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Survival Time Analysis of Multiple Myeloma Patients using Type 1 Censored Exponential Distribution Parameter Estimation

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ABSTRACT

Multiple myeloma is a type of blood cancer that attacks plasma cells in the bone marrow and affects the immune system. This study analyzes the survival time of patients with multiple myeloma using Type 1 censored exponential distributed parameter estimation. The data, consisting of 47 patients (35 uncensored and 12 censored), were tested for exponential distribution fit using the Anderson-Darling test, yielding a p-value of 0.495, confirming the suitability of the exponential model. The maximum likelihood estimation method was applied, resulting in a parameter estimate ($\hat{\theta}$) of approximately 54.028 days, representing the mean survival time. Hypothesis testing and confidence intervals were conducted, with the 95% confidence interval for θ_0 ranging between 32 and 53 days. The findings suggest that the exponential distribution effectively models the survival data, providing insights into patient survival trends and supporting clinical decision-making.

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A. INTRODUCTION

Multiple myeloma is a form of blood cancer that originates from abnormal plasma cell proliferation in the bone marrow (Accioly et al., 2024). The disease is characterized by the overproduction of monoclonal immunoglobulins, or M-proteins, leading to various clinical complications such as anemia, renal insufficiency, hypercalcemia, and osteolytic bone lesions (Wijnands et al., 2025). Sensitive monitoring of M-protein is crucial for evaluating therapy effectiveness and detecting disease relapse. Recent advances show that mass spectometry enables earlier and more accurate detection of M-protein than traditional methods like SPEP and IFE (McDonald et al., 2021), enhancing clinicians' ability to track response and anticipate relapse. Epidemiologically, multiple myeloma accounts for approximately 10% of all hematologic magnancies and has an incidence rate that increases with age. Although advances in immunomodulatory and monoclonal antibody-based therapies have prolonged patient survival, disease relapse is almost inevitable (Utsu et al., 2025).

In an effort to understand the course of disease and evaluate the effectiveness of therapy, survival data analysis is a crucial statistical approach. Survival analysis is a class of statistical methods for studying the occurrence of an event (Turkson et al., 2021;Indrayan & Tripathi, 2022). One of the main challenges in survival analysis is the presence of censored data, particularly type 1 censorship, where patient observation stops after a certain predetermined time, regardless of whether a clinical event has occurred or not. This censoring is common in prospective cohort studies with a fixed observation time limit (Nayabuddin, 2025).

The exponential distribution is one of the basic probability models widely used to model time-to-event data in medical contexts (Akbar et al., 2024). This distribution is characterized by a constant event rate over time, making it an ideal initial model, especially when limited data is available or the assumption of constant hazard is considered valid (Nayabuddin, 2025). Parameter estimation of the exponential distribution with type 1 censored data is essential to identify the underlying clinical event rate and support data-driven clinical decision-making. Parameter estimation for the exponential distribution with type 1 censored data can be efficiently performed using maximum likelihood methods, including on progressively censored samples, thus supporting accurate time-to-event analysis in clinical settings (Dutta & Kayal, 2022).

Several previous studies have demonstrated the relevance and application of survival models particularly exponential models in the context of multiple myeloma. Mamudu and Tsokos compared log-normal and Kaplan–Meier methods using data from 48 multiple myeloma patients and found that parametric methods provided higher estimates of survival probability (Mamudu & Tsokos, 2020). In their follow-up study, they developed nonlinear statistical models that demonstrated up to 93% accuracy in predicting survival times based on exponential assumptions (Mamudu & Tsokos, 2021). Additionally, a study by *BMC Medical Research Methodology* evaluated several parametric survival models, including exponential and spline-based models, to extrapolate long-term survival outcomes in multiple myeloma patients, validating predictions against empirical long-term data (Bakker et al., 2023).

