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# Two-Stage Estimation in Copula-Based Bivariate Survival Models with Cox Marginals

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***Abstract***

*This study is motivated by the presence of dependence between event times in bivariate survival data, which cannot be adequately captured by univariate Cox models. A copula-based bivariate survival model with Cox Proportional Hazards marginals is considered. The estimation procedure follows a two-stage approach, where marginal parameters are first obtained using partial likelihood and the baseline survival function is estimated via the Breslow method. In contrast to conventional approaches that treat marginal estimates as final or imposing shared parameter structures, this study introduces a modification in the second stage by performing simultaneous joint estimation of marginal without imposing shared parameter and dependence parameters using the BHHH algorithm. This allows the marginal parameters to be estimated while explicitly accounting for the dependence between event times. The evaluation was conducted via simulation with variation in sample size, censoring, dependency level and copula types. Simulation results show that the proposed method produces stable and reliable parameter estimates while preserving the interpretability of marginal effects, providing a flexible framework for modeling dependent bivariate survival data.*

***Keywords:*** *Bivariate survival, BHHH algorithm, copula, cox proportional hazard, dependence modelling*

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## 1. INTRODUCTION

In many real-world studies, particularly in medical research, the exact timing of an event cannot always be fully observed due to incomplete follow-up or censoring. Survival analysis serves as the main statistical framework for handling such data, with the Cox proportional hazards model widely used to assess the effects of covariates [1], [2]. The Kaplan–Meier estimator is also commonly applied to estimate the survival function in the presence of censored observations [3]. However, the Cox model is generally developed under the assumption of independent survival times. In practice, bivariate survival data are often observed from the same individual, especially in paired organs [4]. In such cases, the assumption of independence is violated due to the presence of dependence between event times, which cannot be adequately addressed using univariate models [5].

Ignoring dependence between event times may lead to biased estimation of covariate effects and misleading inference when the correlation is substantial. Therefore, modeling the dependence structure is crucial to obtain more accurate and reliable conclusions in survival studies involving paired or clustered data [6]. To accommodate this dependence, copula-based survival models have been widely employed, as they allow the construction of a joint distribution based on marginal distributions and a dependence parameter. Compared to alternative approaches such as frailty models or multivariate survival models, copulas offer greater flexibility in representing various forms of dependence [7].

In this framework, marginal distributions are commonly modeled using the Cox proportional hazards model and subsequently combined through a specified copula function to form a bivariate survival model. Among various copula families, Archimedean copulas, such as Gumbel, Clayton, Frank, and Joe are frequently used due to their flexibility and tractability. In addition, dependence measures such as Kendall's $\tau$ can be directly expressed as functions of the copula parameters in many Archimedean copula models [8].

Despite their flexibility, parameter estimation in copula-based bivariate Cox survival models remains challenging due to the presence of censoring and the complexity of the joint likelihood function. A commonly used approach is the Inference Functions for Margins (IFM), where marginal parameters are estimated separately in the first stage and subsequently treated as fixed when estimating the dependence parameter in the second stage [9]. This approach may fail to account for the influence of dependence on the estimation of marginal parameters. As an extension of IFM, the two-stage method proposed by Sun and Ding [10] performs joint estimation of the marginal parameters and the dependence parameter in the second stage. However, this approach typically assumes an identical parameter structure across the two margins ($\beta_1 = \beta_2$), thereby limiting the ability to capture differences in covariate effects between the margins.

To address these limitations, this study proposes a modification of the two-stage estimation procedure by performing simultaneous joint estimation of the regression parameters for both margins ($\beta_1$ and $\beta_2$) along with the dependence parameter, without imposing equality constraints between them. Thus, the proposed method not only accounts for the influence of dependence during the estimation process but also allows for heterogeneity in covariate effects across the margins.

In its implementation, parameter optimization is carried out using the BHHH algorithm based on the outer product of gradients, making it more computationally stable and not requiring the computation of complex Hessian matrices for the likelihood function with censoring and copula structure [11]. Therefore, the main contribution of this study lies in the development of a more flexible and comprehensive estimation framework for copula-based bivariate survival models. Accordingly, this study aims to develop and evaluate the proposed estimation framework through simulation studies.

