6-8-2021

JMASM 57: Bayesian Survival Analysis of Lomax Family Models with Stan (R)

Mohammed H. A. Abujarad
Aligarh Muslim University, m.jarad@gu.edu.ps

Athar Ali Khan
Aligarh Muslim University, atharkhan1962@gmail.com

Recommended Citation

JMASM 57: Bayesian Survival Analysis of Lomax Family Models with Stan (R)

Mohammed H. A. Abujarad
Aligarh Muslim University
Aligarh, India

Athar Ali Khan
Aligarh Muslim University
Aligarh, India

An attempt is made to fit three distributions, the Lomax, exponential Lomax, and Weibull Lomax to implement Bayesian methods to analyze Myeloma patients using Stan. This model is applied to a real survival censored data so that all the concepts and computations will be around the same data. A code was developed and improved to implement censored mechanism throughout using rstan. Furthermore, parallel simulation tools are also implemented with an extensive use of rstan.

Keywords: Lomax model, exponential Lomax model, Weibull Lomax model, posterior, simulation, RStan, Bayesian inference, R software, HMC

Introduction

Survival analysis is the study of survival times and of the factors that influence them. Types of studies with survival outcomes include clinical trials, time from birth until death. Survival analysis arises in many fields of study including medicine, biology, engineering, public health, epidemiology, and economics. An attempt is made in the current study to outline how a Bayesian approach proceeds to fit Lomax, exponential Lomax, and Weibull Lomax models for lifetime data using Stan. The tools and techniques used are in a Bayesian environment, which are implemented using the rstan package. Stan is a probabilistic programming language for specifying statistical models.

Bayesian inference is based on Bayes' rule which provides a rational method for updating our beliefs in the light of new information. Bayes' rule states that a posterior distribution is the combination of a prior and data information. It does not tell what beliefs should be, it tells how they should change after seeing new

information. The prior distribution is important in Bayesian inference since it influences the posterior.

When no information is available, we need to specify a prior which will not influence the posterior distribution. Such priors are called weakly-informative or non-informative, such as normal, gamma, and half-Cauchy; these types of priors will be used throughout the paper. The posterior distribution contains all the information needed for Bayesian inference and the objective is to calculate the numeric summaries of it via integration. In cases where the conjugate family is considered the posterior distribution is available in a closed form and so the required integrals are straightforward to evaluate. However, the posterior is usually of non-standard form and evaluation of integrals is difficult.

For evaluating such integrals various methods are available such as Laplace's method (see, for example, Carlin & Louis, 2009; Tierney et al., 1989) and numerical integration methods (Evans & Swartz, 1995). Simulation can also be used as an alternative technique. Simulation based on Markov chain Monte Carlo (MCMC) is used when it is not possible to sample θ directly from a posterior $p(\theta \mid y)$. For a wide class of problems, this is the easiest method to get reliable results (Gelman et al., 2004). Gibbs sampling, Hamiltonian Monte Carlo, and Metropolis-Hastings algorithm are the MCMC techniques which render difficult computational tasks quite feasible. A variant of MCMC techniques are performed such as independence Metropolis and Metropolis within Gibbs sampling. To make computation easier, software such as R, Stan (full Bayesian inference using the No-U-Turn sampler (NUTS), a variant of Hamiltonian Monte Carlo (HMC)) are used.

Analysis of Lomax Family of Distributions

Lomax Model

The Lomax model (Lomax, 1954) attracted the attention of researchers due to its applications in various branches of actuarial, medical, biological, engineering, lifetime, and reliability modeling. Atkinson and Harrison (1978) applied the Lomax distribution to income and wealth data. Myhre and Saunders (1982) applied the Lomax distribution in the right censored data. Abd-Elfattah et al. (2007) discussed the Bayesian and non-Bayesian estimation problem of sample size in the case of type-I censored samples. Based on a cumulative exposure model, the optimal times plans of changing stress level of simple stress for the Lomax distribution were determined by Hassan and Al-Ghamdi (2009). The optimal times of changing stress level for k-level step stress accelerated life tests based on adaptive type-II

3

progressive hybrid censoring with product's lifetime following the Lomax distribution have been investigated by Hassan et al. (2016).

The cumulative distribution function (cdf) F(y, α, λ), probability density function (pdf) f(y, α, λ), survival function S(y, α, λ), and hazard function h(y) of the Lomax distribution are given as

$$F\left(y,\alpha,\lambda\right)=1-\left(1+\frac{y}{\lambda}\right)^{-\alpha}; \quad \alpha,\lambda,y>0, \tag{1}$$

$$f\left(y,\alpha,\lambda\right)=\frac{\alpha}{\lambda}\left(1+\frac{y}{\lambda}\right)^{-(\alpha+1)}; \quad \alpha,\lambda,y>0, \tag{2}$$

$$S\left(y,\alpha,\lambda\right)=\left(1+\frac{y}{\lambda}\right)^{-\alpha}; \quad \alpha,\lambda,y>0, \tag{3}$$

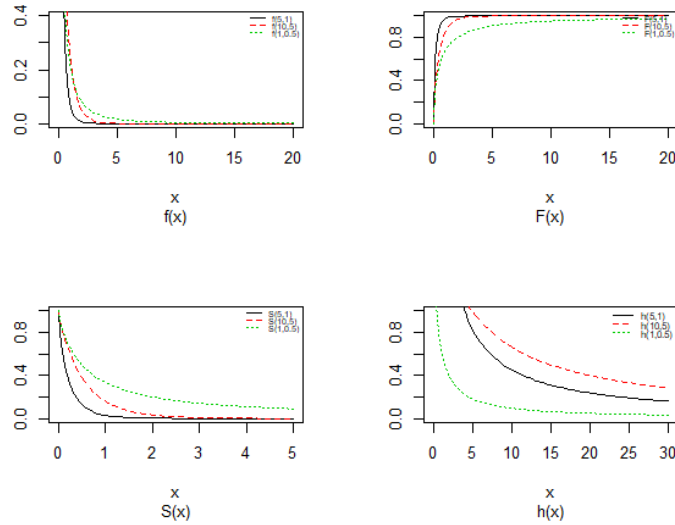$$h\left(y\right)=\frac{f\left(y\right)}{S\left(y\right)}. \tag{4}$$

Figure 1. Probability density plots, cdf, survival, and hazard curves of Lomax distribution for different values of shape and scale

The Exponential Lomax Model

The exponential and Lomax distributions are used widely. The cumulative distribution function (cdf) F(*y*, *v*, *α*, *λ*), probability density function (pdf) f(*y*, *v*, *α*, *λ*), survival function S(*y*, *v*, *α*, *λ*), and hazard function h(*y*) of the exponential Lomax model are given as

$$F\left(y, v, \alpha, \lambda\right) = \left[1 - \left(1 + \frac{y}{\lambda}\right)^{-\alpha}\right]^{v}; \quad \alpha, \lambda, v, y > 0, \tag{5}$$

$$f\left(y, v, \alpha, \lambda\right) = \frac{v\alpha}{\lambda}\left(1 + \frac{y}{\lambda}\right)^{-(\alpha+1)}\left[1 - \left(1 + \frac{y}{\lambda}\right)^{-\alpha}\right]^{v-1}; \quad \alpha, \lambda, v, y > 0, \tag{6}$$

$$S\left(y, v, \alpha, \lambda\right) = 1 - \left[1 - \left(1 + \frac{y}{\lambda}\right)^{-\alpha}\right]^{v}; \quad \alpha, \lambda, v, y > 0, \tag{7}$$
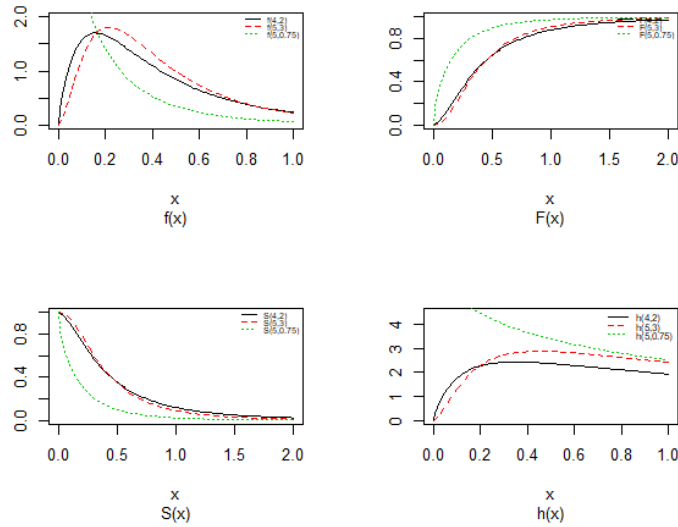

Figure 2. Probability density plots, cdf, survival, and hazard curves of exponential Lomax distribution for different values of shapes and at scale = 1

$$h(y) = \frac{f(y)}{S(y)}. \tag{8}$$

Taking $v = 1$ in equations (5), (6), and (7), we get equations (1), (2), and (3), respectively.

