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Research Article

Estimation of Two Parameter Birnbaum-Saunders Distribution Based on Type-II Right Censored Reliability Data Using Genetic Algorithm

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Abstract. The *Birnbaum-Saunders* (BS) distribution is a common reliability distribution used in scientific studies. There have been studies in the literature on parameter estimates for this distribution. Furthermore, in many studies, it is recommended to use *Genetic Algorithm* (GA) optimization methods for parameter estimation in modeling. This article focuses on estimating the model parameters of a two-parameter Birnbaum-Saunders distribution for Type II right censored reliability data. For parameter estimation of the Birnbaum-Saunders distribution, we propose the *Genetic Algorithm* (GA) method as an alternative to the *Maximum Likelihood* (ML) estimation method. Psi31 data is often used as an example to show the limitations of prediction methods when using inaccurate data. In addition, the performances of ML and GA methods were investigated through Monte Carlo simulation with different sample sizes and censorship rates.

Keywords. Birnbaum-Saunders distribution, Genetic Algorithm, Maximum Likelihood, Type-II right censored data

Mathematics Subject Classification (2020). 62H12, 68W50

1. Introduction

The Birnbaum-Saunders distribution was first proposed by Birnbaum and Saunders [3] in 1969. This distribution is used to model fatigue fractures. The Birnbaum-Saunders model has many desirable features and is a well-suited asymmetric two-parameter unimodal distribution with non-negative support. This distribution can help researchers design models for different applications, including survival, lifetime, and environmental data analysis. As mentioned in the

article by Johnson *et al*. [5], there are many references in the literature about the properties, implications, and applications of the Birnbaum-Saunders distribution. Also, to find out more about the characteristics and generalizations of the Birnbaum-Saunders distribution, readers can read the articles by Ng *et al*. [9], and Kundu *et al*. [6]. A computationally analytical EM-type algorithm is developed for computing maximum likelihood estimates of Birnbaum-Saunders distribution for the unobserved error terms in nonlinear regression models (Naderi *et al*. [8]).

A suitable optimization method should serve two opposite purposes: explore the solution domain (ergodicity property) and use the best solutions found. The *Genetic Algorithm* (GA), which is based on the theory of evolution, is commonly used in stochastic optimization applications. The algorithm is run on a population of N individuals (also known as 'chromosomes'), each characterized by a gene (a component of the vector). Identifying the most functionally productive individual is a complex task that requires careful consideration of a variety of factors. Generations of individuals are followed by each other, with the most productive members continuing to produce until a limit is reached. The transition from one generation to the next is carried out through 'operators', which are divided into several categories. Recent studies have found that the GA method is a useful tool for estimating parameters in statistical models. Lee *et al*. [7] studied the effects of a new diet on people's health. They found that the diet was effective in reducing the risk of various diseases. Also, Lee *et al*. [7] used a GA approach for two parameters in a mesoscale meteorological model. A genetic algorithm is used along with Bayes' information criteria to identify the best periodic autoregressive models with one exogenous variable (Ursu and Pereau [11]). Tekeli and Yüksel [10] used a genetic algorithm to estimate the parameters of a twofold Weibull mixture model. Akay *et al*. [1] proposed optimal clustering of units using the GA approach.

The purpose of this article is to estimate the parameters of a two-parameter Birnbaum-Saunders distribution using a genetic algorithm and compare it with the results of the maximum likelihood estimation of right-censored reliability data. The article is organized as follows. Section 2 provides information on the properties of the two-parameter Birnbaum-Saunders distribution. One of the methods used to estimate the parameters, the maximum likelihood estimation method under Type II censorship, is described in Section 3. Section 4 proposes a genetic algorithm-based method, and compares its results with those of the maximum likelihood method using a real dataset. Section 5 conducts a Monte Carlo simulation to evaluate the performance of the methods under different conditions. The simulation results are presented in this section. Finally, the numerical results are interpreted in Section 6.

2. Two Parameter Birnbaum-Saunders Distribution

We would like to remind you that if a random variable X follows the Birnbaum-Saunders distribution with shape α and scale β, where $\alpha, \beta > 0$, then the notation used is $X \sim BS(\alpha, \beta)$. By choosing a random variable T according to the standard normal distribution, i.e., a normal distribution with zero mean and a variance that drops to one, one gets:

$$T = \frac{1}{\alpha}\left(\sqrt{\frac{X}{\beta}} - \sqrt{\frac{\beta}{X}}\right). \tag{1}$$

Random variables $X \sim BS(\alpha,\beta)$ and $T \ldots N(0,1)$ remain connected by the monotone transformation. However, we can say that any random variable X with a Birnbaum-Saunders distribution can be obtained as a transformation of another random variable T with a standard normal distribution. Thus,

$$X = \beta\left(\frac{\alpha T}{2} + \sqrt{\left(\frac{\alpha T}{2}\right)^2 + 1}\right)^2, \tag{2}$$

where α and β are the shape and scale parameters, respectively.

