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A Hybrid Support Vector Machine–Genetic Algorithm Framework Approach for Parameters Estimation for the [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process in nonhomogenous Poisson Process

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Abstract The estimation of three unknown parameters of [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process of nonhomogeneous Poisson Process (TNHIRP). It discusses nine of those estimation methods, which are the maximum likelihood, maximum product spacing, Anderson Darling, Right Anderson-Darling, ordinary least squares, weighted least squares, Cramer-von Mises, Hybrid Support Vector Machine–Genetic Algorithm, and percentiles to estimate points. These estimators were compared in terms of bias and mean squared errors using detailed analysis and a lot of simulation experiments. According to the simulation outcomes, all the estimators work well under these considerations and show similar values in case of large sample size. There are also some statistical properties of the new distribution derived. The estimators were also applied to two real life datasets and the values of the Kolmogorov-Smirnoff statistics reported. Lastly, the [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh process was tested on two real world datasets, and the performance was compared with other well-known extensions of Inverse Rayleigh process using four selection criteria.

Keywords Truncated, Survival estimation, Inverse Rayleigh Process, Newton Raphson, SVM-GA, nonhomogeneous Poisson Process, Simulation

AMS 2010 subject classifications 60J80, 60J85, 60K10

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1. Introduction

The simulation and analysis of real-world data is important in various areas including medicine engineering and finance. The correct choice of a probabilistic model for data analysis is essential because various lifetime distributions have been used to model different types of data throughout history. This research led to the development of multiple probability distribution families together with their corresponding methodological framework. The recent research contributions until now show active research interest in developing complex and general modeling systems. The actual data distributions found in multiple real-world data sets do not conform to

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established distribution patterns. The present paper introduces eight estimation techniques for the [0,1] Truncated Nadarajah Haghighi Rayleigh distribution which enable researchers to analyze data that remains unclassifiable by traditional methods [1, 2, 3, 4].

The Non-Homogeneous Poisson Processes (NHPPs) have been greatly utilized in the time dependent event occurrences describing reliability engineering, survival analysis, telecommunications, and finance. The models used in existing NHPP models normally involve intensity functions based on classical lifetime distributions like exponential, Weibull, log-normal and Rayleigh type models. Although these models offer mathematical tractability, their constraining nature of the hazard structure can be a significant limitation to their application in the case of real-world data that have complex time-varying failure [5, 6]. A number of studies have tried to enhance flexibility through the use of longer or compounded lifetime distributions; nevertheless, a significant number of these techniques are still insufficient in the case of limited or terminated data that is frequently found in the real world. The NHPP has a number of valuable applications in many disciplines, such as reliability engineering, finance, and telecommunications [7, 8, 9].

The NHPP is often employed in modeling the time dependence of the failure rate of systems in reliability engineering, but the failure rate is time-dependent, because of the aging of the system or other effects [5, 10]. Finance The arrival rate of financial transactions or the probability of a market event occurring over time is represented by the NHPP in finance [6, 7, 11] Telecommunications NHPP can be used to model the call or message arrival rate in communication networks [12, 13]. The second property that is relevant to the NHPP is that it is Markov, that is, the probability of the events happening depends on the present instead of the history of past conditions of the process [14, 15]. This fact renders the NHPP especially applicable to the modeling of complex systems and processes. It is difficult to estimate the intensity function parameters, due to the temporal variation of the NHPP and the complexity of the intensity function; however, different approaches to estimating such parameters have been suggested: Maximum Likelihood Estimation (MLE), Bayesian Inference, and Intelligent techniques, such as Genetic Algorithms (GA) and Neural Networks [16, 17, 18].

The Rayleigh and Inverse Rayleigh distribution have been of much interest because of its applicability in reliability and survival modeling. Many extensions have been suggested based on the Rayleigh model to allow greater flexibility, or Marshall–Olkin extensions have been suggested to modify the shape of the tail [19, 20, 21]. Despite the fact that these models enhance the adaptability of hazard shapes, the majority of them are characterized on infinite supports, hence are not applicable in modeling data that are restricted in finite intervals [22, 23]. Moreover, they are only applied in NHPP frameworks with limited cases, especially in cases of truncation [24].

To take care of the case that observations are truncated by physical, experimental, or administrative reasons, truncated and bounded lifetime distributions have been proposed. There is a relative lack of research that examines truncated Rayleigh-type processes in an NHPP environment despite their significance [12, 25, 26]. The current truncated models usually concentrate on distributional properties only without integrating them into stochastic processes, which restricts their use in the context of recurrent event data. This shows that there is a serious literature void in flexible NHPP models that can accommodate limited lifetimes [27, 28, 29, 30].

Some of the limitations of the traditional methods that have been used to estimate the parameters of an extended Rayleigh distribution have not been explicitly discussed in these past studies [31, 32, 33]. This paper would fill the gap in the traditional methods by introducing and comparing techniques, such as the maximum likelihood, maximum product spacing, Anderson-Darling, Right Anderson-Darling, ordinary least squares, weighted least squares, Cramer-von Mises, and percentiles as tools to analyze and model non-traditional data that are not observed under standard probability models.

This paper introduces a hybrid estimation model of Non-Homogeneous Poisson Processes (NHPPs) using a Support Vector machine Genetic Algorithm (SVMGA) model with a combination of [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Inverse Rayleigh (TNHIRP) distribution. The framework is very malleable as it is possible to model both monotonic and non-monotonic hazard behavior and global metaheuristic optimization itself is able to overcome the complexities which have made other strategies of estimation difficult. Moreover, the quantification of uncertainty is accomplished with the help of a Bayesian Neural Network (BNN), which is capable of not only estimating the points but also giving credible intervals and reliability scores because network weights are modeled as random variables. This probabilistic treatment also differentiates the method to the previous deterministic or heuristic methods, which are usually limited in terms of accuracy and goodness-of-fit.

The rest of this paper will be organized in the following way. Section 2 offers a detailed introduction and motivation, including how the current distributions based on the Rayleigh model are limited and how a more flexible model should be created in order to accommodate truncated and bounded lifetime data. Section 3 provides the methodological development of the proposed [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process (TNHIRP) including its probability density and cumulative distribution functions and major mathematical properties. Section 4 addresses the statistical characteristics and derivations in terms of moments that define the theoretical basis of the new model. Section 5 presents the hybrid estimation framework, in which the Support Vector Machine–Genetic Algorithm (SVM–GA) is presented as a smart alternative to classical estimation methods, in addition to the maximum likelihood and other eight rival estimation methods. Section 6 provides the simulation design and results and compares all estimators on the existing bias, mean squared error, and mean relative error, thus showing their consistency and asymptotic efficiency. Section 7 illustrates the practical implementation of the TNHIRP model on two empirical data sets and measures the adequacy of models in terms of log-likelihood and information (AIC, BIC, CAIC, HQIC) and compares it to other existing lifetime distributions. The discussion of results is made in detail in section 7.3, in which the superiority of intelligent SVM–GA Lastly, Section 8 ends the paper by presenting the key findings, theoretical contributions, and practical implications, with followed research suggestions, such as the design of full extensions of Bayesian inference, introducing covariates, and investigating more in-depth neural architectures.

1.1. Motivation

Actual data demonstrates that both lifespan and reliability information exists in multiple fields which include biomedical survival analysis and engineering reliability and financial risk modeling but the data itself suffers from intrinsic restrictions and incomplete records. The standard lifetime distribution models together with the non-homogeneous Poisson process (NHPP) framework fail to offer sufficient modeling capacity for these restricted patterns because their hazard rate dynamics follow intricate monotonic and non-monotonic development paths. The maximum likelihood estimation (MLE) method together with all other traditional parameter estimation techniques exhibit numerical instability because they reach only local maximum points which results in poor performance during small and moderate sample size testing on complex likelihood surfaces. The existing limitations force researchers to develop new lifetime procedures which include estimation systems that handle truncated data together with nonlinear optimization challenges.

1.2. Main Contributions

- A new lifetime model is proposed, which we call the [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process (TNHIRP), which is defined in the framework of a non-homogeneous Poisson process and can imply more flexibility in modeling truncated and bounded lifetime data.
- The probability density function and cumulative distribution function, quantile function, and moment of the TNHIRP model are computed in closed-form.
- The proposed model is studied in terms of nine parameter estimation methods that include classical algorithms and intelligent optimization-based algorithms.
- A new hybrid Support Vector Machine-Genetic Algorithm (SVM-GA) estimation scheme is created to overcome the numerical and optimization difficulties of the likelihood functions of a complex nature.
- Simulation studies are done at large lengths to compare the performance of all estimators in terms of bias, mean squared error, and mean relative error, which proves that SVM-GA is a more stable and accurate method, especially in the small and moderate sample sizes.
- The utility of the proposed TNHIRP model in practice is demonstrated with the help of two real-world datasets, where it beats many popular competitor lifetime distributions based on various goodness-of-fit metrics.

2. Methodology

The methodology framework that has been used to assess the proposed model is shown in Figure 1 which shows the steps involved. The analysis was carried out in a systematic manner guided by this framework and the equations as provided in the computational analysis subsection.

