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Modeling and Forecasting the Prevalence of Human Immuno-Deficiency Virus (HIV) in Birnin Gwari Local Government Area of Kaduna State

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ABSTRACT

Human immunodeficiency virus (HIV) has been prevalent in millions of people worldwide for more than 50 years. Therefore, its prevalence must be monitored to make well-informed decisions and create efficient health plans. This paper dwelt on the modeling and prediction of the prevalence of HIV among inpatients and outpatients visiting Jibril Mai-Gwari I Memorial Hospital in Birnin Gwari Local Government Area of Kaduna State. An expo-facto research methodology was adopted for this study through the collection of twelve (12) years of monthly data spanning the period 2010-2021 as extracted from the hospital's inpatient and outpatient department records. Box and Jenkins analytical approach was used to model the data due to its presence of unit root, as a non-stationarity data cannot be modeled using the conventional time series models. Iterative methods were applied in the identification of several ARIMA models as ARIMA (2, 1, 5) model was found to be the best fit among the 25 iterated models based on its higher loglikelihood (-435.57), lower variance (24.95) and lower AIC (887.13). More so, the model was found to scale through the portmanteau tests of residual independence (Ljung-Box Chi-square 5.9261, p-value > 0.05) and normality (Wilk 0.9830, p-value > 0.05), a confirmatory test of model reliability and accuracy. Although the prognosis suggests that HIV prevalence may not change significantly in the upcoming years, the expanding uncertainty band suggests that it will be challenging to estimate HIV prevalence in the future with high confidence. To manage prevalence and lower the chance of an unanticipated increase, public health measures must be consistent and effective.

INTRODUCTION

As the name implies, Human Immunodeficiency Virus (HIV) is a retrovirus that infects immune cells and destroys their functions. A retrovirus is a virus that uses RNA instead of DNA as its genetic material. It incorporates itself into the host cells' DNA by the use of an enzyme known as reverse transcriptase, this allows several copies of the virus to be produced in the host cells. Unlike certain other diseases, the human body cannot dispose of HIV. That indicates that once you get HIV, you have it forever. HIV is widespread all across the world, with Sub-Saharan Africa accounting for 70% of new infections each year (Awoleye & Thron, 2015; Kapila *et al*., 2016).

Heterosexual transmission is the most common method of transmission, which account for about 85% of all HIV infections. Southern Africa remains the epicenter of the pandemic, with significant rates of new HIV infections (Simon *et al*., 2006). Furthermore, studies revealed that Sub-Saharan Africa tends to bear a significant amount of the worldwide HIV burden. In 2010, Sub-Saharan Africa was home to 68% of all HIV-positive individuals. In 2012, it was projected that 3.5 million people in Nigeria live with the virus, putting Nigeria the third among countries with the highest burden of HIV infection after India and South Africa (Awoleye & Thron, 2015). In 2021, 1.9 million Nigerians were living with HIV. In addition, 170,000 children up to the age of 14 were HIV positive (UNAIDS, 2021).

HIV is most commonly transmitted through sexual contact. It can also be passed from mother to child, during pregnancy or childbirth (by blood or fluid exposure), or through nursing. Non-sexual Transmission can also occur by sharing injection equipment, most commonly needles (Umunna & Olanrewaju, 2020).

In Nigeria, nearly 80% of new HIV infections are transmitted through heterosexual intercourse, with mother-to-child transmission following closely behind, 38% of new adult infections are attributable to female sex workers (FSW), injecting drug users (IDU), and men having sex with men (MSM), accounting for 3.5% of the adult population (Awoleye & Thron, 2015; Ummuna & Olanrewaju, 2020).

Therefore, an epidemiological prediction of this virus is crucial to formulate policies and develop effective strategies; it is clearly advantageous to have a clear picture of its future occurrence, spread, and impact. This contributes to public health decision-making, resource allocation, and other intervention plans.

Several studies have been written on HIV in Nigeria, the prevalence, the knowledge, awareness, factors responsible for its prevalence, and numerous further in the literature. However, only very few have been predictive in nature or forecast the prevalence or trend of HIV in Nigeria in the coming years.

