

Resampling Methods for Survival Parameter Estimation in a Two-Parameter Exponential Model

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	ABSTRACT
Received: 12 July 2026	This study compares Bootstrap, Jackknife Delete-1, Delete-2, Delete-3 and a K-level Delete-r procedure for estimating parameters of a two-parameter exponential survival model. Monte Carlo simulation used $n = 10,30,70$, $\theta = 0,1,2$, $\lambda = 0.5,1,2$, and 200 replications per scenario, followed by an NCCTG lung-cancer application. Delete-1 generally produced the smallest bias, variance and MSE, while Bootstrap showed greater variability. The K-level Delete-r method remained competitive and stable. The study provides practical evidence for selecting resampling methods and clarifies the distinction between direct Delete-r and recursive K-repeated jackknifing. Future work should examine censoring, larger sample size and other survival distributions.
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INTRODUCTION

Survival data arise whenever the outcome of interest is the time until an event occurs, such as death, failure, relapse or system breakdown. A central problem in survival analysis is the reliable estimation of model parameters when the available sample is limited and the estimator may be affected by sampling variability or finite sample bias. The two-parameter exponential distribution is useful in this setting because, in addition to the rate parameter, it includes a location or threshold parameter that allows the distribution to begin at a non-zero time. This makes the model relevant to lifetime, reliability and survival applications where an event cannot occur before a minimum threshold (Goel et al., 2025; Soori et al., 2025). In the present study, the parameters of interest are the location parameter θ , the rate parameter λ , and the corresponding survival probability.

Resampling methods provide a practical way of studying the behaviour of estimators without relying entirely on large sample approximations. Their usefulness has also been demonstrated in applied statistical modelling, including comparative assessment of bootstrap and jackknife procedures in logistic regression (Usman et al., 2021). The bootstrap approximates the sampling distribution by repeated sampling with replacement, while the jackknife systematically recalculates an estimator after deleting observations from the original sample. Recent work has continued to demonstrate the usefulness of these approaches for bias reduction and inference. Jiang and Zhang (2019), for example, examined the use of the jackknife for correcting bias in maximum likelihood estimation, while Ahmed Abdulhadi et al. (2024) showed that bias correction procedures can improve finite sample estimation. Marta (2023) discussed the broader role of resampling in statistical estimation, and Limozin et al. (2025) compared bootstrap and jackknife based inference for survival outcomes. These studies support the continued relevance of resampling methods, although their performance can vary with the estimator, sample size and data structure. An especially relevant study is Adewara and Mbata (2014), who compared bootstrap, jackknife and K-repeated jackknife methods for survival estimation under a two-parameter exponential model. Their study reported that the K-repeated jackknife reduced mean squared error relative to the other methods considered. However, the K-repeated

procedure described by Adewara and Mbata is an iterative procedure in which the results from one stage are used in constructing the next stage. The present study does not reproduce that recursive procedure. Instead, it considers Delete-1, Delete-2 and Delete-3 directly from the original sample, evaluates all possible deletion subsets at each level, and then averages the resulting level specific estimates to obtain a K-level Delete-r estimator. This distinction is central to the contribution of the present work.

Despite the continuing use of bootstrap and jackknife methods, there is still limited comparative evidence on how ordinary MLE, Delete-1, higher-order direct Delete-r, and bootstrap perform together for the two-parameter exponential survival model across different finite sample sizes. The gap is not simply the absence of another resampling method; rather, it concerns the lack of a transparent comparison in which the deletion level, number of resulting subsamples, aggregation of the levels, and distinction between recursive and non-recursive procedures are explicitly defined. The present study therefore investigates whether systematic direct Delete-r resampling can provide competitive and stable parameter estimation relative to the ordinary MLE and bootstrap method.

The aim of the study is to compare the finite sample performance of the ordinary maximum likelihood estimator, jackknife Delete-1, Delete-2, Delete-3, the combined K-level Delete-r estimator with $K = 3$, and bootstrap estimation for the two-parameter exponential survival model. The study asks the research question: Which of the competing resampling procedures provides the most accurate and stable estimation of the location and rate parameters of the two-parameter exponential survival model under the simulated conditions and the empirical NCCTG lung cancer data? The investigation uses Monte Carlo simulation with sample sizes $n = 10,30,70$, parameter values $\theta = 0,1,2$ and $\lambda = 0.5,1,2$, followed by an empirical analysis using NCCTG lung cancer survival data. Estimator performance is assessed through bias, variance, MSE and percentage error in the simulation, and through parameter estimates, standard errors, confidence intervals, stability and sensitivity to resampling in the real-data analysis.

The study matters because it provides evidence that can help researchers choose an appropriate resampling strategy when

estimating survival model parameters in finite samples. It also clarifies an important methodological issue that can easily be overlooked: a higher deletion level is not automatically an improvement, and a multi-level Delete-r procedure should not be described as recursive when each deletion level is constructed directly from the original observations. The remainder of the paper presents the model and resampling methods first, followed by the simulation design, the real data application, the results and discussion, and the conclusion.

MATERIAL AND METHODS

Two-Parameter Exponential Distribution

The two-parameter exponential distribution, an extension of the standard one-parameter exponential distribution, is widely used in lifetime modelling and reliability theory because it incorporates a location (threshold) parameter in addition to the scale parameter, making it more flexible for modelling failure-time data (Goel et al., 2025). It is defined by two parameters: a location parameter, θ , also called the minimum threshold or the initial shift parameter, and a rate parameter, λ . Statistically, it describes a random variable X such that X is greater than θ , meaning that no event occurs before the threshold θ . After this point, the waiting time follows an exponential pattern. This makes the model suitable for situations where a process begins after a fixed delay, such as delayed system failure or survival time after a certain starting point (Soori et al., 2025)

Probability Density Function, Cumulative Distribution Function and Survival Function of the Two-Parameter Exponential Distribution

Let X be a random variable following a two-parameter exponential distribution with location (shift) parameter θ and rate parameter λ , where

$$\theta \geq 0, \lambda > 0.$$

The distribution can be expressed as

$$X = \theta + Y,$$

where

$$Y \sim \text{Exponential}(\lambda).$$

Thus, the two-parameter exponential distribution has a lower threshold at θ , below which the event cannot occur.

i. Probability Density Function (PDF)

The probability density function is

$$f(x; \theta, \lambda) = \begin{cases} \lambda \exp[-\lambda(x - \theta)], & \text{if } x \geq \theta, \\ 0, & \text{and } 0 \text{ if } x < \theta. \end{cases} \quad 1$$

Here, θ determines the starting point or threshold of the distribution, while λ controls the rate at which the density decreases.

ii. Cumulative Distribution Function (CDF)

The cumulative distribution function is

$$F(x; \theta, \lambda) = \begin{cases} 0, & x < \theta, \\ 1 - \exp[-\lambda(x - \theta)], & x \geq \theta. \end{cases} \quad 2$$

Thus, $F(x) = 0$ for values below the threshold because the event cannot occur before θ .

iii. Survival Function (Reliability Function)

The survival function is defined as

$$S(t; \theta, \lambda) = P(X > t) = \begin{cases} 1, & t < \theta, \\ \exp[-\lambda(t - \theta)], & t \geq \theta. \end{cases} \quad (3)$$

For $t < \theta$, $S(t) = 1$ because no event can occur before the threshold. For $t \geq \theta$ theta, the survival probability decreases exponentially as t increases beyond the threshold. Hence, θ determines the minimum possible event time, whereas λ determines the rate of decline in survival probability.

