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Estimation of the Three-Parameter Inverse Rayleigh Distribution Parameters for Guinea Pig Survival Data

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Abstract

The Generalized Transmuted Inverse Rayleigh Function (GTIR) distribution is an extension of the inverse Rayleigh distribution, which is commonly used to model reliability and survival data. By incorporating an additional shape parameter ($\hat{\alpha}$) and a transmutation parameter ($\hat{\lambda}$) alongside the scale parameter ($\hat{\sigma}$), this distribution offers greater flexibility in handling skewed data or data with a non-monotonic hazard function. The parameters of the GTIR distribution are estimated using the Maximum Likelihood Estimation (MLE) method; however, they must be solved implicitly through numerical procedures. In this study, the GTIR distribution was employed to analyze the survival data of guinea pigs infected with tuberculosis. The primary objective of this analysis was to estimate the distribution parameters and to provide an overview of the survival pattern. The application of the GTIR distribution to the survival and hazard functions demonstrated that guinea pigs experience a sharp decline in survival probability at the onset of tuberculosis infection, followed by a gradual decrease in the risk of mortality over time. The hazard rate pattern, which initially increases and then decreases, indicates that the most critical period occurs immediately after infection. Parameter estimation of the GTIR distribution using the MLE approach yielded estimates of $\hat{\lambda}$ = 0.781, $\hat{\alpha}$ = 10.135, and $\hat{\sigma}$ = 12.319, confirming that this model effectively captures the complex survival pattern with high accuracy.

Keywords: GTIR, survival analysis, MLE, tuberculosis infection

1. Introduction

Scientifically, the guinea pig has the Latin name *Cavia porcellus* and belongs to the Caviidae family, which is also known as the guinea pig family (Gotch, 1979). This animal originates from the mountainous regions of South America. Extensive breeding has resulted in various color variations and fur characteristics. The most common breeds include the American, which has short and smooth fur, and the Teddy, known for its diverse fur colors (Riggs, 2009). Guinea pigs are docile, easy to care for, and their immune system shares many similarities with humans, although the availability of specific reagents is still limited. The main advantage of this animal is its ability to mimic the pathology of viral diseases in humans, both grossly and histologically. They are often used for studies of negative-strand DNA and RNA viruses because infections in ferrets exhibit clinical symptoms and disease profiles similar to those in humans (Baxter & Griffin, 2016). This makes it an effective model for testing potential therapies and understanding the factors that influence survival in an infection.

Tuberculosis (TB) is a directly contagious disease caused by an infection of the *Mycobacterium tuberculosis* bacteria. TB is a disease that is easily transmitted through the air from the source of transmission, which is a patient with positive pulmonary TB who, when coughing or sneezing, spreads germs into the air in the form of sputum droplets. One cough can produce about 3,000 sputum droplets. Pulmonary TB is the most commonly encountered form, accounting for about 80% of all cases (Tan, 2016). The public generally only knows that TB attacks the lungs, but TB can also affect other organs besides the lungs, which is called extrapulmonary TB. Extrapulmonary TB occurs when TB bacteria spread to other parts of the body through the bloodstream (Osamor, 2014). About 75% of TB patients are in the most economically productive age group (15-50 years) (Sandhu, 2011).

The Rayleigh distribution is a special case of the Weibull distribution that has been widely used for modeling lifetime data in various fields such as survival analysis (Badmus *et al*., 2017). Voda (1972) pioneered the one-parameter Inverse Rayleigh (IR) distribution. The Inverse Rayleigh distribution is one of the comprehensive and

relevant lifetime models, with applications in reliability and survival data. Many studies have been conducted on the Inverse Rayleigh distribution in the literature. One of the developments of this distribution is the Generalized Rayleigh distribution. The Generalized Rayleigh distribution is a generalization of the Rayleigh distribution obtained by raising the Rayleigh distribution to a new parameter. The Transmuted Generalized Rayleigh distribution is an extension of the Generalized Rayleigh distribution formed using the Quadratic Rank Transmutation Maps (QRTM) method (Andaryani, 2015). QRTM is used to create a new distribution that is more flexible than the base distribution by adding parameters. The parameters added in QRTM are called transmuted parameters (Nurrohmah *et al.*, 2016). These parameters influence how the base distribution is altered or transformed into a new distribution.

This research is motivated by the importance of a deep understanding of survival patterns in guinea pigs infected with virulent Tubercle bacilli, considering that these animals are effective subjects in the study of tuberculosis, which resembles conditions in humans. The dataset used contains information on the survival times of 72 guinea pigs after infection, which serves as a crucial basis for accurate statistical modeling. The authors are interested in applying the three-parameter Rayleigh distribution, specifically the Generalized Transmuted Inverse Rayleigh (GTIR) model, because this distribution offers greater flexibility in describing the complex variations in lifespan within survival data. By estimating the parameters of this distribution, the study aims to determine the parameter estimates of the Generalized Transmuted Inverse Rayleigh (GTIR) distribution and provide insights into survival patterns that can support the further development of understanding in the field of health.

