Development and characterization of a flexible three-parameter lifetime distribution: theoretical properties and real-world applications

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Abstract

In this article, we propose a new three-parameter lifetime distribution and derive some of its properties. This new distribution is suitable for analyzing failure time data with decreasing or unimodal-shaped hazard rates. Although the moment generating function of the distribution does not exist in closed-form, all moments exist and have closed-form expressions. The nice expressions for its density function, distribution function, hazard function, and quantile function make the distribution attractive to researchers in reliability and life testing experiments. Various structural properties, including moment generating function, mean deviations, entropy measures, tail behavior, and density-quantile function, are studied. The distribution can be classified as short- or long-tailed based on the density-quantile function. We first consider maximum likelihood and Bayesian methods of estimation for complete samples and study two different real-life applications. Then, we consider the maximum likelihood and Bayesian methods for censored samples with and without cure fraction, with and without covariates, and study one real-life application in this scenario.

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1. INTRODUCTION

It is a well-known fact that the addition of one or more shape/skewness parameters to a distribution improves its flexibility to model different data and that no single distribution can be sufficient for all purposes. Consequently, new distributions are being introduced to model diverse datasets [Ley 2014, Rasekhi et al. 2016, Rasekhi et al. 2017, Das et al. 2023].

Various methods are available for incorporating additional parameter(s) into a baseline distribution. The most important among these methods are proportional hazards model, proportional reversed hazards model, proportional odds model, power transformation, Kumaraswamy generalized model, beta generalized model, transmuted model, among others. The proportional odds model is used in failure time studies to compare two or more groups of subjects. Marshall and Olkin [1997] used this idea to introduce a shape parameter to a baseline distribution and introduced the

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extensions of the exponential and Weibull distributions. Since then, many important new distributions have been introduced in statistical literature by applying this particular approach [Cordeiro et al. 2013, Kundu and Nanda 2017, Mohtashami-Borzadaran et al. 2020, Handique et al. 2020, Klakattawi et al. 2022, Escobar-Bach and Helali 2023]. The idea of proportional hazards (PH) model was first introduced by Cox [1972], and his PH model is the most celebrated model in survival analysis. Like the proportional odds model, the PH model is used in failure time studies to compare two or more groups of subjects by introducing the proportionality constant to a baseline hazard function. The same idea can be used to compare the parametric hazard function that is proportional to some baseline parametric hazard function. Important applications of this method are Burr type XII and Lomax distributions that can be obtained from baseline survival functions $(1+u^c)^{-1}$ and $(1+u/\delta)^{-1}$ respectively. The reversed hazard function is often used in reliability analysis, particularly when the lifetimes are left censored, and the time scale is reversed. Several distributions, known as exponentiated distributions, have been introduced and studied in statistical literature using the proportional reversed hazards approach. Important examples include exponentiated exponential, exponentiated Weibull, exponentiated Burr type XII, exponentiated gamma, among others [Mudholkar and Srivastava 1993, Gupta et al. 1998, Gupta and Kundu 1999, Nadarajah and Kotz 2006, Barreto-Souza et al. 2010, Cordeiro et al. 2013].

Eugene et al. [2002] introduced the beta generalized class of distributions for adding two additional shape parameters to a baseline distribution, unifying the proportional hazards and proportional reversed hazards models. Consider a random variable U with $g_U(u)$ and $G_U(u)$ as the baseline density and distribution functions, respectively. The distribution function of a new random variable T using the beta generator with two additional parameters ϕ and ψ can be obtained from

$$F_T(t) = \frac{1}{B(\phi,\psi)} \int_0^{G_U(t)} \varepsilon^{\phi-1}(1-\varepsilon)^{\psi-1} d\varepsilon = \frac{B_{G_U(t)}(\phi,\psi)}{B(\phi,\psi)} = I_{G_U(t)}(\phi,\psi), \quad (1)$$

where $B(\phi,\psi)$ denotes the complete beta function with parameters $\phi > 0$ and $\psi > 0$, $B_{G_U(t)}(\phi,\psi)$ the lower incomplete beta function, and $I_{G_U(t)}(\phi,\psi)$ the regularized incomplete beta function. The density function corresponding to the above distribution function is

$$f_T(t) = \frac{g_U(t)}{B(\phi,\psi)} [G_U(t)]^{\phi-1} [1-G_U(t)]^{\psi-1}; \quad \phi > 0, \quad \psi > 0. \quad (2)$$

The generator approach of Eugene et al. [2002] has garnered considerable

attention from researchers across various applied fields, including survival analysis, insurance, and finance. The beta-generated transformation method has recently been instrumental in the development of various new distributions across diverse fields. For example, Alexander et al. [2012] introduced a generalized beta-generated distribution to model financial data, effectively capturing the complexities of asset return behaviors. In survival analysis, Smith and Jones [2014] proposed a beta-generated Weibull distribution, achieving a superior fit compared to traditional models. To address heavy tails in insurance claim data, Lee et al. [2016] formulated a beta-generated Burr type XII distribution, demonstrating its robustness in risk assessment. Kumar and Singh [2018] expanded the application of this approach by developing a beta-generated gamma distribution tailored for reliability analysis, showcasing its adaptability in multiple contexts. In environmental data modeling, Rodriguez and Martinez [2020] utilized a beta-generated log-normal distribution, which more accurately represented skewness and kurtosis than conventional methods. Most recently, Chen et al. [2022] applied a beta-generated generalized normal distribution to synthetic aperture radar image processing, significantly enhancing the modeling of backscatter coefficients. These advancements underscore the beta-generated transformation's effectiveness in generating flexible and application-specific distributions.

2. MODEL FORMULATION

Ahmad and Danish (2024) introduced a new four-parameter lifetime distribution with density function

$$f_Z(z;a,b,c,k) = \frac{ck(kz)^{ca-1}}{B(a,b)(1+kz)^{ca+1}}\left[1-\frac{z^c}{\left(k^{-1}+z\right)^c}\right]^{b-1}; z>0,\ a>0,\ b>0,\ c>0,\ k>0, \tag{3}$$

applying the generator approach of Eugene et al. [2002] to a baseline distribution with density function

$$g_Y(y) = \frac{ck(ky)^{c-1}}{(1+ky)^{c+1}}; \quad y>0, \quad c>0, \quad k>0. \tag{4}$$

In this article, we study the sub-model of the distribution corresponding to $a=1$. The density function of the proposed distribution, named SMD distribution, is

$$f_Z(z;b,c,k) = \frac{bck(kz)^{c-1}}{(1+kz)^{c+1}}\left[1-\frac{(kz)^c}{(1+kz)^c}\right]^{b-1}; \quad b>0, \quad c>0, \quad k>0. \tag{5}$$

It may be noted that the distribution function corresponding to the density function in (5) is not in closed form like the well-known gamma distribution. However, the distribution function corresponding to the density function in (5) has a nice closed-form expression like the Weibull distribution, and it is given by

$$F_Z(z;b,c,k) = 1 - \left[1 - \frac{(kz)^c}{(1+kz)^c}\right]^b. \tag{6}$$

We plot the density function in (5) for selected combinations of parameters. The flexibility of the distribution to model different data is clear from a variety of curve shapes in Figure 1. The hazard function of the SMD distribution is

$$h(z) = \frac{bck(kz)^{c-1}}{(1+kz)^{c+1}}\left[1 - \left(\frac{kz}{1+kz}\right)^c\right]^{-1}. \tag{7}$$

We plot the hazard function for specific parameter values in Figure 2. We see that the hazard function is decreasing for $c \leq 1$ and is unimodal for $c > 1$.

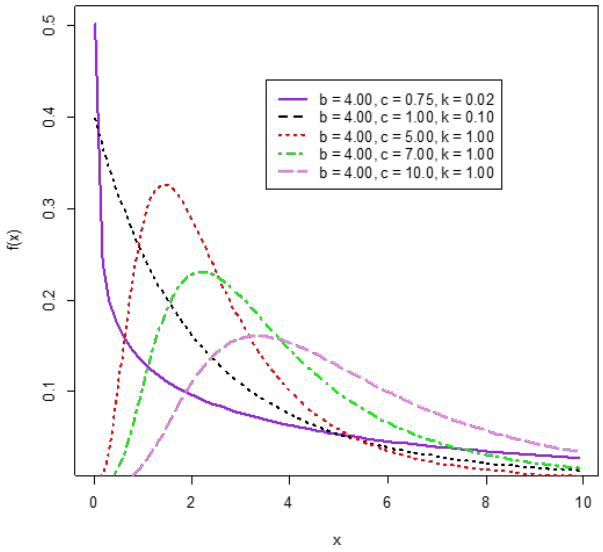

Fig. 1. Density plots of the SMD distribution.

