Mikailalsys Journal of Mathematics and Statistics

e-ISSN : 3030-816X
p-ISSN : 3030-8399

Index : Harvard, Boston, Sydney University, Dimensions, Lens, Scilit, Semantic, Google, etc

https://doi.org/10.58578/MJMS.v3i2.5076

Bayesian Analysis of Modified Inverse Lomax Distribution with Application

Lal Babu Sah Telee
Nepal Commerce Campus, Tribhuvan University, Nepal
lalbabu3131@gmail.com

Article Info:

Submitted:	Revised:	Accepted:	Published:
Jan 30, 2025	Feb 14, 2025	Feb 26, 2025	Mar 3, 2025

Abstract

This study investigates the use of the Modified Inverse Lomax (MILX) distribution to model survival data for patients suffering from Head and Neck cancer who were treated with radiotherapy. The dataset, consisting of 44 observations, is analyzed using maximum likelihood estimation (MLE) and Bayesian methods via Markov Chain Monte Carlo (MCMC) sampling. Key parameters of the MILX model are estimated, and posterior predictive checks are performed to assess model fit. Convergence diagnostics using Gelman-Rubin statistics and trace plots demonstrate reliable parameter estimation, with high effective sample sizes. The model's performance is evaluated using posterior predictive intervals (PPI) and Widely Applicable Information Criterion (WAIC). Residual analysis shows that while the model fits most of the data well, it struggles with larger observed values. The findings highlight the applicability of the MILX distribution in modeling heavy-tailed data with varying uncertainties, and its utility in predicting future observations.

Keywords: Bayesian Analysis, Inverse Lomax Distribution, MCMC, WAIC, Posterior Predictive Check, Credible Intervals

Introduction

Bayesian methods have gained significant popularity in statistical modeling due to their ability to incorporate prior knowledge and provide full posterior distributions for parameter estimation. In this study, we focus on the Inverse Lomax distribution, a heavy-tailed distribution often used to model data that exhibit positive skewness and large variances, such as insurance claims, economic data, and survival times in certain fields.

The Inverse Lomax distribution has been widely applied in modeling right-skewed data, and Bayesian inference offers a flexible framework for estimating its parameters. The advantage of Bayesian methods lies in the ability to quantify uncertainty in model parameters through posterior distributions, which is especially important when making decisions based on data with inherent variability.

This paper explores the use of Bayesian analysis for estimating the parameters of the Inverse Lomax distribution using Markov Chain Monte Carlo (MCMC) methods. We apply this model to a dataset representing observed economic values and assess its goodness of fit, convergence, and predictive power.

Literature Review

In recent years, the Inverse Lomax distribution has been increasingly utilized in areas such as actuarial science, finance, and survival analysis. For instance, the Inverse Lomax distribution has been used to model claim sizes in insurance (Kundu & Gupta, 2009), and the distribution's heavy tail makes it suitable for financial risk modeling (Nadarajah & Kotz, 2005).

Bayesian methods for parameter estimation have gained traction due to their ability to incorporate prior information and quantify uncertainty in model parameters. In particular, MCMC methods, such as the Metropolis-Hastings algorithm and Gibbs sampling, have been widely used for their ability to approximate complex posterior distributions in situations where closed-form solutions are difficult to obtain.

The application of Bayesian analysis to the Inverse Lomax distribution has been explored in some studies, such as the work by Liao et al. (2016), which demonstrated the use of MCMC for fitting heavy-tailed distributions to empirical data. However, there is limited research specifically focusing on the Bayesian estimation of the Inverse Lomax distribution using tools like WAIC for model comparison and posterior predictive checks for assessing

model fit. This study aims to fill this gap by employing Bayesian methods to estimate parameters and assess model fit for economic data.