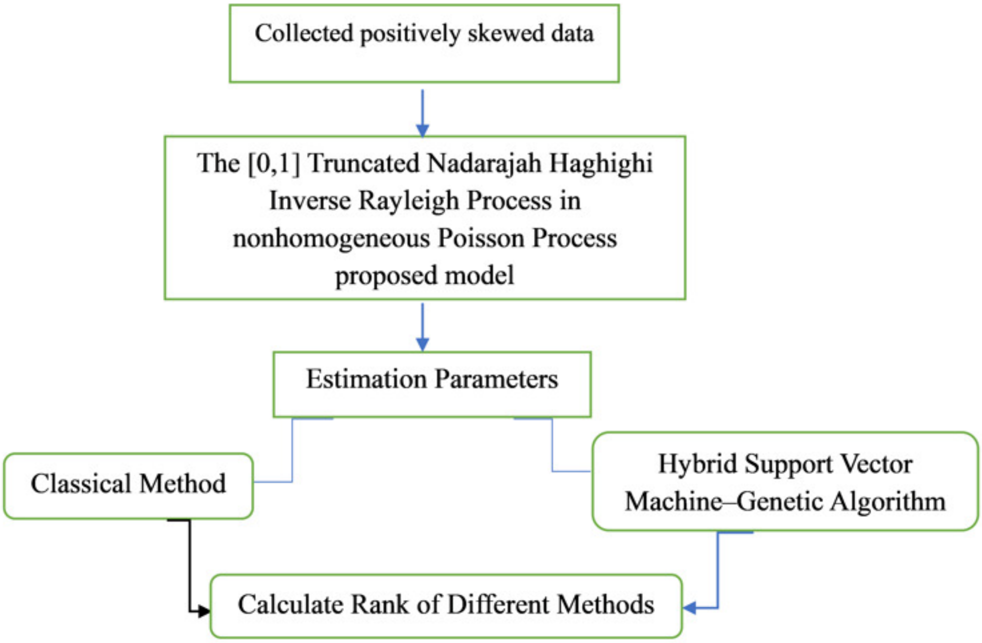

Figure 1. Workflow of current Research

2.1. *The [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process (Proposed Model)*

The inverse Rayleigh (IR) distribution is a general and highly practical continuous probability distribution model that has earned much interest in different reliability studies and life test operations. Particularly, it is helpful in the modelling of the time rate of occurrence of the non-homogeneous Poisson processes leading to a new process, thus called the Inverse Rayleigh process. The IR distribution is unimodal, is a member of the exponential family, and is useful in the modelling and prediction of the failure rates of complex systems. It can be applied in the manufacturing, engineering, and healthcare industries to make better decisions. We proposed that the Inverse Rayleigh process is a nonhomogeneous Poisson process with the time rate of occurrence defined by:

$$\lambda\left(t\right)=2\alpha t^{-3},0<t<\infty \tag{1}$$

where $\alpha>0$ represent scale parameter.

The process parameter $m(t)$ represents the mean rate, is the cumulative function of the time rate of occurrence and is given by [10, 34].

$$m\left(t\right)=\int\limits_{0}^{t}\lambda\left(u\right)du,0<t<\infty. \tag{2}$$

$$=\int\limits_{0}^{t}\frac{2\alpha}{u^{3}}du. \tag{3}$$

After a change of variable, the expression for $m(t)$ becomes:

$$m(t) = -\alpha t^{-2}; 0 < t < t_0, \tag{4}$$

where $t_{\,0}$ represent the time of occurrence of the event. The inter-arrival process for the Inverse Rayleigh process is distribution as:

$$f\left(t\right) = \lambda\left(t\right) e^{-\int\limits_{0}^{t} \lambda(u) du}, \tag{5}$$

which simplifies to:

$$f\left(t\right) = \frac{2\alpha^2}{t^3} e^{-\alpha^2 t^{-2}}, t > 0. \tag{6}$$

Let Y be a random variable. The cumulative distribution function (CDF) and probability density function (PDF) of the [0,1] Truncated Nadarajah–Haghighi–G family of distributions are given in Equation 1 and Equation 2 respectively.

$$F(y)_{TNH-G} = \frac{1 - e^{1-(1+bG(y,\varphi))^a}}{1 - e^{1-(1+b)^a}}, \tag{7}$$

$$f(y)_{TNH-G} = \frac{ab(1 + bG\left(y, \varphi\right))^{a-1} e^{1-(1+bG(y,\varphi))^a} g\left(y, \varphi\right)}{1 - e^{1-(1+b)^a}}, \tag{8}$$

where $G\left(y, \varphi\right)$ and $g\left(y, \varphi\right)$ are CDF and PDF of the base distribution. Inverse Rayleigh process will be used as the baseline Non-Homogeneous Poisson Process in this paper, and the CDF and PDF can be provided as follows:

$$G\left(y, \alpha\right) = e^{-\frac{\alpha}{y^2}}; y \geq 0, \alpha > 0, \tag{9}$$

$$g\left(y, \alpha\right) \ = \frac{2\alpha}{\mathrm{y}^3} e^{-\frac{\alpha}{y^2}}; y \geq 0, \alpha > 0. \tag{10}$$

By substituting the functions in Equation 9 and Equation 10 into Equation 7 and Equation 8, the cumulative distribution function (CDF), probability density function (PDF), and quantile function of the [0,1] TNH Inverse Rayleigh Process (TNHIRP) distribution are obtained, as presented in Equation 11, Equation 12, and Equation 13 respectively.

$$F(y; a, b, \alpha)_{[0,1]TNHIRay} = \frac{1 - e^{1-\left(1+b\left(e^{-\frac{\alpha}{y^2}}\right)\right)^a}}{1 - e^{1-(1+b)^a}}; y \geq 0, a, b, \alpha > 0, \tag{11}$$

$$f(y; a, b, \alpha)_{[0,1]TNHIRay} = \frac{\frac{2\alpha}{\mathrm{y}^2}\left(1 + b\left(e^{-\frac{\alpha}{y^2}}\right)\right)^{a-1} e^{\left(1-\left(1+b\left(e^{-\frac{\alpha}{y^2}}\right)\right)^a\right)} e^{-\frac{\alpha}{y^2}}}{1 - e^{(1-(1+b)^a)}}, \tag{12}$$

$$Q(u)_{[0,1]TNHIR} = \sqrt{-\frac{\alpha}{\ln\left(\frac{(1-\ln\left(1-u\left(1-e^{(1-(1+b)^a)}\right)\right)^{\frac{1}{a}}-1}{b}\right)}}; 0 < u < 1. \tag{13}$$

2.2. *Moments*

The r^{th} moment of [0,1] TNHI-Ray process can be derived from the following relation:

$$\mu_r = \int\limits_{-\infty}^{\infty} x^r f(y)\, dy,$$

Where $f(y)$ is given in Equation 12, so that:

$$\mu_r = \int\limits_{0}^{\infty} x^r \frac{\frac{2\alpha \mathrm{y}}{\mathrm{y}^3}\left(1+b\left(e^{-\frac{\alpha}{y^2}}\right)\right)^{a-1} e^{\left(1-\left(1+b\left(e^{-\frac{\alpha}{y^2}}\right)\right)^{a}\right)} e^{-\frac{\alpha}{y^2}}}{1-e^{\left(1-(1+b)^a\right)}} dy, \tag{14}$$

after some simplifications,

$$\mu_r = E\left(X^r\right) = \frac{x^r \sqrt{\alpha} e}{1-e^{\left(1-(1+b)^a\right)}} \int\limits_{0}^{\infty} s^{-1/2}\left(1+be^{-s}\right)^{a-1} e^{-s-\left(1+be^{-s}\right)^a} ds. \tag{15}$$

3. Genetic Algorithm Applications

The initial form of stochastic, population-based variants of optimization algorithms called Genetic Algorithms (GAs) was coined by [16, 35, 36] and is based on Darwinian principles of natural selection and evolution. Their basic concept is to successively mutate a population of candidate solutions to increasingly fitter in terms of some objective function. GA due to their strength and versatility have been extensively applied to science, engineering, and data-driven modeling especially nonlinear, multimodal and non-analytically graded problems [37, 38].

3.1. *Mathematical Formulation*

Let the optimization problem be defined as:

$$\min_{x \in {}^d} f(x), \tag{16}$$

$f(x)$ is the objective (fitness) function, and $x = [x_1, x_2, \ldots, x_d]$ is a decision vector, d-dimensional. GA evolves a population $P^{(t)} = \left\{x_1^{(t)}, x_2^{(t)}, \ldots, x_N^{(t)}\right\}$ of N individuals at generation t, to which a candidate solution corresponds. The overall evolution process is composed of three main genetic operators: selection, crossover, and mutation.

