International Journal of Scientific Research in Mathematical and Statistical Sciences
Volume-5, Issue-5, pp.243-252, October (2018)
Research Paper
E-ISSN: 2348-4519

Stochastic Modeling of Viral Replication and Lysing CD_4^+T Cells in the HIV Infection

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Available online at: www.isroset.org

Received: 03/Aug/2018, Accepted 23/Aug/2018, Online 31/Oct/2018

Abstract-The existing models of HIV infection are non-linear system of differential equations. Solving system of differential equations is very difficult task and also drawing inference is not easy. Therefore, an attempt has been made to estimate the HIV replication periodically using Markov processes in the condition of decay of CD_4^+T cells. The proposed model is illustrated in this paper.

Keywords- *CD_4^+ T cell, HIV and Markov processes*

I. INTRODUCTION

In the viral dynamic study, the HIV infection spread in the human being is very vast in the world. It is a major epidemic in the world now days.HIV infection is naturally distory the human the immune system, in particularly by depleting the CD_4^+ T cells. The HIV transmission system has biologic and social determinants. Biologic determinants include characteristics of the pathogen, the host, and biomedical interventions. Social determinants include individual-level, pair wise and community-level processes that affect behavior, and thus the structure and dynamics of the transmission networks. In the 1990s, the time to development of AIDS after initial infection with the virus is approximately 10 to 12 years. In the mid 1980s, however, the average time from infection to AIDS was 8 to 10 years (Klatt, 1998). This improvement in time to development of AIDS is due, in part, to improved diagnosis, increased use of antiretroviral therapy and improved management of opportunistic infections.At this stage of infection, viral load in an individual may be extremely high, around one million copies/ml, although individual variation is significant. Although CD_4^+ T cell counts may also vary, individuals with CD_4^+ counts below 200 *cells/mm3* are at the greatest risk of developing opportunistic infections (note that CD_4^+ T cell counts of healthy individuals are usually above 1000 cells/mm3) (Chibatamoto, 1996).The overall effect of infection with HIV and its interaction with the body's natural response mechanisms is severe damage to the immune system, destroying by the means which the human body naturally defends itself against infections. Following entry into the host is disseminated via the blood and circulatory system to different tissues in the body. From this moment of infection, the virus is replicating at extremely rapid rates. As the virus replicates and spreads throughout the body.

Effectively, the virus has now hijacked the host cell's own replication system. As a result, when the cellular DNA is transcribed, so the viral DNA to form an RNA transcript. Further processing of this RNA into messenger RNA (mRNA) and genomic viral RNA occurs. The viral mRNA is then translated into viral proteins, which along with the genomic RNA, are assembled into new virus particles. This last stage requires the viral enzyme, protease (Marr, 1998). Finally, the new viral particles are released from the infected cell and go on to infect other cells in the body.

This paper concentrated to the periodically viral replication of infected persons. The stochastic models are designed for the viral replication in the CD_4^+ T cells and lysing CD_4^+ T cells count and illustrated.

Singer et al. (2007) have explained the point of departure for this study was the gross misunderstanding among researchers concerning which stochastic matrices are compatible with a continuous-time Markov process having stationary transition probabilities. **Myron S. Cohen et al. (2008)** have given several behavioral and structural strategies have made a difference male circumcision provides substantial protection from sexually transmitted diseases, including HIV-1, and the for prevention holds great promise.**Cassels et al. (2012)** have discussed mathematical models provide a way to examine the potential effects of the proximate biologic and behavioral determinants of HIV transmission dynamics, alone and in combination. The purpose of this article is to show how mathematical modeling studies have contributed to our understanding of the dynamics and disparities in the global spread of HIV.**Mbogoet al. (2013)** have explained stochastic model for in-host