2. Literature Review

2.1 Guinea Pig

The guinea pig (*Cavia porcellus*) is a rodent belonging to the Caviidae family, originating from the mountainous regions of South America, and has been domesticated for approximately 3,000 years. In the wild, guinea pigs live in groups, which is why they are more comfortable when kept with other individuals of the same species. Guinea pigs have a broad body, short legs, a flat nose, laterally positioned eyes, and hairless ears. The anatomical characteristics that distinguish members of the Caviidae family include having four toes on the forelimbs and three toes on the hind limbs, with an adult guinea pig's body weight ranging from 700 to 1,200 grams. The average lifespan of a pet guinea pig is 5–7 years (Riggs, 2009).

Furthermore, guinea pigs possess an immune system that is quite similar to humans and exhibit pathological responses that resemble human disease symptoms, both grossly and histologically (Baxter & Griffin, 2016). In addition to being docile and easy to handle, these animals are also highly susceptible to various infections, particularly respiratory infections.

2.2 Tuberculosis

Tuberculosis (TB) is a chronic infectious disease caused by bacteria belonging to the *Mycobacterium tuberculosis* complex, specifically *Mycobacterium tuberculosis*, *Mycobacterium bovis*, and *Mycobacterium africanum*. In developing countries, children are particularly susceptible to *M. bovis* infection through the consumption of unpasteurized milk (Martin & Oxman, 1988). This disease primarily affects the lungs, but it can also disseminate to other organs, such as the lymph nodes (Bowling, 2015). The discovery by Robert Koch in 1882 provided definitive evidence that TB is an infectious disease caused by bacteria, building upon Villenim's earlier demonstration that TB could be transmitted from one individual to another.

Since the time of Robert Koch, guinea pigs have been widely employed as biological models for *Mycobacterium tuberculosis* infection due to their high susceptibility, even to minimal exposure to the pathogen. Today, guinea pigs remain indispensable for investigating TB pathology and serve as a primary preclinical model for evaluating next-generation TB vaccines. Two main modelling approaches are commonly utilized: the long-term disease model, which assesses disease progression following vaccination; and the short-term mycobacterial load model, which measures a vaccine's efficacy in reducing bacterial burden after aerosol challenge with a virulent *M. tuberculosis* strain (Padilla-Carlin, McMurray, & Hickey, 2008). The pronounced sensitivity of guinea pigs to TB infection, combined with the similarity of their immune and histopathological responses to humans, underscores their relevance as a robust preclinical tool in the development of TB control strategies.

2.3 Generalized Transmuted Inverse Rayleigh (GTIR) Distribution

The inverse Rayleigh distribution is a continuous probability distribution that is widely utilized in reliability and survival data analysis due to its suitability for modeling the failure times of systems. This distribution has been extended to the Generalized Inverse Rayleigh (GIR) distribution by incorporating additional parameters, and further

enhanced through the introduction of a transmutation parameter using the Quadratic Rank Transmutation Map (QRTM) technique (Jan *et al.*, 2018). However, the GIR and its transmuted variants still present certain limitations when handling complex datasets, particularly those characterized by high skewness or non-monotonic hazard functions (Shala & Merovci, 2024).

To overcome these limitations, the Generalized Transmuted Inverse Rayleigh (GTIR) distribution has been proposed. This distribution introduces two additional parameters namely a shape parameter (α) and a transmutation parameter (λ) alongside the existing scale parameter (σ). The inclusion of these three parameters enhances the flexibility of the GTIR distribution, enabling it to better accommodate highly skewed data and to adapt its probability density function more effectively to varying data characteristics (Shala & Merovci, 2024).

2.4 Probability Density Function (PDF)

A Probability Density Function (PDF) is a function used to describe the probability distribution of a continuous random variable. The conditions of a probability density function are as follows:

Given: The Cumulative Distribution Function (CDF) is defined as follows:

$$F(x;\lambda,\alpha,\sigma) = (1+\lambda)e^{-\alpha(\frac{\sigma}{x})^2} - \lambda e^{-2\alpha(\frac{\sigma}{x})^2}$$