Selection: The selection operator biases preferentially those individuals who are more fit to transmit genetic material to the following generation. Assuming that f_i is the fitness of individual i its selection probability is:

$$p_i = \frac{f_i}{\sum_{j=1}^{N} f_j}. \tag{17}$$

Crossover: Crossover (also recombination) is the combination of two parent solutions with the goal of producing offspring and so purposes the exploration of the search space. Given that x_p and x_q, are two parents, arithmetic crossover may be defined as follows:

$$x_{\text{child}} = \alpha x_p + (1-\alpha) x_q, \tag{18}$$

where $\alpha \in [0,1]$ is a random blending coefficient. Other types of crossovers are a one point, two point and uniform crossover schemes [39].

Mutation: The mutation operator applies random variations to the individual parameters in order to keep the diversity and avoid early convergence. One of the formulations of real-valued GAs is:

$$x_i^{(t+1)} = x_i^{(t)} + \sigma \mathcal{N}(0,1), \tag{19}$$

where σ controls the mutation rate and $\mathcal{N}(0,1)$ represents a standard normal random variable. The iterative GA process can be summarized as:

$$P^{(t+1)} = \text{Mutation}\left(\text{Crossover}\left(\text{Selection}\left(P^{(t)}\right)\right)\right). \tag{20}$$

The process of evolutionary change proceeds in this manner until some convergence criterion, e.g. a maximal number of generations or a threshold of fitness, is achieved.

4. Support Vector Machine (SVM)

In this part, we provide a brief description of the Support Vector Machine (SVM) algorithm as well as its theoretical background. To be treated holistically the reader is sent [13, 14, 39]. The binary classification problem is considered to have a dataset, $\{(a_i, b_i)\}_{i=1}^{l}$, with class labels $b_i \in \{-1, +1\}$. SVM aims at identifying a linear classifier with the minimal overall generalization error, based on the Structural Risk Minimization (SRM) principle [13, 40]. The best separating hyperplane is the one which maximizes the margin- the perpendicular distance between the hyperplane and the closest data points, which are called support vectors [15, 26, 41]. This margin maximization improves not only the accuracy of the classification, but has also a better generalization capacity of the model, which is in accordance with the statistical learning theory. In case the data is not linearly separable, SVM proposes a soft- margin model that simultaneously maximizes the margin and minimizes the classification error. It is done by optimizing a Quadratic Programming (QP) problem with a regularization constant $C > 0$ that balances between these conflicting aims. The decision function is of the form:

$$f(y) = \text{sign}\left(\sum_{i=1}^{l} \beta_i a_i y_i^T y + b\right), \tag{21}$$

and β_i are the linear classifier coefficients. In order to generalize SVMs to nonlinear issues, the input vectors $y \in R^d$, are transformed into a larger-dimensional feature space by a nonlinear transformation.

$$z(y) = (\phi_1(y), \ldots, \phi_n(y)) \in R^n, \tag{22}$$

that makes it possible to perform linear separation in the transformed space [13, 42, 43], showed that this mapping could be trained implicitly using kernel functions $K(y, y_i)$, which compute inner products in the feature space without actually performing the transformation-a phenomenon called the kernel trick. The nonlinear decision function is thus given as:

$$f(y) = \text{sign}\left(\sum_{i=1}^{l} \beta_i a_i K(y, y_i) + b\right), \tag{23}$$

in which $K(.,.)$ is a symmetric, positive-definite kernel that characterizes the measure of similarity among samples. Practically, the choice of the parameters of the kernel and the regularization constant C are very crucial in the performance of SVMs. genetic Algorithms (GA), which is an evolutionary optimization technique based on a population, has demonstrated great success in tuning these hyperparameters. The hybrid SVM-GA model allows combining SVM-GA framework to gain the global search of GA and the powerful classification of SVM. GA optimizes sets of the candidate parameters (e.g. C, kernel width, or shape parameters) to minimize classification error or to maximize model accuracy, so that it avoids local minima and the convergence to good model configurations. Such hybridization provides adaptive choice of models and also improves predictive behavior particularly when the data environment is complex, nonlinear or high-dimensional.

5. Parameters Estimation

In this section, a study on parameters estimation of the [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process (TNHIRP) distribution is conducted on nine different estimation methods. The overall goal is to come up with correct and valid parameter estimates of the [0,1] TNHIRP distribution by using these varied estimation methods. Their comparative effectiveness is assessed through the extensive simulation studies whose findings are summarized in a comparative ranking framework in order to determine the most appropriate technique. Special attention is given to the determination of the efficiency of each estimation technique with references to the distributional properties of the [0,1] TNHIRP model as well as the effects of the sample size n.

5.1. The Ordinary Least Squares (OLS) Method

The OLS estimates of the [0,1] TNHIRP distribution are obtained by minimizing the following objective function:

$$V\left(a,b,\alpha\right)=\sum_{j=1}^{n}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}-\frac{j}{n+1}\right)^2 \tag{24}$$

Equivalently, the estimates may be derived by solving the system of nonlinear Equation 26 – Equation 28.

$$\sum_{j=1}^{n}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}-\frac{j}{n+1}\right)\Delta_s\left(y_j\right)=0, s=1,2,3 \tag{25}$$

where $\left(y_i\setminus a,b,\alpha\right),\Delta_2\left(y_i\right)=\Delta_2\left(y_i\setminus a,b,\alpha\right),\Delta_3\left(y_i\right)=\Delta_3\left(x_i\setminus a,b,\alpha\right)$ are defined as follows:

$$\Delta_1\left(y_i\right)=\frac{\partial}{\partial a}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}\right)=\frac{\left(1-e^{1-(1+b)^a}\right)e^{1-\left(1+be^{-\alpha/y_i^2}\right)^a}\left(1+be^{-\alpha/y_i^2}\right)^a\ln\left(1+be^{-\frac{\alpha}{y_i^2}}\right)}{\left(1-e^{1-B^a}\right)^2}$$

$$-\frac{\left(1-e^{1-\left(1+be^{-\alpha/y_i^2}\right)^a}\right)e^{1-(1+b)^a}\left(1+b\right)^a\ln\left(1+b\right)}{\left(1-e^{1-B^a}\right)^2}. \tag{26}$$

$$\Delta_2\left(y_i\right)=\frac{\partial}{\partial b}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}\right)$$

$$=\frac{a}{\left(1-e^{1-B^a}\right)^2}\left[\left(1-e^{1-B^a}\right)e^{-\alpha/y_i^2}A(y_i)^{a-1}e^{1-A(y_i)^a}-\left(1-e^{1-A(y_i)^a}\right)B^{a-1}e^{1-B^a}\right] \tag{27}$$

where $B=1+b, A\left(y_i\right)=1+be^{-\alpha/y_i^2}$.

$$\Delta_3\left(y_i\right)=\frac{\partial}{\partial\alpha}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}\right)=-\frac{ab}{y_i^2}\frac{e^{-\frac{\alpha}{y_i^2}}\left(1+be^{-\frac{\alpha}{y_i^2}}\right)^{a-1}e^{1-\left(1+be^{-\frac{\alpha}{y_i^2}}\right)^a}}{1-e^{1-(1+b)^a}}. \tag{28}$$

5.2. The Weighted Least-Squares (WLS) Method

The WLS estimators of [0,1] TNHIRP distribution are developed by minimizing the following objective function:

$$W\left(a,b,\alpha\right)=\sum_{j=1}^{m}\frac{\left(m+1\right)^2\left(m+2\right)}{j\left(m-j+1\right)}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}-\frac{j}{m+1}\right)^2 \tag{29}$$

The WLS estimates can alternatively be determined by solving the corresponding non-linear equations.

$$\sum_{j=1}^{m}\frac{(m+1)^2(m+2)}{j(n-j+1)}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{y_j{}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}-\frac{j}{n+1}\right)\Delta_s(y_j)=0, s=1,2,3 \tag{30}$$

where $\Delta_1(y_i)=\Delta_1(y_i\setminus a,b,\alpha), \Delta_2(y_i)=\Delta_2(y_i\setminus a,b,\alpha), \Delta_3(y_i)=\Delta_3(x_i\setminus a,b,\alpha)$ are defined in Equation 26 - Equation 28.

5.3. *Maximum Product Spacing (MPS)*

Let $y_1<\ldots<y_n$ be a random sample of size n. The uniform spacings of the TNHIRP distribution are then given by: $D_i(a,b,\alpha)=F(y_j)-F(y_{j-1}); j=1,\ldots,n+1$, where $F\left(y_{(0)}\right)=0, F\left(y_{(n+1)}\right)=1, \& \sum_{j=1}^{n+1}D_j=1$.
The MPS Estimates of the TNHR distribution parameters can be obtained by maximizing the corresponding objective function.

$$G(a,b,\alpha)=\frac{1}{n+1}\sum_{j=1}^{n+1}\log\{D_j\}. \tag{31}$$

This can be determined by solving the corresponding non-linear equations.

$$G(a,b,\alpha)=\frac{1}{n+1}\sum_{j=1}^{n+1}\frac{1}{D_j}\left(\Delta_s(y_j,a,b,\alpha)-\Delta_s(y_{j-1},a,b,\alpha)\right)=0, s=1,2,3, \tag{32}$$

where $\Delta_1(y_i)=\Delta_1(y_i\setminus a,b,\alpha), \Delta_2(y_i)=\Delta_2(y_i\setminus a,b,\alpha), \Delta_3(y_i)=\Delta_3(x_i\setminus a,b,\alpha)$ are defined in Equation 26 - Equation 28.