Using the two-parameter Birnbaum-Saunders distribution, we define the probability density function of a random variable X by:

$$f_X(x;\alpha,\beta) = \frac{1}{2\sqrt{2\pi}\alpha\beta}\left[\left(\frac{\beta}{x}\right)^{\frac{1}{2}} + \left(\frac{\beta}{x}\right)^{\frac{3}{2}}\right]\exp\left[-\frac{1}{2\alpha^2}\left(\frac{x}{\beta}+\frac{\beta}{x}-2\right)\right], \quad x>0,\ \alpha>0,\ \beta>0, \tag{3}$$

where $\psi(\cdot)$ is the standard normal cumulative distribution function,

$$\varphi(t) = t^{\frac{1}{2}} - t^{-\frac{1}{2}}, \quad t>0 \tag{4}$$

and

$$\varphi'(t) = \frac{1}{2}(t^{-\frac{1}{2}} + t^{-\frac{3}{2}}).$$

Using the transformation theorem of random variables, eq. (3) is easy can be obtained, and using eq. (1), the probability density function is given as follows:

$$\phi(T) = \frac{1}{\sqrt{2\pi}}\exp\left(-\frac{1}{2}T^2\right). \tag{5}$$

As the random variable Xhas the BS distribution in eq. (1), then the corresponding *cumulative distribution function* (*cdf*) is

$$F_X(x;\alpha,\beta) = \psi\left[\frac{1}{\alpha}\left\{\left(\frac{x}{\beta}\right)^{\frac{1}{2}} - \left(\frac{\beta}{x}\right)^{\frac{1}{2}}\right\}\right], \quad 0<x<\infty,\ \alpha,\beta>0, \tag{6}$$

where

$$\psi(T) = \int_{-\infty}^{T}\phi(t)dt, \quad T\in\mathbb{R} \tag{7}$$

is the standard normal cumulative distribution function. The mean and variance can be given as follows:

$$E(T) = \beta\left(1+\frac{\alpha^2}{2}\right) \tag{8}$$

and

$$\mathrm{Var}(T) = (\alpha\beta)^2\left(1+\frac{5}{4}\alpha^2\right). \tag{9}$$

3. Estimation of Maximum Likelihood under Censored Type II

Consider $\{t_{(1)}, t_{(2)}, \ldots, t_{(s)}\}$ for a right-censored ordered random sample of Type II defined from n units chosen on a lifetime test experiment in which each unit has its lifetime according to the distribution of Birnbaum-Saunders with pdf as indicated in eq. (3), with the largest $(n-s)$ lifetimes having been censored. Then, the likelihood function is given by Balakrishnan and

Cohen [2],

$$L=\frac{n(n-1)!}{(n-s)(n-s-1)!}\left\{1-\psi\left[\frac{1}{\alpha}\varphi\left(\frac{t_{(s)}}{\beta}\right)\right]\right\}^{n-s}\left\{\frac{1}{(\alpha\beta\sqrt{2\pi})^{s}}\left[\prod_{i=1}^{s}\varphi'\left(\frac{t_{(i)}}{\beta}\right)\right]\exp\left[-\frac{1}{2\alpha^2}\sum_{i=1}^{s}\varphi^2\left(\frac{t_{(i)}}{\beta}\right)\right]\right\}. \tag{10}$$

However, the log-likelihood function is

$$\ln L=c+(n-s)\ln\left\{1-\psi\left[\frac{1}{\alpha}\varphi\left(\frac{t_{(s)}}{\beta}\right)\right]\right\}-s\ln\alpha sl\sum_{i=1}^{s}\varphi'\left(\frac{t_{(i)}}{\beta}\right)-\frac{1}{2\alpha^2}\sum_{i=1}^{s}\varphi^2\left(\frac{t_{(s)}}{\beta}\right) \tag{11}$$

with $\varphi^2(t)=t+t^{-1}-2$ and c is a constant.

Let us denote by $x=(x_1,\ldots,x_n)$ a random sample of size n following the Birnbaum-Saunders distribution with a vector of unknown parameter $\theta=(\alpha,\beta)$. We will consider the estimation of the parameters of the BS distribution by the maximum likelihood method. The likelihood function for a parameter θ is defined as

$$L(\theta)=\prod_{i=1}^{n}L_i(\theta), \tag{12}$$

where $L_i(\theta)=f_X(x,\theta)$ is the individual contribution of each observation to the likelihood function. Retaining that the likelihood function and its natural logarithm (log-likelihood) reach their maximum values at the same points, working with the log-likelihood function because of its mathematical treatability is often called upon. Therefore, the log-likelihood function for θ is given in general by

$$\mathcal{L}(\theta)=\sum_{i=1}^{n}\log(f_X(x_i;\theta)). \tag{13}$$

We maximize the log-likelihood function by taking member by member the first derivative of eq. (12) with respect to α and β, which gives us

$$-n\log(\alpha\beta)+\sum_{i=1}^{n}\log\left[\left(\frac{\beta}{x_i}\right)^{\frac{1}{2}}+\left(\frac{x_i}{\beta}\right)^{\frac{3}{2}}\right]-\frac{1}{2\alpha^2}\sum_{i=1}^{n}\left(\frac{x_i}{\beta}+\frac{\beta}{x_i}-2\right). \tag{14}$$

Thus,

$$\frac{\partial\mathcal{L}(\theta)}{\partial\alpha}=\frac{1}{\alpha^3}\sum_{i=1}^{n}\left(\frac{x_i}{\beta}+\frac{\beta}{x_i}\right)-\frac{n}{\alpha}-\frac{2n}{\alpha^3}, \tag{15}$$

$$\frac{\partial\mathcal{L}(\theta)}{\partial\beta}=\sum_{i=1}^{n}\frac{1}{x_i+\beta}+\frac{1}{2\alpha^2}\sum_{i=1}^{n}\left(\frac{x_i}{\beta^2}+\frac{1}{x_i}\right)-\frac{n}{2\beta}. \tag{16}$$

