Electronic Research Archive

https://www.aimspress.com/journal/era

ERA, 34(9): 6573–6613.
DOI: 10.3934/era.2026288
Received: 02 July 2026
Revised: 24 July 2026
Accepted: 27 July 2026
Published: 03 August 2026

Research article

Modeling cure fractions in interval-censored competing risks data: An AFT mixture approach

Yijun Wang[1,2,3], **Bing Zhou**[1], **Chenghui Fu**[1] **and Xuan Xu**[4,*]

[1] School of Statistics and Data Science, Zhejiang Gongshang University, Hangzhou 310018, China
[2] Collaborative Innovation Center of Statistical Data Engineering, Technology & Application, Zhejiang Gongshang University, Hangzhou 310018, China
[3] Laboratory for Statistical Monitoring and Intelligent Governance of Common Prosperity, Zhejiang Gongshang University, Hangzhou 310018, China
[4] Asset and Laboratory Management Office, Zhejiang University of Finance and Economics, Hangzhou 310018, China

* **Correspondence:** Email: xuxuan@zufe.edu.cn.

Abstract: This paper proposes a parametric mixture cure model within the accelerated failure time (AFT) framework for interval-censored data with competing risks. The model integrates multinomial logistic regression for the incidence of various event types (including cure) and AFT models for the latency among susceptible individuals. We consider three lifetime distributions (Weibull, lognormal, loglogistic) and develop an expectation-maximization (EM) algorithm for estimation. The large-sample properties of the proposed estimators are established and validated through comprehensive simulations, which show minimal bias, well-aligned standard errors, and coverage probabilities reaching the nominal level. In an empirical application to Lending Club personal loan data, our model, which accounts for default and prepayment as competing risks, reveals distinct covariate mechanisms overlooked by models ignoring competition: Annual income symmetrically "delays default while accelerating prepayment", while loan amount consistently accelerates only prepayment. Model comparison based on Akaike information criterion (AIC) selects the Weibull distribution as optimal.

Keywords: mixture cure model; interval censoring data; competing risks; accelerated failure time; EM algorithm

1. Introduction

In survival analysis, a substantial proportion of individuals may never experience the event of interest despite extended follow-up periods. These individuals are typically characterized as a "cured fraction",

representing a subpopulation inherently immune to the event. To analyze data containing such cured individuals, the mixture cure model (MCM), pioneered by Boag [1] and subsequently developed by Berkson and Gage [2], provides a robust analytical framework. The survival function in this model is defined as $S(t) = p + (1 - p)S_0(t)$, where p denotes the proportion of cured individuals, and $S_0(t)$ describes the survival probability of susceptible individuals. Subsequently, Kuk and Chen [3] proposed a hybrid framework combining logistic regression with the Cox model. Building on this, Peng and Dear [4] developed a nonparametric mixture cure model. Meanwhile, Sy and Taylor [5] incorporated the Cox model into the latency component and provided standard error estimation, while Fang et al. [6] further established the large-sample theory for this class of models. In addition, Zhang and Peng [7] proposed a semiparametric estimation method for the accelerated failure time (AFT) mixture cure model. These advances have progressively refined the methodological framework of mixture cure models from various perspectives, greatly enriching both their methodology and applications.

Besides the population heterogeneity induced by cured individuals, practical survival studies often encounter another layer of complexity arising from observational mechanism imperfections, namely interval censoring, where the exact event time is unobserved but known to occur within a specific time interval. Such data frequently arise in clinical trials, financial markets, social sciences, and various other fields. Seminal work by Lindsey and Ryan [8] introduced systematic methods for handling interval-censored data. Finkelstein [9] developed regression methods for proportional hazards models with left-, right-, and interval-censored observations. Kooperberg and Clarkson [10] extended hazard regression to address the non-concave likelihood and numerical challenges posed by interval censoring. Additionally, Finkelstein and Wolfe [11] constructed semiparametric models for interval-censored data, while Rabinowitz et al. [12] and Odell et al. [13] investigated AFT models in this context. Betensky et al. [14] further developed computationally efficient methods for fitting AFT models to interval-censored data.

The literature on cure-rate models for interval-censored data has grown considerably, reflecting a sustained effort to address the complexities of this data type. The evolution of methodologies ranges from early adaptations of approximate likelihood techniques by Kim and Jhun [15] to more sophisticated approaches. These include models for clustered data by Xiang et al. [16], multiple-imputation algorithms for efficient estimation by Zhou et al. [17], and flexible semiparametric extensions that incorporate Bayesian methods and generalized accelerated-hazards structures to capture nonlinear and time-dependent effects by Liu [18]. A recent innovation by Li and Ma [19] further tackles partly interval-censored data using penalized likelihood and Gaussian basis functions. Collectively, these works represent a nuanced and progressive refinement of statistical techniques, underscoring the field's focus on improving model accuracy and flexibility in the presence of a cured fraction.

In recent years, machine learning has been introduced into cure rate modeling for interval-censored data to overcome the linearity restriction of the logistic function on the classification boundary. Specifically, Pal et al. [20] proposed a support vector machine (SVM) -based mixture cure model, using the SVM to capture nonlinear effects of covariates on the cure probability while retaining a proportional hazards structure for the latency part. On this basis, Pal and Aselisewine [21] extended the framework to mixed-case interval-censored data and adopted Platt scaling to estimate the cure probability. Furthermore, Aselisewine and Pal [22] developed a more general two-component SVM framework, again for mixed-case interval-censored data, and demonstrated its superiority over traditional logistic-link and spline-based models. In addition to SVM-based modeling strategies, alternative frameworks combining

boosting algorithms and the AFT model have been developed to handle complex interval-censored data. Chen and Qiu [23] proposed an AFT modeling approach for partly interval-censored survival data with length-biased sampling and covariate measurement error, where the simulation and extrapolation (SIMEX) method and boosting procedure are adopted for measurement error correction and variable selection. Chen and Qiu [24] further developed the R package SIMEXBoost to implement the proposed algorithms for analyzing high-dimensional error-prone data.

A further layer of complexity arises from competing risks, where each subject may experience an event from one of several mutually exclusive causes. This setting introduces considerable complexity, as the occurrence of any one event precludes observation of others, and each cause of failure constitutes a competing risk. Methodological developments in this area include a class of tests proposed by Gray [25] for comparing cumulative incidence functions across groups with right-censored competing risks data. Fine and Gray [26] proposed a subdistribution proportional hazards model to directly assess covariate effects on cumulative incidence. Coviello and Boggess [27] developed the Stata command stcompet to estimate cumulative incidence with standard errors and confidence intervals. Klein and Andersen [28] used pseudovalues and generalized estimating equations to model cumulative incidence directly, applying their method to bone marrow transplant data. These studies advanced cumulative incidence modeling in competing risks. Austin et al. [29] further explored the use of this function in estimating crude incidence rates. Through illustrative examples and real-data applications, Huebner et al. [30] compared standard survival approaches with methods designed for competing risks, highlighting biases in the Kaplan-Meier estimator under such settings. Additionally, Beyersmann et al. [31] provided a framework for simulating competing risks data using cause-specific hazards that may vary over time.

The integration of mixture cure models with competing risks frameworks provides a robust analytical approach for time-to-event data, particularly in studies involving cured subpopulations and multiple failure causes. This unified methodology enables more accurate estimation of cause-specific event probabilities and enhances the evaluation of risk factors. Semiparametric estimation techniques have been advanced through the works of Choi et al. [32] and Chen et al. [33], while Basu and Tiwari [34] contributed a Bayesian perspective. Building on these developments, Choi et al. [35] proposed a cure-mixture competing risks model that combines semiparametric AFT models for cause-specific survival functions with a multinomial logistic incidence structure. Wang et al. [36] proposed a unified proportional hazards mixture cure model for clustered survival data with incurable competing risks.

Most existing studies only address one or two of these data characteristics separately. In practical observational research, interval censoring, competing risks, and cure heterogeneity frequently coexist, creating compound statistical challenges that cannot be fully resolved by models designed for only one or two features. Specifically, interval censoring results in unobserved exact failure times, competing risks induce mutually exclusive event structures, and cure stratification partitions the population into susceptible and immune subgroups. The superposition of these three features drastically complicates likelihood construction and parameter estimation, forming a prevalent yet highly challenging data structure in survival analysis. Current methodological developments for such complex data mainly include nonparametric estimation and various semiparametric regression approaches, such as generalized odds-rate models and methods for progressively censored data. Nevertheless, the existing literature is dominated by semiparametric frameworks, and a unified, fully parametric AFT modeling system with clear probabilistic interpretations remains absent. Such a framework would characterize the incidence probabilities of distinct events among susceptible subjects via multinomial logistic regression while

simultaneously fitting cause-specific latency distributions. This parametric framework offers high computational efficiency, intuitive probabilistic interpretations, and superior finite-sample stability, thus holding great practical value.

Motivated by these considerations, this study proposes a unified parametric mixture cure model for interval-censored data with competing risks. Our model integrates a multinomial logistic regression to estimate the incidence of uncured events with AFT models for the conditional latency distribution. The AFT framework offers a direct link between latent failure times and covariates, ensuring intuitive interpretability. Section 2 elaborates on the structure of the proposed multinomial logistic-AFT mixture cure model. Section 3 outlines the maximum likelihood estimation methodology. Section 4 establishes the asymptotic properties of the estimators. Section 5 assesses the finite-sample performance of the model through comprehensive simulations. Section 6 illustrates the model's practical utility in an analysis of Lending Club data. Finally, Section 7 provides concluding remarks and future research directions.

2. Model

Consider a study where each individual may experience one of K mutually exclusive event types, or remain event-free (i.e., "cured"). Let the discrete random variable $U \in \{0, 1, \ldots, K\}$ denote the eventual outcome, where $U = k$ indicates the occurrence of the k-th event type, and $U = 0$ denotes a cured individual who will never experience any event. In practice, $K = 2$ is the most common and practically relevant scenario in competing risks analysis. Researchers typically focus on one specific event type, while grouping all other competing events into a single "other" category. Therefore, for simplicity, we assume two competing events ($K = 2$), with event 1 representing the outcome of primary interest and event 2 encompassing all other failure types.

To model this complex structure, define T_k as the latent failure times for each event type $k = 1, 2$. For a cured individual ($U = 0$), these latent times are conceptually infinite. For a susceptible individual who ultimately fails from cause k ($U = k$), we only observe the failure time for the actual cause k. Thus, the failure time T for each individual is defined by the equation:

$$T = T_1 \times I(U = 1) + T_2 \times I(U = 2) + \infty \times I(U = 0), \tag{2.1}$$

where $I(\cdot)$ is the indicator function. In addition, the observed data may be subject to interval censoring due to discrete observations. The exact failure time T cannot be observed; instead, only an interval $[L, R)$ in which the event occurred is observed, or the event is right-censored if it has not occurred by the last observation time L. The censoring indicator is defined as

$$\delta = \begin{cases} 1, & \text{if the event is interval-censored } (T \in [L, R)), \\ 0, & \text{if the observation is right-censored } (T \geq L,\ R \to \infty). \end{cases}$$

Note that $L = 0$ if the subject is left-censored, so it belongs to a special interval censoring, that is, $T \in [0, R)$. Critically, for a right-censored individual ($\delta = 0$), the true failure type U is naturally unknown, as the event has not yet been observed.

For the latent failure times among susceptible individuals, we adopt the AFT model. The model assumes a linear relationship between the log-transformed latent failure times and covariates X:

$$\log(T_k) = \beta_k^\top X + \varepsilon_k, \quad \text{for } k = 1, 2, \tag{2.2}$$

where β_k is a vector of regression parameters corresponding to event k, and ε_k represents the error term. The distribution of ε_k determines the parametric family for T_k. The nomenclature of the AFT model is determined by the distribution of T_k itself, rather than that of $\log T_k$. Commonly used parametric distributions in the AFT framework include the Weibull, log-normal, and log-logistic distributions; these correspond to ε_k following Gumbel, normal, and logistic distributions, respectively. In each case, a_k and b_k denote the location and scale parameters of the error distribution. The corresponding survival functions $S_k(t;\beta_k, a_k, b_k)$ are standard results and are omitted here.

Compared with the conventional Cox proportional hazards model, the AFT model offers several distinct advantages that motivated its use in this study. First, the AFT model does not require the proportional hazards assumption, which is often violated in practice; instead, it directly models the effect of covariates on the survival time, providing a more intuitive interpretation. Second, the AFT framework accommodates flexible parametric distributions, allowing a better fit to the underlying survival process and more efficient estimation when the distribution is correctly specified. In contrast, when the PH assumption is violated, the Cox model can produce biased estimates and less reliable inferences. Therefore, the AFT model was selected as the primary analytical approach for its robustness, interpretability, and appropriateness for the observed survival data.

In the incidence part, we consider a multinomial logistic regression model to formally characterize the relationship between the discrete event probability π_k and the covariate vector Z. Note that X and Z may overlap or differ. Let γ_k denote the p_z-dimensional regression coefficient vector corresponding to the covariates Z in the incidence component, and let β denote the p_x-dimensional regression coefficient vector corresponding to the covariates X in the latency component. The model is specified as follows:

$$\pi_k = P(U = k \mid Z) = \frac{\exp(\gamma_k^\top Z)}{1 + \sum_{j=1}^{2} \exp(\gamma_j^\top Z)}, \quad \text{for } k = 1, 2, \tag{2.3}$$

$$\pi_0 = 1 - \pi_1 - \pi_2 = \frac{1}{1 + \sum_{j=1}^{2} \exp(\gamma_j^\top Z)}, \tag{2.4}$$

where γ_k is a vector of regression coefficients corresponding to event k. Under these model assumptions, the overall survival function for T has the following mixture representation:

$$S_T(t;\Theta) \equiv P(T \geq t \mid Z, X) = \pi_0 + \pi_1 S_1(t;\beta_1, a_1, b_1) + \pi_2 S_2(t;\beta_2, a_2, b_2), \tag{2.5}$$

where the full parameter vector is given by $\Theta = (\gamma_1, \gamma_2, \beta_1, a_1, b_1, \beta_2, a_2, b_2)$.

3. Estimation

The construction of the likelihood must account for the different types of observations. For an interval-censored individual ($\delta_i = 1, U_i = k$), we know the event occurred in $[L_i, R_i)$ and was of type k. The likelihood contribution is the probability of this joint event: $\pi_k \cdot [S_k(L_i) - S_k(R_i)]$. For a right-censored individual ($\delta_i = 0$), we only know that no event had occurred by time L_i. This individual could be cured, or susceptible, but their event time is beyond L_i. Therefore, the likelihood contribution is the probability of surviving beyond L_i from all causes, which is $\pi_0 + \sum_{k=1}^{K} \pi_k S_k(L_i)$.

Let $U_i \in \{0, 1, 2\}$ denote the event indicator. The observed data for subject i are given by $O_i = \{L_i, R_i, \delta_i, \delta_i U_i, X_i, Z_i\}$ for $i = 1, \ldots, n$. Note that U_i is observable only when $\delta_i = 1$. The likelihood function takes the form:

$$L(\Theta) = \prod_{i=1}^{n}\Bigg(\prod_{k=1}^{2}\Big\{\pi_k[S_k(L_i;\beta_k,a_k,b_k) - S_k(R_i;\beta_k,a_k,b_k)]\Big\}^{\delta_i I(U_i=k)} \times \Big\{\pi_0 + \pi_1 S_1(L_i;\beta_1,a_1,b_1) + \pi_2 S_2(L_i;\beta_2,a_2,b_2)\Big\}^{(1-\delta_i)}\Bigg). \tag{3.1}$$

Direct maximization of the likelihood function (3.1) is computationally challenging due to the complicated structure of the finite mixture cure model. Choi et al. [35] pointed out that the layered mixture structure leads to poor convergence and numerical instability of maximum likelihood estimation under right-censored competing risks. Different from their work restricted to right-censored observations, this paper targets the more complex interval-censored competing risk data. The corresponding likelihood function involves nested integrals and coupled parameters, which further increases the difficulty of numerical optimization. To tackle this issue, we treat the event indicator U_i as a latent variable and adopt the expectation maximization (EM) algorithm for iterative estimation to avoid computational defects of direct likelihood maximization. The complete-data likelihood function is presented as follows:

$$L(\Theta) = \prod_{i=1}^{n}\Bigg(\prod_{k=1}^{2}\Big\{\pi_k\left[S_k(L_i;\beta_k,a_k,b_k) - S_k(R_i;\beta_k,a_k,b_k)\right]\Big\}^{\delta_i I(U_i=k)} \times \Big[\pi_0^{I(U_i=0)}\left\{\pi_1 S_1(L_i;\beta_1,a_1,b_1)\right\}^{I(U_i=1)}\left\{\pi_2 S_2(L_i;\beta_2,a_2,b_2)\right\}^{I(U_i=2)}\Big]^{(1-\delta_i)}\Bigg). \tag{3.2}$$

Taking the logarithm of (3.2) yields the complete-data log-likelihood:

$$\begin{aligned}\ell(\Theta) = \sum_{i=1}^{n}\Bigg(\sum_{k=1}^{2}\delta_i I(U_i=k)\log\left\{\pi_k\left[S_k(L_i;\beta_k,a_k,b_k) - S_k(R_i;\beta_k,a_k,b_k)\right]\right\} \\ + (1-\delta_i)\Big[I(U_i=0)\log\pi_0 + I(U_i=1)\log\left\{\pi_1 S_1(L_i;\beta_1,a_1,b_1)\right\} \\ + I(U_i=2)\log\left\{\pi_2 S_2(L_i;\beta_2,a_2,b_2)\right\}\Big]\Bigg).\end{aligned} \tag{3.3}$$

Then, we decompose the log-likelihood function (3.3) into three separate expressions that contain only $\gamma_1, \gamma_2, \beta_1, a_1, b_1$, and β_2, a_2, b_2, respectively:

$$\ell(\Theta) = \ell_{\gamma_1,\gamma_2}(\Theta) + \ell_{\beta_1,a_1,b_1}(\Theta) + \ell_{\beta_2,a_2,b_2}(\Theta),$$

$$\ell_{\gamma_1,\gamma_2}(\Theta) = \sum_{i=1}^{n}\Big[(1-\delta_i)I(U_i=0)\log\pi_0 + I(U_i=1)\log\pi_1 + I(U_i=2)\log\pi_2\Big], \tag{3.4}$$

$$\begin{aligned}\ell_{\beta_1,a_1,b_1}(\Theta) = \sum_{i=1}^{n}\Big[\delta_i I(U_i=1)\log\left\{S_1(L_i;\beta_1,a_1,b_1) - S_1(R_i;\beta_1,a_1,b_1)\right\} \\ + (1-\delta_i)I(U_i=1)\log S_1(L_i;\beta_1,a_1,b_1)\Big],\end{aligned} \tag{3.5}$$

$$\ell_{\beta_2,a_2,b_2}(\Theta) = \sum_{i=1}^{n}\Bigg[\delta_i I(U_i = 2)\log\{S_2(L_i;\beta_2,a_2,b_2) - S_2(R_i;\beta_2,a_2,b_2)\} + (1-\delta_i)I(U_i = 2)\log S_2(L_i;\beta_2,a_2,b_2)\Bigg]. \tag{3.6}$$

The EM algorithm is employed to efficiently maximize the observed data log-likelihood. The algorithm iterates between two key steps to progressively optimize model parameters.

