

Bayesian Methods of Estimation of HIV Replication in a CD_4^+T Using Rayleigh Distribution under the Various Loss Function Approach

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Abstract- Human Immuno Deficiency Virus (HIV) infection of humans represents a complex biological system and a great challenge to public health. Novel approaches for analysis and prediction of the infection dynamics based on a multi-scale integration of virus ontogeny and immune reactions are needed to deal with the system complexity. It is known from the literature survey that HIV replication models are represented as first order differential equations. It gives only rate of change of HIV replication with respect to time. But, the parameter estimation and analytical solution of the differential equations are very difficult. So, in this paper, the Bayesian Methodology is used to estimate the HIV replication for the future period per infected CD_4^+T cell. In the Bayesian Methodology, the prior and current sample information simultaneously is used to obtain the posterior estimation of the parameter which gives effective information for future. In the HIV life cycle, there are seven different stages, such as binding, fusion, reverse transcription, integration, replication, assembly and budding. At the stage of binding, the various viral components bind with the CD_4^+T cell. Such as a-Surface glycoprotein (gp_{120}), b - transmembrane glycoprotein (gp_{41}) CCR₅, c - reverse transcriptase (P_{66}/P_{51}) are considered to estimate the HIV replication. Therefore, in this paper, a new risk function derived to use the components a, b and c. Finally, posterior parameter of HIV replication in a CD_4^+T cell is estimated. The estimated parameter is compared with some standard parameter using various loss functions.

Keywords: HIV Replication, New loss function, Bayes estimator, Risk function.

I. INTRODUCTION

Human Immune Deficiency Virus (HIV) infection represents a complex biological system [4,9,8,11] and a great challenge for cure strategies [12,20]. Past three decades HIV infected patients suffered a lot due to the non-availability of proper medicine to cure. In this context, finding appropriate medicine to resist the HIV replication of the infected patient is needed. So, the estimation of the HIV replication of infected per CD_4^+T cell for future period is very much essential to extent their life time and for the determination of medicine quantity and also classifies the medicine quantity if more than one categories available. This paper, concentrates on estimation of posterior parameter among the various component of a complex biological system. So, the estimation of parameter is involving various loss function as a biological components in the life cycle of the HIV replication per infected CD_4^+T cell. Naturally HIV infection is monotonically increasing nature after the infection takes place in a CD_4^+T cell. So, the number of replicated virus per CD_4^+T cell is considered as random variable of the Rayleigh distribution [10]. Rayleigh distribution's origin and properties are discussed in [1], the importance of this distribution in electro vacuum devices and communication engineering are notified in [2] and [3]. Rayleigh distribution is a particular case of weibull distribution, this was first introduced by Lord Rayleigh [18]. It is applied in several areas such as health science, agriculture, biology and other sciences. One major application of this distribution is used for analysis of the wind speed data is discussed in [14]. Therefore, in this paper the viral replication in a CD_4^+T cell is assumed to be Rayleigh distribution.

Section I : Explains the introduction of Bayesian estimation of HIV replication using Rayleigh distribution.

Section II : Contains literature review of Rayleigh distribution and its related works.

Section III : Gives Bayesian Methodology is used to estimate the HIV replication for future by period using various loss function.

Section IV : Shows that tables and graphs.

Section V : Gives conclusion of this paper.

II. REVIEW OF LITERATURE

Dey (2012) has obtained Bayes estimator of parameter and reliability function of inverse Rayleigh distribution under two loss functions and also obtained associated risk functions of the Bayes estimator. **Ahmed et al. (2013)** have obtained Bayes estimate of parameter of Rayleigh distribution using Jeffrey's and extension of Jeffrey's prior under Squared error and Al-Bayyati's loss function. One major application of this model is used in analyzing wind speed data. Recently Bayesian estimation approach has received great attention by most researchers. Bayesian analysis is an important approach to statistics, which formally seeks use of prior information. Bayes Theorem provides the formal basis for using this information. In this approach, parameters are treated as random variables and data is treated fixed. Ghafoor et al. (2001)] and Rahul *et al.* (2009) have discussed the application of Bayesian methods. **R. Lakshmajayam and G.Meenakshi (2014)** developed a model of HIV replication for the succeeding period, which is numerically illustrated by David et al. (1995). **R. Lakshmajayam and G.Meenakshi (2015)** described the model for HIV replication in the infected CD4+ T -cells, under the assumption of law of mass action by using truncated logistic distribution and numerically illustrated the replication of viral load for the future period. **G.Meenakshi, Habineza Alexis and R. Lakshmajayam (2015)** discussed a model of HIV replication where infected cells considered as a truncated logistic distribution can be used for future studies of HIV intracellular replication. **Paresh Sanat et.al (2015)** explained the Rayleigh distribution is often observed when the overall magnitude of a vector is related to its directional components. One example, where the Rayleigh distribution naturally arises when velocity is analyzed into its orthogonal 2-dimensional components. **Ferreira et al. (2016)** have proposed Bayes estimators including shrinkage estimators of the unknown parameter of the censored Rayleigh distribution using Al-Bayyati loss function considering different objective prior distribution. **Sanat et al. (2016)** have proposed Bayes estimate of parameter of Rayleigh distribution using Quasi prior under different loss functions. **G Meenakshi and S Lakshmi Priya (2017)** have derived the predictive distribution of viral load for the future period using Exponential Distribution as Prior by the Bayesian methodology. **G Meenakshi and S.Lakshmi Priya (2018)** derived statistical model for HIV replication in each stages of a CD_4^+T cell. This paper concentrates on viral replication per CD_4^+T cell is estimated by Bayesian methodology with various loss function by using Rayleigh distribution.