Bashorun *et al*. (2014) carried out a cross-sectional

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study that involved pregnant women who attended Antenatal Clinics in 160 sentinel facilities for 10 years. The national and state prevalence were ascertained using unlinked-anonymous HIV testing (UAT), consecutive sampling, and Epi-Info. The burden of infection was also prognosticated using The Estimation and Projection Package with Spectrum. The results between the years 2001 and 2010 showed pivotal differences in the epidemic in different states. There was elevated HIV prevalence in eight countries and a reduction of more than 2% in six countries. States in the middle and south of Nigeria also had an advanced prevalence of HIV.

Badru *et al*. (2020) used cross-sectional data to examine comprehensive HIV knowledge, stigma, and comprehension of the threat of HIV among youthful adolescents. The data were obtained from the 2017 Akwa Ibom AIDS Indicator Survey. Data were scrutinized using descriptive statistics, Chi-square test or Fisher's exact test, and multivariable logistic retrogression models were used to determine associations with the study issues. The results of the study indicated that there was significantly low comprehensive HIV knowledge among youthful adolescents, the majority of youthful adolescents reported stigmatizing tendencies towards people living with HIV, and most adolescents do not perceive themselves to be at threat of HIV, and HIV Prevalence among youthful adolescents was at 0.6.

Onovo *et al*. (2023) conducted a study to decide the level of state HIV seropositivity rates by scrutinizing the Nigeria HIV testing services (HTS) data for Nigeria from October 1, 2020, to September 30, 2021. The study used a Bayesian direct model with normal prior distribution and a Markov Chain Monte Carlo approach to estimate the HIV state-level prevalence for all the states in Nigeria, including FCT. The HIV seropositivity rates as the outcome variable were well acclimated for demographic, economic, biological, and societal covariates. The result shows a national HIV prevalence of 2.1% among grown-ups aged 15 – 49 times in Nigeria, which corresponds to roughly 2 million people living with HIV. It also shows a state-varied HIV prevalence in Nigeria, with Benue having the highest prevalence, followed by Rivers, Akwa Ibom, Edo, and Taraba, placing fourth and fifth independently. Jigawa had the smallest HIV prevalence.

Isichei *et al*. (2015) also carried out a cross-sectional study to examine the prevalence of HIV infection and associated risk factors among pregnant women in the Plateau state. 248 pregnant village women in prenatal clinics in five villages of Mangu Local Government area of Plateau State, North Central Nigeria were recruited for the study. The results show a high prevalence of HIV in the area, at 3.2%. It also showed that there was an advanced rate of HIV infection among women who did not hesitate from sexual intercourse during gestation and women in polygamous marriages. Parous women were also noticed to be significantly more likely to be infected than nulliparous women.

Adeoye *et al*. (2021) assessed the prevalence of HIV among the crucial populations in Nigeria using HIV Testing Services handed by the Society for Family Health intervention, and data from the intervention between the times 2019 and 2020 were analyzed with SPSS interpretation 20. The results show an advanced prevalence of HIV among those 40 years and above, the male gender, and men who have coitus with men (MSM). Box- Jenkins ARIMA fashion in prognosticating the number of adults who will be infected with HIV annually in Nigeria over the given period of 2019 to 2030 was applied by Nyoni and Nyoni (2020). The result of their study shows that the prevalence of new HIV infections in Nigerian adults will increase between the time 2019 and 2030 having an estimated figure of 101754 new HIV infections in Nigeria in 2019 and 114883 by 2030. However, this study is the only study in the literature that attempts to prognosticate the estimated rise and trend of HIV in Nigeria.

There remains a significant gap in the literature when it comes to forecasting the rise in HIV prevalence in Nigeria, underscoring the need for this study. This research aims to inform and influence programs focused on the prevention and control of HIV in the country. By applying an epidemiological prediction model such as the Autoregressive Integrated Moving Average (ARIMA), this study seeks to provide a clearer understanding of future HIV trends in Nigeria. The findings could play a crucial role in shaping national strategies aimed at reducing new infections and improving health outcomes for those living with HIV. This research intends to fill the current gap and serve as a valuable tool for public health planning and intervention in the study area. This study aims to model the prevalence of HIV infection among outpatients visiting Jibril Mai-Gwari I Memorial Hospital, Birnin Gwari, Kaduna State, Nigeria.

