SURVIVAL OF DISEASE HIV THROUGH STATISTICAL MODEL USING SOURCE OF DISTRIBUTION

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Abstract

Public health issues are very important in our society, particularly the AIDS virus (HIV) infected with HIV. If leave HIV had become be leading cause of deaths because of increased life anticipation. Derived statistical tools from theoretical modelling of solid epidemiological although some adjustments were made because of the unique nature of HIV infection. In this paper shock model to assess the threshold level is been derived by three parameter ExponentiatedWeibull distribution. Information collected in secondary data fitted for this model will be used to support the development of the model.

INTRODUCTION

A mathematical model based on the basic transmission of HIV may help doctors and community. Such modeling continues to be important to monitor how the changes in various parameters and assumptions affect the course of the epidemic. Therefore, the development of such mathematical models, we can do some extent expected to spread in the population difference and evaluate the effectiveness of the potential difference to bring the epidemic under control and makes 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. Threshold beyond which the human immune system cannot be wise and be expressed as the sum of two random variables. One can see more details on Esary et al, (1973) and Pandiyan et al. (2014) mentioned about time, is expected to cross the threshold of the seroconversion period. In this chapter and the random pattern is said to be considering the fact that a person is exposed to two different modes of transmission of HIV and the time expected. seroconversion are derived.

ASSUMPTIONS OF THE MODEL

- sexual contact is the only source of people infected with HIV.
- The second criterion of any person, is a random variable.
- If the total damage across the threshold Y, which itself is a random variable. seroconversion Happened and who is recognized as being infected.
- Interarrival time between the successive contacts are at random variable which are identically.

MODEL DESCRIPTION

The Cumulative density function (CDF) of the three parameter ExponentiatedWeibull distribution

$$F(x,\theta) = \left[1 - e^{-\left(\frac{x}{\lambda}\right)^{k}}\right]^{\alpha} \; ; \qquad x > 0$$

The corresponding survival function isis given in equation (1), on simplification

$$\bar{H}(x) = e^{-\left(\frac{x}{\lambda_1}\right)^{\beta_1}} + e^{-\left(\frac{x}{\lambda_2}\right)^{k_2}} - e^{-\left(\frac{x}{\lambda_1}\right)^{\beta_1}} e^{-\left(\frac{x}{\lambda_2}\right)^{\beta_2}} \qquad \ldots (1)$$

The shock survival probability is given by

$$P(X_i < Y) = \int_0^\infty g^*(x)\, \bar{H}(x)\, dx$$

Now the threshold Y is such that it has two contacts namely $Y_1$and Y_2. Transfer of Immune system from Y_1 to Y_2 is also possible. We have the threshold level of seroconversion is given by $Y = max(Y_1, Y_2)$.

$$P[max(Y_1, Y_2)] = P[(Y_1 < y) \cap (Y_2 < y)] = P[Y_1 < y]P[Y_2 < y]$$

Now that, Y_1 and Y_2 follow three parameter ExponentiatedWeibull distribution with parameter λ, β and α . The continous random variable denotes the threshold level. the survivor function i.e$P(T > t)$.

$$P(T > t) = \sum_{k=0}^{\infty} V_k(t)\, P\left(\sum_{i=1}^{k_i} X_i < max\, Y_1, Y_2\right) (2)$$

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).