E-step. Compute the conditional expectation of the latent event indicator $I(U_i = k)$ given the observed data and current parameter estimates $\hat{\Theta}$:

$$\hat{\mu}_{ki} \equiv P(U_i = k \mid O_i, \hat{\Theta}) = \delta_i I(U_i = k) + (1-\delta_i)\psi_k(t_i;\hat{\Theta}), \quad k = 0,1,2, \tag{3.7}$$

where for $k = 1, 2$:

$$\psi_k(t_i;\hat{\Theta}) = P(U_i = k \mid O_i, \hat{\Theta}, \delta_i = 0) = \frac{\pi_k S_k(t_i;\beta_k,a_k,b_k)}{\pi_0 + \pi_1 S_1(t_i;\beta_1,a_1,b_1) + \pi_2 S_2(t_i;\beta_2,a_2,b_2)},$$

and $\psi_0(t_i;\hat{\Theta}) = 1 - \psi_1(t_i;\hat{\Theta}) - \psi_2(t_i;\hat{\Theta})$. Here, $\psi_k(t)$ represents the posterior probability that a patient belongs to event type k given survival up to time t. The conditional probabilities $\hat{\mu}_{ki}$ facilitate inference about potential failure events when exact event types are unobserved.

M-step. Maximize the conditional expectation of the complete-data log-likelihood:

$$E[\ell(\Theta) \mid O_i, \hat{\Theta}] = E[\ell_{\gamma_1,\gamma_2}(\Theta) \mid O_i, \hat{\Theta}] + E[\ell_{\beta_1,a_1,b_1}(\Theta) \mid O_i, \hat{\Theta}] + E[\ell_{\beta_2,a_2,b_2}(\Theta) \mid O_i, \hat{\Theta}]. \tag{3.8}$$

Let $\hat{\Theta}^{(s)} = \{\hat{\gamma}_1^{(s)}, \hat{\gamma}_2^{(s)}, \hat{\beta}_1^{(s)}, \hat{a}_1^{(s)}, \hat{b}_1^{(s)}, \hat{\beta}_2^{(s)}, \hat{a}_2^{(s)}, \hat{b}_2^{(s)}\}$ denote the parameter estimates after the s-th iteration. Convergence is assessed by comparing successive estimates; the algorithm terminates when $\|\Theta^{(s+1)} - \Theta^{(s)}\| < \varepsilon$ for a predefined threshold ε. The EM algorithm proceeds as follows:

Step 1. Initialize parameters:

$$\Theta^{(0)} = \left\{\gamma_1^{(0)}, \gamma_2^{(0)}, \beta_1^{(0)}, a_1^{(0)}, b_1^{(0)}, \beta_2^{(0)}, a_2^{(0)}, b_2^{(0)}\right\},$$

For the AFT latency parameters $\beta_k^{(0)}, a_k^{(0)}, b_k^{(0)}$ $(k = 1, 2)$, we fitted a standard AFT model using only the observations that we considered likely to be uncured and used those estimates as initial values. For the cure fraction parameters $\gamma_1^{(0)}$ and $\gamma_2^{(0)}$ in the multinomial logistic part, we adopted a simpler approach: we treated all right?censored observations as if they were cured and then fitted a multinomial logistic regression based on that crude classification to obtain starting values. This initialization strategy was applied consistently in both the simulation study and the real data analysis.

Step 2. At iteration s, maximize (3.8) to obtain updated estimates:

$$\hat{\gamma}_1^{(s)}, \hat{\gamma}_2^{(s)}, \hat{\beta}_1^{(s)}, \hat{a}_1^{(s)}, \hat{b}_1^{(s)}, \hat{\beta}_2^{(s)}, \hat{a}_2^{(s)}, \hat{b}_2^{(s)}.$$

Step 3. Update conditional probabilities $\hat{\mu}_{ki}$ using (3.7) for all i and $k = 1, 2$.

Step 4. Evaluate convergence criteria. The algorithm stops when both (i) the relative change in the parameter vector satisfies $\|\Theta^{(s+1)} - \Theta^{(s)}\|/\|\Theta^{(s)}\| < 10^{-4}$, and (ii) the absolute change in the log-likelihood satisfies $|\ell(\Theta^{(s+1)}) - \ell(\Theta^{(s)})| < 10^{-4}$. If convergence is not achieved, set $s = s + 1$ and return to Step 2.

It is worth noting that the maximum likelihood estimates $\hat{\theta}$ obtained solely via the EM algorithm cannot be directly employed for cross-model comparisons, since increasing the number of model parameters can mechanically inflate the likelihood value. To overcome this limitation, we further adopt the Akaike information criterion (AIC) to conduct a comparative analysis of models under different distributional assumptions. This criterion provides a quantitative assessment of statistical models' relative performance by simultaneously balancing goodness-of-fit against parametric complexity [37]. Widely adopted in model selection, the AIC is founded on the principle that models with smaller values achieve a superior trade-off between fitting accuracy and complexity.

The AIC is calculated as follows:

$$\mathrm{AIC} = -2\log(L) + k \cdot p, \tag{3.9}$$

where L denotes the maximized value of the likelihood function obtained upon convergence of the EM algorithm, p represents the number of estimated parameters, and k is a scaling constant (typically set to 2).

4. Asymptotic properties of the mixture cure AFT model

In this section, we establish the consistency of the maximum likelihood estimator for the proposed model. We clarify that all asymptotic results in this section are derived under the standard fixed-dimensional setting, where the overall parameter dimension d remains fixed and finite as the sample size $n \to \infty$; accordingly, the asymptotic conclusions are independent of the specific value of d.

Let the true parameter vector be

$$\Theta^* = (\gamma_1^*,\ \gamma_2^*,\ \beta_1^*,\ a_1^*,\ b_1^*,\ \beta_2^*,\ a_2^*,\ b_2^*) \in \mathcal{B},$$

where $\mathcal{B} \subset \mathbb{R}^d$ is a compact parameter space. The observed data $O_i = (L_i, R_i, \delta_i, \delta_i U_i, X_i, Z_i),\ i = 1, \ldots, n$ are independent and identically distributed. Denote the likelihood contribution of a single observation by $\ell(O_i; \Theta)$ as defined in Eq (3.1), and let $Q(\Theta) = \mathbb{E}[\log \ell(O_1; \Theta)]$ be the expected log-likelihood. The MLE is defined as $\hat{\Theta}_n = \arg\max_{\Theta \in \mathcal{B}} \prod_{i=1}^n \ell(O_i; \Theta)$. If the EM algorithm converges to a stationary point of the observed likelihood and the model is identifiable, $\hat{\Theta}_n$ is taken as that point. The following regularity conditions are stated for the first.

Condition 1 (Compactness) $\mathcal{B}$ is compact, and Θ^* lies in its interior.

Condition 2 (Identifiability) If $\Theta \neq \Theta^*$, then $\ell(O; \Theta) \neq \ell(O; \Theta^*)$ almost surely. This implies that the multinomial logistic coefficients (γ_1, γ_2) and the AFT parameters (β_k, a_k, b_k) are uniquely determined, e.g., by imposing a label constraint such as $\beta_{11} > \beta_{21}$ or fixing $\gamma_{1,1} = 0$.

Condition 3 (Bounded covariates) The supports of X and Z are compact. The observed intervals satisfy $0 \leq L < R \leq \tau$ almost surely for some $\tau < \infty$.

Condition 4 (Non-informative censoring) The censoring time C is independent of the true failure time T and the event type U. Moreover, $P(L < R) = 1$.

Condition 5 (Continuity and integrability) For almost every O, the map $\Theta \mapsto \log \ell(O;\Theta)$ is continuous on $\mathcal{B}$, and there exists an integrable dominating function $M(O)$ such that $|\log \ell(O;\Theta)| \le M(O)$ for all $\Theta \in \mathcal{B}$.

Condition 6 (Uniform law of large numbers)

$$\sup_{\Theta\in\mathcal{B}}\Big|\frac{1}{n}\sum_{i=1}^{n}\log \ell(O_i;\Theta) - Q(\Theta)\Big| \xrightarrow{P} 0.$$

Condition 7 (Unique maximum) $Q(\Theta)$ attains a unique maximum at Θ^*; i.e., $Q(\Theta) < Q(\Theta^*)$ for all $\Theta \neq \Theta^*$.

Theorem 4.1 (Consistency of the MLE)**.** *Under Conditions 1–7, the MLE $\hat{\Theta}_n$ is weakly consistent:*

$$\hat{\Theta}_n \xrightarrow{P} \Theta^* \qquad (n \to \infty).$$

Theorem 4.2 (Asymptotic normality)**.** *We adopt the method suggested by Sy and Taylor [38] and the conclusion of Louis [39] to express the observed information matrix as the difference between the expected complete-data information and the missing information. For our model, the observed information matrix is*

$$-\frac{\partial^2 \log L(\Theta;O)}{\partial\Theta\partial\Theta^\top} = -\frac{\partial^2}{\partial\Theta\partial\Theta^\top}\mathbb{E}[\log L_c(\Theta;O,U)\mid O,\hat{\Theta}] - \mathrm{Var}\Big[\frac{\partial}{\partial\Theta}\log L_c(\Theta;O,U)\mid O,\hat{\Theta}\Big], \tag{4.1}$$

where $O = \{L_i, R_i, \delta_i, \delta_i U_i, X_i, Z_i\}_{i=1}^n$, U_i are the latent event indicators, and $\hat{\Theta}$ denotes the parameter estimates after convergence of the EM algorithm. The complete-data log-likelihood $\log L_c$ is given in Eq (3.3). Because it can be decomposed into three independent parts, the observed information matrix has a block-diagonal structure:

$$I_{obs}(\Theta) = \mathrm{diag}(I_{obs}^{(\gamma)},\ I_{obs}^{(\psi_1)},\ I_{obs}^{(\psi_2)}),$$

where $\psi_1 = (\beta_1, a_1, b_1)$ and $\psi_2 = (\beta_2, a_2, b_2)$. We derive each block separately. The overall observed information matrix is

$$I_{obs}(\hat{\Theta}) = \begin{pmatrix} I_{obs}^{(\gamma)} & 0 & 0 \\ 0 & I_{obs}^{(\psi_1)} & 0 \\ 0 & 0 & I_{obs}^{(\psi_2)} \end{pmatrix}.$$

The asymptotic covariance matrix of $\hat{\Theta}$ is estimated by $\widehat{\mathrm{Cov}}(\hat{\Theta}) = I_{obs}(\hat{\Theta})^{-1}$. Standard errors are the square roots of the diagonal elements. All quantities π_{ki}, $\hat{\mu}_{ki}$, V_{ki}, and W_{ki} are evaluated at the final EM estimate $\hat{\Theta}$.

5. Simulation studies

5.1. Simulation settings

The simulation procedure generates interval-censored survival data with competing risks and a cure fraction through the following steps. First, a multinomial logistic model with covariate vector Z classifies

each subject into one of three groups: non-diseased (cured, $U = 0$), event type 1 ($U = 1$), or event type 2 ($U = 2$). For each subject i, a visit/censoring time C_i is generated from a uniform distribution $U[0, 10]$, while the true survival time T_i is generated from a specified parametric distribution.

If $T_i > C_i + 40$, the observation is treated as right-censored, with $L_i = C_i + 40$ and $R_i = \infty$. Otherwise, the exact interval containing T_i is determined as follows: Given a fixed interval length d and an initial endpoint e, if $0 < T_i \leq e$, the interval is set to $[h, e]$, where h is a machine-precision constant approximating zero. If $T_i > e$, we compute $k = \lfloor (T_i - e)/d \rfloor + 1$ and define the interval as $[e + (k-1)d, e + kd]$.

The final dataset includes interval-censored event times, event indicators, true survival times, covariate vectors, and relevant summary statistics, providing a realistic foundation for analyzing cure fraction models under interval censoring and competing risks. We vary the parameters γ_1 and γ_2 in three distinct configurations to achieve the different right-censoring proportions reported in Table 1. For each parameter scenario, we simulate 200 datasets with sample sizes $n = 200$, $n = 500$, $n = 800$, and $n = 1000$ to evaluate finite-sample performance.

Table 1. Parameter values for three levels of right-censoring.

	Scenario 1	Scenario 2	Scenario 3
Right-Censoring	20%	30%	40%
γ_{11}	1	1	1
γ_{12}	2	0.5	0.5
γ_{21}	1.5	1.5	1
γ_{22}	1.5	1.5	1

We generate covariates $Z_i = (Z_{1i}, Z_{2i})$, where Z_{1i} is from the standard normal distribution and Z_{2i} from the Bernoulli distribution with the same probability for 0 and 1. For the survival function part, we specify the parameters as follows: $a_1 = 2, \beta_1 = (1, 1.5)^\top$, $b_1 = 1$ and $a_2 = 1.5, \beta_2 = (1, 1)^\top$, $b_2 = 2$. The survival functions for the two events under the three distributions are given by the following formulas:

(a) Weibull distribution

$$S_1(t_i, \beta_1, a_1, b_1) = \exp\left\{-\left(\frac{t_i}{\exp(X_{1i} + 1.5X_{2i} + 2)}\right)\right\},$$
$$S_2(t_i, \beta_2, a_2, b_2) = \exp\left\{-\left(\frac{t_i}{\exp(X_{1i} + X_{2i} + 1.5)}\right)^{1/2}\right\}.$$

(b) Log-normal distribution

$$S_1(t_i, \beta_1, a_1, b_1) = 1 - \Phi\left(\log t_i - (X_{1i} + 1.5X_{2i} + 2)\right),$$
$$S_2(t_i, \beta_2, a_2, b_2) = 1 - \Phi\left(\frac{\log t_i - (X_{1i} + X_{2i} + 1.5)}{2}\right).$$

(c) Log-logistic distribution

$$S_1(t_i, \beta_1, a_1, b_1) = \left[1 + \left(\frac{t_i}{\exp(X_{1i} + 1.5X_{2i} + 2)}\right)\right]^{-1},$$

$$S_2(t_i, \beta_2, a_2, b_2) = \left[1 + \left(\frac{t_i}{\exp(X_{1i} + X_{2i} + 1.5)}\right)^{1/2}\right]^{-1}.$$

where $X_i = (X_{1i}, X_{2i})$ and $X_{1i} \sim \mathcal{N}(0, 1)$ and $X_{2i} \sim \text{Binomial}(1, 0.5)$ are independent.

5.2. Simulation results

A comprehensive simulation study was conducted to evaluate the performance of the proposed estimation method using multiple metrics: bias, empirical standard error (ESE), average estimated asymptotic standard error (ASE), mean square error (MSE), and the empirical coverage probability (CP) of nominal 95% confidence intervals.

As summarized in Tables 2–4, the proposed estimators exhibit minimal finite-sample bias across all parameters, indicating that the estimation procedure accurately recovers the true data-generating values. The close agreement between the ESE and ASE suggests that the large-sample variance estimator reliably reflects the actual variability of the estimates. Moreover, the empirical coverage probabilities are consistently near the nominal 95% level, confirming that the Wald-type confidence intervals are well calibrated. As expected, increases in sample size lead to systematic decreases in bias, standard errors, and MSE, which aligns with the established asymptotic properties of the proposed estimators.

Figures 1–9 depict the estimated survival functions for the overall survival function (S_T), superimposed on their true counterparts and accompanied by pointwise 95% confidence intervals. The estimated survival curves show excellent agreement with the true functions across all scenarios. The observed discrepancies diminish as the sample size increases, further underscoring the consistency of the estimators. These results collectively indicate that the proposed method performs reliably and satisfactorily across the range of sample sizes considered in this study.

Simulation results under 20% right-censoring (Table 2) indicate that the proposed estimator performs satisfactorily across all sample sizes ($n = 200, 500, 800, 1000$) for the Weibull, log-normal, and log-logistic distributions. As the sample size increases, the bias, ESE, and MSE decrease uniformly across parameters, demonstrating the consistency and efficiency of the estimator. Moreover, the empirical CPs of the 95% confidence intervals remain close to the nominal 0.95 level, confirming that interval estimation is well calibrated under moderate censoring.

These findings are visually supported by Figures 1–3, where the estimated survival curves align closely with the true functions across all distributions. The 95% pointwise confidence intervals tightly envelope the true curves, further validating the reliability of the proposed method.

Similar trends are observed under 30% right-censoring (Table 3), though a slight increase in ESE and MSE reflects the expected loss of information under heavier censoring. Despite this, CP values remain near the nominal level for larger sample sizes ($n \geq 500$), and estimated survival functions (Figures 4–6) continue to track the true curves accurately, with only minor instability in the distribution tails.

Under a 40% right-censoring rate (Table 4), the estimator remains consistent across distributions and sample sizes, with bias, ESE, and MSE decreasing as n increases. However, the higher censoring proportion leads to noticeably larger standard errors and MSEs compared to lighter censoring scenarios, reflecting the increased estimation difficulty under substantial information loss. At small sample sizes ($n = 200$), certain parameters (e.g., b_1 and b_2 in the Weibull model) exhibit under-coverage, which is largely remedied when $n \geq 500$.

