nigeria's six geopolitical zones. These records were obtained from the database of the National Center for Disease Control (NCDC), which serves as the authoritative source for tracking and reporting infectious disease cases in the country. The NCDC database provides detailed daily counts of COVID-19 infections reported by healthcare facilities and laboratories across all states within each geopolitical zone. This readily accessible database offers disaggregated daily case counts for each state within their respective geopolitical zone.

Data Analysis

The data analysis process employed a multi-pronged approach to comprehensively understand the spatial distribution of COVID-19 infection patterns across Nigeria's geopolitical zones.

To analyze the data, a series of statistical methods were employed. Initially, a descriptive statistics analysis was conducted to characterize the active cases variable. Subsequently, various count models, including Poisson, Negative Binomial, Zero-Inflated Poisson, Zero-Inflated Negative Binomial, and Generalized Poisson, were fitted to the infection data. For this research, the R-Package was employed for model fitting and selection, facilitating a comprehensive analysis of the dataset.

Descriptive Statistics

The initial phase involved conducting a descriptive statistics analysis. This analysis aimed to characterize the central tendency (average level) and variability (spread) of daily COVID-19 cases within each of the six geopolitical zones. Common summary measures employed for this purpose included the mean (average number of daily cases), median (middle value when cases are ordered from lowest to highest), and standard deviation (measure of how spread out the data is from the mean). Analyzing these measures provided valuable insights into the overall burden and variation of COVID-19 cases across the different zones.

Count Distribution Modeling

The core component of the analysis involved fitting various count distribution models to the daily COVID-19 case data for each zone. This comparative approach aimed to identify the model that best represents the underlying distribution of infection rates within each zone. The R statistical software package (version number) was chosen for model fitting and selection due to its extensive functionalities for statistical analysis.

Poison

The Poisson distribution describes the probability of a given number of events occurring in a fixed interval of time or space. It is characterized by a single parameter, μ, representing the average rate of occurrence.

Let Y be a random variable having a Poison distribution with parameter μ. It takes integer value (0,1,2…) with Probability Mass Function (P.M.F.)

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

The mean and variance of the distribution are equal, i.e.

$$\mathrm{E(Y) = Var\ (Y)} = \mu$$

Negative Binomial

The Negative Binomial distribution is used to model over-dispersed count data and accounts for variability in the data through an additional parameter, α.

The Negative Binomial model can be obtained from the mixture of Poison and Gamma distributions. It is widely used in modeling over-dispersed count data. It is probability distribution is given by

$$P(Y=y)=\frac{\Gamma(y+\alpha)}{y!\,\Gamma(\alpha)}\left(\frac{\Gamma}{\lambda+\alpha}\right)^{\alpha}\left(\frac{\lambda}{\lambda+\alpha}\right)^{y}, y=0,1,\dots\lambda,\alpha>1$$

$\lambda=E(Y)$, α =shape parameter

Generalized Poison (GP) Distribution

The GP distribution is a flexible count model that allows for both under-dispersion and over-dispersion by incorporating a shape parameter, θ.

$$f(y;\theta,\lambda)=\frac{\theta(\theta+\lambda y)^{y-1}\ell^{-\theta-\lambda y}}{y!} \qquad y = 0,1,2,\dots$$

$$\theta>0,\ 0\le\lambda\le1$$

Where,

$\lambda=E(Y)$, which is the average rate;

θ =Shape parameter,

Zero-Inflated Poison (ZIP)

This model account for excess zeros in the data, which may arise due to both genuine absence of events and excess zeros.

This was developed by Lambert (1992), given the responses

Y = (Y_1,…..,Y_n) which are independent, the assumption of the model is that with probability P the only possible is 0, and with probability (1- p), a Poison (μ) random variable is observed in Y. The P.m.f of Y is given by

$$Y_i=\begin{cases}0, with\,\rho robability\,\rho_i+\left(1-\rho_i\right)e^{-\lambda_i}\\ k, with\,\rho robability\left(1-\rho_i\right)\dfrac{e^{-\lambda_i}\lambda_i^{yi}}{y_!}, k=1,2,\dots\end{cases}$$

The mean and the variance are

$E(Y_i) = (1 - p_i)\lambda_i$ and $Var(Y_i) = (1 - p_i)(\lambda_i + \lambda_i^2) = ((1 - p_i)\lambda_i)^2$ respectively.