From a methodological standpoint, several recent studies have focused on refining parameter estimation techniques for the exponential distribution under type I censoring. A study published by *MDPI* employed a minimum message length (MML) approach, demonstrating its superiority over traditional maximum likelihood estimation, especially in small sample settings (Makalic & Schmidt, 2021). Other efforts, such as those by Dutta & Kayal and the Pakistani Journal of Statistics and Operations Research, emphasized how type I progressive censoring can be effectively addressed using likelihood-based and Bayesian methods (Dutta & Kayal, 2022*;* Ashour & Nassar, 2014).

Along with the complexity of multiple myeloma, statistical approaches are also evolving to deal with mode complex disease dynamics. Joint Bayesian models, which combine analysis of longitudinal biomarker data and survival data, have been used to improve prediction of therapy transition and mortality risk in multiple myeloma patients (Alvares et al., 2024). This strategy allows for more personalized clinical predictions based on the evolution of individual biomarkers such as M-protein levels and response to new lines of therapy.

In addition to classical survival analysis, developments in minimal residual disease (MRD) monitoring have opened new avenues in evaluating the depth of therapeutic response in

multiple myeloma. MRD detection using next-generation cell flow technology or deep sequencing has shown a strong correlation with long-term patient outcomes (Caroni et al., 2025). In this context, censored data-based estimation of survival distribution parameters provides an important framework for understanding when relapse is likely to occur and how treatment can be optimized.

Given the importance of estimating survival distribution parameters in the management of multiple myeloma disease, as well as the special challenges posed by censored data type 1, it is necessary to develop and apply accurate and efficient estimation methods. Therefore, this article will discuss the methodology of estimating exponential distribution parameters with type 1 censored data, with specific application to multiple myeloma patient data, and examine the clinical relevance of the estimation results in the context of disease management (Jayakodi et al., 2022).

B. METHODS

Research methods are techniques for collecting data and analyzing data. Research methods allow research to be carried out in an organized, planned, neutral, and valueable manner (Magister et al., 2023). This technique is carried out as a strategy in collecting data and finding solutions to problems based on existing facts. A high-quality systematic review uses explicit and reproducible methods to systematically search, critically appraise, and synthesize evidence on a specific issue, adhering to a strict scientific design based on pre-specified procedures (Turkson et al., 2021).

Survival analysis is a statistical technique for conducting tests related to the survival or reliability of component (Proust, 2024). Life test analysis is also an event time analysis, where the occurance of the desired event is called failure time or survival time (Insan Firsawan et al., 2022). While commonly applied in clinical settings to model time to death or relapse, survival analysis has also found use in broader contexts, such as evaluating user retention in mobile applications, where it serves as a useful indicator to monitor promotional effectiveness (Lin et al., 2020).

This study uses secondary data of multiple myeloma patients from the Mayo Clinic (2019). The average survival time of patients diagnosed with Multiple Myeloma is measured from the time the patient is diagnosed until the patient dies. With the research variables of patient survival time (time) and death status (status). Patients with uncensored survival with 1 and patients with censored survival with 0 indicating that the patient lived for more than 91 days, as shown in Table 1.

Table 1. Survival Time Data of Patients with Multiple Myeloma

Time	**Status** ($\boldsymbol{d_i}$)
1	1
1	1
1	1
⋮	⋮
91	0
91	0
91	0

1. Type 1 Censored Data

Data is categorized as censored when the known lifetime or observation occurs at a predetermined time, while the information to be known dozes not occur within that interval (Insan Firsawan et al., 2022). Type I censored is when the experiment is terminated after reaching a predetermined time to end all and the data is categorized as censored. If there are no sudden missing individuals, the life time of the censored observation is equal to the length of the observation time. This is a form of right censoring, which occurs when the event of interest does not happen during the study period. For example, if a subject does not ecperience a recurrence of disease throughout the 1-year observation period, the subject is considered right-censored at the last visit (Barrajón & Barrajón, 2020). Right censoring is the most common type of censoring in clinical trials.

