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MATHEMATICAL MODELING OF HIV TRANSMISSION DYNAMICS USING THE CONCEPTS OF PROBABILITY DISTRIBUTIONS AND KOLMOGOROV DIFFERENTIAL EQUATIONS

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ABSTRACT
The negative impact of HIV/AIDS in our society cannot be over-emphasized. Many industries are faced with decrease in manpower leading to low productivity and revenue generation as a result of their staffs being afflicted with HIV related diseases. Hence, developing mathematical models which determine the level at which the virus will pose a risk to humans and at what rate the HIV- infected adults and children finally develop AIDS then die is very crucial. In this research, we extend existing models by applying the concept of inverse probabilities to construct HIV transmission pattern in the past in order to predict future infectious cases. Secondly, Komolgorov differential equations involving probability generating function is applied to derive the mean and variance of the HIV virus persons infected in a given population. The mathematical models presented in this paper have advantage over existing ones because if the relevant data are available, the models can be used to determine epidemiological parameters such as the expectation and variance of the HIV transmission and its subsequent progression to AIDS. Also, the research identifies what data is needed so that predictions of future infection can be more precise. This will make the relevant agencies to predict HIV/AIDS transmission patterns for many decades ahead and formulate future policies meant to curb the epidemic.

Keywords: HIV/AIDS, transmission, patients, infection, population.

1 INTRODUCTION
Epidemiology is the study of disease transmission in human populations. AIDS which is also referred to as acquired immune-deficiency syndrome was first discovered in 1981 in the United State of America (USA) among homosexuals as reported in [1]. As contained in [2], more than seventeen million people had been infected with the virus with over sixteen million adults among them. In [3], HIV was classified into four hierarchies of clinical immunological dysfunctions. Group 1 was referred to as Sero-conversion stage, Group 2 is asymptomatic stage. Group 3 is referred to as progressive generalized lymphadenopathy while group 4 is referred to as clinical manifestation stage. The group 4 is where we have AIDS patients. The three major ways HIV can be transmitted according to laboratory and epidemiological research are: (i) sexual intercourse (ii) blood transfusion and (iii) mother- to-child. Seventy-five percent (75%) cases of HIV transmission is attributed to sexual intercourse. There are different methods that can be used to predict and estimate the rate of HIV transmission as contained in [4]. These are: (a) Extrapolation Method, (b) Back-calculation Approach, (c) The Use of Dynamic Models, and (d) Automata Network Model. A frame work to guide and interpret observed trends can be provided by mathematical models as reported in [5].

The authors in [6] remarked that HIV transmission among heterosexual and intravenous drug users has constituted a major concern to curbing the menace of the virus. Hence, it is

very essential to have data related to the long term pattern of the transmission of HIV among sex- workers, and intravenous drug users in order to curb the AIDS epidemic. The level at which the virus will pose a risk to humans and the rate at which the HIV- infected adults and children finally develop AIDS then die have been uncertain due to the social stigma associated with those infected with it.

National HIV/AIDS 2023 Surveillance Report

The rate at which diseases are transmitted from one person to another depends on the contact rate between the number of the susceptible and infectious persons. HIV/AIDS Surveillance is a system which deals with collection of HIV data including their analysis, interpretation and uses for the purpose of improving the health of people. Data are usually collected from clinical care centers by client-monitoring team who use them to guide the national response team in understanding the epidemic trend. There are three major surveillances which help in tracking HIV related data as stated in [7]. These are (a) Recent infection surveillance of HIV-1, (b) Case Base Surveillance and (c) Mortality Surveillance. Mortality Surveillance is used to evaluate the transmission patterns in order to know the causes of death in population of people infected with HIV, how the patients can be treated and how to curb further transmission. For example, in [8], Verbal Autopsy (VA) instrument is used to analyze information obtained from member of family who were close to the decease before his or her death. The collected data from verbal autopsy is usually uploaded into smart VA analysis to determine the cause of death. The Fig 1 below shows HIV- 1 Surveillance chart.