5.4. *Cramér-Von Mises (CVM)*

Under the Cramer von Mises (CVM) test, the estimates of the parameters are derived by estimating the difference between the cumulative and empirical distribution functions. In particular, CVM estimates of the parameters of the distribution [0,1] TNHIRP are obtained in favor of this discrepancy.

$$C(a,b,\alpha)=\frac{1}{12m}+\sum_{j=1}^{m}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{y_j{}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}-\frac{2j-1}{2m}\right)^2. \tag{33}$$

With respect to a,b,α, the CVM estimates can be obtained by solving the corresponding non-linear equations.

$$\sum_{j=1}^{m}\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{y_j{}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}-\frac{2j-1}{2m}\right)\Delta_s(y_j)=0, s=1,2,3, \tag{34}$$

where $\Delta_1(y_i)=\Delta_1(y_i\setminus a,b,\alpha), \Delta_2(y_i)=\Delta_2(y_i\setminus a,b,\alpha), \Delta_3(y_i)=\Delta_3(x_i\setminus a,b,\alpha)$ are defined in Equation 26 - Equation 28.

5.5. *Anderson- Darling (ADE)*

The ADE estimates of the [0,1] TNHIRP distribution parameters are estimated by reducing the objective function associated with them:

$$A(a,b,\alpha)=-m$$

$$-\frac{1}{m}\sum_{j=1}^{m}(2j-1)\left(\log\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}\right)-\log\left(\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}-e^{1-(1+b)^a}\right)\right), \tag{35}$$

With respect to a, b, α , these estimates can be obtained by solving the corresponding non-linear equations:

$$\sum_{j=1}^{m}(2j-1)\left(\frac{\Delta_s\left(y_j\right)}{F\left(y_j\right)}-\frac{\Delta_i\left(y_{m+1-j}\right)}{S\left(y_{m+1-j}\right)}\right)=0, s=1,2,3, \tag{36}$$

where $\Delta_1\left(y_i\right)=\Delta_1\left(y_i \setminus a,b,\alpha\right), \Delta_2\left(y_i\right)=\Delta_2\left(y_i \setminus a,b,\alpha\right), \Delta_3\left(y_i\right)=\Delta_3\left(x_i \setminus a,b,\alpha\right)$ are defined in Equation 26 - Equation 28.

5.6. *Right-Tail Anderson-Darling (RTADE)*

The RTADE estimates of the [0,1] TNHIRP distribution parameters are obtained by minimizing the associated objective function.

$$R\left(a,b,\alpha\right)=\frac{m}{2}-2\sum_{j=1}^{m}\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}}{1-e^{1-(1+b)^a}}$$

$$-\frac{1}{m}\sum_{j=1}^{m}(2j-1)\log\left\{\frac{1-e^{1-\left(1+b\left(e^{-\frac{\alpha}{{y_j}^2}}\right)\right)^a}-e^{1-[1+b]^a}}{1-e^{1-[1+b]^a}}\right\}. \tag{37}$$

Alternatively, the estimates can be obtained by solving the corresponding non-linear equations.

$$-2\sum_{j=1}^{m}\Delta_s\left(y_j\right)+\frac{1}{m}\sum_{j=1}^{m}(2j-1)\frac{\Delta_S\left(y_{m+1-j}\right)}{S\left(y_{m+1-j}\right)}=0, s=1,2,3, \tag{38}$$

where $\Delta_1\left(y_i\right)=\Delta_1\left(y_i \setminus a,b,\alpha\right), \Delta_2\left(y_i\right)=\Delta_2\left(y_i \setminus a,b,\alpha\right), \Delta_3\left(y_i\right)=\Delta_3\left(x_i \setminus a,b,\alpha\right)$ are defined in Equation 26 - Equation 28.

5.7. *Percentile (PC) Method*

To estimate of the parameters of a distribution, the percentile (PC) or minimum quantile estimation (MQE) can be used. Because$d_i=\frac{i}{n+1}$ is the uniform estimator of $\left(y_{(j)} \mid a,b,\alpha\right)$, the PC estimates of [0,1] TNHIRP distribution parameters are the results of optimizing the objective function.

$$P\left(a,b,\alpha\right)=\sum_{i=1}^{n}\left(-2\alpha^{-2}\left(\ln\left\{1-\frac{1}{b}\left(\left(1-\ln\left\{1-u\left(1-e^{1-(1+b)^a}\right)\right\}\right)^{\frac{1}{a}}-1\right)\right\}\right)\right)^{1/2}. \tag{39}$$

5.8. *Maximum Likelihood Estimation (MLE)*

Suppose an independent random sample of size n that is $Y_1, Y_2, Y_3 \dots Y_n$ is selected from a, b, α. The Likelihood function is defined as:

$$L=\prod_{i=1}^{n}f\left(Y;\alpha,a,B\right), a,b,\alpha>0. \tag{40}$$

By substituting Equation 12 into the preceding expression, we obtain the following result:

$$L=\prod_{i=1}^{n}\frac{\frac{2\alpha}{\mathrm{y}^2}\left(1+b\left(e^{-\frac{\alpha}{{y_i}^2}}\right)\right)^{a-1}e^{\left(1-\left(1+b\left(e^{-\frac{\alpha}{{y_i}^2}}\right)\right)^a\right)}e^{-\frac{\alpha}{{y_i}^2}}}{1-e^{(1-(1+b)^a)}}, \tag{41}$$

the log-likelihood function for the complete case $\ell(\theta)$ is given by:

$$\ell(\theta) = n\ln(2\alpha) - 2\sum_{i=1}^{n}\ln(y_i) + (a-1)\sum_{i=1}^{n}\ln\left(1+be^{-\frac{\alpha}{y_i^2}}\right)$$
$$+\sum_{i=1}^{n}\left[1-\left(1+be^{-\frac{\alpha}{y_i^2}}\right)^{a}\right] - \alpha\sum_{i=1}^{n}\frac{1}{y_i^2} - n. \tag{42}$$

In order to get the estimates of the parameters, we differentiate the log-likelihood with respect to parameters a, b, c, α partially and set them equal to zero.

$$\frac{d\ell(\theta)}{d\alpha} = \frac{n}{\alpha} - \sum_{i=1}^{n}\frac{1}{y_i^2} + \sum_{i=1}^{n}\frac{be^{-\alpha/y_i^2}}{y_i^2}\,\frac{a\left(1+be^{-\alpha/y_i^2}\right)^{a}-(a-1)}{1+be^{-\alpha/y_i^2}}, \tag{43}$$

$$\frac{d\ell(\theta)}{db} = \sum_{i=1}^{n}\frac{e^{-\alpha/y_i^2}\left((a-1)-a\left(1+be^{-\alpha/y_i^2}\right)^{a}\right)}{1+be^{-\alpha/y_i^2}}, \tag{44}$$

$$\frac{d\ell(\theta)}{da} = \sum_{i=1}^{n}\ln\left(1+be^{-\frac{\alpha}{y_i^2}}\right)\left[1-\left(1+be^{-\frac{\alpha}{y_i^2}}\right)^{a}\right]. \tag{45}$$

The maximum likelihood estimations $\hat{a}, \hat{b}, \hat{\alpha}$ of $[0,1]$ Truncated Nadarajah-Haghighi Inverse Rayleigh Process are either written as the maximization of the Equation 42 or by simultaneously solving the following Equation 43 - Equation 45. Nevertheless, the MLEs do not have any closed-form analytical solutions of these equations. To compute the MLEs, therefore, a numerical approach is required, e.g. a Newton-Raphson-type algorithm. It is possible to apply this procedure by means of several software packages such as MATLAB2020a.

5.9. Modified SVM–GA Hybrid Estimation for Model (SVM–GA)

Input:

- Observed data $\{x_i\}_{i=1}^{n}$.
- Model parameters $\Theta = (x;\alpha,a,b)$.
- Parameter bounds $\Theta_{\min}, \Theta_{\max}$.
- Number of training samples N_S.
- Population size N_P, and maximum generations G_{max}.

Step 1: Define Negative Log-Likelihood (NLL)

- Define $\mathcal{L}(\Theta) = -\sum\limits_{i=1}^{n}\log h(x_i;\alpha,a,b)$, where $h(.)$ is the model PDF.

Step 2: Generate Initial Samples

- Generate N_S random samples $\Theta^{(j)} \in [\Theta_{\min}, \Theta_{\max}], j = 1, 2, \ldots, N_s$.
- Evaluate each sample $y^{(j)} = \mathcal{L}\left(\Theta^{(j)}\right)$ form training set $\mathcal{D} = \left\{\left(\Theta^{(j)}, y^{(j)}\right)\right\}$.

