



Cessation Point of HIV Transmission through Stochastic Approach

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Abstract: A stochastic model in this paper possesses the survival of the human system to withstand the threshold level. This model will apply for any environmental population to accesses when the virus damages the human system in the time period. Through shock model approach in stochastic process we find out the mean along with numerical simulations are concluded.

Keywords: Distribution, Human system, Modelling, Time period, Virus.

1. INTRODUCTION

Infection by the human immunodeficiency virus (HIV) gradually evolves to the acquired immune deficiency syndrome (AIDS), and AIDS evolves to death if not handled carefully. Considering this progress of HIV infection to AIDS and then to death as a stochastic process. By splitting the progression into various states of the disease based on the immunological indicators namely CD4+ count including death as one state [1]. Mathematical/Statistical models paly and important role in human biological system, the models make it possible to predict the behavior of the human biological system. HIV and CD4 cells still been a major area of findings through modelling [2,3,4]. The stochastic process with differential equation model through HIV internal viral dynamics by [5] used two types of infected cells, latently infected cells and actively infected cells.

In this paper, we present the results of modelling of the progression of HIV/ AIDS so as to predict the future threshold level and survival probability of a patient. These are: the conditional probability that an HIV/AIDS patient given that he/she is infected with disease, after a period of time interval, the patients threshold level is calculated; and the probability that an HIV/AIDS patient survives for a specific time given his/her starting state of the disease. Dalal, Greenhalgh and Mao, (2007) [6], pointed the real benefits gained through stochastic rather than deterministic model. Different cells and infective virus elements react in the same environment of gives different results. Similar finding of stochastic model related to the expected time/ withstand of threshold, one can refer to [7,8,9,10,11].

2. DESCRIPTION OF THE STOCHASTIC MODEL

The human system been observed with the virus assumed from time $t = 0$. Further his/her sexual contacts occur at random time points which follow the Alpan-poisson distribution with parameters 'a' and 'α' which is given in equation (1), and the inter arrival time between the contacts follows mittag-leffler distribution.

$$(p_{a,\alpha})^{(n,t)} = \sum_{k=0}^{\infty} (-1)^k \binom{k+n}{k} \frac{(at)^\alpha (k+n)}{\Gamma(\alpha(k+n) + 1)}, \quad a > 0, 0 \leq 1; n = 0,1,2 \dots \quad (1)$$

The time of the HIV transmission in the human system be represented by random variable T. We obtain the distribution of HIV transmission by a stochastic model based on the following assumptions.



- i) Sexual contact is the only source of HIV transmission.
- ii) Transmission of HIV at each contact of inter arrival time are independently identical random variables.
- iii) The damage process acting on the human system of an infected individual is non-linear and cumulative.
- iv) The total damage caused exceeds a threshold level Y which itself is a random variable.
- v) The process that generates the contacts, the sequence of damages and threshold are mutually independent.

Let X_i – The virus arising due to HIV spread during i^{th} contact.

$G(\cdot)$ – Distribution function of X_i

$g(\cdot)$ – The probability density function of X_i ; $g^*(s)$ – Laplace transformation of $g(\cdot)$

$g^k(\cdot)$ – The probability density functions of the random variable $\sum_{i=1}^k X_i$, which is the K Convolution of $g(\cdot)$.

Y – Random variable denoting the human system to withstand the threshold, which follows three parameter weibull distribution.

$F(\cdot)$ – The probability density function of human system to withstand the threshold.

The model parameters are

A – Total damage .

α – human system to withstand the threshold

λ – time

3. DISTRIBUTION OF SEROCONVERSION TIME

A. Theorem

If the number of contacts is an Alpha Process with parameters ‘ a ’ and ‘ α ’ and inter contact time is a Mittag–leffler distribution while the threshold level is three parameter weibull distribution with parameter ‘ μ ’ then the probability density function of the seroconversion time is a modified form the distribution.

Proof

Lack of treatment for many reasons cannot be assessed for the patient, so the patient depends only on the present state and not his/her previous history. Individually evolution of the HIV is random regardless to time. The prevalence function $L(t) = 1 - S(t)$, where

$S(t) = \{T > t\}$ = probability that the human system does not take before t .

$S(t) = \sum_{k=1}^{\infty} p \left(\text{No human system affected before } \frac{t}{\text{exactly}} k \text{ contact in } (0, t] \text{ with intensity } \alpha \right)$

* P [Exactly k contacts in $(0, t]$ with intensity α]

$$= \sum_{k=1}^{\infty} V_k(t) P\left\{\sum_{i=1}^k X_i < Y\right\}$$

Where $V_k(t)$ – probability of exactly k contacts in $(0, t]$ with intensity ‘ α ’ . Therefore,

$$P[X > Y] = \int_0^{\infty} 1 - e^{-\left(\frac{t}{\beta}\right)^x} \left[1 + \frac{at}{b}\right]^{\left(\frac{b}{\alpha^2}\right)-1} e^{-\frac{t}{\alpha}} dt$$

$$= \int_0^{\infty} e^{-\frac{t}{\alpha}} \frac{t}{b} \left[1 + \frac{at}{b}\right]^{\left(\frac{b}{\alpha^2}\right)-1} dt - \int_0^{\infty} e^{-t\left(\frac{1}{\beta} + \frac{1}{\alpha}\right)} \frac{t}{b} \left[1 + \frac{at}{b}\right]^{\left(\frac{b}{\alpha^2}\right)-1} dt$$

