Modification of Cox-Snell and Martingale Residual for Estimating Change Point in a Covariate within the Cox Proportional Hazard Model

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***Abstract*—The Cox Proportional Hazard (Cox-PH) model can be segmented into two parts if there is an indication of a change point. A method is developed to detect a change point through the residuals of the Cox-PH model. These residuals are modified to obtain the optimal estimate for the Cox-PH model with a change point. The modification is carried out by calculating the residuals based on the Kaplan-Meier estimator and the Koziol-Green model instead of the Nelson-Aalen estimator. The presence of a change point is tested by calculating the empirical likelihood ratio of the residuals. The distribution of the proposed test statistic is analyzed using P-P plots from the simulation data. The performance of the Cox-PH model with an estimated change point was evaluated through simulations. For real data application, PBC data is analyzed using the proposed method, and the results are compared with the results of previous studies with the same dataset.**

***Index Terms*—Cox-PH, Change point, Empirical likelihood ratio, Residuals, Kaplan-Meier, Koziol-Green.**

I. Introduction

In survival analysis, the observed data is the time to event and its censoring status. This allows for the estimation of the hazard function that indicates the risk level at t. In some cases, covariates are also analyzed. If so, the Cox-Proportional Hazard (Cox-PH) Model is commonly used. In practice, the hazard function can undergo drastic changes due to changes in the covariate values. Failure to anticipate these changes can lead to analysis results that may not accurately reflect the actual conditions and could endanger patients in care. On the other hand, determining life insurance premiums must also consider these changes to ensure fairer premiums for the patients. A similar issue has also been discussed regarding the lifetime of components in an adjacent parallel structure [1]. So, estimating the covariate value that will change the hazard function drastically is essential. The occurrence of these changes is referred to as change points.

Previous studies have explored the estimation of change points in the Cox-PH model. The change point estimation can be conducted for the time variable [2], [3]. The Cox-PH model was upgraded to include a change point parameter in both studies. Therefore, the partial likelihood function will also undergo adjustments. Estimations are those that maximize the partial likelihood function. Liu et al. (2008) performed a Monte Carlo simulation to detect change points in the same model [4]. Modifications can also be made to the Cox-PH model to allow the detection of change points in its covariate [5], [6]. The estimation of the change point parameters are those that maximize the partial likelihood function. A further advanced study was carried out by Jensen and Lütkebohmert (2008), enabling the detection of more than one change point in a single covariate [7]. Change point detection can also be conducted by performing a likelihood ratio test [8]. This test relies on the partial likelihood function of the Cox-PH model, which includes change point parameters.

A common aspect of the previous studies is modifying the Cox-PH model to include change point parameters before estimating these parameters. Some modifications often have complex forms. In this paper, we will attempt to estimate the change point based on the basic form of the Cox-PH model without needing to add a change point parameter. If there is a sample consisting of time t, censoring status δ, and a single covariate x, written as $(t_i, \delta_i, x_i)_{i=1}^n$ such that $x_i \leq x_{i+1}$ and the suspected change point is x_k, with $i = 1, 2, ..., k, k+1, ..., n$, then the model to be discussed in this paper is

$$h(t_i|x_i) = \begin{cases} h_0(t_i)_A \exp(\beta_1 x_i)|_{i=1}^k \\ h_0(t_i)_B \exp(\beta_2 x_i)|_{i=k+1}^n \end{cases} \quad (1)$$

Because there is no change point parameter, the change point is determined by trying each possible value of k in the model (1). An empirical likelihood ratio test will test whether x_k is a change point. This procedure was inspired by the studies by Liu and Qian (2010), who applied it to a linear model with a single covariate [9]. Gamage and Ning (2021) also used it in an autoregressive model [10]. In both studies, change point detection was performed by calculating the likelihood ratio of the model's residuals. The empirical likelihood ratio is calculated because the residuals are not assumed to follow a specific distribution. However, the residuals in the Cox-PH model have a different formula. There are several formulas for the Cox-PH residuals. In this paper, the martingale residual formula will be discussed. Therneau et al. (1990) have shown that martingale residuals can detect the presence of outliers in a sample [11]. If there are outliers, a specific Cox-PH model can be estimated. This aligns with the idea of the change point. Farrington (2000) indicates that the martingale residual is a modified version of the Cox-Snell residuals [12]. Therefore, the Cox-Snell

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residual will also be discussed in this paper.

This study will attempt to detect and estimate a change point in a single covariate using Cox-Snell and martingale residuals. Both residuals are formed based on the Nelson-Aalen estimator for the cumulative hazard function. Modifications will be made to the cumulative hazard function for both residuals to obtain the best residuals for the change point estimation. We will modify by changing Nelson-Aalen with another estimator, such as Kaplan-Meier [13] and the Koziol-Green model [14]. Modifying the estimator of the hazard function using the Koziol-Green model can lead to a better model [15]. On the other hand, the Kaplan-Meier estimator has its strengths and weaknesses compared to Nelson-Aalen, depending on the data characteristics[16]. Also, the Kaplan-Meier is one of the most used techniques in survival analysis [17].

The structure of this paper is as follows. Section II discusses Cox-Snell and martingale residuals for the Cox-PH model with a single covariate. Section III provides the detection and estimation of a change point by calculating the empirical likelihood ratio of both residuals and then defining a statistic to test for the presence of a change point. The distribution of this statistic was examined through simulation. In Section IV, modifications are made to the Cox-Snell and martingale residuals by substituting their cumulative baseline hazard functions with other estimators than Nelson-Aalen. These modifications are used to detect and estimate a change point. In Section V, we conduct simulations and real data analysis. Also, we calculate the average remaining lifetime based on covariate intervals constructed based on the estimated change points to illustrate the implementation of change point estimation in healthcare and insurance fields. Section VI contains a discussion.

II. Residual for Cox-PH Model

A. Cox-Snell Residual

Let t_i and x_i be time-to-event and covariate values for i-th observations, respectively, for $i = 1, 2, ..., n$. A Cox-PH regression model with a single covariate x can be formulated as

$$h(t_i|x_i) = h_0(t_i)\exp(\beta x_i) \tag{2}$$

$h_0(t_i)$ is the baseline hazard before the covariate effect is added into the model, and β is the Cox-PH's parameter. The cumulative of the baseline hazard is written as $H_0(t)$. The distribution for the cumulative baseline hazard is exponential ($\lambda = 1$). By estimating β and $H_0(t)$, the Cox-Snell residual for Eq. (2) is

$$\hat{\varepsilon}_{CSi} = \hat{H}_0(t_i)\exp(\hat{\beta}x_i) \tag{3}$$

Therefore we can see that $E(\hat{\varepsilon}_{CSi}) = \exp(\hat{\beta}\bar{x})$. The estimation for the cumulative baseline hazard is defined as [18]

$$\hat{H}_0(t) = \sum_{t_i \le t} \frac{d_i}{W(t_i, \hat{\beta})} \tag{4}$$

d_i is the number of events at t_i and $W(t_i, \hat{\beta}) = \sum_{j \in R(t_i)} \exp\left(\hat{\beta}x_j\right)$, with $R(t_i)$ is the number of objects at risk, at t_i. If there are no covariates, the Eq. (4) will take the form of the Nelson-Aalen estimator for the cumulative hazard function. Therefore, the Cox-Snell residual become

$$\hat{\varepsilon}_{CSi} = \sum_{t_i \le t} \frac{d_i}{R(t_i)} \tag{5}$$

B. Martingale Residual

The martingale residual is calculated using a counting process approach that counts the number of objects experiencing the event in the interval $[0, t)$. For $i = 1, 2, ..., n$ and $t \ge 0$, we define the counting process $N_i(t) = I[T_i \le t, \delta_i = 1]$ so that $N(t) = \sum_{i=1}^{n} N_i(t) = \sum_{t_i \le t} \delta_i$ represents the number of events at time t or before t. Let $Y_i(t) = I[T_i \ge t]$ be an indicator that object number i is at risk on t so that $Y_i(t) = 1$ for $t_i \ge t$. By looking at the Cox-PH model with a single covariate, the intensity function for the counting process $N_i(t)$ is defined using the following equation [19]

$$\lambda_i(t) = Y_i(t)h(t|x) \tag{6}$$

The cumulative function for the intensity function is

$$\begin{aligned} \Lambda_i(t) &= \int_0^\infty Y_i(t)h(t|x)dt \\ &= \int_0^\infty Y_i(t)\exp(\beta x)d(H_0(t)) \\ &= H_0(t)\exp(\beta x) \end{aligned} \tag{7}$$

The difference between the counting process and the cumulative intensity function is called the Martingale. By estimating $H_0(t)$ and β, we will obtain the formula for the Martingale residual.

$$\begin{aligned} \hat{\varepsilon}_{Mi} &= N_i(t) - \hat{H}_0(t_i)\exp(\hat{\beta}x_i) \\ &= \delta_i - \hat{\varepsilon}_{CSi} \end{aligned} \tag{8}$$

Based on the estimated Cox-PH model, the Martingale residual can be interpreted as the difference between the actual number of events and the expected number of events. Mathematically, the Martingale residual is the difference between the censoring indicator (δ_i) and the Cox-Snell residual $(\hat{\varepsilon}_{CSi})$. Therefore, the expected value for the Martingale residual is $E(\hat{\varepsilon}_{Mi}) = E(\delta_i) - \exp(\hat{\beta}\bar{x})$. Assuming that δ_i is Bernoulli (θ), the value of $E(\delta_i) = \theta$ is the proportion of the uncensored objects.

