Chapter 5

Four Stage HIV/AIDS Epidemic Model

5.1 Introduction

Large number of models have been developed to study the transmission dynamics of HIV/AIDS epidemic and its applications to projecting HIV infections and AIDS cases. Many of these investigations are based on empirical data set or statistical and mathematical models. Brookemeyer and Gail (See [74, 75, 119]) introduced back-calculation method to reconstruct the past pattern of HIV infections from the empirical data and used to predict the AIDS cases. The method is based on the distribution of infections, assumed distribution of incubation period and observed counts of AIDS cases over the time. Recently Nagaraj Rao and Srivenkatramana (See [120]) have noticed uncertainties and difficulties in using back-calculation method for the analysis of Indian data, specifically on the choice of infection density, distribution of incubation period and inaccuracy in AIDS counts. They have proposed an alternative method to projecting HIV infec-
tions using the information on seropositivity rate of infection. However, it is simple and sufficient to give an estimate of the number of HIV infections based on the population size, only when the rate of seropositivity is assumed to be precise and the interest is only to project HIV infections alone. More recently Thomas and Pandey (See [121, 122]) have used the EM Algorithm approach to estimate HIV infections for a group of per 10,00,000 hypothetical susceptible population over the period of 15 years of time (1984 to 1999) for the estimated effective contact rate in four risk groups: pregnant women, sex workers, intravenous drug users and STI patients to the Indian data. In another study, Anbupalam, Rvanan and Venkatesan (See [123]) have used the back calculation method to estimate HIV and AIDS cases in Tamil Nadu. Usefulness of these methods are limited and restricted generally to short-term projections.

Isham (See, [34]), Bailey (See, [35]), Anderson (See, [36]) and others have studied transmission dynamics of HIV/AIDS epidemic using deterministic models. They have shown that, the significance of variable infectiousness to the course of the epidemic can be assessed through the basic reproductive rate of infection, $R_0$ and also doubling time $t_d$ for the incidence of AIDS in the early stage of the epidemic.

On the other hand, stochastic models have been developed on par with deterministic models by presuming variables as random variables, which has some advantages over the deterministic approach (See [20]). Usually this kind of models were found to be potentially powerful for long-term prediction purposes but more difficult to derive explicit solution. Billiard and Zhao [79], proposed a method for estimating AIDS cases, and is based on the multiple-stage compartmental model of type Right-shift process. They investigated in particular five-stage and four-stage models with time dependent rates, which are linear functions of the variables. These models have been fitted to the
actual data set, giving number of AIDS cases in USA, reported by the Center for Disease Control (CDC) [80] for US male homosexual, US blood transfusion, New York State, San Francisco and US populations.

In the present chapter we have made an attempt to describe more extensively the four-stage HIV/AIDS epidemic model originally developed by Tan and Hsu [73], introducing modified infection rate as proposed by Frank Ball and Philip O'Neill [63] and different distribution of incubation period, such as: exponential and Wiebull distributions. This model has been fitted to the actual data set on the number of AIDS cases in India.

This chapter consists of six Sections. After presenting introduction in Section 5.1, notations and assumptions are stated in Section 5.2. The next section gives formulation of deterministic model. Its behaviour has been studied by deriving threshold parameter: Basic Reproduction Number $R_0$. Section 5.4 deals with formulation of stochastic model and obtained solution using the method proposed by Billiard and Zhao [79]. We have also compared the expected values of AIDS cases obtained from the special case of the stochastic model with the reported AIDS cases in India. We conclude the chapter with discussion on long-term projection of HIV/AIDS epidemic in Section 5.5.

5.2 Notations and assumptions

Denote $S(t)$ as the number of individuals at time $t$, who are susceptible to infection and can contract the disease if they have an effective contact with an infected individual or source. Let $L(t)$ be the number of individuals at time $t$ in the latent period, during which a previously susceptible individual has become infected but not yet infectious.
I(t) represents the number of infectious individuals at time t and they have passed out latent period and developed the HIV symptoms. A(t) represents the number of AIDS cases at time t. The present epidemic problem can be described completely in terms of four stage Markov Process, moving from lowest stage to the highest, as follows $S \rightarrow L \rightarrow I \rightarrow A$. Let $(S(0), L(0)) = (m, n)$, then for given $\{S(t), L(t), I(t)\}$, transitions among these states during the interval $(t, t + \delta t)$ is described as follows.

The infection of a susceptible with probability

$$\lambda_i(x, t) \delta t + o(\delta t)$$  \hspace{1cm} (5.1)

An individual moving into the third stage (infectious) with probability

$$\lambda_i(x, t) \delta t + o(\delta t)$$  \hspace{1cm} (5.2)

Diagnosis of an HIV infected individual as having AIDS with probability

$$\lambda_a(x, t) \delta t + o(\delta t)$$  \hspace{1cm} (5.3)

where $\lambda_i(x, t)$'s are infinitesimal transition rates of individuals in a given stage $i$ can move into stage $i + 1$, with $x = (s, l, i, a)$ as a particular realization of $X = (S(t), L(t), I(t), A(t))$ and $o(\delta t)$ is defined by $\lim_{\delta t \to 0} \frac{o(\delta t)}{\delta t} = 0$.

5.3 The deterministic model

Following the usual procedure and assumptions, the deterministic version of the model is constructed by identifying the conditional mean of the change in the state during an infinitesimal time interval $(t, t + \delta t)$. Let $\{(S(t), L(t), I(t)), t \in R^+\}$ denotes the
resulting process for the number of susceptible, individuals in the latent period and HIV infected cases respectively, at time $t$. Let $(S(0), L(0)) = (m, n)$ be the initial size of susceptible and individuals in the latent period. Then $A(t) = m + n - S(t) - L(t) - I(t)$ represent the number of AIDS cases at time $t$. Now following the assumptions 5.1 to 5.3, suppose that, the incidence of infection occurs at the rate $\lambda_1(x, t) = \frac{as(x,t)}{N(t)}$, where $\frac{as(x)}{N(t)}$ represents the infection rate exerted by each infective on any given susceptible at time $t$ and $N(t) = S(t) + L(t) + I(t)$, this follows from Ball and O'Neill [63]. Also assume that, an individual moving from latent stage to infectious stage at the rate $\lambda_2(x, t) = \gamma L(t)$ and diagnosis of HIV individual to AIDS with rate $\lambda_3(x, t) = \delta I(t)$, where $\frac{1}{\gamma}$ and $\frac{1}{\delta}$ are the latent and infectious periods respectively. The change in the state of the system can be described using the following system of non-linear differential equations:

\[
\frac{d}{dt} S(t) = -\frac{\beta S(t) I(t)}{N(t)} \\
\frac{d}{dt} L(t) = \frac{\beta S(t) I(t)}{N(t)} - \gamma L(t) \\
\frac{d}{dt} I(t) = \gamma L(t) - \delta I(t) \\
\frac{d}{dt} A(t) = \delta I(t)
\]  