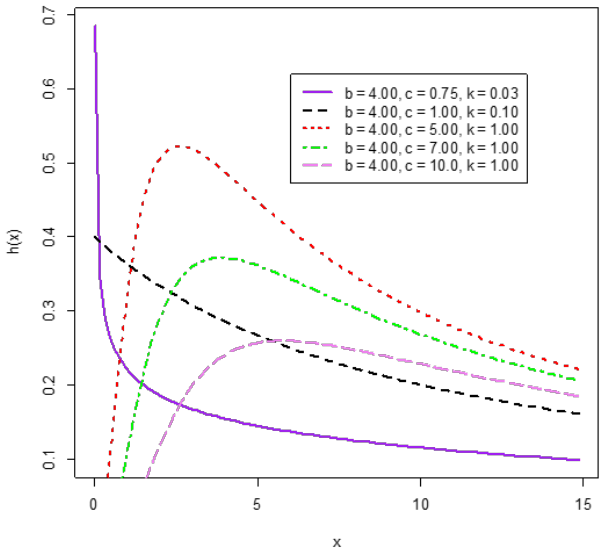

Fig. 2. Plot of hazard function for the SMD distribution.

The rth moment about zero of the SMD distribution is

$$\mu'_r = E(Z^r) = bck \int_0^\infty z^r \frac{(kz)^{c-1}}{(1+kz)^{c+1}} \left[1 - \left(\frac{kz}{1+kz}\right)^c\right]^{b-1} dz. \tag{8}$$

Using the transformation $\varepsilon = \left(\frac{kz}{1+kz}\right)^c$, we get

$$\mu'_r = \frac{b}{k^r} \int_0^1 \varepsilon^{1+\frac{r}{c}-1} (1-\varepsilon)^{b-1} \left(1-\varepsilon^{\frac{1}{c}}\right)^{-r} d\varepsilon.$$

Now using the series expansion of $\left(1-\varepsilon^{\frac{1}{c}}\right)^{-r}$ for $|\varepsilon| < 1$, we get

$$\mu'_r = \frac{b}{k^r} \sum_{j=0}^{\infty} \binom{r+j-1}{j} \int_0^1 \varepsilon^{1+\frac{r}{c}+\frac{j}{c}-1} (1-\varepsilon)^{b-1} d\varepsilon$$

$$= \frac{b}{k^r} \sum_{j=0}^{\infty} \binom{r+j-1}{j} B\left(1+\frac{r}{c}+\frac{j}{c}, b\right). \tag{9}$$

The remainder of this paper is organized as follows. Sections 2 and 3 present the proposed model along with its theoretical properties. Maximum likelihood (ML) estimation for complete samples is discussed in Section 4. In Section 5, model

selection criteria are outlined, followed by the application of these criteria to real data analysis in Section 6. The ML estimation procedures for incomplete samples and cure model are detailed in Sections 7 and 8, with corresponding empirical analyses provided in Section 9. Finally, the conclusions of the study are summarized in Section 10.

3. PROPERTIES

The moment generating function of a random variable plays an important role in statistics and uniquely determines the corresponding distribution function. The first four moments are often used to describe the location, scale, skewness, and kurtosis of a distribution. For this, we need the following theorem.

Theorem 1. If $f_Z(z;b,c,k)$ is the density function of the SMD distribution, we have a mixture representation of $f_Z(z;b,c,k)$ in terms of the baseline distribution in (4) as

$$f_Z(z;b,c,k) = \sum_{j=0}^{\infty} w_j g_Z(z;c(1+j),k), \tag{10}$$

where w_j are mixture weights given by

$$w_j = w_j(b) = \sum_{j=0}^{\infty} \frac{(-1)^j b!}{(j+1)!(b-j-1)!} \tag{11}$$

and $g_Z(z;c(a+j),k)$ are the mixture components given by

$$g_Z(z;c(1+j),k) = c(1+j)k\frac{(kz)^{c(1+j)-1}}{(1+kz)^{c(1+j)+1}}. \tag{12}$$

Proof. The density function of the SMD distribution is

$$f_Z(z;b,c,k) = \frac{bck(kz)^{c-1}}{(1+kz)^{c+1}}\left[1-\frac{(kz)^c}{(1+kz)^c}\right]^{b-1}.$$

Using the series expansion of $\left[1-\frac{(kz)^c}{(1+kz)^c}\right]^{b-1}$ for $\left\|\frac{(kz)^c}{(1+kz)^c}\right\| < 1$, we get

$$f_Z(z;b,c,k) = \sum_{j=0}^{\infty} \frac{(-1)^j b!}{(j+1)!(b-j-1)!} c(1+j)k\frac{(kz)^{c(1+j)-1}}{(1+kz)^{c(1+j)+1}}$$

$$= \sum_{j=0}^{\infty} w_j g_Z(z;c(1+j),k). \tag{13}$$

3.1. The Moment Generating Function

The moment generating function of the SMD distributed random variable Z can be written as

$$M_0(t) = E\left[\exp(tZ)\right] = \int_0^\infty \exp(tz) f_Z(z;b,c,k)dz.$$

Using the series expansion of $f_Z(z;b,c,k)$, we get

$$M_0(t) = \int_0^\infty \exp(tz) \sum_{j=0}^{\infty} \frac{(-1)^j b!}{(j+1)!(b-j-1)!} c(1+j)k \frac{(kz)^{c(1+j)-1}}{(1+kz)^{c(1+j)+1}} dz$$

$$= \sum_{j=0}^{\infty} \frac{(-1)^j b!}{(j+1)!(b-j-1)!} M_j(t) = \sum_{j=0}^{\infty} w_j M_j(t), \tag{14}$$

where $M_j(t)$ is the moment generating function of $Z \sim g_Z(z;c(1+j),k)$ and can be computed as follows.

$$M_j(t) = \int_0^\infty \exp(tz) c(1+j)k \frac{(kz)^{c(1+j)-1}}{(1+kz)^{c(1+j)+1}} dz.$$

Substituting $kz = y$, we have

$$M_j(t) = c(1+j) \int_0^\infty \exp\left(\frac{t}{k}y\right) y^{c(1+j)-1} (1+y)^{-c(1+j)-1} dy. \tag{15}$$

We need the following result from Prudnikov et al. [1986] which holds for γ and δ positive integers, $\eta > 0$ and $\xi > -1$.

$$I\left(\eta, \xi, \frac{\gamma}{\delta}, \tau\right) = \int_0^\infty \exp(-\eta y) y^\xi \left(1 + y^{\frac{\gamma}{\delta}}\right)^\tau dy$$

$$= \frac{\delta^{-\tau} \gamma^{\xi+\frac{1}{2}}}{(2\pi)^{\frac{(\gamma-1)}{2}} \Gamma(-\tau) \eta^{\xi+1}} G^{\delta,\delta+\gamma}_{\delta+\gamma,\delta}\left(\frac{\gamma^\gamma}{\eta^\gamma}\middle\| \begin{matrix} \Delta(\gamma,-\xi), \Delta(\delta,\tau+1) \\ \Delta(\delta,0) \end{matrix}\right), \tag{16}$$

where

$$G^{m,n}_{p,q}\left(y\middle\| \begin{matrix} a_1,a_2,\ldots,a_p \\ b_1,b_2,\ldots,b_q \end{matrix}\right) = \frac{1}{2\pi i} \int_L \frac{\prod_{j=1}^m \Gamma(b_j+t) \prod_{j=1}^n \Gamma(1-a_j-t)}{\prod_{j=n+1}^p \Gamma(a_j+t) \prod_{m+1}^q \Gamma(1-b_j-t)} y^{-t} dt,$$

$$\Delta(\delta,b) = \frac{b}{\delta}, \frac{b+1}{\delta}, \frac{b+2}{\delta}, \ldots, \frac{b+\delta}{\delta},$$

$i = \sqrt{-1}$ and L is the integral path. Interested readers are referred to [Gradshteyn

and Ryzhik 2000] and [Paranaíba et al. 2011] for further details. Now taking $\frac{\gamma}{\delta} = 1$ and $t < 0$ in (16), we can compute the moment generating function $M_j(t)$ as

$$M_j(t) = c(1+j)I\left(-\frac{t}{k}, c(1+j)-1, \frac{1}{1}, -c(1+j)-1\right).$$

Finally, the moment generating function in (14) of the SMD distribution for $t < 0$ is

$$M_0(t) = c\sum_{j=0}^{\infty}(1+j)w_j I\left(-\frac{t}{k}, c(1+j)-1, \frac{1}{1}, -c(1+j)-1\right). \tag{17}$$

