BIS 537 Final Project Report

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1. Introduction

While the ideal setting to conduct causal inference on survival outcomes are randomized experiments, as is true for most areas of research, it is often the case that such an experimental setting is difficult or impossible to achieve. As such, when treatment and control groups are not exchangeable, it may be necessary to implement causal inference methods to address the absence of direct counterfactual proxies.

Time-to-event outcomes are of great interest to investigators across a variety of clinical settings, however present analytical difficulties even within the constrains of a randomized controlled trial. In particular, the non-observation of an event yet loss of a subject's data, or censoring, presents another missing data issue that the investigator has need to consider. This issue is compounded in the setting of a non-randomized or observational study, where exchangeability between treatment groups cannot be assumed of the collected data.

Several procedures addressing this dual-level missing data issue in the estimation of time-to-event causal effects have been explored previously. Some of these procedures extend the idea of inverse probability weighting to the setting of survival analysis in constructing a combined treatment and censoring weights (Hernan 2000, Cheng 2022) to approximate exchangeability and estimating the causal estimand through a weighted estimator. Other methods approach the problem by obtaining survival outcomes for each subject through a jackknife procedure (Andersen 2010) and estimate

the causal estimand based on those pseudo-observed endpoints. The pseudo-observaions approach has been further improved upon with the employment of propensity score weighting to close the distance between the collected sample and the target population (Li 2021) as well as with the recent proposal of a doubly-robust estimation technique (Wang 2023) to allow for some flexibility with regards to model misspecification.

In this study, we are interested in revisiting the weighting methods and are proposing a new procedure in which model misspecification may be implicitly adjusted for. In doing so, we will first employ the two-arm weighting method established by Cheng et.al (2022), in which weights based on the probability of treatment and the probability of censoring are calculated and used together in estimating the causal estimand of interest. We will then compare its performance to the results obtained from a single-arm sequential weighting method that we have developed, where weights are constructed iteratively, and the final compositely-weighted dataset will then be used to estimate the causal estimand.

The remainder of this report is organized as follows: in section 2, we introduce our causal survival estimand; in section 3, we discuss our simulation design; in section 4, we illustrate our results from simulation study; and section 5 concludes with a discussion.

2. Methods

2.1 Causal Survival Estimand

While there are several causal estimands that could be of interest, we will be focusing our study on the restricted average causal effect (RACE) for ease of interpretation. In Mao et al. (2018), this was defined as follows:

$$\begin{aligned}\Delta_{RACE} &= \frac{E[\omega(e_i)\min(T_{1i}, t^*)]}{E[\omega(e_i)]} - \frac{E[\omega(e_i)\min(T_{0i}, t^*)]}{E[\omega(e_i)]} \\ &= \int_0^{t^*} S_1(t)dt - \int_0^{t^*} S_0(t)dt\end{aligned}$$

This estimand is interpreted as the average difference in survival time between the treatment and control groups, if both potential outcomes are observed, under the upper bound time restriction of t^*.

In this study, we are interested in the upper bound time restriction of 5 – thus, our estimand will take the following form:

$$\begin{aligned}\Delta_{RACE} &= \frac{E[\omega(e_i)\min(T_{1i}, 5)]}{E[\omega(e_i)]} - \frac{E[\omega(e_i)\min(T_{0i}, 5)]}{E[\omega(e_i)]} \\ &= \int_0^5 S_1(t)dt - \int_0^5 S_0(t)dt\end{aligned}$$

2.2 Causal Estimators

In the separate weighting procedure, to incorporate both the inverse probability treatment weights (IPTW) and the inverse probability of censoring weights (IPCW), we employed the usage of the non-parametric weighted Kaplan-Meier estimator defined by Cheng et al. (2022). This estimator is defined as follows:

$$\begin{aligned}\hat{\Delta}(t) &= \hat{S}(1) - \hat{S}(0) \\ &= \left(1 - \frac{\sum_{i=1}^n \omega_{IPTW_i} Z_i \delta_i I(U_i \leq t)\omega_{IPCW_i}}{\sum_{i=1}^n \omega_{IPTW_i} Z_i}\right) - \left(1 - \frac{\sum_{i=1}^n \omega_{IPTW_i}(1-Z_i) \delta_i I(U_i \leq t)\omega_{IPCW_i}}{\sum_{i=1}^n \omega_{IPTW_i}(1-Z_i)}\right)\end{aligned}$$

where T_i^S is the event time of interest, T_i^C is the censoring time, $U_i = min(T_i^S, T_i^C)$ is the observed time in study, δ_i is the censoring indicator, Z_i is the treatment indicator, $I(U_i \leq t)$ is the indicator for the observed time being less than the upper limit of time t, and ω_{IPTW_i} and ω_{IPCW_i} are IPTW and IPCW respectively. Then, our estimator would be defined as follows, at $t = 5$:

$$\hat{\Delta}(5) = \left(1 - \frac{\sum_{i=1}^n \omega_{IPTW_i} Z_i \delta_i I(U_i \leq 5)\omega_{IPCW_i}}{\sum_{i=1}^n \omega_{IPTW_i} Z_i}\right) - \left(1 - \frac{\sum_{i=1}^n \omega_{IPTW_i}(1-Z_i) \delta_i I(U_i \leq 5)\omega_{IPCW_i}}{\sum_{i=1}^n \omega_{IPTW_i}(1-Z_i)}\right)$$