(5.4)

The above system of non-linear differential equations does not admit closed form solution. However, the behavior of the model can be studied through a threshold parameter, known as Basic Reproduction Number-$R_0$, giving the average number of secondary infection produced when one infected individual is introduced into a host virgin population. This is useful for its clear exhibition of the bifurcation phenomenon that corresponds to a threshold for the deterministic model. The derivation of the threshold parameter $R_0$, using the final state of the epidemic and stability analysis as well are given in next sub-sections.
5.3.1 Final state and threshold behavior

Let \( \{ S(\infty), L(\infty), I(\infty), A(\infty)\} = \lim_{t \to \infty} \{ S(t), L(t), I(t), A(t)\} \) be the final state of the epidemic. Ultimately at the final state of the epidemic, there will be no more Latent individuals and HIV infective present in the population, that is \( L(\infty) = 0 \) and \( I(\infty) = 0 \), then the total number of AIDS cases in the population will be

\[
A(\infty) = m + n - S(\infty)
\] (5.5)

Now from first and last equations of the system 5.4, we have

\[
\frac{S(t)}{m} = \left\{ 1 - \frac{A(t)}{m + n} \right\}^{R_0}
\] (5.6)

where \( R_0 = \frac{\beta}{\gamma} \). Then from equations 5.5 and 5.6, we see that \( S(\infty) \) is a solution to the equation

\[
\frac{x}{m} = \left\{ \frac{x}{m + n} \right\}^{R_0} \text{ for } 0 \leq x \leq m
\] (5.7)

Let \( \overline{S(\infty)} = \frac{S(\infty)}{m+n} \) be the final proportion of susceptible in the whole population, then from equation 5.7, \( \overline{S(\infty)} \) is a solution to the equation

\[
\left\{ \frac{(m+n)y}{m} \right\}^{R_0} = y \text{ for } 0 \leq y \leq \frac{m}{m+n}
\] (5.8)

The graph of the function on the left-hand side (with orange color) and the function on the right hand side (with black color) of equation 5.8 are shown in figures 5.3.1 and 5.3.1 separately for \( R_0 < 1 \) and \( R_0 \geq 1 \). Obliviously \( \left\{ \frac{(m+n)y}{m} \right\}^{R_0} \) increases in \( R_0 \) when \( R_0 < 1 \) and there exists two intersection points, one such point is zero and one another lies in between \( 0 \leq y \leq \frac{m}{m+n} \). For the later case, zero is the only point of intersection. More interestingly the value of \( S(\infty) \) decreases with \( R_0 \), then we can deduce directly that

\[
\overline{S(\infty)} = 0, \quad \text{If} \quad R_0 \geq 1
\] (5.9)
Figure 5.1: Representation of equation 5.8, when $R_0 < 1$

$$S(\infty) = m \left( \frac{m}{m+n} \right)^{\frac{R_0}{R_0-1}}, \quad \text{If} \quad R_0 < 1 \quad (5.10)$$

Note that when $R_0 \geq 1$, all the susceptible will ultimately contract with AIDS, which is rather uncommon for real-life situation.
Figure 5.2: Representation of equation 5.8, when $R_q > 1$
5.3.2 Linearized stability of the model

The method of Linearized Stability Principle (LSP), proposed by Grimshaw [102] has been used to derive the Basic Reproduction Number (BRN) and also to study the stability of any system containing nonlinear ordinary differential equations of the form:

\[
y'(t) = f(y(t)), \quad t \in [0, T]
\]
\[
y(0) = y_0, \quad y \in \mathbb{R}^n, \quad f : \mathbb{R}^n \to \mathbb{R}^n
\]

As per LSP, if the eigenvalues of the Jacobian matrix evaluated at the stationary point say \( y^* \), have negative real value, then \( y^* \) is said to be locally asymptotically stable.

The first three equations of the system 5.4 contain no \( A(t) \) term, this allows us to reduce the system 5.4 to

\[
\begin{align*}
\frac{d}{dt}S(t) &= -\frac{\beta S(t)I(t)}{N(t)} \\
\frac{d}{dt}L(t) &= \frac{\beta S(t)I(t)}{N(t)} - \gamma L(t) \\
\frac{d}{dt}I(t) &= \gamma L(t) - \delta I(t)
\end{align*}
\]

This system has only one equilibrium point at \( P = (m, 0, 0) \) and it corresponds to, infection free state. The Jacobian Matrix of the system 5.11 is given by

\[
J = \begin{pmatrix}
-\frac{\beta N(t)I(t)}{N(t)^2} & \frac{\beta S(t)I(t)}{N(t)^2} & -\frac{\beta N(t)S(t) + \beta S(t)I(t)}{N(t)^2} \\
\frac{\beta N(t)S(t) + \beta S(t)I(t)}{N(t)^2} & \frac{\beta S(t)I(t)}{N(t)^2} & \frac{\beta S(t)I(t)}{N(t)^2} - \gamma \\
0 & \gamma & \delta
\end{pmatrix}
\]

Now evaluating the jacobian matrix at the equilibrium point \( P \), we have

\[
J(P) = \begin{pmatrix}
0 & 0 & -\beta \\
0 & -\gamma & \beta \\
0 & \gamma & -\delta
\end{pmatrix}
\]
One of the eigenvalue of $J(P)$ is 0 and other eigen values are the roots of the following quadratic equation in $\lambda$:

$$\gamma\beta - (\lambda + \gamma)(\lambda + \delta) = 0$$

(5.12)

It is observed from 5.12 that, the roots have negative real part if and only if $\beta - \delta < 0$, implying that the point is locally asymptotically stable if and only if

$$\frac{\beta}{\delta} < 1$$

(5.13)

Thus the threshold parameter $R_0$ is given by

$$R_0 = \frac{\beta}{\delta}$$

(5.14)

If $R_0 > 1$, then the point $P$ becomes unstable and at the initial stage of the epidemic, the infected fraction of the population at risk may rise exponentially. However, the endemic equilibrium point does not exist for the model to analyze the stability of the system in the endemic region. This stability analysis shows that the bifurcation occurs at $R_0 = 1$ and this leads to an interpretation that the condition $R_0$ assures that the disease cannot invade the population, and invasion occurs only when $R_0 > 1$, hence $R_0 = 1$ is the threshold point of the deterministic model.

