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Kappa Model with Laplace Approximation: A Bayesian Study

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Abstract: This paper covers Kappa model in Bayesian perspective to check whether these distributions truly work well for Prognosis for women with Breast cancer Data. The main objective is to quantitatively assess the prognostic performance of the Kappa model for right-censored survival data using advanced Bayesian techniques. Laplace Approximation analytically approximates the posterior distribution of parameters and Markov chain Monte Carlo (MCMC) methods simulate samples from posterior and both approaches in the LapalcesDemon package in R. Weakly informative normal and half-Cauchy priors are employed to ensure numerical stability and robustness of posterior estimates. The methodology will be applied to a real-case survival problem of patients with breast cancer in relation to their tumor staining status. The performance of this model will show that it can deliver accurate results in terms of estimating parameters using a Bayesian Kappa model, thus being a good alternative model in survival studies for medical prognosis.

Keywords: Bayesian Statistics, LaplaceApproximation, LaplacesDemon, JAGS, R.

1. Introduction

Many researchers such as [5, 16, 19] have attempted to introduce three- and four-parameter kappa distributions using the maximum entropy principle as a tool to reduce precision under constraints. The maximum entropy (ME) is an inference tool in uncertainty, and many authors [2, 18] use (ME) to estimate four- and three-parameter kappa distributions. This paper covers Kappa model in Bayesian perspective to check whether these distributions truly work well for Prognosis for women with Breast cancer Data. We use the Kappa model and the Bayes method to evaluate the survival of the Kappa model using the Laplace approximation.

A statistical technique called survival analysis is issued to analyse data related to the timing of events, where the main outcome variable is the time at which an event takes place. Such events. are often referred to as failures, and examples of this could include the duration until an electrical device stops working and the interval until a tumour reappears following the initial treatment are examples of time-to-event data that are frequently examined using survival analysis techniques.

It is possible that a failure time will not be observed due to random censoring, or deliberately by design, for example, if a patient is still alive at the end of a clinical trial period or has been lost to follow-up, their survival time is said to be censored. To accommodate censoring, specialized models and procedures have been developed, which is the primary reason for the development of survival analysis. In addition to medicine, biology, and engineering, survival analysis is also applied in public health, epidemiology, economics, psychology, and demography. Survival analysis commonly uses models like gamma, Weibull, and normal distributions. The Kappa distribution is another significant model used for survival data. It is a two-parameter family of models that is flexible. In this paper, we examine a Bayesian methodology for fitting the Kappa distribution to lifetime data. The methodology used involves the Laplace approximation, which requires maximizing the joint log posterior densities. This approach aims to improve our understanding of using Kappa distribution in survival analysis and provide practical guidance for its implementation.

A method based on Bayesian principles has been devised to estimate the Kappa distribution for lifetime data by employing The Laplace approximation method requires the capability to optimize the log posterior densities jointly. The statistical tools and methods are based on a Bayesian framework, and the computations are carried out using the LaplacesDemon package developed by [17]. The package's objective is to offer a user-friendly and self-contained Bayesian environment in R. It achieves this by utilizing MCMC algorithms are utilized to approximate the posterior densities.

The Laplace Approximation function, a part of the LaplacesDemon package, approximates the posterior results analytically

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and then produces simulated results by utilizing the sampling importance resampling (SIR) method after the convergence is reached. In the Laplace Approximation function, the argument called "Method," and (TR) Trust Region algorithm developed by [7] applied to approximate the posterior density. The TR algorithm employed by LaplacesDemon strives to accomplish its objective using the minimum iterations possible., making it highly efficient and safe. This is especially useful when evaluating complex models that require a considerable amount of computation. In addition to the TR algorithm, another important function of the Laplaces Demon package is LaplacesDemon, this function is particularly useful for complex models where direct calculation of the posterior density is infeasible. By using MCMC algorithms, LaplacesDemon can approximate the posterior distribution of the parameters of interest. However, the censoring mechanism is not explicitly covered by this package. However, to account for this, a separate function has been created to handle censored data effectively during survival data analysis. To provide practical illustrations, real survival data is frequently utilized for demonstration purposes, and the methods and techniques discussed in this paper avoid bias and utilize the partial information available on a subject or item. The procedures presented here are more powerful than those that treat incomplete data as missing data and omit them from the analysis, resulting in the loss of partial information and introducing systematic error. Survival analysis is a vital tool for analysing time-to-event data and has numerous applications in various fields, including economics, medicine, biology, engineering, public health, epidemiology, psychology, and demography. By incorporating specialized models and procedures that accommodate censoring, such as the Kappa distribution, and using Bayesian approaches and efficient algorithms like TR and MCMC, we can avoid bias and obtain more powerful and accurate results.

