USE OF GENERATING FUNCTIONS

IN

HIV/AIDS TRANSMISSION MODELS

BY

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DECLARATION

I certify that this project does not incorporate without acknowledgment any material previously submitted for a degree or diploma in any universities; and that to the best of my knowledge and belief it does not contain any material previously published or written by another person except where due reference is made in the text.

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DEDICATION

Dedicated to my brother; Tim, mother; Agnes

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Abstact

This study is concerned with the mathematical modeling for human immunodefi ciency virus (HIV) transmission epidemics. The mathematical models are specified by stochastic differential equations. The differential equations are solved by use of Generating Functions (GF).In the process of literature review, a conceptual framework is drawn which summarizes the literature on HIV/AIDS transmission epidemic models. 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) are developed and the expectations and variances of Susceptible (S) persons, Infected (I) persons and AIDS cases found. It is shown from the combined model that MTCT and Heterosexual models are special cases of the combined model.

General aspects of modeling HIV/AIDS are described in chapter 1, Chapter 2 focuses on the literature review. MTCT model is formulated in chapter 3. Heterosexual model is developed in chapter 4, Chapter 5 focuses on the development of the Combined model. Chapter 6 concludes the study.

Chapter 1

GENERAL INTRODUCTION

1.1 BACKGROUND OF THE STUDY

This chapter deals with the general introduction of HIV/AIDS and how it is spread. Generating function (GF) which is the main tool used to solve the differential equations derived in the study is introduced in this chapter. several Epidemic models are also introduced in this chapter.

1.1.1 Introduction

Mathematical modeling plays an essential role in bridging the gap between the mathematical theory and public health practice, and it is this aspect that motivates the present discussion. We attempt to promote the use of mathematical modeling that provides practical insight and guidance for the disease control, with emphasis on identifying issues that have not been addressed adequately. While deterministic models can serve as a guide towards parameter estimates,the need to quantify the precision of estimates and the variation in data imply that stochastic models are the natural basis for the analysis of infectious disease data. The approach to modeling HIV/AIDS is to

use HIV transmission dynamics models which include the progression to AIDS. These models often have the population divided into compartments consisting of those who are Susceptible(persons without the HIV virus), infected but without symptoms and those who have developed the full blown symptoms (it can take around 7-10 years to develop full blown AIDS symptoms after infection with HIV). In deterministic transmission models, the movements between these compartments by becoming infected, progressing to the next stage or AIDS, migrating or dying are specified by systems of difference or differential equations. Some HIV transmission dynamics models are stochastic with probabilities of moving to the next stage at each time step. The study of HIV/AIDS requires various aspects of academic disciplines. Developing mathematical modeling is therefore important in understanding or explaining the progression of HIV from Susceptible to infective and then to AIDS case (those who have developed full blown AIDS symptoms).

1.1.2 Modes of HIV/AIDS Transmission

Introduction

The last ten years has witnessed a veritable explosion of research on disease called acquired immunodificiency syndrome (AIDS) that was first identified in the summer of 1981 in USA. We realize that a large range of problems remain to be resolved. Understanding and controlling the H I V epidemic is a paticularly difficult challenge .The long and variable period between H I V infection and clinical diseases makes it difficult both to forecast the future magnitude of the epidermic , which is important for health care planning , and to estimate the number infected in the last several years , which is equally important for monitoring the current status of the epidemic. In such a situation mathematical and statistical modeling are of help. HIV is transmitted through shared bodily fluid such as semen and vaginal fluids, infected blood and blood products.

Modes of transmission

Sexual Transmission

Sexual Transmission is the most important mode of transmission of AIDS infection and accounts for 75 percent of cases of AIDS globally. AIDS could be transmitted by both heterosexual and homosexual transmission.

•Heterosexual intercourse

Heterosexual transmission is the dominant mode of transmission of AIDS infection in Asia and Africa. The current worldwide expansion of the AIDS epidemic is primarily driven by the sexual transmission of human immunodeficiency virus (HIV), and its future will be determined largely by the degree to which sexual transmission can be reduced.

•Homosexual intercourse

Homosexual transmission of AIDS is another mode of sexual transmission and occurs when a male has anal intercourse with another male. As this virus is carried in the semen, if one male is already having AIDS, the second male contacts this disease. This mode of transmission is more common in Europe and United States as compared to Asia and Africa.

Transfusion of infected blood or blood products

This occurs when infected HIV positive blood is transfused into a normal patient. Many blood products in common use today such as platelet concentrates, factor VIII concentrate, etc. also can transmit the virus. Therefore it is important to screen all blood for presence of HIV before transfusion is given. Transfusions are given to increase the blood's ability to carry oxygen, restore the body's blood volume, improve immunity, and correct clotting problems.The transfusion of blood can transmit an infectious disease carried in the donor's blood. That's why health officials have stepped

up their screening of blood donors and made blood testing more thorough. Today, all blood donations are tested for viral hepatitis, AIDS, syphilis, and selected other viruses. There is a very high probability of infection through the transmission of blood and other blood products if the original product is HIV-infected. Thus the rate of transition from uninfected to infected depends upon the number of transfusions received by a person and the conditional probability that if a transfusion takes place it involves infected blood or blood products. The probability of becoming infected during the time interval $(t, t + \Delta t)$ is proportional to the fraction of the total population eligible for blood donation who are infected. Blood transfusion now is very rarely in countries where blood is screened for HIV antibodies)

Vertical transmission (Mother-to-child)

Mother-to-child transmission (MTCT) is by far the largest source of HIV infection in children under the age of 15.In the absence of preventive intervention, the probability that an HIV-positive woman's baby will become infected ranges from 15% to 25% in industrialized countries and 25% to 35% in developing countries. The virus may be transmitted to the newborn babies during pregnancy(foetus), labor, delivery(in utero) (through contamination by blood or other fluids during birth), or after the child's birth during breastfeeding. Among infected infants who are not breastfed, about two-thirds of cases of MTCT occur around the time of delivery and the rest during the pregnancy (mostly during the last 2 months). In populations where breastfeeding is the norm, it accounts for more than one-third of all transmission.Thus the rate of transmission from uninfected to infected depends upon the health status of the mother and the conditional probability that an infected mother will transmit the virus to either the foetus or newborn in utero, during or shortly after delivery.

Intravenous (IV) drug users

These comprise an important group in the chain of transmission of HIV. Drug users usually inject a variety of substances into the blood and often use or share the same

needle. If any one of the drug users has HIV, this virus is transmitted to all those who use the same syringe and needle. Also as the drug users get infected and they pass this infection to their spouse. Thus a male drug abuser who has AIDS can infect his wife, she in turn infects the children born after she has contracted AIDS. Thus the whole family could be involved, if either the husband or wife abuses drugs. The children born before the wife is infected will not develop AIDS by mother to child transmission; only those children born after the wifes infection acquire HIV from their mother. This is discussed in detail below (mother to infant transmission).

1.1.3 Generating functions (GF)

Generating functions are important tools for some areas of applied probability and statistics. since GF is going to be the core tool in this study, it is in order to describe it briefly.

The method of generating functions is one of the most important analytic tools in the study of stochastic processes with discrete sample spaces. It has been used in differential and integral calculus and in combinatorial analysis. The generating function of an integer-valued random variable completely determines its probability distribution and provides convenient ways to obtain the moments of the distribution. Furthermore, certain important relations among random variables may be simply expressed in terms of generating functions. In population studies, the generating function technique has been used to study life tables, the effects of family size under various controlling conditions, the survival of family names, kinship theory, stable population theory, the impact of family planning programmes on fertility, the human reproduction process, etc. Use of Generating functions has also been made in studying group-screening designs with random group-sizes and with repeated testing.

Definition

let $a_0, a_1, a_2, \ldots$ be a sequence of real numbers. If $A(s) = a_1 + a_2 s^2 + a_3 s^3 + \ldots = \sum_{k=0}^{\infty} a_k s^k$ converges/exists in some interval $-s_0 < s < s_1$, then

$$A(s) = \sum_{k=0}^{\infty} a_k s^k \tag{1.1}$$

is called the Generating function of the sequence $\{a_k\}$.

Probability Generating Function(PGF)

Definition

Probability generating function (pgf) is a special case of a generating function.

Let the sequence $\{a_k\}$ satisfy the following two conditions:

(i) $0 \leq a_k \leq 1$

(ii) $\sum_{k=0}^{n} a_k = 1$

This means that $\{a_k\}$ is a probability mass function. Then the corresponding $A(s)$ is called a probability generating function of $\{a_k\}$.

Mean and Variance of generating functions

getting the derivative of equation (1.1) we have

$$A'(s) = \sum_{k=0}^{\infty} k a_k s^{k-1}$$

Putting $s = 1$ we have

$$A'(1) == \sum_{k=0}^{\infty} k a_k = E(X)$$

This is the expectation of the distribution.

To obtain variance of X we have to add $E(X) - E^2(X)$ which leads us to

$$var(X) = A''(1) + A'(1) - A'^2(1)$$

1.1.4 Partial Differential Equations (PDE)

The partial differential equations encountered in this project are linear differential equations of the first order with two independent variables. The typical equation

involving two independent variables is

$$P\frac{\delta z}{\delta x} + Q\frac{\delta z}{\delta y} = R \tag{1.2}$$

subject to appropriate secondary conditions, where P, Q, and R are functions of x,y, and z. Corresponding to (1.2), there are two ordinary differential equations, known as auxiliary or subsidiary equations

$$\frac{dx}{P} = \frac{dy}{Q} = \frac{dz}{R} \tag{1.3}$$

any function $u(x, y, z) = constant$ or $v(x, y, z) = constant$ that satisfies (1.3) is also a solution of (1.2). Therefore, instead of solving the partial differential equation directly, we solve the ordinary differential equations. To obtain the general solution, we make one constant a function of the other, that is,

$$u = \phi(v)$$

the particular solution is determined by the appeal to the initial boundary conditions.

1.1.5 Epidemic models

Introduction

It is in order to briefly review the basic ideas involved in the epidemiology of infectious diseases before we discuss HIV/AIDS transmission models.
to begin with we suppose that we have a group of Susceptible (non-infected)individuals all mixing homogeneously together. One or more from this group then contracts a certain infectious disease which may in due course be passed on to the other Susceptibles.

In general we assume that after the receipt of infectious material, there is a latent period during which the disease develops purely internally within the infected person. The latent period is followed by an infectious period, during which the infected person or infective as he is then called, is able to dicharge infectious matter in some way and possibly communicate to other susceptibles. Sooner or later the symptoms appear in the infective and he is removed from circulation amongst the Infectives until he either dies or recovers. This removal brings the infectious period effectiveness or an end(at least so far as the possibility of spreading the disease is concerned). The time interval between the receipt of the infection and the appearance of symptoms is the incubation period.

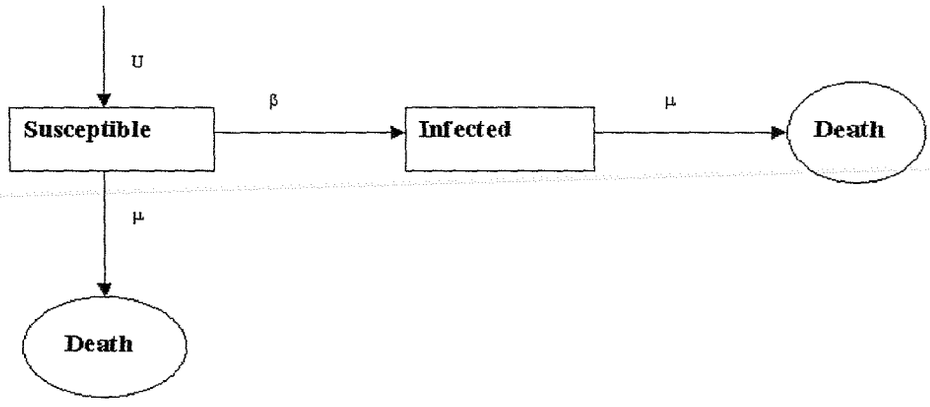
The Epidemiology of infectious diseases

A number of epidemic models have been developed for various infectious diseases. With the emergence of HIV/AIDS, it has been necessary to re-examine these models so as to come up with appropriate models for HIV/AIDS transmission. A brief description of these models follow:

I. SI Models with vital dynamics

In this model,the study population in SI model is divided into two compartments; Susceptibles (S):-those persons who are free of the disease but can contract it from an infected person, and Infectives (I):- those persons who have the disease and can pass it on to susceptible persons. In the simple SI model with no cure, everyone eventually gets the disease no matter what treatment strategy is applied. The infected is assumed to die.

Figure 1.1: SI model



The equations for SI models with vital dynamics are:

$$\begin{aligned} dS/dt &= U - \mu S - \beta S, \\ dI/dt &= \beta S - \mu I, \end{aligned}$$

where $N = S + I$

$$\beta = \frac{\lambda c S I}{N}$$

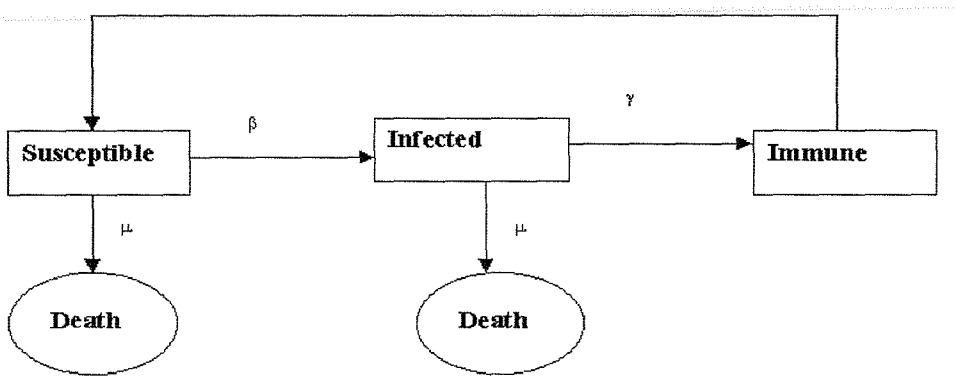
Application of the SI model is in Influenza disease spread, where the model divides the population into two groups:Susceptibles or those who may contract the disease, and infecteds or those infected and experiencing severe symptoms.

II. SIS Models with vital dynamics

This model is an improvement of the SI model. it is not true for all diseases that infected persons die, in most diseases, the infected recover and again they become susceptibles. The study population is divided into two classes; Susceptible and Infected in which susceptibles (S) become infected (I) and recover without immunity and so are again susceptible. Assume S are the susceptibles and I are the infecteds and infectious individuals. The connectivity diagram is as shown below. The rate of recovery per infected is γ, a constant and the rate coefficient for infection, called the force of infection β, where

$$\beta = \lambda c$$

Figure 1.2: SIS model



The equations for SIS model are given by:

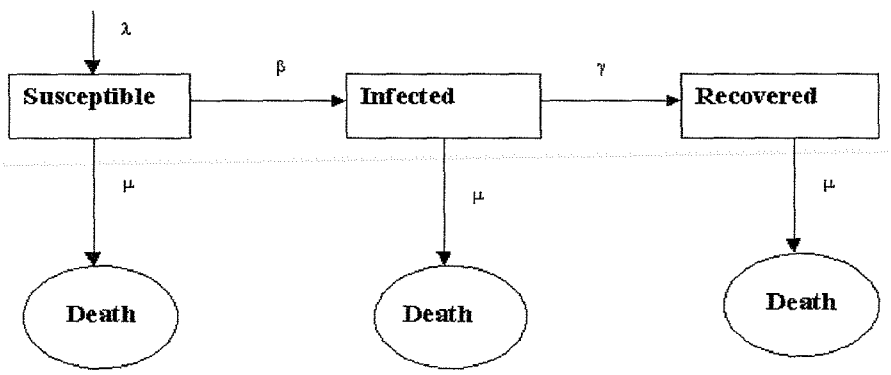
$$\begin{aligned} dS/dt &= U - \mu S - \beta IS/N, \\ dI/dt &= \beta IS/N - \mu I - \gamma I \end{aligned}$$

where $S(t)$, and $I(t)$ are the numbers in these classes, so that $S(t) + I(t) = N(t)$ Application of this model SIS is in the spread of Gonorrhea, where the model divides the population into two groups: susceptibles or those who may contract the disease, infecteds or those infected and experiencing severe symptoms,the infecteds recover without immunity and so are again susceptible.

III. SIR Model with vital dynamics

The most fundamental mathematical model of the spread of disease is the susceptible/ infective/recovered or SIR model. In this model a population is divided into three classes according to their status in relation to the disease of interest: susceptible (S), meaning they are free of the disease but can catch it, infective (I), meaning they have the disease and can pass it on to others, and recovered (R), meaning they have recovered from the disease and can not longer pass it on. There is a fixed probability per unit time that an infective individual will pass the disease to a susceptible individual with whom they have contact, rendering that individual infective. Individuals who contract the disease remain infective for a certain time period before recovering and losing their infectivity. This model is a bit more complicated in that there is a constant recruitment of new susceptibles at rate U and there is a background mortality rate coefficient,μ , which is the same for susceptibles, infecteds and immunes, i.e. there are no extra deaths due to the disease. The force of infection,λ , is a function of X, Y and Z. We shall use the SIR model to show how one writes the equations and then use it to develop some of the most important ideas in the epidemiology of infectious diseases. Suppose each susceptible makes c contacts per unit of time that are of the disease transmitting type. Then the susceptibles make cS contacts per unit time. Assume the contacts are at random with members of the total population, N=S+I+R. Then only the fraction I/N of the contacts are with infectious individuals. Let β be the probability of transmission in a contact between an infected and a susceptible. Then the rate susceptibles become infected must be, $\frac{\beta cSI}{N}$

Figure 1.3: SIR model



The equations for SIR models are:

$$\begin{aligned} dS/dt &= U - \mu S - \lambda S, \\ dI/dt &= \lambda S - (\mu + \gamma) I, \\ dR/dt &= \gamma R - \mu R \end{aligned}$$

where

$$\lambda = \frac{\beta c S I}{N}$$

This model can be applied in the spread of Measles, where the model divides the population into three groups: susceptibles or those who may contract the disease, infecteds or those infected and experiencing severe symptoms, and partial immunes(recovered) or those infected but experiencing only mild symptoms.

IV. SEIR Model with vital dynamics

This model is an extension of SIR model. Assume a given population may be divided into the following categories:

Susceptibles-those capable of contracting the disease,

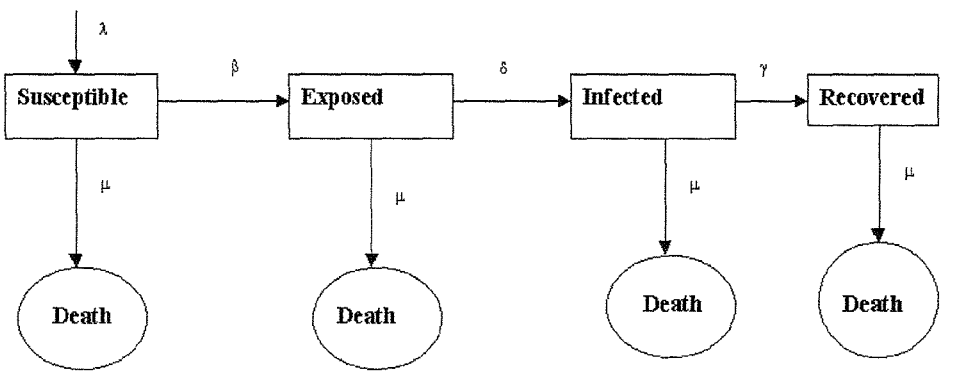
Expossed- those who are infected but not infectious,

Infectives- those capable of transmitting the disease,

Recovered- those who are immune.

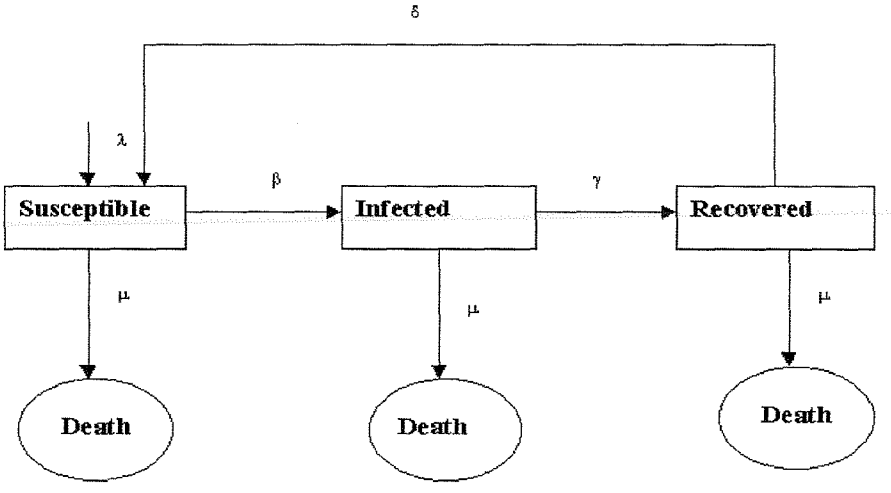
The connectivity diagram shown below is for a constant, open population with births and deaths.