The Weibull Lomax Model

A random variable y with the Weibull Lomax distribution has four parameters: v, η, α, and λ. The cumulative distribution function (cdf) $F(y, v, \eta, \alpha, \lambda)$, probability density function (pdf) $f(y, v, \eta, \alpha, \lambda)$, survival function $S(y, v, \eta, \alpha, \lambda)$, and hazard function $h(y)$ of the Weibull Lomax model are given as

$$F(y, v, \eta, \alpha, \lambda) = 1 - \exp\left[-v\left(\left(1 + \frac{y}{\lambda}\right)^{-\alpha} - 1 \right) \right]^{\eta}; \quad \alpha, \lambda, v, \eta, y > 0, \tag{9}$$
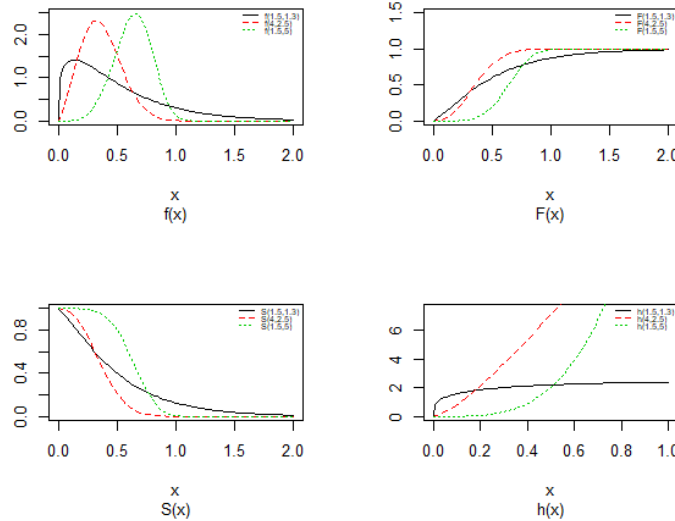

Figure 3. Probability density plots, cdf, survival, and hazard curves of Weibull Lomax distribution for different values and $\alpha = 0.75$, $\lambda = 0.5$

$$f(y,v,\eta,\alpha,\lambda) = \frac{v\eta\alpha}{\lambda}\left(1+\frac{y}{\lambda}\right)^{(\eta\alpha-1)}\left[1-\left(1+\frac{y}{\lambda}\right)^{-\alpha}\right]^{\eta-1}$$
$$\times\exp\left\{-v\left[\left(1+\frac{y}{\lambda}\right)^{\alpha}-1\right]^{\eta}\right\}; \quad \alpha,\lambda,v,\eta,y>0 \tag{10}$$

$$S(y,v,\eta,\alpha,\lambda) = \exp\left\{-v\left[\left(1+\frac{y}{\lambda}\right)^{\alpha}-1\right]^{\eta}\right\}; \quad \alpha,\lambda,v,\eta,y>0, \tag{11}$$

$$h(y) = \frac{f(y)}{S(y)}. \tag{12}$$

Bayesian Inference

Some preliminary considerations:

- Prior distribution p(θ): The parameter θ can set a prior distribution that uses probability as a means of quantifying uncertainty about θ before taking the data into account.
- Likelihood p($y \mid \theta$): A likelihood function for variables related in the full probability model.
- Posterior distribution p($\theta \mid y$): The joint posterior distribution that expresses uncertainty about parameter θ after taking into account information about the prior and the data, as in the following equation:

$$p(\theta \mid y) = p(y \mid \theta) \times p(\theta). \tag{13}$$

The Prior Distributions

Bayesian inference has the prior distribution which represents the information about an uncertain parameter θ that is combined with the probability distribution of data to get the posterior distribution p($\theta \mid y$). For the Bayesian paradigm, it is important to specify prior information with the value of the specified parameter or information which are obtained before analyzing the experimental data by using a probability distribution function which is called the prior probability distribution

7

(or the prior). In this paper, we use two types of priors, which are the half-Cauchy prior and the normal prior. The simplest of all priors is conjugate prior which makes posterior calculations easy. Also, a conjugate prior distribution for an unknown parameter leads to a posterior distribution for which there is a simple formula for posterior means and variances. Abujarad and Khan (2018b) used the half-Cauchy distribution with scale parameter $\alpha = 25$ as prior distribution for scale parameters.

Weakly Informative Priors for the Parameters

Consider the types of prior distribution, which are the half-Cauchy prior and the normal prior. First, the probability density function of half-Cauchy distribution with scale parameter α is given by

$$\mathrm{f}\left(x\right) = \frac{2\alpha}{\pi\left(x^2 + \alpha^2\right)}; \quad x > 0, \alpha > 0.$$

The mean and variance of the half-Cauchy distribution do not exist, but its mode is equal to 0. The half-Cauchy distribution with scale $\alpha = 25$ is a recommended, default, weakly informative prior distribution for a scale parameter. At this scale, $\alpha = 25$, the density of half-Cauchy is nearly flat but not completely (see Figure 4); prior distributions that are not completely flat provide enough information for the numerical approximation algorithm to continue to explore the target density, the posterior distribution. The inverse-gamma is often used as a non-informative prior distribution for the scale parameter. However, this model creates a problem for scale parameters near zero. Gelman and Hill (2006) recommend that the uniform or, if more information is necessary, the half-Cauchy is a better choice. Thus, in this paper, the half-Cauchy distribution with scale parameter $\alpha = 25$ is used as a weakly informative prior distribution.

Second, in the normal (or Gaussian) distribution, each parameter is assigned a weak informative Gaussian prior probability distribution. In this paper, we use the parameters β_i which are independently normally distributed with mean = 0 and standard deviation = 1000, that is, $\beta_i \sim N(0, 1000)$, as this obtains a flat prior. From Figure 4, we see the large variance indicates a lot of uncertainty about each parameter and hence, a weakly informative distribution.
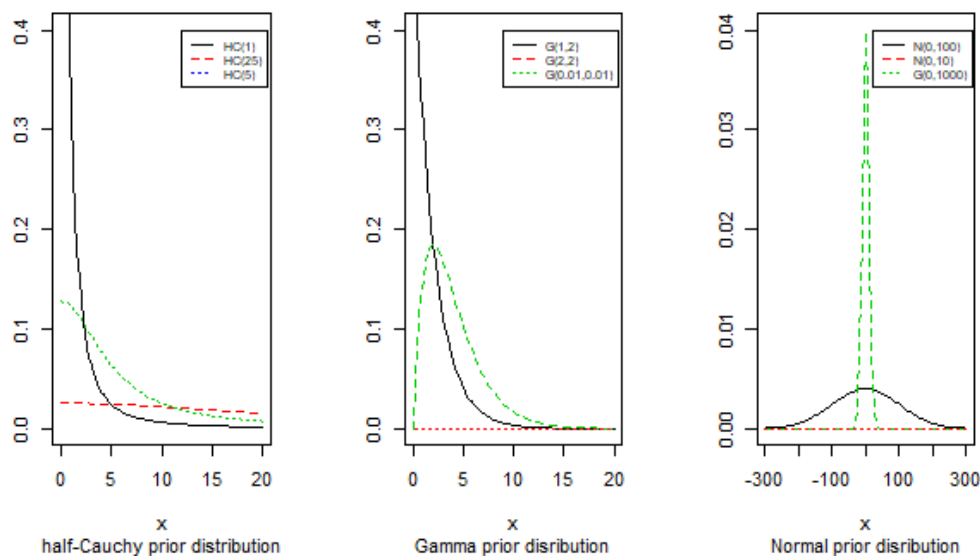
Figure 4. Weakly informative priors