III. Detecting Change Point via Cox-PH Residual

Using the residual formula of Cox-PH, we propose the procedure to estimate the change point at the covariate x. The proposed method is inspired by the work of Liu and Qian (2010), which calculates the empirical likelihood ratio of the linear model's residual to detect the existence of a change point in a single covariate [9].

Let $(t_i, \delta_i, x_i)_{i=1}^n$ is the observation sorted by x so that $x_i \le x_{i+1}$. Then the observation is divided into two parts so we will get $(t_i, \delta_i, x_i)_{i=1}^k$ and $(t_i, \delta_i, x_i)_{i=k+1}^n$. Then, the segmented Cox-PH model we get is as in Eq. (1). For each segment, the parameter β is estimated so that the Cox-Snell residual for (1) is

$$\hat{\varepsilon}_{CSi}(k) = \begin{cases} \left[\sum_{i=1}^{k} \frac{d_i}{W(t_i, \hat{\beta}_1)}\right] \exp(\hat{\beta}_1 x_i)\big|_{i=1}^{k} \\ \left[\sum_{i=k+1}^{n} \frac{d_i}{W(t_i, \hat{\beta}_2)}\right] \exp(\hat{\beta}_2 x_i)\big|_{i=k+1}^{n} \end{cases} \tag{9}$$

When there is no change point, we will get $\beta_1 \approx \beta_2 \approx \beta$. If so, the Eq. (9) can be written as

$$\tilde{\varepsilon}_{CSi}(k) = \begin{cases} \left[\sum_{i=1}^{k} \frac{d_i}{W(t_i,\hat{\beta}_2)}\right] \exp(\hat{\beta}_2 x_i)\big|_{i=1}^{k} \\ \left[\sum_{i=k+1}^{n} \frac{d_i}{W(t_i,\hat{\beta}_1)}\right] \exp(\hat{\beta}_1 x_i)\big|_{i=k+1}^{n} \end{cases} \tag{10}$$

Under the null hypothesis $H_0 : \beta_1 = \beta_2$ the expected value of $\tilde{\varepsilon}_{CSi}(k)$ would be $E(\tilde{\varepsilon}_{CSi}(k)) = E(\hat{\varepsilon}_{CSi}) = \exp(\hat{\beta}\bar{x})$. When the null hypothesis is true, x_k is not the change point. We will use the empirical likelihood ratio to test the hypothesis [9], [10].

Suppose the switched Cox-Snell residuals $(\tilde{\varepsilon}_{CS1}, ..., \tilde{\varepsilon}_{CSn})$ are sample from population with unknown distribution function so that $p_i = P(\varepsilon_{CSi} = \tilde{\varepsilon}_{CSi})$, then its empirical likelihood function is

$$L(F) = \prod_{i=1}^{n} p_i \tag{11}$$

Since p_i is probability then it holds both $p_i \geq 0$ and $\sum_{i=1}^{n} p_i = 1$. Since the Cox-Snell residual has an expected value $E(\hat{\varepsilon}_{CSi}) = \exp(\hat{\beta}\bar{x})$, the empirical likelihood ratio is defined as [20],

$$-2\log \Re(k) = -2\sup\left\{\sum_{i=1}^{n} \log(np_i)\right\} \tag{12}$$

where $\sum_{i=1}^{n} p_i \tilde{\varepsilon}_{CSi}(k) = \exp(\hat{\beta}\bar{x})$. To calculate $-2\log \Re(k)$, we need to estimate p_i first. For that purpose, the Lagrange function is formulated as,

$$R = \sum_{i=1}^{n} \log np_i - n\alpha\left(\sum_{i=1}^{n} p_i \tilde{\varepsilon}_{CSi}(k) - \exp(\hat{\beta}\bar{x})\right) - \gamma\left(\sum_{i=1}^{n} p_i - 1\right) \tag{13}$$

α and γ are the Lagrange multiplier. The values of p_i that optimize $\sum_{i=1}^{n} \log(np_i)$ can be obtained by solving $\partial R/\partial p_i = 0$ for $i = 1, ..., n$.

$$1 - n\alpha p_i \tilde{\varepsilon}_{CSi}(k) - \gamma p_i = 0 \tag{14}$$

By taking $\gamma = n$ the estimation for p_i is

$$\hat{p}_i = \frac{1}{n(\alpha\tilde{\varepsilon}_{CSi}(k) + 1)} \tag{15}$$

To determine $\hat{p}_i$, we need to estimate α. Substituting Eq. (15) into Eq. (12) we will obtain

$$-2\log \Re(k) = 2\left[\sum_{i=1}^{n} \log(\alpha\tilde{\varepsilon}_{CSi}(k) + 1)\right] \tag{16}$$

The value of α that optimizes the empirical likelihood ratio can be obtained by solving

$$\frac{\partial(-2\log \Re(k))}{\partial\alpha} = 2\left[\sum_{i=1}^{n} \frac{\tilde{\varepsilon}_{CSi}(k)}{(\alpha\tilde{\varepsilon}_{CSi}(k) + 1)^2}\right] = 0 \tag{17}$$

The second derivative of $-2\log \Re(k)$ for α will be negative, so the estimated α will maximize $-2\log \Re(k)$.

Now, we will explain the change point detection using martingale residual. For each segment of the Cox-PH model, the martingale residual is

$$\hat{\varepsilon}_{Mi}(k) = \begin{cases} \left(\delta_i - \left[\sum_{i=1}^{k} \frac{d_i}{W(t_i,\hat{\beta}_1)}\right] \exp(\hat{\beta}_1 x_i)\right)\big|_{i=1}^{k} \\ \left(\delta_i - \left[\sum_{i=k+1}^{n} \frac{d_i}{W(t_i,\hat{\beta}_2)}\right] \exp(\hat{\beta}_2 x_i)\right)\big|_{i=k+1}^{n} \end{cases} \tag{18}$$

Then, when there is no change point, the martingale residual can be written as

$$\tilde{\varepsilon}_{Mi}(k) = \begin{cases} \left(\delta_i - \left[\sum_{i=1}^{k} \frac{d_i}{W(t_i,\hat{\beta}_2)}\right] \exp(\hat{\beta}_2 x_i)\right)\big|_{i=1}^{k} \\ \left(\delta_i - \left[\sum_{i=k+1}^{n} \frac{d_i}{W(t_i,\hat{\beta}_1)}\right] \exp(\hat{\beta}_1 x_i)\right)\big|_{i=k+1}^{n} \end{cases} \tag{19}$$

Using similar steps, the empirical likelihood ratio for the martingale residual is

$$-2\log \Re^*(k) = -2\sup\left\{\sum_{i=1}^{n} \log(np_i^*)\right\} \tag{20}$$

where $\sum_{i=1}^{n} p_i^* \tilde{\varepsilon}_{Mi}(k) = \theta - \exp(\hat{\beta}\bar{x}), p_i^* \geq 0, \sum_{i=1}^{n} p_i^* = 1$, and p_i^* is the distribution for $(\tilde{\varepsilon}_{M1}, ..., \tilde{\varepsilon}_{Mn})$. Using the Lagrange method, we can obtain that

$$\hat{p}_i^* = \frac{1}{n(\alpha^*\tilde{\varepsilon}_{Mi}(k) + 1)}$$

Thus, the empirical likelihood ratio for $(\tilde{\varepsilon}_{M1}, ..., \tilde{\varepsilon}_{Mn})$ will become

$$-2\log \Re^*(k) = 2\left[\sum_{i=1}^{n} \log(\alpha^*\tilde{\varepsilon}_{Mi}(k) + 1)\right] \tag{21}$$

with α^* is the Lagrange multiplier that can be estimated.

If the empirical likelihood ratio is not sufficiently large, then hypothesis H_0 is not rejected, indicating that x_k is not the change point. Under the null hypothesis not rejected, the ratio will be sufficiently small. The empirical likelihood ratio is calculated for every possible value of k. To test the hypothesis, a test statistic called "Change-Point Test (CP_{test})" is determined using both residuals. Based on Liu and Qian (2010), the test statistics are [9].

$$CP_{test}(\text{Cox-Snell}) = \sqrt{\max_{LB \leq k \leq UB}(-2\log \Re(k))} \tag{22}$$

$$CP_{test}(\text{Martingale}) = \sqrt{\max_{LB \leq k \leq UB}(-2\log \Re^*(k))} \tag{23}$$

LB and UB are the lower bound and upper bound for k respectively. There are no specific rules to determine LB and UB. We decide that $LB = (\log n)^2$ and $UB = n - LB$. If the test result shows that H_0 is not rejected for all k within the interval $k \in [LB, UB]$ then there is no change point within observation $(t_i, \delta_i, x_i)_{i=1}^{n}$.