Zero-Inflated Negative Binomial

These models account for excess zeros in the data, which may arise due to both genuine absence of events and excess zeros.

$$P(Y = y) = \begin{cases} \rho + (1-\rho_i)\left(1+\dfrac{\lambda}{\alpha}\right)^{-\alpha}, & y = 0 \\ (1-\rho)\dfrac{\Gamma(y+\alpha)}{y!\Gamma(\alpha)}\left(1+\dfrac{\lambda}{\alpha}\right)^{-\alpha}\left(1+\dfrac{\lambda}{\alpha}\right)^{-y}, & y = 1, 2, \ldots \end{cases}$$

In order to estimate α and β as in the Poison model, the iteration procedure or method of Newton Raphson is applied.

Model Selection and Rationale

Five candidate count distribution models were considered for this analysis:

Poisson Regression: This commonly used model assumes a constant rate of new COVID-19 cases over time. However, it might not be suitable for data with over-dispersion, where the variance is greater than the mean.

Negative Binomial Regression: This model addresses the limitation of the Poisson model by allowing for over-dispersion. It is often preferred for count data with a higher degree of variability than expected under a Poisson distribution.

Zero-Inflated Poisson (ZIP) Regression: This model specifically caters to scenarios where there is an excess of zeros in the data. This could be relevant for some zones that may have experienced periods with very low or zero reported cases, particularly in the early stages of the pandemic.

Zero-Inflated Negative Binomial (ZINB) Regression: This model combines the strengths of the ZIP and Negative Binomial models, accounting for both over-dispersion and an excess of zeros. It offers a more flexible approach when these characteristics are present in the data.

Generalized Poisson (GP) Regression: This model provides more flexibility in capturing various shapes of count data distributions compared to the other models. It might be useful if the daily case data exhibits a non-standard distribution pattern.

Model Selection Criteria

The Akaike Information Criterion (AIC) served as the primary metric for model selection. AIC is a statistical measure that balances model fit with model complexity. The model with the lowest AIC value for each zone was considered the best fit for the daily COVID-19 case data within that zone. Choosing the model with the lowest AIC ensures a balance between accurately representing the data and avoiding overly complex models.

Justification for Model Selection

The selection of these specific count distribution models was guided by the potential characteristics of the daily COVID-19 case data. It is likely that the number of daily cases would exhibit over-dispersion due to factors like population density, healthcare access, and testing capacity varying across zones. Additionally, the possibility of encountering zones with a significant number of zero cases early in the pandemic motivated the inclusion of Zero-Inflated models (ZIP and ZINB). Finally, the Generalized Poisson model offered a versatile option for accommodating potentially non-standard distribution patterns in the data.

Hypothesis Testing

Hypothesis

Null Hypothesis (H_o); The distribution fits the infection data well.

Alternative Hypothesis (H_a); The distribution does not fit the infection data well.

Level of Significance:

The level of significance (α) is set at 5%.

Decision Rule:

The null hypothesis (H0) will be rejected if the p-value is less than α, indicating that the chosen distribution does not fit the infection data well. Conversely, if the p-value is greater than or equal to α, the null hypothesis will not be rejected, signifying a good fit of the distribution to the infection data.

RESULTS

On analysis of dataset on number of COVID-19 infections across the six geopolitical zones. Table 1 provides an overview of COVID-19 infection records categorized by varying counts of cases within Nigeria's Geopolitical Zones. Each row in the table represents a distinct count of cases, spanning from 0 to 8, while each column corresponds to a specific Geopolitical Zone. The figures within each cell represent the count of COVID-19 infection records within that zone associated with the specified count of cases.

Table 1: Number of COVID-19 infections records for each Geopolitical Zone in Nigeria

NUMBER OF CASES RECORDS	NORTH-EAST		NORTH-CENTRAL		NORTH-WEST		SOUTH-WEST		SOUTH-EAST		SOUTH-SOUTH	
	Count	**(%)**	**Count**	**(%)**	**Count**	**(%)**	**Count**	**(%)**	**Count**	**(%)**	**Count**	**(%)**
0	366	53.6	288	45.6	183	36.2	176	33.4	198	37.7	166	33.0
1	127	18.6	118	18.7	109	21.6	125	23.7	112	21.3	137	27.3
2	81	11.9	78	12.4	84	16.6	89	16.9	94	17.9	86	17.1
3	40	5.9	52	8.2	61	12.1	56	10.6	59	11.2	53	10.5
4	29	4.2	38	6.0	34	6.7	40	7.6	38	7.2	25	5.0
5	13	1.9	28	4.4	25	5.0	22	4.2	15	2.9	15	3.0
6	12	1.8	12	1.9	5	1.0	12	2.3	5	1.0	12	2.4
7	10	1.5	12	1.9	3	0.6	5	0.9	3	0.6	7	1.4
>7	5	0.7	5	0.8	1	0.2	2	0.4	1	0.2	2	0.4
TOTAL	683		631		505		527		525		503	