Stan Modeling

Stan is a high-level language written in a C++ library for Bayesian modeling and inference that primarily uses the No-U-Turn sampler (NUTS) (Hoffman & Gelman, 2014) to obtain posterior simulations given a user-specified model and data. A statistical model through a conditional probability function $p(\theta \mid y, x)$ can be defined by the Stan program, where θ is a sequence of modeled unknown values, y is a sequence of modeled known values, and x is a sequence of un-modeled predictors and constants (e.g., sizes, hyperparameters). A Stan program imperatively defines a log probability function over parameters conditioned on specified data and constants. Stan provides full Bayesian inference for continuous-variable models through Markov chain Monte Carlo methods (Metropolis et al., 1953), an adaptive form of Hamiltonian Monte Carlo sampling (Duane et al., 1987). Stan can be called from R using the rstan package, and through Python using the pystan package. All interfaces support sampling and optimization-based inference with diagnostics and posterior analysis. rstan and pystan also provide access to log probabilities, parameter transforms, and specialized plotting. Stan programs consist of variable type declarations and statements. Variable types include constrained and unconstrained integer, scalar, vector, and matrix types. Variables are declared in

9

blocks corresponding to the variable use: data, transformed data, parameter, transformed parameter, or generated quantities.

Bayesian Approach

Obtain the marginal posterior distribution of the particular parameters of interest. In principle, the route to achieving this aim is clear; first, we require the joint posterior distribution of all unknown parameters, then, we integrate this distribution over the unknowns parameters that are not of immediate interest to obtain the desired marginal distribution. Or equivalently, using simulation, we draw samples from the joint posterior distribution, then, we look at the parameters of interest and ignore the values of the other unknown parameters.

Lomax Model

The probability density function (pdf) is given by

$$f\left(y,\alpha,\lambda\right) = \frac{\alpha}{\lambda}\left(1+\frac{y}{\lambda}\right)^{-(\alpha+1)}.$$

Also, the survival function is given by

$$S\left(y,\alpha,\lambda\right) = 1 - F\left(y\right) = \left(1+\frac{y}{\lambda}\right)^{-\alpha}.$$

Write the likelihood function for right censored (as is our case the data are right censored) as

$$L = \prod_{i=0}^{n} p\left(y_i,\delta_i\right)$$

$$= \prod_{i=0}^{n}\left[f\left(y_i\right)\right]^{\delta_i}\left[S\left(y_i\right)\right]^{1-\delta_i}$$

where δ_i is an indicator variable which takes the value 0 if the observation is censored and 1 if the observation is uncensored. Thus, the likelihood function is given by

$$L = \prod_{i=0}^{n} \left[\frac{\alpha}{\lambda}\left(1+\frac{y}{\lambda}\right)^{-(\alpha+1)} \right]^{\delta_i} \left[\left(1+\frac{y}{\lambda}\right)^{-\alpha} \right]^{1-\delta_i} \tag{14}$$

and the joint posterior density is given by Abujarad and Khan (2018a):

$$p(\alpha,\beta \mid y,X) \propto L(y \mid X,\alpha,\beta) \times p(\beta) \times p(\alpha)$$

$$\propto \prod_{i=0}^{n} \left[\frac{\alpha}{e^{X\beta}}\left(1+\frac{y}{e^{X\beta}}\right)^{\alpha-1} \right]^{\delta_i} \left[\left(1+-\frac{y}{e^{X\beta}}\right)^{-\alpha} \right]^{1-\delta_i} \tag{15}$$

$$\times \prod_{j=0}^{J} \frac{1}{\sqrt{2\pi \times 10^3}} \exp\left(-\frac{1}{2}\frac{\beta_j^2}{10^3}\right) \times \frac{2 \times 25}{\pi\left(\alpha^2 + 25^2\right)}$$

To perform Bayesian inference in the Lomax model, we must specify a prior distribution for α and the βs. We discussed the issue associated with specifying prior distributions in a previous section, but for simplicity at this point, we assume that the prior distribution for α is half-Cauchy on the interval [0, 5] and for β is normal on [0, 5]. Elementary application of Bayes' rule as displayed in (13), applied to (14), then gives the posterior density for α and β as equation (15). The result for this marginal posterior distribution results in a high-dimensional integral over all model parameters β_j and α; for solving this integral we use the approximated using Markov chain Monte Carlo methods. However, due to the availability of computer software package like rstan, this required model can be easily fitted in Bayesian paradigm using Stan as well as MCMC techniques.

Exponential Lomax Model

The probability density function (pdf) is given by

$$f(y,v,\alpha,\lambda) = \frac{v\alpha}{\lambda}\left(1+\frac{y}{\lambda}\right)^{-(\alpha+1)} \left[1-\left(1+\frac{y}{\lambda}\right)^{-\alpha} \right]^{v-1}.$$

Also, the survival function is given by

$$S(y,v,\alpha,\lambda) = 1 - \left[1-\left(1+\frac{y}{\lambda}\right)^{-\alpha} \right]^{v}.$$

11

Write the likelihood function for right censored (as is our case the data are right censored) as

$$L = \prod_{i=0}^{n} p(y_i, \delta_i)$$

$$= \prod_{i=0}^{n} \left[f(y_i) \right]^{\delta_i} \left[S(y_i) \right]^{1-\delta_i}$$

where δ_i is an indicator variable which takes the value 0 if the observation is censored and 1 if the observation is uncensored. Thus, the likelihood function is given by

$$L = \prod_{i=0}^{n} \left[\frac{v\alpha}{\lambda} \left(1 + \frac{y}{\lambda} \right)^{-(\alpha+1)} \left(1 - \left(1 + \frac{y}{\lambda} \right)^{-\alpha} \right)^{v-1} \right]^{\delta_i} \left[1 - \left(1 - \left(1 + \frac{y}{\lambda} \right)^{-\alpha} \right)^{v} \right]^{1-\delta_i} \quad (16)$$

and the joint posterior density is given by

$$p(\alpha, v, \beta \mid y, X) \propto L(y \mid X, \alpha, v, \beta) \times p(\beta) \times p(\alpha) \times p(v)$$

$$\propto \prod_{i=0}^{n} \left[\frac{v\alpha}{e^{X\beta}} \left(1 + \frac{y}{e^{X\beta}} \right)^{-(\alpha+1)} \left(1 - \left(1 + \frac{y}{e^{X\beta}} \right)^{-\alpha} \right)^{v-1} \right]^{\delta_i}$$

$$\times \prod_{i=0}^{n} \left[1 - \left(1 - \left(1 + \frac{y}{e^{X\beta}} \right)^{-\alpha} \right)^{v} \right]^{1-\delta_i} \quad (17)$$

$$\times \prod_{j=0}^{J} \frac{1}{\sqrt{2\pi \times 10^3}} \exp\left(-\frac{1}{2} \frac{\beta_j^2}{10^3} \right) \times \frac{2 \times 25}{\pi \left(\alpha^2 + 25^2 \right)} \times \frac{2 \times 25}{\pi \left(v^2 + 25^2 \right)}$$

To perform Bayesian inference on the exponential Lomax model, we must specify a prior distribution for α, v, and the βs. Assume the prior distribution for α and v is half-Cauchy on the interval [0, 5] and for β is Normal on [0, 5]. Elementary application of Bayes' rule as displayed in (13), applied to (16), gives the posterior density for α, v, and β as equation (17). The result for this marginal posterior distribution is a high-dimensional integral over all model parameters β_j, v, and α. For solving this integral we approximate using Markov chain Monte Carlo methods.

