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Modelling The Prevalence of Some Infectious Diseases Among Farmers in Benue using Poisson Autoregressive Model

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RESEARCH ARTICLE

Abstract

The aim of this work is to model the infection rates of some infectious diseases among farmers in Benue state using Poisson autoregressive model (PAR (1)). The study utilizes monthly secondary data on serologically confirmed infection cases of Human Immunodeficiency Virus (HIV), tuberculosis (TB) and viral hepatitis (VHP). The data span from January, 2010 to December, 2022. The study employs summary statistics and Anderson-Darling normality test, time plots, bar graphs and Poisson autoregressive model as the principal methods of investigation. Results show that HIV, TB and VHP have positive and increasing trends over time with non-Gaussian tendencies. All the three infections peaked between 2017 and 2019 and had their lowest occurrence in 2010, indicating a potential common relationship in occurrence and trend among them. The results of PAR (1) model indicate positive time trends in the HIV, TB and VHP infection rates, suggesting that infections are increasing over time. The results further revealed significant monthly increase of 2.25% in HIV, 1.22% in TB and 12.08% in VHP respectively over the study period. The coefficient of determinations of the models explained 83.3%, 78.8% and 80.8% of the variability in the HIV, TB and VHP data indicating better fit for all the fitted models. However, the Anderson test revealed that the data did not follow a normal distribution. The positive time trend suggests that monitoring the infection rates over time is crucial. The findings highlight the importance to address the non-normality of the data, which is a limitation of the research and the need for further research to identify factors contributing to the transmission of these infections. Public health strategies need to account for this increasing trend and aim to reverse it.

Keywords: Farmers, HIV, Hepatitis B, Hepatitis C, Modelling, Model, Data, Prevalence, Poisson autoregressive model, and Tuberculosis.

1. Introduction

Human Immune-Deficiency Virus (HIV) represents a significant global health challenge, affecting around 70 million individuals worldwide and resulting in substantial morbidity and mortality (Omondi

et al., 2018). The majority of HIV cases are concentrated in the Sub-Saharan African region, where over two-thirds of affected individuals reside (Amuche *et al*., 2017). According to the Center for Disease Control and Prevention, individuals with HIV who do not receive antiretroviral therapy (ART) progress through three disease stages: acute HIV infection, clinical latency (HIV dormancy), and acquired immunodeficiency syndrome (AIDS). (Yeom *et al.,* 2024)

The widespread adoption of antiretroviral therapy has significantly reduced mortality rates among individuals living with HIV/AIDS globally, transforming the disease from fatal to a manageable long-term condition. (Lindegger 2024). However, the emergence of co-infections such as tuberculosis (TB), hepatitis B virus (HBV), and hepatitis C virus (HCV) presents a serious health challenge for people living with HIV/AIDS. TB is the primary cause of mortality among this population, even among those receiving antiretroviral treatment (Furin *et al*., 2015). The HIV virus infects CD4 cells, CD4 cells are responsible for fighting disease causing organisms, during this infection, these CD4 cells are destroyed (Rafaqat *et al.,* 2024). As HIV progresses, the immune system becomes more weakened, making it difficult for the body to fight opportunistic infections such as Tuberculosis and viral hepatitis. (Bekker *et al.*, 2023), Therefore making Co-infections of viral hepatitis and TB to worsen prognosis compared to HIV mono-infections alone (WHO, 2016).

Globally, opportunistic infections are the leading causes of morbidity and mortality among HIV infected children, contributing to more than 90% of HIV-related deaths (Mekonnen *et al.,* 2023). Occurrence of HIV in Benue state has been costly in terms of time spent on care, funerals and mourning (Iliya 2024). This has affected income and productivity of the farmers affected with HIV and opportunistic infections that come with it.

2. Materials and Methods

2.1 Data Source

The data used in this work comprised monthly time series secondary count data on the serologically confirmed cases of HIV, Tuberculosis (TB) and Viral Hepatitis (VHP) infections in Benue state. The data spanned from January 2010 to December, 2022 and was obtained from Benue State Epidemiological Unit. The following statistical tools have been employed for analysis of data in this work.

1. Descriptive statistics and normality measures

The mean of any given set of data is computed as:

$$\bar{Y} = \frac{1}{n}\sum_{i=1}^{n} Y_i \tag{1}$$

(Tsay, 2014).

The sample standard deviation is computed as:

$$\hat{\sigma} = \sqrt{\frac{1}{n-1}\sum_{i=1}^{n}\left(Y_i - \bar{Y}\right)^2} \tag{2}$$

where $\bar{Y}$ is the mean, n is the sample size.