## 2. METHOD

### 2.1. Copula-Based Bivariate Survival Model

A copula-based bivariate Cox survival model is a statistical approach that employs a copula function to combine two marginal survival functions into a joint survival function, where the dependence parameter ($\eta$) quantifies the strength of dependence between the two marginal distributions [12]. Let $T_1$ and $T_2$ be continuous random variables representing the survival times of two observed units. The corresponding marginal survival functions are defined as $S_1(t_1) = P(T_1 \geq t_1)$ and $S_2(t_2) = P(T_2 \geq t_2)$. The joint survival function conditional on covariates $(\boldsymbol{x}_1, \boldsymbol{x}_2)$ can be expressed as follows [13]:

$$S(t_1, t_2|\boldsymbol{x}_1, \boldsymbol{x}_2) = C_\eta\big(S_1(t_1|\boldsymbol{x}_1), S_2(t_2|\boldsymbol{x}_2)\big);\ t_1, t_2 \geq 0. \tag{1}$$

Here, $C_\eta(\cdot,\cdot)$ denotes the copula function that links the marginal survival functions $S_1(t_1)$ and $S_2(t_2)$, while $\boldsymbol{x}_1$ and $\boldsymbol{x}_2$ respectively denote the covariate vectors for the first and second margins. In this study, $S_1(t_1|\boldsymbol{x}_1)$ and $S_2(t_2|\boldsymbol{x}_2)$ are specified through Cox proportional hazards models, where the effects of covariates are captured by regression parameters $\boldsymbol{\beta}_1$ and $\boldsymbol{\beta}_2$, as detailed in Section 2.2. The corresponding joint density function is given by [14]:

$$f(t_1, t_2|\boldsymbol{x}_1, \boldsymbol{x}_2) = c_\eta\big(S_1(t_1|\boldsymbol{x}_1), S_2(t_2|\boldsymbol{x}_2)\big) f_1(t_1|\boldsymbol{x}_1) f_2(t_2|\boldsymbol{x}_2);\ t_1, t_2 \geq 0. \tag{2}$$

Where $c_\eta(u_1, u_2) = \partial^2 C_\eta(u_1, u_2)/\partial u_1 \partial u_2$ denotes the second-order partial derivative of the copula function, $\eta$ denotes the dependence parameter and $f_k(t_k) = h_{0k}(t_k) S_k(t_k)$ is the marginal density function.

In this study, the Clayton copula is employed due to its ability to capture lower tail dependence and its analytical tractability [15]. Also, the Joe copula is considered to represent upper tail dependence, enabling the proposed method to be evaluated under contrasting dependence structures [16]. The Clayton and Joe copula functions are each presented by the following **Equation (3)** and **Equation (4)**:

$$C_\eta(u_1, u_2) = \big(u_1^{-\eta} + u_2^{-\eta} - 1\big)^{-\frac{1}{\eta}};\quad \eta > 0. \tag{3}$$

$$C_\eta(u_1, u_2) = 1 - ((1-u_1)^\eta + (1-u_2)^\eta - (1-u_1)^\eta (1-u_2)^\eta)^{\frac{1}{\eta}};\quad \eta \geq 1. \tag{4}$$

Although other copula families exist, these two copulas are selected to balance model flexibility and computational simplicity while maintaining focus on the proposed estimation framework.

### 2.2. Marginal Survival Function under the Cox Proportional Hazards Model

The marginal survival function $S_k(t_k|\boldsymbol{x}_k)$ under the Cox proportional hazards model with covariates $\boldsymbol{x}_k$ is given by [17]:

$$S_k(t_k|\boldsymbol{x}_k) = \exp\left(-\int_0^{t_k} h_{0k}(u)\, exp\left(\boldsymbol{x}_{\boldsymbol{k}}^T\boldsymbol{\beta}_{\boldsymbol{k}}\right) du\right) = \exp\left(-H_{0k}(t_k)\exp\left(\boldsymbol{x}_{\boldsymbol{k}}^T\boldsymbol{\beta}_{\boldsymbol{k}}\right)\right). \quad (5)$$

Where $h_{0k}(t_k)$ denotes the baseline hazard function for the $k$-th margin, $H_{0k}(t_k)$ represents the cumulative baseline hazard function for the $k$-th margin, with $k = 1{,}2$, and $\boldsymbol{\beta}_k$ is a $p \times 1$ vector of regression parameters associated with the covariates $\boldsymbol{x}_k$.

