

Causal survival analysis

Estimation of the Average Treatment Effect (ATE): Practical Recommendations

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Abstract

Causal survival analysis combines survival analysis and causal inference to evaluate the effect of a treatment or intervention on a time-to-event outcome, such as survival time. It offers an alternative to relying solely on Cox models for assessing these effects. In this paper, we present a comprehensive review of estimators for the average treatment effect measured with the restricted mean survival time, including regression-based methods, weighting approaches, and hybrid techniques. We investigate their theoretical properties and compare their performance through extensive numerical experiments. Our analysis focuses on the finite-sample behavior of these estimators, the influence of nuisance parameter selection, and their robustness and stability under model misspecification. By bridging theoretical insights with practical evaluation, we aim to equip practitioners with both state-of-the-art implementations of these methods and practical guidelines for selecting appropriate estimators for treatment effect estimation. Among the approaches considered, G-formula two-learners, AIPCW-AIPTW, Buckley-James estimators, and causal survival forests emerge as particularly promising.

Keywords: Restricted Mean Survival Time, Randomized Control Trial, Observational Study, Censoring

Contents

1	Introduction	2
1.1	Context and motivations	2
1.2	Definition of the estimand: the RMST	3
1.3	Organisation of the paper	5
1.4	Notations	5

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2	Causal survival analysis in Randomized Controlled Trials	6
2.1	Independent censoring: the Kaplan-Meier estimator	7
2.2	Conditionally independent censoring	9
2.2.1	The G-formula and the Cox Model	10
2.2.2	Censoring unbiased transformations	11
2.2.3	Augmented corrections	16
3	Causal survival analysis in observational studies	16
3.1	Independent censoring	17
3.2	Conditional independent censoring	18
3.2.1	IPTW-IPCW transformations	19
3.2.2	IPTW-BJ transformations	20
3.2.3	Double augmented corrections	21
4	Implementation	21
4.1	Summary of the estimators	21
4.2	Implementation of the estimators	22
4.3	Available packages	36
5	Simulations	37
5.1	RCT	37
5.2	Observational data	43
5.3	Mispecification of nuisance components	46
6	Conclusion	49
	References	52
7	Appendix A: Proofs	54
7.1	Proofs of Section 2.1	54
7.2	Proofs of Section 2.2	55
7.3	Proofs of Section 3.1	57
7.4	Proofs of Section 3.2	57
8	Appendix B: Descriptive statistics	59
8.1	RCT	59
8.2	Observational study with linear relationship	61
8.3	Observational study with interaction	63
	Session information	65

1 Introduction

1.1 Context and motivations

Causal survival analysis is a growing field that integrates causal inference (D. B. Rubin 1974; Hernán and Robins 2010) with survival analysis (Kalbfleisch and Prentice 2002) to evaluate the impact of treatments on time-to-event outcomes, while accounting for censoring situations where only partial information about an event’s occurrence is available.

Being a relatively new domain, the existing literature, though vast, remains fragmented. As a result, a clear understanding of the theoretical properties of various estimators is challenging to obtain.

Moreover, the implementation of proposed methods is limited, leaving researchers confronted with a range of available estimators and the need to make numerous methodological decisions. There is a pressing need for a comprehensive survey that organizes the available methods, outlines the underlying assumptions, and provides an evaluation of estimator performance — particularly in finite sample settings. Such a survey also has the potential to help identify remaining methodological challenges that need to be addressed. This need becomes increasingly urgent as causal survival analysis gains traction in both theoretical and applied domains. For instance, its applications to external control arm analyses are particularly relevant in the context of single-arm clinical trials, where traditional comparator arms are unavailable. Regulatory guidelines have begun to acknowledge and support such semi-experimental approaches, reflecting the broader evolution of trial design and therapeutic innovation in precision medicine, see for instance (European Medicines Agency 2024).

By synthesizing the theoretical foundations, assumptions, and performance of various estimators, a survey on existing causal survival analysis methods would provide researchers and practitioners with the necessary tools to make informed methodological choices. This is crucial for fostering robust and reliable applications of causal survival analysis in both academic research and practical settings, where precise and valid results are paramount.

In this paper, we focus our attention to the estimation of the Restricted Mean Survival Time (RMST), a popular causal measure in survival analysis which offers an intuitive interpretation of the average survival time over a specified period. In particular, we decided to not cover the estimation of Hazard Ratio (HR), which has been prominently used but often questioned due to its potential non-causal nature (Martinussen, Vansteelandt, and Andersen 2020). Additionally, unlike the Hazard Ratio, the RMST has the desirable property of being a collapsible measure, meaning that the population effect can be expressed as a weighted average of subgroup effects, with positive weights that sum to one (Huitfeldt, Stensrud, and Suzuki 2019).

1.2 Definition of the estimand: the RMST

We set the analysis in the potential outcome framework, where a patient, described by a vector of covariates $X \in \mathbb{R}^p$, either receives a treatment ($A = 1$) or is in the control group ($A = 0$). The patient will then survive up to a certain time $T(0) \in \mathbb{R}^+$ in the control group, or up to a time $T(1) \in \mathbb{R}^+$ in the treatment group. In practice, we cannot simultaneously have access to $T(0)$ and $T(1)$, as one patient is either treated or control, but only to T defined as follows:

Assumption. (Stable Unit Treatment Value Assumption: SUTVA)

$$T = AT(1) + (1 - A)T(0). \quad (1)$$

Due to potential censoring, the outcome T is not completely observed. The most common form of censoring is right-censoring (also known as type II censoring), which occurs when the event of interest has not taken place by the end of the observation period, indicating that it may have occurred later if the observation had continued (Turkson, Ayiah-Mensah, and Nimoh 2021). We focus in this study on this type of censoring only and we assume that we observe $\tilde{T} = T \wedge C = \min(T, C)$ for some censoring time $C \in \mathbb{R}^+$. When an observation is censored, the observed time is equal to the censoring time.

We also assume that we know whether an outcome is censored or not. In other words, we observe the censoring status variable $\Delta = \mathbb{I}\{T \leq C\}$, where $\mathbb{I}\{\cdot\}$ is the indicator function. Δ is 1 if the true outcome is observed, and 0 if it is censored.

We assume observing a n -sample of variables $(X, A, \tilde{T}, \Delta)$ stemming from an n -sample of the partially unobservable variables $(X, A, T(0), T(1), C)$. A toy example of such data is given in Table 1.

Table 1: Example of a survival dataset. In practice, only X , A , \tilde{T} and Δ are observed.

ID	Co-variates			Treat-ment	Cen-soring	Status	Poten-tial out-comes		True out-come	Ob-served out-come
i	X_1	X_2	X_3	A	C	Δ	$T(0)$	$T(1)$	T	\tilde{T}
1	1	1.5	4	1	?	1	?	200	200	200
2	5	1	2	0	?	1	100	?	100	100
3	9	0.5	3	1	200	0	?	?	?	200

Our aim is to estimate the Average Treatment Effect (ATE) defined as the difference between the Restricted Mean Survival Time of the treated and controls (Royston and Parmar 2013).

Definition 1.1. (Causal effect: Difference between Restricted Mean Survival Time)

$$\theta_{\text{RMST}} = \mathbb{E}[T(1) \wedge \tau - T(0) \wedge \tau],$$

where $a \wedge b := \min(a, b)$ for $a, b \in \mathbb{R}$.

We define the survival functions $S^{(a)}(t) := \mathbb{P}(T(a) > t)$ for $a \in \{0, 1\}$, i.e., the probability that a treated or non-treated individual will survive beyond a given time t . Likewise, we let $S(t) := \mathbb{P}(T > t)$, and $S_C(t) := \mathbb{P}(C > t)$. We also let $G(t) := \mathbb{P}(C \geq t)$ be the left-limit of the survival function S_C . Because $T(a) \wedge \tau$ are non-negative random variables, one can easily express the restricted mean survival time using the survival functions:

$$\mathbb{E}(T(a) \wedge \tau) = \int_0^\infty \mathbb{P}(T(a) \wedge \tau > t) dt = \int_0^\tau S^{(a)}(t) dt. \quad (2)$$

Consequently, θ_{RMST} can be interpreted as the mean difference between the survival function of treated and control until a fixed time horizon τ . A difference in RMST $\theta_{\text{RMST}} = 10$ days with $\tau = 200$ means that, on average, the treatment increases the survival time by 10 days at 200 days. We give a visual interpretation of RMST in Figure 1.

Although the present work focuses on the estimation of the difference in RMST, we would like to stress that the causal effect can be assessed through other measures, such as for instance the difference of the survival functions

$$\theta_{\text{SP}} := S^{(1)}(\tau) - S^{(0)}(\tau)$$

for some time τ , see for instance (Ozenne et al. 2020). As mentionned in Section 1.1, another widely used measure (though not necessarily causal) is the hazards ratio, defined as

$$\theta_{\text{HR}} := \frac{\lambda^{(1)}(\tau)}{\lambda^{(0)}(\tau)},$$

where the hazard function $\lambda^{(a)}$ is defined as

$$\lambda^{(a)}(t) := \lim_{h \rightarrow 0^+} \frac{\mathbb{P}(T(a) \in [t, t+h) | T(a) \geq t)}{h}.$$

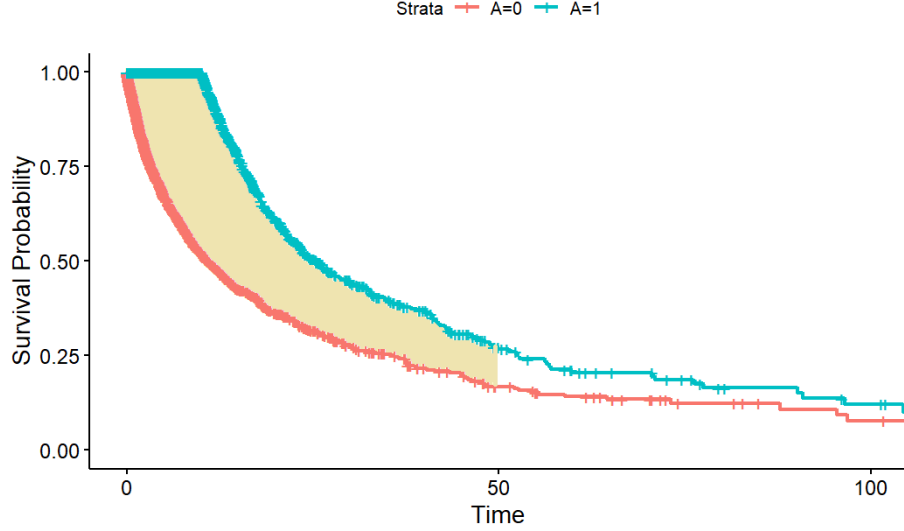


Figure 1: Plot of the estimated survival curves on synthetic toy-data. The θ_{RMST} at $\tau = 50$ corresponds to the yellow shaded area between the two survival curves. The curves have been estimated using Kaplan-Meier estimator, see Section 2.1.

in a continuous setting, or as $\lambda^{(a)}(t) := \mathbb{P}(T(a) = t | T(a) \geq t)$ when the survival times are discrete. The hazard functions and the survival functions are linked through the identities

$$S^{(a)}(t) = \exp(-\Lambda^{(a)}(t)) \quad \text{where} \quad \Lambda^{(a)}(t) := \int_0^t \lambda^{(a)}(s) ds, \quad (3)$$

in the continuous case. The functions $\Lambda^{(a)}$ are call the cumulative hazard functions. In the discrete case, we have in turn

$$S^{(a)}(t) = \prod_{t_k \leq t} (1 - \lambda^{(a)}(t_k)), \quad (4)$$

where $\{t_1, \dots, t_K\}$ are the atoms of $T^{(a)}$. These hazard functions are classically used to model the survival times and the censoring times, see Section 2.2.1.

1.3 Organisation of the paper

In this paper, we detail the minimal theoretical framework that allows the analysis of established RMST estimators in the context of both Randomized Controlled Trials (Section 2) and observational data (Section 3). We give their statistical properties (consistency, asymptotic normality) along with proofs when possible. We then conduct in Section 5 a numerical study of these estimators through simulations under various experimental conditions, including independent and conditionally independent censoring and correct and incorrect model specifications. We conclude in Section 6 with practical recommendations on estimator selection, based on criteria such as asymptotic behavior, computational complexity, and efficiency.

1.4 Notations

We provide in Table 2 a summary of the notation used throughout the paper.

Table 2: Summary of the notations.

Symbol	Description
X	Covariates
A	Treatment indicator ($A = 1$ for treatment, $A = 0$ for control)
T	Survival time
$T(a), a \in \{0, 1\}$	Potential survival time respectively with and without treatment
$S^{(a)}, a \in \{0, 1\}$	Survival function $S^{(a)}(t) = \mathbb{P}(T(a) > t)$ of the potential survival times
$\lambda^{(a)}, a \in \{0, 1\}$	Hazard function $\lambda^{(a)}(t) = \lim_{h \rightarrow 0^+} \mathbb{P}(T(a) \in [t, t+h] T(a) \geq t) / h$ of the potential survival times
$\Lambda^{(a)}, a \in \{0, 1\}$	Cumulative hazard function of the potential survival times
C	Censoring time
S_C	Survival function $S_C(t) = \mathbb{P}(C > t)$ of the censoring time
G	Left-limit of the survival function $G(t) = \mathbb{P}(C \geq t)$ of the censoring time
\tilde{T}	Observed time ($T \wedge C$)
Δ	Censoring status $\mathbb{I}\{T \leq C\}$
Δ^τ	Censoring status of the restricted time $\Delta^\tau = \max\{\Delta, \mathbb{I}\{\tilde{T} \geq \tau\}\}$
$\{t_1, t_2, \dots, t_K\}$	Discrete times
$e(x)$	Propensity score $\mathbb{E}[A X = x]$
$\mu(x, a), a \in \{0, 1\}$	$\mathbb{E}[T \wedge \tau X = x, A = a]$
$S(t x, a), a \in \{0, 1\}$	Conditional survival function, $\mathbb{P}(T > t X = x, A = a)$.
$\lambda^{(a)}(t x), a \in \{0, 1\}$	Conditional hazard functions of the potential survival times
$G(t x, a), a \in \{0, 1\}$	left-limit of the conditional survival function of the censoring $\mathbb{P}(C \geq t X = x, A = a)$
$Q_S(t x, a), a \in \{0, 1\}$	$\mathbb{E}[T \wedge \tau X = x, A = a, T \wedge \tau > t]$

2 Causal survival analysis in Randomized Controlled Trials

Randomized Controlled Trials (RCTs) are the gold standard for establishing the effect of a treatment on an outcome, because treatment allocation is controlled through randomization, which ensures (asymptotically) the balance of covariates between treated and controls, and thus avoids problems of confounding between treatment groups. The core assumption in a classical RCT is the random assignment of the treatment (D. B. Rubin 1974).

Assumption. (Random treatment assignment) There holds:

$$A \perp\!\!\!\perp T(0), T(1), X \quad (5)$$

We also assume that there is a positive probability of receiving the treatment, which we rephrase under the following assumption.

Assumption. (Trial positivity)

$$0 < \mathbb{P}(A = 1) < 1 \quad (6)$$

Under Assumptions 5 and 6, classical causal identifiability equations can be written to express θ_{RMST} without potential outcomes.

$$\begin{aligned}
 \theta_{\text{RMST}} &= \mathbb{E}[T(1) \wedge \tau - T(0) \wedge \tau] \\
 &= \mathbb{E}[T(1) \wedge \tau | A = 1] - \mathbb{E}[T(0) \wedge \tau | A = 0] \quad (\text{Random treatment assignment}) \\
 &= \mathbb{E}[T \wedge \tau | A = 1] - \mathbb{E}[T \wedge \tau | A = 0]. \quad (\text{SUTVA})
 \end{aligned} \quad (7)$$

However, Equation 7 still depends on T , which remains only partially observed due to censoring. To ensure that censoring does not compromise the identifiability of treatment effects, we must impose certain assumptions on the censoring process, standards in survival analysis, namely, independent censoring and conditionally independent censoring. These assumptions lead to different estimation approaches. We focus on two strategies: those that aim to directly estimate $E[T \wedge \tau | A = a]$ directly (e.g., through censoring-unbiased transformations, see Section 2.2), and those that first estimate the survival curves to derive RMST via Equation 2 (such as the Kaplan-Meier estimator and all its variants, see the next Section).

2.1 Independent censoring: the Kaplan-Meier estimator

In a first approach, one might assume that the censoring times are independent from the rest of the variables.

Assumption. (Independent censoring)

$$C \perp\!\!\!\perp T(0), T(1), X, A. \quad (8)$$

Under Equation 8, subjects censored at time t are representative of all subjects who remain at risk at time t . Figure 2 represents the causal graph when the study is randomized and outcomes are observed under independent censoring.

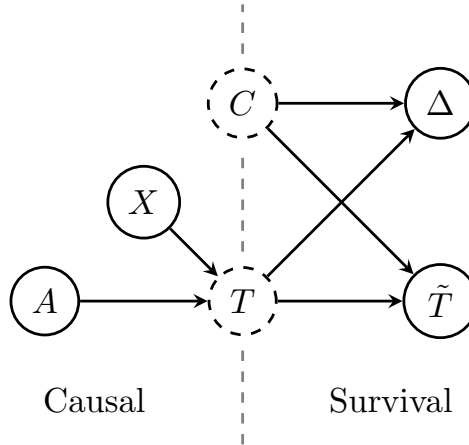


Figure 2: Causal graph in RCT survival data with independent censoring.

We also assume that there is no almost-sure upper bound on the censoring time before τ , which we rephrase under the following assumption.

Assumption. (Positivity of the censoring process) There exists $\varepsilon > 0$ such that

$$G(t) \geq \varepsilon \quad \text{for all } t \in [0, \tau). \quad (9)$$

If indeed it was the case that $P(C < t) = 1$ for some $t < \tau$, then we would not be able to infer anything on the survival function on the interval $[t, \tau]$ as all observation times \tilde{T}_i would be in $[0, t]$ almost surely. In practice, adjusting the threshold time τ can help satisfy the positivity assumption. For instance, in a clinical study, if a subgroup of patients has zero probability of remaining uncensored at a given time, τ can be modified to ensure that participants have a feasible chance of remaining uncensored up to the revised threshold.

The two Assumptions 8 and 9 together allow the distributions of $T(a)$ to be identifiable, in the sense that there exists an identity that expresses $S^{(a)}$ as a function of the joint distribution of $(\tilde{T}, \Delta, A = a)$,

see for instance Ebrahimi, Molefe, and Ying (2003) for such a formula in a non-causal framework. This enables several estimation strategies, the most well-known being the Kaplan-Meier product-limit estimator.

To motivate the definition of the latter and explicit the identifiability identity, we set the analysis in the discrete case. We let $\{t_k\}_{k \geq 1}$ be a set of positive and increasing times and assume that $T \in \{t_k\}_{k \geq 1}$ almost surely. Then for any $t \in [0, \tau]$, it holds, letting $t_0 = 0$ by convention, thanks to Equation 4,

$$\begin{aligned} S(t|A = a) &= \mathbb{P}(T > t|A = a) = \prod_{t_k \leq t} (1 - \mathbb{P}(T = t_k|T > t_{k-1}, A = a)) \\ &= \prod_{t_k \leq t} \left(1 - \frac{\mathbb{P}(T = t_k, A = a)}{\mathbb{P}(T \geq t_k, A = a)}\right). \end{aligned}$$

Using Assumptions 8 and 9, we find that

$$\frac{\mathbb{P}(T = t_k, A = a)}{\mathbb{P}(T \geq t_k, A = a)} = \frac{\mathbb{P}(T = t_k, C \geq t_k, A = a)}{\mathbb{P}(T \geq t_k, C \geq t_k, A = a)} = \frac{\mathbb{P}(\tilde{T} = t_k, \Delta = 1, A = a)}{\mathbb{P}(\tilde{T} \geq t_k, A = a)}, \quad (10)$$

yielding the final identity

$$S(t|A = a) = \prod_{t_k \leq t} \left(1 - \frac{\mathbb{P}(\tilde{T} = t_k, \Delta = 1, A = a)}{\mathbb{P}(\tilde{T} \geq t_k, A = a)}\right). \quad (11)$$

Notice that the right hand side only depends on the distribution of the observed tuple (A, \tilde{T}, Δ) . This last equation suggests in turn to introduce the quantities

$$D_k(a) := \sum_{i=1}^n \mathbb{I}(\tilde{T}_i = t_k, \Delta_i = 1, A = a) \quad \text{and} \quad N_k(a) := \sum_{i=1}^n \mathbb{I}(\tilde{T}_i \geq t_k, A = a), \quad (12)$$

which correspond respectively to the number of deaths $D_k(a)$ and of individuals at risk $N_k(a)$ at time t_k in the treated group ($a=1$) or in the control group ($a=0$).

Definition 2.1. (Kaplan-Meier estimator, Kaplan and Meier (1958)) With $D_k(a)$ and $N_k(a)$ defined in Equation 12, we let

$$\hat{S}_{KM}(t|A = a) := \prod_{t_k \leq t} \left(1 - \frac{D_k(a)}{N_k(a)}\right). \quad (13)$$

The associated RMST estimator is then simply defined as

$$\hat{\theta}_{KM} = \int_0^\tau \hat{S}_{KM}(t|A = 1) - \hat{S}_{KM}(t|A = 0) dt. \quad (14)$$

The Kaplan-Meier estimator is the Maximum Likelihood Estimator (MLE) of the survival functions, see for instance Kaplan and Meier (1958). Furthermore, because $D_k(a)$ and $N_k(a)$ are sums of i.i.d. random variables, the Kaplan-Meier estimator inherits some convenient statistical properties.

Proposition 2.1. Under Assumptions 1, 5, 6, 8 and 9, and for all $t \in [0, \tau]$, the estimator $\hat{S}_{KM}(t|A = a)$ of $S^{(a)}(t)$ is strongly consistent and admits the following bounds for its bias:

$$0 \leq S^{(a)}(t) - \mathbb{E}[\hat{S}_{KM}(t|A = a)] \leq O(\mathbb{P}(N_k(a) = 0)),$$

where k is the greatest time t_k such that $t \geq t_k$.

Gill (1983) gives a more precise lower-bound on the bias in the case of continuous distributions, which was subsequently refined by Zhou (1988). The bound we give, although slightly looser, still exhibits the same asymptotic regime. In particular, as soon as $S^{(a)}(t) > 0$ (and Assumption 9 holds), then the bias decays exponentially fast towards 0. We give in Section 7.1 a simple proof of our bound in our context.

Proposition 2.2. *Under Assumptions 1, 5, 6, 8 and 9, and for all $t \in [0, \tau]$, $\hat{S}_{\text{KM}}(t|A = a)$ is asymptotically normal and $\sqrt{n}(\hat{S}_{\text{KM}}(t|A = a) - S^{(a)}(t))$ converges in distribution towards a centered Gaussian of variance*

$$V_{\text{KM}}(t|A = a) := S^{(a)}(t)^2 \sum_{t_k \leq t} \frac{1 - s_k(a)}{s_k(a)r_k(a)},$$

where $s_k(a) = S^{(a)}(t_k)/S^{(a)}(t_{k-1})$ and $r_k(a) = \mathbb{P}(\tilde{T} \geq t_k, A = a)$.

The proof of Proposition 2.2 can be found in Section 7.1. Because $D_k(a)/N_k(a)$ is a natural estimator of $1 - s_k(a)$ and, $\frac{1}{n}N_k(a)$ a natural estimator for $r_k(a)$, the asymptotic variance of the Kaplan-Meier estimator can be estimated with the so-called Greenwood formula, as already derived heuristically in Kaplan and Meier (1958):

$$\widehat{\text{Var}}(\hat{S}_{\text{KM}}(t|A = a)) := \hat{S}_{\text{KM}}(t|A = a)^2 \sum_{t_k \leq t} \frac{D_k(a)}{N_k(a)(N_k(a) - D_k(a))}. \quad (15)$$

We finally mention that the KM estimator as defined in Definition 2.1 still makes sense in a non-discrete setting, and one only needs to replace the fixed grid $\{t_k\}$ by the values at which we observed an event ($\tilde{T}_i = t_k, \Delta_i = 1$). We refer to Breslow and Crowley (1974) for a study of this estimator in the continuous case and to Aalen, Borgan, and Gjessing (2008), Sec 3.2 for a general study of the KM estimator through the prism of point processes.