The Anderson-Darling (AD) test is used to test if a sample of data comes from a population with a specific distribution. Its most common use is for testing whether a sample data comes from a normal distribution (Ma *et al.*,2024). The AD test statistic is defined by:

$$A^2 = AD = -n - \frac{1}{n}\sum_{i=1}^{n}(2i-1)\left[\ln F\left(Y_i\right) + \ln\left(1 - F\left(Y_{n-i+1}\right)\right)\right] \quad (3)$$

where F is the cumulative distribution function of the specified distribution, Y_i are the ordered data. The Anderson-Darling normality test tests the following pair of hypotheses:

H_0: The data followed a normal distribution

H_a: The data did not follow a normal distribution

The AD test rejects the null hypothesis if the p-value of the test statistic is less than $\alpha = 0.05$, indicating that the data is statistically different from a normal distribution. On the other hand, if the p-value of the AD test statistic is greater than 0.05, it can be concluded that the data is statistically not different from a normal distribution.

Skewness is a statistical measure that describes the asymmetry of a probability distribution. It indicates whether the data points in a distribution are concentrated more on one side than the other. Positive skewness indicates a longer right tail, while negative skewness indicates a longer left tail. (Papadopoulos and Parmeter, 2024). The sample skewness is computed as:

$$\text{Sample Skewness} = \frac{1}{n}\sum_{i=1}^{n}\left(\frac{Y_i - \bar{Y}}{s^3}\right)^3 \quad (4)$$

(Tsay, 2014).

Kurtosis is a statistical measure that describes the distribution of data in terms of the tails and the central peak. It assesses whether the data are heavy-tailed or light-tailed compared to a normal distribution. Positive kurtosis indicates heavier tails while negative kurtosis indicates lighter tails than a normal distribution. The sample kurtosis is computed as:

$$\text{Sample Skewness} = \frac{1}{n}\sum_{i=1}^{n}\left(\frac{Y_i - \bar{Y}}{s^4}\right)^4$$

(Tsay, 2014).

2.2 Time Plots of the Original Series

We first examine the data in level and plot the series against time to assess the pattern of trend movement and to see whether any structural breaks, outliers or data errors occur. This step may also reveal whether there is a significant seasonal pattern in the series.

2.3 Poisson Autoregressive Model

A Poisson autoregressive (PAR) model is a type of statistical model used for analyzing and forecasting count data that exhibit serial correlation. These models are particularly useful when the data are non-negative integers, such as the number of events occurring in a fixed period of time (e.g., number of daily hospital admissions, counts of traffic accidents, etc.). The key characteristic of a Poisson autoregressive model is that the current value of the count variable is influenced by its past values, similar to how autoregressive models work in time series analysis (Greene, 2012).

A Poisson autoregressive model of order one PAR (1) with a time component can be specified as follows:

$$Y_t \left| F_{t-1} \sim Poisson\left(\lambda_t\right) \right. \text{ where } \lambda_t = \alpha + \beta_1 Y_{t-1} + \gamma t + \varepsilon_t \quad (6)$$

A Poisson autoregressive model of order one PAR (2) can be specified as:

$$\lambda_t = \alpha + \beta_1 Y_{t-1} + \beta_2 Y_{t-2} + \gamma t + \varepsilon_t \quad (7)$$

where

Y_t is the count variable at time t.

F_{t-1} represents the information set available at time $t-1$.

λ_t is the expected infection rate at time t.

β_1, β_2 are the coefficients for the previous period's infection rates corresponding to time $t-1$ and $t-2$ respectively.

γ is the coefficient for the time component.

ε_t is the error term, assumed to be white noise.

2.4 Estimation Procedure

The PAR (1) model with a time component can be estimated using various methods, including Ordinary Least Squares (OLS) and Maximum Likelihood Estimation (MLE). It is however, more beneficial to use MLE, especially when dealing with models that might involve more complex error structures or when the assumptions of OLS do not hold (Greene, 2012).