2. Exponential Distribution

The exponential distribution is one of the most commonly used probability distribution in survival analysis. It is one of the continuous distributions to find the time difference that occurs in the probability of a certain region (Triana & Purwadi, 2019). This distribution is particularly useful in modelling situations where the event of interest is equally likely to occur at any moment (Pushpanjali & Vijayalakshmi, 2022). Several generalizations of the exponential distribution have been developed to improve model flexibility and goodness-of-fit. For example, the WLLE distribution demonstrates superior performance in modelling real-world data compared to other commonly used models (Job & Solomon Ogunsanya, 2022). A continous random variable X is said to be exponentially distributed with parameter $\theta > 0$ when it has a distribution function:

$$f(x;\theta) = \begin{cases} \frac{1}{\theta} e^{\frac{x}{\theta}}, & x < 0 \\ 0, & x \geq 0 \end{cases} \quad (1)$$

where θ is the parameterized rate and the cummulative distribution function is:

$$F(X;\theta) = 1 - e^{-\frac{x}{\theta}}; \quad x > 0 \quad (2)$$

3. Likelihood Function

The likelihood function is a joint probability function that depends on the parameters, it's value indicates the likelihood of the observed data. There are always merits in obtaining raw data (i.e., exact individual failure times) rather than grouped data, because given raw data, we can always construct grouped data, but the converse is typically not true (Etikan, 2018). Therefore, this study focuses on the use of raw. Type I censored data to estimate parameters using maximum likelihood estimation (MLE), which allows for consistent inference based on observed and censored survival times (Jia et al., 2018). The data in this study uses type one censored data whose likelihood equation is:

$$L(\theta) = \prod_{i=1}^{n} f(t_i)^{d_i} \cdot S(t_i)^{1-d_i} \tag{3}$$

4. Hypothesis Test and Cofidence Interval

Hypothesis testing aims to determine whether an assumption (hypothesis) related to a population can be accepted or must be rejected based on the sample data that has been collected. The parameter tested is θ which is the distribution in the model used in this study. The decision to accept or reject the null hypothesis is based on an analysis that measures how consistent the data is with the hypothesis. The parameters hypothesis test θ is formulated with H_0 and H_1 as follows:

$$\begin{aligned} H_0&: \theta = \theta_0 \\ H_1&: \theta \neq \theta_0 \end{aligned} \tag{4}$$

From the two hypothesis it will be seen whether the simple model (under H_0) is still good enough or should use more complex model (under H_1). Therefore, the test statistic will be used, namely:

$$\Lambda = -2\log\left(\frac{L(\theta_0)}{L(\hat{\theta})}\right) \tag{5}$$

Desciption:

Λ = The chi-square distribution test statistic

$L(\theta_0)$ = Value of likelihood function parameter θ_0 (under H_0)

$L(\hat{\theta})$ = The value of the likelihood function in the parameter $\hat{\theta}$ (under H_1, value that maximizes the likelihood)

Rejected criteriaH_0: $\Lambda < {\chi^2}_{\frac{\alpha}{2}}(1)$ or $\Lambda > {\chi^2}_{1-\frac{\alpha}{2}}(1)$ which is a chi-distribution square with 1 degree of freedom. The confidence interval θ is determined by finding the value of θ_0 which makes the sttaistic Λ is in the range:

$${\chi^2}_{\frac{\alpha}{2}}(1) < \Lambda < {\chi^2}_{1-\frac{\alpha}{2}}(1) \tag{6}$$

The criterion for acceptance of the null hypothesis in a two-sided test is if the value Λ falls between the two limits of the chi-square critical value. If Λ is too small or too large drom this range, the null hypothesis is rejected.

C. RESULT AND DISCUSSION

This study uses patient survival data classified into two categories based on event status: censored (status = 0) and uncensored (status = 1).

1. Descriptive Statistics

Based on secondary data from the Mayo Clinic (2019), as cited in the article (Pradana & Sofro, 2019), the following results were obtained, as shown in Table 2.