Figure 1.4: SEIR model



Further modification of the SIR model is by adding an immediate return path, δR, back to the susceptibles following the concept that partial immunity is not immediately acquired. The connectivity diagram is as shown below:

Figure 1.5: SIRS model with vital dynamics



The differential equations from the diagram are:

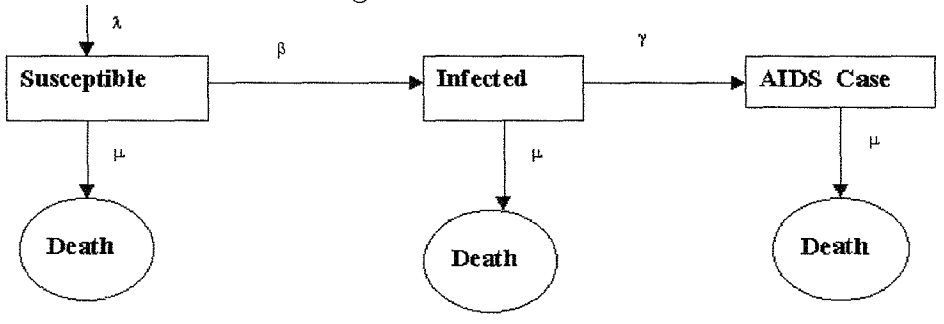
$$\begin{aligned}
\frac{dS}{dt} &= U - \mu S - \lambda S + \delta R; \\
\frac{dI}{dt} &= \lambda S - (\mu + \gamma) I; \\
\frac{dR}{dt} &= \gamma I - \mu R - \delta R
\end{aligned}$$

Application of this model in in Malaria spread.

V. SIA Model

These models are just like SIS models but instead of infectives recovering, they develop AIDS symptoms.The population in this model is divided into three classes: Susceptibles (S), Infective (I) and AIDS case (A).

Figure 1.6: SIA model



A key characteristic of HIV is its long infection time (anywhere from a few months to years) before the onset of AIDS. In fact, some individuals may carry the disease but never develop AIDS. During this infection time the individual is infective and may infect others. Here it will be assumed that once an individual progresses from this infective stage to AIDS, the individual will no longer be sexually active and cannot infect others. The big task now in most countries is to combat the spread of the epidemic. The age structure of the population is changing drastically fast: the sexually active age-group is the one most affected and, as a consequence, the workforce is being reduced and the number of orphans is growing very fast. Thus, it is important, for the purpose of economic and social planning, to have an idea of the age structure of a population. This is what prompted the researcher to look at a three stage groups model, a population under consideration is divided into three age-groups:

$0 - a_1$ (the pre-school age group), $a_1 - a_2$ (the age group between 5 and 15 years, school age) and a_2 and more years (From 15 years). In each age-group, the population is divided into: S (Susceptible)[An S person does not carry the AIDS virus but can contract it from an I person] ,I (Infectives) [An I person has been transmitted with the AIDS virus and carries the AIDS virus and can transmit the virus to S persons. There is a chance that he will develop AIDS symptoms to become an AIDS case or remain non-infectious. Non-infectious person has the virus, which he can contract to uninfected person, but he does not develop the AIDS symptoms] and A (AIDS case) [An AIDS case person is a person who has developed AIDS symptoms, Since there is no effective cure for AIDS at the present time, there is high probability that this person will die from AIDS]. It is the third age group that is sexually mature and active and, therefore, capable of reproduction. It is also this group that is responsible for the horizontal transmission of the epidemic through heterosexual activities and for vertical transmission to the first group by infected mothers. The other modes of transmission of HIV, such as use of unsterilized needles or instruments in hospitals/clinics and through blood transfusion has been reduced drastically to almost 0% presently. In group 1, the only possible mode is the vertical transmission: HIV/AIDS infected mothers pass the virus to their newly born babies. In the model presented in this work, we shall assume that all those born infected with the HIV will die before the school age a_1. Thus, Group II will be free of the HIV/AIDS. However, it should be noted that, according to recent clinical research results, some children born with antibodies against the HIV do lose the antibodies after some time and they never get the HIV [2]. In this case, those who survive the developmental period $(0, a_1)$ years can be accounted for by the value of the parameter for the proportion of the newly born babies by infected mothers that do not have the HIV.

1.2 STATEMENT OF THE PROBLEM

Generating functions have been applied extensively in population studies, especially in branching processes, human reproduction process, Birth and Death process etc. There is need to extend the application of generating functions to HIV transmission models. In the literature, this approach has not been used extensively by researchers to study epidemic processes. Most of the researchers have focused their research on deterministic models. 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 then solve them by using Generating functions.

1.3 PURPOSE OF THE STOCHASTIC HIV/AIDS MODELING

Our research was basically 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) As we shall see, under some special conditions, the deterministic approach is equivalent to working with the expected values of the stochastic models. In this sense, then, the deterministic approach is a special case of the stochastic models if one is only interested in the expected values.

1.4 OBJECTIVES OF THE STUDY

The primary objective of the study is to apply generating function (GF) technique in modeling HIV/AIDS transmission. The study has the following specific research objectives.

(i) To identify some deterministic and stochastic models that have been developed For HIV/AIDS transmission dynamics.

(ii) Modify these equations and formulate stochastic differential equation versions from these ordinary differential equations.

(iii) Apply Generating function technique (GF) in:

- Mother to child transmission model.
- Heterosexual Model.
- Combined model.

The major significance of the study is to show how Generating functions (GF) can be applied in HIV/AIDS transmission models. The models are tested by simulation so as to study the patterns of the population; the susceptibles, infecteds and AIDS cases, by changing parameter values under study. The study helps the author develop a proposal for Ph.D work in this area.

The project's thoroughness and depth of coverage will make this area of research a valuable reference for researchers at the frontiers of the field; since the field is full of potential for future developments in mathematical modeling and empirical application.The work on stochastic process would also make the analysis of HIV/AIDS pandemic straightforward.

Chapter 2

LITERATURE REVIEW

2.1 INTRODUCTION

In this chapter, we are highlighting various epidemic models on HIV/AIDS by various researchers and use of Generating functions. These models are based on homosexual and heterosexual populations. For each population, we have considered deterministic and stochastic approaches. From the literature, it is seen that little has been done on the use of generating functions. It is only Tan and Hsu (1989) who used Generating function but did not consider Mother-to-child Transmission(MTCT) which has become a major mode of HIV/AIDS transmission. Since litle is done on use of generating functions in epidemiology, the author tries to review the deterministic and stochastic models which have been studied in HIV/AIDS.

2.2 HOMOSEXUAL POPULATION

Many mathematical models for HIV transmission and AIDS incidence have dealt primarily with one homogeneously mixing risk group which usually consists of highly

sexually-active homosexual men. Some of these modeling efforts are described below.

2.2.1 Deterministic Models

Anderson *et al.*(1986) described some preliminary attempts to use mathematical models for HIV transmission in a homosexual community. The epidemic data available on HIV infection and the incidence of AIDS was surveyed. After the risk groups and transmission mechanisms were described, doubling times for AIDS incidence were given for risk groups in various geographic locations. Some data were also given for the HIV infection period, the proportion who develop AIDS, and measures of sexual activity. Models of the early stages of the AIDS epidemic in homosexual men were used to find the reproductive number from the distribution of the AIDS incubation period and the initial doubling time. These more complex models showed that heterogeneity in sexual behavior can greatly influence the predictions, with more heterogeneity implying decreased magnitude of the AIDS epidemic. This result is reasonable since high heterogeneity implies that the few very sexually active people are removed rapidly from the infectious pool. Anderson emphasized that uncertainty in parameter values implies that the models are not suitable for prediction. The purpose of their modeling was to investigate the effects of various parameters and help improve our general understanding of the transmission dynamics of HIV infection. Areas of biological uncertainty, future data needs, and public health policy implications were discussed.

Pickering *et al.*(1986) formulated a model for the spread of HIV and AIDS incidence in the homosexual male population in three large cities.They used a discrete time nonlinear model for the sexual transmission of HIV with several possible courses of progression after infection. They gave some preliminary forecasts for San Francisco, Los Ageles and New York city but concluded that there were insufficient data to choose between radically different forecasts.

2.2.2 Stochastic models

May and Anderson (1987) presented some simple HIV transmission models to help clarify the effects of various factors on the overall pattern of the AIDS epidemic.They began by defining the basic reproductive number as the product of three parameters and then obtained estimates of these three parameters from various data sources. They showed that if the probability of developing AIDS increases linearly with tine since infection, then the distribution of the AIDS incubation period is a Weibull distribution. Their calculations assumed that 30% of HIV infecteds eventually develop AIDS, but we now know that this percentage is too low. They considered a model for heterosexual transmission where infection comes from the homosexual male population through bisexuals and found that the doubling times would be significantly larger in the heterosexual population than in the homosexual population. At present, this is not a realistic model for the sexual transmission of HIV in Africa, since most heterosexual transmission is to sexual partners (man and a woman). In their discussion, they emphasized the uncertainty of the parameter values and the need for better data in several areas.Anderson's(1992) epidemiological model has the form $R_0 = \beta c \delta$, where R_0 is the reproductive rate of the epidemic, that is, the number of new infectious that result from each infected individual. β is the probability of the virus being transimited by sexual patnership; c is the number of sexual patners or patner" changes" δ is the duration of infectiousness of seropositive individuals.

What this model indicate is HIV will spread more rapdely in a porpulation where the per-patner probability of transimition is high where the number of sexual patners is large, and where the duration of infectiousness is length.

The mean of c and its variance are positively correlated and the actual impact of c on the transmission rate is:

$$c = m + \frac{\delta^2}{m}$$

where m and δ^2 are the mean and variance of c respectively.

Blythe and Anderson (1988) considered HIV transmission models with four forms for

the distribution of AIDS incubation period (exponential, Weibull, gamma and rectangular). As in most models, the HIV infections period was assumed to be equal to the AIDS incubation period. The impact of the four distributions on HIV transmission dynamics in male homosexual communities was assessed by examining the equilibrium states and their local stability in a model with constant recruitment of susceptibles. In their discussion of the relative merits of the four distributions of the AIDS incubation period, they concluded that, for qualitative purposes, it may be sufficient to consider only these four distributions(if their means coincided with the observed value).

Castillo-Chavez *et al.*(1989a,b,c) extended the above results to arbitrary distributions and analyzed a model where the mean rate of acquisition of new partners depends on the size of the sexually active population. Their results are further described in Castillo-Chavez*et al.*(1989d). In his model, the sexually active homosexual population is subdivided into three groups: S (Susceptible), I (HIV infectious), and A (AIDS infectious). He assumed that A- individuals are sexually inactive and hence do not contribute to disease dynamics. He also assumed that sexually active individuals choose their partners at random. The demographic parameters are given by Λ, the recruitment rate into S; μ, the sexual activity removal rate; d, the AIDS-induced mortality rate, and λ, the transmission rate per infectious partner. $C(T)$ denotes the mean number of sexual partners that an average individual has per unit time, given that the sexually active population is $T = S+I$. It is reasonable to expect that in general $C(T)$ increases linearly for small T and saturates for large T. He further assumed that the incidence rate $B(t)$- the number of new cases per unit time is proportional to $C(T)$, to S, and to the sexually active infected fraction: $B(t) = \lambda C(T)S(t)\frac{I(t)}{T(t)}$. $P(s)$ is the proportion of individuals that are infected at time t and that, if alive, are still infectious at time $t+s$. The distribute-delay model for the sexual spread of HIV/AIDS is therefore given

by the following systems of integro-differential equations:

$$\begin{aligned}
\tfrac{dS(t)}{dt} &= \Lambda - B(t) - \mu S(t), \\
I(t) &= I_0(t) + \textstyle\int_0^t B(x)e^{-\mu(t-x)}P(t-x)dx, \\
A(t) &= A_0(t) + A_1 e^{-dt} + \textstyle\int_0^t \Big\{ \int_0^\tau B(x)e^{-\mu(\tau-x)}[-P'(\tau-x)e^{-d(t-\tau)}]dx \Big\} d\tau
\end{aligned}$$

This model generalizes the models developed by Anderson and May(1987), and Blythe and Anderson(1988). Later Castillo-Chaves reduced the above model to the following system of ordinary differential equations:

$$\begin{aligned}
\tfrac{dS(t)}{dt} &= \Lambda - B(t) - \mu S(t), \\
\tfrac{dI_1(t)}{dt} &= B(t) - (a_1 + \mu) I_1(t), \\
\tfrac{dI_2(t)}{dt} &= a_1 I_1(t) - (a_2 + \mu) I_2(t), \\
\tfrac{dI_3(t)}{dt} &= a_2 I_2(t) - (a_3 + \mu) I_3(t), \\
\tfrac{dA(t)}{dt} &= a_3 I_3(t) - dA(t)
\end{aligned}$$

Where $a_i, i = 1, 2, 3$ denote the rate at which new AIDS cases occur.

Bailey (1989) presented a model for HIV infection and AIDS in which infected people proceeded through a sequence of stages to AIDS and then to Death.The model is given by a system of $m + 2$ nonlinear differential equations with mass-action incidence term and negative exponential waiting times in the infected stages, which correspond to a gamma distribution for the AIDS incubation period. He used data on HIV prevalence in the San Francisco city Clinic cohort of 7,000 people and the reported AIDS incidence in all San Francisco and obtained a best (minimum chi-square) fit of his model. The best fit yielded a gamma distribution with $m = 7$ for the AIDS incubation period.

Mode *et al.* (1989) considered a stochastic population model of an AIDS epidemic in a population of male homosexuals. Computer intensive methods were used to study more properties of the model statistically. A numerical factorial experiment was used to study three factors of importance in the evaluation of the AIDS epidemic. These factors were the distribution of the latent period of HIV, the probability of infection with HIV per sexual contact with an infected individual, and the distribution of the number of contacts per sexual partner per month. They found that the latent period

of the HIV infection had a decisive impact, but the impact depended crucially on the other factors. The monte Carlo experiment showed that the deterministic,nonlinear differential equations using expected values gave more pessimistic predictions than the stochastic population process. Their latent period of HIV would more properly be called the incubation period for AIDS. They used the Weibull and gamma distributions for this AIDS incubation period. The infectivity of HIV-positive individuals was taken to be constant and then zero when they developed AIDS. Since longer mediam AIDS incubation period implies a longer infectious period, their conclusion that the HIV prevalence is much higher for longer median AIDS incubation period seems reasonable.

Tan and Hsu (1989) used a stochastic model for the spread of the AIDS virus in a homosexual population. In this model, susceptible (S) persons become HIV latent (L), infective (I) and then develop AIDS (A). Transitions between these groups were governed by probabilities with constant rate and two transmission rates. The probability generating function (PGF) of the number of Latent persons, Infective persons, and AIDS case was derived. The expected numbers, and variances and covariances of these persons satisfy some ordinary differential equations. These equations are solved numerically to assess the effects of various factors on AIDS spread.

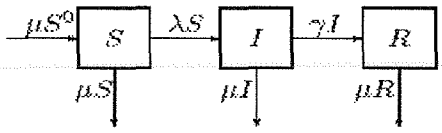
Kaplan (1989) developed dynamic models that apply to needle sharing populations. He made the assumption that a susceptible individual using an infected needle removes the virus from the needle. Kaplan performed extensive simulations illustrating the sensitivity of the model to various parameters and computed the basic reproduction number for this model. He also discussed the effect of possible intervention strategies. the model described by Kaplan is similar to the model considered by Hethcote and Van Ark (1987). at time t, the population contains $n(t)$ gay men. This population is divided into m subpopulations, with $n_i(t)$ men in subpopulation i.Immigration to subpopulation i occurs at a constant rate of N_i men per year, μ is the mortality rate per man per year.

A general model for HIV transmission and AIDS has been formulated by Hethcote

(1987, 1989a).The comprehensive model proposed contains all known transmission routes including homosexual and heterosexual intercourse, needle sharing among intravenous drug users, blood transfusions, blood factor concentrates to hemophiliacs, and perinatal infections. The primary risk groups in the model were sexually active homosexual and bisexual men, prostitutes, sexually active heterosexual women and men, and intravenous drug using women and men. The secondary risk groups were transfusion recipients,hemophiliacs, monogamous partners and children born to women in a previous risk group. For each risk group, there was a differential equation incorporating the inflow and out flow. The progression from HIV infection to AIDS was modeled by a unidirectional flow in a sequence of stages. No attempt was made to estimate parameter values or to apply the model.

Hethcote (1989b) formulated an HIV transmission and AIDS model as a system of nonlinear difference equations with a time step of one month.Parameters were estimated and Hethcote (1989c) estimated more parameters and applied the model to Homosexual males in San Francisco. Jan P. Medlock (2000) formulated an SIR model for the Transmission of HIV. he considered a population of homosexual men, this population was subdivided into S (Susceptibles), I (infectives), and R (individuals removed from infective class).He assumed a constant migration of individuals into the high-risk population as new susceptibles, that is, into S, $\mu S^0 > 0$.Further, he assumed a constant natural death rate which is proportional to the number of individuals in the group, μS, μI and μR, where $\mu > 0$. The number of individuals removed from the infective class into the removed class (by progression from HIV to AIDS) is proportional to the number of individuals in the infective class, γI and the infection rate, λ, depends on the number of partners per individual per unit time, $r > 0$, the transmission probability per partner, $\beta > 0$, and the proportion of infected individuals to sexually active individuals, $I/(S+I)$. Note here that the removed individuals are taken to be sexually inactive so that there are no new infections due to the removed class. The following is the flow diagram which he came up with.

Figure 2.1: SIR model



The following system of ODEs describes this SIR model:

$$\begin{aligned}
\frac{dS}{dt} &= \mu(S^0 - S(t)) - \lambda(t)S(t), \\
\frac{dI}{dt} &= \lambda(t)S(t) - (\mu + \gamma)I(t), \\
\frac{dR}{dt} &= \gamma I(t) - \mu R(t)
\end{aligned}$$

where

$$\lambda(t) = \frac{r\beta I(t)}{S(t) + I(t)}$$

Note that most of these models are continous in nature and not descrete.

2.3 HETEROSEXUAL POPULATION

The AIDS models described above have involved only one population. Clearly, HIV transmission takes place in populations that are heterogeneous in a variety of ways. The contacts between people can be homosexual, heterosexual, or by needle sharing among intravenous drug users; some groups have higher contact rates than others; people may have contacts primarily with others who are similar or with a wide variety of partners; and behavior is not uniform geographically or temporally. One way in which this heterogeneity can be modeled is to consider models with multiple groups. Another possibility is to use continuous distributions of behaviors instead of discrete groups with different behaviors. Some recent models of these types for sexually transmitted diseases and AIDS will now be described.

Recently, multigroup models have been used for AIDS by several different authors. Hyman and Stanley (1988,1989) formulated and used several models to study questions related to the AIDS epidemic. Their τ-dependent model, where τ denotes time since infection, includes variable infectivity as a function of τ. This model is given by a system of nonlinear integro-differential equations for the distribution of infecteds and AIDS cases as a function of time and age since infection. Sample calculations showed that the infectivity profile could dramatically change the rate at which the susceptible population is infected. In their models, they used a Weibull distribution for the AIDS incubation period, and initial cubic growth of the AIDS cases and inverse quartic distributions for the number of sexual partners per unit time. They also used risk-based models with random (proportionate) mixing and biased (preferred) mixing. With random mixing, their numerical simulations showed that the disease progresses rapidly in both the high and low risk populations, but with biased (like-to-like) mixing, the disease progresses rapidly in the high risk populations and more slowly in the low risk populations. The random mixing result seems inconsistent with data. They also noted that if the difference between the male-to-female and female-to-male infectivities is large, then the lower of these two infectivities tends to determine heterosexual spread. The number of infected people as a function of time can be determined by a convolution integral from the AIDS incidence as a function of time and the distribution of the AIDS incubation period. They found that, if people select partners with very similar risk behavior, then the epidemic grows much more slowly than if they were more random in selecting partners.

Blower S. M.,*et al.*(1991) formulated a data-based mathematical model to assess the epidemiological consequences of heterosexual, intravenous drug use and perinatal transmission in New York City. The model was analyzed to clarify the relationship between heterosexual and IVD Use transmission and to provide qualitative and quantitative insights into the HIV epidemic in New York City. The results demon strated the significance of the dynamic interaction of heterosexual and intravenous drug use transmission. Scenario analysis of the model was used to suggest a new ex planation for the

stabilization of the seroprevalence level that has been observed in the New York City intravenous drug use community; the proposed explanation does not rely upon any intravenous drug use or sexual behavioural changes. Gender-specific risks of hetero-sexual transmission in intravenous drug users were also explored by scenario analysis. The model was used to predict future numbers of adult and pe diatric AIDS cases; a sensitivity analysis of the model showed that the confidence intervals on these estimates were extremely wide. This prediction variability was due to the uncertainty in estimating the values of the model's thirty variables. However,the sensitivity analysis revealed that only a few key variables were significant in con tributing to the AIDS case prediction variability; partial rank correlation coefficients were calculated and used to identify and to rank the importance of these key variables. The model consists of thirty-four ordinary differential equations.

Luboobi(1994) formulated a three age-groups model for the HIV/AIDS epidemic. In his model, he subdivided each age group into susceptibles, infecteds, and AIDS cases.The equations of his model are delayed differential equations.He used the method of steps in obtaining bounding functions for the HIV prevalence.

Jacquez and Koopman [6] used multi -group compartmental models for HIV with constant recruitment into the susceptible classes and variable infectivity in the infectious stages to analyze the effects of different mixing pattern.

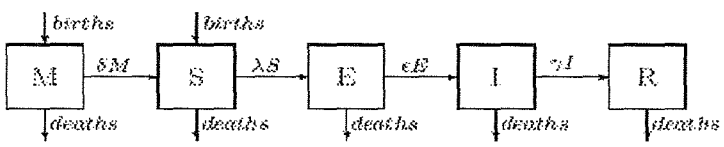
Hyman and Stanley [7] have considered both continuous and discrete HIV/AIDS models with heterogeneity and different mixing structures. They have analyzed the spread from high to low risk groups, the effects of variable infectivity and the instability of the back calculation procedure. The formulation of the models in this study is similar to that of Hethcote et al. [1].