- The first step in the process is to establish a Bayesian model, which involves specifying the likelihood function and prior. This is a very important part in Bayesian analysis, as it determines the framework for making statistical inferences based on the available data.
- Once the Bayesian model has been defined, the next step is to implement the model using R code. This involves using Laplace approximation and simulation tools to approximate the posterior distribution of the model parameters. This step is essential for obtaining numerical estimates of the model parameters.
- The last step in the process is to summarize the posterior distributions obtained in step 2. This includes both numeric summaries of the posterior distributions, as well as graphic summaries. These summaries provide insights into the uncertainty associated with the model parameters and help to identify potential issues with the model fit.

Despite the general popularity of the application of the classical survival models like Weibull, Gamma, and Log-normal distributions, these models seem inadequate and are often not flexible enough for the modeling of complex survival functions that are applied on real survival medical datasets. Even though the Kappa distribution has been recognized for its successful application on reliability and hydrological data and was noted for its flexibility properties, the application of the Kappa survival model for censored datasets on the Bayesian platform has yet to gain popularity on the medical platforms. Equally unexplored is the application of the Bayesian estimation for the Kappa survival model using the Laplace Approximation and MCMC algorithms.

2. Kappa Distribution

Kappa distribution is a flexible distribution commonly used in survival analysis. It is a two-parameter distribution that can be used to model lifetime data in survival analysis. The Kappa distribution is recognized as a flexible and reliable model for analyzing lifetime data. The Kappa model has demonstrated its effectiveness across various fields, including medicine, engineering, economics, and more.

Probability density function of Kappa distribution is given by:

$$f(t)=\frac{a}{\lambda}\left[a+\left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(-\left(\frac{a+1}{a}\right)\right)}, \quad a,\lambda,t\geq 0 \tag{1}$$

Where shape is a is, scale is λ parameter. The corresponding cumulative distribution function is;

$$F(t)=\frac{t}{\lambda}\left[a+\left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(\frac{1}{a}\right)} \tag{2}$$

The Survival function of Kappa Distribution is given by

$$S(t) = 1 - F(t) = 1 - \frac{t}{\lambda}\left[a + \left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(\frac{1}{a}\right)} \tag{3}$$

Mathematically, the hazard function is expressed as $h(t) = \dfrac{f(t)}{S(t)}$

$$= \frac{\frac{a}{\lambda}\left[a + \left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(-\left(\frac{a+1}{a}\right)\right)}}{1 - \frac{t}{\lambda}\left[a + \left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(\frac{1}{a}\right)}} \tag{4}$$

These functions provide a useful mathematical description of the Kappa distribution, which is commonly used in reliability analysis and survival modelling. The distribution finds application in different fields including survival analysis, engineering and reliability.

3. Prior Distribution

In Bayesian analysis, it is crucial to incorporate prior knowledge of the problem by specifying a probability distribution function known as the prior distribution. This distribution encapsulates the existing information regarding the parameter before analysing the experimental data. There are various types of prior distributions, each serving a specific purpose in subsequent Bayesian reliability models. The selection of a suitable prior distribution depends upon the nature and availability of prior information. In this context, the present study discusses different prior distributions used in Bayesian reliability models, emphasizing their applications and implications. By incorporating prior knowledge, the Bayesian approach allows for a more informative and accurate analysis of the experimental data.