III. METHODOLOGY

Let as assume that random variable X is considered as number of replicated virus in a CD_4^+T cell, which is distributed as Rayleigh and its conjugate prior distribution of average replication is considered as gamma distribution. Then, the posterior distribution is derived and estimate the posterior parameter. Finally, a new Bayes parameter is estimated using various loss function. The various biological terms involved in the HIV replication cycle of the viral components such as a- Surface glycoprotein (gp_{120}), b - transmembrane glycoprotein (gp_{41}) CCR_5 , c - reverse transcriptase (P_{66}/P_{51}) in a infected CD_4^+T cell is considered as the coefficient of parameters of the loss function. The estimated new parameters are compared with the standard parameter. Finally, the Mean Square error of the parameter is found.

Let X_1, X_2, \dots, X_n be a random sample of size n from Rayleigh distribution is considered as HIV replications per ml of the HIV infected patients CD_4^+T cells. The likelihood function is given by

$$L(X, \theta) = (2\theta)^n \prod_{i=1}^n x_i e^{-\theta \sum x_i^2}$$

The conjugate prior density of the parameter θ is assumed to be r (scale parameter) is given by

$$g(\theta/r) = \frac{e^{-\theta} \theta^{r-1}}{\Gamma r}, \quad r > 0, \theta > 0$$

The posterior density of θ given X is given by

$$p(\theta/x) \propto L(X, \theta) * g(\theta/r)$$

$$= (2\theta)^n \prod_{i=1}^n x_i e^{-\theta \sum x_i^2} * \frac{e^{-\theta} \theta^{r-1}}{\Gamma r}, \quad x > 0, r > 0, \theta > 0.$$

$$= k. \theta^{n+r-1} e^{-\theta(\sum x_i^2+1)}$$

where $k = \frac{2^n \prod x_i}{\Gamma r}$,

Thus,

$$\int_0^\infty p(\theta/x) d\theta = \int_0^\infty \theta^{n+r-1} e^{-\theta(\sum x_i^2+1)} d\theta$$

$$= \frac{(\sum x_i^2 + 1)^{n+r}}{\Gamma(n+r)} = d \text{ say,}$$

The posterior density function is given by

$$p(\theta/x) = \frac{k e^{-\theta(\sum x_i^2+1)} \theta^{n+r-1} (\sum x_i^2 + 1)^{n+r}}{\Gamma(n+r)}$$

$$p(\theta/x) = \frac{k}{d} e^{-\theta(\sum x_i^2+1)} \theta^{n+r-1}; \quad \theta > 0, r > 0, x > 0$$

Where

$$\frac{k}{d} = \frac{2^n \prod x_i}{\Gamma r} * \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}}$$

which is independent of θ .

Maximum likelihood estimation of Posterior Parameter:

The average replication of the n CD4⁺T cells per ml blood plasma is denoted by $\theta_1, \theta_2, \dots, \theta_n$, and its density is given by

$$P(\theta_n) = \frac{(\sum x_i^2 + 1)^{n+r}}{\Gamma(n+r)} e^{-\theta_n(\sum x_i^2+1)} \theta_n^{n+r-1}$$

$$\log[P(\theta_n)] = (n+r) \log \left(\sum x_i^2 + 1 \right) - \log \Gamma(n+r) +$$

$$[(n+r) - 1] \log \theta_n - \theta_n \left(\sum x_i^2 + 1 \right)$$

$$\sum_{n=0}^{n-1} \log[P(\theta_n)] = N(n+r) \log \left(\sum x_i^2 + 1 \right) - N \log \Gamma(n+r) +$$

$$[(n + r) - 1] \sum_{n=0}^{n-1} \log \theta_n - \left(\sum x_i^2 + 1 \right) \sum_{n=0}^{n-1} \theta_n$$

On simplification, MLE of θ is $\hat{\theta}$

$$\hat{\theta} = \frac{n + r}{\sum x_i^2 + 1}$$

Loss function - Model I

In this model the biological term such as a-Surface glycoprotein (gp₁₂₀), b - transmembrane glycoprotein (gp₄₁) CCR₅, c - reverse transcriptase (P₆₆ /P₅₁) involved to react and produce a new virus in the cycle of viral replication are considered as function of loss function is given by

$$L(\theta, \hat{\theta}) = (\hat{\theta} - \theta) \left[1 - \left\{ \frac{a}{b} - (\hat{\theta} - \theta) \right\} + c \right]$$

