

An Exploratory Analysis of Human Immunodeficiency Virus (HIV) Prevalence in Nigeria

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ABSTRACT

This paper involved conducting a statistical analysis on the number of individuals living with HIV/AIDS. The University of Ilorin Teaching Hospital (UITH) was chosen as the case study for the years 2014 to 2019, with factors such as year, sex, and age group taken into account. During this six-year period, a total of 2604 cases were recorded at UITH. Among both sexes, females had the highest number of people living with HIV/AIDS. Additionally, the age group of 31-45 had the highest number of individuals affected by the disease. In terms of the specific year, 2016 had the highest number of people living with the disease, totalling 460 cases. A chi-square test of independence was conducted to examine the relationship between the factors, using a significance level of 0.05. The results indicated that all the considered factors were not independent of each other, meaning they were related.

Key Words: Chi-square test, HIV, Prevalence, Test of independency.

1. INTRODUCTION

Human Immunodeficiency Virus (HIV) is a global health concern that has had a significant impact on individuals, communities, and countries worldwide. Since the first reported cases in the early 1980s, HIV has spread rapidly and continues to be a major public health challenge. HIV is a viral infection that attacks the immune system, specifically targeting CD4 cells, which are crucial for the body's defence against infections and diseases. Without treatment, HIV can progress to Acquired Immunodeficiency Syndrome (AIDS), a condition characterized by severe immune system impairment. According to the Joint United Nations Programme on HIV/AIDS (UNAIDS), approximately 38 million people worldwide were living with HIV at the end of 2020 [1].

The distribution of HIV varies significantly across regions, with some areas experiencing higher prevalence rates than others. Sub-Saharan Africa has been disproportionately affected by the HIV epidemic, accounting for approximately two-thirds of the global HIV infections. In this region, southern and eastern African countries have been particularly hard hit, with prevalence rates among the highest in the world [1].

To understand the magnitude of the HIV epidemic, it is essential to consider key statistics related to its prevalence. As of the end of 2020, an estimated 1.5 million people became newly infected with HIV globally (UNAIDS, 2021). Despite significant progress in preventing new infections and expanding access to treatment, certain populations continue to face higher risks. Among them are key populations such as men who have sex with men, people who inject drugs, sex workers, transgender people, and prisoners [1]. Moreover, women and girls bear a disproportionate burden of HIV, particularly in sub-Saharan Africa. In this region, young women aged 15-24 are significantly more likely to acquire HIV compared to their male counterparts [1]. Additionally, HIV prevalence among children remains a concern, with an estimated 160,000 new infections occurring among children under the age of 15 globally in 2020 [1].

The purpose of this study is to conduct a comprehensive statistical analysis of HIV prevalence, aiming to provide valuable insights into the current trends, distribution patterns, and associated risk factors of HIV infection. By leveraging advanced statistical

techniques and utilizing available data, this research aims to contribute to the understanding of the global HIV epidemic and inform evidence-based interventions and prevention strategies.

2. LITERATURE REVIEW

This review aims to provide a detailed overview of studies that have utilized statistical analysis to examine HIV prevalence. It encompasses various methodologies, data sources, and geographical locations, highlighting the advancements in understanding the epidemiology of HIV/AIDS. HIV/AIDS remains a global health challenge, necessitating robust statistical analysis to assess its prevalence accurately. Over the years, numerous studies have been conducted worldwide to examine HIV prevalence rates, risk factors, and trends. This review summarizes key research articles that have employed statistical methods to investigate HIV prevalence.

Regression analysis has been widely employed in HIV prevalence studies to identify risk factors and examine their association with HIV infection rates. Studies have utilized logistic regression to assess the influence of variables such as age, gender, sexual behavior, and drug use on HIV prevalence (e.g., [2,3]). Bogart et al. [2] conducted a cross-sectional study aiming to identify social determinants associated with HIV prevalence among men who have sex with men (MSM). Logistic regression was utilized to assess the impact of age, race, income, education, and sexual behaviors on HIV infection rates. The study found that older age, lower income, and higher numbers of sexual partners were significantly associated with increased HIV prevalence among MSM. This study exemplifies the application of regression analysis in identifying multiple risk factors and their respective contributions to HIV prevalence. Khezri et al. [3] conducted a retrospective cohort study to investigate the risk factors for HIV infection among people who inject drugs (PWID). Logistic regression was employed to analyze variables such as age, gender, drug injection frequency, and engagement in harm reduction services. The study revealed that younger age, female gender, higher frequency of drug injection, and lack of access to harm reduction services were significantly associated with higher HIV prevalence among PWID. The findings of this study underline the utility of regression analysis in uncovering risk factors specific to different populations affected by HIV.

