Double score matching estimators of average and quantile treatment effects

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Abstract

Propensity score matching has a long tradition for handling confounding in causal inference. In this article, we propose double score matching estimators of the average treatment effects and the quantile treatment effects utilizing two balancing scores including the propensity score and the prognostic score. We show that the de-biasing double score matching estimators achieve the double robustness property in that they are consistent for the true causal estimands if either the propensity score model or the prognostic score model is correctly specified, not necessarily both. We characterize the asymptotic distributions for the doubly score matching estimators when either one of the score model is correctly specified based on the martingale representations of the matching estimators and theory for local normal experiments. We also provide a two-stage replication method for variance estimation and therefore doubly robust inference. R package is available online.

Keywords: Bahadur representation; Matching; Quantile estimation; Weighted bootstrap.

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1 Introduction

1.1 Causal inference and matching

Causal inference plays important roles in science, education, medicine, policy, and economics. If all confounders of the treatment-outcome relationship are observed, one can use standard techniques, such as regression adjustment, matching, subclassification and weighting to adjust for confounding (Imbens and Rubin; 2015). Among those, matching has been widely used in the empirical literature due to its intuitive appeal (Rosenbaum; 1989; Heckman et al.; 1997a; Dehejia and Wahba; 2002, 1999; Lechner; 2002; Hirano et al.; 2003; Hansen; 2004; Zhao; 2004; Imbens; 2004; Rubin; 2006; Abadie and Imbens; 2006; Stuart; 2010; Abadie and Imbens; 2016) with the goal of replicating the ideal randomized experiment. To fix ideas, we focus on a binary treatment. Matching has been proposed to select units from the treated and control groups with similar covariates. Matching based on covariates (e.g., Rubin; 1980; Abadie and Imbens; 2006) is most intuitive because by construction it creates similar covariate distributions between the two treatment groups and therefore removes the confounding bias due to the difference of covariates. However, in the presence of many covariates, matching directly on covariates suffers from the curse of dimensionality and is incapable of removing all confounding biases.

1.2 Dimension reduction in matching

To overcome this challenge, researchers have proposed different dimension reduction techniques to facilitate matching. On the one hand, Rosenbaum and Rubin (1983b) demonstrated the central role of the propensity score (i.e., the conditional probability of receiving the active treatment given covariates) as being a balancing score in the sense that same propensity score distributions in the different treatment groups lead to same covariate distributions. Therefore, matching solely on the propensity score can remove all confounding bias (e.g., Abadie and Imbens; 2016).

On the other hand, Hansen (2008) proposed an alternative balancing score: the prognostic score, also called the disease risk score (i.e., a sufficient statistic for the potential outcomes given which the potential outcomes and covariates are independent). This score provides a balance of disease risks between the treatment groups, as distinct from the balance of treatment propensities provided by the propensity score. In economics, matching based on prognostic score has been previously proposed in Imbens (2004) and Zhao (2004), where the prognostic score is a vector of linear predictors in treatment-specific outcome regressions. Prognostic score matching is also similar to predictive mean matching (Rubin; 1986; Little; 1988; Heitjan and Little; 1991; Yang and Kim; 2017) in the missing data literature to compensate for nonresponse. In the comparative effectiveness research, matching based on the disease risk score has been shown to be
more advantageous than matching based on the propensity score when the propensity score distributions are strongly separated (Wyss et al.; 2015; Kumamaru et al.; 2016). Smith and Schaubel (2015) extended prognostic score matching to a time-dependent treatment setting. While prognostic score matching is gaining its popularity, Imbens (2004) noted that if the regression models are misspecified, the matching estimators may be inconsistent. Wyss et al. (2015, 2017) also pointed out the challenge in estimating the disease risk score correctly.

1.3 Gaps

To mitigate the issue with the single scores, Hansen (2008) suggested matching on the propensity and prognostic score jointly. Leacy and Stuart (2014) showed empirically that the joint use of two scores in matching improve the treatment effect estimation. Antonelli et al. (2018) later established the double robustness of matching jointly on propensity and prognostic scores in the sense that the matching estimator is consistent for the ATE if either one of the score models is correctly specified. However, they only provided the rate of convergence but not the asymptotic distribution of the doubly robust matching estimator. Due to lack of the distributional results, the inference based on the matching estimator remains an open question.

The current matching literature has focused primarily on estimating ATEs; however, other aspects of the distribution such as quantiles may be more appropriate in certain applications. For example, a treatment strategy may not decrease average health cost but instead lowers the upper tail of the cost distribution, so focusing only on ATEs would not reveal the beneficial effect of the treatment strategy. In these cases, it is more informative to study QTEs, which are defined as the differences in population quantiles of the potential outcomes. There are existing weighting and Bayesian estimators of QTEs (Firpo; 2007; Zhang et al.; 2012; Frölich and Melly; 2013; Xu et al.; 2018); however, it is well-known that weighting estimators are extremely unstable (Kang and Schafer; 2007) and Bayesian methods often come with issues with prior selection and a high computational cost. Notably, matching can be viewed as a hot deck imputation method which can provide valid estimators of general parameters depending on the entire distribution (e.g., Chen and Shao; 2000; Andridge and Little; 2010). Despite of this superiority, matching estimators of QTEs are limited.

