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A stochastic model for seroconversion time using exponential distribution

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Abstract
The impact of the immune system's cumulative damage as a result of HIV infection is explored. This paper concentrates on the study of shock models and the cumulative damage process. The term "random antigenic diversity threshold" refers to the antigenic diversity threshold that causes seroconversion. Every interaction creates and adds to the antigenic variety, which when it reaches a certain threshold level causes seroconversion in the individual. The exponential distribution is used as the threshold in the statistical analysis of the time to seroconversion for HIV-infected individuals.

Keywords: Antigenic diversity, cumulative damage process, infectivity, seroconversion, human immuno deficiency virus, threshold

1. Introduction
The entire world witnessed a pandemic situation with the advent of the terrible and disastrous disease called Acquired Immune Deficiency Syndrome (AIDS) caused by the Human Immunodeficiency Virus (HIV). HIV is a retrovirus, which is RNA-biased and has no DNA. Antigenic diversity is an important determinant of the outcome of HIV infection. Successive invasion through various modes of HIV transmission may contribute to increased HIV antigenic diversity. The idea of the immune system's antigenic variety threshold has been examined by Nowak and May (1991) [3] and Stilianakis *et al* (1994) [5]. If the overall antigenic diversity produced by HIV exceeds the antigenic diversity threshold, the immune system is unable to defend itself against HIV, which results in immune system collapse and seroconversion occurs rapidly.
The probability of transmission through contact is called infectivity. Shiboski and Jewell (1992) [4] obtained the prevalence function expression using available data from partner studies. In the present study, it is assumed that an HIV-uninfected person is infected by an infected person through sexual contact.
Every encounter results in the transmission of a small number of HIV particles, which in turn add to the antigenic variety throughout the replication process, which is the regenerative process. The seroconversion occurs when and when the total antigenic diversity reaches a certain level due to the decreasing T_4 Cells. The principles of the cumulative damage process and the shock model served as the foundation for the development of the current model. In Esary *et al* (1973) [2], the same was covered in detail. The intercontact times between contacts are considered to be Poisson random variables for the sake of this study. A Generalized Poisson distribution and the uses for it that Anil (2001) [1] mentioned are employed in the creation of the stochastic model. At this point, we assume the following.
We view sexual contact as the only source of HIV transmission and assume that a random amount of HIV is transmitted when an uninfected person has sexual contact with an HIV-infected partner. Thus, the individual in this case is subjected to a process of damage acting on the immune system, and the damage is assumed to be nonlinear and cumulative. The transmission of HIV results in harm to persons at each point of contact, and the intervals between encounters are taken to be Poisson random variables. If the total amount of damage surpasses a predetermined limit, which is also subject to random variables. The seroconversion takes place, and the individual is identified as seropositive.

We also assume that the process that creates contacts, the order of damages, and the threshold are independent of one another.

We use the symbol Xi to indicate the rise in antigenic diversity brought on by HIV transmission during the ith interaction. Assumed to be continuous random variables are X1, X2,... Let's assume that the antigenic diversity threshold's random variable, Y, has an exponential distribution with parameter. Let G(.) stand for the Xi distribution function and g(.) for the associated p.d.f. The distribution function of the random variable indicating the intervals between subsequent encounters is denoted by the letter F(.). Let gk(.) be the random variable's p.d.f $\sum_{i=1}^{k} X_i$. To denote the Laplace transform of g(x), we will use g*(s). Assume that T represents the period until seroconversion and is a continuous random variable.