2.4.1 Maximum Likelihood Estimation (MLE)

Maximum Likelihood Estimation is a method that estimates the parameters of a model by maximizing the likelihood function, which measures how likely it is to observe the given data under different parameter values (Tsay, 2014). The PAR (1) model with a time component can be specified as:

$$\lambda_t = \alpha + \beta Y_{t-1} + \gamma t + \varepsilon_t \quad (8)$$

where $\varepsilon_t \sim N\left(0, \sigma^2\right)$ are i.i.d. normally distributed error terms with mean zero and variance σ^2. The likelihood function $L(\theta)$ represents the probability of observing the given data $Y = (Y_1, Y_2, \ldots, Y_n)$ given the parameters $\theta = (\alpha, \beta, \gamma, \sigma^2)$. For the normal distribution, the probability density function for an observation Y_t is:

$$f\left(Y_t | \alpha, \beta, \gamma, \sigma^2\right) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{\left(Y_t - \left(\alpha + \beta Y_{t-1} + \gamma t\right)\right)^2}{2\sigma^2} \right)$$

The likelihood function $L(\theta)$ for the entire dataset is the product of the individual densities:

$$L(\theta) = \prod_{t=2}^{n} f(Y_t | \alpha, \beta, \gamma, \sigma^2)$$

To simplify the optimization, we take the natural logarithm of the likelihood function, resulting in the log-likelihood function:

$$\log L(\theta) = \sum_{t=2}^{n} \log f(Y_t | \alpha, \beta, \gamma, \sigma^2)$$

Substituting the probability density function, we get:

$$\log L(\theta) = \sum_{t=2}^{n} \left(-\frac{1}{2}\log(2\pi\sigma^2) - \frac{(\mathrm{Y}_t - (\alpha + \beta \mathrm{Y}_{t-1} + \gamma t))^2}{2\sigma^2} \right)$$

Simplifying, we obtain:

$$\log L(\theta) = -\frac{n-1}{2}\log(2\pi\sigma^2) - \frac{1}{2\sigma^2}\sum_{t=2}^{n}(\mathrm{Y}_t - \alpha - \beta \mathrm{Y}_{t-1} - \gamma t)^2$$

To find the MLE estimates, we need to maximize the log-likelihood function with respect to the parameters α, β, γ and σ^2. This is equivalent to minimizing the negative log-likelihood (Enders, 2014).

$$-\log L(\theta) = -\frac{n-1}{2}\log(2\pi\sigma^2) + \frac{1}{2\sigma^2}\sum_{t=2}^{n}(\mathrm{Y}_t - \alpha - \beta \mathrm{Y}_{t-1} - \gamma t)^2$$

Compute the partial derivatives of the negative log-likelihood function with respect to α, β, γ and σ^2 and set them to zero to find the critical points. This involves solving:

$$\frac{\partial(-\log L)}{\partial \alpha} = 0, \frac{\partial(-\log L)}{\partial \beta} = 0, \frac{\partial(-\log L)}{\partial \gamma} = 0, \frac{\partial(-\log L)}{\partial \sigma^2} = 0.$$

Given the complexity of these equations, we typically use numerical optimization methods such as the Broyden-Fletcher-Goldfarb-Shanno (BFGS) algorithm, which is implemented in various statistical software packages.

2.5 Model Diagnostic Checks

After estimating the parameters, it is crucial to check the adequacy of the model. This involves several diagnostic checks:

2.5.1 Goodness-of-Fits

Assess the goodness-of-fit using measures such as deviance tests, this evaluates if the models capture variance.

2.5.2 Residual Analysis

Analyze the residuals to check for any patterns that might indicate model misspecification. Residuals should ideally be uncorrelated and follow a Poisson distribution with mean zero.

2.5.3 Autocorrelation

Check the autocorrelation function (ACF) and partial autocorrelation function (PACF) of residuals to ensure no significant autocorrelations remain.

Lower deviance indicates a better fit, as it means the model's predictions are closer to the observed values. Deviance is also used in hypothesis tests (like the deviance chi-square test) to compare models. (de León-Delgado *et al.*, 2024).

3. Results and Discussion

3.1 Descriptive Statistics and Normality Measures

The descriptive statistics and normality measures are computed and reported in Table 1. The descriptive statistics presented in Table 1 reveal that the monthly averages of HIV, TB, and VHP are all positive, indicating an increase in infection cases for these diseases during the reviewed period. The high standard deviations suggest significant dispersion from the monthly average infection cases for the diseases over the investigation period. The considerable gaps between the maximum and minimum values further support the high variability of the diseases in the study area during the specified period.

Positive skewness coefficients for all infections indicate that their distributions among the population in Benue State are substantially positively skewed. Kurtosis, which measures the thickness of the distribution tail and is approximately 3 for a normal distribution, is below 3 for all study variables in this research. The skewness and kurtosis coefficients indicate that the infection cases do not follow normal distributions. Additionally, the Anderson-Darling test rejects the null hypothesis of normality at a 5% significance level, as the *p*-values for the test statistics of all variables are less than 0.05 $(p < 0.05)$.