3.0 Weakly Informative Priors (WIPs)

WIP are prior distributions used in Bayesian statistics to balance prior information and the influence of observed data on the posterior distribution. Their purpose is to prevent outcomes that contradict existing knowledge while avoiding the use of non-existent information.

WIP [4], commonly used as an estimate for mean and measurement, is a distribution with a mean of 0 and a variance of 10,000, which means standard deviation of 100 or an accuracy of 1.0 x 10^-4.

$$\theta \sim N(0,10000)$$

Weakly informative priors are broad enough to allow for a wide range of plausible parameter values and are typically chosen based on expert knowledge or previous research. The use of weakly informative priors has become increasingly popular in Bayesian statistics as a way to incorporate prior knowledge without overly influencing the posterior distribution. By using weakly informative priors, researchers can ensure that their results are not driven solely by the prior distribution, but rather a combination of prior knowledge and the observed data.

3.1 The half-Cauchy Priors distributions

The half-Cauchy distribution is a commonly used weakly informative prior in Bayesian statistics. It belongs to the Cauchy distribution family, which has heavy tails and is considered a non-informative prior because it allows for a wide range of plausible values. The half-Cauchy distribution has a truncated version of the Cauchy distribution, where it only takes on non-negative values. Its pdf is

$$f(x) = \frac{2\alpha}{\pi(x^2 + \alpha^2)}, \qquad x > 0, \alpha > 0.$$

Where x is the random variable, α is the scale parameter, and $f(x)$ is probability density function. The half-Cauchy distribution is commonly employed as a prior distribution for variance parameters in normal distribution models, primarily because it allows for the inclusion of large values. It has a mode of 0, while the mean and variance are undefined. However, when it comes to non-informative priors for scale parameters, the scale parameter of 25 is often suggested for the half-Cauchy distribution. It provides sufficient information for numerical approximation algorithms to explore the posterior distribution. This is particularly advantageous as the inverse-gamma, another non-informative prior for scale parameters, poses challenges for parameters close to zero. In summary, the half-Cauchy distribution is a valuable tool for incorporating weak prior information in Bayesian analysis.

4. Laplace Approximation

In Bayesian statistics, the Laplace approximation is a statistical technique utilized to approximate the posterior distribution of a parameter. This method approximates the moments and marginal densities of the unimodal posterior by fitting a normal distribution. It is applicable when the posterior distribution is smooth and unimodal. The approach involves determining The Laplace approximation estimates the mode of the posterior distribution and approximates its neighborhood by employing a second-order Taylor expansion. This approximation yields a normal distribution with the mean equal to the mode and the variance equal to the inverse of the curvature of the log-posterior at the mode. The Laplace approximation is commonly utilized when calculating the posterior distribution is challenging or when dealing with a high number of parameters. It is particularly beneficial for peaked posterior distributions or when the sample size is large. It is essential to note that the Laplace approximation assumes a symmetric and unimodal posterior distribution. Accuracy may be compromised if the posterior is not unimodal or skewed. In such cases, alternative methods like the Markov chain Monte Carlo, such as the one proposed by [13], might be more suitable.

Let's consider $-h(\theta)$ is a smooth, bounded unimodal function, this function has a maximum at $\hat{\theta}$, where θ is a scalar. By utilizing Laplace method, In the work of [9], they specifically discuss the evaluation of the integral.

$$I = \int f(\theta)\exp[-nh(\theta)]d\theta$$

can be approximated by

$$\hat{I} = f(\hat{\theta})\sqrt{\frac{2\pi}{n}}\sigma \exp[-nh(\hat{\theta})],$$

where

$$\sigma = \left[\frac{\partial^2 h}{\partial \theta^2}\Big|_{\hat{\theta}}\right]^{-1/2}.$$

As presented in Wallace and Mosteller (1964), Laplace method is to expand about $\hat{\theta}$ to obtain:

$$I \approx \int f(\hat{\theta})\exp\left(-n\left[h(\hat{\theta}) + (\theta-\hat{\theta})h'(\hat{\theta}) + \frac{(\theta-\hat{\theta})^2}{2}h''(\hat{\theta})\right]\right)d\theta.$$