Bayesian estimation of θ under loss function

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} L(\theta, \hat{\theta}) * p(\theta/x) d\theta$$

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} \left\{ (\hat{\theta} - \theta) \left[1 - \left\{ \frac{a}{b} - (\hat{\theta} - \theta) \right\} + c \right] \right\} \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$= \frac{\hat{\theta}k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} - \frac{ka\hat{\theta}}{db} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{ka}{db} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}}$$

$$+ \frac{k\hat{\theta}^2}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k2\hat{\theta}}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} + \frac{k}{d} \frac{\Gamma(n+r+2)}{(\sum x_i^2 + 1)^{n+r+2}}$$

$$+ \frac{ck}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}}$$

Differentiating w.r.to $\hat{\theta}$ and equating to 0 is given by

$$\frac{k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{ka}{db} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{2\hat{\theta}k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k2}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} = 0$$

On simplification, MLE of θ is $\hat{\theta}$

$$\hat{\theta} = \left[\frac{2(n+r)}{2(\sum x_i^2 + 1)} + \frac{a}{2b} - \frac{1}{2} \right]$$

Thus Bayes Estimator of $\hat{\theta}$ is

$$\hat{\theta}_{BL} = \left[\frac{(n+r)}{(\sum x_i^2 + 1)} + \frac{a}{2b} - \frac{1}{2} \right]$$

Loss function - Model II

In this model, the loss function only considered as the average number of replication per CD₄⁺T cell is given by

$$L(\theta, \hat{\theta}) = (\hat{\theta} - \theta) \left\{ 1 + \frac{(\hat{\theta} - \theta)}{\hat{\theta}} \right\}$$

Bayesian Estimation of θ under loss function

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} L(\theta, \hat{\theta}) * p(\theta/x) d\theta$$

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} \left\{ (\hat{\theta} - \theta) \left\{ 1 + \frac{(\hat{\theta} - \theta)}{\hat{\theta}} \right\} \right\} \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$= \frac{\hat{\theta}k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} + \frac{k\hat{\theta}}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k2}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} + \frac{k}{d\hat{\theta}} \frac{\Gamma(n+r+2)}{(\sum x_i^2 + 1)^{n+r+2}}$$

Differentiating w.r.to $\hat{\theta}$ and equating to 0 is given by

$$\frac{k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k}{d\hat{\theta}^2} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} = 0$$

On simplification, MLE of θ is $\hat{\theta}$

$$\hat{\theta} = \sqrt{\frac{(n+r+1)(n+r)}{2(\sum x_i^2 + 1)^2}}$$

Thus Bayes Estimator of $\hat{\theta}$ is

$$\hat{\theta}_{BL} = \sqrt{\frac{(n+r+1)(n+r)}{2(\sum x_i^2 + 1)^2}}$$

Loss function - Model III

In this model, various proportion of the component a- Surface glycoprotein (gp₁₂₀), b - transmembrane glycoprotein (gp₄₁) CCR₅, c - reverse transcriptase (P₆₆/P₅₁) are reacted with the cycle of modifications in the HIV replication in the loss function is given by

$$L(\theta, \hat{\theta}) = (\hat{\theta} - \theta) \left[1 - \left\{ \frac{a}{b} - c(\hat{\theta} - \theta) \right\} \right]$$

Bayesian Estimation of θ under loss function

$$E[L(\theta, \hat{\theta})] = \int_0^\infty L(\theta, \hat{\theta}) * p(\theta/x) d\theta$$

$$E[L(\theta, \hat{\theta})] = \int_0^\infty \left\{ (\hat{\theta} - \theta) \left[1 - \left\{ \frac{a}{b} - c(\hat{\theta} - \theta) \right\} \right] \right\} \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$\begin{aligned} &= \frac{\hat{\theta}k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} - \frac{ka\hat{\theta}}{db} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{ka}{db} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} \\ &\quad + \frac{ck\hat{\theta}^2}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{ck2\hat{\theta}}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} + \frac{ck}{d} \frac{\Gamma(n+r+2)}{(\sum x_i^2 + 1)^{n+r+2}} \end{aligned}$$

Differentiating w.r.to $\hat{\theta}$ and equating to 0 is given by

$$\frac{k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{ka}{db} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{2\hat{\theta}kc}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k2c}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} = 0$$

On simplification, MLE of θ is $\hat{\theta}$

$$\hat{\theta} = \left[\frac{(n+r)}{(\sum x_i^2 + 1)} + \frac{a}{2bc} - \frac{1}{2c} \right]$$

Thus Bayes Estimator of $\hat{\theta}$ is

$$\hat{\theta}_{BL} = \left[\frac{(n+r)}{(\sum x_i^2 + 1)} + \frac{a}{2bc} - \frac{1}{2c} \right]$$

Loss function - Model IV

In this model, the loss function only consider the reaction with c - reverse transcriptase (P₆₆/P₅₁) and the average replication is represented as

$$L(\theta, \hat{\theta}) = e^{c(\hat{\theta}-\theta)} - \frac{(\hat{\theta} - \theta)}{c}$$