Step 3: Train Surrogate Model

- Fit a surrogate $\hat{\mathcal{L}}(\Theta)$ to approximate the true NLL surface using. Support Vector Regression (SVR) with a radial basis function (RBF) kernel $\hat{\mathcal{L}}(\Theta) \approx \mathcal{L}(\Theta)$.

Step 4: Global Search via Genetic Algorithm (GA)

1. Initialize population $\{\Theta_i\}_{i=1}^{N_p}$ within parameter bounds $g = 1$ to G_{max}.

2. Evaluate fitness using surrogate $f_i = \hat{\mathcal{L}}\left(\Theta_i\right)$.
3. Apply GA operators:
    - Selection (prefer individuals with lower f_i).
    - Crossover (combine two parents).
    - Mutation (introduce random perturbations).
4. Update population and record best solution Θ^*_{GA}.

Step 5: Local Refinement (MLE)

- Refine Θ^*_{GA} by minimizing the true NLL $\Theta^* = \arg\min_{\Theta} \mathcal{L}\left(\Theta\right)$.
- Using the Nelder-Mead simplex method. Obtain final estimates $\left(\hat{\alpha}, \hat{a}, \hat{b}\right) = \Theta^*$.

Step 6: Model Evaluation

- Compute $log-$likelihood $\log L = -\mathcal{L}\left(\hat{\Theta}\right)$.
- Calculate information criteria:
  $\mathrm{AIC} = -2\log L + 2k$
  $\mathrm{BIC} = -2\log L + k\log n$
  $\mathrm{CAIC} = -2\log L + k\left(\log n + 1\right)$
  $\mathrm{HQIC} = -2\log L + 2k\log\left(\log n\right)$

Step 7: Goodness-of-Fit and Visualization

1. Compute fitted PDF and CDF $\hat{f}\left(x\right) = f(x; \hat{a}, \hat{b}, \hat{\alpha})_{[0,1]TNHIRay}, \hat{F}\left(x\right) = \int\limits_0^x \hat{f}\left(t\right)dt$.
2. Compare empirical and fitted distributions using: KS, Anderson-Darling, and Cramér-von Mises tests. amér-von Mises tests.
3. Plot empirical vs. model PDF and CDF curves.

Output:

- Parameter estimates $\hat{\alpha}, \hat{a}, \hat{b}$.
- Minimum NLL value.
- Information criteria (AIC, BIC, CAIC, HQIC).
- Goodness-of-fit statistics.
- Diagnostic plots (PDF, CDF).

6. Simulations

In the simulation study, the performance of the estimation methods is evaluated according to the mean values of these three quantities:

- Absolute Bias: $|\mathrm{Bias}\tau| = \frac{1}{M}\sum\limits_{j=1}^{M} |\hat{\tau} - \tau|$,
- Mean Square Error (MSE): $MSE = \frac{1}{M}\sum\limits_{j=1}^{M} (\hat{\tau} - \tau)^2$,
- Mean Relative Error (MRE): $MRE = \frac{1}{M}\sum\limits_{j=1}^{M} \left|\hat{\tau} - \tau\right| / \tau$.

The observations are obtained with the [0, 1] TNHIRP model by applying the quantile function in Equation 12, in which [0,1] is the uniform random variable 6. Out of 5000 observations $n = 5000$, they are randomly sampled $n = 30, 50, 80, 120, 200$. The possible parameter settings are $a = 1.5, 3, 0.75$ and $b = 3, 0.5, 1.75$ and $\alpha = 0.4, 1.6, 3$. The parameters of [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process are estimated using these parameter combinations and sample sizes, and the performance of the estimators is measured using Absolute Bias, Mean Squared Error (MSE), and Mean Relative Error (MRE).

Practically, calculating a reasonable sample size involves a tradeoff between feasibility, cost and the desired level of precision. Although a sample of $n = 25$ can be adequate in some studies, it might be insufficient to obtain highly accurate and generalizable outcomes, especially when it comes to large population as the one taken into account in the present study. It is important to note though that the difference between $n = 25$ and $n = 30$ can often be small and the best option would be based on the particular circumstances and goals of the simulation study. The process of the selection of estimation values is a careful process that incorporates the comprehension of the problem, the available data and expert knowledge, the range of variables, the exploration of other possible scenarios, and the determination of the parameters values that reflect realistic conditions. Table 1 provide the results of the relevant simulations.

To make the simulation valid and effective, accuracy, precision, and recall are some of the important performance factors that were considered. The scope of the suggested distribution is positive in nature, and findings are consistent. MATLAB 2020a software environment was used in all the analyses. Table 1 shows the rank of every estimator in its respective row as superscripts. The Σ Ranks column is the cumulative rank of estimators for every sample size. In general, the findings suggest that the different estimation methods have similar performance in the various settings of the parameters.

7. Application

In this section the focus of analysis is based on the practical uses of data in the real world using [0,1] Truncated Nadarajah-Haghighi Inverse Rayleigh distribution (referred to as [0,1] TNHIRP) under non-homogeneous framework. The main objective would be to show the goodness of fit that is much better with the proposed distribution than with the available alternatives. In order to measure the performance of the [0, 1] TNHIRP model, one uses a number of established statistical criteria such as the negative log-likelihood (-LL), the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC), and the Hannan Quinn Information Criterion (HQIC). A thorough comparative study is then done to determine the relative performance of [0,1] TNHIRP distribution with the other competing models including Beta Rayleigh (BER), Kumaraswamy Rayleigh (KUR), Truncated Nadarajah Haghighi Rayleigh (TNHR), Exponential Generalized Rayleigh (EGR), Weibull Rayleigh (WER), Gompertz Rayleigh (GOR), Marshall Olkin Rayleigh (MOR), and Exponentiated Rayleigh (ER) distributions. The findings of such a comparison point to the strength and flexibility of the suggested [0,1] TNHIRP distribution to the modeling of various real data structures.

7.1. Data Set 1

The first dataset, previously analyzed by [18], comprises the survival times (in years) of patients who underwent chemotherapy treatment only, without any adjunct therapeutic intervention.

Table 2 - Table 4 distinctly present the statistical superiority of the proposed TNHIRP model in the estimation framework of the Support Vector Machine paired with Genetic Algorithm (SVM-GA) framework. The intelligent approach results in significantly smaller AIC, BIC and HQIC values, and a significantly large increase in the log-likelihood, which proves that the balance between the goodness-of-fit and model parsimony is better than in the case of the clever approach. By contrast, the traditional MLE method is plagued by increased information criteria, convergence to nonoptimal local minima in the complicated likelihood surface. Therefore, the SVM-GA-based estimation is not only more numerically stable and globally optimized, but also accounts for the nonlinear dependency structure of the patients under treatment with chemotherapy. As a result, intelligent hybrid estimation is

Table 1. Simulated results of the [0,1] TNHIRP for $\delta = (a = 1.5, b = 3, \alpha = 0.4)^T$