Suppose that there are $V$ distinct event times among $n$ observed individuals. Let $t_1, t_2, \ldots, t_V$ denote the ordered event times, where $t_v$ represents the $v$-th event time, for $v = 1{,}2, \ldots, V$. At each event time $t_v$, let $R(t_v)$ denotes the corresponding risk set of individuals who remain at risk of the event at time $t_v$, then the regression parameters $\boldsymbol{\beta}_k$ are estimated using the partial likelihood [18] in the Equation (6). Subsequently, the cumulative baseline hazard function $H_{0k}(t_k)$ is estimated using the Breslow estimator as in Equation (7) [19]:

$$L(\boldsymbol{\beta}_k) = \prod_{i=1}^{n}\left(\frac{\exp\left(\boldsymbol{x}_{ki}^T\boldsymbol{\beta}_k\right)}{\sum_{r\in R(t_{kv})}\exp\left(\boldsymbol{x}_{kr}^T\boldsymbol{\beta}_k\right)}\right)^{\delta_{ki}};\, k = 1, 2. \quad (6)$$

$$\widehat{H}_{0k}(t_k) = \sum_{v:t_{kv}\le t_k}\frac{d_{kv}}{\sum_{r\in R(t_{kv})}\exp\left(\boldsymbol{x}_{kr}^T\widehat{\boldsymbol{\beta}}_k\right)};\, v = 1, 2, \ldots, V. \quad (7)$$

Where $\delta_{ki} = I(T_{ki} \le C_{ki})$ is an indicator function that equals to 1 if the condition is true and 0 otherwise, $\boldsymbol{x}_{kr}$ represents the covariate vector for the $k$-th margin of an individual who remains at risk at time $t_{kv}$ with $r = 1{,}2, \ldots, N\left(R(t_{kv})\right)$ and $d_{kv}$ denotes the number of events occuring at time $t_{kv}$.

### 2.3. Existing Two-Stage Estimation Approaches

Two-stage estimation procedures are widely used in copula-based bivariate survival models to simplify the estimation of complex likelihood functions. Let $\boldsymbol{\theta} = (\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \eta)$ denote the unknown parameter, and $Y_{ki} = \min(T_{ki}, C_{ki})$ denotes the observation time for an individu, then the individual likelihood for copula-based survival with semiparametric marginal [17] showed by Equation (8). These approaches generally separate the estimation of marginal and dependence parameters, thereby reducing computational burden.

$$L_i(\boldsymbol{\theta}) = f(y_{1i}, y_{2i}|\boldsymbol{x}_{1i}, \boldsymbol{x}_{2i})^{\delta_{1i}\delta_{2i}} \times \left(-\frac{\partial S(y_{1i}, y_{2i}|\boldsymbol{x}_{1i}, \boldsymbol{x}_{2i})}{\partial y_{1i}}\right)^{\delta_{1i}(1-\delta_{2i})}$$
$$\times \left(-\frac{\partial S(y_{1i}, y_{2i}|\boldsymbol{x}_{1i}, \boldsymbol{x}_{2i})}{\partial y_{2i}}\right)^{(1-\delta_{1i})\delta_{2i}} \times S(y_{1i}, y_{2i}|\boldsymbol{x}_{1i}, \boldsymbol{x}_{2i})^{(1-\delta_{1i})(1-\delta_{2i})} \quad (8)$$

Where $(\delta_{1i}, \delta_{2i}) \in \{(0{,}0), (0{,}1), (1{,}0), (1{,}1)\}$ represent the censoring indicators for the two margins for $i = 1, 2, \ldots, n$.

#### 2.3.1. Inference Functions for Margins (IFM)

The inference functions for margins (IFM) method, introduced by Shih and Louis (1995), estimates marginal and dependence parameters in a sequential manner. In the first stage, the regression parameters $\boldsymbol{\beta}_k$ for each margin are estimated using the Cox partial likelihood, followed by the estimation of the cumulative baseline hazard function $H_{0k}(t_k)$ using the Breslow estimator [9]. In the second stage, the estimated marginal survival functions $S_k(t_k|x_k)$ are constructed and substituted into the copula-based likelihood to estimate the dependence parameter $\eta$.

