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MATHEMATICAL MODELING FOR HUMAN IMMUNODEFICIENCY VIRUS (HIV) TRANSMISSION USING GENERATING FUNCTION APPROACH

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ABSTRACT. This study is concerned with the mathematical modeling for human immunodeficiency virus (HIV) transmission epidemics. The mathematical models are specified by stochastic differential equations that are solved by use of Generating Functions (GF). Models based on Mother to child transmission (MTCT) (age group 0-5 years), Heterosexual transmission (age group 15 and more years) and combined case (incorporating all groups and the two modes of transmission) were developed and the expectations and variances of Susceptible (S) persons, Infected (I) persons and AIDS cases were found. The $S_1(t)$ Susceptible model produces a constant expectation and increasing variance. It was shown that Mother to Child transimission and Heterosexual models are special cases of the Combined model.

1. INTRODUCTION

Generating functions have been applied extensively in population studies, especially in branching processes, human reproduction process, birth and death process etc. In this study, generating function (GF) technique was used in modeling HIV/AIDS transmission. In the literature, this approach has not been used extensively by researchers to study epidemic processes. There is need to extend the application of generating functions to HIV transmission models in modern day work. Jewel

(1990) studied compartmental and empirical modeling approaches. In recent time, most of the researchers have focused on deterministic models and various approaches for studing epidemiology of infectious diseases, AIDS inclusive, have also been developed. In this study we proceed to study the deterministic models, then develop a stochastic differential equations from the deterministic models for the spread of the HIV/AIDS virus in a heterosexual population and then solve the equations by using the approach of probability generating functions. We are motivated by the following considerations.

(i) Many biological factors such as incubation periods and social factors affecting HIV/AIDS spread are subjected to considerable random variation so that the spread of the AIDS virus is in essence a stochastic process.

(ii) Stochastic models provide more information than deterministic models; for example, besides the expected values, one may also compute the variances and covariances and assess effects of various factors on these variances and covariances.

(iii) Under certain special conditions, the deterministic approach is equivalent to working with the expected values of the stochastic models. In this sense, the deterministic approach is a special case of the stochastic models if one is only interested in the expected values.

The section two of the work focuses on Mother-to-Child Transmission Models while section three examined the Heterosexual Model. In section four the combined model was discussed and section five gave the concluding remarks.

1.1. ASSUMPTIONS AND NOTATIONS FOR THE MODEL

Let

m_1—Survival rate of children between ages $0-5$ years

m_2—Survival rate of children in ages $5-15$ years

m_3—Survival rate of young adults and obove

μ— the death(death unrelated to HIV/AIDS) or emigration rate (migrate out of the population because of fear of HIV/AIDS),where $k = 1, 2, 3$ (the different age groups have different per capita mortality rates).

ϑ_i^{-1}—Average Incubation period in stage i

λ—birth rate for sexually mature persons per person per time.

α — the immigration rate for the sexually mature persons be α per time, this is independent of the population

t—Present time

x_1—starting time

x_2—future time (in years)

$a(t)$– The expected rate of new AIDS incidences at time t.

$h(t)$–The expected number of new incidences of HIV infection at time t.

$Y(t)$–Random variable corresponding to the number of newly diagnosed
AIDS incidences at time t

Thus the probability that a birth will occur in the heterosexual population during the time interval $(t, t + \Delta t)$ is $\lambda\Delta t + o(\Delta t)$

Let the sexual contact rate between a matually sexual S person and an I person be ω where $\omega \geq 0$.

$S(t)$: denote the number of persons in group S at time t

$I(t)$: denote the number of persons in group I at time t

$A(t)$: denote the number of persons in group AIDS case at time t

It is reasonable to assume that at the beginning of the epidemic, at $t = 0$, that $S(0)$ is large, that $I(0)$ is fairly small, and that $A(0) = 0$. At time t, let $N(t)$ represent the size of the population. Therefore the total population consists of

$$N(t) = S(t) + I(t) + A(t)$$

(a) If the population size is $n(n > 0)$ at time t, during the small interval of time $(t, t + \Delta t)$, the probability that "birth"(an increase to the population) will occur is $\lambda_n(t)\Delta t + o(\Delta t)$. The probability of no "birth"occuring in that small interval is $1 - \lambda_n(t)\Delta t + o(\Delta t)$ and the probability of more than one"birth"occurring is $o(\Delta t)$. "birth"occuring in $(t, t + \Delta t)$ are independent of time since the last occurence.

(b)The probability that "death"will occur in a small interval of time $(t, t + \Delta t)$ is $\mu_n(t)\Delta t + o(\Delta t)$,the probability of no "death"occuring is $1 - \mu_n(t)\Delta t + o(\Delta t)$ and the probability that more that one "death"occurs is $o(\Delta t)$. "death"occuring in $(t, t + \Delta t)$ are independent of time since the last occurence.

(c) $n = 0$ is an absorbing state of the process.
(d) For the same population size, the "birth"and "death"occur independently of each other.