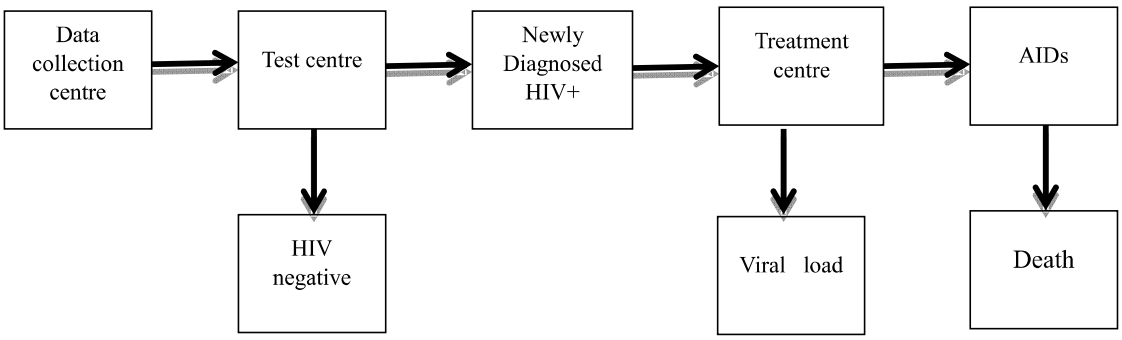

Fig 1: HIV- 1 Surveillance chart

HIV/AIDS Statistical Data

HIV/AIDS prevalence in Nigeria varies from one state to another. For example, the 2023 NAIIS report in [9] shows that Akwa-Ibom and Benue States have the highest HIV/AIDS prevalence estimates in Nigeria while Jigawa and Katsina States have the lowest prevalence. According to United Nation AIDS (2024) report, 39.8 million people lived with HIV in the year 2023 while people who were newly infected with it were estimated to be 1.3 million. In 2023, the number of HIV/AIDS patients who accessed antiretroviral therapy were 30.7 million while 630, 000 died from HIV/AIDS related diseases. Epidemiological report in [10], shows that the five major causes of death are AIDS (24%), Malaria (12%), Stroke (5%), Road accidents (4%) and Pneumonia (2%). Since the emergence of HIV/AIDS epidemic, 88.5 million people have been infected while 42.4 million people lost their lives due to HIV/AIDS related diseases. The people who are mostly infected by HIV are homosexuals, lesbians, sex workers, transgender, prisoners and people who are injected with drugs as stated in [11] and [12] while the report in [10], shows that girls and women of different ages make up the 44 % people who are newly infected with HIV. In Africa Sub-Sahara, about 62

% newly infected people are girls and women while in other part of the world, 73% of newly infected people are boys and men.

Problem Definition

The major problems confronting relevant stakeholders tackling the menace of HIV/AIDS are:

(i) Inadequate and substandard diagnostic equipment and inaccurate reporting of AIDS cases. HIV rate of infection is largely silent in Nigeria.

(ii) The social stigma associated with those infected with HIV/AIDS infection. Hence, there is hardly any accurate data on transmission cases.

(iii) A research conducted in [13] shows that the two main impacts of HIV/AIDS on business operations are time lost to HIV/AIDS related sicknesses and the cost of medical care for HIV/AIDS patients. This is one of the crucial reasons why mathematical models such as the ones developed in this research containing the essential epidemiological parameters of the relationship between HIV transmission and its subsequent progressions to AIDS are needed. Our models identify the types of data required to predict future infection rate. This assists in formulation of future policies, clarify observed trends and make predictions for many decades ahead.

2 LITERATURE REVIEW

The authors in [14] stated that Daniel Bernoulli (a mathematician and physician) was the first to apply mathematics to the study of diseases in 1760. He invented the formula to evaluate the benefit in life expectancy if smallpox were eradicated from the human population. This was closely followed by the science of bacteriology research work reported in [14]. The author in [15] developed a deterministic mathematical model which deals with malaria transmission with mosquitoes as vectors. His model predicts the future rate of infection among susceptible and infectious persons including recovery, birth and death rates. Hence, his model became a mathematical tool in epidemiological research.