Table 2. Results of 200 simulations with right-censoring rate 20%.

	n = 200					n = 500					n = 800					n = 1000				
Par.	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP
Weibull																				
γ_{11}	0.0450	0.2824	0.2502	0.0818	0.915	0.0203	0.1390	0.1548	0.0197	0.980	-0.0062	0.1226	0.1213	0.0151	0.955	0.0089	0.1088	0.1089	0.0117	0.955
γ_{12}	0.0668	0.4253	0.3985	0.1853	0.945	0.0337	0.2288	0.2448	0.0535	0.960	0.0056	0.1695	0.1912	0.0288	0.965	0.0345	0.1597	0.1722	0.0267	0.965
γ_{21}	0.0509	0.2924	0.2694	0.0881	0.950	0.0286	0.1618	0.1674	0.0270	0.940	-0.0033	0.1340	0.1308	0.0180	0.940	0.0136	0.1122	0.1175	0.0128	0.955
γ_{22}	0.0797	0.4565	0.4222	0.2148	0.935	0.0264	0.2462	0.2602	0.0613	0.955	0.0058	0.1846	0.2032	0.0341	0.970	0.0232	0.1720	0.1831	0.0301	0.955
a_1	-0.0428	0.2236	0.2027	0.0518	0.920	-0.0164	0.1274	0.1278	0.0165	0.955	-0.0121	0.0940	0.0993	0.0090	0.955	-0.0021	0.0968	0.0890	0.0094	0.935
β_{11}	0.0148	0.1528	0.1364	0.0236	0.925	0.0003	0.0859	0.0844	0.0074	0.940	-0.0011	0.0648	0.0654	0.0042	0.940	0.0007	0.0570	0.0584	0.0033	0.955
β_{12}	0.0205	0.2848	0.2473	0.0816	0.920	0.0178	0.1452	0.1554	0.0214	0.960	0.0131	0.1208	0.1210	0.0148	0.940	-0.0032	0.1157	0.1084	0.0134	0.940
b_1	-0.0205	0.1233	0.1137	0.0156	0.890	0.0037	0.0696	0.0724	0.0049	0.950	-0.0085	0.0537	0.0563	0.0030	0.955	-0.0036	0.0538	0.0506	0.0029	0.935
a_2	-0.0723	0.5132	0.4433	0.2686	0.910	0.0179	0.2988	0.2759	0.0896	0.915	0.0048	0.2081	0.2175	0.0433	0.960	-0.0116	0.2124	0.1994	0.0452	0.945
β_{21}	0.0378	0.3101	0.2890	0.0976	0.935	0.0163	0.1884	0.1763	0.0358	0.945	0.0028	0.1448	0.1381	0.0210	0.950	0.0051	0.1334	0.1257	0.0178	0.945
β_{22}	0.0481	0.5434	0.5141	0.2975	0.920	0.0078	0.3318	0.3259	0.1101	0.940	-0.0136	0.2670	0.2558	0.0715	0.920	0.0013	0.2444	0.2339	0.0597	0.935
b_2	-0.1006	0.3137	0.2923	0.1085	0.895	-0.0399	0.1924	0.1859	0.0386	0.900	-0.0394	0.1392	0.1459	0.0209	0.960	-0.0008	0.1393	0.1348	0.0194	0.950
Lognormal																				
γ_{11}	0.0640	0.2286	0.2502	0.0564	0.965	0.0006	0.1460	0.1535	0.0213	0.950	0.0140	0.1201	0.1216	0.0146	0.950	0.0046	0.1009	0.1087	0.0102	0.960
γ_{12}	0.0499	0.3644	0.3930	0.1353	0.960	0.0233	0.2390	0.2436	0.0576	0.945	0.0367	0.1829	0.1928	0.0348	0.965	0.0111	0.1541	0.1712	0.0239	0.970
γ_{21}	0.0600	0.2696	0.2699	0.0763	0.955	0.0088	0.1666	0.1659	0.0278	0.940	-0.0017	0.1228	0.1310	0.0151	0.970	0.0127	0.1067	0.1174	0.0115	0.960
γ_{22}	0.0347	0.4048	0.4178	0.1650	0.970	0.0143	0.2596	0.2591	0.0676	0.960	0.0273	0.2026	0.2048	0.0418	0.960	0.0066	0.1665	0.1821	0.0278	0.975
a_1	0.0159	0.2059	0.1979	0.0426	0.940	-0.0084	0.1133	0.1256	0.0129	0.980	0.0073	0.0939	0.0988	0.0089	0.955	-0.0085	0.0879	0.0885	0.0078	0.955
β_{11}	0.0021	0.1375	0.1358	0.0189	0.950	0.0012	0.0830	0.0854	0.0069	0.935	-0.0106	0.0634	0.0670	0.0041	0.965	0.0055	0.0632	0.0599	0.0040	0.955
β_{12}	-0.0130	0.2575	0.2521	0.0665	0.935	0.0067	0.1493	0.1595	0.0223	0.970	-0.0101	0.1260	0.1257	0.0160	0.940	0.0146	0.1065	0.1123	0.0115	0.965
b_1	-0.0240	0.0976	0.0976	0.0101	0.915	-0.0064	0.0617	0.0624	0.0039	0.950	-0.0020	0.0505	0.0493	0.0026	0.955	-0.0072	0.0416	0.0439	0.0018	0.950
a_2	0.0103	0.4604	0.4438	0.2120	0.940	-0.0362	0.2953	0.2849	0.0885	0.955	-0.0316	0.2342	0.2231	0.0558	0.930	0.0038	0.1839	0.1967	0.0338	0.965
β_{21}	0.0077	0.3113	0.2941	0.0970	0.945	-0.0070	0.1798	0.1886	0.0324	0.955	-0.0059	0.1696	0.1468	0.0288	0.925	-0.0147	0.1350	0.1299	0.0184	0.935
β_{22}	0.0609	0.5514	0.5532	0.3078	0.965	0.0259	0.3814	0.3560	0.1461	0.925	0.0374	0.2779	0.2785	0.0786	0.950	-0.0087	0.2321	0.2467	0.0539	0.955
b_2	-0.0706	0.2579	0.2558	0.0715	0.910	0.0018	0.1724	0.1673	0.0297	0.925	-0.0201	0.1285	0.1306	0.0169	0.945	-0.0234	0.1253	0.1156	0.0162	0.915
Loglogistic																				
γ_{11}	0.0231	0.2435	0.2488	0.0598	0.960	0.0265	0.1482	0.1555	0.0227	0.970	0.0130	0.1258	0.1219	0.0160	0.940	0.0163	0.1034	0.1090	0.0109	0.955
γ_{12}	0.0877	0.4115	0.3981	0.1770	0.965	0.0489	0.2425	0.2462	0.0612	0.960	0.0141	0.1829	0.1918	0.0337	0.960	0.0176	0.1647	0.1720	0.0274	0.945
γ_{21}	0.0401	0.2574	0.2685	0.0679	0.965	0.0308	0.1697	0.1676	0.0298	0.955	0.0060	0.1278	0.1314	0.0164	0.960	0.0231	0.1147	0.1177	0.0137	0.955
γ_{22}	0.0847	0.4339	0.4224	0.1955	0.955	0.0651	0.2479	0.2609	0.0657	0.965	0.0184	0.1857	0.2036	0.0348	0.980	0.0249	0.1844	0.1826	0.0346	0.950
a_1	0.0055	0.3261	0.3179	0.1064	0.940	0.0068	0.2150	0.2023	0.0463	0.915	-0.0016	0.1493	0.1599	0.0223	0.965	-0.0033	0.1546	0.1435	0.0239	0.950
β_{11}	0.0128	0.1975	0.2209	0.0392	0.975	-0.0075	0.1365	0.1395	0.0187	0.965	0.0156	0.1118	0.1103	0.0128	0.945	0.0035	0.1014	0.0987	0.0103	0.930
β_{12}	0.0233	0.4364	0.4168	0.1910	0.940	-0.0097	0.2716	0.2654	0.0739	0.950	-0.0190	0.1896	0.2089	0.0363	0.970	0.0010	0.1826	0.1879	0.0334	0.965
b_1	-0.0270	0.1143	0.1165	0.0138	0.900	-0.0090	0.0709	0.0749	0.0051	0.960	-0.0097	0.0642	0.0585	0.0042	0.920	-0.0031	0.0524	0.0526	0.0028	0.940
a_2	-0.0263	0.7157	0.7115	0.5130	0.955	-0.0130	0.4513	0.4499	0.2039	0.950	0.0192	0.3509	0.3520	0.1235	0.955	-0.0085	0.3302	0.3121	0.1091	0.945
β_{21}	0.0160	0.4906	0.4834	0.2410	0.965	0.0111	0.2802	0.3044	0.0787	0.980	0.0172	0.2509	0.2402	0.0633	0.940	0.0108	0.2075	0.2127	0.0432	0.955
β_{22}	0.0858	0.9842	0.9254	0.9760	0.960	-0.0291	0.6028	0.5870	0.3643	0.955	-0.0415	0.4602	0.4612	0.2135	0.950	0.0347	0.4390	0.4097	0.1939	0.935
b_2	-0.0630	0.2894	0.3080	0.0877	0.905	-0.0006	0.1959	0.2007	0.0384	0.945	0.0005	0.1477	0.1512	0.0218	0.955	-0.0102	0.1220	0.1323	0.0150	0.950

Bias: empirical bias; **ESE**: empirical standard error; **ASE**: the average of the estimated asymptotic standard error; **MSE**: mean square error; **CP**: 95% coverage probability.

Table 3. Results of 200 simulations with right-censoring rate 30%.

	n = 200					n = 500					n = 800					n = 1000				
Par.	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP
Weibull																				
γ_{11}	0.0029	0.2403	0.2499	0.0577	0.960	0.0183	0.1551	0.1570	0.0244	0.955	0.0073	0.1203	0.1238	0.0145	0.955	0.0081	0.1143	0.1109	0.0131	0.950
γ_{12}	0.0177	0.3709	0.3641	0.1378	0.940	0.0199	0.2338	0.2277	0.0551	0.920	0.0015	0.1798	0.1794	0.0323	0.960	0.0239	0.1650	0.1616	0.0278	0.920
γ_{21}	0.0027	0.2316	0.2512	0.0537	0.980	0.0161	0.1582	0.1578	0.0253	0.965	0.0201	0.1204	0.1246	0.0149	0.955	0.0130	0.1136	0.1114	0.0131	0.920
γ_{22}	0.0277	0.3322	0.3245	0.1111	0.950	0.0194	0.1947	0.2033	0.0383	0.980	0.0114	0.1556	0.1600	0.0243	0.965	0.0453	0.1381	0.1441	0.0211	0.965
a_1	-0.0279	0.2807	0.2534	0.0796	0.925	-0.0194	0.1747	0.1634	0.0309	0.945	-0.0198	0.1333	0.1289	0.0181	0.950	-0.0065	0.1243	0.1155	0.0155	0.930
β_{11}	0.0117	0.2044	0.1736	0.0419	0.900	-0.0018	0.1143	0.1082	0.0131	0.920	0.0110	0.0851	0.0850	0.0074	0.935	-0.0057	0.0796	0.0786	0.0064	0.940
β_{12}	0.0040	0.3402	0.3070	0.1157	0.920	0.0047	0.2045	0.1986	0.0419	0.950	0.0160	0.1578	0.1570	0.0252	0.935	-0.0034	0.1466	0.1422	0.0215	0.960
b_1	-0.0658	0.1395	0.1391	0.0238	0.875	-0.0185	0.1009	0.0919	0.0105	0.910	-0.0072	0.0733	0.0730	0.0054	0.940	-0.0126	0.0704	0.0669	0.0051	0.930
a_2	-0.0584	0.3969	0.3832	0.1609	0.925	0.0028	0.2400	0.2377	0.0576	0.960	0.0025	0.1762	0.1877	0.0310	0.965	-0.0016	0.1750	0.1727	0.0306	0.940
β_{21}	0.0057	0.2661	0.2443	0.0708	0.950	-0.0051	0.1473	0.1488	0.0217	0.945	-0.0020	0.1171	0.1185	0.0137	0.965	0.0139	0.1162	0.1113	0.0137	0.950
β_{22}	0.0141	0.4621	0.4465	0.2138	0.925	0.0000	0.2753	0.2789	0.0758	0.945	0.0148	0.2134	0.2205	0.0458	0.960	-0.0157	0.2150	0.2037	0.0465	0.950
b_2	-0.0606	0.2272	0.2544	0.0553	0.925	-0.0396	0.1544	0.1598	0.0254	0.935	-0.0337	0.1199	0.1263	0.0155	0.950	0.0025	0.1204	0.1214	0.0145	0.965
Lognormal																				
γ_{11}	0.0555	0.2586	0.2548	0.0699	0.940	0.0235	0.1527	0.1578	0.0239	0.955	0.0132	0.1348	0.1239	0.0184	0.915	0.0093	0.1068	0.1105	0.0115	0.960
γ_{12}	0.0677	0.3822	0.3678	0.1507	0.960	0.0082	0.2151	0.2283	0.0464	0.955	0.0092	0.1658	0.1792	0.0276	0.970	0.0082	0.1600	0.1603	0.0257	0.950
γ_{21}	0.0833	0.2684	0.2575	0.0790	0.945	0.0292	0.1527	0.1586	0.0242	0.950	0.0133	0.1254	0.1245	0.0159	0.955	0.0209	0.1051	0.1112	0.0115	0.965
γ_{22}	0.0699	0.3266	0.3294	0.1116	0.970	0.0269	0.2127	0.2035	0.0460	0.940	0.0075	0.1572	0.1600	0.0248	0.970	0.0083	0.1400	0.1432	0.0197	0.970
a_1	-0.0029	0.2666	0.2573	0.0711	0.955	-0.0040	0.1693	0.1619	0.0287	0.930	-0.0178	0.1236	0.1283	0.0156	0.960	0.0053	0.1046	0.1138	0.0110	0.970
β_{11}	-0.0009	0.1752	0.1762	0.0307	0.955	0.0080	0.1210	0.1112	0.0147	0.930	0.0037	0.0934	0.0870	0.0087	0.940	-0.0032	0.0777	0.0769	0.0060	0.960
β_{12}	-0.0131	0.3187	0.3229	0.1017	0.945	-0.0136	0.2252	0.2055	0.0509	0.925	0.0228	0.1633	0.1625	0.0272	0.950	-0.0020	0.1418	0.1442	0.0201	0.945
b_1	-0.0421	0.1316	0.1226	0.0191	0.890	-0.0151	0.0847	0.0801	0.0074	0.915	-0.0073	0.0579	0.0635	0.0034	0.965	-0.0158	0.0637	0.0564	0.0043	0.915
a_2	0.0071	0.3853	0.3810	0.1485	0.960	0.0224	0.2424	0.2386	0.0592	0.935	0.0042	0.1983	0.1907	0.0393	0.960	-0.0083	0.1796	0.1710	0.0323	0.925
β_{21}	0.0084	0.2521	0.2550	0.0636	0.945	-0.0026	0.1649	0.1586	0.0272	0.945	-0.0073	0.1226	0.1254	0.0151	0.935	-0.0041	0.1161	0.1134	0.0135	0.915
β_{22}	-0.0464	0.4864	0.4763	0.2387	0.960	-0.0172	0.3224	0.2990	0.1042	0.900	0.0078	0.2300	0.2391	0.0530	0.950	0.0130	0.2281	0.2143	0.0522	0.940
b_2	-0.0446	0.2364	0.2231	0.0579	0.895	-0.0359	0.1418	0.1408	0.0214	0.935	-0.0067	0.1033	0.1126	0.0107	0.965	-0.0054	0.1082	0.1015	0.0117	0.920
Loglogistic																				
γ_{11}	0.0286	0.2564	0.2535	0.0665	0.950	0.0168	0.1424	0.1577	0.0206	0.970	0.0217	0.1355	0.1242	0.0188	0.945	0.0131	0.1111	0.1106	0.0125	0.930
γ_{12}	0.0208	0.3787	0.3662	0.1438	0.955	0.0267	0.2116	0.2271	0.0455	0.955	0.0271	0.1786	0.1798	0.0326	0.960	0.0134	0.1380	0.1602	0.0192	0.985
γ_{21}	0.0521	0.2556	0.2556	0.0680	0.955	0.0210	0.1502	0.1586	0.0230	0.960	0.0252	0.1356	0.1251	0.0190	0.920	0.0154	0.1057	0.1112	0.0114	0.955
γ_{22}	0.0326	0.3289	0.3267	0.1092	0.975	0.0189	0.1842	0.2031	0.0343	0.985	0.0179	0.1656	0.1609	0.0278	0.950	0.0140	0.1303	0.1432	0.0172	0.965
a_1	-0.0383	0.4598	0.4196	0.2129	0.905	0.0028	0.2527	0.2633	0.0639	0.960	-0.0102	0.1981	0.2068	0.0393	0.965	-0.0159	0.1891	0.1850	0.0360	0.940
β_{11}	0.0628	0.2892	0.2922	0.0876	0.945	0.0055	0.1771	0.1808	0.0314	0.965	0.0057	0.1453	0.1437	0.0211	0.950	0.0027	0.1327	0.1276	0.0176	0.940
β_{12}	0.0193	0.5905	0.5435	0.3491	0.925	-0.0198	0.3274	0.3440	0.1076	0.945	0.0367	0.2619	0.2714	0.0699	0.970	0.0421	0.2428	0.2419	0.0607	0.945
b_1	-0.0472	0.1535	0.1487	0.0258	0.895	-0.0057	0.0990	0.0970	0.0098	0.950	-0.0002	0.0835	0.0770	0.0070	0.925	-0.0056	0.0676	0.0674	0.0046	0.925
a_2	-0.0544	0.6546	0.6134	0.4314	0.965	0.0224	0.4017	0.3802	0.1618	0.940	-0.0026	0.3139	0.3019	0.0985	0.930	0.0149	0.2844	0.2675	0.0811	0.920
β_{21}	-0.0138	0.4302	0.4153	0.1853	0.955	0.0104	0.2818	0.2609	0.0795	0.930	0.0093	0.2178	0.2057	0.0475	0.940	0.0030	0.1912	0.1812	0.0366	0.940
β_{22}	0.0434	0.8648	0.7975	0.7498	0.930	-0.0250	0.5253	0.4994	0.2765	0.935	-0.0051	0.4279	0.3958	0.1831	0.930	-0.0204	0.3603	0.3510	0.1302	0.940
b_2	-0.0354	0.2574	0.2701	0.0675	0.920	-0.0175	0.1801	0.1703	0.0327	0.930	-0.0118	0.1439	0.1348	0.0208	0.910	-0.0172	0.1218	0.1133	0.0151	0.915

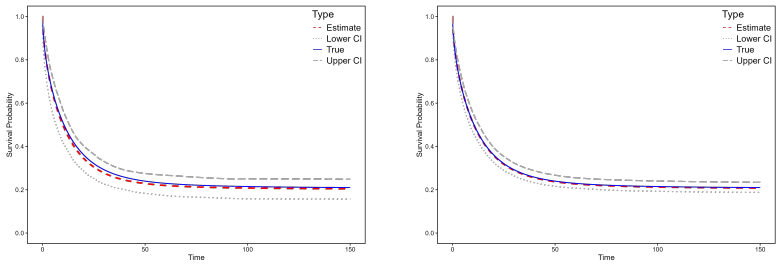
Bias: empirical bias; **ESE**: empirical standard error; **ASE**: the average of the estimated asymptotic standard error; **MSE**: mean square error; **CP**: 95% coverage probability.

Table 4. Results of 200 simulations with right-censoring rate 40%.