Table 2. Descriptive Statistics

Variable	Mean	StDev	Minimum	Median	Maximum
Survival Time	22.83	24.19	1.00	14.00	91.00

Descriptive statistics of survival time were calculated based on uncensored patients (status = 1) to avoid bias due to incomplete data in censored patients. Table 2 shows the average survival time (in days) for patients with multiple myeloma until death was 22.83 days. The fastest survival time was 1 day and the longest survival time was 91 days.

2. Exponential Distribution Testing

Before estimating the parameters of the survival data, the Anderson Darling test is used to determine whether a data has a certain distribution. In this study, data analysis was carried out on the exponential distribution (Jäntschi & Bolboacă, 2018).

Hypothesis:

H_0: Data is exponentially distributed

H_1: Data is not exponentially distributed

Critical region: Reject H_0 if P-Value $< \alpha = 5\%$

The following is a meta-analysis: accuracy level of the radial basis function method in time series prediction, as shown in Figure 1.

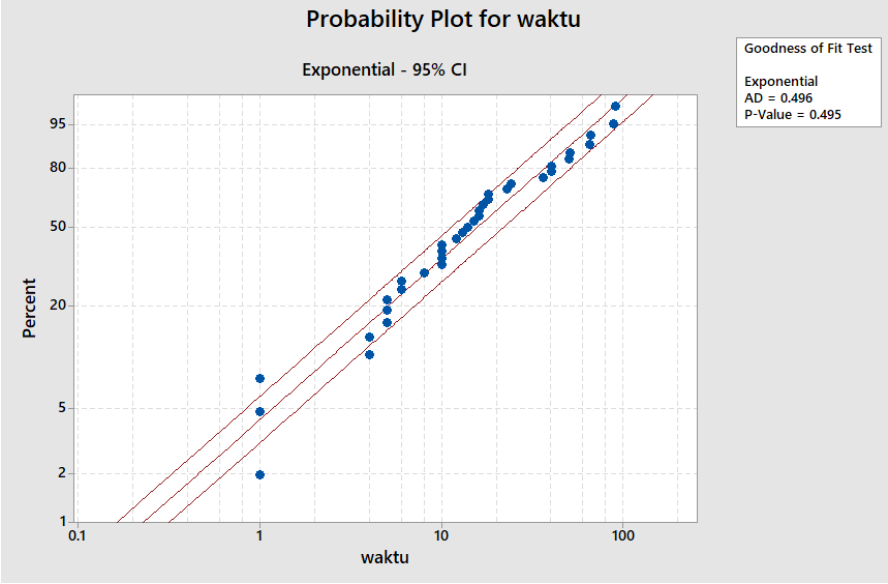

Figure 1. Anderson Darling Test Plot of Multiple Myeloma Patient Survival Time

Based on Figure 1, the P-Value shows $0.495 > \alpha = 5\%$. So the decision taken is to fail to reject H_0. Thus, it can be concluded that the survival time data of patients with multiple myeloma follow an exponential distribution. Therefore, this data is suitable for analyzed further, especially in the context of estimating the parameters of the type 1 censored exponential distribution as raised in this study.

3. Parameter Estimation Using the Derivative of the Likelihood Function

In type 1 censored data, the observation of the 1st, 2nd, …, n individual is limited by the observation time $L_1, L_2, \dots, L_n$ and can only be observed if the individual survival time T_i satisfies the condition $T_i \leq L_i$. When the data pair (T_i, L_i), for $i = 1, 2, \dots, n$ are independent of each other then:

$$t_i = \min(T_i, L_i)$$
$$d_i = \begin{cases} 1, & t_i = T_i \text{ jika } T_i \leq L_i \\ 0, & t_i = L_i \text{ jika } T_i > L_i \end{cases}$$

The variable d_i indicates whether the individual's life time is censored or not. Thus, it can be simplified to:

$$d_i = \begin{cases} 1, & \text{if the data is not censored (observed)} \\ 0, & \text{if the data is censored (unobserved)} \end{cases}$$