Bayesian Estimation of θ under loss function

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} L(\theta, \hat{\theta}) * p(\theta/x) d\theta$$

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} \left\{ e^{c(\hat{\theta}-\theta)} - \frac{(\hat{\theta} - \theta)}{c} \right\} \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$= \frac{k}{d} e^{c\hat{\theta}} \frac{\Gamma(n+r)}{(\sum x_i^2 + c + 1)^{n+r}} - \frac{k\hat{\theta}}{cd} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{k}{cd} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}}$$

Differentiating w.r.to $\hat{\theta}$ and equating to 0 is given by

$$\frac{ck}{d} e^{c\hat{\theta}} \frac{\Gamma(n+r)}{(\sum x_i^2 + c + 1)^{n+r}} - \frac{k}{cd} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} = 0$$

On simplification, MLE of θ is $\hat{\theta}$

$$e^{c\hat{\theta}} = \frac{(\sum x_i^2 + c + 1)^{n+r}}{c^2(\sum x_i^2 + 1)^{n+r}}$$

Taking log on both sides

$$c\hat{\theta} = \log \left[\frac{(\sum x_i^2 + c + 1)^{n+r}}{c^2(\sum x_i^2 + 1)^{n+r}} \right]$$

$$\hat{\theta} = \frac{\log \left[\frac{(\sum x_i^2 + c + 1)^{n+r}}{c^2 (\sum x_i^2 + 1)^{n+r}} \right]}{c}$$

Thus Bayes Estimator of $\hat{\theta}$ is

$$\hat{\theta}_{BL} = \frac{\log \left[\frac{(\sum x_i^2 + c + 1)^{n+r}}{c^2 (\sum x_i^2 + 1)^{n+r}} \right]}{c}$$

Loss function - Model V

In this model, the loss function considered only the proportional changes of the a- Surface glycoprotein (gp₁₂₀), b - transmembrane glycoprotein (gp₄₁) CCR₅, c - reverse transcriptase (P₆₆/P₅₁) are represented as

$$L(\theta, \hat{\theta}) = (\hat{\theta} - \theta) \left[1 - \left\{ \frac{a}{b} - \frac{(\hat{\theta} - \theta)}{c} \right\} \right]$$

Bayesian Estimation of θ under loss function

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} L(\theta, \hat{\theta}) * p(\theta/x) d\theta$$

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} \left\{ (\hat{\theta} - \theta) \left[1 - \left\{ \frac{a}{b} - \frac{(\hat{\theta} - \theta)}{c} \right\} \right] \right\} \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$\begin{aligned} &= \frac{\hat{\theta}k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} - \frac{k a \hat{\theta}}{d b} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{k a}{d b} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} \\ &\quad + \frac{k \hat{\theta}^2}{c d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k 2 \hat{\theta}}{c d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} + \frac{k}{c d} \frac{\Gamma(n+r+2)}{(\sum x_i^2 + 1)^{n+r+2}} \end{aligned}$$

Differentiating w.r.to $\hat{\theta}$ and equating to 0 is given by

$$\frac{k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k a}{d b} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{2 \hat{\theta} k}{c d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k 2}{c d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} = 0$$

On simplification, MLE of θ is $\hat{\theta}$

$$\hat{\theta} = \left[\frac{(n+r)}{(\sum x_i^2 + 1)} + \frac{a c}{2 b} - \frac{c}{2} \right]$$

Thus Bayes Estimator of $\hat{\theta}$ is

$$\hat{\theta}_{BL} = \left[\frac{(n+r)}{(\sum x_i^2 + 1)} + \frac{ac}{2b} - \frac{c}{2} \right]$$

Loss function - Model VI

In this, model a- Surface glycoprotein (gp₁₂₀), b - transmembrane glycoprotein (gp₄₁) CCR₅, c - reverse transcriptase (P₆₆/P₅₁) involved various proportional changes in the loss function is given by

$$L(\theta, \hat{\theta}) = (\hat{\theta} - \theta) \left[\left\{ \frac{(\hat{\theta} - \theta)}{c} \right\} - \left\{ \frac{a}{b} + 1 \right\} \right]$$

Bayesian Estimation of θ under loss function

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} L(\theta, \hat{\theta}) * p(\theta/x) d\theta$$

$$E[L(\theta, \hat{\theta})] = \int_0^{\infty} \left\{ (\hat{\theta} - \theta) \left[\left\{ \frac{(\hat{\theta} - \theta)}{c} \right\} - \left\{ \frac{a}{b} + 1 \right\} \right] \right\} \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$\begin{aligned} &= \frac{\hat{\theta}^2 k}{cd} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{2\hat{\theta}k}{cd} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} + \frac{k}{cd} \frac{\Gamma(n+r+2)}{(\sum x_i^2 + 1)^{n+r+2}} - \frac{ka\hat{\theta}}{bd} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} \\ &+ \frac{ak}{bd} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} - \frac{k\hat{\theta}}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} + \frac{k}{d} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} \end{aligned}$$