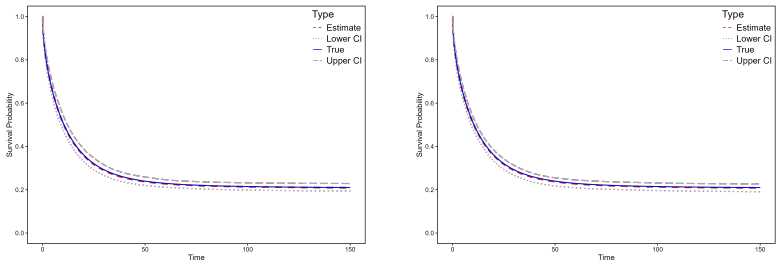
	n = 200					n = 500					n = 800					n = 1000				
Par.	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP	Bias	ESE	ASE	MSE	CP
Weibull																				
γ_{11}	0.0130	0.2205	0.2261	0.0488	0.955	0.0269	0.1435	0.1421	0.0213	0.960	0.0083	0.1096	0.1117	0.0121	0.960	0.0023	0.0950	0.0997	0.0090	0.955
γ_{12}	0.0066	0.2919	0.3171	0.0853	0.965	0.0278	0.2008	0.1975	0.0411	0.955	0.0307	0.1460	0.1561	0.0223	0.960	0.0153	0.1293	0.1399	0.0170	0.955
γ_{21}	0.0316	0.2077	0.2185	0.0441	0.985	0.0248	0.1317	0.1373	0.0180	0.960	0.0077	0.1046	0.1078	0.0110	0.950	0.0087	0.0848	0.0962	0.0073	0.985
γ_{22}	0.0251	0.2866	0.2923	0.0827	0.950	0.0135	0.1842	0.1829	0.0341	0.955	0.0289	0.1381	0.1444	0.0199	0.950	0.0269	0.1150	0.1291	0.0139	0.985
a_1	0.0042	0.2141	0.2270	0.0459	0.960	-0.0033	0.1669	0.1566	0.0279	0.925	-0.0077	0.1297	0.1250	0.0169	0.960	-0.0189	0.1168	0.1108	0.0140	0.945
β_{11}	-0.0061	0.1619	0.1536	0.0263	0.950	0.0147	0.1511	0.1363	0.0231	0.905	0.0038	0.1087	0.1074	0.0118	0.950	0.0091	0.0944	0.0896	0.0090	0.945
β_{12}	-0.0110	0.2733	0.2769	0.0748	0.945	0.0004	0.2296	0.2239	0.0527	0.935	-0.0019	0.1820	0.1781	0.0331	0.935	0.0259	0.1594	0.1517	0.0261	0.950
b_1	-0.0485	0.1287	0.1274	0.0189	0.875	-0.0213	0.1198	0.1096	0.0148	0.910	-0.0052	0.0878	0.0878	0.0077	0.950	-0.0026	0.0744	0.0739	0.0055	0.935
a_2	-0.0386	0.4394	0.4075	0.1946	0.955	0.0395	0.2537	0.2736	0.0659	0.955	-0.0060	0.2174	0.2225	0.0473	0.950	0.0047	0.2040	0.1937	0.0416	0.930
β_{21}	-0.0165	0.2678	0.2577	0.0720	0.945	0.0028	0.1950	0.1992	0.0380	0.965	0.0073	0.1662	0.1600	0.0277	0.920	-0.0073	0.2506	0.2352	0.0628	0.945
β_{22}	0.0560	0.5153	0.4758	0.2687	0.930	-0.0424	0.3519	0.3382	0.1256	0.940	0.0021	0.2703	0.2733	0.0731	0.940	-0.0055	0.1572	0.1608	0.0248	0.955
b_2	-0.1050	0.2755	0.2688	0.0869	0.890	-0.0426	0.2365	0.2398	0.0578	0.935	0.0106	0.1961	0.1957	0.0386	0.960	0.0025	0.1204	0.1214	0.0145	0.965
Lognormal																				
γ_{11}	0.0373	0.2400	0.2271	0.0590	0.925	0.0138	0.1359	0.1410	0.0186	0.950	0.0152	0.1152	0.1122	0.0135	0.920	0.0243	0.0962	0.1001	0.0098	0.965
γ_{12}	0.0330	0.3200	0.3165	0.1035	0.950	0.0177	0.1992	0.1979	0.0400	0.935	0.0168	0.1605	0.1562	0.0260	0.960	0.0230	0.1390	0.1403	0.0198	0.940
γ_{21}	0.0468	0.2476	0.2196	0.0635	0.920	0.0011	0.1382	0.1359	0.0191	0.945	0.0177	0.1118	0.1083	0.0128	0.955	0.0155	0.0958	0.0964	0.0094	0.950
γ_{22}	0.0251	0.2895	0.2929	0.0845	0.955	0.0201	0.1732	0.1826	0.0304	0.960	0.0177	0.1489	0.1443	0.0225	0.940	0.0351	0.1366	0.1294	0.0199	0.935
a_1	-0.0355	0.2468	0.2389	0.0622	0.940	-0.0015	0.1561	0.1488	0.0244	0.925	-0.0085	0.1192	0.1173	0.0143	0.960	0.0067	0.1014	0.1052	0.0103	0.975
β_{11}	0.0184	0.2049	0.1835	0.0423	0.945	-0.0039	0.1120	0.1065	0.0126	0.940	0.0085	0.0889	0.0857	0.0080	0.955	-0.0025	0.0728	0.0774	0.0053	0.970
β_{12}	0.0508	0.3392	0.3193	0.1176	0.940	0.0069	0.2043	0.1923	0.0418	0.925	0.0176	0.1634	0.1528	0.0270	0.925	-0.0081	0.1225	0.1381	0.0151	0.965
b_1	-0.0324	0.1447	0.1361	0.0220	0.895	-0.0045	0.0763	0.0795	0.0058	0.940	-0.0106	0.0623	0.0646	0.0040	0.940	-0.0031	0.0630	0.0587	0.0040	0.935
a_2	-0.0604	0.4755	0.4392	0.2297	0.935	-0.0364	0.2730	0.2701	0.0759	0.955	-0.0258	0.2104	0.2127	0.0449	0.980	-0.0035	0.1832	0.1872	0.0336	0.955
β_{21}	0.0207	0.2973	0.3072	0.0888	0.975	0.0059	0.1819	0.1839	0.0331	0.960	0.0136	0.1458	0.1463	0.0214	0.950	-0.0112	0.1283	0.1290	0.0166	0.935
β_{22}	0.0515	0.5843	0.5495	0.3440	0.925	0.0448	0.3291	0.3382	0.1103	0.960	0.0093	0.2484	0.2669	0.0618	0.950	0.0119	0.2319	0.2358	0.0539	0.955
b_2	-0.0326	0.3204	0.3140	0.1037	0.920	0.0060	0.1816	0.1798	0.0330	0.940	0.0061	0.1472	0.1455	0.0217	0.920	-0.0210	0.1239	0.1300	0.0158	0.960
Loglogistic																				
γ_{11}	0.0113	0.2428	0.2257	0.0591	0.940	0.0248	0.1476	0.1425	0.0224	0.935	0.0065	0.1107	0.1117	0.0123	0.965	0.0180	0.0979	0.1001	0.0099	0.945
γ_{12}	0.0060	0.3010	0.3165	0.0907	0.970	0.0202	0.1897	0.1987	0.0364	0.955	0.0289	0.1584	0.1563	0.0259	0.945	0.0265	0.1346	0.1397	0.0188	0.960
γ_{21}	0.0115	0.2192	0.2176	0.0482	0.965	0.0169	0.1357	0.1373	0.0187	0.950	0.0192	0.1072	0.1080	0.0119	0.945	0.0144	0.0896	0.0965	0.0082	0.975
γ_{22}	0.0278	0.2729	0.2912	0.0752	0.965	0.0323	0.1682	0.1832	0.0293	0.975	0.0292	0.1376	0.1446	0.0198	0.970	0.0331	0.1293	0.1291	0.0178	0.945
a_1	-0.0307	0.3496	0.3848	0.1232	0.975	0.0014	0.2443	0.2388	0.0597	0.960	0.0066	0.1717	0.1866	0.0295	0.965	0.0028	0.1802	0.1660	0.0325	0.935
β_{11}	0.0190	0.2707	0.2660	0.0736	0.930	0.0005	0.1638	0.1659	0.0268	0.945	-0.0091	0.1302	0.1303	0.0170	0.945	0.0125	0.1213	0.1174	0.0149	0.940
β_{12}	0.0181	0.4780	0.4993	0.2289	0.960	-0.0107	0.3344	0.3113	0.1119	0.950	-0.0229	0.2390	0.2452	0.0576	0.965	-0.0160	0.2264	0.2185	0.0515	0.950
b_1	-0.0156	0.1486	0.1401	0.0223	0.900	-0.0111	0.0923	0.0921	0.0086	0.950	-0.0022	0.0787	0.0734	0.0062	0.930	-0.0089	0.0605	0.0661	0.0037	0.960
a_2	0.0685	0.6798	0.6469	0.4668	0.940	0.0149	0.4138	0.4129	0.1714	0.960	-0.0561	0.3268	0.3358	0.1099	0.950	0.0003	0.2827	0.2960	0.0799	0.950
β_{21}	0.0157	0.4409	0.4491	0.1946	0.960	0.0042	0.3018	0.2845	0.0911	0.935	0.0001	0.2532	0.2283	0.0641	0.930	0.0224	0.1830	0.2036	0.0340	0.970
β_{22}	-0.0646	0.8825	0.8492	0.7831	0.960	-0.0133	0.5336	0.5416	0.2849	0.965	0.0633	0.3977	0.4365	0.1622	0.960	-0.0254	0.3636	0.3863	0.1329	0.955
b_2	-0.0521	0.2923	0.2924	0.0882	0.910	-0.0180	0.2213	0.2044	0.0493	0.940	0.0170	0.1737	0.1666	0.0305	0.955	0.0011	0.1511	0.1500	0.0228	0.950

Bias: empirical bias; **ESE**: empirical standard error; **ASE**: the average of the estimated asymptotic standard error; **MSE**: mean square error; **CP**: 95% coverage probability.

Survival function estimates (Figures 7–9) show good overall fit but increased variability in the tails, particularly for longer survival times. Nevertheless, the pointwise confidence intervals maintain reasonable coverage, supporting the methods usability even under high censoring, provided the sample size is sufficient.



(a) $n = 200$, S_T **(b)** $n = 500$, S_T



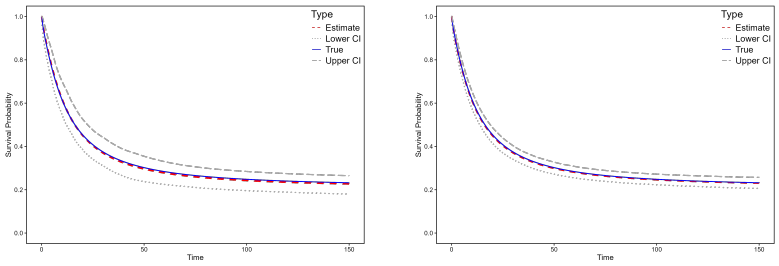
(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 1. Under a censoring rate of 20%, the overall survival function (S_T) estimated based on the Weibull distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).

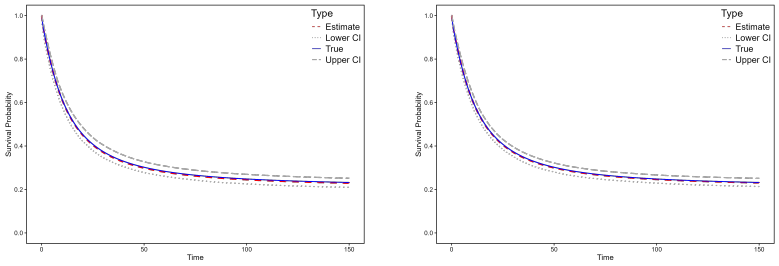
Table 5 presents the simulation results of model misspecification under 20% right-censoring with a sample size of 500. All simulated datasets are generated from the Weibull distribution, and three distributions (Weibull, lognormal, and log-logistic) are employed as working models for estimation respectively. When the working model matches the true data-generating distribution, the estimation biases of all parameters remain at a low level, the ESEs align well with the ASEs, and the empirical CPs of the 95% confidence intervals are close to the nominal level, showing estimation performance consistent with correctly specified settings. Under model misspecification, the multinomial logistic regression parameters γ and the regression coefficients β of the AFT model exhibit certain robustness, with relatively limited increases in estimation bias, and the CPs of confidence intervals for most parameters remain within an acceptable range.

Meanwhile, Figure 10 presents the estimated overall survival functions under different model specifications. As can be seen from the figure, even under distributional misspecification, there is no apparent deviation between the estimated and true survival functions, further indicating that the misspecification considered herein has only a negligible impact on the estimation of the overall survival function.

The proposed estimator demonstrates strong robustness across varying censoring rates (20%–40%), sample sizes, and lifetime distributions. Performance is excellent under light to moderate censoring

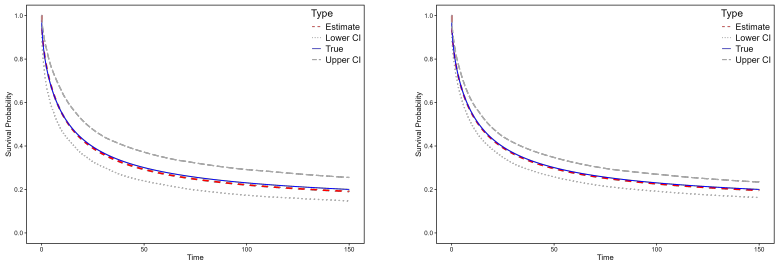


(a) $n = 200$, S_T **(b)** $n = 500$, S_T

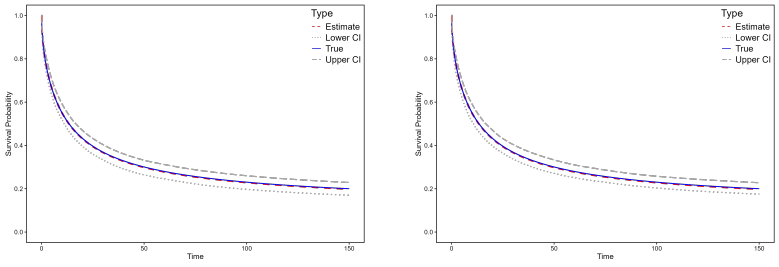


(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 2. The overall survival function (S_T) estimated based on the lognormal distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).

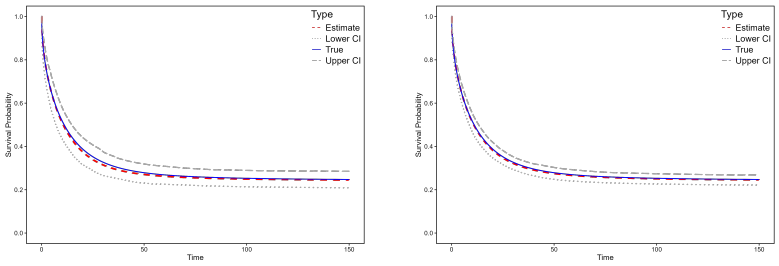


(a) $n = 200$, S_T **(b)** $n = 500$, S_T

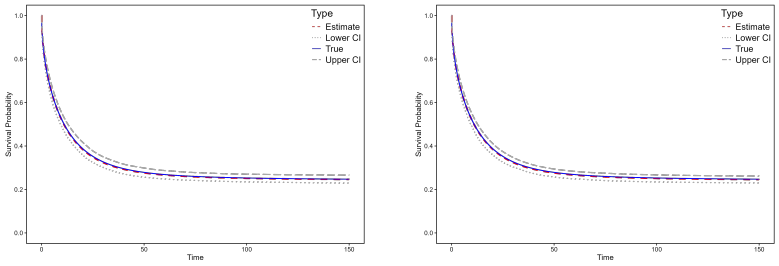


(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 3. Under a censoring rate of 20%, the overall survival function (S_T) estimated based on the loglogistic distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).

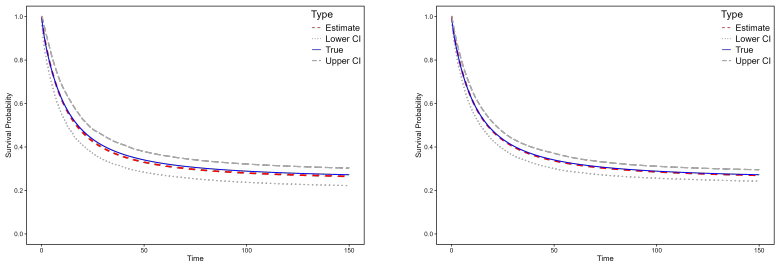


(a) $n = 200$, S_T **(b)** $n = 500$, S_T

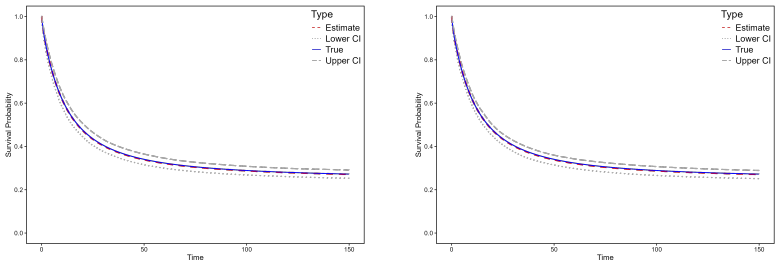


(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 4. Under a censoring rate of 30%, the overall survival function (S_T) estimated based on the Weibull distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).

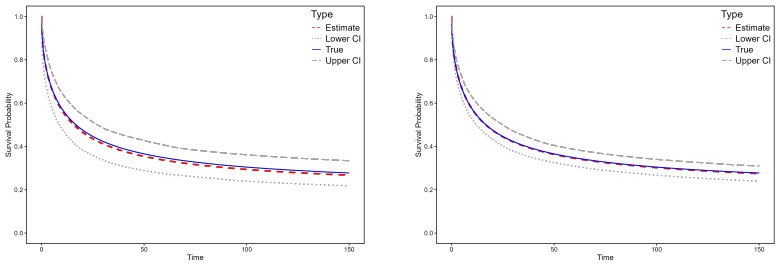


(a) $n = 200$, S_T **(b)** $n = 500$, S_T

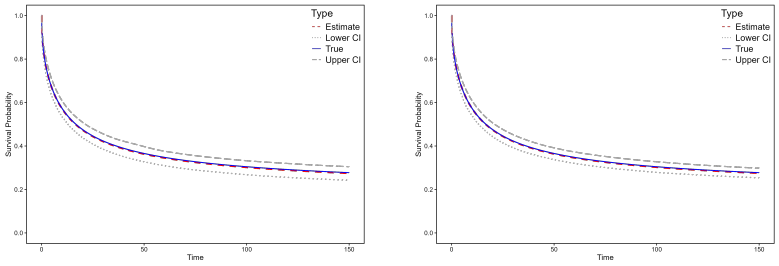


(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 5. Under a censoring rate of 30%, the overall survival function (S_T) estimated based on the lognormal distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).

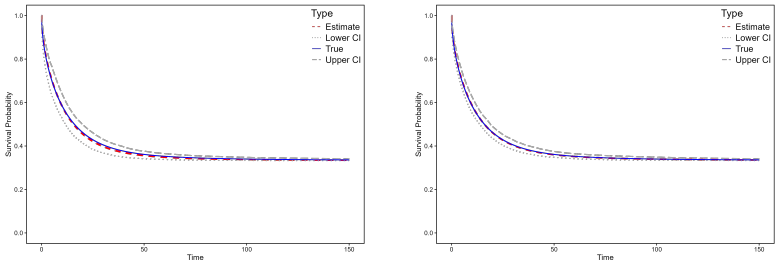


(a) $n = 200$, S_T **(b)** $n = 500$, S_T

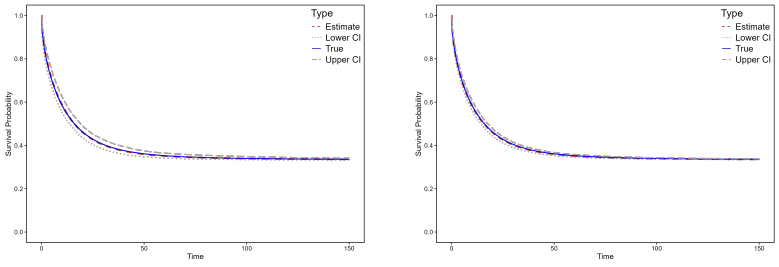


(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 6. Under a censoring rate of 30%, the overall survival function (S_T) estimated based on the loglogistic distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).