The estimators used in the sequentially weighted procedure will similarly be weighted Kaplan-Meier estimators – however, these will be distinct from the previously defined estimator in that there will be the need to adjust for one set of weights only. The estimator will thus have the

following form, both generally and at $t = 5$:

$$\begin{aligned}
\hat{\Delta}(t) &= \hat{S}(1) - \hat{S}(0) \\
&= \left(1 - \frac{\sum_{i=1}^{n} \omega_{IPTW \circ IPCW_i} Z_i \delta_i I(U_i \leq t)}{\sum_{i=1}^{n} \omega_{IPTW \circ IPCW_i} Z_i}\right) - \left(1 - \frac{\sum_{i=1}^{n} \omega_{IPTW \circ IPCW_i} (1 - Z_i) \delta_i I(U_i \leq t)}{\sum_{i=1}^{n} \omega_{IPTW \circ IPCW_i} (1 - Z_i)}\right) \\
\hat{\Delta}(5) &= \hat{S}(1) - \hat{S}(0) \\
&= \left(1 - \frac{\sum_{i=1}^{n} \omega_{IPTW \circ IPCW_i} Z_i \delta_i I(U_i \leq 5)}{\sum_{i=1}^{n} \omega_{IPTW \circ IPCW_i} Z_i}\right) - \left(1 - \frac{\sum_{i=1}^{n} \omega_{IPTW \circ IPCW_i} (1 - Z_i) \delta_i I(U_i \leq 5)}{\sum_{i=1}^{n} \omega_{IPTW \circ IPCW_i} (1 - Z_i)}\right)
\end{aligned}$$

where $\omega_{IPTW \circ IPCW_i}$ is the composite treatment and censoring weight and all other notation is the same as defined previously.

2.3 Weighting Procedures

Critical to the construction of the causal estimators are the weighting procedures underlying the construction of the inverse probability weights of both treatment assignment and censoring indication. The goal for both of the procedures that are the subject of investigation in this study is covariate balance between treatment and control groups, such that the study sample would mimic the distribution of the theoretical larger population that it is drawn from.

All weights constructed in this study were inverse probability weights – in particular, for the construction of a weight on indicator variable R, the weights w_{IPRW_i} for a given subject i were constructed as follows:

$$\mathbb{E}[R|\mathbf{X}] = e_R(\mathbf{X}), \quad \text{where } \mathbf{X} \text{ is the vector of covariate values}$$

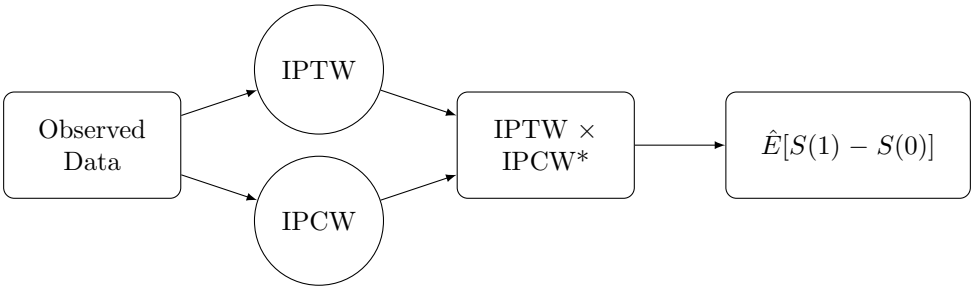
$$w_{IPRW_i} = \begin{cases} \frac{1}{e_R(\mathbf{X})}, & \text{if R} = 1 \\ \frac{1}{1 - e_R(\mathbf{X})}, & \text{if R} = 0 \end{cases}$$

In the estimated propensity score models, all available baseline covariates (which does exclude treatment assignment and censoring indication) were included as model predictors, irrespective of how the true propensity score model was generated. Though this by default produces a misspecified

model, our intent was to replicate and examine situations that may occur in practice, where the data generation procedure is unknown and it may seem reasonable to the investigator to include all collected baseline characteristics. We will explore the impact of this decision in the Discussion section of this paper.

2.3.1 Separate Weighting

The first weighting procedure is to estimate IPTW and IPCW separately. Then the two weights are used together in the estimator described in the previous section to estimate our target estimand (see the diagram below).