Recalling that $h'(\hat{\theta}) = 0$,

we have

$$I \approx \int f(\hat{\theta})\exp\left[-n\left(h(\hat{\theta}) + \frac{(\theta-\hat{\theta})^2}{2}h''(\hat{\theta})\right)\right]d\theta$$

$$= f(\hat{\theta})\exp[-nh(\hat{\theta})]\int \exp\left(\frac{-n(\theta-\hat{\theta})^2}{2\sigma^2}\right)d\theta$$

$$= f(\hat{\theta})\sqrt{\frac{2\pi}{n}}\sigma \exp[-nh(\hat{\theta})].$$

if exp $[-nh(\theta)]$ is very peaked about $\hat{\theta}$, then the integral can be well approximated by the behavior of the integrand near $\hat{\theta}$. More formally, it can be shown that

$$I = \hat{I}\left[1 + O\left(\frac{1}{n}\right)\right].$$

To compute moments of posterior distributions, it is necessary to evaluate expressions such as:

$$\mathrm{E}[g(\theta)] = \frac{\int g(\theta)\exp[-nh(\theta)]d\theta}{\int \exp[-nh(\theta)]d\theta},$$

where $\exp[-nh(\theta)] = L(\theta|y)p(\theta)$.

5. Bayesian Analysis of Kappa Model

For more than a century, the kappa distribution family has captured the interest of numerous researchers in various fields, particularly in reliability and survival analysis. The Kappa distribution is recognized as a flexible and reliable model for analyzing lifetime data.

Its successful application has been observed in a wide range of fields, including medicine, engineering, and economics.

5.1. Code in R for Random Number Generation

```
rkappa <- function(n,a,lambda){
   u <- runif(n)
   x <- lambda*((u^(-a)-1)/a)^-(1/a)
return(x)
}
```

5.2. Likelihood Function of Kappa Model with Censoring

To construct a kappa regression model, for right-censored data, we can formulate the likelihood function of the Kappa model to account for the specific censoring mechanism.

$$L = \prod_{i=1}^{n} [f(t_i)]^{\delta_i}\,[S(t_i)]^{1-\delta_i},$$

where x_i is the observed time, δ_i is a pointer variable that takes a value of 1 if x_i is observed and 0 if it is right-censored

$$L = \prod_{i=1}^{n}\left[\frac{a}{\lambda}\left[a + \left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(-\left(\frac{a+1}{a}\right)\right)}\right]^{\delta_i}\left[1 - \frac{t}{\lambda}\left[a + \left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(\frac{1}{a}\right)}\right]^{1-\delta_i},$$

In Bayesian analysis, in order to proceed with the analysis, it is necessary to select suitable prior distributions for the regression coefficients. β_s as well as the shape parameter a. The choice of prior is often problem-specific and requires careful consideration. For example, we can use normal priors with mean 0 and large variance 10000 and a half-Cauchy prior with scale = 25.

According to Bayes' theorem, $Psoterior \propto Likelihood \times Prior$

$$p(\beta, a \mid t, X) \propto L(t, X \mid \beta, a) \times p(\beta) \times p(a)$$

Where $L(t, X|\beta, a)$ is the likelihood function, and $p(\beta)$, and $p(a)$ are the prior distributions for model of $Kappa(a, \lambda$ respectively.

$$p(\beta,a\,|\,t,X)\propto\prod_{i=1}^{n}\left[\frac{a}{\lambda}\left[a+\left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(-\left(\frac{a+1}{a}\right)\right)}\right]^{\delta_i}\times\left[1-\frac{t}{\lambda}\left[a+\left(\frac{t}{\lambda}\right)^{a}\right]^{-\left(\frac{1}{a}\right)}\right]^{1-\delta_i}$$

$$\times\prod_{j=1}^{J}\frac{1}{\sqrt{2\pi\times10^3}}\exp\left(-\frac{1}{2}\frac{\beta_j^2}{10^3}\right)\times\frac{2\times25}{\pi(a^2+25^2)}.$$

Closed-form solutions are not accessible for obtaining the posterior densities of Kappa (a,λ). However; these densities can be obtained through numerical integration or Markov chain Monte Carlo (MCMC) methods.