In the North-East, the region accounts for a total of 683 COVID-19 infection records. These records are distributed as follows: 53.6% of the records have 0 cases, 18.6% have 1 case, 11.9% have 2 cases, and 5.9% have 3 cases. Moving to the North-Central zone, the records are distributed as follows: 45.6% with 0 cases, 18.7% with 1 case, 12.4% with 2 cases, and 8.2% with 3 cases throughout the study period. In the North-West zone, the distribution is as follows: 36.2% of the records have 0 cases, 21.6% have 1 case, 16.6% have 2 cases, and 12.1% have 3 cases.

For the South-West zone, the distribution stands at: 33.4% with 0 cases, 23.7% with 1 case, 16.9% with 2 cases, and 10.6% with 3 cases. In the South-East, the distribution is as follows: 37.7% with 0 cases, 21.3% with 1 case, 17.9% with 2 cases, and 11.2% with 3 cases. Lastly, in the South-South zone, with a total of 503 COVID-19 infection records, the distribution is: 33.0% with 0 cases, 27.3%

with 1 case, 17.1% with 2 cases, and 10.5% with 3 cases.

The data reveals that both the North-East and North-Central zones have the highest number of infection records across all counts of cases, suggesting a higher frequency of COVID-19 infections in these regions. Furthermore, there is a noticeable variation in the distribution of infection records among different zones. The South-West and South-South zones, in particular, exhibit relatively lower counts of infection records across all counts of cases compared to the North-East, North-Central, and North-West zones. It is worth noting that the majority of infection records are concentrated around lower counts of cases (ranging from 1 to 3), indicating that most Geopolitical Zones experienced a higher number of instances with relatively fewer COVID-19 cases.

Table 2 presents key results for the dataset of COVID-19 infections in North-East, Nigeria. The observed mean of COVID-19 infections is 1.1303, and the observed variance is 2.8877. These statistics offer insights into the data's distribution. When the observed mean and variance significantly differ, it indicates over-dispersion in the data. Over-dispersion occurs when the observed variance exceeds what would be expected from a Poisson distribution.

Table 2: The goodness-of-fit and estimation models with parameter for dataset of number of COVID-19 infections in North-East, Nigeria

X	COUNT	PD	NB	GP	ZIP	ZINB
0	366	220.5638	360.9949	356.5746	166.0002	365.9997
1	127	249.3050	142.3100	151.5186	105.3617	125.5618
2	81	140.8957	74.3887	74.2907	105.4615	78.9154
3	40	53.0852	42.0712	39.9938	70.3743	47.4015
4	29	15.0006	24.6948	22.8921	35.2205	27.8125
5	13	3.3911	14.8126	13.6765	14.1015	16.0866
6	12	0.6388	9.0119	8.4320	4.7050	9.2148
7	10	0.1032	5.5379	5.3253	1.3455	5.2418
>7	5	0.0146	3.4286	3.4277	0.3367	2.9662
TOTAL	683	683	683	683	683	683
PARAMETER (S)	$x=1.1303$ $\sigma^2=2.8877$	$\lambda=1.1303$	$r=0.6053$ $p=0.6512$	$\lambda=1.130$ $\alpha=3.0243$	$\lambda=2.0019$ $p=0.2253$	$\lambda=1.3065$ $\alpha=0.4550$ $p=0.2777$
CHI-SQUARE VALUE		3081.836	8.684592	12.82043	63.6937	**8.4257**
P-VALUE		0.0000	0.0123	0.0251	0.0000	**0.0772**
AIC		2355.760	1996.5698	2002.780	2006.027	**1994.154**

The analysis computes the expected number of zero counts based on the observed mean using the formula 683 * e^(-1.1303), resulting in approximately 220.57. However, the actual number of zero counts in the data is 366. This substantial difference between the expected and actual zero counts suggests the presence of excess zeros in the dataset. Excess zeros occur when there are more zeros in the data than expected from a typical distribution.

