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# Change Point Analysis of the Time to Recurrence in Colon Cancer Patients

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**Abstract:** Change point analysis is essential in the identification of shifts in disease progression, particularly in assessing recurrence risk in cancer patients. This study evaluated whether the likelihood of colon cancer recurrence remains constant over time or changes across time. The Likelihood Ratio Test (LRT) was applied to detect significant changes in the hazard function, and maximum likelihood estimation was used to estimate the change points. A bootstrap resampling scheme generated the empirical distribution of the LRT statistic under the null hypothesis of no change. Simulation studies assessed the power of the LRT, showing improved accuracy with increased sample size, larger hazard differences, and centrally located change points. The proposed method was applied to a real colon cancer dataset comprising 888 patients, of whom 446 experienced recurrence. Four covariates—treatment type, number of positive nodes, extent of local spread, and time to registration—were found to be significant and were included in the change point detection analysis. Each covariate showed one significant change point based on the LRT exceeding the bootstrap critical value. In the Cox Proportional Hazards model, treatment was associated with a greater reduction in hazard after the change point, while the other covariates were associated with increased recurrence risk, with stronger effects post-change. In the Weibull Accelerated Failure Time (AFT) model, treatment was associated with a reduced hazard, while the covariates linked to increased hazard exhibited slightly weaker effects after the change. Model adequacy was evaluated using Cox–Snell and deviance residuals, Schoenfeld residuals, quantile–quantile plots, and the Grambsch–Therneau test. Models with change points performed better across all checks, except the Weibull AFT model, which failed the quantile–quantile plot test. Overall, the Cox Proportional Hazards model with covariate-specific change points provided the best fit, offering critical insight into dynamic recurrence risk patterns in colon cancer patients. These findings provide a basis for cancer surveillance agencies and public health organizations to refine screening programs and allocate resources efficiently by focusing on high-risk periods.

**Keywords:** Change Point, Cox Proportional Hazards, Weibull AFT, Hazard Function, Bootstrap Resampling, Colon Cancer Recurrence

## 1. Introduction

Change is a fundamental aspect of life, manifesting in various domains such as personal behavior, health, technology, finance, and industry. Whether sudden, like a shift in stock prices or the impact of a lottery win, or gradual, such as academic improvement, climate shifts, or recovery from illness; change often occurs subtly, with its effects becoming evident only over time. In many cases, the precise point at which change occurs is of great interest, particularly because the consequences can be long-lasting and sometimes delayed. In healthcare, for example, the initial high mortality rate among Human Immunodeficiency Virus (HIV) patients starting antiretroviral therapy may drop significantly after a certain period, and cancer patients may experience improved outcomes during recovery phases. Identifying these critical moments of change is essential for timely intervention and informed decision-making in both clinical and non-clinical contexts.

In survival analysis, the change point problem involves detecting a shift in the distribution of time-to-event data across a sequence of ordered observations. A commonly used approach for analyzing such data is the semiparametric Cox proportional hazards (Cox PH) model [6]. However, this model requires the key assumption that the hazard ratio function is constant over time, which may be violated in survival data, as a lag period before an experimental treatment takes effect is possible [13]. A parametric alternative to the semi-parametric proportional hazards model is the accelerated failure time model, which requires distributional assumptions and instead of assuming that a covariate has a multiplicative effect on the hazard, assumes that a covariate accelerates the hazard by a constant.

Cancer remains a leading global cause of death, with approximately 20 million new cases and 9.7 million cancer-related deaths reported in 2022 alone [3]. Colorectal cancer, in particular, ranks as the third most commonly diagnosed cancer and the second leading cause of cancer-related mortality, accounting for around 2 million new cases and 900,000 deaths globally. Despite treatment, recurrence is a major concern, especially for patients with stage II and III colon cancer, with 20-30$\%$ experiencing a return of the disease within five years of surgery most commonly within the first two years [2]. Recurrence is associated with significantly higher mortality and places a substantial economic and social burden on patients, families, and healthcare systems, including financial hardship, decreased quality of life, and productivity losses due to premature death. Conventional survival analysis methods typically provide an overall recurrence risk and may not capture changes in risk over time, thus missing critical high-risk periods. This study applies change point analysis to time-to-recurrence data in colon cancer patients to detect when shifts in recurrence risk occur and identify factors influencing these changes. Understanding these patterns can support timely interventions, improve surveillance strategies, and ultimately enhance patient survival outcomes.

Change point detection in survival analysis involves testing whether a change in the hazard function occurs over time. This is typically framed as a hypothesis test, with the null hypotheses indicating no change and the alternative suggesting the presence of a change. If the null hypothesis is not rejected, the procedure concludes; otherwise, the next step is to estimate the point in time at which the change occurs. Several statistical methods are used for detecting such changes, including the likelihood ratio test, the Wald test, and the maximal score test. Reference [20] adapted the change point concept to survival data by proposing a likelihood ratio test and a score test to evaluate constant hazard functions against alternatives with a single change point. Their findings indicated that the likelihood ratio test outperformed the score test in terms of power. Reference [17] noted that while the maximal score test can be sensitive to the location of the change point, the maximal Wald test generally performs well even with moderate sample sizes. Reference [18] extended the analysis to include the likelihood ratio test, highlighting its practical advantage of not requiring the variance-covariance matrix, unlike the Wald and score tests. Reference [21] conducted a simulation study to assess the power of the likelihood ratio test (LRT) in detecting change points. Their results showed that the test's power increases with larger sample sizes, greater differences between hazard rates before and after the change, and when the change occurs near the center of the observation period. The findings align with those reported in [22].

However, complexities in determining the null distribution arise in the absence of a change point, making it difficult to derive an exact theoretical distribution. To address this, Monte Carlo simulations are often used to estimate the null distribution by generating data under the null hypothesis, while resampling methods such as bootstrapping provide empirical estimates to support statistical inference. Reference [10] recommended using bootstrap-based resampling to estimate the null distribution of the likelihood ratio test in survival change point analysis, offering a practical solution to this challenge.

Locating the change point, once a shift in the hazard function has been identified, is crucial for understanding variations in risk patterns over time. In this study, we propose a maximum likelihood estimation approach for identifying a change point, since the likelihood function of survival distributions has an explicit form. Moreover, maximum likelihood estimates (MLEs) are consistent, meaning they converge to the true parameter values as the sample size increases. This approach is supported by findings in previous studies, including those reported in [5, 14, 15, 19].

The Accelerated Failure Time model with a Weibull distribution offers a great flexibility since it includes the exponential distribution as a special case and is the only continuous distribution that simultaneously supports both the proportional hazards and accelerated failure time models (AFT) models. The Weibull AFT model accommodates hazard rates that may increase or decrease over time, making it suitable for a wide range of survival data. Furthermore, it can be simplified into a piecewise constant hazard model or re-parameterized into a change point model within the proportional hazards framework. These features make the Weibull AFT model particularly useful in change point analysis, as demonstrated in [10].

Existing literature on change point estimation in survival analysis has predominantly concentrated on single-covariate models, with a particular emphasis on binary variables such as gender or treatment allocation. While these studies have provided valuable insights, they often neglect the influence of other clinically or biologically relevant covariates that may modulate the timing or presence of a structural shift in the hazard function. This limited scope may obscure complex interactions or mask secondary patterns of change that are driven by additional covariate effects. In this study, we extend the methodological framework to examine how additional clinical and pathological covariates, beyond those traditionally considered, to include variables such as lymph involvement, duration post surgery to registration and extent of spread which may also affect the estimation and interpretation of change points.

Furthermore, consistent with the recommendations in [10], model adequacy is evaluated through residual diagnostics and formal statistical tests to ensure that the identified change points represent genuine structural changes in the hazard function rather than false signals caused by model mis-specification. In addition, while existing literature has predominantly employed either the Cox proportional hazards model or the Weibull AFT model in isolation, this study extends prior work by applying both approaches. This dual-model framework allows for a more comprehensive analysis of change point behavior and enhances the robustness and credibility of the resulting inferences.

The remainder of this paper is organized as follows: Section 2 represents the methodology of the study including the overview of the piecewise constant single change point model, likelihood ratio test, maximum likelihood estimation method, Cox PH model, Weibull AFT model, and the methods for checking the adequacy of the fitted models including the residuals analysis and statistical tests. Section 3 discusses the results of simulated data and the application of the model specifications to a real data of colon cancer. Finally, Section 4 summarizes the conclusions and offers suggestions for future research.

# 2. Methodology

### *2.1. Change Point Detection in the Hazard Function*

Change point detection involves testing whether a change exists in the hazard function, that is, a null hypothesis indicating no change and the alternative hypothesis of a change has occurred are tested. An equivalent hypothesis would involve testing whether the hazard rates before and after the specified points are equivalent. Let $\lambda_1$ denote the hazard rate before the change point and $\lambda_2$ denote the hazard rate after the change point. Then the hypotheses can be written as;

$$\begin{aligned} H_0 &: \lambda_1 = \lambda_2 = \lambda \\ H_1 &: \lambda_1 \neq \lambda_2 \end{aligned} \tag{1}$$

If the alternative hypothesis is rejected, then the change does not exist. Otherwise, a change has occurred.

### *2.2. Piece-wise Constant Single Change Point Model*

Take into account a sample of $n$ distinct individuals with the hazard rate function described in equation (1). Let $T_i^0$ represent the survival time of subject $i$ which is frequently subjected to random right censoring. The Pairs $(T_i, \delta_i)$, $i = 1, 2, \cdots, n$ are recorded, with the assumption that $C_i$ is independent of $T_i^0$. In the event that the survival time $T_i^0$ is right-censored at time $C_i$, the observed time is $T_i = \min(T_i^0, C_i)$, for $i = 1, 2, \ldots, n$. The indicator variable

$$\delta_i = \begin{cases} 1 & \text{if} \quad T_i^0 \leq C_i \text{ (failure)}, \\ 0 & \text{if} \quad T_i^0 > C_i \text{ (censored)} \end{cases} \tag{2}$$

takes the value 1 if an individual has failed and 0 if the individual is censored. The pairs $(T_i, \delta_i)$, $i = 1, 2, \ldots, n$ are recorded, with the assumption that $C_i$ is independent of $T_i^0$.

The piece-wise constant single shift point model is employed to analyze the duration until the event under study happens by assuming that the hazard rate of an event remains unchanged throughout certain periods but experiences a single, abrupt change at an uncertain point , referred to as the point of change. That is, the model assumes a constant hazard rate function $\lambda = \lambda_1$ up to an unknown time $\tau$ which needs to be estimated. At time $\tau$, $\lambda$ shifts to $\lambda_2$ and then remains constant thereafter. Therefore, the hazard rate function is described as;

$$h(t, \lambda, \tau) = \begin{cases} \lambda_1, & 0 \leq t \leq \tau \\ \lambda_2, & t > \tau \end{cases} \tag{3}$$

where $\lambda_1 > 0$, $\lambda_2 > 0$, and $\tau$ is the unknown change point, the key parameter under study.

This method gives a direct estimation of the hazard function as opposed to other survival models such as the Cox PH model which centers on assessing the impact of predictor factors on the hazard function without directly estimating it.

The cumulative hazard function for the hazard function given in (3), is given by;

$$H(t, \lambda, \tau) = \begin{cases} \lambda_1 t, & 0 \leq t \leq \tau \\ \lambda_1 \tau + \lambda_2 (t - \tau)), & t > \tau \end{cases} \tag{4}$$

The survival functions with a change point for a random variable $T$ is defined as;

$$S(t, \lambda, \tau) = \begin{cases} exp(-\lambda_1 t), & 0 \leq t \leq \tau \\ exp(-\lambda_1 \tau - \lambda_2 (t - \tau)), & t > \tau \end{cases} \tag{5}$$

### *2.3. Likelihood Ratio Test*

Let $t_1, t_2, \ldots, t_n$ represent the observed $n$ survival times. Under the null hypothesis stated in (1), the likelihood function takes the form;

$$L_0(\lambda) = \prod_{i=1}^{n} \left[\lambda e^{-\lambda t_i}\right]^{\delta_i} \left[e^{-\lambda t_i}\right]^{1-\delta_i} \tag{6}$$

where $\delta_i$ is the event indicator for the $i^{\text{th}}$ individual, taking the value 1 if the observation corresponds to an event and 0 if it is censored.

If the alternative hypothesis holds, the likelihood is of the form;

$$L_1(\lambda_1,\lambda_2,\tau)=\prod_{i=1}^{n}\left[\lambda_1 e^{-\lambda_1 t_i}I_{(t\le\tau)}+\lambda_2 e^{-\lambda_1\tau-\lambda_2(t_i-\tau)}I_{(t>\tau)}\right]^{\delta_i}\times\prod_{i=1}^{n}\left[e^{-\lambda_1 t_i}I_{(t\le\tau)}+e^{-\lambda_1\tau-\lambda_2(t_i-\tau)}I_{(t>\tau)}\right]^{1-\delta_i} \quad (7)$$

where $I(\cdot)$ denotes the indicator function that returns 1 if the specified condition is satisfied and 0 otherwise. The indicator function values $I_{(t\le\tau)}$ takes the value 1 when $t$ is in the interval [0,$\tau$] and 0 otherwise while $I_{(t>\tau)}$ takes the value 1 when $t>\tau$ and 0 otherwise.

The likelihood ratio statistic is defined by:

$$\wedge_\tau=-2\log\left[\frac{L_0(\lambda)}{L_1(\lambda_1,\lambda_2,\tau)}\right] \quad (8)$$

$$\begin{aligned}\wedge_\tau &= 2\sum_{i=1}^{n}\left\{\delta_i\left(\log\frac{\lambda_2}{\lambda_1}+(\lambda_1-\lambda_2)(t_i-\tau)\right)I_{t_i>\tau}\right.\\ &\quad\left.+(1-\delta_i)(t_i-\tau)(\lambda_1-\lambda_2)I_{t_i>\tau}\right\} \quad (9)\\ &= 2\sum_{i=1}^{n}d_i\end{aligned}$$

where

$$d_i=\begin{cases}\log\frac{\lambda_2}{\lambda_1}+(\lambda_1-\lambda_2)(t_i-\tau), & t_i>\tau, \quad \delta_i=1\\ (\lambda_1-\lambda_2)(t_i-\tau), & t_i>\tau, \quad \delta_i=0\\ 0, & otherwise\end{cases} \quad (10)$$

Under the null hypothesis, the test statistic $\wedge_\tau$ asymptotically follows a chi-square distribution with degrees of freedom equal to the difference in the number of parameters between the two models, which in this case is 2. Thus, $H_0$ is rejected at significance level $\alpha$ when $\wedge_\tau\ge\chi^2_\alpha(2)$, indicating a significant change in the hazard function at some point $\tau$. When the exact distribution of the LRT statistic under the null is difficult to determine, methods such as bootstrap resampling or Monte Carlo simulation can be used.