The authors in [16] applied the model in [15] to males and females human population with respect to sexually transmitted diseases. Models which deal with sexually transmitted diseases, especially gonorrhea are reported in [17] and [18]. In recent years, there has been an upsurge of interest in mathematical models relating to epidemics of which majority of them focused on HIV/AIDS epidemic. For example, the first mathematical model on the dynamics of HIV transmission was developed in [5] and it was a deterministic model. Other methods used in literature in studying HIV transmission are Markov chains used for evaluating the rate of spread, Fuzzy Arithmetic Techniques used in estimating dates of infection, as stated in [18]. The authors in [19] stated that back-calculation method is often used because few assumptions are required about the infection curve shape, data of the AIDS incidence and the incubation estimation distribution period.

The four types of mathematical models that can be used to study HIV transmission as reported in [4], are statistical, deterministic, stochastic and state-space. In stochastic models, it is assumed that the response variable is randomly indexed. Hence the HIV epidemic transmission rate is based on probability distribution process. The authors in [20] opined that people infected with HIV go through four irreversible stages. These are: (a) susceptible (b) infection onset (c) infectious (d) symptoms appearance. For example, HIV models which consider the infection at the early stages, the dynamics of prevalence and control of the HIV/AIDS are reported in [21] and [22]. Statistical models on HIV epidemic uses back-calculation to construct trends of HIV infections in the past in order to predict future infectious cases, their impacts and control as reported in [23]. State-space (a computational scheme) method estimates HIV infection and incubation distributions, the susceptible and the infected persons as discussed in [2]. A mathematical model of the

transmission dynamics of HIV/AIDS epidemic through female sex workers using fourth-order Runge-Kutta method is developed in [24]. The authors in {25} present a deterministic HIV transmission model which has a unique epidemic equilibrium point showcasing the impact of counseling and treatment.

According to the authors in [26], [27] and [28], HIV/AIDS is yet to get a cure but its treatment is usually carried out by using anti-retroviral (ARV) drugs which help in prolonging the life of the patient. The HIV transmission model developed by the authors in [28] consists of three stages: (i) Susceptible, (ii) Infection and (iii) AIDS. Their model was later extended in [29] by inclusion of Treatment stage. HIV mathematical models relating to microbiology and immunology, globally stable endemic, HIV stability analysis are discussed in [29], [30] and [31]. Models for infectious diseases containing information related to changes in patterns of contacts are studied in [32], [33] and [35]. HIV and shifting of epicenters for optimal control and the danger of late diagnosis of the dynamics of HIV/AIDS models are contained in [36] and [37]. Compartmental models which consist of reproduction numbers and sub-thresholds to describe HIV transmission endemic equilibrium are reported in [38].

The Shortcoming of the Existing Models

Many of the existing mathematical models used for projecting cases of HIV/AIDS transmission use the incubation period. This approach involves projecting AIDS cases only from the infection that has already occurred within the last two years without providing information on the future infection incidence in terms of age, risk, and treatment. Epidemic models aim at revealing the reason for new AIDS cases in order to tackle its transmission properly in term of cure and prevention. Hence, there is need to develop a more comprehensive model which involves the different stages of HIV/ AIDS transmission such as the one presented in this paper.

3 METHODS/ PROCEDURE

Methodology: In this research, we apply the concept of inverse probability which has been known for its applications in determining unknown probabilities based on the information provided by either past records or experiments. The Inverse probabilities are to be used in constructing transmission pattern of HIV infections in the past in order to predict future infectious cases. Secondly, Komolgorov differential equation using probability generating function is applied to determine the mean and variance of the number of persons infected with HIV virus in a given population.

Materials: In this research, we use the year 2023 statistical data on HIV/AIDS prevalence in Nigeria as contained in NAIIS, 2023 report. HIV prevalence by sex and age classification reported in NAIIS, 2018 and United Nation AIDS (2024) report on the number of people living with HIV, number of people who were newly infected, number of HIV/AIDS patients who accessed antiretroviral therapy and the number of people who died from HIV/AIDS related diseases.

Table 1: Below shows global data on HIV prevalence from year 2000 to 2023.