Given the evidence of both over-dispersion and excess zeros, it is clear that the Poisson model is not appropriate for this dataset. The Poisson distribution assumes equal mean and variance, which is not the case due to over-dispersion, and it does not handle excess zeros well. Furthermore, the presence of more than 35% zeros indicates an excess of zeros.

Based on the p-values in Table 2, we have sufficient statistical evidence to reject the null hypothesis for Poisson regression (p-value = 0.0000), Generalized Poisson (p-value = 0.0251), Negative Binomial (p-value = 0.0123), and Zero-inflated Poisson regression (p-value = 0.0000). Therefore, we conclude that these distributions do not fit the data at the 5% level of significance.

However, based on the p-value from Table 2, we have enough statistical evidence not to reject the null hypothesis for the Zero-Inflated Negative Binomial (p-value = 0.0772). Consequently, we conclude that this distribution fits the data at the 5% level of significance.

In summary, the Zero-Inflated Negative Binomial distribution is the best fit for the dataset of COVID-19 infections in North-East, Nigeria. This conclusion is based on evidence of over-dispersion, excess zeros, chi-square goodness-of-fit tests, and model comparison using the Akaike Information Criterion (AIC). The ZINB distribution stands out with the lowest AIC value (1994.154) compared to other competing models in Table 2.

Table 3 displays the goodness-of-fit results for different models applied to the COVID-19 infection data in North-Central Nigeria. The table presents counts for various infection levels ranging from 0 to 8, along with the respective model predictions for each distribution. For each infection level (x), the table provides the observed count and the model predictions for the Poisson (PD), Negative Binomial (NB), Generalized Poisson (GP), Zero-Inflated Poisson (ZIP), and Zero-Inflated Negative Binomial (ZINB) distributions. These predictions represent the expected number of infections for each distribution.

When examining the p-values in Table 3, we find that there is substantial statistical evidence to reject the null hypothesis for the Poisson regression (p-value = 0.0000), Generalized Poisson (p-value = 0.0008), Negative Binomial (p-value = 0.0039), and Zero-Inflated Poisson regression (p-value = 0.0200). This leads us to conclude that these distributions do not adequately fit the data at a 5% level of significance.

However, based on the p-value in Table 3, we have sufficient statistical evidence not to reject the null hypothesis for the Zero-Inflated Negative Binomial (p-value = 0.2090). Consequently, we conclude that this distribution fits the data at a 5% level of significance.

In summary, the Zero-Inflated Negative Binomial distribution is the best fit based on the evidence provided by p-values, AIC, and chi-square values. With an AIC value of 1700.9593, it offers a better balance between fit and model complexity compared to other distributions. This makes it the most suitable choice for modeling the COVID-19 infection data in North-Central Nigeria, accounting for observed over-dispersion and potential excess zeros.

In Table 4, we observe that the mean and variance of the data are 1.4548 and 3.5086, respectively. The substantial difference between the variance and mean indicates over-dispersion, suggesting that the Poisson distribution's assumption of equal mean and variance is not met. This highlights the need for alternative models capable of accommodating the data's characteristics. Models designed to handle over-dispersion are essential for an accurate fit. Additionally, the presence of more than 35% zeros indicates an excess of zeros.

Table 3: The goodness-of-fit and estimation models with parameter for dataset of number of COVID-19 infections in North-Central, Nigeria

X	COUNT	PD	NB	GP	ZIP	ZINB
0	183	107.7705	170.0574	166.4639	183.0001	183.0001
1	109	166.4574	135.2994	139.4147	92.1109	103.5516
2	84	128.5513	86.6248	87.9959	98.3882	92.5821
3	61	66.1848	50.9737	50.5379	70.0623	61.9667
4	34	25.5565	28.6747	27.9004	37.4185	34.5116
5	25	7.8947	15.6851	15.1292	15.9874	16.8939
6	5	2.0322	8.4172	8.1380	5.6923	7.5104
7	3	0.4484	4.4547	4.3636	1.7372	3.0977
>7	1	0.0865	2.3329	2.3385	0.4639	1.2031
TOTAL	**505**	**505**	**505**	**505**	**505**	**505**
PARAMETER (S)	x=1.5445 σ^2=2.6771	λ=1.5456	r=1.6411 p= 0.4848	λ=1.5445 α=1.9370	λ=2.1363 p= 0.2770	λ=7.1349 α= 0.7802 p= 0.2316
CHI-SQUARE VALUE		156.5338	17.29505	20.8011	13.3876	5.8709
P-VALUE		0.0000	0.0039	0.0008	0.0200	0.2090
AIC		1812.491	1714.195	1717.990	1704.690	1700.9593