Differentiating w.r.to $\hat{\theta}$ and equating to 0 is given by

$$\frac{2\hat{\theta}k}{cd} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{2k}{cd} \frac{\Gamma(n+r+1)}{(\sum x_i^2 + 1)^{n+r+1}} - \frac{ka}{bd} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} - \frac{k}{d} \frac{\Gamma(n+r)}{(\sum x_i^2 + 1)^{n+r}} = 0$$

On simplification, MLE of θ is $\hat{\theta}$

$$\hat{\theta} = \frac{(n+r)}{(\sum x_i^2 + 1)} + \frac{ac}{2b} + \frac{c}{2}$$

Thus Bayes Estimator of $\hat{\theta}$ is

$$\hat{\theta}_{BL} = \frac{(n + r)}{(\sum x_i^2 + 1)} + \frac{ac}{2b} + \frac{c}{2}$$

Loss function - Model VII

In this model, only considered the c - reverse transcriptase (P₆₆/P₅₁) as coefficient of parameter in the loss function is given by

$$L(\theta, \hat{\theta}) = \frac{e^{c(\hat{\theta}-\theta)}}{c} - 1$$

Bayesian Estimation of θ under loss function

$$E[L(\theta, \hat{\theta})] = \int_0^\infty L(\theta, \hat{\theta}) * p(\theta/x) d\theta$$

$$E[L(\theta, \hat{\theta})] = \int_0^\infty \left\{ \frac{e^{c(\hat{\theta}-\theta)}}{c} - 1 \right\} \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$= \frac{k}{d} e^{c\hat{\theta}} \frac{\Gamma(n + r)}{(\sum x_i^2 + c + 1)^{n+r}} - \frac{k}{d} \frac{\Gamma(n + r)}{(\sum x_i^2 + 1)^{n+r}}$$

Differentiating w.r.to $\hat{\theta}$ and equating to 0 is given by

$$\frac{ck}{d} e^{c\hat{\theta}} \frac{\Gamma(n + r)}{(\sum x_i^2 + c + 1)^{n+r}} = 0$$

$$e^{c\hat{\theta}} = \frac{d(\sum x_i^2 + c + 1)^{n+r}}{ck\Gamma(n + r)}$$

On simplification, MLE of θ is $\hat{\theta}$

$$\hat{\theta}_{BL} = \frac{\log \left[\frac{d(\sum x_i^2 + c + 1)^{n+r}}{ck\Gamma(n+r)} \right]}{c}$$

Thus Bayes Estimator of $\hat{\theta}$ is

$$\hat{\theta}_{BL} = \frac{\log \left[\frac{d(\sum x_i^2 + c + 1)^{n+r}}{ck\Gamma(n+r)} \right]}{c}$$

Mean square error

$$L(\hat{\theta}, \theta) = \frac{(\hat{\theta} - \theta)^2}{c^2}$$

$$E(L(\hat{\theta}, \theta)) = \int_0^\infty \frac{(\hat{\theta} - \theta)^2}{c^2} \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$\hat{\theta} = \frac{(n+r)}{(\sum x_i^2 + 1)}$$

$$L(\hat{\theta}, \theta) = \left[\frac{\theta}{b} - \frac{(\hat{\theta} - \theta)}{c} \right]^2$$

$$E(L(\hat{\theta}, \theta)) = \int_0^\infty \left[\frac{\theta}{b} - \frac{(\hat{\theta} - \theta)}{c} \right]^2 \frac{k}{d} e^{-\theta(\sum x_i^2 + 1)} \theta^{n+r-1} d\theta$$

On simplification,

$$\hat{\theta} = \frac{c(n+r)}{(\sum x_i^2 + 1)}$$

IV. CALCULATION

Estimation of parameters with different loss functions by Bayesian methodology using R-software, generated random observations from Rayleigh distribution and derived the MLE of parameter for the different loss functions.

Table 1: $\hat{\theta}$ variation for the seven loss function model when $\Theta = 0.5$

n (sample size)	$\hat{\theta}_{ML}$	$\hat{\theta}_{MSE}$	$\hat{\theta}_{BL_1}$	$\hat{\theta}_{BL_2}$	$\hat{\theta}_{BL_3}$	$\hat{\theta}_{BL_4}$	$\hat{\theta}_{BL_5}$	$\hat{\theta}_{BL_6}$	$\hat{\theta}_{BL_7}$

5	3.8603	0.8603	3.7353	2.9483	3.7353	1.2944	3.7353	4.7355	0.0769
10	6.0010	0.0010	5.8759	4.4319	5.8759	2.0799	5.8759	6.8760	0.0047
15	4.6548	0.6548	4.5298	3.3920	4.5298	1.2199	4.5298	5.5298	0.0021
20	7.1996	0.1996	7.0746	5.2106	7.0746	2.6885	7.0746	8.0746	0.0001
25	5.7612	0.7612	5.6362	4.1514	5.6362	3.0014	5.6362	6.6363	0.0009
30	5.8113	0.8113	5.6530	4.1750	5.6530	2.3132	5.6530	6.6864	0.0007