$$[1 - G(t)] = \left[\frac{e}{b}\right]^{\frac{t}{\alpha^2}} (at + b) e^{-\frac{(at+b)}{\alpha^2}}$$

$$\text{Therefore, } G(t) = \left(1 + \frac{at}{b}\right)^{\frac{t}{\alpha^2}}$$

The probability density function of t is given by

$$g(t) = \frac{-b}{\alpha^2} \left[1 + \frac{at}{b}\right]^{\left(\frac{b}{\alpha^2}\right)-1} \left(\frac{\alpha}{b}\right) e^{-\frac{t}{\alpha}} + e^{-\frac{t}{\alpha}} \left[1 + \frac{at}{b}\right]^{\left(\frac{b}{\alpha^2}\right)}$$

$$g(t) = \frac{t}{b} \left[1 + \frac{at}{b}\right]^{\left(\frac{b}{\alpha^2}\right)-1} \frac{-1}{e^{\alpha}}$$

As a special case taking $a = \frac{1}{\mu}$ and $b = \frac{1}{\mu^2}$



$$G(t) = \frac{1}{(\mu t + 1)e^{-\mu t}} \tag{2}$$

Above equation (2) is the distribution function if the Erland-2 distribution, and does not satisfy the lack of memory property.

4. RESULTS

The probability that the human system develop a single contact does not cross the threshold level is given by

$$P[T > t] = \int_0^{\infty} F(x)g(x)dx$$

Therefore

Now, if we was assume that human system’s threshold induced by a single contact follows exponential distribution with mean β , then we have

$$\begin{aligned} P[T > t] &= \sum_0^{\infty} P\{\text{There are exactly } k \text{ contacts in } (0,t]\} \times \{\text{the threshold is not crossed}\} \\ &= \sum_0^{\infty} V_k(t) P[X < Y] \\ &= e^{-(\lambda t)^\alpha} e^{[(\lambda t)^\alpha A]} \end{aligned}$$

$$\begin{aligned} H(t) &= P[T \leq t] \\ &= 1 - e^{-(\lambda t)^\alpha [A-1]} \end{aligned}$$

$$\frac{d}{dt} H(t) = -\alpha \lambda^\alpha t^{\alpha-1} (A - 1) e^{-\lambda^\alpha (A-1) t^\alpha}$$

Assuming that $b = \alpha^2$ on simplification, it can be shown that

$$P[X > Y] = \frac{\alpha^2 + 2\beta\alpha}{(\beta + \alpha)^2} \text{ on simplification}$$

$$\text{Let } A = \frac{\alpha^2 + 2\beta\alpha}{(\beta + \alpha)^2}$$

When there are k contact we have

$$P[X_1 + X_2 + \dots + X_k < Y] = \left[\frac{\alpha^2 + 2\beta\alpha}{(\beta + \alpha)^2} \right]^k$$

Now the total probability that the total virus has not crossed the threshold level before the time ‘t’ is given by

$$h(t) = \alpha \lambda^\alpha t^{\alpha-1} (1 - A) e^{-\lambda^\alpha (1-A) t^\alpha}$$

$$E(T) = \int_0^{\infty} t \alpha \lambda^\alpha t^{\alpha-1} (1 - A) e^{-\lambda^\alpha (1-A) t^\alpha} dt$$

$$\text{Let } C = \lambda^\alpha (1 - A), t^\alpha = \frac{y}{C}, t = \left(\frac{y}{C}\right)^{\frac{1}{\alpha}}$$

$$\alpha t^\alpha dt = \left(\frac{y}{C}\right)^{\frac{1}{\alpha}} \frac{dy}{C}$$

$$E(T) = C \alpha \int_0^{\infty} t^\alpha e^{-y} dy$$

$$E(t) = \frac{1}{[\lambda^\alpha (1-A)]^{\frac{1}{\alpha}}} \Gamma\left(\frac{1}{\alpha} + 1\right) \tag{3}$$



5. CONCLUSION

General equations are verified for the rates of individually method and combined to formulate a numerical model consisting of equations for each assumed variables. From equation (3) we observe the threshold of human system to withstand the virus through numerical illustration as observed in the below table 1. Table 1 observes the various change when the parameter values are fixed in different period of time. The total damage $A=0.8$ is been fixed to show there is no damage occurs from other source to the human system. When λ the time period of infected human system to withstand threshold α increases, the expected count of virus decreases in all the cases. In the initial state when $\alpha = 0.5$, we observe the total counts in the human system (i.e., 50) as time period increases we find the counts decreasing. In the second state when $\alpha = 1$, we find that almost 90% of the cells been destroyed by the virus showing there is no chance of the human system to survive for a long period of time.

Table 1. Survival of human system

A=0.8			
λ	$\alpha = 0.5$	$\alpha = 1$	$\alpha = 1.5$
1	50	5	2.64
2	35.355	2.5	0.933
3	28.868	1.667	0.508
4	25	1.25	0.33
5	22.361	1	0.236
6	20.412	0.833	0.18
7	18.898	0.714	0.143
8	17.678	0.625	0.117
9	16.667	0.556	0.098
10	15.811	0.5	0.083

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