2.2 Conditionally independent censoring

An alternative hypothesis in survival analysis that relaxes the assumption of independent censoring is conditionally independent censoring, also referred sometimes as *informative censoring*. It allows to model more realistic censoring processes, in particular in situations where there are reasons to believe that C may be dependent from A and X (for instance, if patient is more like to leave the study when treated because of side-effects of the treatment).

Assumption. (Conditionally independent censoring)

$$C \perp\!\!\!\perp T(0), T(1) \mid X, A \quad (16)$$

Under Equation 16, subjects within a same stratum defined by $X = x$ and $A = a$ have equal probability of censoring at time t , for all t . In case of conditionally independent censoring, we also need to assume that all subjects have a positive probability to remain uncensored at their time-to-event.

Assumption. (Positivity / Overlap for censoring) There exists $\varepsilon > 0$ such that for all $t \in [0, \tau]$, it almost surely holds

$$G(t|A, X) \geq \varepsilon. \quad (17)$$

Figure 3 represents the causal graph when the study is randomized with conditionally independent censoring.

Under dependent censoring, the Kaplan-Meier estimator as defined in Definition 2.1 can fail to estimate survival, in particular because Equation 10 does not hold anymore. Alternatives include plug-in G-formula estimators (Section 2.2.1) and unbiased transformations (Section 2.2.2).

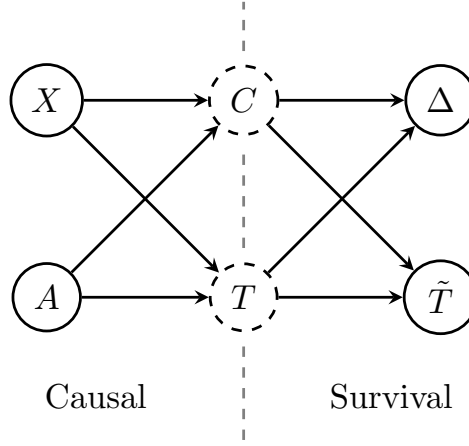


Figure 3: Causal graph in RCT survival data with dependent censoring.

2.2.1 The G-formula and the Cox Model

Because the censoring is now independent from the potential outcome conditionally to the covariates, it would seem natural to model the response of the survival time conditionally to these covariates too:

$$\mu(x, a) := \mathbb{E}[T \wedge \tau | X = x, A = a].$$

Building on Equation 7, one can express the RMST as a function of μ :

$$\theta_{\text{RMST}} = \mathbb{E}[\mathbb{E}[T \wedge \tau | X, A = 1]] - \mathbb{E}[T \wedge \tau | X, A = 0]] = \mathbb{E}[\mu(X, 1) - \mu(X, 0)].$$

An estimator $\hat{\mu}$ of μ would then straightforwardly yield an estimator of the difference in RMST through the so-called *G-formula* plug-in estimator:

$$\hat{\theta}_{\text{G-formula}} = \frac{1}{n} \sum_{i=1}^n \hat{\mu}(X_i, 1) - \hat{\mu}(X_i, 0). \quad (18)$$

We would like to stress that a G-formula approach works also in an observational context as the one introduced in Section 3.2. However, because the estimation strategies presented in the next sections relies on estimating nuisance parameters, and that this latter task is often done in the same way as we estimate the conditional response μ , we decided to not delay the introduction of the G-formula any further, and we present below a few estimation methods for μ . These methods are sub-divided in two categories: *T-learners*, where $\mu(\cdot, 1)$ is estimated separately from $\mu(\cdot, 0)$, and *_S-learners*, where $\hat{\mu}$ is obtained by fitting a single model based on covariates (X, A) .

Cox's Model. There are many ways to model μ in a survival context, the most notorious of which being the Cox proportional hazards model (Cox 1972). It relies on a semi-parametric modelling the conditional hazard functions $\lambda^{(a)}(t|X)$ as

$$\lambda^{(a)}(t|X) = \lambda_0^{(a)}(t) \exp(X^\top \beta^{(a)}),$$

where $\lambda_0^{(a)}$ is a baseline hazard function and $\beta^{(a)}$ has the same dimension as the vector of covariate X . The conditional survival function then take the simple form (in the continuous case)

$$S^{(a)}(t|X) = S_0^{(a)}(t)^{\exp(X^\top \beta^{(a)})},$$

where $S_0^{(a)}(t)$ is the survival function associated with $\lambda_0^{(a)}$. The vector $\beta^{(a)}$ is classically estimated by maximizing the so-called *partial likelihood* function as introduced in the original paper of Cox (1972):

$$\mathcal{L}(\beta) := \prod_{\Delta_i=1} \frac{\exp(X_i^\top \beta)}{\sum_{\tilde{T}_j \geq \tilde{T}_i} \exp(X_j^\top \beta)},$$

while the cumulative baseline hazard function can be estimated through the Breslow's estimator (Breslow 1974):

$$\hat{\Lambda}_0^{(a)}(t) = \sum_{\Delta_i=1, \tilde{T}_i \leq t} \frac{1}{\sum_{\tilde{T}_j \geq \tilde{T}_i} \exp(X_j^\top \hat{\beta}^{(a)})}$$

where $\hat{\beta}^{(a)}$ is a partial likelihood maximizer. One can show that $(\hat{\beta}^{(a)}, \hat{\Lambda}_0^{(a)})$ is the MLE of the true likelihood, when $\hat{\Lambda}_0^{(a)}$ is optimized over all step functions of the form

$$\Lambda_0(t) := \sum_{\Delta_i=1} h_i, \quad h_i \in \mathbb{R}^+.$$

This fact was already hinted in the original paper by Cox and made rigorous in many subsequent papers, see for instance Fan, Feng, and Wu (2010). Furthermore, if the true distribution follows a Cox model, then both $\hat{\beta}^{(a)}$ and $\hat{\Lambda}_0^{(a)}$ are strongly consistent and asymptotically normal estimator of the true parameters $\beta^{(a)}$ and $\Lambda^{(a)}$, see Kalbfleisch and Prentice (2002), Sec 5.7. When using a *T*-learner approach, one simply finds $(\hat{\beta}^{(a)}, \hat{\Lambda}_0^{(a)})$ for $a \in \{0, 1\}$ by considering the control group and the treated group separately. When using a *S*-learner approach, the treatment status A becomes a covariate and the model becomes

$$\lambda(t|X, A) = \lambda_0(t) \exp(X^\top \beta + \alpha A). \quad (19)$$

for some $\alpha \in \mathbb{R}$. One main advantage of Cox's model is that it makes it very easy to interpret the effect of a covariate on the survival time. If indeed $\alpha > 0$, then the treatment has a negative effect on the survival times. Likewise, if $\beta_i > 0$, then the i -th coordinate of X has a negative effect as well. We finally mention that the hazard ratio takes a particularly simple form under the later model since

$$\theta_{\text{HR}} = e^\alpha.$$

In particular, it does not depend on the time horizon τ , and is thus sometimes referred to as *proportional hazard*. Figure 4 illustrates the estimation of the difference in Restricted Mean Survival Time using G-formula with Cox models.

Weibull Model. A popular parametric model for survival is the Weibull Model, which amounts to assume that

$$\lambda^{(a)}(t|X) = \lambda_0^{(a)}(t) \exp(X^\top \beta)$$

where $\lambda_0^{(a)}(t)$ is the instant hazard function of a Weibull distribution, that is to say a function proportional to t^γ for some shape parameter $\gamma > 0$. We refer to Zhang (2016) for a study of this model.

Survival Forests. On the non-parametric front, we mention the existence of survival forests (Ishwaran et al. 2008).

2.2.2 Censoring unbiased transformations

Censoring unbiased transformations involve applying a transformation to T . Specifically, we compute a new time T^* of the form

$$T^* := T^*(\tilde{T}, X, A, \Delta) = \begin{cases} \phi_0(\tilde{T} \wedge \tau, X, A) & \text{if } \Delta^\tau = 0, \\ \phi_1(\tilde{T} \wedge \tau, X, A) & \text{if } \Delta^\tau = 1. \end{cases} \quad (20)$$

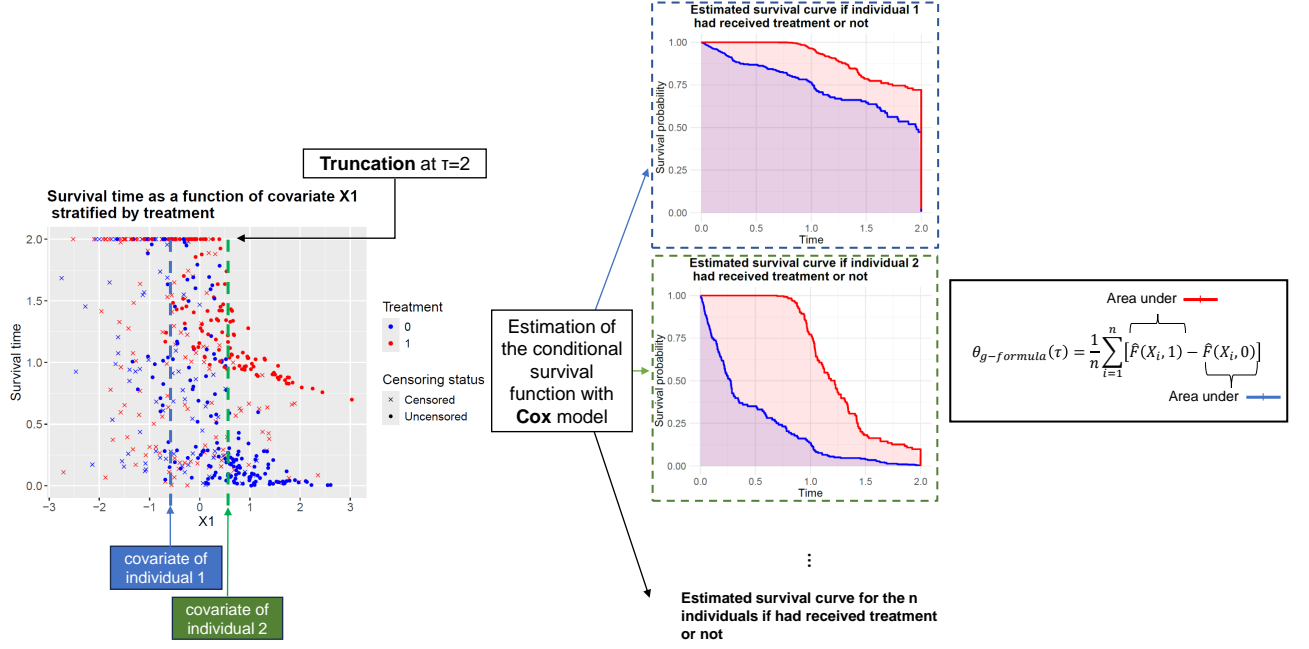


Figure 4: Illustration of the G-formula for estimating θ_{RMST} in an RCT when only one covariate X_1 influences the outcome.

for two wisely chosen transformations ϕ_0 and ϕ_1 , and where

$$\Delta^\tau := \mathbb{I}\{T \wedge \tau \leq C\} = \Delta + (1 - \Delta)\mathbb{I}(\tilde{T} \geq \tau) \quad (21)$$

is the indicator of the event where the individual is either uncensored or censored after time τ . The idea behind the introduction of Δ^τ is that because we are only interested in computing the expectation of the survival time thresholded by τ , any censored observation coming after time τ can in fact be considered as uncensored ($\Delta^\tau = 1$).

A censoring unbiased transformation T^* shall satisfy: for $a \in \{0, 1\}$, it holds

$$\mathbb{E}[T^*|A = a, X] = \mathbb{E}[T(a) \wedge \tau | X] \quad \text{almost surely.} \quad (22)$$

A notable advantage of this approach is that it enables the use of the full transformed dataset (X_i, A_i, T_i^*) as if no censoring occurred. Because it holds

$$\mathbb{E}[\mathbb{E}[T^*|A = a, X]] = \mathbb{E}\left[\frac{\mathbb{I}\{A = a\}}{\mathbb{P}(A = a)} T^*\right], \quad (23)$$

there is a very natural way to derive an estimator of the difference in RMST from any censoring unbiased transformation T^* as:

$$\hat{\theta} = \frac{1}{n} \sum_{i=1}^n \left(\frac{A_i}{\pi} - \frac{1 - A_i}{1 - \pi} \right) T_i^* \quad (24)$$

where $\pi = \mathbb{P}(A = 1) \in (0, 1)$ by Assumption 6 and where $T_i^* = T^*(\tilde{T}_i, X_i, A_i, \Delta_i)$. We easily get the following result.

Proposition 2.3. *Under Assumptions 5 and 6, the estimator $\hat{\theta}$ derived as in Equation 24 from a square integrable censoring unbiased transformations satisfying Equation 22 is an unbiased, strongly consistent, and asymptotically normal estimator of the difference in RMST.*

Square integrability will be ensured any time the transformation is bounded, which will always be the case of the ones considered in this work. It is natural in a RCT setting to assume that probability of being treated π is known. If not, it is usual to replace π by its empirical counterpart $\hat{\pi} = n_1/n$ where $n_a = \sum_i \mathbb{1}\{A = a\}$. The resulting estimator takes the form

$$\hat{\theta} = \frac{1}{n_1} \sum_{A_i=1} T_i^* - \frac{1}{n_0} \sum_{A_i=0} T_i^*. \quad (25)$$

Note however that this estimator is slightly biased due to the estimation of π (see for instance Colnet et al. (2022), Lemma 2), but it is still strongly consistent and asymptotically normal, and its bias is exponentially small in n .

Proposition 2.4. *Under Assumptions 5 and 6, the estimator $\hat{\theta}$ derived as in Equation 25 from a square integrable censoring unbiased transformations satisfying Equation 22 is a strongly consistent, and asymptotically normal estimator of the difference in RMST.*

The two most popular transformations are Inverse-Probability-of-Censoring Weighting (Koul, Susarla, and Ryzin (1981)) and Buckley-James (Buckley and James (1979)), both illustrated in Figure 5 and detailed below. In the former, only non-censored observations are considered and they are weighted while in the latter, censored observations are imputed with an estimated survival time.

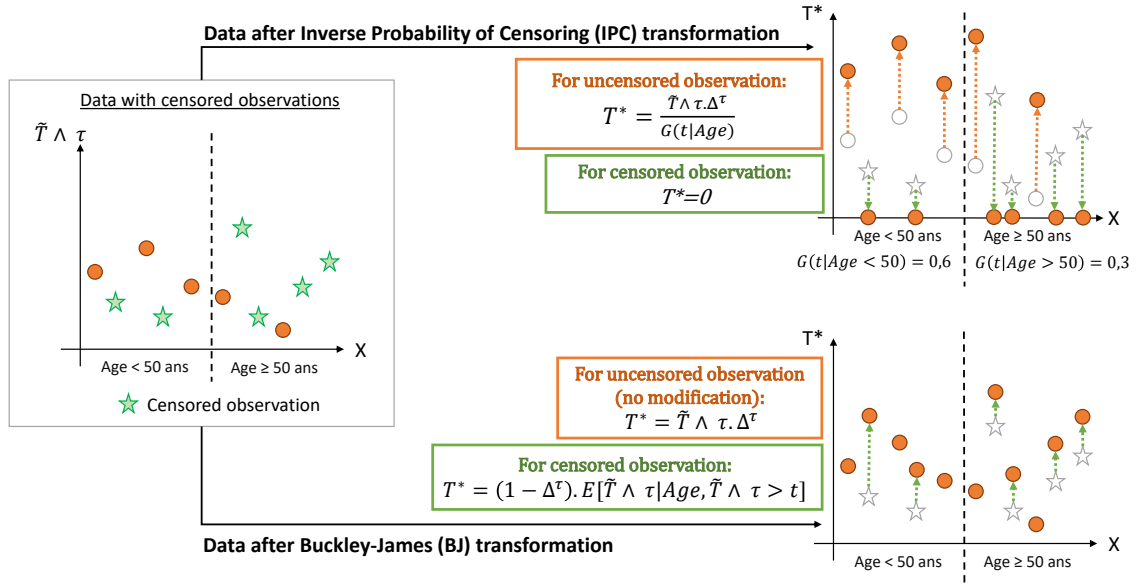


Figure 5: Illustration of Inverse-Probability-of-Censoring and Buckley-James transformations.

The Inverse-Probability-of-Censoring Weighted transformation

The Inverse-Probability-of-Censoring Weighted (IPCW) transformation, introduced by (Koul, Susarla, and Ryzin (1981)) in the context of censored linear regression, involves discarding censored observations and applying weights to uncensored data. More precisely, we let

$$T_{IPCW}^* = \frac{\Delta^\tau}{G(\tilde{T} \wedge \tau | X, A)} \tilde{T} \wedge \tau, \quad (26)$$

where we recall that $G(t|X, A) := P(C \geq t|X, A)$ is the left limit of the conditional survival function of the censoring. This estimator assigns higher weights to uncensored subjects within a covariate

group that is highly prone to censoring, thereby correcting for conditionally independent censoring and reducing selection bias (Howe et al. 2016).

Proposition 2.5. *Under Assumptions 1, 5, 6, 16 and 17, the IPCW transform 26 is a censoring unbiased transformation in the sense of Equation 22.*

The proof of Proposition 2.5 is in Section 7.2. The IPCW depends on the unknown conditional survival function of the censoring $G(\cdot|X, A)$, which thus needs to be estimated. Estimating conditional censoring or the conditional survival function can be approached similarly, as both involve estimating a time—whether for survival or censoring. Consequently, we can use semi-parametric methods, such as the Cox model, or non-parametric approaches like survival forests, and we refer to Section 2.2.1 for a development on these approaches. Once an estimator $\hat{G}(\cdot|A, X)$ of the later is provided, one can construct an estimator of the difference in RMST based on Equation 24 or Equation 25

$$\hat{\theta}_{\text{IPCW}} = \frac{1}{n} \sum_{i=1}^n \left(\frac{A_i}{\pi} - \frac{1-A_i}{1-\pi} \right) T_{\text{IPCW},i}^* \quad (27)$$

or

$$\hat{\theta}_{\text{IPCW}} = \frac{1}{n_1} \sum_{A_i=1} T_{\text{IPCW},i}^* - \frac{1}{n_0} \sum_{A_i=0} T_{\text{IPCW},i}^* \quad (28)$$

where we recall that $n_a := \#\{i \in [n] \mid A_i = a\}$. By Proposition 2.3, Proposition 2.4 and Proposition 2.5, we easily deduce that $\hat{\theta}_{\text{IPCW}}$ is asymptotically consistent as soon as \hat{G} is.

Corollary 2.1. *Under Assumptions 1, 5, 6, 16 and 17, if \hat{G} is uniformly weakly (resp. strongly) consistent then so is $\hat{\theta}_{\text{IPCW}}$, either as in defined in Equation 27 or in Equation 28.*

This result simply comes from the fact that $\hat{\theta}_{\text{IPCW}}$ depends continuously on \hat{G} and that G is lower-bounded (Assumption 17). Surprisingly, we found limited use of this estimator in the literature, beside its first introduction in Koul, Susarla, and Ryzin (1981). This could potentially be explained by the fact that, empirically, we observed that this estimator is highly variable. Consequently, we do not explore its properties further and will not include it in the numerical experiments. A related and more popular estimator is the IPCW-Kaplan-Meier, defined as follows.

Definition 2.2. (IPCW-Kaplan-Meier) We let again $\hat{G}(\cdot|X, A)$ be an estimator of the (left limit of) the conditional censoring survival function and we introduce

$$D_k^{\text{IPCW}}(a) := \sum_{i=1}^n \frac{\Delta_i^\tau}{\hat{G}(\tilde{T}_i \wedge \tau | X_i, A = a)} \mathbb{I}(\tilde{T}_i = t_k, A_i = a)$$

and $N_k^{\text{IPCW}}(a) := \sum_{i=1}^n \frac{\Delta_i^\tau}{\hat{G}(\tilde{T}_i \wedge \tau | X_i, A = a)} \mathbb{I}(\tilde{T}_i \geq t_k, A_i = a),$

be the weight-corrected numbers of deaths and of individual at risk at time t_k . The IPCW version of the KM estimator is then defined as:

$$\hat{S}_{\text{IPCW}}(t|A = a) = \prod_{t_k \leq t} \left(1 - \frac{D_k^{\text{IPCW}}(a)}{N_k^{\text{IPCW}}(a)} \right).$$

Note that the quantity π is not present in the definition of $D_k^{\text{IPCW}}(a)$ and $N_k^{\text{IPCW}}(a)$ because it would simply disappear in the ratio $D_k^{\text{IPCW}}(a)/N_k^{\text{IPCW}}(a)$. The subsequent RMST estimator then take the form

$$\hat{\theta}_{\text{IPCW-KM}} = \int_0^\tau \hat{S}_{\text{IPCW}}(t|A = 1) - \hat{S}_{\text{IPCW}}(t|A = 0) dt. \quad (29)$$

Like before for the classical KM estimator, this new reweighted KM estimator enjoys good statistical properties.

Proposition 2.6. *Under Assumptions 1, 5, 6, 16 and 17, and for all $t \in [0, \tau]$, the oracle estimator $S_{\text{PCW}}^*(t|A = a)$ defined as in Definition 2.2 with $\hat{G} = G$ is a strongly consistent and asymptotically normal estimator of $S^{(a)}(t)$.*

The proof of Proposition 2.6 can be found in Section 7.2. Because the evaluation of $N_k^{\text{PCW}}(a)$ now depends on information gathered after time t_k (through the computation of the weights), the previous proofs on the absence of bias and on the derivation of the asymptotic variance unfortunately do not carry over in this case. Whether its bias is exponentially small and whether the asymptotic variance can be derived in a closed form are questions left open. We are also not aware of any estimation schemes for the asymptotic variance in this context. In the case where we do not have access to the oracle survival function G , we can again still achieve consistency if the estimator $\hat{G}(\cdot|A, X)$ that we provide is consistent.

Corollary 2.2. *Under Assumptions 1, 5, 16 and 17, if \hat{G} is uniformly weakly (resp. strongly) consistent then so is $\hat{S}_{\text{PCW}}(t|A = a)$.*

This corollary ensures that the corresponding RMST estimator defined in Equation 29 will be consistent as well.

The Buckley-James transformation

One weakness of the IPCW transformation is that it discards all censored data. The Buckley-James (BJ) transformation, introduced by (Buckley and James (1979)), takes a different path by leaving all uncensored values untouched, while replacing the censored ones by an extrapolated value. Formally, it is defined as follows:

$$T_{\text{BJ}}^* = \Delta^\tau(\tilde{T} \wedge \tau) + (1 - \Delta^\tau)Q_S(\tilde{T} \wedge \tau|X, A), \quad (30)$$

where, for $t \leq \tau$,

$$Q_S(t|X, A) := \mathbb{E}[T \wedge \tau|X, A, T \wedge \tau > t] = \frac{1}{S(t|X, A)} \int_t^\tau S(u|X, A) du$$

where $S(t|X, A = a) := \mathbb{P}(T(a) > t|X)$ is the conditional survival function. We refer again to Figure 5 for a diagram of this transformation.

Proposition 2.7. *Under Assumptions 1, 5, 16 and 17, the BJ transform 30 is a censoring unbiased transformation in the sense of Equation 22.*

The proof of Proposition 2.7 can be found in Section 7.2. Again, the BJ transformation depends on a nuisance parameter (here $Q_S(\cdot|X, A)$) that needs to be estimated. We again refer to Section 2.2.1 for a brief overview of possible estimation strategies for Q_S . Once provided with an estimator $\hat{Q}_S(\cdot|A, X)$, a very natural estimator of the RMST based on the BJ transformation and on Equation 24 or Equation 25 would be

$$\hat{\theta}_{\text{BJ}} = \frac{1}{n} \sum_{i=1}^n \left(\frac{A_i}{\pi} - \frac{1 - A_i}{1 - \pi} \right) T_{\text{BJ},i}^*, \quad (31)$$

or

$$\hat{\theta}_{\text{BJ}} = \frac{1}{n_1} \sum_{A_i=1} T_{\text{BJ},i}^* - \frac{1}{n_0} \sum_{A_0=1} T_{\text{BJ},i}^*. \quad (32)$$

Like for the IPCW transformation, the BJ transformation yields a consistent estimate of the RMST as soon as the model is well-specified.