Table 4: The goodness-of-fit and estimation models with parameter for dataset of number of COVID-19 infections in North-West, Nigeria

X	COUNT	PD	NB	GP	ZIP	ZINB
0	288	147.3001	277.5859	271.6486	287.9995	287.9992
1	118	214.2917	140.9850	150.3232	79.6907	110.5987
2	78	155.8833	81.6858	83.1152	97.3838	86.7712
3	52	75.5948	49.2750	47.8540	79.3367	58.9257
4	38	27.4945	30.3111	28.5613	48.4756	36.9087
5	28	7.9999	18.8623	17.5432	23.6953	21.9503
6	12	1.9397	11.8278	11.0244	9.6520	12.5913
7	12	0.4031	7.4570	7.0564	3.3700	7.0330
>7	5	0.0733	4.7204	4.5851	1.0296	3.8489
	631	631	631	631	631	631
PARAMETER (S)	x=1.4548 σ^2=3.5086	λ=1.4548	r= 0.7803 p= 0.6508	λ=1.4548 α=2.9798	λ=2.4440 p= 0.4048	λ=2.351 α= 0.5318 p= 0.2972
CHI-SQUARE VALUE		994.7953	13.6188	21.5480	72.7226	7.7755
P-VALUE		0.0000	0.0182	0.0006	0.0000	0.1002
AIC		2422.357	2093.000	2102.539	2120.179	2081.5399

Based on the results in Table 3, we find significant statistical evidence to reject the null hypothesis for Poisson regression (p-value = 0.0000), Generalized Poisson (p-value = 0.0006), Negative Binomial (p-value = 0.0182), and Zero-Inflated Poisson regression (p-value = 0.0000). This implies that these distributions do not fit the data at a 5% level of significance.

However, based on the p-value from Table 3, we find sufficient statistical evidence not to reject the null hypothesis for the Zero-Inflated Negative Binomial (p-value = 0.1002), indicating that this distribution fits the data at a 5% level of significance.

In summary, the analysis shows that the Zero-Inflated Negative Binomial (ZINB) model is a better fit for the data compared to other models like Poisson (PD), Negative Binomial (NB), and Zero-Inflated Poisson (ZIP). This determination is based on a p-value greater than 0.05, indicating that the ZINB model statistically fits the data better. Additionally, the lower AIC value for the ZINB model (2081.5399) suggests a better balance between model complexity and data fit.

In conclusion, based on the evidence from p-values, AIC, and chi-square values, the Zero-Inflated Negative Binomial (ZINB) distribution provides the best fit for the dataset of COVID-19 infections in North-West Nigeria. It effectively accounts for over-dispersion and the presence of excess zeros, making it a suitable choice for modeling the data.

Table 5 presents the results for assessing the goodness-of-fit of various models applied to the dataset of COVID-19 infections in South-West Nigeria. The observed mean and variance for COVID-19 infections in this region are 1.6394 and 2.9724, respectively. The larger variance compared to the mean indicates the presence of over-dispersion in the data. As a result, the Negative Binomial (NB), Generalized Poisson (GP), and Zero-Inflated Negative Binomial (ZINB) distributions provide a better fit to the data compared to other models, unlike the Poisson (PD) and Zero-Inflated Poisson (ZIP) distributions, where the p-value falls below the 5% significance level.

Based on the p-values from Table 5, we find sufficient statistical evidence to reject the null hypothesis for Poisson regression (p-value = 0.0000) and Zero-Inflated Poisson regression (p-value = 0.0000), indicating that these distributions do not fit the data at the 5% significance level.

However, based on the p-values in Table 5, we find enough statistical evidence not to reject the null hypothesis for Generalized Poisson (p-value = 0.1696), Negative Binomial (p-value = 0.3666), and Zero-Inflated Negative Binomial (p-value = 0.6058), suggesting that these distributions fit the data at the 5% significance level.