	2000	2005	2010	2020	2022	2023
People with HIV	27.3 million	29.5 million	32.1 million	38.8 million	39.6 million	39.6 million
People newly infected HIV	2.7 million	2.6 million	2.2 million	1.6 million	1.5 million	1.4 million
Deaths due to AIDS	1.9 million	2.1 million	1.4 million	731 000	671 000	631 000
(Adults, aged 15+) newly infected with HIV	2.3 million	2.0 million	1.8 million	1.3 million	1.2 million	1.2 million
(Children, aged 0-14) newly infected with HIV	530 000	470 000	300 000	150 000	130 000	120 000
People who have access to antiretroviral therapy	512 000	2.0 million	7.8 million	26.3 million	29.4 million	30.8 million
Available resources	US $5.2 billion	US $ 9.4 billion	US$ 16.8 billion	US$ 21.6 billion	US$ 20.9 billion	US$ 19.9 billion

In Table 1, we observe that the number of people living with HIV increases rapidly in the early years and later declines in the later years. The same trend is applicable to people who are newly infected with HIV and the number of HIV related deaths per year. This trend could be attributed to HIV/AIDS campaign awareness and the use of antiretroviral drugs. On the other hand, the number of people accessing the antiretroviral drugs increases in all the years under consideration without declining. This trend is also similar to the amount of money (in dollars) spent per year to tackle the HIV epidemic as shown in the last row of Table 1.

Table 2 shows global World Health Organization's report on HIV regional cumulative data as at 2023. According to the report, 39.8 million people lived with HIV, number of newly infected people were 1.4 million and the number of AIDS related deaths was 0.63 million.

Table 2: HIV Regional Cumulative Data as at the Year 2023

	People living with HIV	New HIV Infections	New HIV Infections (Adults, aged 15+)	New Infections (Children, aged 0-14)	AIDS-related deaths
Global	39.8 million	1.4 million	1.3 million	121 000	631 000
Asia and the Pacific	6.8 million	301 000	291 000	11 000	152 000
Caribbean	341 000	16 000	14 000	1 400	5 200
Eastern and Southern Africa	20.9 million	451 000	401 000	51 000	261 000
Eastern Europe and central Asia	2.2 million	141 000	141 000	1 400	45 000
Latin America	2.4 million	121 000	120 000	4 000	31 000
Middle East and North Africa	210 000	23 000	21 000	1 900	6 200
Western and central Africa	5.2 million	191 000	141 000	49 000	131 000
Western and central Europe and North America	2.4 million	57 000	57 000	_	14 000

Table 3 shows global data on treatment of HIV coverage per region as at year 2023. According to World Health Organization report, among people living with HIV (adults, aged

15+) who access antiretroviral treatment is 75% while it is 57% for children aged 0-14 as at year 2023.

Table 3: Treatment of HIV Coverage Per Region at at 2023

	Among people living with HIV, the percent on ART (Adults, aged15+)	Among people living with HIV, the percent on ART (Children, aged 0-14)	Among people living with HIV, the percent on ART
Global	78%	58%	78%
Asia and the Pacific	68%	76%	68%
Caribbean	72%	40%	71%
Eastern and Southern Africa	85%	66%	84%
Eastern Europe and central Asia	51%	74%	51%
Latin America	75%	39%	74%
Middle East and North Africa	51%	36%	50%
Western and central Africa	80%	36%	77%
Western and central Europe and North America	78%	-	78%

Model Mathematical Symbols and Notations

$P_j(t)$ = Probability that *j* population is infected at time *t*.
$P_{j+1}(t)$ = Probability that *j+1* population are infected at time *t*.
$P_{j-1}(t)$ = Probability the *j–1* population are infected at time t.
$P_j(t + \Delta t)$ = Probability that *j* population are infected at time interval $(t + \Delta t)$.
$1 - (j\emptyset\Delta t + 0\Delta t)$=probability of no birth.
$1 - (j\psi\Delta t + 0\Delta t)$ = Probability of no death.
$j\emptyset\Delta t + 0\Delta t$ = probability of birth.
$j\psi\Delta t + 0\Delta t$ = probability of death.
k = average number of sexual partners per unit time.
d = death rate as a result of AIDS.
r_1 = rate of transition from infection stage to AID stage.
r_2 = rate of transition from infection stage to treatment stage.
v = natural mortality rate.
H = rate of sexual contact between two persons say male *(m)* and female *(f)*.
u = rate of treatment for aids category.
b = rate of HIV/AIDS infection.
S = number of adults that survive after treatment.
s = number of children that survive after treatment.