Bootstrap Estimation Methods

The bootstrap method, according to Marta (2023), replaces the unknown population distribution with the empirical distribution that assigns equal probability to each observed value. The practical use of bootstrap and jackknife procedures

for assessing estimator performance has also been demonstrated in applied statistical modelling (Usman et al., 2021). By repeatedly sampling with replacement from the data, it approximates the sampling distribution of an estimator. This approach enables data driven estimation and evaluation of performance measures for survival estimators without requiring strong parametric assumptions.

For each sample $X_1^{*(b)}, X_2^{*(b)}, \dots, X_n^{*(b)}$ is obtained from the original observations with replacement.

For each bootstrap sample, the two-parameter exponential maximum likelihood estimators are calculated as

$$\theta^{*(b)} = \min(X_1^{*(b)}, \dots, X_n^{*(b)}) \quad 4$$

and

$$\lambda^{*(b)} = \frac{n-1}{\sum_{i=1}^n (X_i^{*(b)} - \theta^{*(b)})} \quad 5$$

The corresponding estimated survival probability at t is calculated as

$$\hat{S}^{*(b)}(t; \theta^{*(b)}, \lambda^{*(b)}) = \exp[-\lambda^{*(b)}(t - \theta^{*(b)})], \quad \forall t \geq \theta^{*(b)} \quad 6$$

Then the bootstrap estimates are the arithmetic means, thus;

$$\hat{\theta}_{boot} = \frac{1}{B} \sum_{b=1}^B \hat{\theta}^{*(b)} \quad 7$$

$$\hat{\lambda}_{boot} = \frac{1}{B} \sum_{b=1}^B \hat{\lambda}^{*(b)} \quad 8$$

$$\hat{S}_{boot}(t) = \frac{1}{B} \sum_{b=1}^B \hat{S}^{*(b)}(t) \quad 9$$

The bootstrap estimate of bias is defined as

$$\widehat{Bias}_{boot}(\hat{S}(t)) = \hat{S}^*(t) - \hat{S}(t) \quad 10$$

where

$$\hat{S}^*(t) = \frac{1}{B} \sum_{b=1}^B \hat{S}^{*(b)}(t).$$

The bootstrap variance is similarly estimated by

$$\widehat{Var}_{boot}(\hat{S}(t)) = \frac{1}{B-1} \sum_{b=1}^B (\hat{S}^{*(b)}(t) - \hat{S}^*(t))^2 \quad 11$$

Consequently, the bootstrap mean square error (MSE) is given by

$$\widehat{MSE}_{boot}(\hat{S}(t)) = \widehat{Var}_{boot}(\hat{S}(t)) + [\widehat{Bias}_{boot}(\hat{S}(t))]^2 \quad 12$$

For interval estimation, the bootstrap provides several approaches. The percentile bootstrap confidence interval for $S(t)$ is constructed from the ordered bootstrap replicates. Thus Let $\hat{S}^{*(\alpha/2)}(t)$ and $\hat{S}^{*(1-\alpha/2)}(t)$ denote the empirical quantiles of the bootstrap distribution. Then a $(1-\alpha)100\%$ confidence interval is given by

$$[\hat{S}^{*(\alpha/2)}(t), \hat{S}^{*(1-\alpha/2)}(t)]. \quad 13a$$

Alternatively, the normal approximation interval is

$$\hat{S}(t) \pm Z_{\alpha/2} \sqrt{\widehat{Var}_{boot}(\hat{S}(t))} \quad 13b$$

where $Z_{\alpha/2}$ is the standard normal quantile.

Finally, the bootstrap framework allows for computation of percentage error, which measures the relative magnitude of estimation error. Therefore, the bootstrap estimate of percentage error for the survival functions is expressed as

$$\widehat{PE}_{boot}(t) = \frac{\sqrt{\widehat{MSE}_{boot}(\hat{S}(t))}}{\hat{S}(t)} \times 100\% \quad 14$$

This quantity provides a scale-free assessment of estimator accuracy and is particularly informative when comparing performance across different time points, t .

Jackknife Delete-One Estimation Method

The jackknife delete-one resampling method, repeatedly recompute the estimator after omitting one observation at a time (resample without replacement).

For the original sample of size n , $X_1, X_2, \dots, X_n$, the i^{th} jackknife pseudo-sample is obtained by deleting observation X_i :

$$X_{(-i)} = (X_1, \dots, X_{i-1}, X_{i+1}, \dots, X_n) \quad \forall i = 1, 2, \dots, n$$

Consequently, each delete-one pseudo-sample contains $n - 1$ observations. For every delete-one pseudo-sample, the two-parameter exponential maximum likelihood estimators were recalculated. Thus;

$$\hat{\theta}_{(-i)} = \min(X_{(-i)}) \quad 15$$

$$\hat{\lambda}_{(-i)} = \frac{(n-1) - 1}{\sum_{X_j \in X_{(-i)}} (X_j - \hat{\theta}_{(-i)})}$$

Equivalently,

$$\hat{\lambda}_{(-i)} = \frac{n-2}{\sum_{X_j \in X_{(-i)}} (X_j - \hat{\theta}_{(-i)})} \quad 16$$

The corresponding survival estimate at a given t is given as

$$\hat{S}_{-i}(t; \theta_{-i}, \lambda_{-i}) = \exp[-\lambda_{-i}(t - \theta_{-i})], \quad \forall t \geq \theta_{-i} \quad 17$$

Table 1: Jackknife Delete-one Estimates of Location Parameter ($\hat{\theta}_{(i)}$), Rate Parameter ($\hat{\lambda}_{(i)}$) and Survival Function $\hat{S}_{(i)}(t)$ for the Two-Parameter Exponential Distribution