Given a sexual contact between an S person and an I person during $(t, t + \Delta t)$, we let δ be the probability that this I person will transmit the AIDS virus to the S person. This event converts the S person to an I person. $\omega\delta = \sqrt{\omega_m \delta_m \omega_f \delta_f}$ where $\omega_m \delta_m$ is the probability that an I male transmit the AIDS virus to an S female and $\omega_f \delta_f$ is the probability that an I female transmit the AIDS virus to an S male.

Let the rate at which an infected mother does not transmitting the HIV virus to the newborn be β
Let the transition rate from infective to AIDS case be γ.
The changes of the population for Susceptible,Infected and AIDS cases assume Birth and Death process.

2. MOTHER-TO-CHILD TRANSMISSION MODELS

The purpose of this Section is to develop the Mother-to-child Transmission (MTCT) model. The study population consists of the pre-school age group (0-5 years), these are the children born of infected and susceptible mothers in group three (15 and more years). The population is divided into those children born free of HIV virus but can contract the virus from their mothers through breast milk (susceptibles), those who contact the virus from their infected mothers (infectives), and the former infectives who develop full blown symptoms (AIDS cases).

2.1. $S_1(t)$ SUSCEPTIBLE MODEL

The change in population size during the time interval $(t, t + \Delta t)$ is governed by the

following conditional probabilities;

$$\begin{aligned}
P_r\{S_1(t+\Delta t)=n+1/S_1(t)=n\} &= nS_3\lambda\Delta t + nI_3\beta\lambda\Delta t + o(\Delta t)\\
P_r\{S_1(t+\Delta t)\geq n+2/X(t)=n\} &= o(\Delta t)\\
P_r\{S_1(t+\Delta t)=n-1/S_1(t)=n\} &= np_1S_1 + nS_1\mu_1\Delta t + o(\Delta t)\\
P_r\{S_1(t+\Delta t)\leq n-2/S_1(t)=n\} &= o(\Delta t)\\
P_r\{S_1(t+\Delta t)=n/S_1(t)=n\} &= 1 - nS_3\lambda\Delta t - nI_3\beta\lambda\Delta t\\
&- np_1S_1 - nS_1\mu_1\Delta t - o(\Delta t)
\end{aligned}$$

Now

$$\begin{aligned}
\lambda_n(t) &= nS_3\lambda + nI_3\beta\lambda\\
\mu_n(t) &= np_1S_1 + nS_1\mu_1
\end{aligned}$$

then from the given rules we have the following Kolmogorov forward differential equations:

$$\begin{aligned}
S_{1_n}'(t) &= -[nS_3\lambda + nS_1\mu_1 + nI_3\beta\lambda + np_1S_1]S_{1n}(t)\\
&+ [(n-1)S_3\lambda + (n-1)I_3\beta\lambda]S_{1n-1}(t) \qquad \text{for n} \geq 1 \qquad (2.1)\\
&+ [(n+1)p_1S_1 + (n+1)S_1\mu_1]S_{1n+1}(t),
\end{aligned}$$

$$S_0'(t) = [p_1S_1 + S_1\mu_1]S_1(t), \quad \text{for n} = 0 \qquad (2.2)$$

where the primes indicate differentiation with respect to t. Using GF technique to solve the differential equation gives:

$$G_{S_1}(Z,t) = \left(\frac{\mu_S(e^{(\eta_S-\mu_S)t}-1) - (\mu_S e^{(\eta_S-\mu_S)t} - \eta_S)Z}{(\eta_S e^{(\eta_S-\mu_S)t} - \mu_S) - \eta_S Z(e^{(\eta_S-\mu_S)t}-1)}\right)^i \qquad (2.3)$$

This is the PGF of the differential equation (2.1)

By expanding the PGF we shall obtain the probability distribution $S_1(t)$.

Differentiating the PGF in (2.3) with respect to Z, we find the expectation and variance of $S_1(t)$:

$$E[S_1(t)] = i\frac{1-A(t)}{1-B(t)} = ie^{(\eta_S-\mu_S)t} \qquad (2.4a)$$

and

$$\begin{aligned}
\delta^2_{S_1} &= i\tfrac{(1-A(t))(A(t)+B(t))}{(1-B(t))^2}\\
&= i(\tfrac{\eta_S+\mu_S}{\eta_S-\mu_S})e^{(\eta_S-\mu_S)t}[e^{(\eta_S-\mu_S)t}-1]. \qquad (2.4b)
\end{aligned}$$

by taking the limits as $\mu_S \to \eta_S$ (where η_S is birth rate for both infected and Susceptible mothers) we find that

$$E[S_1(t)] = i \qquad (2.5a)$$

and

$$\delta^2_{S_1} = 2\eta_S t \qquad (2.5b)$$

Thus when $\eta_S = \mu_S$ the population size has a constant expectation but an increasing variance. Where