A. The Distribution of the CP_{test}

The CP_{test} statistic has been obtained by calculating the maximum value of the residual's empirical likelihood ratio. To utilize the CP_{test} statistic, the distribution of the CP_{test} should be known. As for the linear model, the statistic to detect the change point is Gumbel extreme value distributed [9]. The Gumbel extreme value distribution is a case of the

generalized extreme value distribution (gev). The probability distribution function for gev is given by

$$f(x;\mu,\sigma,\zeta) = \exp\left\{-\left[1+\zeta\left(\frac{x-\mu}{\sigma}\right)\right]^{-1/\zeta}\right\} \quad (24)$$

with $-\infty < x < \infty$ and $1+(x-\mu)\zeta/\sigma > 0$. The location, scale, and shape parameters are $\mu \in (-\infty,\infty), \sigma > 0$, and $\zeta \in (-\infty,\infty)$ respectively. When the shape parameter is close to zero, the gev will become Gumbel extreme value distribution. The residuals for the Cox-PH model are formulated differently, so it needs to be investigated whether the statistic still has the same distribution in the linear model. We will simulate whether the CP_{test} statistic follows the generalized extreme value distribution. The simulation is designed to include a time variable T, a censoring status δ, and a covariate X. Additionally, some observations will be censored in the simulation to mimic real observations in survival analysis. The algorithm for the simulation is as follows.

1) Generating data using the following model: $T = 2X + \epsilon$. There is no particular reason to use that linear model except to generate data. X is generated from an exponential distribution with $\lambda = 1/5$, and ϵ is generated from normal distribution with $\mu = 10$ and $\sigma = 3$. We also need a censor status variable (δ) to have (T,δ,x). δ is generated from a Bernoulli distribution with $p = 0.7$. The generated sample size is $n = 200$, resulting in $(T_i,\delta_i,x_i)_{i=1}^{200}$.
2) Resampling via the bootstrap method with 600 iterations for $(T_i,\delta_i,x_i)_{i=1}^{200}$. The sample size for each iteration is 200 to have $(T_{ij},\delta_{ij},x_{ij})_{i=1}^{200}; j = 1,2,...,600$.
3) For each iteration, the CP_{test} statistics is calculated to have $(CP_{\text{test}j})_{j=1}^{600}$. Then, the parameters of the gev distribution are estimated using the maximum likelihood method.
4) Creating the P-P plots of $(CP_{\text{test}j})_{j=1}^{600}$ to investigate whether $CP_{\text{test}j}$ follow the gev distribution. P-P Plot can show the cumulative relationship between $CP_{\text{test}j}$ and the theoretical distribution, making it more sensitive to small differences that may not be visible in a histogram.

The P-P plots of the calculated CP_{test} using Cox-Snell and Martingale residuals are presented on **Fig**. 1 and **Fig**. 2. The P-P plot indicates that the observed probability of the CP_{test} approximates the expected probability using gev distribution. Thus, the CP_{test} is a generalized extreme value distributed. Let GEV_α represent the critical value for the CP_{test} at significance level α, denoted as $P(CP_{test} \geq GEV_\alpha) = \alpha$. If the statistics CP_{test} exceeds GEV_α, then the null hypothesis is rejected at the significance level α, indicating the presence of a change point for covariate x. For $k^* \in [LB,UB]$, if $CP_{test} = \sqrt{-2\log\Re(k^*)}$ then the estimation for the covariate change point is the corresponding value to x_{k^*}. So, the model will be

$$h(t_i|x_i) = \begin{cases} h_0(t_i)_A \exp(\beta_1 x_i); x_i \leq x_{k^*} \\ h_0(t_i)_B \exp(\beta_2 x_i); x_i > x_{k^*} \end{cases} \quad (25)$$

IV. Modification of the Cox-PH Residual

The Cox-Snell and Martingale residuals are calculated using the Nelson-Aalen estimator for the cumulative hazard function. When covariates are not present, the Cox-Snell residual can be calculated by estimating the Nelson-Aalen cumulative hazard function as in Eq (5). Meanwhile, the Martingale residual can be calculated by taking the difference between the censoring status of each observation and the Cox-Snell residual. In addition to Nelson-Aalen, there are other estimators for the cumulative hazard function. In this article, the Cox-Snell and Martingale residuals will be calculated by modifying the estimation of its baseline cumulative hazard function $(\hat{H}_0(t))$. This modification is executed by estimating $(\hat{H}_0(t))$ using estimators other than Nelson-Aalen, which are Kaplan-Meier and Koziol-Green. The results of these modifications will be compared to determine a better estimation for the change point.

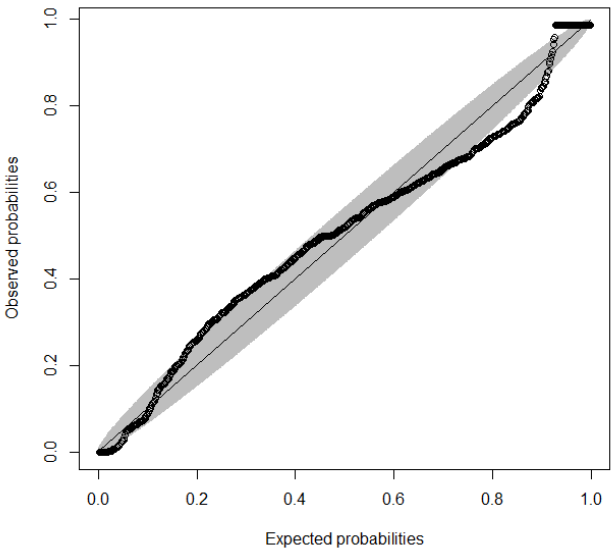

Fig. 1: the P-P plot of the CP_{test} using Cox-Snell residuals

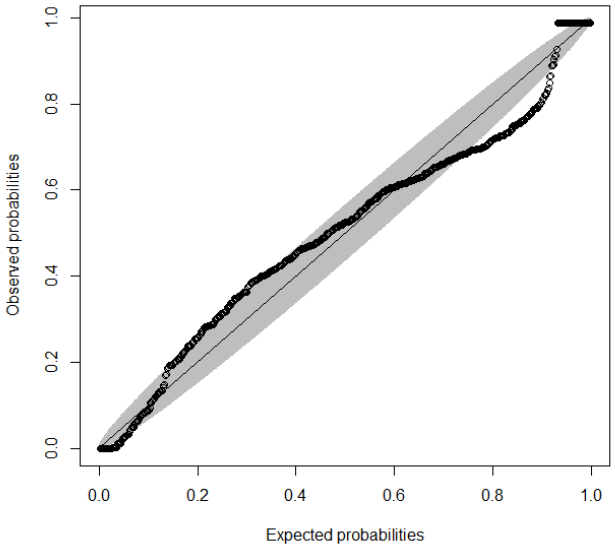

Fig. 2: the P-P plot of the CP_{test} using Martingale residuals

A. Modification using Kaplan-Meier

Given $t_1,...,t_n$ with $t_i \leq t_{i+1}$ representing the times of occurred event for n objects. For $t_n \leq t$, the Kaplan-Meier

(KM) estimator for the survival probability is [13]

$$\hat{S}(t)_{KM} = \prod_{t_i \leq t} \left(1 - \frac{d_i}{R(t_i)}\right) \tag{26}$$

By knowing that $H(t) = -\log S(t)$, the Kaplan-Meier estimator for the cumulative hazard function is

$$\hat{H}(t)_{KM} = -\sum_{t_i \leq t} \log\left(1 - \frac{d_i}{R(t_i)}\right) \tag{27}$$

To modify the cumulative baseline hazard $\hat{H}_0(t)$, we have to recall that in the absence of covariates, the Cox-Snell residual can be calculated using Eq. (5), that is the Nelson-Aalen's hazard cumulative. Suppose we modify by replacing the Nelson-Aalen with the Kaplan-Meier estimator. In that case, when there are no covariates, the formula for the Cox-Snell residual will be the same as the Eq. (27). Both equations (5) and (27) share the same characteristics as both of them consist of d_i and $R(t_i)$. By looking at the original formula of the baseline hazard cumulative in Eq. (4), then the formula of the baseline hazard cumulative using the Kaplan-Meier estimator can be written as

$$\hat{H}_0(t)_{KM} = -\sum_{t_i \leq t} \log\left(1 - \frac{d_i}{W(t_i, \hat{\beta})}\right) \tag{28}$$

with $W(t_i, \hat{\beta}) = \sum_{j \in R(t_i)} \exp\left(\hat{\beta} x_j\right)$.

B. Modification using Koziol-Green

Modifications will also be made using the estimation of cumulative hazard function based on the Koziol-Green (KG) model. Let Y denote the duration until an object experiences an event, and C represents the censoring time for each object. The cumulative distribution functions for Y and C are denoted $F(t)$ and $G(t)$, respectively. Let $T_i = \min(Y_i, C_i)$ be a random variable representing the survival data. If $T_i = Y_i$, then the i-th observation is uncensored; conversely, if $T_i = C_i$, the i-th observation is right censored. The cumulative distribution for T is

$$K(t) = P(T \leq t) = 1 - (1 - F(t))(1 - G(t)) \tag{29}$$

If $\delta = 1$, then $T = Y$ or $Y \leq C$. Let the cumulative distribution function for T under the condition $T = Y$ be $F_1(t) = P(T \leq t | Y \leq C)$. The probability density function for $(T = Y | Y \leq C)$ is

$$dF_1(t) = \lim_{\Delta t \to 0} \frac{P(t \leq Y \leq t + \Delta t)}{\Delta t P(Y \leq C)} \tag{30}$$

Since $T = Y$ and according to Eq.(29)

$$P(T \leq t) = P(Y \leq t) = F(t) = 1 - (1 - F(t))(1 - G(t))$$

will hold if and only if $(1 - G(t)) = 1$. Therefore, the probability density function for Y can be written as

$$\lim_{\Delta t \to 0} \frac{P(t \leq Y \leq t + \Delta t)}{\Delta t} = (1 - G(t)) dF(t) \tag{31}$$