### *2.4. Maximum Likelihood Estimation of the Change Point*

Maximum likelihood estimation method is a point estimation procedure employed to determine the parameter values that maximize the likelihood function, indicating that the observed data is most likely under the given statistical model. Within the context of change point analysis, the likelihood function is modified to take into consideration a possible shift in the hazard function at an unspecified time point, denoted as $\tau$ (the change point). It is assumed that the hazard function changes at time $\tau$, creating two distinct hazard rates prior to and subsequent to the change point as shown in (1). Proceeding from (10), when $\lambda_1$ and $\lambda_2$ are known, $d_i$ is linear in the change point $\tau$, $\wedge_\tau$ is linear between any two sequentially recorded survival times, and therefore, its maximum occurs at an observed survival time, denoted as $T_i$, which is the $m^{th}$ ordered survival time, $T_m$. For every $k\le m$, the value of $d_k$ associated with the order statistic $T_k$ is 0. Thus, the MLE of the change point $\tau$ is

$$\widehat{\tau}=T_{\widehat{m}}, \quad \widehat{m}=arg\max_m\sum_{i=m+1}^{n}d_i \quad (11)$$

This maximization of the likelihood is often performed numerically, as the likelihood function can be complex.

When $\lambda_1$ and $\lambda_2$ are not known, they need to be estimated alongside the point of change $\tau$. The candidate values of $\tau$ are in the set specified by:

$$\tau\in\{T_2^-,T_2,\cdots,T_{n-1}^-,T_{n-1}\} \quad (12)$$

where $T_2,\cdots,T_{n-1}$ are the ordered event times (except the last one $T_n$) while $T_r^-$ represents a value just below $T_r$, which allows for the possibility that the change point occurs immediately before an observed event time. In the piecewise constant model, the log-likelihood function, expressed when $\lambda_1\ne\lambda_2$ is;

$$\begin{aligned}l_1(\lambda_1,\lambda_2,\tau) &= \sum_{i=1}^{n}\delta_i log\left[\lambda_1 e^{-\lambda_1 t_i}I_{(t\le\tau)}+\lambda_2 e^{-\lambda_1\tau-\lambda_2(t_i-\tau)}I_{(t>\tau)}\right]\\ &\quad+\sum_{i=1}^{n}(1-\delta_i)log\left[e^{-\lambda_1 t_i}I_{(t\le\tau)}+e^{-\lambda_1\tau-\lambda_2(t_i-\tau)}I_{(t>\tau)}\right] \quad (13)\end{aligned}$$

The MLEs of $\lambda_1$, $\lambda_2$, and $\tau$ were obtained by minimizing the negative log-likelihood function in (13) using the Nelder–Mead optimization algorithm, as the equation does not have a closed-form solution.

### *2.5. Survival Regression Models*

#### *2.5.1. Cox Proportional Hazards Model*

The Cox proportional hazards model, proposed by [6], is a special case of the proportional hazards model. It is semi-parametric, allowing the assessment of the association between survival time and one or more explanatory variables without requiring assumptions about the baseline hazard function. The hazard function of the Cox PH model is given by;

$$h(t; X_i) = h_0(t) \exp(\beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p) = h_0(t) \exp(\boldsymbol{\beta' X_i}) \tag{14}$$

where $h(t; X_i)$ denotes the hazard function at time $t$, $h_0(t)$ is the baseline hazard, $\boldsymbol{\beta} = (\beta_1, \beta_2, \ldots, \beta_p)'$ is the vector of regression coefficients, and $\mathbf{X_i} = (x_1, x_2, \ldots, x_p)'$ represents the covariate values for individual $i$. The model assumes that the hazard ratio comparing any two individuals is constant over time.

For a single covariate $X$, the hazard ratio (HR) comparing an individual with $X = 1$ to one with $X = 0$ is given by

$$HR = \frac{h(t|X=1)}{h(t|X=0)} = \frac{h_0(t)\exp(\beta)}{h_0(t)\exp(0)} = \exp(\beta) \tag{15}$$

which is independent of $t$. Here, $HR = 1$ indicates no effect of the covariate, $HR < 1$ indicates a reduction in hazard, and $HR > 1$ indicates an increased hazard.

To estimate the regression coefficients $\boldsymbol{\beta}$, and hence the hazard ratios, the Cox PH model uses the partial likelihood approach, which does not require specifying the baseline hazard. Assuming that $u_1, u_2, \cdots, u_j$ represent the $j$ ordered distinct death times, the partial likelihood is given by;

$$L(\boldsymbol{\beta}) = \prod_{i=1}^{j} \left[ \frac{\exp(\boldsymbol{\beta' } X_i)}{\sum_{l \in R(u_i)} \exp(\boldsymbol{\beta' } X_l)} \right] \tag{16}$$

where $R(u_i)$ denotes the risk set at time $u_i$. The estimate of $\boldsymbol{\beta}$ is obtained by maximizing this partial likelihood.

The proportional hazards assumption may not hold when a structural change occurs in the likelihood of the event at an unspecified time, referred to as the change point. A Cox PH model with a change point accounts for this shift by estimating separate hazard functions before and after the change point. Incorporating a change point allows for a better understanding of the dynamic nature of risk factors and their effects on the event of interest. The hazard function for a model with a change point and a common baseline hazard is defined as;

$$h(t; X_i) = \begin{cases} h_0(t)\exp(\boldsymbol{\beta}_1^{'} X_i), & 0 \le t \le \tau \\ h_0(t)\exp(\boldsymbol{\beta}_2^{'} X_i), & t > \tau \end{cases} \tag{17}$$

where $\boldsymbol{\beta_1'}$ and $\boldsymbol{\beta_2'}$ are the vectors of coefficients before and after the change point $\tau$, respectively, and $h_0(t)$ is the common baseline hazard. Let $\ominus = (\tau, \boldsymbol{\beta_1}, \boldsymbol{\beta_2})$ denote the vector of unknown parameters, where the effect of covariate $X_i$ changes at $\tau$.

Under the hazard of the Cox PH model with a shift point defined in (17), the survival function $S(t; X_i)$ is defined as follows:

$$S(t; X_i) = \begin{cases} \exp\Big( - t\, h_0(t)\, \exp\big(\boldsymbol{\beta}_1' X_i\big)\Big), & 0 \le t \le \tau, \\ \exp\Big( - \tau\, h_0(t)\, \exp\big(\boldsymbol{\beta}_1' X_i\big) \\ \quad -(t-\tau)\, h_0(t)\, \exp\big(\boldsymbol{\beta}_2' X_i\big)\Big), & t > \tau. \end{cases} \tag{18}$$

The likelihood function of the Cox PH model with a change point is defined as follows:

$$L(\ominus) = \prod_{i=1}^{n} h(t; X_i)^{\delta_i} S(t; X_i) \tag{19}$$

The corresponding log-likelihood is:

$$\begin{aligned} l(\ominus) = &\sum_{i=1}^{n} \delta_i \log\Big(h_0(t)\exp\left(\boldsymbol{\beta}_1^{'} X_i\right)\Big) - t h_0(t)\exp\left(\boldsymbol{\beta}_1^{'} X_i\right)\Big|_{0 \le t \le \tau} \\ &+ \sum_{i=1}^{n} \delta_i \log\Big(h_0(t)\exp\left(\boldsymbol{\beta}_2^{'} X_i\right)\Big) - \tau h_0(t)\exp\left(\boldsymbol{\beta}_1^{'} X_i\right) - (t-\tau) h_0(t)\exp\left(\boldsymbol{\beta}_2^{'} X_i\right)\Big|_{t > \tau}. \end{aligned} \tag{20}$$

Differentiating the logarithmic likelihood function obtained in equation (20) with regard to $\beta_1$ and $\beta_2$ and setting to zero, the following score equations are obtained as in (21) and (22) respectively:

$$\frac{\partial l(\ominus)}{\partial \beta_1} = \sum_{i=1}^{n} \Big(\delta_i X_i - t h_0(t) X_i \exp(\beta_1' X_i)\Big)\Big|_{(0 \le t \le \tau)} - \tau h_0(t) X_i \exp(\beta_1' X_i)\Big|_{(t > \tau)} = 0 \tag{21}$$

$$\frac{\partial l(\ominus)}{\partial \beta_2} = \sum_{i=1}^{n} (\delta_i X_i - X_i (t-\tau) h_0(t) exp(\beta_2' X_i))|_{(t > \tau)} = 0 \tag{22}$$

For a given change point model, the parameter vector $\widehat{\boldsymbol{\theta}} = (\widehat{\tau}, \widehat{\beta}_1, \widehat{\beta}_2)$ is estimated by maximizing the log-likelihood via the Nelder–Mead simplex algorithm. This derivative-free method minimizes the negative log-likelihood by iteratively adjusting simplex vertices, making it suitable for non-smooth likelihoods with respect to $\tau$. The change point is determined by searching a finely spaced grid of $\tau$ values and selecting the one with the highest likelihood.

Due to the complexities surrounding the empirical distribution of the likelihood ratio test in the change point setting, the bootstrap resampling scheme, as explained in [8], was applied to approximate the distribution of the test statistic under the null hypothesis.

### *2.5.2. The Accelerated Failure Times Model*

The Accelerated Failure Times model provides an alternative to the Cox proportional hazard model since it assumes that the influence of a covariate either speeds up or slows down the failure times by constant factor [16].

The underlying assumption of the AFT model can be expressed as follows:

$$S(t; X) = S_0(texp(\boldsymbol{\beta}\mathbf{X})) \tag{23}$$

where the survival function, $S(t; X)$, represents the likelihood of survival at time $t$ while $S_0(texp(\boldsymbol{\beta}\mathbf{X}))$ denotes the baseline survival function assessed at time $t$. The term $exp(\boldsymbol{\beta}\mathbf{X})$ from (23) is referred to as the acceleration factor which speeds up the survival function when the explanatory variable $X = 0$.

The model considers the log of survival time as the dependent variable and incorporates a residual term that is presumed to follow a specific distribution. The model for an $i^{th}$ individual can be represented in its generalized log-linear form as follows:

$$\log T_i = \beta_0 + \beta_1 X_{1i} + \cdots + \beta_p X_{pi} + \sigma\epsilon_i \tag{24}$$

where $\log\ T_i$ is the logarithm of the transformed survival time, $X_1, X_2, \cdots, X_p$ are covariates with corresponding coefficients $\beta_1, \beta_2, \cdots, \beta_p$, while $\beta_0$ and $\sigma$ represent the intercept and scale parameters respectively. $\epsilon_i$ represents the error term or residual assumed to follow specific distributions such as the extreme value, normal, or logistic distributions corresponding to survival times $T_i$ that follow Weibull, log-normal, or log-logistic distributions, respectively. The survival function of $T_i$ can be represented by the survival function of $e_i$ (error term) as follows;

$$\begin{aligned} S_i(t) &= P(T \geq t) \\ &= P(logT \geq logt) \\ &= P(\beta_0 + \beta_1 X_{1i} + \cdots + \beta_p X_{pi} + \sigma\epsilon_i \geq logt) \\ &= P\left(e_i \geq \frac{logt - \beta_0 - \beta_1 X_1 - \cdots - \beta_p X_p}{\sigma}\right) \\ &= S_{\epsilon_i}\left(\frac{logt - \beta_0 - \beta_1 X_1 - \cdots - \beta_p X_p}{\sigma}\right) \\ &= S_{\epsilon_i(t)} \end{aligned} \tag{25}$$

The AFT model family encompasses the exponential, Weibull, log-logistic, log-normal, and gamma distributions. Detecting a change point in the Weibull AFT model is ideal due to its flexibility to model increasing ($\lambda > 1$), decreasing ($\lambda < 1$), or constant hazard rates ($\lambda = 1$). Moreover, the Weibull distribution is unique among continuous distributions in that the AFT model can be restructured to become a proportional hazards model.

Time ratio is used to assess whether a covariate will accelerate or decelerate the failure times of an individual for the accelerated failure time model. The time ratio compares two categories of a covariate ($X_i = 1$) versus ($X_1 = 0$) which is defined as:

$$TR = \frac{exp(\beta_i | X_i = 1)}{exp(\beta_i | X_i = 0)} = exp(\beta_i) \tag{26}$$

which is perceived as the calculated ratio of the expected survival times between the two groups. A time ratio greater than 1 for the explanatory variable suggests that this predictor factor extends the duration to event, while a time ratio less than 1 signifies a higher likelihood of the event occurring earlier.

*Weibull AFT distribution*

Let the survival time $T$ be distributed according to the Weibull distribution characterized by a scale parameter, the hazard function for the $i^{th}$ person is defined as;

$$h(t; X_i) = exp(\boldsymbol{\beta'} X_i)\lambda\alpha(t)^{\alpha-1}, \lambda > 0, \alpha > 0 \tag{27}$$

where:$\lambda$ is the scale, $\alpha$ is the shape parameter. If $\alpha = 1$, then the equation of the hazard conforms to that of the exponential model. If $\alpha > 1$, the hazard intensifies as time progresses while if $\alpha < 1$, the hazard reduces as time advances. The survival function of the Weibull AFT model is given by;

$$S(t; X_i) = exp\{-\lambda t^{\alpha} exp(\boldsymbol{\beta'} X_i)\} \tag{28}$$

In the change point model, the assumption is that the shape parameter and the covariate effects will remain unchanged and only the changes in the scale parameter ($\lambda$) will be detected. Therefore;

$$\lambda(t) = \begin{cases} \lambda_1, & 0 \leq t \leq \tau \\ \lambda_2. & t > \tau \end{cases} \tag{29}$$

where $\lambda(t)$ is the function for the scale parameter, while $\lambda_1$ and $\lambda_2$ are the values of the scale parameter prior to and subsequent to the change point $\tau$. The Weibull AFT model with one point of change and without any covariates is given by;

$$h(t) = \begin{cases} \lambda_1\alpha t^{\alpha-1}, & 0 \leq t \leq \tau \\ \lambda_2\alpha t^{\alpha-1}, & t > \tau \end{cases} \tag{30}$$

The model with a single shift point involving a binary covariate is given by;

$$h(t; X_i) = \begin{cases} exp(\boldsymbol{\beta'} X_i)\lambda_1\alpha t^{\alpha-1}, & 0 \leq t \leq \tau \\ exp(\boldsymbol{\beta'} X_i)\lambda_2\alpha t^{\alpha-1}, & t > \tau \end{cases} \tag{31}$$

where $\lambda_1$ and $\lambda_2$ are the scale parameters prior to and following the point of change respectively. The unknown parameter vector is $\theta = (\tau, \lambda_1, \lambda_2)$.

The cumulative hazard function,$H(t; X_i)$, is represented as;

$$H(t; X_i) = \begin{cases} \lambda_1 exp(\boldsymbol{\beta'} X_i) t^\alpha, & 0 \le t \le \tau \\ \lambda_1 exp(\boldsymbol{\beta'} X_i) \tau^\alpha + \lambda_2 exp(\boldsymbol{\beta'} X_i)(t^\alpha - \tau^\alpha), & t > \tau \end{cases} \tag{32}$$

The survival function is expressed as;

$$S(t; X_i) = \exp\big(-H(t; X_i)\big) = \begin{cases} \exp(-\lambda_1 \exp(\boldsymbol{\beta}' X_i)\, t^\alpha)\,, & 0 \le t \le \tau, \\ \exp\Big(-\lambda_1 \exp(\boldsymbol{\beta}' X_i)\, \tau^\alpha - \lambda_2 \exp(\boldsymbol{\beta}' X_i)\, (t^\alpha - \tau^\alpha)\Big), & t > \tau. \end{cases} \tag{33}$$

Here $\tau \in (0, T]$ is the change point within the observation window.