Hethcote (2000) came up with a MSEIR epidemiological model for Infectious Diseases.He assumed a constant birth rate b and death rate d, so the population size $N(t)$ satisfies $N'(t) = (b-d)N$. Thus the population is growing, constant, or decaying if the net change rate $q = b - d$ is positive, zero, or negative, respectively. In this MSEIR epidemiological model, the transfer out of the passively immune class is δM,

the transfer out of the exposed class is ϵE, and the recovery rate from the infectious class is $\gamma I.\lambda$ is the force of infection, hence the number of new cases per unit time is $\lambda S = \frac{\beta SI}{N}$,. Below is the flow diagram:

The system of differential equations for the numbers in the epidemiological classes

Figure 2.2: Transfer diagram for the MSEIR model with the passively immune class M, the susceptible class S, the exposed class E, the infective class I, and the recovered class R.



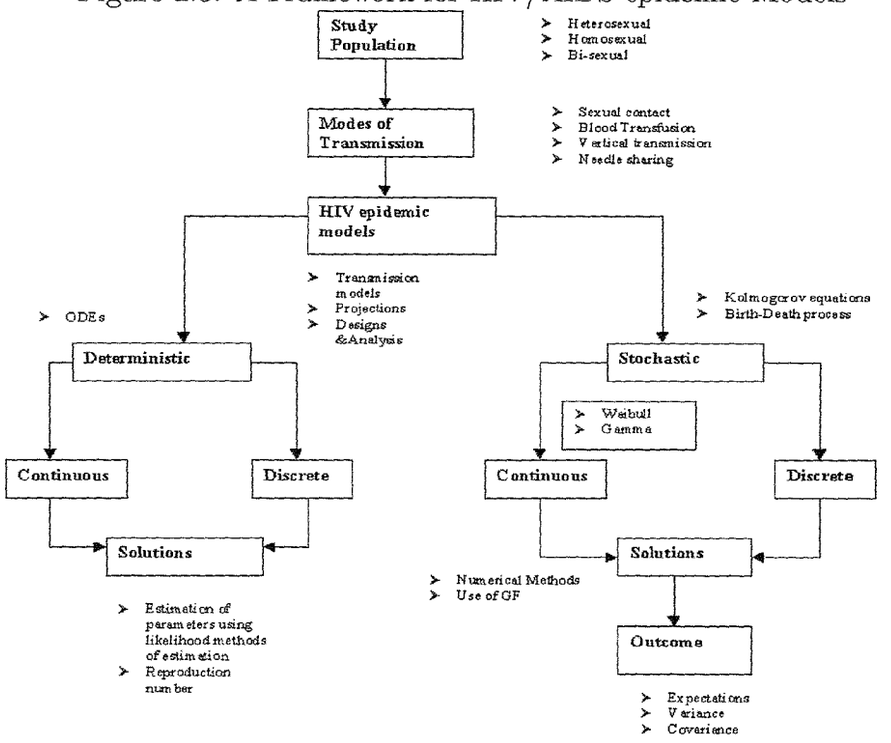
and the population size is:

$$\begin{aligned}
\frac{dM}{dt} &= b(N-S) - (\delta + d)M, \\
\frac{dS}{dt} &= bS + \delta M - \frac{\beta SI}{N} - dS, \\
\frac{dE}{dt} &= \frac{\beta SI}{N} - (\epsilon + d)E, \\
\frac{dI}{dt} &= \epsilon E - (\gamma + d)I, \\
\frac{dR}{dt} &= \gamma I - dR, \\
\frac{dN}{dt} &= (b-d)N.
\end{aligned}$$

2.4 A General Framework for HIV/AIDS model studies

From the above literature, a number of issues emerging can be summerized in the following framework.

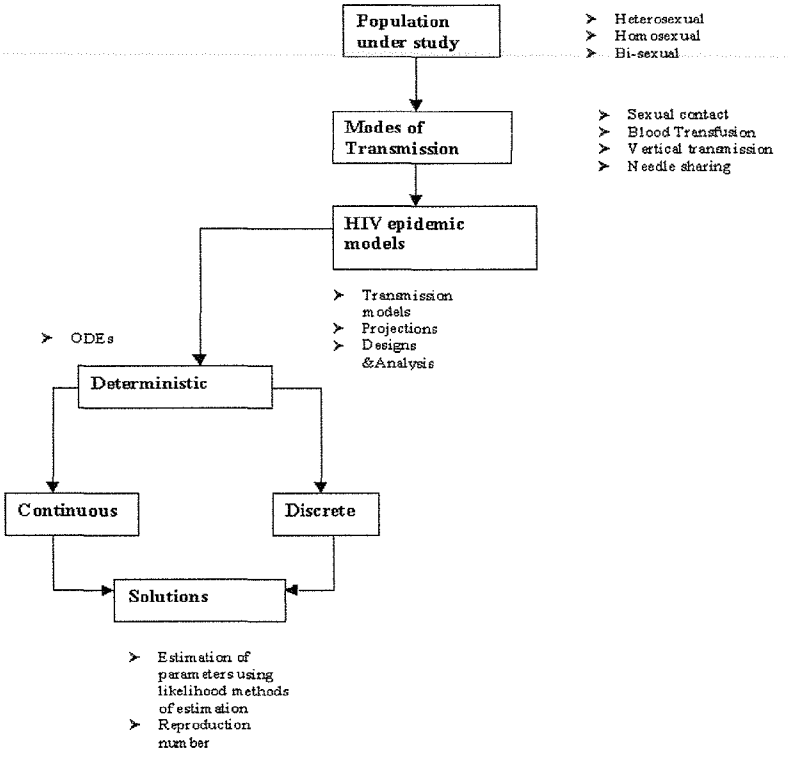
Figure 2.3: A Framework for HIV/AIDS epidemic Models



source: Author

From above framework, We can see which route each researcher followed. Most of the researchers have followed the deterministic route,that is:

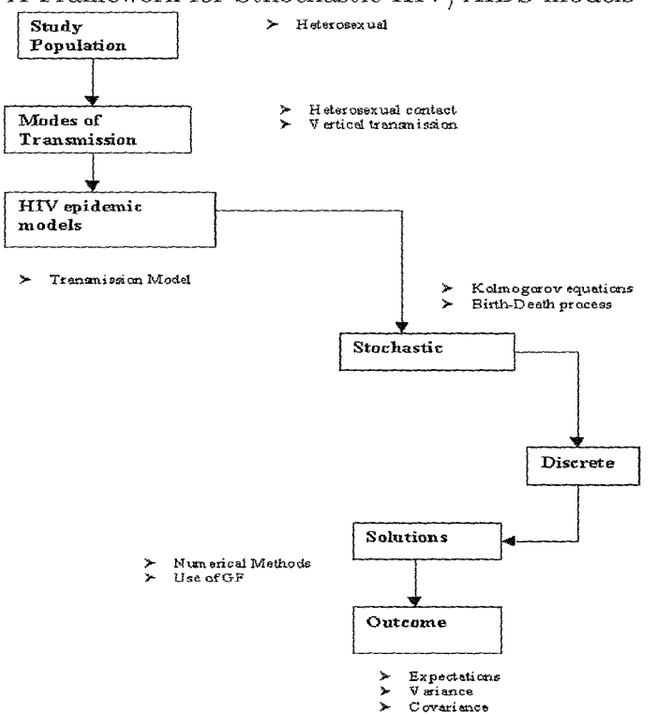
Figure 2.4: A Framework for Deterministic HIV/AIDS Models



source: Author

From the literature, it is seen that little has been done on generating functions. It is only Tan and Hsu (1989) who used Generating function but did not consider Mother-to-child Transmission(MT CT) which has become a major mode of HIV/AIDS transmission. The author bases the study on this and on what Luboobi did. It is clear from the general framework that this study will follow the stochastic route.the following Framework summarizes the authors study:

Figure 2.5: A Framework for Sthochastic HIV/AIDS models



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Chapter 3

MTCT MODELS

3.1 Introduction

The purpose of this chapter is to develop the Mother-to-child Transmission (MTCT) model also called Vertical transmission 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) and the mothers in the age group (15 and more years).The population is divided into those children born free of HIV virus (susceptibles), those who contact the virus from their infected mothers (Infectives), and the former infectives who develop full blown symptoms (AIDS cases).

The mode of HIV/AIDS transmission in this group is Mother-to-child transmission (MTCT). The virus may be transmitted to the newborn babies during pregnancy(in utero), labor, delivery (through contamination by blood or other fluids during birth), or after the child's birth during breastfeeding. Among infected infants who are not breastfed, about two-thirds of cases of MTCT occur around the time of delivery and the rest during the pregnancy (mostly during the last 2 months). In populations where breastfeeding is the norm, it accounts for more than one-third of all transmission.Thus the rate of transmission from uninfected to infected depends upon the health status of

the mother and the conditional probability that an infected mother will transmit the virus to either the foetus or newborn in utero, during or shortly after delivery which is 21-43%.

Assumptions and notations

The pre-school age group (0-5 years) at time t is subdivided into $S_1(t)$ Non-infected (those infants free of HIV), $I_1(t)$ infectives (infected by infected mothers), and $A_1(t)$ AIDS cases (those who have developed full blown AIDS symptoms but are still alive).

Let the rate at which an infected mother does not transmitting the HIV virus to the newborn be β.Thus the probability that a child born by infected mother will not contract the HIV virus during $(t, t+\Delta t)$ is $\beta\lambda\Delta t + o(\Delta t)$, where λ is the birth rate. The probability that the child born by infected mother is HIV positive is $(1-\beta)_a\lambda\Delta t+o(\Delta t)$, where a= transmission during pregnancy (which is 15-30%), delivery or breastfeeding (which is 10-15%).

Let the transition rate from infective to AIDS case γ. Thus , during $(t, t+\Delta t)$, the probability of that a transition will occur is $\gamma\Delta t + o(\Delta t)$ so that the incubation (infectious) period is $1/\gamma$

Let the death(death unrelated to HIV/AIDS) rate be μ_1 per person per time. Thus an individual existing at time t has a chance $\mu_1\Delta t + o(\Delta t)$ of dying during the time interval $(t, t+\Delta t)$. Hence the mean life expectancy is $1/\mu_1$.

since the rate of natural death is very much smaller than the rate of death from AIDS, we assume that those children with full blown symptoms die at the same rate μ_1

Let survival rate from age group 1 to group 2 be p_1,thus , during $(t, t+\Delta t)$, the probability that a person in age group 1 will survive the development period (0-5)years to age group 2 is $p_1\Delta t + o(\Delta t)$ Total population for the age group 1 at time t is assumed to be $N(t) = S_1(t) + I_1(t) + A_1(t)$

3.2 Susceptible population model

In this model, changes in the numbers of Susceptible persons are treated as a birth and death process; the "birth"are the births by both non and infected mothers and "death"are the natural deaths and the proportion of children who survive the development period to the next age group. 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 birth from non or infected mothers during the time interval $(t, t+\Delta t)$
(iii) That there are $n+1$ individuals by time t and 1 dies or survives to the next age group during the time interval $(t, t+\Delta t)$
In the model, we study the Mother-to-child transmission (MTCT). The change in population size during the time interval $(t, t+\Delta t)$ is governed by the following conditional probabilities;

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

Let the probability distribution of the population size at time t be denoted by
$S_{1n}(t) = P_r\{S_1(t) = n/S_1(0) = i\}$, $i < n$ and $i = 0, 1, ...$

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

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

Where

$$S_K = \frac{S_k(t)}{n \cdot}, \qquad I_k = \frac{I_k(t)}{n}, and \quad A_k = \frac{A_k(t)}{n}$$

proportions of Susceptibles, infecteds, and AIDS case respectively, where $k = 1, 2, 3$ Let $S_{1n}(t)$ be the probability that the population size $N_1(t)$ has the value n at time t, $S_{1n-1}(t)$ the probability that the population size $N_1(t)$ has the value $n-1$ at time t, and $S_{1n+1}(t)$ the probability that the population size $N_1(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned}S_{1n}(t+\Delta t) &= [1 - nS_3\lambda\Delta t - nI_3\beta\lambda\Delta t - np_1S_1 - nS_1\mu_1\Delta t - o(\Delta t)]S_{1n}(t) \\ &+ [(n-1)S_3\lambda\Delta t + (n-1)I_3\beta\lambda\Delta t + o(\Delta t)]S_{1n-1}(t) \\ &+ [(n+1)p_1S_1 + (n+1)S_1\mu_1\Delta t + o(\Delta t)]S_{1n+1}(t)\end{aligned}$$

which gives

$$\begin{aligned}S_{1n}(t+\Delta t) - S_{1n}(t) &= [-nS_3\lambda\Delta t - nI_3\beta\lambda\Delta t - np_1S_1 - nS_1\mu_1\Delta t - o(\Delta t)]S_{1n}(t) \\ &+ [(n-1)S_3\lambda\Delta t + (n-1)I_3\beta\lambda\Delta t + o(\Delta t)]S_{1n-1}(t) \\ &+ [(n+1)p_1S_1 + (n+1)S_1\mu_1\Delta t + o(\Delta t)]S_{1n+1}(t)\end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we have the following Kolmogorov forward equations:

$$\begin{aligned}S_{1n}'(t) &= -[nS_3\lambda + nS_1\mu_1 + nI_3\beta\lambda + np_1S_1]S_{1n}(t) \\ &+ [(n-1)S_3\lambda + (n-1)I_3\beta\lambda]S_{1n-1}(t) \qquad \text{for } n \geq 1 \qquad (3.2.1) \\ &+ [(n+1)p_1S_1 + (n+1)S_1\mu_1]S_{1n+1}(t),\end{aligned}$$

$$S_0'(t) = [p_1S_1 + S_1\mu_1]S_1(t), \quad \text{for } n = 0 \qquad (3.2.2)$$

Where the primes indicate differentiation with respect to t In equation (3.2.1), there are 3 unknown probabilities; $S_{1n}(t)$, $S_{1n-1}(t)$, and $S_{1n+1}(t)$. Therefore these equation

cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_S(Z,t) = \sum_{n=0}^{\infty} S_{1n}(t)Z^n$$

. With $n = 0$,in equation (3.2.2) $S_{1-1}(t)$ is identically Zero. The coefficient of $S_{1n-1}(t)$ arises from considering the conditional probability of "birth"into the population given that the population size is $n-1$. Multiplying equation (3.2.1) by Z^n and sum over $n = 1$, we have

$$\begin{aligned} \textstyle\sum_{n=1}^{\infty} S'_{1n}(t)Z^n &= -[S_3\lambda + I_3\beta\lambda + S_1\mu_1 + p_1S_1]\textstyle\sum_{n=1}^{\infty} nS_{1n}(t)Z^n \\ &+ [S_3\lambda + I_3\beta\lambda]\textstyle\sum_{n=1}^{\infty}(n-1)S_{1n-1}(t)Z^n \\ &+ (p_1+\mu_1)S_1\textstyle\sum_{n=1}^{\infty}(n+1)S_{1n+1}(t)Z^n \end{aligned} \tag{3.2.3}$$

Define

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} S'_{1n}(t)Z^n \\ \tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nS_{1n}(t)Z^n \\ G(Z,t) &= \textstyle\sum_{n=0}^{\infty} S_{1n}(t)Z^n \end{aligned}$$

Therefore equation (3.2.3) becomes

$$\begin{aligned} \tfrac{\partial G}{\partial t} - S'_0(t) &= -[S_3\lambda + I_3\beta\lambda + S_1\mu_1 + p_1S_1]Z\tfrac{\partial G}{\partial Z} \\ &+ (S_3\lambda + I_3\beta\lambda)Z^2\tfrac{\partial G}{\partial Z} \\ &+ [p_1+\mu_1]S_1(\tfrac{\partial G}{\partial Z} - S_1(t)) \end{aligned}$$

From equation (3.2.2) we have

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= -[S_3\lambda + I_3\beta\lambda + S_1\mu_1 + p_1S_1]Z\tfrac{\partial G}{\partial Z} \\ &+ (S_3\lambda + I_3\beta\lambda)Z^2\tfrac{\partial G}{\partial Z} \\ &+ (p_1+\mu_1)S_1\tfrac{\partial G}{\partial Z} \end{aligned}$$

$$\frac{\partial G}{\partial t} = -(1-Z)[(S_3\lambda + I_3\beta\lambda)Z - (p_1+\mu_1)S_1]\frac{\partial G}{\partial Z}$$

Therefore

$$\frac{\partial G}{\partial t} + (1-Z)[(S_3\lambda + I_3\beta\lambda)Z - (p_1+\mu_1)S_1]\frac{\partial G}{\partial Z} = 0$$

The auxiliary equations are:

$$\frac{dt}{1} = \frac{dZ}{(1-Z)[(S_3\lambda + I_3\beta\lambda)Z - (p_1+\mu_1)S_1]} = \frac{dG}{0}$$

Considering

$$\frac{dG}{0} = \frac{dt}{1}$$

Therefore

$$G(Z,t) = C_1$$

Next we consider

$$\frac{dt}{1} = \frac{dZ}{(1-Z)[(S_3\lambda + I_3\beta\lambda)Z - (p_1+\mu_1)S_1]}$$

On integration and using partial fractions we have

$$\Big(\frac{1-Z}{(S_3\lambda + I_3\beta\lambda)Z - (p_1+\mu_1)S_1}\Big)e^{[(S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1]t} = C_2$$

Where C_1 and C_2 are constants of integration. Setting C_1 as a function of C_2,we arrive at the most general solution

$$G_{S_1}(Z,t) = f\{(\frac{1-Z}{[(S_3\lambda + I_3\beta\lambda)Z - (p_1+\mu_1)S_1]})e^{[(S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1]t}\}$$

Where f is an arbitrary differentiable function. We had denoted that $S_1(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let the initial population at time $t = 0$ be $S_1(0) = i$ then

$$G_{S_1}(Z,0) = Z^i$$

Therefore

$$f\{\frac{1-Z}{[(S_3\lambda + I_3\beta\lambda)Z - (p_1+\mu_1)S_1]}\} = Z^i \tag{3.2.4}$$

Let

$$\eta_S = (S_3\lambda + I_3\beta\lambda) \tag{3.2.5a}$$

and

$$\mu_S = (p_1+\mu_1)S_1 \tag{3.2.5b}$$

then equation (3.2.4) becomes

$$f\{\frac{1-Z}{[\eta_S Z-\mu_S]}\}$$

This is for $|Z|<1$. For any θ,

$$\theta=\frac{1-Z}{\eta_S Z-\mu_S}$$

We have

$$Z=\frac{1+\mu_S\theta}{1+\eta_S\theta}$$

Hence we have

$$f(\theta)=\{\frac{1+\mu_S\theta}{1+\eta_S\theta}\}^i$$

Now replacing θ by $\frac{1-Z}{\eta_S Z-\mu_S}$ we have

$$G_{S_1}(Z,t)=\left(\frac{(\eta_S Z-\mu_S)+\mu_S(1-Z)e^{(\eta_S-\mu_S)t}}{(\eta_S Z-\mu_S)+\eta_S(1-Z)e^{(\eta_S-\mu_S)t}}\right)^i \tag{3.2.5}$$

Rewriting equation (3.2.5) in a suitable form, we get

$$G(Z,t)=\left(\frac{\mu_S(e^{(\eta_S-\mu_S)t}-1)-(\mu_S e^{(\eta_S-\mu_S)t}-\eta_S)Z}{(\eta_S e^{(\eta_S-\mu_S)t}-\mu_S)-\eta_S Z(e^{(\eta_S-\mu_S)t}-1)}\right)^i \tag{3.2.6}$$

but

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

and

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

Then equation (3.2.6) becomes

$$G(Z,t)=\left(\frac{(p_1+\mu_1)S_1(e^{((S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1)t}-1)-((p_1+\mu_1)S_1e^{((S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1)t}-(S_3\lambda+I_3\beta\lambda)Z(e^{((S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)}\right. \tag{3.2.7}$$

We let

$$A(t)=(p_1+\mu_1)S_1\frac{1-e^{(S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1)t}}{(p_1+\mu_1)S_1-S_3\lambda+I_3\beta\lambda)e^{(S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1)t}}$$

and

$$B(t)=\frac{S_3\lambda+I_3\beta\lambda)}{(p_1+\mu_1)S_1}A(t)$$

Hence equation (3.2.7) becomes

$$G_{S_1}(Z,t) = \left(\frac{A(t) + [1 - A(t) - B(t)]Z}{1 - B(t)Z}\right)^i \tag{3.2.8}$$

This is the PGF of the differential equation (3.2.1)

Now it is a simple matter of expanding the PGF to obtain the probability distribution $S_1(t)$.

Differentiating the PGF in (3.2.7) with respect to Z, we find the expectation and variance of $S_1(t)$:

$$\begin{aligned} E[S_1(t)] &= i\tfrac{1-A(t)}{1-B(t)} \\ &= ie^{(\eta_S - \mu_S)t} \\ &= ie^{(S_3\lambda + I_3\beta\lambda) - (p_1+\mu_1)S_1)t} \end{aligned} \tag{3.2.9a}$$

and

$$\begin{aligned} \delta^2_{S_1} &= i\tfrac{(1-A(t))(A(t)+B(t))}{(1-B(t))^2} \\ &= i(\tfrac{\eta_S+\mu_S}{\eta_S-\mu_S})e^{(\eta_S-\mu_S)t}[e^{(\eta_S-\mu_S)t} - 1] \\ &= i(\tfrac{S_3\lambda+I_3\beta\lambda)+(p_1+\mu_1)S_1}{S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1})e^{(S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1)t}[e^{(S_3\lambda+I_3\beta\lambda)-(p_1+\mu_1)S_1)t} - 1]. \end{aligned} \tag{3.2.9b}$$

by taking the limits as $(p_1 + \mu_1)S_1 \rightarrow S_3\lambda + I_3\beta\lambda)$ (where $S_3\lambda + I_3\beta\lambda)$ is birth rate for both infected and Susceptible mothers) we find that

$$E[S_1(t)] = i \tag{3.2.9a}$$

and

$$\delta^2_{S_1} = 2(S_3\lambda + I_3\beta\lambda)t \tag{3.2.9b}$$

Thus when $S_3\lambda + I_3\beta\lambda) = (p_1 + \mu_1)S_1$ the population size has a constant expectation but an increasing variance.