MATERIALS AND METHODS

This paper adopts expo-facto research design. Monthly HIV prevalence data were collected from Jibril Mai-Gwari I Memorial Hospital, Birnin Gwari, Kaduna State, over 12 years from 2010 to 2021. Unit root test was applied to the data calibrate the data for model-building development. We use the Augmented Dickey-Fuller unit root test to validate this property of stationarity in time series data. The ADF equation is given as:

$$\Delta_{y_t} = a_0 + a_1 y_{t-1} + \sum_{i=1}^{p} a_i \Delta_{y_{t-i}} + \varepsilon_i \qquad (1)$$

We reject the null hypothesis of no unit root if the p-value of Dickey-Fuller test statistic is less than the level of significance 0.05.

The method of data analysis used in the study is Autoregressive Integrated Moving Average (ARIMA) Model, which is a crucial method for modeling non-stationary time series data. ARIMA models consist of three components: autoregressive (AR), differencing (I), and moving average (MA). The AR component regresses the time series on its lagged values, the I component involves differencing the series to achieve stationarity, and the MA component models the relationship between the series and past forecast errors. The model is expressed as ARIMA(p, d, q), where 'p' is the number of lag observations in the model, 'd' is the degree of differencing, and 'q' is the size of the moving average window.

The specific ARIMA model developed for this study is given by:

$$Y_t = \mu + \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \cdots + \phi_p Y_{t-p} + \varepsilon_t - \theta\varepsilon_{t-1} - \theta_2\varepsilon_{t-2} - \ldots - \theta_q \varepsilon_{t-q} \qquad (2)$$

Where:

μ is the mean of the series

Y_t,Y_{t-1} represent the occurrence of period t and t−1, respectively.

ε_t, ε_{t-1} are residuals (errors) of period t and t−1.

Φ_1, Φ_1 are coefficients of autoregressive and moving average processes, respectively.

Once stationarity was confirmed, the ARIMA (p, d, q) model was fitted to the data, and the final model used for forecasting was determined.

Model Selection Criteria

Based on the Loglikelihood approach and the Akaike Information Criterion (AIC), the best fitting model out of multiple iterated models was selected. The AIC using maximum likelihood case is defined as:

$$AIC = 2 \log(\text{maximum likelihood}) + 2k \qquad (3)$$

Where,

k = p + q + 1 if the model contains a constant term and k =p+q otherwise. Then, the addition of 2(p+q+1) or 2(p+q) acts as a “penalty function” helps to guarantee the selection of economic models and prevent models with an excessive number of parameters.

Residual Analysis and Diagnostic Check

To ensure the validity of model, we conducted a diagnostic test using Shapiro Wilk and Ljung-Box test on the residuals of the fitted model.

Shapiro-Wilk Test

To assess the normality of the residuals, we applied the Shapiro-Wilk test. The test statistic W for the Shapiro-Wilk is calculated as follows:

$$w = \frac{\left(\sum_{i=1}^{n} a_i x_{(i)}\right)^2}{\sum_{i=1}^{n}(x_i - x)^2} \qquad (4)$$

Where:

x_i are the ordered residuals (from smallest to largest),

a_i are constants derived from the covariance matrix of the residuals,

$\bar{\mathbf{x}}$ is the mean of residuals,

n is the sample size.

Ljung-Box Test

To check for autocorrelation in the residuals, we performed the Ljung-Box test. The Ljung-Box test statistic Q is given by:

$$Q = n(n+2)\sum_{k=1}^{n} \frac{\widehat{P_k^2}}{n-k} \qquad (5)$$

Where,

n is the number of observations,

h is the number of lags being tested,

$\widehat{P_k^2}$ is the autocorrelation of the residuals at lag k.

RESULTS AND DISCUSSION

(4)