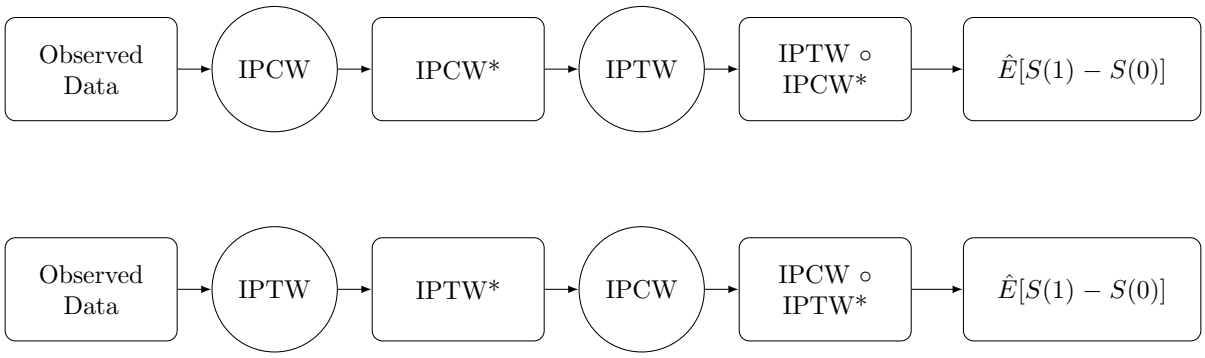


We estimated IPTW using logistic regression with covariates X_1, X_2, and X_3. In separate weighting procedure, we used both logistic regression and Cox-Exponential regression with covariates X_1, X_2, and X_3 to estimate IPCW. All simulations and analyses were conducted in R. The logistic regressions were fitted using `glm` function and Cox-exponential model using `ipcw` from `riskRegression` R package.

2.3.2 Sequential Weighting

In this second weighting procedure, weights are first constructed based on either treatment assignment or censoring indication propensity scores. After this, the weighted dataset would be used to generate weights based on the indication that was not used in the first step of weighting. The causal estimand would be estimated using the second set of weights applied to to the weighted dataset from the first step of weighting.

The weighting processes were conducted as depicted in the following diagram, where circles indicate where weighting occurred and boxes marked with asterisks indicate pseudo-populations:



We have considered the utility of both indicator variables (treatment assignment and censoring indication) as weighting starting points because the relationship between censoring indication and treatment assignment causes it to be difficult to favor one sequential weighting pathway over the other. Some may prefer the sequential weighting procedure that calculates treatment weights first, on the basis of observational temporality – however, while it is true that treatment assignment is observed by the researcher prior to censoring time, if the subject indeed is censored, it seems that the timeline of the conduct of the actual study may not necessarily be the best guideline in determining the order of how weights are calculated, especially if it is assumed that censoring time and treatment assignment are independent of each other, as is commonly assumed and has been maintained in this study. In such a case, when censoring time is a quantity that is generated without respect to treatment assignment, the censoring indicator variable would be related to treatment assignment indirectly, through the effect that the assigned treatment would have on survival time; this is a rather complex relationship to evaluate

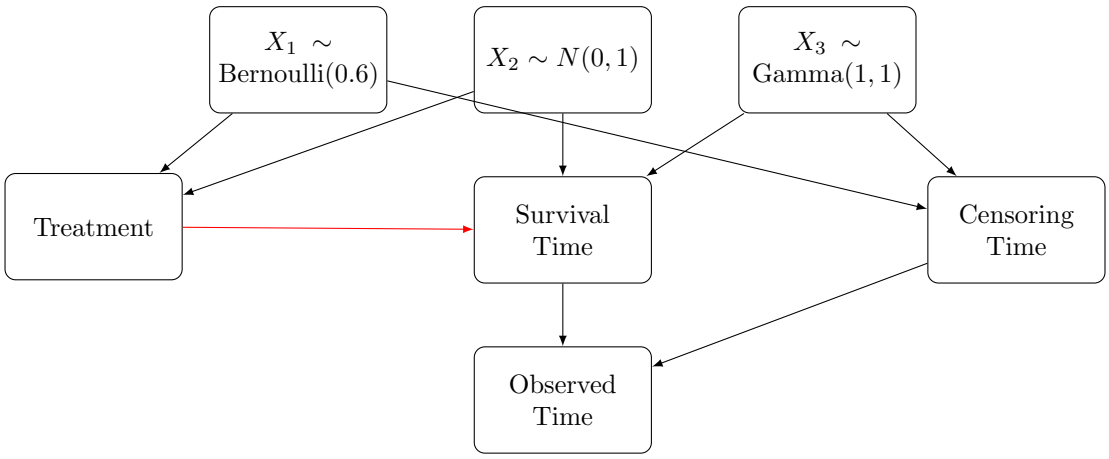
Thus, in this study, we have considered and presented results for both options of sequential weighting, allowing room for investigators interested in this method of inverse probability weighting adjustment to select the method most suitable for the parameters of their studies.

In the implementation of both procedures, the treatment weights were obtained through a logistic regression in `R`, using the `glm` function in base `R` with a logit link function, and the censoring weights were obtained through two Cox-Exponential regressions, which were separated by treatment group, through the `ipcw` function in the `riskRegression` package. In the establishment of

the IPTW ∘ IPCW procedure, the censoring weights were directly identified in the `glm` function call. In the establishment of the IPCW ∘ IPTW procedure, as the `ipcw` function does not take in weights, the treatment-weighted dataset was expanded, using the `expandRows` function from the `splitstackshape` package, according to the calculated treatment weights in order to obtain the second set of weights for censoring indication.

3. Data Generation

We will generate data in accordance with the following relationships, and the causal effect of interest is highlighted in red:



Each component will be described in further detail in the following sections.