HIV dynamics that included combined therapeutic treatment and intracellular delay between the infection of a cell and the emission of viral particles. This is model included dynamics of three compartments the number of healthy CD4 cells, the number of infected CD4 cells, and the HIV virons and it described HIV infection of CD4 T cells before and during therapy. **Tang Ning et al.(2013)**have studied the non-Markovian dynamical properties of a two-level system coupled to a zero-temperature structured environment under the NRWA.They derived the TCL master equation in the limit of weak coupling between the system and its environment. **Doss et al. (2014)** have briefed out the Continuous-time linear birth–death-immigration (BDI) processes are frequently used in ecology and epidemiology to model stochastic dynamics of the population of interest. In clinical settings, multiple birth–death processes can describe disease trajectories of individual patients, allowing for estimation of the effects of individual covariates on the birth and death rates of the process.**Leonid et al. (2015)** have considered a stochastically perturbed Nowak–May model of virus dynamics within a host. Using the direct Lyapunov method, they found sufficient conditions for the stability in probability of equilibrium states of this model. Mathematical model for the spread of HIV and AIDS amongst PWIDs. Stochasticity into their model by using the standard technique of parameter perturbation. The spread of the disease amongst PWIDs can be described by the differential equation the fraction of PWIDs who must clean their needles after use, the effects of HIV testing, or the amount that PWIDs need to decrease their syringe sharing rates in order to reduce beneath one and eliminate disease. **Liang et al. (2016).O Abu et al. (2016)** have discussed stochastic differential equation models for vertical and heterosexual transmission dynamics of HIV/AIDS in a population are formulated and investigated. The models were solved numerically to investigate the effects of ART, condom use and both on the transmission dynamics and to also examine the model performance. **Precharattana et al.(2016)**have given the infection of human immunodeficiency virus type 1(HIV-1), causing acquired immunodeficiency syndrome (AIDS), is responsible for millions of deaths worldwide. Pathogenesis medical professionals use the CD4 count and viral load in HIV-1 patient blood to refer the stage of disease progression and to decide when to begin treatment. **Konstantina Palla et al. (2017)** have illustrated Bayesian nonparametric prior over feature allocations for sequential data, the birth death feature allocation process (BDFP). The BDFP models the evolution of the feature allocation of a set of N objects across a covariate (e.g. time) by creating and deleting features. **Joseph N. Inungu et al. (2017)** have explained the understanding of the lifecycle of the HIV was a turning application of antiretroviral agents point that provided researchers with the knowledge and tools needed to prosecute drug discovery efforts focused on targeted inhibition with specific pharmacological agents. The following models explain the natural replication of HIV in the CD_4^+ T cells.

II. MODELING OF HIV REPLICATION

Let $X_{t,s}(t)$- is denoted by the random variable as the viral replication at time t and state S. Where, S-state space represents number of replicated virus, Time space t is each succeeding periods. If $X_{01}^{(t)} = i, X_{12}^{(t)} = j, X_{23}^{(t)} = k$; $t = 0,1,2,$ ...denotes, each succeeding period viral replication. The conditional probability of AIDS stage infected person is denote by,

$$P_{i,i+a}[X(t) = j/X(t) = i] > P[X(t) = i] \quad ; \; i = 0,1,2 P_{i+a,i+2a}[X(t) = k/X(t) = i + a] > P_{i,i+a}[X(t) = j/X(t) = i] > P[X(t) = i]$$

Since i, j, k, Considered as states of non-infection, infection, become critical AIDS.A time space represents the each succeeding period (i.e.) every three month.

$X_{1,2}(t)$ →Current infection stage $(i - k)$.There are n stages available in between [i, k] n stage may be time period. Where, $a = a_1 + a_2 + \cdots + a_n ; a_1 > a_2 > a_3 > a_4 > \cdots > a_n \geq \sum_{i=1}^{n} a_i$

$If\, a_{n+1} \geq \sum_{i=1}^{n} a_i \,, X(t_i) = k.$, j state classified as n intervals.$(n+1)^{th}$State.

Where $X(t_i)$is the state space of the random variable. (Viral replication).The transition probability is given by

$$P[X(t_2) = j/X(t_1) = i] = P_{ij}$$

$P[X(t_3) = k/X(t_2) = i] = P_{jk}$,Where,$P_{ij} < P_{jk}$.