However, due to the availability of computer software packages like rstan, this required model can be easily fitted in Bayesian paradigm using Stan as well as MCMC techniques.

Weibull Lomax Model

The probability density function (pdf) is given by

$$f\left(y,v,\eta,\alpha,\lambda\right)=\frac{v\eta\alpha}{\lambda}\left(1+\frac{y}{\lambda}\right)^{\left(\eta\alpha-1\right)}\left[1-\left(1+\frac{y}{\lambda}\right)^{-\alpha}\right]^{\eta-1}\exp\left\{-v\left[\left(1+\frac{y}{\lambda}\right)^{\alpha}-1\right]^{\eta}\right\}.$$

The survival function is given by

$$S\left(y,v,\eta,\alpha,\lambda\right)=\exp\left\{-v\left[\left(1+\frac{y}{\lambda}\right)^{\alpha}-1\right]^{\eta}\right\}.$$

Write the likelihood function for right censored (as is our case the data are right censored) as

$$L=\prod_{i=0}^{n}p\left(y_i,\delta_i\right)$$
$$=\prod_{i=0}^{n}\left[f\left(y_i\right)\right]^{\delta_i}\left[S\left(y_i\right)\right]^{1-\delta_i}$$

where δ_i is an indicator variable which takes the value 0 if the observation is censored and 1 if the observation is uncensored. Thus, the likelihood function is given by

$$L=\prod_{i=0}^{n}\left[\frac{v\eta\alpha}{\lambda}\left(1+\frac{y}{\lambda}\right)^{\left(\eta\alpha-1\right)}\left(1-\left(1+\frac{y}{\lambda}\right)^{-\alpha}\right)^{\eta-1}\exp\left\{-v\left[\left(1+\frac{y}{\lambda}\right)^{\alpha}-1\right]^{\eta}\right\}\right]^{\delta_i}$$
$$\times\prod_{i=0}^{n}\left[\exp\left\{-v\left[\left(1+\frac{y}{\lambda}\right)^{\alpha}-1\right]^{\eta}\right\}\right]^{1-\delta_i}$$

(18)

13

and the joint posterior density is given by

$$p(\alpha, \nu, \beta \mid y, X) \propto L(y \mid X, \alpha, \eta, \nu, \beta) \times p(\beta) \times p(\alpha) \times p(\nu) \times p(\eta)$$

$$\propto \prod_{i=0}^{n} \left[\frac{\nu \eta \alpha}{\lambda} \left(1 + \frac{y}{\lambda}\right)^{(\eta \alpha - 1)} \left(1 - \left(1 + \frac{y}{\lambda}\right)^{-\alpha}\right)^{\eta - 1} \exp\left\{-\nu \left[\left(1 + \frac{y}{\lambda}\right)^{\alpha} - 1\right]^{\eta}\right\} \right]^{\delta_i}$$

$$\times \prod_{i=0}^{n} \left[\exp\left\{-\nu \left[\left(1 + \frac{y}{\lambda}\right)^{\alpha} - 1\right]^{\eta}\right\} \right]^{1-\delta_i} \tag{19}$$

$$\times \prod_{j=0}^{J} \frac{1}{\sqrt{2\pi \times 10^3}} \exp\left(-\frac{1}{2} \frac{\beta_j^2}{10^3}\right) \times \frac{2 \times 25}{\pi(\alpha^2 + 25^2)}$$

$$\times \frac{2 \times 25}{\pi(\nu^2 + 25^2)} \times \frac{2 \times 25}{\pi(\eta^2 + 25^2)}$$

To perform Bayesian inference on the Weibull Lomax model, we must specify a prior distribution for α, ν, η, and the βs. Assume the prior distribution for α, η, and ν is half-Cauchy on the interval $[0, 5]$ and for β is Normal on $[0, 5]$. Elementary application of Bayes' rule as displayed in (13), applied to (18), gives the posterior density for α, ν, η, and β as equation (19). The result for this marginal posterior distribution is a high-dimensional integral over all model parameters β_j, ν, η, and α. For solving this integral we approximate using Markov chain Monte Carlo methods. However, due to the availability of computer software packages like rstan, this required model can be easily fitted in Bayesian paradigm using Stan as well as MCMC techniques.

Lung Cancer Survival Data

The data in Table 1 are from a more comprehensive set given by Krall et al. (1975). The problem is to relate survival times for multiple myeloma patients to a number of prognostic variables. The data given here show survival times, in months, for 65 patients and include measurements on each patient for the following five covariates:

x_1 Logarithm of a blood urea nitrogen measurement at diagnosis.
x_2 Hemoglobin measurement at diagnosis.
x_3 Age at diagnosis.

x_4 Sex: 0, male; 1, female.

x_5 Serum calcium measurement at diagnosis.

Table 1. Lung cancer survival data

t	x_1	x_2	x_3	x_4	x_5	t	x_1	x_2	x_3	x_4	x_5
1	2.218	9.4	67	0	10	26	1.230	11.2	49	1	11
1	1.940	12.0	38	0	18	32	1.322	10.6	46	0	9
2	1.519	9.8	81	0	15	35	1.114	7.0	48	0	10
2	1.748	11.3	75	0	12	37	1.602	11.0	63	0	9
2	1.301	5.1	57	0	9	41	1.000	10.2	69	0	10
3	1.544	6.7	46	1	10	42	1.146	5.0	70	1	9
5	2.236	10.1	50	1	9	51	1.568	7.7	74	0	13
5	1.681	6.5	74	0	9	52	1.000	10.1	60	1	10
6	1.362	9.0	77	0	8	54	1.255	9.0	49	0	10
6	2.114	10.2	70	1	8	58	1.204	12.1	42	1	10
6	1.114	9.7	60	0	10	66	1.447	6.6	59	0	9
6	1.415	10.4	67	1	8	67	1.322	12.8	52	0	10
7	1.978	9.5	48	0	10	88	1.176	10.6	47	1	9
7	1.041	5.1	61	1	10	89	1.322	14.0	63	0	9
7	1.176	11.4	53	1	13	92	1.431	11.0	58	1	11
9	1.724	8.2	55	0	12	4	1.945	10.2	59	0	10
11	1.114	14.0	61	0	10	4*	1.924	10.0	49	1	13
11	1.230	12.0	43	0	9	7*	1.114	12.4	48	1	10
11	1.301	13.2	65	0	10	7*	1.532	10.2	81	0	11
11	1.508	7.5	70	0	12	8*	1.079	9.9	57	1	8
11	1.079	9.6	51	1	9	12	1.146	11.6	46	1	7
13	0.778	5.5	60	1	10	11*	1.613	14.0	60	0	9
14	1.398	14.6	66	0	10	12*	1.398	8.8	66	1	9
15	1.602	10.6	70	0	11	13*	1.663	4.9	71	1	9
16	1.342	9.0	48	0	10	16*	1.146	13.0	55	0	9
16	1.322	8.8	62	1	10	19*	1.322	13.0	59	1	10
17	1.230	10.0	53	0	9	19*	1.322	10.8	69	1	10
17	1.591	11.2	68	0	10	28*	1.230	7.3	82	1	9
18	1.447	7.5	65	1	8	41*	1.756	12.8	72	0	9
19	1.079	14.4	51	0	15	53*	1.114	12.0	66	0	11
19	1.255	7.5	60	1	9	57*	1.255	12.5	66	0	11
24	1.301	14.6	56	1	9	77*	1.079	14.0	60	0	12
25	1.000	12.4	67	0	10						

Note: t = Days of survival

Implementation using Stan

Bayesian modeling of the Lomax family in the rstan package includes the creation of blocks, data, transformed data, parameter, transformed parameter, or generated quantities. To use the method for Lomax model, exponential Lomax, and Weibull Lomax, first you must build a function for the model containing the following objects:

- Define the log survival.
- Define the log hazard.
- Define the sampling distributions for right censored data.