Corollary 2.3. *Under Assumptions 1, 5, 16 and 17, if \hat{Q}_S is uniformly weakly (resp. strongly) consistent then so is $\hat{\theta}_{BJ}$ defined as in Equation 31 or Equation 32.*

The proof is again a mere application of Propositions 2.3, 2.4 and 2.7, and relies on the continuity of $S \mapsto Q_S$. The BJ transformation is considered as the best censoring transformation of the original response in the following sense.

Theorem 2.1. *For any transformation T^* of the form 20, it holds*

$$\mathbb{E}[(T_{BJ}^* - T \wedge \tau)^2] \leq \mathbb{E}[(T^* - T \wedge \tau)^2].$$

This result is stated in Fan and Gijbels (1994) but without a proof. We detail it in Section 7.2 for completeness.

2.2.3 Augmented corrections

The main disadvantage of the two previous transformations is that they heavily rely on the specification of good estimator \hat{G} (for IPCW) or \hat{S} (for BJ). In order to circumvent this limitation, D. Rubin and Laan (2007) proposed the following transformations, whose expression is based on theory of semi-parametric estimation developed in Laan and Robins (2003),

$$T_{DR}^* = \frac{\Delta^{\tau} \tilde{T} \wedge \tau}{G(\tilde{T} \wedge \tau | X, A)} + \frac{(1 - \Delta^{\tau}) Q_S(\tilde{T} \wedge \tau | X, A)}{G(\tilde{T} \wedge \tau | X, A)} - \int_0^{\tilde{T} \wedge \tau} \frac{Q_S(t | X, A)}{G(t | X, A)^2} d\mathbb{P}_C(t | X, A), \quad (33)$$

where $d\mathbb{P}_C(t | X, A)$ is the distribution of C conditional on the covariates X and A . We stress that this distribution is entirely determined by the $G(\cdot | X, A)$, so that this transformation only depends on the knowledge of both conditional survival functions G and S , will be thus sometimes denoted $T_{DR}^*(G, S)$ to underline this dependency. This transformation is not only a censoring unbiased transform in the sense of Equation 22, but is also doubly robust in the following sense.

Proposition 2.8. *We let F, R be two conditional survival functions. Under Assumptions 1, 5, 6, 16 and 17, if F also satisfies Assumption 17, and if $F(\cdot | X, A)$ is absolutely continuous wrt $G(\cdot | X, A)$, then the transformation $T_{DR}^* = T_{DR}^*(F, R)$ is a censoring unbiased transformation in the sense of Equation 22 whenever $F = G$ or $R = S$.*

The statement and proof of this results is found in D. Rubin and Laan (2007) in the case where C and T are continuous. A careful examination of the proofs show that the proof translates straight away to our discrete setting.

3 Causal survival analysis in observational studies

Unlike RCT, observational data — such as from registries, electronic health records, or national healthcare systems — are collected without controlled randomized treatment allocation. In such cases, treated and control groups are likely unbalanced due to the non-randomized design, which results in the treatment effect being confounded by variables influencing both the survival outcome T and the treatment allocation A . To enable identifiability of the causal effect, additional standard assumptions are needed.

Assumption. (Conditional exchangeability / Unconfoundedness) It holds

$$A \perp\!\!\!\perp T(0), T(1) | X \quad (34)$$

Under Equation 34, the treatment assignment is randomly assigned conditionally on the covariates X . This assumption ensures that there are no unmeasured confounder as the latter would make it impossible to distinguish correlation from causality.

Assumption. (Positivity / Overlap for treatment) Letting $e(X) := \mathbb{P}(A = 1|X)$ be the *propensity score*, there holds

$$0 < e(X) < 1 \quad \text{almost surely.} \quad (35)$$

The Equation 35 assumption requires adequate overlap in covariate distributions between treatment groups, meaning every observation must have a non-zero probability of being treated. Because Assumption 5 does not hold anymore, neither does the previous idenfiability Equation 7. In this new context, we can write

$$\begin{aligned} \theta_{\text{RMST}} &= \mathbb{E}[T(1) \wedge \tau - T(0) \wedge \tau] \\ &= \mathbb{E}[\mathbb{E}[T(1) \wedge \tau|X] - \mathbb{E}[T(0) \wedge \tau|X]] \\ &= \mathbb{E}[\mathbb{E}[T(1) \wedge \tau|X, A = 1] - \mathbb{E}[T(0) \wedge \tau|X, A = 0]] \quad (\text{unconfoundness}) \\ &= \mathbb{E}[\mathbb{E}[T \wedge \tau|X, A = 1] - \mathbb{E}[T \wedge \tau|X, A = 0]]. \quad (\text{SUTVA}) \end{aligned} \quad (36)$$

In another direction, one could wish to identify the treatment effect through the survival curve as in Equation 2:

$$S^{(a)}(t) = \mathbb{P}(T(a) > t) = \mathbb{E}[\mathbb{P}(T > t|X, A = a)]. \quad (37)$$

Again, both identities still depend on the unknown quantity T and suggest two different estimation strategies. These strategies differ according to the censoring assumptions and are detailed below.

3.1 Independent censoring

Figure 6 illustrates a causal graph in observational survival data with independent censoring (Assumption 8).

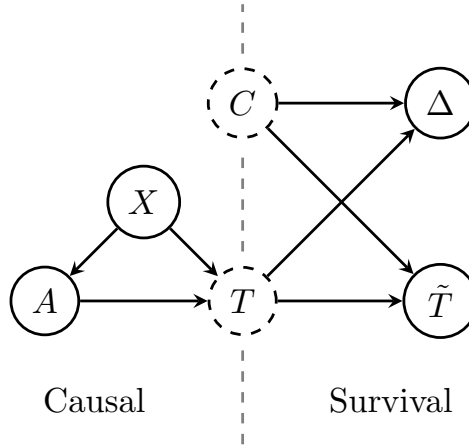


Figure 6: Causal graph in observational survival data with independent censoring.

Under Assumption 8, we saw in Section 2.1 that the Kaplan-Meier estimator could conveniently handle censoring. Building on Equation 37, we can write

$$S^{(1)}(t) = \mathbb{E} \left[\frac{\mathbb{E}[\mathbb{I}\{A = 1, T > t\}|X]}{\mathbb{E}[\mathbb{I}\{A = 1\}|X]} \right] = \mathbb{E} \left[\frac{A \mathbb{I}\{T > t\}}{e(X)} \right],$$

which suggests to adapt the classical KM estimator by reweighting it by the propensity score. The use of propensity score in causal inference has been initially introduced by Rosenbaum and Rubin (1983) and further developed in Hirano, Imbens, and Ridder (2003). It was extended to survival analysis by Xie and Liu (2005) through the adjusted Kaplan-Meier estimator as defined below.

Definition 3.1. (IPTW Kaplan-Meier estimator) We let $\hat{e}(\cdot)$ be an estimator of the propensity score $e(\cdot)$. We introduce

$$D_k^{\text{IPTW}}(a) := \sum_{i=1}^n \left(\frac{a}{\hat{e}(X_i)} + \frac{1-a}{1-\hat{e}(X_i)} \right) \mathbb{I}(\tilde{T}_i = t_k, \Delta_i = 1, A_i = a)$$

and $N_k^{\text{IPTW}}(a) := \sum_{i=1}^n \left(\frac{a}{\hat{e}(X_i)} + \frac{1-a}{1-\hat{e}(X_i)} \right) \mathbb{I}(\tilde{T}_i \geq t_k, A_i = a),$

be the numbers of deaths and of individual at risk at time t_k , reweighted by the propensity score. The Inverse-Probability-of-Treatment Weighting (IPTW) version of the KM estimator is then defined as:

$$\hat{S}_{\text{IPTW}}(t|A=a) = \prod_{t_k \leq t} \left(1 - \frac{D_k^{\text{IPTW}}(a)}{N_k^{\text{IPTW}}(a)} \right). \quad (38)$$

We let $S_{\text{IPTW}}^*(t|A=a)$ be the oracle KM-estimator defined as above with $\hat{e}(\cdot) = e(\cdot)$. Although the reweighting slightly changes the analysis, the good properties of the classical KM carry on to this setting.

Proposition 3.1. *Under Assumptions 1, 34, 35, 8 and 9 The oracle IPTW Kaplan-Meier estimator $S_{\text{IPTW}}^*(t|A=a)$ is a strongly consistent and asymptotically normal estimator of $S^{(a)}(t)$.*

The proof of this result simply relies again on the law of large number and the δ -method and can be found in Section 7.3. Because now S_{IPTW}^* is a continuous function of $e(\cdot)$, and because e and $1-e$ are lower-bounded as per Assumptions 35, we easily derive the following corollary.

Corollary 3.1. *Under the same assumptions as Proposition 3.1, if $\hat{e}(\cdot)$ satisfies $\|\hat{e} - e\|_\infty \rightarrow 0$ almost surely (resp. in probability), then the IPTW Kaplan-Meier estimator $\hat{S}_{\text{IPTW}}(t|A=a)$ is a strongly (resp. weakly) consistent estimator of $S^{(a)}(t)$.*

The resulting RMST estimator simply takes the form:

$$\hat{\theta}_{\text{IPTW-KM}} = \int_0^\tau \hat{S}_{\text{IPTW}}(t|A=1) - \hat{S}_{\text{IPTW}}(t|A=0) dt. \quad (39)$$

which will be consistent under the same Assumptions as the previous Corollary. Note that, we are not aware of any formal results concerning the bias and the asymptotic variance of the oracle estimator $S_{\text{IPTW}}^*(t|A=a)$, and we refer to Xie and Liu (2005) for heuristics concerning these questions.

3.2 Conditional independent censoring

Under Assumptions 34 (uncounfoundedness) and 16 (conditional independent censoring), the causal effect is affected both by confounding variables and by conditional censoring. The associated causal graph is depicted in Figure 7. In this setting, one can still use the G-formula exactly as in Section 2.2.1.

A natural alternative approach is to weight the IPCW and BJ transformations from Section 2.2.2 by the propensity score to disentangle both confounding effects and censoring at the same time.

We mention that the G-formula approach developed in Section 2.2.1 does work in that context. In particular, Chen and Tsiatis (2001) prove consistency and asymptotic normality results for Cox estimators in an observational study, and they give an explicit formulation of the asymptotic variance as a function of the parameters of the Cox model. In the non-parametric world, Foster, Taylor, and Ruberg (2011) and Künzel et al. (2019) empirically study this estimator using survival forests, with the former employing it as a T-learner (referred to as *Virtual Twins*) and the latter as an S-learner.

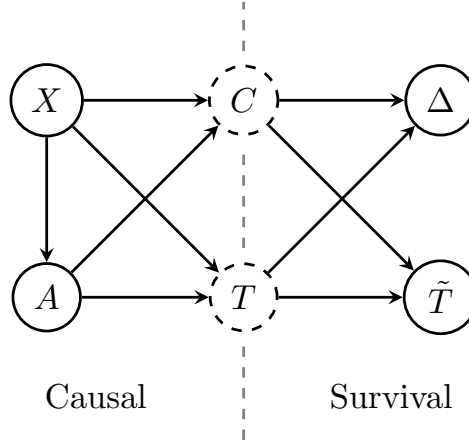


Figure 7: Causal graph in observational survival data with dependent censoring.

3.2.1 IPTW-IPCW transformations

One can check that the IPCW transformation as introduced in Equation 26 is also a censoring unbiased transformation in that context.

Proposition 3.2. *Under Assumptions 1, 34, 35, 16 and 17, the IPTW-IPCW transform 26 is a censoring unbiased transformation in the sense of Equation 22.*

The proof of Proposition 3.2 can be found in Section 7.4. Deriving an estimator of the difference in RMST is however slightly different in that context. In particular, Equation 23 rewrites

$$\mathbb{E}[\mathbb{E}[T^*|X, A = 1]] = \mathbb{E}\left[\frac{A}{e(X)}T^*\right],$$

Which in turn suggests to define

$$\hat{\theta}_{\text{IPTW-IPCW}} = \frac{1}{n} \sum_{i=1}^n \left(\frac{A}{e(X)} - \frac{1-A}{1-e(X)} \right) T_{\text{IPCW},i}^*. \quad (40)$$

This transformation now depends on two nuisance parameters, namely the conditional survival function of the censoring (through T_{IPCW}^*) and the propensity score. Once estimators of these quantities are provided, one could look at the corresponding quantity computed with these estimators.

Proposition 3.3. *Under Assumptions 1, 34, 35, 16 and 17, and if $\hat{G}(\cdot|X, A)$ and $\hat{e}(\cdot)$ are uniformly weakly (resp. strongly) consistent estimators, then estimator 40 defined with \hat{e} and \hat{G} is a weakly (resp. strongly) consistent estimator of the difference in RMST.*

The proof of Proposition 3.3 can be found in Section 7.4. We can also use the same strategy as for the IPCW transformation and incorporate the new weights into a Kaplan-Meier estimator.

Definition 3.2. (IPTW-IPCW-Kaplan-Meier) We let again $\hat{G}(\cdot|X, A)$ and $\hat{e}(\cdot)$ be estimators of the conditional censoring survival function and of the propensity score. We introduce

$$D_k^{\text{IPTW-IPCW}}(a) := \sum_{i=1}^n \left(\frac{A_i}{\hat{e}(X_i)} + \frac{1-A_i}{1-\hat{e}(X_i)} \right) \frac{\Delta_i^\tau}{\hat{G}(\tilde{T}_i \wedge \tau | X_i, A = a)} \mathbb{I}(\tilde{T}_i = t_k, A_i = a)$$

and

$$N_k^{\text{IPTW-IPCW}}(a) := \sum_{i=1}^n \left(\frac{A_i}{\hat{e}(X_i)} + \frac{1-A_i}{1-\hat{e}(X_i)} \right) \frac{\Delta_i^\tau}{\hat{G}(\tilde{T}_i \wedge \tau | X_i, A = a)} \mathbb{I}(\tilde{T}_i \geq t_k, A_i = a),$$

be the weight-corrected numbers of deaths and of individual at risk at time t_k . The IPTW-IPCW version of the KM estimator is then defined as:

$$\hat{S}_{\text{IPTW-IPCW}}(t|A=a) = \prod_{t_k \leq t} \left(1 - \frac{D_k^{\text{IPTW-IPCW}}(a)}{N_k^{\text{IPTW-IPCW}}(a)} \right).$$

The difference in RMST estimated with IPTW-IPCW-Kaplan-Meier survival curves is then simply as

$$\hat{\theta}_{\text{IPTW-IPCW-KM}} = \int_0^\tau \hat{S}_{\text{IPTW-IPCW}}(t|A=1) - \hat{S}_{\text{IPTW-IPCW}}(t|A=0) dt. \quad (41)$$

Proposition 3.4. *Under Assumptions 1, 34, 35, 16 and 17, and for all $t \in [0, \tau]$, if the oracle estimator $S_{\text{IPTW-IPCW}}^*(t|A=a)$ defined as in Definition 3.2 with $\hat{G}(\cdot|A, X) = G(\cdot|A, X)$ and $\hat{e} = e$ is a strongly consistent and asymptotically normal estimator of $S^{(a)}(t)$.*

The proof of Proposition 3.4 can be found in Section 7.4. Under consistency of the estimators of the nuisance parameters, the previous proposition implies that this reweighted Kaplan-Meier is a consistent estimator of the survival curve, which in turn implies consistency of $\hat{\theta}_{\text{IPTW-IPCW-KM}}$.

Corollary 3.2. *Under Assumptions 1, 34, 35, 16 and 17, and for all $t \in [0, \tau]$, if the nuisance estimators $\hat{G}(\cdot|A, X)$ and \hat{e} are weakly (resp. strongly) uniformly consistent, then $\hat{S}_{\text{IPTW-IPCW}}(t|A=a)$ is a weakly (resp. strongly) consistent estimator of $S^{(a)}(t)$.*

We are not aware of general formula for the asymptotic variances in this context. We mention nonetheless that Schaubel and Wei (2011) have been able to derive asymptotic laws in this framework in the particular case of Cox-models.

3.2.2 IPTW-BJ transformations

Like IPCW transformation, BJ transformation is again a censoring unbiased transformation in an observational context.

Proposition 3.5. *Under Assumptions 1, 34, 35, 16 and 17, the IPTW-BJ transform 30 is a censoring unbiased transformation in the sense of Equation 22.*

The proof of Proposition 3.5 can be found in Section 7.4. The corresponding estimator of the difference in RMST is

$$\hat{\theta}_{\text{IPTW-BJ}} = \frac{1}{n} \sum_{i=1}^n \left(\frac{A}{e(X)} - \frac{1-A}{1-e(X)} \right) T_{\text{BJ},i}^*. \quad (42)$$

This transformation depends on the conditional survival function S (through T_{BJ}^*) and the propensity score. Consistency of the nuisance parameter estimators implies again consistency of the RMST estimator.

Proposition 3.6. *Under Assumptions 1, 34, 35, 16 and 17, and if $\hat{S}(\cdot|X, A)$ and $\hat{e}(\cdot)$ are uniformly weakly (resp. strongly) consistent estimators, then $\hat{\theta}_{\text{IPTW-BJ}}$ defined with \hat{S} and \hat{e} is a weakly (resp. strongly) consistent estimator of the RMST.*

The proof of Proposition 3.6 can be found in Section 7.4.

3.2.3 Double augmented corrections

Building on the classical doubly-robust AIPTW estimator from causal inference (Robins, Rotnitzky, and Zhao 1994), we could incorporate the doubly-robust transformations of Section 2.2.3 to obtain a *quadruply robust* transformation

$$\Delta_{\text{QR}}^* = \Delta_{\text{QR}}^*(G, S, \mu, e) := \left(\frac{A}{e(X)} - \frac{1-A}{1-e(X)} \right) (T_{\text{DR}}^*(G, S) - \mu(X, A)) + \mu(X, 1) - \mu(X, 0),$$

where we recall that T_{DR}^* is defined in Section 2.2.3. This transformation depends on four nuisance parameters: G and S through T_{DR}^* , and now the propensity score e and the conditional response μ . This transformation doesn't really fall into the scope of censoring unbiased transform, but it is easy to show that Δ_{QR}^* is quadruply robust in the following sense.

Proposition 3.7. *Let F, R be two conditional survival function, p be a propensity score, and v be a conditional response. Then, under the same assumption on F, R as in Proposition 2.8, and under Assumptions 1, 34, 35, 16 and 17, the transformations $\Delta_{\text{QR}}^* = \Delta_{\text{QR}}^*(F, R, p, v)$ satisfies, for $a \in 0, 1$,*

$$\mathbb{E}[\Delta_{\text{QR}}^*|X] = \mathbb{E}[T(1) \wedge \tau - T(0) \wedge \tau|X] \quad \text{if} \quad \begin{cases} F = G & \text{or} & R = S & \text{and} \\ p = e & \text{or} & v = \mu. \end{cases}$$

This result is similar to Ozenne et al. (2020), Thm 1, and its proof can be found in Section 7.4. Based on estimators $(\hat{G}, \hat{S}, \hat{\mu}, \hat{e})$ of (G, S, μ, e) , one can then propose the following estimator of the RMST, coined the AIPTW-AIPCW estimator in Ozenne et al. (2020):

$$\begin{aligned} \hat{\theta}_{\text{AIPTW-AIPCW}} &:= \frac{1}{n} \sum_{i=1}^n \Delta_{\text{QR},i}^*(\hat{G}, \hat{S}, \hat{\mu}, \hat{e}) \\ &= \frac{1}{n} \sum_{i=1}^n \left(\frac{A_i}{\hat{e}(X_i)} - \frac{1-A_i}{1-\hat{e}(X_i)} \right) (T_{\text{DR}}^*(\hat{G}, \hat{S})_i - \hat{\mu}(X_i, A_i)) + \hat{\mu}(X_i, 1) - \hat{\mu}(X_i, 0). \end{aligned} \tag{43}$$

This estimator enjoys good asymptotic properties under parametric models, as detailed in Ozenne et al. (2020).

4 Implementation

In this section, we first summarize the various estimators and their properties. We then provide custom implementations for all estimators, even those already available in existing packages. These manual implementations serve two purposes: first, to make the methods accessible to the community when no existing implementation is available; and second, to facilitate a deeper understanding of the methods by detailing each step, even when a package solution exists. Finally, we present the packages available for directly computing θ_{RMST} .

4.1 Summary of the estimators

Table 3 provides an overview of the estimators introduced in this paper, along with the corresponding nuisance parameters needed for their estimation and an overview of their statistical properties in particular regarding their sensitivity to misspecification of the nuisance parameters.

Table 3: Estimators of the difference in RMST and nuisance parameters needed to compute each estimator. Empty boxes indicate that the nuisance parameter is not needed in the estimator thus misspecification has no impact. Estimators in italic are those that are already implemented in available packages.

Estimator	RCT	Obs	Ind Cens	Dep Cens	Outcome model	Censor- ing model	Treat- ment model	Robust- ness
<i>Unadjusted KM</i>	X		X					
IPCW-KM	X		X	X		G		
BJ	X		X	X	S			
<i>IPTW-KM</i>	X	X	X				e	
IPCW-IPTW-KM	X	X	X	X		G	e	
IPTW-BJ	X	X	X	X	S		e	
<i>G-formula</i>	X	X	X	X	μ			
AIPTW-AIPCW	X	X	X	X	S, μ	G	e	X (Prp 3.7)

4.2 Implementation of the estimators

Across different implementations, we use the following shared functions provided in the `utility.R` file.

- `estimate_propensity_score`: function to estimate propensity scores $e(X)$ using either parametric (i.e. logistic regression with the argument `type_of_model = "glm"`) or non-parametric methods (i.e. probability forest with the argument `type_of_model = "probability forest"` based on the `probability_forest` function from the [grf](#) (Tibshirani et al. 2017) package). This latter can include cross-fitting (`n.folds 1`).
- `estimate_survival_function`: function to estimate the conditional survival model, which supports either Cox models (argument `type_of_model = "cox"`) or survival forests (argument `type_of_model = "survival forest"`) which uses the function `survival_forest` from the [grf](#) (Tibshirani et al. 2017) package. This latter can include cross-fitting (`n.folds 1`). The estimation can be done with a single learner (argument `learner = "S-learner"`) or two learners (argument `learner = "T-learner"`).
- `estimate_hazard_function`: function to estimate the instantaneous hazard function by deriving the cumulative hazard function at each time point. This cumulative hazard function is estimated from the negative logarithm of the survival function.
- `Q_t_hat`: function to estimate the remaining survival function at all time points and for all individuals which uses the former `estimate_survival_function`.
- `Q_Y`: function to select the value of the remaining survival function from `Q_t_hat` at the specific time-to-event.
- `integral_rectangles`: function to estimate the integral of a decreasing step function using the rectangle method.
- `expected_survival`: function to estimate the integral with x, y coordinate (estimated survival function) using the trapezoidal method.
- `integrate`: function to estimate the integral at specific time points `Y.grid` of a given integrand function which takes initially its values on times using the trapezoidal method.