Then $E\left(X_{n+1}(t)\right) = \sum_{i=1}^{n} a_i P_{ij}$ and $P_{ii} = 0, P[X(t) = j/X(t) = i] = P_{ij} \sim$ Binomial distribution. In the every period initial infection of CD_4^+T is distributed as binomial, and end period viral replication is distributed as Poisson.

The conditional density of viral replication of current period is given by

$$P(x(t) = j/x(t) = i) = \frac{P[(x(t) = j) \cap (x(t) = i)]}{\sum_{i=1}^{n}[P(x(t) = j) \times P(x(t) = i)]}$$

$$P(X = i) = \sum_{j=0}^{\infty} P(X = i, Y = j) = \sum_{j=0}^{\infty} P(X = i/Y = j)P(Y = j)$$

$$= \sum_{j=i}^{\infty} \binom{j}{i} P^i (1-P)^{j-i} \frac{e^{-j}\lambda^j}{j!} if j < i \geq 0$$

$$= \frac{(\lambda p)^i e^{-\lambda}}{i!} \sum_{j=i}^{\infty} \frac{\left((1-p)\lambda\right)^{j-i}}{(j-i)!}$$

$$= \frac{(\lambda p)^i e^{-\lambda}}{i!} e^{(1-p)\lambda}$$

$= \frac{(\lambda p)^i e^{-\lambda p}}{i!}$ [Which is distributed as Poisson with parameter λp.]

Let as assume that Succeeding period viral load $\{X_{t,s}\}$ is random variable which is distributed as exponential with parameter $\theta = \sum a_i/n$ and Transition probability of succeeding periods is given by

$$t_1 \quad t_2 \ldots \quad t_n$$

$$P_{t,s} = \lambda_{ij} = \begin{bmatrix} \lambda_{11} & \lambda_{12} \ldots & \lambda_{1n} \\ \vdots & \vdots & \vdots \\ \lambda_{N1} & \lambda_{N2} \ldots & \lambda_{Nn} \end{bmatrix}$$

The State space is viral replication ever the n period is given by

$$A_{ij} = \begin{bmatrix} a_{11} & a_{12} \ldots & a_{1n} \\ \vdots & \vdots & \vdots \\ a_{N1} & a_{N2} \ldots & a_{Nn} \end{bmatrix}$$

and

The Time space has n- period is denoted by

$$[t_1 \quad t_2 \ldots \quad t_n]$$

HIV replication is treated as the markov chain, the sequence of random variable the time space and state space is finite. Time space-is treated as every period of (every three months) monitoring viral level. $a_i (i = 1,2, \ldots, n)$ State space-is treated as viral load per period say $(a_1, a_2, \ldots a_n)$

Viral replication is random variable which is considered as rapid growth. It is monotonically increasing function and also infect to rapidly to CD_4^+T cells. Which is distributed as exponential with rate of replication per period is considered as

$\theta_i a_i i = 1,2, \dots, n$ and $a_i's$ state.$\{X_i, a_i\}$ is said to be the viral replication in the blood plasma of HIV infected person. The probability matrix of the "N" infected persons and their n period viral replication is given by.

$$P_{ji} = \begin{bmatrix} \lambda_1 a_1 & \lambda_1 a_2 \dots & \lambda_1 a_n \\ \vdots & \vdots & \vdots \\ \lambda_N a_1 & \lambda_N a_2 \dots & \lambda_N a_N \end{bmatrix}$$

Where,$\lambda_j a_i \cap \lambda_j a_{i+1,} i = 1,2, \dots, n,\ j = 1,2, \dots N$and $0 < \lambda_i < 1,\ a_i > 0.$

$\{X_i a_i\}$ is said to be continuous time markov chain and its time space is stationary steady state (every three month).but the state space is the increasing order of the exponential growth $a_1 < a_2 < a_3 \dots < a_i \dots < a_n$ .The transition probability of the j[th] patient i[th] period viral replication is denoted by $\lambda_j a_i . \lambda_j \rightarrow$is j[th] patient's probability that to replicate the virus in the CD_4^+T cell. a_i is viral load per period. $(0 < \lambda_i < 1,\ a_i > 0)$ Let as assume that viral replication is towards constant rate for successions periods, $\lambda_j = {lna_i}/{10^2}$.