Because the value of T_i as the actual time is only known with certainty. If the data is not censored, then the construction of the likelihood function is carried out based on the actually observed data, namely the observation time t_i and the sensor status d_i. By considering that the survival data follows an exponential distribution, the joint likelihood density function (joint pdf) of the t_i and d_i can be expressed as follows:

$$f(t_i, d_i) = f(t_i)^{d_i} \cdot S(t_i)^{1-d_i}$$

The form unifies two conditions: if the data is uncensored, then $f(t_i, d_i) = f(t_i)$, which is the density function of the event time. Meanwhile, if the data is censored, then $f(t_i, d_i) = S(t_i)$ which is the survival function of the observation time (Su, 2015). Assuming that each individual is independent, the likelihood function of all data is:

$$L(\theta) = \prod_{i=1}^{n} f(t_i)^{d_i} \cdot S(t_i)^{1-d_i}$$

It is known that $f(t_i) = \frac{1}{\theta} e^{-t_i/\theta}$ and $S(t_i) = 1 - F(t_i)$

$$S(t_i) = 1 - \int_0^{t_i} \frac{1}{\theta} e^{-x/\theta}\, dx$$

For example, $-x/\theta = y$ and $dx = -\theta dy$

$$S(t_i) = 1 - \int_0^{t_i} \left(\frac{1}{\theta} e^{y}\right) - \theta dy$$

$$S(t_i) = 1 - \left(- \int_0^{t_i} e^y \, dy \right)$$
$$S(t_i) = [1 + e^y]_0^{t_i}$$
$$S(t_i) = \left[1 + e^{-x/\theta}\right]_0^{t_i}$$
$$S(t_i) = 1 + e^{-t_i/\theta} - 1$$
$$S(t_i) = e^{-t_i/\theta}$$

Thus, the form of the likelihood function can be rewritten as:

$$L(\theta) = \prod_{i=1}^{n} f(t_i)^{d_i} \cdot S(t_i)^{1-d_i}$$
$$L(\theta) = \prod_{i=1}^{n} \left(\frac{1}{\theta} e^{-t_i/\theta}\right)^{d_i} \left(e^{-t_i/\theta}\right)^{1-d_i}$$
$$L(\theta) = \prod_{i=1}^{n} \frac{1}{\theta^{d_i}} e^{-t_i/\theta}$$
$$L(\theta) = \frac{1}{\theta^{\sum_{i=1}^{n} d_i}} e^{-\frac{\sum_{i=1}^{n} t_i}{\theta}}$$

where $\sum_{i=1}^{n} d_i$ is the amount of uncensored data and n is the amount of overall data.

$$L(\theta) = \frac{1}{\theta^{35}} e^{-\frac{\sum_{i=1}^{n} t_i}{\theta}}$$

To maximize the likelihood function, $\ln L(\theta)$ is differentiated with respect to θ, and the result is set to zero (Alomari, 2023).

$$0 = \frac{\partial \ln L(\theta)}{\partial \theta}$$
$$0 = \frac{\partial \ln \left(\frac{1}{\theta^{35}} e^{-\frac{\sum_{i=1}^{n} t_i}{\theta}} \right)}{\partial \theta}$$
$$0 = \frac{\partial \left(-35 \ln \theta - \frac{\sum_{i=1}^{n} t_i}{\theta} \right)}{\partial \theta}$$
$$0 = -\frac{35}{\theta} + \frac{\sum_{i=1}^{n} t_i}{\theta^2}$$
$$0 = \frac{-35\theta + \sum_{i=1}^{n} t_i}{\theta^2}$$
$$35\theta = \sum_{i=1}^{n} t_i$$

The estimator value of the exponential distribution parameter is:

$$\hat{\theta} = \frac{\sum_{i=1}^{n} t_i}{35}$$

4. Average Survival Time (in days) of Patients with Multiple Myeloma to Death

From the parameter estimator values that have been obtained, we can calculated the average survival time (in days) of patients with multiple myeloma until they die, which is as follows:

$$\hat{\theta} = \frac{\sum_{i=1}^{47} t_i}{35}$$
$$\hat{\theta} = \frac{1891}{35}$$

$$\hat{\theta} \approx 54{,}028$$

so, the average survival time (in days) of patients with multiple myeloma to death was 54.028 days.