Among the distributions that fit the data well, the ZINB model is the preferred choice. This preference is supported by the smallest chi-square value and the highest p-value (0.6058), indicating a good fit as the p-value is greater than 0.05 (5% significance level).

The AIC values further support the preference for the Zero-Inflated Negative Binomial (ZINB) distribution. The fact that the ZINB model has the smallest AIC value (1831.3818) compared to the other models suggests that it is the most suitable model according to this criterion.

In conclusion, based on the evidence from p-values, AIC, and chi-square values, the Zero-Inflated Negative Binomial (ZINB) distribution provides the best fit for the dataset of COVID-19 infections in South-West Nigeria. This distribution effectively accounts for observed over-dispersion and the presence of potential excess zeros, making it a suitable choice for modeling the data.

Table 5: The goodness-of-fit and estimation models with parameter for dataset of number of COVID-19 infections in South-West, Nigeria

X	COUNT	PD	NB	GP	ZIP	ZINB
0	176	102.2818	167.6486	164.5370	176.0001	176.0000
1	125	167.6878	139.3709	143.3202	97.2252	119.6053
2	89	137.4595	92.2826	93.5175	106.1963	95.4853
3	56	75.1202	55.8992	55.3329	77.3300	62.2333
4	40	30.7893	32.2842	31.4356	42.2327	36.0001
5	22	10.0956	18.0992	17.4810	18.4518	19.2420
6	12	2.7585	9.9426	9.6431	6.7181	9.7206
7	5	0.6461	5.3818	5.2988	2.0966	4.7072
>7	2	0.1324	2.8806	2.9084	0.5725	2.2055
TOTAL	527	527	527	527	527	527
PARAMETER (S)	x=1.6394 $\sigma^2=2.9724$	$\lambda=1.6395$	r=1.6864 p= 0.4929	$\lambda=1.6395$ $\alpha=1.9836$	$\lambda=2.1845$ p= 0.2495	$\lambda=3.4525$ $\alpha= 0.6414$ p= 0.1507
CHI-SQUARE VALUE		146.1064	5.4215	7.7648	29.1358	2.7196
P-VALUE		0.0000	0.3666	0.1696	0.0000	0.6058
AIC		1950.248	1834.8136	1837.7897	1849.344	1831.3818

The results in Table 6 assess the goodness-of-fit of various models to the dataset of COVID-19 infections in South-East Nigeria. The observed mean and variance for COVID-19 infections in this region are 1.4533 and 2.4506, respectively. The larger variance compared to the mean indicates the presence of over-dispersion. Furthermore, the existence of more than 35% zeros suggests an excess of zeros (0's).

Table 6: The goodness-of-fit and estimation models with parameter for dataset of number of COVID-19 infections in South-East, Nigeria

X	COUNT	PD	NB	GP	ZIP	ZINB
0	198	122.7396	184.3077	180.8182	198.0005	198.0009
1	112	178.3815	143.5297	147.6343	100.6602	109.9161
2	94	129.6239	89.1974	90.4169	101.9440	96.6193
3	59	62.7956	50.7556	50.2511	68.8295	62.3977
4	38	22.8157	27.5506	26.8011	34.8537	33.0309
5	15	6.6317	14.5214	14.0245	14.1193	15.1643
6	5	1.6064	7.5017	7.2741	4.7665	6.2566
7	3	0.3335	3.8191	3.7589	1.3792	2.3730
>7	1	0.0606	1.9229	1.9405	0.3492	0.8407
TOTAL	525	525	525	525	525	525
PARAMETER (S)	x=1.4533 $\sigma^2=2.4506$	$\lambda=1.4533$	r=1.6777 p= 0.4641	$\lambda=1.4533$ $\alpha=1.8591$	$\lambda=2.0255$ p= 0.2825	$\lambda=8.8012$ $\alpha= 0.8207$ p= 0.2445
CHI-SQUARE VALUE		144.5888	14.9731	17.9663	6.7682	1.4963
P-VALUE		0.0000	0.0105	0.0029	0.2384	0.82728
AIC		1822.539	1732.832	1736.237	1719.9020	1718.0877

Based on the p-values in Table 5, there is compelling statistical evidence to reject the null hypothesis for Poisson regression (p-value = 0.0000), Negative Binomial (p-value = 0.0105), and Generalized Poisson regression (p-value = 0.0029). Consequently, we conclude that these distributions do not fit the data at a 5% level of significance.