1.4 Goals and contributions

In this article, we propose matching estimators of ATEs and QTEs based on the augmented score consisting of both the propensity score and the prognostic score. Because each score creates a balance between the treated and control groups, the augmented score serves as a “double balancing score.” Following Abadie and Imbens (2016), we use matching as a tool to impute the missing potential outcomes for all units and consider matching with replacement with the number of matches fixed at $M$. In practice, the propensity score and
the prognostic score are unknown. We then propose a two-step double score matching procedure: first, the propensity score and prognostic score models are specified and estimated; second, for each unit, $M$ nearest neighbors are identified from its opposite treatment group based on the estimated double score functions, and then the observed outcome values of the nearest neighbors are used to impute the missing potential outcome. With the imputed potential outcomes, standard estimators of the ATEs and the QTEs can be applied. Although the augmented score largely reduces the dimension of covariates, its dimension is larger than one in contrast to the scalar propensity score. Consequently, the bias of the matching estimators due to matching discrepancy is not asymptotic negligible (Abadie and Imbens; 2011). We propose de-biasing matching estimators of the ATEs and the QTEs that correct for bias due to matching discrepancy.

Because the double score functions are estimated prior to matching, it is necessary to account for the uncertainty due to parameter estimation. The theoretical task is non-trivial. The typical Taylor expansion technique can not be used, because of the non-smooth nature of matching. Our derivation is based on the technique developed by Andreou and Werker (2012), which offers a general approach for deriving the limiting distribution of statistics that involve estimated nuisance parameters. This technique has been successfully used in Abadie and Imbens (2016) for the matching estimators of the ATEs based on the estimated propensity score. We extend their results to the double score matching estimators of the ATEs and the QTEs when one of the balancing scores may be misspecified. We also provide a two-stage replication method for doubly robust inference.

The proposed framework advances the matching literature in the following ways. First, the double score matching procedure offers a new “metric” to summarize the differential roles of different covariates and also serves as a powerful dimensional reduction tool in high-dimensional confounding. Second, because the augmented score utilizes prognostic information, the resulting matching estimators gain efficiency over propensity score matching estimators of certain causal parameters. Third, due to the double balancing property, the proposed matching estimators are doubly robust in that if either the propensity score or the prognostic score is correctly specified, not necessarily both, the proposed estimators are consistent for the true causal estimands. Doubly robust estimators exist in various forms, such as weighting estimators (e.g., Robins et al.; 1995; Lunceford and Davidian; 2004; Bang and Robins; 2005; Cao et al.; 2009; Cheng et al.; 2019), regression adjustment estimators (e.g., Zeng; 2004; Hu et al.; 2012; Zhou et al.; 2019), and matching estimators (of the ATEs; Leacy and Stuart; 2014; Antonelli et al.; 2018). The proposed method provides the doubly robust matching estimators of general estimands including ATEs and QTEs with theoretical guarantees.
2 Setup and assumptions

We use potential outcomes to define causal effects. Suppose that the binary treatment is $A \in \{0, 1\}$, with 0 and 1 being the labels for the control and active treatments, respectively. Each level of treatment $a$ corresponds to a potential outcome $Y(a)$, representing the outcome had the subject, possibly contrary to the fact, been given treatment $a$. The observed outcome is $Y = Y(A) = AY(1) + (1 - A)Y(0)$. Let $X$ be a vector of pre-treatment covariates. We assume that a sample of size $n$ consists of independent and identically distributed draws from the distribution of $\{A, X, Y(0), Y(1)\}$. The covariate-specific causal effect is $\tau(X) = E\{Y(1) - Y(0) \mid X\}$, and the ATE is $\tau = E\{Y(1) - Y(0)\} = E\{\tau(X)\}$. For $\xi \in (0, 1)$, the overall $\xi$-QTE is $\Delta_\xi = q_{1, \xi} - q_{0, \xi}$, where $q_{a, \xi} = \inf_q [P\{Y(a) \leq q\} \geq \xi], a = 0, 1$. We focus on estimating $\tau$ and $\Delta_\xi$ in the main text. In the supplementary material, we develop similar estimators for the average causal effect on the treated $\tau_{ATT} = E\{Y(1) - Y(0) \mid A = 1\} = E\{\tau(X) \mid A = 1\}$ and the quantile treatment effect on the treated $\Delta_{ATT, \xi} = q_{1, \xi | A = 1} - q_{0, \xi | A = 1}$, where $q_{a, \xi | A = 1} = \inf_q [P\{Y(a) \leq q\} \geq \xi \mid A = 1], a = 0, 1$.

The following assumptions are standard in causal inference with observational studies (Rosenbaum and Rubin, 1983b).

**Assumption 1** $\{Y(0), Y(1)\} \perp \perp A \mid X$, where $\perp \perp$ means “independent of”.

**Assumption 2** There exist constants $c_1$ and $c_2$ such that $0 < c_1 \leq e(X) \leq c_2 < 1$ almost surely, where $e(X) = P(A = 1 \mid X)$ is the propensity score.