Omitted Observation (i)	Reduced Sample $\hat{t}_{(-i)}$	$\hat{\theta}_{(-i)}$	$\hat{\lambda}_{(-i)}$	$\hat{S}_{(-i)}(t)$
Omit t_1	$t_2, t_3, \dots, t_n$	$\hat{\theta}_{(1)}$	$\hat{\lambda}_{(1)}$	$\text{Exp}[-\hat{\lambda}_1(t - \hat{\theta}_{(1)})]$
Omit t_2	$t_1, t_3, \dots, t_n$	$\hat{\theta}_{(2)}$	$\hat{\lambda}_{(2)}$	$\text{Exp}[-\hat{\lambda}_2(t - \hat{\theta}_{(2)})]$
Omit t_3	$t_1, t_2, t_4, \dots, t_n$	$\hat{\theta}_{(3)}$	$\hat{\lambda}_{(3)}$	$\text{Exp}[-\hat{\lambda}_3(t - \hat{\theta}_{(3)})]$
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
Omit t_n	$t_1, t_2, t_4, \dots, t_{n-1}$	$\hat{\theta}_{(n)}$	$\hat{\lambda}_{(n)}$	$\text{Exp}[-\hat{\lambda}_n(t - \hat{\theta}_{(n)})]$

The delete-one estimates are obtained by averaging the estimates from all n delete-one pseudo samples;

$$\hat{\theta}_{D1} = \frac{1}{n} \sum_{i=1}^n \hat{\theta}_{(-i)} \quad 18$$

$$\hat{\lambda}_{D1} = \frac{1}{n} \sum_{i=1}^n \hat{\lambda}_{(-i)} \quad 19$$

and

$$\hat{S}_{D1} = \frac{1}{n} \sum_{i=1}^n \hat{S}_{(-i)}(t) \quad 20$$

The jackknife estimate of bias of $\hat{S}(t)$ is given by

$$\widehat{Bias}_{jack}(t) = (n-1)[\hat{S}_{(i)}(t) - \hat{S}(t)] \quad 21$$

Which follows directly from the linear approximation principle underlying the jackknife method.

The jackknife estimate of variance is

$$\widehat{Var}_{jack}(t) = \frac{n-1}{n} \sum_{i=1}^n (\hat{S}_{(i)}(t) - \hat{S}(t))^2. \quad 22$$

These expressions provide a complete second-order assessment of the estimator's accuracy, consistent with the general resampling context emphasised by Marta (2023), where the jackknife approximates the sampling distribution through deterministic sampling. For interval estimation, an approximate $(1-\alpha)100\%$ confidence interval for $S(t)$ can be constructed using the asymptotic normality of the jackknife estimator:

$$\hat{S}(t) \pm Z_{\alpha/2} \sqrt{\widehat{Var}_{jack}(t)} \quad 23$$

where $Z_{\alpha/2}$ is the upper $\alpha/2$ quantile of the standard normal distribution. This interval relies on the consistency of the jackknife variance estimator and is appropriate when the sample size is moderate or large. Alternatively, bias-corrected versions may be formed by replacing

$$\hat{S}(t) - \widehat{Bias}_{jack}(t) \text{ in the interval construction.}$$

Lastly, the percentage error of the jackknife estimator can be expressed as

$$PE_{jack}(t) = \frac{\widehat{Bias}_{jack}(t)}{\hat{S}(t)} \times 100\% \quad 24$$

K-Level Delete-R Jackknife Resampling Estimation Method

The classical jackknife is commonly formulated as a delete-one procedure in which one observation is omitted at a time and the statistic of interest is recalculated from each resulting sample as discusses above. The proposed Delete-r resampling procedure extends the ordinary Delete-One jackknife by considering several deletion levels.

More generally, this can be obtained by deleting (r) observations simultaneously from the original sample and evaluating the estimator on every resulting reduced sample.

For a sample $X = (X_1, X_2, \dots, X_n)$, let D_r denote a subset of r observations selected for deletion. The corresponding pseudo-sample $X_{(-D_r)} = \{X_i: i \notin D_r\}$.

The size of every delete r pseudo-sample is therefore

$$m = n - r$$

For each deletion level r , all possible subsets were considered. The number of possible delete- r subset is

$$N_r = \binom{n}{r}$$

For each delete- r pseudo-sample, the two-parameter exponential MLE are recalculated. if the remaining sample has size $m = n - r$, then

$$\hat{\theta}_{(-D_r)} = \text{Min}(X_{(-D_r)}), \quad 25$$

$$\hat{\lambda}_{(-D_r)} = \frac{m-1}{\sum_{X_i \in X_{(-D_r)}} (X_i - \hat{\theta}_{(-D_r)})} \quad 26$$

The corresponding survival estimate at time t is

$$\hat{S}_{-D_r}(t; \theta_{-D_r}, \lambda_{-D_r}) = \exp[-\lambda_{-D_r}(t - \theta_{-D_r})], \quad \forall t \geq \theta_{-D_r} \quad 27$$

Consequently, each delete- (r) reduced sample produces an independently recalculated estimate of the survival probability.

Stage- (r) Estimator

For each deletion level r , the estimates are averaged across all possible deletion subsets. Thus

The average survival estimate at deletion level (r) is defined as

$$\hat{S}_{Dr}(t) = \frac{1}{\binom{n}{r}} \sum_{D_r} \hat{S}_{(-D_r)}(t) \quad 28$$

Similarly, the corresponding stage estimates of the location and rate parameters are

$$\hat{\theta}_{Dr} = \frac{1}{\binom{n}{r}} \sum_{D_r} \hat{\theta}_{(Dr)}(t) \quad 29$$

and

$$\hat{\lambda}_{Dr} = \frac{1}{\binom{n}{r}} \sum_{D_r} \hat{\lambda}_{(Dr)}(t) \quad 30$$

Thus, the three quantities that must be distinguished at every deletion level are:

- Deletion level (r):* the number of observations removed from the original sample;
- Remaining sample size ($n - r$):* the number of observations retained in every reduced sample;

- iii. Number of reduced samples $\binom{n}{r}$: the number of distinct deletion subsamples evaluated at level r .

Note: The r quantities should not be interpreted as the number of observations deleted repeatedly from changing pseudo-samples. At r , the number of generated *delete* – r sample is

$$N_r = \binom{n}{r}$$

Consequently,

$$N_1 = \binom{n}{1}, \quad N_2 = \binom{n}{2}, \quad N_3 = \binom{n}{3}, \quad \dots,$$

and the general $N_r = \binom{n}{r}$.

The table 2 and 2 below illustrates the multi-level stages of the approach.