$$\eta_S = (S_3\lambda + I_3\beta\lambda)$$

and

$$\mu_S = (p_1 + \mu_1)S_1$$

2.2. $I_1(t)$(INFECTION) MODEL

The change in population size during the time interval $(t, t + \Delta t)$ is governed by the following conditional probabilities;

$$\begin{array}{lcl} P_r\{X(t+\Delta t) = n+1/X(t) = n\} & = & nI_3(1-\beta)_a\lambda\Delta t + o(\Delta t) \\ P_r\{X(t+\Delta t) \geq n+2/X(t) = n\} & = & o(\Delta t) \\ P_r\{X(t+\Delta t) = n-1/X(t) = n\} & = & nI_1\mu_1\Delta t + nI_1\gamma\Delta t + o(\Delta t) \\ P_r\{X(t+\Delta t) \leq n-2/X(t) = n\} & = & o(\Delta t) \\ P_r\{X(t+\Delta t) = n/X(t) = n\} & = & 1 - nI_3(1-\beta)_a\lambda\Delta t - nI_1\gamma\Delta t \\ & - & nI_1\mu_1\Delta t - o(\Delta t) \end{array}$$

Now

$$\begin{array}{lcl} \lambda_n(t) & = & nI_3(1-\beta)_a\lambda \\ \mu_n(t) & = & nI_1\gamma + nI_1\mu_1 \end{array}$$

Then from the given rules we have the following Kolmogorov forward differential equations:

$$\begin{array}{rcll} I_n'(t) & = & -[nI_1\mu_1 + nI_3(1-\beta)_a\lambda + nI_1\gamma]I_n(t) & \\ & + & [(n-1)I_3(1-\beta)_a\lambda+]I_{1n-1}(t) & \text{for n} \geq 1 \\ & + & [(n+1)I_1\gamma + (n+1)I_1\mu_1]I_{1n+1}(t), & \end{array} \tag{2.6}$$

$$I_0'(t) = [I_1\mu_1 + I_1\gamma]I_1(t), \quad \text{for n} = 0 \tag{2.7}$$

Where the primes indicate differentiation with respect to t. GF was used to solve the differential equations and the results are shown below:

$$G_{I_1}(Z,t) = \left(\frac{\mu_I(1-e^{(\eta_I-\mu_I)t}) - (\eta_I - \mu_I e^{(\eta_I-\mu_I)t}}{\mu_I - \eta_I e^{(\eta_I-\mu_I)t} - \eta_I Z(1-e^{(\eta_I-\mu_I)t})}\right) \tag{2.8}$$

This is the PGF of the differential equation (2.6)

. Now by simply expanding the PGF we obtain the probability distribution $I_1(t)$. Differentiating the PGF in (2.8) with respect to Z, we find the expectation and variance of $I_1(t)$:

$$E[I_1(t)] = \frac{1-B(t)}{1-C(t)} = e^{(\eta_I-\mu_I)t} \tag{2.9}$$

and

$$\begin{aligned}\delta^2_{I_1} &= \tfrac{(1-B(t))(B(t)+C(t))}{(1-C(t))^2} \\ &= (\tfrac{\eta_I+\mu_I}{\eta_I-\mu_I})e^{(\eta_I-\mu_I)t}[e^{(\eta_I-\mu_I)t}-1].\end{aligned} \tag{2.10}$$

by taking the limits as $\mu_I \to \eta_I$ (where η_I is birth rate for both infected and Susceptible mothers) we find that

$$E[I_1(t)] = 1$$

and

$$\delta^2_{I_1} = 2\eta_I t$$

Thus when the $\eta_I = \mu_I$, the population size has a constant expectation but an increasing variance. Where $\eta_I = I_3(1-\beta)_a\lambda$ and $\mu_I = I_1(\mu_I + \gamma)$

2.3. $A_1(t)$ (AIDS CASE) MODEL

The change in population size during the time interval $(t, t+\Delta t)$ is governed by the following conditional probabilities;

$$\begin{aligned}
P_r\{X(t+\Delta t) = n+1/X(t) = n\} &= nI_1\gamma\Delta t + o(\Delta t) \\
P_r\{X(t+\Delta t) \geq n+2/X(t) = n\} &= o(\Delta t) \\
P_r\{X(t+\Delta t) = n-1/X(t) = n\} &= nA_1\mu_1\Delta t + o(\Delta t) \\
P_r\{X(t+\Delta t) \leq n-2/X(t) = n\} &= o(\Delta t) \\
P_r\{X(t+\Delta t) = n/X(t) = n\} &= 1 - nI_1\gamma\Delta t - nA_1\mu_1\Delta t - o(\Delta t)
\end{aligned}$$

Now

$$\begin{aligned}\lambda_n(t) &= nI_1\gamma \\ \mu_n(t) &= nA_1\mu_1\end{aligned}$$