Further the value of $R_0$ obtained in Sections 5.3.1 and 5.3.2 are same and are independent of the parameter $\gamma$ (where, $\frac{1}{\delta}$ is the mean latent period following exponential distribution). This assures that, during the latent period of an infective, even though the susceptible have an effective contact with an infective, will not contract the disease.

### 5.3.3 Doubling time

From the above discussion, we have noticed that at the initial stage of the epidemic the infected fraction of the population at risk rises exponentially and is given by $\exp \left( (\beta - \delta) t \right)$
when $R_0 > 1$. At the early stage of an epidemic, assume everyone is susceptible, then the doubling time $t_d$ defined as the time taken for doubling of the infected number and is given by

$$t_d = \frac{\ln 2}{\delta(R_0 - 1)}$$  \hspace{1cm} (5.15)

Thus the basic reproduction rate $R_0$, doubling time $t_d$ and the mean infectious period $\frac{1}{\delta}$ are inter related, and it can be rewritten as

$$R_0 = 1 + \frac{1}{\delta t_d} \ln 2$$  \hspace{1cm} (5.16)

Note that the expression 5.16 for $R_0$ is more refined estimate than the estimates of May and Anderson [33], and is used by Srinivasa Rao. (See Table-2 of [124]) for estimating $R_0$ by taking 9 years as incubation period for adults in developing countries. The UNAIDS Reference Group on Estimates [125], for different doubling times. Since the incubation period is the sum of latent period and infectious period, and during the latent period the infected individual is unable to spread the disease because the infectious symptom is still under developmental stage in his body. As per the estimates mean latent period is found to be 6 months (See, J. V. Koenig [126]). Considering this fact, and taking mean infectious period of 8.5 years instead of incubation period of 9 years as a whole, we have estimated $R_0$ values for different doubling times, given in Table 5.1 along with the estimates of Srinivasa Rao [124].

The results from the table 5.1 indicate that, the estimates of Srinivasa Rao [124] under estimates $R_0$ to the extent of latent period included in the incubation period.
Table 5.1: Basic reproduction number for varying doubling times.

<table>
<thead>
<tr>
<th>Sl.No</th>
<th>$t_d$</th>
<th>$R_0^*$</th>
<th>$R_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1.0</td>
<td>1.077</td>
<td>1.082</td>
</tr>
<tr>
<td>2</td>
<td>1.5</td>
<td>1.051</td>
<td>1.054</td>
</tr>
<tr>
<td>3</td>
<td>2.0</td>
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</tr>
<tr>
<td>4</td>
<td>2.5</td>
<td>1.031</td>
<td>1.033</td>
</tr>
<tr>
<td>5</td>
<td>3.0</td>
<td>1.026</td>
<td>1.027</td>
</tr>
<tr>
<td>6</td>
<td>3.5</td>
<td>1.022</td>
<td>1.023</td>
</tr>
</tbody>
</table>

* See Table 2. of Srinivasa Rao [124], estimated values of $R_0$

5.4 Stochastic model

We now turn our attention to the stochastic model. Let $X(t) = \{S(t), L(t), I(t), A(t)\}$ be a four-tuple random vector having their usual meaning as defined in Section 5.2, with $x = (s, l, i, a)$ as particular realization of the process $X(t)$. Define $e_i$ as the four component vector with elements $e_{iv} = \delta_{iv}$, where $i, v = 4, \cdots, 1$. For example, $e_4 = (1, 0, 0, 0)$ and $e_1 = (0, 0, 0, 1)$. Now restating the equations 5.1 to 5.3, we have

$$
\Pr \left\{ X(t + \delta t) = x - e_4 + e_3 \big| X(t) = x \right\} = \lambda_1(x, t) \delta t + o(\delta t)
$$

$$
\Pr \left\{ X(t + \delta t) = x - e_3 + e_2 \big| X(t) = x \right\} = \lambda_2(x, t) \delta t + o(\delta t)
$$

$$
\Pr \left\{ X(t + \delta t) = x - e_2 + e_1 \big| X(t) = x \right\} = \lambda_3(x, t) \delta t + o(\delta t)
$$

and

$$
\Pr \left\{ X(t + \delta t) = x \big| X(t) = x \right\} = 1 - \sum_{i=1}^3 \lambda_i(x, t) \delta t + o(\delta t)
$$

Let $p_{x_0, x}(t_0, t)$ be conditional probability of finding the process is in state $x$ at time $t$, given that at previous instant it was in the state $x_0$. 

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Denote,
\[ p(x, t) = \begin{cases} 
  \pi_{x_0, x}(t_0, t) & \text{for } x \in \Gamma \\
  0 & \text{for } x \notin \Gamma 
\end{cases} \quad (5.17) \]

where
\[ \Gamma = \{ x : 0 \leq s \leq m, 0 \leq l \leq m + n, 0 \leq i \leq m + n, 0 \leq a \leq m + n, s + l + i + a = m + n \} \quad (5.18) \]

Then the Kolmogorov forward differential difference equation for the system is given by,
\[
\frac{d}{dt} p(x, t) = - \sum_{i=1}^{3} \lambda_i(x, t) p(x, t) + \lambda_1(x + e_4 - e_3, t) p(x + e_4 - e_3, t) + \lambda_2(x + e_3 - e_2, t) p(x + e_3 - e_2, t) + \lambda_3(x + e_2 - e_1, t) p(x + e_2 - e_1, t) \quad \text{for } x \in \Gamma \quad (5.19)
\]

and zero otherwise.

To find the explicit solution to the system 5.19 no straightforward method exists, therefore, we use Severo's method called as Right Shift Process [71, 72] to transformer the system 5.19 into a triangular array to solve recursively. However, in particular, when lower triangular matrix of coefficients is time dependent we cannot use Severo's [72] recursion theorem. Since, the system 5.19 corresponds to a right shift process [71] with transition to the right adjacent category only, therefore we can readily use the method developed by Billard and Zhao [78, 79] to find the solution.

Let us define the following transformation to express the state probabilities in a triangular form
\[ p(x, t) = Z_k(j) \quad (5.20) \]
with each \( x \) corresponds uniquely to a \( k(x) \) and hence to a \( k(j) \), where \( j = (j_1, j_2, j_3) \).