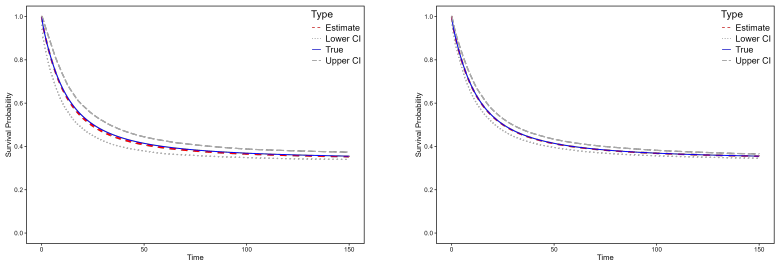


(a) $n = 200$, S_T **(b)** $n = 500$, S_T

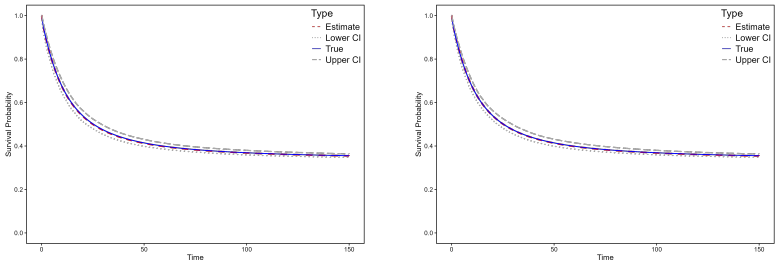


(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 7. Under a censoring rate of 40%, the overall survival function (S_T) estimated based on the Weibull distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).

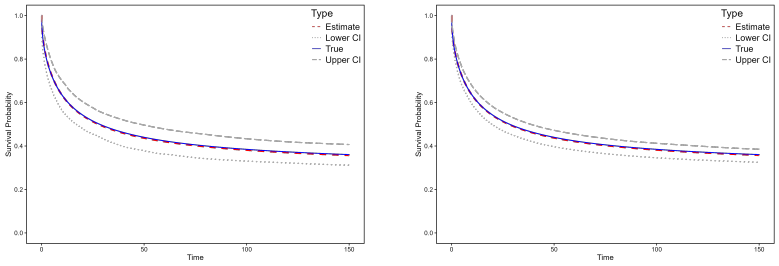


(a) $n = 200$, S_T **(b)** $n = 500$, S_T

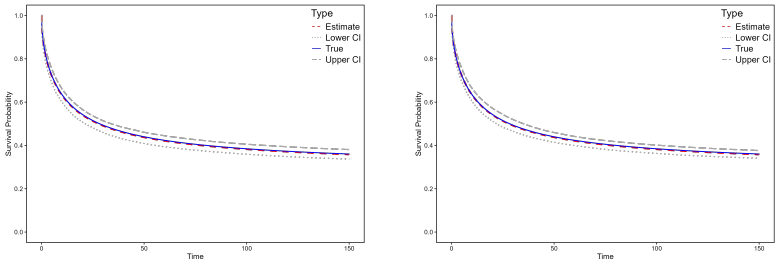


(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 8. Under a censoring rate of 40%, the overall survival function (S_T) estimated based on the lognormal distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).



(a) $n = 200$, S_T **(b)** $n = 500$, S_T



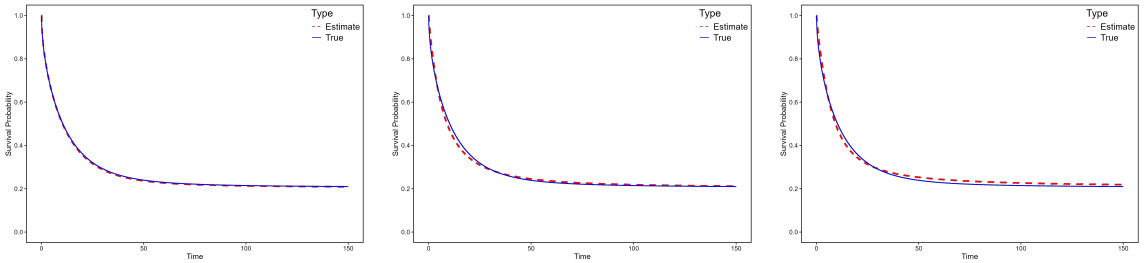
(c) $n = 800$, S_T **(d)** $n = 1000$, S_T

Figure 9. Under a censoring rate of 40%, the overall survival function (S_T) estimated based on the loglogistic distribution (red dashed line), with 95% pointwise confidence intervals (long dashed and dotted lines), and the corresponding true survival function (blue solid line).

Table 5. Model misspecification simulation results with 20% right-censoring (Weibull true distribution, n = 500).

Par.	Bias	ESE	ASE	MSE	CP
Weibull					
γ_{11}	0.0032	0.1553	0.1540	0.0241	0.950
γ_{12}	-0.0025	0.2472	0.2421	0.0611	0.935
γ_{21}	-0.0061	0.1764	0.1658	0.0311	0.945
γ_{22}	0.0112	0.2713	0.2569	0.0737	0.935
a_1	-0.0226	0.1358	0.1269	0.0190	0.930
β_{11}	-0.0001	0.0859	0.0831	0.0074	0.935
β_{12}	0.0298	0.1578	0.1541	0.0258	0.930
b_1	-0.0105	0.0774	0.0714	0.0061	0.925
a_2	-0.0204	0.2802	0.2764	0.0789	0.955
β_{21}	0.0266	0.1783	0.1755	0.0325	0.955
β_{22}	0.0406	0.3304	0.3241	0.1108	0.930
b_2	-0.0584	0.1763	0.1844	0.0345	0.935
Lognormal					
γ_{11}	0.0091	0.1623	0.1552	0.0264	0.930
γ_{12}	0.0458	0.2446	0.2457	0.0619	0.955
γ_{21}	0.0100	0.1735	0.1670	0.0302	0.945
γ_{22}	0.0480	0.2612	0.2607	0.0705	0.935
a_1	-0.4812	0.1446	0.1482	0.2525	0.040
β_{11}	-0.0063	0.1012	0.0959	0.0103	0.935
β_{12}	-0.0049	0.1731	0.1789	0.0300	0.960
b_1	0.0491	0.0765	0.0721	0.0083	0.920
a_2	-0.7038	0.3113	0.3067	0.5923	0.330
β_{21}	-0.0304	0.1886	0.1881	0.0365	0.955
β_{22}	-0.0051	0.3470	0.3519	0.1205	0.940
b_2	-0.1858	0.1528	0.1729	0.0578	0.770
Loglogistic					
γ_{11}	0.0255	0.1526	0.1550	0.0239	0.960
γ_{12}	0.0282	0.2310	0.2440	0.0541	0.960
γ_{21}	0.0260	0.1718	0.1672	0.0302	0.960
γ_{22}	0.0205	0.2362	0.2593	0.0562	0.960
a_1	-0.4284	0.1500	0.1479	0.2061	0.140
β_{11}	0.0103	0.1045	0.0984	0.0110	0.955
β_{12}	-0.0136	0.1768	0.1804	0.0315	0.965
b_1	-0.3906	0.0454	0.0472	0.1546	0.000
a_2	-0.6162	0.3136	0.3029	0.4780	0.485
β_{21}	-0.0286	0.2118	0.1953	0.0457	0.925
β_{22}	-0.0916	0.3716	0.3580	0.1464	0.935
b_2	-0.9486	0.1014	0.1109	0.9101	0.000

Bias: empirical bias; **ESE**: empirical standard error; **ASE**: the average of the estimated asymptotic standard error; **MSE**: mean square error; **CP**: 95% coverage probability.



(a) Weibull, S_T **(b)** Lognormal, S_T **(c)** Loglogistic, S_T

Figure 10. Estimated overall survival function S_T under different distributional assumptions with a 20% censoring rate. The Weibull distribution is correctly specified, while the lognormal and loglogistic distributions are misspecified. The blue solid line represents the true survival function.

and remains reliable under heavy censoring when sample sizes are adequate. The method provides accurate point and interval estimates, making it suitable for practical applications where censoring is non-negligible.

6. Empirical application: P2P lending data

6.1. Data source and context

Fixed-rate peer-to-peer (P2P) lending provides an ideal setting for validating the proposed mixture cure model with competing risks. This study utilizes data from Lending Club, one of the world's largest P2P lending platforms, which offers loan products with standard terms of 36 and 60 months.We focus specifically on 36-month loans issued in 2017, and restrict our analysis to borrowers within credit grade E—a segment characterized by lower credit scores and elevated default risk, thus representing a typical high-risk population in consumer lending.

Throughout the loan term, borrowers are obligated to make fixed monthly payments. A loan is classified as a right-censored observation if the borrower completes all 36 scheduled payments without any early termination. Conversely, early termination occurs if the borrower either defaults or fully prepays the loan before the maturity date.

A strict criterion for default is adopted: Any loan with a delinquency status (including "current" loans with a recorded delinquency amount) is classified as a default event. Prepayment is defined as the full repayment of outstanding principal before contractual maturity. To capture the temporal uncertainty of these events, both default and prepayment are treated as interval-censored data—specifically, we can only ascertain that each event occurred within a one-month interval around the observed payment failure or early settlement date. The rationale for this monthly interval specification is that in credit risk management practice, key post-loan decisions—such as risk alerting, collection scheduling, and provisioning—are all made on a monthly cycle; aggregating event times to the monthly level aligns model output with operational decision frequency, enhancing practical deployability. This approach provides a solid foundation for the subsequent survival models that explicitly account for temporal uncertainty in event occurrence.

Since default and prepayment are mutually exclusive events, and both lead to the early termination

of loans, it is methodologically reasonable to adopt a competing risks model for empirical analysis. After data cleaning, the final sample consists of 2067 loan records in the default group and 3709 loan records in the prepayment group. Further Schoenfeld residual tests indicate that both the default and prepayment events significantly violate the Cox proportional hazards assumption, rendering the traditional Cox model inappropriate. Therefore, this paper adopts the AFT model, which does not require the proportional hazards constraint, for modeling within the competing risks framework. For empirical analysis, we select three core risk factors: loan amount, annual income, and interest rate. These variables capture distinct dimensions of borrower risk:

- **Loan amount** directly reflects the borrower's debt leverage level. Higher amounts imply greater monthly payment obligations, increasing the probability of future cash flow shortfall.
- **Annual income** serves as a key indicator of repayment capacity. Higher income provides a larger buffer against financial shocks, thereby reducing relative default risk.
- **Interest rate** embodies the platform's pricing of the borrower's credit risk. Higher rates not only increase the repayment burden but also signal potential credit deficiencies.

Collectively, these variables form a foundational framework for modeling the incidence of default and prepayment.

6.2. Model specifications

We develop three mixture cure model variants to capture different immune mechanisms:

(A) **Model A: Fully competing risk mixture cure model** Accommodates loans susceptible to both default and prepayment, plus an "immune" fraction never at risk of either event. The survival function is given by

$$S_T(t|Z,X) = \pi_0(Z) + \pi_1(Z)S_1(t|X) + \pi_2(Z)S_2(t|X).$$

(B) **Model B: Default-specific mixture cure model** Assumes a subpopulation immune to default and considers default as the sole risk. The survival function is given by

$$S_T(t|Z,X) = \pi_0(Z) + [1-\pi_0(Z)]\,S_1(t|X).$$

(C) **Model C: Prepayment-specific mixture cure model** Assumes a subpopulation immune to prepayment and considers prepayment as the sole risk. The survival function is given by

$$S_T(t|Z,X) = \pi_0(Z) + [1-\pi_0(Z)]\,S_2(t|X).$$

The standardized covariates $Z = (z_1, z_2, z_3)$ (loan amount, annual income, interest rate) determine event timing, while $X = (z_1, z_2)$ influences classification probabilities.

Figure 11 illustrates monthly proportions of defaulted and prepaid loans, where an event in month i corresponds to $t_i \in (i-1, i]$. These models enable financial institutions to predict borrower behavior more accurately and inform differentiated credit policies. Based on this data structure, we first obtain the overall survival curve via the Turnbull nonparametric estimator (Figure 12). The results show that the curve exhibits a stable plateau, indicating that a subset of borrowers never experienced any competing events throughout the observation period, which reflects a clear cure characteristic in the data.

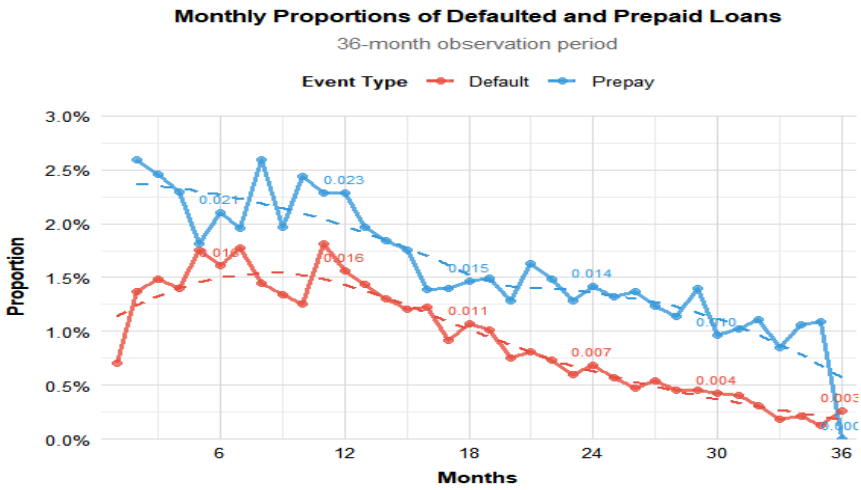


Figure 11. Proportions of defaulted and prepaid loans.

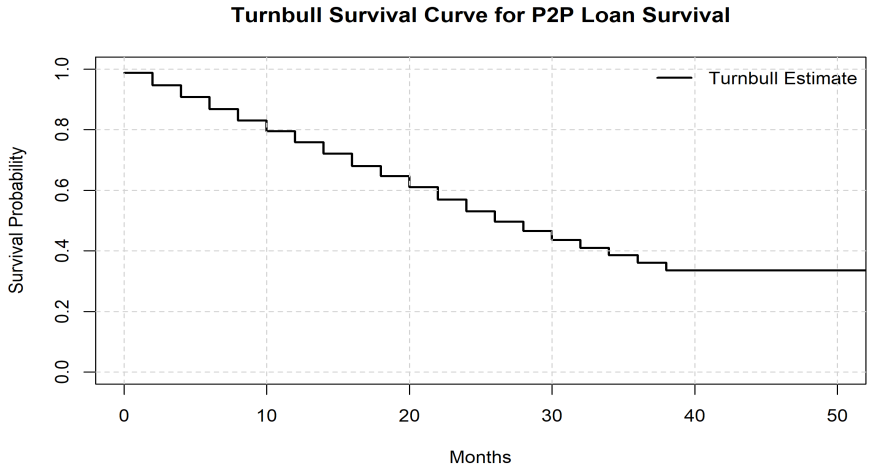


Figure 12. Turnbull survival curve for P2P lending data.

6.3. Distributional performance and model selection

Based on the comprehensive regression results (Tables 6–8) and the corresponding survival curves (Figures 13–15), the Weibull distribution consistently demonstrates superior performance across all models above.

In the competing risks (Model A) framework (Table 6), the Weibull specification exhibits exceptional estimation precision, with all standard errors confined within the narrow range of 0.010–0.037. Notably, 11 out of 14 parameters are statistically significant, ensuring reliable inference. In contrast, both the lognormal and log-logistic distributions show substantially higher standard errors and critical significance issues in key parameters (e.g., β_{11} and β_{12} in lognormal, $p > 0.7$), undermining their practical utility.

This superiority persists in the mixture cure models (Models B and C). For default risk (Table 7), all cure model covariates (γ_{11}, γ_{12}, γ_{13}) under the Weibull distribution are highly significant. Although β_{11} is non-significant across distributions, β_{12} remains significant ($p = 0.0138$) with a substantially lower standard error (0.0112) compared to lognormal (0.0832), indicating superior precision. For prepayment risk (Table 8), the Weibull distribution again shows the lowest standard errors and high significance for β_{22} ($p < 0.0001$), while the lognormal distribution performs poorest with non-significant parameters and abnormally high standard errors (e.g., 0.0903 for β_{21}). The significant differences in scale parameter estimates (e.g., b_2 values: 0.7367, 0.9910, 0.5612) further reflect fundamental differences in how these distributions capture risk timing dynamics.

Figures 13–15 demonstrate that the Weibull-based survival curves closely follow the empirical pattern across all models. The narrow confidence bands are consistent with the low standard errors, confirming the distribution's precision and stability. In contrast, alternative distributions (e.g., lognormal) exhibit visible deviations and wider confidence bands. These results collectively validate the Weibull distribution's superior performance in characterizing risk duration dynamics.

6.4. Influence mechanisms of covariates under the AFT framework

The AFT model results elucidate distinct influence mechanisms of covariates on the timing of loan default and prepayment.

Loan amount exhibits divergent effects: It shows no significant impact on default timing (β_{11}) but a consistent positive trend on prepayment timing (β_{21}), suggesting borrowers with larger loans may delay prepayment.

Annual income demonstrates a particularly revealing pattern, similar as [40, 41]. It exerts a symmetrically opposing influence: The coefficient is significantly positive for default risk (β_{12}), indicating higher income delays default due to stronger repayment capacity, while being significantly negative for prepayment risk (β_{22}), reflecting that higher-income borrowers prepay earlier based on capital opportunity cost considerations. This "high income late default, early prepayment" duality robustly captures the variable's dual regulatory effect on credit behavior.

6.5. Necessity of the competing risks mixture cure framework

The parameter estimates underscore the critical necessity of employing a mixture cure model that incorporates both default and prepayment as competing risks. The results reveal fundamentally different data-generating processes for each risk, which would be obscured in separate, single-risk models.

Table 6. Parameter estimates and bootstrap (200 replications) inference results for Model A.

