Smoothed Bootstrap for Right-Censored Data

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Abstract

A smoothed bootstrap method is introduced for right-censored data based on the right-censoring-$A_{(n)}$ assumption introduced by Coolen and Yan (2004), which is a generalization of Hill's $A_{(n)}$ assumption (Hill, 1968) for right-censored data. The smoothed bootstrap method is compared to Efron's method for right-censored data (Efron, 1981) through simulations. The comparison is conducted in terms of the coverage of percentile confidence intervals for the quartiles. From the study, it is found that the smoothed bootstrap method mostly performs better than Efron's method, in particular for small data sets. We also illustrate the use of the method for survival function inference and compare it to a smoothed Kaplan-Meier bootstrap method through simulations.

Keywords: Banks' bootstrap, Efron's bootstrap, Hill's $A_{(n)}$ assumption, nonparametric predictive inference, right-censored data, right-censoring-$A_{(n)}$ assumption.

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1. Introduction

The bootstrap approach, as presented by Efron (1979), is a nonparametric method proposed to measure the variability of sample estimates. Due to its simplicity to apply and efficiency to provide good estimates, the method has been widely used for a variety of statistical problems (Efron and Tibshirani, 1993). If one has little information about a suitable distribution, powerful nonparametric methods, e.g. the bootstrap method, are of great practical use (Davison and Hinkley, 1997).

Efron (1979) presented the bootstrap method for univariate real-valued data, and the method is described with real world applications in many references, e.g. Berrar (2019), Davison and Hinkley (1997) and Efron and Tibshirani (1993). The method creates multiple bootstrap samples by sampling with replacement from the original data set, and the statistic of interest is calculated based on each bootstrap sample. The empirical distribution of the resulting values can be used as a good proxy for the distribution of the statistic of interest.

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For random variables with finite support, Banks (1988) presented a smoothed bootstrap method by linear interpolation between consecutive observations. Suppose that there are n observed data points, Banks' bootstrap method starts with ordering the data and creating $n+1$ intervals. This method assigns probability $\frac{1}{n+1}$ to each interval. To create one Banks' bootstrap sample, n intervals are drawn with replacement, then one observation is sampled uniformly from each chosen interval; if an interval has been sampled twice or more times, multiple observations will be sampled from that interval. It should be noted that this method allows to sample from the whole support and ties do not occur in the bootstrap samples. This is contrary to Efron's method, where the process is restricted to sampling with replacement from the original data set (Efron, 1979). Coolen and BinHimd (2020) generalized Banks' bootstrap method for data in the case of underlying distributions with infinite support by assuming distribution tail(s) for the last interval(s).

For univariate right-censored data, Efron (1981) generalized the bootstrap method by the empirical distribution assigning probability $\frac{1}{n}$ to each data point, regardless whether the observation is an event time or a right-censored time. To create one bootstrap sample, n observations are sampled with replacement from the original data set, then the Kaplan-Meier estimator is used to compute the statistic of interest. This bootstrap method leads to bootstrap samples including ties and right-censored observations, which can cause complications in computations. Moreover, Dobler (2019) showed that the method can provide poor results when the sample size is small.

This paper presents a smoothed bootstrap method based on the right-censoring-$A_{(n)}$ assumption introduced by Coolen and Yan (2004). As shown in this paper, this method has three advantages over Efron's bootstrap in case of right-censored data. First, the new method tends to provide better results than Efron's method, in particular for small data sets and large censoring proportions. Secondly, the new method avoids ties and right-censored observations in the bootstrap samples, which may simplify further computations based on those samples. Thirdly, the new method provides a nearly smooth estimate of the survival function.

This paper is organized as follows. In Section 2, Efron's bootstrap methods for real-valued data and right-censored data are reviewed (Efron, 1979, 1981), along with Banks' bootstrap method for real-valued data (Banks, 1988). Section 3 presents the smoothed bootstrap method for right-censored data based on the right-censoring-$A_{(n)}$ assumption introduced by Coolen and Yan (2004). In Section 4, the smoothed bootstrap method is compared to Efron's bootstrap method in terms of the coverage of the bootstrap confidence intervals through simulation studies. A brief comparison of the smoothed bootstrap method and the well-known Kaplan-Meier estimator of the survival function is given in Section 5. The smoothed bootstrap method is compared to a smoothed Kaplan-Meier bootstrap method in Section 6. The final section provides some concluding remarks.

2. Bootstrap methods

This section introduces different bootstrap methods for real-valued data and right-censored data. Let $Y_1, Y_2, \ldots, Y_n$ be random quantities, which are independent and identically distributed from a distribution F supported on the finite interval $[a, b]$. Furthermore, let $y_1, y_2, \ldots, y_n$ be the observations corresponding to $Y_1, Y_2, \ldots, Y_n$ and $\theta(F)$ be the statistic of interest.

For real-valued data, Efron (1979) presented the bootstrap method based on the empirical cumulative distribution function. This distribution assigns probability $\frac{1}{n}$ to each observed data point. To apply the bootstrap method, multiple samples of size n are created by sampling with replacement from the observed data. Based on each bootstrap sample, the statistic of interest is calculated. The empirical distribution of the resulting values is used as a proxy for the sampling distribution of $\theta(F)$.

Banks (1988) presented a smoothed bootstrap method for real-valued data by linear interpolation between consecutive observations. Banks' bootstrap method partitions the support into $n+1$ intervals based on the observed data points and assigns probability $\frac{1}{n+1}$ to each interval. To create one bootstrap sample, n intervals are sampled with replacement from the created intervals, then one observation is drawn uniformly from each chosen interval. It is true that if an interval is chosen twice or multiple times during the procedure, the observations will be sampled from that interval. Based on this bootstrap sample, the statistic of interest is computed. These two steps are performed multiple times to create multiple bootstrap samples along with their statistics of interest. The empirical distribution of the resulting values is used as a proxy for the sampling distribution of $\theta(F)$.

Efron's bootstrap method for right-censored data (Efron, 1981) is quite similar to the standard bootstrap method for univariate real-valued data (Efron, 1979). The method assigns probability $\frac{1}{n}$ to each observation, regardless whether it is an observed event time or a right-censored observation. Suppose that the random variables $T_1, T_2, \ldots, T_n$ are independent and identically distributed from a distribution H supported on $\mathbb{R}$ and the censored random variables $C_1, C_2, \ldots, C_n$ are independent and identically distributed from a distribution G supported on $\mathbb{R}$. The right-censored random variables are of the form $(X_1, D_1), (X_2, D_2), \ldots, (X_n, D_n)$, where the pair (X_i, D_i), for $i = 1, 2, \ldots, n$, is defined as

$$X_i = \min(T_i, C_i), \text{ for } \; i = 1, 2, \ldots, n \tag{1}$$

$$D_i = \begin{cases} 1 & \text{if } \; X_i = T_i \;\; \text{(uncensored)} \\ 0 & \text{if } \; X_i = C_i \;\; \text{(censored)} \end{cases} \tag{2}$$

Suppose that $(x_1, d_1), (x_2, d_2), \ldots, (x_n, d_n)$ are the observations of the corresponding random quantities $(X_1, D_1), (X_2, D_2), \ldots, (X_n, D_n)$ and $\theta(H)$ is the statistic of interest, which can be estimated through $\theta(\hat{H})$. Efron's bootstrap procedure for right-censored data is described as follows (Efron, 1981):

(i) Sample n pairs (x_i, d_i) with replacement from the original data set, which has n observations. The bootstrap sample is denoted by $D^*_{boot}=\{(x^*_1, d^*_1), (x^*_2, d^*_2), \ldots, (x^*_n, d^*_n)\}$.

(ii) Calculate the statistic of interest $\hat{\theta}^* = \hat{\theta}(D^*_{boot})$ based on D^*_{boot} sample and the Kaplan-Meier estimator (Kaplan and Meier, 1958).

(iii) Perform steps (i) and (ii) B times; this leads to $\hat{\theta}^{*1}, \hat{\theta}^{*2}, \ldots, \hat{\theta}^{*B}$.

Two points should be noted in this bootstrap procedure. First, due to the process of this bootstrap method, Efron's bootstrap samples have to include ties and right-censored observations, which may cause some complications in computations, in particular when the sample size is small and the censoring proportion is large. Secondly, if the censoring proportion in the original data set is zero, Efron's bootstrap method for right-censored data will be reduced to Efron's bootstrap method for univariate real-valued data presented in (Efron, 1979).

3. The smoothed bootstrap method for right-censored data

Hill (1968, 1988) assumed that the observable random variables X_1,X_2, …,X_n are exchangeable with no ties, and the $A_{(n)}$ assumption provides a partial specification of a probability distribution for the next future observation X_{n+1} based on n observed data points. This assumption orders the observations, then it assigns probability $\frac{1}{n+1}$ for the next observation to be between any consecutive observations. This can be written as

$$P\left(X_{n+1} \in (x_{(i)}, x_{(i+1)})\right) = \frac{1}{n+1} \tag{3}$$

for all $i = 0, 1, 2, \ldots, n$, where $x_{(0)} = -\infty$ and $x_{(n+1)} = +\infty$ (for non-negative random quantities, $x_{(0)} = 0$ and $x_{(n+1)} = +\infty$).

Coolen and Yan (2004) provided a partial specification of a probability distribution for a real-valued random quantity X based on mass-function, M-function, values assigned to open intervals conducted between consecutive observations, without any further restriction on the spread of the probability mass within each interval. The M-function values are basic probability assignments following the general theory introduced by Shafer (1976); they are within $[0, 1]$, and they all sum up to one.