Making $\frac{\partial\mathcal{L}(\theta)}{\partial\alpha}=0$ and $\frac{\partial\mathcal{L}(\theta)}{\partial\beta}=0$, we obtain the log-likelihood equations,

$$\widehat{\alpha}=\left(\frac{1}{n}\sum_{i=1}^{n}\left(\frac{x_i}{\widehat{\beta}}+\frac{\widehat{\beta}}{x_i}\right)\right)^{\frac{1}{2}}, \tag{17}$$

$$\widehat{\beta}=\left(\frac{\sum_{i=1}^{n}x_i}{\sum_{i=1}^{n}\frac{1}{x_i}-2\widehat{\alpha}^2\sum_{i=1}^{n}\frac{1}{x_i+\widehat{\beta}}+\frac{\widehat{\alpha}n}{\widehat{\beta}}}\right)^{\frac{1}{2}}. \tag{18}$$

4. Proposed Method and Example of Application

4.1 Genetic Algorithm (GA)

The use of *Genetic Algorithms* (GA) to solve problems is the origin of research by Holland *et al*. [5] at the University of Michigan who have proposed genetic algorithms since 1960. This new research group's novelty was the addition of the cross-over operator to their model of mutation. This operator is often used to find the optimum of a function by combining the genes of different individuals in the population. The first result of this research was 'Adaptation in Natural and Artificial Systems' (Holland [4]). GA's are often used in machine learning and optimization practices. The GA algorithm is designed to find the best solution among many possible ones. Overall, we start with a population of strings of characters, each corresponding to a chromosome. In genetic algorithms, the genes stored in a given population are best suited to the environmental needs of the species. Indeed, certain gene variations give individuals who possess them a competitive advantage over the rest of the population. This competitive advantage results in better reproduction of these individuals, which can be passed on to the entire population in successive generations. The principle of genetic algorithms is to try different operations to see which ones produce the best results. Genetic algorithms can be used to solve problems effectively. However, the use of these methods must be conditioned by specific characteristics of the problem. The computational time of the fitness function for the evaluation should be reasonably short. In fact, it is rated many times.

4.2 Numerical Example

The psi31 data used in our article was taken from the study of Birnbaum and Saunders [3]. The dataset has been used in the past in the nucleic acid research study. This data illustrates the proposed method.

Table 1. Psi31 data

Uncensored					Censored	
70	112	124	132	141	151	168
90	112	124	132	141	152	170
96	113	124	133	142	155	174
97	114	128	134	142	156	196
99	114	128	134	142	157	212
100	114	129	134	142	157	
103	116	129	134	142	157	
104	119	130	134	142	157	
104	120	130	136	144	158	
105	120	130	136	144	159	
107	120	131	137	145	162	
108	121	131	137	146	163	

In Table 1, there are 101 observations, with 80 of them describing the raw data and 21 of them describing the censored data. Use the Logrank test (a nonparametric test for skewed and censored data) to compare the hazard function of the two groups at each time point of

the observed event. The test is built by counting the number of observed and expected events in one of the groups at each time of the observed event, then calculating an overall summary at all the times when there is an event. The Logrank test is based on the same assumptions as the Kaplan-Meier survival curve, which states that the survival probabilities are the same for subjects recruited early and late in the year. The study was conducted at the specified times. Deviations from these assumptions are significant if they are fulfilled differently in the comparison groups, for example if censorship is more likely in one group than in another. We also used the two-sample Kolmogorov-Smirnov test, which is one of the most useful and general nonparametric methods for comparing two samples, since it is sensitive to differences in the position and shape of the accumulated empirical data of the distribution functions of the two samples. The test statistics are given in Table 2.

Table 2

Structure of chromosome $[\alpha, \beta]$	
Population	30
Iteration count	30
Mutation rate	0.1
Fitness function	max(log-likelihood)

The model's performance was compared to that of the MLE method, and the results are shown in Table 3. Cross-validation helps to create several sets of data that can be used to estimate the accuracy of a model more accurately, with less bias and variation. With k-block cross-validation, we divide the original sample into k-samples, and choose one of the samples as the validation set while the other $k-1$ samples form the training set. After training, the validation efficiency can be calculated. The validation process is repeated by selecting another validation sample from among the predefined blocks. At the end of the procedure, we obtained k performance scores for each block. The mean and standard deviation of the k performance scores can be used to estimate the bias and variance of validation performance. In order to ensure the validity of the estimate and to increase the reliability of the model performance comparison, a 5-fold cross-validation is used in the MLE and GA methods. In the cross-validation procedure, the data is divided into five parts, and each part is used to validate the accuracy of the model. Four of the data points were used to develop models, and the other data point was used to assess the performance of the models. Five different parts were used to perform the test data five times. The fitness averages of the models in each iteration with the training and test data are statistically analyzed using the Log-rank test.