Then from the given rules we have the following Kolmogorov forward differential equations:

$$\begin{aligned}A'_{1_n}(t) &= -[nI_1\gamma + nA_1\mu_1]A_{1n}(t) \\ &+ [(nI_1\gamma]A_{1n-1}(t) \qquad \text{for n} \geq 1 \\ &+ (n+1)A_1\mu_1 A_{1n+1}(t),\end{aligned} \tag{2.11}$$

$$A'_0(t) = [A_1\mu_1]A_1(t), \quad \text{for n} = 0 \tag{2.12}$$

Where the primes indicate differentiation with respect to t. By using the GF technique to solve the differential equation gives:

$$G_{A_1}(Z,t) = 1$$

3. HETEROSEXUAL MODELS

In this section,we consider a population consisting of the adults(15 and more years). Since the age group 2 consists of HIV free population and it is the survivors of this subgroup over the developmental period (5,15) that generate age group 3, hence we include the survivors in the Susceptible model.

3.1. $S_3(t)$ MODEL

The change in population size during the time interval $(t, t+\Delta t)$ is governed by the following conditional probabilities;

$$\begin{array}{lcl} P_r\{S_3(t+\Delta t) = n+1/S_3(t) = n\} & = & p_2 S_2^* \Delta t + o(\Delta t) \\ P_r\{S_3(t+\Delta t) \geq n+2/S_3(t) = n\} & = & o(\Delta t) \\ P_r\{S_3(t+\Delta t) = n-1/S_3(t) = n\} & = & nS_3(\omega\delta + \mu_3)\Delta t + o(\Delta t) \\ P_r\{S_3(t+\Delta t) \leq n-2/S_3(t) = n\} & = & o(\Delta t) \\ P_r\{S_3(t+\Delta t) = n/S_3(t) = n\} & = & 1 - p_2 S_2^* \Delta t - nS_3(\omega\delta + \mu_3)\Delta t \\ & - & o(\Delta t) \end{array}$$

Now

$$\lambda_n(t) = p_2 S_2^* \Delta t$$

$$\mu_n(t) = nS_3(\omega\delta + \mu_3)\Delta t$$

Then from the given rules we get the following Kolmogorov forward differential equations:

$$\begin{array}{lcll} S_{3_n}'(t) & = & -[p_2 S_2^* + nS_3(\omega\delta + \mu_3)]S_{3n}(t) & \\ & + & p_2 S_2^* S_{3n-1}(t) & \text{for n} \geq 1 \\ & + & (n+1)S_3(\omega\delta + \mu_3)S_{3n+1}(t), & \end{array} \tag{3.1}$$

$$S_0'(t) = -p_2 S_2^* S_{30}(t) + S_3(\omega\delta + \mu_3)S_{31}(t), \quad \text{for n} = 0 \tag{3.2}$$

where the primes indicate differentiation with respect to t. Using Gf technique we get:

$$\begin{array}{lcl} G_{S_3}(Z,t) & = & \left(1 + (Z-1)e^{-S_3(\omega\delta+\mu_3)t}\right)^i \\ & \{ & exp\{-(\frac{p_2 S_2^*}{s_3(\omega\delta+\mu_3)})(Z-1)(e^{-S_3(\omega\delta+\mu_3)t} - 1)\}\} \end{array} \tag{3.3}$$

Now it is a simple matter of expanding the PGF to obtain the probability distribution $S_3(t)$.

Differentiating the PGF in equation (3.3) with respect to Z, we find the expectation and variance of $S_3(t)$:

$$E[S_3(t)] = \frac{p_2 S_2^*}{s_3(\omega\delta + \mu_3)}(1 - e^{-S_3(\omega\delta+\mu_3)t}) + ie^{-S_3(\omega\delta+\mu_3)t} \tag{3.4}$$

and

$$\delta^2(S_3(t)) = ie^{-S_3(\omega\delta+\mu_3)t}[1 - e^{-S_3(\omega\delta+\mu_3)t}] + \frac{p_2 S_2^*}{s_3(\omega\delta + \mu_3)}[1 - e^{-S_3(\omega\delta+\mu_3)t}] \tag{3.5}$$

3.2. $I_3(t)$ (INFECTED) MODEL

The change in population size during the time interval $(t, t + \Delta t)$ is governed by the following conditional probabilities;

$$\begin{array}{lcl}
P_r\{I_3(t+\Delta t) = n+1/I_3(t) = n\} & = & +nI_3\omega\delta\Delta t + o(\Delta t) \\
P_r\{I_3(t+\Delta t) \geq n+2/I_3(t) = n\} & = & o(\Delta t) \\
P_r\{I_3(t+\Delta t) = n-1/I_3(t) = n\} & = & nI_3\mu_3\Delta t + nI_3\gamma\Delta t + o(\Delta t) \\
P_r\{I_3(t+\Delta t) \leq n-2/I_3(t) = n\} & = & o(\Delta t) \\
P_r\{I_3(t+\Delta t) = n/I_3(t) = n\} & = & 1 - nI_3\omega\delta\Delta t - nI_3\gamma\Delta t - nI_3\mu_3\Delta t - o(\Delta t)
\end{array}$$