6. Description of Data: Prognosis for women with Breast cancer Data

Breast cancer is a commonly occurring type of cancer among women in Western countries. A research study was conducted to investigate a specific histochemical marker called Helix pomatia agglutinin (HPA), which can differentiate between primary breast cancer with metastasis and without. HPA is obtained from the albumin gland of the Helix pomatia, also known as the Roman snail. It functions by binding to breast cancer cells that are linked to the spread of the disease to nearby lymph nodes. enables their identification under microscopic examination.

In the provided data set, which is taken from "Modelling survival data in medical research [3]", referred to as In Table 1, the study focuses on the survival times of women who underwent either a simple or radical mastectomy for Grade II, III, or IV tumours during the period from January 1969 to December 1971. The table classifies the survival times into different categories based on the presence or absence of positive staining for the tumor.

* Indicate the Censored survival times.

Table 1: Survival durations of women with tumours categorized as negative or positive for HPA staining

Staining Status	**Survival Times**
Negatively Stained	23, 47, 69, 70*, 71*, 100*, 101, 148, 181, 198*, 208*, 212*, 224*, 61, 225*
Positively Stained	5, 8, 10*, 13, 18, 24, 26, 26, 31, 35, 40, 41, 48, 50, 59, 68, 71, 76*, 105*, 107*, 109*, 113, 116*, 118, 143, 154*, 162*, 188*, 212*, 217*

7. Model Implementation

7.1.0 Analysis using LaplacesDemon

The LaplacesDemon package offers a Bayesian Kappa distribution model, which involves a series of steps including data creation, model specification, and fitting to survival data using the LaplacesDemon and Laplace Approximation functions. This package provides R code implementation for all these functions.

7.1.1 Fitting with LaplaceApproximation

The LaplacesDemon package encompasses various functionalities, such as model specification, data creation, and initial value setup, to facilitate model fitting.

7.1.2 Model Specification

To utilize the LaplaceApproximation function, a Bayesian model must be specified with a specified likelihood and prior, as demonstrated by [14].

$$y\sim kappa(a,\lambda),$$

and log link function is used

$$\log(\lambda)=X\beta,$$

$$\lambda=\exp(X\beta),$$

where a is shape parameter, λ is scale parameter The logarithm of $\lambda$is expressed as the inner product of the design matrix $X$and the transpose of the parameter vector β.

Priors for β and a are specified as:

$$\beta_j \sim N(0{,}1000), \qquad j = 1, \dots, J,$$

$$a \sim HC(25)$$

In the analysis conducted by [17], a large variance or small precision in the prior distribution indicates a substantial degree of uncertainty associated with each observation. This choice of prior is considered weakly informative. Additionally, the half-Cauchy distribution is utilized as a weakly informative prior in the analysis.

Consequently, the complete code for the regression analysis of the Bayesian model is presented below.

```
Model <- function(parm,Data) {

#Parameters

beta <- parm[Data$pos.beta]

a <- exp(parm[Data$pos.a])

# Log(Prior Densities)

beta.prior <- sum(dnormv(beta,0,1000,log=TRUE))

a.prior <- dhalfcauchy(a, 25, log=TRUE)

# Log-likelihood

Mu <- tcrossprod(beta, Data$X)

Lambda <- exp(mu)

F <- a/lambda*(a+(y/lambda)^a)^(-((a+1)/a))

S <- 1-y/lambda*(a+(y/lambda)^a)^(-(1/a))

LL <- censor*log(f)+(1-censor)*log(s)

LL <- sum(LL)

LP <- LL + beta.prior + a.prior

Modelout<-list(LP=LP,Dev= *LL,Monitor=c(LP,a),yhat=rkappa(length(y),a,lambda),parm=parm)

return(Modelout)

}
```

The "Model" function has two arguments - "parm" and "Data." "Parm" represents the set of parameters, while "Data" represents the list of data. The function has two parameters - "beta" and "alpha" - which have priors "beta.prior" and "alpha.prior," respectively. The "LL" object represents the log-likelihood, while the "LP" object represents the log-posterior. The "Model" function returns the "Modelout" object, and several objects listed in order: log-posterior ="LP," deviance = "Dev," monitor parameter "Monitor," fitted values "yhat,", parameter estimates "parm."