Then for each point on the state space \( \Gamma \), there exists a unique counting co-ordinate

\[
k(x) = k(j)
\]

given by

\[
k(j) = \begin{cases} 
  j_1 - \binom{j_2}{1} + \frac{(j_2 - 1)}{2} - \binom{j_1 + 1}{2} + \binom{j_1 + 2}{3}, & \text{if } n = 0; \\
  j_1 - \binom{j_2}{1} + \frac{(j_2 - 1)}{2} - \binom{n + j_1 + 1}{2} + \binom{n + j_1 + 2}{3} - \binom{n + 2}{3}, & \text{if } n > 0.
\end{cases}
\]

(5.21)

with \( s = m + 1 - i_1; \quad l = n + j_1 - j_2; \quad i = j_2 - j_3; \quad a = j_3 - 1, \) where

\( j_1 = 1, 2, \ldots, m + 1; \quad j_2 = 1, 2, \ldots, j_1 + n; \quad j_3 = 1, 2, \ldots, j_2. \)

Following Billard and Zhao [78, 79], in order to account for the initial state \((m,n,o)\) in 5.21 for the numbering, the quantity \( \binom{n+2}{3} \) has to be subtracted from the original formula to modify accordingly (See. equation 2.3 of [78]). In particular \((m,n,o,o)\) is numbered as, \( k(m,n,o,o) = 1. \) the last state \( k(o,o,m+n) \) as

\[
\binom{m-n+3}{3} - \binom{n+2}{3} = k_f \quad \text{(say)}.
\]

The point \( x \) defines the co-ordinate \( k(j) \), where \( j = (j_1, j_2, j_3) \), likewise the point \( x + e_b - e_c \) defines the co-ordinate

\[
k(x + e_b - e_c) = \begin{cases} 
  k(j_1 - 1, j_2, j_3), & \text{if } b = 4 \text{ and } c = 3; \\
  k(j_1, j_2 + 1, j_3), & \text{if } b = 3 \text{ and } c = 2; \\
  k(j_1, j_2, j_3 - 1), & \text{if } b = 2 \text{ and } c = 1.
\end{cases}
\]

(5.22)

Now by applying the transformation defined in 5.20, the system of equation 5.19 becomes,

\[
\frac{d}{dt} Z_{k(j_1,j_2,j_3)}(t) = -\sum_{i=1}^{3} \lambda_i(j_1,j_2,j_3,t) Z_{k(j_1,j_2,j_3)}(t) + \lambda_1(j_1 - 1, j_2, j_3, t) Z_{k(j_1 - 1,j_2,j_3)}(t) \\
+ \lambda_2(j_1, j_2 - 1, j_3, t) Z_{k(j_1,j_2 - 1,j_3)}(t) \\
+ \lambda_3(j_1, j_2, j_3 - 1, t) Z_{k(j_1,j_2,j_3 - 1)}(t) \quad \text{for } k = 1, 2, \ldots, k_f \quad (5.23)
\]
In matrix form, the system of equation 5.23 can be written as

$$\frac{d}{dt} Z(t) = BZ(t) \quad (5.24)$$

where $Z(t) = (Z_1(t), Z_2(t), \ldots, Z_k(t))'$. Before going to find the solution to the equation 5.24, we shall consider the structure of matrix $B$.

5.4.1 Structure of the coefficient matrix $B$

The matrix $B$ of coefficients is of the order $k_f \times k_f$, lower triangular matrix. We partition this matrix into a nested system of sub blocks as illustrated by Billard [70, 79] to facilitate to apply the method developed by Severo [71] and Billard and Zhao [79] to find the solution easily.

The first partition of $B$ gives

$$B = \left( B\left(j_1, j'_1 \right), j_1, j'_1 = 1, \ldots, m + 1 \right)$$

again the elements of $B$ are in matrix form, can be portioned further to give

$$B\left(j_1, j'_1 \right) = \left( \begin{array}{c} B\left(j_1, j_2; j'_1, j'_2 \right), j_2 = 1, \ldots, j_1 + n, j'_2 = 1, \ldots, j'_1 + n \end{array} \right)$$

with 'elements'

$$B\left(j_1, j_2; j'_1, j'_2 \right) = \left( \begin{array}{c} B\left(j_1, j_2, j_3; j'_1, j'_2, j'_3 \right), j_3 = 1, \ldots, j_2, j'_3 = 1, \ldots, j'_2 \end{array} \right)$$

Thus the co-ordinates of $B$ are given by

$$B\left(j_1, j_2, j_3; j'_1, j'_2, j'_3 \right)$$

where

$$\begin{align*}
  j_1 &= 1, 2, \ldots, m + 1 & j'_1 &= 1, 2, \ldots, m + 1 \\
  j_2 &= 1, 2, \ldots, j_1 + n & j'_2 &= 1, 2, \ldots, j'_1 + n \\
  j_3 &= 1, 2, \ldots, j_2 & j'_3 &= 1, 2, \ldots, j'_2
\end{align*}$$
Then using block arrangements, the non-zero elements of $B$ are given by

$$B(j_1, j_2, j_3; j_1, j_2, j_3) = -\sum_{i=1}^{3} \lambda_i(j_1, j_2, j_3, t)$$

$$B(j_1, j_2, j_3; j_1 - 1, j_2, j_3) = \lambda_1(j_1 - 1, j_2, j_3, t)$$

$$B(j_1, j_2, j_3; j_1, j_2 - 1, j_3) = \lambda_2(j_1, j_2 - 1, j_3, t)$$

$$B(j_1, j_2, j_3; j_1, j_2, j_3 - 1) = \lambda_3(j_1, j_2, j_3 - 1, t)$$

Now we can prove the following theorem.

**Theorem 5.1** The solution of equation 5.24 i.e., $\frac{d}{dt}Z(t) = BZ(t)$ with initial condition $Z(0) = (a_1, a_2, \cdots, a_k)^T$, is given recursively by

$$Z_{k(j_1, j_2, j_3)}(t) = \exp \left[ -\int_{0}^{t} \sum_{i=1}^{3} \lambda_i(j_1, j_2, j_3, u) du \right] \left( a_{k(j_1, j_2, j_3)} \right)$$

$$+ \int_{0}^{t} \left\{ \lambda_1(j_1 - 1, j_2, j_3, u) Z_{k(j_1 - 1, j_2, j_3)}(t) + \lambda_2(j_1, j_2 - 1, j_3, u) Z_{k(j_1, j_2 - 1, j_3)}(t) 
+ \lambda_3(j_1, j_2, j_3 - 1, u) Z_{k(j_1, j_2, j_3 - 1)}(t) \right\} \exp \left[ -\int_{0}^{u} \sum_{i=1}^{3} \lambda_i(j_1, j_2, j_3, v) dv \right] du \right) \quad (5.25)$$

for $j_1 = 1, 2, \cdots, m + 1; \quad j_2 = 1, 2, \cdots, n + j_1; \quad$ and $\quad j_3 = 1, 2, \cdots, j_2$.