3.3 Asymptomatic (Infection) Model

In this model, changes in the numbers of persons infected are treated as a birth and death process; the "birth"are the new infections from infected mother to child and

"death"are the children who develop AIDS symptoms or die. The probability that there are n individuals in the infective 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 HIV transmission,immigration or Mother-to child transmission during the time interval $(t, t+\Delta t)$

(iii) That there are $n+1$ individuals by time t and 1 dies or converts to AIDS 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;

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

Let the probability distribution of the population size at time t be denoted by $I_{1n}(t) = P_r\{I_1(t) = n/I_1(0) = 1\}$, We seek to find this distribution by deriving a system of differential equations from the assumptions above. Now

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

Let $I_{1n}(t)$ be the probability that the population size $N_1(t)$ has the value n at time t, $I_{1n-1}(t)$ the probability that the population size $N_1(t)$ has the value $n-1$ at time t, and $I_{1n+1}(t)$ the probability that the population size $N_1(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned}
I_n(t+\Delta t) &= [1 - (nI_1\mu_1 + nI_3(1-\beta)_a\lambda + nI_1\gamma)\Delta t + o(\Delta t)]I_n(t) \\
&+ ([(n-1)I_3(1-\beta)_a\lambda]\Delta t + o(\Delta t))I_{1n-1}(t) \\
&+ ([(n+1)I_1\gamma + (n+1)I_1\mu_1]\Delta t + o(\Delta t))I_{1n+1}(t)
\end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we have the following Kolmogorov forward equations:

$$\begin{aligned} I_n'(t) &= -[nI_1\mu_1 + nI_3(1-\beta)_a\lambda + nI_1\gamma]I_n(t) \\ &+ [(n-1)I_3(1-\beta)_a\lambda+]I_{1n-1}(t) \qquad \text{for } n \geq 1 \\ &+ [(n+1)I_1\gamma + (n+1)I_1\mu_1]I_{1n+1}(t), \end{aligned} \tag{3.3.1}$$

$$I_0'(t) = [I_1\mu_1 + I_1\gamma]I_1(t), \quad \text{for } n = 0 \tag{3.3.2}$$

Where the primes indicate differentiation with respect to t In equation (3.3.1), there are 3 unknown probabilities; $I_n(t)$, $I_{1n-1}(t)$, and $I_{1n+1}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_S(Z,t) = \sum_{n=0}^{\infty} I_n(t)Z^n$$

. With $n = 0$,in equation (3.3.2) $I_{1-1}(t)$ is identically Zero. The coefficient of $I_{1n-1}(t)$ arises from considering the conditional probability of "birth"into the population given that the population size is $n-1$. Multiplying equation (3.3.1) by Z^n and sum over $n = 1$, we have

$$\begin{aligned} \textstyle\sum_{n=1}^{\infty} I_n'(t)Z^n &= -[I_1\mu_1 + I_3(1-\beta)_a\lambda + I_1\gamma]\textstyle\sum_{n=1}^{\infty} nI_n(t)Z^n \\ &+ ((1-\beta)_a\lambda)I_1\textstyle\sum_{n=1}^{\infty}(n-1)I_{1n-1}(t)Z^n \\ &+ [\mu_1+\gamma]I_1\textstyle\sum_{n=1}^{\infty}(n+1)I_{1n+1}(t)Z^n \end{aligned} \tag{3.3.3}$$

Define

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} I_n'(t)Z^n \\ \tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nI_n(t)Z^n \\ G(Z,t) &= \textstyle\sum_{n=0}^{\infty} I_n(t)Z^n \end{aligned}$$

Therefore equation (3.3.3) becomes

$$\begin{aligned} \tfrac{\partial G}{\partial t} - I_0'(t) &= -(I_1\mu_1 + I_3(1-\beta)_a\lambda + I_1\gamma)Z\tfrac{\partial G}{\partial Z} \\ &+ ((1-\beta)_a\lambda)I_1Z^2\tfrac{\partial G}{\partial Z} \\ &+ (\mu_1+\gamma)(\tfrac{\partial G}{\partial Z} - I_1(t)) \end{aligned}$$

From equation (3.3.2) we have

$$\begin{aligned}\frac{\partial G}{\partial t} &= -(I_3(1-\beta)_a\lambda + I_1\mu_1 + I_1\gamma)Z\frac{\partial G}{\partial Z} \\ &+ ((1-\beta)_a\lambda)I_1Z^2\frac{\partial G}{\partial Z} \\ &+ (\mu_1+\gamma)I_1\frac{\partial G}{\partial Z}\end{aligned}$$

$$\frac{\partial G}{\partial t} = -(1-Z)[((1-\beta)_a\lambda)I_1Z - (\mu_1+\gamma)I_1]\frac{\partial G}{\partial Z}$$

Therefore

$$\frac{\partial G}{\partial t} + (1-Z)[((1-\beta)_a\lambda)I_1Z - (\mu_1+\gamma)I_1]\frac{\partial G}{\partial Z} = 0$$

The auxiliary equations are:

$$\frac{dt}{1} = \frac{dZ}{(1-Z)[((1-\beta)_a\lambda)I_1Z - (\mu_1+\gamma)I_1]} = \frac{dG}{0}$$

Considering

$$\frac{dG}{0} = \frac{dt}{1}$$

Therefore

$$G(Z,t) = C_1$$

Next we consider

$$\frac{dt}{1} = \frac{dZ}{(1-Z)[((1-\beta)_a\lambda)I_1Z - (\mu_1+\gamma)I_1]}$$

On integration and using partial fractions we have

$$\left(\frac{1-Z}{(1-\beta)_a\lambda)I_1Z - (\mu_1+\gamma)I_1}\right)e^{[(1-\beta)_a\lambda)I_1-(\mu_1+\gamma)I_1]t} = C_2$$

Where C_1 and C_2 are constants of integration. Setting C_1 as a function of C_2,we arrive at the most general solution

$$G_{I_1}(Z,t) = f\{(\frac{1-Z}{[((1-\beta)_a\lambda)I_1Z - (\mu_1+\gamma)I_1]})e^{[(1-\beta)_a\lambda)I_1-(\mu_1+\gamma)I_1]t}\}$$

Where f is an arbitrary differentiable function. We had denoted that $I_1(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let the initial population at time $t = 0$ be $I_1(0) = 1$ then

$$G_{I_1}(Z,0) = Z$$

Therefore

$$f\{\frac{1-Z}{[((1-\beta)_a\lambda)I_1Z-(\mu_1+\gamma)I_1]}\}=Z \tag{3.3.4}$$

Let $\eta_I = I_3(1-\beta)_a\lambda$ and $\mu_I = I_1(\mu_I+\gamma)$ then equation (3.3.4) becomes

$$f\{\frac{1-Z}{[\eta_I Z-\nu]}\}=Z$$

This is for $|Z|<1$. For any θ,

$$\theta=\frac{1-Z}{\eta_I Z-\mu_I}$$

We have

$$Z=\frac{1+\mu_I\theta}{1+\eta_I\theta}$$

Hence we have

$$f(\theta)=\{\frac{1+\mu_I\theta}{1+\eta_I\theta}\}$$

Now replacing θ by $\frac{1-Z}{\eta_I Z-\mu_I}$ we have

$$G_{I_1}(Z,t)=\left(\frac{(\eta_I Z-\mu_I)+\mu_I(1-Z)e^{(\eta_I-\mu_I)t}}{(\eta_I Z-\mu_I)+\eta_I(1-Z)e^{(\eta_I-\mu_I)t}}\right) \tag{3.3.5}$$

Rewriting equation (3.3.5) in a suitable form, we get

$$G(Z,t)=\left(\frac{\mu_I(1-e^{(\eta_I-\mu_I)t})-(\eta_I-\mu_I e^{(\eta_I-\mu_I)t}}{\mu_I-\eta_I e^{(\eta_I-\mu_I)t}-\eta_I Z(1-e^{(\eta_I-\mu_I)t})}\right) \tag{3.3.6}$$

but $\eta_I = I_3(1-\beta)_a\lambda$ and $\mu_I = I_1(\mu_I+\gamma)$ Then equation (3.2.6) becomes

$$G(Z,t)=\left(\frac{I_1(\mu_I+\gamma)(1-e^{(I_3(1-\beta)_a\lambda-I_1(\mu_I+\gamma))t})-(I_3(1-\beta)_a\lambda-I_1(\mu_I+\gamma)e^{(I_3(1-\beta)_a\lambda-I_1(\mu_I+\gamma))t}}{I_1(\mu_I+\gamma)-I_3(1-\beta)_a\lambda e^{(I_3(1-\beta)_a\lambda-I_1(\mu_I+\gamma))t}-I_3(1-\beta)_a\lambda Z(1-e^{(I_3(1-\beta)_a\lambda-I_1(\mu_I+\gamma))t})}\right) \tag{3.3.6}$$

We let

$$B(t)=I_1(\mu_I+\gamma)\frac{1-e^{(I_3(1-\beta)_a\lambda-I_1(\mu_I+\gamma))t}}{I_1(\mu_I+\gamma)-I_3(1-\beta)_a\lambda e^{(I_3(1-\beta)_a\lambda-I_1(\mu_I+\gamma))t}}$$

and

$$C(t)=\frac{I_3(1-\beta)_a\lambda}{I_1(\mu_I+\gamma)}B(t)$$

Hence equation (3.3.6) becomes

$$G_{I_1}(Z,t)=\left(\frac{B(t)+[1-B(t)-C(t)]Z}{1-C(t)Z}\right) \tag{3.3.7}$$

This is the PGF of the differential equation (3.3.1)

Now it is a simple matter of expanding the PGF to obtain the probability distribution $I_1(t)$.

Differentiating the PGF in (3.3.7) with respect to Z, we find the expectation and variance of $I_1(t)$:

$$E[I_1(t)] = \frac{1 - B(t)}{1 - C(t)} = e^{(I_3(1-\beta)_a\lambda - I_1(\mu_I+\gamma))t} \tag{3.3.8}$$

and

$$\begin{aligned} \delta^2_{I_1} &= \tfrac{(1-B(t))(B(t)+C(t))}{(1-C(t))^2} \\ &= (\tfrac{I_3(1-\beta)_a\lambda + I_1(\mu_I+\gamma)}{I_3(1-\beta)_a\lambda - I_1(\mu_I+\gamma)}) e^{(I_3(1-\beta)_a\lambda - I_1(\mu_I+\gamma))t}[e^{(I_3(1-\beta)_a\lambda - I_1(\mu_I+\gamma))t} - 1]. \end{aligned} \tag{3.3.9}$$

by taking the limits as $I_1(\mu_I + \gamma) \rightarrow I_3(1-\beta)_a\lambda$ (where $I_3(1-\beta)_a\lambda$ is birth rate for both infected and Susceptible mothers) we find that

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

and

$$\delta^2_{I_1} = 2I_3(1-\beta)_a\lambda t$$

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

3.4 Symptomatic (AIDS case) model

In this model, changes in the numbers of AIDS case are treated as a birth and death process; the "birth"are the children who become symptomatic and "death"are the deaths. The probability that there are n individuals in the symptomatic stage 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 developing the symptoms

during the time interval $(t, t+\Delta t)$

(iii) That there are $n+1$ individuals by time t and 1 dies 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;

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

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

$A_{1n}(t) = P_r\{A_1(t) = n/A_1(0) = 0\}$,

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

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

Let $A_{1n}(t)$ be the probability that the population size $N_1(t)$ has the value n at time t, $A_{1n-1}(t)$ the probability that the population size $N_1(t)$ has the value $n-1$ at time t, and $A_{1n+1}(t)$ the probability that the population size $N_1(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned}
A_{1n}(t+\Delta t) &= [1 - nI_1\gamma\Delta t - nA_1\mu_1\Delta t - o(\Delta t)]A_{1n}(t) \\
&+ (n-1)I_1\gamma\Delta t + o(\Delta t)]A_{1n-1}(t) \\
&+ [(n+1)A_1\mu_1\Delta t + o(\Delta t)]A_{1n+1}(t)
\end{aligned}$$

which gives

$$\begin{aligned}
A_{1n}(t+\Delta t) - A_{1n}(t) &= [-nI_1\gamma\Delta t - nA_1\mu_1\Delta t - o(\Delta t)]A_{1n}(t) \\
&+ nI_1\gamma\Delta t + o(\Delta t)]A_{1n-1}(t) \\
&+ [(n+1)A_1\mu_1\Delta t + o(\Delta t)]A_{1n+1}(t)
\end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we have the following Kolmogorov forward equations:

$$\begin{aligned} A_{1_n}'(t) &= -[nI_1\gamma + nA_1\mu_1]A_{1n}(t) \\ &+ [(nI_1\gamma]A_{1n-1}(t) \qquad \text{for } n \geq 1 \qquad (3.4.1) \\ &+ (n+1)A_1\mu_1 A_{1n+1}(t), \\ A_0'(t) &= [A_1\mu_1]A_1(t), \quad \text{for } n = 0 \qquad (3.4.2) \end{aligned}$$

Where the primes indicate differentiation with respect to t In equation (3.4.1), there are 3 unknown probabilities; $A_{1n}(t)$, $A_{1n-1}(t)$, and $A_{1n+1}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_A(Z,t) = \sum_{n=0}^{\infty} A_{1n}(t)Z^n$$

. With $n = 0$,in equation (3.4.2) $A_{1-1}(t)$ is identically Zero. The coefficient of $A_{1n-1}(t)$ arises from considering the conditional probability of "birth"into the population given that the population size is $n-1$. Multiplying equation (3.4.1) by Z^n and sum over $n = 1$, we have

$$\begin{aligned} \textstyle\sum_{n=1}^{\infty} A_{1_n}'(t)Z^n &= -[I_1\gamma + A_1\mu_1]\textstyle\sum_{n=1}^{\infty} nA_{1n}(t)Z^n \\ &+ I_1\gamma\textstyle\sum_{n=1}^{\infty}(n-1)A_{1n-1}(t)Z^n \qquad (3.4.3) \\ &+ A_1\mu_1\textstyle\sum_{n=1}^{\infty}(n+1)A_{1n+1}(t)Z^n \end{aligned}$$

Define

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} A_{1_n}'(t)Z^n \\ \tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nA_{1n}(t)Z^n \\ G(Z,t) &= \textstyle\sum_{n=0}^{\infty} A_{1n}(t)Z^n \end{aligned}$$

Therefore equation (3.4.3) becomes

$$\begin{aligned} \tfrac{\partial G}{\partial t} - A_0'(t) &= -[I_1\gamma + A_1\mu_1]Z\tfrac{\partial G}{\partial Z} \\ &+ I_1\gamma Z^2\tfrac{\partial G}{\partial Z} \\ &+ A_1\mu_1(\tfrac{\partial G}{\partial Z} - A_1(t)) \end{aligned}$$

From equation (3.4.2) we have

$$\begin{aligned}\frac{\partial G}{\partial t} &= -[I_1\gamma + A_1\mu_1]Z\frac{\partial G}{\partial Z} \\ &+ I_1\gamma Z^2\frac{\partial G}{\partial Z} \\ &+ A_1\mu_1\frac{\partial G}{\partial Z}\end{aligned}$$

$$\frac{\partial G}{\partial t} = -(1-Z)[I_1\gamma Z - A_1\mu_1]\frac{\partial G}{\partial Z}$$

Therefore

$$\frac{\partial G}{\partial t} + (1-Z)[I_1\gamma Z - A_1\mu_1]\frac{\partial G}{\partial Z} = 0$$

The auxiliary equations are:

$$\frac{dt}{1} = \frac{dZ}{(1-Z)[I_1\gamma Z - A_1\mu_1]} = \frac{dG}{0}$$

Considering

$$\frac{dG}{0} = \frac{dt}{1}$$

Therefore

$$G(Z,t) = C_1$$

Next we consider

$$\frac{dt}{1} = \frac{dZ}{(1-Z)[I_1\gamma Z - A_1\mu_1]}$$

On integration and using partial fractions we have

$$\left(\frac{1-Z}{I_1\gamma Z - A_1\mu_1}\right)e^{[I_1\gamma - A_1\mu_1]t} = C_2$$

Where C_1 and C_2 are constants of integration. Setting C_1 as a function of C_2,we arrive at the most general solution

$$G_{A_1}(Z,t) = f\{(\frac{1-Z}{[I_1\gamma Z - A_1\mu_1]})e^{[I_1\gamma - A_1\mu_1]t}\}$$

Where f is an arbitrary differentiable function. We had denoted that $A_1(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let the initial population at time $t = 0$ be $A_1(0) = 0$ then

$$G_{A_1}(Z,0) = 1$$

Therefore

$$f\{\frac{1-Z}{[I_1\gamma Z - A_1\mu_1]}\} = 1 \tag{3.4.4}$$

This is for $|Z| < 1$. For any θ,

$$\theta = \frac{1-Z}{I_1\gamma Z - \mu}$$

We have

$$Z = \frac{1 + A_1\mu_1\theta}{1 + I_1\gamma\theta}$$

Hence we have

$$f(\theta) = 1$$

Therefore

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

3.5 NUMERICAL ILLUSTRATIONS

To demonstrate the applications of results of sections 2-4, in this section we assume some parameter values and solve for the expectations numerically. By this approach, one may then assess effects of various factors on the expected values, and the variance of the numbers of S persons, I persons and AIDS cases. To see the effects of drugs on the MTCT, we vary the value of β and compute the expected values of S persons, and I persons. Use of the drugs say, Azidovudine (AZT) and Nevirapine, reduces the rate at which the babies contract the virus from their infected mothers, that is it reduces $(1-\beta)$ which is the same as increasing β. From figure (3.1), we can see that with the introduction of the drugs for Prevention of mother to child Transmission (PMTCT), the number of Susceptible infants born by infected mothers increase. Figure (3.2) below shows that with PMTCT, MTCT decrease. That is there are few newborns who contract the disease from their infected mothers. Numerically we have:

Table 3.1: Effects Changing β

λ	μ	P1	β	t=Months	E[S1(t)]	E[I1(t)]	E[A1(t)]
0.36	0.112	0.5	0.32	20	8,650	118	
0.36	0.112	0.5	0.60	20	14,310	71	
0.36	0.112	0.5	0.73	20	18,090	56	
0.36	0.112	0.5	0.91	20	25,010	41	
S(t0)=100,000, I(t0)=100, Sk=Sk(t)/n=0.60, Ik=0.25, Ak=0.15 where k=1,2,3							