Thus, we obtain:

$$\begin{aligned}
\frac{d}{dx}\left((1+\lambda)e^{-\alpha\left(\frac{\sigma}{x}\right)^2}\right) &= (1+\lambda)e^{-\alpha\left(\frac{\sigma}{x}\right)^2}\cdot\frac{d}{dx}\left(-\alpha\left(\frac{\sigma}{x}\right)^2\right)\cdot\frac{d}{dx}(\sigma x^{-1}) \\
&= (1+\lambda)e^{-\alpha\left(\frac{\sigma}{x}\right)^2}\cdot -\alpha\cdot 2\left(\frac{\sigma}{x}\right)\cdot -\frac{\sigma}{x^2} \\
&= (1+\lambda)e^{-\alpha\left(\frac{\sigma}{x}\right)^2}\cdot\frac{2\alpha\sigma^2}{x^3} \\
&= \frac{2\alpha(1+\lambda)\sigma^2}{x^3}e^{-\alpha\left(\frac{\sigma}{x}\right)^2} \\
\frac{d}{dx}\left(-\lambda e^{-2\alpha\left(\frac{\sigma}{x}\right)^2}\right) &= -\lambda e^{-2\alpha\left(\frac{\sigma}{x}\right)^2}\cdot\frac{d}{dx}\left(-2\alpha\left(\frac{\sigma}{x}\right)^2\right)\cdot\frac{d}{dx}(\sigma x^{-1}) \\
&= -\lambda e^{-2\alpha\left(\frac{\sigma}{x}\right)^2}\cdot -2\alpha\cdot 2\left(\frac{\sigma}{x}\right)\cdot -\frac{\sigma}{x^2} \\
&= -\lambda e^{-2\alpha\left(\frac{\sigma}{x}\right)^2}\cdot -\frac{4\alpha\sigma}{x}\cdot -\frac{\sigma}{x^2} \\
&= -\frac{4\alpha\lambda\sigma^2}{x^3}e^{-2\alpha\left(\frac{\sigma}{x}\right)^2}
\end{aligned}$$

Based on the derivative of the Cumulative Distribution Function (CDF), the Probability Density Function (PDF) is obtained as follows:

$$\begin{aligned}
f(x;\lambda,\alpha,\sigma) &= \frac{d}{dx}\left((1+\lambda)e^{-\alpha\left(\frac{\sigma}{x}\right)^2}\right) + \frac{d}{dx}\left(-\lambda e^{-2\alpha\left(\frac{\sigma}{x}\right)^2}\right) \\
&= \frac{2\alpha(1+\lambda)\sigma^2}{x^3}e^{-\alpha\left(\frac{\sigma}{x}\right)^2} - \frac{4\alpha\lambda\sigma^2}{x^3}e^{-2\alpha\left(\frac{\sigma}{x}\right)^2}, x>0, \alpha>0, \sigma>0, |\lambda| \le 1
\end{aligned}$$

From this point onward, the variable *x* will be denoted as *t*, as it represents a specific point in time in the context of survival analysis.

2.5 Survival Function

The survival function represents the probability that an individual survives up to a certain time point, namely time *t* (Yanuar *et al*., 2011). In this context, the lifetime is considered a random variable denoted by *T*, with values in the interval [0,∞). Accordingly, *f(t)* is defined as the probability density function of *T*, and the cumulative distribution function is expressed as follows:

$$F(t) = P(T \le t) = \int_0^t f(x)\,dx. \tag{1}$$

Mathematically, the survival function *S(t)* can be expressed as follows:

$$\begin{aligned} S(t) &= P(T \geq t) \\ &= \int_t^{\infty} f(x)\, dx. \end{aligned} \tag{2}$$

Thus, the equation that describes the relationship between the survival function and the cumulative distribution function is obtained as follows:

$$S(t) = 1 - F(t) \tag{3}$$

where *S(t)* denotes the probability of an individual surviving up to time *t*. The value of the survival function is non-increasing over time, since the probability of survival cannot increase as time progresses.

$$S(t) = \begin{cases} 1, & \text{untuk } t = 0 \\ 0, & \text{untuk } t = \infty \end{cases} \tag{4}$$

This means that the probability of surviving at least until time $t = 0$ is 1, and the probability of surviving indefinitely, as time approaches infinity ($t \to \infty$), is 0.