Then the distribution should be based on the function definition blocks. The function definition block contains user defined functions. The data block declares the required data for the model. The transformed data block allows the definition of constants and transforms of the data. The parameters block declares the model's parameters. The transformed parameters block allows variables to be defined in terms of data and parameters that may be used later and will be saved. The model block is where the log probability function is defined.

Model Specification

Now look for the posterior estimates of the parameters when the Lomax, exponential Lomax and Weibull Lomax models are fitted to the above data. The first most requirement for the Bayesian fitting is the definition of the likelihood. Here, we have likelihood as:

$$
\begin{aligned}
L(\theta \mid t) &= \prod_{i=1}^{n} f(t_i)^{\delta_i} S(t_i)^{1-\delta_i} \\
&= \prod_{i=1}^{n} \left(\frac{f(t_i)^{\delta_i}}{S(t_i)} S(t_i) \right) \\
&= \prod_{i=1}^{n} h(t_i)^{\delta_i} S(t_i)
\end{aligned}
$$

Thus, our log-likelihood becomes

$$\log L = \sum_{i=1}^{n} \left(\log \left[h(t_i) \right]^{\delta_i} + \log(S_t) \right).$$

Lomax Model

The first model is Lomax:

$$y \sim \text{Lomax}(\alpha, \lambda),$$

where $\lambda = \exp(X\beta)$. The Bayesian framework requires the specification of prior distributions for the parameters. Here, we stick to subjectivity and thus introduce weakly informative priors for the parameters. Priors for the βs and α are taken to be normal and half-Cauchy as follows:

$$\beta_j \sim \text{N}(0,5); \quad j = 1, 2, 3, \ldots, J$$
$$\alpha \sim \text{HC}(0,5)$$

Finally, the fitting is done with the Stan function using the following commands:

```
library(rstan)
model_code1="
functions{
//defined survival, shape= , scale= .
vector log_s(vector t, real shape, vector scale){
vector[num_elements(t)] log_s;
for(i in 1:num_elements(t)){
log_s[i]=log((1+t[i] / scale[i])^-shape);}
return log_s;}
//define log_ft, shape= , scale= .
vector log_ft(vector t, real shape, vector scale){
vector[num_elements(t)] log_ft;
for(i in 1:num_elements(t)){
log_ft[i]=log((shape / scale[i]) * (1+t[i] / scale[i])^-
      (shape+1));}
return log_ft;}
//define log hazard, shape= , scale= .
```

```
vector log_h(vector t, real shape, vector scale){
vector[num_elements(t)] log_h;
vector[num_elements(t)] logft;
vector[num_elements(t)] logs;
logft=log_ft(t,shape,scale);
logs=log_s(t,shape,scale);
log_h=logft-logs;
return log_h;}
//define the sampling distribution , shape=alpha, scale=lambda.
real surv_lom_lpdf(vector t, vector d, real shape, vector scale){
vector[num_elements(t)] log_lik;
real prob;
log_lik=d .* log_h(t,shape,scale)+log_s(t,shape,scale);
prob=sum(log_lik);
return prob;}}
```

Therefore, obtain the survival and hazard of the Lomax model.

Exponential Lomax Model

The second model is exponential Lomax:

$$y \sim \mathrm{EL}\left(v, \alpha, \lambda\right),$$

where $\lambda = \exp(X\beta)$. The Bayesian framework requires the specification of prior distributions for the parameters. Here, we stick to subjectivity and thus introduce weakly informative priors for the parameters. Priors for the βs, α, and v are taken to be normal and half-Cauchy as follows:

$$\beta_j \sim \mathrm{N}\left(0,5\right); \quad j = 1,2,3,\ldots,J$$
$$\alpha, v \sim \mathrm{HC}\left(0,5\right)$$

Finally, the fitting is done with the Stan function using the following commands:

```
model_code1="
functions{
//defined survival, shape1= ,shape2=  , scale=
vector log_s(vector t, real shape1, real shape2 ,vector scale){
```

```
vector[num_elements(t)] log_s;
for(i in 1:num_elements(t)){
log_s[i]=log(1-(1-(1+t[i] / scale[i])^-shape1)^shape2);}
return log_s;}
//define log_ft, shape1= ,shape2=  , scale=
vector log_ft(vector t, real shape1, real shape2 , vector scale){
vector[num_elements(t)] log_ft;
for(i in 1:num_elements(t)){
log_ft[i]=log((shape1*shape2/scale[i])*(1+t[i]/scale[i])^-
    (shape1+1)*(1-(1+t[i]/scale[i])^(-shape1))^(shape2-1));}
return log_ft;}
//define log hazard, shape1= ,shape2=  , scale=
vector log_h(vector t, real shape1, real shape2 , vector scale){
vector[num_elements(t)] log_h;
vector[num_elements(t)] logft;
vector[num_elements(t)] logs;
logft=log_ft(t,shape1,shape2,scale);
logs=log_s(t,shape1,shape2,scale);
log_h=logft-logs;
return log_h;}
//define the sampling distribution
real surv_lomE_lpdf(vector t, vector d, real shape1, real
    shape2 , vector scale){
vector[num_elements(t)] log_lik;
real prob;
log_lik=d .*
    log_h(t,shape1,shape2,scale)+log_s(t,shape1,shape2,scale);
prob=sum(log_lik);
return prob;}}
```

Therefore, obtain the survival and hazard of the exponential Lomax model.

Weibull Lomax Model

The third model is Weibull Lomax:

$$y \sim \mathrm{WL}(v,\eta,\alpha,\lambda),$$

where $\lambda = \exp(X\beta)$. The Bayesian framework requires the specification of prior distributions for the parameters. Here, we stick to subjectivity and thus introduce weakly informative priors for the parameters. Priors for the βs, α, v, and η are taken to be normal and half-Cauchy as follows:

$$\beta_j \sim N(0,5); \quad j=1,2,3,\ldots,J$$
$$\alpha,v,\eta \sim HC(0,5)$$

Finally, the fitting is done with the Stan function using the following commands:

```
model_code1="
functions{
//defined survival, shape1= ,shape2= , shape3=  ,scale=
vector log_s(vector t, real shape1, real shape2 ,real shape3,
    vector scale){
vector[num_elements(t)] log_s;
for(i in 1:num_elements(t)){
log_s[i]=log(exp(-shape1*(((1+t[i] / scale[i])^shape3)-
    1)^shape2));}
return log_s;}
//define log_ft shape1= ,shape2= , shape3=  ,scale=
vector log_ft(vector t, real shape1, real shape2, real shape3,
    vector    scale){
vector[num_elements(t)] log_ft;
for(i in 1:num_elements(t)){
log_ft[i]=log((shape1*shape2*shape3/scale[i])*((1+t[i]/scale[i])^
    (shape2*shape3-1))*((1-(1+t[i]/scale[i])^(-shape3))^(shape2-
    1))*exp(-shape1*(((1+t[i]/scale[i])^(shape3))-1)^shape2));}
return log_ft;}
//define log hazard shape1= ,shape2= , shape3=  ,scale=
vector log_h(vector t, real shape1, real shape2 ,real shape3,
    vector scale){
vector[num_elements(t)] log_h;
vector[num_elements(t)] logft;
vector[num_elements(t)] logs;
logft=log_ft(t,shape1,shape2,shape3,scale);
logs=log_s(t,shape1,shape2,shape3,scale);
```

```
log_h=logft-logs;
return log_h;}
//define the sampling distribution
real surv_lomW_lpdf(vector t, vector d, real shape1, real
    shape2 ,real shape3, vector scale){
vector[num_elements(t)] log_lik;
real prob;
log_lik=d.*log_h(t,shape1,shape2,shape3,scale)+log_s(t,shape1,sha
    pe2,shape3,scale);
prob=sum(log_lik);
return prob;}}
```

Therefore, obtain the survival and hazard of the Exponential Lomax model.