Unadjusted Kaplan-Meier

Although Kaplan-Meier is implemented in the survival package (Therneau 2001), we provide a custom implementation, `Kaplan_meier_handmade`, for completeness. The difference in Restricted Mean Survival Time, estimated using Kaplan-Meier as in Equation 14 can then be calculated with the `RMST_1` function.

```
source("utility.R")
# Kaplan-Meier estimator handmade implementation
# The database 'data' must be in the same form as that shown in
# notation (Table 1) and with the same variable names (status, T_obs)
Kaplan_meier_handmade <- function(data,
                                   status = data$status,
                                   T_obs = data$T_obs) {

  # Sort unique observed times
  Y.grid <- sort(unique(T_obs))

  # Initialize vectors for number of events, number at risk, and survival
  # probability
  d <- rep(NA, length(Y.grid)) # Number of events at time Y.grid[i]
  n <- rep(NA, length(Y.grid)) # Number at risk just before time Y.grid[i]
  S <- rep(NA, length(Y.grid)) # Survival probability at time Y.grid[i]

  # Loop over each unique observed time
  for (i in 1:length(Y.grid)) {
    d[i] <- sum(T_obs == Y.grid[i] & status == 1, na.rm = TRUE) # Count events
    n[i] <- sum(T_obs >= Y.grid[i]) # Count at risk

    # Calculate survival probability
    S[i] <- cumprod(1 - d / n)[i]
  }

  # Create a dataframe with the results
  df <- data.frame(d = d, n = n, S = S, T = Y.grid)

  return(df)
}

# Function to calculate RMST (Restricted Mean Survival Time):
# Two possibilities for computing RMST:
# - in using directly S_A1 and S_A0 (survival function of treated and control)
# - in using the dataframe and the function computes the survival functions
RMST_1 <- function(data = NULL, A1 = 1, A0 = 0, tau, S_A1 = NULL, S_A0 = NULL) {
  if (is.null(S_A1) & is.null(S_A0)) {
    # Subset data for treatment groups
    data1 <- data[data$A == A1,]
    data0 <- data[data$A == A0,]

    # Calculate Kaplan-Meier survival estimates
    S_A1 <- Kaplan_meier_handmade(data1, status = data1$status,
```

```

      T_obs = data1$T_obs)
S_A0 <- Kaplan_meier_handmade(data0, status = data0$status,
      T_obs = data0$T_obs)

# Restrict observations to those less than or equal to tau
Y.grid1 <- data1$T_obs[data1$T_obs <= tau]
Y.grid0 <- data0$T_obs[data0$T_obs <= tau]
} else {
  # Restrict observations to those less than or equal to tau
  Y.grid1 <- S_A1$T[S_A1$T <= tau]
  Y.grid0 <- S_A0$T[S_A0$T <= tau]
}

# Filter survival estimates to restricted observations
S_A1 <- S_A1 %>%
  dplyr::filter(T %in% Y.grid1)
S_A0 <- S_A0 %>%
  dplyr::filter(T %in% Y.grid0)

# Check if there is any event at tau for S_A1
if (!any(S_A1$T == tau)) {
  new_row <- tibble(T = tau, S = S_A1$S[nrow(S_A1)])
  S_A1 <- dplyr::bind_rows(S_A1, new_row)
}

# Check if there is any event at tau for S_A0
if (!any(S_A0$T == tau)) {
  new_row <- tibble(T = tau, S = S_A0$S[nrow(S_A0)])
  S_A0 <- dplyr::bind_rows(S_A0, new_row)
}

# Calculate integrals from 0 to tau of survival probabilities
intA1 <- integral_rectangles(S_A1$T, S_A1$S)
intA0 <- integral_rectangles(S_A0$T, S_A0$S)
RMST1 <- intA1 - intA0

return(list(RMST=RMST1, intA1=intA1,intA0=intA0))
}

```

As an alternative, one can also use the `survfit` function in the `survival` package (Therneau 2001) for Kaplan-Meier and specify the `rmean` argument equal to τ in the corresponding summary function:

```

# Alternative code to estimate Kaplan-Meier estimator with survival package
# instead of handmade KM
RMST_alternative <- function(data, A1 = 1, A0 = 0, tau){
  # Estimate Kaplan-Meier estimator with survfit function on data subset
  # Groupe A = 0
  fit0 <- survfit(Surv(T_obs, status) ~ 1, data = data[data$A == A0,])
  # Groupe A = 1
  fit1 <- survfit(Surv(T_obs, status) ~ 1, data = data[data$A == A1,])

```



```

# Estimate the RMST with rmean
summary_fit0 <- summary(fit0, rmean = tau) # RMST for A = 0
summary_fit1 <- summary(fit1, rmean = tau) # RMST for A = 1

# Extract the RMST from the summary objects
rmst0 <- summary_fit0$table["rmean"][[1]]
rmst1 <- summary_fit1$table["rmean"][[1]]

# Compute the difference of RMST between the two groups
difference_rmst <- rmst1 - rmst0
return(difference_rmst)
}

```

IPCW Kaplan-Meier

We first provide an `adjusted.KM` function which is then used in the `IPCW_Kaplan_meier` function to estimate the difference in RMST $\hat{\theta}_{\text{IPCW}}$ as in Equation 29. The survival censoring function $G(t|X)$ is computed with the `estimate_survival_function` utility function from the `utility.R` file.

```

# Kaplan-Meier adjusted
# Times of event
# Failures: 1 if event, 0 if censored
# Variable: 1 if treated, 0 if control
# Weights: Weight of the individual
adjusted.KM <- function(times, failures, variable, weights = NULL) {
  # Sanity checks
  if (sum(times < 0) > 0) {
    stop("Error: times must be positive")
  }
  if (!is.null(weights) && sum(weights < 0, na.rm = TRUE) > 0) {
    stop("Error: weights must be superior to 0")
  }
  if (sum(failures != 0 & failures != 1) > 0) {
    stop("Error: failures must be a vector of 0 or 1")
  }
  # If 'weights' is NULL, initialize 'w' with ones of the same length as 'times',
  # otherwise use 'weights'
  w <- if (is.null(weights)) rep(1, length(times)) else weights

  # Create a DataFrame 'data' with columns t (times), f (failures),
  # v (stratification variable: often treatment variable), and w (weights)
  data <- data.frame(t = times, f = failures, v = variable, w = w)

  # Remove rows from the DataFrame where the stratification variable is NA
  data <- data[!is.na(data$v),]

  # Initialize an empty DataFrame to store the Kaplan-Meier results
  table_KM <- data.frame(times = NULL, n.risk = NULL, n.event = NULL,
    survival = NULL, variable = NULL)

  # Loop over each unique value of the stratification variable

```

```

for (i in unique(variable)) {
  # Subset the data for the current stratification variable value
  d <- data[data$v == i,]

  # Create a sorted vector of unique event times, including time 0 and the
  # maximum time
  tj <- c(0, sort(unique(d$t[d$f == 1])), max(d$t))

  # Calculate the number of events at each time point
  dj <- sapply(tj, function(x) {
    sum(d$w[d$t == x & d$f == 1])
  })

  # Calculate the number of individuals at risk at each time point
  nj <- sapply(tj, function(x) {
    sum(d$w[d$t >= x])
  })

  # Compute the cumulative product for the survival probabilities
  st <- cumprod((nj - dj) / nj)

  # Append the results to the Kaplan-Meier table
  table_KM <- rbind(table_KM, data.frame(T = tj, n = nj, d = dj,
                                          S = st, variable = i))
}
return(table_KM)
}

# IPCW Kaplan-Meier estimator with restricted tau
IPCW_Kaplan_meier <- function(data, tau,
                              X.names.censoring,
                              nuisance_censoring = "cox",
                              n.folds = NULL) {

  # Compute of truncated T_obs, status and censored status
  data$T_obs_tau <- ifelse(data$T_obs >= tau, tau, data$T_obs)
  data$censor.status_tau <- 1 - as.numeric((data$T_obs >= tau) |
                                          (data$T_obs < tau & data$status == 1))
  data$status_tau <- as.numeric((data$T_obs >= tau) |
                               (data$T_obs < tau & data$status == 1))
  Y.grid <- sort(unique(data$T_obs_tau))

  # Estimate probability of remaining uncensored based on nuisance model
  S_C_hat <- estimate_survival_function(data = data, X.names = X.names.censoring,
                                       Y.grid = Y.grid, T_obs = "T_obs_tau",
                                       status = "censor.status_tau",
                                       type_of_model = nuisance_censoring,
                                       n.folds = n.folds)

```

```

# Select the probability of censoring for each observed T_obs_tau from the
# curve
data$S_C <- S_C_hat$S_hat[cbind(1:nrow(data), match(data$T_obs_tau, Y.grid))]

# Compute IPC weights
data$weights <- data$status_tau / data$S_C

# Compute the adjusted IPCW Kaplan-Meier
S <- adjusted.KM(times = data$T_obs, failures = data$status,
                 variable = data$A, weights = data$weights)

# Compute difference of RMST between the two groups
RMST <- RMST_1(S_A1 = S[S$variable == 1,], S_A0 = S[S$variable == 0,], tau = tau)

return(list(RMST = RMST$RMST,
           intA1 = RMST$intA1,
           intA0 = RMST$intA0,
           weights = data$weights))
}

```

One could also use the `survfit` function in the `survival` package (Therneau 2001) in adding IPCW weights for treated and control group and specify the `rmean` argument equal to τ in the corresponding summary function:

```

# Alternative code to estimate IPCW Kaplan-Meier, IPTW Kaplan-Meier or
# IPTW-IPCW Kaplan-Meier estimator with survival package instead of using
# handmade adjusted.KM function (the weights need to be calculated before).

# Weights0 corresponds to weights of the control and weights1 of treated
Adjusted_Kaplan_meier_alternative <- function(data, A1 = 1, A0 = 0, tau,
                                             weights0, weights1){
  # Estimate Kaplan-Meier estimator with survfit function on data subset
  # Groupe A = 0
  fit0 <- survfit(Surv(T_obs, status) ~ 1, data = data[data$A == A0,], weights = weights0)
  # Groupe A = 1
  fit1 <- survfit(Surv(T_obs, status) ~ 1, data = data[data$A == A1,], weights = weights1)

  # Estimate the RMST with rmean
  summary_fit0 <- summary(fit0, rmean = tau) # RMST for A = 0
  summary_fit1 <- summary(fit1, rmean = tau) # RMST for A = 1

  # Extract the RMST from the summary objects
  rmst0 <- summary_fit0$table["rmean"][[1]]
  rmst1 <- summary_fit1$table["rmean"][[1]]

  # Compute the difference in RMST between the two groups
  difference_rmst <- rmst1 - rmst0
  return(difference_rmst)
}

```

This alternative approach for IPCW Kaplan-Meier would also be valid for IPTW and IPTW-IPCW

Kaplan-Meier.

Buckley-James based estimator

The function BJ estimates θ_{RMST} by implementing the Buckley-James estimator as in Equation 31. It uses two functions available in the utility.R file, namely Q_t_hat and Q_Y.

```
# Compute the Restricted Mean Survival Time (RMST) difference
BJ <- function(data, tau, X.names.outcome = c("X1", "X2", "X3", "X4"),
               nuisance = "cox", n.folds = NULL) {
  # Truncate observed times at tau
  data$T_obs_tau <- ifelse(data$T_obs >= tau, tau, data$T_obs)
  Y.grid <- sort(unique(data$T_obs_tau))

  # Censoring status at tau
  data$status_tau <- as.numeric((data$T_obs >= tau) |
                                (data$T_obs < tau & data$status == 1))

  # Compute Q_t for all time points
  Q_t <- Q_t_hat(data, tau, X.names.outcome, nuisance, n.folds)
  data$Q_y <- Q_Y(data, tau, Q_t)

  # Split data by treatment group
  data_treated <- data %>% dplyr::filter(A == 1)
  data_not_treated <- data %>% dplyr::filter(A == 0)

  # Calculate Restricted Survival Time (RST) for each group
  data_treated$RST <- data_treated$status_tau * data_treated$T_obs_tau +
    (1 - data_treated$status_tau) * data_treated$Q_y

  data_not_treated$RST <- data_not_treated$status_tau * data_not_treated$T_obs_tau +
    (1 - data_not_treated$status_tau) * data_not_treated$Q_y

  # Calculate RMST difference between treated and not treated
  RMST <- mean(data_treated$RST) - mean(data_not_treated$RST)

  # Return RMST and other relevant metrics
  return(list(
    RMST = RMST,
    ATE_treated = mean(data_treated$RST),
    ATE_not_treated = mean(data_not_treated$RST)
  ))
}
```

IPTW Kaplan-Meier

The function IPTW_Kaplan_meier implements the IPTW-KM estimator in Equation 39. It uses the estimate_propensity_score function from the utility.R.

```
# Function to calculate IPTW Kaplan-Meier
IPTW_Kaplan_meier <- function(data, tau, X.names.propensity,
                              nuisance_propensity = "glm", n.folds = NULL) {
  # Estimate propensity scores
```

```

data$e_hat <- estimate_propensity_score(
  data,
  treatment_covariates = X.names.propensity,
  type_of_model = nuisance_propensity,
  n.folds = n.folds)

# Truncate observed times at tau
data$T_obs_tau <- pmin(data$T_obs, tau)

# Define censoring status at tau
data$status_tau <- as.numeric((data$T_obs >= tau) |
  (data$T_obs < tau & data$status == 1))

# Calculate weights
data$weights <- (data$A) * (1 / data$e_hat) + (1 - data$A) / (1 - data$e_hat)

# Adjusted Kaplan-Meier estimator
S <- adjusted.KM(
  times = data$T_obs,
  failures = data$status,
  variable = data$A,
  weights = data$weights)

# Calculate RMST from the adjusted survival curves
RMST <- RMST_1(S_A1 = S[S$variable == 1,],
  S_A0 = S[S$variable == 0,],
  tau = tau)

return(list("intA0" = RMST$intA0, "intA1" = RMST$intA1, "RMST" = RMST$RMST))
}

```

G-formula

We implement two versions of the G-formula: `g_formula_T_learner` and `g_formula_S_learner`. In `g_formula_T_learner`, separate models estimate survival curves for treated and control groups, whereas `g_formula_S_learner` uses a single model incorporating both covariates and treatment status to estimate survival time. The latter approach is also available in the RISCA package but is limited to Cox models.

```

# Function to estimate the g-formula Two-learner.
g_formula_T_learner <- function(data,
  X.names.outcome,
  tau,
  nuisance_survival = "cox",
  n.folds = NULL) {
  # Compute min(T_obs,tau)
  data$T_obs_tau <- ifelse(data$T_obs >= tau, tau, data$T_obs)

  # Y.grid is the grid of time points where we want to estimate the
  # survival function.
  Y.grid <- sort(unique(data$T_obs_tau))

```

```

S_hat <- estimate_survival_function(data, X.names.outcome,
                                   Y.grid,
                                   type_of_model = nuisance_survival,
                                   T_obs = "T_obs",
                                   status = "status",
                                   n.folds = n.folds)

# Compute the area under each survival curve up to max(Y.grid) = tau.
E_hat1 <- expected_survival(S_hat$S_hat1, Y.grid)
E_hat0 <- expected_survival(S_hat$S_hat0, Y.grid)

# Calculate the mean difference.
theta_g_formula <- mean(E_hat1 - E_hat0)

return(theta_g_formula)
}

# Function to estimate the g-formula Single-learner.
g_formula_S_learner <- function(data,
                                X.names.outcome,
                                tau,
                                nuisance_survival = "cox",
                                n.folds = NULL) {
  # Compute min(T_obs, tau)
  data$T_obs_tau <- ifelse(data$T_obs >= tau, tau, data$T_obs)

  # Y.grid is the grid of time points where we want to estimate the
  # survival function.
  Y.grid <- sort(unique(data$T_obs_tau))

  S_hat <- estimate_survival_function(data, X.names.outcome,
                                      Y.grid,
                                      type_of_model = nuisance_survival,
                                      learner = "S-learner",
                                      T_obs = "T_obs",
                                      status = "status",
                                      n.folds = n.folds)

  # Compute the area under each survival curve until max(Y.grid) = tau.
  E_hat1 <- expected_survival(S_hat$S_hat1, Y.grid)
  E_hat0 <- expected_survival(S_hat$S_hat0, Y.grid)

  # Calculate the mean difference.
  theta_g_formula <- mean(E_hat1 - E_hat0)

  return(theta_g_formula)
}

```

IPTW-IPCW Kaplan-Meier

The `IPTW_IPCW_Kaplan_meier` function implements the IPTW-IPCW Kaplan Meier estimator from Equation 41. It uses the utility functions from the `utility.R` file `estimate_propensity_score` and `estimate_survival_function` to estimate the nuisance parameters, and the function `adjusted.KM` which computes an adjusted Kaplan Meier estimator using the appropriate weight.

```
IPTW_IPCW_Kaplan_meier <- function(data,
                                   X.names.propensity,
                                   X.names.censoring,
                                   tau,
                                   nuisance_propensity = "glm",
                                   nuisance_censoring = "cox",
                                   n.folds = NULL) {
  # Censoring time to tau if observed time exceeds tau
  data$T_obs_tau <- ifelse(data$T_obs >= tau, tau, data$T_obs)

  # Create censoring status for tau
  data$censor.status_tau <- 1 - as.numeric((data$T_obs >= tau) |
                                           (data$T_obs < tau & data$status == 1))

  # Create status at tau
  data$status_tau <- as.numeric((data$T_obs >= tau) |
                                (data$T_obs < tau & data$status == 1))

  # Grid of unique observed times truncated at tau
  Y.grid <- sort(unique(data$T_obs_tau))

  # Estimate propensity scores
  data$e_hat <- estimate_propensity_score(data,
                                         treatment_covariates = X.names.propensity,
                                         type_of_model = nuisance_propensity,
                                         n.folds = n.folds)

  # Estimate survival function for censoring
  S_C_hat <- estimate_survival_function(data, X.names = X.names.censoring,
                                       Y.grid = Y.grid, T_obs = "T_obs_tau",
                                       status = "censor.status_tau",
                                       type_of_model = nuisance_censoring,
                                       n.folds = n.folds)

  # Get estimated survival probabilities for censoring
  data$S_C <- S_C_hat$S_hat[cbind(1:nrow(data), match(data$T_obs_tau, Y.grid))]

  # Calculate weights
  data$weights <- data$status_tau / data$S_C *
    (data$A * (1 / data$e_hat) +
     (1 - data$A) * (1 / (1 - data$e_hat)))

  # Compute adjusted Kaplan-Meier estimator
  S <- adjusted.KM(times = data$T_obs,
                  failures = data$status,
```

```

        variable = data$A,
        weights = data$weights)

# Compute Restricted Mean Survival Time (RMST)
RMST <- RMST_1(S_A1 = S[S$variable == 1, ],
              S_A0 = S[S$variable == 0, ],
              tau = tau)

# Return RMST and ATE for treated and not treated groups
return(list(RMST = RMST$RMST, ATE_treated = RMST$intA1,
           ATE_not_treated = RMST$intA0))
}

```

IPTW-BJ estimator

The IPTW_BJ implements the IPTW-BJ estimator in Equation 42. It uses the utility functions, from the utility.R file, `estimate_propensity_score`, `Q_t_hat` and `Q_Y` to estimate the nuisance parameters.

```

IPTW_BJ <- function(data,
                    X.names.propensity,
                    X.names.outcome,
                    tau,
                    nuisance_propensity = "glm",
                    nuisance = "cox",
                    n.folds = NULL) {
  # Minimum of T_obs and tau
  data$T_obs_tau <- ifelse(data$T_obs >= tau, tau, data$T_obs)

  # Grid of unique observed times truncated at tau
  Y.grid <- sort(unique(data$T_obs_tau))

  # Indicator for min(T, tau) < C
  data$status_tau <- as.numeric((data$T_obs >= tau) |
                                (data$T_obs < tau & data$status == 1))

  # Estimate propensity scores
  data$e_hat <- estimate_propensity_score(data,
                                         treatment_covariates = X.names.propensity,
                                         type_of_model = nuisance_propensity,
                                         n.folds = n.folds)

  # Estimation of Q_s
  Q_t <- Q_t_hat(data, tau, X.names.outcome, nuisance, n.folds)
  data$Q_y <- Q_Y(data, tau, Q_t)

  # BJ transformation
  data$Y <- data$status_tau * data$T_obs_tau +
            (1 - data$status_tau) * data$Q_y
}

```



```

# IPTW on BJ transformation
data$RST <- data$Y * (data$A/data$e_hat-(1-data$A)/(1-data$e_hat))

RMST <- mean(data$RST)

# Return RMST
return(RMST)
}

```

AIPTW-AIPCW

The AIPTW_AIPCW function implements the AIPTW_AIPCW estimator in Equation 43 using the utility function from the utility.R file estimate_propensity_score, Q_t_hat, Q_Y, and estimate_survival_function to estimate the nuisance parameters.

```

# DR censoring transformation
AIPCW <-function(data,
                 tau,
                 X.names.censoring = c("X1","X2","X3","X4"),
                 X.names.outcome = c("X1","X2","X3","X4"),
                 nuisance_Qt = "cox",
                 nuisance_censoring = "cox",
                 n.folds = NULL,
                 h_C_hat = NULL,
                 method_aipw = 1) {

# Truncate observed times at tau
data$T_obs_tau <- pmin(data$T_obs, tau)

# Define status at tau
data$status_tau <- as.numeric((data$T_obs > tau) |
                             (data$T_obs <= tau & data$status == 1 ))

data$censor.status_tau <- 1- as.numeric(
  (data$T_obs > tau) | (data$T_obs <= tau & data$status == 1 ))

Y.grid <- sort(unique(data$T_obs_tau))

# Estimate survival function for censoring
S_C_hat <- estimate_survival_function(data = data,X.names.censoring,
                                     type_of_model = nuisance_censoring,
                                     n.folds = n.folds,
                                     Y.grid = Y.grid,
                                     T_obs = "T_obs_tau",
                                     status = "censor.status_tau")

Y.index <- findInterval(data$T_obs_tau, Y.grid)

data$S_C_hat_T_obs_tau <- S_C_hat$S_hat[cbind(seq_along(Y.index), Y.index)]

```

```

if (is.null(h_C_hat)) {
  h_C_hat <- estimate_hazard_function(S_C_hat$S_hat,Y.grid)
}

# Compute Q.t.hat
Q.t.hat <- Q_t_hat(data = data,
                   X.names = X.names.outcome,
                   tau = tau,
                   nuisance = nuisance_Qt,
                   n.folds = n.folds)

# Compute Q.Y.hat
data$Q.Y.hat <- Q_Y(data = data, tau, Q.t.hat)

# Compute first term
data$first_term <- (data$T_obs_tau * data$status_tau) /
  data$S_C_hat_T_obs_tau

# Compute second term
data$second_term <- (data$Q.Y.hat * (1 - data$status_tau)) /
  data$S_C_hat_T_obs_tau

Y.diff <- diff(c(0, Y.grid))

# Compute integrand for the third term
integrand <- sweep( ( h_C_hat) / S_C_hat$S_hat ) * (Q.t.hat), 2, Y.diff, "*")

# Compute third term
data$third_term <- integrate(integrand, Y.grid, data$T_obs_tau)

# Compute pseudo outcome
pseudo_outcome <- data$first_term + data$second_term - data$third_term

return(pseudo_outcome)
}

AIPTW_AIPCW <- function(data,
                        tau,
                        X.names.propensity = c("X1", "X2", "X3", "X4"),
                        X.names.censoring = c("X1", "X2", "X3", "X4"),
                        X.names.outcome = c("X1", "X2", "X3", "X4"),
                        nuisance_propensity = "glm",
                        nuisance_regression = "cox",
                        nuisance_censoring = "cox",
                        nuisance_Qt = "cox",
                        n.folds = NULL) {

# Estimate propensity scores

```

```

data$e_hat <- estimate_propensity_score(
  data = data,
  treatment_covariates = X.names.propensity,
  type_of_model = nuisance_propensity,
  n.folds = n.folds
)

# Prepare data for censoring model
data$T_obs_tau <- ifelse(data$T_obs >= tau, tau, data$T_obs)

data$censor.status_tau <- 1 - as.numeric((data$T_obs >= tau) |
                                         (data$T_obs < tau & data$status == 1))

data$status_tau <- as.numeric((data$T_obs >= tau) |
                              (data$T_obs < tau & data$status == 1))

# Create unique time grid
Y.grid <- sort(unique(data$T_obs_tau))

S_hat <- estimate_survival_function(data, X.names.outcome,
                                   type_of_model = nuisance_regression,
                                   Y.grid = Y.grid,
                                   T_obs = "T_obs",
                                   status = "status",
                                   n.folds = n.folds)

# Compute area under the survival curve up to tau
data$E_hat1 <- expected_survival(S_hat$S_hat1, Y.grid)
data$E_hat0 <- expected_survival(S_hat$S_hat0, Y.grid)

# Compute IPW-weighted residuals
data$IPW_res <- data$E_hat1 * (1 - data$A / data$e_hat) -
  data$E_hat0 * (1 - (1 - data$A) / (1 - data$e_hat))

# Compute AIPCW weights
TDR <- AIPCW(
  data = data,
  tau = tau,
  X.names.censoring = X.names.censoring,
  X.names.outcome = X.names.outcome,
  nuisance_Qt = nuisance_Qt,
  nuisance_censoring = nuisance_censoring,
  n.folds = n.folds
)

data$TDR <- TDR

# Compute AIPCW-weighted residuals
data$AIPCW_w <- data$TDR * (data$A / data$e_hat -
                           (1 - data$A) / (1 - data$e_hat))

```

```

# Compute regression residuals
data$reg <- data$E_hat1 - data$E_hat0
data$reg_res <- data$A / data$e_hat * (data$TDR - data$E_hat1) -
  (1 - data$A) / (1 - data$e_hat) * (data$TDR - data$E_hat0)

# Compute estimators
# na.rm = TRUE to remove NA for the mean calculation
AIPTW_AIPCW_IPW_res <- mean(data$AIPCW_w + data$IPW_res, na.rm = TRUE)
AIPTW_AIPCW_reg_res <- mean(data$reg + data$reg_res, na.rm = TRUE)

return(list(AIPTW_AIPCW_reg_res = AIPTW_AIPCW_reg_res,
            AIPTW_AIPCW_IPW_res = AIPTW_AIPCW_IPW_res))
}

```

4.3 Available packages

Currently, there are few sustained implementations available for estimating RMST in the presence of right censoring. Notable exceptions include the packages [survRM2](#) (Hajime et al. 2015), [grf](#) (Tibshirani et al. 2017) and [RISCA](#) (Foucher, Le Borgne, and Chatton 2019). Those packages are implemented in the `utility.R` files.