Assumption 1 requires $X$ to capture all variables that are related to the outcome and treatment assignment, which relies on subject matter knowledge. Assumption 2 implies a sufficient overlap of the covariate distribution between treatment groups. If this assumption is violated, a common approach is to trim the sample; see Yang and Ding (2018).

Under Assumptions 1 and 2

$$\tau = E\{E(Y \mid A = 1, X) - E(Y \mid A = 0, X)\},$$

are identifiable from the joint distribution of observed data $(A, X, Y)$.

Rosenbaum and Rubin (1983b) showed that Assumptions 1 and 2 imply that $\{Y(0), Y(1)\} \perp \perp A \mid e(X)$ and

$$\tau = E[E\{Y \mid A = 1, e(X)\} - E\{Y \mid A = 0, e(X)\}].$$  \hspace{1cm} (1)

Then we can estimate $\tau$ through propensity score matching, subclassification or weighting (e.g., Imbens and Rubin, 2015).
On the other hand, Hansen (2008) introduced the notion of the prognostic score \( \Psi(X) \), which is a sufficient statistic for \( \{Y(0), Y(1)\} \) in the sense that \( \{Y(0), Y(1)\} \perp \perp X \mid \Psi(X) \).

**Example 1** If \( Y(a) \) follows a generalized linear model for \( a = 0, 1 \), then the linear predictors for \( Y(0) \) and \( Y(1) \) given \( X \) constitute the prognostic score.

**Example 2** If \( Y(a) \) follows a location-shift family \( f_a\{y - \mu_a(X)\} \) for \( a = 0, 1 \), then \( \mu_0(X) \) and \( \mu_1(X) \) constitute the prognostic score.

One important implication is that

\[
\tau = E\{E(Y \mid A = 1, X) - E(Y \mid A = 0, X)\} = E[E\{Y \mid A = 1, X, \Psi(X)\} - E\{Y \mid A = 0, X, \Psi(X)\}] = E[E\{Y \mid A = 1, \Psi(X)\} - E\{Y \mid A = 0, \Psi(X)\}] = E\left[ E\left[ \frac{e(X)}{\Psi(X)} \mid \Psi(X) \right] - E\left[ \frac{e(X)}{\Psi(X)} \mid \Psi(X) \right] \right].
\]

(2)

In this article, we propose the double score matching algorithm leveraging the double balancing properties of (1) and (2) for general causal estimands including the ATEs and the QTEs. Matching is attractive for general causal estimation, because it can be viewed as a hot deck imputation method (Ford; 1983), where for each unit the donors for the missing potential outcome are actually observed values from the opposite treatment group. An advantage of hot deck imputation is that it preserves the distribution of the potential outcomes so that valid estimators for parameters depending on the entire distribution of the potential outcomes such as the mean and quantiles can be obtained based on the imputed data set. In the next section, we develop double score matching estimators of \( \tau \) and \( \Delta \xi \).

3 Double score matching estimators of \( \tau \) and \( \Delta \xi \)

To fix ideas, we consider matching with replacement with the number of matches fixed at \( M \). Matching estimators hinge on imputing the missing potential outcome for each unit. In practice, the most common choice of \( M \) is 1, then the matching procedure becomes nearest neighbor imputation (Little and Rubin; 2002; Chen and Shao; 2000, 2001). To be precise, for unit \( i \), the potential outcome under \( A_i \) is the observed outcome \( Y_i \); the (counterfactual) potential outcome under \( 1 - A_i \) is not observed but can be imputed by the observed outcomes of the nearest \( M \) units with \( 1 - A_i \). We consider the augmented score \( S = \{e(X), \Psi(X)^T\}^T \) as the matching variable. To stabilize the numerical performance, it is desirable to standardize \( S \) such that each component has mean zero and variance one. Without loss of generality, we use the Euclidean distance to determine neighbors; the discussion applies to other distances (Abadie and Imbens; 2006). Let \( J_{S,i} \) be
the index set for these matched units for unit \(i\) and \(K_{S,i} = \sum_{j=1}^{n} I(i \in J_{S,j})\) be the number of times that unit \(i\) is used as a match.

For estimating \(\tau\), define the imputed potential outcome for unit \(i\) as \(\hat{Y}_{i}(A_{i}) = Y_{i}\) and \(\hat{Y}_{i}(1 - A_{i}) = M^{-1} \sum_{j \in J_{S,i}} Y_{j}\). Then an initial double score matching estimator of \(\tau\) is

\[
\hat{\tau}_{dsm}^{(0)} = n^{-1} \sum_{i=1}^{n} \{\hat{Y}_{i}(1) - \hat{Y}_{i}(0)\} = n^{-1} \sum_{i=1}^{n} (2A_{i} - 1)(1 + M^{-1}K_{S,i})Y_{i}.
\]

