Propensity score weighting for causal inference with multi-stage clustered data

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Abstract

Propensity score weighting is a tool for causal inference to adjust for measured confounders. Survey data are often collected under complex sampling designs such as multi-stage cluster sampling, which presents challenges for propensity score modeling and estimation. In addition, for clustered data, there may also be unobserved cluster effects related to both the treatment and the outcome. When such unmeasured confounders exist and are omitted in the propensity score model, the subsequent propensity score adjustment will be biased. We propose a calibrated propensity score weighting adjustment for multi-stage clustered data in the presence of unmeasured cluster-level confounders. The propensity score is calibrated to balance design-weighted covariate distributions and cluster effects between treatment groups. In particular, we consider a growing number of calibration constraints increasing with the number of clusters, which is necessary for removing asymptotic bias that is associated with the unobserved cluster-level confounders. We show that our estimator is robust in the sense that the estimator is consistent without correct specification of the propensity score model. We extend the results to the multiple treatments case. In simulation studies we show that the proposed estimator is superior to other competitors. We estimate the effect of School Body Mass Index Screening on prevalence of overweight and obesity for elementary schools in Pennsylvania.

Keywords: Causality; Covariate Balance; Double Robustness; Unmeasured Confounder.
1 Introduction

The gold standard for evaluating effects of treatments is using randomized controlled trials. However, this approach may not be applicable due to practical constraints or ethical issues. Observational studies become useful in these settings. In observational studies, there often is confounding by indication: some covariates are predictors of both the treatment and the outcome. One implication is that the covariate distributions differ between treatment groups. Under the assumption of unconfoundedness or ignorable treatment assignment, causal effect of treatments can be obtained by comparing the outcomes for units from different treatment groups, adjusting for the observed confounders. Rosenbaum and Rubin (1983) further introduced the central role of the propensity score, and showed that adjusting for the propensity score is sufficient to remove bias due to all observed confounders. An extensive literature thereafter proposed a number of estimators based on the propensity score. In particular, propensity score weighting can be used to create a weighted population where the covariate distributions are balanced between treatment groups, and the comparison between the weighted outcomes has a causal interpretation (Hirano and Imbens; 2001; Hirano et al.; 2003; Imbens and Rubin, 2015).

Survey data are observational in nature, and are often collected under complex sampling designs. In complex surveys, each unit is associated with a design weight, which approximates the number of units that this unit represents in the finite population. Also, the data often undergo other weighting adjustments such as calibration, nonresponse adjustment, poststratification, raking, weight trimming, and etc. Propensity score methods for causal inference are well-developed for non-survey data; there is however much less literature that focuses on how to adopt these methods for complex survey data, with exceptions including Zanutto et al. (2005); Zanutto (2006); Li et al. (2013), and DuGoff et al. (2014). These researchers suggested that design weights should be incorporated in propensity score modeling or the weighting estimators. For clustered data, Li et al. (2013) investigated the performance of the propensity score weighting estimator and the doubly robust estimator under generalized linear mixed effect models for the propensity score and the outcome, and showed that at least either the propensity score model or the weighting estimator should take the sampling design into account in order to avoid bias.

Another challenge with complex survey data is that the sampled data are often collected at multi-stages. For example, for two-stage cluster sampling, clusters are selected at the first stage,
and then for the sampled clusters, units are selected at the second stage. The multi-stage sampling
design makes the propensity score modeling difficult. Moreover, even we collect a rich set of
unit-level covariates, there may be unobserved cluster effects related to both the treatment and
the outcome. When such unmeasured confounders exist and are omitted in the propensity score
model, the subsequent analysis will be biased.

The goal of this article is to develop propensity score weighting for complex survey data with
multi-stage clustered data structure in the presence of unmeasured cluster-level confounders. We
focus on two-stage cluster sampling. The key insight is based on the central role of the propensity
score in balancing the covariate distributions between treatment groups in the finite population. In
survey sampling, calibration is widely used to integrate auxiliary data, see for example, Chen and
Sitter (1999); Wu and Sitter (2001); Chen et al. (2002); and Kim (2009), or to handle nonresponse
in survey sampling, see for example, Kott (2006); Chang and Kott (2008); and Kim et al. (2016).
In causal inference, calibration has been used such as Constrained Empirical Likelihood (Qin
and Zhang, 2007), Entropy Balancing (Hainmueller, 2012), Inverse Probability Tilting (Graham
et al., 2012), and Covariate Balance Propensity Score of (Imai and Ratkovic, 2014). Chan et al.
(2015) showed that estimation of average treatment effects by empirical balancing calibration
weighting can achieve global efficiency. However, all these works are developed for simple
settings with independent and identically distributed (iid) random variables and they assume that
there are no unmeasured confounders. We adopt calibration for causal inference with clustered
data, to handle unmeasured cluster effects that may confound the causal relationship between
the treatment and the outcome. Based on the sample, we impose the design-weighted covariate
balancing constraints, and also certain design-weighted balancing constraints for each cluster. In
particular, we consider a growing number of calibration constraints increasing with the number of
clusters, which is necessary for removing asymptotic bias that is associated with the unobserved
cluster-level confounders.

The organization of this paper is as follows. Section 2 provides the basic setup. Section 3
introduces the proposed calibration propensity score weighting estimator and the computational
aspect in light of exponential titling. In Section 4, main results are presented. Under certain
conditions, we show that the proposed estimator is consistent for the average treatment effect in
the presence of unmeasured cluster-level confounders, without requiring correctly specification
of the propensity score model and the outcome model, and therefore is robust. Imposing calibration conditions also improves the efficiency of the estimator. In Section 5, we extend the results to the multiple treatments case. In Section 6, we examine the consistency and robustness of the proposed estimator in finite samples by simulation. In Section 7, we estimate the effect of School Body Mass Index Screening on prevalence of overweight and obesity for elementary schools in Pennsylvania, and discussions are made in Section 8.

2 Basic Setup

We use the potential outcome framework (Rubin; 1974), which has been commonly adopted in the causal inference literature. Consider a finite population with \( M \) clusters and \( N_i \) units in the \( i \)th cluster. Therefore, the population size is \( N = \sum_{i=1}^{M} N_i \). For unit \( j \) in cluster \( i \), we observe a vector of pre-treatment variables \( X_{ij} \), a binary treatment \( A_{ij} \) with 0 indicating the control treatment and 1 indicating the active treatment, and lastly an outcome variable \( Y_{ij} \). We assume that there is no interference between units and no versions of each treatment level (the Stable Unit Treatment Value assumption, Rubin; 1978). Under this assumption, each unit has two potential outcomes: \( Y_{ij}(0) \), the outcome that would be realized if the unit received the control treatment, and \( Y_{ij}(1) \), the outcome that would be realized if the unit received the active treatment. We assume that the observed outcome is the potential outcome corresponding to the treatment received, i.e., \( Y_{ij} = Y_{ij}(A_{ij}) \) (the Consistency assumption, Rubin; 1974).