Build the Stan

Stan contains a set of blocks as described before; the first block to work on is data block. In this block create a number of observations that include observed times, a censoring indicator (1 = observed, 0 = censored), a number of covariates, and build the matrix of covariates (with *N* rows and *M* columns). Then, create the parameter in block parameters because there is more than one parameter. Then, do some transformations of the parameters in blocks of transformed parameters. Finally, create the models in blocks Model. In these blocks, put the prior for the parameters and the likelihood in this block to get the posterior distribution for this model. After this, save the work in a file to use in the rstan package.

Lomax Model

```
//data block
data {
int N;                              // number of observations
vector<lower=0>[N] y;          // observed times
vector<lower=0,upper=1>[N] censor;//censoring indicator
    (1=observed, 0=censored)
int M;                              // number of covariates
matrix[N, M] x;  }          // matrix of covariates (with N rows
    and M columns)
parameters {
```

```
vector[M] beta; // Coefficients in the linear predictor
    (including intercept)
real<lower=0> shape; }   // shape parameter
transformed parameters {
vector[N] linpred;
vector[N] scale;
linpred = x*beta;
for (i in 1:N) {
scale[i] = exp(linpred[i]);}}
model {
shape ~ cauchy(0,25);
beta  ~ normal(0,5);
y ~ surv_lom(censor, shape, scale);}
"
```

Exponential Lomax Model

```
//data block
data {
int N;                              // number of observations
vector<lower=0>[N] y;          // observed times
vector<lower=0,upper=1>[N] censor;//censoring indicator
    (1=observed, 0=censored)
int M;                              // number of covariates
matrix[N, M] x; }          // matrix of covariates (with N rows
    and M columns)
parameters {
vector[M] beta; // Coefficients in the linear predictor
    (including intercept)
real<lower=0> shape1;    // shape parameter
real<lower=0> shape2; }   // shape parameter
transformed parameters {
vector[N] linpred;
vector[N] scale;
linpred = x*beta;
for (i in 1:N) { scale[i] = exp(linpred[i]); }}
model {
shape1 ~ cauchy(0,25);
shape2 ~ cauchy(0,25);
```

```
beta   ~ normal(0,25);
y ~ surv_lomE(censor, shape1,shape2, scale);}
"
```

Weibull Lomax Model

```
//data block
data {
int N;                              // number of observations
vector<lower=0>[N] y;          // observed times
vector<lower=0,upper=1>[N] censor;//censoring indicator
    (1=observed, 0=censored)
int M;                              // number of covariates
matrix[N, M] x; }          // matrix of covariates (with N rows
    and M columns)
parameters {
vector[M] beta; // Coefficients in the linear predictor
    (including intercept)
real<lower=0> shape1;     // shape1 parameter
real<lower=0> shape2;     // shape2 parameter
real<lower=0> shape3; }   // shape3 parameter
transformed parameters {
vector[N] linpred;
vector[N] scale;
linpred = x*beta;
for (i in 1:N) { scale[i] = exp(linpred[i]); }}
model {
shape1 ~ cauchy(0,25);
shape2 ~ cauchy(0,25);
shape3 ~ cauchy(0,25);
beta ~ normal(0,5);
y ~ surv_lomW(censor, shape1,shape2,shape3, scale); }
"
```

Creation of Data for Stan

Now create the data to use for analysis; data creation requires model matrix **X**, a number of predictors *M*, and information regarding the censoring and response variable. The number of observations is specified by *N*, that is, 65. Censoring is

taken into account, where 0 stands for censored and 1 for uncensored values. Finally, all these operations are combined in a listed form as dat.

```
y<-
    c(1,1,2,2,2,3,5,5,6,6,6,6,7,7,7,9,11,11,11,11,11,13,14,15,16,
    16,17,17,18,19,19,24,25,26,32,35,37,41,42,51,52,54,58,66,67,8
    8,89,92,4,4,7,7,8,12,11,12,13,16,19,19,28,41,53,57,77)
x1<-
    c(2.218,1.940,1.519,1.748,1.301,1.544,2.236,1.681,1.362,2.114
    ,1.114,1.415,1.978,1.041,1.176,1.724,1.114,1.230,1.301,1.508,
    1.079,0.778,1.398,1.602,1.342,1.322,1.230,1.591,1.447,1.079,1
    .255,1.301,1.000,1.230,1.322,1.114,1.602,1.000,1.146,1.568,1.
    000,1.255,1.204,1.447,1.322,1.176,1.322,1.431,1.945,1.924,1.1
    14,1.532,1.079,1.146,1.613,1.398,1.663,1.146,1.322,1.322,1.23
    0,1.756,1.114,1.255,1.079)
x2<-
    c(9.4,12.0,9.8,11.3,5.1,6.7,10.1,6.5,9.0,10.2,9.7,10.4,9.5,5.
    1,11.4,8.2,14.0,12.0,13.2,7.5,9.6,5.5,14.6,10.6,9.0,8.8,10.0,
    11.2,7.5,14.4,7.5,14.6,12.4,11.2,10.6,7.0,11.0,10.2,5.0,7.7,1
    0.1,9.0,12.1,6.6,12.8,10.6,14.0,11.0,10.2,10.0,12.4,10.2,9.9,
    11.6,14.0,8.8,4.9,13.0,13.0,10.8,7.3,12.8,12.0,12.5,14.0)
x3<-
    c(67,38,81,75,57,46,50,74,77,70,60,67,48,61,53,55,51,43,65,70
    ,51,60,60,70,48,62,53,68,65,51,60,56,67,49,46,48,63,69,70,74,
    60,49,42,59,52,47,63,58,59,49,48,81,57,46,60,66,71,55,59,69,8
    2,72,66,66,60)
x4<-
    c(0,0,0,0,0,1,1,0,0,1,0,1,0,1,1,0,0,0,0,0,1,1,0,0,0,1,0,0,1,0
    ,1,1,0,1,0,0,0,0,1,0,1,0,1,0,0,1,0,1,0,1,1,0,1,1,0,1,1,0,1,1,
    1,0,0,0,0)
x5<-
    c(10,18,15,12,9,10,9,9,8,8,10,8,10,10,13,12,10,9,10,12,9,10,1
    0,11,10,10,9,10,8,15,9,9,10,11,9,10,9,10,9,13,10,10,10,9,10,9
    ,9,11,10,13,10,11,8,7,9,9,9,9,10,10,9,9,11,11,12)
censor<-
    c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1
    ,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,
    0,0,0,0,0)
```

```
x <- cbind(1,x1,x2,x3,x4,x5)
N = nrow(x)
M = ncol(x)
event=censor
dat <- list( y=y, x=x, event=event, N=N, M=M)
```

Running the Model using Stan for Lomax Model

```
#regression coefficient with log(y) as a guess to initialize
beta1=solve(crossprod(x),crossprod(x,log(y)))
#convert matrix to a vector
beta1=c(beta1)
M00<-
    stan(model_code=model_code1,init=list(list(beta=beta1)),data=
    dat,iter=1000,chains=1)
```

Summarizing Output

The function rstan approximates the posterior density of the fitted model and the posterior summaries can be seen in the following tables. Table 2 contains summaries for all chains merged and individual chains, respectively. Included in the summaries are quantiles, means, standard deviations (sd), effective sample sizes (n_eff), and split (Rhats) (the potential scale reduction derived from all chains after splitting each chain in half and treating the halves as chains). For the summary of all chains merged, Monte Carlo standard errors (se_mean) are also reported.