### 2.3.2. Two-Stage Approach with Joint Estimation

An extension of the IFM approach was proposed by Sun and Ding [10] which introduces a joint estimation step in the second stage. In the first stage, the IFM procedure is applied to obtain initial estimates of the marginal parameters and baseline hazard functions. These estimates are then used as initial values for the second stage.

In the second stage, the dependence parameter $\eta$ is estimated jointly with the marginal parameters by maximizing the copula-based joint likelihood. However, this joint estimation is performed under constraints, such as assuming a shared parameter structure ($\boldsymbol{\beta}_1 = \boldsymbol{\beta}_2$) [20]. To provide a clearer comparison of these approaches, the main differences are summarized in **Table 1**.

**Table 1. Comparison of Existing and Proposed Two-Stage Estimation Methods**

| Aspect | IFM | Two-Stage (Sun & Ding) | Proposed Method |
|---|---|---|---|
| Stage 1 | Estimated marginals | Same as IFM | Same as Sun & Ding |
| Stage 2 | Estimated $\eta$ only | Joint estimation | Joint estimation |
| Marginal Parameters | Fixed | Updated with constraint | Fully updated |
| Dependence Parameter | Ignored in marginals | Incorporated | Incorporated |
| Constraint | None | $\beta_1 = \beta_2$ | No constraint |

Despite these developments, existing two-stage approaches either treat marginal parameters as fixed or allow only limited updating under restrictive assumptions. Consequently, the estimated marginal effects may not fully reflect the underlying dependence structure.

## 2.4. Proposed Modified Two-Stage Estimation Approach

To address the limitations of existing two-stage approaches, this study proposes a modified two-stage estimation procedure that allows full joint updating of both marginal and dependence parameters in the second stage without imposing shared parameter constraints.

The first stage follows the approach of Sun and Ding [10], where marginal parameters are estimated and used as initial values. In the second stage, all parameters $\boldsymbol{\theta}$ are estimated jointly using the copula-based likelihood, allowing the marginal parameters to adapt to the underlying dependence structure. As highlighted in **Table 1**, the proposed method differs from existing approaches by removing restrictive assumptions and enabling greater flexibility in modeling heterogeneous covariate effects across margins.

### 2.5. BHHH-Based Joint Estimation Algorithm

Since the joint likelihood function does not have a closed-form solution, both the estimation of the dependence parameter $\eta$ in the first stage and the joint estimation in the second stage are carried out using numerical optimization methods. The optimization is performed using the Berndt–Hall–Hall–Hausman (BHHH) algorithm, a quasi-Newton method that updates parameter estimates based on the outer product of gradients [21].

To enhance numerical stability and ensure convergence of the optimization procedure, a backtracking line search strategy is incorporated into the BHHH update. This approach helps prevent overshooting and improves the robustness of the estimation, particularly in scenarios with complex likelihood surfaces or limited information [22].

Let $\boldsymbol{\theta} = (\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \eta)$ denote the vector of parameters. The individual log-likelihood function is denoted by $\ell_{\mathrm{i}}(\boldsymbol{\theta})$, and the estimation algorithm for stage two as follows [21]:

1. Set initial values for the parameter vector $\boldsymbol{\theta}^{(0)}$, obtained from the first-stage estimation.
2. Compute the individual log-likelihood based on the copula-based model.
$$\begin{aligned}\ell_i(\boldsymbol{\theta}) = d_{1i}d_{2i}&\left(\log\frac{\partial^2 C_\eta(u_{1i},u_{2i})}{\partial u_{1i}\partial u_{2i}} + \log f_{1i} + \log f_{2i}\right)\\ &+ d_{1i}(1-d_{2i})\left(\log\frac{\partial C_\eta(u_{1i},u_{2i})}{\partial u_{1i}} + \log f_{1i}\right)\\ &+ d_{2i}(1-d_{1i})\left(\log\frac{\partial C_\eta(u_{1i},u_{2i})}{\partial u_{2i}} + \log f_{2i}\right)\\ &+ (1-d_{1i})(1-d_{2i})\log C_\eta(u_{1i},u_{2i})\end{aligned} \tag{9}$$
where $(u_1, u_2) = \big(S_1(t_1|\boldsymbol{x}_1), S_2(t_2|\boldsymbol{x}_2)\big)$.
3. Evaluate the score vector $\boldsymbol{s}(\boldsymbol{\theta}) = \boldsymbol{\Sigma}_{\boldsymbol{i}}\boldsymbol{s}_{\boldsymbol{i}}(\boldsymbol{\theta})$, where $\boldsymbol{s}_{\boldsymbol{i}}(\boldsymbol{\theta}) = \left[\frac{\partial \ell_i(\boldsymbol{\theta})}{\partial \boldsymbol{\beta}_1} \quad \frac{\partial \ell_i(\boldsymbol{\theta})}{\partial \boldsymbol{\beta}_2} \quad \frac{\partial \ell_i(\boldsymbol{\theta})}{\partial \eta}\right]^T$.
4. Construct the approximation of the information matrix using the outer product gradients:
$$\boldsymbol{H}(\boldsymbol{\theta}) = -\left[\sum\nolimits_{i=1}^{n} \boldsymbol{s}_i(\boldsymbol{\theta})[\,\boldsymbol{s}_i(\boldsymbol{\theta})]^T\right]. \tag{10}$$
5. Parameter iteratively update using the following scheme:
$$\widehat{\boldsymbol{\theta}}^{(m+1)} = \widehat{\boldsymbol{\theta}}^{(m)} - \alpha^{(m)}\boldsymbol{H}\big(\boldsymbol{\theta}^{(m)}\big)^{-\mathbf{1}}\boldsymbol{s}\big(\boldsymbol{\theta}^{(m)}\big), \quad m = 0, 1, 2, \ldots \tag{11}$$
where $0 \le \alpha^{(m)} \le 1$ is a step size determined by a backtracking line search procedure to ensure sufficient improvement in the log-likelihood.
6. Repeat steps 2-5 until convergence criteria are satisfied.

### 2.6. Simulation Study Design and Evaluation Metrics

Survival times were generated from a copula-based bivariate model with exponential marginal distributions and a specified dependence structure. Dependent uniform variables were simulated from the copula and transformed into survival times using the inverse transform method. Covariates were generated from a standard normal and a Bernoulli distribution, and right censoring was introduced using an exponential distribution. All combinations of copula types (Clayton and Joe), dependence parameters ($\eta$ = 2 and 5), sample sizes (n = 100 and 500), and censoring levels (10% and 40%) were considered. The detailed simulation settings are provided in Table 2.

**Table 2. Simulation Settings**

| Component | Description |
|---|---|
| Sample size | 100 and 500 |
| True Parameters | $\boldsymbol{\beta}_1 = 0.5$; $\boldsymbol{\beta}_2 = -0.5$ |
| Covariates | $X_1 \sim N(0,1)$ and $X_2 \sim Bernoulli(0,6)$ |
| Dependence parameter | $\eta$ = 2 and 5 |
| Copula type | Clayton and Joe |
| Baseline rate ($\lambda$) | $\lambda_1 = 0.1$ and $\lambda_2 = 0.2$ |
| Censoring mechanism | 10% and 40% |
| Convergence criteria | $\left\|\widehat{\boldsymbol{\theta}}^{(m+1)} - \widehat{\boldsymbol{\theta}}^{(m)}\right\| \leq 10^{-6}$ |

The performance of the proposed method is evaluated using bias and root mean square error (RMSE), which are commonly employed measures in simulation studies to assess estimation accuracy and precision. The bias and MSE in the estimation of parameters are given, respectively, by,

$$\widehat{Bias}(\widehat{\boldsymbol{\theta}}) = \frac{1}{N}\sum_{i=1}^{N}(\widehat{\boldsymbol{\theta}}^{(i)} - \boldsymbol{\theta}) \tag{10}$$

$$\widehat{RMSE}(\widehat{\boldsymbol{\theta}}) = \sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(\widehat{\boldsymbol{\theta}}^{(i)} - \boldsymbol{\theta}\right)^2} \tag{11}$$

where $\widehat{\boldsymbol{\theta}}^{(i)}$ denote the estimated parameter and $N$ is the number of simulated samples.