Now

$$\begin{array}{lcl}
\lambda_n(t) & = & nI_3\omega\delta \\
\mu_n(t) & = & nI_3(\gamma\delta + \mu_3)\Delta t
\end{array}$$

Then from the given rules we get the difference equations:

$$\begin{array}{rcll}
I_n'(t) & = & -[nI_3\mu_3 + nI_3\omega\delta + nI_3\gamma]I_n(t) & \\
& + & [(n-1)I_3\omega\delta+]I_{n-1}(t) & \text{for n} \geq 1 \\
& + & [(n+1)I_3(\gamma + \mu_3)]I_{n+1}(t), &
\end{array} \tag{3.6}$$

$$I_0'(t) = [I_3\mu_3 + I_3\gamma]I_3(t), \quad \text{for n} = 0 \tag{3.7}$$

where the primes indicate differentiation with respect to t. With the application of GF technique we have:

$$G_{I_3}(Z,t) = \left(\frac{(\eta Z - \nu) + \nu(1-Z)e^{(\eta-\nu)t}}{(\eta Z - \nu) + \eta(1-Z)e^{(\eta-\nu)t}}\right) \tag{3.8}$$

We let

$$\alpha_(t) = \nu\frac{1 - e^{(\eta-\nu)t}}{\nu - \eta e^{(\eta-\nu)t}}$$

and

$$\omega(t) = \frac{\eta}{\nu}\alpha_(t)$$

Hence equation (4.8) becomes

$$G_{I_3}(Z,t) = \left(\frac{\alpha_(t) + [1-\alpha_(t) - \omega(t)]Z}{1-\omega(t)Z}\right) \tag{3.9}$$

This is the PGF of the differential equation (3.1)

Now it is a simple matter of expanding the PGF to obtain the probability distribution $I_3(t)$.

Differentiating the PGF in (3.9) with respect to Z, we find the expectation and variance of $I_3(t)$:

$$\begin{aligned} E[I_3(t)] &= \frac{1-\alpha_(t)}{1-\omega(t)} \\ &= e^{(\eta-\nu)t} \end{aligned} \tag{3.10}$$

and

$$\begin{aligned} \delta^2_{I_3} &= \frac{(1-\alpha_(t))(\alpha_(t)+\omega(t))}{(1-\omega(t))^2} \\ &= (\frac{\eta+\nu}{\eta-\nu})e^{(\eta-\nu)t}[e^{(\eta-\nu)t}-1]. \end{aligned} \tag{3.11}$$

by taking the limits as $\nu \to \eta$ (where η is birth rate for both infected and non infected mothers) we find that

$$E[I_3(t)] = 1$$

and

$$\delta^2_{I_3} = 2\eta t$$

Thus when the birth rate is equal to the death rate, the population size has a constant expectation but an increasing variance.

3.3. $A_3(t)$ (AIDS CASE) MODEL

The change in population size during the time interval $(t, t+\Delta t)$ is governed by the following conditional probabilities;

$$\begin{aligned} P_r\{A_3(t+\Delta t) = n+1/A_3(t) = n\} &= nI_3\gamma\Delta t + o(\Delta t) \\ P_r\{A_3(t+\Delta t) \geq n+2/A_3(t) = n\} &= o(\Delta t) \\ P_r\{A_3(t+\Delta t) = n-1/A_3(t) = n\} &= nA_3\mu_3\Delta t + o(\Delta t) \\ P_r\{A_3(t+\Delta t) \leq n-2/A_3(t) = n\} &= o(\Delta t) \\ P_r\{A_3(t+\Delta t) = n/A_3(t) = n\} &= 1 - nI_3\gamma\Delta t - nA_3\mu_3\Delta t - o(\Delta t) \end{aligned}$$

Now

$$\begin{aligned} \lambda_n(t) &= nI_3\gamma \\ \mu_n(t) &= nA_3\mu_3 \end{aligned}$$

Then from the given rules we get the Kolmogorov forward diffential equations:

$$\begin{aligned} A'_{1n}(t) &= -[nI_3\gamma + nA_3\mu_3]A_{1n}(t) \\ &+ [(nI_3\gamma]A_{1(n-1)}(t) \qquad \text{for n} \geq 1 \\ &+ (n+1)A_3\mu_3 A_{1(n+1)}(t), \end{aligned} \tag{3.12}$$

$$A'_0(t) = [A_3\mu_3]A_3(t), \quad \text{for n} = 0 \tag{3.13}$$

Where the primes indicate differentiation with respect to t. solving these equations by GF technique we have:

$$G_{A_3}(Z,t) = 1$$

4. COMBINED MODELS

In this section,we consider a model which combines both the two modes of transmission (that is, Heterosexual transmission and the Mother-to-child transmission (MTCT) and the age groups. The population is subdivided into Susceptibles, Infectives and AIDS cases. We assume that there is homogeneous mixing among S persons and I persons.