5. Hypothesis Testing and Confidence Intervals

Hypothesis testing is used to determine whether there is enough evidence in the sample data to reject the initial conjecture (H_0) about the value of a population parameter. The parameter hypothesis θ is formulated as follows:

$$H_0 : \theta = \theta_0$$
$$H_1 : \theta \neq \theta_0$$

The test statistics used are:

$$\Lambda = -2 \log\left(\frac{L(\theta_0)}{L(\hat{\theta})}\right)$$

The H_0 rejection criteria are:

$$\Lambda < \chi^2_{\alpha/2}(1) \text{ atau } \Lambda > \chi^2_{1-\alpha/2}(1)$$

The first step to calculating test statistics is to find the value of $\log L(\hat{\theta})$ with a value of $\hat{\theta} = 54{,}02857$:

$$\log(L(\hat{\theta})) = \log\left(\frac{1}{54{,}028^{35}} e^{-\frac{1891}{54{,}028}}\right)$$
$$\log(L(\hat{\theta})) = -75{,}842$$

Then find the $\log L(\theta_0)$ value by using the initial value of θ_0 as the initial guess value to be tested. The value of θ_0 to be used is based on the value of θ_0 around $\hat{\theta}$. We will use the value of $\theta_0 = 40$ which is the average survival value of all patients with censored and uncensored data status. The $\log L(\theta_0)$ value with $\theta_0 = 40$ are as follows:

$$\log(L(\theta_0)) = \log\left(\frac{1}{40^{35}} e^{-\frac{1891}{40}}\right)$$
$$\log(L(\theta_0)) = -76{,}603$$

The test statistic values are obtained as follows:

$$\Lambda = -2(\log L(\theta_0) - \log L(\hat{\theta}))$$
$$\Lambda = -2(-76{,}603 + 75{,}842)$$
$$\Lambda = 1{,}522$$

so that a decision can be made to fail to reject H_0 because $\chi^2_{\alpha/2}(1) = 0{,}001 < \Lambda = 1{,}522 < \chi^2_{1-\alpha/2}(1) = 5{,}024$ which means that the data is obtained consistent with the assumption that the level of accuracy of parameter estimation $\hat{\theta}$ is equal to the initial expected value θ_0. Furthermore, to determine the level of accuracy of parameter estimation $\hat{\theta}$ obtained, it is necessary to calculated the confidence interval from θ with a confidence level of 95%. Search for θ_0 which makes the value of Λ fall within the interval boundary:

$$\chi^2_{\alpha/2}(1) < \Lambda(\theta_0) < \chi^2_{1-\alpha/2}(1)$$

Calculating the test statistic

$$\Lambda(\theta_0) = -2(\log L(\theta_0) - \log L(\hat{\theta}))$$

To test $\Lambda(\theta_0)$, the value of θ_0 that satisfies the interval limit of $0{,}001 < \Lambda(\theta_0) < 5{,}024$ is tested.

Upper limit of the interval θ_0

- $\theta_0 = 54$

$$\Lambda(\theta_0) = -2(\log L(54) - \log L(54{,}028))$$
$$\Lambda(\theta_0) = -2(-75{,}84213 + 75{,}84212)$$
$$\Lambda(\theta_0) = 0{,}00002$$

The result show that $\Lambda(\theta_0)$ is outside the interval, so it is necessary to check the value of other θ_0 to know the upper limit of θ_0.