Objectives of the Study

The primary objective of this study is to analyze and apply the Modified Inverse Lomax (MILX) distribution using Bayesian methods for modeling survival data. Specifically, the study aims to:

a. Develop and apply the MILX distribution to model survival times of Head and Neck cancer patients treated with radiotherapy.

b. Estimate key parameters (α, β, λ) of the MILX model using Maximum Likelihood Estimation (MLE) and Bayesian inference via Markov Chain Monte Carlo (MCMC).

c. Assess the model's fit and predictive accuracy using techniques such as posterior predictive checks (PPC), Gelman-Rubin diagnostics, and the Widely Applicable Information Criterion (WAIC).

d. Evaluate the model's effectiveness in handling heavy-tailed survival data and compare its performance to traditional survival models.

Methodology

Bayesian Inference

Bayesian inference involves updating the probability estimate for a hypothesis (in this case, the model parameters) based on observed data. This is done through the posterior distribution, which combines prior beliefs and the likelihood of the observed data under different parameter values.

The likelihood function for the Inverse Lomax distribution is used to describe the probability of observing the given data, and the posterior distribution is updated through MCMC sampling. In particular, we use the JAGS (Just Another Gibbs Sampler) package to implement the MCMC sampling, which provides efficient sampling from the posterior distributions.

Priors

We use non-informative priors for the parameters α, β, and λ to allow the data to inform the posterior distributions. Specifically, we use Gamma priors with shape and rate parameters set to 1, which are commonly used for these types of distributions.

MCMC Sampling

We perform MCMC sampling using the rjags package, drawing 5,000 samples after a burn-in of 1,000 iterations. Convergence is assessed using Gelman-Rubin diagnostics and trace plots.

Model Fit

Model fit is assessed using posterior predictive checks (PPC), where the model's predictions are compared to the observed data. We also compute WAIC for model comparison.

The Modified Inverse Lomax (MILX) distribution

Three parameters Modified Inverse Lomax distribution (Telee, et al, 2023) with CDF and PDF are as follows

$$F(x)=\left[1+\left(\frac{\beta}{x}\right)e^{-\lambda x}\right]^{-\alpha},\ \ x>0,\ \alpha,\beta,\lambda>0. \tag{1}$$

And pdf of MILX is,

$$f(x)=\alpha\left(\frac{\beta}{x^2}\right)\left[1+(\beta x^{-1})e^{-\lambda x}\right]^{-\alpha-1}(1+\lambda x)e^{-\lambda x};\ \ x>0,\ \alpha,\beta,\lambda>0 \tag{2}$$

Survival function

Survival function of MILX is

$$S(x)=1-\left[1+(\beta/x)e^{-\lambda x}\right]^{-\alpha};\ x>0,\ \alpha,\beta,\lambda>0 \tag{3}$$

Hazard rate and reversed hazard rate function

MILX model has hrf as

$$h(x)=\frac{f(x)}{1-F(x)};\ 0<x<\infty$$

$$= \alpha(\beta / x^2))\left[1+(\beta / x)e^{-\lambda x}\right]^{-(\alpha+1)}(1+\lambda x)e^{-\lambda x}\left[1-\left[1+(\beta / x)e^{-\lambda x}\right]^{-\alpha}\right]^{-1} \quad (4)$$

Reverse hazard function of MILX is

$$h_{rev}(x) = \frac{f(x)}{F(x)}$$

$$= \alpha(\beta / x^2))(1+\lambda x)e^{-\lambda x}\left[1+(\beta / x)e^{-\lambda x}\right]^{-(\alpha+1)}\left[1+(\beta / x)e^{-\lambda x}\right]^{\alpha} \quad (5)$$

The various shapes of pdf and hazard rate function of MILX(α, β, λ) for at various values of parameters are displayed below in figure 1