3.2. Mean Deviations

The mean deviation from mean (μ) and the mean deviation from median (ν) are often used to measure the dispersion of the data assumed to follow some distribution. In this subsection, we derive these measures for the SMD distribution. The mean deviation from mean, say ρ_1, is defined by

$$\rho_1 = E|Z-\mu| = \int_0^{\infty}|z-\mu|f_Z(z)dz$$

$$= -\int_0^{\mu}(z-\mu)f_Z(z)dz + \int_{\mu}^{\infty}(z-\mu)f_Z(z)dz$$

$$= -\int_0^{\mu}zf_Z(z)dz + \int_0^{\mu}\mu f_Z(z)dz + \int_{\mu}^{\infty}zf_Z(z)dz - \int_{\mu}^{\infty}\mu f_Z(z)dz$$

$$= \mu\left(\int_0^{\mu}f_Z(z)dz - 1 + \int_0^{\mu}f_Z(z)dz\right) + 2\int_{\mu}^{\infty}zf_Z(z)dz$$

$$= 2\mu F_Z(\mu) - 2\mu + 2\Upsilon(\mu),$$

where

$$\Upsilon(\mu) = \int_{\mu}^{\infty}zf_Z(z)dz.$$

The mean deviation from median, say ρ_2, is defined by

$$\rho_2 = E|Z-\nu| = \int_0^{\infty}|z-\nu|f_Z(z)dz$$

$$= -\int_0^{\mu}(z-\nu)f_Z(z)dz + \int_{\mu}^{\infty}(z-\nu)f_Z(z)dz$$

$$= -\int_0^{\nu} z f_Z(z)dz + \int_0^{\nu} \nu f_Z(z)dz + \int_{\nu}^{\infty} z f_Z(z)dz - \int_{\nu}^{\infty} \nu f_Z(z)dz$$

$$= 2\Upsilon(\mu) - \mu.$$

We can compute the distribution function $F_Z(\mu)$ at mean $\mu = \mu_1'$ from (6) and the quantity $\Upsilon(\mu)$ as follows. Using the series form of the SMD density function, we have

$$\Upsilon(\mu) = \int_{\mu}^{\infty} z f_Z(z)dz = \sum_{j=0}^{\infty} w_j \int_{\mu}^{\infty} zc(1+j)k \frac{(kz)^{c(1+j)-1}}{(1+kz)^{c(1+j)+1}} dz.$$

Now using the transformation $x = kz$, we have

$$\Upsilon(\mu) = \frac{c}{k} \sum_{j=0}^{\infty} w_j (1+j) \int_{k\mu}^{\infty} x^{c(1+j)} (1+x)^{-c(1+j)-1} dx. \tag{18}$$

The integral in the last expression can be calculated using the procedure suggested by Paranaíba et al. [2011].

3.3. Entropy Measures

Entropy is a measure of uncertainty or disorder; it measures the degree to which the probability of the system is spread out over different possible states. Different measures of entropy are studied in the literature. We discuss the most important of them, namely, Shannon entropy and Rényi entropy for the Danish distribution. The Shannon entropy, say E_S, is defined by

$$E_S = E\left[-\log\left(f(Z)\right)\right]$$

$$= -E\left[\log\left(bck \frac{1}{(1+kz)^2}\left(\frac{kz}{1+kz}\right)^{c-1}\left[1-\left(\frac{kz}{1+kz}\right)^{c}\right]^{b-1}\right)\right]$$

$$= -\log(bck) + 2E\left[\log(1+kZ)\right] - (c-1)E\left[\log\left(\frac{kZ}{1+kZ}\right)\right] - (b-1)E\left[\log\left\{1-\left(\frac{kZ}{1+kZ}\right)^{c}\right\}\right],$$

where

$$E\left[\log\left\{1-\left(\frac{kZ}{1+kZ}\right)^{c}\right\}\right] = \int_0^{\infty} \log\left\{1-\left(\frac{kz}{1+kz}\right)^{c}\right\} bck \frac{(kz)^{c-1}}{(1+kz)^{c+1}}\left[1-\left(\frac{kz}{1+kz}\right)^{c}\right]^{b-1} dz$$

$$= b\int_0^1 \log(1-y)(1-y)^{b-1}dy = \left\{\Psi(b) - \Psi(1+b)\right\},$$

$$E\left[\log\left(\frac{kZ}{1+kZ}\right)\right] = \int_0^{\infty} \log\left(\frac{kz}{1+kz}\right) bck \frac{(kz)^{c-1}}{(1+kz)^{c+1}}\left[1-\left(\frac{kz}{1+kz}\right)^{c}\right]^{b-1} dz$$

$$= \frac{b}{c}\int_0^1 \log(y)(1-y)^{b-1}dy = \frac{1}{c}\left\{\Psi(1)-\Psi(1+b)\right\},$$

and

$$E\left[\log(1+kZ)\right] = \int_0^\infty \log(1+kz)bck\frac{(kz)^{c-1}}{(1+kz)^{c+1}}\left[1-\left(\frac{kz}{1+kz}\right)^c\right]^{b-1}dz$$

$$= -b\int_0^1 \log\left(1-y^{\frac{1}{c}}\right)(1-y)^{b-1}dy$$

$$= E_1\left\{\log\left(1-Y^{\frac{1}{c}}\right)\right\}, \tag{19}$$

$$= \frac{\sum_{i=M+1}^{N}\log\left(1-y_i^{\frac{1}{c}}\right)}{N-M} = A_1, \tag{20}$$

where E_1 in (19) denotes the expectation with respect to the beta distribution with parameters 1 and b, expression in (20) follows from the Gibbs sampling procedure with burn-in M and $\Psi(.)$ denotes the digamma function. So, the Shannon entropy can be obtained from

$$E_S = -\log(bck) + 2A_1 - \left(1-\frac{1}{c}\right)\left\{\Psi(1)-\Psi(1+b)\right\} - (b-1)\left\{\Psi(b)-\Psi(1+b)\right\}.$$

The Rényi entropy, say E_R, is defined by

$$E_R = \frac{1}{1-\delta}\log\left[\int_0^\infty \left\{f(z)\right\}^{\delta-1}dz\right], \quad \delta > 0 \quad \& \quad \delta \neq 1.$$

The definite integral can be evaluated as

$$\int_0^\infty \left\{f(z)\right\}^{\delta}dz = \int_0^\infty \left\{bck\frac{(kz)^{c-1}}{(1+kz)^{c+1}}\left[1-\left(\frac{kz}{1+kz}\right)^c\right]^{b-1}\right\}^{\delta}dz$$

Using the transformation $y = \left(\frac{kz}{1+kz}\right)^c$, we get

$$\int_0^\infty \left\{f(z)\right\}^{\delta}dz = (bck)^{\delta-1}\int_0^1 \left(1-y^{\frac{1}{c}}\right)^{2(\delta-1)} y^{\delta(1-\frac{1}{c})+\frac{1}{c}-1}(1-y)^{\delta(b-1)+1-1}dy$$

$$= (bck)^{\delta-1}E_2\left\{\left(1-Y^{\frac{1}{c}}\right)^{2(\delta-1)}\right\}, \tag{21}$$

$$= \frac{(ck)^{\delta-1}}{B^{\delta-1}(a,b)} \frac{\sum_{i=M+1}^{N} \left(1 - y_i^{\frac{1}{c}}\right)^{2(\delta-1)}}{N-M}, \tag{22}$$

where E_2 in (21) denotes the expectation with respect to the beta distribution with parameters $\delta(1-\frac{1}{c})+\frac{1}{c}$ and $\delta(b-1)+1$ and expression in (22) follows accordingly. So, the Shannon entropy can be obtained from

$$E_R = \frac{1}{1-\delta} \log \left[(bck)^{\delta-1} \frac{\sum_{i=M+1}^{N} \left(1 - y_i^{\frac{1}{c}}\right)^{2(\delta-1)}}{N-M} \right]. \tag{23}$$

3.4. Tail Behavior

Tail behavior of a probability distribution plays an important role in statistics, particularly in reliability and extreme value theories. A distribution can be classified into one of the three categories depending on its tail behavior. There are many distribution classification criteria in statistical literature. Parzen [1979] introduced the density-quantile function to classify the category of a distribution and showed that the density-quantile function of many distributions is of the form

$$fQ(u) \sim (1-u)^{\alpha}, \tag{24}$$

where f is the density function, Q the quantile function, α is called the tail exponent parameter, and $f1(u) \sim f2(u)$ denotes that the ratio $\frac{f2(u)}{f2(u)}$ tends to a positive finite constant as u approaches 1. A distribution is said to be short-, medium-, or long-tailed according to $\alpha < 1$, $\alpha = 1$, or $\alpha > 1$ respectively. A more precise statement corresponding to (24) is given by Rojo and Ott [2010] as

$$fQ(u) = L(u)(1-u)^{\alpha}, \tag{25}$$

where $L(.)$ is a slowly varying function from the left at 1.

The quantile functions of the SMD distribution is

$$Q(u) = \frac{1}{k} \frac{\left\{1 - (1-u)^{\frac{1}{b}}\right\}^{1/c}}{\left[1 - \left\{1 - (1-u)^{\frac{1}{b}}\right\}^{1/c}\right]}$$

and the corresponding density-quantile function is

$$fQ(u) = bck\left\{1-(1-u)^{\frac{1}{b}}\right\}^{1-\frac{1}{c}}\left[1-\left\{1-(1-u)^{\frac{1}{b}}\right\}^{\frac{1}{c}}\right]^2(1-u)^{1-\frac{1}{b}}$$

$$= \begin{cases} L(u)(1-u)^{1-\frac{1}{b}}; & b>1 \\ bk(1-u)^{1+\frac{1}{b}}; & c=1 \end{cases} \tag{26}$$

where

$$L(u) = bck\left\{1-(1-u)^{\frac{1}{b}}\right\}^{1-\frac{1}{c}}\left[1-\left\{1-(1-u)^{\frac{1}{b}}\right\}^{\frac{1}{c}}\right]^2.$$

The expressions in (26) indicate that the distribution can have short- or long-tailed based on the density-quantile function classification criterion.

