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VARIATION OF CONTINUOUS PROBABILITY DISTRIBUTION PARAMETERS WITH LARGE MATRIX OF HIV CD4 COUNT DATA

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ABSTRACT: Over the past era of HIV, statisticians, researchers and policy makers have put a great amount of efforts in developing and comparing suitable probability models for the analysis of large matrix of HIV CD4 count data and other markers of HIV progression. These models must be general enough to allow for different pattern of changes in the immunological, clinical and virological markers data. As per the literature, some probabilistic models have been developed with lower precision and lesser accuracy [5-6]. In this paper we fitted different probability distribution models and are to find out the parameter variations with respect to CD4 count of PLHIV at the time of inception of HAART.

Key words: HAART, HIV, CD4 count, AIDS

1. INTRODUCTION

The Probability distribution models of HIV infection and diseases serve as illuminating caricatures, as foundation to build on, as analytical tool for the estimation of epidemiological parameters, and as guides to the information need for improving epidemiological understanding and in planning, implementation of new innovative programme for HIV associated illness and infection control. Many authors developed a probability distribution models by using different approaches like epidemic and the HIV pathogenesis in HIV infected individuals. Since the AIDS epidemic is basically a descriptive model approach as many risk variables subjected to extraneous variations. Some probabilistic models have been developed with lower precision and lesser accuracy (8-9). The present study aims to simulate the different probability distributions and are to find out the parameter variations with respect to CD4 count of PLHIV at the time of inception of HAART therapy.

2. METHODS

The cluster differential cell CD4 count (micro/dl) was determined by using inflow cytometric techniques of people living with HIV at onset of inception of antiretroviral therapy (HAART). Total 300 eligible ANC patients were recruited with written consent, prospectively ART follow up for the accrual period of two years, Demographic profile, and clinical profile like adverse and serious adverse drug reaction and laboratory parameters were collected systematically. The collected data were simulated in MATLAB -10.30 versions.

Parametric variations of continuous distributions like Normal, lognormal and Chi-squared distributions were observed with different mean values and SD deviations of CD4 count at inception of HAART. The discrepancy or probability gap of different parameters were simulated and correlated with mean values and SD.

3. MODEL FORMULATION FOR NORMAL DISTRIBUTION

Let "X" be a r.v with mean CD4 count at different intervals $-\infty < X < \infty$, $F(x)$, is the probability density functions $pdf = \int_{-\infty}^{+\infty} f(x)\,dx = 0$ area under *pdf* is being equated to 1. Two years follow up on CD4 count of PLHIV was

considered for model formulation, and then the projected model density function is given by $P(Xi > a) = \int_a^{\infty} f(x)dx$ Where as Xi = Mean CD4 count at the time of inception of ART therapy at different intervals like i= <100,150-250 and >250 micro per Dl. $P(Xi < a) = \int_{-a}^{\infty} f(x)\,dx$, $P(a < x < b) = \int_a^b f(x)dx$, then the probability $P(X \geq a) = P(X > a)$. The cumulative density function was calculated by $P(a < X < b) = P(X \leq b) - P(X \leq a) = F(b) - F(a)$. The fitted model hypothesis is tested by the probability values (P<0.05)

4. MODEL FORMULATION FOR LOG-NORMAL DISTRIBUTION

A random variable "*Xi*", where *i* = Mean CD4 count at different intervals" with parameter $\mu \in R$ and $\sigma > 0$ if ln(x) $N\sim(\mu, \sigma)$, σ equivalently $X = e^Y$. The fitted model pdf is given by

$$f(x) = \frac{1}{\sqrt{2\pi\sigma x}} \exp\left(\frac{\ln(X - \mu 2)}{2\sigma^2}\right),\ X > 0,\ \Pr \mid Xi \leq a \mid = \Pr \log(x) \leq \log(a) = \varphi\left(\frac{\log(x) - \mu}{\sigma}\right).$$

The model was demonstrated with different criteria $P = (X = a)$, $P = (X < a)$, $P = (a < X < b)$, $P = (X < a$ or $X > b)$ and determined their probability values.

5. MODEL FORMULATION FOR CHI-SQUARE DISTRIBUTION

The X_i is a standard normal (SND) distribution, where *i* = CD4 count of PLHIV than the distribution of $y = x^2$ is called the chi squared distribution for one df, the pdf is given by $f_{y(Y)} = f_x\left(\sqrt{y}\right) \Big/ \sqrt{y}, = \frac{1}{\sqrt{2\pi}} y^{-1\ 2} e^{-\frac{y}{2}}$ from,

$$\frac{1}{\sqrt{2\pi}} y^{-1/2} e^{-1\,2} = \frac{\left(\frac{1}{2}\right)1/2}{r\left(\frac{1}{2}\right)} y^{-1/2} e^{-1/2}.$$

