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Review Article

A STOCHASTIC MODEL FOR HIV PATIENTS USING THREE SOURCE OF TRANSMISSION

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Abstract

There is no medical treatment and cure against HIV/AIDS, till date. It is very much important to take remedial measure as well as preventive measures to reduce or avoid the risks associated with the disease. In this paper, we adopted stochastic models to obtain the expected lifetime of HIV infected people, which is predicted with three sources of transmission.

Key words: Shock model, Exponential, Erlang, HIV, Threshold.

INTRODUCTION

Globally, 35 million people were living with HIV at the end of 2013 (WHO). An estimated 0.8% of adults aged 15-49 years worldwide are living with HIV, although the burden of the epidemic continues to vary considerably between counties and regions. It is a well known fact that there is an increase of late in the number of persons infected with human immunodeficiency virus (HIV). The situation warrants immediate need for quick diagnosis, monitoring and antiretroviral therapy. HIV a retrovirus, mainly targets the CD4 T lymphocytes. These cells are most widely available white blood cells of human immune system. HIV infects the other cells as well. But it causes great damage and reduction to the in CD4 T cells and there by weaken resistance of the immune system. To comprehend HIV dynamics, its progression, anti-retroviral prophylaxis and so on a number of mathematical models have been put forward. Since the day the virus was discovered, HIV has been spreading in different directions. To put more precisely, our perception of the reason and the place where HIV spreads has been shifting in the course of years. In the beginning more number of men were infected with HIV compared to women along with the youth and poor who are the worst affected group. The present paper attempts to develop a stochastic model to obtain the expected time to reach the threshold level in the context of HIV/AIDS. erlane distribution Esary *et al.,* provides more details regarding the present study in the area. One can refer to willcox, R.R (1976) and Palanivel *et al* 2010 for obtaining details on expected time. The data for the present study from TRICH region and fitted.

Assumption of the Model

- An uninfected partner has sexual contacts with an infected person,
- unsterile needles for drug abuse
- Transfusion of infected blood products.

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- On every occasion of the above three behaviors there is a random amount of transmission of HIV, which together contributes to the antigenic diversity.
- The damages due to the events namely sexual contacts, sharing of needles and blood products are statistically independent
- If the cumulative damage due to successive events crosse0s the antigenic diversity threshold level the seroconversion takes place. The inter-arrival times between contacts, sharing needles and blood products are statistically independent.

Model description

The Cumulative density function (CDF) of the Distribution function Exponential with parameter θ,

$$F(x;\lambda) = 1 - e^{-\lambda x} \qquad x \geq 0 \qquad (1)$$

The Cumulative density function (CDF) of the Distribution function Erlang Distribution with parameter θ,

$$F(x;k,\lambda) = 1 - \sum_{n=0}^{k-1} \frac{1}{n!} e^{-\lambda x} (\lambda x)^n \qquad (2)$$

The continous random variable denotes the threshold level. the survivor function i.e $P(T > t)$. Is to be found from equation (1) & (2)

$$P(T > t) = \sum_{k=0}^{\infty} V_k(t)\, P\left(\sum_{i=1}^{k_i} X_i < max\, Y_1, Y_2, Y_3 \right) \qquad (3)$$

To find expected time of the threshold we D.r.to S=0 in equation in equation (3). Let the random variable U denoting inter arrival time which follows exponential with parameter c. Now $f^*(s) = \left(\frac{c}{c+s}\right)$, substituting in the above equation (4).

Table 1. Expected Time

Age	Time interval of CD4 count C	μ Platelet count	λ_1 Activated Partial Thromboplastin Time	λ_2 Prothrombine Tim	λ_3 Viral RNA
34	405	230	22.6	16.1	1360
27	706	210	25.6	18	1556
30	516	260	58.2	22.3	1650
45	945	246	70.6	27.6	1959
28	146	205	20.6	21.3	612
42	590	340	59.7	29.4	1552
33	242	225	27.1	14.6	812
30	415	175	19.5	13.9	1293
28	253	190	31.8	11.4	673
47	346	148	28.4	12.4	994
32	526	250	85.4	15.8	1267
44	80	110	22.7	26.4	268
38	256	240	22.6	14.5	689
55	430	210	17.3	16	1750
39	530	179	26.8	19.6	1681
52	600	416	120.4	26.9	1908
29	297	199	30.4	18.3	853
33	458	160	27.3	15.4	1548
38	269	176	19.9	11.8	759
46	556	256	46.8	16.3	1761
47	526	350	60.9	22.4	1689
52	340	195	35	11.5	879
35	310	169	42.6	14.6	794
34	405	210	43.6	15.9	1268
46	425	280	34.2	11.7	1164

