Global Journal of Mathematical Sciences: Theory and Practical.
ISSN 0974-3200 Volume 4, Number 1 (2012), pp. 43-48

http://www.irphouse.com

Estimation of the Generalized Logistic Distribution based on the Expected Time in Shock Model

Subramanian C., Rajivgandhi R.* and Vinoth R.

Department of Statistics, Annamalai University,
Annamalai Nagar-608 002, Tamil Nadu, India
**Corresponding Author E-mail: statrajiv@gmail.com*

Abstract

A stochastic model based on the shock model approach for the expected time to seroconversion of the immune system is presented in this paper. The time to cross the threshold of the infected person is a vital event in seroconversion. Tools were derived from the firmly established theory of epidemic modeling, although some adjustments became necessary, because of specific characteristics of HIV infection. From simulations with the stochastic model expressed for threshold of HIV is shown. However, most of the behavior in this stochastic model for the expected time strongly depends on initial conditions.

Keywords: Expected Time, Inter arrival Time, Seroconversion, Threshold.

Introduction

Every day, over 6,800 persons become infected with HIV and over 5,700 persons die from AIDS, mostly because of inadequate access to HIV prevention and treatment services (JUNA, 2007). Infection with human immunodeficiency virus frequently causes seroconversion illness characterized by fever, rash and lymphadenopathy, usually lasting less than 2 weeks although durations of up to 10 weeks have been reported Schaker et al. (1996).

Mathematical model is obtained for the expected time of breakdown point to reach the seroconversion threshold level. In the context of HIV/AIDS, the assumptions that the times between decision period are independent and identically distributed (i.i.d) random variable. One can see for more detail about the expected time to cross the threshold level of seroconversion period in Esary et al. (1973), Sathiyamoorthi (1980), Rajivgandhi et al. (2010), Pandiyan et al., (2010), Subramanian and Rajivgandhi (2011).

Assumptions

These assumptions are somewhat artificial, but are made because of the lack of detailed real-world information on one hand and in order to illustrate the proceedings on the other hand.

- Sexual contacts are the only source of HIV infection.
- The antigenic diversity threshold of any individual is a random variable.
- If the total damage crosses a threshold level Y which itself is a random variable, the seroconversion occurs and a person is recognized as an infected.
- The inter-arrival times between successive contacts, the sequence of damage and the threshold are mutually independent.

Notations

X_i : a continuous random variable denoting the amount of contribution to the threshold due to the HIV transmitted in the i^{th} contact, in other words the damage caused to the immune system in the i^{th} contact, with p.d.f g (.) and c.d.f G (.).

Y : a continuous random variable denoting the threshold which follows Generalized logistic distribution.

U_i : a random variable denoting the inter-arrival times between contact with c.d.f. $F_i(.)$, $i = 1,2,3 \ldots k$.

$g(.)$: The probability density functions of X_i

$g^*(.)$: Laplace transform of g (.)

$g_k(.)$: The k- fold convolution of g (.) i.e., p.d.f. of $\sum_{j=1}^{k} X_i$

$f(.)$: p.d.f. of random variable denoting between successive contact with the corresponding c.d.f. F (.)

$F_k(.)$: k-fold convolution of F (.)

$V_k(t)$: Probability of exactly k successive contact.

$S(.)$: Survival function, i.e., $P[T > t]$

$L(t)$: 1 - S (t)

Result

A generalized logistic distribution is proposed, based on the fact that the difference of two independent Gumbel-distributed random variables has the standard logistic distribution. The shape parameters have been specifically designed to modify the behavior of the curve in the extreme-probability regions where problems of lack of fit may occur, while allowing for asymmetric treatment of the two tails, Stukel (1988). In this paper we made an attempt when the shape parameter $\alpha = 1$

Let Y be the random variable which has the cdf defined as

$$F(x, \alpha, \lambda) = \left(1 + e^{-\lambda x}\right)^{-\alpha}, -\infty < x < \infty$$

and has the probability density function (p.d.f)

$$f(x, \alpha, \lambda) = \alpha\lambda\left(1 + e^{-\lambda x}\right)^{-\alpha-1} e^{-\lambda x}, -\infty < x < \infty$$

The corresponding survival function is $\bar{H}(x) = 1 - F(x)$

$$= \frac{e^{-\lambda x}}{1 + e^{-\lambda x}} \tag{1}$$

One is interested in an item for which there is a significant individual variation in ability to withstand shocks. There may be no practical way to inspect an individual item to determine its threshold y. In this case, the threshold must be a random variable. The shock survival probability are given by

$$P(X_i < Y) = \int_0 g_k(x)\, \bar{H}(x) dx$$

$$= \left\{ g^* \left[\frac{\lambda}{1+\lambda} \right] \right\}^k \; by\; convolation \tag{2}$$

Therefore $S(t) = P[T > t]$is the survival function which gives the probability that the cumulative antigenic diversity will fail only after time t.