- $\theta_0 = 53$

$$\Lambda(\theta_0) = -2(\log L(53) - \log L(54{,}028))$$
$$\Lambda(\theta_0) = -2(-75{,}84495 + 75{,}84212)$$
$$\Lambda(\theta_0) = 0{,}004$$

The result show that $\Lambda(\theta_0)$ is inside the interval, so it is decided that $\theta_0 = 53$ is the upper bound of θ_0.

Lower limit of the interval θ_0.

- $\theta_0 = 31$

$$\Lambda(\theta_0) = -2(\log L(31) - \log L(54{,}028))$$
$$\Lambda(\theta_0) = -2(-78{,}68962 + 75{,}84212)$$
$$\Lambda(\theta_0) = 5{,}695$$

The result show that $\Lambda(\theta_0)$ is outside the interval, so it is necessary to check the value of other θ_0 to know the lower limit of θ_0.

- $\theta_0 = 32$

$$\Lambda(\theta_0) = -2(\log L(32) - \log L(54{,}028))$$
$$\Lambda(\theta_0) = -2(-78{,}34433 + 75{,}84212)$$
$$\Lambda(\theta_0) = 5{,}004$$

The result show that $\Lambda(\theta_0)$ is inside the interval, so it is decided that $\theta_0 = 32$ is the lower bound of θ_0. So, it can be concluded that the confidence interval for θ_0 is:

$$32 < \theta_0 < 53$$

Thus, it can be concluded that at the confidence level 95%, the value of θ_0 is between 32 and 53. Although the maximum estimate value of $\hat{\theta} = 54.028$ is outside the interval, this does not contradict the test method used, because $\hat{\theta}$ is the value that maximizes the likelihood function, while the confidence interval is formed based on values of θ_0 which is not statisfically significantly different from $\hat{\theta}$. This relatively short survival time likely reflects patients in advanced stages of multiple myeloma or those with serious comorbidities such as renal impairment. According to the NCCN Clinical Practice Guidelines (2024), patients who receive standard therapy including immunomodulatory drugs (IMiDs), proteasome inhibitors, and autologous stem cell transplantation (ASCT) can achieve a median overall survival of up to 67 months (Raje et al., 2014). In their 2023 update, the IMWG recommends immediate initiation of bortezomib-based regimens in patients presenting with renal dysfunction, as this approach promotes renal recovery and enhances survival outcomes (Dimopoulos et al., 2023). Additionally, Faiman (2011) emphasize that patients who recover renal function through aggressive intervention can achieve survival rates similar to those without renal complications. These findings support policy recommendations such as early renal screening, broader access to effective therapies, and the establishment of a national multiple myeloma registry to monitor outcomes and guide evidence-based care strategies.

D. CONCLUSION AND SUGGESTIONS

Research data of patients with *multiple myeloma* are classified into 2 categories, namely censored data and uncensored (observed) data. In the data obtained as many as 47 patients with 35 patients died in the observation period (not censored) and 12 patients were still alive until the end of the observation period (censored). The results of the analysis show that the average survival time of patients with *multiple myeloma* is 22.83 days with a standard deviation of 24.19. Furthermore, the data is tested using the Anderson-Darling Test and shows

that the data is exponentially distributed with a p-value of 0.495> 5%, which means that the data is exponentially distributed and is considered suitable for estimating the type 1 censored exponential distribution parameters. Then the estimator value of the exponential distribution parameter $(\hat{\theta})$ is 54.028. After knowing the value of $\hat{\theta}$, the test is carried out hypothesis and the confidence interval of θ_0. The hypothesis test results show that the conjecture parameter value $\theta_0 = 40$ is acceptable with the confidence interval of θ_0 being within the interval of 32 to 53 days. For future research, studies can explore more flexible models like the Weibull or log-normal distribution, especially if the exponential distribution assumptions are not fully met. Researchers can also include other factors that influence patient survival using models such as Cox regression. In addition, newer approaches like machine learning (e.g., survival forests or deep learning models) could be used to improve prediction accuracy and tailor treatment plans more effectively for each patient.

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