**Proof** The proof of this theorem follows from Billard and Zhao (See, Theorem 1 of [79]).

Once we get state probabilities of all states with recursive equation 5.25 we can compute the expected number of AIDS cases using the expression

$$E\{A(t)\} = \sum_{k=1}^{k_f} (j_3 - 1) Z_{k(j_1, j_2, j_3)}(t) \quad (5.26)$$

and the expression for variance is given by

$$Var\{A(t)\} = \sum_{k=1}^{k_f} (j_3 - 1)^2 Z_{k(j_1, j_2, j_3)}(t) - \left[ \sum_{k=1}^{k_f} (j_3 - 1) Z_{k(j_1, j_2, j_3)}(t) \right]^2 \quad (5.27)$$

Now we shall examine this AIDS epidemic model under varied assumptions on infection rate and distribution of incubation period considering them as different cases.
Case i. Suppose that the incidence of infection occurs at the rate $\lambda_1(j_1, j_2, j_3, t) = \beta S(t) I(t)$, where $\beta$ is the rate of infection. Let an individual moving from latent stage to infectious stage at the rate $\lambda_2(j_1, j_2, j_3, t) = \gamma L(t)$ and an individual moving from the state of an HIV individual to as having AIDS at the rate $\lambda_3(j_1, j_2, j_3, t) = \delta I(t)$, where $\frac{1}{\gamma}$ and $\frac{1}{\delta}$ are the mean latent and infectious periods, both following exponential distribution.

Then the equation 5.25 becomes,

$$
Z_{k(j_1,j_2,j_3)}(t) = \exp \left[ - \int_0^t \left\{ \beta (m + 1 - j_1)(j_2 - j_3) + \gamma (n - j_1 - j_2) + \delta (j_2 - j_3) \right\} \, du \right] 
\times \left( a_{k(j_1,j_2,j_3)} + \int_0^t \left\{ \beta (m + 2 - j_1)(j_2 - j_3) Z_{k(j_1,j_2,j_3)}(t) 
+ \gamma (n - j_1 - j_2 + 1) Z_{k(j_1,j_2-1,j_3)}(t) + \delta (j_2 - j_3 + 1) Z_{k(j_1,j_2,j_3-1)}(t) \right\} \, du \right)
\times \exp \left[ - \int_0^t \left\{ \beta (m + 1 - j_1)(j_2 - j_3) + \gamma (n - j_1 - j_2) + \delta (j_2 - j_3) \right\} \, du \right] 
\text{for } k = 1, 2, \ldots, k_f \quad (5.28)
$$

Using the equation 5.28 we can compute $E\{A(t)\}$ and $Var\{A(t)\}$

Case ii. Here we assume that the rate of infection and the rate that an individual moving from latent stage to infectious stage are remain same as defined in the Case i, but the diagnosis of an HIV individual as AIDS cases at the rate $\lambda_3(j_1, j_2, j_3, t) = \delta I(t)$, and the period of infectious follows Weibull distribution (See,[77, 127, 128]), given by

$$
f(t, \delta) = \theta \delta^\theta t^{\theta - 1}, \quad \text{with } \delta = 2 \quad (5.29)
$$
Then equation 5.25 becomes,

\[
Z_{k(j_1,j_2,j_3)}(t) = \exp \left[ - \int_0^t \left\{ \beta (m + 1 - j_1)(j_2 - j_3) + \gamma (n + j_1 - j_2) + \delta (j_2 - j_3) \right\} du \right]
\times \left( a_{k(j_1,j_2,j_3)} + \int_0^t \left\{ \beta (m + 2 - j_1)(j_2 - j_3) Z_{k(j_1-1,j_2,j_3)}(t) \right. \right.
\quad + \left. \gamma (n + j_1 - j_2 + 1) Z_{k(j_1,j_2-1,j_3)}(t) + \delta (j_2 - j_3 + 1) Z_{k(j_1,j_2,j_3-1)}(t) \right\} du \right) 
\times \exp \left[ - \int_0^t \left\{ \beta (m + 1 - j_1)(j_2 - j_3) + \gamma (n + j_1 - j_2) + \delta (j_2 - j_3) \right\} du \right]
\quad \text{for } k = 1, 2, \cdots, k_f \quad (5.30)
\]

Again mean and variance of \( A(t) \) can be obtained from equations 5.26 and 5.27.

**Case iii.** Suppose that, the incidence of infection occurs at the rate of \( \lambda_1(j_1, j_2, j_3, t) = \frac{bN}{N(t)} \), where \( \frac{bN}{N(t)} \) represents the infection rate exerted by each infective an any given susceptible at time \( t \) and \( N(t) = S(t) + L(t) + I(t) \equiv m + n + 1 - j_3 \), (as in Ball and O’Neill [63]). Also assume that an individual moving from latent stage to infectious stage at the rate \( \lambda_2(j_1, j_2, j_3, t) = \gamma L(t) \) and diagnosis of HIV individual to AIDS at the rate \( \lambda_3(j_1, j_2, j_3, t) = \delta I(t) \) as in Case i. Then equation 5.25, becomes

\[
Z_{k(j_1,j_2,j_3)}(t) = \exp \left[ - \int_0^t \left\{ \beta \frac{(m + 1 - j_1)(j_2 - j_3)}{m + n + 1 - j_3} + \gamma (n + j_1 - j_2) + \delta (j_2 - j_3) \right\} du \right]
\times \left( a_{k(j_1,j_2,j_3)} + \int_0^t \left\{ \beta \frac{(m + 2 - j_1)(j_2 - j_3)}{m + n + 1 - j_3} Z_{k(j_1-1,j_2,j_3)}(t) \right. \right.
\quad + \left. \gamma (n + j_1 - j_2 + 1) Z_{k(j_1,j_2-1,j_3)}(t) + \delta (j_2 - j_3 + 1) Z_{k(j_1,j_2,j_3-1)}(t) \right\} du \right) 
\times \exp \left[ - \int_0^t \left\{ \beta \frac{(m + 1 - j_1)(j_2 - j_3)}{m + n + 1 - j_3} + \gamma (n + j_1 - j_2) + \delta (j_2 - j_3) \right\} du \right]
\quad \text{for } k = 1, 2, \cdots, k_f \quad (5.31)
\]