Where$\lambda_1 > \lambda_2 > \lambda_j > \lambda_{j+1} > \lambda_{j+2} > \cdots > \lambda_{j+n}$ for a particular patient probability of the (n+1)[th] period is denoted by

$\lambda_{n+1} = 1 - \sum_{j=1}^{n} {\lambda_j}/{n}$; $0 < \sum \lambda_j < 1$ and $\sum_{j=1}^{n+1} \lambda_j = 1$

Under the assumption, of

(1) (j+1)[th] probability will be maximum.
(2) $a_{n+1} \geq (\sum_{i=1}^{n} a_i)/n$
(3) $a_n < (\sum_{i=1}^{n} a_i)/n$

The average viral replication of the I[st] patient is denoted by,$E(X_{t,s})_1 = \sum_{i=1}^{n} \lambda_{1i} a_{1i}$at first patient average viral replicate at i[th] period,

$E(X_{t_1 s})_N = \sum_{i=1}^{n} \lambda_{Ni} a_{Ni}$,denoted the n periods average viral replication of N[th] patients.

$E(X_{t_1 s})$ at (n+1)[th] period is consider as the future prediction of viral replication. That is $E(X_{t_1 s})_{n+1} = \lambda_{n+1} a_{n+1}$,

Where, $a_n = \sum_{i=1}^{n} a_i$, $a_{n+1} \geq a_n$, $\lambda_{n+1} = 1 - \lambda_\alpha$ and $\lambda_\alpha = \sum_{i=1}^{n} {\lambda_{ij}}/{n}, \alpha = 1,2,3, \dots, N$
Where λ_α is the average of probability n period a particular patient.

Let $a_{ij} > 0$, it is distributed as Poisson random variable j[th] patient i[th] period average replication. The average replication of (n+1) period is denoted by, $E(X_{t,s})_{at\,(n+1)} = (1 - \lambda_\alpha) a_n$
Where a_n is poisson random variable and λ_α is exponential random variable,

$$\left\{\left\{E(X_{t_1 s})_j\right\}^1, j > 0, t > 0, s > 0\right\} i = 1,2, \dots, n, j = 1,2, \dots, N.$$

Homogeneous t is stationary (time space) probability equal interval. (Every month) s is dependent to the previous state. (Viral load per period) is stochastic processes. In which viral replication is continuous time markov chain. Therefore Average replication of first person n period is denoted by

$$A_{1i}\lambda_{1i}^{'} = [a_{11} \quad a_{12} \quad \cdots \quad a_{1n}] \begin{bmatrix} \lambda_{11} \\ \lambda_{12} \\ \vdots \\ \lambda_{1n} \end{bmatrix}$$

$$A_{1i}\lambda_{1i}^{'} = [a_{11}\lambda_{11} + \quad a_{12}\lambda_{12} + \cdots \quad + a_{1n}\lambda_{1n}]$$

The average replication of N^{th} patients first period average replication is given.

$$\lambda_{j1}^{'} A_{j1} = \begin{bmatrix} \lambda_{11}\lambda_{12} \ldots \lambda_{j1} \ldots \lambda_{N1} \end{bmatrix} \begin{bmatrix} a_{11} \\ a_{21} \\ \vdots \\ a_{j1} \\ \vdots \\ a_{N1} \end{bmatrix}$$

$$\lambda_{j1}^{'} A_{j1} = \begin{bmatrix} \lambda_{11}a_{11} + \lambda_{21}a_{21} + \lambda_{ji}a_{ji} + \cdots + \lambda_{N1}a_{N1} \end{bmatrix}$$