SurvRM2

The difference in RMST with Unadjusted Kaplan-Meier $\hat{\theta}_{KM}$ (Equation 14) can be obtained using the function `rmst2` which takes as arguments the observed time-to-event, the status, the arm which corresponds to the treatment and τ .

RISCA

The RISCA package provides several methods for estimating θ_{RMST} . The difference in RMST with Unadjusted Kaplan-Meier $\hat{\theta}_{KM}$ (Equation 14) can be derived using the `survfit` function from the `survival` package (Therneau 2001) which estimates Kaplan-Meier survival curves for treated and control groups, and then the `rmst` function calculates the RMST by integrating these curves, applying the rectangle method (`type="s"`), which is well-suited for step functions.

The IPTW Kaplan-Meier (Equation 38) can be applied using the `ipw.survival` and `rmst` functions. The `ipw.survival` function requires user-specified weights (i.e. propensity scores). To streamline this process, we define the `RISCA_ipw` function, which combines these steps and utilizes the `estimate_propensity_score` from the `utility.R` file.

A single-learner version of the G-formula, as introduced in Section 2.2.1, can be implemented using the `gc.survival` function. This function requires as input the conditional survival function which should be estimated beforehand with a Cox model via the `coxph` function from the `survival` package (Therneau 2001). Specifically, the single-learner approach applies a single Cox model incorporating both covariates and treatment, rather than separate models for each treatment arm. We provide a function `RISCA_gf` that consolidates these steps.

grf

The `grf` package (Tibshirani et al. 2017) enables estimation of the difference between RMST using the Causal Survival Forest approach (Cui et al. 2023), which extends the non-parametric causal forest framework to survival data. The RMST can be estimated with the `causal_survival_forest` function, requiring covariates X , observed event times, event status, treatment assignment, and the

time horizon τ as inputs. The `average_treatment_effect` function then evaluates the treatment effect based on predictions from the fitted forest.

5 Simulations

We compare the behaviors and performances of the estimators through simulations conducted across various experimental contexts. These contexts include scenarios based on RCTs and observational data, with both independent and dependent censoring. We also use semi-parametric and non-parametric models to generate censoring and survival times, as well as logistic and nonlinear models to simulate treatment assignment.

5.1 RCT

Data Generating Process

We generate RCTs with independent censoring (Scenario 1) and conditionally independent censoring (Scenario 2). We sample n iid datapoints $(X_i, A_i, C, T_i(0), T_i(1))_{i \in [n]}$ where $T_i(0), T_i(1)$ and C follows Cox's models. More specifically, we set

- $X \sim \mathcal{N}(\mu, \Sigma)$ where $\mu = (1, 1, -1, 1)$ and $\Sigma = \text{Id}_4$.
- The hazard function of $T(0)$ is

$$\lambda^{(0)}(t|X) = 0.01 \exp\{\beta_0^\top X\} \quad \text{where} \quad \beta_0 = (0.5, 0.5, -0.5, 0.5).$$

- The survival times in the treatment group are given by $T(1) = T(0) + 10$.
- The hazard function of the censoring time C is simply taken as $\lambda_C(t|X) = 0.03$ in Scenario 1, and in Scenario 2 as

$$\lambda_C(t|X) = 0.03 \cdot \exp\{\beta_C^\top X\} \quad \text{where} \quad \beta_C = (0.7, 0.7, -0.25, -0.1).$$

- The treatment allocation is independent of X : $e(X) = 0.5$.
- The threshold time τ is set to 25.

```
##### RCT
# RCT1: Random treatment assignment + independent censoring
# RCT2: Random treatment assignment + dependent censoring (conditional on X
# and A)
simulate_data_RCT <- function(n, mu = c(1, 1, -1, 1),
                              sigma = diag(4),
                              colnames_cov = c("X1", "X2", "X3", "X4"),
                              tau,
                              coefT0 = 0.01,
                              parsS = c(0.5, 0.5, -0.5, 0.5),
                              coefC = 0.03,
                              parsC = c(0.7, 0.3, -0.25, -0.1),
                              parsC_A = c(-0.2),
                              scenario = "RCT2",
                              mis_specification="none") {

  # Generate X from a multivariate normal distribution
```

```

X <- MASS::mvrnorm(n, mu, sigma)
X <- as.data.frame(X)
colnames(X) <- colnames_cov

# Treatment variable selection: all X
X_treatment <- as.matrix(X)

# Propensity score: constant for random assignment
e <- rep(0.5, n)

# Random treatment assignment
A <- sapply(e, FUN = function(p) rbinom(1, 1, p))

# Outcome variable selection: all X
X_outcome <- as.matrix(X)

# Simulate the outcome using the cumulative hazard inversion method
epsilon <- runif(n, min = 1e-8, max = 1)
T0 <- -log(epsilon) / (coefT0 * exp(X_outcome %*% parsS))

if (scenario == "RCT1") {
  # Simulate independent censoring time
  epsilon <- runif(n, min = 1e-8, max = 1)
  C <- -log(epsilon) / coefC
}
else if (scenario == "RCT2") {
  # Simulate dependent censoring time
  X_censoring <- as.matrix(cbind(X,A))
  parsC <- c(parsC,parsC_A)

  epsilon <- runif(n, min = 1e-8, max = 1)
  C <- -log(epsilon) / (coefC * exp(rowSums(X_censoring %*% diag(parsC))))
}
# T(1) = T(0) + 10
T1 <- T0 + 10

# True survival time
T_true <- A * T1 + (1 - A) * T0

# Observed time
T_obs <- pmin(T_true, C)

# Status indicator
status <- as.numeric(T_true <= C)
censor.status <- as.numeric(T_true > C)

# Restricted survival time
T_obs_tau <- pmin(T_obs, tau)
status_tau <- as.numeric((T_obs > tau) | (T_obs <= tau & status == 1))

```

```

# Combine all data into a single data frame
data_target_population <- data.frame(X, tau, A, T0, T1, C, T_obs, T_obs_tau,
                                     status, censor.status, status_tau, e)

return(data_target_population)
}

```

The descriptive statistics of the two datasets are displayed in Annex (Section 8.1). The graph of the difference in RMST as a function of τ for the two scenarios are displayed below; θ_{RMST} is the same in both settings.

```

# Function to calculate ground truth for RCT and Observational data
ground_truth <- function(tau,
                        data) {
  # Compute RMST with the true T1
  data$T1_tau <- ifelse(data$T1 >= tau, tau, data$T1)

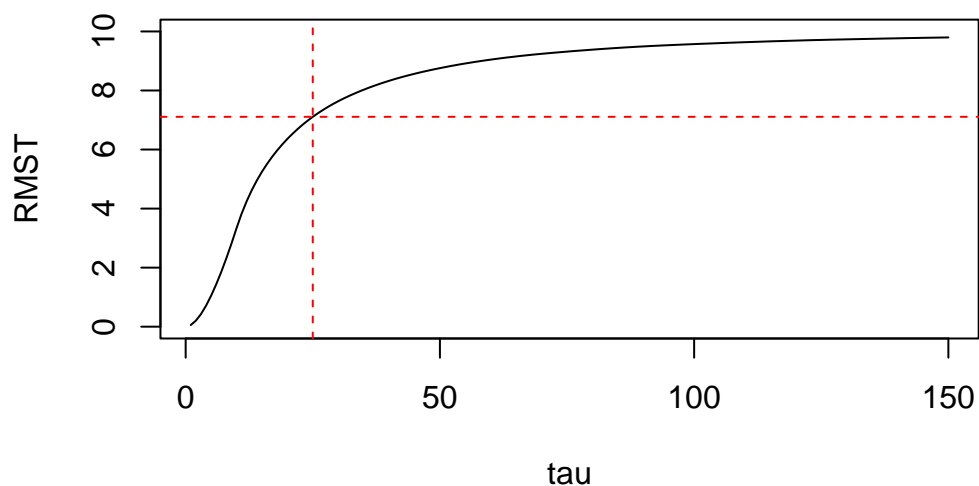
  # Compute RMST with the true T0
  data$T0_tau <- ifelse(data$T0 >= tau, tau, data$T0)

  # Compute the difference in RMST if everyone had the treatment
  # and if everyone had the control
  truth <- mean(data$T1_tau) - mean(data$T0_tau)

  return(truth)
}

```

True difference in RMST for RCT scenario 1



```
[1] "The ground truth for RCT scenario 1 and 2 at time 25 is 7.1"
```

Estimation of the RMST

For each Scenario, we estimate the difference in RMST using the methods summarized in Section 4.1. The methods used to estimate the nuisance components are indicated in brackets: either logistic

regression or random forests for propensity scores and either cox models or survival random forests for survival and censoring models. A naive estimator where censored observations are simply removed and the survival time is averaged for treated and controls is also provided for a naive baseline.

Figure 8 shows the distribution of the difference in RMST for 100 simulations in Scenario 1 and different sample sizes: 500, 1000, 2000, 4000. The true value of θ_{RMST} is indicated by red dotted line.

```
# Update the theme to center the plot title
theme_update(plot.title = element_text(hjust = 0.5))

# Define the desired order of the estimators

desired_order <- c(
  "Naive",
  "KM",
  "SurvRM2 - KM",
  "IPTW KM (Log. Reg.)",
  "RISCA - IPTW KM (Log. Reg.)",
  "IPCW KM (Cox)",
  "BJ (Cox)",
  "IPTW-BJ (Cox & Log. Reg.)",
  "IPTW-IPCW KM (Cox & Log. Reg.)",
  "G-formula (Cox/ T-learners)",
  "G-formula (Cox/ S-learner)",
  "RISCA - G_formula (S-learner)",
  "AIPTW-AIPCW (Cox & Cox & Log. Reg.)",
  "grf - Causal Survival Forest",
  "IPTW KM (Forest)",
  "RISCA - IPTW KM (Forest)",
  "IPCW KM (Forest)",
  "BJ (Forest)",
  "IPTW-BJ (Forest)",
  "IPTW-IPCW KM (Forest)",
  "G-formula (Forest/ T-learners)",
  "G-formula (Forest/ S-learner)",
  "AIPTW-AIPCW (Forest)")

# Convert sample size to a factor with levels sorted in decreasing order
simulation_rct1$sample.size <- factor(
  simulation_rct1$sample.size,
  levels = sort(unique(simulation_rct1$sample.size), decreasing = FALSE)
)

# Convert estimator column to a factor with the specified order
simulation_rct1$estimator <- factor(simulation_rct1$estimator,
  levels = desired_order)

# Create the plot for RCT + independent censoring
simulation_graph_rct1 <- simulation_rct1 %>%
  ggplot(aes(
```



```

    x = estimator, y = estimate,
    fill = factor(sample.size, levels = rev(levels(sample.size)))
  )) +
  scale_fill_brewer(palette = "Accent") +
  geom_boxplot(alpha = 0.9, show.legend = TRUE, position = "dodge") +
  xlab("") + # Change x-axis label
  ylab("ATE") + # Change y-axis label
  stat_boxplot(geom = "errorbar") +
  geom_hline(
    yintercept = truth_tau1, linetype = "dashed", color = "red",
    alpha = 0.8, size = 0.8
  ) +
  theme(
    legend.title = element_blank(), legend.position = "bottom",
    legend.box = "vertical", legend.text = element_text(size = 18),
    axis.text.x = element_text(angle = 35, vjust = 1, hjust = 1),
    # Adjust text angle for better visibility
    axis.text = element_text(size = 15, face = "bold"),
    axis.title.x = element_text(size = 16, face = "bold"),
    plot.margin = margin(t = 10, r = 10, b = 50, l = 10) # Add margin
  ) +
  coord_cartesian(ylim = c(0, 15))

```

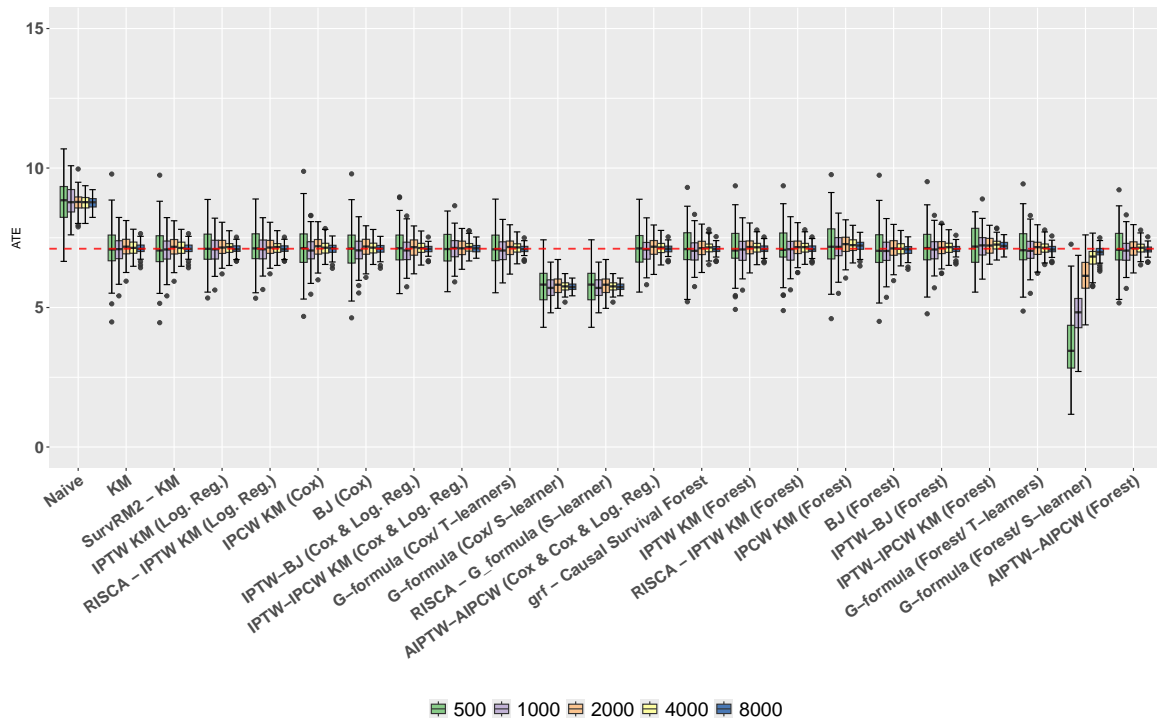


Figure 8: Results of the ATE for the simulation of a RCT with independent censoring.

In this setting, and in accordance with the theory, the simplest estimator (unadjusted KM) performs just as well as the others, and presents an extremely small bias (as derived in Section 2.1).

The naive estimator is biased, as expected, and the bias in both the G-formula (RISCA) and the

manual G-formula S-learner arises because the treatment effect is additive $T(1) = T(0) + 10$ and violates the assumption that T would follow a Cox model in the variables (X, A) . However, $T|A = a$ is a Cox-model for $a \in \{0, 1\}$, which explain the remarkable performance of G-formula (Cox/T-learners) and some of the other models based on a Cox estimation of S .

Other estimators (IPTW KM (Reg.Log), IPCW KM (Cox), IPTW-IPCW KM (Cox & Log.Reg), IPTW-BJ (Cox & Log.Reg), AIPTW-AIPCW (Cox & Cox & Log.Reg)) involve unnecessary nuisance parameter estimates, such as propensity scores or censoring models. Despite this, their performance remains relatively stable in terms of variability, and there are roughly no differences between using (semi-)parametric or non-parametric estimation methods for nuisance parameters except for IPCW KM and IPTW-IPCW KM where there is a slight bias when using forest-based methods.

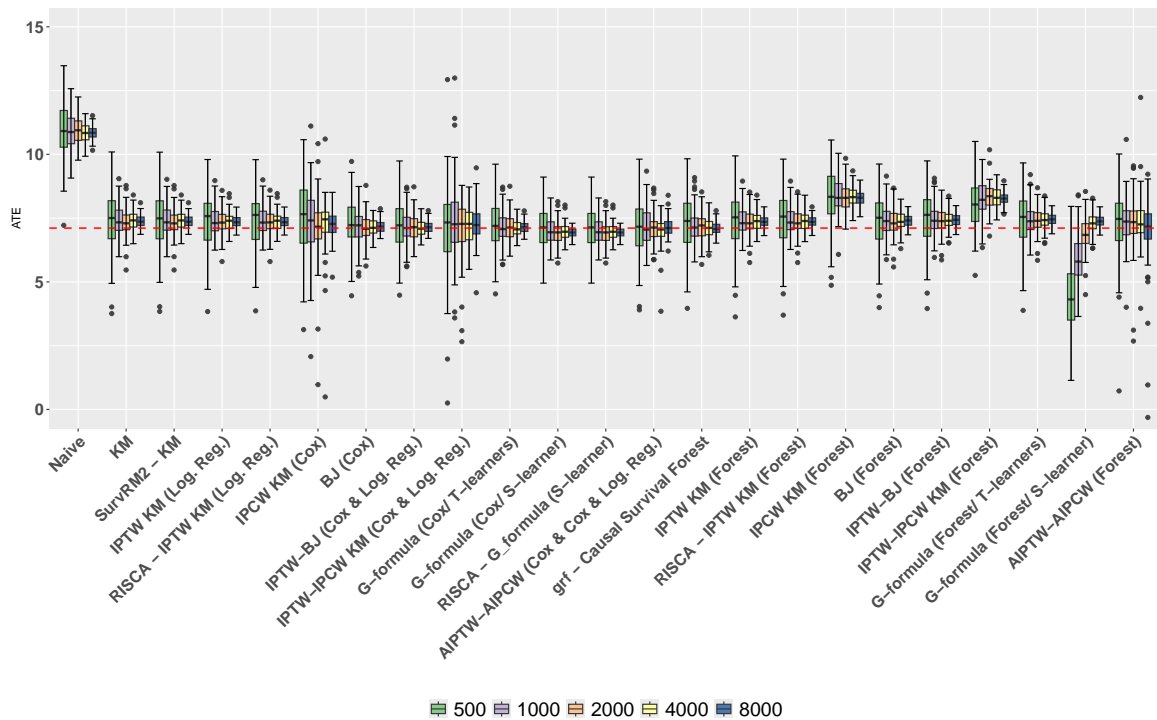


Figure 9: Estimation results of the ATE for the simulation of a RCT with dependent censoring.

Figure 9 shows the results for the RCT simulation with conditionally independent censoring (Scenario 2). In this setting, the Naive estimator remains biased. Similarly, both the unadjusted Kaplan-Meier (KM) and its SurvRM2 equivalent, as well as the treatment-adjusted IPTW KM and its RISCA equivalent, are biased due to their failure to account for dependent censoring. As in Scenario 1, G-formula (Cox/ S-learner) and its RISCA equivalent also remain biased. The IPCW KM (Cox) is slightly biased up to 4,000 observations and quite variable due to extreme censoring probabilities. IPTW-IPCW KM (Cox & Log.Reg.) is not biased but shows high variance. In contrast, the Buckley-James estimator BJ (Cox) is unbiased even with as few as 500 observations. The BJ estimator also demonstrates smaller variance than IPCW methods. G-formula (Cox/ T-learners) and AIPCW-AIPTW (Cox & Cox & Log.Reg.) estimators seem to perform well, even in small samples. The forest versions of these estimators seem more biased, except Causal Survival Forest and the AIPTW-AIPCW (Forest). Notably, all estimators exhibit higher variability compared to Scenario 1.

5.2 Observational data

Data Generating Process

As for Scenarii 1 and 2, we carry out two simulations of an observational study with both independent and conditional independent censoring. The only difference lies in the simulation of the propensity score, which is no longer constant. For the simulation, an iid n -sample $(X_i, A_i, C, T_i(0), T_i(1))_{i \in [n]}$ is generated as in Section 5.1, except for the treatment allocation process that is given by:

$$\text{logit}(e(X)) = \beta_A^\top X \quad \text{where} \quad \beta_A = (-1, -1, -2.5, -1),$$

where we recall that $\text{logit}(p) = \log(p/(1-p))$. The descriptive statistics for the two observational data with independent (Obs1) and conditionally independent censoring (Obs2) are displayed in Appendix (Section 8.2). Note that we did not modify the survival distribution, the target difference in RMST is thus the same.

```
# Obs1: Treatment assignment dependent on X + independent censoring
# Obs2: Treatment assignment dependent on X + dependent censoring (conditional
# on X)

# Function to simulate observational data for two scenarios: Obs1 and Obs2
simulate_data_obs <- function(n,
                              mu = c(1, 1, -1, 1),
                              sigma = diag(4),
                              colnames_cov = c("X1", "X2", "X3", "X4"),
                              tau,
                              coefT0 = 0.01,
                              parsS = c(0.5, 0.5, -0.5, 0.5),
                              parsA = c(-1, -1, -2.5, -1),
                              parsC_A = c(0),
                              coefC = 0.03,
                              parsC = c(0.7, 0.3, -0.25, -0.1),
                              scenario = "Obs2") {

  # Generate covariates X from a multivariate normal distribution
  X <- mvrnorm(n, mu, sigma)
  X <- as.data.frame(X)
  colnames(X) <- colnames_cov

  # Propensity score model based on X
  e <- rowSums(as.matrix(X) %*% diag(parsA))
  e <- plogis(e) # Transform to probability scale

  # Treatment assignment based on the propensity score
  A <- sapply(e, FUN = function(p) rbinom(n = 1, size = 1, prob = p))

  # Outcome model based on X
  X_outcome <- as.matrix(X)
  epsilon <- runif(n, min = 0.00000001, max = 1)
  T0 <- -log(epsilon) / (coefT0 * exp(X_outcome %*% parsS))
```

```

# Define treatment effect (shift in survival time due to treatment)
T1 <- T0 + 10

if (scenario == "Obs1") {
  # Scenario 1: Independent censoring
  C <- -log(runif(n, min = 0.00000001, max = 1)) / coefC

} else if (scenario == "Obs2") {
  # Scenario 2: Dependent censoring based on X
  X_censoring <- as.matrix(cbind(X,A))
  parsC <- c(parsC,parsC_A)

  C <- -log(runif(n, min = 0.00000001, max = 1)) /
    (coefC * exp(rowSums(X_censoring %*% diag(parsC))))

} else {
  stop("Invalid scenario. Choose 'Obs1' or 'Obs2'.")
}

# Determine the true survival time based on treatment
T_true <- A * T1 + (1 - A) * T0

# Observed time is the minimum of the true survival time and censoring time
T_obs <- pmin(T_true, C)

# Status indicator: 1 if the event (death) occurred, 0 if censored
status <- as.numeric(T_true <= C)

# Restricted survival time (censored at tau)
T_obs_tau <- pmin(T_obs, tau)
status_tau <- as.numeric((T_obs > tau) | (T_obs <= tau & status == 1))

# Compile the simulated data into a data frame
DATA_target_population <- data.frame(X, tau, A, T0, T1, C, T_obs, T_obs_tau,
                                     status, status_tau, e)

return(DATA_target_population)
}

[1] "The ground truth for Obs scenario 1 at time 25 is 7.1"
[1] "The ground truth for Obs scenario 2 at #time 25 is 7.1"

```

Estimation of the RMST

Figure 10 below shows the distribution of the estimators of θ_{RMST} for the observational study with independent censoring.