$$= \sum_{k=0} P \; \{\text{there are exactly k contacts in } (0, t]$$

$$* \; P \; (\text{the total cumulative antigenic diversity } (0, t]\}$$

It may happen that successive shocks become increasingly effective in causing damage, even though they are independent. This means that $V_k(t)$, the distribution function of the k^{th} damage is decreasing in k = 1,2, ...for each t. A renewal process is a counting process such that the time until the first event occurs has some distribution F, the time between the first and second event has, independently of the time of the first event, the same distribution F, and so on. When an event occurs, we say that a renewal has taken place. It is also known from renewal process that

$P(\text{exactly k policy decesions in } (0, t]) = F_k(t) - F_{K+1}(t)$ with $F_0(t) = 1$

$$P(T > t) = \sum_{k=0} V_k(t)\, P(X_i < Y)$$

Data that measure "the length of time" until the occurrence of an event are called lifetimes, failure times or survival data. $L(T) = 1 - S(t)$

Taking Laplace transform of $L(T)$, we get

$$= 1 - \left\{ \sum_{k=0} F_k(t) - F_{k+1}(t) \left(g^* \left\{ \frac{\lambda}{1+\lambda} \right\} \right)^k \right\}$$

$$= 1 - 1$$

$$+ \left[1 - g^* \left(\frac{\lambda}{1+\lambda} \right) \right] \sum_{k=1} F_k(t) \left(g^* \left\{ \frac{\lambda}{1+\lambda} \right\} \right)^k \tag{3}$$

Laplace transform $l^*(s)$ is given as

$$l^*(s) = \frac{\left[1 - g^*\left(\frac{\lambda}{1+\lambda}\right)\right] f^*(s)}{\left[1 - g^*\left(\frac{\lambda}{1+\lambda}\right) f^*(s)\right]} \tag{4}$$

$$E(T) = -\frac{d}{ds} l^*(s) \; given \; s = 0$$

$$E(T^2) = \frac{d^2}{ds^2} l^*(s) \; given \; s = 0$$

From which $V(T)$ can be obtained.

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) we get,

$$l^*(s) = \frac{c\left[1 - g^*\left(\frac{\lambda}{1+\lambda}\right)\right]}{\left[c + s - g^*\left(\frac{\lambda}{1+\lambda}\right) c\right]}$$

$$E(T) = \frac{1}{c\left[1 - g^*\left(\frac{\lambda}{1+\lambda}\right)\right]} \quad on \; simplification \tag{5}$$

$$E(T^2) = \frac{2}{c^2\left[1 - g^*\left(\frac{\lambda}{1+\lambda}\right)\right]^2}$$

$$V(T) = E(T^2) - [E(T)]^2$$

$$= \frac{2}{c^2\left[1 - g^*\left(\frac{\lambda}{1+\lambda}\right)\right]^2} - \left[\frac{1}{c\left[1 - g^*\left(\frac{\lambda}{1+\lambda}\right)\right]}\right]^2 \quad on \; simplification \tag{6}$$

The inter-arrival time of the threshold follows exponential distribution. The Laplace transformation of the exponential is given by $\left[\mu/\mu + \lambda\right]$.

$$g^*(.) \sim exp(\mu), g^*(\mu) \sim exp\left(\frac{\mu}{\mu + \lambda}\right)$$

$$E(T) = \frac{2\mu + \lambda}{c[\mu + \lambda]} \quad on \; simplification \tag{7}$$

$$V(T) = \left[\frac{(2\mu + \lambda)^2}{c^2(\mu + \lambda)^2}\right] \quad on \; simplification \tag{8}$$

Numerical Illustration

Simulation models are particularly useful in studying in small damaged organism where random fluctuations are likely to be more serious. The theory developed was tested using stimulated data in MathCAD software. To illustrate the method described in this paper, we give some limited simulation results in the figures given.

Conclusion

When μ is kept fixed the inter-arrival time $'c'$ which follows exponential distribution, is an increasing case by the process of renewal theory. Therefore, the value of the expected time $E(T)$ to cross the threshold of seroconversion is found to be decreasing, in all the cases of the parameter value $\mu = 0.5,1,1.5,2$. When the value of the parameter μ increases, the expected time is found increasing, this is observed in Figure 1. The same case is found in Variance V (T) which is observed in Figure 3.

When λ is kept fixed and the inter-arrival time $'c'$ increases, the value of the expected time E (T) to cross the threshold of seroconversion is found to be decreasing, in all the cases of the parameter value $\lambda = 0.5, 1,1.5, 2$. When the value of the parameter λ increases, the expected time is found decreasing, this is indicated in Figure 2. The same case is observed in the threshold of seroconversion of Variance V (T) which is observed in Figure 4.