6. RESULTS-SIMULATION

Tabble 1: Probability Distribution Fitted Models

SL	Probability distribution	Characteristics	Descriptive statistics value		Parameter		Probability value
			Mean-CD4 count @inception of HAART therapy	SD	a	b	
01	ND	P=(X=a)	189.00000	63.00000	0.50	0.00	0.000*
		P=(X<a)	189.00000	63.00000	0.50	0.00	0.00139*
		P=(X<a)	189.00000	63.00000	0.50	0.00	0.99861
		P=(a<X<b)	189.00000	63.00000	0.50	0.72	0.00001*
		P=(X<a or X>b)	189.00000	63.00000	0.50	0.72	0.99999
02	Log ND	P=(X=a)	189.00000	63.00000	0.50	0.00	0.00*
		P=(X<a)	189.00000	63.00000	0.50	0.00	0.00131*
		P=(X<a)	189.00000	63.00000	0.50	0.00	0.99869
		P=(a<X<b)	189.00000	63.00000	0.50	0.72	0.00002*
		P=(X<a or X>b)	189.00000	63.00000	0.50	0.72	0.99998

Table 1 Cont'd

03	Chi-square distribution	P=(X=a)	189.00000	63.00000	0.50	0.00	0.00000*
		P=(X<a)	189.00000	63.00000	0.50	0.00	0.00000**
		P=(X<a)	189.00000	63.00000	0.50	0.00	1.00000
		P=(a<X<b)	189.00000	63.00000	0.50	0.72	0.00000**
		P=(X<a or X>b)	189.00000	63.00000	0.50	0.72	1.00000

*, Significant @0.05 level ($p<0.05$)

7. DISCUSSION

The choice of model of distribution for a particular response variable *'X'* is usually based on how well it fits the data as judged by the fitted model deviance. The normal, log normal and chi-squared distribution parameters ($a = 0.50$ $b = 0.72$, Mean CD4 count 189.0 micro /dl SD = 63.0 micro/dl) was considered. The pdf of fitted models like P = (X = a), P = (X < a) and P = (a < X < b) is found to be statistically significant ($p < 0.05$). As per the fitted model lower CD4 count at inception of HAART therapy likely to be get Opportunistic infections and AIDS defining illness.

The present work provides parameter variations set against which the robustness of an expected CD4 count and the rate of opportunistic infections can be tested. Our model adequately represents the natural trend of immunological marker at inception of HAART therapy. Our model suggests a number of conclusions about the dynamics of HIV as it interacts with the immune system and the evolutionary drift of the virus frequency to evade the immune response, eventually resulting in declined of CD4 count. The higher the variance, ?2, the wider the distribution and the further away the new rate is from the original. For a given parameter, a, we can choose ? so that the new rate is within a factor " a & b" of the original probability 50%, since for a standard normal distribution, 75% of the density is below $\Phi - 1$ (0.72) = 0.66449.The model was clearly depicted that 66.49 % variation were observed between the two parameters "a and b"

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9. CONCLUSION

This deterministic continuous probabilistic model allows a straightforward measure of the diversity of CD4 count at onset of HAART therapy and reproduces the observed probability values varied with different parameters. The fitted model can able to reproduce simulation with large matrix of Biological data with greater accuracy

REFERENCES

[1] P. Nelson, J. Mittler, A. Perelson, "Effect of Drug Efficacy and the Eclipse Phase of the Viral Life Cycle on Estimates of HIV-1 Viral Dynamic Parameters", *J. AIDS* 26 (2001) 405.

[2] S.M. Ross, "Introduction to Probability Models", *Academic Press*, 1993.

[3] A. Perelson, P. Nelson, "Mathematical Models of HIV Dynamics in Vivo", SIAM Review 41 (1999) 3.

[4] R. Culshaw, S. Ruan, A Delay-differential Equation Model of HIV Infection of CD4þ T-cells", Math. Biosci. 165 (2000) 27

[5] Gilbert, P. B., Self, S. and Ashby, M. (1998). "Statistical Methods for Assessing Differential Vaccine Protection Against Human Immunodefficiency Virus Types. Biometrics 54, 799-814.

[6] Sun, Y. and Gilbert, P. B. (2012). "Estimation of Stratited Mark-specific Proportional Hazards Models with Missing Marks". *Scandinavian Journal of Statistics*, 39 34-52.

[7] Sun, Y., Gilbert, P. B. and McKeague, I. W. (2009). "Proportional Hazards Models with Continuous Marks". *The Annals of Statistics*, 37, 394-426.

[8] Damgaard, C.K., Andersen, E.S., Knudsen, B., Gorodkin, J., Kjems, J.,2004. "RNA Interactions in the 5 Region of HIV-1 Genome. J. Mol.Biol. 336, 369-379

[9] Abbink, T.E., Berkhout, B., 2003. "A Novel Long Distance Base-pairing Interaction in Human Immunodeficiency Virus Type 1 RNA Occludes the Gag Start Codon". J. Biol Chem. 278, 11601-11611.