In the simulation of an observational study with independent censoring, confounding bias is introduced, setting it apart from RCT simulations. As expected, estimators that fail to adjust for this bias, such as unadjusted Kaplan-Meier (KM), IPCW KM (Cox), and their equivalents, are biased. However, estimators like IPTW KM (Log.Reg.), IPTW-IPCW KM (Cox & Log. Reg.) are unbiased,

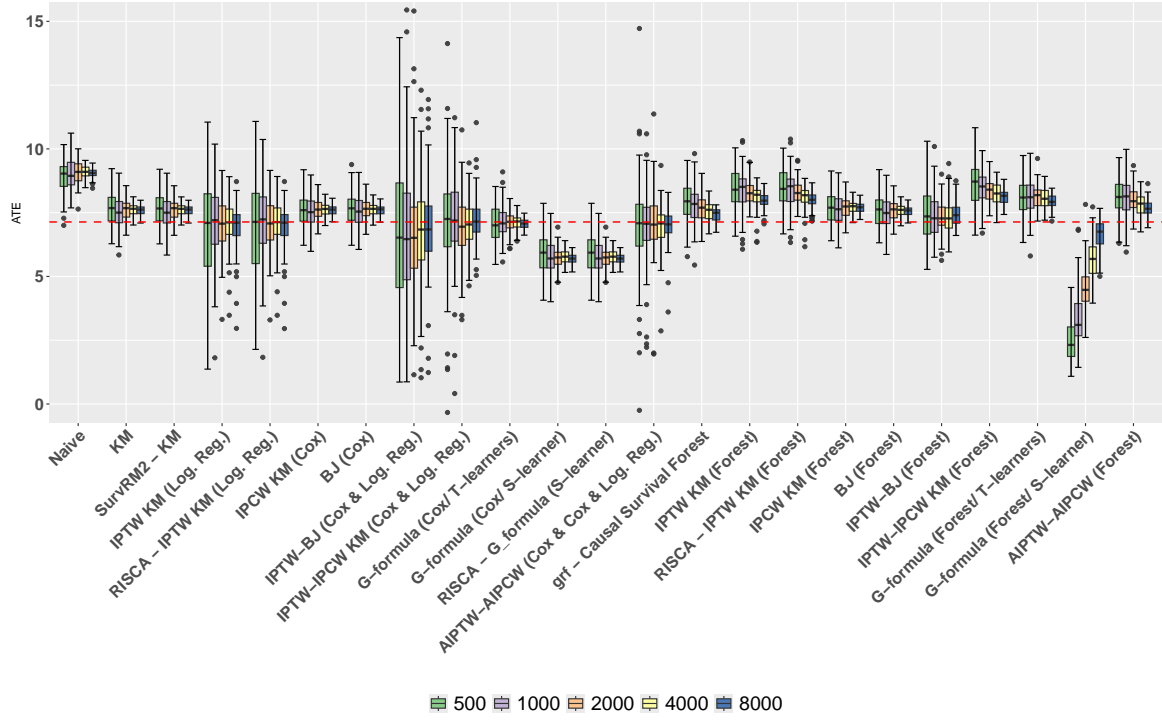


Figure 10: Estimation results of the ATE for the simulation of an observational study with independent censoring.

even if the latter estimate unnecessary nuisance components. Results with IPTW BJ (Cox & Log.Reg) are extremely variable.

The top-performing estimators in this scenario are G-formula (Cox/ T-learners) and AIPCW-AIPTW (Cox & Cox & Log.Reg.), which are unbiased even with 500 observations. The former has the lowest variance. All estimators that use forests to estimate nuisance parameters are biased across sample sizes from 500 to 8000. Although Causal Survival Forest and AIPW-AIPCW (Forest) are expected to eventually converge, they remain extremely demanding in terms of sample size. This setting thus highlights that one should either have an a priori knowledge on the specification of the models or large sample size.

Figure 11 below shows the distribution of the θ_{RMST} estimates for the observational study with conditionally independent censoring. The red dashed line represents the true θ_{RMST} for $\tau = 25$.

In the simulation of an observational study with conditionally independent censoring, estimators that do not account for both censoring and confounding bias, such as KM, IPCW KM, IPTW KM, and their package equivalents, are biased. The top-performing estimators in this scenario are G-formula (Cox/ T-learners) and AIPCW-AIPTW (Cox & Cox & Log.Reg.), which are unbiased even with 500 observations. The former has the lowest variance as expected, see Section 2.2.1. Surprisingly, the G-formula (Cox/S-learner) and its equivalent from the RISCA package perform quite competitively, showing only a slight bias despite the violation of the proportional hazards assumption. All estimators that use forests to estimate nuisance parameters are biased across sample sizes from 500 to 8000. Although Causal Survival Forest and AIPW-AIPCW (Forest) are expected to eventually converge, they remain extremely demanding in terms of sample size.

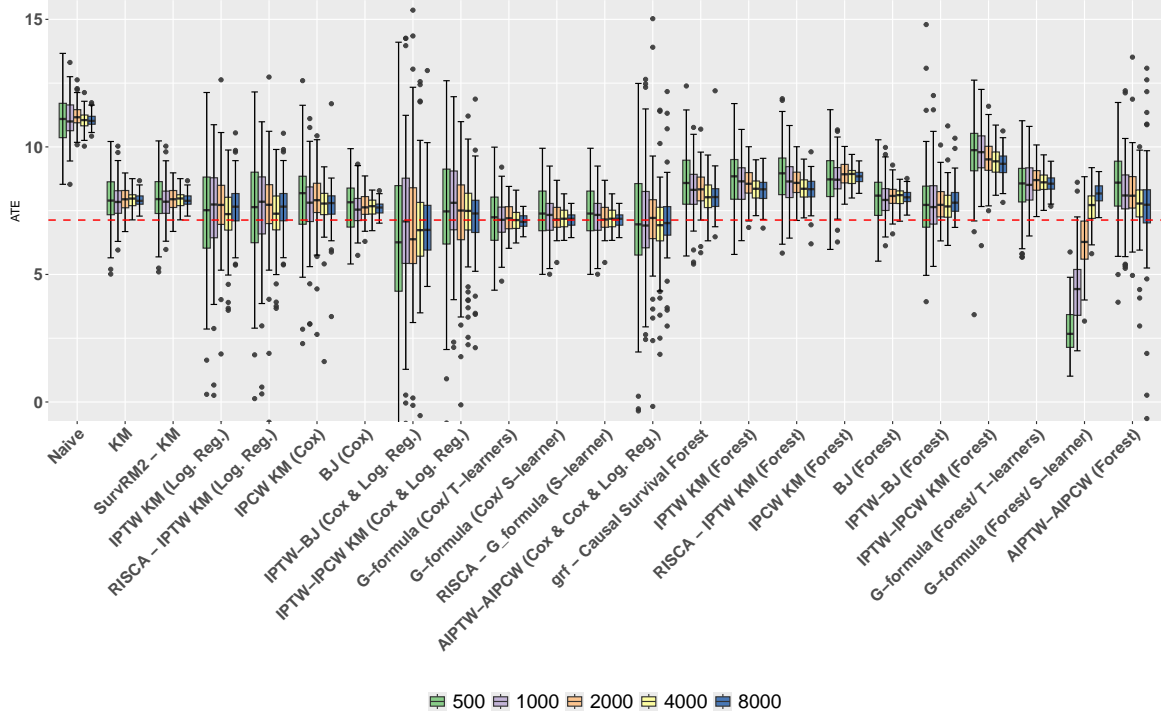


Figure 11: Estimation results of the ATE for the simulation of an observational study with dependent censoring.

5.3 Misspecification of nuisance components

Data Generating Process

We generate an observational study with covariate interactions and conditionally independent censoring. The objective is to assess the impact of misspecifying nuisance components; specifically, we will use models that omit interactions to estimate these components. This approach enables us to evaluate the robustness properties of various estimators. In addition, in this setting forest based methods are expected to behave better.

We generate n samples $(X_i, A_i, C, T_i(0), T_i(1))$ as follows:

- $X \sim \mathcal{N}(\mu, \Sigma)$ and $\mu = (0.5, 0.5, 0.7, 0.5)$, $\Sigma = \text{Id}_4$.
- The hazard function of $T(0)$ is given by

$$\lambda^{(0)}(t|X) = \exp\{\beta_0^\top Y\} \quad \text{where} \quad \beta_0 = (0.2, 0.3, 0.1, 0.1, 1, 0, 0, 0, 0, 1),$$

$$\text{and} \quad Y = (X_1^2, X_2^2, X_3^2, X_4^2, X_1 X_2, X_1 X_3, X_1 X_4, X_2 X_3, X_2 X_4, X_3 X_4).$$

- The distribution of $T(1)$ is the one of $T(0)$ but shifted: $T(1) = T(0) + 1$.
- The hazard function of C is given by

$$\lambda_C(t|X) = \exp\{\beta_C^\top Y\} \quad \text{where} \quad \beta_C = (0.05, 0.05, -0.1, 0.1, 0, 1, 0, -1, 0, 0).$$

- The propensity score is

$$\text{logit}(e(x)) = \beta_A^\top Y \quad \text{where} \quad \beta_A = (0.05, -0.1, 0.5, -0.1, 1, 0, 1, 0, 0, 0).$$

When the model is well-specified, the full vector (X, Y) is given as an input of the nuisance parameter models. When it is not, only X and the first half of Y corresponding to $(X_1^2, X_2^2, X_3^2, X_4^2)$ is given as an input.

```
# DGP for misspecification
simulate_data_mis <- function(n,
                               mu = c(0.5, 0.5, 0.7, 0.5),
                               sigma = matrix(c(1, 0, 0, 0,
                                                  0, 1, 0, 0,
                                                  0, 0, 1, 0,
                                                  0, 0, 0, 1),
                                              nrow = 4, byrow = TRUE),
                               colnames_cov = c("X1", "X2", "X3", "X4"),
                               parsA = c(0.05, -0.1, 0.5, -0.1),
                               tau){

  # Generate X from a multivariate normal distribution
  X <- MASS::mvrnorm(n, mu, sigma)
  X <- as.data.frame(X)
  colnames(X) <- colnames_cov

  # Treatment variable selection: all X
  X_treatment <- as.matrix(X)

  # Propensity score model based on X
  e <- parsA[1]*X_treatment[, "X1"]^2 + parsA[2]*X_treatment[, "X2"]^2 +
    parsA[3]*X_treatment[, "X3"]^2 + parsA[4]*X_treatment[, "X4"]^2 -
    X_treatment[, "X1"]*X_treatment[, "X2"] +
    X_treatment[, "X1"]*X_treatment[, "X4"]

  # Logistic regression
  e <- plogis(e)

  # Treatment assignment based on the propensity score
  A <- sapply(e, FUN = function(p) rbinom(n = 1, size = 1, prob = p))

  # Outcome variable selection: all X
  X_outcome <- as.matrix(X)

  lambda <- exp(0.2*X[,1]^2 + 0.3*X[,2]^2 + 0.1*X[,3]^2 + 0.1*X[,4]^2 +
               X[,1] * X[,2] + X[,3] * X[,4])
  # Simulate the outcome using the cumulative hazard inversion method
  epsilon <- runif(n, min = 1e-8, max = 1)
  T0 <- -log(epsilon) / lambda

  # Simulate independent censoring time
  censoring_lambda <- exp(0.05*X[,1]^2 + 0.05*X[,2]^2 - 0.1*X[,3]^2 + 0.1*X[,4]^2 +
                        X[,3] * X[,1] - X[,2]*X[,4])
  epsilon <- runif(n, min = 1e-8, max = 1)
  C <- -log(epsilon) / censoring_lambda
```

```

# T(1) = T(0) + 1
T1 <- T0 + 1

# True survival time
T_true <- A * T1 + (1 - A) * T0

# Observed time
T_obs <- pmin(T_true, C)

# Status indicator
status <- as.numeric(T_true <= C)
censor.status <- as.numeric(T_true > C)

# Restricted survival time
T_obs_tau <- pmin(T_obs, tau)
status_tau <- as.numeric((T_obs > tau) | (T_obs <= tau & status == 1))
# Compile the simulated data into a data frame
DATA_target_population <- data.frame(X, tau, A, T0, T1, C, T_obs, T_obs_tau,
                                     status, status_tau, censor.status, e)

return(DATA_target_population)
}

```

The descriptive statistics are given in Appendix (Section 8.3).

```
[1] "The ground truth for mis scenario at time 0.45 is 0.26"
```

Estimation of the RMST

First, we estimate θ_{RMST} without any model misspecification to confirm the consistency of the estimators under correctly specified nuisance models. More specifically, it means that for parametric propensity score models, semi-parametric censoring and survival models, we use models including interactions and squared assuming knowledge on the data generating process.

Next, we introduce misspecification individually for the treatment model, censoring model, and outcome model (Figure 13), i.e., we use models without interaction to estimate parametric and semi-parametric nuisance components while the data are generated with interactions.

We further examine combined misspecifications for pairs of models: treatment and censoring, treatment and outcome, and outcome and censoring. Finally, we assess the impact of misspecifying all nuisance models simultaneously (Figure 14).

When there is no misspecification in Figure 12, as expected, IPTW-BJ (Cox & Log.Reg), G-formula (Cox/ T-learners) and AIPTW-AIPCW (Cox & Cox & Reg.Log) are unbiased. IPTW-IPCW KM (Cox & Log.Reg) exhibits a bias but seems to converge at larger sample size. Regarding forest-based methods, IPTW-BJ (Forest), AIPTW-AIPCW (Forest) and Causal Survival Forest estimate accurately the difference in RMST. Surprisingly, G-formula (Forest/ T-learners), G-formula (Forest/ S-learner) and IPTW-IPCW KM (Forest) exhibit small bias but are expected to eventually converge at large sample size.

Figure 13 shows that AIPTW-AIPCW (Cox & Cox & Reg.Log) is convergent when there is one nuisance misspecification. In contrary, the other estimators are biased when one of its nuisance

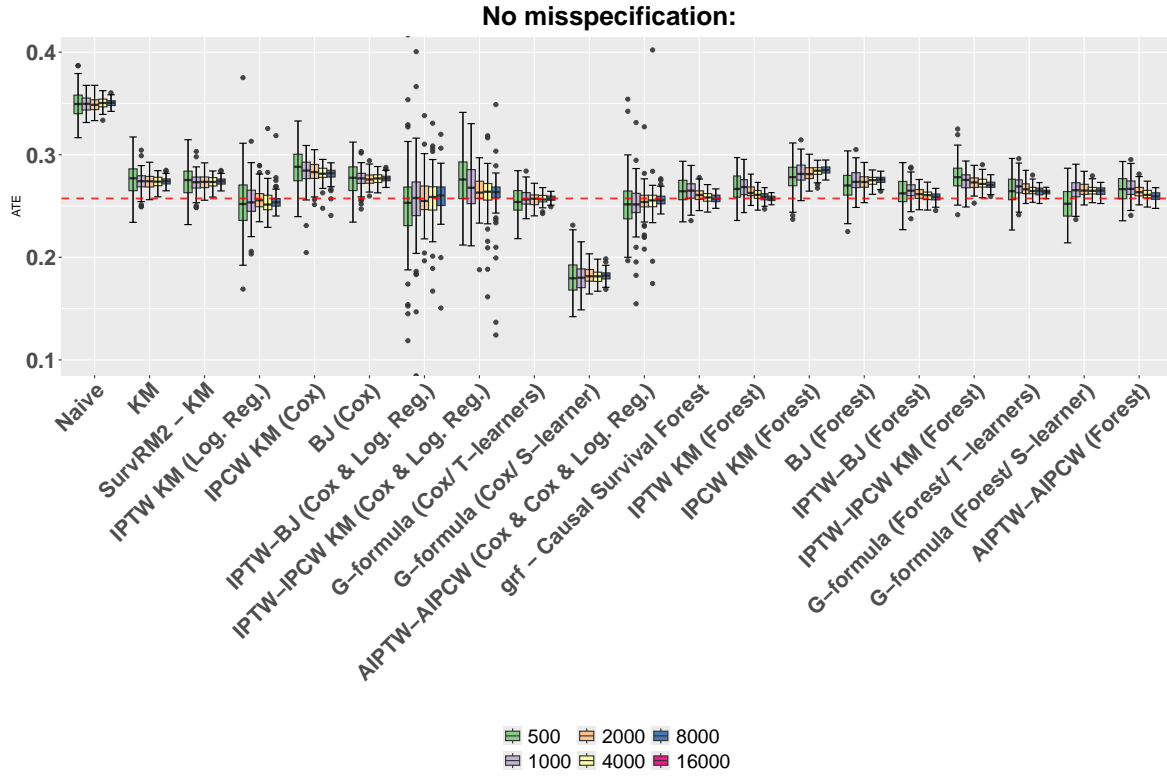


Figure 12: Estimation results of the ATE for the simulation of an observational study with dependent censoring and non linear relationships.

parameter is misspecified.

Figure 14 shows that, as expected, when all nuisance models are misspecified, all estimators exhibit bias. AIPTW-AIPCW (Cox & Cox & Reg.Log) seems to converge in case where either the outcome and censoring models, or the treatment and censoring models are misspecified which deviates from initial expectations. It was anticipated that AIPTW-AIPCW would converge solely when both the censoring and treatment models were misspecified.

6 Conclusion

Based on the simulations and theoretical results, it might be advisable to stay away from the IPCW and IPTW-IPCW estimators, as they often exhibit excessive variability. Instead, we recommend implementing BJ which seems like a more stable transformation as IPCW, as well as Causal Survival Forest, G-formula (T-learners), IPTW-BJ, and AIPTW-AIPCW in both their Cox, Logistic Regression and forest versions. By qualitatively combining the results from these more robust estimators, we can expect to gain a fairly accurate understanding of the treatment effect.

It is important to note that our simulations utilize large sample sizes with relatively simple relationships, which may not fully capture the complexity of real-world scenarios. In practice, most survival analysis datasets tend to be smaller and more intricate, meaning the stability of certain estimators observed in our simulations may not generalize to real-world applications. Testing these methods on real-world datasets would provide a more comprehensive evaluation of their performance in practical settings.

An interesting direction for future work would be to focus on variable selection. Indeed, there is no

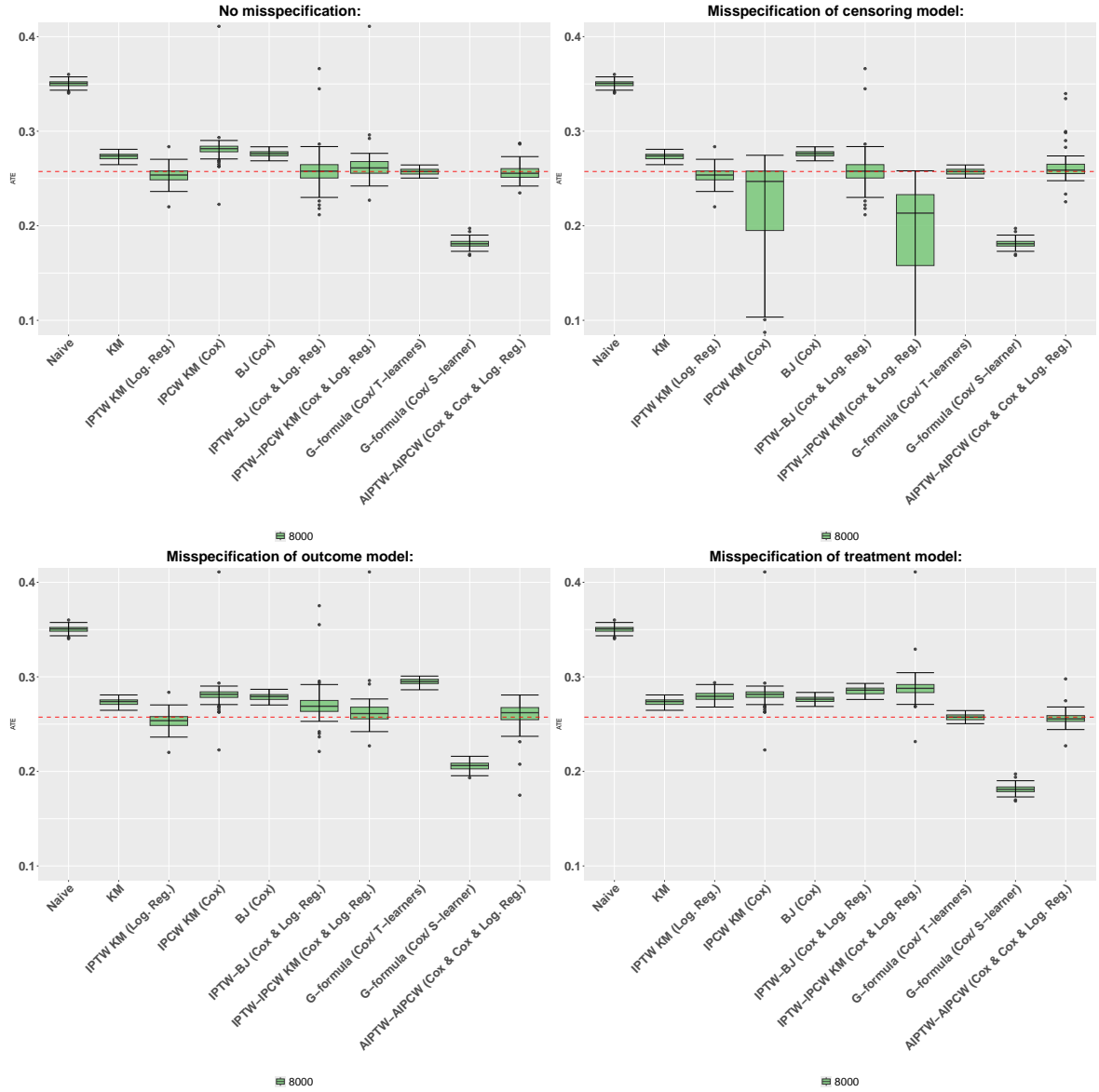


Figure 13: Estimation results of the ATE for an observational study with dependent censoring in case of a single misspecification.

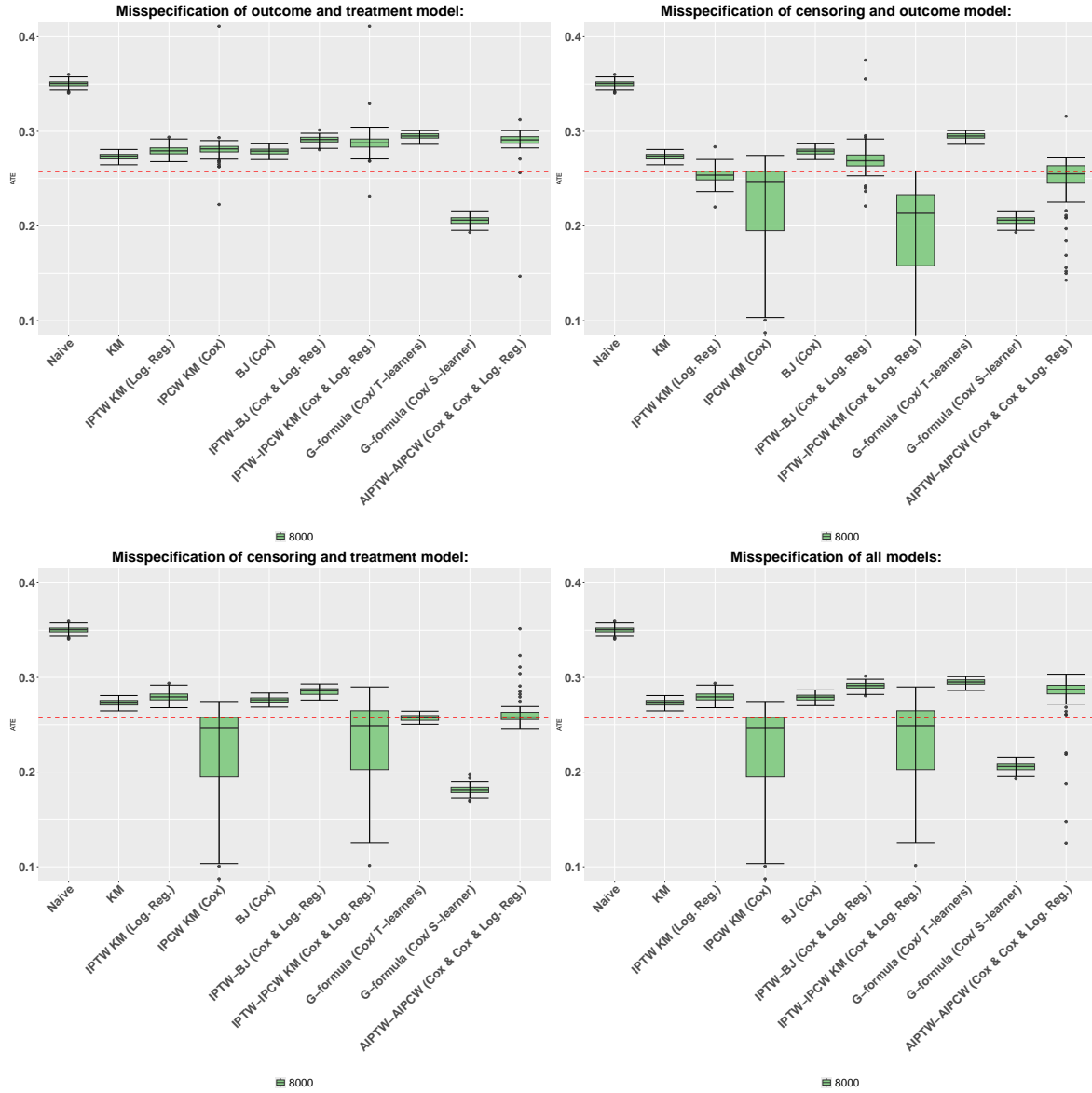


Figure 14: Estimation results of the ATE for an observational study with dependent censoring in case of a two or more misspecifications.

reason to assume that the variables related to censoring should be the same as those linked to survival or treatment allocation. We could explore differentiating these sets of variables and study the impact on the estimators' variance. Similarly to causal inference settings without survival data, we might expect, for instance, that adding precision variables—those solely related to the outcome—could reduce the variance of the estimators.