Therefore, the survival function for the Generalized Time Inverse Rayleigh (GTIR) distribution with three parameters $(\lambda, \alpha, \sigma)$ is given as follows:

$$\begin{aligned} S(t) &= 1 - F(t) \\ &= 1 - \left((1+\lambda) e^{-\alpha\left(\frac{\sigma}{t}\right)^2} - \lambda e^{-2\alpha\left(\frac{\sigma}{t}\right)^2} \right) \\ S(t) &= 1 - (1+\lambda) e^{-\alpha\left(\frac{\sigma}{t}\right)^2} + \lambda e^{-2\alpha\left(\frac{\sigma}{t}\right)^2} \end{aligned}$$

2.6 Hazard Function

The hazard function represents the instantaneous probability that an individual experiences failure in a short time interval from *t* to $t + \Delta t$, given that the individual has survived up to time *t*. Mathematically, the hazard function *h(t)* can be expressed as follows:

$$\begin{aligned} h(t) &= \frac{f(t)}{1 - F(t)} \\ h(t) &= \frac{f(t)}{S(t)} \end{aligned} \tag{5}$$

where:
$f(t)$: probability density function
$F(t)$: cumulative distribution function
$S(t)$: survival function

Based on the above equation, the hazard function for the GTIR distribution with parameters $(\lambda, \alpha, \sigma)$ is given as follows:

$$h(t) = \frac{f(t)}{S(t)} = \frac{\frac{2\alpha(1+\lambda)\sigma^2}{t^3} e^{-\alpha\left(\frac{\sigma}{t}\right)^2} - \frac{4\alpha\lambda\sigma^2}{t^3} e^{-2\alpha\left(\frac{\sigma}{t}\right)^2}}{1 - (1+\lambda) e^{-\alpha\left(\frac{\sigma}{t}\right)^2} + \lambda e^{-2\alpha\left(\frac{\sigma}{t}\right)^2}}$$

2.7 *Maximum Likelihood Estimation* (MLE)

Maximum Likelihood Estimation (MLE) is a statistical method used to estimate parameters by maximizing the likelihood function based on observed data. This method was first introduced by Sir Ronald A. Fisher in 1922. The objective of MLE is to determine the parameter values that maximize the likelihood function, which represents the probability of obtaining the observed data given certain parameter assumptions. The parameter values that maximize this function are referred to as the maximum likelihood estimators. Mathematically, the likelihood function can be expressed as follows:

$$L(\theta) = f(x_1; \theta) \ldots (x_n; \theta) = \prod_{i=1}^{n} f(x_i; \theta) \tag{6}$$

Thus, the Maximum Likelihood Estimators (MLEs) for the GTIR distribution with parameters $(\lambda, \alpha, \sigma)$ are obtained as follows:

$$\begin{aligned} L(x; \lambda, \alpha, \sigma) &= \prod_{i=1}^{n} f(x; \lambda, \alpha, \sigma) \\ &= \prod_{i=1}^{n} \frac{2\alpha(1+\lambda)\sigma^2}{x^3} e^{-\alpha\left(\frac{\sigma}{x}\right)^2} - \frac{4\alpha\lambda\sigma^2}{x^3} e^{-2\alpha\left(\frac{\sigma}{x}\right)^2} \end{aligned}$$

$$= \prod_{i=1}^{n} \frac{2\alpha\sigma^2}{{x_i}^3} e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2} \left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]$$

$$= \prod_{i=1}^{n} \frac{2\alpha\sigma^2}{{x_i}^3} \prod_{i=1}^{n} e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2} \prod_{i=1}^{n} \left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]$$

To simplify the calculation process, a natural logarithm transformation is applied. The natural logarithm form of the likelihood function for the three-parameter GTIR distribution can be written as follows:

$$\ln(L(f(x;\lambda,\alpha,\sigma) = ln\prod_{i=1}^{n} \frac{2\alpha\sigma^2}{{x_i}^3} + ln\prod_{i=1}^{n} e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2} + ln\prod_{i=1}^{n} \left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]$$

$$= ln(2\alpha\sigma^2)^n - ln\prod_{i=1}^{n} x_i^3 + \ln e^{-\alpha\prod_{i=1}^{n}\left(\frac{\sigma^2}{x_i^2}\right)} + \ln\prod_{i=1}^{n} \left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]$$

$$= \ln 2^n + \ln \alpha^n + \ln \sigma^{2n} - \sum_{i-1}^{n} \ln x_i^3 - \alpha \sum_{i=1}^{n} \frac{\sigma^2}{x_i} \ln e + \sum_{i=1}^{n} ln\left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]$$

$$= n\ln(2) + n\ln(\alpha) + 2n\ln(\sigma) - 3\sum_{i=1}^{n} \ln(x_i) - \alpha\sigma^2 \sum_{i=1}^{n} \frac{1}{{x_i}^2} + \sum_{i=1}^{n} ln\left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]$$

After obtaining the natural logarithm of the likelihood function, the next step is to perform differentiation with respect to each of the specified parameters.