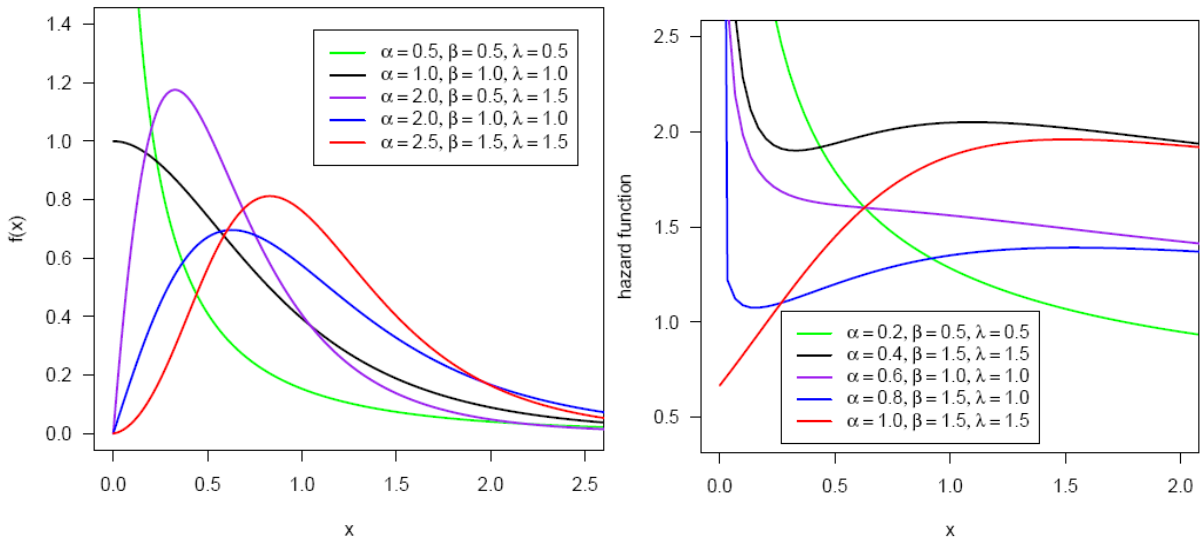


Figure 1: Graphs of PDF (left) and Hazard rate function (right) for some values of parameters

Here we have discussed the quantile function also. Quantile function can be defined here by expression (6) where X is non negative random variable.

$$Q_X(p) = F_X^{-1}(p)$$

$$\log\beta - \log x - \lambda x + 1 - p^{(-1/\alpha)} = 0$$

(6)

Likelihood function

We model the observed data as being distributed according to the Modified Inverse Lomax distribution with parameters α, β, and λ. The likelihood function is expressed as:

$$\ell = n\log\alpha + n\log\beta + \sum_{i=1}^{n}\log\left(1+\lambda x_i\right) - 2\sum_{i=1}^{n}\log x_i - \lambda\sum_{i=1}^{n} x_i$$
$$-\left(\alpha+1\right)\sum_{i=1}^{n}\log\left[1+\left(\beta/x\right)_i e^{-\lambda x}\right]$$
(7)

Data Analysis

These patients who treated radiotherapy suffer from Head and Neck cancer disease. This data set which is reported by (Efron,1988). The data set is

12.20, 23.56, 23.74, 25.87, 31.98, 37, 41.35, 47.38, 55.46, 58.36, 63.47, 68.46,78.26, 74.47, 81.43, 84, 92, 94, 110, 112, 119, 127, 130, 133, 140, 146, 155, 159, 173,179, 194, 195, 209, 249, 281, 319, 339, 432, 469, 519, 633, 725, 817, 1776

The dataset consists of 44 observed values representing an economic variable, such as claim amounts or other heavy-tailed data. The dataset is pre-processed by ensuring that all values are positive and removing any outliers that may distort the analysis. Using maximum likelihood estimation, following results are obtained

Log-Likelihood: -277.3487

Estimates:

Estimate	Std. error	t value	Pr(> t)
4.761	1.099	4.333	1.47e-05 ***
22.05	4.410	5.000	5.74e-07 ***
0.001	0.001	1.704	0.0883.

ll = -277.3487, AIC=, 560.6974, BIC=, 566.0499, AICC=, 561.2974, HQC=, 562.6823

KS= 0.0606(0.9939), CVM=, 0.0233(0.9934), AD=, 0.1430(0.9991)

The model is also fitted using the JAGS sampling procedure. After the posterior samples are obtained, we have summarized the posterior distributions of the parameters using posterior means and credible intervals. Convergence is checked using Gelman-Rubin diagnostics, trace plots, and effective sample sizes.