4. COMPLETE SAMPLE ESTIMATION

For an observed sample, say $O = \{x_i; i = 1,2,\ldots,n\}$, of size n from the SMD distribution, the likelihood function denoted by $l(\omega\|O)$ is

$$l(\omega\|O) = \prod_{i=1}^{n} f_X(x_i;\omega) = \prod_{i=1}^{n} bck\frac{(kx_i)^{c-1}}{(1+kx_i)^{c+1}}\left[1-\left(\frac{kx_i}{1+kx_i}\right)^c\right]^{b-1}$$

$$= (bck)^n\prod_{i=1}^{n}(kx_i)^{c-1}\prod_{i=1}^{n}(1+kx_i)^{-c-1}\prod_{i=1}^{n}\left(1-\left(\frac{kx_i}{1+kx_i}\right)^c\right)^{b-1}. \tag{27}$$

where $\omega' = (b,c,k)$. The log-likelihood function, say $L(\omega\|O)$, is

$$L(\omega\|O) = n\ln(c) + n\ln(k) + n\ln(b) + (b-1)\sum_{i=1}^{n}\ln\left\{1-\left(\frac{kx_i}{1+kx_i}\right)^c\right\}$$
$$+ (c-1)\sum_{i=1}^{n}\ln(kx_i) - (c+1)\sum_{i=1}^{n}\ln(1+kx_i)$$

The ML estimates are solutions to the following score equations

$$\frac{\partial L}{\partial b} = n\Psi(1+b) - n\Psi(b) - \sum_{i=1}^{n}\ln\left\{1-\left(\frac{kx_i}{1+kx_i}\right)^c\right\} = 0$$

$$\frac{\partial L}{\partial c} = \frac{n}{c} + \sum_{i=1}^{n}\ln(kx_i) - \sum_{i=1}^{n}\ln(1+kx_i) - (b-1)\sum_{i=1}^{n}\frac{\left(\frac{kx_i}{1+kx_i}\right)^c\ln\left(\frac{kx_i}{1+kx_i}\right)}{1-\left(\frac{kx_i}{1+kx_i}\right)^c} = 0,$$

$$\frac{\partial L}{\partial k}=\frac{n}{k}+\frac{n(c-1)}{k}-(c+1)\sum_{i=1}^{n}\frac{x_i}{1+kx_i}-c(b-1)\sum_{i=1}^{n}\frac{\frac{x_i}{(1+kx_i)^2}\left(\frac{kx_i}{1+kx_i}\right)^{c-1}}{1-\left(\frac{kx_i}{1+kx_i}\right)^{c}}=0.$$

We see that the ML estimator does not exist in closed form; we need some statistical computer software to solve the score equations using some iterative procedure. We use R software to find the ML estimate using the Newton-Raphson iterative procedure. Under standard regularity conditions of ML estimators, we can state that

$$\left(\widehat{\Omega}-\omega\right)\sim N_3(0,\Theta),$$

where $\widehat{\Omega}$ denotes the vector estimator corresponding to the vector parameter ω and Θ is the inverse of the negative of the Hessian matrix evaluated at the ML estimate $\widehat{\omega}=\left(\widehat{b},\widehat{c},\widehat{k}\right)$.

For a Bayesian estimation of parameters, one needs prior distributions of these parameters. These prior distributions depend upon the knowledge about the parameters and the experience of similar phenomena. We assume the following independent gamma priors for unknown quantities

$$\left.\begin{aligned}\pi_1(b)&=g(b;a_1,b_1)=\frac{{b_1}^{a_1}}{\Gamma(a_1)}b^{a_1-1}e^{-b_1b};b>0,a_1,b_1>0\\ \pi_2(c)&=g(c;a_2,b_2)=\frac{{b_2}^{a_2}}{\Gamma(a_2)}c^{a_2-1}e^{-b_2c};c>0,a_2,b_2>0\\ \pi_3(k)&=u(k;a_3,b_3)=\frac{1}{b_3-a_3};-\infty<a_3<k<b_3<\infty\end{aligned}\right\}\tag{28}$$

Our prior assumptions of the independent gamma distributions for shape parameters and an independent uniform distribution for the scale parameter are flexible enough to cover informative and noninformative, flat and vague priors. The joint prior density can be written as

$$\pi(\omega)\propto b^{a_1-1}c^{a_2-1}\exp(-b_1b)\exp(-b_2c).\tag{29}$$

The joint posterior distribution can be obtained from (20) and (22) as

$$\pi(\omega\|O)\propto l(\omega\|O)\times\pi(\omega)=(bck)^n\prod_{i=1}^{n}(kx_i)^{c-1}\prod_{i=1}^{n}(1+kx_i)^{-c-1}$$

$$\times\prod_{i=1}^{n}\left(1-\left(\frac{kx_i}{1+kx_i}\right)^{c}\right)^{b-1}b^{a_1-1}c^{a_2-1}\exp(-b_1b)\exp(-b_2c),$$

$$\propto b^{n+a_1-1}\exp\left[-\left\{b_1-\sum_{i=1}^{n}\ln(1-E_i^c)\right\}b\right]$$
$$\times c^{n+a_2-1}\exp\left[-\left\{b_2-\sum_{i=1}^{n}\ln(E_i)\right\}c\right]$$
$$\times k^{-n}\exp\left\{\sum_{i=1}^{n}\ln(E_i)\right\}\exp\left\{-\sum_{i=1}^{n}\ln(1-E_i^c)\right\}.$$

where $E_i=\frac{kx_i}{1+kx_i}$. Thus, the posterior expectation of any function of parameters, say $U(\omega)$, is

$$E\left(U(\omega)\|O\right)=\frac{\int_0^\infty U(\omega)\pi(\omega\|O)\,d\omega}{\int_0^\infty \pi(\omega\|O)\,d\omega}. \tag{30}$$

It is apparent that explicit expressions for the Bayes estimates are not possible; analytical or Markov chain Monte Carlo (MCMC) methods are needed for the Bayes estimates. We propose the MCMC Gibbs sampling method to obtain the Bayes estimate and the associated HPD credible intervals. In the last few years, the MCMC Gibbs sampling scheme has become the most popular method of sampling complex, intractable, and high-dimensional posterior distributions. The package R2OpenBUGS in R statistical software provides an enabling environment for implementing the MCMC Gibbs sampling.

5. MODEL SELECTION CRITERIA

Different model selection criteria are proposed in the literature to compare competing models. The most common classical measure in this regard is the Akaike information criterion (AIC) recognized by

$$AIC=-2L\left(\widehat{\gamma},\widehat{\beta}\middle\|O\right)+2p,$$

where $L\left(\widehat{\gamma},\widehat{\beta}\middle\|O\right)$ is the ML estimate of $L(\gamma,\beta\|O)$ and p implies the dimension of the parameter space corresponding to the model in question. The model which has the least AIC value is preferred. When comparing hierarchical models, researchers often use the deviance information criterion (DIC), which depends on the deviance given by

$$D(\gamma,\beta)=-2L(\gamma,\beta\|O)+c,$$

where $L(\gamma,\beta\|O)$ is as before and c is simply the constant not required for comparing hierarchical models. If we denote the mean of the posterior distribution

by $\left(\widetilde{\gamma},\widetilde{\beta}\right)$, then DIC

$$= D\left(\widetilde{\gamma},\widetilde{\beta}\right) + 2pD,$$

where pD denotes the number of model parameters given by

$$pD = \bar{D} - D\left(\widetilde{\gamma},\widetilde{\beta}\right).$$

The measures $\bar{D}$ and $D\left(\widetilde{\gamma},\widetilde{\beta}\right)$ represent the expectation of the deviance with respect to the posterior distribution and the Bayesian estimate of the deviance at $\left(\widetilde{\gamma},\widetilde{\beta}\right)$, respectively. Like the AIC, the model which has the smallest DIC value is preferred.