Table 2. Summary of the simulated results using rstan function with Mean stands for posterior mean, se_mean, sd for posterior standard deviation, LB, Median, UB are 2.5%, 50%, 97.5% quantiles, n_eff for number effective sample size, and Rhat, respectively

|	Mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
beta[1]	5.6089	0.1240	2.0703	1.5289	4.2831	5.6102	7.0116	9.5042	279	0.9995
beta[2]	-1.5127	0.0312	0.6156	-2.6675	-1.9476	-1.5312	-1.0925	-0.3258	390	0.9983
beta[3]	0.1558	0.0040	0.0678	0.0296	0.1092	0.1544	0.2009	0.2899	281	1.0006
beta[4]	0.0252	0.0008	0.0178	-0.0109	0.0135	0.0256	0.0376	0.0595	489	1.0001
beta[5]	0.1466	0.0192	0.3698	-0.4930	-0.1249	0.1394	0.4029	0.8843	373	0.9980
beta[6]	-0.1163	0.0054	0.1082	-0.3116	-0.1882	-0.1176	-0.0538	0.1249	405	0.9981
shape	13.3384	1.7943	25.5222	2.0063	4.6611	7.2923	13.0081	53.8389	202	0.9997
lp__	-211.7708	0.1160	1.9048	-216.3929	-212.7992	-211.4257	-210.4121	-208.9114	270	0.9990
dev	423.1262	0.2380	3.8849	417.5023	420.4241	422.5258	425.2199	433.6832	266	0.9983
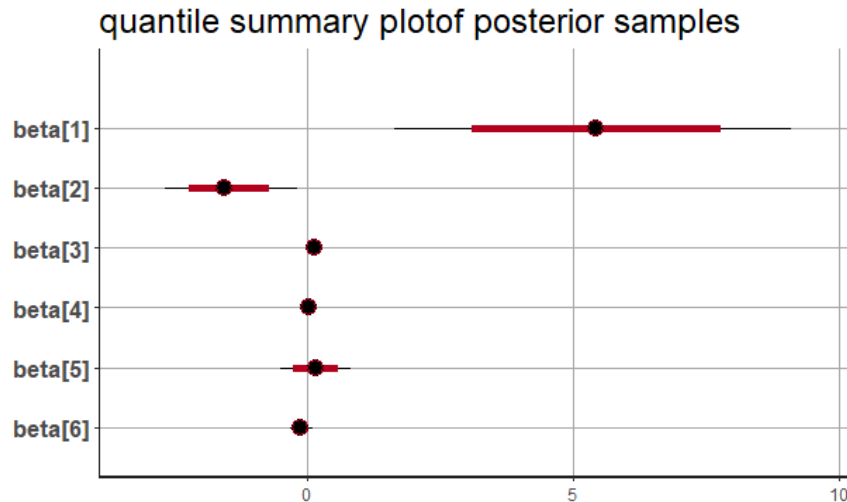
Figure 5. Caterpillar plot for Lomax model

The selection of appropriate regressor variable can also be done by using a caterpillar plot. Caterpillar plots are popular plots in Bayesian inference for summarizing the quantiles of posterior samples. We can see in Figure 5 that the caterpillar plot is a horizontal plot of 3 quantiles of the selected distribution. This may be used to produce a caterpillar plot of posterior samples.

Running the Model using Stan for Exponential Lomax Model

```
#regression coefficient with log(y) as a guess to initialize
beta1=solve(crossprod(x),crossprod(x,log(y)))
#convert matrix to a vector
beta1=c(beta1)
M11<-
    stan(model_code=model_code1,init=list(list(beta=beta1)),data=
    dat,iter=1000,chains=1)
```

Summarizing Output

The function rstan approximates the posterior density of the fitted model and posterior summaries can be seen in the following tables. Table 3 contains summaries for all chains merged and individual chains, respectively. Included in the summaries are quantiles, means, standard deviations (sd), effective sample sizes (n_eff), and split (Rhats) (the potential scale reduction derived from all chains after

splitting each chain in half and treating the halves as chains). For the summary of all chains merged, Monte Carlo standard errors (se_mean) are also reported.

The selection of appropriate regressor variable can also be done by using a caterpillar plot. Caterpillar plots are popular plots in Bayesian inference for summarizing the quantiles of posterior samples. We can see in Figure 6 that the caterpillar plot is a horizontal plot of 3 quantiles of the selected distribution.

Table 3. Summary of the simulated results using rstan function with Mean stands for posterior mean, se_mean, sd for posterior standard deviation, LB, Median, UB are 2.5%, 50%, 97.5% quantiles, n_eff for number effective sample size, and Rhat, respectively

|	Mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
beta[1]	3.5139	0.1745	2.0718	-0.5590	2.1267	3.4463	5.0398	7.5326	141	1.0185
beta[2]	-1.5541	0.0196	0.4393	-2.3904	-1.8659	-1.5400	-1.2403	-0.7263	500	0.9997
beta[3]	0.1594	0.0031	0.0548	0.0546	0.1219	0.1587	0.1920	0.2650	311	1.0025
beta[4]	0.0112	0.0008	0.0144	-0.0161	0.0016	0.0103	0.0204	0.0413	347	0.9988
beta[5]	0.2547	0.0196	0.3123	-0.3490	0.0388	0.2530	0.4781	0.8200	255	1.0011
beta[6]	-0.1606	0.0046	0.0798	-0.3107	-0.2154	-0.1593	-0.1089	0.0042	301	0.9996
shape1	2.6087	0.2872	4.2739	0.8902	1.1702	1.4611	2.3965	10.8118	221	1.0042
shape2	8.7931	2.0758	23.4918	1.2799	2.1065	3.6149	6.6342	41.1162	128	1.0197
lp__	-207.7097	0.1344	1.8616	-212.2721	-208.8383	-207.4109	-206.3405	-204.7106	192	1.0039
dev	416.4598	0.2666	3.5951	410.8526	413.8118	415.9122	418.5855	425.0859	182	1.0102
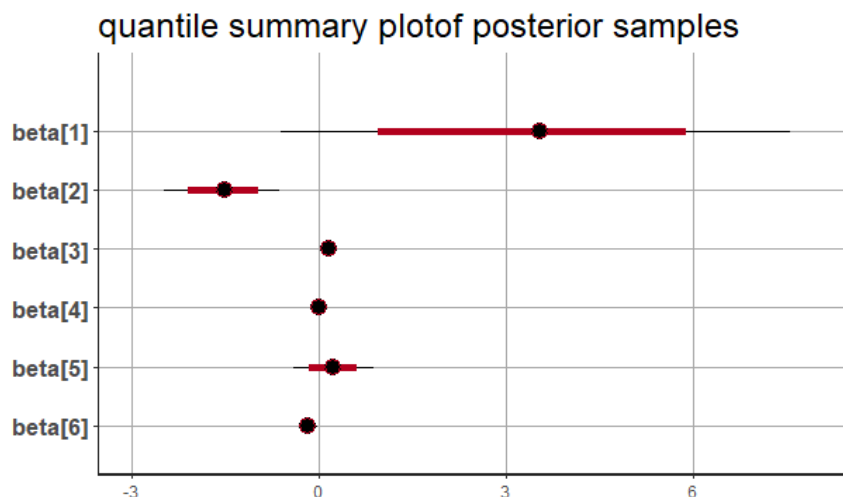
Figure 6. Caterpillar plot for exponential Lomax model

Running the Model using Stan for Weibull Lomax Model

```
#regression coefficient with log(y) as a guess to initialize
beta1=solve(crossprod(x),crossprod(x,log(y)))
#convert matrix to a vector
beta1=c(beta1)
M22<-
    stan(model_code=model_code1,init=list(list(beta=beta1)),data=
    dat,iter=1000,chains=1)
```

Summarizing Output

The function rstan approximates the posterior density of the fitted model and posterior summaries can be seen in the following tables. Table 4 contains summaries for all chains merged and individual chains, respectively. Included in the summaries are quantiles, means, standard deviations (sd), effective sample sizes (n_eff), and split (Rhats) (the potential scale reduction derived from all chains after splitting each chain in half and treating the halves as chains). For the summary of all chains merged, Monte Carlo standard errors (se_mean) are also reported.