The sample is selected according to a two-stage cluster sampling design. Specifically, at the first stage, cluster \( i \) is sampled with the first inclusion probability \( \pi_i \), \( i \in S_I \), where \( S_I \) is the index set for the sampled clusters and we assume that \( S_I = \{1, \ldots m\} \) for simplicity. Let \( \pi_{ij} = \text{pr}(i,j \in S_I) \) be the second inclusion probability for clusters \( i \) and \( j \) being sampled. At the second stage, given that cluster \( i \) was selected at the first stage, unit \( j \) is sampled with conditional probability \( \pi_{j|i} \), \( j = 1, \ldots, n_i \). Let \( \pi_{kl|i} \) be the second inclusion probability for units \( k \) and \( l \) being sampled given that cluster \( i \) was selected. The final sample size is \( n = \sum_{i \in S_I} n_i \). Let the design weight for unit \( j \) in cluster \( i \) be \( \omega_{ij} = (\pi_i \pi_{j|i})^{-1} \), which reflects the number of units for cluster \( i \) in the finite population this unit \( j \) represents. Our goal is to estimate the average treatment effect \( \tau = E\{Y(1) - Y(0)\} \) based on the sample.

Rubin (1974) described the condition for estimating average treatment effect in the setting.
with iid samples, the so-called unconfoundedness or ignorable treatment assignment assumption,

\[ Y(a) \perp A \mid X, \quad (1) \]

for \( a = 0, 1 \). This assumption indicates that there are no unmeasured confounders, which can be achieved by collected a sufficiently rich set of pre-treatment variables that affect both the treatment and the outcome. For clustered data, even we collect all the unit-level confounders, there may be unmeasured cluster effects \( U_i \) that are related to both the treatment and the outcome. In this case, we make the following assumption instead of (1).

**Assumption 1 (Ignorability)** For \( a = 0, 1 \), \( Y_{ij}(a) \perp A_{ij} \mid X_{ij}, U_i \).

Under Assumption 1,

\[
E\{Y_{ij}(a) \mid X_{ij}, U_i\} = E(Y_{ij} \mid A_{ij} = a, X_{ij}, U_i), \quad (2)
\]

so the average of the potential outcomes can be identified if the cluster effects \( U_i \) are observed.

Following Rosenbaum and Rubin (1983), we define the propensity score for our setting.

**Definition 1 (Propensity score)** The propensity score is the conditional probability of receiving the active treatment given the confounders,

\[
e(X_{ij}, U_i) = \Pr(A_{ij} = 1 \mid X_{ij}, U_i). \quad (3)
\]

To estimate the average treatment effect, we make the following identifiable assumptions. First, let us assume that there is sufficient overlap between treatment groups.

**Assumption 2 (Overlap)** For all \( X_{ij} \) and \( U_i \), there exist \( \underline{e} \) and \( \bar{e} \) such that \( 0 < \underline{e} < e(X_{ij}, U_i) < \bar{e} < 1 \).

The above overlap assumption is required; otherwise there exist some units for which we can not estimate the treatment effect without extrapolation assumptions. Secondly, since the cluster effects are never observed, we make the following independence assumption in order to identity the causal parameter.
Assumption 3 The unit-level confounder $X_{ij}$ and the unobserved cluster-level confounder $U_i$ are independent.

The unobserved cluster-level confounder $U_i$ can be viewed as a modeling quantity, which is similar to the role of the random effect in mixed effect models. In practice, the unobserved cluster-level confounder is likely to be associated with the observed confounders. In such cases, we model $U_i$ to be part of the unobserved confounder that is independent of $X_{ij}$. Implicitly, we assume that the other part of the unobserved confounder is fully controlled after adjusting for $X_{ij}$. Figure 1 presents a causal diagram for which Assumptions 1 and 3 are satisfied. In Theorem 1, we show that under Assumptions 1–3, $\tau$ is nonparametrically identifiable.

Notice that the outcome model for (2) and the propensity score model for (3) share the same random effect $U_i$. Such models, the so-called shared parameter or shared random effects models, have been used in the missing data literature for modeling one particular type of nonignorable missingness. Namely, researchers use separate models for the primary response and missingness and link them by a common random parameter. See for example, Follmann and Wu (1995); Gao (2004); Yang et al. (2013); Kim et al. (2016).

Finally, for the asymptotic result, we assume the following moment condition.

Assumption 4 For $a = 0, 1$, $E\{Y(a)^4\} < \infty$.

3 Methodology

For analyzing survey data, design-based approaches are favored in government agencies since they are model-free and thereby avoiding model misspecification (Kish, 1965; Cochran, 2007). The widely used design-based estimator is the Horvitz-Thompson estimator (Horvitz and Thompson, 1952). For example, let $T$ is the population total of $Y_{ij}$, and the Horvitz-Thompson estimator is $\hat{T}_n = \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} Y_{ij}$, which is design-unbiased for $T$.

If the propensity score $e(X_{ij}, U_i)$ is known, the design-based inverse probability of treatment weighting (IPTW) estimator for $\tau$ is

$$\hat{\tau}_{IPTW} = \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij} Y_{ij}}{e(X_{ij}, U_i)} - \frac{(1 - A_{ij}) Y_{ij}}{1 - e(X_{ij}, U_i)} \right\} .$$

(4)
where $\hat{N} = \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij}$. Now the issue is that in observational studies, the true propensity score is usually unknown. For propensity score modeling and estimation, the majority of the literature relies on parametric logistic regression to estimate propensity score. For clustered data, Li et al. (2013) considered different models including fixed effect logistic regression models and random effect logistic regression models. However, it requires assumptions regarding variable selection, the functional form of variables, and specification of interactions. If any of these assumption fail, it may results in bias in effect estimation.

We consider a parametric working model for the propensity score, and calibrate the propensity score to satisfy certain constraints. To motivate these constraints, notice that the central role of the propensity score is to balance the covariate distributions between treatment groups in the population. Specifically, we have

$$E \left\{ \frac{A}{e(X,U)} X \right\} = E \left\{ \frac{1 - A}{1 - e(X,U)} X \right\} = E(X), \quad (5)$$

and

$$E \left\{ \frac{A}{e(X,U)} U \right\} = E \left\{ \frac{1 - A}{1 - e(X,U)} U \right\} = E(U). \quad (6)$$

Based on the sample, for the estimated propensity score $\hat{e}(X_{ij}, U_i)$, we would impose the following design-weighted moment constraints,

$$\sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} X_{ij} = \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} X_{ij}, \quad (7)$$

$$\sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_i)} X_{ij} = \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} X_{ij}, \quad (8)$$

$$\sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \frac{A_{ij}}{\hat{e}(X_{ij}, U_{ij})} U_i = \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} U_i, \quad (9)$$

$$\sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_{ij})} U_i = \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} U_i, \quad (10)$$

which approximate equations in (5) and (6). However, since the cluster effects $U_i$ are unobserved, the constraints (9) and (10) are infeasible. We notice that if

$$\sum_{j=1}^{n_i} \omega_{ij} \frac{A_{ij}}{\hat{e}(X_{ij}, U_{ij})} = \sum_{j=1}^{n_i} \omega_{ij}, \quad (i = 1, \ldots, K), \quad (11)$$

$$\sum_{j=1}^{n_i} \omega_{ij} \frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_{ij})} = \sum_{j=1}^{n_i} \omega_{ij}, \quad (i = 1, \ldots, K), \quad (12)$$
the constraints (9) and (10) are satisfied automatically. Here, we consider a growing number of calibration equations increasing with the number of clusters, as opposed to a fixed number of calibration equations (9) and (10). The growing number of calibration equations is necessary for removing asymptotic bias that is associated with the unobserved cluster-level confounders.

3.1 Computation

We now discuss the specific steps for computation.

Step0. Use a logistic linear fixed effect model with a cluster-level main effect, fitted to \((A_{ij}, X_{ij}, \delta_i)\) where \(\delta_i\) is the cluster indicator. This provides an initial set of inverse propensity score weights \(W^0 = \{d_{ij}; i \in S_I, j = 1, \ldots, n_i\}\), with \(d_{ij} = 1/e_{ij}^0\) if \(A_{ij} = 1\) and \(d_{ij} = 1/(1 - e_{ij}^0)\) if \(A_{ij} = 0\).