## 3. RESULTS AND DISCUSSION

The performance is assessed using bias and root mean square error (RMSE), which reflect the accuracy and precision of the estimators, respectively. The simulation settings are varying as mentioned in Table 2. The bias and RMSE are summarized in Table 3 and Table 4 for all parameters under the considered simulation scenarios for the Clayton and Joe copulas, respectively.

Overall, the results demonstrate a clear improvement in estimation performance as the sample size increases. Moving from $n = 100$ to $n = 500$ consistently reduces both bias and RMSE across all parameters. This indicates that the proposed estimator exhibits desirable large-sample properties. The observed reduction in bias and RMSE as the sample size increases is consistent with the asymptotic properties of maximum likelihood estimators. As $n$ grows, the likelihood function grows more concentrated around the true parameter values, resulting in improved numerical stability and reduced estimation variability.

The influence of censoring is also substantial. Higher censoring levels (40%) lead to noticeable increases in both bias and RMSE compared to the 10% censoring scenario. This effect is particularly more significant for the dependence parameter $\eta$, which shows significantly larger variability under heavy censoring. This behavior is expected as censoring reduces the effective sample size and weakens the information available for capturing dependence between variables. This finding highlights an important practical implication, as many real survival datasets involve moderate to high censoring. Therefore, careful consideration is required when interpreting dependent estimates under such conditions.

**Table 3. Bias and RMSE of Parameter Estimates under Clayton Copula**

| N | %Censored | Parameter | $\eta = 2$ | | $\eta = 5$ | |
|---|---|---|---|---|---|---|
| | | | **Bias** | **RMSE** | **Bias** | **RMSE** |
| 100 | 10% | $\beta_{11}$ | 0.0687 | 0.0315 | 0.0314 | 0.1579 |
| | | $\beta_{12}$ | 0.0749 | 0.0860 | -0.0069 | 0.2912 |
| | | $\beta_{21}$ | 0.0031 | 0.0126 | 0.0190 | 0.1451 |
| | | $\beta_{22}$ | 0.0988 | 0.0693 | 0.0045 | 0.2832 |
| | | $\eta$ | -0.0554 | 0.3615 | -0.2535 | 1.2325 |
| | 40% | $\beta_{11}$ | 0.0568 | 0.2972 | NA | NA |
| | | $\beta_{12}$ | -0.0446 | 0.5753 | NA | NA |
| | | $\beta_{21}$ | 0.0177 | 0.2659 | NA | NA |
| | | $\beta_{22}$ | -0.0532 | 0.5496 | NA | NA |
| | | $\eta$ | 0.3682 | 1.5958 | NA | NA |
| 500 | 10% | $\beta_{11}$ | 0.0089 | 0.0694 | 0.0055 | 0.0644 |
| | | $\beta_{12}$ | -0.0119 | 0.1357 | -0.0078 | 0.1283 |
| | | $\beta_{21}$ | 0.0098 | 0.0679 | 0.0071 | 0.0631 |
| | | $\beta_{22}$ | 0.0024 | 0.1432 | 0.0007 | 0.1270 |
| | | $\eta$ | 0.0036 | 0.2806 | -0.0809 | 0.6064 |
| | 40% | $\beta_{11}$ | 0.0042 | 0.1012 | 0.0019 | 0.0985 |
| | | $\beta_{12}$ | -0.0274 | 0.2379 | -0.0320 | 0.2239 |
| | | $\beta_{21}$ | 0.0087 | 0.1111 | 0.0055 | 0.0998 |
| | | $\beta_{22}$ | -0.0070 | 0.2295 | -0.0184 | 0.2049 |
| | | $\eta$ | 0.0191 | 0.5770 | -0.0357 | 1.0012 |

A more detailed examination reveals that regression parameters ($\beta_{11}, \beta_{12}, \beta_{21}, \beta_{22}$) are generally estimated with relatively small bias, especially under moderate censoring and larger sample sizes. In contrast, the dependence parameter $\eta$ tends to exhibit larger bias and RMSE across most scenarios. This suggests that estimating the dependence structure is inherently more challenging than estimating marginal effects, particularly in copula-based models within survival analysis. This pattern may be attributed to the complexity of the joint likelihood function, where the dependence component is more sensitive to data sparsity and censoring mechanisms compared to marginal components.