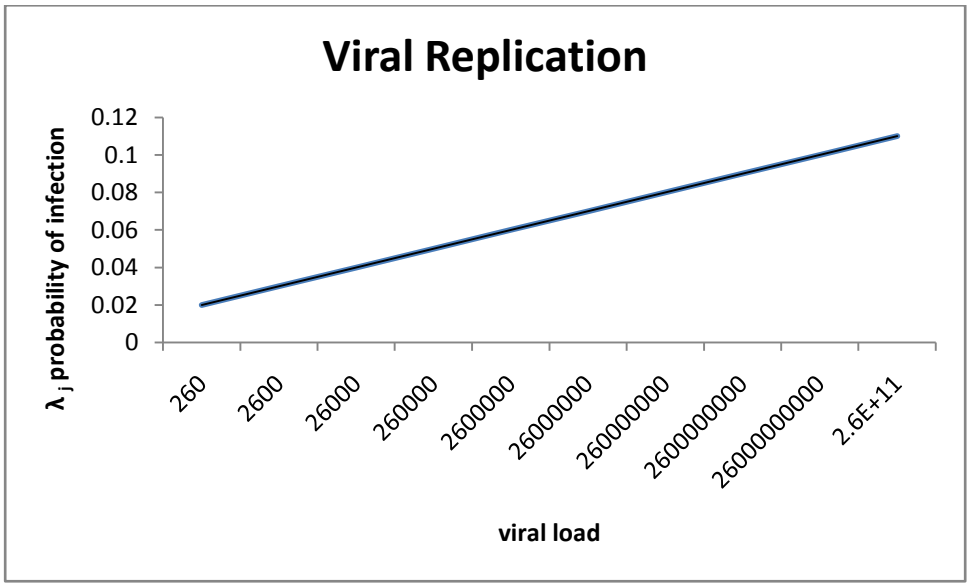
The following table-I explain the exponential nature of the viral replication for the future period is illustrated.

Table-I

Period(x)	**Viral Load(a_i)**	**Probability $\lambda_j = {lna_i}/{100}$**
1	260	0.02
2	2600	0.03
3	26000	0.04
4	260000	0.05
5	2600000	0.06
6	26000000	0.07
7	260000000	0.08
8	2600000000	0.09
9	26000000000	0.10
10	260000000000	0.11

The above model is illustrate through following graph-I

GRAPH I:



Graph I illustrate that viral load is increasing and probability of infection increases by assumption of exponential growth rate of replication.

III. Model for Lysing CD_4^+TCells, Over the n Periods

Viral replication in a individual CD_4^+T calls is denoted bya_{ij}. It is a random variable at time t. The number of CD_4^+T cells that release the virus at time t is denoted byε_{ij}. It also a random variable each lysing individual CD_4^+T is independent identically distributed .which is denoted by

$$P(\varepsilon_{ij}) = P_{ij}, \qquad i = 1,2,\dots,n,\ \ j = 1,2,\dots,k$$

The sequence of $\{\varepsilon_{ij}\}$ lysing CD_4^+Tcell at time interval $(t_1 - t_0)$ is called as discrete state space of stochastic process. The value of ε_{ij} are discrete numbers (i.e.) state space A. Time space is countable$(t_1 - t_0, t_2 - t_1, \dots)$. At time interval $t_1 = (t_1 - t_0)$, assumption that there are two CD_4^+T cells are lysing ((i.e.) ε_{11} andε_{12}, at time interval $t_1$the state space is 2) similarly at $t_2 - t_1$ there five lysing CD_4^+Tcells. (i.e.) $\varepsilon_{21}, \varepsilon_{22}, \varepsilon_{23}, \varepsilon_{24}$and ε_{25} the state space is 5.

The total number of lysing cells at time t_i is denoted by.

$\varepsilon_i = \sum_i \sum_j \varepsilon_{ij}$ at time t_i.