Figure 3.1: Effects of Changing β

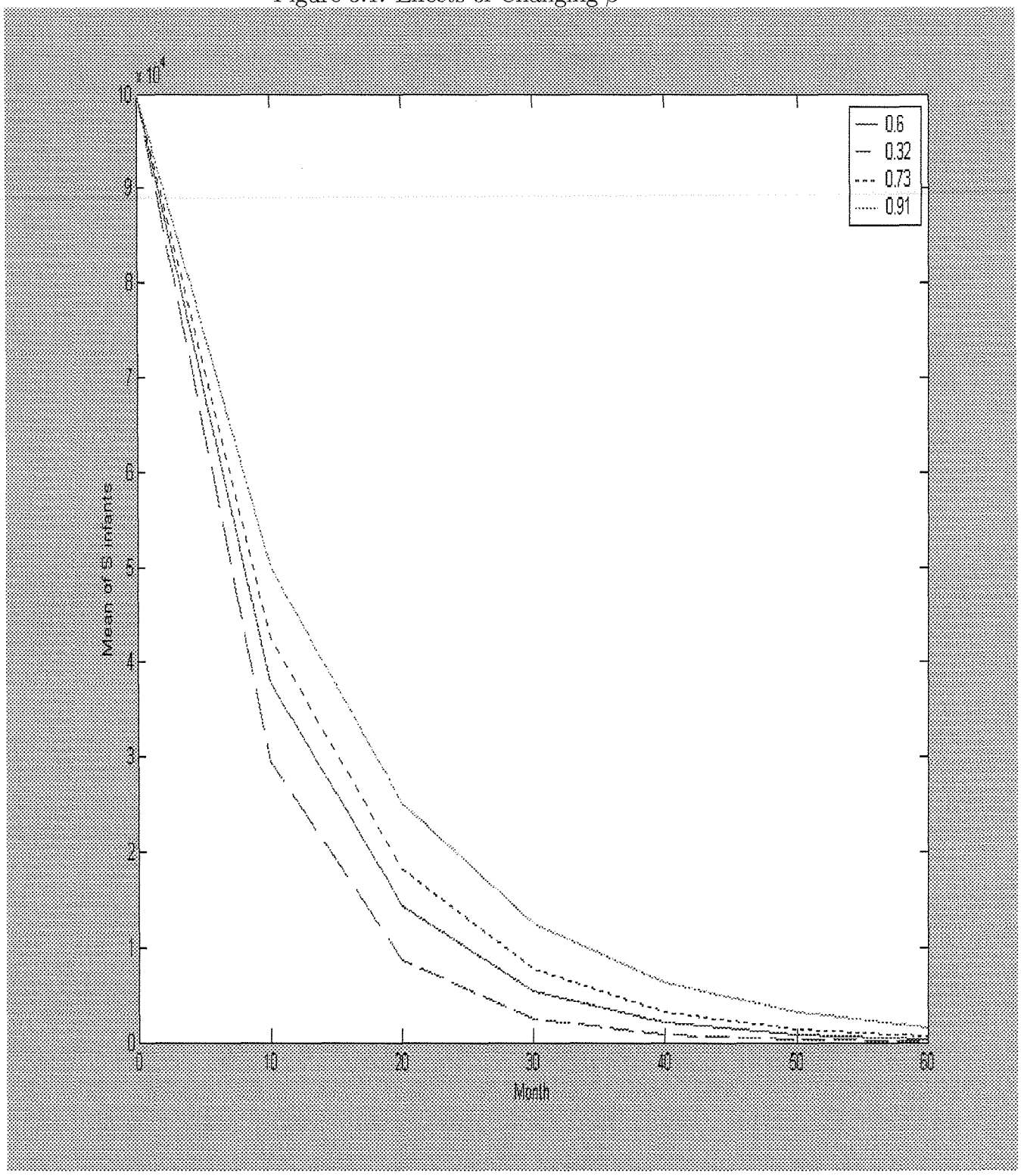
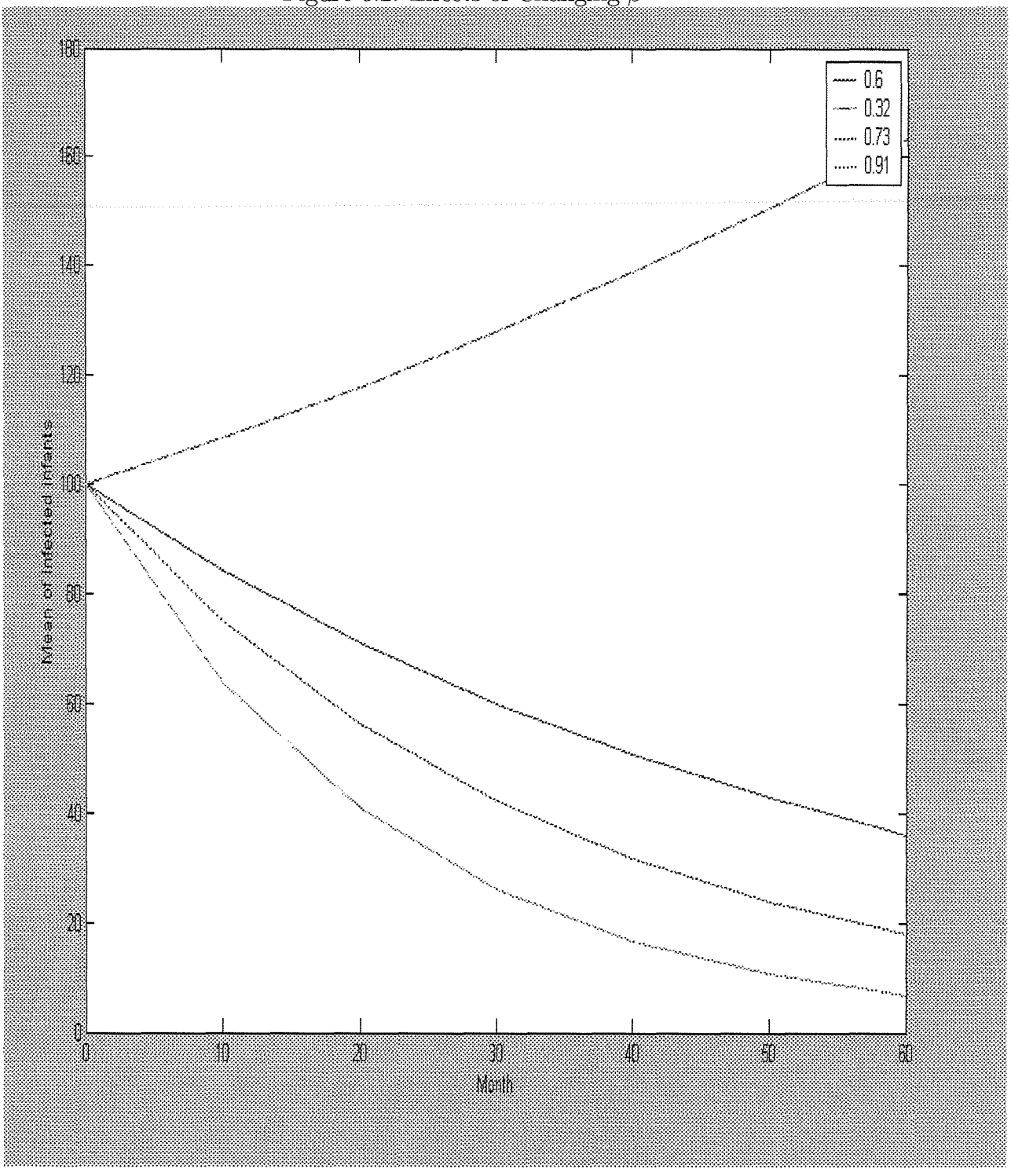


Figure 3.2: Effects of Changing β



Chapter 4

HETEROSEXUAL MODELS

4.1 Introduction

In this chapter,we consider a population consisting of the adults(15 and more years). It is this group that is sexually mature and active and, therefore, capable of reproduction. It is also this group that is responsible for the horizontal transmission of the HIV virus through heterosexual activities and for vertical transmission by infected mothers to their children. 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 its formulation in this chapter as a section.

Assumptions and notations

The population for this group at time t is subdivided into $S_3(t)$ and $S_2^*(t)$ Susceptibles(those free of HIV), $I_3(t)$ infectives (contacted the virus through heterosexual intercourse), and $A_3(t)$ AIDS cases (those who have developed full blown AIDS symptoms but are still alive).

Let the sexual contact rate between a mutually sexual S person and an I person be ω where $\omega \geq 0$. Thus the probability of a sexual contact between an S person and an I person during $(t, t+\Delta t)$ is $\omega\Delta t + o(\Delta t)$ where $\lim_{\Delta t \to 0} \frac{o(\Delta t)}{\Delta t} = 0$

• 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. Then the probability of an S person contracting HIV/AIDS virus from an I person by sexual contact is $\omega\delta\Delta t + o(\Delta t)$ and $\omega\delta = \sqrt{\omega_m\delta_m\omega_f\delta_f}$ 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 transition rate from infective to AIDS case γ. Thus , during $(t, t+\Delta t)$, the probability of that a transition will occur is $\gamma\Delta t + o(\Delta t)$ so that the incubation (infectious) period is $1/\gamma$

Let the death(death unrelated to HIV/AIDS) rate be μ_3 per person per time. Thus the probability that a person will die during the time interval $(t, t+\Delta t)$ is $\mu_1\Delta t + o(\Delta t)$ Hence the mean life expectancy is $1/\mu_3$

Since the rate of natural death is very much smaller than the rate of death from AIDS, we assume that those children with full blown symptoms die at the same rate μ_3

Let survival rate from age group 2 to group 3 be p_2,thus , during $(t, t+\Delta t)$, the probability that a person in age group 2 will survive the development period (5-15)years to age group 3 is $p_2\Delta t + o(\Delta t)$

4.2 Susceptible population model

4.2.1 $S_2^*(t)$ Model

In this section,we consider a population consisting of early non infecteds (5-15 years). It is assumed that the infected of group 1 will die before the age of 5 years. The population consists only of the non infecteds $S_2^*(t)$.

The population increases due to children from group 1 surviving to this group and decreases due to natural death or persons in this group surviving to the next group.

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

$$\begin{aligned}
P_r\{S_2^*(t+\Delta t) = n+1/S_2^*(t) = n\} &= p_1 S_1 \Delta t + o(\Delta t) \\
P_r\{S_2^*(t+\Delta t) \geq n+2/S_2^*(t) = n\} &= o(\Delta t) \\
P_r\{S_2^*(t+\Delta t) = n-1/S_2^*(t) = n\} &= nS_2^*(p_2+\mu_2)\Delta t + o(\Delta t) \\
P_r\{S_2^*(t+\Delta t) \leq n-2/S_2^*(t) = n\} &= o(\Delta t) \\
P_r\{S_2^*(t+\Delta t) = n/S_2^*(t) = n\} &= 1 - p_1 S_1 \Delta t - nS_2^*(p_2+\mu_2)\Delta t - o(\Delta t)
\end{aligned}$$

Let the probability distribution of the population size at time t be denoted by $S_{2n}^*(t) = P_r\{S_2^*(t) = n/S_2^*(0) = i\}$, $i < n$ and $i = 0, 1, ...$

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

$$\begin{aligned}
\lambda_n(t) &= p_1 S_1 \Delta t \\
\mu_n(t) &= nS_2^*(p_2+\mu_2)\Delta t
\end{aligned}$$

Hence

$$\begin{aligned}
S_{2n}^*(t+\Delta t) &= [1 - nS_2^*(p_2+\mu_2)\Delta t - p_1 S_1 \Delta t - o(\Delta t)]S_{2n}^*(t) \\
&+ [p_1 S_1 \Delta t + o(\Delta t)]S_{2n-1}^*(t) \\
&+ (n+1)S_2^*(p_2+\mu_2) + o(\Delta t)]S_{2n+1}^*(t)
\end{aligned}$$

which gives

$$\begin{aligned}
S_{2n}^*(t+\Delta t) - S_{2n}^*(t) &= [-p_1 S_1 \Delta t - nS_2^*(p_2+\mu_2)\Delta t - o(\Delta t)]S_{2n}^*(t) \\
&+ [p_1 S_1 \Delta t + o(\Delta t)]S_{2n-1}^*(t) \\
&+ [(n+1)S_2^*(p_2+\mu_2)\Delta t + o(\Delta t)]S_{2n+1}^*(t)
\end{aligned}$$

The Kolmogorov forward equations are:

$$\begin{aligned}
S_{2n}^{*\prime}(t) &= -[p_1 S_1 + nS_2^*(p_2+\mu_2)]S_{2n}^*(t) \\
&+ p_1 S_1 S_{2n-1}^*(t) \qquad \text{for } n \geq 1 \qquad (4.2.1.1) \\
&+ (n+1)S_2^*(p_2+\mu_2)S_{2n+1}^*(t),
\end{aligned}$$

$$S_0'(t) = -p_1 S_1 S_{20}^*(t) + S_2^*(p_2+\mu_2)S_{21}^*(t), \quad \text{for } n = 0 \qquad (4.2.1.2)$$

Where the primes indicate differentiation with respect to t In equation (1), there are 3 unknown probabilities; $S^*_{2n}(t)$, $S_{n-1}(t)$, and $S^*_{2n+1}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_S(Z,t) = \sum_{n=0}^{\infty} S^*_{2n}(t)Z^n$$

. With $n = 0$,in equation (4.2.1.2) $S_{-1}(t)$ is identically Zero. The coefficient of $S_{n-1}(t)$ arises from considering the conditional probability of "birth"into the population given that the population size is $n-1$. Multiplying equation (4.2.1.1) by Z^n and sum over $n = 1$, we have

$$\begin{aligned} \textstyle\sum_{n=1}^{\infty} S^{*\prime}_{2n}(t)Z^n &= -[S^*_2(p_2+\mu_2)]\textstyle\sum_{n=1}^{\infty} nS^*_{2n}(t)Z^n \\ &+ p_1S_1\textstyle\sum_{n=1}^{\infty} S^*_{2n}(t)Z^n \\ &+ p_1S_1\textstyle\sum_{n=1}^{\infty} S^*_{2n-1}(t)Z^n \\ &+ S^*_2(p_2+\mu_2)\textstyle\sum_{n=1}^{\infty}(n+1)S^*_{2n+1}(t)Z^n \end{aligned} \tag{4.2.1.3}$$

Define

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} S^{*\prime}_{2n}(t)Z^n \\ \tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nS^*_{2n}(t)Z^n \\ G(Z,t) &= \textstyle\sum_{n=0}^{\infty} S^*_{2n}(t)Z^n \end{aligned}$$

Therefore equation (4.2.1.3) becomes

$$\begin{aligned} \tfrac{\partial G}{\partial t} - S'_0(t) &= -S^*_2(p_2+\mu_2)Z\tfrac{\partial G}{\partial Z} \\ &- p_1S_1[G(Z,t) - S_0(t)] + p_1S_1ZG(Z,t) \\ &+ S^*_2(p_2+\mu_2)(\tfrac{\partial G}{\partial Z} - S^*_2(t)) \end{aligned}$$

From equation (4.2.1.2) we have

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= -S^*_2(p_2+\mu_2)Z\tfrac{\partial G}{\partial Z} \\ &- p_1S_1G(Z,t) + p_1S_1ZG(Z,t) \\ &+ S^*_2(p_2+\mu_2)\tfrac{\partial G}{\partial Z} \end{aligned}$$

$$\frac{\partial G}{\partial t} = -(Z-1)(S^*_2(p_2+\mu_2)\frac{\partial G}{\partial Z} + (Z-1)p_1S_1G(Z,t)$$

Therefore

$$\frac{\partial G}{\partial t} + (Z-1)S_2^*(p_2+\mu_2)\frac{\partial G}{\partial Z} = (Z-1)p_1 S_1 G(Z,t)$$

The auxiliary equations are:

$$\frac{dt}{1} = \frac{dZ}{(Z-1)S_2^*(p_2+\mu_2)} = \frac{dG}{(Z-1)p_1 S_1 G(Z,t)}$$

Considering

$$\frac{dG}{(Z-1)p_1 S_1 G(Z,t)} = \frac{dZ}{(Z-1)S_2^*(p_2+\mu_2)}$$

Therefore

$$G(Z,t)e^{-(\frac{p_1 S_1}{S_2^*(p_2+\mu_2)})Z} = C_1$$

Next we consider

$$\frac{dt}{1} = \frac{dZ}{(Z-1)S_2^*(p_2+\mu_2)}$$

On integration we have

$$(Z-1)e^{-S_2^*(p_2+\mu_2)t} = C_2$$

Where C_1 and C_2 are constants of integration. Setting C_1 as a function of C_2,we arrive at the most general solution

$$G_{S_2^*}(Z,t)e^{-(\frac{p_1 S_1}{S_2^*(p_2+\mu_2)})Z} = f\Big((Z-1)e^{-S_2^*(p_2+\mu_2)t}\Big)$$

Where f is an arbitrary differentiable function. We had denoted that $S_2^*(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let the initial population at time $t = 0$ be $S_2^*(0) = i$ then

$$G_{S_2^*}(Z,0) = Z^i$$

Therefore

$$f(Z-1) = Z^i e^{-(\frac{p_1 S_1}{S_2^*(p_2+\mu_2)})Z} \tag{4.2.1.4}$$

This is for $|Z| < 1$. For any θ,

$$\theta = (Z-1)$$

We have

$$Z = 1 + \theta$$

Hence we have

$$f(\theta) = (1+\theta)^i e^{-(\frac{p_1 S_1}{S_2^*(p_2+\mu_2)})1+\theta}$$

but

$$\begin{aligned} G_{S_2^*}(Z,t) &= f\Big(\theta e^{-S_2^*(p_2+\mu_2)t}\Big) \\ &= \Big(1+\theta e^{-S_2^*(p_2+\mu_2)t}\Big)^i e^{-(\frac{p_1 S_1}{S_2^*(p_2+\mu_2)})(1+\theta e^{-S_2^*(p_2+\mu_2)t})} \end{aligned}$$

Now replacing θ by $Z-1$ we have

$$G_{S_2^*}(Z,t) = \Big(1+(Z-1)e^{-S_2^*(p_2+\mu_2)t}\Big)^i exp\{-(\frac{p_1 S_1}{S_2^*(p_2+\mu_2)})(Z-1)(e^{-S_2^*(p_2+\mu_2)t}-1)\} \tag{4.2.1.5}$$

Now it is a simple matter of expanding the PGF to obtain the probability distribution $S_2^*(t)$.

Differentiating the PGF in equation (4.2.1.5) with respect to Z, we find the expectation and variance of $S_2^*(t)$:

$$E[S_2^*(t)] = \frac{p_1 S_1}{S_2^*(p_2+\mu_2)}(1-e^{-S_2^*(p_2+\mu_2)t}) + ie^{-S_2^*(p_2+\mu_2)t} \tag{4.2.1.6}$$

and

$$\delta^2(S_2^*(t)) = ie^{-S_2^*(p_2+\mu_2)t}[1-e^{-S_2^*(p_2+\mu_2)t}] + \frac{p_1 S_1}{S_2^*(p_2+\mu_2)}[1-e^{-S_2^*(p_2+\mu_2)t}] \tag{4.2.1.7}$$

4.2.2 $S_3(t)$ Model

In this model, changes in the numbers of Susceptible persons corresponds to immigration and death process; the "immigration" are the proportion of persons from age group 2 who survive the development period to age group three. "death" are the natural death and persons who contact the HIV virus to become HIV infected. 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 persons from age group

2 entering age group 3 during the time interval $(t, t+\Delta t)$

(iii) That there are $n+1$ individuals by time t and 1 dies or becomes infected during the time interval $(t, t+\Delta t)$

In the model, we study the heterosexual transmission mode. The change in population size during the time interval $(t, t+\Delta t)$ is governed by the following conditional probabilities;

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

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

$S_{3n}(t) = P_r\{S_3(t) = n/S_3(0) = i\}$, $i < n$ and $i = 0, 1, ...$

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

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

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

Let $S_{3n}(t)$ be the probability that the population size of age group 3 $N_3(t)$ has the value n at time t, $S_{3n-1}(t)$ the probability that the population size $N_3(t)$ has the value $n-1$ at time t, and $S_{3n+1}(t)$ the probability that the population size $N_3(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned}
S_{3n}(t+\Delta t) &= [1 - nS_3(\omega\delta + \mu_3)\Delta t - p_2 S_2^* \Delta t - o(\Delta t)]S_{3n}(t) \\
&+ [p_2 S_2^* \Delta t + o(\Delta t)]S_{3n-1}(t) \\
&+ (n+1)S_3(\omega\delta + \mu_3) + o(\Delta t)]S_{3n+1}(t)
\end{aligned}$$

which gives

$$\begin{aligned}
S_{3n}(t+\Delta t) - S_{3n}(t) &= [-p_2 S_2^* \Delta t - nS_3(\omega\delta + \mu_3)\Delta t - o(\Delta t)]S_{3n}(t) \\
&+ [p_2 S_2^* \Delta t + o(\Delta t)]S_{3n-1}(t) \\
&+ [(n+1)S_3(\omega\delta + \mu_3)\Delta t + o(\Delta t)]S_{3n+1}(t)
\end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we get the following Kolmogorov forward equations:

$$\begin{aligned} S_{3_n}'(t) &= -[p_2 S_2^* + nS_3(\omega\delta + \mu_3)]S_{3n}(t) \\ &+ p_2 S_2^* S_{3n-1}(t) \qquad \text{for n} \geq 1 \\ &+ (n+1)S_3(\omega\delta + \mu_3)S_{3n+1}(t), \end{aligned} \tag{4.2.2.1}$$

$$S_0'(t) = -p_2 S_2^* S_{30}(t) + S_3(\omega\delta + \mu_3)S_{31}(t), \quad \text{for n} = 0 \tag{4.2.2.2}$$

Where the primes indicate differentiation with respect to t In equation (4.2.2.1), there are 3 unknown probabilities; $S_{3n}(t)$, $S_{n-1}(t)$, and $S_{3n+1}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_S(Z,t) = \sum_{n=0}^{\infty} S_{3n}(t)Z^n$$

. With $n = 0$,in equation (4.2.2.2) $S_{-1}(t)$ is identically Zero. The coefficient of $S_{n-1}(t)$ arises from considering the conditional probability of immigration into the population given that the population size is $n-1$. Multiplying equation (1) by Z^n and sum over $n = 1$, we have

$$\begin{aligned} \textstyle\sum_{n=1}^{\infty} S_{3_n}'(t)Z^n &= -[S_3(\omega\delta + \mu_3)] \textstyle\sum_{n=1}^{\infty} nS_{3n}(t)Z^n \\ &+ p_2 S_2^* \textstyle\sum_{n=1}^{\infty} S_{3n}(t)Z^n \\ &+ p_2 S_2^* \textstyle\sum_{n=1}^{\infty} S_{3n-1}(t)Z^n \\ &+ S_3(\omega\delta + \mu_3) \textstyle\sum_{n=1}^{\infty}(n+1)S_{3n+1}(t)Z^n \end{aligned} \tag{4.2.2.3}$$

Define

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} S_{3_n}'(t)Z^n \\ \tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nS_{3n}(t)Z^n \\ G(Z,t) &= \textstyle\sum_{n=0}^{\infty} S_{3n}(t)Z^n \end{aligned}$$

Therefore equation (4.2.2.3) becomes

$$\begin{aligned} \tfrac{\partial G}{\partial t} - S_0'(t) &= -S_3(\omega\delta + \mu_3)Z\tfrac{\partial G}{\partial Z} \\ &- p_2 S_2^*[G(Z,t) - S_0(t)] + p_2 S_2^* ZG(Z,t) \\ &+ S_3(\omega\delta + \mu_3)(\tfrac{\partial G}{\partial Z} - S_3(t)) \end{aligned}$$