3.1 Covariates

As described in the previous diagram, we will be utilizing three covariates in this simulation study: X_1, X_2, X_3. These covariates have the following distributions: $X_1 \sim$ Bernoulli(0.6), $X_2 \sim N(0, 1)$, $X_3 \sim$ Gamma$(1, 1)$ and will explicitly be defined to not be time dependent. These distributions were selected to represent different kinds of covariates that may appear in a real-world study and also to a variety of distributional behaviors.

In addition, these three covariates will all affect the critical measures of interest in this study (i.e., treatment, survival time, and censoring time). However, any given measure will only be affected by two of the three covariates and no two measures will be affected by the same combination of covariates.

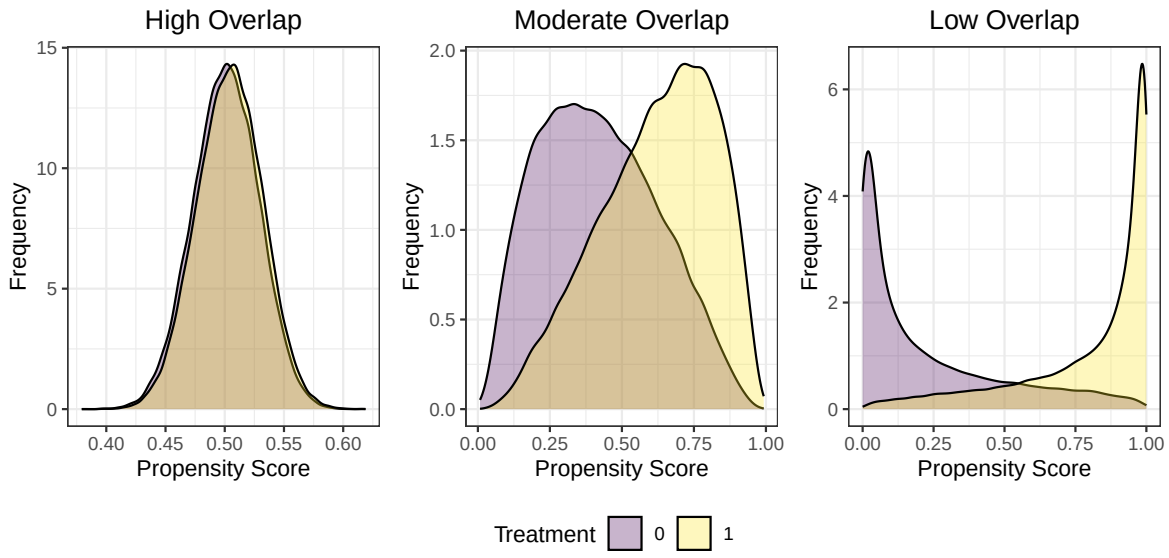
3.2 True Propensity Score Model

The true propensity score model will be defined using the following logistic regression, taking in covariates X_1 and X_2:

$$g^{-1}(E[Z = 1|\mathbf{X}_i]) = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i},$$
$$\text{where } g(\mathbf{X_i}) = \frac{\exp(\boldsymbol{\beta}\mathbf{X}_i^T)}{1 + \exp(\boldsymbol{\beta}\mathbf{X}_i^T)} = E[Z = 1|\mathbf{X}_i] = e(\mathbf{X}_i)$$

In our simulation, β_1, β_2 will be held fixed at $\beta_1 = \beta_2 = 0.1$ for the setting of high overlap of overlap, $\beta_1 = \beta_2 = 1$ for the setting of medium overlap, and $\beta_1 = \beta_2 = 3$ for the setting of low overlap. For each of these settings, the β_0 that would produce an expected treatment proportion of 55% will be obtained through a numerical search over an interval.

The distribution of propensity scores according to each of these settings can be visualized with the following plots, demonstrating that the levels of overlap between treatment groups have indeed been achieved:



3.3 True Survival Time Model

The true survival time model will be defined using the following Cox-Weibull mode, taking in covariates X_1 and X_3:

$$
\begin{aligned}
h(t|\mathbf{X}_i) &= h_0(t)\exp(L_i), \\
\text{where } h_0(t) &= \lambda\nu t^{\nu-1}, \text{ and } L_i = a_0 Z_i + a_1 X_{1i} + a_3 X_{3i} \\
S(T_i^S = t) &= \exp(-\lambda t^v \exp(L_i)) \\
&= 1 - F(t)
\end{aligned}
$$

The survival time for subject i will then be drawn from:

$$
\begin{aligned}
T_i^S &= \left(\frac{-\log(u_i^S)}{\lambda\exp(L_i)}\right)^{1/\nu}, \\
&\text{where } u_i^S \sim \text{Unif}(0,1)
\end{aligned}
$$

From this model, the treatment effect will be determined by α_0. Two settings of α_0 were selected to correspond with a low and high treatment effect respectively.