By assuming the censoring indicator $\delta_i = I(Y_i \leq C_i)$ follows a Bernoulli distribution with the probability of success (uncensored) for $i = 1, 2, ..., n$ is $\gamma = P(Y \leq C)$, we will obtain

$$\begin{aligned} P(Y \leq C) &= \int_0^\infty P(Y \leq C | Y = u) dF(u) \\ &= \int_0^\infty P(u \leq C) dF(u) \\ &= \int_0^\infty (1 - G(u)) dF(u) \end{aligned} \tag{32}$$

Next, the Koziol-Green model is defined as [14]

$$(1 - F(t))^\varphi = (1 - G(t)) \tag{33}$$

with φ as the censoring parameter. Using Eq.(33), γ can be written as

$$\begin{aligned} \gamma &= \int_0^\infty (1 - F(u))^\varphi dF(u) \\ &= \frac{1}{\varphi + 1} \end{aligned} \tag{34}$$

Using Eq.(29),(33), and (34), the survival function based on Koziol-Green model is

$$P(T > t) = (1 - K(t))^\gamma$$

Using the maximum likelihood, the estimation for γ is $(1/n) \sum_{i=1}^{n} \delta_i$. Empirically, the function $K(t)$ can be calculated as $\hat{P}(T \leq t) = (1/n) \sum_{i=1}^{n} I(T_i \leq t)$. Therefore, the estimation of the survival using the Koziol-Green (KG) model is

$$\hat{S}(t)_{KG} = \left(1 - \frac{1}{n} \sum_{i=1}^{n} I(T_i \leq t)\right)^{\frac{1}{n} \sum_{i=1}^{n} \delta_i} \tag{35}$$

The $\hat{\gamma}$ represents the proportion of the uncensored observations. Therefore, when $\hat{\gamma} \approx 1$ (almost no censored observations), the estimation of the Koziol-Green survival function will be the same as the Kaplan-Meier estimator, which is the empirical survival probability $\hat{P}(T > t)$. Then, the estimated cumulative hazard function using Koziol-Green can be written as

$$\hat{H}(t)_{KG} = -\left[\frac{1}{n} \sum_{i=1}^{n} \delta_i\right] \log\left(1 - \frac{1}{n} \sum_{i=1}^{n} I(T_i \leq t)\right) \tag{36}$$

Using Nelson-Aalen and Kaplan-Meier estimators, $R(t)$ is the divisor. Meanwhile, the Koziol-Green estimator uses n as its divisor. The presence of censored observations is accommodated through the parameter γ. By revisiting the Nelson-Aalen's cumulative hazard, the Cox-Snell residual is calculated by modifying $R(t_i)$ to $W(t_i, \hat{\beta})$ (see Eq. (4)), similarly when modification is done with the Kaplan-Meier estimator (see Eq. (28)). In the Koziol-Green estimator, that $W(t_i, \hat{\beta})$ cannot be applied since its divisor is n. Therefore, instead of using $W(t_i, \hat{\beta})$, for the Koziol-Green estimator, we propose the form of $W(\hat{\beta})$.

$$W(\hat{\beta}) = \sum_{i=1}^{n} \exp(\hat{\beta} x_i) \tag{37}$$

The proposed value of $W(\hat{\beta})$ is determined based on the formula of $W(t_i, \hat{\beta})$. The difference is that $W(\hat{\beta})$ is not time-dependent. This is consistent with the estimation using the Koziol-Green model, which uses n, whose value is also not time-dependent. Furthermore, based on Eq. (36) and Eq. (37), by replacing n with $W(\hat{\beta})$, the cumulative baseline hazard function using Koziol-Green model is

$$\hat{H}_0(t)_{KG} = -\hat{\gamma} \log \left(1 - \frac{1}{W(\hat{\beta})} \sum_{i=1}^{n} I(T_i \leq t)\right) \quad (38)$$

with $\hat{\gamma} = (1/n) \sum_{i=1}^{n} \delta_i$ is the proportion of the uncensored observations.

C. Change Point Detection using Modified Residuals

To detect a change point using Cox-Snell residuals, where the baseline cumulative hazard has been modified using Kaplan-Meier, Eq. (9) can be written as

$$\hat{\varepsilon}_{CSKMi}(k) = \begin{cases} \hat{H}_0(t, \hat{\beta}_1)_{KM} \exp(\hat{\beta}_1 x_i)\big|_{i=1}^{k} \\ \hat{H}_0(t, \hat{\beta}_2)_{KM} \exp(\hat{\beta}_2 x_i)\big|_{i=k+1}^{n} \end{cases} \quad (39)$$

where

$$\hat{H}_0(t, \hat{\beta}_p)_{KM} = -\sum_{i=1}^{k} \log \left(1 - \frac{d_i}{W(t_i, \hat{\beta}_p)}\right)$$

for $p = 1, 2$. If the baseline cumulative hazard is estimated using the Koziol-Green, the Cox-Snell residual can be expressed as

$$\hat{\varepsilon}_{CSKGi}(k) = \begin{cases} \hat{H}_0(t, \hat{\beta}_1)_{KG} \exp(\hat{\beta}_1 x_i)\big|_{i=1}^{k} \\ \hat{H}_0(t, \hat{\beta}_2)_{KG} \exp(\hat{\beta}_2 x_i)\big|_{i=k+1}^{n} \end{cases} \quad (40)$$

where

$$\hat{H}_0(t, \hat{\beta}_p)_{KG} = -\gamma_p \log \left[1 - \frac{1}{W(\hat{\beta}_p)} \sum_{i=1}^{k} I(T_i \leq t)\right]$$

for $p = 1, 2$. The estimation for parameters γ_1 and γ_2 are $-(1/k)(\sum_{i=1}^{k} \delta_i)$ and $(1/[n-k])(\sum_{i=k+1}^{n} \delta_i)$, respectively. By referring to Eq.(37), we find that $W(\hat{\beta}_1) = \sum_{i=1}^{k} \exp(\hat{\beta}_1 x_i)$ and $W(\hat{\beta}_2) = \sum_{i=k+1}^{n} \exp(\hat{\beta}_2 x_i)$.

As in Eq.(9) and Eq.(10), if x_k is not a change point, then $\hat{\beta}_1$ and $\hat{\beta}_2$ in Eq.(39) and (40) can be exchanged each other to obtain $\tilde{\varepsilon}_{CSKMi}(k)$ and $\tilde{\varepsilon}_{CSKGi}(k)$.

$$\tilde{\varepsilon}_{CSKMi}(k) = \begin{cases} \hat{H}_0(t, \hat{\beta}_2)_{KM} \exp(\hat{\beta}_2 x_i)\big|_{i=1}^{k} \\ \hat{H}_0(t, \hat{\beta}_1)_{KM} \exp(\hat{\beta}_1 x_i)\big|_{i=k+1}^{n} \end{cases} \quad (41)$$

$$\tilde{\varepsilon}_{CSKGi}(k) = \begin{cases} \hat{H}_0(t, \hat{\beta}_2)_{KG} \exp(\hat{\beta}_2 x_i)\big|_{i=1}^{k} \\ \hat{H}_0(t, \hat{\beta}_1)_{KG} \exp(\hat{\beta}_1 x_i)\big|_{i=k+1}^{n} \end{cases} \quad (42)$$

Since the distribution of the cumulative baseline hazard is exponential ($\lambda = 1$), then $E(\hat{H}_0(t)_{KM}) = E(\hat{H}_0(t)_{KG}) = 1$. Thus, when x_k is not the change point, we will get $E(\tilde{\varepsilon}_{CSKM}(k)) = E(\tilde{\varepsilon}_{CSKG}(k)) = \exp(\hat{\beta}\bar{x})$. Then, the empirical likelihood ratio for the Cox-Snell residual modified using the Kaplan-Meier and the Koziol-Green are

$$-2 \log \Re_{\text{CSKM}}(k) = -2 \sup \left\{ \sum_{i=1}^{n} \log(n p_{\text{KM}i}) \right\} \quad (43)$$

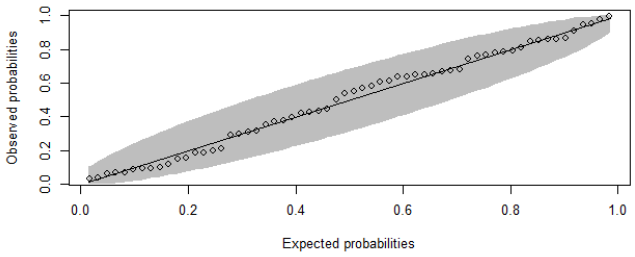

Fig. 3: P-P plot of the CP_{test} using Cox-Snell-Kaplan-Meier residuals, fitted with generalized extreme value distribution

where p_{KM} is the probability distribution for $\tilde{\varepsilon}_{\text{CSKM}}$. As the empirical likelihood ratio of the Cox-Snell modified using the Koziol-Green is

$$-2 \log \Re_{\text{CSKG}}(k) = -2 \sup \left\{ \sum_{i=1}^{n} \log(n p_{\text{KG}i}) \right\} \quad (44)$$

with p_{KG} is the probability distribution for $\tilde{\varepsilon}_{\text{CSKG}}$.

The $-2 \log \Re(k)$'s are calculated for each possible value of k, then used to calculate the statistic CP_{test} by taking the square root in Eq (43) and (44).