Coolen and Yan (2004) generalized the $A_{(n)}$ assumption for data including right-censored observations. They divide the sample space into $n + 1$ intervals, then they assign certain probabilities to those intervals. They first assume that the random quantities $X_1, X_2, \ldots, X_n$ are exchangeable and non-negative and ties occur with probability zero. Suppose that there are n observations including u event times and v right-censored observations, where $n = u + v$. Let $0 < t_{(1)} < t_{(2)} < \ldots < t_{(u)}$ be the event time observations, where $0 \leq u \leq n$, and $0 < c_{(1)} < c_{(2)} < \ldots < c_{(v)}$ be the right-censored observations, where $v = n - u$. Let $I_i = (t_{(i)}, t_{(i+1)})$, for $0 \leq i \leq u$, and denote the ordered right-censoring times within I_i by $c_1^i < c_2^i < \ldots < c_{l_i}^i$, where l_i is the number of right-censored observations in the interval I_i. The sample space is divided into $n+1$ intervals $(t_{(i)}, t_{(i+1)})$ and $(c_k^i, t_{(i+1)})$, where $1 \leq k \leq l_i$, $t_{(0)} = 0$ and $t_{(u+1)} = b$ if the support is $[0, b]$ or $t_{(u+1)} = +\infty$ if the support is $[0, +\infty]$. The probabilities for the next future observation X_{n+1} to be in the intervals $(t_{(i)}, t_{(i+1)})$ and $(c_k^i, t_{(i+1)})$ are referred to by M-function values $M_{X_{n+1}}(t_{(i)}, t_{(i+1)})$ and $M_{X_{n+1}}(c_k^i, t_{(i+1)})$, respectively. These M-function values can be computed by

$$M_{X_{n+1}}(t_{(i)}, t_{(i+1)}) = \frac{1}{n+1} \prod_{\{r: c_{(r)} < t_{(i)}\}} \frac{\tilde{n}_{c_{(r)}} + 1}{\tilde{n}_{c_{(r)}}} \tag{4}$$

$$M_{X_{n+1}}(c_k^i, t_{(i+1)}) = \frac{1}{(n+1)\tilde{n}_{c_k^i}} \prod_{\{r: c_{(r)} < c_k^i\}} \frac{\tilde{n}_{c_{(r)}} + 1}{\tilde{n}_{c_{(r)}}} \tag{5}$$

where $\tilde{n}_{c_{(r)}}$ is the number of individuals remaining at risk (still alive) just before time $c_{(r)}$ plus one, and $\tilde{n}_{c_k^i}$ is the number of individuals remaining at risk just before time c_k^i plus one.

The right-censoring $A_{(n)}$ assumption can be used to develop a smoothed bootstrap method for right-censored data, generalizing Banks' bootstrap method. The smoothed bootstrap (SB) algorithm for right-censored data is as follows:

(i) Sample intervals with replacement n times with the M-function values.

(ii) Sample one observation uniformly from each finite interval. For the case of infinite interval $(x_{(i)}, \infty)$, where $x_{(i)}$ could be either an event time or a right-censored observation, BinHimd (2014) assumed an Exponential tail for any infinite interval with rate parameter $\lambda_{(i)}$ based on the corresponding assignment probabilities $M_{X_{n+1}}(x_{(i)}, \infty)$. The rate parameter $\lambda_{(i)}$ can be estimated by

$$\hat{\lambda}_{(i)} = \frac{-\ln\left(M_{X_{n+1}}(x_{(i)}, \infty)\right)}{x_{(i)}} \tag{6}$$

with $\left(M_{X_{n+1}}(x_{(i)}, \infty)\right)$ from Equations (4) and (5). After assuming the Exponential tail, sample one observation being greater than $x_{(i)}$ from the tail for the infinite interval $(x_{(i)}, \infty)$.

(iii) Calculate the statistic of interest, $\hat{\theta}^*$.

(iv) Perform steps from (i) to (iii) B times. This leads to B smoothed bootstrap samples with their corresponding statistics of interest.

It should be noted that the smoothed bootstrap method uses sampling from the whole data range, so ties can occur in the bootstrap samples with probability zero. Also, all observations generated for the bootstrap samples are event times. This makes the computations straightforward for the statistics of interest, contrary to Efron's bootstrap method, where the KM estimate should be used when the data include censored observations. If the censoring proportion in the original data set is equal to zero, then the smoothed bootstrap method will be reduced to Banks' bootstrap method for univariate real-valued data.

To apply the SB method for the case of original data set including ties, we need to break them, and this can be done by adding a very small number (Gibbons and Chakraborti, 2020). In this paper, we do not go further on this because we think no significant difference will occur with the inferences, the resulting inferences will be nearly identical. If a tie between two event time observations is observed, there will be a positive probability to chose the observation for the SB bootstrap samples. If there is a tie between an event time and a censored time, we assume that the right-censored observation will occur after the event observation. For the case of ties between censored observations, the SB method will not be really affected.

4. Comparison with Efron's method

To compare methods through simulation studies in terms of the coverage probability, statisticians usually consider high levels of confidence, e.g. $90\%, 95\%$ and 99%, and the best method is considered to be the one that leads to lower discrepancy between the actual and nominal coverage levels. However, Banks (1988) proposed to investigate the global coverage accuracy to show the best method that provides lower discrepancy between the actual and nominal coverage levels over the whole range of confidence levels. He generated 20 segments by the quantiles of the statistic of interest with nominal level 0.05, and this can be found by

$$CRL_{(i)} = \left(q_{(\frac{\alpha_{i+1}}{2})}, q_{(\frac{\alpha_i}{2})}\right) \tag{7}$$

$$CRR_{(i)} = \left(q_{(1-\frac{\alpha_i}{2})}, q_{(1-\frac{\alpha_{i+1}}{2})}\right) \tag{8}$$

where $i = 1, 2, \ldots, 10$, $\alpha_{i+1} = \alpha_i - 0.10$, $\alpha_1 = 1$ and $q_{(z)}$ is the z^{th} quantile of functional values, so $CRL_{(i)}$ are the confidence regions presenting the left tail of the global measure of coverage accuracy, and $CRR_{(i)}$ are the confidence regions presenting the right tail of the global measure of coverage accuracy.

Banks (1988) also generated 10 segments with nominal coverage probability 0.10 by

$$CR_{(i)} = \left(q_{(\frac{\alpha_{i+1}}{2})}, q_{(\frac{\alpha_i}{2})}\right) \cup \left(q_{(1-\frac{\alpha_i}{2})}, q_{(1-\frac{\alpha_{i+1}}{2})}\right) \tag{9}$$

where $CR_{(i)} = CRL_{(i)} \cup CRR_{(i)}$ for $i = 1, 2, \ldots, 10$.

These confidence regions are used to test the hypothesis that all segments have equal coverage probabilities for a certain statistic of interest by conducting the chi-squared goodness of fit test (Banks, 1988). This test considers the discrepancy between the actual and nominal coverage probabilities. Banks (1988) used this technique to compare his smoothed bootstrap method to other bootstrap methods, namely Efron's method (Efron, 1979), Rubin's Bayesian bootstrap (Rubin, 1981) and smoothed Rubin's bootstrap (Banks, 1988), where the best method has the lowest chi-squared value. This comparison method will also be used in this section for the case of right-censored data.

To generate data sets containing right-censored observations, three different scenarios are specified in Table 1. In each scenario, two distributions are considered, one is used to generate event observations and the other is used to generate right-censored observations. To create one right-censored data set from any scenario, we generate n observations from each distribution of that scenario, then use Equations (1) and (2). The distributions used for right-censored data sets are presented in Table 1 along with their corresponding parameter values, where the censoring proportion in each scenario is set at 15% (other proportions of right-censored observations are considered in (Al Luhayb, 2021) and the simulation results are similar to the ones presented in this section. For more information on determining the censoring proportions see (Al Luhayb, 2021; Wan, 2017)).

Scenario	Distribution for event times	Distribution for censored times
1	$f(t) = \frac{t^{\alpha-1}(1-t)^{\beta-1}}{\beta(\alpha,\beta)};\ t \in [0,1]$ where $\alpha = 1.2$ and $\beta = 3.2$. [Beta(α,β)]	$g(c) = \frac{1}{b-a};\ c \in [a,b]$ where $a = 0$ and $b = 1.82$. [Uniform(a,b)]
2	$f(t) = \frac{\alpha}{\beta}(\frac{t}{\beta})^{\alpha-1}\exp(-(\frac{t}{\beta})^{\alpha});\ t \in [0,\infty)$ where $\alpha = 1.5$ and $\beta = 1$. [Weibull(α,β)]	$g(c) = \lambda\exp(-\lambda c);\ c \in [0,\infty)$ where $\lambda = 0.187$. [Exponential(λ)]
3	$f(t) = \dfrac{1}{t\sqrt{2\pi}}\exp(-\frac{(\ln(t))^2}{2});\ t \in (0,\infty)$ [Log-Normal$(0,1)$]	$g(c) = \frac{\alpha}{\beta}(\frac{c}{\beta})^{\alpha-1}\exp(-(\frac{c}{\beta})^{\alpha});\ c \in [0,\infty)$ where $\alpha = 3$ and $\beta = 3.7$. [Weibull(α,β)]

Table 1: The density functions for the distributions used in each scenario to generate right-censored data sets.

4.1. First scenario

For the case of finite support, we use the first scenario presented in Table 1 to generate 1000 right-censored data sets of size n. Based on each created data set, we apply each bootstrap method 1000 times and compute the statistic of interest based on each bootstrap sample. Hence, we derive confidence regions specified in Equations (7), (8) and (9). We then count one for the confidence region that includes the true statistic of interest and zero else, the true value of the statistic is the one corresponding to the distribution used to generate the event time observations. We iterate this procedure for each generated data set to define coverage proportions. Based on these coverage proportions, we can compute the chi-squared value corresponding to each bootstrap method.