Spatial analysis techniques, including spatial autocorrelation and cluster analysis, have contributed to understanding the geographical distribution of HIV prevalence. These methods allow researchers to identify high-risk areas, hotspots, and spatial patterns of HIV infection (e.g., [4,5]). Spatial autocorrelation is a powerful tool that allows researchers to explore the degree of similarity or dissimilarity in HIV prevalence across different geographic areas. It assesses whether areas with similar characteristics are clustered together or randomly dispersed. By quantifying the strength and significance of spatial dependence, researchers can identify patterns and detect areas with high or low HIV prevalence. Ying et al. [4] demonstrated the utility of spatial autocorrelation in their study, where they analysed the spatial patterns of HIV cases in a specific region. They found evidence of clustering, indicating localized areas with higher HIV prevalence. This information can be valuable for targeting interventions and resource allocation. Cluster analysis is another important technique in spatial analysis, enabling researchers to identify statistically significant clusters or hotspots of HIV infection. By evaluating the spatial concentration of cases, researchers can identify areas where the disease burden is higher than expected by chance. Ratmann et al. [5] conducted a study that utilized cluster analysis to examine the spatial patterns of HIV prevalence in a large-scale population-based survey. Their findings revealed several significant clusters of high HIV prevalence, highlighting areas where targeted interventions can have a substantial impact on reducing transmission rates. The simultaneous use of spatial autocorrelation and cluster analysis provides a more comprehensive understanding of the geographical distribution of HIV prevalence. Spatial autocorrelation identifies areas with similar characteristics, while cluster analysis identifies areas with a higher disease burden. Integrating these techniques allows researchers to identify both high-risk areas and the extent to which similar areas are clustered together. This information can assist policymakers and public health officials in designing geographically targeted interventions and resource allocation strategies.

Time series analysis has enabled the examination of temporal trends in HIV prevalence, incidence, and mortality rates. These studies employ techniques such as autoregressive integrated moving average (ARIMA) models and joinpoint regression to identify changes over time and forecast future trends (e.g., [6,7]). Kharsany et al. [6] utilized ARIMA modeling to analyze the temporal trends in HIV prevalence among a high-risk population. The study revealed a declining prevalence trend over time, suggesting the effectiveness of HIV prevention strategies implemented in the region. The ARIMA model also enabled the researchers to generate accurate short-term forecasts, aiding in resource allocation and program planning. Lindley et al. [7] employed join point regression analysis to examine the trends in HIV incidence and mortality rates in a national HIV surveillance dataset. The study identified significant joinpoints, indicating changes in the epidemic trajectory. The findings revealed an initial increase in HIV incidence followed by a subsequent decline, possibly attributed to the implementation of prevention and treatment interventions. Joinpoint regression allowed for the identification of these inflection points, providing valuable insights into the effectiveness of public health measures.

Network analysis has proven valuable in understanding HIV transmission dynamics. By analyzing social networks and sexual partnerships, researchers can determine the structure of HIV transmission networks and identify key individuals who play a significant role in spreading the virus (e.g., Wertheim et al., 2017; Goodreau et al., 2018). Network analysis involves examining the relationships and connections among individuals within a given population. By applying this methodology to the study of HIV transmission dynamics, researchers have gained insights into the patterns and pathways of viral spread. Two notable studies, Wertheim et al. (2017) and Goodreau et al. (2018), have made significant contributions to this field. In the study by Wertheim et al. (2017), the researchers used phylogenetic analysis and network modeling to reconstruct transmission networks in a population of HIV-positive individuals. By analysing the genetic sequences of the virus, they were able to identify clusters of closely related strains and infer potential transmission links between individuals. This approach provided a detailed understanding of the interconnectedness of the population and highlighted the role of specific individuals as key transmitters within the network. Goodreau et al. (2018) employed a combination of network analysis and mathematical modelling to investigate the impact of different intervention strategies on HIV transmission. They developed a dynamic network model that simulated the spread of HIV within a population, considering factors such as sexual behavior, partnership dynamics, and the effectiveness of prevention measures. By quantifying the effects of various interventions, such as testing, treatment, and behavioural changes, the study provided valuable insights into the potential effectiveness of different strategies in curbing the epidemic. Both studies demonstrated the power of network analysis in uncovering the hidden structure of HIV transmission networks. By examining the social and sexual connections between individuals, researchers were able to identify key nodes or individuals who played a pivotal role in disseminating the virus. These individuals, often referred to as "bridges" or "super-spreaders," had a disproportionately high number of sexual partnerships or acted as connectors between different subgroups within the network. Understanding the role of these key individuals is crucial for targeting prevention efforts and designing more effective interventions.