Step1. We follow the procedure discussed by Deville and Särndal (1992) to minimize a function of the distance between the initial weights \(W^0\) and the final weights \(W = \{\alpha_{ij}; i \in S_I, j = 1, \ldots, n_i\}\), subject to the calibration constraints. Consider a general distance function

\[
\min \sum_{i \in S_I} \sum_{j=1}^{n_i} G(\alpha_{ij}, \omega_{ij})
\]

subject to the calibration constraints. If \(G(\alpha_{ij}, \omega_{ij}) = \omega_{ij}(\alpha_{ij}/\omega_{ij} - 1)^2\), the minimum distance estimation leads to the generalized regression estimator (Park and Fuller; 2012). If \(G(\alpha_{ij}, \omega_{ij}) = -\omega_{ij} \log(\alpha_{ij}/\omega_{ij})\), this approach leads to empirical likelihood estimation (Newey and Smith; 2004). Calibration using empirical likelihood has been discussed in Hellerstein and Imbens (1999); Tan (2006); Qin and Zhang (2007); Chan et al. (2012); Graham et al. (2012); Han and Wang (2013). We modify the initial set of weights \(W^0\) to a new set of weights \(W = \{\alpha_{ij}; i \in S_I, j = 1, \ldots, n_i\}\) by minimizing the Kullback-Leibler distance (Kullback and Leibler; 1951),

\[
\sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij}\alpha_{ij} \log \frac{\alpha_{ij}}{d_{ij}},
\]

subject to the calibration equations (7), (8), (11) and (12). The Kullback-Leibler minimum distance estimation leads to the exponential tilting estimator (Kitamura and Stutzer; 1997).
An advantage of using the exponential tilting estimator is that the resulting weights are always non-negative. Also, with exponential tilting, the calibration constraints (11) and (12) can be built into a closed form expression for the weights, and thus avoiding solving a large number of equations. See the computation below. This reduces the computation burden greatly when there is a large number of clusters. By Lagrange Multiplier, the solution to (13) is

$$
\alpha_{ij}(\lambda_1, \lambda_2) = \frac{A_{ij} d_{ij} \exp(\lambda_1 X_{ij} A_{ij})}{\sum_{j=1}^{n_i} \omega_{ij} A_{ij} d_{ij} \exp(\lambda_1 X_{ij} A_{ij})} + \frac{(1 - A_{ij}) d_{ij} \exp\left\{\lambda_2 X_{ij} (1 - A_{ij})\right\}}{\sum_{j=1}^{n_i} \omega_{ij} (1 - A_{ij}) d_{ij} \exp\left\{\lambda_2 X_{ij} (1 - A_{ij})\right\}},
$$

where $\hat{N}_i = \sum_{j=1}^{n_i} \omega_{ij}$, and $(\lambda_1, \lambda_2)^T$ is the solution to the following equation

$$
Q(\lambda_1, \lambda_2) = \left( \begin{array}{c} Q_1(\lambda_1, \lambda_2) \\ Q_2(\lambda_1, \lambda_2) \end{array} \right) = \left( \begin{array}{c} \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \left\{ A_{ij} \alpha_{ij}(\lambda_1, \lambda_2) - 1 \right\} X_{ij} \\ \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \left\{ (1 - A_{ij}) \alpha_{ij}(\lambda_1, \lambda_2) - 1 \right\} X_{ij} \end{array} \right) = 0.
$$

From the above calibration algorithm, we obtain an estimate for the propensity score, $\hat{e}(X_{ij}, U_i) = \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2) - A_{ij} \{1 - \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2)\}^{-1} A_{ij}$. The proposed estimator for the average treatment effect $\tau$ is the weighting estimator (4) with the propensity score estimates $\hat{e}(X_{ij}, U_i)$, denoted by $\hat{\tau}_{\text{cal}}$.

**Remark 1** The logistic linear fixed effect model in Step 0 is only a working model, and the proposed estimator $\hat{\tau}_{\text{cal}}$ does not require the specification of this working model to be true. Chan et al. (2015) suggested using an initial set of uniform weights, which controls the dispersion of final weights and is less likely to obtain extreme final weights. Our simulation studies show that the consistency of $\hat{\tau}_{\text{cal}}$ is not sensitive to the choice of the initial set of weights. Therefore, $\hat{\tau}_{\text{cal}}$ is robust to the specification of this working propensity score model.

### 4 Main results

Theorem 1 establishes the unbiasedness of the proposed estimator for the average treatment effect $\tau$, which indicates that $\tau$ is nonparametrically identifiable by $\hat{\tau}_{\text{cal}}$. The proof is given in the Appendix.
**Theorem 1** Under Assumptions 1–3, the proposed estimator $\hat{\tau}_{\text{cal}}$ is unbiased of $\tau$.

**Remark 2** The weighting estimators are often not an efficient estimator. In a special case, we found that the weighting estimator is efficient. Assume that the potential outcome variables follow linear mixed effects models, that is,

$$Y_{ij}(a) = X_{ij}\beta_a + U_i + e_{ij}, \ a = 0, 1,$$

(14)

with unknown parameters $\beta_a$, random effects $U_i$ that have mean zero, and independent errors $e_{ij}$ such that $E(e_{ij} | X_{ij}, U_i) = 0$. The augmented inverse probability of treatment weighting (AIPTW, Lunceford and Davidian 2004; Bang and Robins 2005) estimator of $\tau$ is

$$\hat{\tau}_{\text{AIPTW}} = \frac{1}{N} \sum_{i \in S} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij}Y_{ij}}{\hat{e}(X_{ij}, U_i)} \left(\frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_i)}\right) Y_{ij} - \frac{A_{ij}Y_{ij}}{\hat{e}(X_{ij}, U_i)} \left(\frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_i)}\right) \right\}$$

$$- \frac{1}{N} \sum_{i \in S} \sum_{j=1}^{n_i} \omega_{ij} \frac{A_{ij} - \hat{e}(X_{ij}, U_i)}{\hat{e}(X_{ij}, U_i)} (X_{ij}\hat{\beta}_1 + U_i)$$

$$- \frac{1}{N} \sum_{i \in S} \sum_{j=1}^{n_i} \omega_{ij} \frac{A_{ij} - \hat{e}(X_{ij}, U_i)}{1 - \hat{e}(X_{ij}, U_i)} (X_{ij}\hat{\beta}_0 + U_i),$$

(15)

where $\hat{\beta}_a$ is a consistent estimator of $\beta_a$ for $a = 0, 1$. The AIPTW estimator has been shown to be doubly robust (Robins et al. 1995, 1997; Lunceford and Davidian 2004; Bang and Robins 2005; Kang and Schafer 2007) in the sense that if either the propensity score model or the outcome regression model for $Y_{ij}(a)$ is correctly specified, the estimator is unbiased. Moreover, if both models are correctly specified, the AIPTW estimator is efficient in the setting with iid random variables. Notice that by the constraints (7), (8), (11), and (12), the augmented terms in (15) disappear and therefore $\hat{\tau}_{\text{cal}} = \hat{\tau}_{\text{AIPTW}}$.