Table 1: Summary Statistics and Anderson-Darling Normality Test

Variable	HIV	TB	VHP
Mean	1022.9	371.6	1109.9
Standard deviation	382.6	183.0	382.6
Maximum	2149	894.0	2236
Minimum	176	111	263
Skewness	0.1003	0.8494	0.1003
Kurtosis	0.6378	0.4396	0.6378
AD	2.38	2.14	2.38
p-value	<0.05	<0.05	<0.05
Number of observations	156	156	156

3.2 Graphical Examination of the Series

The first step in analyzing time series data is to plot the original series in level against time and observe its graphical properties. This help in understanding the trend as well as pattern of movement of the original series. Here the original series (monthly infection cases of HIV, TB and VHP infections) has been plotted as a function of time. The time plots of the HIV, TB and VHP original series are presented in Figures 1, 2 and 3.

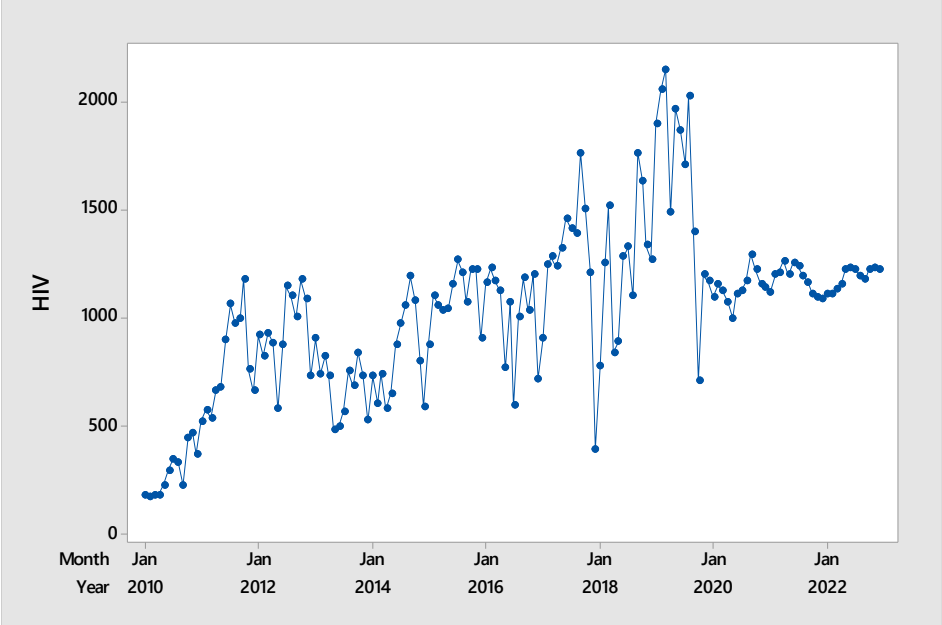

Figure 1: Time Plot of HIV Infection in Benue State from 2010-2022

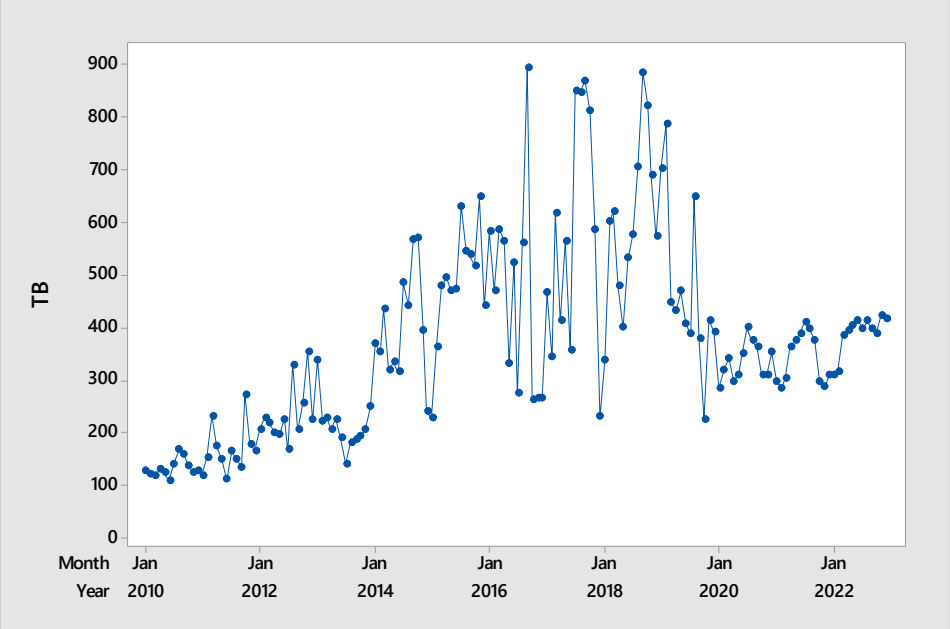

Figure 2: Time Plot of TB Infection in Benue State from 2010-2022

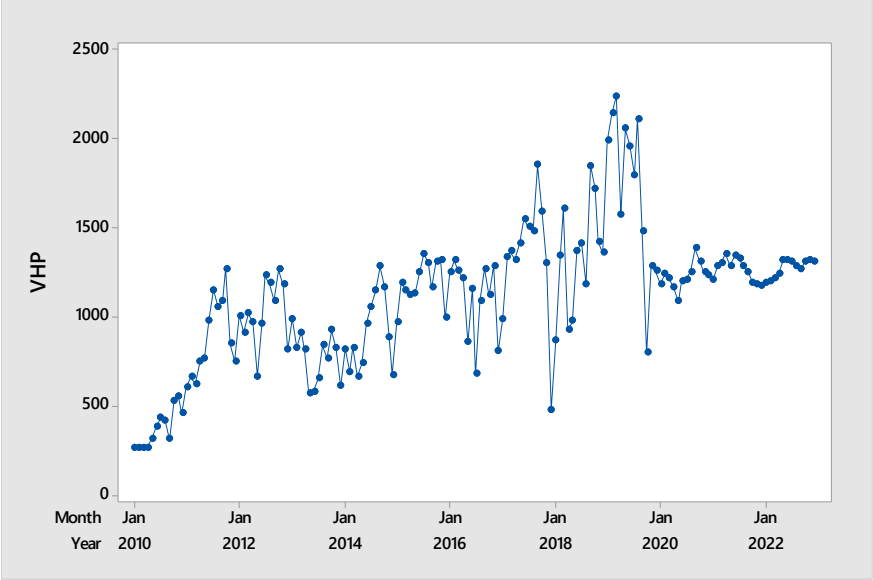

Figure 3: Time Plot of VHP Infection in Benue State from 2010-2022

The time plots in Figures 1, 2 and 3 illustrate the monthly values for HIV, TB, and VHP infections from January 2010 to January 2022. Each disease shows an initial steady increase until around 2012, with HIV and VHP rising to approximately 1,000 infection cases, and TB to around 300 cases. From 2012 to 2017, all the three diseases exhibit considerable fluctuations but continue an overall upward trend: HIV and VHP values reached about 1,500 cases, and TB reached around 600 cases. In 2017-2018, HIV and VHP peaked significantly above 2,000 cases, while TB peaked at about 900 cases. Post-2018, all the three diseases showed a sharp decline followed by continued variability. From 2019 onwards, values for all the diseases stabilized with less extreme fluctuations, indicating a slight downward trend: HIV and VHP averaged between 1,000 and 1,500 cases, while TB fluctuated around 300 to 400 cases.

3.3 Bar Graphs of the Annual Infection Cases

We also consider the bar graphs of each of the infection cases to observe how the infections are distributed across the years annually. The bar graphs for HIV, TB and VHP annual infections are presented in Figures 4, 5 and 6 respectively.