After confirming the method's performance, the last model was created using all the data, omitting any models that appeared during iterations. Therefore, model parameters for the Birnbaum-Saunders distribution were estimated by the MLE and GA methods for the psi31 data. We aimed to maximize the likelihood function as a fitness function in the genetic algorithm method. Log-rank and Kolmogorov-Smirnov were used as performance measures to assess the statistical significance of differences. Although the Kolmogorov-Smirnov value was generally the same in both methods, the logarithmic rank value turned out to be effective in the GA method for some nuclei and the MLE method for some nuclei. Table 3 lists the ranges of GA's success. However, the models obtained by the GA method are more suited for the psi31 data set.

Table 3. Results of MLE and GA methods using different kernels for psi31 data

Kernel	Method	Model		Log-rank	Kolmogorov-Smirnov
		α	β		
T_2	MLE	0.1303	131.3480	**0.0493**	0.2183
	GA	0.1312	132.4502	0.0664	0.2183
T_4	MLE	0.1570	133.2545	0.0904	0.2083
	GA	0.1632	133.0659	**0.0888**	**0.1988**
T_8	MLE	0.1789	133.7577	0.1334	0.1988
	GA	0.1753	134.1157	**0.1312**	0.1988
T_{15}	MLE	0.1850	133.8760	0.1654	0.1988
	GA	0.1835	134.9488	**0.1620**	0.1988
T_{50}	MLE	0.1982	134.3694	**0.2087**	0.1988
	GA	0.1924	135.4835	0.2118	0.1988
T_{100}	MLE	0.2006	134.4090	0.2104	0.1888
	GA	0.1936	135.5795	**0.1898**	0.1888

5. Simulation Study

In this study, we simulate the performance of GA and the current method, ML, to evaluate their relative merits. A number of simulations were run for different sample sizes. In this simulation study, the sample size (n) takes values of 50, 100, 250, and 500, the *censoring rate* (CR) is 10%, 20%, 30%, and 40%, and the value of ν is 5 and 20. The model parameters are $\alpha = 0.3$, $\beta = 60$, and 120. Thus, four different α and β values are investigated. For each case, 100 different synthetic data sets were generated, and bias and MSE values for the parameters were calculated. The *estimated mean square error* (EMSE) and *estimated bias* (EBIAS) for each case are calculated according to the following equation:

$$\text{EMSE}_\alpha = \frac{1}{m}\sum_{i=1}^{m}(\widehat{\alpha}_i - \alpha_i)^2, \tag{19}$$

$$\text{EMSE}_\beta = \frac{1}{m}\sum_{i=1}^{m}(\widehat{\beta}_i - \beta_i)^2, \tag{20}$$

$$\text{EBIAS}_\alpha = \frac{1}{m}\sum_{i=1}^{m}\widehat{\alpha}_i - \alpha, \tag{21}$$

$$\text{EBIAS}_\beta = \frac{1}{m}\sum_{i=1}^{m}\widehat{\beta}_i - \beta \tag{22}$$

with $\theta = (\alpha, \beta)m$ is the number of tests in the simulation. The results are shown in graphs. According to simulation values, the value of ν does not affect the results. As the sample size (n) increased, although the GA method estimated the β parameter better than the ML method, it was seen that there was no difference between the two methods in the estimation of α parameter. In other words, the larger the sample size, the better the GA method can predict.

In Figure 1, according to simulation results, for small samples, we can say that the EMSE_α value calculated by the GA method gives more minor results than EMSE_α values obtained by

the ML method, when $n = 50$, censor rates for 0.1 and 0.2, and $\beta = 60$. Again, when CR = 0.3 and 0.4 are taken, we can say that the EMSE_α values obtained by the GA method are smaller at each α value of $\beta = 120$.

In Figure 2, as the sample size increases, we can say that the GA method for EMSE_α does not differ significantly except in some cases. It can be said that it is recommended to use the ML method as n increases.

If we look at the EMSE_β analysis for $n = 50$, it can be said that the ML estimation gives better results than GA for each censorship rate and each value of α and β. We conclude that in all four cases, α and β for $n = 100$ and CR = 0.1, the EMSE_β value calculated with GA is smaller than the EMSE_β calculated with ML.

In Figure 3, as the sensor ratio increases, we can see that the ML method has a smaller EMSE_β value, except for some cases. When $n = 250$ is taken, the EMSE_β value of the GA method calculated with $\alpha = 0.3$ and $\beta = 120$ and $\alpha = 0.6$ and $\beta = 60$ values for CR = 0.2 is smaller than the EMSE_β values of the ML method. In other cases, we can say that the ML method gives better results.

In Figure 4, When the sample size increases, it can be seen that for $n = 500$, for the values of CR = 0.1 and 0.3, the EMSE_β values obtained with ML are more significant than the EMSE_β values calculated with GA in most of the α and β values. However, this situation is reversed as the censorship rate increases to 0.2 and 0.4.