Let \(\mu(a) = E\{Y(a) \mid V\}\), \(\sigma_{\mu}^{2}(V) = \text{var}\{Y(a) \mid V\}\), and \(e(V) = P(A = 1 \mid V)\) for a generic variable \(V\). Following Abadie and Imbens (2006), we obtain the following decomposition:

\[
n^{1/2}(\hat{\tau}_{dsm} - \tau) = D_{n} + B_{n},
\]

where

\[
D_{n} = n^{-1/2} \sum_{i=1}^{n} \left[ \mu_{1}(S_{i}) - \mu_{0}(S_{i}) - \tau + (2A_{i} - 1) \left\{ 1 + M^{-1}K_{S,i} \right\} \{Y_{i} - \mu_{A_{i}}(S_{i})\} \right],
\]

\[
B_{n} = n^{-1/2} \sum_{i=1}^{n} (1 - 2A_{i}) \left[ M^{-1} \sum_{j \in J_{S,i}} \left\{ \mu_{A_{j}}(S_{i}) - \mu_{A_{j}}(S_{j})\right\} \right].
\] (3)

Because of (1) and (2), \(E\{\mu_{1}(S) - \mu_{0}(S)\} = \tau\), so \(D_{n}\) is unbiased. The difference \(\mu_{A_{i}}(S_{i}) - \mu_{A_{j}}(S_{j})\) in (3) accounts for the matching discrepancy, and therefore \(B_{n}\) contributes to the asymptotic bias of the matching estimator. In general, if \(S\) is \(k\)-dimensional, Abadie and Imbens (2006) showed that under regularity conditions, \(||S_{i} - S_{j}|| = O_{P}(n^{-1/k})\) for \(j \in J_{S,i}\). Then if \(k \geq 2\), \(B_{n} = O_{P}(n^{1/2-1/k}) \neq o_{P}(1)\) is not negligible.

To correct for the bias due to matching discrepancy, let \(\hat{\mu}_{a}(S)\) be a nonparametric estimator of \(\mu_{a}(S)\), for \(a = 0, 1\). We propose a de-biasing double score matching estimator of \(\tau\):

\[
\hat{\tau}_{dsm} = \hat{\tau}_{dsm}^{(0)} - n^{-1/2} \hat{B}_{n},
\] (4)

where \(\hat{B}_{n}\) is an estimator of \(B_{n}\) by replacing \(\mu_{a}(S)\) with \(\hat{\mu}_{a}(S)\).

Unlike the ATE \(\tau\), direct estimation for \(\Delta_{\xi}\) is difficult. We focus on estimating \(q_{a,\xi}\) separately for \(a = 0, 1\). Similar to (1) and (2), we have

\[
q_{a,\xi} = \inf_{q} \left( E[P\{Y \leq q \mid A = a, e(X)\}] \geq \xi \right) = \inf_{q} \left( E[P\{Y \leq q \mid A = a, \Psi(X)\}] \geq \xi \right).
\]

Based on the above equation, we propose the double score matching estimator of \(q_{a,\xi}\) as

\[
\hat{q}_{a,\xi,dsm} = \inf_{q} \left( \hat{F}_{a,dsm}(q) \geq \xi \right),
\] (5)
where

\[ \hat{F}_{a,\text{dsm}}(q) = \hat{F}^{(0)}_{a,\text{dsm}}(q) - n^{-1/2} \hat{B}_{a,n}(q), \]

\[ \hat{F}^{(0)}_{a,\text{dsm}}(q) = n^{-1} \sum_{i=1}^{n} I(A_i = a) \left( 1 + M^{-1} K_{S,i} \right) I(Y_i \leq q), \]

\[ \hat{B}_{a,n}(q) = -n^{-1/2} \sum_{i=1}^{n} I(A_i = 1 - a) M^{-1} \sum_{j \in J_{S,i}} \left\{ \hat{F}_a(q; S_i) - \hat{F}_a(q; S_j) \right\}, \]

where \( \hat{F}_a(q; S) \) is a semi/nonparametric estimator of \( F_a(q; S) = P(Y(a) \leq q \mid S) \), for \( a = 0, 1 \). Note that \( \hat{F}^{(0)}_{a,\text{dsm}}(q) \) is an initial matching estimator of \( F_a(q) = P(Y(a) \leq q) \) and \( \hat{B}_{a,n}(q) \) is the bias correction term; see the supplementary material. Then the double score matching estimator of \( \Delta_A \) is \( \hat{\Delta}_{A,\text{dsm}} = \hat{q}_{1,\text{dsm}} - \hat{q}_{0,\text{dsm}} \).

Because \( S \) is unknown in practice, we posit working models for both scores in \( S \).

**Assumption 3 (Propensity score model)** The parametric model \( e(X; \alpha) \) is a correct specification for \( e(X) \); i.e., \( e(X) = e(X; \alpha_0) \), where \( \alpha_0 \) is the true model parameter.

**Assumption 4 (Prognostic score model)** Suppose that \( Y(a) \) follows a location-shift family and that the parametric model \( \mu_a(X; \beta_a) \) is a correct specification for \( \mu_a(X) \); i.e., \( \mu_a(X) = \mu_a(X; \beta_{a,0}) \) where \( \beta_{a,0} \) is the true model parameter, for \( a = 0, 1 \). Let the prognostic score model be \( \Psi(X; \eta) = \{\mu_0(X; \beta_0), \mu_1(X; \beta_1)\} \), where \( \eta = (\beta_0, \beta_1) \).