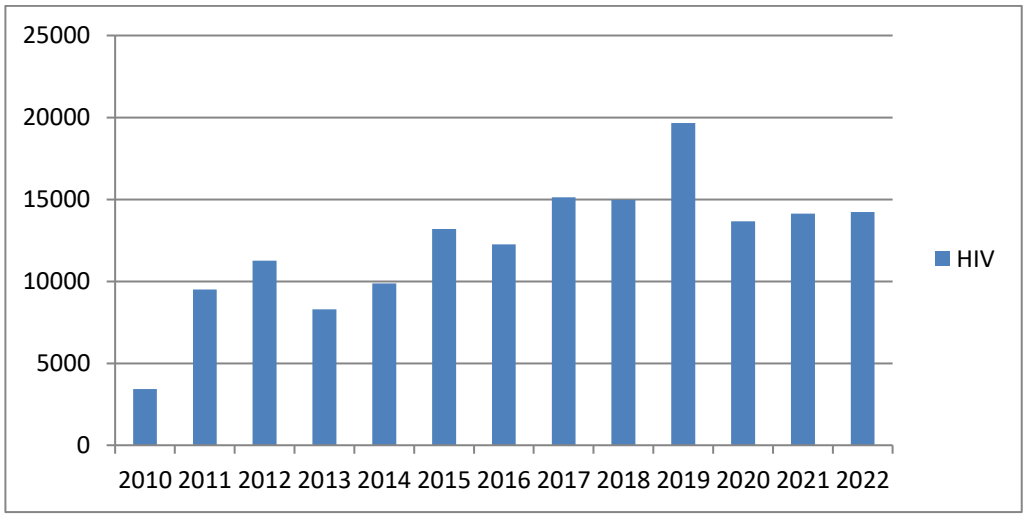

Figure 4: Bar Chart of Annual Cases of HIV in Benue State from 2010-2022

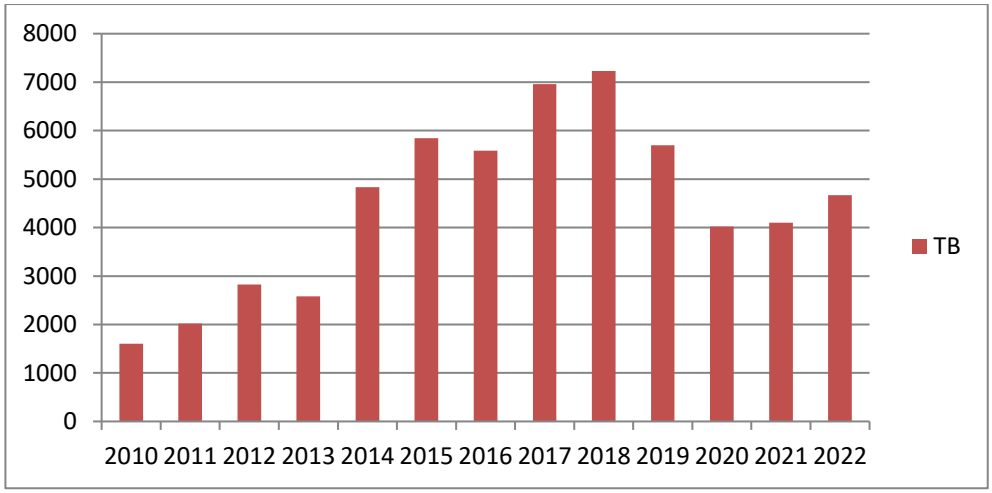

Figure 5: Bar Chart of Annual Cases of Tuberculosis in Benue State from 2010-2022

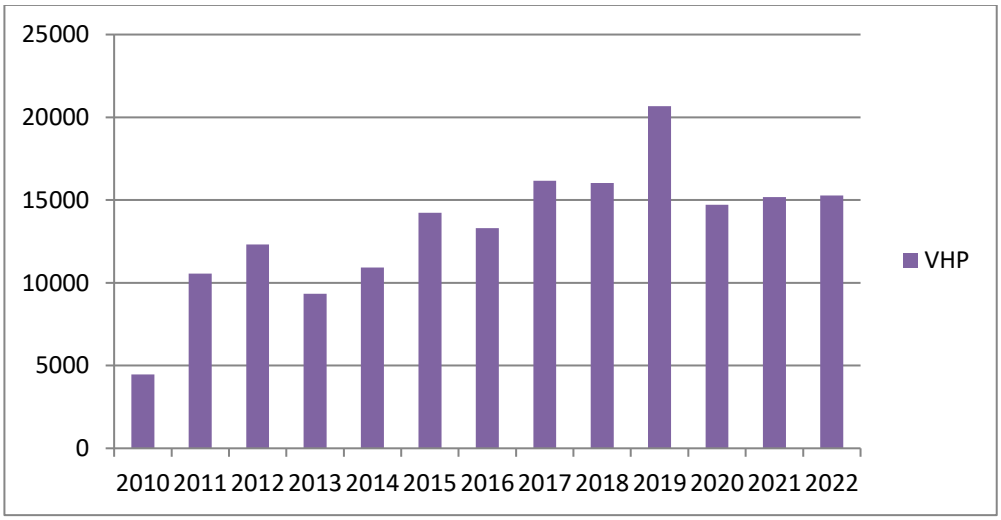

Figure 6: Bar Chart of Annual Cases of Viral Hepatitis in Benue State from 2010-2022

The results of Figures 4, 5 and 6 show the annual distribution of HIV, TB and Viral Hepatitis infection cases in Benue State from 2010 to 2022. The highest cases of HIV and Viral Hepatitis infections are recorded in 2019 while the lowest cases of HIV and Viral Hepatitis infection are recorded in 2019. This high number of cases in the two diseases: HIV and viral hepatitis could be due to their common mode of transmission; unprotected sexual relations and unscreened blood transfusion. PLHIV are at increased risk of acquiring Viral Hepatitis, particularly Hepatitis B and C due to weakened immune system which predisposes them to hepatitis B and C, also HIV infection can accelerate the progression of Viral Hepatitis to liver disease even to liver cancer. (Nelson *et al.*, 2022). The highest cases of TB infection are recorded in 2018 and 2017 while the lowest cases of TB infection are recorded in 2010. All the three infections have their peak period between 2017 and 2019 and their lowest occurrence in 2010. This suggests a common relationship in the occurrence of the three infections and also explains the synergistic effect of HIV on the other two diseases.