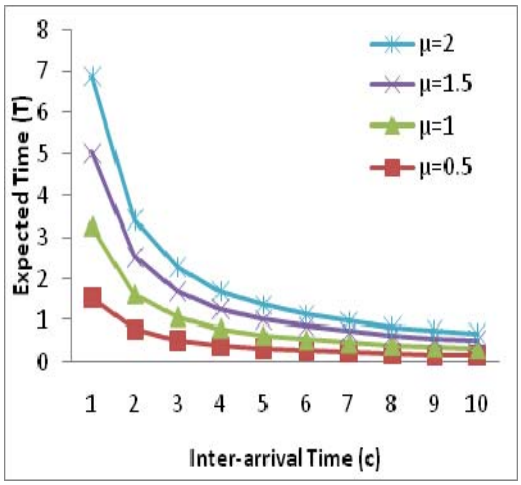

Figure 1

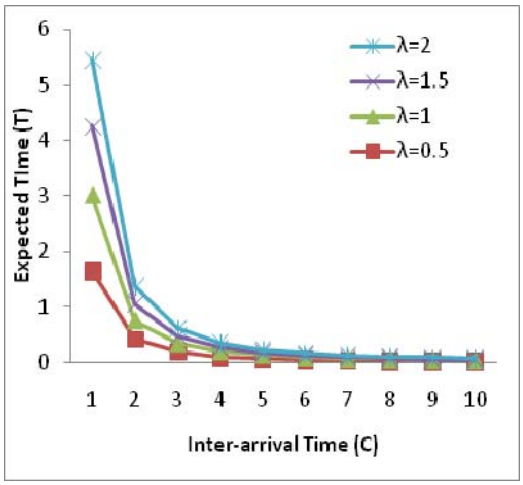

Figure 2

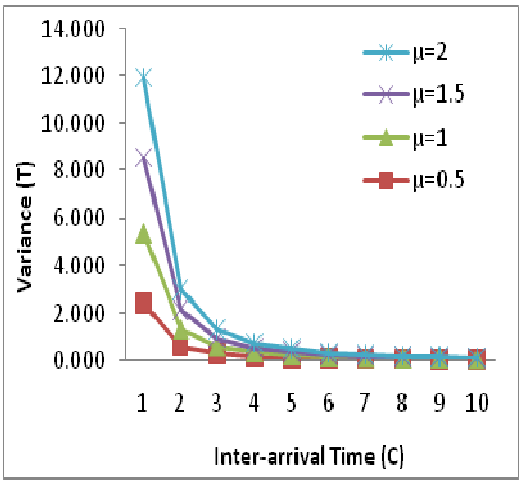

Figure 3

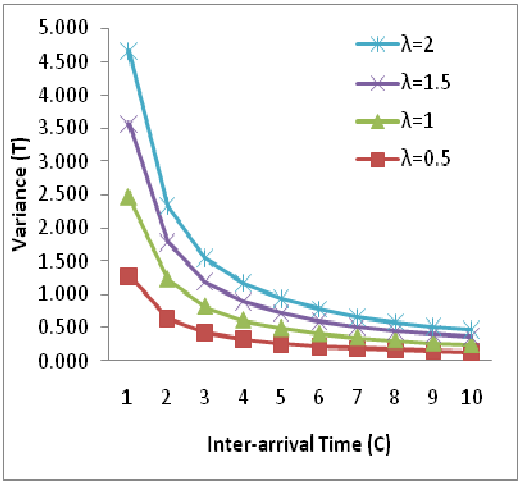

Figure 4

Reference

[1] Esary, J.D., A.W. Marshall and F. Proschan. 1973. Shock models and wear processes. Ann. Probability, 1(4), 627-649.

[2] Joint United Nations Programme on HIV/AIDS 2007. *2007 AIDS epidemic update*.

[3] Pandiyan, P., R. Agasthiya, R.M. Palanivel, K. Kannadasan and R. Vinoth 2010, Expected Time to Attain the Threshold Level Using Multisource of HIV Transmission – Shock Model Approach, Journal of Pharm Tech Research.

[4] Rajivgandhi, R, Ganesan, A, Vinoth, R and K. Kannadasan. 2010. Left and Right Censoring for Expected Time to Seroconversion – A Shock Model Approach. Journal of Recent Research in Science and Technology, 2(3), 80-85.

[5] Sathiyamoorthi R. 1980. Cumulative Damage model with Correlated Inter arrival Time of Shocks. IEEE Transactions on Reliability, R-29, No.3.

[6] Schaker, T, A.C. Collier, J. Hughes, T. Shea, L. Corey, 1996. Clinical and epidemiologic features of primary HIV infection, Ann. Intern. Med. 125, 257–264.

[7] Stukel, T.A., 1988. Generalized Logistic Models. Journal of the American Statistical Association, Vol. 83, No. 402, 426-431.

[8] Subramanian, C and R. Rajivgandhi, 2011. Extremely Prolonged HIV Seroconversion to Estimate the Expected Time through Generalized Rayleigh Distribution. Asian Journal of Science and Technology, 1(4), 041-043.