Table 2: The Multi-Level Stages of K – Level Delete – r Jackknife

Level	Operation	Source of Deleting Data	Observation Retained	Number of Subsample
$r = 1$	Delete-1	Original	$n - 1$	$\binom{n}{1}$
$r = 2$	Delete-2	Original	$n - 2$	$\binom{n}{2}$
$r = 3$	Delete-3	Original	$n - 3$	$\binom{n}{3}$
$r = 4$	Delete-4	Original	$n - 4$	$\binom{n}{4}$
$r = 5$	Delete-5	Original	$n - 5$	$\binom{n}{5}$
$r = k$	Delete-r	Original	$n - r$	$\binom{n}{r}$

The Above is the Multi-Level Stage where Each Branch Starts from the Original Data

Table 3: Illustration of the General Direct Delete-r Structure

Level r	Observation Deleted	Observation Remaining	Number of Subsample
1	1	9	10
2	2	8	45
3	3	7	120
4	4	6	210
5	5	5	252
6	6	4	210
7	7	3	120
8	8	2	45

The simulation in this study uses $K = 3$, comprising Delete-1, Delete-2 and Delete-3.

Definition of (K)

If the procedure considers deletion levels

$$r = 1, 2, \dots, k,$$

then (K) is the number of deletion levels, not the number of observations deleted at every stage.

For the two-parameter exponential model, at least two observations are required for estimation of the location and rate parameters. Therefore, the maximum deletion level that permits estimation of both parameters in the present implementation is

$$K_{max} = n - 2$$

For the simulation and validation procedure, (K) may therefore be selected subject to

$$1 \leq K \leq n - 2$$

Overall K – Level Estimator

After obtaining the stage estimates for $r = 1, 2, \dots, k$,

The K-level Delete-r jackknife is when all possible deletion subsets are considered independently at each deletion level and the resulting delete-1, delete-2, ..., delete-r estimates are subsequently averaged to obtain the final K-level estimator.

That is to say,

the overall K – level Delete – (r) estimate is defined as the arithmetic mean of the stage estimates:

$$\hat{S}_K(t) = \frac{1}{K} \sum_{r=1}^K \hat{S}_r(t) \quad 31$$

similarly,

$$\hat{\theta}_K = \frac{1}{K} \sum_{r=1}^K \hat{\theta}_r \quad 32$$

and

$$\hat{\lambda}_K = \frac{1}{K} \sum_{r=1}^K \hat{\lambda}_r \quad 33$$

The overall estimator therefore combines information from all specified deletion levels while maintaining the defining property that every reduced sample is generated directly from the original observed sample.

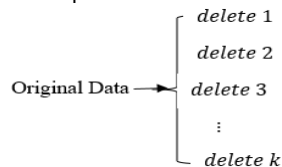
Table 2: Interpretation of the K-level Delete-r Jackknife

Quantity	Meaning
K	Total number of deletion levels Investigated
r	Number of observations deleted at level r
$m = n - r$	Number of observations remaining in each <i>delete</i> – r sample
N_r	Number of <i>delete</i> – r samples generated
$N_r = \binom{n}{r}$	Number of possible deletion subsets
$r = 1$	Delete-one level: one observation is deleted from the original data in every possible way
$r = 2$	Delete-two level: two observation is deleted from the original data in every possible way

Quantity	Meaning
$r = 3$	Delete-three level: three observation is deleted from the original data in every possible way
$\vdots$	$\vdots$
$r = K$	Final deletion level

Important Distinction from Recursive Jackknife

The procedure used in this study is not a recursive pseudo-sample jackknife. In particular, the estimates generated at deletion level (r) are not treated as observations from which the next deletion level is constructed. That is to say, they are not used as input observations for level $r + 1$. Instead, every deletion level is conducted independently from the original Sample.



This distinction is essential. The present method is therefore more accurately characterized as a K-level delete-(r) jackknife resampling procedure (a systematic delete-r resampling scheme), rather than a recursive K-repeated jackknife.

Relationship with Adewara and Mbata (2014)

Adewara and Mbata (2014) introduced and applied a K-repeated jackknife procedure for survival estimation in the two-parameter exponential model. Their approach is an iterative procedure with a recursive structure, where the jackknife estimates obtained at each stage are used as the pseudo-sample for the subsequent stage. The present investigation, a non-recursive multi-level jackknife resampling scheme, does not claim to reproduce the recursive k-repeated jackknife algorithm of Adewara and Mbata (2014). Rather, it adopts their work as an important methodological reference and benchmark and then evaluates a systematic k-level extension of the delete-one jackknife in which the deletion size is increased from one observation to k observations (all deletion direct from the original data) while all possible deletion subsets (subsamples) are considered at each level.

Data Simulation and Estimation of the Parameters

A Monte Carlo Simulation using R software is conducted to evaluate the performance of three resampling techniques: Bootstrap, Jackknife delete-one and K-level Delete-r Jackknife, in estimating parameters of survival data. Survival times were generated under the assumption that they follow a two-parameter exponential distribution defined as

$$X = \theta + Y, \quad Y \sim \text{Exp}(\lambda) \quad 23$$

where θ is the location parameter

λ is the rate parameter

$$X \geq \theta, \quad \theta \geq 0, \quad i = 1, 2, \dots, n.$$

Consequently, the probability density function is $f(x) = \lambda e^{-\lambda(x-\theta)}$, $x > \theta$ and the corresponding survival function is $S(t; \theta, \lambda) \quad \forall t \geq 0$, θ shifts the distribution (starting point) and λ controls the rate (speed of decay).

The simulation considered the following parameter combinations $\theta \in \{0, 1, 2\}$ and $\lambda \in \{0.5, 1, 2\}$. The sample sizes were considered; $n \in \{10, 30, 70\}$.

Therefore, the simulation contained $3 \times 3 \times 3 = 27$ distinct parameter/sample size scenarios.

For each scenario, $R = 200$ independent Monte Carlo replications were performed. The data for each replication were generated as

$$X_i = \theta + Y_i \quad \text{where}$$

$$Y_i \sim \text{Exponential}(\lambda), \quad \forall i = 1, 2, \dots, n.$$

For every generated sample, the ordinary two-parameter exponential MLE was calculated. The estimator of the location parameter was $\hat{\theta} = X_{(1)} = \text{Min}(X_1, \dots, X_n)$, while the estimator of the rate parameter was $\hat{\lambda} = \frac{n-1}{\sum_{i=1}^n (X_i - \hat{\theta})}$. The estimated survival probability was evaluated at $t = 2$. The true probability used for comparison was

$$S(2; \theta, \lambda) = \exp[-\lambda(2 - \theta)] \quad \forall 2 \geq \theta$$

The Delete-1, Delete-2, Delete-3, final K-level Delete-r estimator and bootstrap estimator were then calculated from each simulated sample.