6. COMPLETE SAMPLE REAL DATA ANALYSIS

In this section, we apply the proposed model to real datasets to illustrate its flexibility and appropriateness. The first dataset pertains to the remission times of patients with bladder cancer [Lee and Wang 2013] and is used here for illustration purposes only. The remission times (in months) of 128 patients are 0.08, 2.09, 3.48, 4.87, 6.94, 8.66, 13.11, 23.63, 0.20, 2.23, 3.52, 4.98, 6.97, 9.02, 13.29, 0.40, 2.26, 3.57, 5.06, 7.09, 9.22, 13.80, 25.74, 0.50, 2.46, 3.64, 5.09, 7.26, 9.47, 14.24, 25.82, 0.51, 2.54, 3.70, 5.17, 7.28, 9.74, 14.76, 26.31, 0.81, 2.62, 3.82, 5.32, 7.32, 10.06, 14.77, 32.15, 2.64, 3.88, 5.32, 7.39, 10.34, 14.83, 34.26, 0.90, 2.69, 4.18, 5.34, 7.59, 10.66, 15.96, 36.66, 1.05, 2.69, 4.23, 5.41, 7.62, 10.75, 16.62, 43.01, 1.19, 2.75, 4.26, 5.41, 7.63, 17.12, 46.12, 1.26, 2.83, 4.33, 5.49, 7.66, 11.25, 17.14, 79.05, 1.35, 2.87, 5.62, 7.87, 11.64, 17.36, 1.40, 3.02, 4.34, 5.71, 7.93, 11.79, 18.10, 1.46, 4.40, 5.85, 8.26, 11.98, 19.13, 1.76, 3.25, 4.50, 6.25, 8.37, 12.02, 2.02, 3.31, 4.51, 6.54, 8.53, 12.03, 20.28, 2.02, 3.36, 6.76, 12.07, 21.73, 2.07, 3.36, 6.93, 8.65, 12.63, 22.69. We

obtain the ML estimates (ests) of parameters (pars) and the associated standard errors (SEs) and 95% confidence intervals and report the results in Table 1. For Bayesian estimation, we first check the convergence of the Gibbs sampling procedure by drawing trace plots of parameters for two independent MCMC chains in Figure 3. We see that all the plots show well mixing of the chains and indicate no problem of convergence as they move along their constant means and variances without any serial correlations. We can say that both the chains represent the stationary time series. Next, we draw the

autocorrelation plots at different lags in Figure 4. All the plots start with high autocorrelations and spike out very quickly. We can observe that the sample

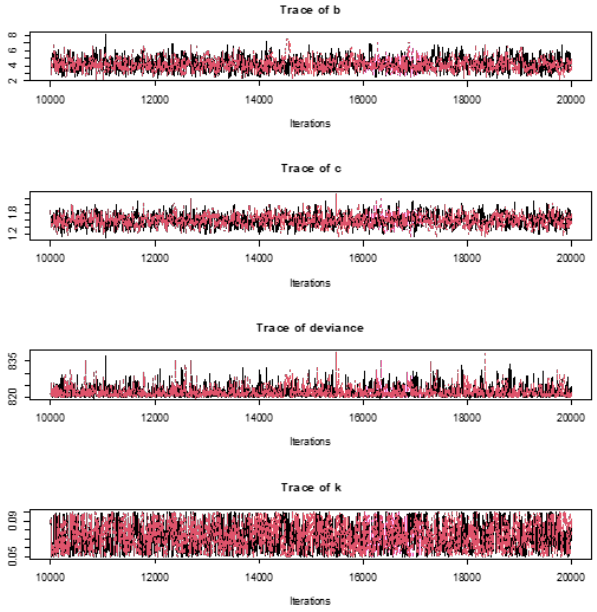

Fig. 3. Trace plots of parameters for two independent chains for remission times data.

autocorrelations are larger at shorter lags and smaller at larger lags and decline to zero very rapidly as the lengths of lags increase. We can say that there is no abnormality with the MCMC Gibbs sampling procedure. Now we obtain Bayesian estimates and associated standard errors and 95% HPD intervals and report the results in Table 1. For goodness of the methods, we compute AIC and DIC measures in Table 1. Based on these measures, we can say that the Bayesian method fits better to this data than the ML method. To further observe the goodness of fit of the proposed distribution, we estimate the survival function of the distribution and fit it to the K-M survival curve in Figure 5. We see that there is a very good agreement between the survival estimates for remission times data.

Since a single dataset is insufficient to assess the appropriateness of the model under investigation, we apply the proposed model to a second real dataset. This second dataset, which pertains to the breaking stress of carbon fibers [Nichols and Padgett 2006] and is used here for just illustration of the proposed methodology. The breaking stress of carbon fibers in Gba are 3.70, 2.74, 2.73, 2.50, 3.60, 3.11, 3.27, 2.87, 1.47, 3.11, 4.42, 2.41, 3.19, 3.22, 1.69, 3.28, 3.09, 1.87, 3.15, 4.90, 3.75, 2.43, 2.95, 2.97, 3.39, 2.96, 2.53, 2.67, 2.93, 3.22, 3.39, 2.81, 4.20, 3.33, 2.55, 3.31, 3.31, 2.85, 2.56,

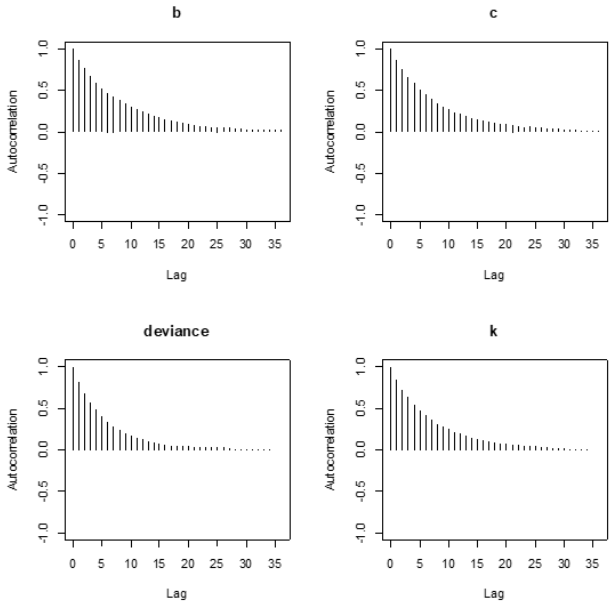

Fig. 4. Autocorrelation plots of parameters and deviance for remission times data.

Table I. ML and Bayesian Estimates with Standard Errors and Confidence Intervals

Parameters	ML Estimates			Bayesian Estimates		
	Est	SE	Confidence Interval	Est	SE	HPD Interval
b	4.2307	1.8033	(0.6961, 7.7652)	4.1562	0.8291	(2.6641, 5.8240)
c	1.5256	0.2747	(0.9872, 2.0639)	1.5891	0.1581	(1.2972, 1.9120)
k	0.0648	0.0420	(0.0000, 0.1471)	0.0728	0.0142	(0.0501, 0.0964)
GoF	AIC = 825.91			DIC = 824.0		

3.56, 3.15, 2.35, 2.55, 2.59, 2.38, 2.81, 2.77, 2.17, 2.83, 1.92, 1.41, 3.68, 2.97, 1.36, 0.98, 2.76, 4.91, 3.68, 1.84, 1.59, 3.19, 1.57, 0.81, 5.56, 1.73, 1.59, 2.00, 1.22, 1.12, 1.71, 2.17, 1.17, 5.08, 2.48, 1.18, 3.51, 2.17, 1.69, 1.25, 4.38, 1.84, 0.39, 3.68, 2.48, 0.85, 1.61, 2.79, 4.70, 2.03, 1.80, 1.57, 1.08, 2.03, 1.61, 2.12, 1.89, 2.88, 2.82, 2.05, 3.65. For this data too, we obtain the ML estimates and the associated standard errors and 95% confidence intervals and report the results in Table 2. As before for Bayesian estimation,

we first check the convergence of the Gibbs sampling procedure by plotting trace

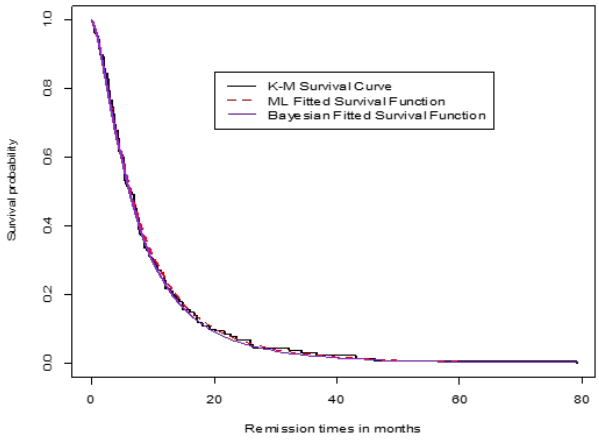

Fig. 5. Estimated survival function of the SMD distribution fitted to K-M survival curve for remission times data.