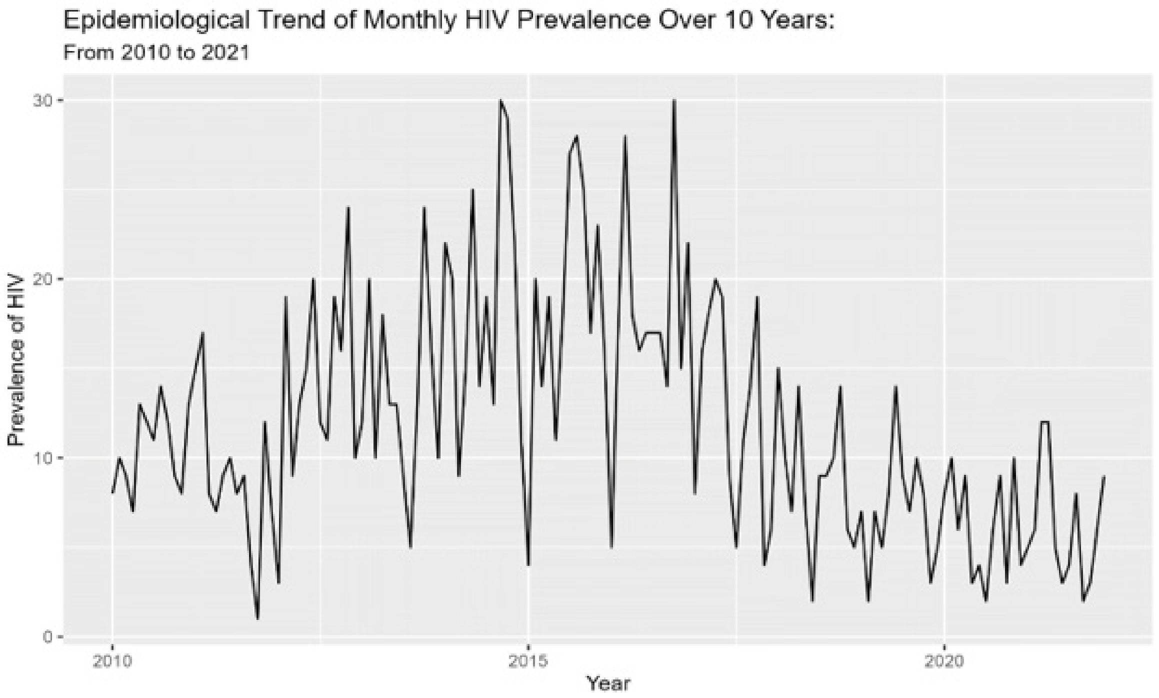

Figure 1: Epidemiological Trend of Monthly HIV Prevalence

(5)

Table 1: Descriptive Statistics of Prevalence of HIV

Descriptive Statistics	**HIV Prevalence**
Observations	144
Min	1
1st Quarter	7
Median	10.5
Mean	11.99
3rd Quarter	16
Max	30
Std.dev	6.647

Source: R-Studio Output

The epidemiological plot of figure 1 shows the monthly prevalence of HIV pattern in Birnin Gwari Local Government area of Kaduna state. The plot indicated that the prevalence of HIV was at its peak in Sep of 2014 and Oct 2016 respectively.

In Table 1, the minimum prevalence of HIV is 1, while the average prevalence of HIV is 11.99 at 25% quantile of 7 and 75% quantile of 16. However, the maximum prevalence of HIV is 30.

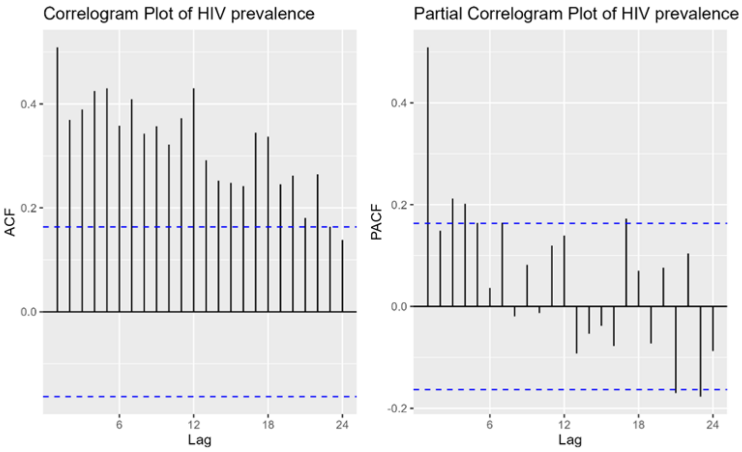

Figure 2: ACF and PACF plot of Human Immunodeficiency Virus Prevalence

Only the final two lags (23 and 24) are within the control limits in the ACF plot of the original HIV prevalence data, showing high non-stationarity that is probably caused by underlying trends or seasonal effects. The other lags show considerable autocorrelations. The data appears to have a significant short-term autocorrelation structure, with

Table 2: Augmented Dickey–Fuller Test for Series Stationarity

Levels	**d.f t-statistic**	**p-value**
Original Series	-2.4235	0.4001
1st difference	-8.3233	0.0100
Source: R-Studio Output		