4.1. $S(t)$ MODEL

The probability that there are n individuals in the Susceptible population during the time interval $(t, t+\Delta t)$ is equal to the probability;

(i)That there are n individuals by time t and nothing happens during the time interval $(t, t+\Delta t)$

(ii)That there are $n-1$ individuals by time t and 1 is added by immigration or birth during the time interval $(t, t+\Delta t)$

(iii) That there are $n+1$ individuals by time t and 1 dies, contracts the HIV virus or migrates from the population during the time interval $(t, t+\Delta t)$

The change in population size during the time interval $(t, t+\Delta t)$ is governed by the following conditional probabilities;

$$\begin{aligned} P_r\{X(t+\Delta t) = n+1/X(t) = n\} &= \alpha\Delta t + nS_3\lambda\Delta t + nI_3\beta\lambda\Delta t + o(\Delta t) \\ P_r\{X(t+\Delta t) \geq n+2/X(t) = n\} &= o(\Delta t) \\ P_r\{X(t+\Delta t) = n-1/X(t) = n\} &= nS_k\mu_k\Delta t + nI_3\omega\delta\Delta t + o(\Delta t) \\ P_r\{X(t+\Delta t) \leq n-2/X(t) = n\} &= o(\Delta t) \\ P_r\{X(t+\Delta t) = n/X(t) = n\} &= 1 - nS_3\lambda\Delta t - \alpha\Delta t - nI_3\beta\lambda\Delta t \\ &- nS_k\mu_k\Delta t - nI_3\omega\delta\Delta t - o(\Delta t) \end{aligned}$$

Let the probability distribution of the population size at time t be denoted by

$S_n(t) = P_r\{S(t) = n/S(0) = m\}$, $m < n$ and $m = 0, 1, ...$

We seek to find this distribution by deriving a system of differential equations from the assumptions above. Now

$$\begin{aligned} \lambda_n(t) &= nS_3\lambda + \alpha + nI_3\beta\lambda \\ \mu_n(t) &= nS_k\mu_k + nI_3\omega\delta \end{aligned}$$

Then from the given rules we have the following Kolmogorov forward diffrential equations:

$$\begin{aligned} S_n'(t) &= -[nS_3\lambda + \alpha + nS_k\mu_k + nI_3\beta\lambda + nI_3\omega\delta]S_n(t) \\ &+ [\alpha + (n-1)S_3\lambda + (n-1)I_3\beta\lambda]S_{n-1}(t) \qquad \text{for n} \geq 1 \qquad (4.1) \\ &+ [(n+1)S_k\mu_k + (n+1)I_3\omega\delta]S_{n+1}(t), \end{aligned}$$

$$S_0'(t) = -\alpha S_0(t) + [S_k\mu_k + I_3\omega\delta]S_1(t), \quad \text{for n} = 0 \qquad (4.2)$$

where the primes indicate differentiation with respect to t.

Using the Generating Function technique we arrive at the generating function, expectation and Variance of the Susceptible persons.

$$G(Z,t) = \frac{(\eta-\nu)^{\alpha/\eta}[(\nu e^{(\eta-\nu)t} - \nu) - Z(\nu e^{(\eta-\nu)t} - \eta)]^m}{[(\eta e^{(\eta-\nu)t} - \nu) - \eta Z(e^{(\eta-\nu)t} - 1)]^{\alpha/\eta+m}} \qquad (4.3)$$

Differentiating the PGF in (4.3) with respect to Z, we find the expectation and variance of $S(t)$:

$$E[S(t)] = me^{(\eta-\nu)t} + \alpha\frac{e^{(\eta-\nu)t} - 1}{(\eta-\nu)} \qquad (4.4)$$

and

$$\delta_S^2 = m(\frac{\eta+\nu}{\eta-\nu})e^{(\eta-\nu)t}[e^{(\eta-\nu)t} - 1] + \alpha\frac{e^{(\eta-\nu)t} - 1}{(\eta-\nu)}. \qquad (4.5)$$

Where $\eta = ((S_3\lambda + I_3\beta\lambda)$ and $\nu = (S_k\mu_k + I_3\omega\delta)$.