7.1.3 Data Creation

To generate the data, we require a model matrix X, the number of predictors Y, parameter naming, details on censoring, and information about the response variable.

```
 library(LaplacesDemon)

# Survival times

y <- c( 23, 47, 69,... ......., 212, 217, 225)

# Binary covariate

x1 <- c(rep(0, 13), rep(1, 32))

# Censoring indicator (1 = observed, 0 = censored)

censor <- c(1, 1, 1, rep(0,4), 1, 1, rep(0,4),rep(1, 18),      rep(0,4), 1, 0, 1, 1, rep(0, 6))
```

```
# Design matrix with intercept

X <- cbind(intercept = 1, x1 = x1)

# Number of regression parameters

J <- ncol(X)

mon.names <- c("LP","a")

parm.names <- as.parm.names(list(beta=rep(0,J),log.a=0))

pos.beta <- grep("beta",parm.names)

pos.a <- grep("log.a",parm.names)

MyData<-
list(J=J,X=X,mon.names=mon.names,parm.names=parm.names,pos.beta=pos.beta,pos.a=pos.a,y=y,censor=censor)
```

The job that we need to do is to define the parameters: beta and alpha, which are to be inserted as vector elements in the list parms.names. There is also the addition of the logposterior LP to the mon.names vector as a monitor. The total number of observations that we have now is 40, and that is denoted by N. We also have censorship, which is indicated by 0 for the censored observations and 1 for the uncensored observations. In a nutshell, these are put into a list called MyData.

7.1.4 Initial Values

When using the Laplace Approximation function, it is necessary to supply a parameter vector containing initial values. Each value acts as a starting point for estimating a specific parameter. In this case, all beta parameters are set to zero, and the alpha parameter is set to zero, which corresponds to log(1). An important thing is that the order in the vector has to reflect the order of appearance of the parameters. Thus, we need to create a vector of starting values as follows.

```
Initial.Values <- c(rep(0, J), log(1))
```

7.1.5 Fitting with Laplace Approximation

To utilize the LaplaceApproximation function, a Bayesian model must be specified with a specified likelihood and prior, as demonstrated by [14].

```
FitKappa <- LaplaceApproximation( Model, Initial.Values, Data = MyData, Method = "TR", Iterations=10000)

# To print the fitted object

Print (FitKappa)
```

7.1.6 Summarizing Output

The function LaplaceApproximation is used to estimate the posterior density of the fitted model, and the outcomes are displayed in two tables. The analytical posterior estimates obtained using Laplace Approximation are summarized in Table 2 and Simulation-based posterior results using the SIR algorithm are presented in Table 3.

Table 2: Asymptotic approximation of Kappa regression parameters obtained using the Laplace Approximation method. Mode indicates for the posterior mode, SD (standard deviation), and LB and UB for 95% credible interval limits.

Parameter	Mode	SD	LB	UB
beta [1]	5.5938414	0.5013726	4.5910963	6.59658652
beta [2]	-1.1870951	0.5833378	-2.3537706	-0.02041956
log. a	0.1849926	0.2952361	-0.4054797	0.77546481

Table 2 represents the results obtained through the LaplaceApproximation function. In Table 2, the regression coefficient β_2 is -1.18, which implies that the exponential value of -1.18 is 3.25. This means that a woman whose tumor is positively stained has 3.25 times the risk of death of a woman whose tumor is negatively stained.

Table 3: Posterior Summary of parameters obtained using the Sampling Importance Resampling (SIR) algorithm based on the Laplace Approximation. MCSE refers to Monte Carlo standard error, and ESS refers to effective sample size.