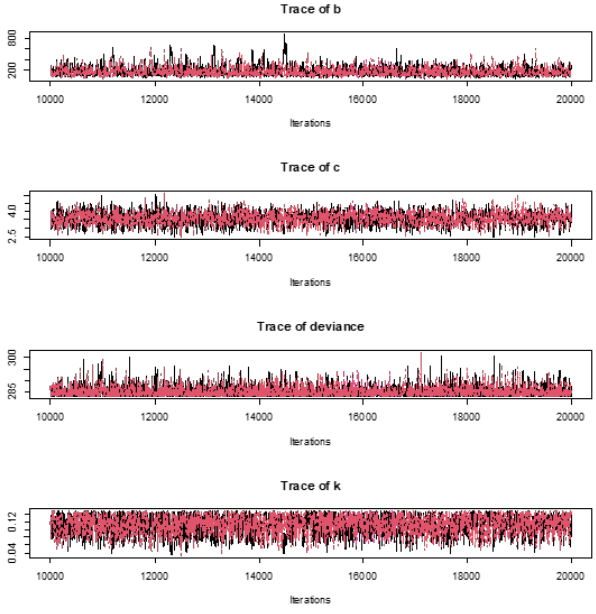

Fig. 6. Trace plots of parameters for two independent chains for breaking stress data.

plots of parameters for two independent MCMC chains in Figure 4. We see that all the

plots indicate no problem of convergence. We can say that both the chains represent the stationary time series. Next, we draw the autocorrelation plots at different lags in Figure 7. We can see that the sample autocorrelations are larger at shorter lags and smaller at larger lags and decline to zero very rapidly as the lengths of lags increase. We can say

Table II. ML and Bayesian Parameter Estimates for Second Model

Parameters	ML Estimates			Bayesian Estimates		
	Est	SE	Confidence Interval	Est	SE	HPD Interval
b	421.56	5.9924	(409.82, 4033.3)	244.56	3.5321	(89.771, 427.11)
c	3.3203	0.3909	(2.5441, 4.0865)	3.2912	0.2615	(2.7932, 3.8224)
k	0.0663	0.0167	(0.0336, 0.0989)	0.0822	0.0123	(0.0593, 0.0997)
GoF	AIC = 288.64			DIC = 286.0		

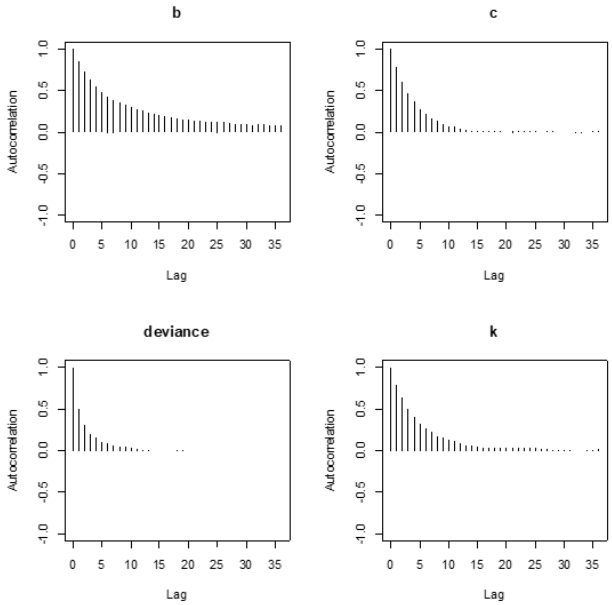

Fig. 7. Autocorrelation plots of parameters and deviance for breaking stress data.

that there is no problem with convergence. Now we obtain Bayesian estimates and associated standard errors and 95% HPD intervals for this data too and report the

results in Table 2. We also compute the AIC and DIC measures in Table 2. Based on these measures, we can say that the Bayesian method fits better to this data too than the ML method. To further observe the goodness of fit of the proposed distribution, we estimate the survival function of the distribution and fit it to the K-M survival curve in Figure 8. We see that there is a very good agreement between the survival estimates for remission times data.

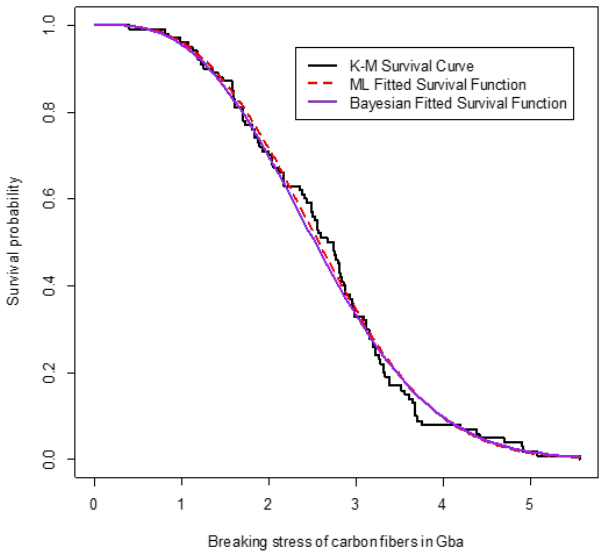

Fig. 8. Estimated survival function of the SMD distribution fitted to K-M survival curve for breaking stress data.

7. CENSORED SAMPLE ESTIMATION

Censoring is an unavoidable feature of reliability and life testing experiments; we, therefore, consider the estimation of our model with censored samples. In this section, we consider the general random censorship model where it is assumed that a sample of n identical patients enter a life testing experiment after some medical treatment and their survival times during the experiment are recorded. It is further assumed that the independent and identically distributed (iid) random variables, say $T_1, T_2, \ldots, T_n$, with distribution function $F_T(.)$ and density function $f_T(.)$ represent their failure times

and the iid random variables, say $C_1, C_2, \ldots, C_n$, with distribution function $F_C(.)$ and density function $f_C(.)$ denote their censoring times. We actually observe iid random pairs (Y_i, D_i), where $Y_i = \min(T_i, C_i)$ and $D_i = I(T_i \leq C_i)$ for $i = 1, 2, \ldots, n$. Usually, the censoring is non-informative, and the censoring time distribution does not contain any parameter of interest. Under the usual independence of censoring and failure time variables, the likelihood function for observed data, say $O = \{y_i, d_i; i = 1, 2, \ldots, n\}$, can be written as

$$l(\omega \| O) = \prod_{i=1}^{n} [f_T(y_i)]^{d_i} [S_T(y_i)]^{1-d_i}$$

$$= \prod_{i=1}^{n} \left[bck \frac{(ky_i)^{c-1}}{(1+ky_i)^{c+1}} \left[1 - \left(\frac{ky_i}{1+ky_i} \right)^c \right]^{b-1} \right]^{d_i} \left[\left\{ 1 - \frac{(ky_i)^c}{(1+ky_i)^c} \right\}^b \right]^{1-d_i} \tag{31}$$

The corresponding log-likelihood function is

$$L(\omega \| O) = \sum_{i=1}^{n} d_i \ln \left\{ bck \frac{(ky_i)^{c-1}}{(1+ky_i)^{c+1}} \right\} + (b-1) \sum_{i=1}^{n} d_i \ln \left\{ 1 - \frac{(ky_i)^c}{(1+ky_i)^c} \right\}$$
$$+ b \sum_{i=1}^{n} (1-d_i) \ln \left\{ 1 - \frac{(ky_i)^c}{(1+ky_i)^c} \right\}.$$

The ML estimate $\widehat{\omega}$ of ω can be obtained by maximizing the log-likelihood function $L(\omega \| O)$. Under standard regularity conditions of ML estimators, we can state that $\left(\widehat{\vartheta} - \omega \right) \sim N(0, V)$, where $\widehat{\vartheta}$ denotes the vector estimator corresponding to the vector parameter ω and V is the inverse of the negative of the Hessian matrix evaluated at the ML estimate $\widehat{\vartheta}$.

For Bayesian estimation, the joint posterior distribution can be obtained by combining the likelihood function in (31) and the joint prior in (29) as

$$\pi(\omega \| O) \propto l(\omega \| O) \times \pi(\omega)$$

$$= \prod_{i=1}^{n} \left[bck \frac{(ky_i)^{c-1}}{(1+ky_i)^{c+1}} \left\{ 1 - \left(\frac{ky_i}{1+ky_i} \right)^c \right\}^{-1} \right]^{d_i} \left\{ 1 - \frac{(ky_i)^c}{(1+ky_i)^c} \right\}^b$$

$$\times b^{a_1 - 1} c^{a_2 - 1} \exp(-b_1 b) \exp(-b_2 c),$$

$$= (bck)^{\sum_{i=1}^{n} d_i} \prod_{i=1}^{n} E_i^{(c-1)d_i} \prod_{i=1}^{n} \{1 - E_i^c\}^{-d_i} \prod_{i=1}^{n} (1 - E_i)^{2d_i}$$

$$\times \prod_{i=1}^{n} \{1-E_i^c\}^b \, b^{a_1-1} c^{a_2-1} \exp(-b_1 b) \exp(-b_2 c),$$

$$\propto b^{a_1+\sum_{i=1}^n d_i-1} \exp\left[-\left\{b_1 - \sum_{i=1}^{n} \ln(1-E_i^c)\right\} b\right]$$

$$\times c^{a_2+\sum_{i=1}^n d_i-1} \exp\left[-\left\{b_2 - \sum_{i=1}^{n} d_i \ln(E_i)\right\} c\right] k^{\sum_{i=1}^n d_i}$$

$$\times exp\left\{-\sum_{i=1}^{n} d_i \ln(E_i) + 2\sum_{i=1}^{n} d_i \ln(1-E_i) - \sum_{i=1}^{n} d_i \ln(1-E_i^c)\right\}.$$

Thus, the posterior expectation of any function of parameters, say $U(\omega)$, is

$$E(U(\omega)\|O) = \frac{\int_0^\infty U(\omega)\pi(\omega\|O)\, d\omega}{\int_0^\infty \pi(\omega\|O)\, d\omega}.$$

We see again that the explicit expressions for the Bayes estimates are not possible; some numerical approximation methods are required for the Bayes estimates. We propose the MCMC Gibbs sampling method to obtain the Bayes estimate and the associated HPD credible intervals. We use the package R2OpenBUGS in R statistical software for the implementation of the MCMC Gibbs sampling.