To establish large-sample properties of our estimator, we assume our sequence of finite populations and samples are as described in Isaki and Fuller (1982), such that the population size $N$ increases but the cluster sample sizes $M_i$ may remain small. In such cases, the number of clusters $K$ increases linearly with $N$. In other cases, $K$ may increase at a slower rate than $N$ does. Assume that the sufficient conditions for the asymptotic normality of the Horvitz-Thompson estimator hold for the sequence of finite populations and the samples, see Fuller (2009). For the sequence of designs, we require that the first-order inclusion probabilities $\pi_i \pi_{ji}$
satisfy \(0 < \pi < \pi_i \pi_{ji} < \bar{\pi} < 1\) for some values \(\pi\) and \(\bar{\pi}\), which prevents producing extremely large design weights that dominate the analyses.

**Theorem 2** Under Assumptions \([7,4]\) and the above regularity conditions on the sequence of populations, samples and designs, the calibrated propensity score weighting estimator in \([4]\), subject to constraints \([7], [8], [11], \) and \([12]\), satisfies

\[
n^{1/2}N^{-1}(\hat{t}_{cal} - \tau) \to \mathcal{N}(0, V),
\]

as \(n \to \infty\), where

\[
V = nN^{-2}\text{var} \left( \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \Phi_{ij} \right),
\]

with \(\Phi_{ij} = \{\alpha_{ij}(\lambda_1^*, \lambda_2^*)A_{ij}(Y_{ij} - B_1^TX_{ij}) + B_1^TX_{ij} - \{\alpha_{ij}(\lambda_1^*, \lambda_2^*)(1 - A_{ij})(Y_{ij} - B_2^TX_{ij}) + B_2^TX_{ij}\},
\)

\[
B_1 = E \left\{ \sum_{i=1}^{M} \sum_{j=1}^{N_i} \alpha_{ij}(\lambda_1^*, \lambda_2^*) \left\{ 1 - \frac{\alpha_{ij}(\lambda_1^*, \lambda_2^*)}{n_i} \right\} A_{ij}Y_{ij}X_{ij}^T \right\}
\times E \left\{ \sum_{i=1}^{M} \sum_{j=1}^{N_i} \alpha_{ij}(\lambda_1^*, \lambda_2^*) \left\{ 1 - \frac{\alpha_{ij}(\lambda_1^*, \lambda_2^*)}{n_i} \right\} A_{ij}X_{ij}X_{ij}^T \right\}^{-1},
\]

\[
B_2 = E \left\{ \sum_{i=1}^{M} \sum_{j=1}^{N_i} \alpha_{ij}(\lambda_1^*, \lambda_2^*) \left\{ 1 - \frac{\alpha_{ij}(\lambda_1^*, \lambda_2^*)}{n_i} \right\} (1 - A_{ij})Y_{ij}X_{ij}^T \right\}
\times E \left\{ \sum_{i=1}^{M} \sum_{j=1}^{N_i} \alpha_{ij}(\lambda_1^*, \lambda_2^*) \left\{ 1 - \frac{\alpha_{ij}(\lambda_1^*, \lambda_2^*)}{n_i} \right\} (1 - A_{ij})X_{ij}X_{ij}^T \right\}^{-1},
\]

and \((\lambda_1^*, \lambda_2^*)^T\) satisfies \(E\{Q(\lambda_1^*, \lambda_2^*)\} = 0\).

See Appendix for the proof. We now discuss variance estimation. Let \(\phi_{ij} = \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2)\{A_{ij}(Y_{ij} - \hat{B}_1^TX_{ij}) - (1 - A_{ij})(Y_{ij} - \hat{B}_2^TX_{ij})\} + (\hat{B}_1 - \hat{B}_2)^TX_{ij},\) where

\[
\hat{B}_1 = \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2) \left\{ 1 - \frac{\alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2)}{n_i} \right\} A_{ij}Y_{ij}X_{ij}^T
\times \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2) \left\{ 1 - \frac{\alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2)}{n_i} \right\} A_{ij}X_{ij}X_{ij}^T,
\]

\[
\hat{B}_2 = \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2) \left\{ 1 - \frac{\alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2)}{n_i} \right\} (1 - A_{ij})Y_{ij}X_{ij}^T
\times \sum_{i \in S_i} \sum_{j=1}^{n_i} \omega_{ij} \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2) \left\{ 1 - \frac{\alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2)}{n_i} \right\} (1 - A_{ij})X_{ij}X_{ij}^T.
\]
Let \( \hat{\tau}_i = \sum_{j=1}^{n_i} \pi_{ji}^{-1} \phi_{ij} \) and
\[
\hat{V}_i = \sum_{k=1}^{n_i} \sum_{l=1}^{n_i} \frac{\pi_{kl|i} - \pi_{k|i} \pi_{l|i}}{\pi_{k|i} \pi_{l|i}} \phi_{ik} \phi_{il}.
\]

The variance estimator is
\[
\hat{V}(\hat{\tau}_{cal}) = \frac{1}{N^2} \left( \sum_{i \in S} \sum_{j \in S_i} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_i \pi_j} \hat{\tau}_i \hat{\tau}_j + \sum_{i \in S_i} \frac{\hat{V}_i}{\pi_i} \right),
\]
which is design-consistent for \( \text{var}(\hat{\tau}_{cal}) \). The above variance estimation uses linearization. Alternatively, we can develop replication methods such as Jackknife variance estimation.

5 Extension to multiple treatments

There is more and more attention nowadays to the setting with more than two treatments, which is important and common in empirical practice. See for example, Imbens (2000); Robins et al. (2000); Lechner (2001); Foster (2003); Hirano and Imbens (2004); Imai and Van Dyk (2012); Cole and Frangakis (2009); Cadarette et al. (2010); Cattaneo (2010); McCaffrey et al. (2013); Rassen et al. (2013); and Yang et al. (2016).

We now extend the potential outcome set up to the case with more than two treatments as in Imbens (2000); Lechner (2001); Imai and Van Dyk (2012); and Cattaneo (2010). The treatment is denoted by \( A \in \mathbb{A} = \{1, \ldots, T\} \). For each unit \( i \) there are \( T \) potential outcomes, one for each treatment level, denoted by \( Y_{ij}(a) \), for \( a \in \mathbb{A} \). The observed outcome for unit \( i \) is the potential outcome corresponding to the treatment received, \( Y_{ij} = Y_{ij}(A_{ij}) \). For the comparison between treatments \( a \) and \( a' \), the average effect is \( \tau(a, a') = E\{Y_{ij}(a) - Y_{ij}(a')\} \). In this setting, we modify Assumption 1 to the following assumption.

Assumption 5 (Ignorability) For \( a \in \mathbb{A} \), \( Y_{ij}(a) \perp A_{ij} \mid X_{ij}, U_i \).

Here, we generalize the propensity score to to the multiple treatments case, following Imbens (2000):

Definition 2 (Generalized Propensity Score) The generalized propensity score is the conditional probability of receiving each treatment level: \( g_a(X_{ij}, U_i) = \text{pr}(A = a \mid X_{ij}, U_i) \).
The overlap assumption is modified as follows.