Model Description: In this research, we consider a HIV/AIDS model in which a heterosexual population is divided into four categories: the susceptible (S), infective (I), Treatment (T) and AIDS (A). The total population in time *t* is denoted by *N(t).* The susceptible population can be infected with HIV through sexual contact with an infected person. An infected mother can infect a child during pregnancy period which is also known as mother-to-child transmission. Individuals that are not infected via mother-to-child transmission could join the susceptible category after a period of time with infant survival rate denoted by *q* and *p*. The individuals in the infected category migrate to join the

treatment class at the rate r_2, while individuals with high degree of infection migrate to join the AIDS category with the rate r_1. *(N* = susceptible + infective+ treatment + AIDS.

Model Formulation

By applying the inverse probability rule of mutually exclusive events probability, we have

$P_j(t+\Delta t) = (1 - j\emptyset\Delta t + 0\Delta t)(1 - j\psi\Delta t + 0\Delta t)P_j + (1 - j\emptyset\Delta t + 0\Delta t)(j\psi\Delta t + 0\Delta t)P_{j+1} +$
$(1 - j\psi\Delta t + 0\Delta t)(j\emptyset\Delta t + 0\Delta t)P_{j-1} + (j\psi\Delta t + 0\Delta t)(j\emptyset\Delta t + 0\Delta t)P_j$ (1)

Equation (1) can be simplified by dividing it through by Δt, neglecting all the terms (0Δt) and allowing limit Δt tend to zero, we obtain equation (2) as follows:

$P_j = -P_j(j\emptyset + j\psi) + (j\psi)P_{j+1} + (j\emptyset)P_{j-1}$ (2)

By differentiating equation (2) with respect to *t*, we have

$$\frac{dP_j(t)}{dt} = -(j\emptyset + j\psi)P_j(t) + (j\psi)P_{j+1}(t) + (j\emptyset)P_{j-1}(t) \quad (3)$$

Susceptible Stage Model

The susceptible population consists of people who are prone or very likely to be infected with the HIV. The change in the susceptible population size in a given time interval (t, t + Δt) is applicable to Baye's theorem of inverse probabilities and could be expressed as stated in any of the following equations (4) – (6) :

$$P\left[H(t, t+\Delta t) = \frac{j+1}{H(t)}\right] = pq + 0\Delta(t) \quad (4)$$

$$P\left[H(t, t+\Delta t) = \frac{j-1}{H(t)}\right] = [w\delta k + v]H + 0\Delta(t) \quad (5)$$

$$P\left[H(t, t+\Delta t) = \frac{j}{H(t)}\right] = 1 - pq - (w\delta + v)H - 0\Delta(t) \quad (6)$$

Equation (4) simply states that the probability of having *j+1* population in the system at time interval (t, t + Δt) is equal to the proportion of children that survive after time *t* multiply by the number of infants who survived mother-to-child transmission in time *t* plus any susceptible individuals at time *t.* Equations (5) simply states that the probability of having *j-1* population in the system at time interval (t, t + Δt) is the sum of the rate at which children are infected plus the rate at which AIDS infected individuals get treated multiply by the number of susceptible in time *t.* Equations (3) simply states that the probability of having *j* population in the system at time interval (t, t + Δt) is one minus the sum of the terms in the RHS of Equations (5) and (6).