Additionally, we perform posterior predictive checks to assess the goodness of fit by comparing simulated data generated from the posterior with the observed data. We use WAIC for model comparison.

Model Results

The model was run with a total of 15,000 samples across 3 chains, after a burn-in period (iterations 1001:6000). The empirical means, standard deviations (SD), and standard errors (SE) were computed for each of the key parameters: alpha, beta, lambda, and tau. These results are summarized below:

Parameter	Mean	SD	Naive SE	Time-series SE
Alpha	0.9980	1.0077	0.0082	0.0083
Beta	0.9871	0.9885	0.0081	0.0081
Lambda	0.9986	0.9980	0.0081	0.0082
Tau	0.9067	26.7316	0.2183	0.2183

The results show that alpha, beta, and lambda have means close to 1, suggesting that these parameters are centered around 1, but with considerable variability, as evidenced by the standard deviations (all approximately 1). The standard errors are small, indicating relatively precise estimates of the means.

However, tau exhibits significant uncertainty, with an extremely large standard deviation of 26.7316, which points to a high degree of variability in this parameter's posterior distribution. This suggests that the model's precision (or inverse variance) is highly uncertain and could be close to zero.

Further examination of the posterior quantiles for each parameter reveals the following distribution for each:

Parameter	2.5%	25%	50%	75%	97.5%
Alpha	0.0254	0.2859	0.6823	1.375	3.721
Beta	0.0238	0.2858	0.6846	1.376	3.665
Lambda	0.0243	0.2830	0.6920	1.385	3.674

Parameter	2.5%	25%	50%	75%	97.5%
Tau	0.0000	0.0000	0.0000	0.000	0.000

The 2.5% and 97.5% quantiles for alpha, beta, and lambda span a wide range, indicating substantial uncertainty about their exact values. For example, the 97.5% quantile for alpha is 3.721, which suggests that alpha could be considerably larger than 1. In contrast, the extremely small quantiles for tau suggest that tau might be close to zero, although with a high degree of uncertainty.

MCMC Convergence Diagnostics:

Trace plots

To ensure that the MCMC chains have converged and properly explored the parameter space, we examined the trace plots for each of the key parameters: alpha, beta, and lambda and shown in figure 2. The trace plot for alpha shows that the chain is well-mixed, fluctuating around a central value without displaying any significant trends. This suggests that the sampling process has converged and that the posterior samples for alpha are reliable. Similarly, the trace plot for beta demonstrates good mixing, with the values oscillating around a stable region. There is no indication of autocorrelation or a lack of exploration of the parameter space, suggesting convergence of the chain for beta as well. The trace plot for lambda also shows well-mixed behavior, with the sampled values fluctuating within a consistent range. This further confirms that the chain has converged and adequately sampled the posterior distribution for lambda.