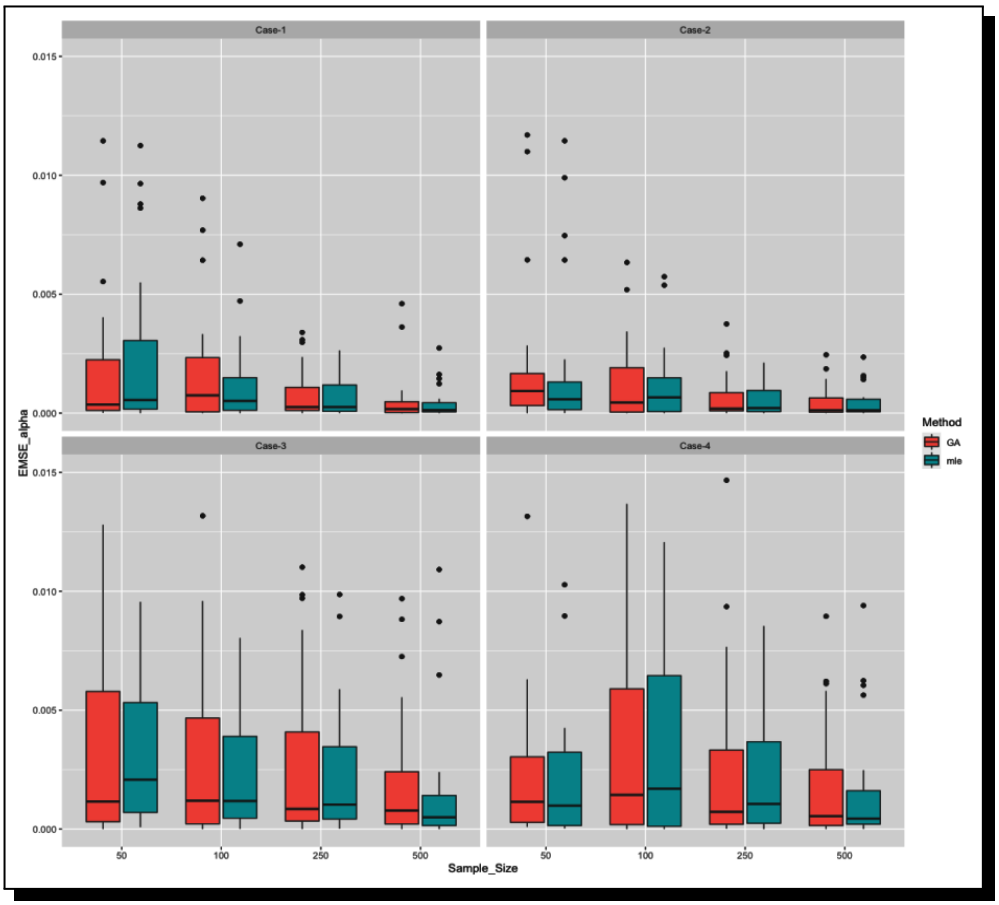

Figure 1. Box plots of EMSE_α according to sample size for CR = 10%

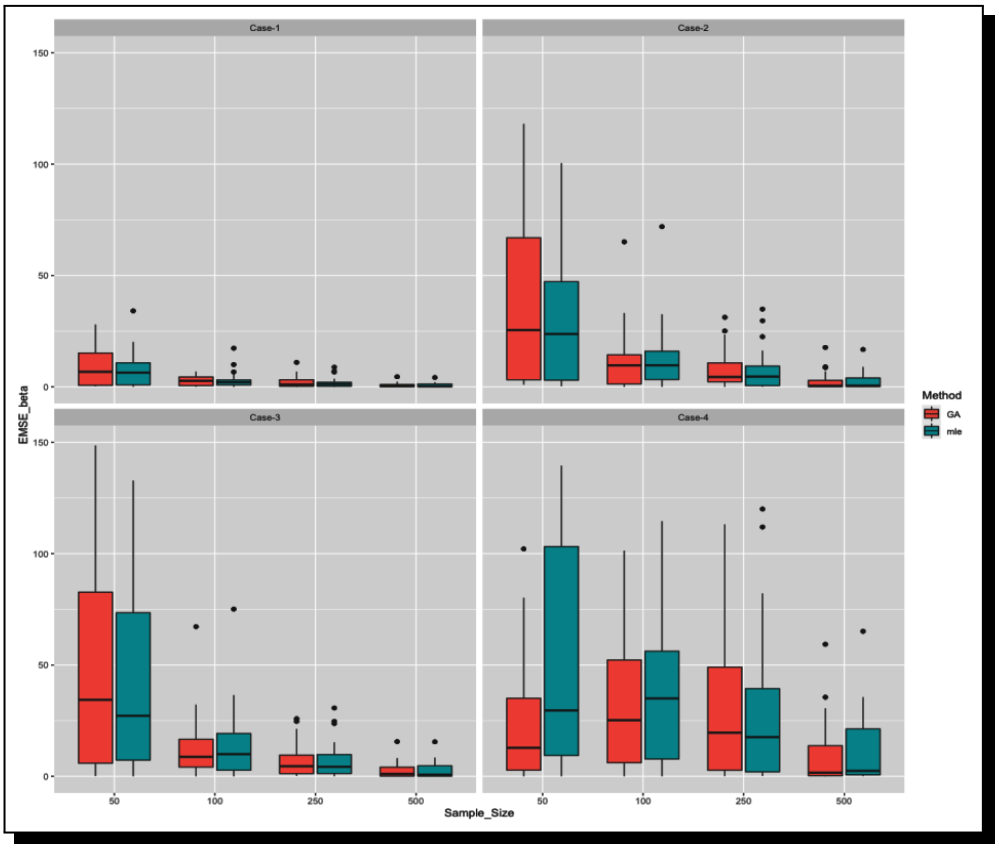

Figure 2. Box plots of EMSE_β according to sample size for CR = 10%

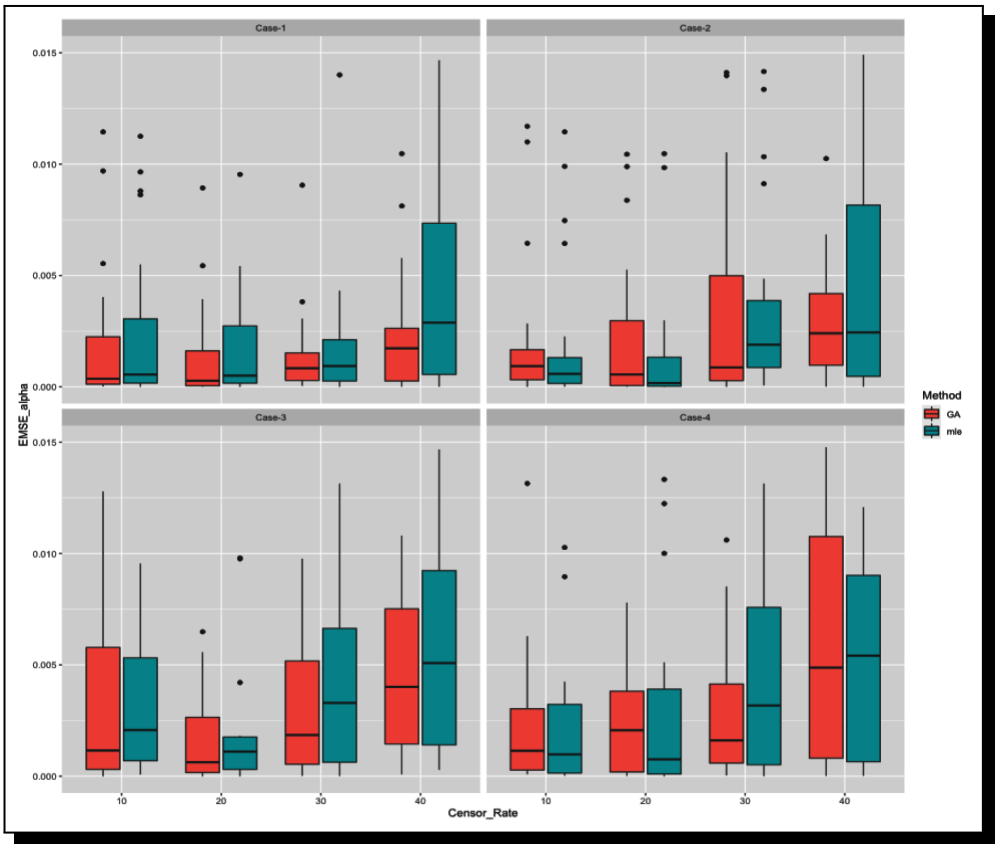

Figure 3. Box plots of EMSE_α according to censor rates

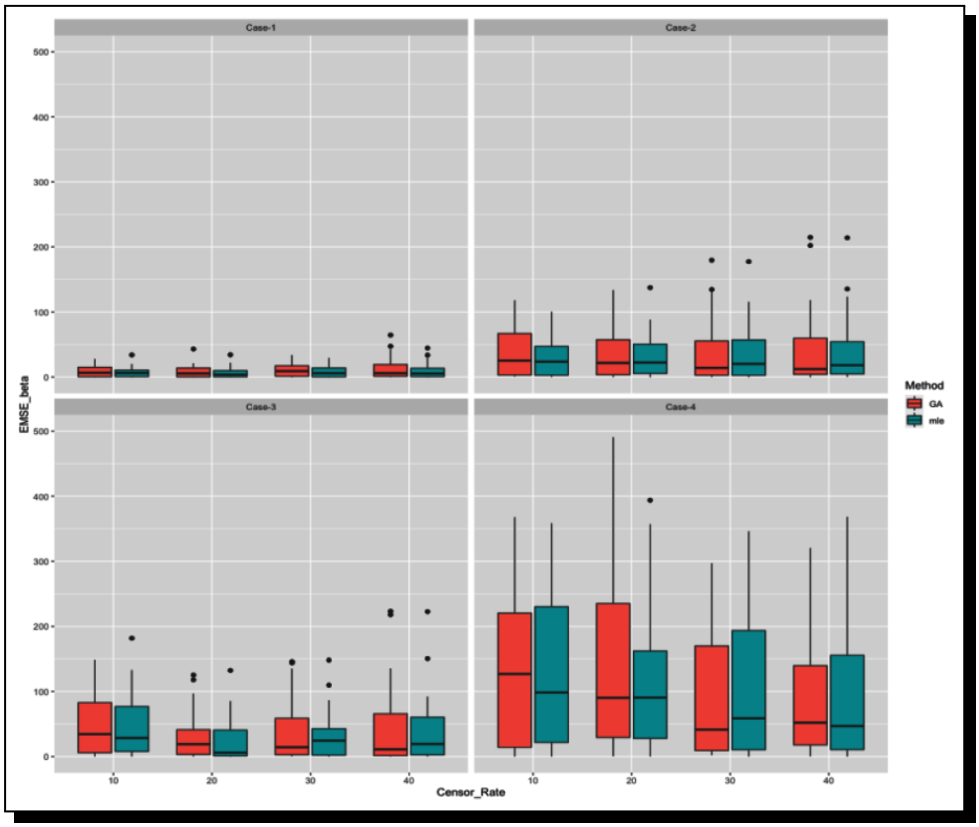

Figure 4. Box plots of EMSE_β according to censor rates

6. Concluding Remarks

As a result, the psi31 data set and simulation study were used to estimate the parameters of the two-parameter Birnbaum-Saunders model. For parameter estimation, we compared the genetic algorithm method proposed by us and the maximum likelihood method used in the literature.