Suppose a change point is to be detected by modifying the Martingale residual. In that case, the modification using the Kaplan-Meier (KM) estimator and Koziol-Green (KG) model can be accomplished by leveraging the results obtained from the modified Cox-Snell residual. Hence, the modification of Martingale residual can be expressed as $\hat{\varepsilon}_{\text{MKM}i} = \delta_i - \hat{\varepsilon}_{\text{CSKM}i}$ and $\hat{\varepsilon}_{\text{MKG}i} = \delta_i - \hat{\varepsilon}_{\text{CSKG}i}$. To test using the modified Martingale residual, whether x_k is a change point or not, the empirical likelihood ratios are

$$-2 \log \Re_{\text{MKM}}(k) = -2 \sup \left\{ \sum_{i=1}^{n} \log(n p^*_{\text{KM}i}) \right\} \quad (45)$$

and

$$-2 \log \Re_{\text{MKG}}(k) = -2 \sup \left\{ \sum_{i=1}^{n} \log(n p^*_{\text{KG}i}) \right\} \quad (46)$$

with p^*_{KM} and p^*_{KG} are the probability distribution for both

$$\tilde{\varepsilon}_{\text{MKM}i}(k) = \delta_i - \tilde{\varepsilon}_{\text{CSKM}i}(k)$$
$$\tilde{\varepsilon}_{\text{MKG}i}(k) = \delta_i - \tilde{\varepsilon}_{\text{CSKG}i}(k)$$

respectively with $i = 1, 2, ..., n$. Thus, the expected values of $\tilde{\varepsilon}_{\text{MKM}i}(k)$ and $\tilde{\varepsilon}_{\text{MKG}i}(k)$ under the null hypothesis of no change point ($H_0 : \beta_1 = \beta_2$) is $\theta - \exp(\hat{\beta}\bar{x})$.

We will investigate whether the CP_{test} statistics obtained by modifying the residuals follow a generalized extreme value distribution. By adjusting the residuals and using the same simulation algorithm as in subsection III.C., the P-P plot of the modified CP_{tests} are shown in the **Fig. 3, 4, 5**, and **6**. The simulation results show that statistics CP_{test} follows the theoretical shape of the gev distribution, suggesting that statistic CP_{test} also follows a gev distribution.

V. Practical Study

A. Simulation

In this section, the performance of the change point estimator using Cox-Snell and Martingale residuals will

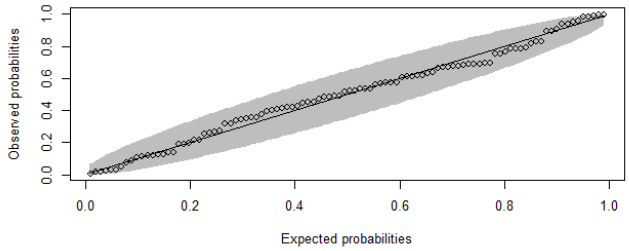

Fig. 4: P-P plot of the CP_{test} using Cox-Snell-Koziol-Green residuals, fitted with generalized extreme value distribution

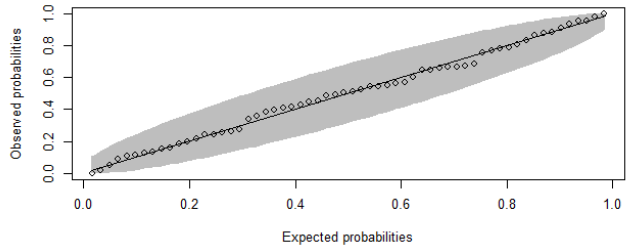

Fig. 5: P-P plot of the CP_{test} using Martingale-Kaplan-Meier residuals, fitted with generalized extreme value distribution

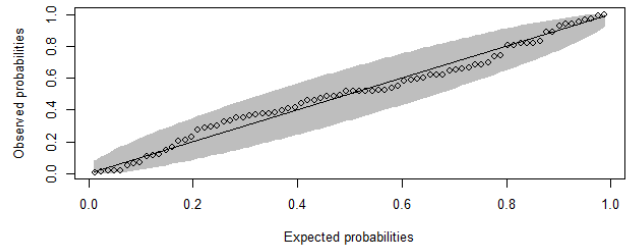

Fig. 6: P-P plot of the CP_{test} using Martingale-Koziol-Green residuals, fitted with generalized extreme value distribution

be compared through simulation. The comparison will be conducted for both the original and modified versions of the residuals in various situations, such as different sample sizes and the proportion of the censored observations.

The random sample of variables (T, δ, x) is generated based on simulation in section III.C. In this section, the covariate x will also be generated from Gamma (shape = 2, scale = 5) and Log-normal $(\mu = 5, \sigma = 1)$ distributions. These distributions, with a domain of $x > 0$, are selected because a numerical variable that serves as a covariate in survival analysis often has positive values. By testing several distributions for the covariate, we seek to understand whether variations in the covariate will affect the goodness of the Cox model with a change point in the covariate. Through this simulation, we want to know whether or not different covariate distributions affect the model with the estimated change point's goodness. The model's goodness will be measured via its Akaike Information Criterion (AIC). The smaller the AIC, the better the model's ability to explain the data [21]. Data generation will be performed using $n = 100$ as the sample size. In addition, the proportion of the uncensored observations (δ) will also be varied to see if the number of censored observations will affect the proposed method's performance. We will perform the simulation for $\delta = (99\%, 80\%, 50\%, 30\%)$. The Cox-PH model's AIC with a change point for x is calculated for each varied sample size and the proportion of censored observations. AIC is used because it can assess the relative quality of the statistical model [22]. AIC helps determine the best and most balanced model to avoid overfitting. Therefore, a model with a lower AIC is better because it could explain data with a minimum number of parameters. The change point is estimated through Cox-Snell and Martingale residuals so that the model will be as on Eq.(25). Modifications on AIC can be made to adjust with the studied model. The AIC is modified for the Cox-PH model with a single change point on covariate x.

$$AIC = 2p - 2[\log(\hat{L}_1) + \log(\hat{L}_2)] \tag{47}$$

with p representing the number of estimated parameters in the model. $\hat{L}_1$ and $\hat{L}_2$ are, respectively, the likelihood values based on the model's parameters, estimated for interval $x \leq x_{k^*}$ and $x > x_{k^*}$. The simulation results are shown in **Fig. 7,8**, and **9**.

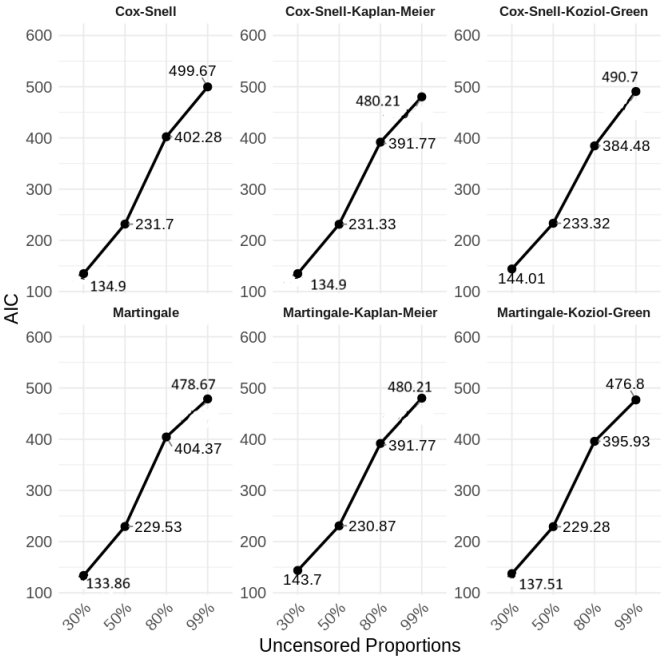

Fig. 7: The AIC of the Cox-PH model with a change point on x, for $x \sim$ exponential$(\lambda = 1/5)$

For all distributions tested in this simulation, the number of uncensored observations positively correlates with the AIC of the Cox-PH model. This also means the more censored observations there are, the smaller the AIC of the model. Thus, estimating the change point using the proposed method will result in a better Cox model in cases where the number of censored observations increases. A significant proportion of censored observations can result in less accurate analysis [23]. By using the proposed method, this issue can be solved. The model estimated based on the estimated change point demonstrates a strong ability to represent the data effectively, as it has a smaller AIC. Based on the residuals tested in this simulation, the Martingale residual with its modification is the most effective in empirically estimating the change point. This applies when the proportion of uncensored observations (δ) is 30% and 50%. For $\delta = 80\%$ and $\delta = 99\%$, the Cox-Snell residual still produces a model with smaller AIC (in the

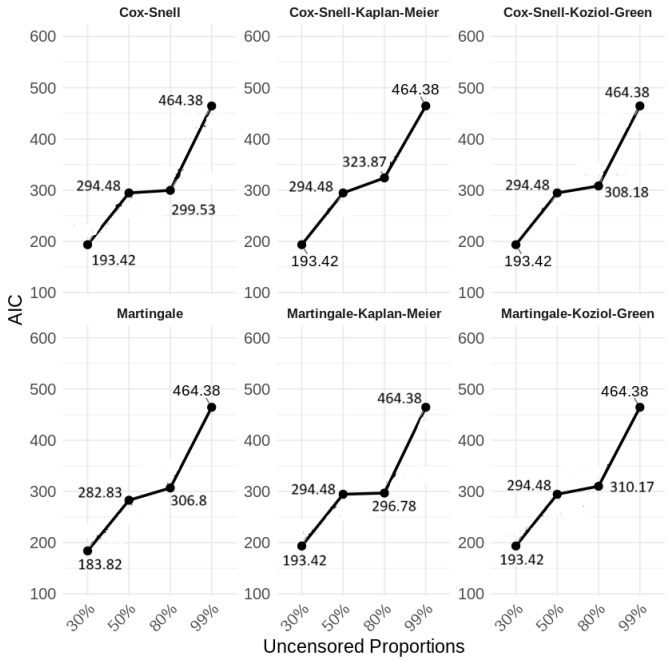

Fig. 8: The AIC of the Cox-PH model with a change point on x, for $x \sim \text{Gamma}(\text{shape} = 2, \text{scale} = 5)$