Simulation Algorithm

To ensure reproducibility of the simulation experiment, R statistical software version 4.5.2 was used and the simulation implementation are summarized as follows: the random number generator was initialized using set.seed(123456). For each parameter combination, the following algorithm was applied:

Step 1: Specify the Simulation Design:

Set seed (123456), $n \in \{10, 30, 70\}$, $\theta \in \{0, 1, 2\}$, $\lambda \in \{0.5, 1, 2\}$ with $R = 200$

Step 2: Generate the data: for each combination of n, θ , and λ , generate $X_i = \theta + Y_i$

where

$Y_i \sim \text{Exponential}(\lambda)$, X_i = survival time, θ = location parameter (minimum threshold), λ = rate parameter. This guarantees that $X_i \geq \theta$

Step 3: Obtain the ordinary maximum likelihood estimators (MLE) for each generated sample:

$$\hat{\theta} = \min(X_1, X_2, \dots, X_n) \quad \text{and} \quad \hat{\lambda} = \frac{n-1}{\sum_{i=1}^n (X_i - \hat{\theta})} \quad \forall i =$$

$1, 2, \dots, n$ and calculate $\hat{S}(t = 2)$ from the estimated parameters.

Step 4: Perform Delete 1:

From the original simulated dataset, generate all $\binom{n}{1}$ possible delete-1 samples. For each sample, calculate the MLE and the survival estimate then average the estimates to obtain $\hat{\theta}_{D1}$, $\hat{\lambda}_{D1}$, and $\hat{S}_{D1}$

Step 5: Perform Delete 2:

Directly from the original simulated dataset, generate all $\binom{n}{2}$ possible delete-2 samples. For each sample, calculate the estimates and average the resulting estimates to obtain $\hat{\theta}_{D2}$, $\hat{\lambda}_{D2}$, and $\hat{S}_{D2}$

Step 6: Perform Delete 3:

Directly from the original simulated dataset,

(a) generate all $\binom{n}{3}$ possible delete-3 samples. Calculate and average the resulting estimates to obtain $\hat{\theta}_{D3}$, $\hat{\lambda}_{D3}$, and $\hat{S}_{D3}(t)$

Step 7: Obtain the Final K-level Delete-r Estimate:

Since $k = 3$, combine the three deletion level,

$$\hat{\theta}_{DK3} = \frac{\hat{\theta}_{D1} + \hat{\theta}_{D2} + \hat{\theta}_{D3}}{3}, \quad \hat{\lambda}_{DK3} = \frac{\hat{\lambda}_{D1} + \hat{\lambda}_{D2} + \hat{\lambda}_{D3}}{3}, \quad \text{and} \quad \hat{S}_{DK3} = \frac{\hat{S}_{D1} + \hat{S}_{D2} + \hat{S}_{D3}}{3}$$

Step 8: Bootstrap:

For each simulated dataset,

- (a) draw $B = 200$ bootstrap samples, each of size n , with replacement from the original simulated sample.
- (b) for each bootstrap sample, compute $\hat{\theta}_{boot}^*$ and $\hat{\lambda}_{boot}^*$
- (c) obtain the average bootstrap estimates $\hat{\theta}_{BOOT} = \frac{1}{B} \sum \hat{\theta}_{boot}^*$, $\hat{\lambda}_{BOOT} = \frac{1}{B} \sum \hat{\lambda}_{boot}^*$
 $\forall i = 1, 2, \dots, B$

Step 9: Repeat step 2 to step 8 for $R = 200$ monte carlo replications within every one of the 27 scenarios. Hence the completed simulation contains $27 \times 200 = 5,400$ datasets.

Step 10: For any estimate ψ , calculated

- (a) $Bias(\hat{\psi}) = \frac{1}{R} \sum_{j=1}^R (\hat{\psi}_j - \psi)$,
- (b) $Variance(\hat{\psi}) = \frac{1}{R-1} \sum_{j=1}^R (\hat{\psi}_j - \bar{\hat{\psi}})^2$
- (c) $MSE(\hat{\psi}) = Var(\hat{\psi}) + [Bias(\hat{\psi})]^2$
- (d) $Percentage\ Error\ (PE) = \left| \frac{\bar{\hat{\psi}} - \psi}{\psi} \right| \times 100$

For parameter values equal to zero, percentage error should be interpreted cautiously because the true value occurs in the denominator. In $\theta = 0$

Step 11: Plot the graph of the metrics against methods to visualize the results.

Real Data Application

The lung cancer dataset from the North Central Cancer Treatment Group (NCCTG), obtained from the survival package in R (Therneau et al., 2026) and archived in the Rdatasets repository (Vincent Arel-Bundock, 2024), which provides survival outcome of 228 patients with advanced lung

cancer was used as a real-life dataset to validate the performance of the proposed resampling methods. The variables that are provided in this dataset include (variable names which are written in *italics*): *Inst*-institution code that is the hospital or the research centre where the patient is treated, *Time*-survival time in days i.e. the time from study entry to death or last follow-up, *Status*- censoring indicator (1=censored i.e. alive or lost to follow-up; 2=event (death) occurred). If the status =2, exact survival time is known but if the status =1, survival time is incomplete (censored), *Sex*-sex of the patient (male=1, female=2), *Ph.ecog* (Eastern Cooperative Oncology Group (ECOG) performance score)- it measures patient's functional status scaled from 0 – 5: (0 = active, 5 = dead), *ph.Karno* (Karnofsky performance score)- doctor's assessment of patient condition ranging from 0 – 100 (≥ 90 : healthy, (≤ 40 :) very ill), *Meal.Cal* (Calories Intake)- daily calories intake consumed at meals which reflect nutritional status: lower values may indicate poor health associated with reduced survival, *Wt.Loss* (Weight Loss (in pounds))- High weight loss/large value indicates serious condition and disease progression while very low value (0) indicates stability. This dataset has been previously used and analysed by Suvilimedu (2017) in survival modelling.

Data preprocessing was carried out on the NCCTG lung cancer dataset, including data cleansing procedure performed on covariates (sex, age, meal.cal, wt.loss) using mean and mode imputation for missing values and winsorization of outliers. Table 2.5 displays the summary of the data. Survival time and censoring indicators were retained in their original forms to preserve the integrity of the survival data.

Table 5: Summary of the NCCTG Lung Cancer Dataset

Variable	Minimum	Maximum	Remark
Inst	1	33	Nominal Codes
Time	5	1,022	Presence of right-censoring
Status	1	2	Binary Category
Age	39	82	Adult Population
Sex	1	2	Binary Category
ph.ecog	0	3	Ordinal performance scale
ph.karno	50	100	Physician-rated health
pat.karno	30	100	Patient-rated health
meal.cal	307	1,535	Wide variability
wt.loss	-24	68	Includes weight gain (negative values)

Table 2.5 presents the descriptive summary of the cleaned lung cancer dataset. The institute code is recorded within the range of 1 - 33, survival time ranges from a minimum of 5 days to a maximum of 1,022 days, indicating the presence of right-censored observations. Status and sex are the binary categories (1 and 2, 1 and 2 respectively), The age distribution (39-82 years) confirms that the dataset consists of adult patients. Clinical performance indicators such as ECOG

scores (0-3) and Karnofsky indices reflect varying health conditions among patients. The physician and patient Karnofsky scores show generally moderate to high functional status. Additionally, calorie intake exhibits wide variability, while weight loss includes both positive and negative values, indicating that some patients experienced weight gain during the study period.