The results show that GA provides a better estimate when the sample size is large. In addition, the log-rank fit test result was found to be the smallest value of the test phase when the entire data set was applied with the GA method. For this reason, it can be said that the model that was established with the GA method performs the best in predicting outcomes.

Besides, a Monte Carlo simulation study was carried out in order to examine the results better. The model's compatibility with the simulation study has been tested for different sample sizes, and it has been found that the models found with the proposed GA method fit the data better when the sample size increases.

Appendix 1

Table A1.1. EBIAS and EMSE for $n = 50$ in simulation ($\nu = 20$)

CR	α	β	MLE				GA			
			BIAS_α	BIAS_β	EMSE_α	EMSE_β	BIAS_α	BIAS_β	EMSE_α	EMSE_β
0.1	0,3	60	0,0205	0,5649	0,0030	7,8339	0,0230	0,9758	0,0034	8,5844
	0,3	120	0,0115	0,5760	0,0019	29,7584	0,0153	1,1121	0,0027	34,3756
	0,6	60	0,0364	3,1430	0,0099	44,3298	0,0225	3,2260	0,0070	48,9484
	0,6	120	0,0295	2,3289	0,0096	137,2190	0,0431	2,0523	0,0111	143,9680

Table Contd.

CR	α	β	MLE				GA			
			$BIAS_\alpha$	$BIAS_\beta$	$EMSE_\alpha$	$EMSE_\beta$	$BIAS_\alpha$	$BIAS_\beta$	$EMSE_\alpha$	$EMSE_\beta$
0.2	0,3	60	0,0081	0,4267	0,0026	7,2874	0,0114	0,8424	0,0020	8,5350
	0,3	120	0,0038	0,8494	0,0015	31,6288	0,0152	0,6878	0,0030	32,7400
	0,6	60	0,0036	0,6684	0,0079	27,1224	0,0142	1,3854	0,0068	34,1012
	0,6	120	0,0016	2,0533	0,0070	135,2965	0,0290	1,3314	0,0114	144,1401
0.3	0,3	60	0,0117	0,4495	0,0025	8,5015	0,0334	1,6938	0,0048	10,6719
	0,3	120	0,0229	1,3087	0,0039	36,6987	0,0272	2,2748	0,0034	38,2205
	0,6	60	0,0133	0,5037	0,0104	31,9327	0,0529	2,4761	0,0160	36,8076
	0,6	120	0,0491	2,2820	0,0144	139,8633	0,0527	4,6486	0,0126	155,6379
0.4	0,3	60	0,0077	0,0529	0,0050	10,0570	0,0364	1,8824	0,0056	13,4630
	0,3	120	0,0086	0,8835	0,0055	40,0596	0,0103	1,8883	0,0034	41,9987
	0,6	60	0,0332	0,7100	0,0205	37,8934	0,0527	2,3496	0,0224	40,8812
	0,6	120	0,0346	2,2388	0,0190	193,2440	0,0336	3,9176	0,0142	190,3549

Appendix 2

Table A2.1. EBIAS and EMSE for $n = 100$ in simulation ($v = 20$)

CR	α	β	MLE				GA			
			$BIAS_\alpha$	$BIAS_\beta$	$EMSE_\alpha$	$EMSE_\beta$	$BIAS_\alpha$	$BIAS_\beta$	$EMSE_\alpha$	$EMSE_\beta$
0.1	0,3	60	0,0174	−0,1593	0,0012	3,0987	0,0230	0,4329	0,0018	2,7314
	0,3	120	0,0171	−0,1446	0,0011	13,0703	0,0194	0,3689	0,0012	12,2567
	0,6	60	0,0415	0,1043	0,0058	13,6092	0,0406	0,6550	0,0050	12,7474
	0,6	120	0,0383	−0,4488	0,0052	48,5017	0,0365	0,1640	0,0051	42,3841
0.2	0,3	60	0,0160	0,0168	0,0014	3,1662	0,0200	0,4719	0,0018	3,5926
	0,3	120	0,0163	−0,1502	0,0014	14,1960	0,0199	0,2412	0,0016	12,4760
	0,6	60	0,0312	0,1326	0,0050	12,5726	0,0332	0,4805	0,0050	12,1026
	0,6	120	0,0275	0,0347	0,0049	49,1496	0,0399	0,8854	0,0062	51,4403
0.3	0,3	60	0,0187	0,1640	0,0016	3,8223	0,0348	0,9936	0,0026	5,5119
	0,3	120	0,0170	0,2077	0,0016	13,2496	0,0211	0,5122	0,0021	12,8348
	0,6	60	0,0396	0,4210	0,0075	15,1177	0,0534	1,2340	0,0087	16,3896
	0,6	120	0,0265	−0,2713	0,0069	50,5689	0,0372	1,6085	0,0086	50,2440
0.4	0,3	60	0,0066	−0,2682	0,0017	3,8734	0,0278	1,1994	0,0026	6,8881
	0,3	120	0,0086	−0,1901	0,0024	11,9040	0,0171	0,7374	0,0026	13,2442
	0,6	60	0,0177	−0,3373	0,0083	14,3330	0,0419	0,9243	0,0108	14,7966
	0,6	120	0,0160	−0,8434	0,0096	50,7946	0,0328	1,2795	0,0094	51,9959