We can compute mean and variance of the number of AIDS cases from expressions 5.26 and 5.27 using state probabilities obtained in equation 5.31.
Case iv. Finally, we assume that the infection rate and the rate that an individual moving from latent stage to infectious stage are remain same as defined in the Case iii, but the diagnosis of an HIV individual as AIDS case at the rate $\lambda_3(j_1, j_2, j_3, t) = \delta t I(t)$, as defined in the Case ii. Then equation (5.25), becomes

$$Z_{k(j_1,j_2,j_3)}(t) = \exp \left[ -\int_0^t \left\{ \frac{\beta (m+1-j_1)(j_2-j_3)}{m+n+1-j_3} + \gamma (n+j_1-j_2) + \delta u(j_2-j_3) \right\} du \right] \times \left( a_{k(j_1,j_2,j_3)} + \int_0^t \left\{ \frac{\beta (m+2-j_1)(j_2-j_3)}{m+n+1-j_3} Z_{k(j_1,j_2,j_3-1)}(t) \right\} \frac{\beta (m+1-j_1)(j_2-j_3)}{m+n+1-j_3} + \gamma (n+j_1-j_2) + \delta u(j_2-j_3) \right) \exp \left[ -\int_0^t \left\{ \frac{\beta (m+1-j_1)(j_2-j_3)}{m+n+1-j_3} + \gamma (n+j_1-j_2) + \delta u(j_2-j_3) \right\} du \right] du \right) \right]$$

for $k = 1, 2, \cdots, k_f$ (5.32)

As in the above cases, here also we can compute mean and variance of number of AIDS cases from expression 5.26 and 5.27 using state probabilities obtained in equation 5.32.

Example : We illustrate the general solution of model in Case (i) for $m = 2$ and $n = 1$ as follows. We suppose that $\beta = 0.6$, $\gamma = 2$ (i.e., mean latent period = 6 months) and $\delta = 0.11765$ (i.e., mean infectious period =8.5 years). The total possible states are $k_f = 19$ and are given in table 5.2. Suppose that the initial condition is $Z(0) = (0,1,0,\cdots,0)$. Substituting into equation 5.28, we can find the solution, and is given below

$$Z_1(t) = \exp (-2t)$$

$$Z_2(t) = 60283.634 \times 10^{-5} \exp (-1.3184t) - 60283.634 \times 10^{-5} \exp (-4.635t)$$

$$Z_3(t) = 3852.512 \times 10^{-5} - 5382.589 \times 10^{-5} \exp (-5.3184t) + 1530.078 \times 10^{-5} \exp (-4.635t)$$

$$Z_4(t) = 0$$

$$Z_5(t) = 8088.608 \times 10^{-5} \exp (-2.7184t) - 17926.885 \times 10^{-5} \exp (-6.753t)$$

$$+ 9838.277 \times 10^{-5} \exp (-10.071t) \times 10^{-5} \exp (-2.7184t)$$
\[ Z_6(t) = 56.6492 \times 10^{-5} \exp(-2t) - 201.714 \times 10^{-5} \exp(-6.718t) + 240.958 \times 10^{-5} \exp(-10.753t) - 95.892 \times 10^{-5} \exp(-14.071t) \]

\[ Z_7(t) = 16614.866 \times 10^{-5} \exp(-1.435t) - 3895.355 \times 10^{-5} \exp(-5.588t) + 4381.762 \times 10^{-5} \exp(-9.618t) - 17101.273 \times 10^{-5} \exp(-12.941t) \]

\[ Z_8(t) = 28.4 \times 10^{-5} \exp(-0.718t) - 56.649 \times 10^{-5} \exp(-2.718t) + 60.056 \times 10^{-5} \exp(-7.435t) - 44.8172 \times 10^{-5} \exp(-11.471t) + 13.630 \times 10^{-5} \exp(-14.788t) \]

\[ Z_9(t) = 2.7191 \times 10^{-5} - 4.610 \times 10^{-5} \exp(-0.718t) + 2.484 \times 10^{-5} \exp(-2.718t) - 0.941 \times 10^{-5} \exp(-7.435t) + 0.455 \times 10^{-5} \exp(-11.471t) - 0.01074 \times 10^{-5} \exp(-14.788t) \]

\[ Z_{10}(t) = 0 \]

\[ Z_{11}(t) = 136.591 \times 10^{-5} \exp(-4.118t) - 710.015 \times 10^{-5} \exp(-10.956t) + 989.470 \times 10^{-5} \exp(-14.988t) - 416.046 \times 10^{-5} \exp(-18.304t) \]

\[ Z_{12}(t) = 0 \]

\[ Z_{13}(t) = 19.485 \times 10^{-5} \exp(-2.235t) - 86.002 \times 10^{-5} \exp(-8.588t) + 215.295 \times 10^{-5} \exp(-15.427t) - 229.795 \times 10^{-5} \exp(-19.459t) + 81.017 \times 10^{-5} \exp(-22.776t) \]

\[ Z_{14}(t) = 2.263 \times 10^{-5} \exp(-2.118t) - 6.01 \times 10^{-5} \exp(-4.953t) + 7.03 \times 10^{-5} \exp(-6.953t) - 3.772 \times 10^{-5} \exp(-11.671t) + 1.979 \times 10^{-5} \exp(-15.704t) - 0.483 \times 10^{-5} \exp(-19.023t) - 0.527 \times 10^{-5} \exp(-6.471t) + 0.0945 \times 10^{-5} \exp(-12.823t) - 1.444 \times 10^{-5} \exp(-19.662t) + 1.253 \times 10^{-5} \exp(-23.694t) - 0.383 \times 10^{-5} \exp(-27.012t) \]
Table 5.2: Possible states of the Four Stage HIV/AIDS epidemic model for $m = 2$ and $n = 1$