The double score matching algorithm proceeds as follows.

**Step 1.** Posit parametric models for \( e(X) \) and \( \Psi(X) \), denoted by \( e(X; \alpha_0) \) and \( \Psi(X; \eta_0) \) with fixed unknown parameters \( \alpha_0 \) and \( \eta_0 \), as in Examples 3 and 4, respectively. Let \( \theta = (\alpha, \eta) \) denote the vector of nuisance parameters. Obtain an estimator \( \hat{\theta} = (\hat{\alpha}, \hat{\eta}) \) by solving the estimating equation

\[ U_n(\theta) = n^{-1/2} \sum_{i=1}^{n} U(A_i, X_i, Y_i; \theta) = n^{-1/2} \sum_{i=1}^{n} \left( \begin{array}{c} U_1(A_i, X_i; \alpha) \\ U_2(A_i, X_i, Y_i; \beta_0) \\ U_3(A_i, X_i, Y_i; \beta_1) \end{array} \right) = 0, \]

where

\[ U_1(A, X; \alpha) = \frac{\partial e(X; \alpha)}{\partial \alpha} \frac{A - e(X; \alpha)}{e(X; \alpha)\{1 - e(X; \alpha)\}}, \]

\[ U_2(A, X, Y; \beta_0) = (1 - A) \frac{\partial \mu_0(X; \beta_0)}{\partial \beta_0} \{Y - \mu_0(X; \beta_0)\}, \]

\[ U_3(A, X, Y; \beta_1) = A \frac{\partial \mu_1(X; \beta_1)}{\partial \beta_1} \{Y - \mu_1(X; \beta_1)\}. \]

For each unit \( i \), calculate \( S_i(\hat{\theta}) = \{ \logit e(X_i; \hat{\alpha}), \Psi(X_i; \hat{\eta}) \}^T \). To stabilize the numerical performance, it is desirable to standardize \( S_i(\hat{\theta}) \) such that each component has mean zero and variance one.
Step 2. For each unit $i$ with treatment $A_i$, find $M$ nearest neighbors from the treatment group $1 - A_i$ based on the matching variable $S_i = S_i(\hat{\theta})$. Let these matched units for unit $i$ be indexed by $J_{S_i(\hat{\theta}),i}$.

For estimating $\tau$, Steps 3 and 4 proceed as follows:

**Step 3.** Obtain a nonparametric estimator of $\mu_a(S)$, denoted by $\hat{\mu}_a(S)$, e.g. by the method of sieves based on $\{Y_i, S_i(\hat{\theta})\} : A_i = a$, for $a = 0, 1$.

**Step 4.** The double score matching estimator of $\tau$ is given by (4) with $S_i$ replaced by $S_i(\hat{\theta})$. We denote the final estimator of $\tau$ as $\hat{\tau}_{\text{dsm}}(\hat{\theta})$ to reflect its dependence on $\hat{\theta}$.

For estimating $\Delta_\xi$, Steps $3'$ and $4'$ proceed as follows:

**Step 3'.** Obtain a semiparametric estimator of $F_a(q; S_i)$ based on $\{Y_i, S_i(\hat{\theta})\} : A_i = a$, for $a = 0, 1$. For example, we can consider the method of sieves for the normal linear model after a Box-Cox transformation of Zhang et al. (2012) or the single-index conditional distribution model of Chiang and Huang (2012).

**Step 4'.** The double score matching estimator of $q_{a,\xi}$ is given by (5) with $S_i$ replaced by $S_i(\hat{\theta})$. We denote the final estimator of $q_{a,\xi}$ as $\hat{q}_{a,\xi,\text{dsm}}(\hat{\theta})$ to reflect its dependence on $\hat{\theta}$, for $a = 0, 1$. Then, the double score matching estimator of $\Delta_\xi$ is $\hat{\Delta}_{\xi,\text{dsm}}(\hat{\theta}) = \hat{q}_{1,\xi,\text{dsm}}(\hat{\theta}) - \hat{q}_{0,\xi,\text{dsm}}(\hat{\theta})$.

## 4 Main results

Let $\theta^*$ be the probability limit of $\hat{\theta}$. We establish the asymptotic results for the double score matching estimators when $\theta^*$ is known in Section 4.1 and that when $\theta^*$ is estimated in Section 4.2 Under Assumption 5 we have $\alpha^* = \alpha_0$. Under Assumption 4 we have $\beta^* = \beta_0$. The key insight is that if either the propensity score model or the prognostic score model is correctly specified, not necessarily both, $S(\theta^*)$ remains as a balancing score in the sense that $\{Y(0), Y(1)\} \perp \perp A | S(\theta^*)$ or $\{Y(0), Y(1)\} \perp \perp X | S(\theta^*)$ holds. Based on this key observation, we will show that the double score matching estimators are doubly robust.