Kolmogorov differential equation is obtained if we substitute Equations (4), (5) and (6) into equation (3) to obtain equation (7) as follows:

$$\frac{dP_j(t)}{dt} = -[(pq + w\delta k + v)H]\,P_j\,(t) - (j+1)(w\delta k + v)HP_{j+1}(t) + (j-1)pqP_{j-1}(t) \quad (7)$$

Equation (7) can be solved by applying probability generating function method. Hence we have:

$$\frac{\partial G(y,t)}{\partial t} = -[pq + (w\delta k + v)H]y\frac{\partial G(y,t)}{\partial y} + (w\partial k + v)H\left[\frac{\partial G(y,t)}{\partial y} - P_1(t)\right] + pqy^n\frac{\partial G(y,t)}{\partial y} \quad (8)$$

Theorem 1: Given any initial state *i* at time *a*, where $a < t$ and $|y| < 1$, then the probability generating function $\mathrm{G(y,t)}$ statisfy the equation is

$$\frac{\partial G(y,t)}{\partial t} = \sum y^n \mathrm{P(j,t/i,a)}\ \{(y-1)\emptyset \mathrm{j(t)} + (\mathrm{y^{-1}} - 1)\psi_j(t)\} \quad (9)$$

By applying the Theorem 1, Equation (9) becomes

$$\frac{\partial G}{\partial t}(y,t) = \frac{\partial G(y,t)}{\partial t}\{(y-1)[ypq + (w\delta k + v)H]\} \quad (10)$$

We can find the general solution of the homogeneous partial differential equation of (10) to obtain:

$$\frac{\partial G(y,t)}{\partial t} - \{(y-1)[ypq + (w\delta k + v)H]\}\frac{\partial G(y,t)}{\partial y} = 0 \quad (11)$$

Given the initial condition: $G(y,0) = y^i$, the auxiliary version of equation (11) is

$$\frac{dt}{1} = \frac{\partial \mathrm{G(y,t)}}{\{(1-y)[ypq+(w\delta \mathrm{k+v})\mathrm{H}]\}} = \frac{\partial G}{1} \quad (12)$$

Equation (12) has two solutions. These are

$$\frac{dt}{1} = \frac{\partial \mathrm{G(y,t)}}{\{(1-y)[ypq+(w\delta k+v)\mathrm{H}\}} \quad (13)$$

and

$$\frac{dt}{1} = \frac{d\mathrm{G(y,t)}}{1} \quad (14)$$

Hence, by simplification of Equation (14), we have

$$d\mathrm{G(y,t)} = ldt \quad (15)$$

By integrating both sides of (15) and let $l\ tends\ to\ zero$ $(l \to 0)$, we have:

$$\int_{G(y,t)=k} d\mathrm{G(y,t)} = \int 0\ dt \quad (16)$$

Solving equation (16) by the method of separation of variables in differential equations, we have equation (17) as follows:

$$G(y,t) = \left[\frac{(w\delta k+v)H\left[e^{[pq-(w\delta k+v)H]t}-1\right]+y\left(pq-(w\delta k+v)\right)He^{[pq-(W\delta k+v)H]t}}{ypq(1-e^{[pq-(w\delta k+v)H]t}+pqe^{[pq-(w\delta k+v)H]t}-(w\delta k+v)H}\right] \quad (17)$$

By differentiating equation (17) with respect to *y* in line with [27] and letting $y \to 1$, we get the expectation (i.e. the mean) as follows:

$$E[G(y,t)] = e^{[pq-(w\delta k+V)H]t} \quad (18)$$

While the variance is

$$Var\ [G(y,t)] = \left[\frac{pq-(w\delta k+v)H}{pq+(w\delta k+v)H}\right]e^{[pq-(w\delta k+v)H]t}\left(e^{[pq-(w\delta k+v)H]t}-1\right) \quad (19)$$

Infection Stage Model

The probability of having *j* individuals in the population of infective in a given time interval $[t, t+\Delta t]$ is equivalent to the probability that there are:

(i) *j* = number of HIV infective at time *t* and there was transmission or death in $(t, \mathrm{t}+\Delta \mathrm{t})$ time interval.

(ii) $j+1$= number of HIV infective at time t and one infective is added by HIV transmission, mother to child migration in $(t, t+\Delta t)$ time interval.

(iii) $j-1$ = number of HIV infective at time *t* and one infective dies or degenerate to AIDS in $(t, t+\Delta t)$ time interval.