In some cases with Efron's bootstrap method, the statistic of interest is not found based on some bootstrap samples and the value of the Kaplan-Meier estimator because there is no inverse for the survival function at the specific probability. This leads us to consider three different suggestions. Suppose that we are interested in the median (the methods are suggested for all quantiles), for any bootstrap sample whose median is not found by the Kaplan-Meier estimator, we neglect these bootstrap samples, so the confidence regions may be based on a number of medians less than 1000. This option is referred to by $\mathrm{E}_{(1)}$. The second option is that we assume the maximum event time of the bootstrap sample whose median is not found is the corresponding median for that bootstrap sample (Efron, 1967), this is denoted by $\mathrm{E}_{(2)}$. The last option is to fit an Exponential distribution to the tail with rate parameter $\hat{\lambda}^* = -\ln(\hat{S}(t_{max}))/t_{max}$, where t_{max} is the maximum event time of the bootstrap sample. Hence, the corresponding median can be found by $X_{med} = -\ln(0.50)/\hat{\lambda}^*$. This last option is described in (Brown et al., 1974), and it is referred to by $\mathrm{E}_{(3)}$. With the last two options, it is assured that the confidence regions are based on 1000 bootstrap samples' medians.

Tables 2, 3 and 4 present the chi-squared values for the quartiles based on the SB method and Efron's bootstrap method. For the first quartile, the SB method performs better in all sample sizes and in both segments' divisions, which are created by Equations

		10 CR				20 CR			
n	measures	SB	$E_{(1)}$	$E_{(2)}$	$E_{(3)}$	SB	$E_{(1)}$	$E_{(2)}$	$E_{(3)}$
6	χ^2	29.92	934.14	933.96	921.52	97.00	2366.84	2373.40	2355.72
	NA	—	1998	0	0	—	1998	0	0
	ABS	—	493	493	493	—	493	493	493
	p-value	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10	χ^2	22.20	876.66	875.62	875.62	57.40	1857.84	1855.64	1855.64
	NA	—	104	0	0	—	104	0	0
	ABS	—	1	1	1	—	1	1	1
	p-value	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000
20	χ^2	11.70	45.98	45.98	45.98	27.44	286.68	286.68	286.68
	NA	—	1	0	0	—	1	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.231	0.000	0.000	0.000	0.095	0.000	0.000	0.000
40	χ^2	11.60	78.76	78.76	78.76	22.48	162.32	162.32	162.32
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.237	0.000	0.000	0.000	0.261	0.000	0.000	0.000
100	χ^2	9.24	14.98	14.98	14.98	28.48	27.52	27.52	27.52
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.415	0.091	0.091	0.091	0.075	0.093	0.093	0.093

Table 2: The chi-squared values for $Q_1 = 0.117$, and their p-values with the corresponding NA and ABS numbers.

(7), (8) and (9), respectively, except when the sample size is 100 and the division is set to 20 confidence regions. In this case, the SB method performs well, but Efron's bootstrap method performs better. For the median, the SB method performs better when the sample size is $6, 10$ and 20 in both divisions. When $n = 40, 100$, both bootstrap methods provide good results, but Efron's bootstrap method mostly performs better. For the last quartile, the SB method performs better when $n = 6, 10, 20, 40$ in both divisions. When $n = 100$, both bootstrap methods provide nearly identical results, but Efron's bootstrap method obtains better results.

In Tables 2, 3 and 4, NA stands for the number of Efron's bootstrap samples for which the KM estimator does not provide their statistics of interest. ABS is the number of Efron's bootstrap samples which created of only right-censored observations. Those samples are replaced by other samples including at least one event time. The NA and ABS numbers are out of 1,000,000. It is obvious from the tables that the NA and ABS numbers decrease as the sample size increases. With the SB method, these measures are not applicable because the bootstrap samples contain event times only.

		10 CR				20 CR			
n	measures	SB	$E_{(1)}$	$E_{(2)}$	$E_{(3)}$	SB	$E_{(1)}$	$E_{(2)}$	$E_{(3)}$
6	χ^2	45.34	207.84	186.38	196.36	55.24	231.48	206.48	223.04
	NA	—	8628	0	0	—	8628	0	0
	ABS	—	493	493	493	—	493	493	493
	p-value	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10	χ^2	22.08	167.86	162.66	158.46	25.76	182.08	179.80	175.08
	NA	—	2332	0	0	—	2332	0	0
	ABS	—	1	1	1	—	1	1	1
	p-value	0.009	0.000	0.000	0.000	0.137	0.000	0.000	0.000
20	χ^2	8.32	58.46	59.44	59.44	20.20	73.64	75.04	75.04
	NA	—	98	0	0	—	98	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.502	0.000	0.000	0.000	0.383	0.000	0.000	0.000
40	χ^2	8.96	6.44	6.44	6.44	12.48	18.12	18.12	18.12
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.441	0.695	0.695	0.695	0.864	0.514	0.514	0.514
100	χ^2	6.94	3.66	3.66	3.66	16.52	10.80	10.80	10.80
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.643	0.932	0.932	0.932	0.622	0.930	0.930	0.930

Table 3: The chi-squared values for $Q_2 = 0.236$, and their p-values with the corresponding NA and ABS numbers.

4.2. Second scenario

For the case of infinite support, we use the second scenario presented in Table 1 to create right-censored data sets. Tables 5, 6 and 7 present the chi-squared values for the quartiles based on the SB method and Efron's bootstrap method. From Table 5, the SB method performs better in comparison to those of Efron's method at all different sample sizes in both divisions. For the second quartile, the SB method provides better results at all different sample sizes and in both divisions, except when the sample size is 100 with 10 confidence regions. Table 7 shows that the SB method performs better when $n = 6, 10$, and as the sample size increases, both bootstrap methods perform well, but Efron's method is better. It is clear from the simulation results for the quartiles that the SB method has reduced the discrepancies between the actual coverage proportions and the nominal sizes, in particular when the sample size is small.

		10 CR				20 CR			
n	measures	SB	$\mathrm{E}_{(1)}$	$\mathrm{E}_{(2)}$	$\mathrm{E}_{(3)}$	SB	$\mathrm{E}_{(1)}$	$\mathrm{E}_{(2)}$	$\mathrm{E}_{(3)}$
6	χ^2	157.04	751.88	678.06	557.32	211.40	1640.24	1628.72	1335.80
	NA	—	52306	0	0	—	52306	0	0
	ABS	—	493	493	493	—	493	493	493
	p-value	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10	χ^2	40.58	108.58	99.38	76.08	62.80	277.60	262.68	211.36
	NA	—	26739	0	0	—	26739	0	0
	ABS	—	1	1	1	—	1	1	1
	p-value	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
20	χ^2	3.78	13.08	12.24	11.54	13.88	58.52	57.2	56.44
	NA	—	5141	0	0	—	5141	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.925	0.159	0.200	0.241	0.791	0.000	0.000	0.000
40	χ^2	6.78	17.20	17.20	17.20	29.20	32.92	32.92	32.92
	NA	—	113	0	0	—	113	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.660	0.046	0.046	0.046	0.063	0.025	0.025	0.025
100	χ^2	12.48	11.74	11.74	11.74	45.56	44.16	44.16	44.16
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.188	0.228	0.228	0.228	0.001	0.001	0.001	0.001

Table 4: The chi-squared values for $Q_3 = 0.396$, and their p-values with the corresponding NA and ABS numbers.

		10 CR				20 CR			
n	measures	SB	$\mathrm{E}_{(1)}$	$\mathrm{E}_{(2)}$	$\mathrm{E}_{(3)}$	SB	$\mathrm{E}_{(1)}$	$\mathrm{E}_{(2)}$	$\mathrm{E}_{(3)}$
6	χ^2	10.58	192.48	180.86	179.30	41.48	255.08	239.28	245.44
	NA	—	5968	0	0	—	5968	0	0
	ABS	—	699	699	699	—	699	699	699
	p-value	0.306	0.000	0.000	0.000	0.002	0.000	0.000	0.000
10	χ^2	6.74	115.10	113.94	117.18	14.12	165.36	161.68	165.20
	NA	—	981	0	0	—	981	0	0
	ABS	—	14	14	14	—	14	14	14
	p-value	0.664	0.000	0.000	0.000	0.777	0.000	0.000	0.000
20	χ^2	13.36	33.40	33.40	33.40	34.52	88.72	88.72	88.12
	NA	—	106	0	0	—	106	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.147	0.000	0.000	0.000	0.016	0.000	0.000	0.000
40	χ^2	16.10	17.76	17.76	17.76	31.48	33.24	33.24	33.24
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.065	0.038	0.038	0.038	0.036	0.023	0.023	0.023
100	χ^2	12.40	6.56	6.56	6.56	24.48	26.16	26.16	26.16
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.192	0.683	0.683	0.683	0.178	0.126	0.126	0.126

Table 6: The chi-squared values for $Q_2 = 0.7832$, and their p-values with the NA and ABS numbers.

		10 CR				20 CR			
n	measures	SB	$E_{(1)}$	$E_{(2)}$	$E_{(3)}$	SB	$E_{(1)}$	$E_{(2)}$	$E_{(3)}$
6	χ^2	36.28	959.10	955.56	955.56	96.04	2171.16	2159.92	2159.72
	NA	—	2051	0	0	—	2051	0	0
	ABS	—	699	699	699	—	699	699	699
	p-value	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10	χ^2	14.48	756.78	752.94	756.78	60.48	1406.24	1404.48	1406.24
	NA	—	124	0	0	—	124	0	0
	ABS	—	14	14	14	—	14	14	14
	p-value	0.106	0.000	0.000	0.000	0.000	0.000	0.000	0.000
20	χ^2	15.58	73.26	73.26	73.26	43.08	343.96	343.96	343.96
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.076	0.000	0.000	0.000	0.001	0.000	0.000	0.000
40	χ^2	7.48	98.82	98.82	98.82	22.08	147.52	147.52	147.52
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.587	0.000	0.000	0.000	0.280	0.000	0.000	0.000
100	χ^2	7.30	13.04	13.04	13.04	23.52	30.88	30.88	30.88
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.606	0.161	0.161	0.161	0.215	0.042	0.042	0.042

Table 5: The chi-squared values for $Q_1 = 0.4358$, and their p-values with NA and ABS numbers.