n	Est.	Est. Par.	Estimation Methods								
			WLSE	OLSE	MLE	MPSE	CVME	ADE	RADE	PCE	SVM-GA
30	BIAS	$\widehat{a}$	0.60748^{6}	0.51649^{5}	1.28733^{9}	0.63243^{7}	0.63487^{8}	0.51166^{4}	0.43017^{2}	0.50089^{3}	0.33015^{1}
		$\widehat{b}$	0.66783^{5}	0.63387^{4}	1.00281^{9}	0.73836^{8}	0.69502^{6}	0.59294^{3}	0.70504^{7}	0.59192^{2}	0.37192^{1}
		$\widehat{\alpha}$	0.02071^{4}	0.01078^{2}	0.34690^{8}	0.02506^{6}	0.3481^{7}	0.01421^{3}	0.02216^{5}	0.00608^{1}	0.35620^{9}
	MSE	$\widehat{a}$	1.16689^{4}	1.04026^{2}	33.89286^{9}	7.73562^{8}	2.48023^{6}	1.17852^{5}	1.08465^{3}	3.00963^{7}	1.02026^{1}
		$\widehat{b}$	2.16466^{3}	2.85819^{4}	19.81177^{9}	3.84077^{5}	7.02539^{7}	1.57507^{2}	11.39344^{8}	6.06509^{6}	1.47506^{1}
		$\widehat{\alpha}$	1.21337^{2}	1.21855^{3}	2.46558^{8}	1.41044^{6}	1.32752^{4}	1.20476^{1}	1.34202^{5}	1.41264^{7}	2.57558^{9}
	MRE	$\widehat{a}$	0.36165^{6}	0.31766^{5}	0.82155^{9}	0.38496^{7}	0.38658^{8}	0.31444^{4}	0.25011^{2}	0.30726^{3}	0.14011^{1}
		$\widehat{b}$	0.12261^{5}	0.11129^{4}	0.23427^{9}	0.15612^{8}	0.13167^{6}	0.18765^{3}	0.13401^{7}	0.18731^{2}	0.17621^{1}
		$\widehat{\alpha}$	0.20176^{5}	0.16694^{3}	0.50551^{9}	0.20265^{7}	0.22702^{8}	0.17552^{4}	0.30539^{5}	0.15519^{2}	0.14419^{1}
	Sigma Ranks		23^{5}	15^{3}	62^{9}	45^{8}	43^{7}	12^{2}	28^{6}	16^{4}	11^{1}
50	BIAS	$\widehat{a}$	0.53336^{7}	0.48359^{5}	0.68037^{8}	0.45193^{3}	0.52861^{6}	0.45438^{4}	0.35070^{1}	0.41749^{2}	0.79147^{9}
		$\widehat{b}$	0.51919^{4}	0.53728^{6}	0.77578^{9}	0.58753^{7}	0.52194^{5}	0.50664^{3}	0.45684^{2}	0.42915^{1}	0.76578^{8}
		$\widehat{\alpha}$	0.09188^{6}	0.08741^{4}	0.12815^{8}	0.08119^{3}	0.09582^{7}	0.08748^{5}	0.07642^{2}	0.07013^{1}	0.08472^{7}
	MSE	$\widehat{a}$	1.14368^{4}	0.83797^{3}	21.28742^{9}	3.48602^{8}	1.22664^{6}	3.17490^{7}	0.48326^{2}	0.41355^{1}	1.01015^{5}
		$\widehat{b}$	1.36913^{4}	1.95062^{5}	16.57927^{9}	2.57858^{8}	2.11165^{6}	2.42732^{7}	1.05340^{2}	0.41893^{1}	1.36405^{3}
		$\widehat{\alpha}$	0.05343^{4}	0.04452^{3}	1.01361^{8}	0.13836^{7}	0.06246^{5}	0.10715^{6}	0.02678^{2}	0.01295^{1}	1.47447^{9}
	MRE	$\widehat{a}$	0.35558^{8}	0.3223^{6}	0.45358^{9}	0.30128^{4}	0.35240^{7}	0.30292^{5}	0.23380^{2}	0.27832^{3}	0.03011^{1}
		$\widehat{b}$	0.16206^{4}	0.16809^{6}	0.21093^{9}	0.18484^{7}	0.16398^{5}	0.15788^{3}	0.14128^{2}	0.13205^{1}	0.16510^{8}
		$\widehat{\alpha}$	0.21870^{7}	0.20753^{5}	0.31026^{9}	0.20187^{4}	0.22579^{8}	0.2077^{6}	0.18005^{2}	0.16433^{1}	0.13318^{3}
	Sigma Ranks		45^{6}	40^{4}	72^{9}	47^{7}	51^{8}	42^{5}	16^{3}	11^{2}	10^{1}
80	BIAS	$\widehat{a}$	0.38206^{7}	0.37875^{6}	0.36795^{5}	0.30086^{2}	0.41530^{8}	0.31705^{4}	0.25676^{1}	0.30052^{3}	0.68147^{9}
		$\widehat{b}$	0.40383^{4}	0.41316^{5}	0.48555^{8}	0.46220^{7}	0.41766^{6}	0.38039^{3}	0.36610^{2}	0.33005^{1}	0.65478^{9}
		$\widehat{\alpha}$	0.06669^{5}	0.06862^{6}	0.07282^{7}	0.05606^{2}	0.07536^{9}	0.06308^{4}	0.05802^{3}	0.05433^{1}	0.07362^{8}
	MSE	$\widehat{a}$	0.36813^{6}	0.46216^{8}	0.41189^{7}	0.20506^{4}	0.70117^{9}	0.23129^{5}	0.17191^{3}	0.16480^{2}	0.01016^{1}
		$\widehat{b}$	0.47325^{5}	0.67486^{8}	0.50038^{7}	0.46312^{4}	0.83289^{9}	0.47787^{6}	0.40657^{3}	0.22017^{1}	0.25405^{2}
		$\widehat{\alpha}$	0.01229^{6}	0.01870^{7}	0.01178^{5}	0.00600^{2}	0.03015^{8}	0.01010^{4}	0.00861^{3}	0.00550^{1}	0.36336^{9}
	MRE	$\widehat{a}$	0.25104^{8}	0.24883^{7}	0.24164^{6}	0.20021^{3}	0.28420^{9}	0.20770^{5}	0.16750^{2}	0.20601^{4}	0.02010^{1}
		$\widehat{b}$	0.12728^{4}	0.13039^{5}	0.15452^{9}	0.14673^{8}	0.13189^{6}	0.12046^{3}	0.11470^{2}	0.10268^{1}	0.15410^{7}
		$\widehat{\alpha}$	0.15847^{6}	0.16330^{7}	0.17381^{8}	0.13016^{3}	0.18014^{9}	0.15010^{5}	0.13654^{4}	0.12757^{2}	0.12217^{1}
	Sigma Ranks		47^{6}	55^{7}	57^{8}	30^{4}	68^{9}	35^{5}	19^{3}	13^{2}	12^{1}
120	BIAS	$\widehat{a}$	0.28209^{6}	0.30748^{7}	0.24654^{5}	0.21309^{2}	0.31285^{8}	0.23876^{4}	0.20118^{1}	0.23053^{3}	0.57046^{9}
		$\widehat{b}$	0.33509^{4}	0.35489^{6}	0.41666^{8}	0.4461^{7}	0.35263^{5}	0.33291^{3}	0.30184^{2}	0.28785^{1}	0.54367^{9}
		$\widehat{\alpha}$	0.04188^{5}	0.04479^{7}	0.04393^{6}	0.03353^{1}	0.05802^{8}	0.04017^{4}	0.03583^{3}	0.03412^{2}	0.06251^{9}
	MSE	$\widehat{a}$	0.18578^{7}	0.20452^{8}	0.13703^{6}	0.10168^{4}	0.23508^{9}	0.12022^{5}	0.08339^{2}	0.08672^{3}	0.01105^{1}
		$\widehat{b}$	0.28387^{4}	0.32179^{6}	0.35582^{9}	0.34293^{7}	0.34789^{8}	0.30092^{5}	0.21029^{3}	0.16536^{2}	0.14304^{1}
		$\widehat{\alpha}$	0.00600^{8}	0.00586^{7}	0.00432^{6}	0.00234^{2}	0.00802^{9}	0.00400^{5}	0.00311^{3}	0.00217^{1}	0.00330^{4}
	MRE	$\widehat{a}$	0.18539^{7}	0.20472^{8}	0.16169^{6}	0.13939^{3}	0.20590^{9}	0.15651^{5}	0.12479^{2}	0.15035^{4}	0.01001^{1}
		$\widehat{b}$	0.10436^{5}	0.11096^{7}	0.13155^{9}	0.12720^{8}	0.11021^{6}	0.10364^{4}	0.10261^{3}	0.08862^{2}	0.04310^{1}
		$\widehat{\alpha}$	0.12120^{6}	0.12847^{8}	0.12633^{7}	0.10031^{2}	0.13655^{9}	0.11442^{5}	0.10608^{4}	0.10180^{3}	0.01106^{1}
	Sigma Ranks		46^{6}	58^{8}	56^{7}	31^{4}	65^{9}	34^{5}	18^{3}	16^{2}	14^{1}
200	BIAS	$\widehat{a}$	0.21013^{7}	0.22815^{8}	0.17064^{4}	0.15822^{3}	0.23393^{9}	0.18027^{6}	0.14099^{2}	0.17008^{5}	0.13088^{1}
		$\widehat{b}$	0.26579^{4}	0.30669^{7}	0.36010^{9}	0.3437^{8}	0.30115^{6}	0.27055^{5}	0.25543^{3}	0.23188^{1}	0.23256^{2}
		$\widehat{\alpha}$	0.04050^{5}	0.04257^{7}	0.04057^{6}	0.03271^{1}	0.04373^{8}	0.03849^{4}	0.03606^{3}	0.03384^{2}	0.05140^{9}
	MSE	$\widehat{a}$	0.08396^{7}	0.10047^{8}	0.05561^{5}	0.04283^{3}	0.11201^{9}	0.06061^{6}	0.03836^{2}	0.04382^{4}	0.00105^{1}
		$\widehat{b}$	0.16062^{3}	0.21005^{7}	0.26892^{9}	0.24090^{8}	0.20288^{6}	0.17054^{5}	0.16180^{4}	0.10656^{2}	0.03203^{1}
		$\widehat{\alpha}$	0.00204^{6}	0.00261^{8}	0.00202^{5}	0.00101^{1}	0.00320^{9}	0.00184^{4}	0.00160^{3}	0.00107^{2}	0.00220^{7}
	MRE	$\widehat{a}$	0.13582^{7}	0.14843^{8}	0.11032^{4}	0.10181^{3}	0.15228^{9}	0.11652^{6}	0.10022^{2}	0.10051^{5}	0.01102^{1}
		$\widehat{b}$	0.08126^{4}	0.10150^{7}	0.11270^{9}	0.10726^{8}	0.10064^{6}	0.08245^{5}	0.07781^{3}	0.07086^{2}	0.03210^{1}
		$\widehat{\alpha}$	0.10038^{6}	0.10806^{8}	0.10306^{7}	0.07342^{2}	0.10106^{9}	0.08787^{5}	0.08179^{4}	0.07875^{3}	0.00105^{1}
	Sigma Ranks		42^{5}	60^{7}	51^{6}	30^{3}	63^{8}	39^{4}	19^{2}	20^{3}	17^{1}

proposed as a strong alternative to classical MLE that is scientifically superior in its ability to model any truncated lifetime process, including the TNHIRP.