The log-likelihood function of a Weibull AFT model with a change point is expressed as;

$$l(\boldsymbol{\theta}) = \begin{cases} \sum_{i=1}^{n} \delta_i \, \log\big(\exp(\boldsymbol{\beta}' X_i)\, \lambda_1 \alpha\, t^{\alpha-1}\big) - \lambda_1 \exp(\boldsymbol{\beta}' X_i)\, t^\alpha, & (0 \le t \le \tau), \\ \sum_{i=1}^{n} \delta_i \, \log\big(\exp(\boldsymbol{\beta}' X_i)\, \lambda_2 \alpha\, t^{\alpha-1}\big) - \lambda_1 \exp(\boldsymbol{\beta}' X_i)\, \tau^\alpha - \lambda_2 \exp(\boldsymbol{\beta}' X_i)\, (t^\alpha - \tau^\alpha), & (t > \tau). \end{cases} \tag{34}$$

The MLEs for $\lambda_1$ and $\lambda_2$ can be found by differentiating the logarithmic likelihood function given in (34) with respect to $\lambda_1$ and $\lambda_2$ and equating to zero yielding;

$$\widehat{\lambda_1} = \frac{\sum_{i=1}^{n} \delta_i|_{(0 \le t \le \tau)}}{exp(\boldsymbol{\beta'} X_i) t^\alpha|_{(0 \le t \le \tau)} + exp(\boldsymbol{\beta'} X_i) \tau^\alpha|_{(t > \tau)}} \tag{35}$$

where $\sum_{i=1}^{n} \delta_i$ represents the count of failures within the interval $0 \le t \le \tau$.

$$\widehat{\lambda_2} = \frac{\sum_{i=1}^{n} \delta_i}{\sum_{i=1}^{N} exp(\boldsymbol{\beta'} X_i)(t^\alpha - \tau^\alpha)}, \quad t > \tau \tag{36}$$

where $\sum_{i=1}^{n} \delta_i$ represents the failure occurrences within the interval $t > \tau$. Differentiating (34) with respect to $\alpha$ gives;

$$\begin{aligned} \frac{\partial l(\boldsymbol{\theta})}{\partial \alpha} = & \sum_{i=1}^{n} \left[ \delta_i \Big( \tfrac{1}{\alpha} + \log(t_i) \Big) - \lambda_1 \exp(\boldsymbol{\beta'} X_i) t_i^\alpha \log(t_i) \right] (0 \le t \le \tau) \\ & + \sum_{i=1}^{N} \left[ \delta_i \Big( \tfrac{1}{\alpha} + \log(t_i) \Big) - \lambda_1 \exp(\boldsymbol{\beta'} X_i) \tau^\alpha \log(t_i) - \lambda_2 \exp(\boldsymbol{\beta'} X_i) \big( t_i^\alpha - \tau^\alpha \big) \log(t_i) \right] \quad (t > \tau) \end{aligned} \tag{37}$$

Setting (37) to zero and solving for $\widehat{\alpha}$ generally requires numerical methods, as no closed-form solution exists. Differentiating the logarithmic likelihood function in relation to the regression coefficients $\beta$ yields;

$$\begin{aligned} \frac{\partial l(\boldsymbol{\theta})}{\partial \beta} = & \sum_{i=1}^{n} (\delta_i X_i - X_i \exp(\boldsymbol{\beta'} X_i) t_i^\alpha)\ (0 \le t \le \tau) + \sum_{i=1}^{n} \Big( \delta_i X_i - \lambda_1 X_i \exp(\boldsymbol{\beta'} X_i) \tau^\alpha \\ & - \lambda_2 X_i \exp(\boldsymbol{\beta'} X_i)(t^\alpha - \tau^\alpha) \Big)\, (t > \tau) \end{aligned} \tag{38}$$

Numerical optimization is required to estimate $\boldsymbol{\beta}$ as (38) does not have an explicit form because it is non linear in $\beta$ due to the exponential terms. By plugging the estimates of $\lambda_1$ and $\lambda_2$ obtained in (35) and (36) respectively into the log-likelihood function obtained in (34), the profile likelihood for $\alpha$, $\beta$ and $\tau$ can be determined. The nuisance parameters ($\alpha$ and $\beta$) and the change point $\tau$ will be estimated using Nelder-Mead simplex algorithm. Once these estimates are obtained, they can be employed to compute the MLEs of $\lambda_1$ and $\lambda_2$.

Due to the complexities surrounding the empirical distribution of the likelihood ratio test in the change point setting, the following bootstrap scheme as explained in [10] was applied to approximate the distribution of the test statistic under the null hypotheses.

### *2.6. The Adequacy of the Regression Models*

#### *2.6.1. The Cox Proportional Hazards Model*

The techniques employed to check the suitability of the Cox PH models include the Kaplan Meier curves, residual plots and Grambsch and Therneau test for the PH assumption.

*Kaplan–Meier curves*, Kaplan–Meier curves for subgroups with different covariates can be plotted to visualize how these covariates influence survival in relation to the estimated change point. In addition to highlighting differences between subgroups, the curves can help assess whether the change point was correctly estimated by examining the slope of the survival curves before and after the change. If the change point causes a noticeable shift in slope or survival pattern across subgroups, it suggests that the Cox–PH model appropriately reflects interactions between covariates and time (hazard function). Conversely, if the curves for different subgroups are not clearly distinct, show similar slopes before and after the change, or exhibit no noticeable shift at the estimated change point, it may indicate that the interaction between covariates and the change point is not well captured by the model.

*Cox Snells residuals*, The Cox-Snell residuals, introduced by [7], for the $i^{th}$ individual with a recorded time $t_i$ is described as follows:

$$R_i = \widehat{H_i}(t_{i|X_i}) = -log\left[\widehat{S_i}(t_i|X_i)\right] \tag{39}$$

For a person $i$ with observed survival time $t_i$ and a group of predictors $X_i$, the Cox-Snell residual $R_i$ is described as:

$$R_i = \widehat{H_0}(t_i)exp(\widehat{\beta}'X_i) = \widehat{H_i}(t_i) = -log\left[\widehat{S_i}(t_i)\right] \tag{40}$$

where $\widehat{H_0}(t_i)$ is is the estimated cumulative baseline hazard function at time $t_i$ and $exp(\widehat{\beta}'X_i)$ is the calculated relative risk for individual $i$ based on their covariates $X_i$ and the estimated vector of regression coefficients $\widehat{\beta}$. In essence, Cox-Snell residuals represent an individual's cumulative hazard under the fitted model. Plotting the Cox-Snell residuals versus the cumulative hazard function allows for an evaluation of the model's fit. A well-fitting model will display a linear relationship through the point $(0, 0)$ with unity slope. In addition, in the event that the model is well-fitted, the value $\widehat{S_i}(t_i)$ would exhibit features comparable to those of $S_i(t_i)$. If the residuals deviate significantly from this distribution, It implies that the model does not provide a good fit for the data or that there might be model misspecifications including incorrect covariate inclusion or omitted variables.

*Deviance residuals*, The deviance residuals, introduced by [26], is given by;

$$r_{dri} = \text{sign}(r_{mri})\sqrt{-2(r_{mri} + \delta_i log(\delta_i - r_{mri}))} \tag{41}$$

where The sign function, denoted as $sign(r_{mri})$, assigns a value of one if $r_{mri>0}$ and negative one if $r_{mri} < 0$; $r_{mri} = \delta_i - r_{ci}$ represent the Martingale residuals for the $i^{th}$ person where $\delta_i$ takes a value of one for uncensored observations and a value of zero for censored observations. One significant limitation of the martingale residual is its inherent asymmetry; while it has an upper bound of 1, it lacks a defined lower bound. Additionally, Martingale residuals exhibit a skewed distribution with an expected value of zero. The deviance residuals are a standardized transformation of the Martingale residuals, maintaining a zero average. When the fitted model is a good fit, these residuals are roughly symmetrically distributed around zero. Model fit can be assessed via a plot of deviance residuals versus covariates. Unusual patterns in the plot may indicate data features not adequately captured by the model. Exceptionally high or low residual values could indicate potential outliers that require further investigation.

In a fitted Cox proportional hazards model, the hazard of an event for a person at any given time is determined by the risk score, defined as:

$$\text{Risk score} = \exp(\boldsymbol{\beta}'\mathbf{X})$$

A diagnostic plot of deviance residuals versus the risk score can help evaluate how well the model fits each individual. Observations with large absolute deviance residuals may indicate potential outliers. This plot provides valuable insights into the characteristics of observations that are not adequately captured by the model.

*Schoenfeld residuals*, The Martingale and devianced residuals discussed in the subsection above pertain to individual observations. Scoenfeld residuals, introduced by [24], are covariate-specific residuals. Originally referred to as partial residuals, the Schoenfeld residual of the $i^{th}$ person on the $j^{th}$ predictor factor, $X_j$ represents an estimate of element $i$ of the first derivative of the log of the partial likelihood function with regard to $\beta_j$. The logarithmic partial likelihood function is expressed as;

$$\frac{\partial logL(\beta)}{\partial \beta j} = \sum_{i=1}^{p} \delta i(x_{ij} - b_{ij}) \tag{42}$$

Here, $x_{ij}$ represents the value of the $j^{th}$ covariate for individual $i$. Also,

$$a_{ji} = \frac{\sum_{l \epsilon R(t_i)} x_{jl}\text{exp}(\beta' x_i)}{\sum_{l \epsilon R(t_i)} \text{exp}(\beta' x_i)} \tag{43}$$

The $i^{th}$ individual's Schoenfeld residual on the $j^{th}$ covariate, $x_j$, is given by:

$$r_{sji} = \delta_i(x_{ji} - b_{ji}) \tag{44}$$

The Schoenfeld residuals are primarily used to assess the proportional hazards assumption in the Cox model. Under this assumption, the residuals should be independent of time; any systematic trend in a plot of Schoenfeld residuals against time suggests a possible violation. The following statistical test involves a test statistic that quantifies the relationship between each predictor's Schonfeld residuals and its ranked failure times.

*Grambsch and Therneau test*, Reference [12] proposed a test for the nonproportional hazard assumption by utilizing scaled schonfeld residuals. This test involves both the global and covariate specific version. The test statistic for the covariate specific version is given as follows:

$$TG_x = \frac{\{\sum_u (g_x - \overline{g}) sr_x^*\}^2}{uI_j \sum_u (g_x - \overline{g})^2} \tag{45}$$

where $sr_x^*$ represents the scaled schonfeld residual for predictor variable $j$, $g_x$ be the time scale associated with the covariate $x$, $\overline{g}$ represent the average time scale, $I_x$ represent the information matrix for the elements for the covariate $x$ and $u$ represents the event times. In the Grambsch and Therneau test, the distribution of the test statistic follows a Chi-squared distribution. When testing a single covariate, the test statistic has 1 degree of freedom. However, when testing multiple covariates simultaneously, the degrees of freedom correspond to the number of covariates being tested. If the test statistic exceeds the critical value from the Chi-squared distribution at the chosen significance level, It is interpreted as evidence of a violation of the nonproportional assumption for that covariate.

#### *2.6.2. The Weibull Accelerated Failure Times Model*

Methods used to assess the adequacy of AFT models include quantile–quantile (QQ) plots and Cox–Snell residuals.

*Quantile-quantile plot* A QQ plot is constructed to evaluate whether the AFT model adequately fits the data by comparing two distinct population groups. The $p^{th}$ percentile for any $p$ value within the range $(0, 100)$ is defined as;

$$t(p) = S^{-1}\left(\frac{100 - p}{100}\right) \tag{46}$$

Let $t_0(p)$ and $t_1(p)$ denote the $p^{th}$ percentiles derived based on the survival distributions of the two survival data groups and let $S_0(t)$ and $S_1(t)$ denote their respective survival functions. Since $t_0(p)$ and $t_1(p)$ correspond to the same percentile $p$, both survival functions yield the same survival probability when evaluated at these times. Thus;

$$S_1[t_1(p)] = S_0[t_0(p)] \tag{47}$$

Within the framework of the AFT model, $S_i(t) = S_0\left(\frac{t}{exp(\beta' X)}\right)$ Therefore

$$S_1[t_1(p)] = S_0\left[\frac{t_1(p)}{exp(\beta' X)}\right] \tag{48}$$

Therefore;

$$t_0(p) = \frac{t_i(p)}{exp(\beta' X)} \tag{49}$$

For the Weibull AFT distribution;

$$t_i(p) = exp\left[\sigma log\left\{-log\left(\frac{100 - p}{100}\right)\right\} + \beta_0 + \beta' X_i\right] \tag{50}$$

The survival distribution percentiles for two different groups can be determined using the Kaplan-Meier estimates of their corresponding survival functions. If AFT model is appropriate, plotting the percentiles of the two groups against each other should yield an approximately straight line passing through point$(0, 0)$. The gradient of this line estimates the acceleration factor $\frac{1}{exp(\beta' X)}$. *Cox Snells Residuals* Cox-Snell residuals are also implemented to assess the overall adequacy of the AFT model. For the AFT model, the Cox-Snell residuals for participant $i$ with recorded time $t_i$ is described as:

$$\begin{aligned} R_i &= -\log\left[\widehat{S}_i(t_i)\right] \\ &= -\log\left[S_{e_i}\left(\frac{\log(t) - \beta_0 - \beta_1 X_1 - \cdots - \beta_p X_p}{\sigma}\right)\right] \end{aligned} \tag{51}$$

Cox-Snell residual is applicable to any fully parameter-defined model, and the specific form of residuals can be derived for a given AFT model. For instance, in the case of a Weibull AFT model, since $S_{e_i(e)} = exp(-exp(e))$, the Cox-Snell residual is consequently defined as;

$$\begin{aligned} R_i &= -\log\left[\widehat{S}_i(t_i)\right] \\ &= -\log\left[S_{e_i}\left(\frac{\log(t) - \beta_0 - \beta_1 X_1 - \cdots - \beta_p X_p}{\sigma}\right)\right] \\ &= \exp\left(\frac{\log(t) - \beta_0 - \beta_1 X_1 - \cdots - \beta_p X_p}{\sigma}\right). \end{aligned} \tag{52}$$

If the fitted model is suitable, the graph of $log(-log(S(R_i)))$ versus $log(R_i)$ should form a straight line via the point$(0, 0)$ with a slope of one.

## 3. Empirical Results

### *3.1. Simulation Study*

A simulation study was conducted to evaluate the performance of the likelihood ratio test in detecting a change point in the hazard function. A sample was generated from a piecewise exponential distribution characterized by a change in hazard rate at a specified point in time. The study explored the effects of varying sample size, failure rate, and change point location, with each observation subject to fixed Type I censoring. Each simulation scenario was replicated 500 times using Monte Carlo methods to ensure robust and reliable results.