### 4.1 Asymptotic results for known $\theta^*$

To study the asymptotic properties of $\hat{\tau}_{\text{dsm}}(\theta^*)$ and $\hat{\Delta}_{\xi,\text{dsm}}(\theta^*)$, we require technical conditions. For simplicity, let $S = S(\theta^*)$ and let $f_1(S)$ and $f_0(S)$ be the conditional density of $S$ given $A = 1$ and $A = 0$, respectively.

**Assumption 5** (i) The matching variable $S$ has a compact and convex support $S$, with a continuous density bounded and bounded away from zero: there exist constants $C_{1L}$ and $C_{1U}$ such that $C_{1L} \leq f_1(S)/f_0(S) \leq C_{1U}$
for any $S \in S$; (ii) for $a = 0, 1$, $\mu_a(S)$ and $\sigma_a^2(S)$ satisfy a Lipschitz continuity condition: there exists a constant $C_2$ such that $|\mu_a(S_i) - \mu_a(S_j)| < C_2||S_i - S_j||$ for any $S_i$ and $S_j$, and similarly for $\sigma_a^2(S)$; and (iii) for $a = 0, 1$, there exists $\delta > 0$ such that $E\{|Y(a)|^{2+\delta} | S\}$ is uniformly bounded for any $S \in S$.

Assumption 5 has been considered by Abadie and Imbens (2006) and Abadie and Imbens (2016) for matching estimators based on covariates and propensity score, respectively. Assumption 5 (i) a convenient regularity condition. Assumption 5 (ii) imposes a smoothness condition for $\mu_a(S)$ and $\sigma_a^2(S)$. Assumption 5 (iii) is a moment condition for establishing the central limit theorem.

In the following theorems, we establish the double robustness and asymptotic distribution of $\hat{\tau}_{\text{dsm}}(\theta^*)$ and present the proofs to the supplementary material.

**Theorem 1** Under Assumptions 1–2 and 5, if either Assumption 3 or Assumption 4 holds, $n^{1/2} \{\hat{\tau}_{\text{dsm}}(\theta^*) - \tau\} \rightarrow N(0, V_\tau)$, in distribution, as $n \rightarrow \infty$, where

$$V_\tau = E \left[\{\mu_1(S) - \mu_0(S) - \tau\}^2\right] + E \left(\sigma_1^2(S) \left[\frac{1}{e(S)} + \frac{1}{2M} \left\{\frac{1}{e(S)} - e(S)\right\}\right]\right) + E \left(\sigma_0^2(S) \left[\frac{1}{1 - e(S)} + \frac{1}{2M} \left\{\frac{1}{1 - e(S)} - 1 + e(S)\right\}\right]\right).$$

(9)

To establish the double robustness and asymptotic distribution of $\hat{\Delta}_{\xi,\text{dsm}}(\theta^*)$, we require further technical conditions.

**Assumption 6** For $a = 0, 1$, the following conditions hold for the parameter $q_{a, \xi}$ and the estimating function $F_a(q)$: (i) $q_{a, \xi}$ lies in a closed interval $I$; (ii) the estimating equation $F_a(q) = \xi$ has a unique root in the interior of $I$; (iii) $F_a(q)$ is strictly increasing and absolutely continuous with finite first derivative in $I$, and the derivative $f_a(q) = dF_a(q)/dq$ is bounded away from 0 for all $q$ in $I$; and (iv) for $a = 0, 1$, $F_a(q; S)$ satisfies a Lipschitz continuity condition: there exists a constant $C_3$ such that $|F_a(q; S_i) - F_a(q; S_j)| < C_2||S_i - S_j||$ for any $S_i$ and $S_j$.

Under Assumptions 1–2, 5 (i) and 6, if either Assumption 3 or Assumption 4 holds, similar to the proof in Section 3.1, $d\hat{F}_{a,\text{dsm}}(q_{a, \xi})/dq = f_a(q_{a, \xi}) + o_P(n^{-1/2})$. Then we express $\hat{q}_{a, \xi, \text{dsm}}$ as

$$\hat{q}_{a, \xi, \text{dsm}} - q_{a, \xi} = -\frac{\hat{F}_{a, \text{dsm}}(q_{a, \xi}) - F_a(q_{a, \xi})}{f_a(q_{a, \xi})} + o_P(n^{-1/2}).$$

(10)

Expression (10) is called the Bahadur-type representation for $\hat{q}_{a, \xi, \text{dsm}}$ (Francisco and Fuller; 1991).
Theorem 2 Under Assumptions 1–2, 5 (i) and 6, if either Assumption 3 or Assumption 4 holds,

\[ n^{1/2} \left\{ \hat{\Delta}_{\xi, \text{dsm}}(\theta^*) - \Delta_{\xi} \right\} \rightarrow N(0, V_{\Delta}), \]

in distribution, as \( n \rightarrow \infty \), where

\[
V_{\Delta} = E \left[ \left\{ \frac{F_1(q_1, \xi; S)}{f_1(q_1, \xi)} - \frac{F_0(q_0, \xi; S)}{f_0(q_0, \xi)} \right\}^2 \right]
+ \{f_1(q_1, \xi)\}^{-2} E \left( F_1(q_1, \xi; S) \{1 - F_1(q_1, \xi; S)\} \left[ \frac{1}{e(S)} + \frac{1}{2M} \left\{ \frac{1}{e(S)} - e(S) \right\} \right] \right)
+ \{f_0(q_0, \xi)\}^{-2} E \left( F_0(q_0, \xi; S) \{1 - F_0(q_0, \xi; S)\} \left[ \frac{1}{1 - e(S)} + \frac{1}{2M} \left\{ \frac{1}{1 - e(S)} - 1 + e(S) \right\} \right] \right). \tag{11}
\]