	Estimate	SE	CI_lower	CI_upper	z_value	p_value
Weibull						
γ_{11}	0.1773	0.0265	0.1240	0.2317	6.4954	0.0000
γ_{12}	-0.0741	0.0358	-0.1434	-0.0020	-2.4852	0.0129
γ_{13}	0.1147	0.0288	0.0630	0.1729	3.4607	0.0005
γ_{21}	-0.1077	0.0356	-0.1821	-0.0426	-2.9502	0.0032
γ_{22}	0.0853	0.0308	0.0326	0.1458	2.3850	0.0171
γ_{23}	0.0531	0.0352	-0.0101	0.1275	1.2430	0.2139
a_1	2.7162	0.0144	2.6921	2.7442	188.6906	0.0000
β_{11}	-0.0104	0.0139	-0.0379	0.0164	-0.7011	0.4833
β_{12}	0.0264	0.0135	0.0005	0.0549	2.0436	0.0410
b_1	0.6183	0.0103	0.5962	0.6362	60.1232	0.0000
a_2	2.7647	0.0124	2.7404	2.7889	223.2815	0.0000
β_{21}	0.0128	0.0107	-0.0088	0.0323	1.1933	0.2328
β_{22}	-0.0507	0.0115	-0.0730	-0.0306	-4.2969	0.0000
b_2	0.7362	0.0113	0.7134	0.7566	65.1074	0.0000
Lognormal						
γ_{11}	0.1773	0.0265	0.1240	0.2317	6.5101	0.0000
γ_{12}	-0.0740	0.0358	-0.1434	-0.0021	-2.4868	0.0129
γ_{13}	0.1146	0.0287	0.0630	0.1728	3.4677	0.0005
γ_{21}	-0.1076	0.0356	-0.1821	-0.0427	-2.9507	0.0032
γ_{22}	0.0853	0.0307	0.0327	0.1457	2.3908	0.0168
γ_{23}	0.0531	0.0351	-0.0100	0.1274	1.2457	0.2129
a_1	2.3627	0.0263	2.3322	2.4000	89.7528	0.0000
β_{11}	-0.0045	0.0322	-0.0401	0.0313	-0.1981	0.8429
β_{12}	0.0381	0.0847	-0.0069	0.0738	0.3769	0.7062
b_1	0.7632	0.0270	0.7350	0.7860	28.2809	0.0000
a_2	2.3326	0.0167	2.2994	2.3631	139.4221	0.0000
β_{21}	0.0278	0.0168	-0.0048	0.0601	1.6651	0.0959
β_{22}	-0.0730	0.0182	-0.1104	-0.0436	-3.9054	0.0001
b_2	0.9836	0.0143	0.9569	1.0135	69.0766	0.0000
Loglogistic						
γ_{11}	0.1773	0.0265	0.1240	0.2317	6.5101	0.0000
γ_{12}	-0.0740	0.0358	-0.1434	-0.0021	-2.4868	0.0129
γ_{13}	0.1146	0.0287	0.0630	0.1728	3.4677	0.0005
γ_{21}	-0.1076	0.0356	-0.1821	-0.0427	-2.9507	0.0032
γ_{22}	0.0853	0.0307	0.0327	0.1457	2.3908	0.0168
γ_{23}	0.0531	0.0351	-0.0100	0.1274	1.2457	0.2129
a_1	2.4236	0.0190	2.3900	2.4629	127.8287	0.0000
β_{11}	-0.0073	0.0195	-0.0414	0.0327	-0.3343	0.7381
β_{12}	0.0337	0.0178	0.0004	0.0637	1.9890	0.0467
b_1	0.4399	0.0079	0.4241	0.4555	56.1842	0.0000
a_2	2.4453	0.0168	2.4113	2.4771	145.7577	0.0000
β_{21}	0.0270	0.0167	-0.0045	0.0580	1.6228	0.1046
β_{22}	-0.0786	0.0191	-0.1197	-0.0484	-3.9736	0.0001
b_2	0.5607	0.0091	0.5431	0.5786	61.7167	0.0000

Estimate: point estimate of the parameter; **SE**: standard error;

CI_lower/CI_upper: 95% confidence interval bounds;

z_value: Wald test statistic; **p_value**: significance of the null hypothesis test.

Table 7. Parameter estimates and bootstrap (200 replications) inference results for Model B.

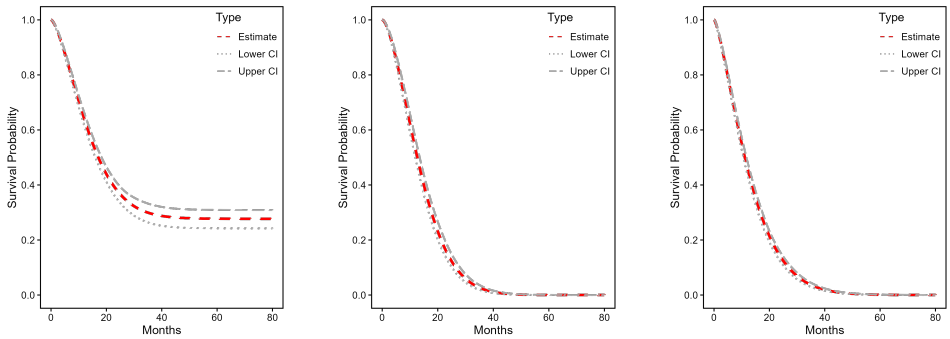
	Estimate	SE	CI_lower	CI_upper	z_value	p_value
Weibull						
γ_{11}	0.3164	0.0405	0.2400	0.3888	7.7956	0.0000
γ_{12}	-0.1467	0.0619	-0.2764	-0.0385	-2.2974	0.0216
γ_{13}	0.1996	0.0427	0.1170	0.2816	4.7567	0.0000
a_1	2.7159	0.0144	2.6897	2.7470	188.0237	0.0000
β_{11}	-0.0110	0.0135	-0.0393	0.0138	-0.7226	0.4699
β_{12}	0.0291	0.0112	0.0082	0.0504	2.4630	0.0138
b_1	0.6188	0.0099	0.6011	0.6369	62.4897	0.0000
Lognormal						
γ_{11}	0.3164	0.0405	0.2400	0.3888	7.7956	0.0000
γ_{12}	-0.1467	0.0619	-0.2764	-0.0385	-2.2974	0.0216
γ_{13}	0.1996	0.0427	0.1170	0.2816	4.7567	0.0000
a_1	2.3619	0.0276	2.3313	2.4007	85.6535	0.0000
β_{11}	-0.0047	0.0320	-0.0420	0.0346	-0.1992	0.8421
β_{12}	0.0426	0.0832	0.0035	0.0662	0.3839	0.7011
b_1	0.7638	0.0272	0.7371	0.7900	28.0609	0.0000
Loglogistic						
γ_{11}	0.3164	0.0405	0.2400	0.3888	7.7956	0.0000
γ_{12}	-0.1467	0.0619	-0.2764	-0.0385	-2.2974	0.0216
γ_{13}	0.1996	0.0427	0.1170	0.2816	4.7567	0.0000
a_1	2.4229	0.0181	2.3913	2.4597	134.1842	0.0000
β_{11}	-0.0078	0.0194	-0.0430	0.0269	-0.3247	0.7454
β_{12}	0.0378	0.0148	0.0070	0.0638	2.3959	0.0166
b_1	0.4403	0.0079	0.4258	0.4559	55.9791	0.0000

Estimate: point estimate of the parameter; **SE**: standard error;
CI_lower/CI_upper: 95% confidence interval bounds;
z_value: Wald test statistic; **p_value**: significance of the null hypothesis test.

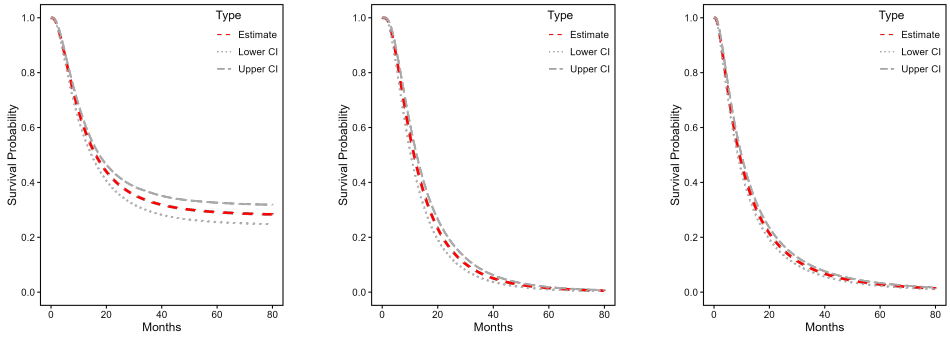
Table 8. Parameter estimates and bootstrap (200 replications) inference results for Model C.

	Estimate	SE	CI_lower	CI_upper	z_value	p_value
Weibull						
γ_{21}	-0.1381	0.0368	-0.2043	-0.0689	-4.0468	0.0001
γ_{22}	0.0828	0.0295	0.0240	0.1345	3.1175	0.0018
γ_{23}	0.0022	0.0317	-0.0522	0.0591	-0.2593	0.7954
a_2	2.7647	0.0122	2.7393	2.7868	226.1526	0.0000
β_{21}	0.0132	0.0113	-0.0061	0.0354	1.1283	0.2592
β_{22}	-0.0503	0.0108	-0.0735	-0.0308	-4.5663	0.0000
b_2	0.7367	0.0106	0.7175	0.7586	69.3028	0.0000
Lognormal						
γ_{21}	-0.1384	0.0366	-0.2040	-0.0689	-4.0665	0.0000
γ_{22}	0.0831	0.0294	0.0242	0.1345	3.1306	0.0017
γ_{23}	0.0020	0.0318	-0.0578	0.0591	-0.2582	0.7963
a_2	2.3361	0.0302	2.2988	2.3716	77.2007	0.0000
β_{21}	0.0166	0.0903	0.0171	0.0599	0.3093	0.7571
β_{22}	-0.0818	0.0729	0.1124	-0.0409	-0.9725	0.3308
b_2	0.9910	0.0489	0.9565	1.0199	20.1657	0.0000
Loglogistic						
γ_{21}	-0.1384	0.0366	-0.2040	-0.0689	-4.0665	0.0000
γ_{22}	0.0831	0.0294	0.0242	0.1345	3.1306	0.0017
γ_{23}	0.0020	0.0318	-0.0578	0.0591	-0.2582	0.7963
a_2	2.4455	0.0162	2.4104	2.4745	151.2089	0.0000
β_{21}	0.0281	0.0179	-0.0056	0.0630	1.5141	0.1300
β_{22}	-0.0771	0.0171	-0.1109	-0.0481	-4.4464	0.0000
b_2	0.5612	0.0088	0.5447	0.5796	64.1981	0.0000

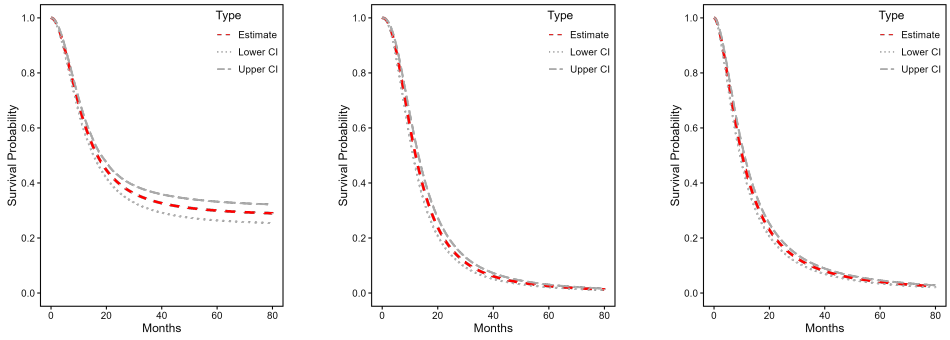
Estimate: point estimate of the parameter; **SE**: standard error;
CI_lower/CI_upper: 95% confidence interval bounds;
z_value: Wald test statistic; **p_value**: significance of the null hypothesis test.



(a) Weibull,S_T **(b)** Weibull,S_1 **(c)** Weibull,S_2

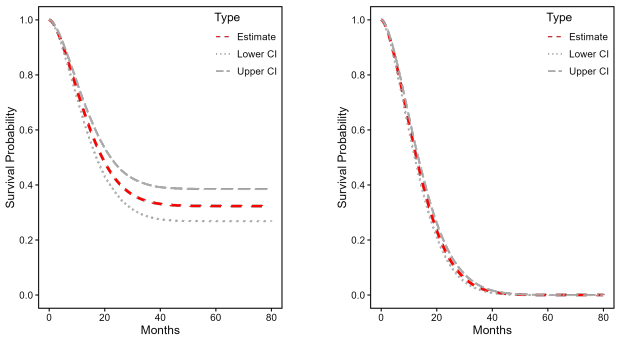


(d) Lognormal,S_T **(e)** Lognormal,S_1 **(f)** Lognormal,S_2

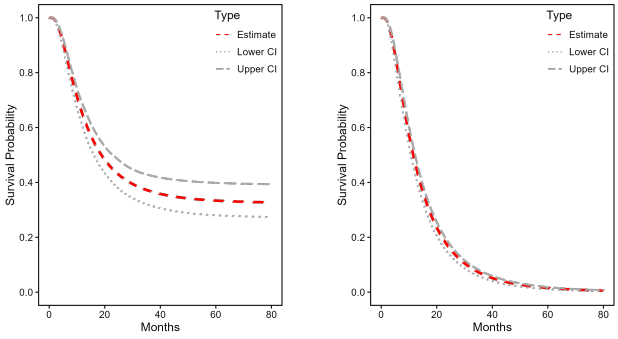


(g) Loglogistic,S_T **(h)** Loglogistic,S_1 **(i)** Loglogoistic,S_2

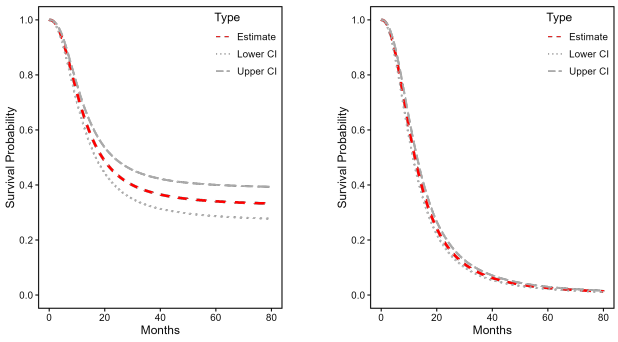
Figure 13. The overall survival function (S_T) and the survival functions for the two event types (S_1 and S_2) estimates (red dashed line) with 95% pointwise confidence intervals (long dashed and dotted lines) for Model A.



(a) Weibull,S_T **(b)** Weibull,S_1

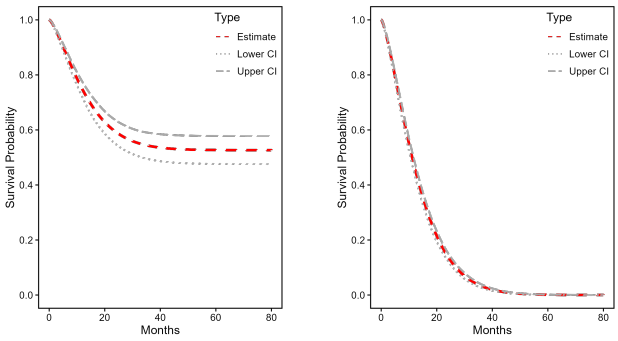


(c) Lognormal,S_T **(d)** Lognormal,S_1

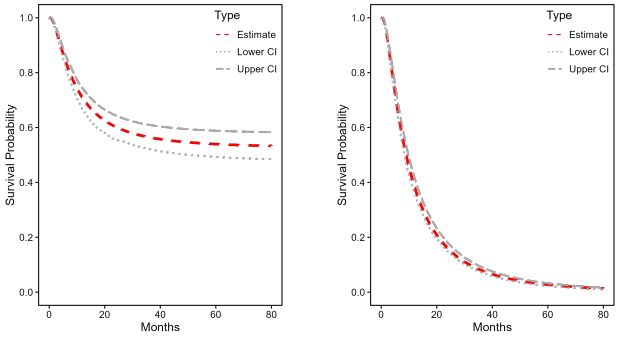


(e) Loglogistic,S_T **(f)** Loglogistic,S_1

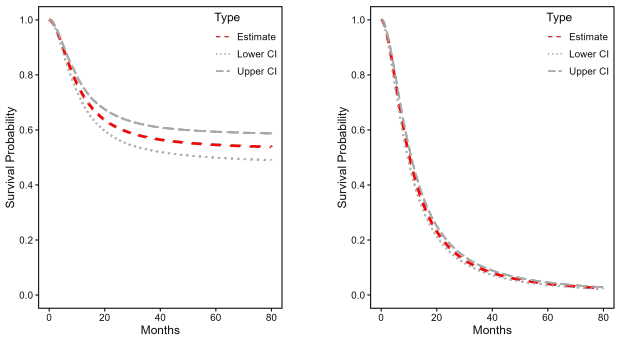
Figure 14. The overall survival function (S_T) and the survival functions for default (S_1) estimates (red dashed line) with 95% pointwise confidence intervals (long dashed and dotted lines) for Model B.



(a) Weibull,S_T **(b)** Weibull,S_2



(c) Lognormal,S_T **(d)** Lognormal,S_2



(e) Loglogistic,S_T **(f)** Loglogistic,S_2

Figure 15. The overall survival function (S_T) and the survival functions for prepayment (S_2) estimates (red dashed line) with 95% pointwise confidence intervals (long dashed and dotted lines) for Model C.

The cure model components show distinct significance patterns between covariates affecting default probability (γ_{11}, γ_{12}, γ_{13} are all significant) and those influencing prepayment probability (γ_{23} is consistently insignificant). This indicates essential differences in the factors determining the "cure" or immune status for each risk.

Furthermore, the latency models capture opposing temporal dynamics. As detailed above, annual income has diametrically opposite effects on the timing of each risk. Developing separate models would fail to incorporate the competitive relationship between these risks, leading to biased estimates of event timing. The competing risks mixture cure model successfully captures the dynamic characteristics of default and prepayment as interdependent events, providing a more faithful representation of true credit risk structure and offering superior reliability for risk management decision-making.

6.6. Comparative results

Table 9 presents the AIC values for the candidate models based on the Weibull, lognormal, and log-logistic distributions. According to the results, the model based on the Weibull distribution yields the lowest AIC value (46732.24), which is substantially smaller than those of the lognormal (48013.68) and log-logistic (47993.16) distributions. This significant difference underscores the pronounced advantage of the Weibull distribution according to the AIC metric.

Table 9. Akaike information criterion (AIC) values for the compared models.

Distribution	Log-Likelihood	Number of Parameters	AIC
Weibull	-23352.12	14	46732.24
Lognormal	-23992.84	14	48013.68
Log-logistic	-23983.58	14	47993.16

Following the conventional interpretation of the AIC in model selection [37], the competing risks mixture cure model constructed using the Weibull distribution is identified as the optimal choice among the candidates. This conclusion is not isolated; it corroborates findings from earlier analyses concerning parameter estimation stability and economic significance. The consistency across these diverse evaluation metrics reinforces the reliability and persuasiveness of selecting the Weibull-based model, thereby providing a robust foundation for subsequent analytical inferences and conclusions.

7. Conclusions

This paper introduces a novel mixture cure model that integrates multinomial logistic regression with the AFT framework, specifically designed for interval-censored competing-risk data. The model provides an analytically transparent structure with clear physical interpretations, addressing complex censoring mechanisms commonly encountered in practical applications.

We systematically evaluate three prevalent lifetime distributions-Weibull, log-normal, and log-logistic—to encompass diverse risk patterns including early failure, random failure, and wear-out failure scenarios. A comprehensive simulation study examines model performance under constrained sample sizes and intricate censoring mechanisms, incorporating right-censoring rates of 20%, 30%, and 40% alongside sample sizes of 200, 500, and 800 observations.

The results demonstrate that parameter estimation bias, confidence-interval CP, and convergence

speed remain within statistically acceptable ranges, confirming the method's robustness and validity. During empirical analysis, we utilize Lending Club personal loan data to compare mixture cure models incorporating competing risks against their single-risk counterparts.

Future research can be extended along several complementary directions. One natural avenue is to relax the parametric error distribution assumption by introducing semi-parametric or non-parametric specifications, thereby enhancing model robustness and applicability. Although existing methods that leave the error distribution unspecified have not yet simultaneously accommodated interval censoring, cure fraction, and competing risks, extending our framework toward such flexible settings remains a worthwhile pursuit. In addition, when the number of competing event types grows, parameter estimation becomes more challenging; penalized estimation techniques could be adopted to regularize the parameters and achieve stable estimation with effective event-type selection. Moreover, adapting the model to handle reliability data such as [42], would further broaden its applicability.