- Derivation of the transmutation parameter ($\hat{\lambda}$)

$$\frac{d\ln(x;\lambda,\alpha,\sigma)}{d\lambda} \Rightarrow \frac{d}{d\lambda}\left(n\ln(2) + n\ln(\alpha) + 2n\ln(\sigma) - 3\sum_{i=1}^{n} \ln(x_i) - \alpha\sigma^2 \sum_{i=1}^{n} \frac{1}{{x_i}^2} + \sum_{i=1}^{n} ln\left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]\right)$$

$$\frac{d\ ln(x;\lambda,\alpha,\sigma)}{d\lambda} \Rightarrow \sum_{i=1}^{n}\left(\frac{1 - 2e^{-\frac{\alpha\sigma^2}{{x_i}^2}}}{1 + \lambda - 2\lambda e^{-\frac{\alpha\sigma^2}{{x_i}^2}}}\right) = 0$$

$$\frac{d\ ln(x;\lambda,\alpha,\sigma)}{d\lambda} \Rightarrow \sum_{i=1}^{n}\left(\frac{1}{1 + \lambda - 2\lambda e^{-\frac{\alpha\sigma^2}{{x_i}^2}}}\right).\left(1 - 2e^{-\frac{\alpha\sigma^2}{{x_i}^2}}\right) = 0$$

The derivative of the log-likelihood function for the parameter λ results in a highly complex equation, where λ appears both inside the logarithmic expression and in the denominator of a fractional function involving exponentials. This form cannot be solved algebraically, as λ cannot be isolated explicitly. Therefore, the estimate of the parameter $\hat{\lambda}$ must be obtained using numerical methods, such as the Newton-Raphson algorithm.

- Derivation of the shape parameter ($\hat{\alpha}$)

$$\frac{d\ ln(x;\lambda,\alpha,\sigma)}{d\alpha} \Rightarrow \frac{d}{d\alpha}\left(n\ ln(2) + n\ ln(\alpha) + 2n\ ln(\sigma) - 3\sum_{i=1}^{n} ln(x_i) - \alpha\sigma^2 \sum_{i=1}^{n} \frac{1}{{x_i}^2} + \sum_{i=1}^{n} ln\left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]\right)$$

$$\frac{d}{d\alpha} ln \Rightarrow \frac{n}{\alpha} - \sigma^2 \sum_{i=1}^{n}\left(\frac{1}{{x_i}^2}\right) + \sum_{i=1}^{n}\left(\frac{2\lambda\sigma^2 e^{-\frac{\alpha\sigma^2}{{x_i}^2}}}{{x_i}^2\left(1 + \lambda - 2\lambda e^{-\frac{\alpha\sigma^2}{{x_i}^2}}\right)}\right) = 0$$

$$\frac{d}{d\alpha} ln \Rightarrow \frac{n}{\alpha} - \sigma^2 \sum_{i=1}^{n}\left(\frac{1}{{x_i}^2}\right) + \sum_{i=1}^{n}\left(\frac{1}{{x_i}^2\left(1 + \lambda - 2\lambda e^{-\frac{\alpha\sigma^2}{{x_i}^2}}\right)}\right).\left(2\lambda\sigma^2 e^{-\frac{\alpha\sigma^2}{{x_i}^2}}\right) = 0$$

The derivative of the log-likelihood function for the parameter α results in a highly complex equation, where α appears both inside the logarithmic expression and in the denominator of a fractional function involving exponentials. This form cannot be solved algebraically, as α cannot be isolated explicitly. Therefore, the estimate of the parameter $\hat{\alpha}$ must be obtained using numerical methods, such as the Newton-Raphson algorithm.

- Derivation of the scale parameter ($\hat{\sigma}$)

$$\frac{d\ ln(x;\lambda,\alpha,\sigma)}{d\sigma} \Rightarrow \frac{d}{d\sigma}\left(n\ ln(2) + n\ ln(\alpha) + 2n\ ln(\sigma) - 3\sum_{i=1}^{n} ln\,(x_i) - \alpha\sigma^2 \sum_{i=1}^{n} \frac{1}{{x_i}^2} + \sum_{i=1}^{n} ln\left[1 + \lambda - 2\lambda e^{-\alpha\left(\frac{\sigma}{x_i}\right)^2}\right]\right)$$

$$\frac{d}{d\sigma} ln \Rightarrow \frac{2n}{\alpha} - 2\alpha\sigma^2 \sum_{i=1}^{n}\left(\frac{1}{{x_i}^2}\right) + \sum_{i=1}^{n}\left(\frac{4\lambda\alpha\sigma e^{-\frac{\alpha\sigma^2}{{x_i}^2}}}{{x_i}^2\left(1 + \lambda - 2\lambda e^{-\frac{\alpha\sigma^2}{{x_i}^2}}\right)}\right) = 0$$

$$\frac{d}{d\sigma} ln \Rightarrow \frac{2n}{\alpha} - 2\alpha\sigma^2 \sum_{i=1}^{n}\left(\frac{1}{{x_i}^2}\right) + \sum_{i=1}^{n}\left(\frac{1}{{x_i}^2\left(1 + \lambda - 2\lambda e^{-\frac{\alpha\sigma^2}{{x_i}^2}}\right)}\right).\left(4\lambda\alpha\sigma e^{-\frac{\alpha\sigma^2}{{x_i}^2}}\right) = 0$$