<table>
<thead>
<tr>
<th>$k$</th>
<th>Susceptibles</th>
<th>latents</th>
<th>Infectious</th>
<th>AIDS cases</th>
<th>$j_1$</th>
<th>$j_2$</th>
<th>$j_3$</th>
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<td>0</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>4</td>
</tr>
</tbody>
</table>
\[
Z_{15}(t) = 0.2850 \times 10^{-5} \exp(-2t) - 0.0646 \times 10^{-5} \exp(-6.118t) \\
+ 0.1017 \times 10^{-5} \exp(-8.953t) - 0.0924 \times 10^{-5} \exp(-10.953t) \\
+ 0.0325 \times 10^{-5} \exp(-15.671t) - 0.0132 \times 10^{-5} \exp(-19.706t) \\
- 0.0027 \times 10^{-5} \exp(-23.023t) + 0.0073 \times 10^{-5} \exp(-10.471t) \\
- 0.0075 \times 10^{-5} \exp(-16.823t) + 0.0078 \times 10^{-5} \exp(-23.662t) \\
- 0.0057 \times 10^{-5} \exp(-27.694t) + 0.0016 \times 10^{-5} \exp(-31.002t)
\]

\[
Z_{16}(t) = 6.914 \times 10^{-5} \exp(-0.353t) - 15.0561 \times 10^{-5} \exp(-2.941t) \\
+ 19.2372 \times 10^{-5} \exp(-9.294t) - 27.2875 \times 10^{-5} \exp(-16.133t) \\
+ 23.1978 \times 10^{-5} \exp(-20.165t) - 7.0055 \times 10^{-5} \exp(-23.482t)
\]

\[
Z_{17}(t) = 3.92085 \times 10^{-5} \exp(-0.118t) - 2.0243 \times 10^{-5} \exp(-2.353t) \\
+ 2.370465 \times 10^{-5} \exp(-5.188t) - 1.98835 \times 10^{-5} \exp(-7.188t) \\
+ 0.63995 \times 10^{-5} \exp(-11.906t) - 0.250126 \times 10^{-5} \exp(-15.941t) \\
+ 0.050506 \times 10^{-5} \exp(-19.259t) + 0.15987 \times 10^{-5} \exp(-6.706t) \\
- 0.01461 \times 10^{-5} \exp(-13.059t) + 0.14598 \times 10^{-5} \exp(-19.897t) \\
- 0.105242 \times 10^{-5} \exp(-23.929t) + 0.028227 \times 10^{-5} \exp(-27.247t) \\
- 5.18566 \times 10^{-5} \exp(-0.588t) + 1.7373 \times 10^{-5} \exp(-3.176t) \\
- 0.721409 \times 10^{-5} \exp(-9.529t) + 0.59259 \times 10^{-5} \exp(-16.368t) \\
- 0.40368 \times 10^{-5} \exp(-20.4t) + 1.0477 \times 10^{-5} \exp(-23.718t)
\]
\[ Z_{18}(t) = 2.1922 \times 10^{-5} \exp(-0.118t) - 0.026915 \times 10^{-5} \exp(-2.235t) + 0.020735 \times 10^{-5} \exp(-6.353t) - 0.022422 \times 10^{-5} \exp(-9.188t) + 0.016688 \times 10^{-5} \exp(-11.188t) - 0.0068855 \times 10^{-5} \exp(-17.059t) + 0.00089979 \times 10^{-5} \exp(-31.237t) - 3.92085 \times 10^{-5} \exp(-0.353t) + 0.1928 \times 10^{-5} \exp(-2.588t) - 0.105123 \times 10^{-5} \exp(-5.423t) + 0.06404 \times 10^{-5} \exp(-7.423t) - 0.012524 \times 10^{-5} \exp(-12.141t) + 0.003665 \times 10^{-5} \exp(-16.176t) - 0.00061332 \times 10^{-5} \exp(-19.494t) - 0.0055127 \times 10^{-5} \exp(-6.941t) + 0.00026083 \times 10^{-5} \exp(-13.294t) - 0.00171837 \times 10^{-5} \exp(-20.133t) + 0.0010298 \times 10^{-5} \exp(-24.165t) - 0.0002427 \times 10^{-5} \exp(-27.482t) + 1.72855 \times 10^{-5} \exp(-0.823t) - 0.124092 \times 10^{-5} \exp(-3.412t) + 0.017596 \times 10^{-5} \exp(-9.765t) - 0.008458 \times 10^{-5} \exp(-16.603t) + 0.0046295 \times 10^{-5} \exp(-20.635t) - 0.010343 \times 10^{-5} \exp(-23.953t) \]
\[ Z_{19}(t) = 115.516 \times 10^{-7} - 292.2 \times 10^{-7} \exp(-0.118t) + 0.12587 \times 10^{-7} \exp(-2.235t) \]
\[ -0.038399 \times 10^{-7} \exp(-6.353t) + 0.028714 \times 10^{-7} \exp(-9.187t) \]
\[ -0.01755 \times 10^{-7} \exp(-11.188t) + 0.0030416 \times 10^{-7} \exp(-15.906t) \]
\[ -0.007827 \times 10^{-7} \exp(-19.941t) - 0.0001183 \times 10^{-7} \exp(-23.259t) \]
\[ +0.001518 \times 10^{-7} \exp(-10.706t) - 0.000611 \times 10^{-7} \exp(-17.059t) \]
\[ +0.00325 \times 10^{-9} \exp(-23.897t) - 0.0174 \times 10^{-9} \exp(-27.929t) \]
\[ +0.00376 \times 10^{-9} \exp(-31.237t) + 1.307 \times 10^{-5} \exp(-0.353t) \]
\[ -87.637 \times 10^{-9} \exp(-2.588t) + 22.804 \times 10^{-9} \exp(-5.423t) \]
\[ -10.149 \times 10^{-9} \exp(-7.423t) + 1.214 \times 10^{-9} \exp(-12.141t) \]
\[ -0.267 \times 10^{-9} \exp(-16.176t) + 0.037 \times 10^{-9} \exp(-19.494t) \]
\[ +0.934 \times 10^{-9} \exp(-6.941t) - 0.023 \times 10^{-9} \exp(-13.294t) \]
\[ +0.1004 \times 10^{-9} \exp(-20.133t) - 0.0501 \times 10^{-9} \exp(-24.165t) \]
\[ +0.0104 \times 10^{-9} \exp(-27.482t) - 2469.4 \times 10^{-9} \exp(-0.823t) \]
\[ +42.79 \times 10^{-9} \exp(-3.412t) - 212.0 \times 10^{-9} \exp(-9.765t) \]
\[ +0.599 \times 10^{-9} \exp(-16.603t) - 0.264 \times 10^{-9} \exp(-20.635t) \]
\[ +0.5080 \times 10^{-9} \exp(-23.953t) \]
Case v. Special case of the model

In view of the complexity that exists in calculating the expected number of individuals in each stage and various statistics, we assume the following transition rates as particular case of the model.