Use of AI tools declaration

The authors declare they have not used Artificial Intelligence (AI) tools in the creation of this article.

Acknowledgments

This work was partially supported by the Zhejiang Provincial Natural Science Foundation under Grant No. LMS25G010001, the National Bureau of Statistics of China under Grant No. 2025LZ023. Additional support was provided by the Characteristic & Preponderant Discipline of Key Construction Universities in Zhejiang Province (Zhejiang Gongshang University-Statistics) , the Fundamental Research Funds for the Provincial Universities of Zhejiang (2025ZDPY06) and First Class Discipline of Zhejiang-A (Zhejiang University of Finance and Economics-Statistics).

Conflict of interest

The authors declare there is no conflicts of interest.

References

1. J. W. Boag, Maximum likelihood estimates of the proportion of patients cured by cancer therapy, *J. R. Stat. Soc. B*, **11** (1949), 15–53. https://doi.org/10.1111/j.2517-6161.1949.tb00020.x
2. J. Berkson, R. P. Gage, Survival curve for cancer patients following treatment, *J. Am. Stat. Assoc.*, **47** (1952), 501–515. https://doi.org/10.1080/01621459.1952.10501187
3. A. Y. C. Kuk, C. H. Chen, A mixture model combining logistic regression with proportional hazards regression, *Biometrika*, **79** (1992), 531–541. https://doi.org/10.1093/biomet/79.3.531
4. Y. Peng, K. B. G. Dear, A nonparametric mixture model for cure rate estimation, *Biometrics*, **56** (2000), 237–243. https://doi.org/10.1111/j.0006-341X.2000.00237.x
5. J. P. Sy, J. M. G. Taylor, Estimation in a Cox proportional hazards cure model, *Biometrics*, **56** (2000), 227–236. https://doi.org/10.1111/j.0006-341X.2000.00227.x

6. H. Fang, G. Li, J. Sun, Maximum likelihood estimation in a semiparametric logistic/proportional-hazards mixture model, *Scand. J. Stat.*, **32** (2005), 59–75. https://doi.org/10.1111/j.1467-9469.2005.00415.x
7. J. Zhang, Y. Peng, A new estimation method for the semiparametric accelerated failure time mixture cure model, *Stat. Med.*, **26** (2007), 3157–3171. https://doi.org/10.1002/sim.2748
8. J. C. Lindsey, L. M. Ryan, Methods for interval-censored data, *Stat. Med.*, **17** (1998), 219–238. https://doi.org/10.1002/9780470317053
9. D. M. Finkelstein, A proportional hazards model for interval-censored failure time data, *Biometrics*, **42** (1986), 845–854. https://doi.org/10.2307/2530698
10. C. Kooperberg, D. B. Clarkson, Hazard regression with interval-censored data, *Biometrics*, **53** (1997), 1485–1494. https://doi.org/10.2307/2533514
11. D. M. Finkelstein, R. A. Wolfe, A semiparametric model for regression of interval-censored failure time data, *Biometrics*, **41** (1985), 933–945. https://doi.org/10.2307/2531335
12. D. Rabinowitz, A. Tsiatis, J. Aragon, Regression with interval-censored data, *Biometrika*, **82** (1995), 501–513. https://doi.org/10.1093/biomet/82.3.501
13. P. M. Odell, K. M. Anderson, R. B. D'Agostino, Maximum likelihood estimation for interval-censored data using a Weibull-based accelerated failure time model, *Biometrics*, **48** (1992), 951–959. https://doi.org/10.2307/2532360
14. R. A. Betensky, D. Rabinowitz, A. A. Tsiatis, Computationally simple accelerated failure time regression for interval censored data, *Biometrika*, **88** (2001), 703–711. https://doi.org/10.1093/biomet/88.3.703
15. Y. J. Kim, M. Jhun, Cure rate model with interval censored data, *Stat. Med.*, **27** (2010), 3–14. https://doi.org/10.1002/sim.2918
16. L. Xiang, X. Ma, K. K. W. Yau, Mixture cure model with random effects for clustered interval-censored survival data, *Stat. Med.*, **30** (2011), 995–1006. https://doi.org/10.1002/sim.4170
17. J. Zhou, J. Zhang, A. C. McLain, B. Cai, A multiple imputation approach for semiparametric cure model with interval censored data, *Comput. Stat. Data Anal.*, **99** (2016), 105–114. https://doi.org/10.1016/j.csda.2016.01.013
18. X. Liu, Z. Szabo, L. Xiang, A double-semiparametric approach for extending mixture cure models with interval-censored data, *Stat. Methods Med. Res.*, **35** (2026), 1281–1294. https://doi.org/10.1177/09622802261442911
19. J. Li, J. Ma, Mixture cure semiparametric additive hazard models under partly interval censoring—a penalized likelihood approach, *Stat. Comput.*, **35** (2025), 1–18. https://doi.org/10.1007/s11222-025-10622-w
20. S. Pal, Y. Peng, W. Aselisewine, S. Barui, A support vector machine-based cure rate model for interval censored data, *Stat. Methods Med. Res.*, **32** (2023), 2405–2422. https://doi.org/10.1177/09622802231210917
21. S. Pal, W. Aselisewine, A Support vector machine-based mixture cure model for mixed case interval censored data, *Stat. Comput.*, **36** (2026), 63. https://doi.org/10.1007/s11222-025-10796-3
22. W. Aselisewine, S. Pal, Machine learning approach for analyzing mixed case interval censored data with a cured subgroup, *AStA Adv. Stat. Anal.*, (2025), 1–24. https://doi.org/10.1007/s10182-025-00544-3

23. L. P. Chen, B. Qiu, Analysis of length-biased and partly interval-censored survival data with mismeasured covariates, *Biometrics*, **79** (2023), 3929–3940. https://doi.org/10.1111/biom.13898
24. L. Chen, B. Qiu, SIMEXBoost: An R package for analysis of high-dimensional error-prone data based on boosting method, *R J.*, **15** (2024), 5–20. https://doi.org/10.32614/RJ-2023-080
25. R. J. Gray, A class of K-sample tests for comparing the cumulative incidence of a competing risk, *Ann. Stat.*, **16** (1988), 1141–1154.
26. J. P. Fine, R. J. Gray, A proportional hazards model for the subdistribution of a competing risk, *J. Am. Stat. Assoc.*, **94** (1999), 496–509. https://doi.org/10.1080/01621459.1999.10474144
27. V. Coviello, M. Boggess, Cumulative incidence estimation in the presence of competing risks, *Stata J.*, **4** (2004), 103–112. https://doi.org/10.1177/1536867x0400400201
28. J. P. Klein, P. K. Andersen, Regression modeling of competing risks data based on pseudovalues of the cumulative incidence function, *Biometrics*, **61** (2005), 223–229. https://doi.org/10.1161/CIRCULATIONAHA.115.017719
29. P. C. Austin, J. P. Fine, D. S. Lee, Introduction to the analysis of survival data in the presence of competing risks, *Circulation*, **133** (2016), 601–609. https://doi.org/10.1002/sim.3516
30. M. Huebner, M. Wolkewitz, M. Enriquez-Sarano, M. Schumacher, Competing risks need to be considered in survival analysis models for cardiovascular outcomes, *J. Thorac. Cardiovasc. Surg.*, **153** (2017), 1427–1431. https://doi.org/10.1016/j.jtcvs.2016.12.039
31. J. Beyersmann, A. Latouche, A. Buchholz, M. Schumacher, Simulating competing risks data in survival analysis, *Stat. Med.*, **28** (2009), 956–971. https://doi.org/10.1002/sim.3516
32. S. Choi, X. Huang, J. N. Cormier, Efficient semiparametric mixture inferences on cure rate models for competing risks, *Can. J. Stat.*, **43** (2015), 420–435. https://doi.org/10.1002/cjs.11256
33. C. M. Chen, P. S. Shen, C. C. Lin, C. C. Wu, Semiparametric mixture cure model analysis with competing risks data: Application to vascular access thrombosis data, *Stat. Med.*, **39** (2020), 4086–4099. https://doi.org/10.1002/sim.8711
34. S. Basu, R. C. Tiwari, Breast cancer survival, competing risks and mixture cure model: a Bayesian analysis, *J. R. Stat. Soc. A*, **173** (2010), 307–329. https://doi.org/10.1111/j.1467-985X.2009.00618.x
35. S. Choi, L. Zhu, X. Huang, Semiparametric accelerated failure time cure rate mixture models with competing risks, *Stat. Med.*, **37** (2018), 48–59. https://doi.org/10.1002/sim.7508
36. Y. Wang, J. Li, Q. Zhou, W. Wang, A unified framework for complex survival data: accounting for clustering, cure fractions, and competing risks, *BMC Med. Res. Methodol.*, **26** (2026). https://doi.org/10.1186/s12874-026-02842-z
37. W. Zucchini, An introduction to model selection, *J. Math. Psychol.*, **44** (2000), 41–61. https://doi.org/10.1006/jmps.1999.1276
38. J. P. Sy, J. M. G. Taylor, Standard errors for the Cox proportional hazards cure model, *Math. Comput. Modell.*, **33** (2001), 1237–1251. https://doi.org/10.1016/S0895-7177(00)00312-5
39. T. A. Louis, Finding the observed information matrix when using the EM algorithm, *J. R. Stat. Soc. B*, **44** (1982), 226–233. https://doi.org/10.1111/j.2517-6161.1982.tb01203.x
40. Y. Zhu, M. Chen, M. Pan, Z. Ren, Beyond funding: How income inequality shapes international clean energy finance's influence on ecological carrying capacity in 114 developing countries, *J. Environ. Manage.*, **393** (2025), 127045. https://doi.org/10.1016/j.jenvman.2025.127045

41. Y. Zhu, R. Shen, Y. Yue, Green credit policies and corporate green innovation: An empirical study based on A-share listed companies, *Emerging Mark. Finance Trade*, (2025), 1–17. https://doi.org/10.1080/1540496X.2025.2563152
42. A. Xu, Y. Miu, J. Sun, S. Zhou, Y. Tang, A hierarchical Bayesian multivariate Wiener process model with dependent degradation rates and volatilities, *IEEE Trans. Reliab.*, **75** (2026), 1420–1433. https://doi.org/10.1109/TR.2026.3674703
43. C. F. J. Wu, On the convergence properties of the EM algorithm, *Ann. Stat.*, **11** (1983), 95–103. https://doi.org/10.1214/aos/1176346060

Appendix

Proof of Theorem 4.1

By Condition 5, $Q(\Theta)$ is continuous. Conditions 2 and 7 together with the information inequality imply that Θ^* is the unique maximizer of Q on $\mathcal{B}$. Condition 6 provides uniform convergence of the empirical log-likelihood to Q. For any $\varepsilon > 0$, define

$$\mathcal{B}_\varepsilon = \{\Theta \in \mathcal{B} : \|\Theta - \Theta^*\| \geq \varepsilon\}.$$

Because $\mathcal{B}_\varepsilon$ is compact,

$$\delta = Q(\Theta^*) - \max_{\Theta \in \mathcal{B}_\varepsilon} Q(\Theta) > 0.$$

Uniform convergence then guarantees that, with probability tending to one, the empirical log-likelihood at Θ^* exceeds its value on $\mathcal{B}_\varepsilon$ by at least $\delta/2$. Hence the maximizer $\hat{\Theta}_n$ must fall inside the ε-neighborhood of Θ^*, yielding $\|\hat{\Theta}_n - \Theta^*\| < \varepsilon$ with probability approaching one. Since ε is arbitrary, $\hat{\Theta}_n \xrightarrow{P} \Theta^*$.

Under the same regularity conditions, the EM algorithm used for computation is guaranteed to converge to a stationary point of the observed likelihood [43]. If the likelihood has a unique maximum (as implied by Condition 7) and the algorithm is started from a suitable initial value, the EM sequence converges to the MLE, and hence inherits the consistency property. In practice, multiple random initializations are recommended to assess global convergence.

Proof of Theorem 4.2

This appendix provides the explicit analytic expressions for the observed Fisher information matrix $\mathbf{J}(\Theta)$ under the AFT model. All quantities are evaluated at the final EM estimate $\hat{\Theta}$, and the posterior probabilities $\hat{\mu}_{ki} = P(U_i = k \mid O_i, \hat{\Theta})$ are obtained from the E-step (Eq (3.7)). The matrix is block-diagonal due to the independence structure of the complete-data log-likelihood; all cross-parameter blocks are zero.

Block structure.

$$\mathbf{J}(\Theta) = \begin{pmatrix} \mathbf{J}^{(\gamma)} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{J}^{(\psi_1)} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{J}^{(\psi_2)} \end{pmatrix},$$

with $\psi_1 = (\beta_1, a_1, b_1)$ and $\psi_2 = (\beta_2, a_2, b_2)$. The detailed non-zero entries are given below.

Information for the incidence parameters (γ_1, γ_2)

Let $\gamma = (\gamma_1^\top, \gamma_2^\top)^\top$. The contribution of a single individual to the incidence part of the complete-data log-likelihood is

$$\ell_{\gamma,i} = I(U_i = 1)\log \pi_{1i} + I(U_i = 2)\log \pi_{2i} + I(U_i = 0)\log \pi_{0i},$$

where $\pi_{ki} = \pi_k(Z_i; \gamma)$ as defined in Eq (2.3). The first and second derivatives are standard for multinomial logistic regression.

The conditional expectations in Eq (4.1) rely on the posterior distribution of U_i. Denote

$$\hat{\mu}_{1i} = P(U_i = 1 \mid O_i, \hat{\Theta}), \quad \hat{\mu}_{2i} = P(U_i = 2 \mid O_i, \hat{\Theta}), \quad \hat{\mu}_{0i} = 1 - \hat{\mu}_{1i} - \hat{\mu}_{2i}.$$

For interval-censored individuals ($\delta_i = 1$), the event type is observed, so $\hat{\mu}_{1i} = I(U_i = 1)$, $\hat{\mu}_{2i} = I(U_i = 2)$. For right-censored individuals ($\delta_i = 0$),

$$\begin{aligned}
\hat{\mu}_{1i} &= \frac{\pi_{1i} S_1(t_i; \beta_1, a_1, b_1)}{\pi_{0i} + \pi_{1i} S_1(t_i; \beta_1, a_1, b_1) + \pi_{2i} S_2(t_i; \beta_2, a_2, b_2)}, \\
\hat{\mu}_{2i} &= \frac{\pi_{2i} S_2(t_i; \beta_2, a_2, b_2)}{\pi_{0i} + \pi_{1i} S_1(t_i; \beta_1, a_1, b_1) + \pi_{2i} S_2(t_i; \beta_2, a_2, b_2)}, \\
\hat{\mu}_{0i} &= 1 - \hat{\mu}_{1i} - \hat{\mu}_{2i}.
\end{aligned}$$

where $t_i = L_i$ (the last observation time). The expected complete-data information matrix is

$$I_{\text{com}}^{(\gamma)} = \sum_{i=1}^{n} \begin{pmatrix} \pi_{1i}(1 - \pi_{1i}) & -\pi_{1i}\pi_{2i} \\ -\pi_{1i}\pi_{2i} & \pi_{2i}(1 - \pi_{2i}) \end{pmatrix} \otimes (Z_i Z_i^\top).$$

The missing information is the conditional variance of the score:

$$I_{\text{mis}}^{(\gamma)} = \sum_{i=1}^{n} \begin{pmatrix} \hat{\mu}_{1i}(1 - \hat{\mu}_{1i}) & -\hat{\mu}_{1i}\hat{\mu}_{2i} \\ -\hat{\mu}_{1i}\hat{\mu}_{2i} & \hat{\mu}_{2i}(1 - \hat{\mu}_{2i}) \end{pmatrix} \otimes (Z_i Z_i^\top).$$

Hence,

$$I_{\text{obs}}^{(\gamma)} = I_{\text{com}}^{(\gamma)} - I_{\text{mis}}^{(\gamma)}.$$

A.1 Incidence part (parameters γ_1, γ_2)

The matrices $J_{\gamma_1\gamma_1}$, $J_{\gamma_1\gamma_2}$, and $J_{\gamma_2\gamma_2}$ are expressed in terms of the model probabilities π_{ki} and the posterior probabilities $\hat{\mu}_{ki}$. For right-censored individuals ($\delta_i = 0$), the posterior probabilities are computed as

$$\hat{\mu}_{1i} = \frac{\pi_{1i} S_1(t_i)}{\pi_{0i} + \pi_{1i} S_1(t_i) + \pi_{2i} S_2(t_i)}, \quad \hat{\mu}_{2i} = \frac{\pi_{2i} S_2(t_i)}{\pi_{0i} + \pi_{1i} S_1(t_i) + \pi_{2i} S_2(t_i)}, \quad \hat{\mu}_{0i} = 1 - \hat{\mu}_{1i} - \hat{\mu}_{2i},$$

where $t_i = L_i$ is the last observation time. The expressions are:

$$J_{\gamma_1,\gamma_1} = \sum_{i=1}^{n} \Big[- \{(1 - \delta_i)\hat{\mu}_{0i} + \hat{\mu}_{1i} + \hat{\mu}_{2i}\} \pi_1(\pi_0 + \pi_2) \Big] z_i \cdot z_i^T,$$

$$J_{\gamma_1\gamma_2} = \sum_{i=1}^{n} \Big[\{(1-\delta_i)\hat{\mu}_{0i} + \hat{\mu}_{1i} + \hat{\mu}_{2i}\}\, \pi_1\pi_2 \Big] z_i \cdot z_i^T,$$

$$J_{\gamma_2\gamma_2} = \sum_{i=1}^{n} \Big[-\{(1-\delta_i)\hat{\mu}_{0i} + \hat{\mu}_{1i} + \hat{\mu}_{2i}\}\, \pi_2(\pi_0+\pi_1) \Big] z_i \cdot z_i^T.$$

Information for the survival parameters $\psi_k = (\beta_k, a_k, b_k)$ $(k = 1, 2)$

For each event type $k = 1, 2$, the contribution of a single individual to the corresponding part of the complete-data log-likelihood is

$$\ell_{\psi_k,i} = \delta_i I(U_i = k) \log(S_k(L_i;\beta_k,a_k,b_k) - S_k(R_i;\beta_k,a_k,b_k)) + (1-\delta_i) I(U_i = k) \log S_k(L_i;\beta_k,a_k,b_k).$$

Define the first-derivative vector

$$V_{ki} = \delta_i \frac{\partial}{\partial \psi_k} \log(S_k(L_i;\beta_k,a_k,b_k) - S_k(R_i;\beta_k,a_k,b_k)) + (1-\delta_i) \frac{\partial}{\partial \psi_k} \log S_k(L_i;\beta_k,a_k,b_k),$$

and the second-derivative matrix

$$W_{ki} = \delta_i \frac{\partial^2}{\partial \psi_k \partial \psi_k^\top} \log(S_k(L_i;\beta_k,a_k,b_k) - S_k(R_i;\beta_k,a_k,b_k)) + (1-\delta_i) \frac{\partial^2}{\partial \psi_k \partial \psi_k^\top} \log S_k(L_i;\beta_k,a_k,b_k).$$

In Eq (4.1), the expected complete-data information part becomes

$$-\mathbb{E}\Big[\frac{\partial^2 \ell_{\psi_k}}{\partial \psi_k^2}\Big| O\Big] = -\sum_{i=1}^{n} \hat{\mu}_{ki} W_{ki},$$

where $\hat{\mu}_{ki} = P(U_i = k \mid O_i, \hat{\Theta})$ are the posterior probabilities obtained from the E-step. The missing information part is the conditional variance of the score:

$$\mathrm{Var}\Big[\frac{\partial \ell_{\psi_k}}{\partial \psi_k}\Big| O\Big] = \sum_{i=1}^{n} \hat{\mu}_{ki}(1-\hat{\mu}_{ki}) V_{ki} V_{ki}^\top.$$

Therefore, the observed information block for ψ_k is

$$I_{\mathrm{obs}}^{(\psi_k)} = -\sum_{i=1}^{n} \hat{\mu}_{ki} W_{ki} \; - \; \sum_{i=1}^{n} \hat{\mu}_{ki}(1-\hat{\mu}_{ki}) V_{ki} V_{ki}^\top.$$

For interval-censored individuals ($\delta_i = 1$), if $U_i = k$, then $\hat{\mu}_{ki} = 1$ and the second term vanishes; if $U_i \neq k$, then the whole contribution is zero. For right-censored individuals, the posterior probabilities $\hat{\mu}_{ki}$ are used as given by the E-step.