The derivative of the log-likelihood function for the parameter σ results in a highly complex equation, where σ appears both inside the logarithmic expression and in the denominator of a fractional function involving exponentials. This form cannot be solved algebraically, as σ cannot be isolated explicitly. Therefore, the estimate of the parameter $\hat{\sigma}$ must be obtained using numerical methods, such as the Newton-Raphson algorithm.

3. Materials and Methods

3.1 Data and Sources

In this study, the data used is an actual dataset obtained from Bjerkedal's study. The dataset contains information on the survival time (measured in days) of 72 guinea pigs after being infected with virulent *Tubercle bacilli*. In other words, the data represents the number of days each animal survived from the time of infection until death during the observation period. This study aims to estimate the parameters of the Generalized Transmuted Inverse Rayleigh (GTIR) distribution and to provide insight into the survival pattern of the guinea pigs. The dataset used in this study is presented as follows:

Table 1. *Guinea Pigs* Data

12	15	22	24	24	32	32	33
34	38	38	43	44	48	52	53
54	54	55	56	57	58	58	59
60	60	60	60	61	62	63	65
65	67	68	70	70	72	73	75
76	76	81	83	84	85	87	91
95	96	98	99	109	110	121	127
129	131	143	146	146	175	175	211
233	258	258	263	297	341	341	376

3.2 Stages of Analysis

This study was conducted through several systematic steps to evaluate the goodness-of-fit of the three-parameter Generalized Transmuted Inverse Rayleigh (GTIR) distribution to the guinea pig survival data. The analysis was carried out using the RStudio programming environment, version 4.4.2. The stages of the analysis are as follows:

1) Importing Data and Libraries

This stage of this study were carried out through a series of systematic steps to apply the three-parameter Generalized Transmuted Inverse Rayleigh (GTIR) distribution to the survival data of guinea pigs. The analysis process was conducted using the Rstudio programming application, version 4.4.2.

2) Defining the PDF & *Log-Likelihood* Functions

At this stage, the probability density function (PDF) and log-likelihood function for the three-parameter GTIR distribution were formulated mathematically.

3) Parameter Estimation

The next step involved estimating the parameters of the GTIR distribution using numerical approach, namely the Maximum Likelihood Estimation (MLE) method. The GTIR distribution incorporates three key parameters: the transmutation parameter ($\hat{\lambda}$), the scale parameter ($\hat{\sigma}$), and the shape parameter ($\hat{\alpha}$), where $\alpha > 0$, $\sigma > 0$, dan $|\lambda| \leq 1$.

4) Constructing the Survival & Hazard Functions

The GTIR survival function calculates the probability of surviving up to a given time *x*. This function is derived based on the theoretical formulation. The hazard function is obtained by dividing the PDF by the survival function at a specific time point, indicating the instantaneous risk of the event (death) occuring at that time

5) Visualization

Subsequently, plots of the survival and hazard functions were generated based on the estimated parameter values. These plots serve to visualize the characteristics of the survival pattern and the risk dynamics in the guinea pig survival data.

6) Interpretation of Results

The final stage of the study involved analyzing and interpreting the estimated parameters. This interpretation includes assessing the goodness-of-fit of the GTIR distribution to the data based on the parameter values. The results of this interpretation provide the basis for concluding the effectiveness of the model in describing the survival parttern of the guinea pigs.

4. Results and Discussion

4.1 Parameter Estimation for the Generalized Transmuted Inverse Rayleigh (GTIR) Distribution

In this study, the parameters of the Generalized Transmuted Inverse Rayleigh (GTIR) distribution were estimated using the Maximum Likelihood Estimation (MLE) approach. The MLE procedure involves determining the parameter values that maximize the likelihood function, which represents the probability of observing the given data under specified GTIR distribution model. In this context, the parameters estimated include the transmutation parameter ($\hat{\lambda}$), the scale parameter ($\hat{\sigma}$), and the shape parameter ($\hat{\alpha}$) of the GTIR distribution.