8. CURE MODEL FOR LONG-TERM SURVIVORS

In this section, we consider the promotion time cure model (PTCM) where it is assumed that for a subject in a group of patients, the count of carcinogenic cells left active after some medication is a variate, say N, distributed as Poisson. It is further assumed that for the ith cell, Z_i represents the random time taken to create cancer disease for $i = 1,2,3,\ldots$ according to some probability distribution $F_Z(.)$ independent of N. Then $T = \min\{Z_i, 0 \le i \le N\}$ with $P(Z_0 = \infty) = 1$ can be considered as the time to recurrence of cancer for the subject, where Z_0 denotes the time when there is no cancer. The population PTCM is defined by Chen et al. [1999] as

$$S_p(t) = \exp(-\theta + \theta S_Z(t)) = \exp(-\theta F_Z(t)) = p^{F_Z(t)}, \tag{32}$$

where $p = \exp(-\theta)$. The density function corresponding to the survival function in (32) is $f_p(t) = \theta f_Z(t) \exp(-\theta F_Z(t))$ and the hazard function is $h_p(t) = \theta f_Z(t)$. One can note that $S_p(\infty) \neq 1$, which otherwise indicates that $S_p(t)$ is not a proper survival

function. Actually, $S_p(\infty) = \exp(-\theta)$ represents the proportion of patients that are cured in the study. We link the cure rate parameter θ in (32) to the covariates vector W as $\ln(\theta(W)) = W'\beta$, where β denotes the corresponding regression parameters. The cure fraction can be obtained from $p = \exp(-\exp(W'\beta))$. When we have only one covariate with two values, zero and one, representing the group identification, then $p_0 = \exp(-\exp(b_0))$ and $p_1 = \exp(-\exp(b_0 + b_1))$ provide the cure fractions in the respective groups.

The population survival function $S_p(t)$ with the SMD distribution as the baseline can be obtained as

$$S_p(t;b,c,k,\beta\|W) = \exp\left[-\exp\left(W'\beta\right)\left(1-\left\{1-\frac{(kt)^c}{(1+kt)^c}\right\}^b\right)\right], \tag{33}$$

The corresponding population density function is

$$\begin{aligned} f_p(t;b,c,k,\beta\|W) = &\exp\left[-\exp\left(W'\beta\right)\left(1-\left\{1-\frac{(kt)^c}{(1+kt)^c}\right\}^b\right)\right] \\ &\times \exp\left(W'\beta\right)\frac{bck(kt)^{c-1}}{(1+kt)^{c+1}}\left[1-\left(\frac{kt}{1+kt}\right)^c\right]^{b-1}. \end{aligned} \tag{34}$$

The likelihood function for the observed data, say $O = \left\{y_i, d_{]i}, w_i; i = 1,2,\ldots,n\right\}$, can be written as

$$l(\tau\|O) = \prod_{i=1}^{n}\left[f_p(y_i)\right]^{d_i}\left[S_p(y_i)\right]^{1-d_i} = \prod_{i=1}^{n}\left[h_p(y_i)\right]^{d_i}S_p(y_i), \tag{35}$$

where $\tau' = (\omega,\beta) = (b,c,k,b_0,\ldots,b_k)$. Replacing $f_p(.)$ and $S_p(.)$ from (33) and (34) in (35), we have the likelihood function for the PTCM based on the SMD distribution as

$$\begin{aligned} l(\tau\|O) = \prod_{i=1}^{n}\Bigg\{ &\left[\exp\left(\sum_{j=0}^{k}B_j w_{ji}\right)\frac{bck(ky_i)^{c-1}}{(1+ky_i)^{c+1}}\left(1-\frac{(ky_i)^c}{(1+ky_i)^c}\right)^{b-1}\right]^{d_i} \\ &\times \exp\left[-\exp\left(\sum_{j=0}^{k}B_j w_{ji}\right)\left(1-\left(1-\frac{(ky_i)^c}{(1+ky_i)^c}\right)^b\right)\right]\Bigg\} \end{aligned} \tag{36}$$

The corresponding log-likelihood function is

$$
\begin{aligned}
L(\tau\|O) = & \sum_{i=1}^{n} d_i \left(\sum_{j=0}^{k} B_j w_{ji} \right) + \ln(bck) \sum_{i=1}^{n} d_i \\
& + (c-1) \sum_{i=1}^{n} d_i \ln(ky_i) - (c+1) \sum_{i=1}^{n} d_i \ln(1+ky_i) \\
& + (b-1) \sum_{i=1}^{n} d_i \ln \left(1 - \frac{(ky_i)^c}{(1+ky_i)^c} \right) \\
& - \sum_{i=1}^{n} \exp \left(\sum_{j=0}^{k} B_j w_{ji} \right) \\
& - \sum_{i=1}^{n} \exp \left(\sum_{j=0}^{k} B_j w_{ji} \right) \left(1 - \frac{(ky_i)^c}{(1+ky_i)^c} \right)^b .
\end{aligned}
$$

where k denotes the number of covariates, w_0 the vector of 1's, w_j's the covariates, B_0 the intercept term, and B_j's the regression coefficients. The maximum likelihood estimate $\widehat{\tau}$ can be obtained by maximizing the log-likelihood function $L(\tau\|O)$. Under standard regularity conditions of ML estimators, we can state that the vector $(\widehat{\tau} - \tau) \sim N(0, V)$, where $\widehat{\tau}$ denotes the vector estimator corresponding to the vector parameter τ and Ω is the inverse of the negative of the Hessian matrix evaluated at the ML estimate $\widehat{\tau}$.

For a Bayesian estimation of parameters, we assume independent gamma priors for the shape parameters b and c as in (28), independent uniform priors over some suitable intervals for the scale k and the regression parameters $B_0, B_1, .., B_k$. The joint posterior distribution can be obtained from (27) and (36) as

$$
\pi(\omega,\beta\|O) \propto l(\omega,\beta\|O) \times \pi(\omega,\beta) \propto \prod_{i=1}^{n} \left\{ \left[\exp \left(\sum_{j=0}^{k} B_j w_{ji} \right) \frac{bck(ky_i)^{c-1}}{(1+ky_i)^{c+1}} \left(1 - \frac{(ky_i)^c}{(1+ky_i)^c} \right)^{b-1} \right]^{d_i} \right.
$$

$$
\left. \exp \left[-\exp \left(\sum_{j=0}^{k} B_j w_{ji} \right) \left(1 - \left(1 - \frac{(ky_i)^c}{(1+ky_i)^c} \right)^b \right) \right] \right\} b^{a_1-1} c^{a_2-1} \exp(-b_1 b) \exp(-b_2 c),
$$

$$
\propto \prod_{i=1}^{n} \left\{ \exp \left(d_i \sum_{j=0}^{k} B_j w_{ji} \right) (bck)^{d_i} (1-E_i)^{2d_i} E_i^{(c-1)d_i} (1-E_i^c)^{(b-1)d_i} \right\}.
$$

$$
\exp \left(-\exp \left(\sum_{j=0}^{k} B_j w_{ji} \right) \left(1 - (1-E_i^c)^b \right) \right) \right\} b^{a_1-1} c^{a_2-1} \exp(-b_1 b) \exp(-b_2 c),
$$

where $E_i = \frac{kx_i}{1+kx_i}$. Thus, the posterior expectation of any function of parameters, say $U(\omega)$, is

$$E\left(U(\omega)\,\|O\right) = \frac{\int_0^\infty U(\omega)\pi\left(\omega\|O\right)d\omega}{\int_0^\infty \pi\left(\omega\|O\right)d\omega}.$$

We consider the MCMC Gibbs sampling method to obtain the Bayes estimate and the associated HPD credible intervals. For this, we use the package R2OpenBUGS in R statistical software.

9. CURED FRACTION REAL DATA ANALYSIS

In this real data analysis, we first illustrate the estimation of PTCM based on the SMD distribution when there are no covariates in the study. For this purpose, we use the bone marrow transplant data from patients with refractory acute lymphoblastic leukemia from Cai [2009]. The study includes 46 patients who received allogeneic treatment and 45 patients who received autologous treatment. Among these, 33 patients in the allogeneic group and 35 patients in the autologous group experienced leukemia recurrence. The survival times (in days) for patients in each treatment group are presented below.

Allogeneic treatment group: 11, 14, 23, 31, 32, 35, 51, 59, 62, 78, 78, 79, 87, 99, 100, 141, 160, 166, 216, 219, 235, 250, 270, 313, 332, 352, 368, 468, 491, 511, 557, 628+, 726+, 819, 915+, 966+, 1109+, 1158+, 1256, 1614+, 1619+, 1674+, 1712+, 1745+, 1820+, 1825.

Autologous treatment group: 21, 40, 42, 50, 53, 54, 56, 61, 64, 67, 73, 76, 79, 81, 88, 95, 98, 98, 99, 104, 105, 106, 112, 131, 147, 171, 172, 179, 189, 195, 199, 213, 223, 224, 277, 724+, 729+, 734, 1053+, 1094+, 1192+, 1475+, 1535+, 1535+, 1845+.