Additionally, the estimators of the Restricted Mean Survival Time (RMST) provide a valuable alternative to the Hazard Ratio. The analysis and code provided with this article enables further exploration of the advantages of the estimators of RMST for causal analysis in survival studies. This could lead to a deeper understanding of how these estimators can offer more stable and interpretable estimates of treatment effects, particularly in complex real-world datasets.

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7 Appendix A: Proofs

7.1 Proofs of Section 2.1

Proof. (Proposition 2.1). Consistency is a trivial consequence of the law of large number and the identity 11. To show that \hat{S}_{KM} is unbiased, let us introduce \mathcal{F}_k be the filtration generated by the set of variables

$$\{A_i, \mathbb{I}\{\tilde{T}_i = t_j\}, \mathbb{I}\{\tilde{T}_i = t_j, \Delta_i = 1\} \mid j \in [k], i \in [n]\}.$$

which corresponds to the known information up to time t_k , so that $D_k(a)$ is \mathcal{F}_k -measurable but $N_k(a)$ is \mathcal{F}_{k-1} -measurable. One can write that, for $k \geq 2$

$$\begin{aligned} \mathbb{E}[\mathbb{I}\{\tilde{T}_i = t_k, \Delta_i = 1, A_i = a\} \mid \mathcal{F}_{k-1}] &= \mathbb{E}[\mathbb{I}\{\tilde{T}_i = t_k, \Delta_i = 1, A_i = a\} \mid \mathbb{I}\{\tilde{T}_i \geq t_k\}, A_i] \\ &= \mathbb{I}\{A_i = a\} \mathbb{E}[\mathbb{I}\{T_i = t_k, C_i \geq t_k\} \mid \mathbb{I}\{T_i \geq t_k, C_i \geq t_k\}, A_i] \\ &= \mathbb{I}\{A_i = a\} \mathbb{I}\{C_i \geq t_k\} \mathbb{E}[\mathbb{I}\{T_i = t_k\} \mid \mathbb{I}\{T_i \geq t_k\}, A_i] \\ &= \mathbb{I}\{\tilde{T}_i \geq t_k, A_i = a\} \left(1 - \frac{S^{(a)}(t_k)}{S^{(a)}(t_{k-1})}\right), \end{aligned}$$

where we used that $T_i(a)$ is independent from A_i by Assumption 5. We then easily derive from this that

$$\mathbb{E} \left[\left(1 - \frac{D_k(a)}{N_k(a)}\right) \mathbb{I}\{N_k(a) > 0\} \mid \mathcal{F}_{k-1} \right] = \frac{S^{(a)}(t_k)}{S^{(a)}(t_{k-1})} \mathbb{I}\{N_k(a) > 0\},$$

and then that

$$\mathbb{E} \left[\hat{S}_{KM}(t_k \mid A = a) \mid \mathcal{F}_{k-1} \right] = \frac{S^{(a)}(t_k)}{S^{(a)}(t_{k-1})} \hat{S}_{KM}(t_{k-1} \mid A = a) + O(\mathbb{I}\{N_k(a) = 0\}),$$

By induction, we easily find that

$$\mathbb{E}[\hat{S}_{\text{KM}}(t|A = a)] = \prod_{t_j \leq t} \frac{S^{(a)}(t_j)}{S^{(a)}(t_{j-1})} + O\left(\sum_{t_j \leq t} \mathbb{P}(N_j(a) = 0)\right) = S^{(a)}(t) + O(\mathbb{P}(N_k(a) = 0))$$

where t_k is the greatest time such that $t_k \leq t$. \square

Proof. (Proposition 2.2). The asymptotic normality is a mere consequence of the joint asymptotic normality of $(N_k(a), D_k(a))_{t_k \leq t}$ with an application of the δ -method. To access the asymptotic variance, notice that, using a similar reasoning as in the previous proof:

$$\begin{aligned} \mathbb{E}[(1 - D_k(a)/N_k(a))^2 | \mathcal{F}_{k-1}] &= \mathbb{E}[1 - D_k(a)/N_k(a) | \mathcal{F}_{k-1}(a)]^2 + \frac{1}{N_k(a)^2} \text{Var}(D_k(a) | \mathcal{F}_{k-1}) \\ &= s_k^2(a) + \frac{s_k(a)(1 - s_k(a))}{N_k(a)} \mathbb{I}\{N_k(a) > 0\} + O(\mathbb{I}\{N_k(a) = 0\}). \end{aligned}$$

Now we know that $N_k(a) = nr_k(a) + \sqrt{n}O_{\mathbb{P}}(1)$, with the $O_{\mathbb{P}}(1)$ having uniformly bounded moments. So that we deduce that

$$\mathbb{E}[(1 - D_k(a)/N_k(a))^2 | \mathcal{F}_{k-1}] = s_k^2(a) + \frac{s_k(a)(1 - s_k(a))}{nr_k(a)} + \frac{1}{n^{3/2}} O_{\mathbb{P}}(1),$$

where $O_{\mathbb{P}}(1)$ has again bounded moments. Using this identity, we find that

$$\begin{aligned} n\text{Var}\hat{S}_{\text{KM}}(t|A = a) &= n(\mathbb{E}S_{\text{KM}}(t|A = a)^2 - S^{(a)}(t)^2) \\ &= nS^{(a)}(t)^2 \left(\mathbb{E} \left[\prod_{t_k \leq t} \left(1 + \frac{1}{n} \frac{1 - s_k(a)}{s_k(a)r_k(a)} + \frac{1}{n^{3/2}} O_{\mathbb{P}}(1) \right) \right] - 1 \right). \end{aligned}$$

Expanding the product and using that the $O_{\mathbb{P}}(1)$'s have bounded moments, we finally deduce that

$$\mathbb{E} \left[\prod_{t_k \leq t} \left(1 + \frac{1}{n} \frac{1 - s_k(a)}{s_k(a)r_k(a)} + \frac{1}{n^{3/2}} O_{\mathbb{P}}(1) \right) \right] - 1 = \frac{1}{n} \sum_{t_k \leq t} \frac{1 - s_k(a)}{s_k(a)r_k(a)} + \frac{1}{n^{3/2}} O(1),$$

$$n\text{Var}\hat{S}_{\text{KM}}(t|A = a) = V_{\text{KM}}(t|A = a) + O(n^{-1/2}),$$

which is what we wanted to show. \square

7.2 Proofs of Section 2.2

Proof. (Proposition 2.5). Assumption 17 allows the tranformation to be well-defined. Furthermore, it holds

$$\begin{aligned} E[T_{\text{IPCW}}^* | A = a, X] &= E \left[\frac{\Delta^\tau \times \tilde{T} \wedge \tau}{G(\tilde{T} \wedge \tau | A, X)} \middle| A = a, X \right] \\ &= E \left[\frac{\Delta^\tau \times T(a) \wedge \tau}{G(T(a) \wedge \tau | A, X)} \middle| A = a, X \right] \\ &= E \left[E \left[\frac{\mathbb{I}\{T(a) \wedge \tau \leq C\} \times T(a) \wedge \tau}{G(T(a) \wedge \tau | A, X)} \middle| A, X, T(1) \right] \middle| A = a, X \right] \\ &= E[T(a) \wedge \tau | A = a, X] \\ &= E[T(a) \wedge \tau | X]. \end{aligned}$$

We used in the second equality that on the event $\{\Delta^\tau = 1, A = a\}$, it holds $\tilde{T} \wedge \tau = T \wedge \tau = T(a) \wedge \tau$. We used in the fourth equality that $G(T(a) \wedge \tau | A, X) = E[\mathbb{I}\{T(a) \wedge \tau \leq C\} | X, T(a), A]$ thanks to Assumption 16, and in the last one that A is independent from X and $T(a)$ thanks to Assumption 5. \square

Proof. (Proposition 2.6). Similarly to the computations done in the proof of Proposition 2.5, it is easy to show that

$$\mathbb{E} \left[\frac{\Delta_i^\tau}{G(\tilde{T} \wedge \tau | X, A)} \mathbb{I}(\tilde{T}_i = t_k, A = a) \right] = \mathbb{P}(A = a) \mathbb{P}(T(a) = t_k),$$

and likewise that

$$\mathbb{E} \left[\frac{\Delta_i^\tau}{G(\tilde{T} \wedge \tau | X, A)} \mathbb{I}(\tilde{T}_i \geq t_k, A = a) \right] = \mathbb{P}(A = a) \mathbb{P}(T(a) \geq t_k),$$

so that $\hat{S}_{\text{IPCW}}(t)$ converges almost surely towards the product limit

$$\prod_{t_k \leq t} \left(1 - \frac{\mathbb{P}(T(a) = t_k)}{\mathbb{P}(T(a) \geq t_k)} \right) = S^{(a)}(t),$$

yielding strong consistency. Asymptotic normality is straightforward. \square

Proof. (Proposition 2.7). There holds

$$\begin{aligned} \mathbb{E}[T_{\text{BJ}}^* | X, A = a] &= \mathbb{E} \left[\Delta^\tau T(a) \wedge \tau + (1 - \Delta^\tau) \frac{\mathbb{E}[T \wedge \tau \times \mathbb{I}\{T \wedge \tau > C\} | C, A, X]}{\mathbb{P}(T > C | C, A, X)} \middle| X, A = a \right] \\ &= \mathbb{E}[\Delta^\tau T(a) \wedge \tau | X] + \underbrace{\mathbb{E} \left[\mathbb{I}\{T \wedge \tau > C\} \frac{\mathbb{E}[T \wedge \tau \times \mathbb{I}\{T \wedge \tau > C\} | C, A, X]}{\mathbb{E}[\mathbb{I}\{T \wedge \tau \geq C\} | C, A, X]} \middle| X, A = a \right]}_{(\star)}. \end{aligned}$$

Now we easily see that conditioning wrt X in the second term yields

$$\begin{aligned} (\star) &= \mathbb{E} [\mathbb{E}[T \wedge \tau \times \mathbb{I}\{T \wedge \tau > C\} | C, A, X] | X, A = a] \\ &= \mathbb{E}[(1 - \Delta^\tau) T \wedge \tau | X, A = a] \\ &= \mathbb{E}[(1 - \Delta^\tau) T(a) \wedge \tau | X], \end{aligned}$$

ending the proof. \square

Proof. (Theorem 2.1). We let $T^* = \Delta^\tau \phi_1 + (1 - \Delta^\tau) \phi_0$ be a transformation of the form Equation 20. There holds

$$\mathbb{E}[(T^* - T \wedge \tau)^2] = \mathbb{E}[\Delta^\tau (\phi_1 - T \wedge \tau)^2] + \mathbb{E}[(1 - \Delta^\tau) (\phi_0 - T \wedge \tau)^2].$$

The first term is non negative and is zero for the BJ transformation. Since ϕ_0 is a function of (\tilde{T}, X, A) and that $\tilde{T} = C$ on $\{\Delta^\tau = 0\}$, the second term can be rewritten in the following way. We let R be a generic quantity that does not depend on ϕ_0 .

$$\begin{aligned} \mathbb{E}[(1 - \Delta^\tau) (\phi_0 - T)^2] &= \mathbb{E} [\mathbb{I}\{T \wedge \tau > C\} \phi_0^2 - 2\mathbb{I}\{T \wedge \tau > C\} \phi_0 T \wedge \tau] + R \\ &= \mathbb{E} [\mathbb{P}(T \wedge \tau > C | C, A, X) \phi_0^2 - 2\mathbb{E}[T \wedge \tau \mathbb{I}\{T \wedge \tau > C\} | C, A, X] \phi_0] + R \\ &= \mathbb{E} \left[\mathbb{P}(T \wedge \tau > C | C, A, X) \left(\phi_0 - \frac{\mathbb{E}[T \wedge \tau \mathbb{I}\{T \wedge \tau > C\} | C, A, X]}{\mathbb{P}(T \wedge \tau > C | C, A, X)} \right)^2 \right] + R. \end{aligned}$$

Now the first term in the right hand side is always non-negative, and is zero for the BJ transformation. \square

7.3 Proofs of Section 3.1

Proof. (Proposition 3.1). The fact that it is strongly consistent and asymptotically normal is again a simple application of the law of large number and of the δ -method. We indeed find that, for $t_k \leq \tau$

$$\begin{aligned} \mathbb{E} \left[\frac{1}{e(X_i)} \mathbb{1}_{\{\tilde{T}_i = t_k, \Delta_i = 1, A_i = 1\}} \right] &= \mathbb{E} \left[\frac{A_i}{e(X_i)} \mathbb{1}_{\{T_i = t_k, C_i \geq t_k\}} \right] \\ &= \mathbb{E} \left[\mathbb{E} \left[\frac{A_i}{e(X_i)} \mathbb{1}_{\{T_i = t_k, C_i \geq t_k\}} \middle| X_i \right] \right] \\ &= \mathbb{E} \left[\mathbb{E} \left[\frac{A_i}{e(X_i)} \middle| X_i \right] \mathbb{P}(T_i = t_k | X_i) \mathbb{P}(C_i \geq t_k) \right] \\ &= \mathbb{P}(T_i = t_k) \mathbb{P}(C_i \geq t_k), \end{aligned}$$

where we used that A is independent from T conditionnaly on X , and that C is independent from everything. Likewise, one would get that

$$\mathbb{E} \left[\frac{1}{e(X_i)} \mathbb{1}_{\{\tilde{T}_i \geq t_k, A_i = 1\}} \right] = \mathbb{P}(T_i \geq t_k) \mathbb{P}(C_i \geq t_k).$$

Similar computations hold for $A = 0$, ending the proof. \square

7.4 Proofs of Section 3.2

Proof. (Proposition 3.2). On the event $\{\Delta^\tau = 1, A = 1\}$, there holds $\tilde{T} \wedge \tau = T \wedge \tau = T(1) \wedge \tau$, whence we find that,

$$\begin{aligned} \mathbb{E}[T_{\text{IPCW}}^* | X, A = 1] &= \mathbb{E} \left[\frac{A}{e(X)} \frac{\mathbb{I}\{T(1) \wedge \tau \leq C\}}{G(T(1) \wedge \tau | X, A)} T(1) \wedge \tau \middle| X \right] \\ &= \mathbb{E} \left[\frac{A}{e(X)} \mathbb{E} \left[\frac{\mathbb{I}\{T(1) \wedge \tau \leq C\}}{G(T(1) \wedge \tau | X, A)} \middle| X, A, T(1) \right] T(1) \wedge \tau \middle| X \right] \\ &= \mathbb{E} \left[\frac{A}{e(X)} T(1) \wedge \tau \middle| X \right] \\ &= \mathbb{E} [T(1) \wedge \tau | X], \end{aligned}$$

and the same holds on the event $A = 0$. \square

Proof. (Proposition 3.3). By consistency of $\hat{G}(\cdot | X, A)$ and \hat{e} and by continuity, it suffices to look at the asymptotic behavior of the oracle estimator

$$\theta_{\text{IPTW-IPCW}}^* = \frac{1}{n} \sum_{i=1}^n \left(\frac{A_i}{e(X_i)} - \frac{1 - A_i}{1 - e(X_i)} \right) \frac{\Delta_i^\tau}{G(\tilde{T}_i \wedge \tau | A_i, X_i)} \tilde{T}_i \wedge \tau.$$

The later is converging almost towards its mean, which, following similar computations as in the previous proof, write

$$\begin{aligned} \mathbb{E} \left[\left(\frac{A}{e(X)} - \frac{1 - A}{1 - e(X)} \right) \frac{\Delta^\tau}{G(\tilde{T} \wedge \tau | A, X)} \tilde{T} \wedge \tau \right] &= \mathbb{E} \left[\left(\frac{A}{e(X)} - \frac{1 - A}{1 - e(X)} \right) T \wedge \tau \right] \\ &= \mathbb{E} [T(1) \wedge \tau] - \mathbb{E} [T(0) \wedge \tau]. \end{aligned}$$

\square

Proof. (Proposition 3.4). Asymptotic normality comes from a mere application of the δ -method, while strong consistency follows from the law of large number and the following computations. Like for the proof of Proposition 2.6, one find, by first conditioning wrt $X, A, T(a)$, that, for $t_k \leq \tau$,

$$\mathbb{E} \left[\left(\frac{A}{e(X)} + \frac{1-A}{1-e(X)} \right) \frac{\Delta^\tau}{G(\tilde{T} \wedge \tau | A, X)} \mathbb{I}\{\tilde{T} = t_k, A = a\} \right] = \mathbb{P}(T(a) = t_k)$$

and likewise that

$$\mathbb{E} \left[\left(\frac{A}{e(X)} + \frac{1-A}{1-e(X)} \right) \frac{\Delta^\tau}{G(\tilde{T} \wedge \tau | A, X)} \mathbb{I}\{\tilde{T} \geq t_k, A = a\} \right] = \mathbb{P}(T(a) \geq t_k)$$

so that indeed $S_{\text{IP}^*_{\text{TW-IPCW}}}(t|A=a)$ converges almost surely towards $S^{(a)}(t)$. \square

Proof. (Proposition 3.5). We write

$$\mathbb{E}[T_{\text{IP}^*_{\text{TW-BJ}}}^* | X, A = 1] = \mathbb{E} \left[\frac{A}{e(X)} \Delta^\tau \times \tilde{T} \wedge \tau \middle| X \right] + \mathbb{E} \left[\frac{A}{e(X)} (1 - \Delta^\tau) Q_S(\tilde{T} \wedge \tau | A, X) \middle| X \right].$$

On the event $\{\Delta^\tau = 1, A = 1\}$, there holds $\tilde{T} \wedge \tau = T \wedge \tau = T(1) \wedge \tau$, whence we find that the first term on the the right hand side is equal to

$$\begin{aligned} \mathbb{E} \left[\frac{A}{e(X)} \Delta^\tau \times \tilde{T} \wedge \tau \middle| X \right] &= \mathbb{E} \left[\frac{A}{e(X)} \Delta^\tau \times T(1) \wedge \tau \middle| X \right] \\ &= \mathbb{E} [\Delta^\tau \times T(1) \wedge \tau | X]. \end{aligned}$$

For the second term in the right hand side, notice that on the event $\{\Delta^\tau = 0, A = 1\}$, there holds $\tilde{T} = C < T(1) \wedge \tau$, so that

$$\begin{aligned} &\mathbb{E} \left[\frac{A}{e(X)} \mathbb{I}\{C < T(1) \wedge \tau\} \frac{\mathbb{E}[T(1) \wedge \tau \times \mathbb{I}\{C < T(1) \wedge \tau\} | X, A, C]}{\mathbb{P}(C < T(1) \wedge \tau | C, X, A)} \middle| X \right] \\ &= \mathbb{E} \left[\frac{A}{e(X)} \mathbb{E}[T(1) \wedge \tau \times \mathbb{I}\{C < T(1) \wedge \tau\} | X, A, C] \middle| X \right] \\ &= \mathbb{E} [T(1) \wedge \tau \times \mathbb{I}\{C < T(1) \wedge \tau\} | X] \\ &= \mathbb{E} [(1 - \Delta^\tau) T(1) \wedge \tau | X], \end{aligned}$$

and the same holds on the event $\{A = 0\}$, which ends the proof. \square

Proof. (Proposition 3.6). By consistency of $\hat{G}(\cdot | X, A)$ and \hat{e} and by continuity, it suffices to look at the asymptotic behavior of the oracle estimator

$$\theta_{\text{IP}^*_{\text{TW-BJ}}}^* = \frac{1}{n} \sum_{i=1}^n \left(\frac{A_i}{e(X_i)} - \frac{1-A_i}{1-e(X_i)} \right) (\Delta_i^\tau \times \tilde{T}_i \wedge \tau + (1 - \Delta_i^\tau) Q_S(\tilde{T}_i \wedge \tau | A_i, X_i)).$$

The later is converging almost towards its mean, which, following similar computations as in the previous proof, is simply equal to the difference in RMST. \square

Proof. (Proposition 3.7). We can write that

$$\Delta_{\text{QR}}^* = \underbrace{\frac{A}{p(X)} (T_{\text{DR}}^*(F, R) - v(X, 1)) + v(X, 1)}_{(A)} - \underbrace{\left(\frac{1-A}{1-p(X)} (T_{\text{DR}}^*(F, R) - v(X, 0)) + v(X, 0) \right)}_{(B)}.$$

Focusing on term (A), we easily find that

$$\begin{aligned} E[(A)|X] &= E \left[\frac{A}{p(X)} (T_{DR}^*(F, R) - v(X, 1)) + v(X, 1) \middle| X \right] \\ &= \frac{e(X)}{p(X)} (\mu(X, 1) - v(X, 1)) + v(X, 1). \end{aligned}$$

Where we used that $T_{DR}^*(F, R)$ is a censoring unbiased transform when $F = G$ or $R = S$. Now we see that if $p(X) = e(X)$, then

$$E[(A)|X] = \mu(X, 1) - v(X, 1) + v(X, 1) = \mu(X, 1),$$

and if $v(X, 1) = \mu(X, 1)$, then

$$E[(A)|X] = \frac{e(X)}{p(X)} \times 0 + \mu(X, 1) = \mu(X, 1).$$

Likewise, we would show that $E[(B)|X] = \mu(X, 0)$ under either alternative, ending the proof. \square

8 Appendix B: Descriptive statistics

8.1 RCT

The summary by group of treatment of the generated (observed and unobserved) RCT with independent censoring is displayed below:

[1] "Descriptive statistics for group A=0: 998"

X1	X2	X3	X4
Min. :-2.9557	Min. :-1.8789	Min. :-4.4758	Min. :-2.4151
1st Qu.: 0.3221	1st Qu.: 0.3453	1st Qu.: -1.7095	1st Qu.: 0.2812
Median : 1.0153	Median : 1.0232	Median : -0.9612	Median : 0.9916
Mean : 1.0019	Mean : 1.0329	Mean : -0.9797	Mean : 0.9600
3rd Qu.: 1.7051	3rd Qu.: 1.7121	3rd Qu.: -0.2730	3rd Qu.: 1.6060
Max. : 4.2736	Max. : 3.9007	Max. : 2.5640	Max. : 4.0861

C	T1	T0	status
Min. : 0.08041	Min. : 10.00	Min. : 0.0004	Min. : 0.0000
1st Qu.: 10.13480	1st Qu.: 13.11	1st Qu.: 3.1084	1st Qu.: 0.0000
Median : 24.33376	Median : 18.08	Median : 8.0838	Median : 1.0000
Mean : 33.88556	Mean : 31.57	Mean : 21.5732	Mean : 0.6984
3rd Qu.: 48.13172	3rd Qu.: 30.36	3rd Qu.: 20.3569	3rd Qu.: 1.0000
Max. : 230.11350	Max. : 466.71	Max. : 456.7149	Max. : 1.0000

T_tild

Min. : 0.00037
1st Qu.: 2.31667
Median : 5.79778
Mean : 10.51124
3rd Qu.: 12.65494
Max. : 84.20756

[1] "Descriptive statistics for group A=1: 1002"

X1	X2	X3	X4
Min. :-2.7508	Min. :-1.9131	Min. :-5.2005	Min. :-2.7113

1st Qu.: 0.3697	1st Qu.: 0.3861	1st Qu.: -1.6777	1st Qu.: 0.3113
Median : 1.0705	Median : 0.9665	Median : -1.0123	Median : 0.9578
Mean : 1.0672	Mean : 0.9930	Mean : -0.9949	Mean : 0.9898
3rd Qu.: 1.7906	3rd Qu.: 1.6155	3rd Qu.: -0.3572	3rd Qu.: 1.7003
Max. : 4.4438	Max. : 4.0436	Max. : 2.1473	Max. : 4.4019

C	T1	T0	status
Min. : 0.06705	Min. : 10.01	Min. : 0.0067	Min. : 0.000
1st Qu.: 9.14730	1st Qu.: 12.61	1st Qu.: 2.6074	1st Qu.: 0.000
Median : 23.25464	Median : 18.08	Median : 8.0819	Median : 1.000
Mean : 32.83999	Mean : 31.56	Mean : 21.5642	Mean : 0.504
3rd Qu.: 45.00530	3rd Qu.: 31.07	3rd Qu.: 21.0683	3rd Qu.: 1.000
Max. : 206.61098	Max. : 610.80	Max. : 600.8020	Max. : 1.000

T_tild

Min. : 0.06705

1st Qu.: 9.14730

Median : 12.63556

Mean : 16.47238

3rd Qu.: 20.36879

Max. : 157.38231

Covariates are balanced between groups, and censoring times are the same (independent censoring). However, there are more censored observations in the treated group ($A = 1$) than in the control group ($A = 0$). This is due to the higher instantaneous hazard of the event in the treated group (with $T_1 = T_0 + 10$) compared to the constant hazard of censoring.

