
ABSTRACT

The present piece of work deals with two segments of the study, the first segment related to the lifetime study and the second segment related to the ecological study based on statistical models. The lifetime study in the thesis belongs to **Chapter 2, 3, and 4** and the ecological modeling-based study belongs to **Chapters 5**. In this context, experimenters/doctors are dealing with lifetime data for patients' survival time. They are facing the difficulty of losing to follow-up of the patient, it is the problem of censoring. When patients are lost to follow-up in the duration of treatment due to unforeseen reasons which are beyond the control of experimenter/doctors such an appropriate censoring is known as progressive Type-II censoring with binomial removals. Such problems are shared in consecutive **Chapter**. **Chapter 2** deals with Bayesian estimation of the parameter of Weibull Poisson distribution under different loss functions using the Expectation-Maximization algorithm. A bladder cancer patient data has been used to show their applicability on Weibull Poisson distribution. **Chapter 3** presents Bayesian and E-Bayesian estimations for Poisson Inverted Exponential distribution under different loss functions. This approach allows and facilitate multiple myeloma patients' data. **Chapter 4**, covers Empirical Bayesian estimation under Linear Exponential loss function for Kumaraswamy distribution parameter, reliability, and hazard function. Also, ulcer patients' data are included in that **Chapter**. The problems their relations are presented at the end of the **Chapter**. Thus we cover all the aforesaid Chapters based on statistical inference of the lifetime models parameter used progressive censoring with Binomial removals. Last **Chapter 5**, concerned with the estimation of the number of species using Poisson Lindley as a stochastic abundance model. We have considered the classical estimation based on profile likelihood, conditional likelihood. For Bayesian estimation, Jeffery's priors and Bernardo's reference prior based on this **Chapter**. The proposed methods are illustrated through a microbial organisms species data.

The statistical **R** software is used for computation purposes in the thesis. The thesis contains a list of references at the end. We recognize that a comprehensive list of sources linked to

the issues mentioned in the thesis would be too long to present here. As a result, we've only included references that are cited in the thesis and are directly linked to our research.