Table 2: $\hat{\theta}$ variation for the seven loss function model when $\Theta=1.5$

n (sample size)	$\hat{\theta}_{ML}$	$\hat{\theta}_{MSE}$	$\hat{\theta}_{BL_1}$	$\hat{\theta}_{BL_2}$	$\hat{\theta}_{BL_3}$	$\hat{\theta}_{BL_4}$	$\hat{\theta}_{BL_5}$	$\hat{\theta}_{BL_6}$	$\hat{\theta}_{BL_7}$
5	0.2132	0.0603	0.0882	0.1629	0.0882	0.0910	0.0882	1.0882	6.2297
10	0.1862	0.0010	0.0612	0.1375	0.0612	0.0801	0.0612	1.0612	3.3719
15	0.2683	0.0548	0.1433	0.1955	0.1433	0.1155	0.1433	1.1433	6.5897
20	0.3970	0.0996	0.2720	0.2873	0.2720	0.1708	0.2720	1.2720	16.9540
25	0.3221	0.0612	0.1971	0.2321	0.1971	0.1390	0.1971	1.1971	23.4128
30	0.2820	0.0113	0.1570	0.2026	0.1570	0.1219	0.1570	1.1570	29.7806

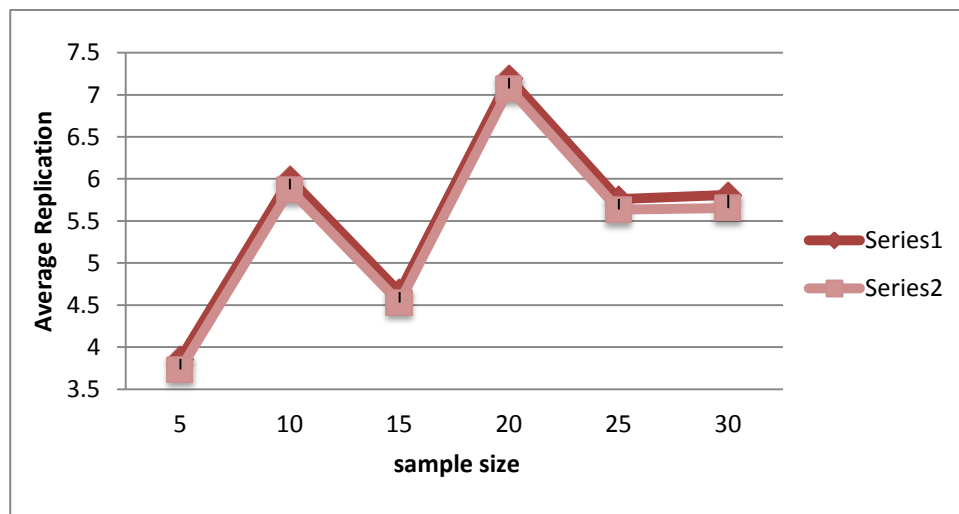


Figure 1: loss function of the model I

Series 1: Maximum likelihood function

Series 2: Loss function model I

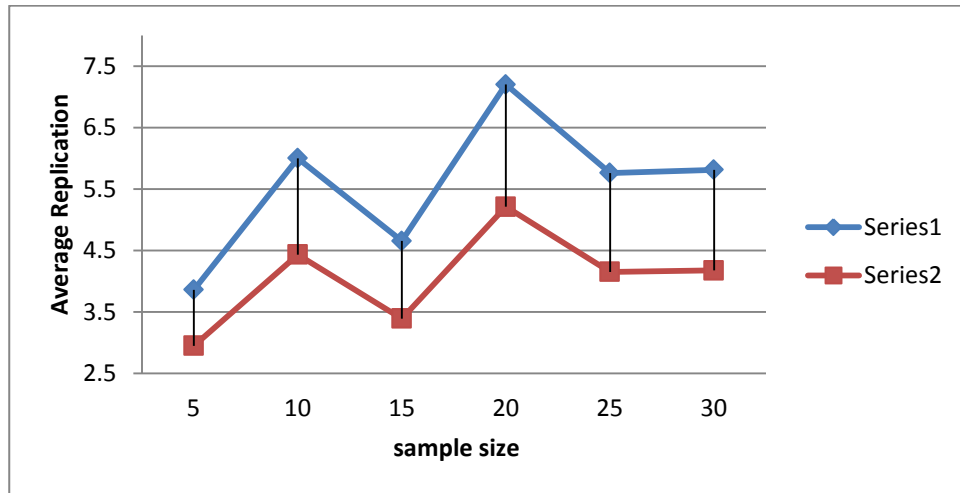


Figure 2: loss function of the model II