The probability of the random variable $\{\varepsilon_{ij}\}$ to be lysing is denoted by $\{P_{ij}\} i = 1,2,\dots,n,$

$j = 1,2,\dots,k$. It is the stationary distribution over the period.

$$\sum_i \sum_j P(\varepsilon_{ij}) = 1.(i.e.) \sum_i \sum_j P_{ij} = 1.$$

The number of virus released by CD_4^+Tcells is denoted by $\{b_{t_i}\}$,at time t_i. The interval of time $t_0 < t_1 < t_2 < t_3 \dots <$ t_{n+1} the values of b_{t_i} at each time interval independent $b_{t_0}, b_{t_1}, b_{t_2}, b_{t_3}, \dots, b_{t_n}, (i.e)\{b_t, t \in T\}$ is independent increment Stochastic Process, that is given by,

$$P(b_{t_{n+1}}/b_{t_m} = x_n, b_{t_{n-1}} = x_{n-1}, \dots, b_{t_0} = x_0).$$

The state space A and time space $t \in T$. $\{b_t, t \in T\}, T \in (0, \infty)$ for every three months. Interval, is markov process, and $b_{t_0} < b_{t_1} < b_{t_2} < \cdots < b_{t_n}$. Then

$$E\left(b_{t_{n+1}} / b_{t_n} = x_n \ldots b_{t_0} = x_0\right) = x_n.$$

Where, $E\left(b_{t_n} / b_{t_n} = x_n \ldots b_{t_0} = x_0\right) = b_{t_n}$.

The expected number of replication at t_{n+1} is same as the t_n is called as martingale process. The stationary probability matrix of succeeding time periods of CD_4^+T cells.

The transition stationary probability matrix is illustrated below.

$$P_{ij} = \begin{bmatrix} 1 & 0 & 0 & 0 & \ldots & 0 \\ 0.4 & 0.6 & 0 & 0 & \ldots & 0 \\ 0.1 & 0.3 & 0.6 & 0 & \ldots & 0 \\ 0.1 & 0.2 & 0.3 & 0.4 & \ldots & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0.05 & 0.05 & 0.15 & 0.25 & \ldots & 0.50 \end{bmatrix}$$

$$i = 1,2, \ldots, n \;\; ; j = 1,2, \ldots, n.$$

Every succeeding period the number of CD_4^+T cells lysing is usually increased, the stationary probability will be also increased. At time t_i, $\{b_{t_i}, i = 1,2, \ldots, n\}$ is random variable it value $x_{t_i} = \sum_i \sum_j b_{ij\ (\varepsilon_{t_i})}$, the state space of $\{b_{t_i}\}$ is given by

$$\varepsilon_{ij} = \begin{bmatrix} b_{11} & b_{12} \ldots & b_{1n} \\ \vdots & \vdots & \vdots \\ b_{n1} & b_{n2} \ldots & b_{mn} \end{bmatrix} x_{ij} < x_{ij+1}; \;\; i = 1,2, \ldots, n; \;\; j = 1,2, \ldots, n$$

$$E\left(b_{t_{n+1}}\right) = \sum_{i=1}^{n} P_{ij} \;\; \varepsilon_{t_{ij}}$$

The number of lysing CD_4^+T cells is denoted by ε_{ij} . The viral replication of individual CD_4^+T cell is independent and identicatically distributed.

Random variable $\{\varepsilon_{ij}\}, i = 1,2, \ldots, n$, cells number of lysing with probability at time t_i.

$$P\{\varepsilon_{ij} = b_i\} = P_i, P\{\varepsilon_1 = b_1\} = P_1, P\{\varepsilon_2 = b_2\} = P_2,$$

$$\sum_{i=1}^{n} P_k = 1, \qquad i = 1,2, \ldots, n, \qquad j = 1,2, \ldots, k$$

Let us assume that, at time t_1, there a two cells lysing namely,

$$\varepsilon_{11} = 500, \varepsilon_{22} = 1500$$

$$P(\varepsilon_{11}) = 0.1, P(\varepsilon_{12}) = 0.9$$

$$X_{11} = b_{1_{\varepsilon_1}} + b_{2_{\varepsilon_2}}$$

At t_2,there a five cells lysing

$$b_{21} = 200, b_{22} = 500, b_{23} = 300, b_{24} = 400, b_{25} = 1500.$$

$$P(\varepsilon_{21}) = 0.2, P(\varepsilon_{22}) = 0.3, P(\varepsilon_{23}) = 0.1, P(\varepsilon_{24}) = 0.1, P(\varepsilon_{25}) = 0.2.$$

$$X_2 = b_{1_{\varepsilon_2}} + b_{2_{\varepsilon_2}} + b_{3_{\varepsilon_2}} + \cdots + b_{n_{\varepsilon_2}}.$$