RESULTS AND DISCUSSION

Simulation Results

Table 6: Average Absolute Bias, Mean Variance, Mean Squared Error and Mean Absolute Percentage Error for θ , λ and $S(t)$ Across the Resampling Methods

Method	Estimand	Mean Abs. Bias	Mean Variance	Mean MSE	Mean Absolute PE
Bootstrap	lambda	0.186895924	0.212126689	0.287684223	16.114477
Bootstrap	survival	0.005409206	0.003581408	0.003682321	5.686148
Bootstrap	theta	0.090163600	0.009302131	0.025651406	6.720880
Delete-1	lambda	0.067290454	0.144828104	0.154134331	5.788474
Delete-1	survival	0.008190707	0.003521475	0.003704369	6.666229
Delete-1	theta	0.062449246	0.008138253	0.016275323	4.634990

Method	Estimand	Mean Abs. Bias	Mean Variance	Mean MSE	Mean Absolute PE
Delete-2	lambda	0.076756625	0.151156375	0.163949783	6.620531
Delete-2	survival	0.008934293	0.003560313	0.003789222	7.226001
Delete-2	theta	0.068233844	0.008406185	0.018449031	5.072596
Delete-3	lambda	0.089913266	0.160880033	0.179590633	7.772217
Delete-3	survival	0.009888479	0.003612183	0.003908172	7.942382
Delete-3	theta	0.075599906	0.008832310	0.021641699	5.630425
Delete-r-K3	lambda	0.077986782	0.151997710	0.165314124	6.727074
Delete-r-K3	survival	0.009004493	0.003562645	0.003796300	7.278204
Delete-r-K3	theta	0.068760999	0.008406591	0.018643703	5.112670

The overall comparison shows that Jackknife Delete-1 demonstrated the best performance, recording the lowest bias, variance, MSE, and percentage error for most measures. Delete-2 and the $K = 3$ Delete-r procedure also performed well, with $K3$ providing a stable aggregated estimate that remained close to the stronger individual jackknife methods. In contrast, Bootstrap generally showed higher bias, variance, MSE, and percentage error, particularly for λ . The advantage of Delete-1 became more pronounced as sample size increased. At $n = 70$, its estimates were highly accurate, whereas at $n = 10$, precision declined and higher deletion

levels, such as Delete-3, performed worse. Thus, increasing the deletion level does not necessarily improve estimation. Generally, the findings indicate that Delete-1 is the most efficient individual jackknife method, while the proposed $K = 3$ Delete-r estimator offers a reliable and competitive alternative, particularly for λ , and generally outperforms Bootstrap. The simulation was successfully validated across 27 scenarios, 200 replications per scenario, 32,400 method-level estimation records, and 486 performance records, with all structural and finite estimate checks passing.

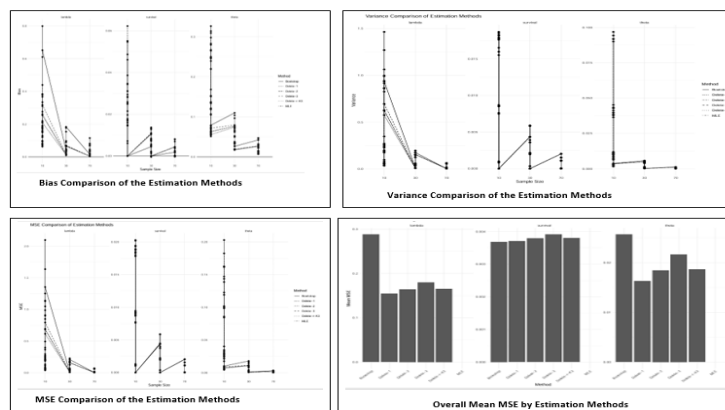


Figure 1: The Plots of the Biases, Variances and MSEs Comparison of the Resampling Methods

Figure 1 shows a clear improvement in estimation performance as sample size increases from $n = 10$ to $n = 30$ and $n = 70$. The bias plots show that bias is generally highest at $n = 10$, particularly for λ and θ , and declines substantially as sample size increases, with the Delete-r methods generally remaining closer to zero than Bootstrap. The MSE plots similarly show a pronounced reduction in MSE with increasing sample size, while Bootstrap exhibits the largest MSE at $n = 10$; this agrees with the simulation results in table 6, where the resampling methods with lower bias and variability produce smaller MSE values. The variance plots confirm the same pattern, with variability markedly higher for the smaller sample and falling considerably at $n = 30$ and $n = 70$. Finally, the overall mean MSE plot shows that Delete-1 has the lowest overall MSE among the displayed resampling methods, followed by Delete-2 and Delete-r $K = 3$, whereas Bootstrap has the highest overall MSE, supporting the table 6 presentation and conclusion that Delete-r resampling, particularly at the lower deletion level, provides more stable estimation than Bootstrap, with the advantage becoming more evident as sample size increases.

Discussion of the Simulated Results

The simulation results show that Delete-1 generally provided the best overall performance, with the lowest average absolute bias and MSE for θ and survival, while Delete-2 remained competitive and Delete-3 tended to perform less well, especially at $n = 10$. The combined Delete-r, $K = 3$ estimator also performed reasonably well, whereas Bootstrap recorded higher bias and MSE, particularly for λ . Figure 1 further shows that bias, variance and MSE decreased as the sample size increased from $n = 10$ to $n = 30$ and $n = 70$, confirming improved estimation with more observations. These findings differ somewhat from Adewara and Mbata (2014), who reported reduced MSE with their recursive K-repeated jackknife; the present study uses a non-recursive direct Delete-r procedure and shows that increasing the deletion level does not necessarily improve performance. This finding is consistent with Jiao and Han (2020), who demonstrated that different delete-d choices can produce substantially different jackknife behaviour. The results therefore support the effectiveness of jackknife resampling, particularly Delete-1, and are consistent with previous evidence that jackknife methods can reduce finite sample estimation error, while bootstrap estimates may exhibit greater variability (Jiang & Zhang, 2019; Ahmed Abdulhadi et al., 2024; Limozin et al., 2025).