Appendix 3

Table A3.1. EBIAS and EMSE for $n = 250$ in simulation ($\nu = 20$)

CR	α	β	MLE				GA			
			BIAS_α	BIAS_β	EMSE_α	EMSE_β	BIAS_α	BIAS_β	EMSE_α	EMSE_β
0.1	0,3	60	0,0173	−0,1012	0,0006	1,8500	0,0194	0,2962	0,0008	2,1694
	0,3	120	0,0177	−0,2621	0,0006	7,6492	0,0197	−0,4029	0,0007	7,9614
	0,6	60	0,0344	−0,1140	0,0022	7,0492	0,0356	−0,0156	0,0026	7,1125
	0,6	120	0,0364	−0,4429	0,0025	28,9340	0,0375	−0,1432	0,0026	30,3716
0.2	0,3	60	0,0190	−0,1674	0,0006	1,8631	0,0219	0,5951	0,0008	2,7524
	0,3	120	0,0190	−0,3355	0,0007	7,6374	0,0194	−0,1744	0,0007	7,5077
	0,6	60	0,0390	−0,2406	0,0027	7,2035	0,0382	0,0082	0,0029	6,9840
	0,6	120	0,0392	−0,5107	0,0028	27,0372	0,0380	−0,2564	0,0026	31,0835
0.3	0,3	60	0,0159	−0,1310	0,0005	1,7773	0,0320	0,8263	0,0017	4,5721
	0,3	120	0,0170	−0,1513	0,0006	7,0226	0,0209	0,2097	0,0007	8,7711
	0,6	60	0,0381	−0,1999	0,0028	7,1546	0,0462	0,4153	0,0038	8,1626
	0,6	120	0,0301	−0,7312	0,0022	28,1480	0,0405	0,4490	0,0029	29,4637
0.4	0,3	60	0,0156	−0,2170	0,0008	1,7828	0,0246	0,7618	0,0012	3,5249
	0,3	120	0,0143	−0,3787	0,0007	8,1642	0,0238	0,5055	0,0011	8,8527
	0,6	60	0,0328	−0,4308	0,0031	7,2640	0,0387	0,3307	0,0038	6,6391
	0,6	120	0,0323	−0,7351	0,0029	33,6439	0,0437	0,4144	0,0038	31,5758

Appendix 4

Table A4.1. EBIAS and EMSE for $n = 500$ in simulation ($\nu = 20$)

CR	α	β	MLE				GA			
			BIAS_α	BIAS_β	EMSE_α	EMSE_β	BIAS_α	BIAS_β	EMSE_α	EMSE_β
0.1	0,3	60	0,0147	−0,2046	0,0004	0,6617	0,0163	0,2274	0,0006	0,7095
	0,3	120	0,0133	−0,4043	0,0004	2,5768	0,0153	−0,4148	0,0005	2,5546
	0,6	60	0,0279	−0,4013	0,0017	2,6272	0,0328	−0,2688	0,0020	2,4320
	0,6	120	0,0257	−0,9642	0,0016	11,2665	0,0289	−0,8576	0,0018	10,1097
0.2	0,3	60	0,0105	−0,2250	0,0003	0,6526	0,0151	0,4214	0,0005	1,7869
	0,3	120	0,0103	−0,5558	0,0003	2,9039	0,0126	−0,2633	0,0004	3,0530
	0,6	60	0,0232	−0,5494	0,0015	2,8302	0,0278	−0,2527	0,0018	2,8893
	0,6	120	0,0209	−1,1914	0,0013	11,2624	0,0237	−0,8918	0,0015	11,0077

Table Contd.

CR	α	β	MLE				GA			
			BIAS_α	BIAS_β	EMSE_α	EMSE_β	BIAS_α	BIAS_β	EMSE_α	EMSE_β
0.3	0,3	60	0,0144	−0,1133	0,0006	0,7231	0,0184	0,6179	0,0009	2,6941
	0,3	120	0,0143	−0,3146	0,0006	2,5978	0,0163	−0,0847	0,0006	2,5345
	0,6	60	0,0279	−0,2426	0,0023	2,5354	0,0366	−0,0018	0,0025	2,3388
	0,6	120	0,0277	−0,7001	0,0022	10,5295	0,0333	−0,2857	0,0027	10,0050
0.4	0,3	60	0,0144	−0,1260	0,0005	1,5825	0,0265	0,7647	0,0011	3,6343
	0,3	120	0,0118	−0,2868	0,0004	2,6385	0,0195	0,2615	0,0006	3,3184
	0,6	60	0,0244	−0,4495	0,0022	2,5008	0,0320	−0,0646	0,0028	2,5958
	0,6	120	0,0184	−1,1371	0,0029	11,3287	0,0329	−0,5660	0,0031	9,9236

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Competing Interests

The authors declare that they have no competing interests.

Authors' Contributions

All the authors contributed significantly in writing this article. The authors read and approved the final manuscript.

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