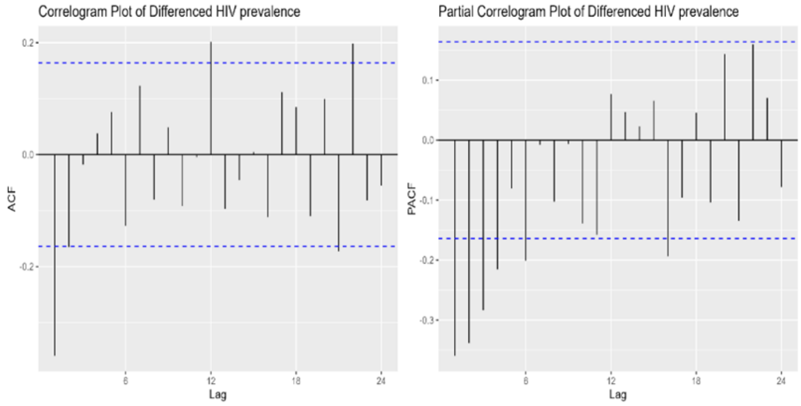

Figure 3: ACF and PACF plot of Differenced Human Immunodeficiency Prevalence

influence waning after these initial lags, according to the PACF plot, which only reveals six lags that exceed the control limits. These patterns suggest that differencing is necessary to ensure stationarity before applying an ARIMA model (Adeboye & Ogunnusi, 2020).

The data's non-stationarity was further confirmed in Table 2 with an ADF value of -2.4235 and an associated p-value (0.4001 > 0.05 significance level). However, after differencing the ADF value of -8.3233 with a p-value (0.01<0.05) confirmed the stationarity of the data at 1st differencing. Model identification can now take place.

Table 3: Iterated ARIMA Models

Models	**LL**	**AIC**	**σ^2**
ARIMA(1,1,1)	-441.93	889.87	28.09
ARIMA(1,1,2)	-441.06	890.13	27.73
ARIMA(1,1,3)	-440.64	891.27	27.56
ARIMA(1,1,4)	-440.57	893.14	27.54
ARIMA(1,1,5)	-439.8	893.6	27.23
ARIMA(2,1,1)	-440.69	889.38	27.59
ARIMA(2,1,2)	-440.55	891.09	27.53
ARIMA(2,1,3)	-439.01	890.01	26.27
ARIMA(2,1,4)	-440.46	894.92	27.49
ARIMA(2,1,5)	-435.57	887.13	24.95
ARIMA(3,1,1)	-440.52	891.03	27.52
ARIMA(3,1,2)	-440.51	893.03	27.52
ARIMA(3,1,3)	-439.16	892.32	26.67
ARIMA(3,1,4)	-437.81	891.61	25.86
ARIMA(3,1,5)	-435.36	888.72	24.87
ARIMA(4,1,1)	-440.51	893.03	27.52
ARIMA(4,1,2)	-439.92	893.83	27.28
ARIMA(4,1,3)	-438.02	892.04	25.97
ARIMA(4,1,4)	-437.76	893.52	25.83
ARIMA(4,1,5)	-436.93	893.96	25.47
ARIMA(5,1,1)	-440.47	894.93	27.5
ARIMA(5,1,2)	-439.53	895.06	27.13
ARIMA(5,1,3)	-435.29	888.58	24.84
ARIMA(5,1,4)	-435.28	890.57	24.84
ARIMA(5,1,5)	-437.83	897.65	26.38

LL = Log Likelihood, AIC = Akaike Information Criterion, σ2 = Variance

Source: R-studio Output

Table 3 shows the model identification. Twenty-Five (25) model was computed to select the best-fit model with the minimum AIC. Out of the computed model, ARIMA(2,1,5) with AIC (887.13) happens to be the best model of fit for the forecast of Human Immunodeficiency Virus prevalence in Birnin Gwari LGA, Kaduna State. Following the rule of parsimony which states that the simplest model should be chosen provided all necessary conditions are met. ARIMA(2,1,5) whose parameters were tested for significance in Table 4 below.