**Assumption 6 (Overlap)** For \( a \in A \), \( \frac{g_a(X_{ij}, U_i)}{X_{ij}} > \xi > 0 \).

We consider a parametric working model for the generalized propensity score, and calibrate the generalized propensity score to satisfy certain constraints. Since we have

\[
E \left\{ I(A = a) \frac{X}{g_a(X, U)} \right\} = E(X), \quad E \left\{ I(A = a) \frac{U}{g_a(X, U)} \right\} = E(U), \quad a \in A.
\]

Based on the sample, for the estimated generalized propensity score \( \hat{g}_a(X_{ij}, U_i) \), we would impose the following constraints,

\[
\sum_{i \in S} \sum_{j=1}^{n_i} \omega_{ij} I(A_{ij} = a) \frac{X_{ij}}{g_a(X_{ij}, U_i)} = \sum_{i \in S} \sum_{j=1}^{n_i} \omega_{ij} X_{ij}, \quad (16)
\]

\[
\sum_{j=1}^{n_i} \omega_{ij} I(A_{ij} = a) \frac{X_{ij}}{g_a(X_{ij}, U_i)} = \sum_{j=1}^{n_i} \omega_{ij}, \quad (i = 1, \ldots, K, a \in A). \quad (17)
\]

We now discuss the specific steps for computation.

**Step 0.** Consider a working model, for example a fixed effect multinomial logistic regression model with a cluster-level main effect, fitted to \( (A_{ij}, X_{ij}, \delta_i) \) where \( \delta_i \) is the cluster indicator. We obtain an initial estimate for the generalized propensity score,

\[
g_0^a(X_{ij}, U_i) = \frac{\exp(X_{ij} \hat{\beta}_a + \hat{\gamma}_i)}{\sum_{a=1}^T \exp(X_{ij} \hat{\beta}_a + \hat{\gamma}_i)}, \quad a \in A,
\]

where \( (\hat{\beta}_1, \ldots, \hat{\beta}_T) \) and \( (\hat{\gamma}_1, \ldots, \hat{\gamma}_m) \) are the fitted estimates. This provides an initial set of inverse propensity score weights \( \mathbb{W}^0 = \{d_{ij}; i \in A_I, j = 1, \ldots, n_i\} \), with \( d_{ij} = 1/g_0^a(X_{ij}, U_i) \).

**Step 1.** We modify the initial set of weights \( \mathbb{W}^0 \) to a new set of weights \( \mathbb{W} = \{\alpha_{ij}; i \in S_I, j = 1, \ldots, n_i\} \), by minimizing the Kullback-Leibler distance,

\[
\sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \alpha_{ij} \log \frac{\alpha_{ij}}{d_{ij}},
\]

subject to the calibration equations (16) and (17). By Lagrange Multiplier, the solution is

\[
\alpha_{ij}(\lambda) = \tilde{N}_i \sum_{a=1}^T I(A_{ij} = a) d_{ij} \exp(\lambda_a^T X_{ij} A_{ij}) \frac{1}{\sum_{j=1}^{n_i} \omega_{ij} I(A_{ij} = a) d_{ij} \exp(\lambda_a^T X_{ij} A_{ij})},
\]
Theorem 3

Under Assumptions 3–6, and the same regularity conditions as in Theorem 2, the calibrated propensity score weighting estimator

\[ \hat{\tau}_{\text{cal}}(a, a') = \sum_{i \in S_l} \sum_{j=1}^{n_i} \omega_{ij} \left( I(A_{ij} = a) \frac{Y_{ij}}{\hat{g}_a(X_{ij}, U_i)} - I(A_{ij} = a') \frac{Y_{ij}}{\hat{g}_{a'}(X_{ij}, U_i)} \right). \]  

(19)

The proof of Theorem 3 is similar to that of Theorems 1 and 2, and therefore is omitted to avoid redundancy. Similarly, the variance estimator of \( \hat{\tau}_{\text{cal}}(a, a') \) can be developed accordingly.

Let \( \phi_{ij}(a, a') = \alpha_{ij}(\lambda_1, \lambda_2) \{ I(A_{ij} = a)(Y_{ij} - \hat{B}_a X_{ij}) - I(A_{ij} = a')(Y_{ij} - \hat{B}_{a'} X_{ij}) \} + (\hat{B}_a - \hat{B}_{a'})^2 \).
\( \hat{B}_a^T X_{ij} \), where

\[
\hat{B}_a = \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2) \left\{ 1 - \frac{\alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2)}{n_i} \right\} I(A_{ij} = a) Y_{ij} X_{ij}^T
\]

\times \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2) \left\{ 1 - \frac{\alpha_{ij}(\hat{\lambda}_1, \hat{\lambda}_2)}{n_i} \right\} I(A_{ij} = a) X_{ij} X_{ij}^T.
\]

Let \( \hat{\tau}_i(a, a') = \sum_{j=1}^{n_i} \pi_{ij}^{-1} \phi_{ij}(a, a') \) and

\[
\hat{V}_i(a, a') = \sum_{k=1}^{n_i} \sum_{l=1}^{n_i} \frac{\pi_{kl|i}}{\pi_{k|i}} \phi_{ik}(a, a') \frac{\phi_{lj}(a, a')}{\pi_{l|i}}.
\]

The variance estimator is

\[
\hat{V} \left\{ \hat{\tau}_{cal}(a, a') \right\} = \frac{1}{N^2} \left\{ \sum_{i \in S_f} \sum_{j \in S_f} \frac{\pi_{ij}}{\pi_{i|i}} \frac{\hat{\tau}_i(a, a') \hat{\tau}_j(a, a')}{\pi_i \pi_j} + \sum_{i \in S_f} \hat{V}_i(a, a') \right\}.
\]

6 Simulation Study

We conducted two simulation studies to evaluate the finite-sample performance of the proposed estimator. We first generated finite populations and then selected a sample from each finite population using a two-stage cluster sampling design.

In the first setting, the potential outcomes were generated according to linear mixed effect models, \( Y_{ij}(0) = X_{ij} + U_i + e_{ij} \) and \( Y_{ij}(1) = X_{ij} + \tau + \tau U_i + e_{ij} \), with \( \tau = 2, U_i \sim N(0,1), X_{ij} \sim N(0,1), e_{ij} \sim N(0,1), U_i, X_{ij}, e_{ij} \) are independent, \( i = 1, \ldots, M = 10,000, j = 1, \ldots, N_i \), and \( N_i \) is the integer part of \( 500 \exp(2 + U_i) / \{1 + \exp(2 + U_i)\} \). The population cluster sizes range from 100 to 500. The parameter of interest is \( \tau = E\{Y_{ij}(1) - Y_{ij}(0)\} \). We considered three propensity score models, \( \text{pr}(A_{ij} = 1 \mid X_{ij}; U_i) = h(\gamma_0 + \gamma_1 U_i + X_{ij}) \), with \( h(\cdot) \) being the inverse logit, probit and complementary log-log link function. The observed outcome is \( Y_{ij} = A_{ij} Y_{ij}(1) + (1 - A_{ij}) Y_{ij}(0) \). From each realized population, \( m \) clusters were sampled by PPS (Probability-Proportional-to-Size) sampling with the measure of size \( N_i \). So the first-order inclusion probability of selecting cluster \( i \) is equal to \( \pi_i = m N_i / \sum_{i=1}^{M} N_i \), which implicitly depends on the unobserved random effect. Once the clusters were sampled, the \( n_i \) units in the \( i \)th sampled cluster were sampled by Poison sampling with the corresponding first-order inclusion probabilities \( \pi_{j|i} = n z_{ij} / (\sum_{j=1}^{M_i} z_{ij}) \), where \( z_{ij} = 0.5 \) if \( e_{ij} < 0 \) and 1 if \( e_{ij} > 0 \). With this
sampling design, the units with $e_{ij} > 0$ were sampled with a chance twice as big as the units with $e_{ij} < 0$. We considered three combinations of the number of clusters $m$ and the cluster size $n$: (i) $(m, n) = (50, 50)$; (ii) $(m, n) = (100, 30)$, with a large number of small clusters; and (iii) $(m, n) = (30, 100)$, with a small number of large clusters.