With respect to the dependence strength, stronger dependence ($\eta = 5$) generally leads to increased estimation variability compared to moderate dependence ($\eta = 2$). This pattern is more evident in smaller samples and under higher censoring, indicating that complex dependence structures amplify estimation difficulty when data are limited. Unlike regression parameters $\boldsymbol{\beta}$, which are informed by marginal likelihood contributions, the dependence parameter $\eta$ is identified solely through the copula component. Consequently, its estimation is more sensitive to censoring and data sparsity, leading to higher variability and bias, especially in small samples.

**Table 4.** Bias and RMSE of Parameter Estimates under Joe Copula

| N | % Censored | Parameter | $\eta = 2$ | | $\eta = 5$ | |
|---|---|---|---|---|---|---|
| | | | Bias | RMSE | Bias | RMSE |
| 100 | 10% | $\beta_{11}$ | 0.0075 | 0.1916 | 0.0111 | 0.1820 |
| | | $\beta_{12}$ | 0.0868 | 0.3872 | 0.0578 | 0.3577 |
| | | $\beta_{21}$ | 0.0268 | 0.2011 | 0.0189 | 0.1999 |
| | | $\beta_{22}$ | 0.0340 | 0.3220 | 0.0258 | 0.2757 |
| | | $\eta$ | 0.1059 | 0.3493 | -0.0119 | 0.7436 |
| | 40% | $\beta_{11}$ | 0.0304 | 0.2484 | 0.0024 | 0.2478 |
| | | $\beta_{12}$ | -0.0465 | 0.6045 | -0.131 | 0.5486 |
| | | $\beta_{21}$ | 0.0311 | 0.2150 | 0.0294 | 0.2251 |
| | | $\beta_{22}$ | -0.0672 | 0.3826 | -0.1774 | 0.4660 |
| | | $\eta$ | 0.4016 | 0.6762 | 0.5517 | 1.3987 |
| 500 | 10% | $\beta_{11}$ | -0.0086 | 0.0576 | 0.0022 | 0.0593 |
| | | $\beta_{12}$ | 0.0035 | 0.1143 | 0.0199 | 0.0973 |
| | | $\beta_{21}$ | 0.0036 | 0.0582 | 0.0134 | 0.0585 |
| | | $\beta_{22}$ | 0.0464 | 0.1156 | 0.0364 | 0.0922 |
| | | $\eta$ | 0.0946 | 0.1536 | 0.1611 | 0.3810 |
| | 40% | $\beta_{11}$ | 0.0014 | 0.0828 | 0.0196 | 0.0937 |
| | | $\beta_{12}$ | 0.01128 | 0.1865 | 0.0080 | 0.1371 |
| | | $\beta_{21}$ | 0.0636 | 0.1195 | 0.0390 | 0.1094 |
| | | $\beta_{22}$ | 0.0412 | 0.1916 | -0.0001 | 0.1708 |
| | | $\eta$ | 0.1359 | 0.2115 | 0.2479 | 0.4554 |

The comparison between the two copula families reveals a trade-off between bias and variability. While the Joe copula tends to show slightly higher bias compared to the Clayton copula in the same simulation setting, it often produces lower RMSE values. This indicates that the Joe copula produces more stable estimates with lower variability, albeit slightly more biased. The difference may be related to how each copula captures dependence. The Joe copula focuses on upper tail dependence, meaning it captures the relationship when both survival times are relatively long. This tends to produce more stable estimates with lower variability. On the other hand, the Clayton copula focuses on lower tail dependence, which can lead to higher variability in the estimates. This highlights the importance of considering both bias and RMSE when evaluating estimator performance, as relying on a single metric may lead to incomplete conclusions.

The most challenging scenario is observed when $n = 100$ and the censoring level is 40%, which serves as a stress-test condition. In this case, both bias and RMSE increase substantially, and instability is observed in certain parameter estimates, including missing values in some configurations under the Clayton copula. The occurrence of missing values (NA) under high censoring and small sample size suggests numerical instability in the optimization procedure. This may be due to flat or ill-behaved likelihood surfaces, which are common in copula-based survival models under heavy censoring.