Table 2. Evaluating the Goodness-of-Fit of the TNHIRP Model for Bladder Cancer Data Using Support Vector Machine with Genetic Algorithm

Model	MLEs	- l	AIC	CAIC	BIC	HQIC
TNHIRP	$\hat{a} = 1.082$ $\hat{b} = 0.449$ $\hat{\lambda} = 0.025$	26.035	58.070	64.727	61.727	59.085
TNHR [0,1]	$\hat{a} = 0.962$ $\hat{b} = 0.149$ $\hat{\lambda} = 0.508$	34.997	63.995	57.338	60.338	62.980
BER	$\hat{a} = 0.973$ $\hat{b} = 2.011$	52.900	109.80	115.36	113.36	111.12
KUR	$\hat{a} = 0.985$ $\hat{b} = 1.112$ $\hat{\lambda} = 0.327$	14.401	36.803	37.778	44.117	39.543
EGR	$\hat{a} = 0.689$ $\hat{b} = 0.052$ $\hat{\lambda} = 0.011$	58.782	121.56	127.22	125.22	122.93
WER	$\hat{a} = 2.264$ $\hat{b} = 0.477$ $\hat{\lambda} = 0.160$	58.051	122.10	130.58	127.58	124.15
GOR	$\hat{a} = 1.562$ $\hat{b} = 0.004$ $\hat{\lambda} = 0.001$	47.197	100.39	108.88	105.88	102.45
MOR	$\hat{a} = 0.473$ $\hat{b} = 0.618$ $\hat{\lambda} = 0.600$	58.436	122.436	131.35	128.35	124.92
R	$\hat{\lambda} = 0.391$	44.880	91.760	94.588	93.588	92.445

Table 3. The K-S value with its corresponding p-value and W value of D1

Model	w	A	K-S	p-value
TNHIRP	0.0308	0.2012	0.0070	0.6418
[0,1] TNHR	0.0319	0.2112	0.0080	0.6206
BER	0.1115	0.6884	0.1224	0.3550
KUR	0.0785	0.5836	0.1017	0.5678
EGR	0.1122	0.8037	0.1228	0.3510
WER	0.0701	0.5325	0.1083	0.6038
GOR	0.1087	0.7207	0.2700	0.0024
MOR	0.0703	0.5526	0.1350	0.2546
R	0.1176	0.8267	0.3220	0.0006

7.2. Data Set 2

The second dataset pertains to the crude mortality rate (CMR) among individuals who inject drugs and was previously analyzed by [19].

The statistical and computational benefits of the Support Vector Machine paired with Genetic Algorithm to estimate the parameters of the Truncated Nadarajah Haghighi Inverse Rayleigh Process (TNHIRP) model are highlighted by the comparative results in Table 5 - Table 7. With the intelligent scheme, the model suggested

Table 4. Evaluating the Goodness-of-Fit of the TNHIRP Model for Bladder Cancer Data Using Maximum likelihood estimates

Model	MLEs	- l	AIC	CAIC	BIC	HQIC
TNHIRP	$\hat{a} = 0.470$ $\hat{b} = 1.002$ $\hat{\lambda} = 0.055$	46.389	98.779	107.26	104.26	100.83
TNHR [0,1]	$\hat{a} = 1.468$ $\hat{b} = 0.943$ $\hat{\lambda} = 0.015$	57.44	120.88	121.46	126.30	122.90
BER	$\hat{a} = 0.973$ $\hat{b} = 2.011$ $\hat{\lambda} = 0.011$	58.697	123.39	123.98	128.81	125.41
KUR	$\hat{a} = 1.237$ $\hat{b} = 0.173$ $\hat{\lambda} = 0.133$	58.026	122.05	122.63	127.47	124.07
EGR	$\hat{a} = 1.200$ $\hat{b} = 0.872$ $\hat{\lambda} = 0.010$	58.7	123.4	123.98	128.82	125.42
WER	$\hat{a} = 1.000$ $\hat{b} = 0.086$ $\hat{\lambda} = 0.002$	58.123	122.24	122.83	127.66	124.26
GOR	$\hat{a} = 1.132$ $\hat{b} = 0.117$ $\hat{\lambda} = 0.022$	72.257	150.51	151.09	155.93	152.53
MOR	$\hat{a} = 0.983$ $\hat{b} = 0.022$	62.762	129.52	129.8	133.13	158.87
R	$\hat{\lambda} = 0.022$	77.916	157.83	157.92	159.63	158.50

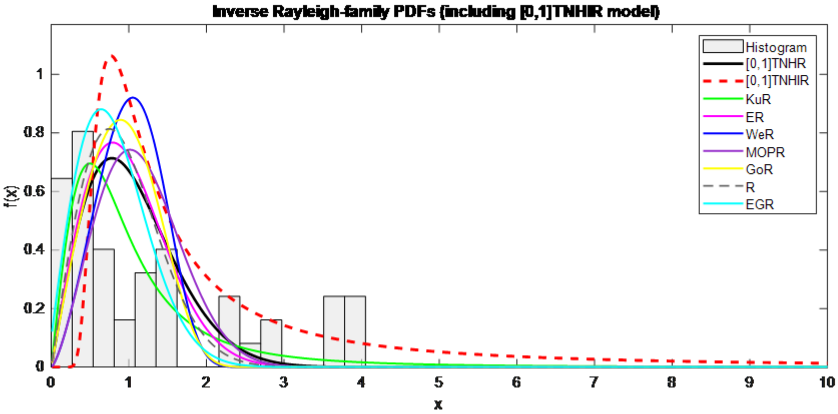

Figure 2. Theoretical and empirical PDF of TNHIRP

is associated with significantly smaller AIC, BIC, and HQIC values, and a significantly greater log-likelihood. The fact that this improvement exceeds 50 percent in all goodness-of-fit measures is an affirmation that the algorithm has a better balance of exploration and exploitation, and also that it can effectively address the nonlinearities inherent in truncated lifetime data. Conversely, the classical MLE approach has greater information criteria and a less positive

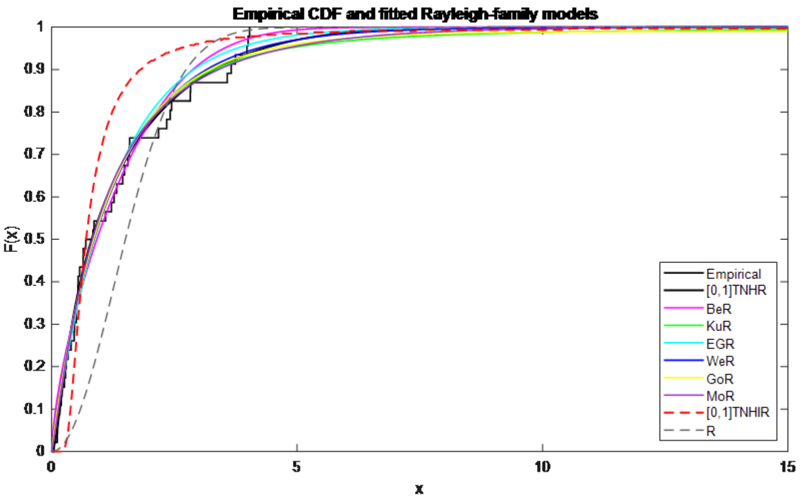

Figure 3. Theoretical and empirical CDF of TNHIRP

Table 5. Evaluating the Goodness-of-Fit of the TNHIRP Model for bank customers Data Using Support Vector Machine with Genetic Algorithm

Model	MLEs	- l	AIC	CAIC	BIC	HQIC
TNHIRP	$\hat{a} = 1.077$ $\hat{b} = 0.471$ $\hat{\lambda} = 0.027$	27.023	60.047	66.704	63.704	61.061
TNHR [0,1]	$\hat{a} = 0.755$ $\hat{b} = 3.880$ $\hat{\lambda} = 0.035$	35.114	76.228	78.646	75.646	71.768
BER	$\hat{a} = 0.723$ $\hat{b} = 0.073$	120.04	244.08	250.40	248.40	245.78
KUR	$\hat{a} = 0.998$ $\hat{b} = 1.054$ $\hat{\lambda} = 0.334$	96.782	201.56	214.263	210.263	204.997
EGR	$\hat{a} = 0.100$ $\hat{b} = 0.140$ $\hat{\lambda} = 0.015$	117.48	238.96	245.24	243.24	240.64
WER	$\hat{a} = 0.555$ $\hat{b} = 0.118$ $\hat{\lambda} = 0.486$	114.73	235.46	244.64	241.64	237.87
GOR	$\hat{a} = 1.716$ $\hat{b} = 0.012$ $\hat{\lambda} = 0.141$	107.33	220.66	230.13	227.13	223.21
MOR	$\hat{a} = 0.869$ $\hat{b} = 0.813$ $\hat{\lambda} = 1.812$	118.98	243.97	253.44	250.44	246.52
R	$\hat{\lambda} = 0.214$	36.224	74.449	77.608	76.608	75.300