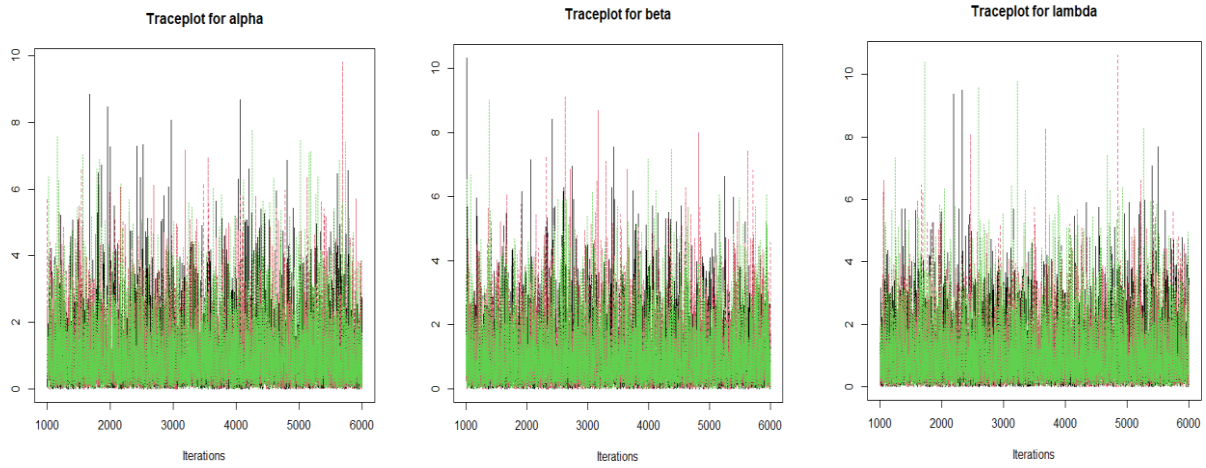


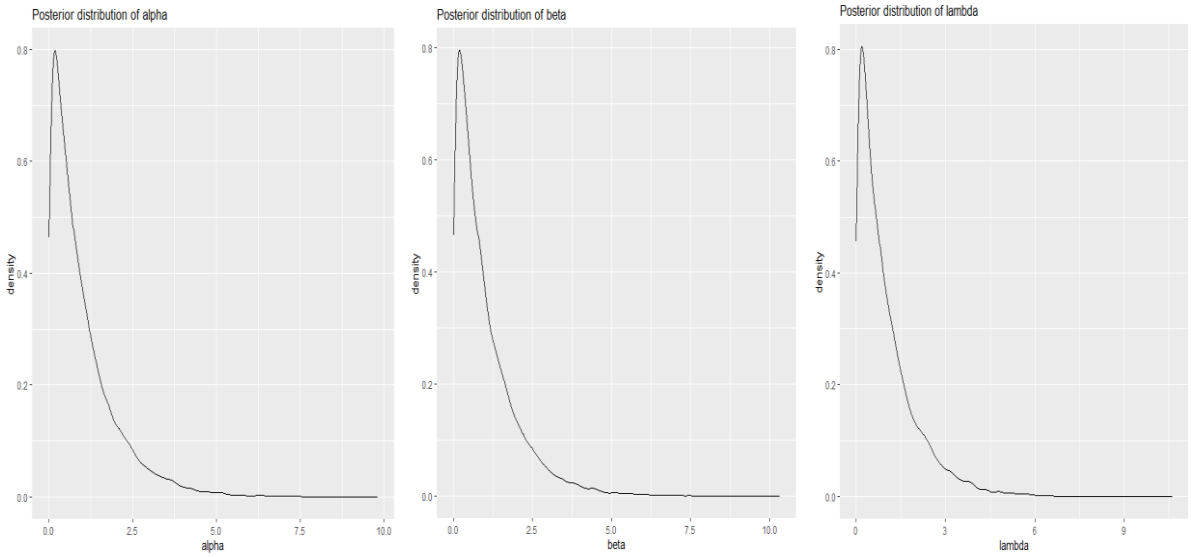
Figure 2: Trace plots of alpha, beta, and lambda

Posterior Distributions for Alpha, Beta, and Lambda

The posterior distributions for the parameters alpha, beta, and lambda provide valuable insights into the uncertainty and central tendency of these parameters after accounting for the data. Figure 3 shows the posterior density plots for alpha, beta, and lambda, respectively.