4.3. Third scenario

In this section, we use the third scenario to create right-censored data sets. The chi-squared values obtained from the actual coverage proportions for the first quartile are presented in Table 8. The SB method provides better results at all different sample sizes except $n = 100$, where Efron's bootstrap method performs better in both confidence region divisions. For the median, Table 9 presents the chi-squared values obtained from the actual coverage proportions based on the SB method and Efron's method. The SB method provides smaller chi-squared values at all different sample sizes and in both divisions of confidence regions. Table 10 presents the chi-squared values for the third quartile. The SB method has less discrepancy between the actual and nominal coverage probabilities when $n = 6, 10, 20, 40$ in both numbers of confidence regions. When $n = 100$, both bootstrap methods provides good results, but Efron's method is better.

		10 CR				20 CR			
n	measures	SB	E$_{(1)}$	E$_{(2)}$	E$_{(3)}$	SB	E$_{(1)}$	E$_{(2)}$	E$_{(3)}$
6	χ^2	23.70	689.00	618.70	549.36	54.96	1323.96	1271.80	1114.52
	NA	—	32959	0	0	—	32959	0	0
	ABS	—	699	699	699	—	699	699	699
	p-value	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10	χ^2	25.50	110.32	109.88	112.62	50.92	181.80	194.68	183.24
	NA	—	15032	0	0	—	15032	0	0
	ABS	—	14	14	14	—	14	14	14
	p-value	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000
20	χ^2	12.20	10.82	10.24	10.56	23.76	25.80	27.36	27.56
	NA	—	3019	0	0	—	3019	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.202	0.288	0.331	0.307	0.206	0.136	0.097	0.092
40	χ^2	11.12	11.26	11.26	11.26	22.64	21.16	21.16	21.16
	NA	—	96	0	0	—	96	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.268	0.258	0.258	0.258	0.254	0.328	0.328	0.328
100	χ^2	12.68	8.76	8.76	8.76	26.24	25.64	25.64	25.64
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.178	0.460	0.460	0.460	0.124	0.141	0.141	0.141

Table 7: The chi-squared values for $Q_3 = 1.2433$, and their p-values with the NA and ABS numbers.

		10 CR				20 CR			
n	measures	SB	E$_{(1)}$	E$_{(2)}$	E$_{(3)}$	SB	E$_{(1)}$	E$_{(2)}$	E$_{(3)}$
6	χ^2	26.10	791.26	746.94	936.34	46.28	879.16	844.68	991.00
	NA	—	50287	0	0	—	50287	0	0
	ABS	—	1207	1207	1207	—	1207	1207	1207
	p-value	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10	χ^2	8.88	116.74	108.60	113.76	26.68	139.08	140.28	146.12
	NA	—	19858	0	0	—	19858	0	0
	ABS	—	145	145	145	—	145	145	145
	p-value	0.448	0.000	0.000	0.000	0.112	0.000	0.000	0.000
20	χ^2	6.80	104.44	103.54	107.36	13.32	135.44	138.48	144.28
	NA	—	2854	0	0	—	2854	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.658	0.000	0.000	0.000	0.822	0.000	0.000	0.000
40	χ^2	4.62	42.76	42.76	42.76	12.04	57.84	57.84	57.84
	NA	—	18	0	0	—	18	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.866	0.000	0.000	0.000	0.884	0.000	0.000	0.000
100	χ^2	5.96	12.02	12.02	12.02	12.88	17.08	17.08	17.08
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.744	0.212	0.212	0.212	0.845	0.584	0.584	0.584

Table 9: The chi-squared values for $Q_2 = 1$, and their p-values with the NA and ABS numbers.

		10 CR				20 CR			
n	measures	SB	E$_{(1)}$	E$_{(2)}$	E$_{(3)}$	SB	E$_{(1)}$	E$_{(2)}$	E$_{(3)}$
6	χ^2	24.06	962.34	946.68	974.80	109.68	2509.36	2460.76	2539.16
	NA	—	5841	0	0	—	5841	0	0
	ABS	—	1207	1207	1207	—	1207	1207	1207
	p-value	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10	χ^2	9.04	917.08	917.62	912.78	67.20	2286.88	2270.72	2287.48
	NA	—	2437	0	0	—	2437	0	0
	ABS	—	145	145	145	—	145	145	145
	p-value	0.434	0.000	0.000	0.000	0.000	0.000	0.000	0.000
20	χ^2	14.80	64.08	64.08	64.08	45.84	154.84	154.84	154.84
	NA	—	11	0	0	—	11	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.097	0.000	0.000	0.000	0.001	0.000	0.000	0.000
40	χ^2	19.04	25.98	25.98	25.98	39.96	59.12	59.12	59.12
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.025	0.002	0.002	0.002	0.003	0.000	0.000	0.000
100	χ^2	9.06	5.84	5.84	5.84	37.60	27.56	27.56	27.56
	NA	—	0	0	0	—	0	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.432	0.756	0.756	0.756	0.007	0.092	0.092	0.092

Table 8: The chi-squared values for $Q_1 = 0.509$, and their p-values with the NA and ABS numbers.

		10 CR				20 CR			
n	measures	SB	E$_{(1)}$	E$_{(2)}$	E$_{(3)}$	SB	E$_{(1)}$	E$_{(2)}$	E$_{(3)}$
6	χ^2	22.44	1670.96	1516.50	352.86	83.92	3478.60	3684.96	1100.52
	NA	—	218705	0	0	—	218705	0	0
	ABS	—	1207	1207	1207	—	1207	1207	1207
	p-value	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10	χ^2	24.04	532.76	590.16	181.30	71.28	1380.88	1706.72	647.64
	NA	—	153425	0	0	—	153425	0	0
	ABS	—	145	145	145	—	145	145	145
	p-value	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000
20	χ^2	10.84	29.80	39.32	28.86	26.40	140.28	177.36	99.56
	NA	—	79850	0	0	—	79850	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.287	0.000	0.000	0.001	0.119	0.000	0.000	0.000
40	χ^2	10.02	10.08	17.74	19.74	33.28	56.60	50.72	47.48
	NA	—	29450	0	0	—	29450	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.349	0.344	0.038	0.020	0.022	0.000	0.000	0.000
100	χ^2	11.94	5.10	6.24	6.24	27.68	23.92	24.36	24.36
	NA	—	2356	0	0	—	2356	0	0
	ABS	—	0	0	0	—	0	0	0
	p-value	0.217	0.826	0.716	0.716	0.090	0.199	0.183	0.183

Table 10: The chi-squared values for $Q_3 = 1.963$, and their p-values with the NA and ABS numbers.

Through simulation studies, some important notes have been observed and they should be mentioned clearly to get insights into the comparisons between the bootstrap methods. First, the SB method creates bootstrap samples with event time observations only. This is contrary to Efron's bootstrap samples, which often include right-censored observations and ties, due to the process of Efron's bootstrap method, which creates the bootstrap samples by sampling with replacement from the original data set. Secondly, the SB method mostly provides better results than those of Efron's method in terms of the coverage probability, in particular when the sample size is small. For very large data sets with a small censoring proportion, the SB method and Efron's bootstrap method will provide nearly identical results because the right-censoring-$A_{(n)}$ assumption will be nearly identical to the cumulative empirical distribution and the differences between the observed data points are very tiny. Thirdly, we proposed three options for Efron's bootstrap method $\mathrm{E}_{(1)}$, $\mathrm{E}_{(2)}$ and $\mathrm{E}_{(3)}$ to create the confidence region divisions because the statistic of interest may not be found based on the Kaplan-Meier estimate, in particular when the sample size is small and the censoring proportion is large. Fourthly, when the sample size is large, the three options $\mathrm{E}_{(1)}$, $\mathrm{E}_{(2)}$ and $\mathrm{E}_{(3)}$ provide nearly identical results because the KM estimator mostly provides the statistic of interest based on each bootstrap sample, NA is equal or approximately equal to zero. Finally, the chi-squared values corresponding to Efron's bootstrap method usually decrease as the sample size increases, while there is no pattern for the SB chi-squared values.

5. Survival function estimates

Analyzing survival data is of interest in many real world applications, e.g. in biology, medicine, engineering and economics. In the literature, the Kaplan-Meier (KM) estimator (Kaplan and Meier, 1958) has been widely used for survival function inferences due to its simplicity to apply and efficiency to provide good survival estimates. In this section, the SB method will be used to estimate the survival function and compare the results to the KM estimator through two real application examples from the literature (Bartholomew, 1957; Therneau, 2020). The $100(1-2\alpha)\%$ bootstrap pointwise confidence intervals will also be derived for the survival function.

Example 1. *Bartholomew (1957) provided a data set for* 10 *pieces of equipment installed in a system. At a later time, some of these pieces had failed and the rest were still in use. He aimed to study the lifetime distribution of the equipment, so he collected the following data points* $2, 4, 14, 21+, 24, 27, 33, 51, 60+, 72+$, *where the + sign means the corresponding number is a right-censored observation. Based on the SB method, the lifetime distribution can be estimated. We first order the data points and define the* 11 *intervals over the real line, and hence we compute their corresponding M-function values by Equations (4) and (5). This is illustrated in Table 11.*

By using the information in Table 11, $B = 1000$ bootstrap samples of size 10 are created by the SB method. Then, we derive the empirical survival function based on each bootstrap sample. At any time t, we have 1000 survival function estimates. To provide a bootstrap

Interval	M-function
(0,2)	0.0909
(2,4)	0.0909
(4,14)	0.0909
(14,24)	0.0909
(21+,24)	0.0130
(24,27)	0.1039
(27,33)	0.1039
(33,51)	0.1039
(51,∞)	0.1039
(60+,∞)	0.0519
(72+,∞)	0.1558

Table 11: The M-function values corresponding to the 11 intervals created by Bartholomew's data set.

estimate at a time t, we take the average of the 1000 survival function estimates at time t. The estimated survival curve based on the SB method is presented in Figure 1.