Parameter	Mode	SD	MCSE	ESS	LB	Median	UB
beta [1]	5.674	0.457	0.014	1000	4.826	5.643	6.746
beta [2]	-1.091	0.702	0.022	1000	-2.501	-1.116	-0.067
log a	0.066	0.295	0.009	1000	-0.346	0.062	0.647

Deviance	315.742	4.504	0.142	1000	311.537	313.942	325.307
LP	-170.31	2.251	0.071	1000	-175.086	-169.408	-168.203
a	1.117	0.345	0.011	1000	0.707	1.064	1.911

The figure 1 indicates that β_1 has a strong and statistically significant influence, with its estimate centered around 6 and the entire uncertainty range above zero. Conversely, β_2 shows a negative effect, with an estimate near –2 and an uncertainty range well below zero, confirming statistical significance once again. This suggests that while β_1 has a positive impact on the outcome, β_2 has a negative one, and both effects are noteworthy and not the product of chance.

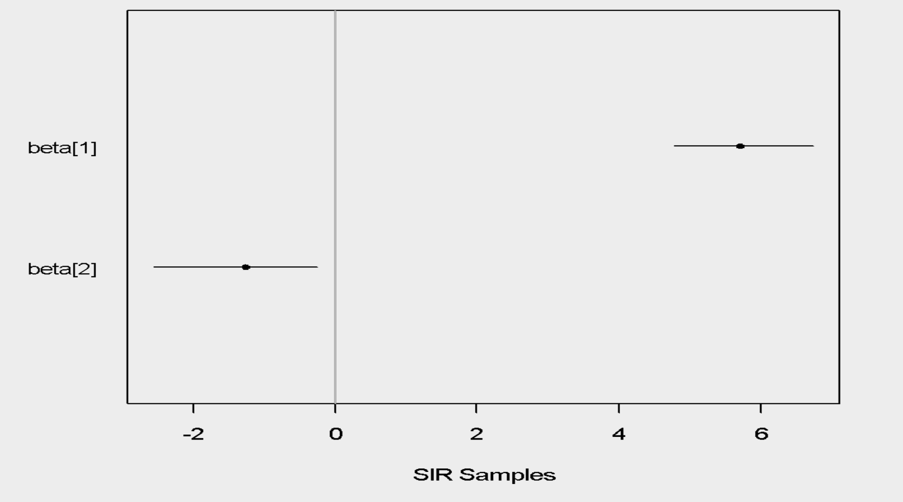

Fig. 1: A caterpillar plot displaying the 95% posterior credible intervals for the regression parameters of the Bayesian Kappa Model identified using the method of Laplace Approximation**.**

7.1.7 Graphical Representation of Posterior Estimates

Caterpillar plots are frequently employed in Bayesian inference to summarize the quantiles of posterior samples. These plots present three quantiles of selected distributions in a horizontal manner. They are particularly useful for visualizing posterior samples of parameters and monitored variables. In a caterpillar plot, the lines representing the following quantiles are displayed for each parameter: 0.025 and 0.975, In the context of estimating unimodal 95% Highest Posterior Density (HPD) intervals for a generic matrix, the plot typically includes a vertical gray line at zero. The median is denoted by a black dot, and the quantile line is also depicted in black. These visual elements help represent the distribution and uncertainty of the estimated intervals. The line begins at the 0.025 quantile and concludes at the 0.975 quantile. By referring to Figure 1, we can observe that for the variable β_1, the 0.025 and 0.975 quantiles are 4.83 and 6.75, respectively. For β_2, the quantiles are -2.50 and -0.07. These horizontal lines, representing the quantiles of the variables, do not cross the line at zero.

As a result, we can conclude that only β_1 and β_2 are statistically significant.