4.2. $I(t)$ MODEL

The change in population size during the time interval $(t, t+\Delta t)$ is governed by the following conditional probabilities;

$$\begin{aligned} P_r\{X(t+\Delta t) = n+1/X(t) = n\} &= \alpha\Delta t + nI_3(1-\beta)_a\lambda\Delta t + nI_3\omega\delta\Delta t + o(\Delta t) \\ P_r\{X(t+\Delta t) \geq n+2/X(t) = n\} &= o(\Delta t) \\ P_r\{X(t+\Delta t) = n-1/X(t) = n\} &= nI_k\mu_k\Delta t + nI_3\gamma\Delta t + o(\Delta t) \\ P_r\{X(t+\Delta t) \leq n-2/X(t) = n\} &= o(\Delta t) \\ P_r\{X(t+\Delta t) = n/X(t) = n\} &= 1 - nI_3(1-\beta)_a\lambda\Delta t - \alpha\Delta t \\ &- nI_3\gamma\Delta t - nS_k\mu_k\Delta t - nI_3\omega\delta\Delta t \end{aligned}$$

Now

$$\begin{aligned}\lambda_n(t) &= \alpha + nI_3(1-\beta)_a\lambda \\ \mu_n(t) &= nI_k\mu_k + nI_3\gamma\end{aligned}$$

Then from the given rules we get the following Kolmogorov forward diffrential equations:

$$\begin{aligned}I_n'(t) &= -[nI_k\mu_k + \alpha + nI_3(1-\beta)_a\lambda + nI_3\omega\delta + nI_3\gamma]I_n(t) \\ &+ [(n-1)I_3(1-\beta)_a\lambda + (n-1)I_3\omega\delta + \alpha]I_{n-1}(t) \qquad \text{for n} \geq 1 \\ &+ [(n+1)I_3\gamma + (n+1)I_k\mu_k]I_{n+1}(t),\end{aligned} \tag{4.6}$$

$$I_0'(t) = -\alpha I_0(t) + [I_k\mu_k + I_3\gamma]S_1(t), \quad \text{for n} = 0 \tag{4.7}$$

Applying the Generating function technique we have:

$$G(Z,t) = \frac{(\kappa-\rho)^{\alpha/\rho}[\kappa e^{(\rho-\kappa)t} - 1) - Z(\kappa e^{(\rho-\kappa)t} - 1)]}{[(\rho e^{(\rho-\kappa)t} - \kappa - \rho Z(e^{(\rho-\kappa)t} - 1)]^{1+\alpha/\rho}} \tag{4.8}$$

Differentiating the PGF in (4.8) with respect to Z, we find the expectation and variance of $S(t)$:

$$E[S(t)] = e^{(\rho-\kappa)t} + \alpha\frac{e^{(\rho-\kappa)t} - 1}{(\rho-\kappa)} \tag{4.9}$$

and

$$\delta_S^2 = (\frac{\rho+\kappa}{\rho-\kappa})e^{(\rho-\kappa)t}[e^{(\rho-\kappa)t} - 1] + \alpha\frac{e^{(\rho-\kappa)t} - 1}{(\rho-\kappa)}. \tag{4.10}$$

where $\rho = ((1-\beta)_a\lambda + \omega\delta)$ and $\kappa = (\mu_k + \gamma)$.

4.3. $A(t)$ MODEL

The change in population size during the time interval $(t, t+\Delta t)$ is governed by the following conditional probabilities;

$$\begin{aligned}P_r\{X(t+\Delta t) = n+1/X(t) = n\} &= \alpha\Delta t + nI\gamma\Delta t + o(\Delta t) \\ P_r\{X(t+\Delta t) \geq n+2/X(t) = n\} &= o(\Delta t) \\ P_r\{X(t+\Delta t) = n-1/X(t) = n\} &= nA\mu_k\Delta t + o(\Delta t) \\ P_r\{X(t+\Delta t) \leq n-2/X(t) = n\} &= o(\Delta t) \\ P_r\{X(t+\Delta t) = n/X(t) = n\} &= 1 - nA\mu_k\Delta t - \alpha\Delta t \\ &- nI\gamma\Delta t - o(\Delta t)\end{aligned}$$

Now

$$\begin{aligned}\gamma_n(t) &= nI\gamma + \alpha \\ \mu_n(t) &= nA\mu_k\end{aligned}$$

Then from the given rules we get the following Kolmogorov forward differential equations:

$$\begin{aligned} A_n'(t) &= -[nA\mu_k + \alpha + nI\gamma]A_n(t) \\ &+ [\alpha + (n-1)I\gamma]A_{n-1}(t) \qquad \text{for n} \geq 1 \\ &+ A\mu_k(n+1)A_{n+1}(t), \end{aligned} \tag{4.11}$$

$$A_0'(t) = -\alpha A_0(t) + A\mu_k A_1(t), \quad \text{for n} = 0 \tag{4.12}$$

Where the primes indicate differentiation with respect to t With the application of GF technique we arrive at:

$$G(Z,t) = \Big(\frac{I\gamma - A\mu}{I\gamma e^{(I\gamma - A\mu)t} - A\mu}\Big)^{\alpha/I\gamma}\Big[1 - \frac{ZI\gamma(e^{(I\gamma - A\mu)t} - 1)}{I\gamma e^{(I\gamma - A\mu)t} - A\mu}\Big]^{-\alpha/I\gamma} \tag{4.13}$$

This is a negative binomial distribution, with

$$p = \Big(\frac{I\gamma - A\mu}{I\gamma e^{(I\gamma - A\mu)t} - A\mu}\Big)$$

and

$$r = \alpha/I\gamma$$

It is of some interest to consider the limiting form of equation (4.13) when $I\gamma < A\mu$ and the time t tends to infinity. The limiting generating function is

$$G(Z,t) = (1 - I\gamma/A\mu)^{\alpha/I\gamma}(1 - I\gamma Z/A\mu)^{-\alpha/I\gamma}$$

and so the mean population size for large t is

$$\frac{\alpha}{(A\mu - I\gamma)}$$

This is related to the stable distribution of population which immigration can just maintain against the excess of $A\mu$ over $I\gamma$.