The survival function estimates based on the SB method and the KM estimator are presented in Figure 1. The bootstrap estimated survival function (orange line) looks smooth; but it is a step function with very small steps, contrary to the KM estimate (black step function), which only decreases at the 7 observed event times $(2, 4, 14, 24, 27, 33, 51)$. Between each two observed data points, the SB estimate goes through the KM estimate, and at each event time, the SB estimate is greater than the KM estimate. Based on the SB method, we derive the 90% confidence intervals for the survival function at times $t = 0, 1, 2, 3, \ldots, 100$, and the bounds of confidence intervals are illustrated by the two green lines. At each time, we order the 1000 survival function estimates, then take the 50th and 950th ordered resulting values to provide the 90% confidence interval for the survival function at that time. Note that the 90% confidence intervals' bounds are step functions due to the empirical survival function at each bootstrap sample taking only one of the 11 values $0, 0.1, \ldots, 0.9, 1$ at any time t.

Example 2. *The lung cancer data set, which was provided by Therneau (2020) in the* `survival` *package in R, will be used to show how the SB method and the KM estimator behave for a large data set, where this data set analyzes the SB method and the KM estimator for large data sets. The data set is for* 138 *patients who are detected to have lung cancer, the time is represented in days. The censoring proportion in the data set is* 0.188*, and there are 17 ties. To apply the SB method, we need to break the ties, and this can be done by adding a very small number to one of the tied observations.*

Based on the SB method and the KM estimator, the estimated survival functions for the lung cancer data are presented in Figure 2. From the figure, it is clear that the estimated survival functions are nearly identical due to the large sample size and small censoring proportion. The 90% bootstrap confidence intervals for the survival function at times t are illustrated by the two green lines. Note that these bootstrap confidence intervals are

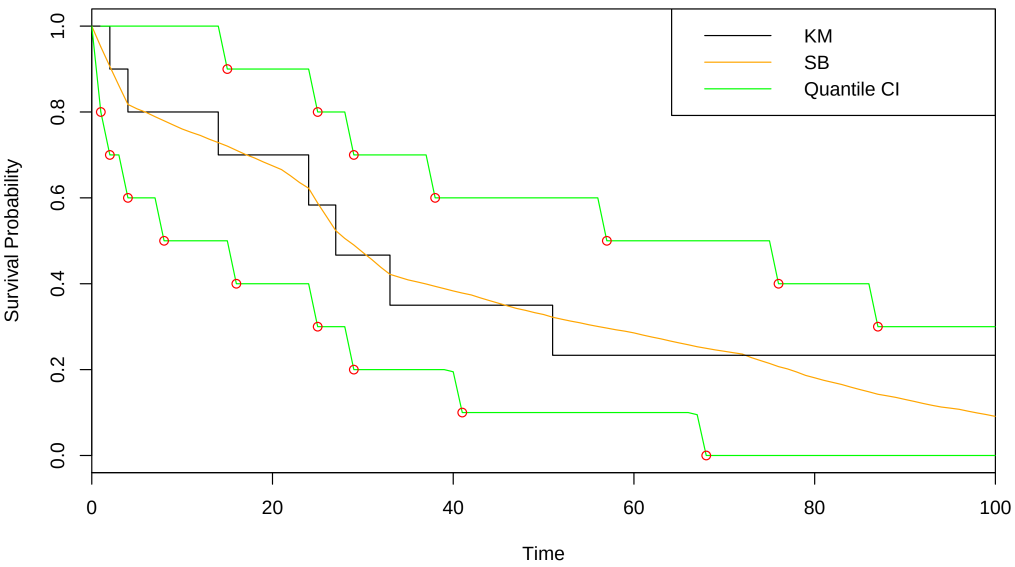

Figure 1: The survival curves for Bartholomew's data set based on the SB method with its 90% bootstrap confidence intervals, and the KM estimate.

narrower than the ones in Example 1, this is due to the large sample size. The bounds of the bootstrap confidence intervals are still step functions, but the steps are small, so that the bounds look smooth. These examples show that the discrepancy between the estimated survival functions based on the SB method and the KM estimator tends to decrease as the sample size increases. For a small data set as in Example 1, the KM estimate decreases only at the event times, so the estimated survival function is a step function with large steps. This is contrary to the estimated survival function based on the SB method, which is quite smooth. For a large data set with a small censoring proportion as in Example 2, the survival function estimates based on the SB method and the KM estimate are nearly identical.

The bounds of bootstrap confidence intervals are step functions as shown in Examples 1 and 2. One can provide smoothed confidence interval's bounds for the survival function, by using the linear and log-transformed confidence intervals presented by Borgan and Liestøl (1990) and Klein and Moeschberger (2003). For confidence level $100(1-2\alpha)\%$, these confidence intervals accomplish that the survival function at time t falls in the intervals with approximately probability $100(1-2\alpha)\%$. Borgan and Liestøl (1990) showed that the log-transformed confidence interval is better than the linear confidence interval in terms of the coverage accuracy, in particular for large confidence levels, e.g. 0.90 or 0.95. The SB and KM estimates will be used to study the performances of linear and log-transformed confidence intervals through simulations in Section 6. The $100(1-2\alpha)\%$ linear confidence interval can be calculated by

$$\hat{S}(t) \mp Z_{(1-2\alpha)} \times SD(\hat{S}(t)) \qquad (10)$$

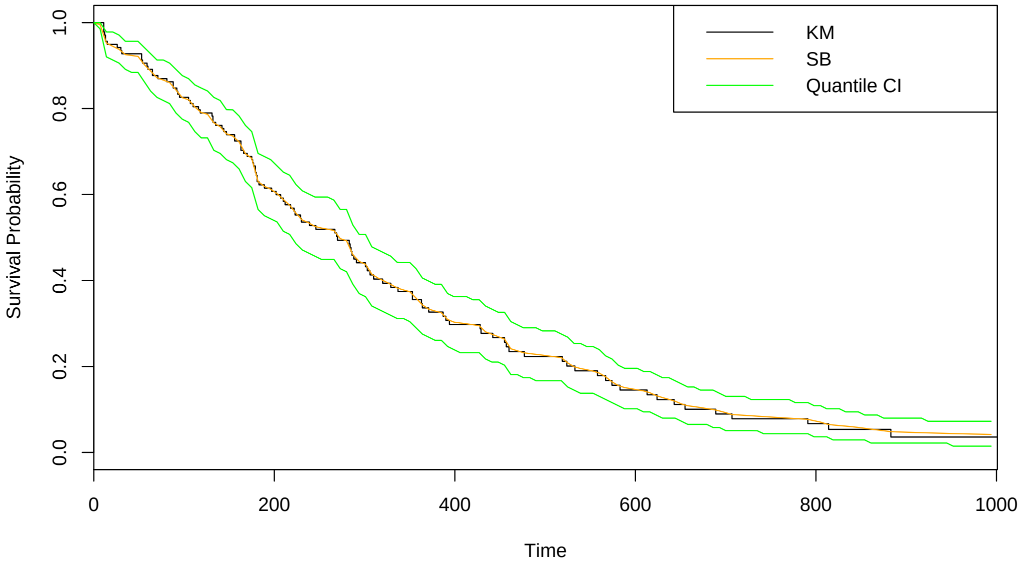

Figure 2: The survival curves for lung cancer data based on the SB method with the 90% bootstrap confidence intervals and the KM estimator.

and the $100(1-2\alpha)\%$ log-transformed confidence interval can be calculated by

$$\left((\hat{S}(t))^{\frac{1}{\theta}}, (\hat{S}(t))^{\theta}\right) \tag{11}$$

where $\theta = \exp(\frac{Z_{(1-2\alpha)} \times SD(\hat{S}(t))}{\hat{S}(t) \times \ln(\hat{S}(t))})$ and $Z_{(1-2\alpha)}$ is the $(1-2\alpha)$ percentile of the standard Normal distribution. $SD(\hat{S}(t))$ is the standard deviation of the estimated survival function, where the estimate can be either based on the SB method or the KM estimate. We restrict the confidence intervals to be within $[0, 1]$. It should be noted that the linear confidence interval is symmetric around the estimated survival function and the confidence interval's bounds are within $[0, 1]$, but the log-transformed confidence interval is not symmetric about the estimated survival function.