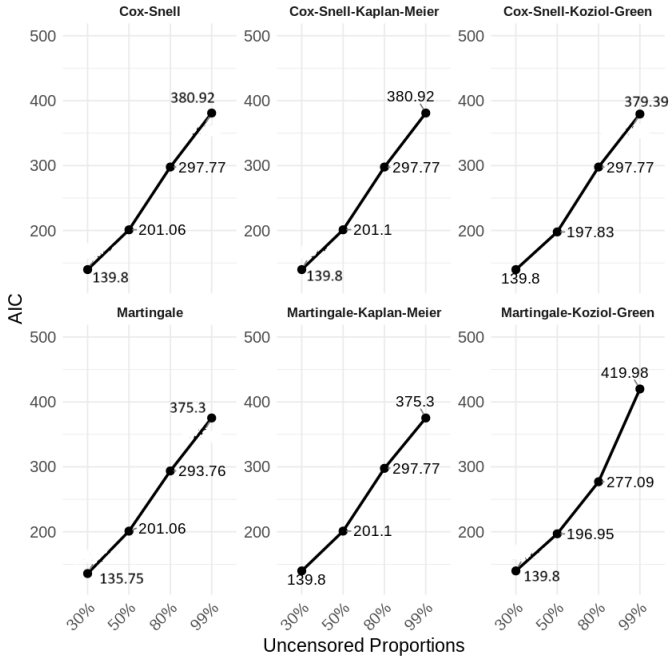

Fig. 9: The AIC of the Cox-PH model with a change point on x, for $x \sim \text{Log-Normal}(\mu = 5, \sigma = 1)$

case of $x \sim$ exponential with $\delta = 80\%$, and $x \sim$ log-normal with $\delta = 99\%$). Meanwhile, in the case $x \sim$ gamma with $\delta = 99\%$, all residuals give a similar change point estimation, resulting in identical models among all residual types.

Based on the modifications applied to the residuals, the modification using the Koziol-Green estimator gives the smallest AIC for the Cox-PH model with a change point. In almost every tested covariate distribution, the residual modification with the Koziol-Green estimator results in the model with the smallest or second-smallest AIC. Only in the case $x \sim$ log-normal with $\delta = 99\%$, the residual modification with the Koziol-Green estimator produces a relatively large AIC. Therefore, it can be concluded that the residual modification with the Koziol-Green estimator will give a good Cox-PH model for cases with a significant number of censored observations.

B. Real data analysis

We applied the proposed method for the Primary Biliary Cirrhosis (PBC) data in [24]. The dataset consists of 418 observations, with 257 of them being right-censored. The variable to be analyzed is the duration (in days) from cirrhosis patients' registration until their death (N.days), along with their censoring status (δ). The covariate to be observed is the bilirubin level (in mg/dl) due to its association with the cirrhosis patients' severity [25]. After estimating the change points for the bilirubin, the Average Remaining lifetime will be calculated for each bilirubin interval.

Before estimating the change point, bilirubin levels must significantly impact the mortality risk of cirrhosis patients, both theoretically and statistically. Additionally, dataset $(\text{N.days}_i, \delta_i, \text{bilirubin}_i)_{i=1}^{418}$ is sorted by the bilirubin variable so that $\text{bilirubin}_i \leq \text{bilirubin}_{i+1}$. By constructing a Cox-PH model, the Wald test statistics for bilirubin levels is 12.26, and it follows a chi-squared distribution with df (degree of freedom) $= 1$ because there is only one covariate being analyzed [26]. For $\alpha = 5\%$, the statistics exceed $\chi^2_{df=1} = 3.84$, indicating that bilirubin levels statistically affect the mortality risk. Therefore, there might be a change point for the bilirubin. The estimated Cox-PH model is

$$h(t|\text{bilirubin}) = h_0(t)\exp(0.142\text{bilirubin})$$

The change point will be estimated using the original and modified version of Cox-Snell and martingale residual. The CP_{test} results are shown in **Table I**.

TABLE I: CP_{test} for change point detection using original and modified Cox-PH residuals

Residuals	CP_{test}	Change Point Candidate	Bilirubin
Cox-Snell (Original)	24.75	bilirubin_{97}	0.7
Cox-Snell (Kaplan-Meier)	52.98	bilirubin_{81}	0.7
Cox-Snell (Koziol-Green)	120.36	bilirubin_{102}	0.8
Martingale (Original)	21.47	bilirubin_{97}	0.7
Martingale (Kaplan-Meier)	52.93	bilirubin_{81}	0.7
Martingale (Koziol-Green)	119.81	bilirubin_{103}	0.8

The CP_{test} statistics using the modified residuals also follow generalized extreme value distribution. At $\alpha = 5\%$, the test indicates that all methods conclude that there is a change point because all of the CP_test exceed $\text{GEV}_{\alpha=5\%} = 2.97$. The potential change point may vary, but based on their bilirubin levels, there are two candidates for the bilirubin change point, 0.7 and 0.8. Thus, if a Cox-PH model was formed with a change point at 0.7 and 0.8, the AICs for both models are shown in **Table II**. As for the original model without a change point, the AIC is 1651.56. It is quite clear that the model with a change point performs better. However, the optimal model is the one with the bilirubin change point at 0.8 mg/dl, estimated via modified Cox-Snell and martingale residual using the Koziol-Green model. The

TABLE II: AIC for the Cox-PH model with a change point in bilirubin

Bilirubin Change Point	AIC
0.7 mg/dl	1548.03
0.8 mg/dl	1518.81

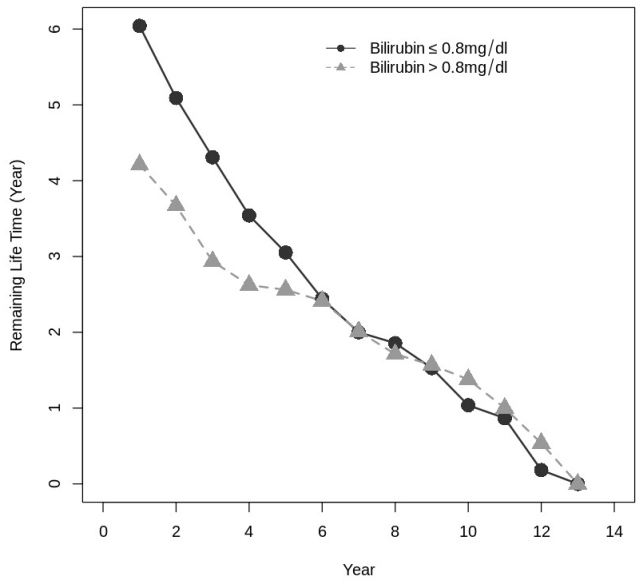

Fig. 10: The Average Remaining lifetime based on Single Change Point of Bilirubin Levels

estimated optimal model is

$$h(t|\text{bilirubin}) = \begin{cases} h_0(t)_A \exp(3.092\text{bilirubin})\big|_{\text{bilirubin}\leq 0.8} \\ h_0(t)_B \exp(0.123\text{bilirubin})\big|_{\text{bilirubin}>0.8} \end{cases}$$

with $h_0(t)_A$ and $h_0(t)_A$ are the baseline hazard corresponding with the bilirubin interval ≤ 0.8 and > 0.8 respectively. The result is theoretically consistent with the fact that normal bilirubin levels do not exceed 1.2 mg/dl [27]. Our results indicate that bilirubin levels above 0.8 mg/dl are already associated with a higher risk of death. Next, we calculate the average remaining lifetime for each bilirubin interval, as shown in **Fig. 10**. We can also construct the mortality tables for each interval, as shown in **Appendixes A** and **B**. The patient with bilirubin levels exceeding 0.8 mg/dl faces a greater risk of death in the early year of the treatment. After six years of treatment, patients in both bilirubin interval groups will have relatively similar remaining lifetimes. Suppose the result is applied to determine the life insurance premiums during the initial six years. In that case, patients with bilirubin levels greater than 0.8 mg/dl should pay higher insurance premiums because their risk is also higher.

The next question is whether the estimated change point significantly affects the changes in the patient's survival. There are 123 patients with bilirubin level $\leq$ 0.8 mg/dl, with 18 patients having complete observations, called O_1. Meanwhile, there are 295 patients with bilirubin levels $>$ 0.8 mg/dl, with 143 patients having complete observations, called O_2. Suppose n_{1t} is the number at risk at t for bilirubin level ≤ 0.8 mg/dl, and n_{2t} is the number at risk at t for bilirubin level > 0.8 mg/dl. Let d_t be the number of events for both categories. The expected value of the occurred event (death) at t for each group is

$$e_{it} = \frac{n_{it}}{\sum_{i=1}^{2} n_{it}} \times d_t; i = 1, 2 \tag{48}$$

The expected value of the event occurrence for both bilirubin categories are $E_1 = \sum_t e_{1t}$ and $E_2 = \sum_t e_{2t}$, respectively. Under the null hypothesis that there is no difference in survival function between categories is [28]

$$W = \sum_{i=1}^{2} \frac{(O_i - E_i)^2}{E_i} \tag{49}$$

The null hypothesis will be rejected at significance level α if $W > \chi^2_{(\alpha,df=1)}$. Using the PBC dataset and significance level 5%, the obtained statistic is $W = 46.3 > \chi^2_{(5\%,df=1)} = 3.84$. Then, based on the log-rank test, we can say there is a significant difference in patient survival for both bilirubin categories.