However, based on the p-values in Table 5, we have adequate statistical evidence not to reject the null hypothesis for Zero-Inflated Poisson (p-value = 0.2384) and Zero-Inflated Negative Binomial (p-value = 0.82728), indicating that these distributions fit the data at a 5% level of significance.

In summary, Zero-Inflated Poisson, Zero-Inflated Negative Binomial, and Negative Binomial distributions provide a good fit to the data at a 5% level of significance, given the observed over-dispersion. These distributions are better suited to capture the variability in the data compared to Poisson and Negative Binomial distributions.

Among the well-fitting distributions, the Zero-Inflated Negative Binomial (ZINB) model is preferred due to having the smallest chi-square value and the highest p-value, signifying a good fit with a p-value greater than 0.05.

When considering AIC values, the ZINB model stands out as the best choice, with the smallest AIC value (1718.0877) among the competing models.

Table 7: The goodness-of-fit and estimation models with parameter for dataset of number of COVID-19 infections in South-South, Nigeria

X	COUNT	PD	NB	GP	ZIP	ZINB
0	166	106.6866	165.4251	163.6056	166.0002	166.0000
1	137	165.4383	136.3764	139.4708	105.3617	135.0187
2	86	128.2722	88.1515	88.6367	105.4615	88.4294
3	53	66.3037	51.7489	50.9384	70.3743	52.1547
4	25	25.7042	28.8436	28.0302	35.2204	29.0613
5	15	7.9719	15.5633	15.1111	14.1012	15.6253
6	12	2.0603	8.2128	8.0663	4.7050	8.1976
7	7	0.4564	4.2643	4.2866	1.3455	4.2244
>7	2	0.0884	2.1871	2.2744	0.3367	2.1475
TOTAL	503	503	503	503	503	503
PARAMETER (S)	x=1.5507 σ^2=2.8415	λ=1.5501	r=1.7602 p= 0.4684	λ=1.5507 α=1.9063	λ=2.0019 p= 0.2253	λ=1.8508 α= 0.5405 p= 0.1437
CHI-SQUARE VALUE		243.7465	4.1375	4.2381	63.6937	4.2995
P-VALUE		0.0000	0.5298	0.5156	0.0000	0.3669
AIC		1808.970	1705.9314	1706.7018	1742.027	1707.9057

Table 7 displays the goodness-of-fit assessment for different models applied to the dataset of COVID-19 infections in South-South Nigeria. The observed mean and variance for COVID-19 infections in this region are 1.5507 and 2.8415, respectively. The larger variance compared to the mean suggests over-dispersion in the data. Notably, the Negative Binomial (NB), Generalized Poisson (GP), and Zero-Inflated Negative Binomial (ZINB) distributions provide a better fit to the data compared to other models such as Poisson (PD) and Zero-Inflated Poisson (ZIP). These distributions are better equipped to handle the increased variability observed in the data.

Based on the p-values in Table 5, there is compelling statistical evidence to reject the null hypothesis for Poisson regression (p-value = 0.0000) and Zero-Inflated Poisson regression (p-value = 0.0000), indicating that these distributions do not fit the data at a 5% significance level.

However, based on the p-values in Table 5, we have adequate statistical evidence not to reject the null hypothesis for Generalized Poisson (p-value = 0.5156), Negative Binomial (p-value = 0.5298), and Zero-Inflated Negative Binomial (p-value = 0.3669), suggesting that these distributions fit the data at a 5% significance level.

In summary, Generalized Poisson, Zero-Inflated Negative Binomial, and Negative Binomial distributions provide a good fit to the data at a 5% significance level, given the observed over-dispersion.

Among the well-fitting distributions, the Negative Binomial (NB) model is preferred. This preference is supported by both the smallest chi-square value (4.1375) and the highest p-value (0.5298), indicating a good fit with a p-value greater than 0.05.

In the context of AIC Model Comparison, the Negative Binomial (NB) model stands out as the best option, with the smallest AIC and BIC values (1705.9314) among the compared models.

In conclusion, we find that the Negative Binomial (NB) distribution is the most suitable model for the dataset of COVID-19 infections in South-South Nigeria. This distribution effectively accounts for over-dispersion and provides a better fit to the data, as supported by both statistical tests and information criteria.

DISCUSSION

The analysis undertaken in this study provides valuable insights into the selection of appropriate statistical models for COVID-19 infection datasets in different regions of Nigeria. It sheds light on the challenges posed by over-dispersion and the presence of excess zero counts, emphasizing the need for models that can effectively handle these complexities.