The following three conditional probabilities can be used to represent the variation in the population size in $(t, t+\Delta t)$ time interval. These are:

$$P\left[x(t, t+\Delta t) = \frac{j+1}{x(t)}\right] = w\delta k + 0\Delta(t) \quad (20)$$

$$P[x\left(t, t+\Delta t=\frac{j-i}{x(t)}\right] = (v + r_1 + r_2)x + 0\Delta(t) \quad (21)$$

$$P\left[x(t, t+\Delta t) = \frac{j}{x(t)}\right] = 1 - w\delta k - (v + r_1 + r_2)x - 0\Delta t \quad (22)$$

If we substitute Equations (20), (21) and (22) into equation (17) we have Kolmogorov differential equation as stated in Equation (23)

$$\frac{\partial P_j(t)}{\partial t} = -j(w\delta k + (v + r_1 + r_2)x)P_j(t) + j + 1(v + r_1 + r_2)x\, P_{j+1}(t) + (j-1)[w\delta k]P_{j-1}(t) \quad \ldots(23)$$

By applying the probability generating function technique on Equation (23), we obtain

$$G_x(y,t) = \left[\frac{yw\delta k-(v+r_1+r_2)x+(v+r_1+r_2)x(1-y)\ell^{(w\delta k-(v+r_1+r_2)x)t}}{yw\delta k-(v+r_1+r_2)x+w\delta k(1-y)\ell^{(w\delta k-(v+r_1+r_2)x}}\right] \quad (24)$$

If we differentiate Equation (24) with respect to *y* and letting $y \to 1$ in line with [17] cited in [27], we obtain the expectation (i.e. mean) as:

$$E[G\ (y,t)] = \ell^{[w\delta k-(v+r_1+r_2)x]t} \quad (25)$$

While the variance is

$$\mathrm{Var}\ [G(y,t)] = \left[\frac{w\delta k-(v+r_1+r_2)x}{\mathrm{w}\delta k+(v+r_1+r_2)x}\right]\ell^{(w\delta k-(v+r_1+r_2)x)t}\left(\ell^{(w\delta k-(v+r_1+r_2)x)t}-1\right) \quad (26)$$

Treatment Model

$$P\left[\beta(t, t+\Delta t) = \frac{j+1}{\beta(t)}\right] = \mathrm{r}_2 x + uA + 0\Delta(t) \quad (27)$$

$$\mathrm{P}\left[\beta(\mathrm{t}, \mathrm{t}+\Delta t) = \frac{\mathrm{j}-1}{\beta(\mathrm{t})}\right] = (\mathrm{v})\beta + 0\Delta(t) \quad (28)$$

$$P\left[\beta(t, t+\Delta t) = \frac{j}{\beta(t)}\right] = 1 - (r_2 - x + uA) - (v)\beta - 0\Delta t \quad (29)$$

If we substitute equations (27), (28) and (29) into (17) we have Kolmogorov differential equation as follows:

$$\frac{\partial \mathrm{G(y,t)}}{\partial t} = -j[r_2 x + uA + (v)\beta]P_j(t) + (j+1)[(v)\beta]P_{j+1}(t) + (j-1)[r_2 x + uA]P_{j-1}(t) \quad (30)$$

By applying probability generating function technique in Equation (30), we have the probability distribution as stated in Equation (31).

$$G_\beta(y,t) = \left[\frac{y(r_2 x + uA - (v)\beta + (c+v)\beta(1-y)\ell^{[r_2 x+uA-(v)\beta]t}}{y(r_2 x + uA) - (v)\beta + (r_2 x + vA)(1-y)\ell^{[r_2 x+uA-(v)\beta]t}}\right] \quad (31)$$

If we differentiate Equation (31) with respect to y and letting $y \to 1$ after simplifying the result, we have the expectation as

$$E[G(y,t)] = \ell^{[r_2 x+uA)-(v)\beta]t} \quad (32)$$

While the variance is

$$\mathrm{Var[G(y,t)]} = \left[\frac{r_2 x+uA=(v)\beta}{r_2 x+uA-(\mathrm{v})\beta}\right]\ell^{[r_2 x+uA-(\mathrm{v})\beta]t}(\ell^{[r_2 x+uA-(\mathrm{v})\beta]t}-1) \quad (33)$$