To obtain the true treatment effects from each of these settings, we started with the conditional

distributions of survival time that would be obtained from the defined Cox-Weibull model:

$$\begin{aligned}
T(1)\Big|(X_1, X_3) &\sim h_{Z=1}(t|X_1, X_3) = \lambda v t^{v-1} \exp(\alpha_0 + \alpha_1 X_1 + \alpha_3 X_3) \\
&= \lambda^* \nu t^{\nu-1}, \text{ where } \lambda^* = \lambda \exp(\alpha_0 + \alpha_1 X_1 + \alpha_3 X_3) \\
T(0)\Big|(X_1, X_3) &\sim h_{Z=0}(t|X_1, X_3) = \lambda v t^{v-1} \exp(\alpha_1 X_1 + \alpha_3 X_3) \\
&= \lambda^* \nu t^{\nu-1}, \text{ where } \lambda^* = \lambda \exp(\alpha_1 X_1 + \alpha_3 X_3)
\end{aligned}$$

Our target estimand is the average causal effect, or $E[T(1) - T(0)]$, which is unconditional on (X_1, X_3). By the law of total expectations and iterated expectations, we see the following:

$$\begin{aligned}
E[T_i] &= E\left[E\Big[T_i|X_1, X_3)\Big]\right] \\
&= \int_{X_1, X_3} E\Big[T_i|X_1 = x_1, X_3 = x_3]P(X_1 = x_1, X_3 = x_3)d\mu(x_1, x_3) \\
&= \int_{X_1, X_3} E\Big[T_i|X_1 = x_1, X_3 = x_3]P(X_1 = x_1)P(X_3 = x_3)d\mu(x_1, x_3)
\end{aligned}$$

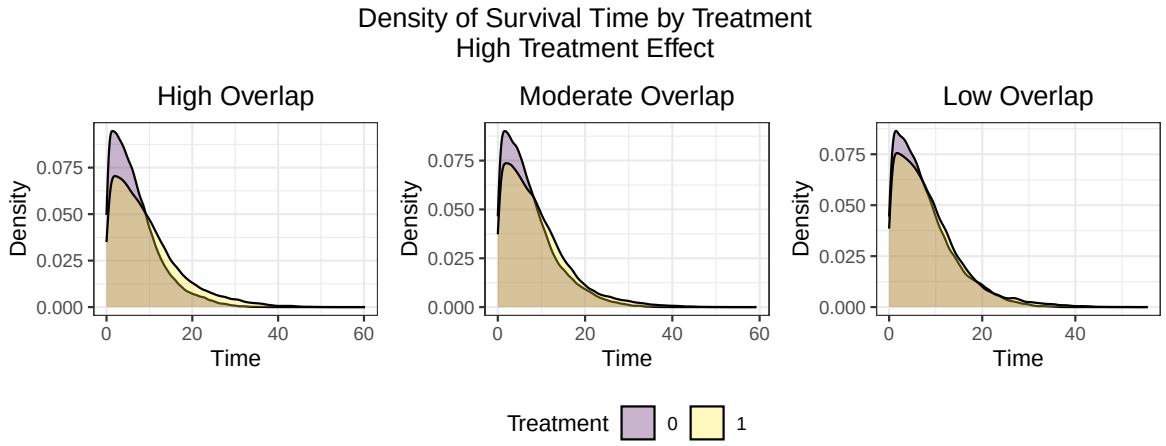
Let $X_{11}, ..., X_{1m} \sim P(X_1)$ and $X_{31}, ..., X_{3m} \sim P(X_3)$. Then, for a sufficiently large m, we note:

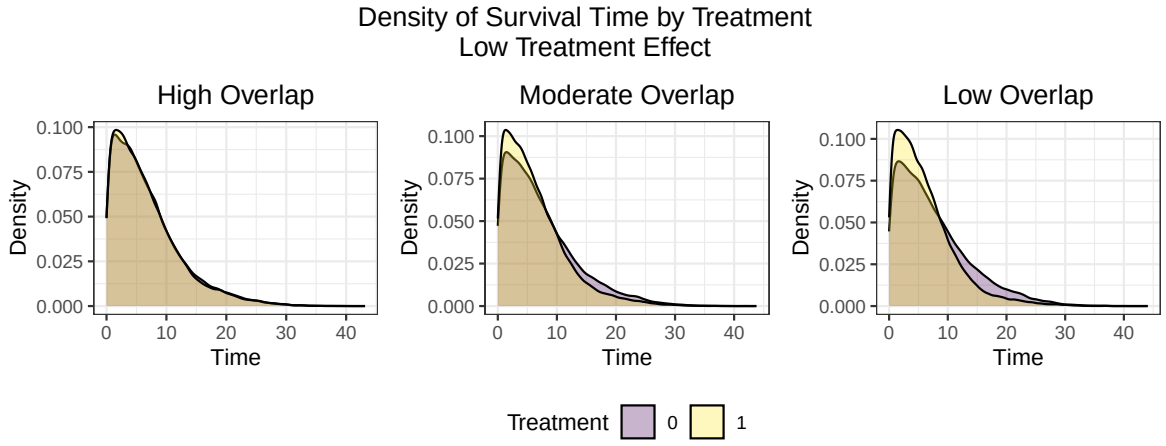
$$\begin{aligned}
E[T_i] &= \int_{X_1, X_3} E\Big[T_i|X_1 = x_1, X_3 = x_3]P(X_1 = x_1)P(X_3 = x_3)d\mu(x_1, x_3) \\
&\approx \sum_{j=1}^{m} E[T_i|X_1 = x_{1j}, X_3 = x_{3j}]
\end{aligned}$$

The true value estimates of $E[T(1)]$ and $E[T(0)]$ will be calculated by taking two samples of size $m = 1000000$ from the distributions of X_1 and X_3 to simulate the distributional behavior of each of these random variables, and sum the computed conditional expectations of $T(1)|(X_{1j}, X_{3j})$ and $T(0)|(X_{1k}, X_{3k})$ for each sample j and k, where $j = k = m$.