The estimation process was carried out with the aid of the Rstudio software, utilizing an optimization algorithm to minimize the log-likelihood function. This approach required an explicit definition of the GTIR probability density function (PDF) and the specification of parameter constraints to ensure that the estimates remain within a valid parameter space. To illustrate the estimation procedure employed in this study, the R syntax used is presented below:

```
# Fungsi PDF GTIR
pdf_gtir <- function(x, lambda, alpha, sigma) {
  term1 <- (2 * alpha * (1 + lambda) * sigma^2 / x^3) * exp(-alpha * (sigma / x)^2)
  term2 <- (4 * alpha * lambda * sigma^2 / x^3) * exp(-2 * alpha * (sigma / x)^2)
  return(term1 - term2)
}

# 3. Fungsi Log-Likelihood negatif
neg_log_likelihood <- function(params) {
  lambda <- params[1]
  alpha <- params[2]
  sigma <- params[3]

  # Cek batas parameter
  if (abs(lambda) > 1 || alpha <= 0 || sigma <= 0) return(Inf)

  pdf_vals <- pdf_gtir(x, lambda, alpha, sigma)

  if (any(pdf_vals <= 0)) return(Inf)

  return(-sum(log(pdf_vals)))
}
```

Figure 1. R syntax

```
# 4. Estimasi parameter dengan optim
set.seed(123)

init_params <- c(lambda = 0.5, alpha = 1, sigma = 1)
result <- optim(par = init_params,
                fn = neg_log_likelihood,
                method = "L-BFGS-B",
                lower = c(-1, 1e-5, 1e-5),
                upper = c(1, Inf, Inf))

# 5. Tampilkan hasil estimasi
cat("Hasil Estimasi Parameter GTIR:\n")
cat("lambda =", result$par[1], "\n")
cat("alpha  =", result$par[2], "\n")
cat("sigma  =", result$par[3], "\n")
```

Figure 2. R syntax

After executing the syntax in RStudio, the estimated parameter values for the GTIR distribution, namely $\hat{\lambda}$, $\hat{\alpha}$, and $\hat{\sigma}$, were obtained. These estimated values are presented in the following table.

Table 2. Parameter Estimation of GTIR Distribution

Parameter Estimation of GTIR Distribution		
$\hat{\lambda}$	$\hat{\alpha}$	$\hat{\sigma}$
- 0.7806525	10.13454	12.31865

Based on the parameter estimation table presented above, the estimated value of the transmutation parameter ($\hat{\lambda}$) is 0.781, the scale parameter ($\hat{\sigma}$) is 12.319, and the shape parameter ($\hat{\alpha}$) is 10.135. The value of $\hat{\lambda}$ being close to 1 indicates a significant transmutation effect on the shape of the distribution, allowing the GTIR distribution to adapt well to the complex characteristics of the data. Meanwhile, the positive values of $\hat{\alpha}$ and $\hat{\sigma}$ confirm that the data's spread and shape align with the underlying assumptions of the GTIR distribution.

The combination of these parameter estimates demonstrates that the GTIR model is capable of capturing the complex patterns present in the survival time data of guinea pigs following infection with virulent *Tubercle bacilli*. This is further supported by the survival and hazard plots interpreted in the previous section. With these parameters, the GTIR model provides a quantitative description on how the risk of mortality and the probability of survival evolve over time within the infected guinea pig population.

4.2 Visualization of The Survival and Hazard Functions

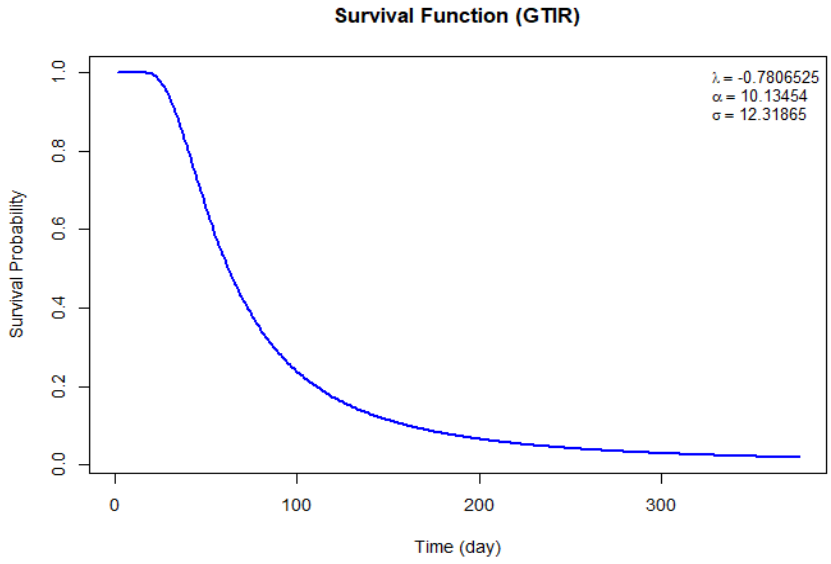

Figure 3. Visualization of The Survival Function

Based on the GTIR survival function plot presented, a visual representation is provided of how the probability of guinea pig remaining alive changes over time following infection with virulent *Tubercle bacilli*. At the onset of infection, nearly all guinea pigs are still alive, as indicated by the survival curve starting very close to 1 on the

probability axis. However, after infection occurs, a marked decline in survival probability is observed, particularly during the first few weeks. This steep drop indicates that most guinea pigs susceptible to the infection succumb within a relatively short period after being infected.