Many countries conduct national surveys to estimate HIV prevalence rates among their populations. These surveys often employ complex sampling techniques, including random cluster sampling, to obtain representative data (e.g., [8,9]). Rucinski et al. [8] conducted a national survey in a large country to estimate HIV prevalence rates among the population. The study employed random cluster sampling, a common sampling technique utilized in large-scale surveys. The research team divided the country into clusters, randomly selected a specific number of clusters, and collected data from within those clusters. By using this sampling technique, the researchers aimed to obtain representative data that could be generalized to the entire population. The study findings indicated an HIV prevalence rate of 3.8% among adults aged 15-49 years. The authors discussed the limitations associated with random cluster sampling, including potential clustering effects and difficulties in ensuring equal probability of selection within clusters. Despite these challenges, the study demonstrated the feasibility and utility of national surveys utilizing random cluster sampling for estimating HIV prevalence rates. The results provided valuable insights into the country's HIV burden, which could inform targeted interventions and resource allocation. In a different country context, Cork et al. [9] conducted a similar national survey to estimate HIV prevalence rates. Their study also employed random cluster sampling to obtain representative data. The researchers stratified the country into various clusters based on geographical regions and randomly selected clusters for data collection. The survey collected information on demographic characteristics, HIV testing, and behavioral risk factors. The study revealed an HIV prevalence rate of 6.2% among the general population. The findings highlighted disparities in HIV prevalence among different regions and identified specific risk factors contributing to the spread of the virus. The research team emphasized the importance of using random cluster sampling in resource-constrained settings to ensure efficiency and cost-effectiveness in data collection.

Longitudinal cohort studies provide valuable insights into the dynamics of HIV prevalence over time. These studies follow individuals at risk for HIV infection and measure prevalence rates at regular intervals (e.g., [10,11]). Longitudinal cohort studies are prospective observational studies that track a group of individuals over an extended period. These studies often involve participants who are at high risk for HIV infection, such as men who have sex with men (MSM), people who inject drugs (PWID), or individuals engaging in unprotected sex with HIV-positive partners. Participants are typically recruited based on specific criteria and followed over time, with regular assessments of HIV prevalence, risk behaviours, and other relevant variables. Valleroy et al. [10] conducted a seminal longitudinal cohort study to examine HIV prevalence dynamics among MSM in a metropolitan area. The study recruited a diverse sample of participants and followed them for several years, collecting data on HIV incidence, risk behaviours, and utilization of preventive measures. The findings highlighted a shift in HIV prevalence rates over time, with an initial increase followed by a subsequent decline. This study emphasized the importance of monitoring changes in risk behaviors and the impact of prevention strategies on HIV transmission dynamics. Davey et al. [11] conducted a longitudinal cohort study focusing on HIV prevalence among PWID. The study aimed to assess the impact of harm reduction interventions on HIV transmission dynamics and to identify factors associated with increased or decreased risk of infection. The findings revealed a decrease in HIV prevalence rates among PWID over the study period, attributed in part to the implementation of needle exchange programs and access to antiretroviral therapy. This study highlighted the effectiveness of harm reduction strategies in reducing HIV transmission and emphasized the importance of addressing social determinants of health in HIV

prevention efforts. Longitudinal cohort studies provide several significant contributions to our understanding of HIV prevalence dynamics. Firstly, they offer a temporal perspective, allowing researchers to observe changes over time and identify trends in HIV incidence and prevalence rates. Secondly, these studies provide valuable data on risk behaviors and factors associated with increased vulnerability to infection, which can inform targeted prevention interventions. Additionally, longitudinal cohort studies shed light on the effectiveness of various interventions, such as harm reduction programs, condom distribution, and antiretroviral therapy, in reducing HIV transmission.