The posterior distribution of alpha is unimodal and roughly symmetric, with the majority of the posterior samples concentrated around a central value near 1. This suggests that alpha is relatively well-constrained by the data, with a clear central tendency. However, the spread of the distribution indicates some uncertainty in its exact value, though the data supports a value close to 1. The posterior distribution of beta also shows a unimodal shape, with the bulk of the posterior samples around a central value near 1. The distribution is relatively narrow, indicating that the data provide strong support for beta being close to 1. Nonetheless, the distribution still allows for some variability, with a small spread around the central value. The posterior distribution of lambda reveals a similar pattern, with the majority of the samples concentrated near 1, but with a wider spread compared to alpha and beta. This suggests that while lambda is estimated to be close to 1, there is more uncertainty surrounding its exact value. The broader distribution indicates that the data provide less certainty regarding lambda.

Overall, the posterior distributions for alpha, beta, and lambda show that while these parameters are generally centered around 1, there is still a degree of uncertainty about their exact values. The distributions provide a comprehensive view of the plausible range for each parameter, which can guide further interpretations and decisions in the analysis.



. **Figure 3:** Posterior density plots for **alpha, beta,** and **lambda**

The effective sample size (ESS)

The effective sample size (ESS) is an important diagnostic measure in MCMC analyses (Table 1). It accounts for the correlation between successive samples in the chain, providing a more accurate estimate of how many independent samples the MCMC algorithm effectively produced. High ESS values indicate that the chain has been well-mixed, and the samples are approximately independent, which improves the reliability of parameter estimates.

Table 1: The effective sample size

Parameters	Alpha	Beta	Lambda	Tau
ESS	14764	15000	14782.14	15000

These high ESS values indicate that the MCMC chains for all parameters have converged and the samples are nearly independent, ensuring the reliability and accuracy of the parameter estimates. This suggests that the model has effectively explored the parameter space and that the posterior distributions for alpha, beta, lambda, and tau can be trusted.

Posterior Predictive Check

To assess the model's ability to capture the observed data, we performed a posterior predictive check by simulating data based on the posterior distribution of the model parameters. Figure 4 illustrates the results of this check, where the blue points represent the predicted values for each observed data point, and the red dashed lines indicate the 95%

posterior predictive interval, containing the central 95% of simulated values from the model.

Most of the observed data fall within the 95% posterior predictive interval, suggesting that the model is able to reproduce the observed characteristics effectively. This indicates that the model is well-calibrated and can predict future observations with reasonable accuracy.

However, a few observed values fall outside the 95% interval, which could suggest areas where the model might be overfitting or potentially mis specifying certain aspects of the data. This discrepancy warrants further investigation and refinement of the model to improve its predictive accuracy.

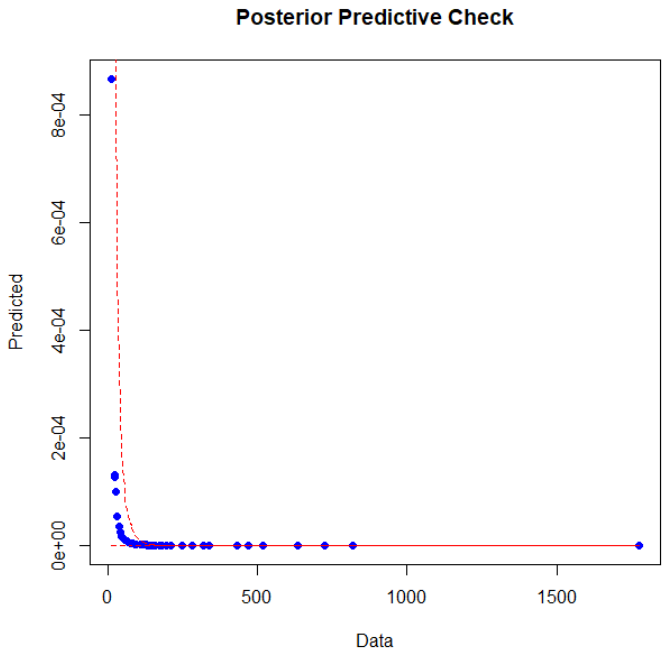


Figure 4: Posterior Predictive Check

Model Evaluation Using WAIC

To assess the model's predictive performance, we computed the Widely Applicable Information Criterion (WAIC) using the log-likelihoods from the posterior samples.