Real Data Analysis

Table 7: Kaplan-Meier Survival Estimates of the Cleaned-Dataset

Time	Survival Probability	Standard Error	Lower C.I	Upper C.I
5.000	0.99561404	0.004395615	0.98707342	1.0000000
11.000	0.98245614	0.008849904	0.96556190	0.9996460
12.000	0.97807018	0.009916654	0.95924368	0.9972662
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
1,022	0.05034557	0.453824434	0.02068546	0.1225342

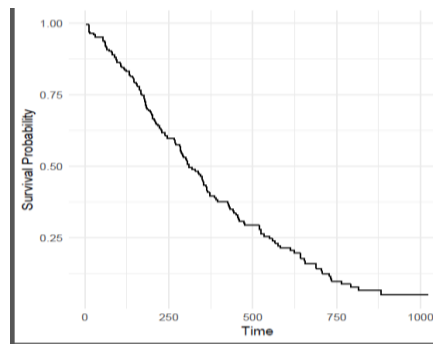


Figure 2: Kaplan-Meier Survival Curve

The Kaplan-Meier survival estimates in Table 7 which display how patients' survival probabilities change over time show that the probability of survival was initially very high, with approximately 99.6% of individuals surviving at the early stage of the study. However, survival probability decreased progressively over time, as visualized in Figure 2, reaching approximately 5.0% at the final observed time point (1,022 days). This indicates a continuous decline in survival as time increases (Kaplan & Meier, 1958).

The number of individuals at risk also decreased over time, contributing to increased variability in the estimates at later stages, as reflected by the larger standard errors and wider confidence intervals (Kleinbaum & Klein, 2012). Additionally, the presence of censored observations confirms that not all individuals experienced the event during the study period. The results suggest a steady increase in mortality risk over time.

Table 8: Empirical Comparison of the Ordinary MLE, Delete-r, and Bootstrap Estimators for the NCCTG Lung Cancer Data

	MLE	Delete-1	Delete-2	Delete-3	Delete-r-K=3	Bootstrap
$\hat{\theta}$	5.00000	5.026316	5.052632	5.078947	5.052632	6.82500
θ_{SE}	0.000000	0.3973597	0.5594922	0.6837044	0.0263158	2.8095986
$\hat{\lambda}$	0.003381	0.003381	0.003381	0.003381	0.003381	0.003405
λ_{SE}	0.00000	1.05E-05	1.48E-05	1.82E-05	2.68E-07	0.00015784
$\hat{S}$	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
θ 95% CI	0.000-0.000	4.247 - 5.805	3.956-6.149	3.739 -6.419	5.001-5.104	1.318-12.332
λ 95% CI	0.000-0.000	0.003-0.003	0.003-0.003	0.003-0.003	0.003-0.003	0.003-0.004
$\hat{\theta} - MLE$	0.0000	0.02631579	0.05263158	0.07894737	0.05263158	1.82500
$\hat{\lambda} - MLE$	0.0000	2.69E-07	5.37E-07	8.06E-07	5.37E-07	2.42E-05

The NCCTG empirical analysis presented in table 8 above shows that the Delete-r procedures are considerably more stable than Bootstrap, particularly for the location parameter θ . Taking the Ordinary MLE as the reference estimator, its estimate of θ is 5.0000, while Delete-1, Delete-2, Delete-3 and the final Delete-r $K = 3$ give 5.0263, 5.0526, 5.0789 and 5.0526, respectively, indicating only small departures from the reference estimate, whereas Bootstrap gives a substantially larger estimate of 6.8250 with a much larger standard error of 2.8096 and a wide 95% confidence interval of 1.3182–12.3318. The standard errors for θ increase from 0.3974 for Delete-1 to 0.5595 for Delete-2 and 0.6837 for Delete-3, while the final Delete-r $K = 3$ substantially reduces this to 0.0263, demonstrating the greater stability of the combined Delete-r estimator. For λ , the estimates from

Ordinary MLE and all Delete-r levels remain almost identical at approximately 0.003381, with the final Delete-r $K = 3$ having an extremely small standard error of 2.68×10^{-7} , compared with 1.58×10^{-4} for Bootstrap; Bootstrap also produces the largest departure from the reference, with $\lambda = 0.003405$. The survival estimates are all equal to 1.0000 because the evaluation time $t = 2$ is below the estimated threshold $\theta \approx 5$, so this estimand does not discriminate between methods in this particular dataset. Hence, these empirical findings reinforce the simulation results by showing that the Delete-r estimators remain close to the reference MLE while exhibiting substantially greater stability than Bootstrap, with the final $K = 3$ estimator providing the most stable combined estimate among the Delete-r procedures.

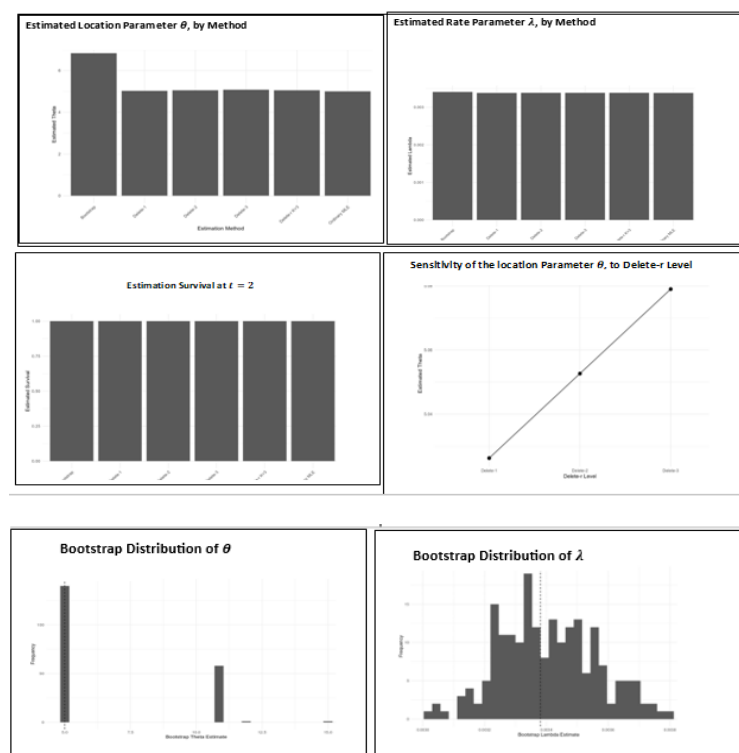


Figure 3: Empirical Plots Comparison of the Estimates of the Location Parameter $\hat{\theta}$, Rate Parameter $\hat{\lambda}$, and Survival Estimates $\hat{S}$ across the Methods for the NCCTG Lung Cancer Data