To derive the linear and log-transformed confidence intervals for a survival function at time t, the standard deviation of the estimated survival function needs to be derived first. For the estimated survival function based on the SB method, the standard deviation can be computed by

$$\hat{\sigma}_{boot}(\hat{S}(t)) = \sqrt{\frac{\sum_{j=1}^{B}(\hat{S}^j(t))^2 - (\sum_{j=1}^{B}\hat{S}^j(t))^2/B}{B-1}} \tag{12}$$

The standard deviation of the KM survival function estimate can be computed by the well-known Greenwood's formula (Greenwood, 1926; Kaplan and Meier, 1958). The estimated survival functions based on the SB method and the KM estimator along with their

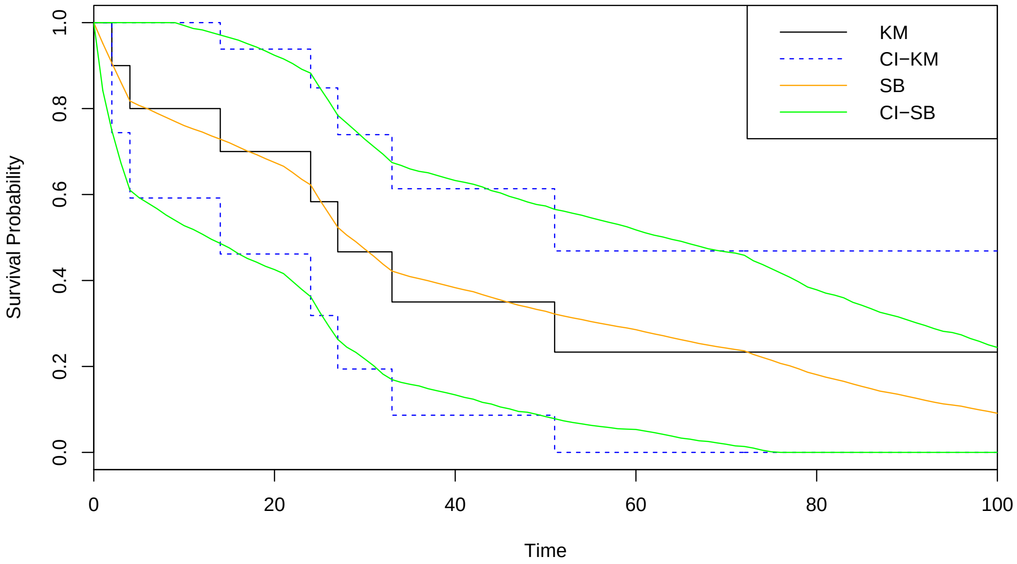

Figure 3: The survival curves for the equipment data based on the smoothed bootstrap method and the KM estimator with their 90% linear confidence intervals.

corresponding standard deviations will be used to obtain the linear and log-transformed confidence intervals. Next, Examples 1 and 2 will be used again to present the linear and log-transformed confidence intervals.

Figure 3 presents the estimated survival functions for the data of Example 1 based on the SB method and the KM estimator along with their corresponding 90% linear confidence intervals. The SB method smooths the bounds of the linear confidence interval for the survival function. In contrast, the KM estimator provides step functions for the confidence interval's bounds due to the fact that the KM method drops only at the event times. For the values of t beyond the largest event time, the KM survival function estimate together with its linear confidence interval remain constant. The estimated survival function for the smoothed bootstrap method decreases beyond the largest event time and its confidence interval becomes more narrow.

For the data in Example 1, Figure 4 presents the SB and KM estimated survival functions with their corresponding log-transformed 90% confidence intervals. The KM estimate leads to the bounds of confidence interval being step functions due to the fact that drops occur only at the event time observations. In contrast, the SB method provides more smooth bounds. From Figures 3 and 4, it is clear that both confidence intervals, regardless of the method being used to estimate the confidence intervals, have nearly identical patterns. The only difference is that the linear confidence interval is symmetric around the survival function as presented in Figure 3 (except in the tails due to the logical restriction to the interval $[0, 1]$) and the symmetry is not observed with the log-transformed confidence interval.

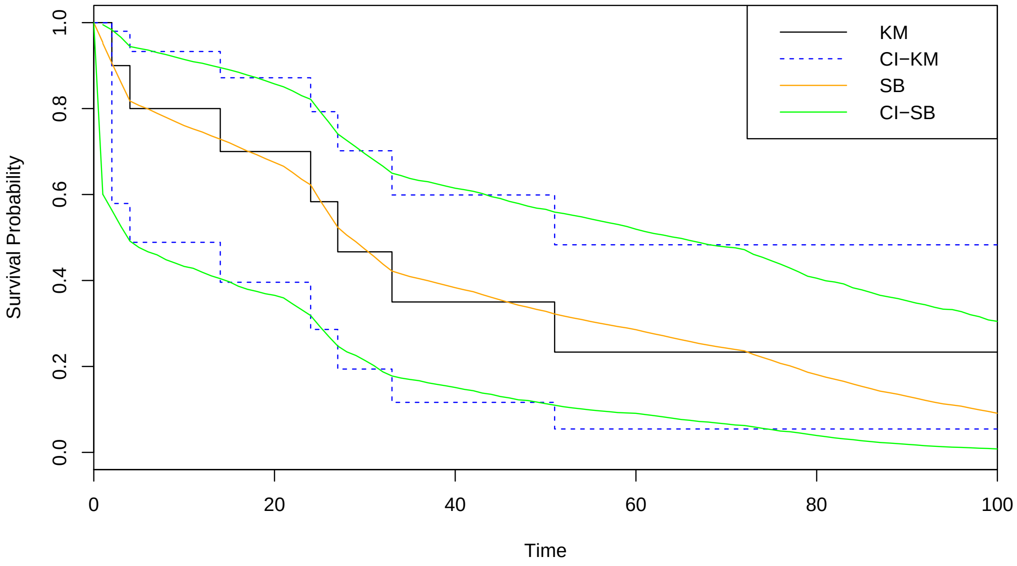

Figure 4: The survival curves for the equipment data based on the smoothed bootstrap method and the KM estimator with their 90% log-transformed confidence intervals.

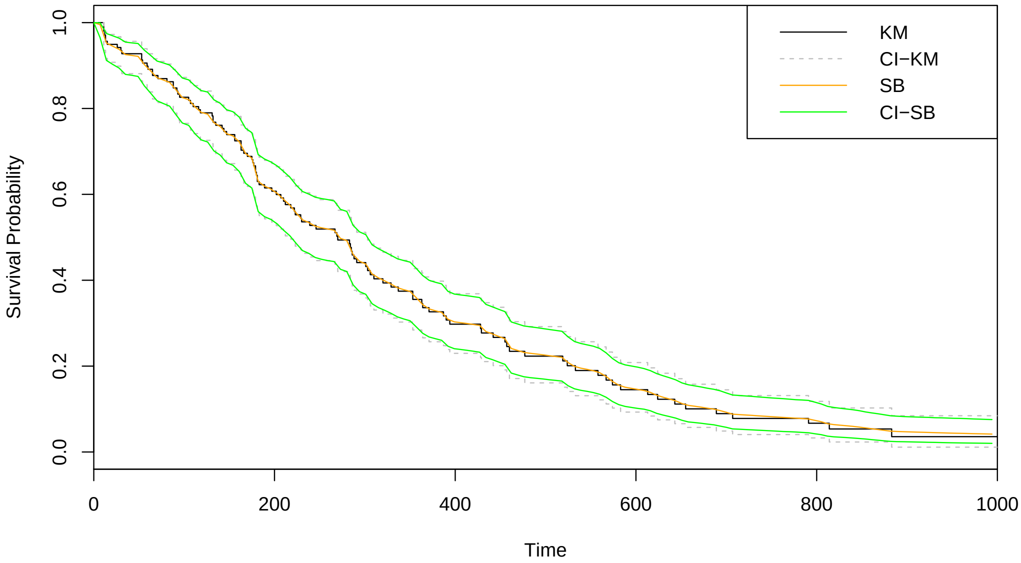

Figure 6: The survival curves for the lung cancer data based on the smoothed bootstrap method and the KM estimator with their 90% log-transformed confidence intervals.

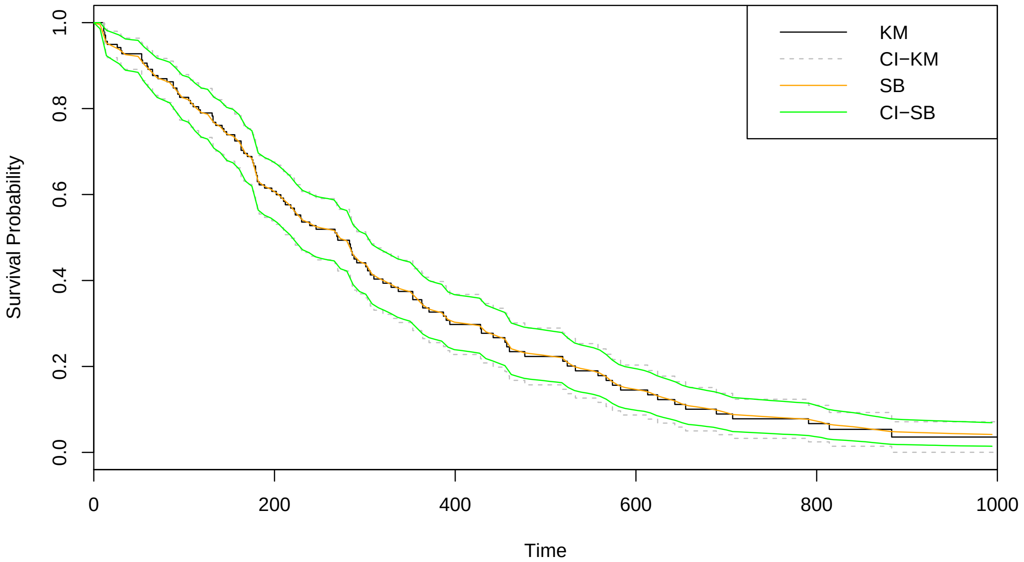

Figure 5: The survival curves for the lung cancer data based on the smoothed bootstrap method and the KM estimator with their 90% linear confidence intervals.

Figures 5 and 6 present the linear and log-transformed confidence intervals, respectively, for the data in Example 2 based on the SB method and the KM estimator. Due to the large sample size, the SB and KM methods provide nearly identical estimates for the survival function as shown in Figure 2. As a consequence, the corresponding confidence intervals are nearly identical as presented in Figures 5 and 6. From this example, we can conclude that the SB and KM methods have about the same behaviour for large data sets with many event time observations. This may be beneficial because the well-known excellent large sample properties of the Kaplan-Meier estimator (Klein and Moeschberger, 2003) seem to hold for the SB method. For the case of large sample size and large censoring proportion, the SB and KM methods may not have the same performance as the censored times seriously affect the estimated survival function based on the KM estimator.