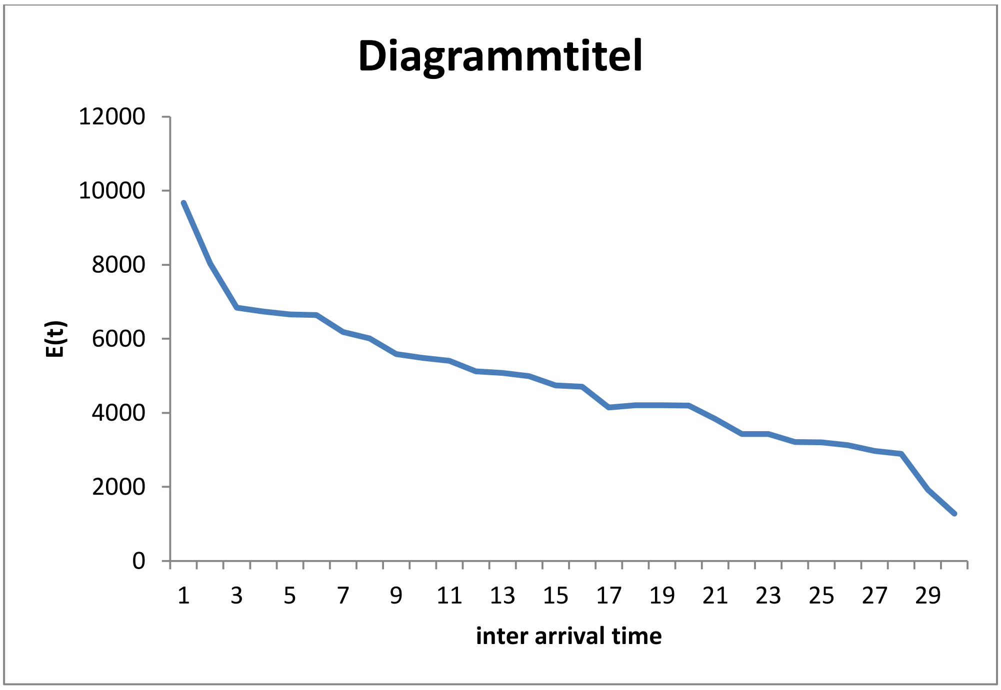
$$l^*(s) = \frac{\left[1 - g^*\left(\frac{1}{\lambda_1}\right)^{\beta_1}\right] f^*(s)}{\left[1 - g^*\left(\frac{1}{\lambda_1}\right)^{\beta_1} f^*(s)\right]} + \frac{\left[1 - g^*\left(\frac{1}{\lambda_2}\right)^{\beta_2}\right] f^*(s)}{\left[1 - g^*\left(\frac{1}{\lambda_2}\right)^{\beta_2} f^*(s)\right]} - \frac{\left[1 - g^*\left(\left(\frac{1}{\lambda_1}\right)^{\beta_1} + \left(\frac{1}{\lambda_2}\right)^{\beta_2}\right)\right] f^*(s)}{\left[1 - g^*\left(\left(\frac{1}{\lambda_1}\right)^{\beta_1} + \left(\frac{1}{\lambda_2}\right)^{\beta_2}\right) f^*(s)\right]} \quad \ldots (3)$$

The inter arrival time which follows exponential distribution is subsisted in Laplace transform of equation. we finally obtain the expected time in the equation(4).

$$E(T) = \frac{{\lambda_1}^{\beta_1}\mu_1 + 1}{c} + \frac{{\lambda_2}^{\beta_2}\mu_2 + 1}{c} - \frac{\left[\mu_1{\lambda_1}^{\beta_1}\mu_2{\lambda_2}^{\beta_2} + \mu_1{\lambda_1}^{\beta_1} + \mu_2{\lambda_2}^{\beta_2} + 1\right]}{c\left[\mu_1{\lambda_1}^{\beta_1} + 1 - \mu_1{\lambda_1}^{\beta_1} - \mu_1\mu_2{\lambda_2}^{\beta_2}{\lambda_1}^{\beta_1}\right]} \ldots (4)$$

Where

C = Time interval of CD4 count, μ_1= Platelet count
μ_2= Activated Partial Thromboplastin Time λ_1= Prothrombine Tim
λ_2= Viral RNA , β_1= CD8 count β_2=protein 24



CONCLUSION

When the CD4 count was resolved by keeping all other parameters platelet count, pothrombin, time and enable time partial thromboplastin time and RNA viruses the inter arrival which follows an exponential distribution with parameter increases. Therefore, the value of the time expected to cross the threshold of seroconversion decreases.If the parameters of the threshold distribution threshold CD4 cell count, RNA, Total leucocytes, Platelet count, CD8 counts, and protein 24 are kept fixed and if the parameter of the inter-arrival time of successive contact increases the Expected time decrease.

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