The presence of a change point in the simulated data was tested using the likelihood ratio test. Under the null hypothesis of no change, a single hazard rate of 0.4 was assumed, while under the alternative hypothesis of a change, the hazard rates were assumed to be $\lambda_1 = 0.35$ and $\lambda_2 = 0.15$, with a change point at $\tau_s = 5$. A sample size of 200 was used for the test. For the null hypothesis (single hazard rate), the optimization was performed using the Brent method [9], which is suitable for single-parameter estimation. For the alternative hypothesis (two hazard rates and a change point), the Nelder-Mead algorithm [25] was used, as it efficiently

optimizes multiple parameters. The estimated value of the change point was $5.14$ which was found to be significant with an LRT statistic of $35.76$ and a p-value of approximately $0.$ since the p-value was less than $0.05$, leading to the rejection of the null hypothesis of no change.

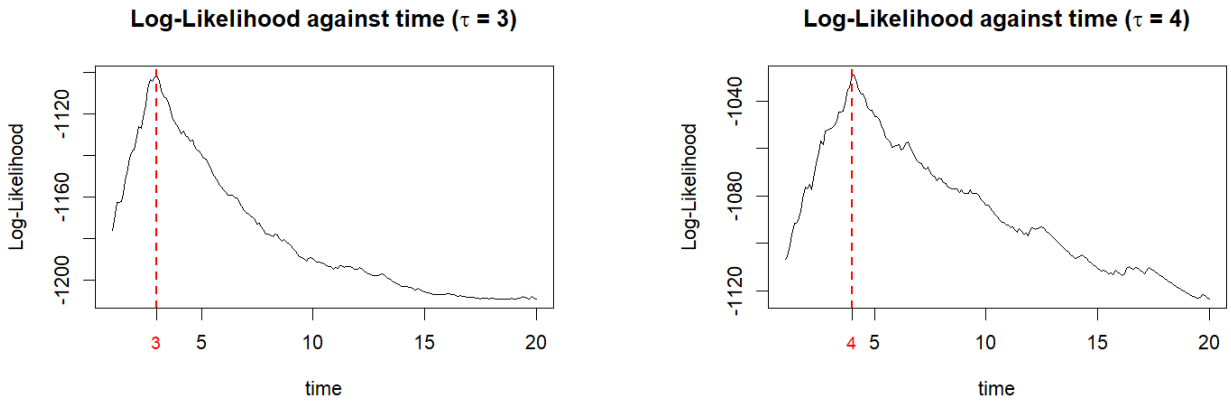
To illustrate the estimation procedure, Figure 1 presents the log-likelihood function plotted against time, showing how the likelihood varied across candidate change points. The estimated change point corresponds to the time that maximized the log-likelihood. This example is based on the scenario with $\lambda_1 = 0.4$, $\lambda_2 = 0.1$, and a sample size of 500.

The properties of the maximum likelihood estimation procedure under different experimental conditions, analyses were conducted using sample sizes of $100$, $200$, $300$, and $500$ and all observations were subject to fixed Type I censoring at time $20$. The maximum likelihood estimates of the parameters were obtained using the Nelder-Mead algorithm. It is important to note that convergence issues occurred in certain scenarios, particularly when the change point was close to the end of the observation period and the hazard rates were similar, resulting in a small magnitude of change of $0.2$. Specifically, estimation difficulties were encountered under a sample size of $500$ with a change point at time $5$, and under sample sizes of $300$ and $500$ with a change point at time $6$, all of which had the smallest magnitude of change of $0.2$. Additionally, issues arose under sample sizes of $100$ and $500$ with a change point at time $6$ when the magnitude of change was $0.35$. Due to the difficulty of reliably identifying change points occurring too close to the beginning or end of the observation period, where few events are observed, these scenarios were excluded from the final results presented. Table 1 presents the results of the maximum likelihood estimation, showing the estimated hazard rates $\lambda_1$ and $\lambda_2$, the estimated change point $\tau_s$, and their corresponding mean squared errors (MSEs) for simulated change points at times $3$, $4$, $5$, and $6$ under three sets of failure rates: (i) $\lambda_1 = 0.45$, $\lambda_2 = 0.10$; (ii) $\lambda_1 = 0.40$, $\lambda_2 = 0.10$; and (iii) $\lambda_1 = 0.35$, $\lambda_2 = 0.15$.

***Table 1.*** *Parameter Estimates of Pre- and Post-Change Hazard Rates with corresponding MSEs.*

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $\lambda_1 = 0.45,\ \lambda_2 = 0.1, \Delta = 0.35$ | | | | | | | | | | | | |
| | $\tau_s = 3$ | | | $\tau_s = 4$ | | | $\tau_s = 5$ | | | $\tau_s = 6$ | | |
| $n$ | $\hat{\lambda}_1$ | $\hat{\lambda}_2$ | $\hat{\tau}_s$ | $\hat{\lambda}_1$ | $\hat{\lambda}_2$ | $\hat{\tau}_s$ | $\hat{\lambda}_1$ | $\hat{\lambda}_2$ | $\hat{\tau}_s$ | $\hat{\lambda}_1$ | $\hat{\lambda}_2$ | $\hat{\tau}_s$ |
| 100 | 0.4413 | 0.0867 | 2.9749 | 0.4341 | 0.0731 | 3.9330 | 0.4213 | 0.0583 | 4.9110 | 0.4080 | 0.0468 | 5.8750 |
| | (0.00256) | (0.00041) | (0.02420) | (0.00236) | (0.00094) | (0.05263) | (0.00254) | (0.00198) | (0.09019) | (0.00246) | (0.00299) | (0.10360) |
| 200 | 0.4427 | 0.0903 | 2.9833 | 0.4305 | 0.0770 | 3.9750 | 0.4203 | 0.0625 | 4.9380 | 0.4080 | 0.0468 | 5.8750 |
| | (0.00114) | (0.00020) | (0.01191) | (0.00135) | (0.00063) | (0.03025) | (0.00170) | (0.00155) | (0.05446) | (0.00246) | (0.00299) | (0.10360) |
| 300 | 0.4444 | 0.0907 | 2.9956 | 0.4320 | 0.0785 | 3.9790 | 0.4215 | 0.0627 | 4.9410 | 0.4092 | 0.0483 | 5.9120 |
| | (0.00080) | (0.00016) | (0.00829) | (0.00089) | (0.00054) | (0.01821) | (0.00134) | (0.00148) | (0.03742) | (0.00219) | (0.00279) | (0.06987) |
| 500 | 0.4446 | 0.0928 | 2.9922 | 0.4328 | 0.0791 | 3.9790 | 0.4200 | 0.0647 | 4.9670 | 0.4092 | 0.0483 | 5.9120 |
| | (0.00052) | (0.00010) | (0.00443) | (0.00071) | (0.00049) | (0.00770) | (0.00124) | (0.00131) | (0.02042) | (0.00219) | (0.00279) | (0.06987) |
| $\lambda_1 = 0.4,\ \lambda_2 = 0.1, \Delta = 0.3$ | | | | | | | | | | | | |
| 100 | 0.4010 | 0.0890 | 2.9625 | 0.3924 | 0.0793 | 3.9496 | 0.3811 | 0.0673 | 4.9350 | 0.3738 | 0.0535 | 5.8340 |
| | (0.00209) | (0.00033) | (0.02754) | (0.00193) | (0.00065) | (0.05809) | (0.00166) | (0.00132) | (0.08748) | (0.00195) | (0.00243) | (0.17440) |
| 200 | 0.3998 | 0.0934 | 2.9774 | 0.3906 | 0.0837 | 3.9860 | 0.3815 | 0.0718 | 4.9520 | 0.3718 | 0.0577 | 5.9920 |
| | (0.00112) | (0.00016) | (0.01521) | (0.00098) | (0.00039) | (0.02446) | (0.00109) | (0.00094) | (0.05063) | (0.00144) | (0.00195) | (0.09633) |
| 300 | 0.3966 | 0.0950 | 2.9923 | 0.3909 | 0.0855 | 3.9800 | 0.3797 | 0.0729 | 4.9710 | 0.3720 | 0.0594 | 5.9340 |
| | (0.00077) | (0.00011) | (0.00900) | (0.00059) | (0.00028) | (0.01870) | (0.00086) | (0.00082) | (0.03341) | (0.00120) | (0.00175) | (0.07160) |
| 500 | 0.3990 | 0.0963 | 2.9914 | 0.3906 | 0.0870 | 3.9900 | 0.3810 | 0.0745 | 4.9730 | 0.3719 | 0.0611 | 5.9530 |
| | (0.00043) | (0.00006) | (0.00507) | (0.00041) | (0.00022) | (0.01164) | (0.00064) | (0.00070) | (0.01984) | (0.00101) | (0.00158) | (0.03684) |
| $\lambda_1 = 0.35,\ \lambda_2 = 0.15, \Delta = 0.2$ | | | | | | | | | | | | |
| 100 | 0.3409 | 0.1175 | 3.0010 | 0.3382 | 0.1053 | 4.0110 | 0.3301 | 0.0915 | 4.9640 | 0.3250 | 0.0787 | 5.9340 |
| | (0.00206) | (0.00126) | (0.04716) | (0.00155) | (0.00223) | (0.07767) | (0.00151) | (0.00371) | (0.11240) | (0.00175) | (0.00541) | (0.18480) |
| 200 | 0.3381 | 0.1203 | 3.0060 | 0.3345 | 0.1090 | 4.0250 | 0.3285 | 0.0954 | 5.0040 | 0.3227 | 0.0817 | 5.9740 |
| | (0.00104) | (0.00100) | (0.02487) | (0.00097) | (0.00181) | (0.06076) | (0.00103) | (0.00313) | (0.06682) | (0.00128) | (0.00484) | (0.09422) |
| 300 | 0.3401 | 0.1221 | 2.9960 | 0.3335 | 0.1106 | 4.0130 | 0.3284 | 0.0969 | 5.0030 | 0.3227 | 0.0817 | 5.9740 |
| | (0.00068) | (0.00084) | (0.01659) | (0.00071) | (0.00163) | (0.02933) | (0.00082) | (0.00292) | (0.04763) | (0.00128) | (0.00484) | (0.09422) |
| 500 | 0.3390 | 0.1240 | 2.9979 | 0.3334 | 0.1116 | 4.0090 | 0.3284 | 0.0969 | 5.0030 | 0.3227 | 0.0817 | 5.9740 |
| | (0.00045) | (0.00071) | (0.01269) | (0.00054) | (0.00152) | (0.01808) | (0.00082) | (0.00292) | (0.04763) | (0.00128) | (0.00484) | (0.09422) |

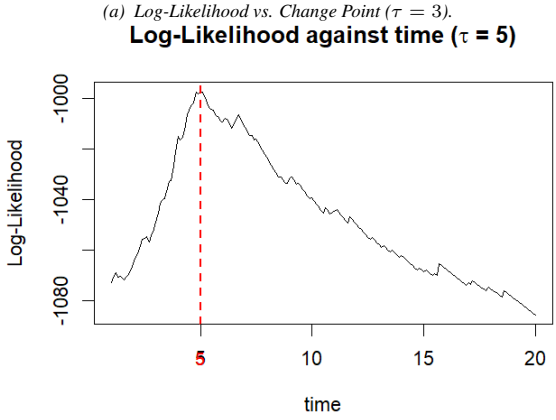
Note: $\lambda_1$ and $\lambda_2$ are the pre- and post-change hazard rates, respectively. $\Delta = \lambda_1 - \lambda_2$ is the change magnitude. $\tau_s$ is the change point. $n$ denotes sample size. Values in parentheses are the corresponding MSEs of the estimates.



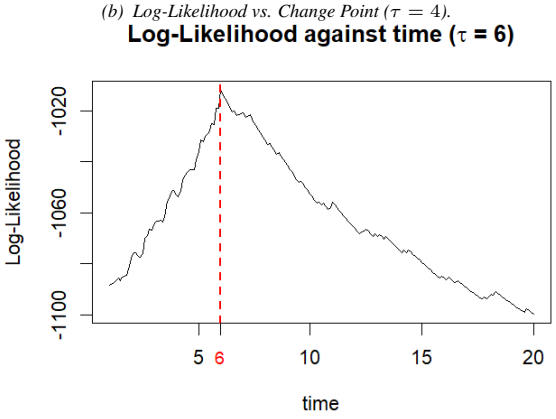

*(a) Log-Likelihood vs. Change Point ($\tau = 3$).*




*(b) Log-Likelihood vs. Change Point ($\tau = 4$).*




*(c) Log-Likelihood vs. Change Point ($\tau = 5$).*




*(d) Log-Likelihood vs. Change Point ($\tau = 6$).*

***Figure 1.*** *Plots of the log-likelihood values evaluated at different candidate change points. The red dashed line indicates the estimated change point that maximizes the log-likelihood.*

The inclusion of MSEs provides measures of estimation variability across the 500 Monte Carlo replications. These results illustrate how estimation accuracy improves with increasing sample size and highlight the influence of different combinations of failure rates and change point locations on the bias and precision of the parameter estimates.

For each simulated sample, censoring was maintained at $5\%$, as higher percentages of censoring leads to higher mean square error of the estimates as noted by [18] as increased censoring leads to fewer observed events, increasing the variance of estimates and potentially introducing bias, both of which contribute to a higher mean square error of the estimates.

The results in Table 1 shows that as the sample size increases, the MLE estimates of $\tau_s$, $\lambda_1$ and $\lambda_2$ converge to their true values for the change point and hazard rates which is consistent with the results obtained by [4, 5, 15, 23]. Hence, $\widehat{\tau_s}$, $\widehat{\lambda_1}$ and $\widehat{\lambda_2}$ are consistent estimators of $\tau_s$, $\lambda_1$ and $\lambda_2$ respectively. In addition, it is evident that estimation precision improved as the magnitude of the change between the pre-change and post-change failure rates increased, even when sample size was held constant. That is, when the two failure rates were more distinct from each other, the maximum likelihood estimation method performed better at identifying both the change point and the hazard rates. Moreover, when the change point occurred closer to the end of the observation period, the MSE of the change point estimate increased, holding the hazard rates and sample size constant.

To further evaluate the power of the likelihood ratio test, its power in detecting a change point was determined by examining how sample size, change point location, and magnitude of change in hazard rates affected the test's performance. The LRTs power was computed as the proportion of simulations in which the estimated change point satisfied the predefined accuracy criterion. That is;

$$\text{Power} = \frac{\text{Number of correct } \tau \text{ estimates}}{\text{Total Monte Carlo runs}} \tag{53}$$

An estimate $\widehat{\tau_s}$ was regarded as correct if: $\frac{|\widehat{\tau_s} - \tau_s|}{\tau_s} \leq 0.1$. This value was chosen to balance computational efficiency and accuracy–small enough to ensure stable parameter estimates, but not so small that it would significantly increase computation time.

To examine the sample size effect, hazard rates were set to ($\lambda_1 = 0.4$, $\lambda_2 = 0.1$), change point at $\tau_s = 5$ while sample sizes ranged from 100 to 500 and the power calculated for each sample. The results are presented in table 2. The results from Table 2 showed that the likelihood ratio tests ability to correctly identify the change point improved substantially with increasing sample size. Figure 2 illustrates this trend, showing that power increased with sample size, approaching 1 for the largest sample considered. This finding is consistent with results reported by [11, 21]. Thus, detecting a change point

is easier with larger samples compared to smaller ones.