6. The Kaplan-Meier smoothed bootstrap method for right-censored data

Efron (1981) introduced the bootstrap method for right-censored data, which has been widely used for survival inferences due to its simplicity to implement and good results, see e.g. Gross and Lai (1996); Mazucheli et al. (2005). The method is used by Bilker and Wang (1997) to provide confidence bands for the estimated survival function and it is used to compare two survival distributions by Heller and Venkatraman (1996). However, for the case of a small data set, Efron's bootstrap method does not perform well due to ties and censored observations, which occur in the bootstrap samples. This motivates development of a smoothed bootstrap method based on the Kaplan-Meier estimator. In this section, we present the KM smoothed bootstrap method, then it will be compared to the smoothed bootstrap method, which is presented in Section 3, through simulations.

The Kaplan-Meier estimate can be used to smooth the bootstrap method for right-censored data. Suppose that a data set of size n includes u event time observations and v right-censored observations, where $n = u + v$, and ties occur with probability 0. First, the n observed data points should be ordered, then we create $u+1$ intervals of the form $(t_{(i)},t_{(i+1)})$ based on the event time observations, where $i = 0, 1, 2, \ldots, u$ and $t_{(0)} = 0$ and $t_{(u+1)} = \infty$. Secondly, we assign a probability $\mathrm{P}_{(i)}$ to each interval of the form $(t_{(i)},t_{(i+1)})$, such that

$$\mathrm{P}_{(i)} = \mathrm{P}(t_{(i)} < T \leq t_{(i+1)}) = \hat{S}(t_{(i)}) - \hat{S}(t_{(i+1)}) \tag{13}$$

where $\hat{S}(t_{(i)})$ and $\hat{S}(t_{(i+1)})$ are the KM estimates for the survival functions at fixed times $t_{(i)}$ and $t_{(i+1)}$, respectively.

For clarity, we present the KM smoothed bootstrap algorithm for right-censored data, which is referred to by SBa, in the following steps:

(i) Order the observed data points and add the end points $t_{(0)} = 0$ and $t_{(u+1)} = +\infty$ (or $t_{(u+1)} = b$ for the case of finite support $[0, b]$). This leads to $t_{(0)} < t_{(1)} < \ldots < t_{(u)} < t_{(u+1)}$.

(ii) Create $u + 1$ intervals of the form $(t_{(i)}, t_{(i+1)})$, where $i = 0, \ldots, u$, based on the u event times.

(iii) Compute the assignment probabilities $\mathrm{P}_{(i)}$ by Equation (13) for the $u + 1$ intervals.

(iv) Sample with replacement n intervals with the assignment probabilities $\mathrm{P}_{(i)}$, then sample one observation uniformly from each finite interval. For the infinite interval $[t_{(u)}, \infty)$, we will fit an Exponential tail for this interval similar as described for the SB method in Section 3. The Exponential tail is fitted with rate parameter (Brown et al., 1974)

$$\hat{\lambda}^* = \frac{-\ln(\hat{S}(t_{(u)}))}{t_{(u)}} \tag{14}$$

This leads to obtain one bootstrap sample of size n.

(v) Calculate the empirical survival function at a fixed time t, $\hat{S}^*(t)$, based on the bootstrap sample.

(vi) Perform steps (iv) and (v) B times in order to have B survival function values at a fixed time t.

In this KM smoothed bootstrap approach, it should be noted that the last interval will not be chosen during the bootstrap implementation if the maximum observation is an event time, in which case the corresponding probability $\mathrm{P}_{(u)}$ is equal to 0. This leads to poor results for the survival function at any time $t > t_{(u)}$, as all survival function values at $t > t_{(u)}$ based on all bootstrap samples will be equal to 0. If the largest observation of the original data set is censored, then the last interval can be chosen in this bootstrap procedure.

To compare the KM smoothed bootstrap method, SBa, to the SB method, which is presented in Section 3, through simulations, we use the second scenario listed in Table

$n =$		6		10		20		40		100	
t	$S(t)$	SB	SBa	SB	SBa	SB	SBa	SB	SBa	SB	SBa
0.138	0.95	0.998	0.994	0.985	0.978	0.993	0.991	0.988	0.986	0.896	0.899
0.223	0.90	0.979	0.954	0.995	0.988	0.918	0.895	0.948	0.944	0.884	0.895
0.298	0.85	0.938	0.877	0.967	0.942	0.894	0.883	0.943	0.942	0.879	0.882
0.368	0.80	0.972	0.956	0.923	0.872	0.890	0.871	0.947	0.936	0.911	0.916
0.436	0.75	0.965	0.913	0.908	0.885	0.886	0.858	0.937	0.932	0.879	0.883
0.503	0.70	0.936	0.855	0.947	0.928	0.930	0.918	0.888	0.890	0.869	0.865
0.570	0.65	0.886	0.881	0.899	0.856	0.872	0.842	0.916	0.909	0.876	0.879
0.639	0.60	0.909	0.857	0.943	0.902	0.925	0.906	0.876	0.873	0.868	0.869
0.710	0.55	0.913	0.819	0.896	0.838	0.870	0.831	0.906	0.897	0.887	0.890
0.783	0.50	0.956	0.897	0.954	0.892	0.879	0.830	0.873	0.862	0.874	0.881
0.861	0.45	0.900	0.821	0.904	0.826	0.880	0.825	0.905	0.885	0.902	0.897
0.943	0.40	0.923	0.772	0.938	0.876	0.878	0.832	0.874	0.844	0.878	0.873
1.033	0.35	0.897	0.691	0.901	0.800	0.918	0.892	0.908	0.899	0.900	0.903
1.132	0.30	0.902	0.765	0.945	0.854	0.880	0.801	0.879	0.859	0.904	0.898
1.243	0.25	0.930	0.694	0.899	0.762	0.868	0.774	0.902	0.883	0.902	0.880
1.373	0.20	0.935	0.601	0.894	0.686	0.877	0.729	0.905	0.865	0.899	0.891
1.533	0.15	0.905	0.552	0.916	0.665	0.937	0.815	0.913	0.835	0.908	0.885
1.744	0.10	0.943	0.422	0.930	0.503	0.896	0.619	0.926	0.818	0.909	0.868
2.078	0.05	0.967	0.230	0.955	0.357	0.925	0.459	0.900	0.617	0.863	0.720

Table 12: The actual coverage proportions for the true survival function at each value of t in the 90% quantile confidence intervals based on the two smoothed bootstrap methods.

1 to create right-censored data sets. We study the coverage proportions for the survival function at 19 distinct fixed times in the quantile, linear and log-transformed confidence intervals based on the SB and SBa methods. The confidence level is set at 90% and the survival functions at the 19 different times are listed in the second column in Tables 12, 13 and 14. These 19 different times are presenting equally spaced quantiles of the event time distribution. By this way, we can discover how the SB and SBa methods perform at different times t.

For the simulations, $N = 1000$ data sets of size n are created to conduct the comparison between the SB and SBa methods. Based on each generated data set, we apply each bootstrap method $B = 1000$ times, and then we derive the empirical survival function based on each bootstrap sample. This leads to 1000 empirical survival functions based on each bootstrap method. For the 90% quantile confidence interval of the survival function at time t, we order the resulting values then compute $\hat{S}^*_{(50)}(t)$, which is the lower bound, and $\hat{S}^*_{(950)}(t)$, which is the upper bound. To conduct the 90% linear and log-transformed confidence intervals of the survival function at time t, we should first calculate the average and the standard deviation of the 1000 survival function estimates, then use Equations (10) and (11). For each confidence interval including the true survival function at time t, we count one; otherwise, we count zero. This is repeated for all generated data sets in order to define the actual coverage proportions for the survival function at a fixed time t.

$n =$		6		10		20		40		100	
t	$S(t)$	SB	SBa	SB	SBa	SB	SBa	SB	SBa	SB	SBa
0.138	0.95	0.998	0.989	0.992	0.985	0.985	0.981	0.954	0.952	0.908	0.903
0.223	0.90	0.987	0.970	0.988	0.973	0.938	0.943	0.905	0.902	0.894	0.897
0.298	0.85	0.981	0.945	0.962	0.951	0.905	0.895	0.898	0.897	0.881	0.881
0.368	0.80	0.969	0.930	0.922	0.922	0.889	0.892	0.898	0.894	0.890	0.886
0.436	0.75	0.955	0.908	0.898	0.872	0.886	0.876	0.909	0.901	0.884	0.888
0.503	0.70	0.935	0.878	0.895	0.862	0.878	0.860	0.891	0.881	0.872	0.863
0.570	0.65	0.911	0.848	0.888	0.852	0.881	0.858	0.882	0.870	0.879	0.877
0.639	0.60	0.895	0.837	0.880	0.846	0.869	0.855	0.880	0.867	0.867	0.871
0.710	0.55	0.913	0.827	0.890	0.827	0.865	0.849	0.873	0.860	0.891	0.892
0.783	0.50	0.918	0.803	0.882	0.837	0.881	0.852	0.866	0.851	0.881	0.875
0.861	0.45	0.910	0.789	0.894	0.812	0.862	0.844	0.861	0.841	0.873	0.871
0.943	0.40	0.899	0.762	0.901	0.796	0.872	0.841	0.876	0.851	0.872	0.864
1.033	0.35	0.906	0.733	0.894	0.791	0.878	0.827	0.882	0.863	0.889	0.868
1.132	0.30	0.919	0.719	0.897	0.771	0.875	0.827	0.881	0.842	0.889	0.870
1.243	0.25	0.926	0.670	0.889	0.740	0.869	0.790	0.870	0.828	0.883	0.863
1.373	0.20	0.936	0.615	0.895	0.716	0.882	0.758	0.860	0.808	0.880	0.855
1.533	0.15	0.950	0.534	0.913	0.654	0.874	0.712	0.868	0.788	0.882	0.860
1.744	0.10	0.955	0.413	0.935	0.544	0.900	0.671	0.882	0.753	0.881	0.830
2.078	0.05	0.974	0.242	0.965	0.361	0.950	0.490	0.914	0.657	0.871	0.743

Table 13: The actual coverage proportions for the true survival function at each value of t in the 90% linear confidence intervals based on the two smoothed bootstrap methods.