AIDS Stage Model

The change in the population size of AIDS category in a given $(t, t+\Delta t)$ time interval can be denoted by conditional probabilities as follows:

$$P\left[\alpha(t, t+\Delta t) = \frac{j+1}{\alpha(t)}\right] = r_1 x + 0\Delta(t) \quad (34)$$

$$P\left[\alpha(t, t+\Delta t) = \frac{j-1}{\alpha(t)}\right] = (d+u+v)\alpha + 0\Delta(t) \quad (35)$$

$$P\left[\alpha(t, t+\Delta t) = \frac{j}{\alpha(t)}\right] = 1 - (r_1 x) - (d+u+v)\alpha - 0\Delta t \quad (36)$$

If we substitute Equations (34), (35) and (36) into Equation (17) we will get Kolmogorov differential equation as follows:

$$\frac{dP_j(t)}{dt} = -j[r_1 x + (d+u+v)\alpha]P_j(t) + (j+1)[(d+u+v)\alpha]P_{j+1}(t) + (j-1)(r_1 x)P_{j-1}(t) \quad (37).$$

If we apply probability generating function technique to Equation (37), we obtain its probability distribution as:

$$G\alpha\,(y, t) = \left(\frac{y(r_1 x) - (d+u+v)\alpha + (d+u+v)\alpha(1-y)\ell^{[(r_1 x)-(d+u+v)\alpha]t}}{y(r_1 x) - (d+u+v)\alpha + (r_1 x)(1-y)\ell^{[(r_1 x)-(d+u+v)\alpha]t}}\right) \quad (38)$$

If we differentiate (38) with respect to y and setting y = 0 we obtain its expectation after simplification as follows:

$$E[G(y,t)] = \ell^{[(r_1 x)=(d+u+v)\alpha]t} \quad (39)$$

While its variance is:

$$\mathrm{Var}[G(y,t)] = \left[\frac{(r_1 x)-(d+u+v)\alpha}{(r_1 x)+(d+u+v)\alpha}\right]\ell^{[(r_1 x)-(d+u+v)\alpha]t}\left(\ell^{[(r_1 x)-(d+u+v)\alpha]t} - 1\right) \quad (40)$$

5 RESULTS/ DISCUSSION

In this research, HIV transmission has be classified into four stages: (i) Susceptible Stage (ii) Infection Stage (iii) Treatment Stage and (4) AIDS Stage. Equations (1)-(3) show the result obtained by applying Theorem 1 to mutually exclusive events. The susceptible model is contained in equation (4) – (19). Equations (18) and (19) are the derived formulas to calculate the mean and variance of the HIV susceptible population. The infection (stage) population derivation procedure is contained in equations (20)-(24). Equations (25) and (26) are the formulas for calculating the mean and variance of the HIV infectious population respectively. HIV treatment stage population derivation is contained in Equations (27)-(31). Equations (32) and (33) are the formulas to calculate the mean and variance of the HIV treatment population. AIDS stage population model derivation is contained in Equations (34)-(40). Equations (39) and (40) are the formulas for calculating the mean and the variance of the AIDS population respectively.

6. CONCLUSION

In this research, we extended the existing models by applying the concept of inverse probability theorem to construct transmission pattern of HIV infections in the past in order to predict future infectious cases. Secondly, Komolgorov differential equations involving probability generating function is applied to derive the formulas for the mean and variance of the number of persons infected with HIV virus in a given population. The models presented in this paper have advantage over existing ones because if the relevant data are available, the models can be used to determine epidemiological parameters such as the expectation and variance of the relationship between HIV transmission and its subsequent progression to AIDS. Also, the research identifies what data is needed so that predictions of future infection can be more precise. This makes the relevant agencies to predict HIV/AIDS transmission patterns for many decades ahead and formulate future policies meant to curb the menace of the epidemic.

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