National and regional HIV surveillance programs collect data from healthcare facilities, clinics, and other sources to monitor HIV prevalence. These data sources often contribute to estimating HIV burden and identifying high-risk populations (e.g., [12,13]) conducted a comprehensive study to assess HIV prevalence and incidence rates in a national HIV surveillance program in a specific country. The study aimed to provide valuable insights into the current state of the HIV epidemic and identify populations at higher risk. The authors utilized data collected from healthcare facilities, clinics, and other relevant sources to estimate HIV burden. The study employed a robust methodology, including a systematic data collection process and rigorous data analysis. The researchers analyzed demographic characteristics, risk factors, and HIV testing patterns among the population. By examining the data, Lot et al. [12] identified key trends, such as an increase in HIV prevalence among specific age groups or geographic regions. They also identified high-risk populations, such as men who have sex with men (MSM) and intravenous drug users. The findings of Lot et al. [12] were instrumental in shaping targeted HIV prevention and control strategies. By identifying the most vulnerable populations, policymakers and healthcare professionals could allocate resources effectively and design interventions that address the specific needs of these populations. Wang et al. [13] conducted a regional study focused on HIV surveillance in a specific area. Their objective was to assess the HIV prevalence among different population subgroups, detect any changes over time, and inform public health policies accordingly. Similar to Lot et al. [12], the authors collected data from multiple sources, including healthcare facilities and clinics, to estimate the HIV burden. The study adopted a comprehensive approach to data analysis, including both descriptive and inferential statistical techniques. Wang et al. [13] investigated factors such as age, gender, sexual behavior, and injection drug use among the study population. They observed changes in HIV prevalence rates over time, as well as disparities between various demographic groups. The results of Wang et al. [13] contributed significantly to the understanding of the regional HIV epidemic. By identifying the specific risk factors associated with HIV transmission, policymakers and public health officials were able to design targeted interventions. The study also emphasized the importance of ongoing surveillance to monitor changes in the epidemic and adapt prevention strategies accordingly.

Many studies on HIV prevalence have focused on Sub-Saharan Africa due to its high burden of HIV/AIDS. These studies often explore factors such as poverty, education, and healthcare access in relation to HIV prevalence (e.g., [14,15]). Many studies have investigated the relationship between HIV prevalence and various socioeconomic factors in Sub-Saharan Africa. One notable study by Okafor et al. [14] explored the association between poverty and HIV/AIDS in a rural community in Nigeria. The study found that individuals from lower socioeconomic backgrounds had a higher risk of HIV infection due to limited access to prevention measures, such as condom use and HIV testing services. Another study conducted by Ratmann et al. [15] focused on the impact of education on HIV prevalence in rural South Africa. The findings revealed a significant inverse relationship between education levels and HIV infection rates. Higher education was associated with better knowledge about HIV transmission, increased condom use, and improved healthcare-seeking behaviors, thereby reducing the risk of HIV transmission. Moreover, several other studies have investigated the influence of healthcare access on HIV prevalence. These studies have highlighted the importance of access to antiretroviral therapy (ART) and regular HIV testing in reducing transmission rates. They have also emphasized the need for comprehensive healthcare services that address both prevention and treatment aspects.

3. METHODS

3.1 Data

The University of Ilorin Teaching Hospital (UITH) was chosen as the case study for the years 2014 to 2019, with factors such as year, sex, and age group taken into account. During this six-year period, a total of 2604 cases were recorded at UITH.

3.2 Poisson modelling

The general form of Poisson regression can be expressed as follows:

$$\log(\lambda) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_k X_k$$

where:

λ represents the expected value (mean) of the response variable.

X_1, X_2, \dots, X_k are the predictor variables.

$\beta_0, \beta_1, \beta_2, \dots, \beta_k$ are the regression coefficients.

Estimating Model Coefficients: The maximum likelihood estimation (MLE) method is commonly used to estimate the regression coefficients in Poisson regression. The MLE procedure seeks the values of the coefficients that maximize the likelihood of observing the given data, assuming a Poisson distribution. **Model Assessment:** Several techniques can be employed to assess the goodness of fit and the overall performance of the Poisson regression model:

Deviance: The deviance statistic compares the fitted model with the saturated model (a model with a separate parameter for each observation). Lower deviance indicates better fit.

Pearson Chi-Square: The Pearson chi-square test compares the observed and expected frequencies based on the fitted model. A non-significant p-value suggests that the model fits well.

Residual Analysis: Residual analysis helps identify influential observations, check for patterns or outliers, and assess model assumptions.

Interpretation of Model Coefficients: The regression coefficients obtained from Poisson regression represent the change in the log of the expected count for a one-unit change in the corresponding predictor variable, while holding other variables constant. Exponentiating the coefficients ($\exp(\beta)$) provides the multiplicative effect on the count variable [16].

4. RESULTS

Table 4.1 summarizes the distribution of the study dataset.

Table 4.1 Data distribution of HIV prevalence across year, age and sex.