Based on the SB and SBa methods, Table 12 presents the coverage proportions for the survival function at different times t in the 90% quantile confidence intervals. When the time t is small, both bootstrap methods provide over-coverage; and as the sample size n increases, the discrepancies between the actual and nominal coverage proportions decrease. For medium and large values of t, the SB method mostly performs better than the SBa method, in particular when the sample size is small. The SB method mostly provides over-coverage regardless to the value of t while the SBa method mostly provides under-coverage when the time t is large, in particular for small data sets. For the largest values of t considered, the SBa method performs poorly while the SB method shows its superiority in making the discrepancy between the actual and nominal coverage probabilities less, particularly for small data sets $n = 6, 10$ and 20. As the sample size increases, the results of SBa method improve, and this is obvious when $n = 40$ and 100.

For the survival function at 19 different values of t, Table 13 presents their actual coverage proportions at the 90% linear confidence intervals based on the SB and SBa methods. When the time t is small, both bootstrap methods provide over-coverage, in particular when the sample size is small. As the sample size increases, the bootstrap methods decrease the discrepancies between the actual and nominal coverage probabilities. For medium and large values of time t, the SB method provides better results than those of the SBa method, in particular for small data sets. For the largest values of time t, the SBa method performs

$n =$		6		10		20		40		100	
t	$S(t)$	SB	SBa	SB	SBa	SB	SBa	SB	SBa	SB	SBa
0.138	0.95	0.919	0.836	0.891	0.863	0.913	0.899	0.924	0.909	0.921	0.917
0.223	0.90	0.922	0.854	0.910	0.877	0.906	0.876	0.925	0.915	0.910	0.907
0.298	0.85	0.936	0.867	0.931	0.877	0.912	0.889	0.914	0.897	0.907	0.900
0.368	0.80	0.941	0.868	0.931	0.876	0.918	0.894	0.918	0.906	0.891	0.884
0.436	0.75	0.945	0.858	0.930	0.876	0.914	0.873	0.909	0.898	0.904	0.897
0.503	0.70	0.941	0.860	0.937	0.869	0.907	0.874	0.904	0.887	0.872	0.869
0.570	0.65	0.948	0.850	0.932	0.869	0.905	0.866	0.899	0.887	0.883	0.876
0.639	0.60	0.952	0.859	0.931	0.863	0.909	0.875	0.891	0.873	0.885	0.881
0.710	0.55	0.968	0.880	0.933	0.861	0.895	0.872	0.884	0.868	0.893	0.888
0.783	0.50	0.973	0.880	0.933	0.868	0.904	0.867	0.881	0.867	0.887	0.883
0.861	0.45	0.972	0.889	0.943	0.855	0.903	0.868	0.882	0.860	0.882	0.879
0.943	0.40	0.969	0.908	0.933	0.860	0.902	0.870	0.892	0.870	0.878	0.871
1.033	0.35	0.973	0.937	0.933	0.870	0.894	0.865	0.890	0.878	0.891	0.879
1.132	0.30	0.985	0.988	0.934	0.882	0.900	0.859	0.899	0.857	0.892	0.881
1.243	0.25	0.982	0.991	0.940	0.921	0.896	0.844	0.876	0.854	0.887	0.867
1.373	0.20	0.974	0.987	0.943	0.970	0.899	0.839	0.868	0.836	0.886	0.871
1.533	0.15	0.972	0.983	0.933	0.965	0.901	0.900	0.879	0.834	0.890	0.870
1.744	0.10	0.954	0.973	0.931	0.962	0.914	0.964	0.888	0.879	0.884	0.858
2.078	0.05	0.936	0.969	0.917	0.950	0.906	0.951	0.895	0.960	0.876	0.847

Table 14: The actual coverage proportions for the true survival function at each value of t in the 90% log-transformed confidence intervals based on the two smoothed bootstrap methods.

poorly because an Exponential tail is assumed for the last interval in only one case, which is the case that the maximum observation is censored; the last interval will not be selected during the bootstrap procedure if the last observation is event due to $\text{P}_{(u)} = 0$. This leads to poor estimated results for the survival function at any time $t \geq t_{(u)}$; the estimated survival function at any time $t \geq t_{(u)}$ is set equal to zero.

Table 14 outlines the actual coverage probabilities for the survival function at different times t in the 90% log-transformed confidence intervals. At different sample sizes n and different times t, the SB method mostly provides better results than the SBa method, in particular for sample sizes 6 and 10. For $n = 6, 10, 20$, the SB method mostly provides over-coverage, but when the sample size is $40, 100$, it mostly provides under-coverage. When the time t is small, e.g. $t = 0.138, 0.223$, the SBa method provides under-coverage when $n = 6, 10$, and as the sample size increases to $20, 40, 100$, it performs well. Overall, the SBa method leads to better coverage in the log-transformed confidence intervals in comparison to the results at the quantile and linear confidence intervals, in particular for small data sets.

For this section, we introduced a smoothed bootstrap method based on the Kaplan-Meier estimate and compared it to the SB method through simulation studies. Based on the simulation results, it is apparent that the SB method mostly provides better coverage. This is because of three reasons; first, the SB method partitions the sample space into

$n+1$ intervals based on all observed data points while the SBa method creates only $u+1$ intervals by the event time observations, where $u \leq n$. The second reason is that with the SB method, we assume an Exponential tail to each infinite interval while with the SBa method, we assume only one Exponential tail to the last interval. Thirdly, the last interval will not be selected during the SBa bootstrap procedure if the maximum observation is an event time due to the fact that $\mathrm{P}_{(u)} = 0$. This leads to poor results for the survival function at times that are greater than $t_{(u)}$.

7. Concluding remarks

This paper has introduced a smoothed bootstrap method for right-censored data (Al Luhayb, 2021) based on the right-censoring $A_{(n)}$ assumption proposed by Coolen and Yan (2004). This method is easy to implement and it provides good results. To investigate its performance, we compared it to Efron's method in terms of the coverage probabilities for the quartiles through simulation studies. The smoothed bootstrap method mostly performs better than Efron's method, in particular for small data sets. For survival inferences, the smoothed bootstrap method has been applied and compared to the Kaplan-Meier estimate through two examples. Then, it is compared to the alternative smoothed bootstrap method based on the Kaplan-Meier estimate. The comparisons were in terms of the coverage of the quantile, linear and log-transformed confidence intervals for the survival function at different times t. The smoothed bootstrap method performs better than the Kaplan-Meier smoothed bootstrap method, in particular when the sample size is small and the time t is large.

Due to the process of Efron's method, which is sampling with replacement from the original data set, the bootstrap samples often include ties and right-censored observations, which may lead to poor results in particular when the sample size is small and the censoring proportion is large. In contrast, the smoothed bootstrap method prevents ties and right-censored observations to occur in the bootstrap samples, and the smoothed bootstrap method samples from the whole data support by using the right-censoring $A_{(n)}$ assumption. For large data sets, Efron's method can provide good accuracy. However, it is not always easy to obtain large data sets for real world applications, e.g. in statistics related to medicines (Freireich et al., 1963; Nahman et al., 1992; Sedmak et al., 1989), so it may be beneficial to use the smoothed bootstrap method instead in such cases.

For survival inferences, the smoothed bootstrap method was used and compared to the Kaplan-Meier estimate through two real applications from the literature. For a small data set, the smoothed bootstrap method provided a smooth survival curve while the Kaplan-Meier estimate decreases only at the event times t. When the sample size is large, the smoothed bootstrap method and the Kaplan-Meier estimate lead to nearly identical estimates of the survival function. Through simulation studies, the smoothed bootstrap method has been compared to the Kaplan-Meier smoothed bootstrap method in terms of the coverage proportions for the survival function at different times t in the quantile, linear and log-transformed confidence intervals. In these confidence intervals, the smoothed bootstrap method mostly provided better results, in particular when the sample size is small and the time t is large. With the smoothed bootstrap method, an Exponential tail is assumed for each infinite interval while only one Exponential tail is assumed for the last interval when the Kaplan-Meier smoothed bootstrap method is applied. With the smoothed bootstrap method based on the Kaplan-Meier estimate, the last interval will not be chosen during the bootstrap procedure if the maximum observation is an event time; it may be selected only if there is at least one right-censored observation greater than the maximum event time.

To implement the smoothed bootstrap method in R software, it requires approximately 15% more time than Efron's method. This is due to the ordering of the observations, computation of the M-function values corresponding to the $n + 1$ intervals and sampling from the intervals to create the bootstrap samples. The Kaplan-Meier smoothed bootstrap method requires similar computation time as the smoothed bootstrap method.

In this paper we have considered the use of the bootstrap method for uncertainty quantification in case of estimation only. Consideration of the use of the bootstrap method for other inferences is also important. One example is the use for hypothesis testing, a detailed study of the newly proposed bootstrap method, with comparison to Efron's bootstrap, applied to hypothesis tests is reported by Al Luhayb (2021). Considering Type-1 errors, the new bootstrap method also provides mostly better results for hypothesis testing than Efron's bootstrap, as for estimation in particular for small data sets and large censoring proportions. Comparing the performances of these bootstrap methods with regard to Type-2 errors for hypothesis tests is an important topic for future research. A further possible use of the smoothed bootstrap method is in reliability applications. For example, Marks et al. (2014) used Efron's bootstrap method for inference on system lifetime distributions for both parallel and series systems. It may be beneficial to use the smoothed bootstrap method instead in such settings, in particular because the resulting survival functions are much smoother.

Conflict of interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

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