From equation (4.2.2.2) we have

$$\begin{aligned}\frac{\partial G}{\partial t} &= -S_3(\omega\delta+\mu_3)Z\frac{\partial G}{\partial Z} \\ &- p_2S_2^*G(Z,t)+p_2S_2^*ZG(Z,t) \\ &+ S_3(\omega\delta+\mu_3)\frac{\partial G}{\partial Z}\end{aligned}$$

$$\frac{\partial G}{\partial t}=-(Z-1)(S_3(\omega\delta+\mu_3)\frac{\partial G}{\partial Z}+(Z-1)p_2S_2^*G(Z,t)$$

Therefore

$$\frac{\partial G}{\partial t}+(Z-1)S_3(\omega\delta+\mu_3)\frac{\partial G}{\partial Z}=(Z-1)p_2S_2^*G(Z,t)$$

The auxiliary equations are:

$$\frac{dt}{1}=\frac{dZ}{(Z-1)S_3(\omega\delta+\mu_3)}=\frac{dG}{(Z-1)p_2S_2^*G(Z,t)}$$

Considering

$$\frac{dG}{(Z-1)p_2S_2^*G(Z,t)}=\frac{dZ}{(Z-1)S_3(\omega\delta+\mu_3)}$$

Therefore

$$G(Z,t)e^{-(\frac{p_2S_2^*}{s_3(\omega\delta+\mu_3)})Z}=C_1$$

Next we consider

$$\frac{dt}{1}=\frac{dZ}{(Z-1)S_3(\omega\delta+\mu_3)}$$

On integration we have

$$(Z-1)e^{-S_3(\omega\delta+\mu_3)t}=C_2$$

Where C_1 and C_2 are constants of integration. Setting C_1 as a function of C_2,we arrive at the most general solution

$$G_{S_3}(Z,t)e^{-(\frac{p_2S_2^*}{s_3(\omega\delta+\mu_3)})Z}=f\Big((Z-1)e^{-S_3(\omega\delta+\mu_3)t}\Big)$$

Where f is an arbitrary differentiable function. We had denoted that $S_3(t)$ is the size of the population at time t for $0\leq t\geq\infty$, let the initial population at time $t=0$ be $S_3(0)=i$ then

$$G_{S_3}(Z,0)=Z^i$$

Therefore

$$f(Z-1) = Z^i e^{-(\frac{p_2 S_2^*}{s_3(\omega\delta+\mu_3)})Z} \tag{4.2.2.4}$$

This is for $|Z| < 1$. For any θ,

$$\theta = (Z-1)$$

We have

$$Z = 1+\theta$$

Hence we have

$$f(\theta) = (1+\theta)^i e^{-(\frac{p_2 S_2^*}{s_3(\omega\delta+\mu_3)})1+\theta}$$

but

$$\begin{aligned} G_{S_3}(Z,t) &= f\Big(\theta e^{-S_3(\omega\delta+\mu_3)t}\Big) \\ &= \Big(1+\theta e^{-S_3(\omega\delta+\mu_3)t}\Big)^i exp\{-(\frac{p_2 S_2^*}{s_3(\omega\delta+\mu_3)})(1+\theta e^{-S_3(\omega\delta+\mu_3)t})\} \end{aligned}$$

Now replacing θ by $Z-1$ we have

$$G_{S_3}(Z,t) = \Big(1+(Z-1)e^{-S_3(\omega\delta+\mu_3)t}\Big)^i exp\{-(\frac{p_2 S_2^*}{s_3(\omega\delta+\mu_3)})(Z-1)(e^{-S_3(\omega\delta+\mu_3)t}-1)\} \tag{4.2.2.5}$$

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

Differentiating the PGF in equation (4.2.2.5) with respect to Z, we find the expectation and variance of $S_3(t)$:

$$E[S_3(t)] = \frac{p_2 S_2^*}{s_3(\omega\delta+\mu_3)}(1-e^{-S_3(\omega\delta+\mu_3)t}) + ie^{-S_3(\omega\delta+\mu_3)t} \tag{4.2.2.6}$$

and

$$\delta^2(S_3(t)) = ie^{-S_3(\omega\delta+\mu_3)t}[1-e^{-S_3(\omega\delta+\mu_3)t}] + \frac{p_2 S_2^*}{s_3(\omega\delta+\mu_3)}[1-e^{-S_3(\omega\delta+\mu_3)t}] \tag{4.2.2.7}$$

4.3 Asymptomatic (Infected) Model

In this model, changes in the numbers of persons infected are treated as a birth and death process; the "birth"are the new infections and "death"are the persons who de-

velop AIDS symptoms or die. The probability that there are n individuals in the infective 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 HIV transmission during the time interval $(t, t+\Delta t)$
(iii) That there are $n+1$ individuals by time t and 1 dies or develops the AIDS symptoms 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;

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

Let the probability distribution of the population size at time t be denoted by $I_{3n}(t) = P_r\{I_3(t) = n/I_3(0) = 1\}$, We seek to find this distribution by deriving a system of differential equations from the assumptions above. Now

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

Let $I_{3n}(t)$ be the probability that the population size of age group 3 $N_3(t)$ has the value n at time t, $I_{3n-1}(t)$ the probability that the population size $N_3(t)$ has the value $n-1$ at time t, and $I_{3n+1}(t)$ the probability that the population size $N_3(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned}
I_n(t+\Delta t) &= [1 - (nI_3\mu_3 + nI_3\omega\delta + nI_3\gamma)\Delta t + o(\Delta t)]I_n(t) \\
&+ ([(n-1)I_3\omega\delta]\Delta t + o(\Delta t))I_{n-1}(t) \\
&+ ([(n+1)I_3(\gamma+\mu_3)]\Delta t + o(\Delta t))I_{n+1}(t)
\end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we get the difference equations:

$$\begin{aligned} I_n'(t) &= -[nI_3\mu_3 + nI_3\omega\delta + nI_3\gamma]I_n(t) \\ &+ [(n-1)I_3\omega\delta+]I_{n-1}(t) \qquad \text{for } n \geq 1 \\ &+ [(n+1)I_3(\gamma+\mu_3)]I_{n+1}(t), \end{aligned} \tag{4.3.1}$$

$$I_0'(t) = [I_3\mu_3 + I_3\gamma]I_3(t), \quad \text{for } n = 0 \tag{4.3.2}$$

Where the primes indicate differentiation with respect to t In equation (4.3.1), there are 3 unknown probabilities; $I_n(t)$, $I_{n-1}(t)$, and $I_{n+1}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_S(Z,t) = \sum_{n=0}^{\infty} I_n(t)Z^n$$

. With $n = 0$,in equation (4.3.2) $I_{-1}(t)$ is identically Zero. The coefficient of $I_{n-1}(t)$ arises from considering the conditional probability of immigration into the population given that the population size is $n-1$. Multiplying equation (1) by Z^n and sum over $n = 1$, we have

$$\begin{aligned} \textstyle\sum_{n=1}^{\infty} I_n'(t)Z^n &= -[I_3\mu_3 + I_3\omega\delta + I_3\gamma]\textstyle\sum_{n=1}^{\infty} nI_n(t)Z^n \\ &+ (\omega\delta)I_3\textstyle\sum_{n=1}^{\infty}(n-1)I_{n-1}(t)Z^n \\ &+ [\mu_3+\gamma]I_3\textstyle\sum_{n=1}^{\infty}(n+1)I_{n+1}(t)Z^n \end{aligned} \tag{4.3.3}$$

Define

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} I_n'(t)Z^n \\ \tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nI_n(t)Z^n \\ G(Z,t) &= \textstyle\sum_{n=0}^{\infty} I_n(t)Z^n \end{aligned}$$

Therefore equation (4.3.3) becomes

$$\begin{aligned} \tfrac{\partial G}{\partial t} - I_0'(t) &= -(I_3\mu_3 + I_3\omega\delta + I_3\gamma)Z\tfrac{\partial G}{\partial Z} \\ &+ (\omega\delta)I_3Z^2\tfrac{\partial G}{\partial Z} \\ &+ I_3(\mu_3+\gamma)(\tfrac{\partial G}{\partial Z} - I_3(t)) \end{aligned}$$

From equation (4.3.2) we have

$$\begin{aligned}\frac{\partial G}{\partial t} &= -(I_3\omega\delta + I_3\mu_3 + I_3\gamma)Z\frac{\partial G}{\partial Z} \\ &+ (\omega\delta)I_3Z^2\frac{\partial G}{\partial Z} \\ &+ (\mu_3+\gamma)I_3\frac{\partial G}{\partial Z}\end{aligned}$$

$$\frac{\partial G}{\partial t} = -(1-Z)[(\omega\delta)I_3Z - (\mu_3+\gamma)I_3]\frac{\partial G}{\partial Z}$$

Therefore

$$\frac{\partial G}{\partial t} + (1-Z)[(\omega\delta)I_3Z - (\mu_3+\gamma)I_3]\frac{\partial G}{\partial Z} = 0$$

The auxiliary equations are:

$$\frac{dt}{1} = \frac{dZ}{(1-Z)[(\omega\delta)I_3Z - (\mu_3+\gamma)I_3]} = \frac{dG}{0}$$

Considering

$$\frac{dG}{0} = \frac{dt}{1}$$

Therefore

$$G(Z,t) = C_1$$

Next we consider

$$\frac{dt}{1} = \frac{dZ}{(1-Z)[(\omega\delta)I_3Z - (\mu_3+\gamma)I_3]}$$

On integration and using partial fractions we have

$$\left(\frac{1-Z}{\omega\delta)I_3Z - (\mu_3+\gamma)I_3}\right)e^{[\omega\delta)I_3-(\mu_3+\gamma)I_3]t} = C_2$$

Where C_1 and C_2 are constants of integration. Setting C_1 as a function of C_2,we arrive at the most general solution

$$G_{I_3}(Z,t) = f\left((\frac{1-Z}{[(\omega\delta)I_3Z - (\mu_3+\gamma)I_3]})e^{[\omega\delta)I_3-(\mu_3+\gamma)I_3]t}\right)$$

Where f is an arbitrary differentiable function. We had denoted that $I_3(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let the initial population at time $t = 0$ be $I_3(0) = 1$ then

$$G_{I_3}(Z,0) = Z$$

Therefore

$$f\Big(\frac{1-Z}{[(\omega\delta)I_3Z-(\mu_3+\gamma)I_3]}\Big)=Z \tag{4.3.4}$$

Let $\eta = I_3\omega\delta$ and $\nu = I_3(\mu_3+\gamma)$ then equation (4.3.4) becomes

$$f\Big(\frac{1-Z}{[\eta Z-\nu]}\Big)$$

This is for $|Z|<1$. For any θ,

$$\theta=\frac{1-Z}{\eta Z-\nu}$$

We have

$$Z=\frac{1+\nu\theta}{1+\eta\theta}$$

Hence we have

$$f(\theta)=\Big(\frac{1+\nu\theta}{1+\eta\theta}\Big)$$

Now replacing θ by $\frac{1-Z}{\eta Z-\nu}$ we have

$$G_{I_3}(Z,t)=\Big(\frac{(\eta Z-\nu)+\nu(1-Z)e^{(\eta-\nu)t}}{(\eta Z-\nu)+\eta(1-Z)e^{(\eta-\nu)t}}\Big) \tag{4.3.5}$$

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 (3.3.5) becomes

$$G_{I_3}(Z,t)=\Big(\frac{\alpha_(t)+[1-\alpha_(t)-\omega(t)]Z}{1-\omega(t)Z}\Big) \tag{4.3.6}$$

This is the PGF of the differential equation (4.3.1)

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

Differentiating the PGF in (4.3.6) with respect to Z, we find the expectation and variance of $I_3(t)$:

$$\begin{aligned} E[I_3(t)] &= \tfrac{1-\alpha_(t)}{1-\omega(t)} \\ &= e^{(\eta-\nu)t} \end{aligned} \tag{4.3.8}$$

and

$$\begin{aligned} \delta^2_{I_3} &= \frac{(1-\alpha_(t))(\alpha_(t)+\omega(t))}{(1-\omega(t))^2} \\ &= (\frac{\eta+\nu}{\eta-\nu})e^{(\eta-\nu)t}[e^{(\eta-\nu)t}-1]. \end{aligned} \tag{4.3.9}$$

by taking the limits as

$$\nu \rightarrow \eta$$

Where $\eta = I_3\omega\delta$ and $\nu = I_3(\mu_3+\gamma)$ 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.

4.4 Symptomatic (AIDS Case) model

In this model, changes in the numbers of AIDS case are treated as a birth and death process; the "birth"are the persons who become symptomatic and "death"are the deaths. The probability that there are n individuals in the symptomatic stage 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 developing the symptoms during the time interval $(t, t+\Delta t)$

(iii) That there are $n+1$ individuals by time t and 1 dies 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;

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

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

$A_{1n}(t) = P_r\{A_3(t) = n/A_3(0) = 0\}$,

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

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

Let $A_{3n}(t)$ be the probability that the population size of age group 3 $N_3(t)$ has the value n at time t, $A_{3n-1}(t)$ the probability that the population size $N_3(t)$ has the value $n-1$ at time t, and $A_{3n+1}(t)$ the probability that the population size $N_3(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned}
A_{1n}(t+\Delta t) &= [1 - nI_3\gamma\Delta t - nA_3\mu_3\Delta t - o(\Delta t)]A_{1n}(t) \\
&+ [(n-1)I_3\gamma\Delta t + o(\Delta t)]A_{1(n-1)}(t) \\
&+ [(n+1)A_3\mu_3\Delta t + o(\Delta t)]A_{1(n+1)}(t)
\end{aligned}$$

which gives

$$\begin{aligned}
A_{1n}(t+\Delta t) - A_{1n}(t) &= [-nI_3\gamma\Delta t - nA_3\mu_3\Delta t - o(\Delta t)]A_{1n}(t) \\
&+ nI_3\gamma\Delta t + o(\Delta t)]A_{1(n-1)}(t) \\
&+ [(n+1)A_3\mu_3\Delta t + o(\Delta t)]A_{1(n+1)}(t)
\end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we get the Kolmogorov forward equations:

$$\begin{aligned}
A'_{1n}(t) &= -[nI_3\gamma + nA_3\mu_3]A_{1n}(t) \\
&+ [(nI_3\gamma]A_{1(n-1)}(t) \qquad \text{for } n \geq 1 \qquad (4.4.1) \\
&+ (n+1)A_3\mu_3A_{1(n+1)}(t),
\end{aligned}$$

$$A_0'(t) = [A_3\mu_3]A_3(t), \quad \text{for } n = 0 \tag{4.4.2}$$

Where the primes indicate differentiation with respect to t In equation (4.4.1), there are 3 unknown probabilities; $A_{1n}(t)$, $A_{1(n-1)}(t)$, and $A_{1(n+1)}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_A(Z,t) = \sum_{n=0}^{\infty} A_{1n}(t)Z^n$$

. With $n = 0$,in equation (4.4.2) $A_{-1}(t)$ is identically Zero. The coefficient of $A_{n-1}(t)$ arises from considering the conditional probability of immigration into the population given that the population size is $n-1$. Multiplying equation (4.4.1) by Z^n and sum over $n = 1$, we have

$$\begin{aligned} \textstyle\sum_{n=1}^{\infty} A_{1n}'(t)Z^n &= -[I_3\gamma + A_3\mu_3]\textstyle\sum_{n=1}^{\infty} nA_{1n}(t)Z^n \\ &+ I_3\gamma\textstyle\sum_{n=1}^{\infty}(n-1)A_{n-1}(t)Z^n \\ &+ A_3\mu_3\textstyle\sum_{n=1}^{\infty}(n+1)A_{n+1}(t)Z^n \end{aligned} \tag{4.4.3}$$

Define

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} A_{1n}'(t)Z^n \\ \tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nA_{1n}(t)Z^n \\ G(Z,t) &= \textstyle\sum_{n=0}^{\infty} A_{1n}(t)Z^n \end{aligned}$$

Therefore equation (4.4.3) becomes

$$\begin{aligned} \tfrac{\partial G}{\partial t} - A_0'(t) &= -[I_3\gamma + A_3\mu_3]Z\tfrac{\partial G}{\partial Z} \\ &+ I_3\gamma Z^2\tfrac{\partial G}{\partial Z} \\ &+ A_3\mu_3(\tfrac{\partial G}{\partial Z} - A_3(t)) \end{aligned}$$

From equation (4.4.2) we have

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= -[I_3\gamma + A_3\mu_3]Z\tfrac{\partial G}{\partial Z} \\ &+ I_3\gamma Z^2\tfrac{\partial G}{\partial Z} \\ &+ A_3\mu_3\tfrac{\partial G}{\partial Z} \end{aligned}$$

$$\frac{\partial G}{\partial t} = -(1-Z)[I_3\gamma Z - A_3\mu_3 mu_1]\frac{\partial G}{\partial Z}$$

Therefore

$$\frac{\partial G}{\partial t} + (1 - Z)[I_3\gamma Z - A_3\mu_3]\frac{\partial G}{\partial Z} = 0$$

The auxiliary equations are:

$$\frac{dt}{1} = \frac{dZ}{(1 - Z)[I_3\gamma Z - A_3\mu_3]} = \frac{dG}{0}$$

Considering

$$\frac{dG}{0} = \frac{dt}{1}$$

Therefore

$$G(Z, t) = C_1$$

Next we consider

$$\frac{dt}{1} = \frac{dZ}{(1 - Z)[I_3\gamma Z - A_3\mu_3]}$$

On integration and using partial fractions we have

$$\left(\frac{1 - Z}{I_3\gamma Z - A_3\mu_3}\right)e^{[I_3\gamma - A_3\mu_3]t} = C_2$$

Where C_1 and C_2 are constants of integration. Setting C_1 as a function of C_2,we arrive at the most general solution

$$G_{A_3}(Z, t) = f\left((\frac{1 - Z}{[I_3\gamma Z - A_3\mu_3]})e^{[I_3\gamma - A_3\mu_3]t}\right)$$

Where f is an arbitrary differentiable function. We had denoted that $A_3(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let the initial population at time $t = 0$ be $A_3(0) = 0$ then

$$G_{A_3}(Z, 0) = 1$$

Therefore

$$f\left(\frac{1 - Z}{[I_3\gamma Z - A_3\mu_3]}\right) = 1 \tag{4.4.4}$$

This is for $|Z| < 1$. For any θ,

$$\theta = \frac{1 - Z}{I_3\gamma Z - \mu}$$

We have

$$Z = \frac{1 + A_3\mu_3\theta}{1 + I_3\gamma\theta}$$

Hence we have

$$f(\theta) = 1$$

Therefore

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

4.5 NUMERICAL ILLUSTRATIONS

In this section, we assume some parameter values and solve for the expectations numerically.The spread of the virus depends more on the number of sexual contacts with different sexual partners per unit time. The use of condoms reduces δ by a factor 0.90 ,if the condoms are used properly and increases the sexual contact rate(ω) because individuals would think that they are protected through the use of condoms.So,because of the possibility of failure of condoms, the improper use of condoms and an increase in ω, there is a possibility that $\omega\delta$ may not reduce much through the use of condoms in a community. Thats why in the figures (4.1) and (4.2), there is no observable changes.