2. Results

S(t) = P(T>t)

= Probability that the seroconversion does not take before t

= $\sum_{k=1}^{\infty} P\{$ no seroconversion before t / exactly k contacts in (0,t]$\}$

*P{ exactly k contacts in (0,t] }

$$= \sum_{k=1}^{\infty} U_k(t)\, P\left\{ \sum_{k=1}^{\infty} Xi < Y \right\}$$

If we assume that the inter–arrival times between contacts follow an exponential distribution.

$$P(X_1+X_2+\ldots.+X_k < Y) = \int_0^{\infty} g_k(x)\, e^{-\theta x} dx$$

$$= g^*_k(\theta)$$

$$= [g^*(\theta)]^k$$

Then

$$S(t) = \sum_{k=0}^{\infty} \frac{e^{-at}(at)^k}{k!} [g^*(\theta)]^k$$

$$= e^{-at} \sum_{k=0}^{\infty} \frac{(at)^k [g*(\theta)]^k}{k!}$$

$$= e^{-at}\left[1 + \frac{atg^*(\theta)}{1!} + \frac{[atg^*(\theta)]^2}{2!} + \ldots.\right]$$

$$= e^{-at} e^{at\, g^*(\theta)}$$

$$S(t) = e^{at[\, g^*(\theta) - 1]}$$

L(T) = 1 – S(T)

$$= 1 - e^{at[\, g^*(\theta) - 1]}$$

$$= 1 - e^{at(\frac{\mu}{\mu+\theta} - 1)}$$

Let g(.) follows an exponential distribution with parameter μ

$$g^*(\theta) = \frac{\mu}{\mu+\theta}$$

$$L(T) = 1 - e^{at(\frac{\theta}{\mu+\theta})}$$

$$\psi(t) = \frac{d}{dt}[L(T)]$$

$$= \frac{d}{dt}\left[1 - e^{at\left(\frac{\theta}{\mu+\theta}\right)}\right]$$

$$\psi(t) = \frac{a\theta}{\mu+\theta}\, e^{-at\left(\frac{\theta}{\mu+\theta}\right)t}$$

The expected time to seroconversion is given by

$$E(T) = \int_0^{\infty} t\psi(t) \qquad (1)$$

$$= \int_0^{\infty} t\left[\frac{a\theta}{\mu+\theta} e^{-\left(\frac{a\theta}{\mu+\theta}\right)t}\right] dt$$

$$= \left(\frac{a\theta}{\mu+\theta}\right) \int_0^t td\left[\frac{e^{-\left(\frac{a\theta}{\mu+\theta}\right)}}{-\left(\frac{a\theta}{\mu+\theta}\right)}\right] \qquad (2)$$

Now $\int_0^{\infty} td\left[\frac{e^{-\left(\frac{a\theta}{\mu+\theta}\right)t}}{-\left(\frac{a\theta}{\mu+\theta}\right)}\right]$

$$= t\left[\frac{e^{-\left(\frac{a\theta}{\mu+\theta}\right)}}{-\left(\frac{a\theta}{\mu+\theta}\right)}\right]_0^{\infty} - \int_0^{\infty} \frac{e^{-\left(\frac{a\theta}{\mu+\theta}\right)t}}{-\left(\frac{a\theta}{\mu+\theta}\right)} t\, dt$$

$$= \frac{\mu+\theta}{a\theta} \int_0^{\infty} e^{-\left(\frac{a\theta}{\mu+\theta}\right)t} dt$$

$$= \frac{\mu+\theta}{a\theta}\left[\frac{e^{-\left(\frac{a\theta}{\mu+\theta}\right)t}}{-\left(\frac{a\theta}{\mu+\theta}\right)}\right]_0^\infty$$

$$= \frac{(\mu+\theta)^2}{(a\theta)^2} \qquad (3)$$

(On Simplification)
Substitute (3) in (2), we get

$$E(T) = \left(\frac{a\theta}{\mu+\theta}\right)\frac{(\mu+\theta)^2}{(a\theta)^2} = \frac{\mu+\theta}{a\theta}$$

$$E(T^2) = \int_0^\infty t^2\psi(t)dt$$

$$= \int_0^\infty t^2\left[\frac{a\theta}{\mu+\theta}e^{-\left(\frac{a\theta}{\mu+\theta}\right)t}\right]dt$$

$$= \left(\frac{a\theta}{\mu+\theta}\right)\int_0^\infty t^2 e^{-\left(\frac{a\theta}{\mu+\theta}\right)t}dt$$