Suppose we create a categorical variable based on the estimated change point for the bilirubin variable. We can construct a Cox-PH model using the new categorical variable to calculate the hazard ratio between categories. The constructed model is

$$h(t|\text{bilirubin}) = h_0(t) \exp(1.55 \times I(\text{bilirubin} > 0.8))$$

A positive regression coefficient indicates that patients with bilirubin levels higher than 0.8 mg/dl have a higher risk of death. To determine how much higher, we will calculate the hazard ratio (HR)

$$HR = \frac{h_0(t) \exp(1.55 \times 1)}{h_0(t) \exp(1.55 \times 0)} = 4.715$$

Through the hazard ratio, the risk can be compared. The interpretation is that patients with bilirubin levels greater than 0.8 mg/dl have a risk of death that is 4.715 times higher compared to patients with bilirubin levels below 0.8 mg/dl.

After obtaining one change point, an interesting thing to be investigated is whether there are also change points in the sub-interval bilirubin ≤ 0.8 and > 0.8. We can apply the proposed method to each sub-interval. Before that, we need to test whether bilirubin levels significantly affect each sub-interval. This is done by creating a Cox-PH model for each sub-interval and then conducting a Wald test. For bilirubin ≤ 0.8 mg/dl, the Wald test statistic is $1.483 < \chi^2_{df=1,\alpha=5\%} = 3.84$, indicating that bilirubin levels do not have a significant effect. Therefore, change point detection and estimation are not needed for this interval. However, for bilirubin > 0.8 mg/dl, the Wald test statistic is $9.712 > \chi^2_{df=1,\alpha=5\%} = 3.84$. Since bilirubin levels have a significant effect, estimating a change point in bilirubin levels within this interval makes sense. The estimated change point is 1.1 mg/dl using the Martingale-Koziol-Green residual. Repeating the same steps, the next change points for bilirubin levels are 1.3 mg/dl, 2.6 mg/dl, and 5 mg/dl. The survival rates of cirrhosis patients can vary depending on their bilirubin levels. If every cirrhosis patient is assumed to have the same survival rate, some patients' conditions may be underestimated, even though their condition has already reached a critical stage. Therefore, creating a mortality table based on these change points can

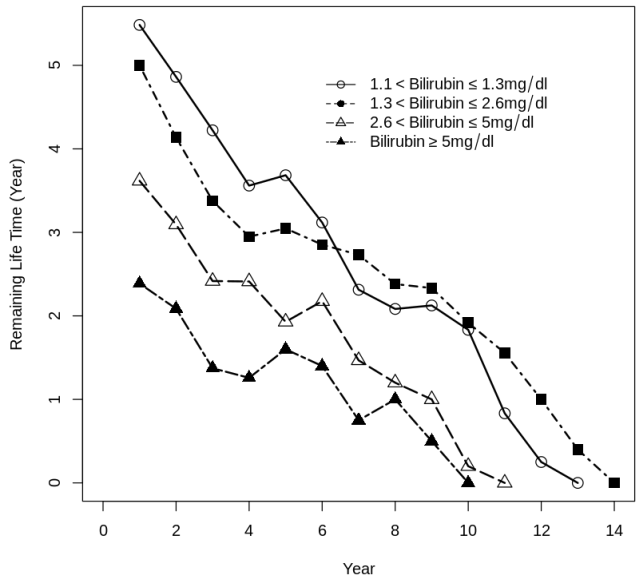

Fig. 11: The Average Remaining lifetime based on Multiple Change Points of Bilirubin Levels

help reduce the risks for the patients. Furthermore, a specific mortality table based on the patient's medical conditions can be used as a reference for determining insurance premiums for patients (see **Appendixes**). It is reasonable for patients with less severe medical conditions to pay lower premium costs. Using the log-rank test, the hazard rate between patients with bilirubin ≤ 8 mg/dl and patients with bilirubin $\in (0.8, 1.1]$ mg/dl is not significantly different because the test statistics $W = 1 < \chi^2_{(5\%,df=1)} = 3.84$. Patients with bilirubin levels $\in (1.1, 1.3]$ mg/dl also do not have a significantly different hazard compared to those with bilirubin ≤ 8 mg/dl and bilirubin $\in (0.8, 1.1]$ mg/dl, as their respective log-rank test statistics are 3.4 and 1.1, both of which are less than $\chi^2_{(5\%,df=1)} = 3.84$. To simplify the interpretation, the plot for the average remaining lifetime for patients with specific bilirubin intervals is only shown for those with significant survival differences, as shown in **Fig 11.** Patients with the shortest remaining lifetime are those with bilirubin levels above 2.6 mg/dl. The remaining lifetime becomes even shorter when it exceeds 5 mg/dl. Therefore, it is reasonable for patients with bilirubin levels below 2.6 mg/dl to pay lower insurance premiums than those with bilirubin levels above 2.6 mg/dl.

The estimated change point we got using our proposed method is consistent with previous studies using the same dataset, which estimated a change point at bilirubin levels of 2.6 mg/dl [8], 2.8 mg/dl [29], and 3 mg/dl [7]. However, using our method, the hazard rate changes can be detected starting from the bilirubin level of 0.8 mg/dl. This can be an early warning for patients with bilirubin levels above 0.8 mg/dl. Patients with bilirubin levels between 0.8 mg/dl and 2.6 mg/dl have a relatively similar remaining lifetime. However, the lifetime decreases when bilirubin levels exceed 2.6 mg/dl.

If we create a new categorical variable for bilirubin levels based on estimated multiple change points and then construct a Cox-PH model using this new categorical variable, the results are shown in **Table III**.

TABLE III: Regression coefficient and Wald Test statistics for each bilirubin level's intervals

Bilirubin Intervals	$\hat{\beta}$	Wald Test Statistics
$0.8 <$ Bilirubin ≤ 1.1	0.330	0.837
$1.1 <$ Bilirubin ≤ 1.3	0.712	0.174
$1.3 <$ Bilirubin ≤ 2.6	1.284	4.348
$2.6 <$ Bilirubin ≤ 5	2.044	7.042
Bilirubin > 5	2.666	9.501

At the significance level 5%, it was found that for Bilirubin $\in (0.8, 1.1]$ and Bilirubin $\in (1.1, 1.3]$, there is no significant effect on the patient mortality, as the Wald Test Statistics for these two intervals is less than $\chi^2_{df=1,\alpha=5\%} = 3.84$. However, in other intervals, there is a significant effect. It can be said that bilirubin levels will only significantly impact after exceeding 1.3, 2.6, and 5. Suppose we take interval bilirubin $\in (1.1, 1.3]$ as the baseline interval for the normal bilirubin level. The hazard ratio will be calculated to determine the increased risk for patients in the intervals that have a significant effect. The hazard ratios are shown on **Table IV**.

TABLE IV: Hazard Ratio between Bilirubin $\in (1.1, 1.3]$ and other significant intervals

Bilirubin Intervals	Hazard Ratio
$1.3 <$ Bilirubin ≤ 2.6	1.771
$2.6 <$ Bilirubin ≤ 5	3.789
Bilirubin > 5	7.057

Patients with bilirubin levels between 1.3 and 2.6 mg/dl have a risk level almost twice that of patients with bilirubin levels between 1.1 and 1.3 mg/dl. If bilirubin levels exceed 2.6 mg/dl, the risk level becomes 3.789 times higher. If it increases to 5, the risk level rises drastically to seven times higher. These results can be a reference for knowing the patient's condition, allowing for appropriate treatment.

VI. Conclusion and Discussion

In this paper, we develop a method for estimating the change point for a single covariate in survival analysis using the residual of the Cox-PH model. The residuals applied are Cox-Snell and martingale. Both residuals are also modified using the Kaplan-Meier and Koziol-Green estimators. To detect a change point, a test statistic is determined based on the likelihood ratio of the residuals. Through simulation, it was established that the distribution of the test statistic is a generalized extreme value. The bootstrap simulation was also performed to evaluate the performance of the proposed change point estimation method. The performance was assessed through AIC of the models. The results show that the proposed method performs exceptionally well when the number of censored observations is relatively high. Change point estimation using martingale residuals produces a Cox-PH model with a smaller AIC. Therefore, when there are many censored observations, martingale residuals are

more effective for change point estimation than Cox-Snell residuals. If modifications are made to both residuals using the Koziol-Green estimator, it will result in a Cox-PH model with a change point and a smaller AIC. This is because the hazard function is also estimated for censored observations, leading to less biased results. Hence, modifications using the Koziol-Green estimator for the residuals give better results for change point estimation.