The blocks for $k = 1$ and $k = 2$ are computed separately, using the respective survival functions S_1, S_2 and the corresponding posterior probabilities $\hat{\mu}_{1i}, \hat{\mu}_{2i}$. For a specific AFT distribution (e.g., Weibull, lognormal, loglogistic), explicit expressions for V_{ki} and W_{ki} can be derived; in practice, numerical differentiation (e.g., using the `numDeriv` package in R) may be employed instead.

A.2 Survival part for event type 1 ($\psi_1 = (\beta_1, a_1, b_1)$)

Define the standardized log-time variables

$$\phi_1(L_i) = \frac{\log(L_i) - \beta_1^T X_i}{b_1}, \qquad \phi_1(R_i) = \frac{\log(R_i) - \beta_1^T X_i}{b_1}.$$

Using the chain rule, the following intermediate quantities are introduced to simplify the second derivatives. They are evaluated at the final estimate $\hat{\Theta}$ and multiplied by the posterior probability $\hat{\mu}_{1i}$.

$$\begin{aligned}
d_{\beta_1\beta_1} &= \left\{\frac{a_1}{b_1} S_1(L_i)\phi_1(L_i)^{2a_1-2} - \frac{a_1-1}{b_1} S_1(L_i)\phi_1(L_i)^{a_1-2}\right\} \\
&\quad - \left\{\frac{a_1}{b_1} S_1(R_i)\phi_1(R_i)^{2a_1-2} - \frac{a_1-1}{b_1} S_1(R_i)\phi_1(R_i)^{a_1-2}\right\}, \\
g_{\beta_1\beta_1} &= \frac{a_1}{b_1} S_1(L_i)\phi_1(L_i)^{a_1-1} - \frac{a_1}{b_1} S_1(R_i)\phi_1(R_i)^{a_1-1}, \\
J_{\beta_1\beta_1} &= \sum_{i=1}^{n}\left[\delta_i \frac{d_{\beta_1\beta_1}\{S_1(L_i) - S_1(R_i)\} - \left\{S_1(L_i)\phi_1(L_i)^{a_1-1} - S_1(R_i)\phi_1(R_i)^{a_1-1}\right\} g_{\beta_1\beta_1}}{\{S_1(L_i) - S_1(R_i)\}^2}\right. \\
&\quad \left. -(1-\delta_i)\frac{a_1-1}{b_1}\phi_1(L_i)^{a_1-2}\right]\frac{a_1}{b_1}\hat{\mu}_{1i} X_i \cdot X_i^T.
\end{aligned}$$

$$\begin{aligned}
d_{\beta_1 a_1} &= S_1(L_i)\phi_1(L_i)^{a_1-1}\{1 - \phi_1(L_i)^{a_1}\}\log\phi_1(L_i) - S_1(R_i)\phi_1(R_i)^{a_1-1}\{1 - \phi_1(R_i)^{a_1}\}\log\phi_1(R_i), \\
g_{\beta_1 a_1} &= S_1(R_i)\phi_1(R_i)^{a_1}\log\phi_1(R_i) - S_1(L_i)\phi_1(L_i)^{a_1}\log\phi_1(L_i), \\
J_{\beta_1 a_1} &= \sum_{i=1}^{n}\left[\delta_i \frac{d_{\beta_1 a_1}\{S_1(L_i) - S_1(R_i)\} - \left\{S_1(L_i)\phi_1(L_i)^{a_1-1} - S_1(R_i)\phi_1(R_i)^{a_1-1}\right\} g_{\beta_1 a_1}}{\{S_1(L_i) - S_1(R_i)\}^2}\right. \\
&\quad \left. + (1-\delta_i)\phi_1(L_i)^{a_1-1}\log\phi_1(L_i)\right]\frac{a_1}{b_1}\hat{\mu}_{1i} X_i.
\end{aligned}$$

$$\begin{aligned}
d_{\beta_1 b_1} &= \left\{\frac{a_1}{b_1} S_1(L_i)\phi_1(L_i)^{2a_1-1} - \frac{a_1-1}{b_1} S_1(L_i)\phi_1(L_i)^{a_1-1}\right\} \\
&\quad - \left\{\frac{a_1}{b_1} S_1(R_i)\phi_1(R_i)^{2a_1-1} - \frac{a_1-1}{b_1} S_1(R_i)\phi_1(R_i)^{a_1-1}\right\}, \\
g_{\beta_1 b_1} &= \frac{a_1}{b_1} S_1(L_i)\phi_1(L_i)^{a_1} - \frac{a_1}{b_1} S_1(R_i)\phi_1(R_i)^{a_1}, \\
J_{\beta_1 b_1} &= \sum_{i=1}^{n}\left[\delta_i \frac{d_{\beta_1 b_1}\{S_1(L_i) - S_1(R_i)\} - \left\{S_1(L_i)\phi_1(L_i)^{a_1-1} - S_1(R_i)\phi_1(R_i)^{a_1-1}\right\} g_{\beta_1 b_1}}{\{S_1(L_i) - S_1(R_i)\}^2}\right. \\
&\quad \left. -(1-\delta_i)\frac{a_1-1}{b_1}\phi_1(L_i)^{a_1-1}\right]\frac{a_1}{b_1}\hat{\mu}_{1i} X_i.
\end{aligned}$$

$$d_{b_1 b_1} = \left\{\frac{a_1}{b_1} S_1(L_i)\phi_1(L_i)^{2a_1-1} - \frac{a_1-1}{b_1} S_1(L_i)\phi_1(L_i)^{a_1-1}\right\}$$

$$
\begin{aligned}
&\quad - \left\{ \frac{a_1}{b_1} S_1(R_i)\phi_1(R_i)^{2a_1-1} - \frac{a_1-1}{b_1} S_1(R_i)\phi_1(R_i)^{a_1-1} \right\}, \\
g_{b_1b_1} &= \frac{a_1}{b_1} S_1(L_i)\phi_1(L_i)^{a_1} - \frac{a_1}{b_1} S_1(R_i)\phi_1(R_i)^{a_1}, \\
J_{b_1b_1} &= \sum_{i=1}^{n} \left[\delta_i \frac{d_{b_1b_1} \{S_1(L_i) - S_1(R_i)\} - \{S_1(L_i)\phi_1(L_i)^{a_1} - S_1(R_i)\phi_1(R_i)^{a_1}\} g_{b_1b_1}}{\{S_1(L_i) - S_1(R_i)\}^2} \right. \\
&\quad \left. - (1-\delta_i) \frac{a_1-1}{b_1} \phi_1(L_i)^{a_1} \right] \frac{a_1}{b_1} \hat{\mu}_{1i}.
\end{aligned}
$$

$$
\begin{aligned}
d_{a_1b_1} &= \left\{ S_1(L_i)\phi_1(L_i)^{a_1} \log \phi_1(L_i) - S_1(L_i)\phi_1(L_i)^{2a_1} \log \phi_1(L_i) \right\} \\
&\quad - \left\{ S_1(R_i)\phi_1(R_i)^{a_1} \log \phi_1(R_i) - S_1(R_i)\phi_1(R_i)^{2a_1} \log \phi_1(R_i) \right\}, \\
g_{a_1b_1} &= S_1(R_i)\phi_1(R_i)^{a_1} \log \phi_1(R_i) - S_1(L_i)\phi_1(L_i)^{a_1} \log \phi_1(L_i), \\
J_{a_1b_1} &= \sum_{i=1}^{n} \left[\delta_i \frac{d_{a_1b_1} \{S_1(L_i) - S_1(R_i)\} - \{S_1(L_i)\phi_1(L_i)^{a_1} - S_1(R_i)\phi_1(R_i)^{a_1}\} g_{a_1b_1}}{\{S_1(L_i) - S_1(R_i)\}^2} \right. \\
&\quad \left. + (1-\delta_i)\phi_1(L_i)^{a_1} \log \phi_1(L_i) \right] \frac{a_1}{b_1} \hat{\mu}_{1i}.
\end{aligned}
$$

$$
\begin{aligned}
d_{a_1a_1} &= S_1(R_i)\phi_1(R_i)^{a_1} \{\log \phi_1(R_i)\}^2 \{1 - \phi_1(R_i)^{a_1}\} - S_1(L_i)\phi_1(L_i)^{a_1} \{\log \phi_1(L_i)\}^2 \{1 - \phi_1(L_i)^{a_1}\}, \\
g_{a_1a_1} &= S_1(R_i)\phi_1(R_i)^{a_1} \log \phi_1(R_i) - S_1(L_i)\phi_1(L_i)^{a_1} \log \phi_1(L_i), \\
J_{a_1a_1} &= \sum_{i=1}^{n} \left[\delta_i \frac{d_{a_1a_1} \{S_1(L_i) - S_1(R_i)\} - \{S_1(L_i)\phi_1(L_i)^{a_1} \log \phi_1(L_i) - S_1(R_i)\phi_1(R_i)^{a_1} \log \phi_1(R_i)\} g_{a_1a_1}}{\{S_1(L_i) - S_1(R_i)\}^2} \right. \\
&\quad \left. - (1-\delta_i)\phi_1(L_i)^{a_1} \{\log \phi_1(L_i)\}^2 \right] \hat{\mu}_{1i}.
\end{aligned}
$$

A.3 Survival part for event type 2 ($\psi_2 = (\beta_2, a_2, b_2)$)

Analogously, define

$$
\phi_2(L_i) = \frac{\log(L_i) - \beta_2^T X_i}{b_2}, \qquad \phi_2(R_i) = \frac{\log(R_i) - \beta_2^T X_i}{b_2}.
$$

The expressions are obtained by replacing subscript 1 with 2 and multiplying by $\hat{\mu}_{2i}$:

$$
\begin{aligned}
d_{\beta_2\beta_2} &= \left\{ \frac{a_2}{b_2} S_2(L_i)\phi_2(L_i)^{2a_2-2} - \frac{a_2-1}{b_2} S_2(L_i)\phi_2(L_i)^{a_2-2} \right\} \\
&\quad - \left\{ \frac{a_2}{b_2} S_2(R_i)\phi_2(R_i)^{2a_2-2} - \frac{a_2-1}{b_2} S_2(R_i)\phi_2(R_i)^{a_2-2} \right\}, \\
g_{\beta_2\beta_2} &= \frac{a_2}{b_2} S_2(L_i)\phi_2(L_i)^{a_2-1} - \frac{a_2}{b_2} S_2(R_i)\phi_2(R_i)^{a_2-1},
\end{aligned}
$$

$$J_{\beta_2\beta_2} = \sum_{i=1}^{n}\Bigg[\delta_i\frac{d_{\beta_2\beta_2}\{S_2(L_i)-S_2(R_i)\}-\left\{S_2(L_i)\phi_2(L_i)^{a_2-1}-S_2(R_i)\phi_2(R_i)^{a_2-1}\right\}g_{\beta_2\beta_2}}{\{S_2(L_i)-S_2(R_i)\}^2}$$
$$-(1-\delta_i)\frac{a_2-1}{b_2}\phi_2(L_i)^{a_2-2}\Bigg]\frac{a_2}{b_2}\hat{\mu}_{2i}X_i\cdot X_i^T.$$

$$d_{\beta_2 a_2} = S_2(L_i)\phi_2(L_i)^{a_2-1}\{1-\phi_2(L_i)^{a_2}\}\log\phi_2(L_i) - S_2(R_i)\phi_2(R_i)^{a_2-1}\{1-\phi_2(R_i)^{a_2}\}\log\phi_2(R_i),$$
$$g_{\beta_2 a_2} = S_2(R_i)\phi_2(R_i)^{a_2}\log\phi_2(R_i) - S_2(L_i)\phi_2(L_i)^{a_2}\log\phi_2(L_i),$$
$$J_{\beta_2 a_2} = \sum_{i=1}^{n}\Bigg[\delta_i\frac{d_{\beta_2 a_2}\{S_2(L_i)-S_2(R_i)\}-\left\{S_2(L_i)\phi_2(L_i)^{a_2-1}-S_2(R_i)\phi_2(R_i)^{a_2-1}\right\}g_{\beta_2 a_2}}{\{S_2(L_i)-S_2(R_i)\}^2}$$
$$+(1-\delta_i)\phi_2(L_i)^{a_2-1}\log\phi_2(L_i)\Bigg]\frac{a_2}{b_2}\hat{\mu}_{2i}X_i.$$

$$d_{\beta_2 b_2} = \left\{\frac{a_2}{b_2}S_2(L_i)\phi_2(L_i)^{2a_2-1}-\frac{a_2-1}{b_2}S_2(L_i)\phi_2(L_i)^{a_2-1}\right\}$$
$$-\left\{\frac{a_2}{b_2}S_2(R_i)\phi_2(R_i)^{2a_2-1}-\frac{a_2-1}{b_2}S_2(R_i)\phi_2(R_i)^{a_2-1}\right\},$$
$$g_{\beta_2 b_2} = \frac{a_2}{b_2}S_2(L_i)\phi_2(L_i)^{a_2}-\frac{a_2}{b_2}S_2(R_i)\phi_2(R_i)^{a_2},$$
$$J_{\beta_2 b_2} = \sum_{i=1}^{n}\Bigg[\delta_i\frac{d_{\beta_2 b_2}\{S_2(L_i)-S_2(R_i)\}-\left\{S_2(L_i)\phi_2(L_i)^{a_2-1}-S_2(R_i)\phi_2(R_i)^{a_2-1}\right\}g_{\beta_2 b_2}}{\{S_2(L_i)-S_2(R_i)\}^2}$$
$$-(1-\delta_i)\frac{a_2-1}{b_2}\phi_2(L_i)^{a_2-1}\Bigg]\frac{a_2}{b_2}\hat{\mu}_{2i}X_i.$$

$$d_{b_2 b_2} = \left\{\frac{a_2}{b_2}S_2(L_i)\phi_2(L_i)^{2a_2-1}-\frac{a_2-1}{b_2}S_2(L_i)\phi_2(L_i)^{a_2-1}\right\}$$
$$-\left\{\frac{a_2}{b_2}S_2(R_i)\phi_2(R_i)^{2a_2-1}-\frac{a_2-1}{b_2}S_2(R_i)\phi_2(R_i)^{a_2-1}\right\},$$
$$g_{b_2 b_2} = \frac{a_2}{b_2}S_2(L_i)\phi_2(L_i)^{a_2}-\frac{a_2}{b_2}S_2(R_i)\phi_2(R_i)^{a_2},$$
$$J_{b_2 b_2} = \sum_{i=1}^{n}\Bigg[\delta_i\frac{d_{b_2 b_2}\{S_2(L_i)-S_2(R_i)\}-\{S_2(L_i)\phi_2(L_i)^{a_2}-S_2(R_i)\phi_2(R_i)^{a_2}\}g_{b_2 b_2}}{\{S_2(L_i)-S_2(R_i)\}^2}$$
$$-(1-\delta_i)\frac{a_2-1}{b_2}\phi_2(L_i)^{a_2}\Bigg]\frac{a_2}{b_2}\hat{\mu}_{2i}.$$

$$d_{a_2 b_2} = \left\{S_2(L_i)\phi_2(L_i)^{a_2}\log\phi_2(L_i)-S_2(L_i)\phi_2(L_i)^{2a_2}\log\phi_2(L_i)\right\}$$
$$-\left\{S_2(R_i)\phi_2(R_i)^{a_2}\log\phi_2(R_i)-S_2(R_i)\phi_2(R_i)^{2a_2}\log\phi_2(R_i)\right\},$$

$$
\begin{aligned}
g_{a_2b_2} &= S_2(R_i)\phi_2(R_i)^{a_2}\log\phi_2(R_i) - S_2(L_i)\phi_2(L_i)^{a_2}\log\phi_2(L_i),\\
J_{a_2b_2} &= \sum_{i=1}^{n}\Bigg[\delta_i\frac{d_{a_2b_2}\{S_2(L_i)-S_2(R_i)\} - \{S_2(L_i)\phi_2(L_i)^{a_2} - S_2(R_i)\phi_2(R_i)^{a_2}\}\, g_{a_2b_2}}{\{S_2(L_i)-S_2(R_i)\}^2}\\
&\quad + (1-\delta_i)\phi_2(L_i)^{a_2}\log\phi_2(L_i)\Bigg]\frac{a_2}{b_2}\hat{\mu}_{2i}.
\end{aligned}
$$

$$
\begin{aligned}
d_{a_2a_2} &= S_2(R_i)\phi_2(R_i)^{a_2}\{\log\phi_2(R_i)\}^2\{1-\phi_2(R_i)^{a_2}\}\\
&\quad - S_2(L_i)\phi_2(L_i)^{a_2}\{\log\phi_2(L_i)\}^2\{1-\phi_2(L_i)^{a_2}\},\\
g_{a_2a_2} &= S_2(R_i)\phi_2(R_i)^{a_2}\log\phi_2(R_i) - S_2(L_i)\phi_2(L_i)^{a_2}\log\phi_2(L_i),\\
J_{a_2a_2} &= \sum_{i=1}^{n}\Bigg[\delta_i\frac{d_{a_2a_2}\{S_2(L_i)-S_2(R_i)\} - \{S_2(L_i)\phi_2(L_i)^{a_2}\log\phi_2(L_i) - S_2(R_i)\phi_2(R_i)^{a_2}\log\phi_2(R_i)\}\, g_{a_2a_2}}{\{S_2(L_i)-S_2(R_i)\}^2}\\
&\quad - (1-\delta_i)\phi_2(L_i)^{a_2}\{\log\phi_2(L_i)\}^2\Bigg]\hat{\mu}_{2i}.
\end{aligned}
$$

All other elements of $\mathbf{J}(\Theta)$ are zero. The expressions above are directly programmable and, when evaluated at the final EM estimate $\hat{\Theta}$, give the observed Fisher information matrix. Its inverse provides the estimated asymptotic covariance matrix of $\hat{\Theta}$, and standard errors are obtained as the square roots of the diagonal elements.

AIMS Press