To investigate the effect of the magnitude of change, the sample size was set to 200, $\tau_s = 5$ while various magnitudes of change varied from $0.27$ to $0.45$. The power was then calculated for each magnitude of change and the results are presented in Table 3.

The results showed that the likelihood ratio tests ability to correctly identify the change point improved as the magnitude of change increased. Figure 3 illustrates this trend, showing that the power of the test rose steadily with larger differences between the pre-change and post-change hazard rates, approaching 1 for the highest magnitudes considered. This finding is consistent with results reported by [1, 11, 21]. Thus, detecting a change point is easier when there is a large difference in hazard rates compared to when the change is small.

To determine the effect of the location of change, the end time was fixed at 20, the sample size was set to 200, and the pre- and post-change hazard rates were set to $0.45$ and $0.15$, respectively. The timing of the change point varied from $0.5$ to $6$. The power was then calculated for each change point location, and the results are presented in Table 4.

The simulation results demonstrates that the power of the likelihood ratio test improved with increasing sample size, greater magnitude of change between hazard rates, and when the change point was located closer to the center of the observation period. These findings affirm the reliability and sensitivity of the test under ideal conditions. In application to real data, the proposed method was used to examine its effectiveness in detecting a change point in colon cancer recurrence survival times.

### 3.2. Application to Real Data

This section investigates significant change points in the hazard function for time to recurrence among colon cancer patients. The presence of a change point was tested using the likelihood ratio test, and if detected, the change point was estimated using the maximum likelihood method. Both the Weibull Accelerated Failure Time model and the Cox Proportional Hazards model were employed to evaluate potential changes in the survival data.

***Table 2.*** *Power Estimates for Different Sample Sizes.*

| **Sample Size (n)** | 100 | 150 | 200 | 250 | 300 | 350 | 400 | 500 |
|---|---|---|---|---|---|---|---|---|
| **Power Estimate** | 0.904 | 0.936 | 0.948 | 0.972 | 0.982 | 0.992 | 0.995 | 0.996 |

***Table 3.*** *Power Estimates for Different Magnitudes of Change.*

| **Magnitude of Change** | 0.27 | 0.29 | 0.30 | 0.33 | 0.35 | 0.37 | 0.40 | 0.45 |
|---|---|---|---|---|---|---|---|---|
| **Power Estimate** | 0.944 | 0.945 | 0.948 | 0.972 | 0.982 | 0.990 | 0.996 | 0.998 |

***Table 4.*** *Power Estimates for Different Timings of Change.*

| $\tau_s$ | 0.5 | 1.0 | 2.0 | 3.0 | 4.0 | 5.0 | 5.5 | 6.0 |
|---|---|---|---|---|---|---|---|---|
| **Power Estimate** | 0.910 | 0.944 | 0.986 | 0.978 | 0.960 | 0.956 | 0.954 | 0.938 |

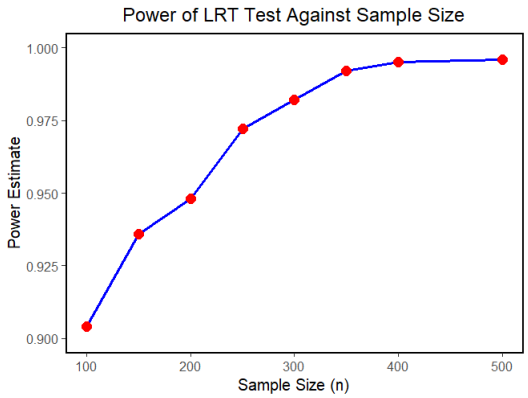



***Figure 2.*** *Power of the Likelihood Ratio Test Against Sample Size.*

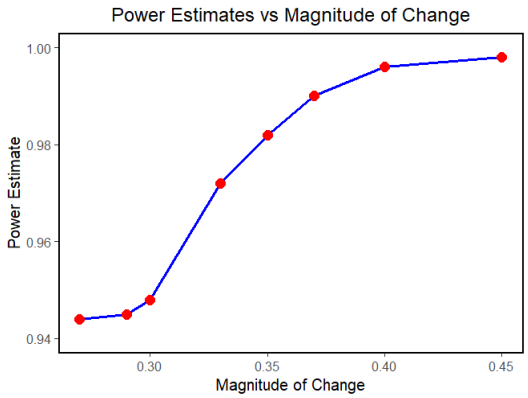



***Figure 3.*** *Power of the Likelihood Ratio Test Against Magnitude of Change.*

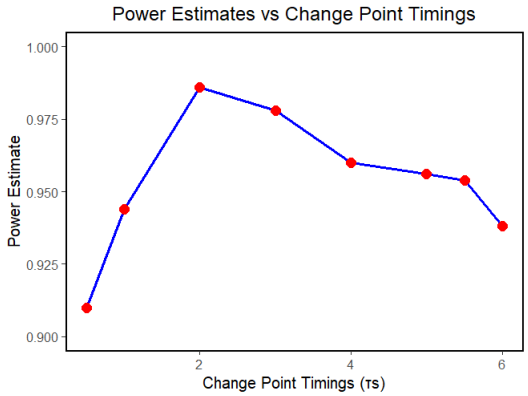



***Figure 4.*** *Power of the Likelihood Ratio Test Against Change Point Locations.*

*Data source and Data Description*

The dataset for this study was sourced from the `R survival` package and includes records for 888 sequential patients diagnosed with stage III colon cancer. While the original dataset contained records for both recurrence and mortality, this study exclusively focused on recurrence events. Individuals who did not experience a recurrence were considered non-informatively censored at the survey date since it occurred due to administrative end of follow-up rather than factors related to the underlying risk of recurrence. In total, 446 patients (50.2%) experienced a recurrence, and 442 (49.8%) were censored. The dataset includes demographic variables (gender and age), treatment assignments (observation only, levamisole alone, or levamisole plus 5-fluorouracil), and various tumor characteristics including obstruction status, perforation, adherence to adjacent organs, extent of local spread, tumor differentiation grade, and number of affected lymph nodes. Additional clinical variables such as time from surgery to registration were also available. The cohort was fairly balanced by gender (51.8% male) and treatment groups (ranging from 32.5% to 34.3% across the three treatment arms).

### *3.3. The Effects of Covariates on Survival Times Using the Cox Proportional Hazard Model*

In this section, the Cox Proportional Hazards model was fitted to examine the effects of covariates on the time to recurrence of colon cancer patients. The primary objective was to identify the statistically significant covariates, which would subsequently be considered in the change point analysis. Focusing on significant variables allowed for a more targeted investigation of potential changes in the hazard function over time.

Table 5 presents the estimated coefficients, standard errors, hazard ratios, and p-values for each covariate included in the Cox Proportional Hazards model. These results provide insight into the strength and significance of the associations between patient characteristics and the risk of cancer recurrence.

***Table 5.*** *Cox PH Model Estimates for Covariates Affecting Survival Time.*

| Covariate | Coefficient | Std.Error | P-Value | Hazard Ratio |
|---|---|---|---|---|
| Gender | -0.128 | 0.096 | 0.182 | 0.880 |
| Treatment type | -0.235 | 0.058 | 0.000 | 0.791 |
| Age | -0.003 | 0.004 | 0.500 | 0.997 |
| Obstruction of tumour | 0.182 | 0.119 | 0.125 | 1.200 |
| Perforation of tumour | 0.213 | 0.257 | 0.406 | 1.238 |
| Adherence to nearby organs | 0.169 | 0.130 | 0.195 | 1.184 |
| Affected lymph nodes | 0.041 | 0.015 | 0.006 | 1.042 |
| Tumor differentiation | 0.136 | 0.098 | 0.166 | 1.145 |
| Extent of local spread | 0.450 | 0.118 | 0.000 | 1.569 |
| Surgery–registration time | 0.232 | 0.104 | 0.025 | 1.262 |
| Positive nodes | 0.573 | 0.141 | 0.000 | 1.773 |

From the results in table 5, the coefficients for the covariates gender, treatment and age were negative indicating that the risk of colon cancer recurrence decreased for male gender, those receiving the new treatment and with increase in age. In contrast, the coefficients associated with all other covariates including obstruction, perforation, adherence, number of positive nodes, differentiation and extent of local cancer spread were positive, suggesting a higher risk of recurrence for individuals associated with these covariates. Furthermore, at a 5% significance level, the covariates treatment, number of positive nodes, extent of local spread, time from surgery to registration and having more than four positive nodes were significant in determining the time to colon cancer recurrence, as their p-values were less than 5% level of significance.

Although tumour perforation is clinically recognised as a risk factor for recurrence, primarily because it may facilitate dissemination of malignant cells into the peritoneal cavity, its effect may not always emerge as statistically significant in multivariable models. In this cohort, patients with perforated tumours may have benefited from complete surgical resection with adequate margins and more aggressive adjuvant therapy, which could have reduced their recurrence risk to levels comparable to patients without perforation. Furthermore, the relatively small number of perforation cases in the dataset,

together with adjustment for other strong prognostic factors such as extent of local spread and lymph node involvement, may have limited the independent contribution of perforation to the hazard of recurrence. Consequently, while the clinical literature supports an elevated risk after perforation, our findings suggest that in this specific patient group, its effect was attenuated and not statistically significant.

*The effects of covariates on the location of the change point using the Cox Proportional Hazard model*

Maximum likelihood estimates for the Cox PH model parameters were obtained using the Nelder–Mead optimization algorithm. Initial values for the parameters $\alpha$ and $\beta$ were estimated using the `survreg` function, while a grid search was conducted to determine initial values for the change point. The likelihood ratio statistic was computed for the original dataset and compared against the empirical distribution of statistics obtained from simulated datasets generated under the null hypothesis.

Using the bootstrap procedure, model parameters were estimated using Maximum Likelihood Estimation method, including change points, coefficients before and after each change point, and corresponding hazard ratios. Table 6 presents the comprehensive change point analysis results, showing estimated change points ($\hat{\tau}$), pre- and post-change coefficients ($\hat{\beta}_1$, $\hat{\beta}_2$) with their hazard ratios ($\mathrm{HR}_1$, $\mathrm{HR}_2$), likelihood ratio test statistics, and bootstrap critical values used to assess statistical significance.

For the treatment type, a change point was identified, indicating that treatment effects on recurrence risk varied over time. Before the change point, the levamisole + 5-FU group showed a stronger protective effect compared to observation only or levamisole alone. After the change point, this protective effect became even more pronounced, suggesting a delayed increase in treatment benefits. The likelihood ratio test confirmed this change was statistically significant.

For the number of positive lymph nodes, a change point was identified, indicating that its effect on recurrence risk varied over time. Before the change point, having more than four positive nodes was associated with an increased risk of recurrence, and this risk became even higher after the change point, suggesting an intensifying detrimental effect. The likelihood ratio test confirmed this change was significant.

For the extent of local cancer spread, a change point was also detected. Initially, greater cancer spread was linked to a moderate increase in recurrence risk, but after the change point, the risk rose further, indicating a stronger adverse effect over time. This change was statistically significant based on the likelihood ratio test.

For time from surgery to registration, a change point indicated varying effects over time. Initially, a shorter time from surgery slightly reduced recurrence risk. However, after the change point, a longer time became associated with a notably increased risk. The likelihood ratio test showed this change in effect was significant.

### 3.4. The Effects of Covariates on Survival Times Using the Weibull Accelerated Failure Time Model

In this section, the Weibull AFT model was fitted to examine the relationship between covariates and survival time. Statistically significant covariates influencing the time to recurrence of colon cancer were identified. These covariates were then used as inputs in the subsequent change point detection analysis, where shifts in their effects on the hazard function over time were explored. Table 7 presents the estimated regression coefficients, corresponding time ratios, standard errors, and p-values for each covariate included in the model.

The results in table 7 indicated that covariates obstruction, perforation, adherence, number of positive nodes, tumor differentiation, extent of local spread, time from surgery to registration, and having more than four positive nodes increased the risk of colon cancer recurrence, as their coefficients were positive and the time ratio was greater than one. However, at a $5\%$ significance level, treatment type, number of positive nodes, extent of local spread, time from surgery to registration, and having more than four positive nodes are statistically significant in determining the time to recurrence.

***Table 6.*** *Change Point Detection Results: Parameter Estimates and Likelihood Ratio Test Statistics.*

| Covariate | $\hat{\tau}$ | $\hat{\beta}_1$ | $\mathrm{HR}_1$ | $\hat{\beta}_2$ | $\mathrm{HR}_2$ | LRT | Bootstrap Critical Value |
|---|---|---|---|---|---|---|---|
| Treatment type | 1055 | -0.107 | 0.899 | -0.382 | 0.682 | 1137.172 | 772.403 |
| Positive nodes | 1086 | 0.561 | 1.753 | 0.593 | 1.810 | 1108.003 | 696.426 |
| Extent of local spread | 1196 | 0.253 | 1.288 | 0.339 | 1.404 | 1127.494 | 265.341 |
| Surgery–registration time | 1098 | -0.058 | 0.944 | 0.616 | 1.852 | 1150.573 | 712.843 |

***Table 7.*** *Weibull AFT Model Estimates for Covariates Affecting Survival Time.*

| Covariate | Coefficient | Std.Error | P-Value | Time ratio |
|---|---|---|---|---|
| Gender | -0.155 | 0.131 | 0.2350 | 0.856 |
| Treatment Type | -0.351 | 0.080 | 0.0000 | 0.704 |
| Age | -0.003 | 0.006 | 0.5591 | 0.997 |

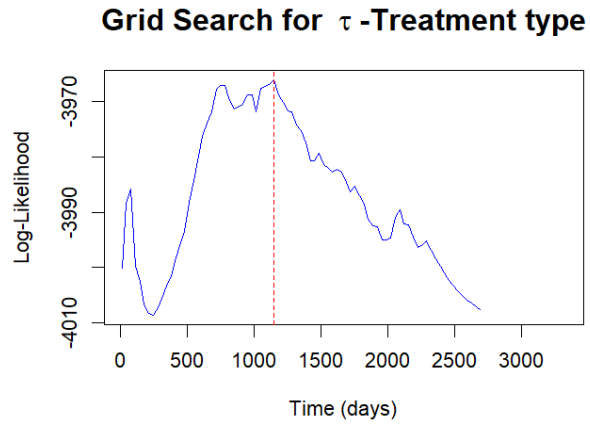
| Covariate | Coefficient | Std.Error | P-Value | Time ratio |
|---|---|---|---|---|
| Obstruction of tumor | 0.218 | 0.163 | 0.1884 | 1.243 |
| Perforation of tumor | 0.336 | 0.352 | 0.3553 | 1.399 |
| Adherence of Tumor | 0.253 | 0.179 | 0.1648 | 1.288 |
| Affected lymph nodes | 0.066 | 0.021 | 0.0035 | 1.068 |
| Tumor differentiation | 0.152 | 0.134 | 0.2567 | 1.164 |
| Extent of local spread | 0.632 | 0.161 | 0.0000 | 1.882 |
| Surgery–registration time | 0.345 | 0.143 | 0.0172 | 1.412 |
| Positive Nodes | 0.788 | 0.196 | 0.0001 | 2.198 |

*The Effects of Covariates on the Timing of the Change Point*

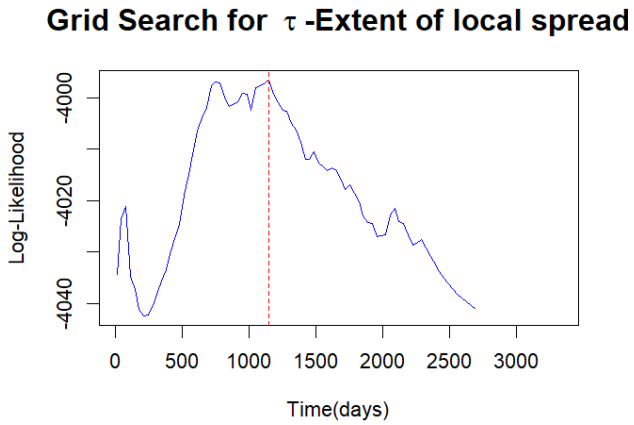
Maximum likelihood estimates for the parameters were obtained using the Nelder-Mead optimization algorithm. Initial values for the shape and regression coefficient parameters were estimated using the survreg function, while a grid search was performed to estimate initial values for the change point as shown in Figure 5.