3.4 Parameter Estimation of PAR (1) Models

Parameter estimates of PAR (1) models for HIV, TB and VHP infection rates are computed and presented in Tables 2, 3 and 4 respectively:

Table 2: Parameter Estimate of PAR (1) Model for HIV Infection Rate

Variable	Coefficient	Std. error	t −statistic	$P > \|t\|$
Constant	0.2507	0.097	2.585	0.012
α	0.7362	0.046	16.004	0.000
γ	0.0225	0.005	4.500	0.000
σ^2	0.1046	0.024	4.358	0.000
R-Squared	0.833			
Adj. R-Squared	0.827			
F-Statistic	211.5		Durbin-Watson	1.834
Prob (F-statistic)	6.40e-32		Jarque-Bera (JB)	16.355
Log-Likelihood	-110.54		Prob (JB)	0.000284
Omnibus	12.582		Skew	-0.645
Prob (Omnibus)	0.003		Kurtosis	4.342

Table 3: Parameter Estimate of PAR (1) Model for TB Infection Rate

Variable	Coefficient	Std. error	t −statistic	$P > \|t\|$
Constant	0.1783	0.107	1.666	0.077
α	0.7036	0.048	14.658	0.000
γ	0.0122	0.004	3.050	0.002
σ^2	0.1247	0.024	5.196	0.000
R-Squared	0.794			
Adj. R-Squared	0.788			
F-Statistic	181.4		Durbin-Watson	1.882
Prob (F-statistic)	1.26e-28		Jarque-Bera (JB)	10.779
Log-Likelihood	-116.33		Prob (JB)	0.00446
Omnibus	8.745		Skew	-0.568
Prob (Omnibus)	0.012		Kurtosis	4.172

Table 4: Parameter Estimate of PAR (1) Model for VHP Infection Rate

Variable	Coefficient	Std. error	t −statistic	$P > \|t\|$
Constant	0.2197	0.103	2.133	0.032
α	0.6718	0.049	13.710	0.000
γ	0.1208	0.005	24.160	0.000
σ^2	0.0984	0.023	4.278	0.000
R-Squared	0.820			
Adj. R-Squared	0.808			
F-Statistic	197.4		Durbin-Watson	1.912
Prob (F-statistic)	3.77e-30		Jarque-Bera (JB)	11.864
Log-Likelihood	-113.58		Prob (JB)	0.00257
Omnibus	9.346		Skew	-0.589
Prob (Omnibus)	0.011		Kurtosis	4.257

From the results of the parameter estimates of PAR (1) models for HIV, TB and VHP infection rates reported in Tables 2, 3 and 4, the intercepts of the models are the base levels of the HIV, TB and VHP infection rates when both the lagged infection rates (Y_{t-1}) and time components (t) are zero. It represents the constant parts of the infection rates that are not influenced by past infection rates or time trends. The baseline infection rates are 0.2507, 0.1783 and 0.2197 for HIV, TB and VHP, respectively

when the lagged infection rates and times are zero. These values are positive and statistically significant and represent the starting levels of the infections without considering past infections or the passage of time.

The lagged HIV, TB and VHP infection rates coefficients are 0.7362, 0.7036 and 0.6718 respectively. These parameters are positive and statistically significant at 1% marginal significance levels and indicate the influence of the previous period's HIV, TB and VHP infection rates (Y_{t-1}) on the current period's infection rates (λ_t). The coefficients of 0.7362, 0.7036 and 0.6718 for the respective infection rates suggest strong positive relationships, meaning that if the infection rates in the previous periods increase by one unit each, the current infection rates will increase by approximately 0.7362, 0.7036 and 0.6718 units respectively for HIV, TB and VHP while holding other factors constant. This shows persistence in the infection rates, where high rates tend to continue. Strong persistence effects in HIV, TB and VHP infections is indicated, where an increase in the previous period's infection rates lead to substantial increases in the current period's rates. This highlights the importance of addressing past infection levels to control current and future infection rates.