Factor	Mean	Standard deviation	95% Confidence Interval	Test of Equality
Year				<i>F(5, 42) = .092, p-value = .993</i>
2014	54.00	37.68	22.50 – 85.50	
2015	55.00	37.38	23.75 – 86.25	
2016	57.50	37.00	26.56 – 88.44	
2017	47.75	34.62	18.81 – 76.69	
2018	51.88	40.99	17.61 – 86.14	
2019	59.63	47.03	20.31 – 98.94	
Age group				<i>F(3, 44) = 85.99, p-value < .001</i>
0 – 15 years	16.58	4.68	13.61 – 19.56	
16 – 30 years	38.92	19.09	26.79 – 51.05	
31 – 45 years	109.17	20.39	96.21 – 122.11	
46+ years	52.50	8.22	47.28 – 57.72	
Sex				<i>t(46) = .160, p-value = .001</i>
Male	46.67	32.22	33.06 – 60.27	
Female	61.92	41.16	44.54 – 79.30	

Table 4.1 presents the data distribution of HIV prevalence across year, age and sex. The results show that there is an increasing trend in the HIV prevalence except in the year 2017 and 2018. However, there is no significant difference in the recorded prevalence of HIV across over the years ($p > .05$). Similarly, HIV is more significantly prevalent among female patients in the age group 31 – 45 years ($p < .001$).

Table 4.2 Poisson regression of HIV prevalence across year, age and sex.

Parameter	B	Std. Error	95% Wald Confidence Interval		Hypothesis Test		
			Lower	Upper	Wald Chi-Square	df	Sig.
(Intercept)	2.652	.0864	2.482	2.821	941.867	1	.000
Year							
2019	.099	.0664	-.031	.229	2.226	1	.136
2018	-.040	.0687	-.175	.095	.341	1	.559
2017	-.123	.0702	-.261	.015	3.067	1	.080
2016	.063	.0670	-.069	.194	.879	1	.349
2015	.018	.0677	-.114	.151	.073	1	.786
2014 (reference)	0 ^a
Sex							
Female	.283	.0396	.205	.360	51.062	1	.000
Male (reference)	0 ^a
Age group							
46+ years	1.152	.0813	.993	1.312	200.843	1	.000
31 – 45 years	1.884	.0761	1.735	2.034	613.504	1	.000
16 – 30 years	.853	.0847	.687	1.019	101.536	1	.000
0 – 15 years (reference)	0 ^a

The Poisson regression results in Table 4.2 shows similar results with the results in Table 4.1. There is significant effect of year on the prevalence of HIV among the study cases ($X^2 = 12.932$, $p = .024$). However, there is no significant of each year on the prevalence of HIV. For Sex effect, the overall effect of sex is significant ($X^2 = 51.06$, $p < .001$). The result also shows that there are more significant HIV cases reported for female than male. For age effect, the overall effect of age is significant ($X^2 = 874.683$, $p < .001$). The result also shows that there are more significant HIV cases reported for those above 30 years compared to those below 30 years.

5. CONCLUSION

In conclusion, the analysis of HIV prevalence data presented this paper reveals several important findings. Firstly, there is an overall increasing trend in HIV prevalence across the years, with the exception of 2017 and 2018. However, statistical tests indicate that the difference in HIV prevalence between the years is not significant, suggesting that the observed fluctuations may be due to random variation rather than a true change in prevalence. Furthermore, the data highlights a significant difference in HIV prevalence based on sex and age. Specifically, HIV is more prevalent among female patients in the age group of 31-45 years. This finding emphasizes the need for targeted interventions and awareness campaigns among this particular population to address the higher risk of HIV infection. The Poisson regression results further support these findings. The analysis reveals a significant effect of the year on HIV prevalence among the study cases. However, when examining the individual years, no specific year demonstrates a significant effect on HIV prevalence.

Regarding the effect of sex, the Poisson regression demonstrates an overall significant effect, with a higher number of significant HIV cases reported among females compared to males. This highlights the importance of gender-specific approaches in HIV prevention and treatment strategies.

Additionally, the Poisson regression analysis underscores the significant effect of age on HIV prevalence. Individuals above 30 years of age exhibit a higher number of significant HIV cases compared to those below 30 years. This finding emphasizes the need for age-specific interventions and targeted healthcare services for different age groups.

In summary, the analysis of both the data distribution and the Poisson regression results support the observed increasing trend in HIV prevalence over time, with exceptions in certain years. The results highlight the significance of sex and age as key factors influencing HIV prevalence, emphasizing the importance of tailored interventions and strategies to address the specific needs of different populations at higher risk of infection. These findings contribute to a better understanding of HIV epidemiology and can guide public health efforts aimed at reducing HIV transmission and improving care for affected individuals.

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