The summary of the generated (observed and unobserved) RCT with conditionally independent censoring stratified by treatment is displayed below.

[1] "Descriptive statistics for group A=0: 1014"

X1	X2	X3	X4
Min. : -1.8896	Min. : -1.9842	Min. : -4.7225	Min. : -2.4215
1st Qu.: 0.2476	1st Qu.: 0.2970	1st Qu.: -1.7013	1st Qu.: 0.3372
Median : 0.9873	Median : 0.9829	Median : -0.9999	Median : 0.9724
Mean : 0.9403	Mean : 1.0060	Mean : -1.0022	Mean : 1.0014
3rd Qu.: 1.6299	3rd Qu.: 1.6525	3rd Qu.: -0.3300	3rd Qu.: 1.6760
Max. : 4.1400	Max. : 5.5345	Max. : 2.1076	Max. : 4.4615

C	T1	T0	status
Min. : 0.0019	Min. : 10.00	Min. : 0.0026	Min. : 0.0000
1st Qu.: 2.3513	1st Qu.: 12.92	1st Qu.: 2.9245	1st Qu.: 0.0000
Median : 7.0890	Median : 18.74	Median : 8.7427	Median : 0.0000
Mean : 16.2008	Mean : 33.33	Mean : 23.3330	Mean : 0.4408
3rd Qu.: 17.5029	3rd Qu.: 34.54	3rd Qu.: 24.5366	3rd Qu.: 1.0000
Max. : 618.2216	Max. : 421.82	Max. : 411.8207	Max. : 1.0000

status_tau	T_tild
Min. : 0.0000	Min. : 0.00188
1st Qu.: 0.0000	1st Qu.: 1.23181
Median : 0.0000	Median : 3.70141
Mean : 0.4783	Mean : 7.96222
3rd Qu.: 1.0000	3rd Qu.: 9.85267
Max. : 1.0000	Max. : 241.77622

```
[1] "Descriptive statistics for group A=1: 986"
```

X1	X2	X3	X4
Min. :-2.3256	Min. :-2.3217	Min. :-4.1564	Min. :-2.8361
1st Qu.: 0.2626	1st Qu.: 0.3277	1st Qu.: -1.6839	1st Qu.: 0.3323
Median : 0.9096	Median : 1.0320	Median : -1.0184	Median : 1.0078
Mean : 0.9277	Mean : 0.9993	Mean : -0.9962	Mean : 0.9884
3rd Qu.: 1.6235	3rd Qu.: 1.6861	3rd Qu.: -0.3001	3rd Qu.: 1.6628
Max. : 4.3415	Max. : 3.7895	Max. : 2.6529	Max. : 4.3211

C	T1	T0	status
Min. : 0.0069	Min. : 10.00	Min. : 0.0004	Min. :0.0000
1st Qu.: 3.3073	1st Qu.: 12.91	1st Qu.: 2.9098	1st Qu.:0.0000
Median : 8.9424	Median : 18.77	Median : 8.7720	Median :0.0000
Mean : 18.6849	Mean : 33.78	Mean : 23.7831	Mean :0.2221
3rd Qu.: 21.7387	3rd Qu.: 34.46	3rd Qu.: 24.4551	3rd Qu.:0.0000
Max. :498.9318	Max. :464.75	Max. :454.7509	Max. :1.0000

status_tau	T_tild
Min. :0.000	Min. : 0.00687
1st Qu.:0.000	1st Qu.: 3.30730
Median :0.000	Median : 8.94239
Mean :0.287	Mean : 12.45445
3rd Qu.:1.000	3rd Qu.: 15.03866
Max. :1.000	Max. :198.71946

Covariates are balanced between the two groups. However, censoring times differ between groups due to conditionally independent censoring based on covariates and treatment group. Indeed, the distribution of C is different between the treatment group.

8.2 Observational study with linear relationship

```
# Observational data with no informative censoring
data_obs1 <- simulate_data_obs(n = 2000, tau = 25, scenario = "Obs1")

# Observational data simulation with dependent censoring
data_obs2 <- simulate_data_obs(n = 2000, tau = 25, scenario = "Obs2",
                                coefC = 0.03, parsC = c(0.7,0.3,-0.25,-0.1))
```

The summary of the generated (observed and unobserved) data set observational study with independent censoring stratified by treatment is displayed below to enhance the difference with the other scenario.

```
[1] "Descriptive statistics for group A=0: 1110"
```

X1	X2	X3	X4
Min. :-1.8667	Min. :-1.4165	Min. :-2.85861	Min. :-1.7909
1st Qu.: 0.5281	1st Qu.: 0.5385	1st Qu.: -1.04179	1st Qu.: 0.5271
Median : 1.1979	Median : 1.2324	Median : -0.52108	Median : 1.1572
Mean : 1.1895	Mean : 1.2241	Mean : -0.49098	Mean : 1.1547
3rd Qu.: 1.8357	3rd Qu.: 1.8978	3rd Qu.: 0.03942	3rd Qu.: 1.8598
Max. : 4.2271	Max. : 4.1827	Max. : 2.37399	Max. : 4.2912

C	T1	T0	status
Min. : 0.00606	Min. : 10.02	Min. : 0.0156	Min. :0.000
1st Qu.: 9.41243	1st Qu.: 12.61	1st Qu.: 2.6086	1st Qu.:0.000

Median : 21.97750	Median : 18.17	Median : 8.1690	Median :1.000
Mean : 31.13134	Mean : 29.55	Mean : 19.5478	Mean :0.682
3rd Qu.: 42.79441	3rd Qu.: 33.00	3rd Qu.: 22.9975	3rd Qu.:1.000
Max. :251.90115	Max. :551.67	Max. :541.6658	Max. :1.000

T_tild

Min. : 0.00606
1st Qu.: 2.04267
Median : 5.69051
Mean : 10.14138
3rd Qu.: 13.32203
Max. :101.80725

[1] "Descriptive statistics for group A=1: 890"

X1	X2	X3	X4
Min. :-1.97991	Min. :-1.97449	Min. :-4.8520	Min. :-1.9872
1st Qu.: 0.03764	1st Qu.: 0.08508	1st Qu.: -2.1841	1st Qu.: 0.1679
Median : 0.69830	Median : 0.74355	Median : -1.6186	Median : 0.8097
Mean : 0.72231	Mean : 0.76693	Mean : -1.6278	Mean : 0.8105
3rd Qu.: 1.34921	3rd Qu.: 1.42976	3rd Qu.: -1.0907	3rd Qu.: 1.4195
Max. : 3.74139	Max. : 4.12392	Max. : 0.4268	Max. : 3.8964

C	T1	T0	status
Min. : 0.00385	Min. : 10.01	Min. : 0.0061	Min. :0.0000
1st Qu.: 9.69811	1st Qu.: 13.00	1st Qu.: 2.9999	1st Qu.:0.0000
Median : 24.51524	Median : 19.33	Median : 9.3318	Median :1.0000
Mean : 34.09568	Mean : 31.42	Mean : 21.4187	Mean :0.5056
3rd Qu.: 46.71067	3rd Qu.: 34.42	3rd Qu.: 24.4175	3rd Qu.:1.0000
Max. :223.99630	Max. :502.44	Max. :492.4397	Max. :1.0000

T_tild

Min. : 0.00385
1st Qu.: 9.69811
Median :13.33370
Mean :16.67190
3rd Qu.:21.07370
Max. :98.10669

The covariates between the two groups of treatment are unbalanced because of dependent treatment assignation. The mean of X1, X2, X3 and X4 is bigger in the control group than in the treated group. The censoring times have the same distribution (independent censoring). There are more censored observation in the treated group (A=1) than in the control group (A=0) for the same reason than in the RCT scenario.

The summary of the generated (observed and unobserved) data set observational study with conditionally independent censoring stratified by treatment is displayed below.

[1] "Descriptive statistics for group A=0: 1079"

X1	X2	X3	X4
Min. :-1.7012	Min. :-2.2524	Min. :-2.83440	Min. :-2.0757
1st Qu.: 0.4614	1st Qu.: 0.6128	1st Qu.: -1.05024	1st Qu.: 0.5266
Median : 1.2076	Median : 1.1950	Median : -0.50517	Median : 1.1470
Mean : 1.1855	Mean : 1.1957	Mean : -0.47302	Mean : 1.1634
3rd Qu.: 1.8810	3rd Qu.: 1.8409	3rd Qu.: 0.04216	3rd Qu.: 1.7990

Max.	: 4.3590	Max.	: 4.0271	Max.	: 2.85214	Max.	: 3.9531
	C		T1		T0		status
Min.	: 0.00035	Min.	: 10.00	Min.	: 0.0016	Min.	:0.0000
1st Qu.:	2.11426	1st Qu.:	12.86	1st Qu.:	2.8629	1st Qu.:	0.0000
Median :	6.64038	Median :	18.53	Median :	8.5288	Median :	0.0000
Mean :	14.48622	Mean :	29.72	Mean :	19.7224	Mean :	0.4337
3rd Qu.:	16.43676	3rd Qu.:	32.04	3rd Qu.:	22.0355	3rd Qu.:	1.0000
Max.	:263.26984	Max.	:370.18	Max.	:360.1836	Max.	:1.0000

	status_tau		T_obs		e
Min.	:0.0000	Min.	: 0.00035	Min.	:0.0000262
1st Qu.:	0.0000	1st Qu.:	1.14757	1st Qu.:	0.0242768
Median :	0.0000	Median :	3.47010	Median :	0.0967140
Mean :	0.4662	Mean :	7.25802	Mean :	0.1993355
3rd Qu.:	1.0000	3rd Qu.:	8.51255	3rd Qu.:	0.2951447
Max.	:1.0000	Max.	:127.28566	Max.	:0.9897459

[1] "Descriptive statistics for group A=1: 921"

	X1		X2		X3		X4
Min.	:-2.38534	Min.	:-2.37074	Min.	:-4.288	Min.	:-2.48186
1st Qu.:	0.09294	1st Qu.:	0.08787	1st Qu.:	-2.245	1st Qu.:	0.05417
Median :	0.74611	Median :	0.75401	Median :	-1.701	Median :	0.73794
Mean :	0.77300	Mean :	0.73981	Mean :	-1.672	Mean :	0.72035
3rd Qu.:	1.45153	3rd Qu.:	1.37168	3rd Qu.:	-1.092	3rd Qu.:	1.37140
Max.	: 3.71673	Max.	: 3.86002	Max.	: 1.205	Max.	: 3.65766

	C		T1		T0		status
Min.	: 0.00468	Min.	: 10.00	Min.	: 0.0007	Min.	:0.0000
1st Qu.:	2.48031	1st Qu.:	13.14	1st Qu.:	3.1381	1st Qu.:	0.0000
Median :	6.48312	Median :	19.17	Median :	9.1743	Median :	0.0000
Mean :	16.00392	Mean :	36.02	Mean :	26.0177	Mean :	0.1835
3rd Qu.:	17.15109	3rd Qu.:	33.56	3rd Qu.:	23.5601	3rd Qu.:	0.0000
Max.	:289.61159	Max.	:741.00	Max.	:730.9985	Max.	:1.0000

	status_tau		T_obs		e
Min.	:0.0000	Min.	: 0.00468	Min.	:0.008566
1st Qu.:	0.0000	1st Qu.:	2.48031	1st Qu.:	0.574571
Median :	0.0000	Median :	6.48312	Median :	0.870434
Mean :	0.2334	Mean :	11.18666	Mean :	0.750833
3rd Qu.:	0.0000	3rd Qu.:	13.65767	3rd Qu.:	0.970773
Max.	:1.0000	Max.	:232.96814	Max.	:0.999914

The covariates between the two groups are unbalanced. The censoring time is dependent on the covariates also, as the covariates are unbalanced between the two groups, the censoring time is also unbalanced. In particular, the mean of X1, X2, X3 and X4 is bigger in the control group than in the treated group. Also, the number of events is bigger in the control than treated group.

8.3 Observational study with interaction

```
mis <- simulate_data_mis(n=2000,tau=0.5)
summary(mis)
```

	X1		X2		X3		X4
Min.	:-2.9158	Min.	:-2.89788	Min.	:-2.66585	Min.	:-2.7603

1st Qu.: -0.1273	1st Qu.: -0.09922	1st Qu.: -0.01735	1st Qu.: -0.1763
Median : 0.5290	Median : 0.56937	Median : 0.66528	Median : 0.4930
Mean : 0.5233	Mean : 0.53603	Mean : 0.64446	Mean : 0.5027
3rd Qu.: 1.1783	3rd Qu.: 1.20148	3rd Qu.: 1.30132	3rd Qu.: 1.2171
Max. : 4.2845	Max. : 3.98276	Max. : 3.76901	Max. : 3.6131

tau	A	T0	T1
Min. : 0.5	Min. : 0.000	Min. : 0.00000	Min. : 1.000
1st Qu.: 0.5	1st Qu.: 0.000	1st Qu.: 0.03341	1st Qu.: 1.033
Median : 0.5	Median : 1.000	Median : 0.18847	Median : 1.188
Mean : 0.5	Mean : 0.581	Mean : 0.92677	Mean : 1.927
3rd Qu.: 0.5	3rd Qu.: 1.000	3rd Qu.: 0.68948	3rd Qu.: 1.689
Max. : 0.5	Max. : 1.000	Max. : 85.51626	Max. : 86.516

C	T_obs	T_obs_tau	status
Min. : 0.0001	Min. : 0.000002	Min. : 0.0000018	Min. : 0.0000
1st Qu.: 0.1249	1st Qu.: 0.048395	1st Qu.: 0.0483946	1st Qu.: 0.0000
Median : 0.5005	Median : 0.226611	Median : 0.2266114	Median : 0.0000
Mean : 5.4494	Mean : 0.538913	Mean : 0.2612059	Mean : 0.4415
3rd Qu.: 1.8525	3rd Qu.: 0.819634	3rd Qu.: 0.5000000	3rd Qu.: 1.0000
Max. : 837.3896	Max. : 29.177705	Max. : 0.5000000	Max. : 1.0000

status_tau	censor.status	e
Min. : 0.0000	Min. : 0.0000	Min. : 0.000696
1st Qu.: 0.0000	1st Qu.: 0.0000	1st Qu.: 0.406083
Median : 1.0000	Median : 1.0000	Median : 0.583381
Mean : 0.5835	Mean : 0.5585	Mean : 0.578583
3rd Qu.: 1.0000	3rd Qu.: 1.0000	3rd Qu.: 0.799478
Max. : 1.0000	Max. : 1.0000	Max. : 0.999990

The summary of the generated (observed and unobserved) data set complex observational study (conditionally independent censoring) stratified by treatment is displayed below.

[1] "Descriptive statistics for group A=0: 838"

X1	X2	X3	C
Min. : -2.8573	Min. : -2.67784	Min. : -2.0794	Min. : 0.0001
1st Qu.: -0.0928	1st Qu.: 0.07166	1st Qu.: -0.1020	1st Qu.: 0.1310
Median : 0.5211	Median : 0.81706	Median : 0.4724	Median : 0.5413
Mean : 0.5285	Mean : 0.75991	Mean : 0.4334	Mean : 4.1779
3rd Qu.: 1.1660	3rd Qu.: 1.45325	3rd Qu.: 0.9888	3rd Qu.: 1.8581
Max. : 4.2845	Max. : 3.69969	Max. : 2.9667	Max. : 352.8472

T1	T0	status	T_obs
Min. : 1.000	Min. : 0.000002	Min. : 0.0000	Min. : 0.000002
1st Qu.: 1.025	1st Qu.: 0.024546	1st Qu.: 0.0000	1st Qu.: 0.017243
Median : 1.153	Median : 0.153370	Median : 1.0000	Median : 0.079083
Mean : 1.606	Mean : 0.605572	Mean : 0.6575	Mean : 0.238527
3rd Qu.: 1.605	3rd Qu.: 0.605294	3rd Qu.: 1.0000	3rd Qu.: 0.278339
Max. : 20.734	Max. : 19.733809	Max. : 1.0000	Max. : 5.297747

status_tau	e
Min. : 0.0000	Min. : 0.000696
1st Qu.: 0.0000	1st Qu.: 0.226983
Median : 1.0000	Median : 0.418088
Mean : 0.7148	Mean : 0.407009


```
3rd Qu.:1.0000 3rd Qu.:0.573608
Max. :1.0000 Max. :0.982719
```

```
[1] "Descriptive statistics for group A=1: 1162"
```

X1		X2		X3		C	
Min.	:-2.9158	Min.	:-2.8979	Min.	:-2.66585	Min.	: 0.0001
1st Qu.	:-0.1509	1st Qu.	:-0.2270	1st Qu.	: 0.09129	1st Qu.	: 0.1206
Median	: 0.5363	Median	: 0.3717	Median	: 0.85363	Median	: 0.4720
Mean	: 0.5196	Mean	: 0.3746	Mean	: 0.79668	Mean	: 6.3664
3rd Qu.	: 1.1807	3rd Qu.	: 1.0114	3rd Qu.	: 1.51072	3rd Qu.	: 1.7938
Max.	: 4.0994	Max.	: 3.9828	Max.	: 3.76901	Max.	:837.3896

T1		T0		status		T_obs	
Min.	: 1.000	Min.	: 0.00001	Min.	:0.0000	Min.	: 0.000115
1st Qu.	: 1.042	1st Qu.	: 0.04212	1st Qu.	:0.0000	1st Qu.	: 0.120552
Median	: 1.215	Median	: 0.21457	Median	:0.0000	Median	: 0.472001
Mean	: 2.158	Mean	: 1.15840	Mean	:0.2857	Mean	: 0.755542
3rd Qu.	: 1.785	3rd Qu.	: 0.78503	3rd Qu.	:1.0000	3rd Qu.	: 1.053869
Max.	:86.516	Max.	:85.51626	Max.	:1.0000	Max.	:29.177705

status_tau		e	
Min.	:0.0000	Min.	:0.08717
1st Qu.	:0.0000	1st Qu.	:0.55174
Median	:0.0000	Median	:0.72520
Mean	:0.4888	Mean	:0.70232
3rd Qu.	:1.0000	3rd Qu.	:0.87989
Max.	:1.0000	Max.	:0.99999

The observations are the same than the previous scenario: The covariates and the censoring time between the two groups are unbalanced. To be able to evaluate the estimators, we need to know the true θ_{RMST} at time τ .

Session information

```
R version 4.2.2 (2022-10-31)
```

```
Platform: x86_64-pc-linux-gnu (64-bit)
```

```
Running under: Ubuntu 22.04.5 LTS
```

```
Matrix products: default
```

```
BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p-r0.3.20.so
```

```
locale:
```

```
[1] LC_CTYPE=C.UTF-8      LC_NUMERIC=C           LC_TIME=C.UTF-8
[4] LC_COLLATE=C.UTF-8    LC_MONETARY=C.UTF-8    LC_MESSAGES=C.UTF-8
[7] LC_PAPER=C.UTF-8      LC_NAME=C              LC_ADDRESS=C
[10] LC_TELEPHONE=C        LC_MEASUREMENT=C.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
```

```
[1] splines stats graphics grDevices datasets utils methods
[8] base
```

other attached packages:

[1] gridExtra_2.3	rms_6.8-1	Hmisc_5.1-3	MASS_7.3-60.0.1
[5] grf_2.3.2	RISCA_1.0.5	mosaicData_0.20.4	ggformula_0.12.0
[9] dplyr_1.1.4	Matrix_1.6-5	ggplot2_3.5.1	lattice_0.22-5
[13] tune_1.2.1	reticulate_1.39.0	relsurv_2.2-9	date_1.2-42
[17] survRM2_1.0-4	survival_3.5-8		

loaded via a namespace (and not attached):

[1] TH.data_1.1-2	cubature_2.1.1	colorspace_2.1-1
[4] class_7.3-22	ggridges_0.5.6	htmlTable_2.4.3
[7] base64enc_0.1-3	rstudioapi_0.16.0	farver_2.1.2
[10] listenv_0.9.1	furrr_0.3.1	MatrixModels_0.5-3
[13] dials_1.3.0	prodlim_2024.06.25	fansi_1.0.6
[16] mvtnorm_1.3-1	lubridate_1.9.3	mosaic_1.9.1
[19] codetools_0.2-19	doParallel_1.0.17	knitr_1.48
[22] Formula_1.2-5	jsonlite_1.8.9	workflows_1.1.4
[25] pROC_1.18.5	caret_6.0-94	cluster_2.1.6
[28] kernlab_0.9-33	png_0.1-8	yardstick_1.3.1
[31] compiler_4.2.2	backports_1.5.0	fastmap_1.2.0
[34] cli_3.6.3	quantreg_5.98	htmltools_0.5.8.1
[37] tools_4.2.2	gtable_0.3.5	glue_1.7.0
[40] reshape2_1.4.4	Rcpp_1.0.13	SuperLearner_2.0-29
[43] DiceDesign_1.10	vctrs_0.6.5	nlme_3.1-164
[46] iterators_1.0.14	parsnip_1.2.1	timeDate_4041.110
[49] gower_1.0.1	xfun_0.47	stringr_1.5.1
[52] globals_0.16.3	timechange_0.3.0	lifecycle_1.0.4
[55] mosaicCore_0.9.4.0	renv_1.0.11	statmod_1.5.0
[58] polyspline_1.1.25	future_1.34.0	zoo_1.8-12
[61] scales_1.3.0	ipred_0.9-15	hms_1.1.3
[64] sandwich_3.1-1	parallel_4.2.2	SparseM_1.84-2
[67] RColorBrewer_1.1-3	yaml_2.3.10	labelled_2.13.0
[70] rpart_4.1.23	gam_1.22-5	stringi_1.8.4
[73] foreach_1.5.2	checkmate_2.3.2	lhs_1.2.0
[76] hardhat_1.4.0	lava_1.8.0	shape_1.4.6.1
[79] rlang_1.1.4	pkgconfig_2.0.3	rsample_1.2.1
[82] evaluate_1.0.0	purrr_1.0.2	labeling_0.4.3
[85] htmlwidgets_1.6.4	recipes_1.1.0	tidyselect_1.2.1
[88] parallelly_1.38.0	plyr_1.8.9	magrittr_2.0.3
[91] R6_2.5.1	generics_0.1.3	nnls_1.5
[94] multcomp_1.4-26	pillar_1.9.0	haven_2.5.4
[97] foreign_0.8-86	withr_3.0.1	nnet_7.3-19
[100] tibble_3.2.1	future.apply_1.11.2	utf8_1.2.4
[103] rmarkdown_2.28	grid_4.2.2	data.table_1.16.0
[106] forcats_1.0.0	ModelMetrics_1.2.2.2	digest_0.6.37
[109] tidyr_1.3.1	stats4_4.2.2	GPfit_1.0-8
[112] munsell_0.5.1	glmnet_4.1-8	