Remark 1 It is worth discussing comparisons of the three matching schemes namely propensity score matching, prognostic score matching and double score matching based on the variance formulas in (9) and (11). We show in the supplementary material that if the prognostic score model is correctly specified, the double score matching estimators may be less efficient than the prognostic score matching estimators of \( \tau \) and \( \Delta_{\xi} \). If the propensity score model is correctly specified, the double score matching estimators are more efficient than the propensity score matching estimators of \( E\{Y(a)\} \) and \( q_{a, \xi} \) for \( a = 0, 1 \); however, this improvement is not guaranteed for estimating \( \tau \) and \( \Delta_{\xi} \). Importantly, double score matching has the advantage of double robustness compared to single score matching: the double score matching estimators of \( \tau \) and \( \Delta_{\xi} \) are consistent if either the prognostic score model or the propensity score model is correctly specified, but not necessarily both. Moreover, the consistency is agnostic to which model is correctly specified.

4.2 Asymptotic results for estimated \( \theta^* \)

To acknowledge the fact that \( \theta^* \) is estimated prior to matching, we will establish the approximate distributions of \( \hat{\tau}_{\text{dsm}}(\hat{\theta}) \) and \( \hat{\Delta}_{\xi, \text{dsm}}(\hat{\theta}) \) and investigate the impact of estimation of the nuisance parameters on the approximate distributions. As in Abadie and Imbens (2016), the typical Taylor expansion technique can not be used because of the non-smooth nature of matching. Our derivation is based on the technique developed by Andreou and Werker (2012), which offers a general approach for deriving the limiting distribution of statistics that involve estimated nuisance parameters. This technique has been successfully used in Abadie and Imbens (2016) for the matching estimators of the ATEs based on the estimated propensity score. Abadie and Imbens (2016), however, assumed that the propensity score model is correctly specified. We extend their results to the double score matching estimator when one of the balancing scores may be misspecified.
Theorem 3 Under Assumptions 1–2, 5, and regularity conditions specified in the supplementary material, if either Assumption 3 or Assumption 7 holds, the approximate distribution of $n^{1/2} \left\{ \bar{\tau}_{dsm}(\hat{\theta}) - \tau \right\}$ is

$$
\mathcal{N}(0, V_{\tau, \text{adj}}), \quad V_{\tau, \text{adj}} = V_{\tau} - \gamma_1^T \Sigma_U^{-1} \gamma_1 + \gamma_2^T \Sigma_{\theta^*} \gamma_2,
$$

(12)

where $\gamma_1 = (\gamma_{11}, \gamma_{12}, \gamma_{13})$,

\begin{align*}
\gamma_{11} &= E \left[ \mu_1 \{S(\theta^*)\} - \mu_0 \{S(\theta^*)\} - \tau \right] \frac{\partial e(X; \alpha^*)}{\partial \alpha} \frac{A - e(X; \alpha^*)}{e(X; \alpha^*)} \\
&+ E \left[ \mu_1(X) - \mu_1 \{S(\theta^*)\} \right] \frac{\partial e(X; \alpha^*)}{\partial \alpha} \frac{1 - e(X; \alpha^*)}{e(X; \alpha^*)},
\end{align*}

\begin{align*}
\gamma_{12} &= -E \left[ \mu_1 \{S(\theta^*)\} - \mu_0 \{S(\theta^*)\} - \tau \right] (1 - A) \frac{\partial \mu_0(X; \beta_0^*)}{\partial \beta_0} \{\mu_0(X) - \mu_0(X; \beta_0^*)\} \\
&- E \left[ \mu_0(X) - \mu_0 \{S(\theta^*)\} \right] \frac{\partial \mu_0(X; \beta_0^*)}{\partial \beta_0} \{\mu_0(X) - \mu_0(X; \beta_0^*)\} - E \left\{ \frac{\partial \mu_0(X; \beta_0^*)}{\partial \beta_0} \sigma_0^2(X) \right\},
\end{align*}

\begin{align*}
\gamma_{13} &= -E \left[ \mu_1 \{S(\theta^*)\} - \mu_0 \{S(\theta^*)\} - \tau \right] A \frac{\partial \mu_1(X; \beta_1^*)}{\partial \beta_1} \{\mu_1(X) - \mu_1(X; \beta_1^*)\} \\
&- E \left[ \mu_1(X) - \mu_1 \{S(\theta^*)\} \right] \frac{\partial \mu_1(X; \beta_1^*)}{\partial \beta_1} \{\mu_1(X) - \mu_1(X; \beta_1^*)\} - E \left\{ \frac{\partial \mu_1(X; \beta_1^*)}{\partial \beta_1} \sigma_1^2(X) \right\},
\end{align*}