Table 4.1: Effects of Changing ω

ω	μ	P1	γ	δ	t=Months	E[S1(t)]	E[I1(t)]	E[A1(t)]
0.01	0.0912	0.5	0.1	0.01	20	33440	38	
0.009	0.0912	0.5	0.1	0.01	20	33440	38	
0.0004	0.0912	0.5	0.1	0.01	20	33440	38	
0.00008	0.0912	0.5	0.1	0.01	20	33440	38	

Table 4.2: Effects of Changing ω and δ

ω	μ	P1	γ	δ	t=Months	E[S1(t)]	E[I1(t)]	E[A1(t)]
0.01	0.0912	0.5	0.1	0.01	20	33480	38	
0.009	0.0912	0.5	0.1	0.006	20	33480	38	
0.0004	0.0912	0.5	0.1	0.00001	20	33480	38	
0.00008	0.0912	0.5	0.1	0.000009	20	33480	38	

Figure 4.1: Effects of Changing ω

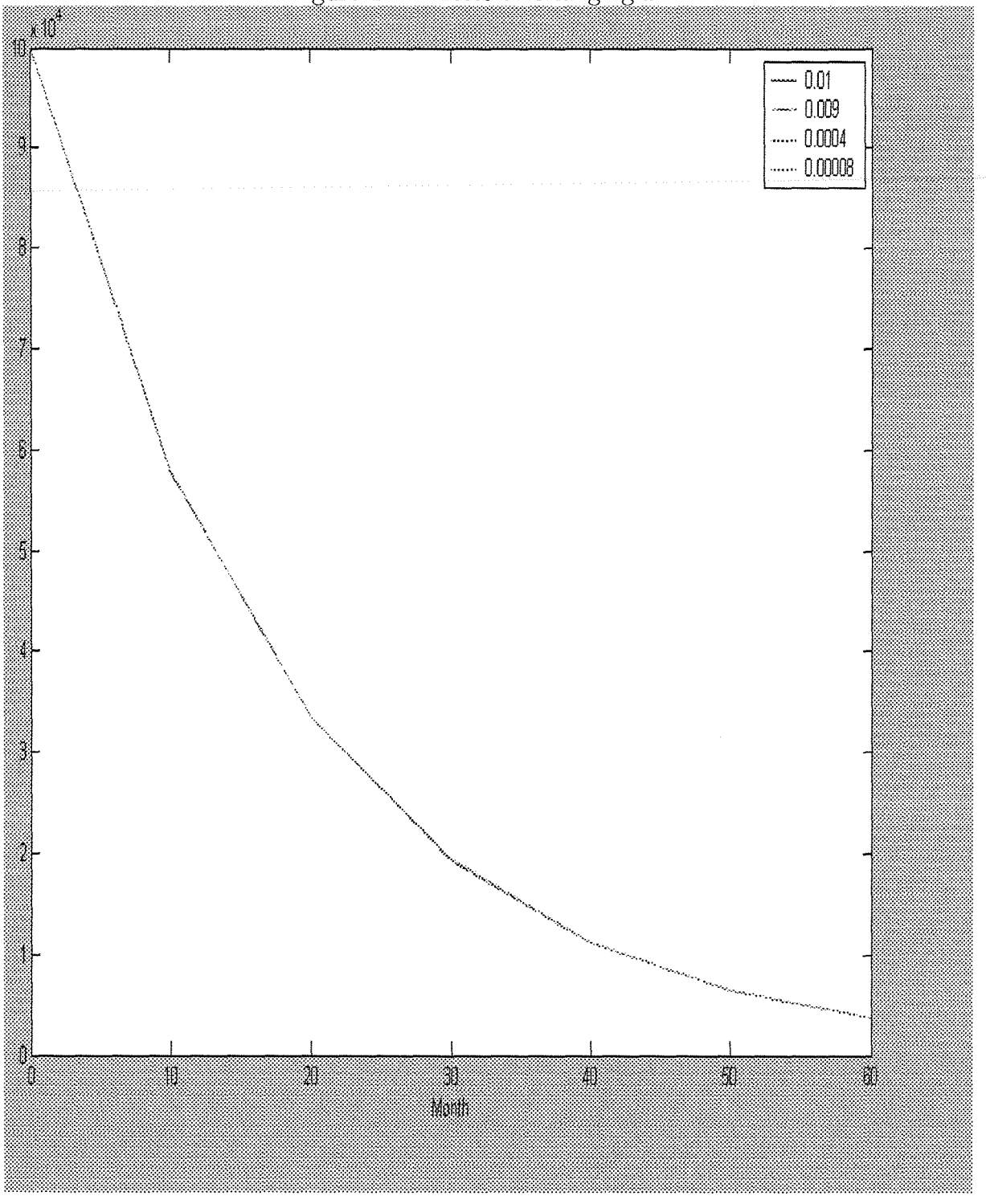
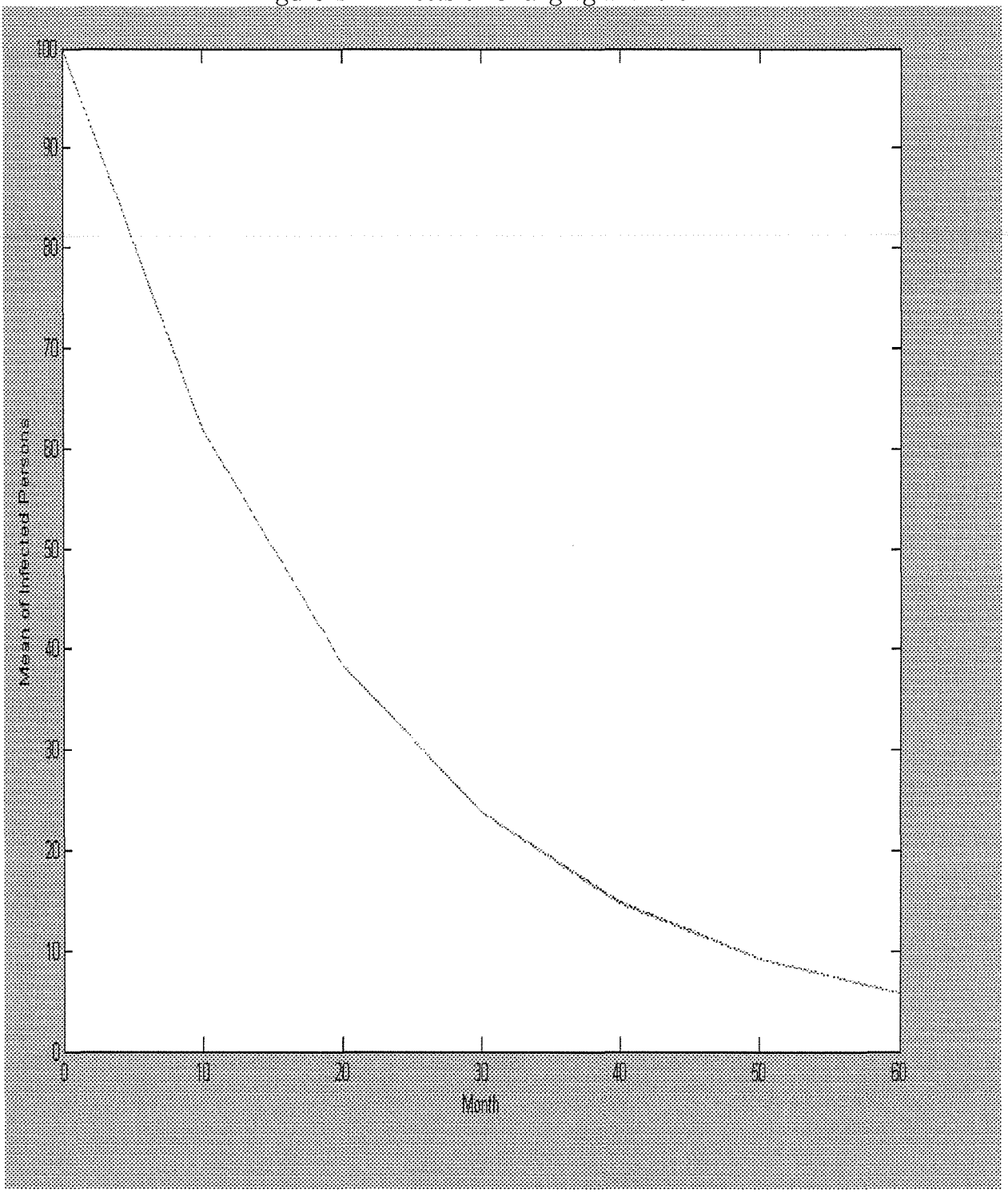


Figure 4.2: Effects of Changing ω and δ



Chapter 5

COMBINED MODEL

5.1 Introduction

In this chapter,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. This is equivalent to assuming that there is an equal probability for each S person to contact any I person.

Let:

$S(t)$: 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

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

Assumptions and notations

(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) With the same population size $n(n > 0)$ at time t, 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.

(i)Let the birth rate for sexually mature persons be λ per person per time. Thus the probability that a birth will occur in the heterosexual population during the time interval $(t, t + \Delta t)$ is $\lambda\Delta t + o(\Delta t)$
(I)Let the death(death unrelated to HIV/AIDS) or emigration rate (migrate out of the population because of fear of HIV/AIDS) be μ_k per person per time, where $k = 1, 2, 3$ (the different age groups have different per capita mortality rates), thus an individual existing at time t has a chance $\mu_k\Delta t+o(\Delta t)$ of dying during the time interval $(t, t+\Delta t)$. Hence the mean life expectancy is $1/\mu_k$
(Ii)Let the immigration rate for the sexually mature persons be α per time, this is

independent of the population, thus the probability that there will be immigration in to the heterosexual population during the time interval $(t, t+\Delta t)$ is $\alpha\Delta t + o(\Delta t)$ in the absence of HIV infection, the subpopulations $n_i(t)$ will approach the steady value of $N = \lambda/\mu_k$

(iv) Assumptions regarding HIV/AIDS spread (S-I): We let the sexual contact rate between a matually sexual S person and an I person be ω where $\omega \geq 0$. Thus the probability of a sexual contact between an S person and an I person during $(t, t+\Delta t)$ is $\omega\Delta t + o(\Delta t)$ where $\lim_{\Delta t \to 0} \frac{o(\Delta t)}{\Delta t} = 0$

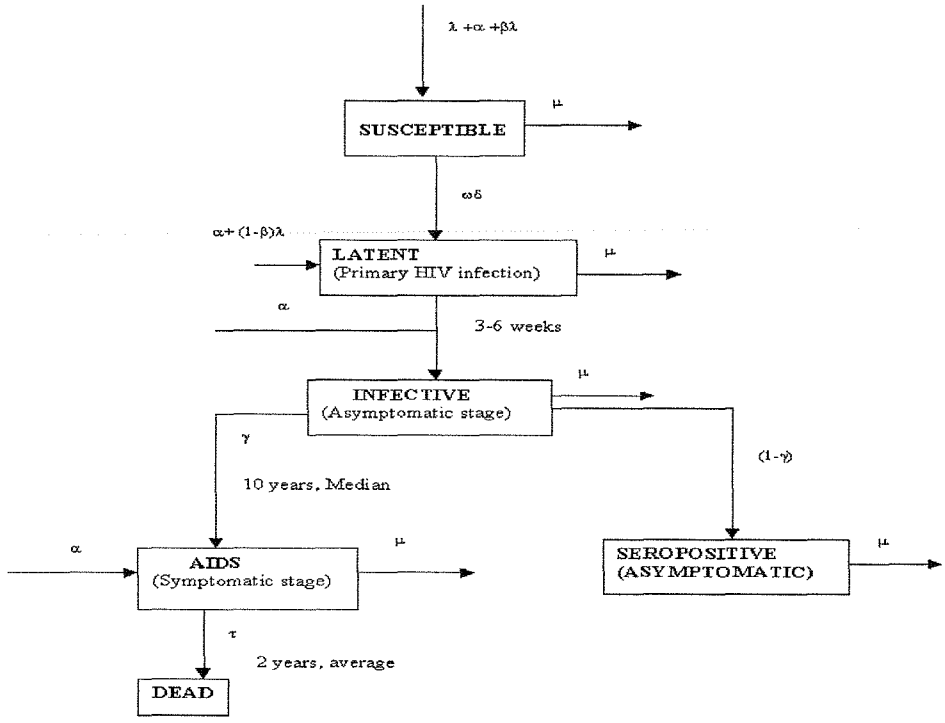
• Given a sexual contact between an S person and an I person during $(t, t+\Delta t)$, we let δ be the probability that this I person will transmit the AIDS virus to the S person. This event converts the S person to an I person. Then the probability of an S person contracting HIV/AIDS virus from an I person by sexual contact is $\omega\delta\Delta t + o(\Delta t)$ and $\omega\delta = \sqrt{\omega_m\delta_m\omega_f\delta_f}$ 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, thus the probability that a child born by infected mother will not contract the HIV virus during $(t, t+\Delta t)$ is $\beta\lambda\Delta t + o(\Delta t)$

The probability that the child born by infected mother is HIV positive is $(1-\beta)_a\lambda\Delta t + o(\Delta t)$

(v)Assumptions regarding incubation (I-A): Let the transition rate from infective to AIDS case γ, thus , during $(t, t+\Delta t)$, the probability of that a transition will occur is $\gamma\Delta t + o(\Delta t)$ so that the incubation (infectious) period is $1/\gamma$

Figure 5.1: HIV/AIDS Epidemic model



From the figure 1 above, Infants who did not get infected from their infected mothers enter the class S of susceptible individuals; that is, those who can become infected. When there is an adequate contact of a susceptible with an infective so that transmission occurs, then the susceptible enters the exposed class L of those in the latent period, who are infected but not yet infectious. After the latent period ends, the individual enters the class I of infectives, who are infectious in the sense that they are capable of transmitting the infection. When the infectious period ends, the individual enters the AIDS class A consisting of those who have acquired full-blown symptoms.

5.2 SUSCEPTIBLE POPULATION MODEL

In this model, changes in the numbers of Susceptible persons are treated as a birth and death process; the "birth"are the immigrants or births by both non and infected mothers and "death" are the natural death, persons who contact the HIV virus or the emigrants . 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 $(t, t + \Delta t)$

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

(Ii) 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 $(t, t + \Delta t)$

In the model, we study the two modes of transmission of the HIV virus: Heterosexual transmission and the Mother-to-child transmission(That is Horizontal and vertical transmission). The change in population size during the time interval $(t, t + \Delta t)$ is

governed by the following conditional probabilities;

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

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

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

Let $S_n(t)$ be the probability that the population size $N(t)$ has the value n at time t, $S_{n-1}(t)$ the probability that the population size $N(t)$ has the value $n-1$ at time t, and $S_{n+1}(t)$ the probability that the population size $N(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned}
S_n(t+\Delta t) &= [1 - nS_3\lambda\Delta t - \alpha\Delta t - nI_3\beta\lambda\Delta t - nS_k\mu_k\Delta t - nI_3\omega\delta\Delta t - o(\Delta t)]S_n(t) \\
&+ [\alpha\Delta t + (n-1)S_3\lambda\Delta t + (n-1)I_3\beta\lambda\Delta t + o(\Delta t)]S_{n-1}(t) \\
&+ [(n+1)S_k\mu_k\Delta t + (n+1)I_3\omega\delta\Delta t + o(\Delta t)]S_{n+1}(t)
\end{aligned}$$

which gives

$$\begin{aligned}
S_n(t+\Delta t) - S_n(t) &= [-nS_3\lambda\Delta t - \alpha\Delta t - nI_3\beta\lambda\Delta t - nS_k\mu_k\Delta t - nI_3\omega\delta\Delta t - o(\Delta t)]S_n(t) \\
&+ [\alpha\Delta t + (n-1)S_3\lambda\Delta t + (n-1)I_3\beta\lambda\Delta t + o(\Delta t)]S_{n-1}(t) \\
&+ [(n+1)S_k\mu_k\Delta t + (n+1)I_3\omega\delta\Delta t + o(\Delta t)]S_{n+1}(t)
\end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we get the following Kolmogorov forward equations:

$$\begin{aligned}
S_n'(t) &= -[nS_3\lambda + \alpha + nS_k\mu_k + nI_3\beta\lambda + nI_3\omega\delta]S_n(t) \\
&+ [\alpha + (n-1)S_3\lambda + (n-1)I_3\beta\lambda]S_{n-1}(t) \qquad \text{for } n \geq 1 \qquad (5.2.1) \\
&+ [(n+1)S_k\mu_k + (n+1)I_3\omega\delta]S_{n+1}(t),
\end{aligned}$$

$$S_0'(t) = -\alpha S_0(t) + [S_k\mu_k + I_3\omega\delta]S_1(t), \quad \text{for n} = 0 \tag{5.2.2}$$

Where the primes indicate differentiation with respect to t In equation (5.2.1), there are 3 unknown probabilities; $S_n(t)$, $S_{n-1}(t)$, and $S_{n+1}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_S(Z,t) = \sum_{n=0}^{\infty} S_n(t)Z^n$$

. With $n = 0$,in equation (5.2.2) $S_{-1}(t)$ is identically Zero. The coefficient of $S_{n-1}(t)$ arises from considering the conditional probability of "birth"into the population given that the population size is $n-1$. Multiplying equation (5.2.1) by Z^n and sum over $n = 1$, we have

$$\begin{aligned}
\textstyle\sum_{n=1}^{\infty} S_n'(t)Z^n &= -[S_3\lambda + I_3\beta\lambda + I_3\omega\delta]\textstyle\sum_{n=1}^{\infty} nS_n(t)Z^n \\
&- \alpha\textstyle\sum_{n=1}^{\infty} S_n(t)Z^n + \alpha\sum_{n=1}^{\infty} S_{n-1}(t)Z^n \\
&+ S_3\lambda\textstyle\sum_{n=1}^{\infty}(n-1)S_{n-1}(t)Z^n + I_3\beta\lambda\sum_{n=1}^{\infty}(n-1)S_{n-1}(t)Z^n \\
&+ S_k\mu_k\textstyle\sum_{n=1}^{\infty}(n+1)S_{n+1}(t)Z^n + I_3\omega\delta\sum_{n=1}^{\infty}(n+1)S_{n+1}(t)Z^n
\end{aligned} \tag{5.2.3}$$

Define

$$\begin{aligned}
\tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} S_n'(t)Z^n \\
\tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nS_n(t)Z^n \\
G(Z,t) &= \textstyle\sum_{n=0}^{\infty} S_n(t)Z^n
\end{aligned}$$

Therefore equation (5.2.3) becomes

$$\begin{aligned}
\tfrac{\partial G}{\partial t} - S_0'(t) &= -\alpha[G(Z,t) - S_0(t)] - [S_3\lambda + I_3\beta\lambda + I_3\omega\delta + S_k\mu_k]Z\tfrac{\partial G}{\partial Z} \\
&+ (S_3\lambda + I_3\beta\lambda)Z^2\tfrac{\partial G}{\partial Z} + \alpha ZG(Z,t) \\
&+ [S_k\mu_k + I_3\omega\delta](\tfrac{\partial G}{\partial Z} - S_1(t))
\end{aligned}$$

From equation (5.2.2) we have

$$\begin{aligned}
\tfrac{\partial G}{\partial t} &= -\alpha G(Z,t) - [S_3\lambda + I_3\beta\lambda + S_k\mu_k + I_3\omega\delta]Z\tfrac{\partial G}{\partial Z} \\
&+ (S_3\lambda + I_3\beta\lambda)Z^2\tfrac{\partial G}{\partial Z} + \alpha ZG(Z,t) \\
&+ (S_k\mu_k + I_3\omega\delta)\tfrac{\partial G}{\partial Z}
\end{aligned}$$

$$\frac{\partial G}{\partial t} = (Z-1)\alpha G(Z,t) + (Z-1)[(S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta)]\frac{\partial G}{\partial Z}$$

Therefore

$$\frac{\partial G}{\partial t} - (Z-1)[(S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta)]\frac{\partial G}{\partial Z} = (Z-1)\alpha G(Z,t)$$

The auxiliary equations are:

$$\frac{dt}{1} = -\frac{dZ}{(Z-1)[(S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta)]} = \frac{dG}{(Z-1)\alpha G(Z,t)}$$

Considering

$$\frac{dZ}{[(S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta)]} = \frac{dG}{\alpha G(Z,t)}$$

and On integration we have

$$((S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta))^{\alpha/(S_3\lambda + I_3\beta\lambda)}G(Z,t) = C_1$$

Next we consider

$$\frac{dt}{1} = -\frac{dZ}{(Z-1)[(S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta)]}$$

On integration we have

$$\left(\frac{[((S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta)]}{Z-1}\right)e^{-[((S_3\lambda + I_3\beta\lambda) - (S_k\mu_k + I_3\omega\delta)]t} = C_2$$

Where C_1 and C_2 are constants of integration. setting C_1 as a function of C_2,we arrive at the most general solution

$$[((S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta)]^{\alpha/((S_3\lambda + I_3\beta\lambda)}G(Z,t)$$

$$= f\left\{\left(\frac{[((S_3\lambda + I_3\beta\lambda)Z - (S_k\mu_k + I_3\omega\delta)]}{Z-1}\right)e^{-[((S_3\lambda + I_3\beta\lambda) - (S_k\mu_k + I_3\omega\delta)]t}\right\}$$

We had denoted that $S(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let the initial population at time $t = 0$ be $S(0) = m$ then

$$G(Z,0) = Z^m$$

Therefore

$$[((S_3\lambda+I_3\beta\lambda)Z-(S_k\mu_k+I_3\omega\delta)]^{\alpha/(S_3\lambda+I_3\beta\lambda)}Z^m = f\Big(\frac{[(S_3\lambda+I_3\beta\lambda)Z-(S_k\mu_k+I_3\omega\delta)]}{Z-1}\Big) \tag{5.2.4}$$

Let $\eta = ((S_3\lambda + I_3\beta\lambda)$ and $\nu = (S_k\mu_k + I_3\omega\delta)$ then equation (5.2.4) becomes

$$(\eta Z-\nu)^{\alpha/\eta}Z^m = f\Big(\frac{\eta Z-\nu}{Z-1}\Big)$$

This is for $|Z| < 1$. For any θ,

$$\theta = \frac{\eta Z-\nu}{Z-1}$$

We have

$$Z = \frac{\nu-\theta}{\eta-\theta}$$

Hence we have

$$\begin{aligned} f(\theta) &= \Big\{\eta\Big(\frac{\nu-\theta}{\eta-\theta}\Big)-\nu\Big\}^{\alpha/\eta}\Big(\frac{\nu-\theta}{\eta-\theta}\Big)^m \\ &= \Big\{\frac{\theta(\nu-\eta)}{\eta-\theta}\Big\}^{\alpha/\eta}\Big(\frac{\nu-\theta}{\eta-\theta}\Big)^m \\ &= \theta^{\alpha/\eta}(\nu-\eta)^{\alpha/\eta}(\eta-\theta)^{-(\alpha/\eta+m)}(\nu-\theta)^m \end{aligned}$$

but

$$(\eta Z-\nu)^{\alpha/\eta}G(Z,t) = f\Big(\theta e^{-(\eta-\nu)t}\Big)$$

Therefore

$$G(Z,t) = (\eta Z-\nu)^{-\alpha/\eta}[\theta e^{-(\eta-\nu)t}]^{\alpha/\eta}(\nu-\eta)^{\alpha/\eta}(\eta-\theta e^{-(\eta-\nu)t})^{-(\alpha/\eta+m)}(\nu-\theta e^{-(\eta-\nu)t})^m \tag{5.2.5}$$

Now replacing θ by $\frac{\eta Z-\nu}{Z-1}$ we have

$$G(Z,t) = \frac{(\eta-\nu)^{\alpha/\eta}[(\nu e^{(\eta-\nu)t}-\nu)-Z(\nu e^{(\eta-\nu)t}-\eta)]^m}{[(\eta e^{(\eta-\nu)t}-\nu)-\eta Z(e^{(\eta-\nu)t}-1)]^{\alpha/\eta+m}} \tag{5.2.6}$$