Series 1: Maximum likelihood function

Series 2: Loss function model II

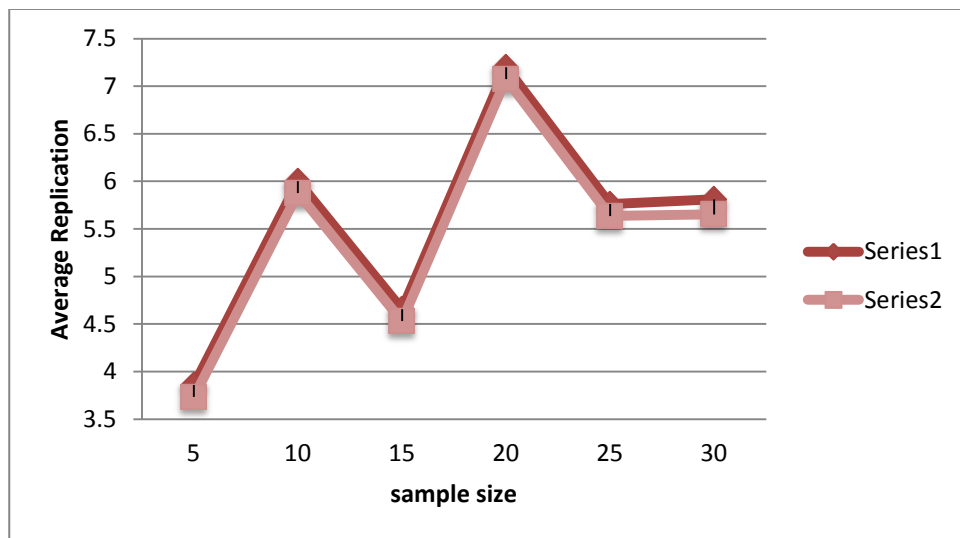


Figure 3: loss function of the model III

Series 1: Maximum likelihood function

Series 2: Loss function model III

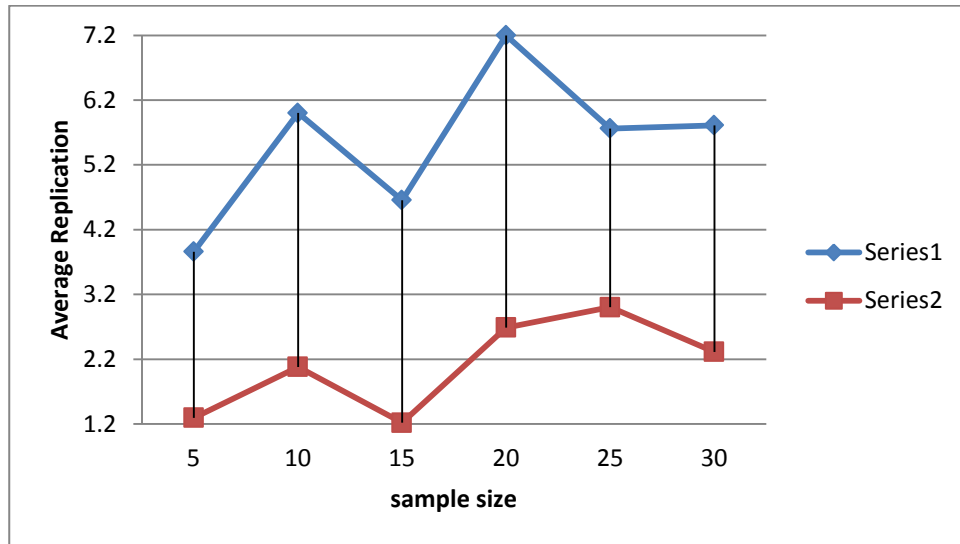


Figure 4: loss function of the model IV

Series 1: Maximum likelihood function

Series 2: Loss function model IV

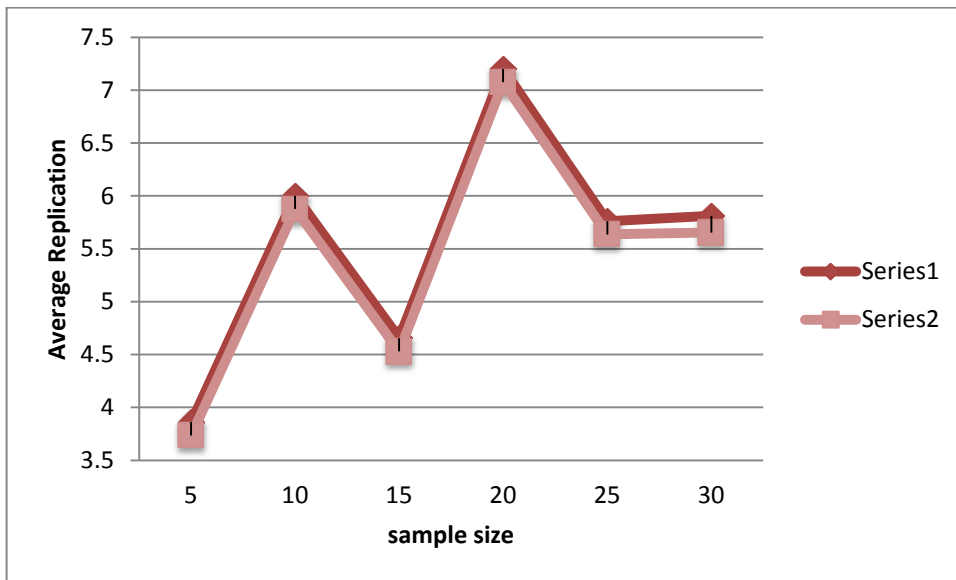


Figure 5: loss function of the model V

Series 1: Maximum likelihood function

Series 2: Loss function model V

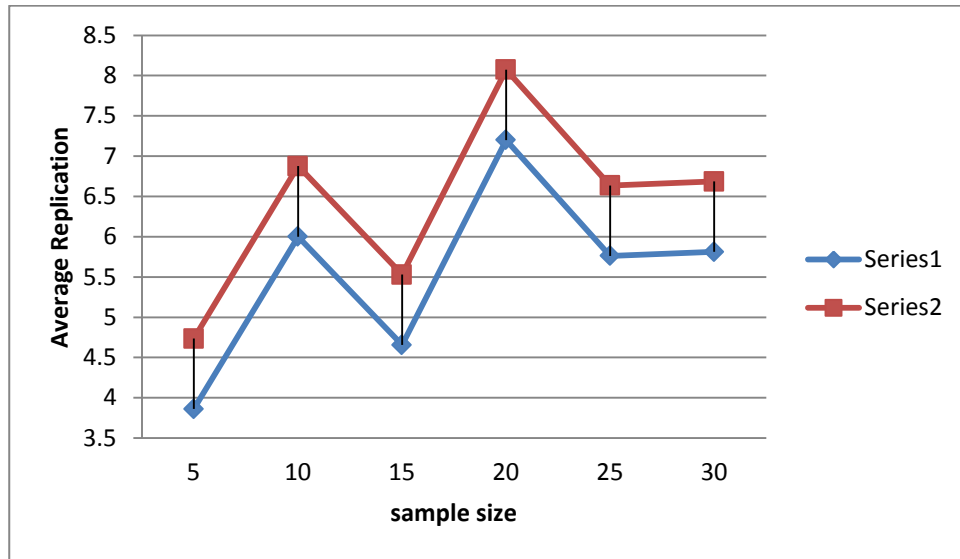


Figure 6: loss function of the model VI

Series 1: Maximum likelihood function

Series 2: Loss function model VI

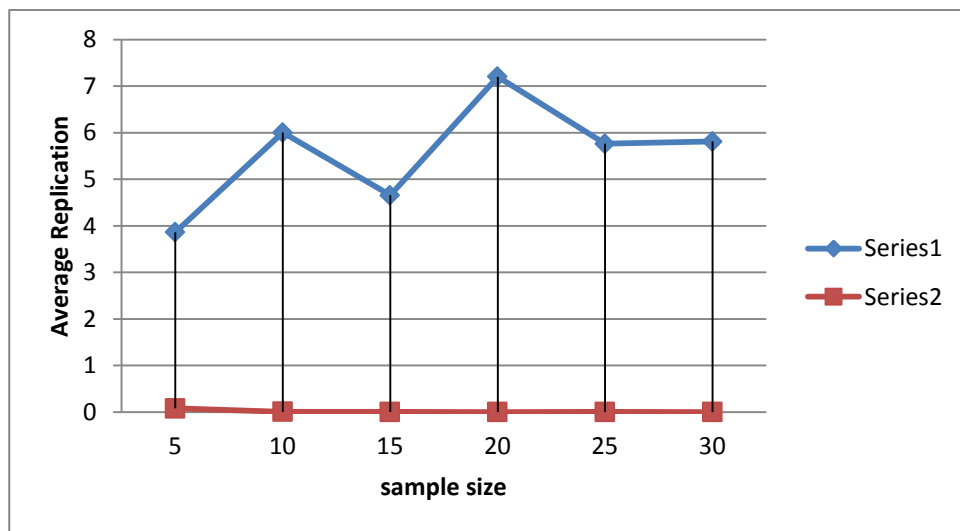


Figure 7: loss function of the model VII

Series 1: Maximum likelihood function

Series 2: Loss function model VII

V. CONCLUSION

In this paper, Bayesian methodology is used for the estimation of parameter using different loss function of Rayleigh distribution. From the posterior parameter of θ , the average replication of HIV per ml CD_4^+ T cell for the future period is obtained. The various loss function of the parameter is considered as function of the biological components such as a- Surface glycoprotein (gp_{120}), b - transmembrane glycoprotein (gp_{41}) CCR_5 , c - reverse transcriptase (P_{66} / P_{51}). Finally, estimated parameters of various models of the loss function compared with MLE and find mean square error and graphically illustrated.

This prediction of viral replication is very much useful to determine the quantity of medicine (ART) for the future period of the patient and classify the quality of medicine if more than one category available. This type of the predetermination of the medicine is very much useful to extend the lifetime of the HIV infected patients.

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