The maximum likelihood estimates of the shape parameter, regression coefficient and change point were obtained using profile likelihood estimation, while the maximum likelihood estimates of the scale parameter for before and after change were obtained based on the estimates of other parameters. The likelihood ratio test was then conducted to check for the presence of a change point in the hazard function.

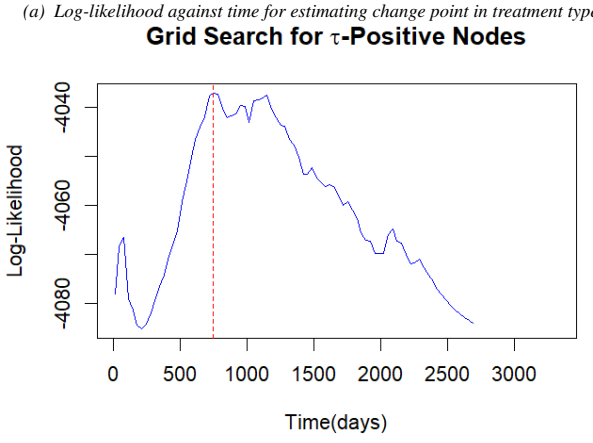
Using the bootstrap procedure, the model parameters were estimated using Maximum Likelihood Estimation, including the change point, the effect of covariates and the hazard estimates before and after the change point respectively.



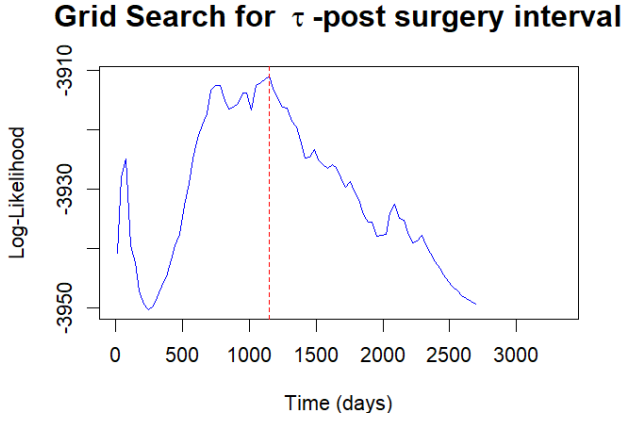

(a) *Log-likelihood against time for estimating change point in treatment type.*




(b) *Log-likelihood against time for estimating change point in Extent of tumour spread.*




(c) *Log-likelihood against time for estimating the change point in number of positive nodes.*




(d) *Log-likelihood against time for estimating the change point in Time post surgery.*

***Figure 5.*** *Grid search for the changepoint ($\tau$) for each of the significant covariates.*

***Table 8.*** *Weibull AFT Change Point Model: Parameter Estimates and Likelihood Ratio Test Statistics.*

| Covariate | $\hat{\tau}$ | $\hat{\alpha}$ | $\hat{\beta}$ | $\hat{\lambda}_1$ | $\hat{\lambda}_2$ | LRT | Bootstrap Critical Value |
|---|---|---|---|---|---|---|---|
| Treatment | 1211 | 0.882 | -0.254 | 0.00153 | 0.000351 | 97.486 | 10.154 |
| Node4 | 752 | 1.081 | 0.886 | 0.000305 | 0.0000578 | 140.470 | 69.779 |
| Extent | 1142 | 0.923 | 0.630 | 0.000150 | 0.0000310 | 112.793 | 48.016 |
| Surg | 1159 | 0.899 | 0.233 | 0.00102 | 0.000217 | 110.477 | 45.620 |

Table 8 presents the comprehensive results of the Weibull AFT change point model, including parameter estimates and likelihood ratio test statistics with bootstrap critical values for change point detection.

For the treatment type, the analysis showed a significant change point, indicating that treatment effects on recurrence risk varied over time. The levamisole + 5-FU group (treatment group) had a stronger protective effect compared to observation only or levamisole alone, with the risk of recurrence decreasing further after the change point. For the number of positive lymph nodes, a change point revealed that patients with more than four positive nodes had an increased risk of recurrence that shifted over time. The hazard was higher before the change point and decreased afterward, although the overall effect remained an increased risk.

For the extent of local cancer spread, the results showed a significant change point. Greater tumor spread initially increased recurrence risk, but the hazard decreased after the change point, though the overall effect remained positive. For time from surgery to registration, a change point indicated that its effect on recurrence risk changed over time. A longer time from surgery was linked to higher risk, which lessened after the change point, underscoring the importance of timely post-surgical follow-up.

Across all covariates, the likelihood ratio tests confirmed that these shifts were statistically significant, demonstrating that their effects on recurrence risk were not constant but changed structurally over time.

### *3.5. Adequacy of the Fitted Regression Models*

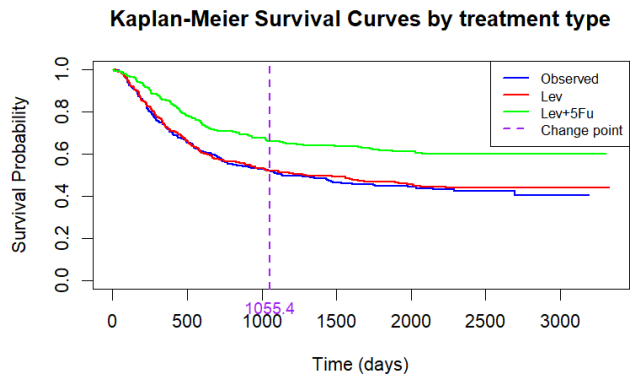
This section presents the diagnostic checks conducted to evaluate the adequacy of the Cox proportional hazards model and the Weibull accelerated failure time model, both with and without the inclusion of covariate-specific change points. The adequacy of each model is examined separately using appropriate graphical and residual-based methods.

#### *3.5.1. The Adequacy of the Cox PH Model with and Without a Change Point*

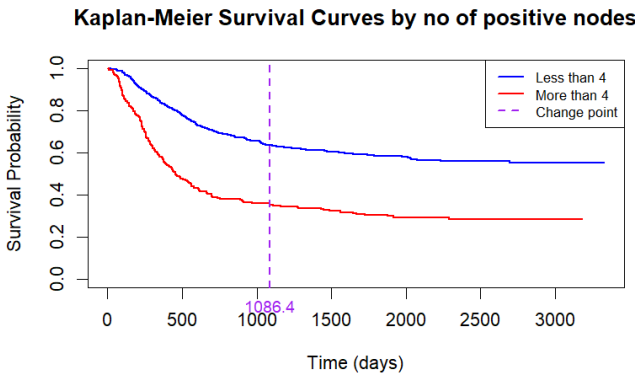
The adequacy of the Cox Proportional Hazards model with and without incorporating covariate specific change point was assessed using both graphical and statistical methods. Kaplan–Meier curves were examined to compare survival experiences across covariate groups. Cox–Snell and deviance residuals were used to evaluate overall model fit, while Schoenfeld residuals and the Grambsch and Therneau test were employed to assess the proportional hazards assumption. Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) were also utilized for model selection.

*Kaplan-Meier Curves*

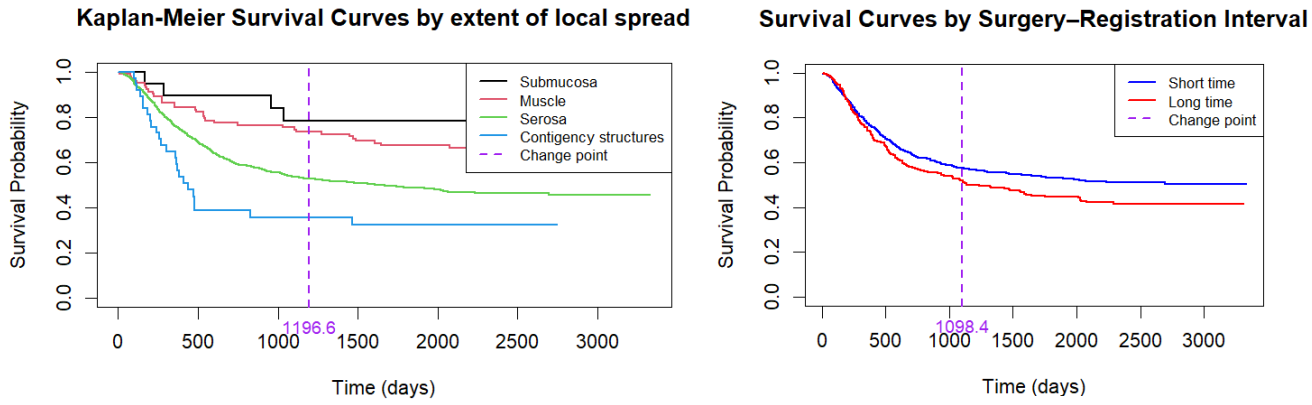
Kaplan–Meier survival curves were plotted for each significant covariate, with a vertical dashed line indicating the estimated change point from the Cox Proportional Hazards model. These plots aided in visually confirming the statistically identified change point. Figure 6 shows the Kaplan–Meier curves stratified by each covariate, with the estimated change point marked.




*(a) Kaplan–Meier curves by treatment type.*




*(b) Kaplan–Meier curves by number of positive nodes.*




*(c) Kaplan–Meier curves by extent of local spread.*

*(d) Kaplan–Meier curves by the time post surgery to registration.*

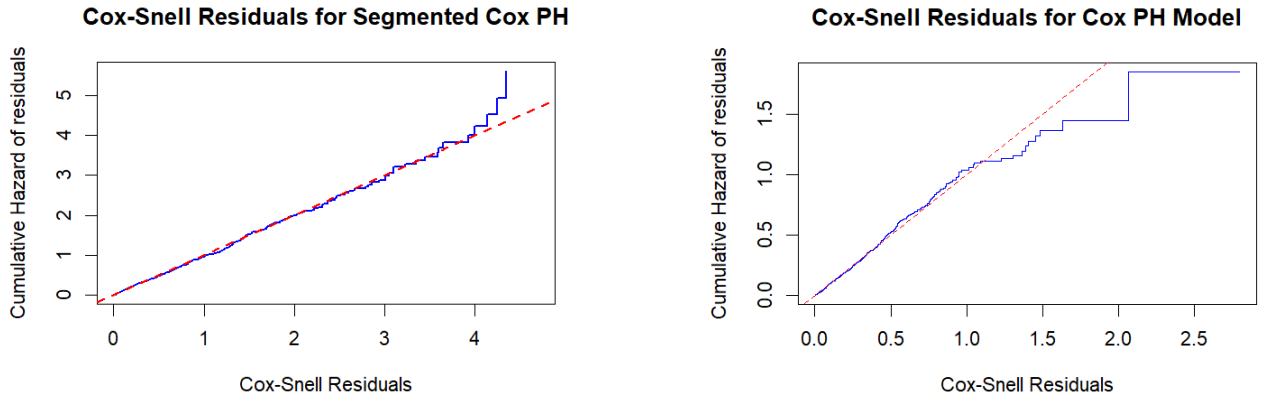
***Figure 6.*** *Survival curves including a change point for each of the significant covariates.*

Figure 6 shows that survival varied across covariates, with clear change points indicating time-varying effects. For treatment (a), patients receiving the new treatment had better survival than those on Levamisole alone or observation, with a steeper decline in survival before the change point at 1055 days. For number of positive nodes (b), patients with fewer than four positive nodes had significantly better survival, with the largest differences occurring before the change point (752 days), after which hazards stabilized. For extent of local spread (c), survival was highest for less invasive cancers, and while advanced stages showed rapid early declines, curves plateaued after 1197 days. For time from surgery to registration (d), shorter durations were linked to slightly better survival, with curves flattening beyond the change point (1159 days), indicating reduced hazard over time. These patterns support the identified change points, suggesting that covariate effects on recurrence risk were not constant but shifted over time. Since the slopes of the survival curves noticeably changed after the estimated change points, this provides visual evidence that the Cox PH model appropriately captured and located the change points in hazard over time.

*CoxSnells residuals*

The Cox–Snell residuals for the Cox PH model with and without change points are compared to assess model adequacy and goodness of fit. Plotting the residuals against the cumulative hazard function provides insights into how well each model fits the data. A model with residuals closely following the 45-degree line indicates better fit. Figure 13 presents the residual plots for both models side by side for comparison.

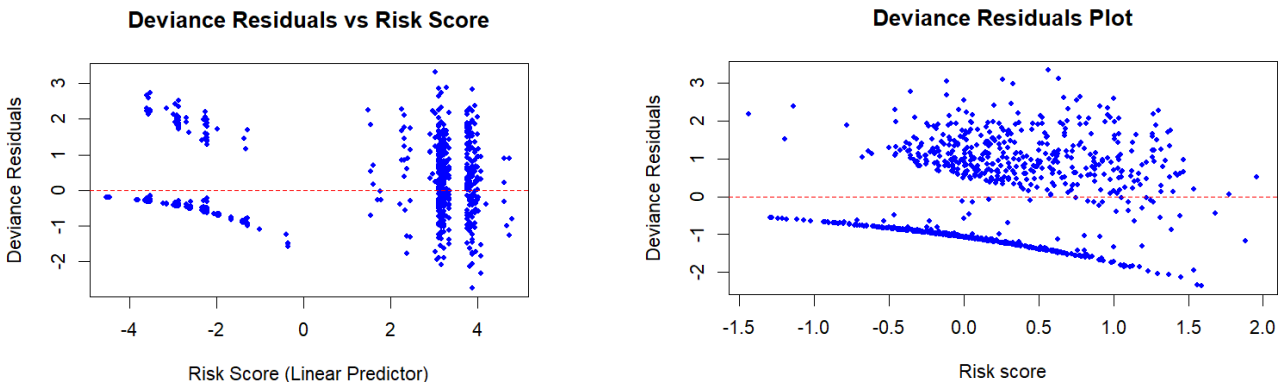
The Cox–Snell residual plot for the model incorporating covariate-specific change points shows a notable improvement in model fit over the Cox PH model without change points. While the general model without change points exhibited clear deviations from the expected 45-degree line at moderate to high residual values, the piecewise model with change points maintains close alignment with the reference line across most of the residual range. Although a slight deviation is observed at the highest residual values, this is expected due to the smaller number of observations in this tail region which leads to increased variability. Overall, the improved alignment indicates that accounting for covariate-specific change points enhances the models ability to capture structural shifts in the hazard function, resulting in a better fit to the data.