Now $\int_0^\infty t^2 e^{-\left(\frac{a\theta}{\mu+\theta}\right)t}dt$

$$= \int_0^\infty t^2 d\left[\frac{e^{-\left(\frac{a\theta}{\mu+\theta}\right)t}}{\left(\frac{-a\theta}{\mu+\theta}\right)}\right]$$

$$= \frac{2(\mu+\theta)^3}{(a\theta)^3} \text{ [on Simplification]}$$

$$\therefore E(T^2) = \left(\frac{a\theta}{\mu+\theta}\right)2\left(\frac{(\mu+\theta)^3}{(a\theta)^3}\right)$$

$$= \frac{2(\mu+\theta)^2}{(a\theta)^2}$$

$$\therefore V(T) = E(T^2) - E(T)^2$$

$$= \frac{2(\mu+\theta)^2}{(a\theta)^2} - \left(\frac{\mu+\theta}{a\theta}\right)^2$$

$$= \frac{(\mu+\theta)^2}{a^2\theta^2}$$

3. Numerical Illustrations

Table 1: Shows the values of statistical measures of seroconversion time

	$\theta = 0.2, \mu = 0.5$	
a	**Mean**	**Variance**
1	0.0600	36.0000
2	0.0300	9.0000
3	0.0200	4.0000
4	0.0150	2.2500
5	0.0120	1.4400
6	0.0100	1.0000
7	0.0086	0.7347
8	0.0075	0.5625
9	0.0067	0.4444
10	0.0060	0.3600

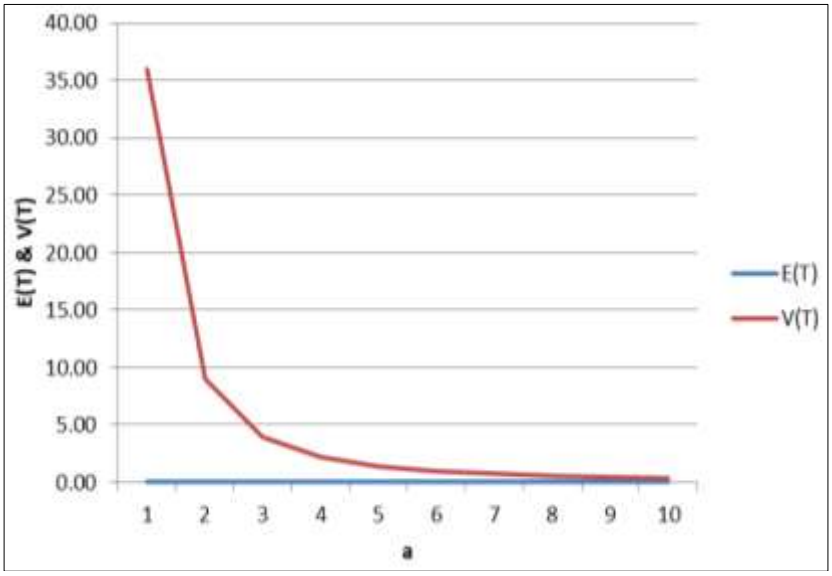

Fig 1: Shows the values of statistical measures of seroconversion time

Table 2: Contribution to the antigenic diversity threshold in which increases then both E(T) and V(T) are increases

	$a = 3, \theta = 0.1$	
μ	**Mean**	**Variance**
0.5	1.3333	4.0000
1.0	2.1667	13.4444
1.5	3.0000	28.4444
2.0	3.8333	49.0000
2.5	4.6667	75.1111
3.0	5.5000	106.7778
3.5	6.3333	144.0000
4.0	7.1667	186.7778
4.5	8.0000	235.1111
5	8.8333	289.0000