\[
\begin{align*}
\lambda_1(x,t) &= \lambda_1 \\
\lambda_2(x,t) &= \lambda_2(t) l \\
\lambda_3(x,t) &= \lambda_3(t) i
\end{align*}
\] (5.33)

where \( \lambda_1 \) is a constant and \( \lambda_2 \) and \( \lambda_3 \) are functions of time \( t \). This model describes the process for which the incidences of new infectives is at a poisson rate and the duration of time in each infective stage follows particular distribution (For example, Exponential or Weibull) with the transition rate proportional to the number of individuals in that stage. Then, the appropriate differential difference equations are given by

\[
\frac{d}{dt} p(x,t) = - \{ \lambda_1 + \lambda_2(t) l + \lambda_3(t) i \} p(x,t) + \lambda_1 p(x + e_4 - e_3, t) + \lambda_2(t) (l + 1) p(x + e_3 - e_2, t) + \lambda_3(t) (i + 1) p(x + e_2 - e_1, t) \quad \text{for } x \in \Gamma
\] (5.34)

Now, we can derive the transition probabilities and hence values for the mean and variance of the model using theorem 2.2. Alternatively, since the transition rates in 5.33 are linear in \( l \) and \( i \), so that we can provide general solution for the model using the probability-generating function method (See, Billard and Zhao [79]) and the solution to the model 5.34 is obtained and are given as follows:

\[
E[L(t)] = E[\text{number of infected individuals}] = \exp \left\{ - \int_0^t \lambda_2(s) ds \right\} \left[ \int_0^t \lambda_1 \exp \left\{ \int_0^s \lambda_2(u) du \right\} ds + 1 \right] (5.35)
\]
\[ E[I(t)] = E[\text{number of infectious individuals}] \]
\[ = \exp\left\{ -\int_0^t \lambda_3(s) ds \right\} \left( \int_0^t \lambda_2(s) \exp\left[ \int_0^s \{\lambda_3(u) - \lambda_2(u)\} du \right] \right. \]
\[ \times \left. \left[ \int_0^u \lambda_1 \exp\left\{ \int_0^u \lambda_2(v) dv \right\} du + 1 \right] ds \right\} \] 
\[ (5.36) \]

\[ E[A(t)] = E[\text{number of AIDS cases}] \]
\[ = \int_0^t \lambda_3(z) \left\{ \exp\left\{ -\int_0^z \lambda_3(s) ds \right\} \left( \int_0^z \lambda_2(s) \exp\left[ \int_0^s \{\lambda_3(u) - \lambda_2(u)\} du \right] \right. \right. \]
\[ \times \left. \left. \left[ \int_0^u \lambda_1 \exp\left\{ \int_0^u \lambda_2(v) dv \right\} du + 1 \right] ds \right\} \right\} dz \] 
\[ (5.37) \]

We use these results for the application to the data on HIV/AIDS epidemic in the Indian context. In particular assuming that the duration time in each infective state follows exponential distribution, i.e., \( \lambda_i(t) = \lambda_i, i = 2, 3 \). Then we can show from equations 5.35, 5.36 and 5.37 that,

\[ E[L(t)] = E[\text{number of infected individuals}] \]
\[ = \lambda_1 \lambda_2^{-1} + (\lambda_2 - \lambda_1) \lambda_2^{-1} \exp(-\lambda_2 t) \] 
\[ (5.38) \]

\[ E[I(t)] = E[\text{number of infectious individuals}] \]
\[ = \lambda_1 \lambda_3^{-1} - \lambda_2 (\lambda_3 - \lambda_1) \lambda_3^{-1} (\lambda_3 - \lambda_2)^{-1} \exp(-\lambda_3 t) \]
\[ + (\lambda_2 - \lambda_1) (\lambda_3 - \lambda_2)^{-1} \exp(-\lambda_2 t) \] 
\[ (5.39) \]

\[ E[A(t)] = E[\text{number of AIDS cases}] \]
\[ = \lambda_1 t - \lambda_1 \lambda_3^{-1} - \lambda_3 (\lambda_2 - \lambda_1) \lambda_3^{-1} (\lambda_3 - \lambda_2)^{-1} \exp(-\lambda_2 t) \]
\[ + \lambda_2 (\lambda_3 - \lambda_1) \lambda_3^{-1} (\lambda_3 - \lambda_2)^{-1} \exp(-\lambda_3 t) + (\lambda_2 - \lambda_1) \lambda_2^{-1} \] 
\[ (5.40) \]
5.4.2 Comparison with reported AIDS cases data in India

Here we have compared expected number of AIDS cases with the reported number of AIDS cases in India (See, UNAIDS [129]). For estimating the parameters of the model, assume that the duration of time in each infective state follows exponential distribution, with mean latent period 6 months [126] and infectious period 8.5 years [124], i.e., $\lambda_2 = 2$ and $\lambda_3 = 0.11765$. Here the incidence function $\lambda_1$ is independent on the size of the population at risk. We use the criterion of minimum sum of squares of error (SSE) with $\lambda_1$ being the expected number of AIDS cases (from equation 5.40) and the actual data to examine the best fit. The estimated value of $\lambda_1$ and the associated minimum SSE are 17905 and $2.10316 \times 10^7$ respectively. The mean number of AIDS cases for Indian population for 1995 to 2004 calculated for the model are plotted in figure 5.3 along with the actual number of reported cases, as reported by UNAIDS [129]. Our results shows that the model under estimate in the beginning period and in the end, but over estimate in middle with actual data (See, Figure 5.3).

5.5 Conclusion

The available data on HIV infections in India represent an incomplete description of the virus spread phenomenon, which is on the whole relatively poorly understood. On the otherhand, the recent data on AIDS are alarming and reveal a frightening trend. In India, the disease is spreading through heterosexual trauma to the general population. It has been estimated that 5.134 million are infected in India [130]. More than 0.6 million Indians were infected with disease in 2003. Likewise, there are many other estimates/projections of HIV/AIDS cases in different regions obtained by various na-
tional/international agencies. These figures differ considerably and also there is a large gap between the actual and estimated numbers. The reason may be the use of different data sets and methodology. As indicated by Nagaraja Rao and Srivenkataramana[120] in a diverse country like India, a state-wise projection of infections is highly desirable, whatever may be the methodology, to obtain the realistic projections. Further more considering separate estimates for sex and urban-rural population will give the more realistic estimations. Thus the state-wise separate estimations for Urban-Male, Urban-Female, Rural-Male and Rural-Female population using the above methodology proposed in the previous section can help to obtain the more realistic results.
Figure 5.3: Mean number of AIDS cases of the model versus reported Indian AIDS cases:
for the estimated parameters $\lambda_1 = 17905$, $\lambda_2 = 2$ and $\lambda_3 = 0.11765$