Our proposed method is designed for a single covariate. If multiple covariates need to be analyzed, they should be handled one at a time. Otherwise, the covariate for which the change point will not be detected can be considered constant. Consider a dataset $(t_i, \delta_i, x_i, y_i)_{i=1}^n$ with two covariates (x and y). If a change point is to be estimated for x, then the dataset must be sorted based on x such that $x_i \leq x_{i+1}$. However, if the change point estimation is intended for y, the condition $y_i \leq y_{i+1}$ must be satisfied for $i = 1, ..., n$. Even the same algorithm can be applied to detect and estimate a change point for time variable t as long as the dataset is sorted by t so that $t_i \leq t_{i+1}$. Next, detecting and estimating a change point is carried out using the residuals from the model. This method can only be used to estimate a single change point. If multiple change points are to be estimated, a one-by-one approach is necessary. For example, let x_k be the change point for covariate x, dividing the existing dataset into $(t_i, \delta_i, x_i)_{i=1}^k$ and $(t_i, \delta_i, x_i)_{i=k+1}^n$. We can also perform change point detection for each of the divided datasets. If a change point is detected on them, then there will be more than one change point within the entire dataset $(t_i, \delta_i, x_i)_{i=1}^n$.

We believe that our method can be applied to actuarial cases. In section V, we obtained intervals for bilirubin levels based on the estimated change points. We also calculated the average remaining lifetime for each bilirubin interval. This can be used as a reference to determine the insurance premiums for patients with specific bilirubin levels. Some insurance premiums are often not adjusted based on the patient's condition [30]. Using the obtained result in this study, further research can be developed to estimate and adjust insurance premiums based on the change point estimations, enabling the calculation of premiums that align with the patient's condition. This approach can also be applied to other diseases, including cirrhosis.

In this paper, the change point is estimated using an empirical method. The change point estimation in data analysis in section V gives such results because those estimated change point values are also present in the dataset. The estimation results are highly dependent on the specific covariate values in the dataset, making the estimation potentially biased or less generalizable if the dataset is not representative. Therefore, we are currently developing a parametric change point estimation method using the same concept in this study for using the Cox-PH's residual. The method we are currently studying employs the idea of Bayesian inference. This concept has been used to estimate the change point for the time-to-event (t) variable without covariates and has shown promising performance [31]. In the case of a survival model with covariates, the Bayesian method can also provide reasonably good model estimation [32], [33]. We plan to use it for change point estimation involving covariates in the model. By adding a change point parameter to one or more covariates, simultaneous change point estimation can likely be achieved. Moreover, it will provide more precise estimates of the change point rather than empirical estimates based solely on the data.

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APPENDIX A
MORTALITY TABLE FOR CIRRHOSIS PATIENTS WITH BILIRUBIN LEVELS < 0.8 MG/DL

Duration of Illness (Years)	l_x (number of living)	d_x (number of dying)	c_x (number of censored)	q_x (proportion of dying)	Average Remaining Lifetime (Years)
0-1	123	1	0	0.0081	6.0407
1-2	122	4	1	0.0329	5.0902
2-3	117	0	6	0.0000	4.3077
3-4	111	1	13	0.0096	3.5405
4-5	97	1	10	0.0109	3.0515
5-6	86	3	13	0.0377	2.4419
6-7	70	4	17	0.0650	2.0000
7-8	49	1	12	0.0233	1.8571
8-9	36	1	8	0.0313	1.5278
9-10	27	1	11	0.0465	1.0370
10-11	15	1	3	0.0741	0.8667
11-12	11	0	9	0.0000	0.1818
12-13	2	0	2	0.0000	0.0000

APPENDIX B
MORTALITY TABLE FOR CIRRHOSIS PATIENTS WITH BILIRUBIN LEVELS ≥ 0.8 MG/DL

Duration of Illness (Years)	l_x (number of living)	d_x (number of dying)	c_x (number of censored)	q_x (proportion of dying)	Average Remaining Lifetime (Years)
0 - 1	295	29	0	0.0983	4.2102
1 - 2	266	16	2	0.0604	3.6692
2 - 3	248	32	15	0.1331	2.9355
3 - 4	201	17	36	0.0929	2.6219
4 - 5	148	14	23	0.1026	2.5608
5 - 6	111	7	15	0.0676	2.4144
6 - 7	89	7	16	0.0864	2.0112
7 - 8	66	6	16	0.1034	1.7121
8 - 9	44	5	10	0.1282	1.5682
9 - 10	29	6	3	0.2182	1.3793
10 - 11	20	2	5	0.1143	1.0000
11 - 12	13	2	4	0.1818	0.5385
12 - 13	7	0	6	0.0000	0.0000

APPENDIX C
MORTALITY TABLE FOR CIRRHOSIS PATIENTS WITH BILIRUBIN LEVELS BETWEEN 0.8 AND 1.1 MG/DL

Duration of Illness (Years)	l_x (number of living)	d_x (number of dying)	c_x (number of censored)	q_x (proportion of dying)	Average Remaining Lifetime (Years)
0 - 1	54	1	0	0.0185	5.7037
1 - 2	53	0	0	0.0000	4.8113
2 - 3	53	0	1	0.0000	3.8113
3 - 4	52	0	9	0.0000	2.8846
4 - 5	43	2	8	0.0513	2.4884
5 - 6	33	3	6	0.1000	2.2424
6 - 7	24	1	3	0.0444	2.0833
7 - 8	20	2	4	0.1111	1.5000
8 - 9	14	1	7	0.0952	1.1429
9 - 10	6	0	1	0.0000	1.6667
10 - 11	5	0	2	0.0000	1.0000
11 - 12	3	0	1	0.0000	0.6667
12 - 13	2	0	2	0.0000	0.0000

APPENDIX D
MORTALITY TABLE FOR CIRRHOSIS PATIENTS WITH BILIRUBIN LEVELS BETWEEN 1.1 AND 1.3 MG/DL

Duration of Illness (Years)	l_x (number of living)	d_x (number of dying)	c_x (number of censored)	q_x (proportion of dying)	Average Remaining Lifetime (Years)
0 - 1	31	2	0	0.0645	5.4839
1 - 2	29	1	1	0.0351	4.8621
2 - 3	27	2	0	0.0741	4.2222
3 - 4	25	2	4	0.0870	3.5600
4 - 5	19	0	2	0.0000	3.6842
5 - 6	17	0	1	0.0000	3.1176
6 - 7	16	0	4	0.0000	2.3125
7 - 8	12	1	3	0.0952	2.0833
8 - 9	8	1	1	0.1333	2.1250
9 - 10	6	0	0	0.0000	1.8333
10 - 11	6	0	2	0.0000	0.8333
11 - 12	4	0	3	0.0000	0.2500
12 - 13	1	0	1	0.0000	0.0000

APPENDIX E
MORTALITY TABLE FOR CIRRHOSIS PATIENTS WITH BILIRUBIN LEVELS BETWEEN 1.3 AND 2.6 MG/DL

Duration of Illness (Years)	l_x (number of living)	d_x (number of dying)	c_x (number of censored)	q_x (proportion of dying)	Average Remaining Lifetime (Years)
0 - 1	75	2	0	0.0267	5.0000
1 - 2	73	4	0	0.0548	4.1370
2 - 3	69	4	6	0.0606	3.3768
3 - 4	59	3	13	0.0571	2.9492
4 - 5	43	5	4	0.1220	3.0465
5 - 6	34	3	5	0.0952	2.8529
6 - 7	26	1	4	0.0417	2.7308
7 - 8	21	2	4	0.1053	2.3810
8 - 9	15	2	1	0.1379	2.3333
9 - 10	12	3	0	0.2500	1.9167
10 - 11	9	1	1	0.1176	1.5556
11 - 12	7	2	0	0.2857	1.0000
12 - 13	5	0	3	0.0000	0.4000
13 - 14	2	0	1	0.0000	0.0000

APPENDIX F
MORTALITY TABLE FOR CIRRHOSIS PATIENTS WITH BILIRUBIN LEVELS BETWEEN 2.6 AND 5 MG/DL

Duration of Illness (Years)	l_x (number of living)	d_x (number of dying)	c_x (number of censored)	q_x (proportion of dying)	Average Remaining Lifetime (Years)
0 - 1	60	7	0	0.1167	3.6167
1 - 2	53	5	0	0.0943	3.0943
2 - 3	48	9	5	0.1978	2.4167
3 - 4	34	3	3	0.0923	2.4118
4 - 5	28	5	6	0.2000	1.9286
5 - 6	17	0	2	0.0000	2.1765
6 - 7	15	2	3	0.1481	1.4667
7 - 8	10	1	3	0.1176	1.2000
8 - 9	6	1	0	0.1667	1.0000
9 - 10	5	3	1	0.6667	0.2000
10 - 11	1	1	0	1.0000	0.0000

APPENDIX G
MORTALITY TABLE FOR CIRRHOSIS PATIENTS WITH BILIRUBIN LEVELS $\geq$ 5 MG/DL

Duration of Illness (Years)	l_x (number of living)	d_x (number of dying)	c_x (number of censored)	q_x (proportion of dying)	Average Remaining Lifetime (Years)
0 - 1	75	17	0	0.2267	2.3867
1 - 2	58	6	1	0.1043	2.0862
2 - 3	51	17	3	0.3434	1.3725
3 - 4	31	9	7	0.3273	1.2581
4 - 5	15	2	3	0.1481	1.6000
5 - 6	10	1	1	0.1053	1.4000
6 - 7	8	3	2	0.4286	0.7500
7 - 8	3	0	1	0.0000	1.0000
8 - 9	2	0	1	0.0000	0.5000
9 - 10	1	0	1	0.0000	0.0000