Table 4: Results of the estimated best-fitted ARIMA (0,0,2)x(0,0,1)12 Model Parameters

Variable	**Parameter**	**Coefficient**	**Std. Error**	**Z-value**	**p-value**
AR(1)	θ_1	-1.6232	0.0305	-53.1672	0.0000***
AR(2)	θ_2	-0.9609	0.0278	-34.5708	0.0000***
MA(1)	Θ_1	0.9814	0.1042	9.4227	0.0000***
MA(2)	Θ_2	-0.3610	0.1283	-2.8125	-0.0049***
MA(3)	Θ_3	-1.0315	0.0989	-10.4264	0.0000***
MA(4)	Θ_4	-0.0924	0.1187	-0.7783	0.4363
MA(5)	Θ_5	0.1604	0.0881	1.8200	0.06876

****represents significant at 1% level* ***represents significant at 5% level*

Source: R-studio Output

The model specification for the identified ARIMA model in table 4 is written as;

$$\boldsymbol{Y_t = \mu + \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \cdots + \phi_p Y_{t-p} + \varepsilon_t - \theta_1 \varepsilon_{t-1}}$$
$$\boldsymbol{-\theta_2 \varepsilon_{t-2} - \cdots - \theta_q \varepsilon_{t-q}}$$

$$Y_t = \mu - 1.6232Y_{t-1} - 0 \cdot 9609Y_{t-2} + \varepsilon_t + 0.9814\varepsilon_{t-1} - 0 \cdot 3610\varepsilon_{t-2}$$
$$-1.0315\varepsilon_{t-3} - 0 \cdot 0924\varepsilon_{t-4} + 0 \cdot 1604\varepsilon_{t-5}$$

In table 4, the estimated parameters of AR(1), AR(2), MA(1), MA(2), and MA(3) are statistically significant with respective p-values < 0.05 level of significance. MA(4) and MA (5) were to contribute to the model insignificantly. Therefore, the model coefficient is sufficient to forecast the prevalence of HIV in Birnin Gwari, Kaduna State.

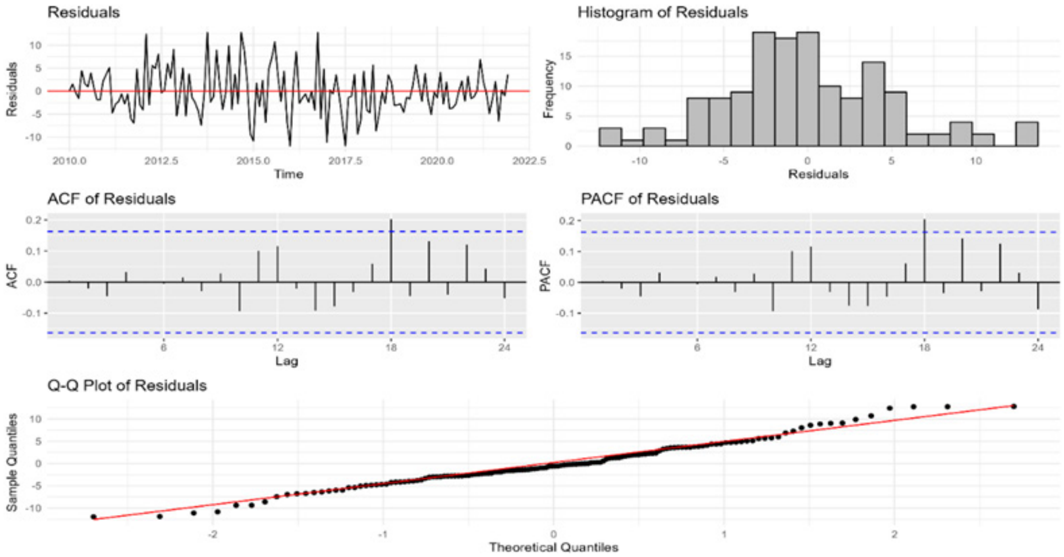

Figure 4: Independency of error term autoregressive conditional heteroskedasticity and ACF/PACF of independency of residual.

Figure 4 shows that the residual of the fitted model met the assumption of the normality test as the qq plot is closely aligned with the reference line and also the histogram appeared symmetrically around zero. The ACF and PACF spike fell within the range. Therefore, it can be said that the ARIMA (2,1,5) appears to provide an adequate predictive model for the prevalence of HIV.

Portmanteau Test on the best fitted ARIMA(2,1,5) Model

There is a necessity to further verify if the model is correctly specified before accepting the fitted model i.e whether assumptions are supported by the data. If some important assumptions are violated, then there is a need to fit a new model and check again until it meets the assumptions and a model that provides an adequate fit to the data is seen. The further diagnostic test for the model are presented below:

The Shapiro-Wilk test of normality of the residual in table 5 above has a test statistic of 0.9830 with corresponding P-values of 0.0732 > 0.05 level of significance where the normality of residuals of the best-fitted ARIMA (2, 1, 5) is not rejected at 1%, 5%, and 10% significance levels. This indicates that the residuals are Independently and Identically Normally Distributed.