In the second setting, all data-generating mechanisms were the same with the first setting, except that the potential outcomes were generated according to logistic linear mixed effect models, $Y_{ij}(0) \sim \text{Bernoulli}(p_{ij}^0)$ with $\text{logit}(p_{ij}^0) = X_{ij} + U_i$ and $Y_{ij}(1) \sim \text{Bernoulli}(p_{ij}^1)$ with $\text{logit}(p_{ij}^1) = X_{ij} + \tau + \tau u_i$, and moreover, in the 2-stage sampling, $\pi_{ji} = n z_{ij} / (\sum_{j=1}^{M_i} z_{ij})$, where $z_{ij} = 0.5$ if $Y_{ij} = 0$ and 1 if $Y_{ij} = 1$. With this sampling design, the units with $Y_{ij} = 1$ were sampled with a chance twice as big as the units with $Y_{ij} = 0$.

We computed four estimators for $\tau$: (i) $\hat{\tau}_{\text{simp}}$, the simple design-weighted estimator without propensity score adjustment; (ii) $\hat{\tau}_{\text{fix}}$, the weighting estimator (4) with the propensity score estimated by a logistic linear fixed effect model with a cluster-level main effect; (iii) $\hat{\tau}_{\text{ran}}$, the weighting estimator (4) with the propensity score estimated by a logistic linear mixed effect model where the cluster effect is random; and (iv) $\hat{\tau}_{\text{cal}}$, the proposed estimator with calibrations. We reported empirical biases, variances, coverages for 95% confidence intervals from 1,000 simulated datasets.

Table 1 shows the simulation results. The simple estimator shows large biases across difference scenarios, even adjusted for sampling design. This suggests that covariate distributions are different between treatment groups in the finite population, contributing to the bias. $\hat{\tau}_{\text{fix}}$ works well under Scenario 1 with the linear mixed effect model for the outcome and the logistic linear mixed effect model for the propensity score; however, its performance is not satisfactory under other scenarios. This is because except for Scenario 1, weighting by the logistic linear fixed effect model does not balance the covariate distributions in the finite population. Moreover, $\hat{\tau}_{\text{fix}}$ shows largest variance among the four estimators. This is because for a moderate or large number of clusters, there are many free parameters and the propensity score estimates may not be stable. For $\hat{\tau}_{\text{ran}}$, we assume that the cluster effect is random, which reduces the number of free parameters greatly. As a result, $\hat{\tau}_{\text{ran}}$ shows less variability than $\hat{\tau}_{\text{fix}}$. Nonetheless, both $\hat{\tau}_{\text{fix}}$ and $\hat{\tau}_{\text{ran}}$ can not control the bias well. The proposed calibrated propensity score weighting estimator is essentially unbiased of $\tau$ under all scenarios, and the empirical coverages are close to the nominal coverage.
Here, we used a working model, a logistic linear fixed effect model, to provide an initial set of weights. But the consistency of the estimator does not rely on this working model. When the true propensity score is probit or complementary log-log model, \( \hat{\tau}_{\text{cal}} \) is still consistent, confirming our theoretical results. We also examined an initial set of uniform weights and did not find results that were meaningfully different from those reported above.

7 An Application

We examined the 2007–2010 BMI surveillance data from Pennsylvania Department of Health to investigate the effect of School Body Mass Index Screening (SBMIS) on the annual overweight and obesity prevalence in elementary schools in Pennsylvania. Early studies have shown that SBMIS has been associated with increased parental awareness of child weight (Harris et al.; 2009; Ebbeling et al.; 2012). However, there have been mixed findings about effects of screening on reducing prevalence of overweight and obesity (Harris et al.; 2009; Thompson and Card-Higgins; 2009).

The data includes 493 school districts in Pennsylvania. The baseline is the school year 2007. The schools are clustered by two factors: location (rural, suburban, and urban), and population density (low, median, and high). This results in five clusters: rural-low, rural-median, rural-high, suburban-high, and urban-high. Let \( A = 1 \) if the school implemented SBMIS, and \( A = 0 \) if the school did not. In this dataset, 63% of schools implemented SBMIS, and the percentages of schools implemented SBMIS across the clusters are from 45% to 70%, indicating cluster-level heterogeneity of treatment. The outcome variable \( Y \) is the annual overweight and obesity prevalence for each district by dividing the number with Body Mass Index (BMI) > 85th by the total number of students screened for each district in the school year 2010. For each school, we obtain individual characteristics including the baseline prevalence of overweight and obesity \( X_1 \), and percentage of reduced and free lunch \( X_2 \).

For a direct comparison, the average difference of the prevalence of overweight and obesity for schools that implemented SBMIS and those that did not is 8.78%. This unadjusted difference in the prevalence of overweight and obesity ignores differences in individual covariates and cluster characteristics. Standard propensity score analyses including \( X_1 \) and \( X_2 \) would account for these observed differences, but there may also be unobserved cluster-level confounders. When
such unmeasured confounders exist but are omitted from the propensity score model, the ensuing analysis will fail to control for the bias.

We consider the propensity score models that also account for cluster effects. Specifically, we consider three methods: (i) a logistic linear fixed effect model with linear predictors including $X_1$, $X_2$, and a fixed intercept for each cluster; (ii) a logistic linear mixed effect model with linear predictors including fixed effects $X_1$, $X_2$, and a random effect for each cluster; (iii) the proposed calibrated propensity score. Using the estimated propensity score, we estimate $\tau = E\{Y(1) - Y(0)\}$ by the weighting method.

Table 2 displays the standardized differences of means for covariates $X_1$ and $X_2$ between the treated and the control for each cluster and the whole population, standardized by the standard errors in the whole population. Without any adjustment, there are large differences in means for $X_1$ and $X_2$. All three propensity score weighting methods improve the balances for $X_1$ and $X_2$. For this specific dataset, the three methods for modeling and estimating the propensity score are similar in balancing the covariate distributions between the treated and the control. Table 3 displays point estimates and variance estimates based on 500 bootstrap replicates. The simple estimator shows that the screening has significant effect in reducing the prevalence of overweight and obesity. However, this may be due to the observed confounders and the unobserved cluster-level confounders. After adjusting for the confounders, the screening does not have significant effect.

8 Discussion

Inverse probability of treatment weighting (IPTW) estimator is not efficient in general. Semiparametric efficiency bounds for estimating the average treatment effects in the setting with iid random variables were derived by Hahn (1998). He showed that the efficient influence function for the average treatment effect depends on both the propensity score and the outcome model. An important implication is that combining the propensity score model and the outcome regression model can improve efficiency of the IPTW estimator. For clustered data, since the data are correlated through the random cluster effects, the efficiency theory established for the iid data is not applicable. Developing semiparametric efficiency theory for clustered data is interesting. This extension will be a subject of future work.
In this article, we assumed that there is no interference between units. This setup is not uncommon. In our application, the treatment was implemented school-wise. The potential outcomes for one school are likely to be unaffected by the treatments implemented at other schools, and therefore the assumption of no interference is likely to hold. However, in other settings this assumption may not hold. A classical example is given in infectious diseases (Ross 1916; Hudgens and Halloran 2008), where whether one person becomes infected depends on who else in the population is vaccinated. Extension of our calibration estimation to take the interference structure into account in these settings is also an interesting topic for future research.