$$l^*(s) = 1 - \left\{ \frac{(1-g^*(\lambda_1))f^*(s)}{(1-g^*(\lambda_1)f^*(s))} + \frac{(1-g^*(\lambda_2))f^*(s)}{(1-g^*(\lambda_2)f^*(s))} + \frac{(1-g^*(\lambda_3))f^*(s)}{(1-g^*(\lambda_3)f^*(s))} - \frac{(1-g^*(\lambda_1+\lambda_2))f^*(s)}{(1-g^*(\lambda_1+\lambda_2)f^*(s))} - \frac{(1-g^*(\lambda_2+\lambda_3))f^*(s)}{(1-g^*(\lambda_2+\lambda_3)f^*(s))} - \frac{(1-g^*(\lambda_3+\lambda_1))f^*(s)}{(1-g^*(\lambda_3+\lambda_1)f^*(s))} + \frac{(1-g^*(\lambda_1+\lambda_2+\lambda_3))f^*(s)}{(1-g^*(\lambda_1+\lambda_2+\lambda_3)f^*(s))} - \left[\frac{(1-g^*(\lambda_3))f^*(s)}{(1-g^*(\lambda_3)f^*(s))} + \frac{(1-g^*(\lambda_2-\lambda_3))f^*(s)}{(1-g^*(\lambda_2-\lambda_3)f^*(s))} + \frac{(1-g^*(\lambda_1-\lambda_3))f^*(s)}{(1-g^*(\lambda_1-\lambda_1)f^*(s))} - \frac{(1-g^*(\lambda_1+\lambda_2+\lambda_3))f^*(s)}{(1-g^*(\lambda_1+\lambda_2+\lambda_3)f^*(s))} \right] \lambda_3 \right\} \quad (4)$$

The inter arrival time which follows exponential distribution is subsisted in Laplace transform of equation. We finally obtain the expected time in the equation (5).

$$E(T) = \frac{1}{c}\left(\frac{\mu+\lambda_1}{\lambda_1} + \frac{\mu+\lambda_2}{\lambda_2} + \frac{\mu+\lambda_3}{\lambda_3} - \frac{\mu+\lambda_1+\lambda_2}{\lambda_1+\lambda_2} - \frac{\mu+\lambda_2+\lambda_3}{\lambda_2+\lambda_3} - \frac{\mu+\lambda_1+\lambda_3}{\lambda_1+\lambda_3} + \frac{\mu+\lambda_1+\lambda_2+\lambda_3}{\lambda_1+\lambda_2+\lambda_3} - \left[\frac{\mu-\lambda_3}{\lambda_3} + \frac{\mu+\lambda_2-\lambda_3}{\lambda_2-\lambda_3} + \frac{\mu+\lambda_1-\lambda_3}{\lambda_1-\lambda_3} - \frac{\mu+\lambda_1+\lambda_2-\lambda_3}{\lambda_1+\lambda_2-\lambda_3} \right] \lambda_3 \right) \quad (5)$$

Where

C = Time interval of CD4 count, μ = Platelet count
λ_1 = Activated Partial Thromboplastin Time λ_2 = Prothrombine Tim
λ_3 = Viral RNA

Data observed of the infected person

RESULTS AND DISCUSSION

Out of the 25 HIV postive patients table given above for observation there were 14 males and 11 females in the age group 26 to 60 . It is observed on the basis of studying the CD4 count of the three variables viz. Platelet count, pothrombin, time and activated partial thromboplastin time and viral RNA that the time to reach threshold is very near once the CD4 count starts decreasing.

It is noticed that once the CD4 count decreases the other cells count also simultaneously decreases. This can be explained by the fact that as the HIV infection progressed, characterized by low CD4 count cells, the infected person with HIV crosses the threshold level more quickly. The model clearly shows that once the person is infected the breakdown of the immune system too starts. Proper medical advice and regular treatment alone can help in extending the span of the infected person.

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