*(a) CoxPH model with Change Point.*

*(b) CoxPH model without Change Point.*

***Figure 7.*** *Cox-Snell Residuals for Cox PH Model with and without Change Points.*




*(a) Deviance Residuals for Cox-PH model with Change Point.*

*(b) Deviance Residuals for Cox-PH model without Change Point.*

***Figure 8.*** *Deviance Residuals for Cox PH Model with and without Change Points.*

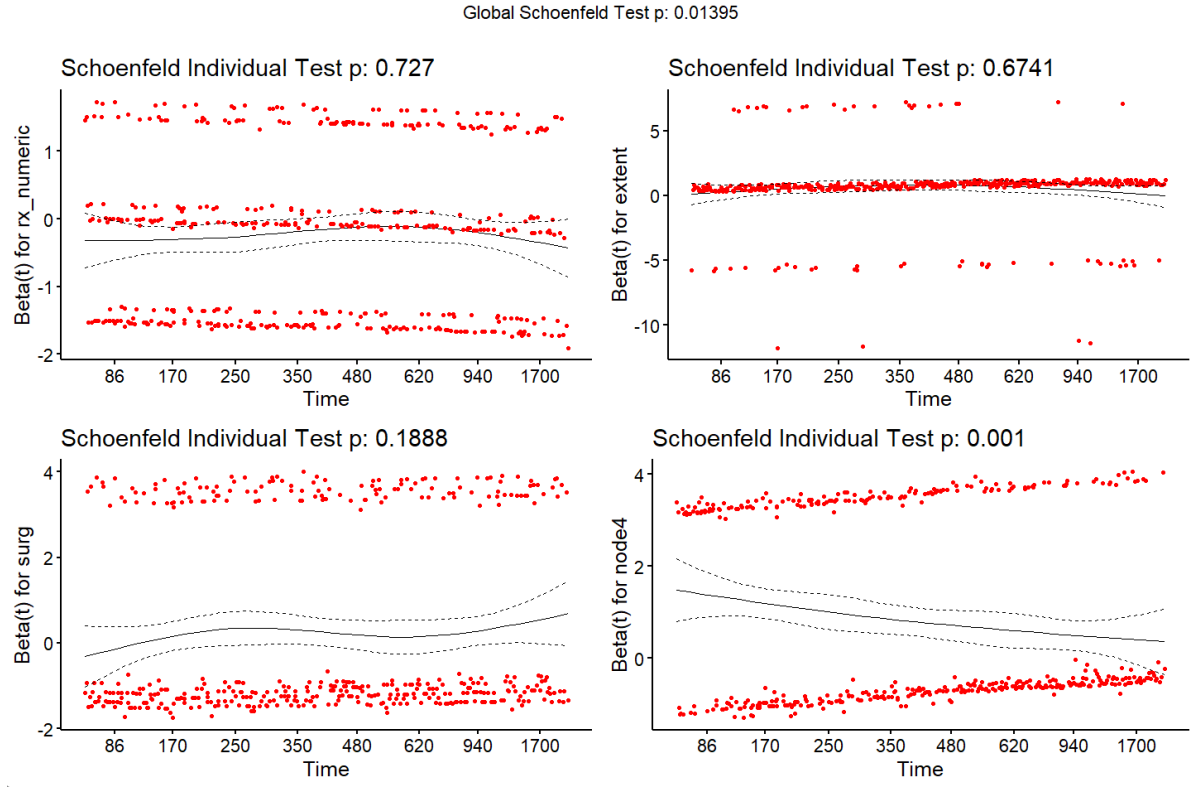



***Figure 9.*** *Schoenfeld residuals for each significant covariate without a change-point.*

*Deviance Residuals*

To further evaluate the effectiveness of the segmented covariate approach, a comprehensive residual analysis was conducted for both the standard Cox proportional hazards model and the model incorporating covariate segmentation.

Figure 8 presents a side-by-side comparison of deviance residuals plotted against risk scores for the Cox proportional hazards model, with and without change points, to assess model adequacy and goodness of fit.The two plots in Figure 8 illustrate the distribution of deviance residuals against risk scores for the Cox proportional hazards model before and after incorporating a change point. In the non-segmented model, a pronounced upward trend in residuals is evident, with low-risk individuals having predominantly negative residuals and high-risk individuals having predominantly positive residuals. This systematic pattern signals a potential misspecification in the model, possibly due to unaccounted heterogeneity or violations of the proportional hazards assumption. In contrast, the segmented model demonstrates a notable improvement in the residual distribution. While some clustering of residuals above the zero line remains for risk scores exceeding two, the overall trend is substantially flattened. This suggests that introducing a change point helps correct for the model's underestimation of risk among high-risk individuals, thereby

enhancing the fit and reliability of the Cox model.

The two plots in Figure 8 illustrate the distribution of deviance residuals against risk scores for the Cox proportional hazards model before and after incorporating a change point. In the non-segmented model, a pronounced upward trend in residuals is evident, with low-risk individuals having predominantly negative residuals and high-risk individuals having predominantly positive residuals. This systematic pattern signals a potential misspecification in the model, possibly due to unaccounted heterogeneity or violations of the proportional hazards assumption. In contrast, the segmented model demonstrates a notable improvement in the residual distribution. While some clustering of residuals above the zero line remains for risk scores exceeding two, the overall trend is substantially flattened. This suggests that introducing a change point helps correct for the model's underestimation of risk among high-risk individuals, thereby enhancing the fit and reliability of the Cox model.

*Sconfeld Residuals*

The impact of change point detection on model fit is assessed by examining Schoenfeld residuals, which are used to evaluate the proportional hazards assumption before and after segmentation. When this assumption holds, Schoenfeld residuals should exhibit no systematic pattern with respect to time. However, if the residuals display time-dependent trends, such as consistently increasing or decreasing values, it suggests a violation of the proportional hazards assumption, indicating that the effect of a covariate may vary over the follow-up period. Figures 10 and 9 present these residuals for the non-segmented and segmented Cox models, respectively. The p-values from the Grambsch and Therneau test assess whether the proportional hazards assumption holds, with values above 0.05 indicating no significant violation.

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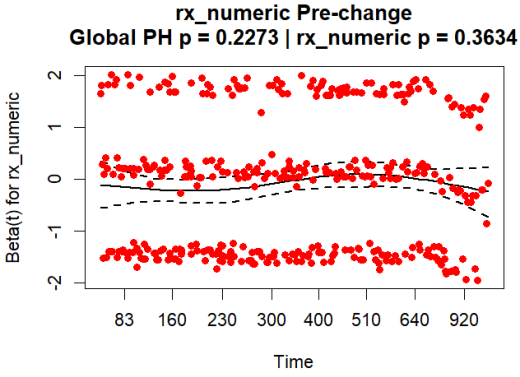
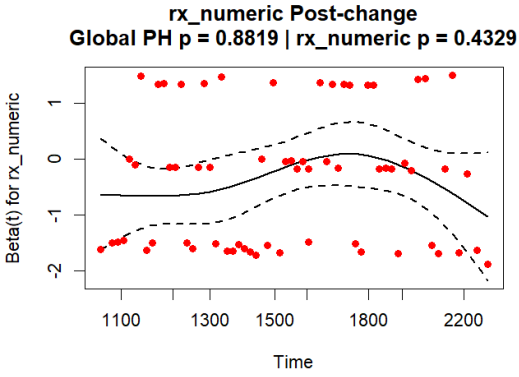
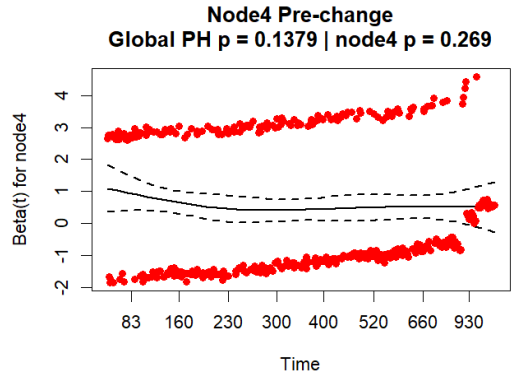


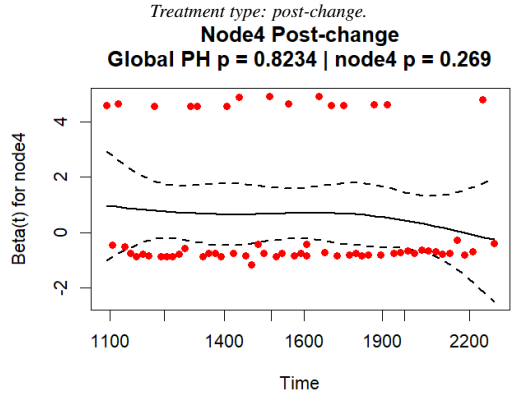

*Treatment type: pre-change.*



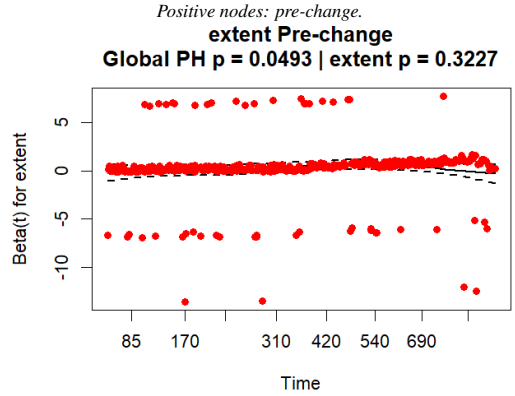

*Treatment type: post-change.*



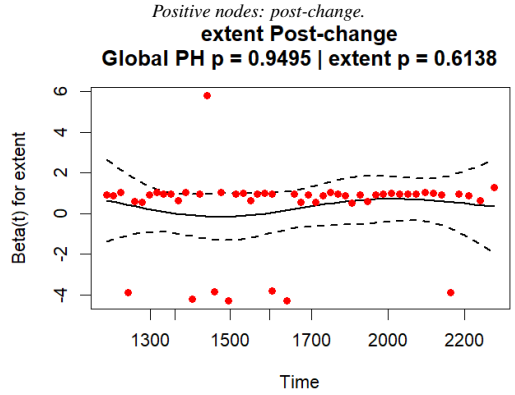

*Positive nodes: pre-change.*



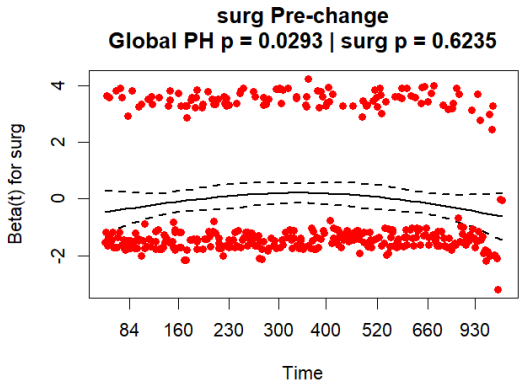

*Positive nodes: post-change.*



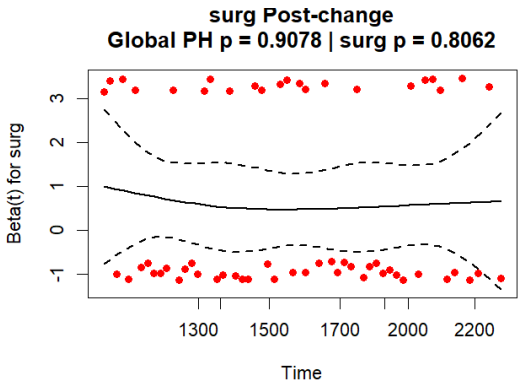

*Extent of local spread: pre-change.*




*Extent of local spread: post-change.*




*Time to registration post-surgery: pre-change.*




*Time to registration post-surgery: post-change.*

***Figure 10.*** *Schoenfeld residuals for treatment type, positive nodes, extent of local spread, and time to registration before and after the change point.*

*Akaike Information Criteria and Bayesian Information Criteria*

The goodness of fit of the Cox proportional hazards models, with and without change points, was assessed using the Akaike Information Criterion and the Bayesian Information Criterion. These measures balance model fit and complexity by penalizing the inclusion of additional parameters. The model with change points achieved substantially lower Akaike Information Criterion and Bayesian Information Criterion values of 4620.43 and 4653.23, respectively, compared to 5646.85 and 5663.25 for the model without change points, indicating improved adequacy in capturing time-dependent effects of covariates on the hazard function despite the increased number of parameters.

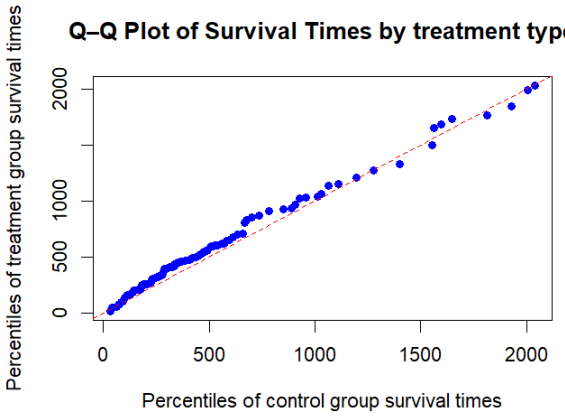
### 3.5.2. The Adequacy of the Weibull AFT Model with and Without a Change Point

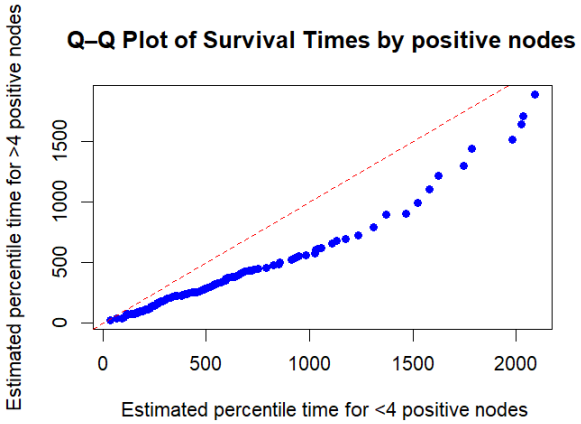
The adequacy of the Weibull Accelerated Failure Time models, with and without covariate–incorporated change points, was assessed using two diagnostic approaches. The Cox–Snell residual analysis was used to evaluate the overall model fit, while quantile–quantile plots were employed to assess the appropriateness of the Weibull distributional assumption. AIC and BIC were also utilized for model selection. The results from these diagnostics are discussed and provide insight into how well each model captures the relationship between covariates and survival time.