As time progresses, the mortality rate begins to decelerate. The survival curve no longer declines as sharply as before, suggesting that guinea pigs that survive the critical early phase of infection have higher chance of living longer. Nonetheless, the survival probability continues to gradually decrease, indicating that risk of death persists as the disease progresses.

Ultimately, after a sufficiently long period, the survival curve approaches zero. This indicates that infection with virulent *Tubercle bacilli* is ultimately fatal for nearly all guinea pigs within observed population. According to the GTIR distribution model applied to this data, the probability of a guinea pig surviving for an extended period post-infection becomes exceedingly low.

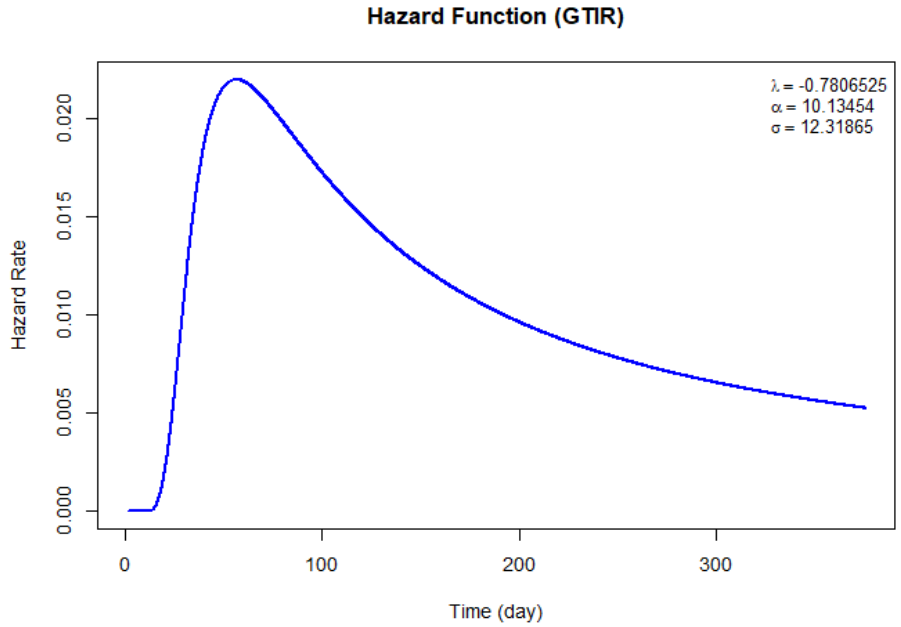

Figure 4. Visualization of The Hazard Function

Based on the GTIR hazard function plot presented, the changing risk of mortality among guinea pigs due to tuberculosis infection over time is illustrated. Initially, the hazard rate rises sharply following infection, reaching its peak at a certain point which indicates the period of highest vulnerability. After this peak, the risk of death per unit time gradually declines. Although the daily risk of mortality decreases, some guinea pigs continue to die, albeit a slower rate.

In the final phase of observation, the daily hazard becomes very low for the guinea pigs that remain alive. This pattern of the hazard rate, characterized by an initial increase followed by a decline, suggests that the most critical period for survival occurs immidiately after infection.

5. Conclusion

The estimated value of the transmutation parameter ($\hat{\lambda}$) was found to be 0.7806525, while the scale parameter ($\hat{\sigma}$) was estimated at 12.318, and the shape parameter ($\hat{\alpha}$) at 10.135. These results provide a quantitative description of the survival time pattern of the guinea pigs. The transmutation parameter ($\hat{\lambda}$) represents the initial point before the risk of mortality begins to increase. The scale parameter ($\hat{\sigma}$) reflects the variability in survival time, whereas the shape parameter ($\hat{\alpha}$) determines the rate at which the risk of death escalates. The combination of these parameter values enables the three-parameter Rayleigh distribution to accurately represent the survival pattern of guinea pigs following infection. The resulting survival and hazard plots illustrate the data's characteristics, such as an initial period of high survival probability followed by a decline in mortality. Therefore, the three-parameter Rayleigh distribution is capable of capturing the survival time dynamics of guinea pigs in this study.

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