Table 6. The K-S statistic, its corresponding p-value, and the W statistic under D2 are reported as follows

Model	w	A	K-S	p-value
TNHIRP	0.0345	0.1864	0.0572	0.9592
[0,1] TNHR	0.0434	0.2842	0.0636	0.9371
BER	0.1010	0.7164	0.1083	0.3010
KUR	0.1600	1.0942	0.1348	0.1141
EGR	0.1154	0.7459	0.1124	0.2643
WER	0.0810	0.5244	0.0946	0.5888
GOR	0.0578	0.3759	0.0964	0.5554
MOR	0.0437	0.2860	0.0630	0.9206
R	0.1122	0.7250	0.1611	0.0413

Table 7. The statistical criteria and the estimated parameter values of the [0,1] Truncated Nadarajah–Haghighi Inverse Rayleigh (TNHIR) Process, along with those of the competing distributions, are presented for Dataset 1. All parameter estimates were obtained using the maximum likelihood estimation (MLE) method

Model	MLEs	- l	AIC	CAIC	BIC	HQIC
TNHIRP	$\hat{a} = 4.658$ $\hat{b} = 0.002$ $\hat{\lambda} = 0.001$	68.705	143.41	152.93	149.93	145.98
TNHR [0,1]	$\hat{a} = 0.866$ $\hat{b} = 4.991$ $\hat{\lambda} = 0.046$	119.03	120.88	121.46	126.30	122.90
BER	$\hat{a} = 0.734$ $\hat{b} = 3.128$ $\hat{\lambda} = 0.022$	121.35	248.70	249.10	255.23	251.28
KUR	$\hat{a} = 0.522$ $\hat{b} = 0.153$ $\hat{\lambda} = 0.549$	123.60	253.20	253.59	259.72	255.77
EGR	$\hat{a} = 2.807$ $\hat{b} = 0.730$ $\hat{\lambda} = 0.026$	121.50	249.00	249.39	255.52	251.57
WER	$\hat{a} = 0.798$ $\hat{b} = 0.699$ $\hat{\lambda} = 0.074$	120.42	246.85	247.24	253.37	249.42
GOR	$\hat{a} = 1.517$ $\hat{b} = 0.284$ $\hat{\lambda} = 0.082$	120.83	247.66	248.06	254.19	250.24
MOR	$\hat{a} = 0.274$ $\hat{b} = 0.046$	119.04	242.09	242.28	246.44	243.81
R	$\hat{\lambda} = 0.093$	123.65	249.30	249.36	251.47	250.16

log-likelihood, which is its vulnerability to local optima in complicated likelihood surfaces. The intelligent SVM-GA approach, therefore, provides a more sound, precise, and worldwide optimal estimation approach showing its potential to be a new generation alternative to conventional estimation approaches in reliable and lifetime modelling.

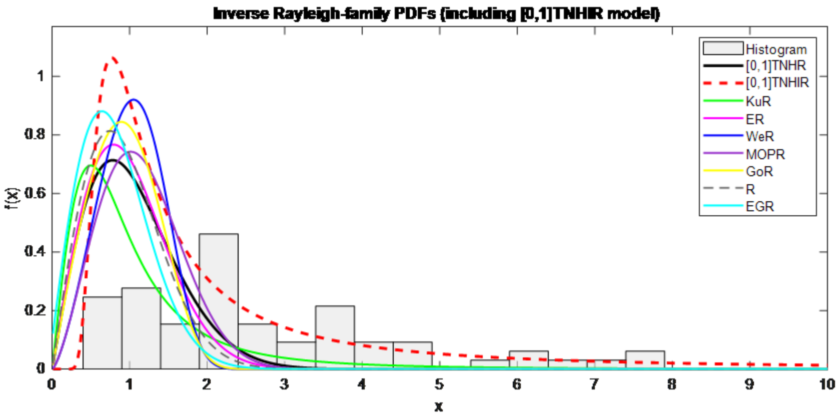

Figure 4. Theoretical and empirical PDF of TNHIRP

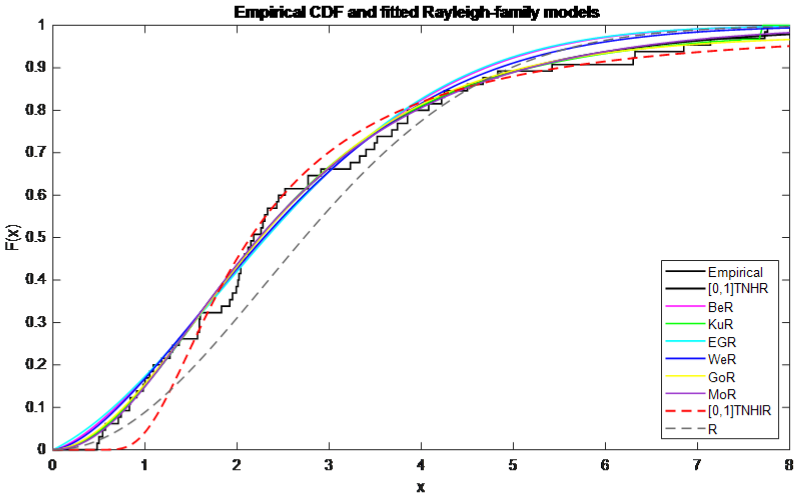

Figure 5. Theoretical and empirical CDF of TNHIRP

7.3. *Discussion of Results*

In this work, the [0,1] Truncated Nadarajah -Haghighi Inverse Rayleigh Process (TNHIRP) with the nine-point estimation techniques are investigated. Some of the basic statistical characteristics of the suggested model are also obtained. A full simulation experiment is carried out to determine the effectiveness and the strength of the estimators. The summarized results in Table 1 show that the bias, mean squared error (MSE), and mean relative error (MRE) of all estimators decreases steadily as the sample size increases, tending to equal zero in larger samples. It proves the consistency and asymptotic efficiency of the estimation procedures suggested. Table 2 and Table 5 shows the descriptive statistics of the two real data under analysis. The result of applying the proposed TNHIRP model to these empirical data sets is that it exhibits better flexibility and goodness of fit than competing distributions based on various selection measures such as AIC, CAIC, BIC, and HQIC (Table 4 and Table 7). In addition, goodness-of-fit tests based on the Anderson-Darling, Cramer-von Mises, and Kolmogorov-Smirnov tests, along with their p-values, are also presented in Table 3 and Table 6. These tests indicate that the proposed distribution has a superior fitting ability compared to the existing ones. Figure 2 and Figure 4 show that both the datasets have positive skew and that the TNHIRP model fits well among the overlaid density plot. On the same note, the empirical and estimated cumulative distribution function (CDF) plots in Figure 3 and Figure 5 further indicate that the best cumulative distribution model that fits both the data sets in the best way possible is the [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process.

8. Conclusions and Future Work

This paper suggested the [0,1] Truncated Nadarajah Haghighi Inverse Rayleigh Process (TNHIRP) as a new and very versatile lifetime distribution, which could be used to analyze truncated and bounded data in a wide range of fields. Nine estimation methods were studied, including classical methods, like Maximum Likelihood Estimation, and smart algorithms (Support Vector Machine with Genetic Algorithm (SVM-GA)). Simulation experiments in MATLAB showed that all the estimators had a uniform behavior with parameter settings, but the SVM-GA approach had better convergence, stability and accuracy to represent the complicated nonlinear form of the likelihood surface. It was verified that the proposed TNHIRP model was more effective than rival distributions,, including [0,1] TNHR, BER, KUR, WER, GOR and MOR in terms of log-likelihood and information criterion (AIC, BIC, CAIC, HQIC). In addition to its statistical performance, the TNHIRP model has useful implications in financial risk management, engineering reliability, and healthcare analytics, where it is essential to model limited risks or survival times. Specifically, its description using normalized incomplete moments and conditional value-at-risk makes it better to interpret and more relevant practically. This work identifies limitations in the sensitivity of computational complexity and estimation sensitivity despite the strengths. Future studies are thus advised to be based on creating full Bayesian hierarchical extensions, covariate structures, and deeper neural architectures to increase predictive generalization. Other possible future research directions are studied regarding the other parameter estimation techniques and the use of the TNHIRP framework for larger data sets in medicine, finance, and industrial quality control, where it is important to have precise modeling of truncated processes.

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Ethical Approval

All the authors demonstrate that they have adhered to the accepted ethical standards of a genuine research study.

Competing Interests

No conflict of interest is declared by authors.

Author contributions

All authors have sufficiently contributed to the study and agreed with the results and conclusions.

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Availability of Data and Materials

The data used to support the findings of this study are included in the article.

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