In Table 2, which pertains to the North-East region, the study revealed that both Poisson models and the Negative Binomial model were not well-suited to address the over-dispersion and excess zero issues within the dataset. However, the Zero-Inflated Negative Binomial (ZINB) model consistently emerged as the superior choice. This preference for ZINB was confirmed through rigorous evaluation, taking into account chi-square statistics, p-values, and AIC values.

Similarly, in Table 3, focusing on the North-Central region, the data exhibited characteristics of over-dispersion and excess zeros. Once again, the ZINB model demonstrated its effectiveness in providing a better fit for the dataset compared to other models.

Table 4, which examined the North-West region, further supported the trend observed in previous tables. Where, ZINB model consistently outperformed other models in addressing the over-dispersion and excess zero counts in the data.

Moving on to Table 5, which pertains to the South-West region, the presence of a larger variance reinforced the notion of over-dispersion in the COVID-19 infection dataset. This region also favored the Negative Binomial and Zero-Inflated Negative Binomial models, with the ZINB model emerging as the best fit, further emphasizing its consistency in handling these complexities.

In Table 6, for the South-East region, the study once again found that the Zero-Inflated Negative Binomial model was the most suitable choice for addressing over-dispersion and excess zero counts.

Finally, in Table 7, representing the South-South region, the analysis pointed to the suitability of the Negative Binomial model, which consistently captured the complexities associated with over-dispersion.

Collectively, this analysis highlights the noteworthy consistency in the suitability of ZINB models for representing COVID-19 infection datasets across various Nigerian regions. These models have proven to be highly effective in accounting for over-dispersion and the presence of excess zero counts, accurately representing the intricate patterns of COVID-19 infections in Nigeria.

This study underscores the importance of choosing statistical models that are not only statistically sound but also capable of accommodating the unique characteristics of the data at hand. It provides valuable guidance for researchers and policymakers seeking to model and understand the spread of COVID-19 across different regions, emphasizing the significance of addressing over-dispersion and excess zero challenges in their analyses.

CONCLUSION

In conclusion, the comprehensive analysis conducted in this study provides valuable insights into the selection of appropriate statistical models for assessing and understanding COVID-19 infection data in Nigeria. The overarching theme that emerges from this analysis is the consistent challenge posed by over-dispersion and the presence of excess zero counts in the dataset. These challenges render the traditional Poisson distribution inadequate for accurately modeling the COVID-19 infection trends across different Nigerian regions.

While the limitations of the Poisson distribution become evident, the study highlights the unwavering performance of the Zero-Inflated Negative Binomial (ZINB) model. In the face of over-dispersion and excess zeros, ZINB consistently excels, offering a superior fit to the data. The ZINB model's remarkable performance is attributed to its ability to simultaneously handle over-dispersion and account for the presence of excess zero counts. This dual capability allows it to effectively capture the complex patterns of COVID-19 infections in Nigeria.

Furthermore, the Negative Binomial model stands out as a suitable choice for regions like the South-South, where excess zero counts are not a prominent feature in the dataset. In such cases, the Negative Binomial model effectively fits the data, providing valuable insights into the dynamics of the pandemic.

Across the diverse Nigerian regions, ZINB and Negative Binomial models consistently deliver results that accurately represent the nuanced trends in COVID-19 infections. These models not only account for over-dispersion but also effectively address the presence of excess zeros, making them valuable tools for policymakers, researchers, and healthcare professionals seeking to gain a deeper understanding of the pandemic's dynamics in different areas.

The insights derived from this analysis have far-reaching implications for public health strategies in the fight against COVID-19 and future infectious and epidemiological diseases. By choosing statistical models that can effectively handle over-dispersion and excess zeros, decision-makers can make more informed and targeted interventions. These findings offer a valuable guide for crafting effective strategies to combat COVID-19 and similar diseases, taking into account the unique challenges presented by different regions within Nigeria.

In summary, the consistent suitability of ZINB models in representing COVID-19 infection datasets across various Nigerian regions, coupled with their ability to handle over-dispersion and excess zeros, underlines their crucial role in understanding the dynamics of the pandemic. These models provide a valuable tool for researchers and policymakers as they work to combat the spread of COVID-19 and other infectious diseases, ultimately contributing to more effective public health strategies and interventions.

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