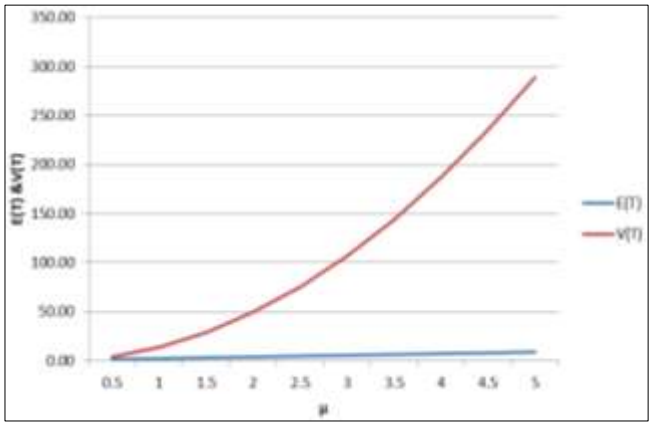

Fig 2: Contribution to the antigenic diversity threshold in which increases then both E(T) and V(T) are increases

Table 3: The value of θ is the parameter of exponential distribution of the threshold increases E(T) and V(T) are decreases

	$a = 2, \mu = 1.5$	
θ	**Mean**	**Variance**
0.1	8.0000	64.0000
0.2	4.2500	18.0625
0.3	3.0000	9.0000
0.4	2.3750	5.6406
0.5	2.0000	4.0000
0.6	1.7500	3.0625
0.7	1.5714	2.4694
0.8	1.4375	2.0664
0.9	1.3333	1.7778
1	1.2500	1.5625

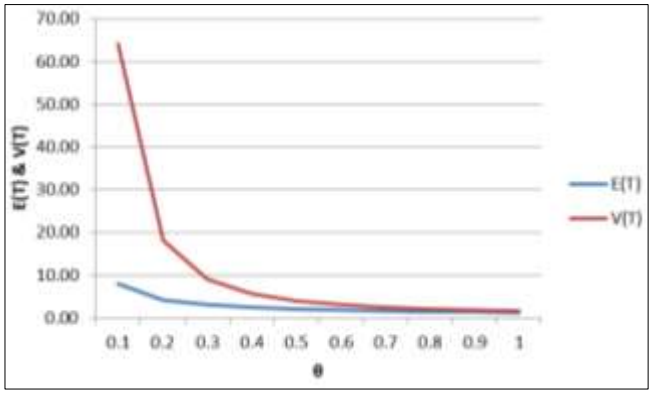

Fig 3: The value of θ is the parameter of exponential distribution of the threshold increases E(T) and V(T) are decreases

4. Conclusion

- In table (1), shows the values of statistical measures of seroconversion time corresponding to the variation in 'a' the parameter of the distribution of inter-arrival time when θ and μ are kept fixed. As 'a' increases, the value of $\frac{1}{a}$ decreases which means the inter-arrival time between contacts becomes smaller and so there is a corresponding decrease in E(T) and V(T).
- It is observed from the contribution to the antigenic diversity threshold which increases then both E(T) and V(T) increases as indicated in the Table (2) and Fig.(2)
- From Table (3), as the value of θ is the parameter of exponential distribution of the threshold increases E(T) and V(T) decreases as indicated in Fig.(3)

5. References

1. Anil V. A Generalized Poisson distribution and its applications. Journal of the Kerala Statistical Association. 2001;12:11-22.
2. Esary JD, Marshall AW, Proschan F. Shock Model and Wear Processes. The Annals of Probability. 1973;1(4):627-649.
3. Nowak MA, May RM. Mathematical Biology of HIV Infection: Antigenic variation and Diversity Threshold. Mathematical Biosciences. 1991;106(1):1-21.
4. Shiboski S. Statistical analysis of HIV Infectivity based on the partner studies Biometrics. 1992;46:1133-1150.
5. Stilianakis N, Schenzle D, Dietz K. On the antigenic diversity threshold model for AIDS. Mathematical Biosciences. 1994;121(2):235-247.