In addition to propensity score weighting, propensity score has been used for subclassification (Rosenbaum and Rubin 1984; Rosenbaum 1991) and matching (Rosenbaum and Rubin 1985; Abadie and Imbens 2006). In the causal inference and missing data literature, previous simulations have found that weighting estimators can have high variability, see for example, Foster (2003) and Frölich (2004) found that the weighting estimator was inferior to matching estimators in terms of mean squared error. Therefore, developing subclassification and matching estimator for clustered data is important, which will be another topic for future research.

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Appendix

Appendix A. Proof of Theorem

Proof 1 Write

\[
E(\hat{r}_{\text{cal}}) = E \left[ \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij} Y_{ij}}{\hat{e}(X_{ij}, U_i)} - \frac{(1 - A_{ij}) Y_{ij}}{1 - \hat{e}(X_{ij}, U_i)} \right\} \right]
\]

\[
= E \left[ \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij} Y_{ij}}{\hat{e}(X_{ij}, U_i)} - Y_{ij}(1) \right\} \right]
\]

\[ - E \left[ \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{(1 - A_{ij}) Y_{ij}}{1 - \hat{e}(X_{ij}, U_i)} - Y_{ij}(0) \right\} \right]
\]

\[ + E \left[ \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \{ Y_{ij}(1) - Y_{ij}(0) \} \right]
\]

\[ \approx E \left[ \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} - 1 \right\} Y_{ij}(1) \right]
\]

\[ - E \left[ \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{(1 - A_{ij})}{1 - \hat{e}(X_{ij}, U_i)} - 1 \right\} Y_{ij}(0) \right] + \tau,
\]

(20)

where \( B \cong C \) means that \( B = C + o_p(1) \) for random variables and \( B = C + o(1) \) for non-random variables, and the approximation in (20) follows from the consistency assumption and that \( \hat{N}^{-1} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \{ Y_{ij}(1) - Y_{ij}(0) \} \) is design-model consistent for \( \tau \). Therefore, to show that \( \hat{r}_{\text{cal}} \) is unbiased for \( \tau \), it is sufficient to show that

\[
E \left[ \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} - 1 \right\} Y_{ij}(1) \right] = 0,
\]

(21)

\[
E \left[ \frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{(1 - A_{ij})}{1 - \hat{e}(X_{ij}, U_i)} - 1 \right\} Y_{ij}(0) \right] = 0.
\]

Since by the calibration equations (11) and (12), for any functions \( \mu_0(U_i) \) and \( \mu_1(U_i) \), we have

\[
\frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} - 1 \right\} \mu_1(U_i) = 0,
\]

(21)

\[
\frac{1}{N} \sum_{i \in S_f} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{(1 - A_{ij})}{1 - \hat{e}(X_{ij}, U_i)} - 1 \right\} \mu_0(U_i) = 0.
\]

(22)
We shall rely on the above equations to show the unbiasedness of \( \hat{\tau}_{\text{cal}} \). Define for \( a = 0, 1 \),

\[
\mu_a(U_i) = \frac{\int q_a(x, U_i) E\{Y_{ij}(a)|x, U_i\} f(x) dx}{\int q_a(x, U_i) f(x) dx},
\]

(23)

where \( f(x) \) is the density of \( X \),

\[
q_1(X_{ij}, U_i) = E\left\{ \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} - 1 \mid X_{ij}, U_i \right\},
\]

and

\[
q_0(X_{ij}, U_i) = E\left\{ \frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_i)} - 1 \mid X_{ij}, U_i \right\}.
\]

Now, following (20),

\[
E(\hat{\tau}_{\text{cal}}) - \tau = E \left[ \frac{1}{N} \sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} - 1 \right\} Y_{ij}(1) \right]

- E \left[ \frac{1}{N} \sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_i)} - 1 \right\} Y_{ij}(0) \right]

+ E \left[ \frac{1}{N} \sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} - 1 \right\} \mu_1(U_i) \right]

+ E \left[ \frac{1}{N} \sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_i)} - 1 \right\} \mu_0(U_i) \right]

+ E \left[ \frac{1}{N} \sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} - 1 \right\} \{Y_{ij}(1) - \mu_1(U_i)\} \right]

+ E \left[ \frac{1}{N} \sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_i)} - 1 \right\} \{Y_{ij}(0) - \mu_0(U_i)\} \right]

= E \left[ \frac{1}{N} \sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{A_{ij}}{\hat{e}(X_{ij}, U_i)} - 1 \right\} \{Y_{ij}(1) - \mu_1(U_i)\} \right]

+ E \left[ \frac{1}{N} \sum_{i \in S_I} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \frac{1 - A_{ij}}{1 - \hat{e}(X_{ij}, U_i)} - 1 \right\} \{Y_{ij}(0) - \mu_0(U_i)\} \right],
\]

(24)
where the second equality follows (27) and (22). Now we first consider the first term in (24),

\[
E \left[ \frac{1}{N} \sum_{i=1}^{M} \sum_{j=1}^{N_i} \omega_{ij} \left\{ \frac{A_{ij}}{e(X_{ij}, U_i)} - 1 \right\} \{Y_{ij}(1) - \mu_1(U_i)\} \right] = E \left[ \frac{1}{N} \sum_{i=1}^{M} \sum_{j=1}^{N_i} \left\{ \frac{A_{ij}}{e(X_{ij}, U_i)} - 1 \right\} \left\{ \{Y_{ij}(1) - \mu_1(U_i)\} \right\} \right] \]

\[
= E \left( \frac{1}{N} \sum_{i=1}^{M} \sum_{j=1}^{N_i} E \left\{ \frac{A_{ij}}{e(X_{ij}, U_i)} - 1 \right\} \left\{ \{Y_{ij}(1) - \mu_1(U_i)\} \right\} \right) \]

\[
= E \left( \frac{1}{N} \sum_{i=1}^{M} \sum_{j=1}^{N_i} q_1(X_{ij}, U_i) \left\{ \{Y_{ij}(1) - \mu_1(U_i)\} \right\} \right) = 0, \tag{25}
\]

where the second equality follows from Assumption 7 (note that \(e(X_{ij}, U_i)\) does not rely on the outcome variable), and the last equality follows from Assumption 3 and the definition of \(\mu_1(U_i)\) in (23). Similarly, we can show that the second term in (24) is zero. Combining the above results with (24), we obtain that \(E(\hat{\tau}_{\text{cal}} - \hat{\tau}) = 0\), leading to \(E(\hat{\tau}_{\text{cal}}) = \tau\).

**Appendix B. Proof of Theorem 2**

**Proof 2** Let \(Q(\lambda_1, \lambda_2) = 0\), and \((\lambda_1^*, \lambda_2^*)\) satisfy \(E\{Q(\lambda_1^*, \lambda_2^*)\} = 0\). By linearization, we obtain

\[
\hat{\tau}_{\text{cal}} = \hat{\tau}_{\text{cal}}(\lambda_1, \lambda_2) \approx \hat{\tau}_{\text{cal}}(\lambda_1^*, \lambda_2^*) - E \left\{ \frac{\partial \hat{\tau}_{\text{cal}}(\lambda_1^*, \lambda_2^*)}{\partial (\lambda_1, \lambda_2)^T} \right\} \left\{ \frac{\partial Q(\lambda_1^*, \lambda_2^*)}{\partial (\lambda_1, \lambda_2)^T} \right\}^{-1} Q(\lambda_1, \lambda_2) \]

\[
\approx \frac{1}{N} \sum_{i \in A_1} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \alpha_{ij}(\lambda_1^*, \lambda_2^*) A_{ij}(Y_{ij} - B_1^T X_{ij}) + B_1^T X_{ij} \right\} \]

\[
- \frac{1}{N} \sum_{i \in A_1} \sum_{j=1}^{n_i} \omega_{ij} \left\{ \alpha_{ij}(\lambda_1^*, \lambda_2^*) (1 - A_{ij})(Y_{ij} - B_2^T X_{ij}) + B_2^T X_{ij} \right\},
\]

\[
= \frac{1}{N} \sum_{i \in A_1} \sum_{j=1}^{n_i} \omega_{ij} \Phi_{ij}.
\]
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Figure 1: A Directed Acyclic Graph illustration for cluster $i$ with two units.
Table 1: Simulation results: bias, variance (var/10^3) and coverage (cvg/100) of 95% confidence intervals based on 1,000 Monte Carlo samples; the outcome is linear and logistic linear mixed effect model and the propensity score is logistic, probit or complementary log-log (C-loglog).