7.2.0 Fitting with LaplacesDemon

To utilize Laplace's Demon, an initial parameter value vector is required for either adaptive chains or non-adaptive Markov chains. If all values are set to zero, Laplace's Demon will optimize them using the LaplaceApproximation function with a resilient backpropagation algorithm. For obtaining initial values from Laplace Approximation, it is recommended to use the Fit object as an input to the as.initial.values function. Another option is to generate initial values randomly using the GIV function. Therefore, to obtain the initial value vector, the as.initial.values function is employed

FitKappald <- LaplacesDemon(Model, Data = MyData, Initial.Values,

Covar= FitKappa$Covar, Iterations=5000, Status=100, Thinning=10, Algorithm="IM", Specs=list(mu=FitKappa$Summary1[1:length(Initial.Values),1]))

FitKappald

7.2.1 Summarizing Output

The regression model was analyzed using the LaplacesDemon function, which employs the Independent Metropolis algorithm to simulate data from the posterior density. The MCMC-based posterior summaries are shown in Table 4.

Table 4: Posterior summaries obtained from MCMC simulation using the LaplacesDemon function with the IM algorithm.

Parameter	**Mean**	**SD**	**MCSE**	**ESS**	**LB**	**Median**	**UB**
beta [1]	5.622	0.290	0.012	500	5.046	5.617	6.201
beta [2]	-1.215	0.335	0.016	500	-1.840	-1.227	-0.583
log a	0.176	0.172	0.009	500	-0.141	0.178	0.492
Deviance	312.307	0.840	0.042	500	311.380	312.091	314.478
LP	-168.588	0.420	0.021	500	-169.678	-168.481	-168.125
a	1.211	0.209	0.011	500	0.869	1.195	1.635

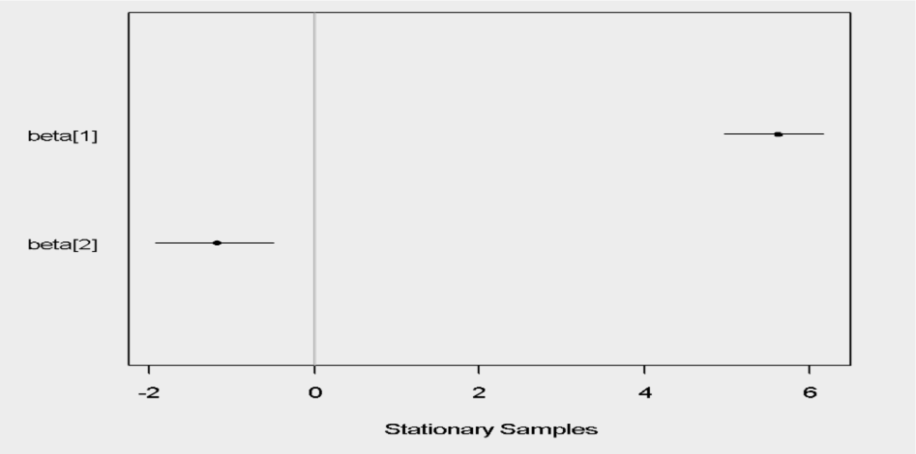

Fig. 2: Caterpillar plot of posterior credible intervals obtained from MCMC simulation using the LaplacesDemon algorithm.

8. Conclusion

This study, the Kappa model is applied as a survival model using a Bayesian approach. The two most important techniques asymptotic approximation and simulation method have been used to solve the high dimensional integration. The models are implemented through the packages R and LaplacesDemon. The LaplaceApproximation function is applied for optimization analytically, whereas LaplacesDemon function is applied for implementation of Markov chain Monte Carlo (MCMC) simulation, in Bayesian atmosphere. The results emphasize that simulation tools provide more precise results in terms of standard error compared to the results obtained through asymptotic approximation. Table 2 shows the results obtained through the LaplaceApproximation function, while Table 3 provides a summary of the simulated results using the Sampling Importance Resampling (SIR) algorithm. In Table 2, the regression coefficient β_2 is -1.18, which implies that the exponential value of -1.18 is 3.25. This indicates that a woman with a positively stained tumor has a 3.25 times higher risk of mortality compared to a woman with a negatively stained tumor. The interpretation of β_2 can be similarly derived from Table 3 and Table 4. Parameter uncertainty is visualized using caterpillar plots in Figure 1 and Figure 2.

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Conflicts of Interest Statement

The authors declare that there is no conflict of interest regarding the publication of this article.

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