The findings of this study are generally consistent with existing literature on copula-based survival models such as Nelsen [23] and Paul Hougaard [24]. It is evident that the observed improvement in bias and RMSE as the sample size increases has also been widely reported, reflecting the desirable large-sample properties of likelihood-based estimators. Also, the impact of censoring on estimation performance observed in this study is consistent with existing results in survival analysis, where higher censoring levels reduce the effective information available for inference and consequently decrease estimation accuracy.

Despite the encouraging results, some limitations of this study must be acknowledged. First, the simulation framework is limited to two copula families that may not fully reflect the various dependence structures encountered in practice. Other copula families with different tail dependence characteristics, such as Gumbel or Frank copulas, or families other than Archimedean, may produce different estimation behaviors. Second, the analysis assumes the correct model specification, whereas in practice, misspecification of the marginal distribution or copula structure can significantly affect estimation accuracy. The numerical instability observed with small sample sizes and heavy censoring indicates that the proposed estimation procedure may be sensitive to optimization settings, such as initial values or convergence criteria. Third, the study considers a limited set of sample sizes and censoring levels, which may not fully reflect more extreme or complex real-world scenarios

In addition, the same simulation scenarios presented in Table 2 were also analyzed using the approach of Sun et al. [20] implemented in the CopulaCenR package. The results indicate that, under the considered settings, the estimated regression parameters tend to be substantially smaller in magnitude compared to the true values (0.5 and −0.5), and the estimated dependence parameter is generally lower than the specified values ($\eta$ = 2 and 5). These findings suggest a tendency toward underestimation in this implementation under the simulated conditions. However, this observation should be interpreted with caution, as it may be influenced by model specification, numerical settings, or implementation details rather than reflecting a general limitation of the method.

Overall, the proposed method demonstrates consistent estimation performance across practically relevant conditions. The estimator shows good overall performance, particularly for the regression parameters, for medium to large sample sizes and at low to moderate levels of censoring, where both bias and variability remain well controlled. However, caution is needed when applying this method to small samples or highly censored data, as the estimation of dependence parameters can become unstable.

## 4. CONCLUSION

This study proposes a copula-based estimation approach for bivariate survival data and evaluates its performance through an extensive simulation study under various scenarios. The results demonstrate that the proposed method performs well in terms of bias and RMSE, particularly as the sample size increases and the censoring level decreases, indicating improved estimation accuracy with more available information. The findings also show that higher censoring levels and stronger dependence structures tend to increase estimation variability, especially for the dependence parameter $\eta$, which is generally more difficult to estimate than the marginal parameters. However, under the most challenging scenario, where the small sample size ($n = 100$) and a high censoring level (40%), the estimation under the Clayton copula exhibits numerical instability, leading to convergence issues in certain cases. In contrast, the method remains more stable under the Joe copula in the same setting. These results indicate that the proposed method is particularly reliable under moderate to large sample sizes and low to moderate censoring levels, where sufficient information is available for stable parameter estimation. Conversely, caution is warranted when applying the method to small samples with high censoring or strong dependence, as these conditions may lead to increased variability and potential convergence difficulties. Overall, the proposed method is a reliable and practical approach for modeling dependence in bivariate survival data, particularly under moderate to favorable data conditions. For future research, further development may include the application of alternative copula families, such as Gumbel, Frank, or other non-Archimedean copulas, to better capture different dependencies. In addition, applying the proposed method to real-world datasets would provide further validation and demonstrate its practical utility in empirical settings.

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**Wahyu Dwi Rahmawati**: Conceptualization, methodology, software, formal analysis, investigation, writing-original draft, writing-review & editing. **Jerry Dwi Trijoyo Purnomo**: Methodology, validation, writing-review & editing, and supervision. **Bambang Widjanarko Otok:** Validation, writing-review & editing, and supervision. All authors discussed the results and contributed to the final manuscript.

## Conflict of Interest Statement
The authors state there is no conflict of interest.

## Data Availability
The data that support the findings of this study were generated through simulation. The simulation procedures are described in detail in this article.

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