| Method     | (m, n) = (50, 50) | (m, n) = (100, 30) | (m, n) = (30, 100) |
|------------|-------------------|--------------------|--------------------|
|            | bias  | var   | cvg  | bias  | var   | cvg  | bias  | var   | cvg  |
| Scenario 1: Linear outcome & Logistic propensity score |
| \( \hat{\tau}_{\text{simp}} \) | -0.37 | 22   | 27.4 | -0.38 | 12   | 8.7  | -0.38 | 35   | 42.3 |
| \( \hat{\tau}_{\text{fix}} \)  | -0.01 | 36   | 95.6 | 0.00  | 21   | 95.6 | -0.01 | 42   | 95.2 |
| \( \hat{\tau}_{\text{ran}} \)  | 0.14  | 26   | 90.2 | 0.21  | 14   | 64.6 | 0.07  | 37   | 94.7 |
| \( \hat{\tau}_{\text{cal}} \)  | 0.01  | 26   | 94.5 | 0.02  | 11   | 95.1 | 0.00  | 33   | 95.6 |
| Scenario 2: Linear outcome & Probit propensity score |
| \( \hat{\tau}_{\text{simp}} \) | -0.29 | 16   | 34.4 | -0.08 | 9    | 2.3  | -0.22 | 30   | 65.6 |
| \( \hat{\tau}_{\text{fix}} \)  | 0.08  | 35   | 90.3 | -0.10 | 19   | 4.5  | 0.12  | 69   | 90.4 |
| \( \hat{\tau}_{\text{ran}} \)  | 0.24  | 28   | 73.9 | -0.07 | 16   | 29.9 | 0.21  | 60   | 85.5 |
| \( \hat{\tau}_{\text{cal}} \)  | 0.01  | 22   | 94.9 | 0.01  | 11   | 95.4 | 0.00  | 33   | 94.6 |
| Scenario 3: Linear outcome & C-loglog propensity score |
| \( \hat{\tau}_{\text{simp}} \) | -0.21 | 20   | 62.0 | -0.21 | 10   | 41.2 | -0.22 | 30   | 65.6 |
| \( \hat{\tau}_{\text{fix}} \)  | 0.12  | 48   | 88.8 | 0.12  | 36   | 82.7 | 0.12  | 69   | 90.4 |
| \( \hat{\tau}_{\text{ran}} \)  | 0.29  | 38   | 69.1 | 0.36  | 22   | 32.5 | 0.21  | 60   | 85.5 |
| \( \hat{\tau}_{\text{cal}} \)  | 0.00  | 21   | 95.3 | 0.00  | 10   | 95.1 | 0.00  | 33   | 94.6 |
| Scenario 4: Logistic outcome & Logistic propensity score |
| \( \hat{\tau}_{\text{simp}} \) | -0.11 | 100  | 9.1  | -0.11 | 540  | 0.5  | -0.11 | 160  | 20.5 |
| \( \hat{\tau}_{\text{fix}} \)  | -0.11 | 44   | 0.3  | -0.11 | 38   | 0.1  | -0.11 | 39   | 0.1  |
| \( \hat{\tau}_{\text{ran}} \)  | -0.09 | 33   | 1.3  | -0.08 | 21   | 0.5  | -0.10 | 34   | 0.3  |
| \( \hat{\tau}_{\text{cal}} \)  | 0.01  | 74   | 96.3 | 0.01  | 55   | 95.2 | 0.01  | 74   | 95.9 |
| Scenario 5: Logistic outcome & Probit propensity score |
| \( \hat{\tau}_{\text{simp}} \) | -0.08 | 58   | 13.1 | -0.08 | 34   | 2.3  | -0.08 | 81   | 25.3 |
| \( \hat{\tau}_{\text{fix}} \)  | -0.10 | 93   | 6.9  | -0.10 | 85   | 4.5  | -0.10 | 73   | 3.8  |
| \( \hat{\tau}_{\text{ran}} \)  | -0.08 | 67   | 23.0 | -0.07 | 48   | 29.9 | -0.09 | 61   | 8.3  |
| \( \hat{\tau}_{\text{cal}} \)  | 0.01  | 89   | 94.7 | 0.01  | 65   | 95.4 | 0.01  | 84   | 95.0 |
| Scenario 6: Logistic outcome & C-loglog propensity score |
| \( \hat{\tau}_{\text{simp}} \) | -0.01 | 62   | 92.5 | -0.01 | 34   | 92.5 | -0.01 | 84   | 93.0 |
| \( \hat{\tau}_{\text{fix}} \)  | -0.03 | 53   | 71.9 | -0.03 | 50   | 69.8 | -0.03 | 50   | 73.7 |
| \( \hat{\tau}_{\text{ran}} \)  | -0.01 | 42   | 98.6 | 0.00  | 33   | 99.6 | -0.02 | 44   | 92.6 |
| \( \hat{\tau}_{\text{cal}} \)  | -0.01 | 81   | 96.0 | -0.01 | 67   | 94.8 | -0.01 | 82   | 94.4 |
Table 2: Balance Check

|              | simple | fixed | random | calibration |
|--------------|--------|-------|--------|-------------|
| Cluster 1    | 1.68   | -0.22 | 0.68   | 0.20        |
| Cluster 2    | 1.21   | 0.10  | -0.41  | 0.10        |
| Cluster 3    | 1.75   | -0.02 | 0.99   | 0.02        |
| Cluster 4    | 0.86   | -0.04 | -1.05  | 0.02        |
| Cluster 5    | -0.36  | 0.37  | -1.39  | 0.33        |
| Whole Pop    | 1.28   | -0.02 | -0.02  | 0           |

| X1            |        |       |        |             |
|---------------|--------|-------|--------|-------------|
| Cluster 1    | 0.48   | 0.02  | 0.30   | 0.03        |
| Cluster 2    | 0.43   | 0.13  | -0.01  | 0.14        |
| Cluster 3    | 0.73   | 0.01  | 0.46   | 0.02        |
| Cluster 4    | 0.18   | -0.08 | -0.34  | -0.07       |
| Cluster 5    | -0.57  | -0.39 | -1.53  | -0.44       |
| Whole Pop    | 0.39   | -0.003 | -0.001  | 0           |

Table 3: Results: estimate, variance estimate (ve) based on 500 bootstrap replicates, and 95% confidence interval (c.i.)

|               | estimate | ve     | 95% c.i. |
|---------------|----------|--------|----------|
| simple        | 8.78     | 2.11   | (5.94, 11.63) |
| fixed         | 0.47     | 0.44   | (-0.83, 1.77)  |
| random        | 0.52     | 0.44   | (-0.77, 1.82)  |
| calibration   | 0.53     | 0.39   | (-0.71, 1.76)  |