At t_i, ε_i,there are n cells lysing,ε_{ij} is the random variable number of CD_4^+T cells lysing out j[th] cells of i[th] time $t_1 < t_2 <, \ldots, < t_{n+1.}$ The $X_i, i = 1,2, \ldots, n$(Number of virus replicated at the time $t_i$of byCD_4^+T calls). $t_1, t_2, t_3, \ldots, t_n$are period of time independent distributed.At time t_{n+1},the number of replicate of virus, is denoted by X_{n+1}

$$X_{n+1} = \sum_{i=1}^{n} X_1 + X_2 + \cdots + X_n + B$$

Where,

$$X_i = \sum_{j=1}^{\varepsilon_i} b_{ij}, \qquad i = 1,2, \ldots, n, \ \ j = 1,2, \ldots, \varepsilon_i.$$

The probability of number of viral replication at $t_{n+1}$is denoted by

$$P\left(X_{t_{n+1}}/X_{t_{n+1}} = b_n, X_{n-1} = b_{n-1}, \ldots, X_n = b_n\right)$$

$p(X_{n+1}\epsilon B/X_n = b_n) = P_{t_{n+1}}$ is a markov process, and its expected number of viral replication is considered as martingale.$E\left[X_{n+1}/X_n = b_n, X_{n-1} = b_{n-1}, \ldots, X_{t_1} = b_1\right]$=$b_n$is martingale.

$$E(X_n) = \sum_{i=1}^{n} X_i P(X_i) = b_n, \qquad i = 1,2, \ldots, n$$

$$E\left(X_{t_{n+1}}\right) = E(X_{n+1}),$$

If $B = 0 \implies E\left(X_{t_{n+1}}\right) = E(X_{n+1})$

If $B > a_n \implies E\left(X_{t_{n+1}}\right) > E(X_n).$

The distribution of lysing CD_4^+Tcells is given in the following matrix over the period of time.

Let $\varepsilon = \begin{bmatrix} \varepsilon_{11} & & & \\ \varepsilon_{21} & \varepsilon_{22} & & \\ \vdots & \vdots & \vdots & \vdots \\ \varepsilon_{n1} & \varepsilon_{n2} & \ldots & \varepsilon_{nn} \end{bmatrix}$ be an infinite matrix of random variables. Let the random variable $\varepsilon_{ji}, 1 \le j \le i, i = 1,2, \ldots$ in each row be independent, and let all of them have finite first through third moments.(i.e.) $E\left(\varepsilon_{ji}\right) = b_{ji}, E\left(\varepsilon_{ji} - b_{ji}\right)^2 = \sigma_{ji}^2, E\left(\left|\varepsilon_{ji} - b_{ji}\right|\right)^3 = v_{ji}$.

Set $b_j = \sum_{j=1}^{i} b_{ji}, \sigma_j^2 = \sum_{j=1}^{i} \sigma_{ji}^2, v_j = \sum_{j=1}^{i} v_{ji}, 1 \le j \le i, i = 1,2, \ldots$

Then under the assumption $\lim_{n\to\infty} v_n\, \sigma_n^{-3} = 0$.