The true RACE values that we computed from this procedure were 0.127 for the "high" treatment effect setting and 0.014 for the "low" treatment effect setting.

The distribution of survival time according to each of these settings and by levels of covariate overlap between treatment groups can be visualized with the following plots:





3.4 True Censoring Model

The censoring model will be defined using the following exponential model, taking in covariates X_2 and X_3, and is generated independently of T_i^C, T_i^S, and Z_i:

$$T_i^C \sim \text{Exponential}(\lambda \exp(K_i)),$$

$$\text{where } K_i = \gamma_0 + \gamma_2 X_{2i} + \gamma_3 X_{3i}$$

Algorithmically, the censoring time for subject i will be drawn from:

$$T_i^C = \frac{-\log(u^C)}{\lambda \exp(K_i)},$$

$$\text{where } u^C \sim \text{Unif}(0, 1)$$

For subject i, the observed time, T^{obs} is the minimum of T_i^C and T_i^S, or $T^{obs} = \min(T_i^C, T_i^S)$. In addition, the censoring indicator for subject i, given the survival time T_i and censoring time T^C, will be assigned as follows:

$$\delta_i(T_i^S, T_i^C) = \begin{cases} 1, & \text{where } T_i^S > T_i^C \\ 0. & \text{where } T_i^S \leq T_i^C \end{cases}$$

It is critical to note that although T_i^C is by definition independent of T_i^S and Z_i, the censoring indication, δ_i is not.

In a similar fashion to how the model intercept was selected in the true propensity score model in order to fix a treatment proportion in expectation, after fixing $\gamma_2 = 2$ and $\gamma_3 = 4$, a numerical search procedure was also run to select a γ_0 so that the proportion of censored subjects could be varied across two levels, corresponding to low (25%) and high (50%) levels of censoring. The selected intercepts varied according to the magnitude of treatment effect, as well as the defined censoring level, consequentially resulting in four defined γ_0 values corresponding to the four treatment effect and censoring level categories. These were as follows: $\gamma_0 = 1.04$ for the high treatment effect with low censoring setting, $\gamma_0 = 1.2$ for the low treatment effect with low censoring setting, $\gamma_0 = 3.35$ for the high treatment effect with high censoring setting, and $\gamma_0 = 3.71$ for the low treatment effect with high censoring setting.

4. Results

4.1 Separate Weighting

We summarized the mean of estimated causal estimand, relative bias and 95% coverage rate from the simulation for separate weighting procedure in Table 1. When using logistic regression to estimate both IPTW and IPCW, we observed smaller relative bias and higher 95% coverage rate among low censoring scenarios regardless of overlap and treatment effect settings. The high overlap scenarios were also observed associated with higher 95% coverage rate. However, such a pattern

was not obvious when using Cox model to estimate IPCW. We also checked covariate balancing by computing absolute standardized difference (ASD) and reported the results in table 2. Contrary to table 1, the performance of the method using logistic regression for IPTW and Cox model for IPCW was better than the model of dual logistic regression in terms of balancing baseline covariates.

Table 1: Separate Weighting Covariate Balance Results (ASD)

	X1			X2			X3		
Scenario[a]	Unweighted	Dual Logistic	Logistic/Cox	Unweighted	Dual Logistic	Logistic/Cox	Unweighted	Dual Logistic	Logistic/Cox
High/High/Low	0.0698	0.1970	0.0272	0.1477	0.2195	0.0377	0.0600	0.1359	0.0263
Med/High/Low	0.4353	0.2046	0.0385	1.1735	0.2493	0.0682	0.0598	0.1454	0.0308
Low/High/Low	0.7229	0.2899	0.1808	1.9886	0.5076	0.4037	0.0587	0.1880	0.0880
High/Low/Low	0.0691	0.2062	0.0274	0.1467	0.2248	0.0413	0.0568	0.1324	0.0254
Med/Low/Low	0.4358	0.2011	0.0375	1.1714	0.2348	0.0707	0.0586	0.1218	0.0308
Low/Low/Low	0.7250	0.2951	0.1837	1.9858	0.5381	0.3948	0.0589	0.1774	0.0870
High/High/High	0.0698	0.1967	0.0427	0.1464	0.3377	0.0553	0.0570	0.1344	0.0220
Med/High/High	0.4343	0.2082	0.0579	1.1740	0.3501	0.0911	0.0598	0.1377	0.0307
Low/High/High	0.7235	0.2966	0.1985	1.9852	0.5636	0.3629	0.0577	0.1830	0.0751
High/Low/High	0.0702	0.1973	0.0478	0.1462	0.3511	0.0566	0.0591	0.1356	0.0235
Med/Low/High	0.4306	0.1990	0.0574	1.1767	0.3530	0.0869	0.0564	0.1363	0.0296
Low/Low/High	0.7214	0.2543	0.2158	1.9860	0.5801	0.3608	0.0605	0.1805	0.0760