The variance of the population size for large t is

$$\frac{\alpha A\mu}{(I\gamma - A\mu)^2}$$

When $A\mu = 0$, (that is, when there are only births and immigration and new infections) it is clear from equation (4.1) that the distribution will still be negative binomial for every finite value of t.

$$G(Z,t) = I\gamma^{\alpha/I\gamma}\Big[1 - Z(1 - e^{-I\gamma t})\Big]^{-\alpha/I\gamma}$$

On the hand, when $I\gamma = 0$,(that is, when there is immigration , emigration and HIV infection)where emigration and HIV infection depends on the population, the distribution assumes a Poisson process.

$$G(Z,t) = e^{\left\{\frac{\alpha}{A\mu}(1-e^{-A\mu t})(Z-1)\right\}}$$

When $t \to \infty$, it gives

$$G(Z) = e^{\{\frac{\alpha}{A\mu}(Z-1)\}}$$

When $I\gamma = 0, A\mu = 0$ (that is, when there is only immigration), the distribution assumes a Poisson process with parameter αt.

$$G(Z,t) = e^{\alpha t(Z-1)}$$

5. CONCLUDING REMARKS

In this paper, we developed HIV/AIDS epidemic models by using Generating functions (GF). We came up with a conceptual framework which summarizes all the concepts of HIV/AIDS transmission models. Stochastic models based on Mother to child transmission(MTCT), Heterosexual transmission and Combined models were developed. By using the stochastic models formulated, we have also demonstrated how various factors affect the expectations of susceptible and infective persons. It is shown from the combined model that Mother to Child transmission and Heterosexual models are special cases of the Combined model. However, in the process of achieving our goals, some problems were encountered; based on the initial condition, it was found that when the initial condition is assumed to be zero (0), in the case of AIDS case, most of the models showed that the Generating function is one (1), this area need further investigation.

References

[1] Anderson, R.M. and May, R.M. (1991): Infectious Diseases of Humans: Dynamics and Control. Oxford University Press, Oxford, UK.

[2] Anderson, R.M. and May, R.M. (1987): "Transmission dynamics of HIV infection", Nature 326, 137-142

[3] Anderson, R.M. , May, R.M. and McLean, A.R. (1988): "Possible demographic consequences of HIV/AIDS epidemics in developing countries", Nature 332,228-234

[4] Anderson, R.M. , May, R.M.,Medley, G.F. and Johnson, A.M. (1986): "A preliminary study of the transmission dynamics of the immunodeficiency virus (HIV)", the causative agent of AID *IMA Journal of Mathematics Applied in Medicine and Biology* 3, 229-263

[5] Anderson, Roy. (1992): "The transmission dynamics of sexually transmitted diseases": The behavor components **pp 23-48** in sexual Behavor and networking: Antropological and socio-cultural studies on the transmission of HIV.

[6] Austin, D.J. and Anderson, R.M. (1999): "Studies of antibiotic resistance within the patient, hospitals and the community using simple mathematical models", *Phil. Trans. R. Soc.* Lond. 354, 721-738.

[7] Bailey(1975): Mathematics for infectious diseases

[8] Bartlett, M.S. (1960): Stochastic Population Models in Ecology and Epidemiology. Methuen, London, UK.

[9] Becker, N.G. (1989): "Analysis of Infectious Disease Data". Chapman and Hall, London.

[10] Chiang,C.L. (1980): An introduction to stochastic processes 2^{nd} edition, Krieger, Newyork.

[11] Hethcote,W.H.(1989): A model for HIV transmission and AIDS. University of Iowa, Iowa City, IA 52242, USA.

[12] Luboobi L.S.(1991): Mathematical models for the dynamics of the AIDS epidemic, in Biometry for Development pp. 76-83, ICIPE Science Press, Nairobi.

[13] Luboobi L.S.(1994): A three Age-group model for HIV/AIDS epidemic and Effects of medical /social interventions" *Mathematical Computational Modeling*, **19**, 91-105.

[14] Muench, H. (1959): "Catalytic Models in Epidemiology". Harvard University Press, Cambridge, USA.

[15] S.self and Y. Panitan (1991): "Modeling a marker of disease progression and onset of disease". University of California. Berkeley,

[16] Woolhouse, M.E.J., Haydon, D.T. and Bundy, D.A.P. (1997): "The design of veterinary vaccination programmes". *Vet. Journal* 153, 41-47.