Table 5: Shapiro-Wilk Test of Normality

Data	**Shapiro-wilk**	**p-value**
HIV	0.9830	0.0732
Source: R-Studio Output		

Ljung-Box test statistic shows a chi-squared statistic of 5.9261 with an associated p-value of 0.9198 > 0.05 level of significance suggesting the acceptance of null hypothesis, which indicates that all autocorrelation functions are zero. Conclusively, there is no evidence for non-zero autocorrelations in the residuals of the fitted model and also ARIMA(2,1,5) model is confirmed to be adequate for predicting the prevalence of HIV in the study area.

Table 6: Ljung Box Test

Test	**Chi-squared**	**degrees of freedom**	**P-value**
Ljung Box test	5.9261	12	0.9198
Source: R-Studio Output			

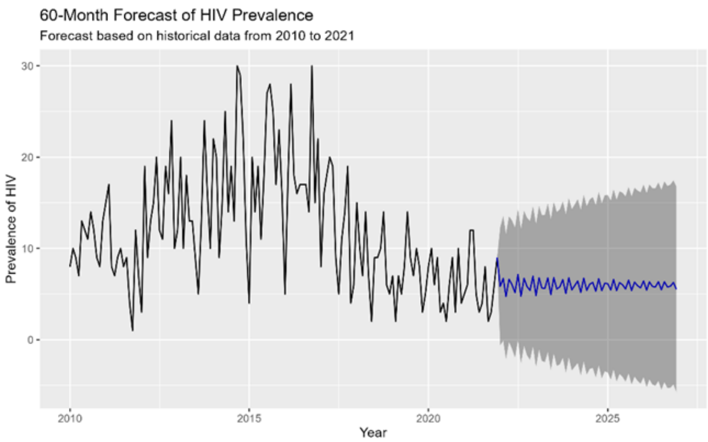

Figure 5: Five (5) years Forecast from the fitted ARIMA(2,1,5) for the Prevalence of HIV

Figure 5 shows the five-year forecast of HIV. The black line represents the actual historical HIV prevalence from 2010 to 2021. It shows significant fluctuations in HIV prevalence during this period, with peaks reaching nearly 30% at certain points. The forecasted trend (in blue) extends from 2022 to 2026. The blue line is relatively flat, indicating a stabilized HIV prevalence rate in this forecast period, as there is no drastic increase or decrease predicted in the upcoming years, suggesting that HIV prevalence is expected to remain relatively steady over this time. The shaded region indicates the 80% (lower side) and 95% (upper side) projection of prediction intervals, indicating the uncertainty range. The widening confidence interval highlights the uncertainty associated with long-term predictions. While the forecast suggests stabilization, there is a chance that HIV prevalence could fluctuate in the future, with possible outcomes ranging from a significant reduction to a moderate rise in prevalence.

CONCLUSION

This research aims to obtain the ARIMA model suitable for predicting the prevalence of Human Immunodeficiency Virus in Birnin Gwari Local Government Area of Kaduna State. The epidemiological plot shows a slight decrease in the trends of the prevalence of HIV over time. Furthermore, the most suitable model for predicting the prevalence of HIV is ARIMA (2,1,5). The predicted values of the fitted model show a gradual decrease in the prevalence of HIV for the predicted years. The relatively stable forecast suggests that if current public health strategies continue, there may be no drastic increases in HIV prevalence. However, the expanding uncertainty range indicates that future changes in prevention strategies, healthcare policies, or socioeconomic factors could significantly impact these trends. While the forecast shows a flat trend, the upper bound of the confidence interval suggests a potential risk of HIV prevalence rising in the worst-case scenario. This underscores the importance of maintaining or strengthening HIV prevention efforts to avoid any upward shift. Therefore, the fitted model is recommended for use by policymakers in Kaduna State Ministry of Health and other concerned agencies that are involved in activities to reduce HIV infection in Nigeria. In the research and academics, further research can be done on the fitted model and data by using more advanced statistical and machine learning algorithms such as Long-Short Time Memory, Artificial Neural Networks, or Recurrent Neural Networks to track the long term prevalence of the series.

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