Differentiating the PGF in (5.2.6) with respect to Z, we find the expectation and variance of $S(t)$:

$$E[S(t)] = me^{(\eta-\nu)t} + \alpha\frac{e^{(\eta-\nu)t}-1}{(\eta-\nu)} \tag{5.2.7}$$

and

$$\delta_S^2 = m(\frac{\eta+\nu}{\eta-\nu})e^{(\eta-\nu)t}[e^{(\eta-\nu)t}-1] + \alpha\frac{e^{(\eta-\nu)t}-1}{(\eta-\nu)}. \tag{5.2.8}$$

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

5.3 ASYMPTOMATIC (INFECTED) MODEL

In this model, changes in the numbers of persons infected are treated as a birth and death process; the "birth"are the new infections(including infected mother to child) and those who migrate to the population , and "death"are the persons who develop AIDS symptoms or die or migrate. The probability that there are n individuals in the infective 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 $(t, t+\Delta t)$
(I)That there are $n-1$ individuals by time t and 1 is added by HIV transmission,immigration or Mother-to child transmission during the time interval $(t, t+\Delta t)$
(Ii) That there are $n+1$ individuals by time t and 1 dies or converts to AIDS 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;

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

Let the probability distribution of the population size at time t be denoted by
$I_n(t) = P_r\{I(t) = n/I(0) = 1\}$,
We seek to find this distribution by deriving a system of differential equations from the assumptions above. Now

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

Let $I_n(t)$ be the probability that the population size $N(t)$ has the value n at time t, $I_{n-1}(t)$ the probability that the population size $N(t)$ has the value $n-1$ at time t,

and $I_{n+1}(t)$ the probability that the population size $N(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned} I_n(t+\Delta t) &= [1-(nI_k\mu_k+\alpha+nI_3(1-\beta)_a\lambda+nI_3\omega\delta+nI_3\gamma)\Delta t+o(\Delta t)]I_n(t) \\ &+ \{[(n-1)I_3\beta\lambda+(n-1)I_3\omega\delta+\alpha]\Delta t+o(\Delta t)\}I_{n-1}(t) \\ &+ \{[(n+1)I_3\gamma+(n+1)I_k\mu_k]\Delta t+o(\Delta t)\}I_{n+1}(t) \end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we get the following Kolmogorov forward equations:

$$\begin{aligned} I_n'(t) &= -[nI_k\mu_k+\alpha+nI_3(1-\beta)_a\lambda+nI_3\omega\delta+nI_3\gamma]I_n(t) \\ &+ [(n-1)I_3(1-\beta)_a\lambda+(n-1)I_3\omega\delta+\alpha]I_{n-1}(t) \qquad \text{for } n \geq 1 \qquad (5.3.1) \\ &+ [(n+1)I_3\gamma+(n+1)I_k\mu_k]I_{n+1}(t), \end{aligned}$$

$$I_0'(t) = -\alpha I_0(t)+[I_k\mu_k+I_3\gamma]S_1(t), \quad \text{for } n=0 \qquad (5.3.2)$$

Where the primes indicate differentiation with respect to t In equation (5.3.1), there are 3 unknown probabilities; $I_n(t)$, $I_{n-1}(t)$, and $I_{n+1}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_S(Z,t) = \sum_{n=0}^{\infty} I_n(t)Z^n$$

. With $n=0$,in equation (5.3.2) $I_{-1}(t)$ is identically Zero. The coefficient of $I_{n-1}(t)$ arises from considering the conditional probability of "birth"into the population given that the population size is $n-1$. Multiplying equation (5.3.1) by Z^n and sum over $n=1$, we have

$$\begin{aligned} \textstyle\sum_{n=1}^{\infty} I_n'(t)Z^n &= -[nI_k\mu_k+nI_3(1-\beta)_a\lambda+nI_3\omega\delta+nI_3\gamma]\textstyle\sum_{n=1}^{\infty} nI_n(t)Z^n \\ &- \alpha\textstyle\sum_{n=1}^{\infty} I_n(t)Z^n \\ &+ \alpha\textstyle\sum_{n=1}^{\infty} I_{n-1}(t)Z^n \\ &+ ((1-\beta)_a\lambda+\omega\delta)I_3\textstyle\sum_{n=1}^{\infty}(n-1)I_{n-1}(t)Z^n+[\mu_k+\gamma]I_k\textstyle\sum_{n=1}^{\infty}(n+1)I_{n+1}(t)Z^n \end{aligned} \qquad (5.3.3)$$

Define

$$\begin{aligned} \tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} I_n'(t)Z^n \\ \tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nS_n(t)Z^n \\ G(Z,t) &= \textstyle\sum_{n=0}^{\infty} S_n(t)Z^n \end{aligned}$$

Therefore equation (5.3.3) becomes

$$\begin{aligned}\frac{\partial G}{\partial t} - I_0'(t) &= -\alpha[G(Z,t) - I_0(t)] - (I_k\mu_k + I_3(1-\beta)_a\lambda + I_3\omega\delta + I_3\gamma)Z\frac{\partial G}{\partial Z} \\ &+ ((1-\beta)_a\lambda + \omega\delta)I_3Z^2\frac{\partial G}{\partial Z} + \alpha ZG(Z,t) \\ &+ (\mu_k + \gamma)(\frac{\partial G}{\partial Z} - I_1(t))\end{aligned}$$

From equation (5.3.2) we have

$$\begin{aligned}\frac{\partial G}{\partial t} &= -\alpha G(Z,t) - ((1-\beta)_a\lambda + \mu_k + \omega\delta + \gamma)I_3Z\frac{\partial G}{\partial Z} \\ &+ ((1-\beta)_a\lambda + \omega\delta)I_3Z^2\frac{\partial G}{\partial Z} + \alpha ZG(Z,t) \\ &+ (\mu_k + \gamma)I_k\frac{\partial G}{\partial Z} \\ \frac{\partial G}{\partial t} &= (Z-1)\alpha G(Z,t) + (Z-1)[((1-\beta)_a\lambda + \omega\delta)I_3Z - (\mu_k + \gamma)I_k]\frac{\partial G}{\partial Z}\end{aligned}$$

Therefore

$$\frac{\partial G}{\partial t} - (Z-1)[((1-\beta)_a\lambda + \omega\delta)I_3Z - (\mu_k + \gamma)I_k]\frac{\partial G}{\partial Z} = (Z-1)\alpha G(Z,t)$$

The auxiliary equations are:

$$\frac{dt}{1} = -\frac{dZ}{(Z-1)[((1-\beta)_a\lambda + \omega\delta)I_3Z - (\mu_k + \gamma)I - k]} = \frac{dG}{(Z-1)\alpha G(Z,t)}$$

Considering

$$\frac{dZ}{[((1-\beta)_a\lambda + \omega\delta)I_3Z - (\mu_k + \gamma)I_k]} = \frac{dG}{\alpha G(Z,t)}$$

and On integration we have

$$(((1-\beta)_a\lambda + \omega\delta)I_3Z - I_k(\mu_k + \gamma)^{\alpha/[(1-\beta)_a\lambda + \omega\delta]I_3}G(Z,t) = C_1$$

Next we consider

$$\frac{dt}{1} = -\frac{dZ}{(Z-1)[((1-\beta)_a\lambda + \omega\delta)I_3Z - (\mu_k + \gamma)I_k]}$$

On integration we have

$$\left(\frac{[((1-\beta)_a\lambda + \omega\delta)I_3Z - (\mu_k + \gamma)I_k]}{Z-1}\right)e^{-[((1-\beta)_a\lambda + \omega\delta)I_3 - (\mu_k + \gamma)I_k]t} = C_2$$

Where C_1 and C_2 are constants of integration. setting C_1 as a function of C_2,we arrive at the most general solution

$$[((1-\beta)_a\lambda + \omega\delta)I_3Z - (\mu_k + \gamma)I_k]^{\alpha/[(1-\beta)_a\lambda + \omega\delta]I_3}G(Z,t) = f\left\{\left(\frac{[((1-\beta)_a\lambda + \omega\delta)I_3Z - (\mu_k + \gamma)I_k]}{Z-1}\right)e^{-}\right.$$

We had denoted that $I(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let there be one infected person at time $t = 0$ that is, $I(0) = 1$ then

$$G(Z, 0) = Z$$

Therefore

$$[((1-\beta)_a\lambda+\omega\delta)I_3Z-(\mu_k+\gamma)I_k]^{\alpha/[(1-\beta)_a\lambda+\omega\delta]I_3}Z = f\Big(\frac{[((1-\beta)_a\lambda+\omega\delta)I_3Z-(\mu_k+\gamma)I_k]}{Z-1}\Big)$$

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

$$(\rho Z - \kappa)^{\alpha/\rho}Z = f\Big(\frac{\rho Z - \kappa}{Z-1}\Big)$$

This is for $|Z| < 1$. For any θ,

$$\theta = \frac{\rho Z - \kappa}{Z-1}$$

We have

$$Z = \frac{\kappa - \theta}{\rho - \theta}$$

Hence we have

$$\begin{aligned} f(\theta) &= \Big\{\rho\Big(\frac{\kappa-\theta}{\rho-\theta}\Big)-\kappa\Big\}^{\alpha/\rho}\Big(\frac{\kappa-\theta}{\rho-\theta}\Big) \\ &= \Big\{\frac{\theta(\kappa-\rho)}{\rho-\theta}\Big\}^{\alpha/\rho}\Big(\frac{\kappa-\theta}{\rho-\theta}\Big) \\ &= \theta^{\alpha/\rho}(\kappa-\rho)^{\alpha/\rho}(\rho-\theta)^{-(1+\alpha/\rho)}(\kappa-\theta) \end{aligned}$$

but

$$(\rho Z - \kappa)^{\alpha/\rho}G(Z,t) = f\Big(\theta e^{-(\rho-\kappa)t}\Big)$$

therefore

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

Now replacing θ by $\frac{\rho Z-\kappa}{Z-1}$ we have

$$G(Z,t) = \frac{(\rho-\kappa)^{\alpha/\rho}[\kappa e^{(\rho-\kappa)t}-1)-Z(\kappa e^{(\rho-\kappa)t}-1)]}{[(\rho e^{(\rho-\kappa)t}-\kappa-\rho Z(e^{(\rho-\kappa)t}-1)]^{1+\alpha/\rho}} \tag{5.2.6}$$

Differentiating the PGF in (5.2.6) with respect to Z, we find the expectation and variance of $S(t)$:

$$E[S(t)] = e^{(\rho-\kappa)t} + \alpha\frac{e^{(\rho-\kappa)t} - 1}{(\rho - \kappa)} \tag{5.2.7}$$

and

$$\delta_S^2 = (\frac{\rho + \kappa}{\rho - \kappa})e^{(\rho-\kappa)t}[e^{(\rho-\kappa)t} - 1] + \alpha\frac{e^{(\rho-\kappa)t} - 1}{(\rho - \kappa)}. \tag{5.2.8}$$

5.4 SYMPTOMATIC (AIDS CASE) MODEL

In this model, changes in the numbers of persons with AIDS symptoms are treated as a birth and death process; the "birth"are the immigrants and persons who transit from infective to AIDS case and "death"" is the death due to AIDS. The probability that there are n individuals in the AIDS case 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 $(t, t + \Delta t)$

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

(Ii) That there are $n + 1$ individuals by time t and 1 dies 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;

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

Let the probability distribution of the population size at time t be denoted by $A_n(t) = P_r\{A(t) = n/A(0) = 0\{$

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

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

Let $A_n(t)$ be the probability that the population size $N(t)$ has the value n at time t, $A_{n-1}(t)$ the probability that the population size $N(t)$ has the value $n-1$ at time t, and $A_{n+1}(t)$ the probability that the population size $N(t)$ has the value $n+1$ at time t, then from the given rules it follows that:

$$\begin{aligned}A_n(t+\Delta t) &= [1 - nA\mu_k\Delta t - nI\gamma\Delta t - \alpha\Delta t - o(\Delta t)]A_n(t) \\ &+ [\alpha\Delta t + (n-1)I\gamma\Delta t + o(\Delta t)]A_{n-1}(t) \\ &+ [A\mu_k\Delta t + o(\Delta t)](n+1)A_{n+1}(t)\end{aligned}$$

which gives

$$\begin{aligned}A_n(t+\Delta t) - A_n(t) &= -[nA\mu_k\Delta t + nI\gamma\Delta t + \alpha\Delta t + o(\Delta t)]A_n(t) \\ &+ [\alpha\Delta t + (n-1)I\gamma\Delta t + o(\Delta t)]A_{n-1}(t) \\ &+ [\mu_k\Delta t + o(\Delta t)](n+1)_A A_{n+1}(t)\end{aligned}$$

Proceeding to the limit as $\Delta t \to 0$, we get the following Kolmogorov forward equations:

$$A_n'(t) = -[nA\mu_k + \alpha + nI\gamma]A_n(t) + [\alpha + (n-1)I\gamma]A_{n-1}(t) + A\mu_k(n+1)A_{n+1}(t), \quad \text{for n} \geq 1 \tag{5.4.1}$$

$$A_0'(t) = -\alpha A_0(t) + A\mu_k A_1(t), \quad \text{for n} = 0 \tag{5.42}$$

Where the primes indicate differentiation with respect to t In equation (5.4.1), there are 3 unknown probabilities; $A_n(t)$, $A_{n-1}(t)$, and $A_{n+1}(t)$. Therefore these equation cannot be solved directly. We resort to the method of Probability generating function (PFG) defined by

$$G_A(Z,t) = \sum_{n=0}^{\infty} A_n(t)Z^n$$

. With $n = 0$,in equation (5.4.2) $A_{-1}(t)$ is identically Zero. The coefficient of $A_{n-1}(t)$ arises from considering the conditional probability of "birth"into the population given

that the population size is $n-1$. Multiplying equation (5.4.1) by Z^n and sum over $n=1$, we have

$$\begin{aligned}
\textstyle\sum_{n=1}^{\infty} A_n'(t)Z^n &= -[A\mu_k + I\gamma]\textstyle\sum_{n=1}^{\infty} nA_n(t)Z^n - \alpha\textstyle\sum_{n=1}^{\infty} A_n(t)Z^n \\
&+ \alpha\textstyle\sum_{n=1}^{\infty} A_{n-1}(t)Z^n \\
&+ I\gamma\textstyle\sum_{n=1}^{\infty}(n-1)A_{n-1}(t)Z^n \\
&+ A\mu_k\textstyle\sum_{n=1}^{\infty}(n+1)A_{n+1}(t)Z^n \\
&= -\alpha\textstyle\sum_{n=1}^{\infty} A_n(t)Z^n - [A\mu_k + I\gamma]\textstyle\sum_{n=1}^{\infty} nA_n(t)Z^n \\
&+ \alpha\textstyle\sum_{n=1}^{\infty} A_{n-1}(t)Z^n \\
&+ I\gamma\textstyle\sum_{n=1}^{\infty}(n-1)A_{n-1}(t)Z^n + A\mu_k\textstyle\sum_{n=1}^{\infty}(n+1)A_{n+1}(t)Z^n
\end{aligned} \tag{5.4.3}$$

Define

$$\begin{aligned}
\tfrac{\partial G}{\partial t} &= \textstyle\sum_{n=0}^{\infty} A_n'(t)Z^n \\
\tfrac{\partial G}{\partial Z} &= \textstyle\sum_{n=0}^{\infty} nA_n(t)Z^n \\
G(Z,t) &= \textstyle\sum_{n=0}^{\infty} A_n(t)Z^n
\end{aligned}$$

Therefore equation (5.4.3) becomes

$$\begin{aligned}
\tfrac{\partial G}{\partial t} - A_0'(t) &= -\alpha[G(Z,t) - A_0(t)] - [A\mu_k + I\gamma]Z\tfrac{\partial G}{\partial Z} \\
&+ \gamma Z^2\tfrac{\partial G}{\partial Z} + \alpha ZG(Z,t) \\
&+ \mu_k(\tfrac{\partial G}{\partial Z} - A_1(t))
\end{aligned}$$

From equation (5.4.2) we have

$$\begin{aligned}
\tfrac{\partial G}{\partial t} &= -\alpha G(Z,t) - [A\mu_k + I\gamma]Z\tfrac{\partial G}{\partial Z} \\
&+ \gamma Z^2\tfrac{\partial G}{\partial Z} + \alpha ZG(Z,t) \\
&+ \mu_k\tfrac{\partial G}{\partial Z} \\
\tfrac{\partial G}{\partial t} &= (Z-1)\alpha G(Z,t) + (Z-1)[I\gamma Z - A\mu_k]\tfrac{\partial G}{\partial Z}
\end{aligned}$$

Therefore

$$\frac{\partial G}{\partial t} - (Z-1)[I\gamma Z - A\mu_k]\frac{\partial G}{\partial Z} = (Z-1)\alpha G(Z,t)$$

The auxiliary equations are:

$$\frac{dt}{1} = -\frac{dZ}{(Z-1)[I\gamma Z - A\mu_k]} = \frac{dG}{(Z-1)\alpha G(Z,t)}$$

Considering

$$\frac{dZ}{[I\gamma Z - A\mu_k]} = \frac{dG}{\alpha G(Z,t)}$$

and On integration we have

$$(I\gamma Z - A\mu_k^{\alpha/\gamma} G(Z,t) = C_1$$

Next we consider

$$\frac{dt}{1} = -\frac{dZ}{(Z-1)[I\gamma Z - A\mu_k]}$$

On integration we have

$$\Big(\frac{[I\gamma Z - A\mu_k]}{Z-1}\Big)e^{-[I\gamma - A\mu_k]t} = C_2$$

Where C_1 and C_2 are constants of integration. setting C_1 as a function of C_2,we arrive at the most general solution

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

We had denoted that $S(t)$ is the size of the population at time t for $0 \leq t \geq \infty$, let there be no individual who has developed full blown symptoms at time $t = 0$ that is, $A(0) = 0$ then

$$G(Z,0) = 1$$

Therefore

$$[I\gamma Z - A\mu_k]^{\alpha/I\gamma}] = f\Big(\frac{[I\gamma Z - A\mu_k]}{Z-1}\Big)$$

This is for $|Z| < 1$. For any ϕ,

$$\phi = \frac{I\gamma Z - A\mu_k}{Z-1}$$

We have

$$Z = \frac{A\mu_k - \phi}{I\gamma - \phi}$$

Hence we have Hence we have

$$f(\phi) = [I\gamma Z - A\mu_k]^{\alpha/I\gamma}]$$

but

$$[I\gamma Z - A\mu_k]^{\alpha/I\gamma}]G(Z,t) = f\Big(\phi e^{-(I\gamma - A\mu)t}\Big)$$

Now replacing ϕ by $\frac{I\gamma Z - A\mu}{Z-1}$ we have

$$G(Z,t) = \Big(\frac{I\gamma - A\mu}{I\gamma e^{(I\gamma - A\mu)t} - A\mu}\Big)^{\alpha/I\gamma}\Big[1 - \frac{ZI\gamma(e^{(I\gamma - A\mu)t} - 1)}{I\gamma e^{(I\gamma - A\mu)t} - A\mu}\Big]^{-\alpha/I\gamma} \tag{5.4.4}$$

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 (5.4.4) 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 (5.4.4) 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 $t \longrightarrow \infty$, 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.

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

5.5 SPECIAL CASES

By assigning values to the parameters , we arrive at some special cases. Allowing α to take the value zero, (that is, no migration into the population $\alpha = 0$) we obtain Generating function, Expectation and Variance for Susceptibles, Infectives and AIDS cases similar to the corresponding Generating function, expectation and Variance of the MTCT model. Hence MTCT models are special cases for the Combined model.

Assuming that $\lambda = 0$, (that is, the birth rate is zero,the population increases due to migration into the population) then the model assumes similar generating function, expectation and variance of the Susceptibles, Infectives and AIDS cases as those of the Heterosexual model. Therefore Heterosexual model is a special case of the Combined model. The simulation of the model will be exactly like for Heterosexual and MTCT models.

Chapter 6

CONCLUSION

6.1 Introduction

In this thesis, our objective was to develop HIV/AIDS epidemic models by using Generating functions (GF). In trying to achieve the goals, the author came up with a conceptual framework which summarizes all the literature on HIV/AIDS transmission models. Stochastic models based on Mother to child transmission(MTCT), Heterosexual transmission and Combined models are 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 MTCT and Heterosexual models are special cases of the Combined model. However, in the process of achieving the author's goal, 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 need further investigation and the author has recommended for further investigation. To test the models, the author used some randomly chosen parameters, which produced some funny results, further work is recommended to study ranges where the parameters work best.

6.2 Further work

• From the study above, the parameters were independent of time, re examination of the models with parameters dependent on time is recommended.

• Since infection in MTCT model can occur in three stages; during pregnancy, during delivery and after birth (breast milk), recommended area or research is to look at the Markov model approach where the transition probability can be dependent of time. Same approach can be applied on the stages of infection in an infected population. Markov chain can be applied in the Combined model where the stages will be the age groups.

• Further investigation is recommended to study why the generating function is unity for some models assuming initial condition to be zero. Also the author recommend further study to find ranges where the model parameters could work best. Generating functions can also be applied Markov transition chain models, especially when considering.

• So far the resulting partial differential equations for probability generating functions have turned out to be of a linear type which is frequently soluble, or at least tractable to yield a number of useful properties. On the other hand, the transition probabilities are usually non-linear functions of the population size, and this leads, even with models that are descriptively very simple to mathematical analyses of considerable complexity.

• So far we have used univariate generating functions. For suitably defined markov chains, there will be need to use multivariate generating functions (Chiang, 1980).

• For literature review, a critical analysis of use of generating functions (both univariate and multivariate in nature) in infectious diseases or in epidemic processes will be necessary since very little has been in the use of generating functions to HIV/AIDS models (Bailey, 1975).

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