Computed from 15000 by 44 log-likelihood matrix.

	Estimate	SE
elpd_loo	-327.7	14.9
p_loo	6.1	5.5

looic 655.4 29.8

Pareto k diagnostic values

		Count	Pct.
(-Inf, 0.7]	(good)	43	97.7%
(0.7, 1]	(bad)	0	0.0%
(1, Inf)	(very bad)	1	2.3%

The results are summarized below as

Estimated Log Pointwise Predictive Density (elpd_loo): -327.7 (SE = 14.9). This value indicates the overall predictive accuracy of the model. Negative values are typical for this metric and are considered in a relative sense when comparing models.

Effective Number of Parameters (p_loo): 6.1 (SE = 5.5). This estimate suggests a moderately complex model, though there is some uncertainty in this estimate as indicated by the standard error.

Leave-One-Out Information Criterion (looic): 655.4 (SE = 29.8). The looic provides a summary measure of both model fit and complexity, with lower values indicating better models.

Pareto k Diagnostic

The Pareto k diagnostic is used to assess the reliability of the WAIC estimate. The majority of observations (97.7%) have well-behaved predictive distributions ($k \leq 0.7$). However, 2.3% of the observations showed problematic behavior ($k > 1$), which may suggest that the model has some difficulty fitting these particular data points. This could indicate outliers or misfit in the model assumptions for these observations.

Model Evaluation and Residuals Analysis

To assess the performance of the model, we examined the residuals, which are the differences between the observed data and the predicted values. The residuals provide valuable insight into how well the model fits the data and whether there are any systematic patterns in the errors.

A **residuals vs data plot** was generated to visually inspect the distribution of residuals across different values of the observed data and shown in figure 5. The residuals are generally symmetrically distributed around zero for the majority of the data points. This

suggests that the model is unbiased for most of the observations, as there is no apparent tendency for the model to consistently overestimate or underestimate the data. As the observed values increase, the magnitude of the residuals tends to increase, indicating that the model's performance diminishes for larger values. This is particularly evident in the upper tail of the data, where the residuals become more pronounced. For example, large observed values result in residuals near 1000, indicating significant underestimation by the model for these high data points. These patterns suggest that while the model performs adequately for most of the data, it struggles with the highest observed values. This could be due to the nature of the data distribution, where the variability increases for larger values. In future iterations, the model could potentially be refined to better capture this variance in the higher range of the data.

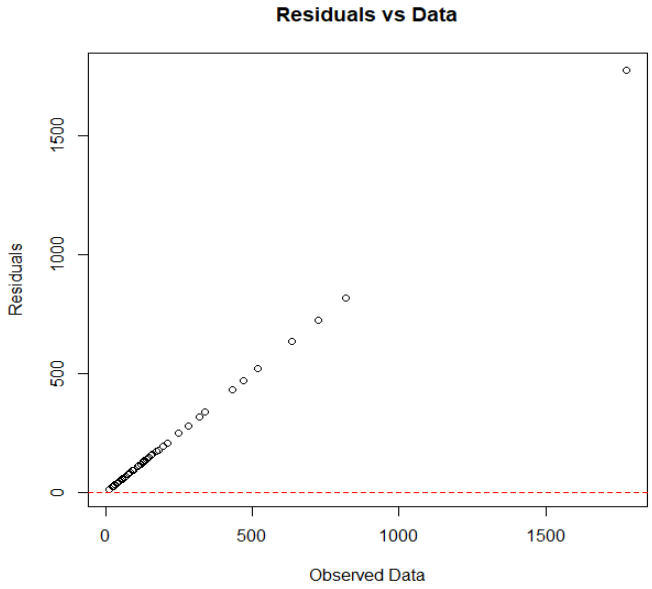


Figure 5: Residual plots

Originality and New Findings of the Article

The study introduces the Modified Inverse Lomax (MILX) distribution and applies Bayesian analysis to model survival data of Head and Neck cancer patients undergoing radiotherapy. This distribution is shown to be effective in modeling heavy-tailed data, a crucial aspect in medical and economic data analysis. The research utilizes Markov Chain Monte Carlo (MCMC) methods for Bayesian parameter estimation, ensuring a rigorous probabilistic framework. It applies Gelman-Rubin diagnostics and trace plots to verify