The selection of appropriate regressor variable can also be done by using a caterpillar plot. Caterpillar plots are popular plots in Bayesian inference for summarizing the quantiles of posterior samples. We can see in Figure 7 that the caterpillar plot is a horizontal plot of 3 quantiles of the selected distribution.

Table 4. Summary of the simulated results using rstan function with Mean stands for posterior mean, se_mean, sd for posterior standard deviation, LB, Median, UB are 2.5%, 50%, 97.5% quantiles, n_eff for number effective sample size, and Rhat, respectively

|	Mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
beta[1]	2.6908	0.2807	2.9114	-2.4083	0.6400	2.6679	4.5507	8.7606	108	0.9993
beta[2]	-1.5325	0.0270	0.4978	-2.4714	-1.8583	-1.5445	-1.2044	-0.5361	339	1.0040
beta[3]	0.1371	0.0032	0.0582	0.0265	0.0996	0.1357	0.1741	0.2578	320	1.0122
beta[4]	0.0185	0.0009	0.0150	-0.0082	0.0083	0.0179	0.0287	0.0496	299	1.0078
beta[5]	0.1174	0.0171	0.3233	-0.4502	-0.1057	0.1027	0.3428	0.7776	356	1.0034
beta[6]	-0.1274	0.0046	0.0939	-0.3117	-0.1925	-0.1227	-0.0633	0.0466	418	0.9991
shape 1	13.5279	2.6027	4.0793	0.2709	2.0477	4.9785	10.3969	61.3541	287	1.0125
shape 2	2.2235	0.1069	1.1900	0.9090	1.2989	1.8814	2.8694	5.2507	124	1.0026
shape 3	1.2650	0.3346	6.3690	0.0693	0.1233	0.2009	0.4644	8.7262	362	0.9982
lp__	-210.0986	0.1596	2.1192	-214.8266	-211.2244	-209.8324	-208.6732	-206.7228	176	1.0091
dev	418.4230	0.3054	3.9798	412.0384	415.4552	418.1524	420.4794	427.7097	170	1.0018
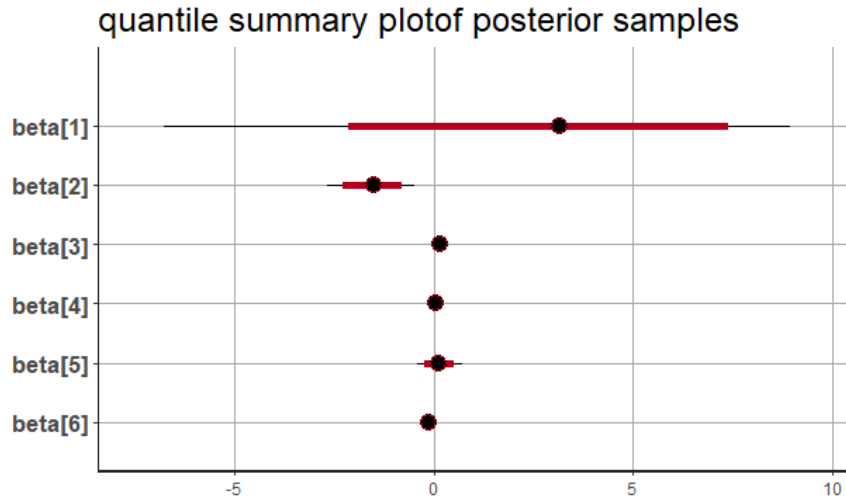
Figure 7. Caterpillar plot for Weibull Lomax model

Conclusion

To select a model for the models discussed in this paper, it is necessary to a draw a comparison among them. the result should be tabulated and analyzed as in Table 5. The exponential Lomax is the most appropriate model for the stan for the data used, as it has a minimum value of deviance as compared with Lomax and Weibull Lomax. The deviance is very good criterion for model comparisons.

Table 5. Model comparison of Lomax, Weibull Lomax, and exponential Lomax models for the myloma data; it is evident from this table that exponential Lomax is much better than Weibull Lomax and Lomax

Model	Stan deviance
Lomax	422.52
Exponential Lomax	415.91
Weibull Lomax	418.15

References

Abd-Elfattah, A. M., Alaboud, F. M., & Alharby, A. H. (2007). On sample size estimation for Lomax distribution. *Australian Journal of Basic and Applied Sciences, 1*(4), 373-378.

Abujarad, M. H., & Khan, A. A. (2018a). Bayesian survival analysis of Topp-Leone generalized family with Stan. *International Journal of Statistics and Applications, 8*(5), 274-290. Retrieved from http://article.sapub.org/10.5923.j.statistics.20180805.06.html

Abujarad, M. H., & Khan, A. A. (2018b). Exponential model: A Bayesian study with Stan. *International Journal of Recent Scientific Research, 9*(8), 28495-28506. Retrieved from http://www.recentscientific.com/exponential-model-bayesian-study-stan

Atkinson, A. B., & Harrison, A. J. (1978). *Distribution of personal wealth in Britain*. Cambridge, UK: Cambridge University Press.

Carlin, B., P., & Louis, T., A. (2009). *Bayesian methods for data analysis* (3rd edition). New York: Chapman and Hall.

Duane, S., Kennedy, A. D., Pendleton, B. J., & Roweth, D. (1987). Hybrid Monte Carlo. *Physics Letters B, 195*(2), 216-222. doi: 10.1016/0370-2693(87)91197-X

Evans, M., & Swartz, T. (1995). Methods for approximating integrals in statistics with special emphasis on Bayesian integration problems. *Statistical Science, 10*(3), 254-272. doi: 10.1214/ss/1177009938

Gelman, A., Carlin, J. B., Stern, H. S., & Rubin, D. B. (2004). *Bayesian data analysis* (2nd edition). New York: Chapman and Hall.

Gelman, A., & Hill, J. (2006). *Data analysis using regression and multilevel/hierarchical models*. Cambridge, UK: Cambridge University Press.

Hassan, A. S., & Al-Ghamdi, A. S. (2009). Optimum step-stress accelerated life testing for Lomax distribution. *Journal of Applied Sciences Research, 5*(12), 2153-2164.

Hassan, A. S., Assar, S. M., & Shelbaia, A. (2016). Optimum step stress accelerated life test plan for Lomax distribution with an adaptive type-II progressive hybrid censoring. *British Journal of Mathematics & Computer Science, 13*(2), 1-19. doi: 10.9734/BJMCS/2016/21964

Hoffman, M. D., & Gelman, A. (2014). The No-U-turn sampler: Adaptively setting path lengths in Hamiltonian Monte Carlo. *Journal of Machine Learning*

Research, 15(47), 1593-1623. Retrieved from
https://www.jmlr.org/papers/v15/hoffman14a.html

Krall, J. M., Uthoff, V. A., & Harley, J. B. (1975). A step-up procedure for selecting variables associated with survival. *Biometrics, 31*(1), 49-57. doi: 10.2307/2529709

Lomax, K. S. (1954). Business failures: Another example of the analysis of failure data. *Journal of the American Statistical Association, 49*(268), 847-852. doi: 10.1080/01621459.1954.10501239

Metropolis, N., Rosenbluth, A. W., Rosenbluth, M. N., Teller, A. H., & Teller, E. (1953). Equation of state calculations by fast computing machines. *The Journal of Chemical Physics, 21*(6), 1087-1092. doi: 10.1063/1.1699114

Myhre, J., & Saunders, S. (1982). Screen testing and conditional probability of survival. In J. Crowley & R. A. Johnson (Eds.), *Survival analysis* (pp. 166-178). Hayward, CA: Institute of Mathematical Statistics.

Tierney, L., Kass, R. E., & Kadane, J. B. (1989). Fully exponential Laplace approximations to expectations and variances of nonpositive functions. *Journal of the American Statistical Association, 84*(407), 710-716. doi: 10.1080/01621459.1989.10478824