The sum $\varepsilon_n = \varepsilon_{n1} + \varepsilon_{n2} + \cdots + \varepsilon_{nn}, n \geq 1$is asymptotically $N(b_n, \sigma_n^2)$distributed.

$$\varepsilon = \begin{bmatrix} 50 & & & \\ 100 & 200 & & \\ \vdots & \vdots & \vdots & \vdots \\ 300 & 200 & \cdots & 50 \end{bmatrix}, \quad E(\varepsilon_{ji}) = \sum \varepsilon_{ji} P(\varepsilon_{ji}) = b_{ji}$$

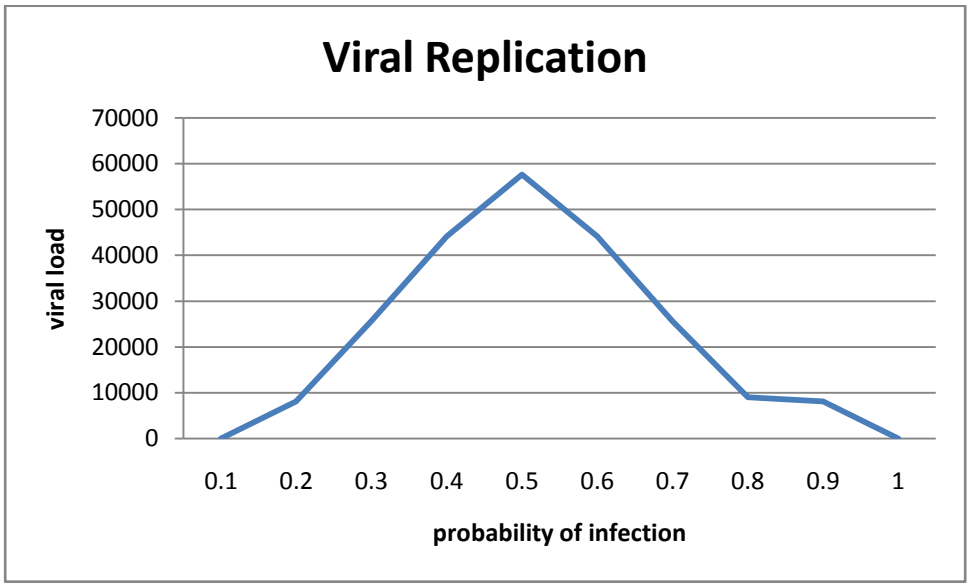
$$i.e)\ b_{ji} = \begin{bmatrix} b_{11} & & & \\ b_{21} & b_{22} & & \\ \vdots & \vdots & \vdots & \vdots \\ b_{n1} & b_{n2} & \cdots & b_{nn} \end{bmatrix} = \begin{bmatrix} 50 & & & \\ 10 & 40 & & \\ \vdots & \vdots & \vdots & \vdots \\ 150 & 80 & \cdots & 30 \end{bmatrix}$$

$$i.e)\ \sigma_{ji}^2 = \begin{bmatrix} \sigma_{11}^2 & & & \\ \sigma_{21}^2 & \sigma_{22}^2 & & \\ \vdots & \vdots & \vdots & \vdots \\ \sigma_{n1}^2 & \sigma_{n2}^2 & \cdots & \sigma_{nn}^2 \end{bmatrix} = \begin{bmatrix} 8100 & & & \\ 25600 & 44100 & & \\ \vdots & \vdots & \vdots & \vdots \\ 122500 & 102400 & \cdots & 72900 \end{bmatrix}$$

$$i.e)V_{ij} = \begin{bmatrix} v_{11} & & & \\ v_{12} & v_{22} & & \\ \vdots & \vdots & \vdots & \vdots \\ v_{n1} & v_{n2} & \cdots & v_{mm} \end{bmatrix} = \begin{bmatrix} 729000 & & & \\ 4096000 & 9261000 & & \\ \vdots & \vdots & \vdots & \vdots \\ 42875000 & 32768000 & \cdots & 19683000 \end{bmatrix}$$

$$b_j = 60, \quad \sigma_j^2 = 62600, \quad v_j = 18235333.33$$

GRAPH II:



The above graph II illustrate that the variation of viral load follows the normal distribution from this we identify the probability of infection is increased.

IV. CONCLUSION

The model which is estimated here to the HIV replication periodically as the Markov processes under the condition of decay of CD_4^+Tcells. This idea will help to the physician those who me treated HIV infected patients to suggest a proper treatment for infected patients in advance. When data in the large size viral load of the infected patients follows normal is distribution in future and the graph II explain the variation of viral load when the probability infection is increased.

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