The empirical plots provide a visual confirmation of the numerical results in the table 8. The estimated location parameter $\hat{\theta}$, shows that Ordinary MLE and the three Delete-r levels are tightly clustered around 5.0, whereas Bootstrap is clearly separated at 6.825, visually confirming its larger departure from the reference estimator. The $\hat{\lambda}$ plot shows almost indistinguishable estimates across all methods, consistent with the table 8 values of approximately 0.003381, although the Bootstrap estimate is slightly higher at 0.003405. The survival plot shows all methods at 1.00, agreeing exactly with the table and reflecting the fact that $t = 2 < \hat{\theta}$. Importantly, the Delete-r sensitivity plot shows a gradual increase in the estimated θ from 5.0263 for Delete-1 to 5.0526 for Delete-2 and 5.0789 for Delete-3, demonstrating that increasing the deletion level introduces some sensitivity, although the estimates remain close to the reference MLE. Finally, the Bootstrap distributions of $\hat{\theta}$ and $\hat{\lambda}$ show considerably greater dispersion, particularly for θ , where most bootstrap estimates are concentrated near 5 but a pronounced right tail extends to much larger values; this corresponds directly to the large Bootstrap standard error of 2.8096 and its wide confidence interval in the table 8. The broader Bootstrap distribution for λ similarly agrees with its much larger standard error of 1.58×10^{-4} , compared with 2.68×10^{-7} for the final Delete-r $K = 3$. Thus, the plots visually support the table-based conclusion and are broadly consistent with the simulation evidence that Delete-r provides greater numerical stability and less sensitivity to resampling than Bootstrap.

RESULTS AND DISCUSSION

Table 6 and Figure 1 provide the main simulation evidence for assessing the study objective. Rather than indicating a universal winner at every parameter combination, they show a consistent difference between the more stable jackknife

procedures and the more variable bootstrap procedure. The bias, variance and MSE plots show the greatest dispersion at $n = 10$, followed by substantial improvement at $n = 30$ and $n = 70$, indicating that sample size is an important determinant of estimator stability. Delete-1 has the lowest overall mean MSE among the displayed resampling methods, while Bootstrap has the highest, with Delete-2 and the combined K-level Delete-r procedure falling between them. This directly addresses the study objective by showing that the choice of resampling method matters most in the smaller finite samples.

The simulation findings also provide a more cautious interpretation of the K-level procedure than would follow from simply assuming that more deletion levels must improve estimation. Delete-2 and Delete-r $K = 3$ remain competitive, but Delete-3 performs less favourably in some small sample settings. The combined procedure therefore appears useful as an aggregated alternative, rather than as an estimator that is uniformly superior to every individual deletion level. This result differs in emphasis from Adewara and Mbata (2014), whose study reported an MSE reduction from their K-repeated jackknife. Their method and the present method should not be treated as identical: Adewara and Mbata used a recursive stage structure, whereas the present analysis forms every deletion level directly from the original sample. The present findings therefore should be interpreted as evidence about a direct K-level Delete-r scheme, not as a reproduction or rejection of the original recursive K-repeated jackknife.

The empirical NCCTG results provide a useful second perspective. Table 8 and Figure 3 show that the Ordinary MLE and Delete-r estimates of θ remain close to one another, whereas Bootstrap produces a much larger estimate and a much wider uncertainty range. The ordinary MLE estimate of θ is 5.0000, compared with 5.0263, 5.0526 and 5.0789 for Delete-1, Delete-2 and Delete-3, while Bootstrap gives

6.8250 with a standard error of 2.8096 and a 95% confidence interval extending from 1.3182 to 12.3318. The final K-level estimator returns 5.0526 with a substantially smaller standard error of 0.0263. For λ , the ordinary MLE and all Delete-r estimates are closely grouped around 0.003381, while Bootstrap is slightly higher at 0.003405 and has a much larger standard error. The survival estimate at $t = 2$ is 1.0000 for every method and therefore does not distinguish the procedures in this particular empirical example.

These empirical results broadly support the simulation findings, but the form of the evidence is different. In the simulation, the generating values of θ , λ and $S(2)$ are known, so genuine Monte Carlo bias and MSE can be calculated. In the NCCTG application, the true parameter values are unknown; consequently, the ordinary MLE is used only as a reference estimator, and the empirical comparison focuses on the magnitude of departures from that reference, standard errors, confidence intervals and sensitivity to resampling. The empirical plots support this interpretation: Figure 3 shows the close clustering of the Delete-r estimates around the MLE, the gradual movement in θ from Delete-1 to Delete-3, and the substantially wider bootstrap distributions. The evidence therefore supports the conclusion that Delete-r methods can provide stable estimates while also showing that the amount of deletion affects sensitivity.

Several limitations should be acknowledged. First, the simulation uses a single distributional family and three sample sizes, so the results should not be generalized automatically to other survival distributions or much larger samples. Secondly, the simulation contains no censoring, whereas the NCCTG data contain right censored observations; the empirical analysis is therefore an application and sensitivity check rather than a direct one to one replication of the simulation conditions. The manuscript documents this distinction in its treatment of the NCCTG status variable and survival data. Furthermore, the Monte Carlo experiment uses 200 replications and a fixed evaluation time of $t = 2$, and alternative replication sizes or evaluation times could give slightly different numerical rankings. Again, the computational burden increases rapidly with n and r , since the number of Delete-r subsets is $\binom{n}{r}$; this places a practical limit on extending the procedure to much larger deletion levels or samples. These limitations do not invalidate the present comparison, but they identify areas where a future study could test the method more broadly, including censored data and alternative distributions such as Weibull, Gamma and log-logistic models.

Therefore, the figures and tables return to the main objective of the study: to determine which resampling approach provides reliable estimation under the two-parameter exponential framework. The evidence does not support the claim that every higher order Delete-r estimator is superior. Instead, it shows that Delete-1 is the strongest individual jackknife procedure in the present simulation, while the direct K-level Delete-r estimator is a competitive aggregated alternative and generally performs better than Bootstrap in the reported settings. This is the principal empirical contribution of the study.

CONCLUSION

The research question asked which of the competing resampling procedures provides the most accurate and stable estimation of the location and rate parameters of the two-parameter exponential survival model. The results provide a clear answer: among the individual resampling procedures examined, Jackknife Delete-1 gives the most consistent overall performance, while the direct K-level Delete-r

estimator with $K = 3$ provides a competitive aggregated alternative; Bootstrap is generally less stable, particularly in the smaller samples. The Monte Carlo study demonstrates that bias, variance and MSE generally decline as sample size increases, while the NCCTG analysis shows that Delete-r estimates remain close to the ordinary MLE reference estimator with considerably less resampling variability than Bootstrap. The study contributes to statistical methodology by providing a transparent definition and empirical assessment of a non-recursive direct Delete-r scheme and by clearly distinguishing it from the recursive K-repeated jackknife of Adewara and Mbata (2014). The combined use of simulation and real survival data also provides evidence on both finite sample performance and empirical stability. Future work should examine the procedure under censoring, alternative lifetime distributions and larger or adaptive resampling designs. Thus, the study shows that careful control of the deletion level is more important than simply increasing the number of deleted observations when seeking stable survival parameter estimation.

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CONFLICT OF INTEREST STATEMENT

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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