The time with + sign indicates censored observation. The p-value of the two-sample log-rank test for this data is 0.106, which indicates that there is no difference in survival experience between the two groups of patients; we, therefore, can merge them and consider one group

of patients for illustration purposes only. The Kaplan-Meier survival curve for the whole group is given in Figure 11, and it shows that the curve levels off at a time substantially greater than 0, which indicates that some of the patients have not experienced a recurrence after the treatments. That is, the data contains a cure fraction, and the analysis of the data without regard to the cure fraction will lead to misleading results. To illustrate this fact, we first fit the random censorship model explained in Section 7 and report the results in Table 3. For this model, the AIC value

Table III. ML and Bayesian Estimates for Additional Parameters

Parameters	ML Estimates			Bayesian Estimates		
	Est	SE	Confidence Interval	Est	SE	HPD Interval
b	0.5275	0.0822	(0.3664, 0.6885)	0.5464	0.0835	(0.3854, 0.7068)
c	17.714	3.8319	(10.203, 25.224)	22.278	8.3681	(6.1950, 37.623)
k	0.2627	0.0781	(0.1096, 0.4159)	0.3264	0.1152	(0.1186, 0.4986)
d	1.5542	0.9783	(0.0000, 3.4716)	0.6113	0.2391	(0.1598, 1.0710)
e	2.8865	1.3713	(0.1988, 5.5743)	47.096	27.218	(2.5350, 93.311)
f	0.0123	0.0121	(0.0000, 0.0359)	0.5039	0.2893	(0.0206, 0.9572)
p	0.2174	0.0528	(0.1141, 0.3209)	0.1668	0.0648	(0.0291, 0.2817)
GoF	AIC = 952.78			DIC = 954.2		

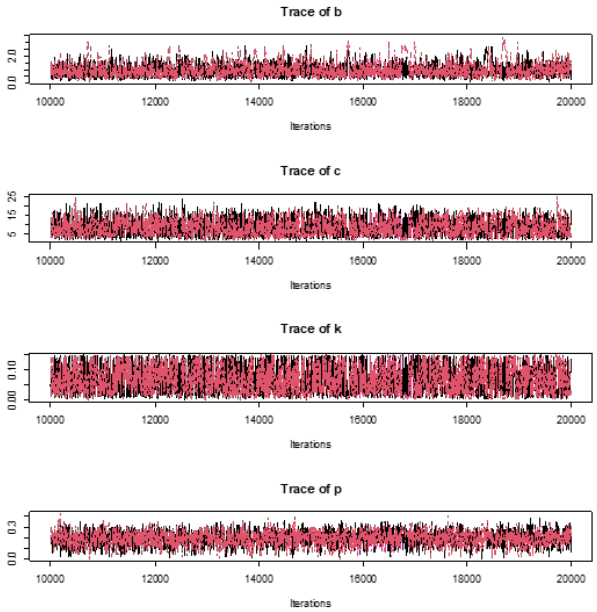

Fig. 9. Trace plots for two independent chains for the bone marrow transplant data.

is 959.60, and its fitness to the Kaplan-Meier survival

curve is shown in Figure 11, which shows a poor fit to the Kaplan-Meier survival curve. Now we analyze the same data assuming the PTCM explained in Section 8 and report the results in Table 3. For this model, the AIC value reduced to 952.78, and its fitness to the Kaplan-Meier survival curve is shown in Figure 11, which shows

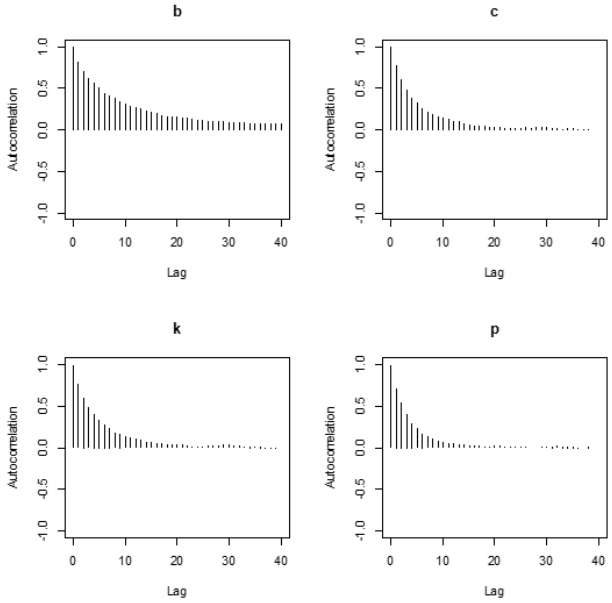

Fig. 10. Autocorrelation plots for the bone marrow transplant data.

a very good fit to the Kaplan-Meier survival curve. For Bayesian estimation, we first check the convergence of the Gibbs sampling procedure by drawing the trace plots of the parameters for two independent MCMC chains in Figure 9. We see that all the plots show well mixing of the chains and indicate no problem of convergence as they move along their constant means and variances without any serial correlations. We can say that both the chains represent the stationary time series. Next, we draw the autocorrelation plots at different lags in Figure 10. All the plots start with high autocorrelations and spike out very quickly. We can observe that the sample autocorrelations are larger at shorter lags and smaller at larger lags and decline to zero very rapidly as the lengths of lags increase. We can say that there is no abnormality with the MCMC Gibbs sampling procedure. Now we obtain Bayesian estimates and associated standard errors and 95% HPD intervals and report the results in Table 3. To further observe the goodness of fit of the proposed distribution, we estimate the survival function of the distribution and fit it to the K-M survival curve in Figure 11. We see that there is a very good agreement between the survival estimates for the bone marrow transplant data.

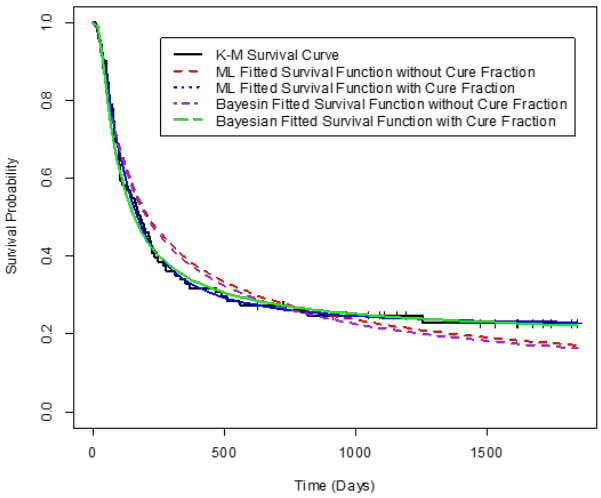

Fig. 11. Estimated survival functions of the random censorship model and PTCM based on the SMD distribution fitted to K-M survival curve for bone marrow transplant data.

10. CONCLUSION

In this article, we have introduced and comprehensively studied a novel three-parameter lifetime distribution, referred to as the SMD distribution. This distribution is specifically designed to model failure time data characterized by decreasing or unimodal-shaped hazard rates, offering a flexible tool for researchers in reliability analysis and life testing experiments. The development of the SMD distribution was motivated by the well-established need for adaptable statistical models that can capture the complexity of real-world phenomena more accurately than traditional distributions.

Our exploration of the SMD distribution encompassed a wide array of structural properties, ensuring a thorough understanding of its behavior and applicability. We derived closed-form expressions for essential functions such as the density, distribution, hazard, and quantile functions, which are crucial for practical applications. Although the moment generating function does not exist in closed form, we demonstrated that all moments of the distribution can be explicitly calculated, providing valuable insights into its statistical characteristics. Additionally, we examined mean deviations, entropy measures, and tail behavior, revealing the

distribution's potential to model both short- and long-tailed data effectively. Various estimation methods, including maximum likelihood and Bayesian approaches, were used for both complete and censored cases. For complete samples, we applied these methods to two distinct real-life datasets, illustrating the flexibility and appropriateness of the SMD distribution in diverse contexts. Our findings indicated that the Bayesian method generally provided a better fit to the data compared to the maximum likelihood approach, as evidenced by lower AIC and DIC values. In scenarios involving censored data, we extended our analysis to incorporate cure fraction models, acknowledging the presence of long-term survivors in certain datasets. By applying the promotion time cure model (PTCM) based on the SMD distribution, we demonstrated its superiority over conventional random censorship models when analyzing survival data with a significant proportion of cured individuals. The improved fit was clearly reflected in both the reduced AIC values and the enhanced alignment with Kaplan-Meier survival curves. Through rigorous empirical analyses, we confirmed the robustness and versatility of the SMD distribution across different types of data and experimental conditions. Furthermore, the estimated survival functions closely matched the non-parametric Kaplan-Meier estimates, underscoring the distribution's ability to provide accurate and meaningful representations of survival experiences.

In summary, the introduction of the SMD distribution marks a significant advancement in the field of lifetime data analysis. Its rich structure and adaptability make it a valuable addition to the existing repertoire of statistical tools, particularly for modeling complex failure time data with varying hazard rate patterns. Future research could explore further extensions of the SMD distribution, such as incorporating additional parameters or integrating it within more sophisticated modeling frameworks, to address even broader classes of problems in reliability and survival analysis.

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