Time component coefficients for HIV, TB and VHP are 0.0225, 0.0122 and 0.1208 respectively and statistically significant at the 1% significance levels. These coefficients represent the influence of time on the HIV, TB and VHP infection rates. The values indicate positive trends over time, meaning that for each additional time period (i.e., each month), and the infection rates increase by 0.0225, 0.0122 and 0.1208 units for HIV, TB and VHP respectively while holding other factors constant. These captured the general trends in the infection rates due to factors not explicitly modeled, such as changes in population behaviour, healthcare policies, or epidemic progression.

These findings indicate positive time trends in the HIV, TB and VHP infection rates, suggesting that infections are increasing over time. This could be due to various factors such as changes in disease transmission dynamics, effectiveness of interventions, or changes in population behaviour.

The Error variances for HIV, TB and VHP infection rates are $\sigma^2 = 0.1046$, $\sigma^2 = 0.1247$ and $\sigma^2 = 0.0984$ respectively with marginal statistically significance at 1% levels. These represent the variances of the error terms ε_t, which captured the variability in the infection rates that are not explained by the models. The respective values of 0.1046, 0.1247 and 0.0984 indicate the extent of this unexplained variability. The relatively low values suggest that the models explained significant portions of the variability in the infection rates, although some random fluctuations still remained.

The models captured most of the variability in the HIV, TB and VHP infection rates, but there are still some random variables not explained by the models. These could be due to random fluctuations, measurement errors, or other unobserved factors.

The Poisson Autoregressive model is not perfect for modelling these diseases although it has served its purpose, the unexplained variability indicates that there are factors that could not be fully captured by the model. This unexplained variability points out the limitation of this research and to better understand this, further research needs to be carried out to identify and possibly reduce this variability.

The Anderson test rejects the null hypothesis of normality thus; the data is not a normal distribution.

3.5 Practical Implications of the Models

The strong persistence effects imply that efforts to reduce HIV, TB and VHP infection rates need to be sustained over time. Short-term reductions may not be sufficient due to the high influence of past infection rates on current rates. The positive time trend suggests that monitoring the infection rates over time is crucial. Public health strategies need to account for this increasing trend and aim to reverse it.

3.6 Goodness-of-Fit Test

The coefficient of determinations for HIV, TB and VHP infection rates models are 0.833, 0.788 and 0.808 respectively indicating that the models explained 83.3%, 78.8% and 80.8% of the variances in the HIV, TB and VHP data. The high percentages of explained variations indicate that the models fit the data well.

3.7 Model Diagnosis

The Omnibus test checks for skewness and kurtosis of residuals. A significant p-value suggests non-normality of residuals. All the p-values of the Omnibus test for the fitted models are statistically significant at 5% levels of significance indicating that the residuals of the fitted models are non-Gaussian. The Durbin-Watson statistic is a test for autocorrelation in residuals. A value close to 2 indicates no autocorrelation in the residuals. Durbin-Watson statistic values for the HIV, TB and VHP infection rates models are 1.834, 1.882 and 1.912 respectively, which are very close to 2 indicating the absence of serial correlations/autocorrelations in the residuals of the estimated models. These also show that the estimated models are non-spurious. The Jarque-Bera statistic is a test for normality of residuals. A significant p-value suggests non-normality. From all the estimated models, the Jarque-Bera statistic p-values are highly statistically significant at the 5% levels, indicating the non-Gaussianity of residuals.

4. Conclusions and Recommendations

4.1 Conclusion

There were increasing trends of the infection rates of the diseases overtime, this implied that if appropriate preventive measures are not put in place, there is a tendency that the diseases will escalate. The upward trend could be due to failure of previous control measures and policies to combat the diseases; the upward trend could also be due to an epidemic or change in individual behavior aggregation to poor health in the population.

Increase in the time components led to corresponding increases in infection rates of the diseases, as shown by the coefficients, 2.25%, 1.22% and 12.08% for HIV, tuberculosis and viral hepatitis. These captured the general trends in the infection rates due to factors not explicitly modeled, such as changes in population behaviour, healthcare policies, or epidemic progression.

The diseases have significant baseline rates which could be as a result of ineffective previous control strategies, unfavourable population behaviour, and lack of good surveillance.

4.2 Recommendations

(i) Strategies to reduce HIV, TB and VHP infection rates need to be sustained over a longer time period, this is because short-term measures are not sufficient due to the high influence of past infection rates on current rates.

(ii) Surveillance of the diseases over time should be carried out using Public Health strategies with an aim of reversing the current and future high trends of the diseases.

(iii) Strategies such as: diseases awareness campaigns, free testing and treatments must be carried out by governments and Non-Governmental Organizations among the affected population, to help shape the behaviour of the population concerning these diseases.

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