*Quantile-Quantile plot*

To evaluate model fit, quantile–quantile plots were constructed comparing survival distributions between groups defined by significant covariates. Figures 12 and 11 show these comparisons for covariates with and without detected change points, respectively. Points lying along the 45-degree reference line indicate similar survival distributions, while deviations suggest model misfit or unaccounted time-varying effects.

The Q–Q plots offer mixed evidence regarding the adequacy of the Weibull AFT model across covariates, highlighting differences between models with and without incorporated change points. For covariates with change points, model fit generally improves pre-change, with treatment type and number of positive nodes showing relatively good alignment with the reference line. However, post-change plots for these covariates reveal increasing deviations especially at higher percentiles–suggesting the presence of group differences and potential model misfit in the extremes. Similarly, extent of local spread and duration from surgery to registration show increased deviations post-change, indicating that the model may inadequately capture changes in survival patterns over time.



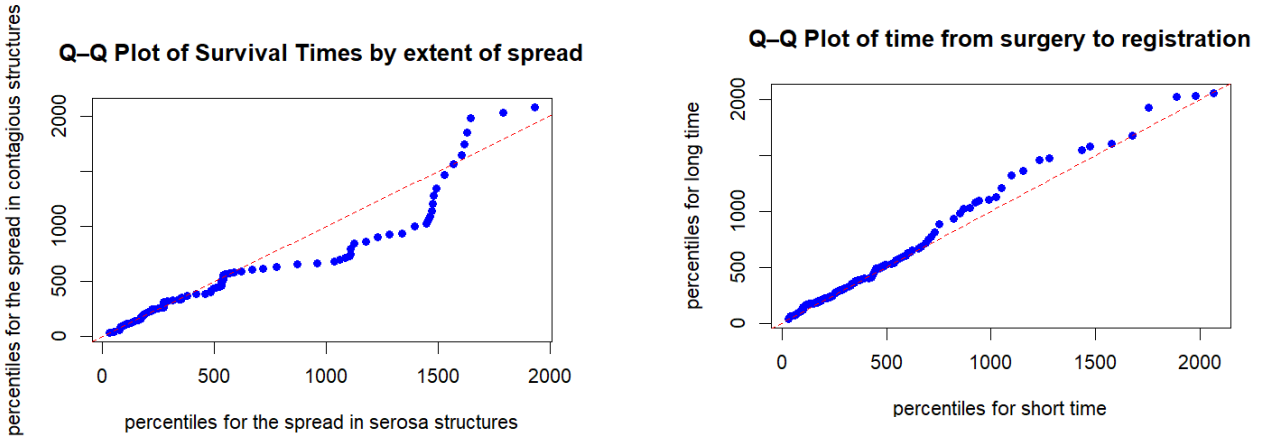
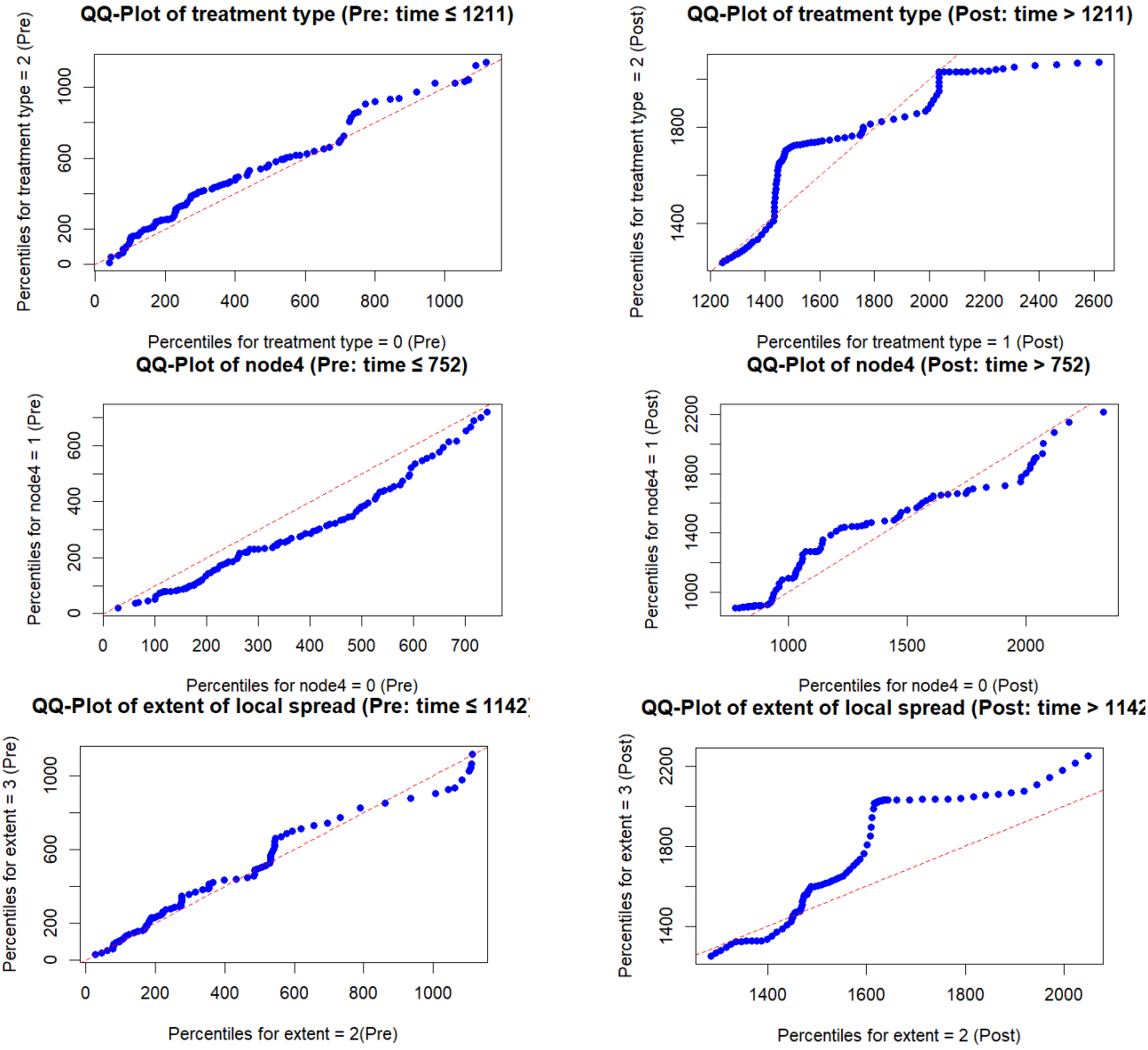



***Figure 11.*** *Q-Q plots comparing survival percentiles under the Weibull AFT model. Slopes indicate acceleration factors.*



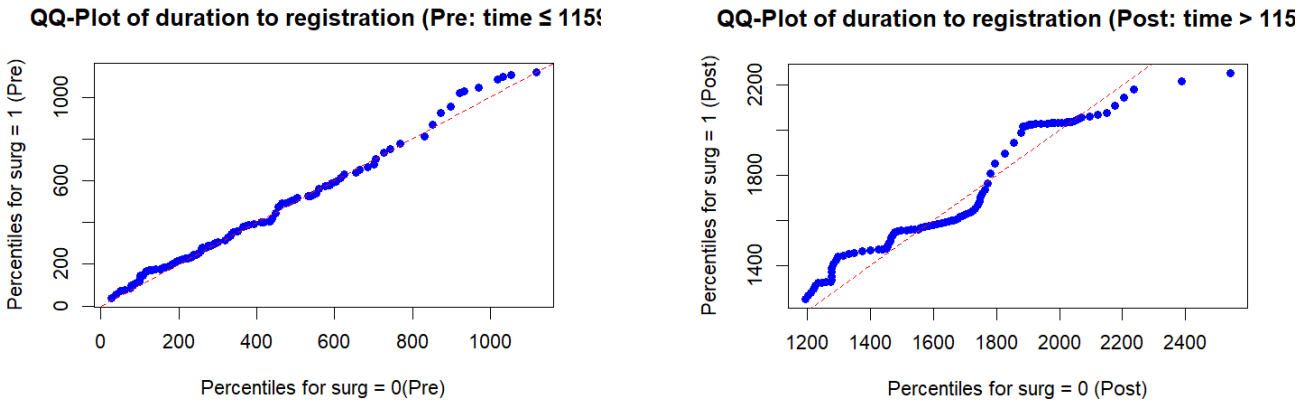


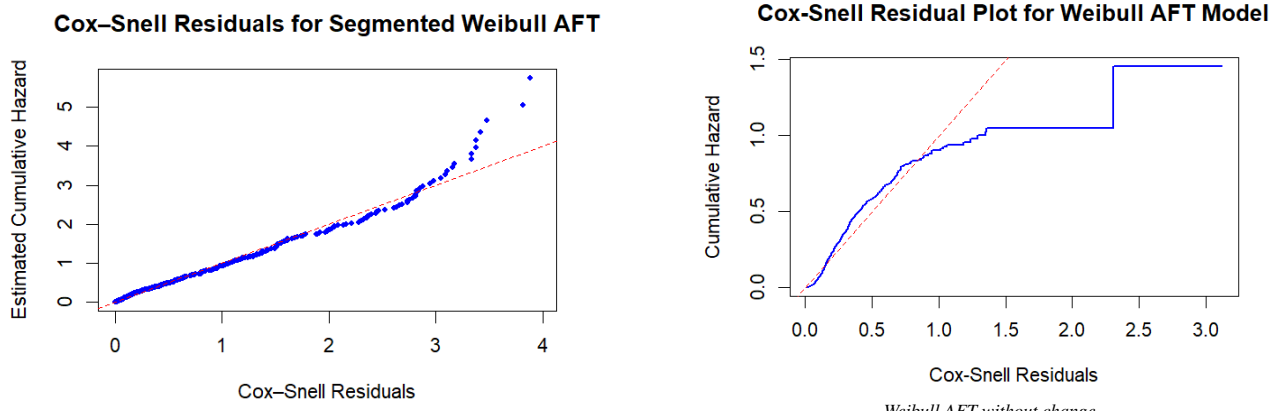

***Figure 12.*** *Q-Q plots comparing pre and post change for the significant covariates under the Weibull AFT model.*

In contrast, the non-segmented model shows better fit for treatment type and time from surgery to registration, with points closely following the 45-degree line, suggesting that the AFT assumption is reasonably met for these covariates. However, for number of positive nodes and extent of local spread, the plots exhibit clear curvature, indicating violations of the AFT assumption. Overall, incorporating change points improves fit in some areas but highlights challenges in modeling extreme survival times, especially in the post-change period.

*Cox-Snells residuals*

To further evaluate the adequacy of the Weibull Accelerated Failure Time models, with and without covariate-incorporated change points, Cox–Snell residuals were computed for all individuals in the dataset. Under a correctly specified model, these residuals are expected to follow a unit exponential distribution. As such, plotting the estimated cumulative hazard function of the Cox–Snell residuals against the residual values should yield a curve that closely follows the 45-degree reference line defined by $y = x$. Deviations from this line indicate potential model misfit and can reveal inadequacies in how the model captures the underlying survival process.

For the piecewise Weibull AFT model, the Cox–Snell residuals closely follow the reference line over a wide range, with only small deviations in the upper tail, an expected outcome due to censoring, which increases variability in the estimated cumulative hazard function. In comparison, the baseline model without change points exhibits more noticeable departures from the theoretical line. This contrast suggests that the piecewise model provides a better fit to the data, as it demonstrates improved alignment with the expected exponential pattern.




*Segmented Weibull AFT.*

*Weibull AFT without change.*

***Figure 13.*** *Cox-Snell Residuals Analysis for Weibull AFT model with and without change points.*

*Akaike Information Criteria and Bayesian Information Criteria*

To assess and compare the goodness of fit of the Weibull Accelerated Failure Time models with and without change points, the Akaike Information Criterion and the Bayesian Information Criterion were computed for both models. These criteria balance model fit and complexity by penalizing the inclusion of additional parameters, with lower values indicating a preferable model. The Weibull AFT model without change points produced an AIC of 7761.277 and a BIC of 7790.011. In contrast, the model incorporating covariate-specific change points achieved an AIC of 6585.608 and a

BIC of 6633.498. These substantially lower values indicate that the piecewise model provides a better fit to the survival data while more accurately capturing time-dependent covariate effects. Both AIC and BIC results support the preference for the change point model despite its increased number of parameters, demonstrating improved model adequacy.

# 4. Conclusions and Recommendations for Further Research

This study aimed to detect a change point in the hazard function of time to recurrence among colon cancer patients using the Likelihood Ratio Test, estimate the location of the change point using maximum likelihood methods, and assess the effects of explanatory variables on the change point using both the Cox Proportional Hazards and Accelerated Failure Time (Weibull) models. The power of the Likelihood Ratio Test in detecting change points was first evaluated through simulations, and the proposed methods were subsequently applied to a real dataset on colon cancer recurrence.

The simulation results demonstrated that larger sample sizes, greater magnitudes of change, and centrally located change points improved the power of the test. Additionally, the bias of the change point estimates decreased with increasing sample size and magnitude of change, while the precision of the estimates improved under the same conditions. Empirical results from the real dataset revealed four significant change points across the covariates, as the likelihood ratio test statistic exceeded the critical values obtained via bootstrap. In the Cox PH model, treatment type had a protective effect that became more pronounced after the change point, while the other covariates increased the hazard of recurrence, with their effects intensifying post-change. In the Weibull AFT model, treatment similarly reduced the hazard, while the other covariates increased the risk of recurrence, although their effects diminished after the change point.

Model adequacy was assessed for both models, with and without change points. The Cox Proportional Hazards and Weibull AFT models incorporating covariate-specific change points demonstrated superior performance over models without change points across various model diagnostics, including Cox-Snell residuals, deviance residuals, Q-Q plots, Schoenfeld residuals, and the Grambsch and Therneau test. However, the Weibull AFT model with change points failed the Q-Q plot check. Overall, the study concludes that the Cox Proportional Hazards model provided a better fit to the data compared to the Weibull AFT model.

Future studies should explore alternative statistical methods for change point detection in survival data to compare their performance with the likelihood ratio test used here, and test for the presence of multiple change points to better understand complex changes in hazard over time, as the hazard function may not change only once but could have several shifts due to factors such as treatment effects wearing off, disease progression, or lifestyle changes.

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# Abbreviations

| | |
|---|---|
| AFT | Accelerated Failure Time |
| AIC | Akaike Information Criterion |
| BIC | Bayesian Information Criterion |
| HIV | Human Immunodeficiency Virus |
| HR | Hazard Ratio |
| LRT | Likelihood Ratio Test |
| MLEs | Maximum Likelihood Estimates |
| MSEs | Mean Squared Errors |
| PH | Proportional Hazards |
| Q-Q | Quantile-Quantile (Plot) |

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# Author Contributions

**Winfred Ngure:** Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Software, Validation, Visualization, Writing - original draft, Writing - review & editing

**Simon Mundia:** Conceptualization, Funding acquisition, Project administration, Resources, Supervision, Writing - review & editing

**Anthony Ngunyi:** Conceptualization, Funding acquisition, Project administration, Resources, Supervision, Writing - review & editing

# Conflicts of Interest

The authors declare no conflicts of interest.

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