[a] Note: scenarios are described by (degree of overlap/treatment effect level/censoring level)

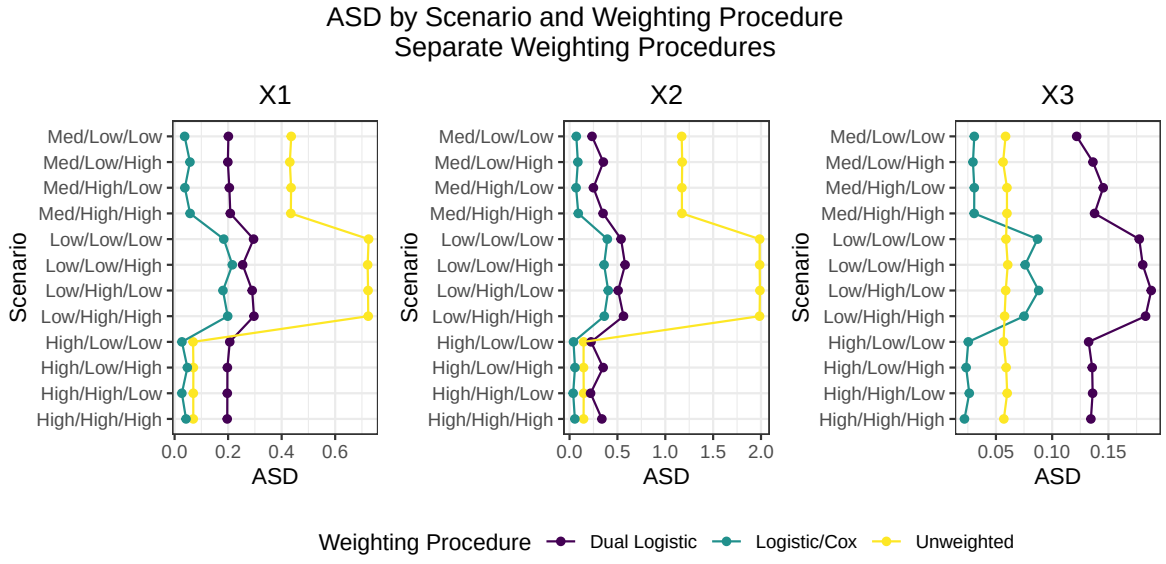


Table 2: Separate Weighting Estimation Results

		Dual Logistic			Logistic/Cox		
Scenario[a]	True ACE	Avg. Estimate	Relative Bias	95% Coverage Rate	Avg. Estimate	Relative Bias	95% Coverage Rate
High/High/Low	0.12	0.1186	-0.0119	0.924	0.0929	-0.2260	0.708
Med/High/Low	0.12	0.1176	-0.0200	0.914	0.0929	-0.2256	0.785
Low/High/Low	0.12	0.1227	0.0227	0.853	0.0965	-0.1956	0.883
High/Low/Low	0.014	0.0165	0.1815	0.918	0.0113	-0.1937	0.938
Med/Low/Low	0.014	0.0130	-0.0720	0.917	0.0109	-0.2194	0.942
Low/Low/Low	0.014	0.0146	0.0460	0.905	0.0167	0.1928	0.894
High/High/High	0.12	0.0797	-0.3362	0.687	0.0552	-0.5401	0.008
Med/High/High	0.12	0.0856	-0.2871	0.676	0.0543	-0.5472	0.023
Low/High/High	0.12	0.0886	-0.2614	0.650	0.0609	-0.4926	0.412
High/Low/High	0.014	0.0097	-0.3088	0.919	0.0064	-0.5410	0.881
Med/Low/High	0.014	0.0096	-0.3165	0.910	0.0055	-0.6106	0.935
Low/Low/High	0.014	0.0159	0.1348	0.893	0.0099	-0.2950	0.914

[a] Note: scenarios are described by (degree of overlap/treatment effect level/censoring level)

4.2 Sequential Weighting

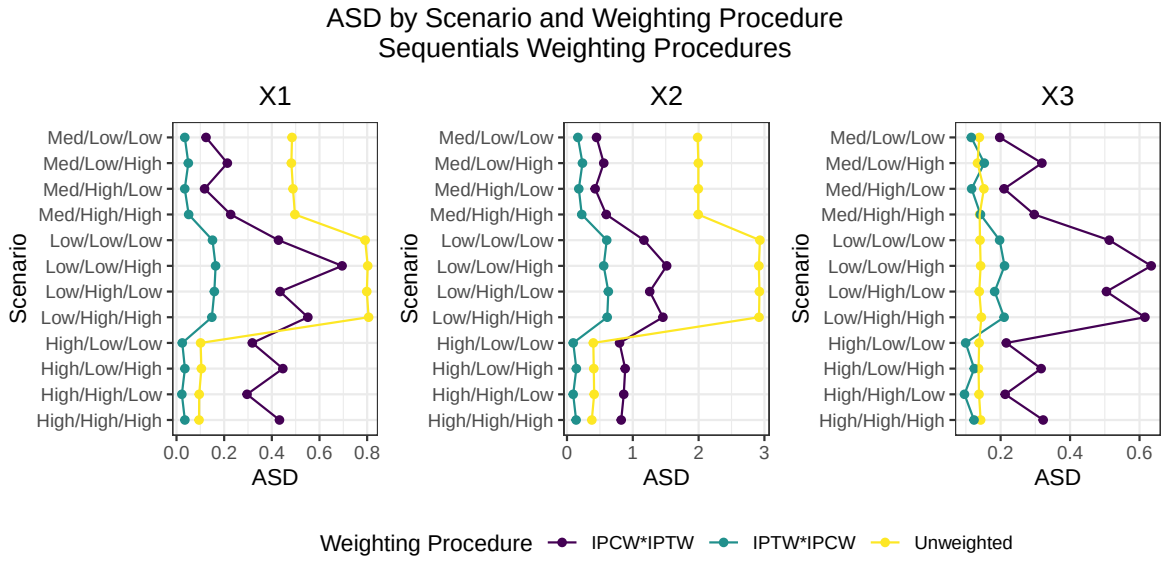
The following table provides results corresponding to how the sequential weighting procedures performed in balancing covariates between the two treatment groups:

Table 3: Sequential Weighting Covariate Balance Results (ASD)[a]

	X1			X2			X3		
Scenario[b]	Unweighted	IPTW∘IPCW	IPCW∘IPTW	Unweighted	IPTW∘IPCW	IPCW∘IPTW	Unweighted	IPTW∘IPCW	IPCW∘IPTW
High/High/Low	0.0952	0.0225	0.2960	0.4127	0.0939	0.8626	0.1378	0.0959	0.2131
Med/High/Low	0.4887	0.0346	0.1178	1.9954	0.1795	0.4275	0.1518	0.1165	0.2100
Low/High/Low	0.7985	0.1588	0.4346	2.9240	0.6283	1.2576	0.1384	0.1828	0.5048
High/Low/Low	0.1011	0.0242	0.3182	0.4002	0.0949	0.7991	0.1381	0.0993	0.2163
Med/Low/Low	0.4846	0.0348	0.1239	1.9852	0.1660	0.4492	0.1387	0.1156	0.1974
Low/Low/Low	0.7916	0.1510	0.4281	2.9317	0.6041	1.1700	0.1407	0.1972	0.5129
High/High/High	0.0945	0.0351	0.4321	0.3772	0.1386	0.8240	0.1425	0.1234	0.3226
Med/High/High	0.4968	0.0510	0.2273	1.9941	0.2244	0.5964	0.1396	0.1419	0.2969
Low/High/High	0.8062	0.1484	0.5512	2.9180	0.6113	1.4578	0.1446	0.2101	0.6156
High/Low/High	0.1044	0.0352	0.4463	0.4069	0.1422	0.8841	0.1365	0.1240	0.3167
Med/Low/High	0.4820	0.0496	0.2134	1.9965	0.2354	0.5590	0.1335	0.1529	0.3189
Low/Low/High	0.8024	0.1641	0.6949	2.9156	0.5579	1.5148	0.1425	0.2113	0.6337

[a] Averaged over 1000 total bootstrapped replicates (100 bootstrap replicates over each of 100 samples)

[b] Scenarios are described by (degree of overlap/treatment effect level/censoring level)



It is apparent that there is improvement across most simulation settings in covariate balance in the IPTW∘IPCW weighting method over the unweighted observed data in covariates X_1 and X_2. This is not the case for the IPCW∘IPTW weighting method, however, as some ASD measures are even larger than what is observable in the

Table 4: Sequential Weighting Estimation Results[a]

		IPTW*circ*IPCW			IPCW*circ*IPTW		
Scenario[b]	True ACE	Avg. Estimate	Relative Bias	95% Coverage Rate	Avg. Estimate	Relative Bias	95% Coverage Rate
High/High/Low	0.12	0.1391	0.1590	0.93	0.1408	0.1731	0.84
Med/High/Low	0.12	0.1307	0.0894	0.91	0.1361	0.1345	0.89
Low/High/Low	0.12	0.1452	0.2096	0.89	0.1396	0.1633	0.91
High/Low/Low	0.014	0.0247	0.7653	0.97	0.0132	-0.0600	0.93
Med/Low/Low	0.014	0.0182	0.3003	0.93	0.0166	0.1864	0.91
Low/Low/Low	0.014	0.0307	1.1927	0.91	0.0215	0.5335	0.91
High/High/High	0.12	0.1148	-0.0430	0.98	0.1233	0.0278	0.95
Med/High/High	0.12	0.1113	-0.0724	0.95	0.1244	0.0363	0.87
Low/High/High	0.12	0.1192	-0.0065	0.95	0.1331	0.1092	0.90
High/Low/High	0.014	0.0152	0.0853	0.94	0.0158	0.1288	0.94
Med/Low/High	0.014	0.0127	-0.0939	0.90	0.0149	0.0637	0.91
Low/Low/High	0.014	0.0085	-0.3926	0.93	0.0112	-0.1973	0.92

[a] Averaged over 1000 total bootstrapped replicates (100 bootstrap replicates over each of 100 samples)

[b] Note: scenarios are described by (degree of overlap/treatment effect level/censoring level)

5. Discussion

6. References

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