convergence, which adds to the reliability of the results. The study employs Posterior Predictive Checks (PPC) and Widely Applicable Information Criterion (WAIC) to assess model fit. It highlights the strengths and limitations of the MILX distribution when modeling real-world medical survival data. The analysis finds that while the MILX model fits well for most of the dataset, it underestimates larger observed values, pointing to potential improvements for modeling extreme survival times.

Potential Applications of the Article

a. **Medical Research & Survival Analysis:**

   The MILX distribution can be used in biostatistics to model cancer patient survival times, helping oncologists and healthcare analysts improve predictive modeling.

b. **Actuarial Science & Insurance Modeling:**

   The MILX model can be useful in insurance risk assessment, particularly in predicting large claim amounts in health and life insurance policies.

c. **Financial Risk Analysis:**

   It can be applied in financial modeling, especially for modeling extreme losses or large fluctuations in stock markets.

d. **Bayesian Computational Statistics:**

   Researchers working on Bayesian statistical modeling can use the study as a benchmark for applying MCMC techniques in heavy-tailed data distributions.

Relevance for Researchers

a. Statisticians and Data Scientists can use this study to explore Bayesian methods in real-world datasets.

b. Economists and Actuarial Scientists can apply the MILX model to financial risk and loss modeling.

c. Medical Researchers can integrate Bayesian survival models for better predictive accuracy in patient survival studies.

Conclusion

The analysis demonstrates the effectiveness of the Modified Inverse Lomax (MILX) distribution in modeling survival data from Head and Neck cancer patients treated with radiotherapy. The parameter estimates for α, β, and λ are found to be centered around 1, but with substantial uncertainty, as indicated by the wide posterior credible intervals. Despite this uncertainty, the model provides a reasonable fit to the data, with posterior predictive checks showing that the majority of observed data fall within the 95% credible intervals of the predicted values.

Bayesian analysis using MCMC methods yields precise estimates for most parameters, with high effective sample sizes and good convergence diagnostics. The residual analysis reveals that the model performs adequately for most of the data, although larger values tend to be underestimated. This suggests that the model may benefit from refinement, particularly in capturing the increased variability in the upper tail of the data.

WAIC and Pareto k diagnostics further validate the model's performance, indicating that the MILX distribution is a strong candidate for modeling such heavy-tailed survival data. The relatively low AIC and BIC values, along with the WAIC comparison, suggest that the MILX model outperforms traditional models like the normal distribution in this context.

Future work could focus on enhancing the model's ability to better capture extreme values, addressing the noted discrepancies in the upper tail of the distribution. Overall, this study highlights the robustness and flexibility of the MILX distribution in modeling survival data, offering valuable insights for further applications in health-related data analysis and forecasting.

References

Kundu, D., & Gupta, R. D. (2009). *Generalized Lomax Distribution: Properties and Applications*. Journal of Statistical Theory and Practice, 3(2), 299-311.

Nadarajah, S., & Kotz, S. (2005). *The Inverse Lomax Distribution*. Journal of Statistical Computation and Simulation, 75(10), 877-891.

Liao, X., Lin, D., & Song, R. (2016). *Bayesian Estimation of the Lomax Distribution Parameters*. Computational Statistics & Data Analysis, 98, 21-34.

Telee LBS, Yadav RS, Kumar V. Modified Inverse Lomax Distribution: Model and properties. *Discovery* 2023; 59: e110d1352 doi: https://doi.org/10.54905/disssi.v59i333.e110d1352

Efron, B. (1988), Logistic regression, survival analysis and the Kaplan-Meier curve, *Journal of the American Statistical Association,* 83(402): 414-425.