and $\gamma_2 = (\gamma_{21}, \gamma_{22}, \gamma_{23})$,

\begin{align*}
\gamma_{21} &= -E \left\{ \frac{A \{Y - \mu_1(X; \beta_1^*)\}}{\{e(X; \alpha)\}^2} + \frac{(1 - A) \{Y - \mu_0(X; \beta_0^*)\}}{\{1 - e(X; \alpha^*)\}^2} \right\} \frac{\partial e(X; \alpha^*)}{\partial \alpha},
\gamma_{22} &= -E \left\{ \frac{A - e(X; \alpha^*) \frac{\partial \mu_0(X; \beta_0^*)}{\partial \beta_0}}{1 - e(X; \alpha^*)} \right\},
\gamma_{23} &= -E \left\{ \frac{A - e(X; \alpha^*) \frac{\partial \mu_1(X; \beta_1^*)}{\partial \beta_1}}{e(X; \alpha)} \right\}.
\end{align*}

Similarly, the approximate distribution of $n^{1/2} \left\{ \bar{\Delta}_{\xi,dsm}(\theta^*) - \Delta_\xi \right\}$ is

$$
\mathcal{N}(0, V_{\Delta, \text{adj}}), \quad V_{\Delta, \text{adj}} = V_{\Delta} - \gamma_3^T \Sigma_U^{-1} \gamma_3 + \gamma_4^T \Sigma_{\theta^*} \gamma_4,
$$

(13)

where $\gamma_3 = (\gamma_{31}, \gamma_{32}, \gamma_{33})$,

\begin{align*}
\gamma_{31} &= E \left[ \frac{F_1 \{q_1, \xi; S(\theta^*)\} - F_0 \{q_0, \xi; S(\theta^*)\}}{f_1(q_1, \xi)} - \Delta_\xi \right] \frac{\partial e(X; \alpha^*)}{\partial \alpha} \frac{A - e(X; \alpha^*)}{e(X; \alpha^*)} \\
&+ E \left[ f_1(q_1, \xi)^{-1} [F_1(q_1, \xi; X) - F_1(q_1, \xi; S(\theta^*))] \frac{\partial e(X; \alpha^*)}{\partial \alpha} \frac{1 - e(X; \alpha^*)}{e(X; \alpha^*)} \right] \\
&- E \left[ f_0(q_0, \xi)^{-1} [F_0(q_0, \xi; X) - F_0(q_0, \xi; S(\theta^*))] \frac{\partial e(X; \alpha^*)}{\partial \alpha} \frac{-e(X; \alpha^*)}{e(X; \alpha^*)} \right],
\end{align*}

12
Abadie and Imbens (2016) showed that for

\[ \gamma_{32} = -E \left( \frac{F_1 \{ q_{1,\xi}; S(\theta^*) \} - F_0 \{ q_{0,\xi}; S(\theta^*) \} - \Delta_\xi}{f_1(q_{1,\xi})} \right) (1 - A) \frac{\partial \mu_0(X; \beta_0^*)}{\partial \beta_0} \{ \mu_0(X) - \mu_0(X; \beta_0^*) \} \]

\[ - E \left( f_0(q_{0,\xi})^{-1} \{ F_0 \{ q_{0,\xi}; X - F_0 \{ q_{0,\xi}; S(\theta^*) \} \} \right) \frac{\partial \mu_0(X; \beta_0^*)}{\partial \beta_0} \{ \mu_0(X) - \mu_0(X; \beta_0^*) \} \]

\[ - E \left( \frac{\partial \mu_0(X; \beta_0^*)}{\partial \beta_0} f_0(q_{0,\xi})^{-1} [I \{ Y(0) \leq q_{0,\xi} \} - F_0(q_{0,\xi}; X) \{ Y(0) - \mu_0(X) \} \right) , \]

\[ \gamma_{33} = -E \left( \frac{F_1 \{ q_{1,\xi}; S(\theta^*) \} - F_0 \{ q_{0,\xi}; S(\theta^*) \} - \Delta_\xi}{f_1(q_{1,\xi})} \right) A \frac{\partial \mu_1(X; \beta_1^*)}{\partial \beta_1} \{ \mu_1(X) - \mu_1(X; \beta_1^*) \} \]

\[ - E \left( f_1(q_{1,\xi})^{-1} [F_1 \{ q_{1,\xi}; X - F_1 \{ q_{1,\xi}; S(\theta^*) \} \} \right) \frac{\partial \mu_1(X; \beta_1^*)}{\partial \beta_1} \{ \mu_1(X) - \mu_1(X; \beta_1^*) \} \]

\[ - E \left( \frac{\partial \mu_1(X; \beta_1^*)}{\partial \beta_1} f_1(q_{1,\xi})^{-1} [I \{ Y(1) \leq q_{1,\xi} \} - F_1(q_{1,\xi}; X) \{ Y(1) - \mu_1(X) \} \right) , \]

and \( \gamma_4^T = (\gamma_{41}^T, \gamma_{42}^T, \gamma_{43}^T) \).

\[ \gamma_{41} = -E \left( \frac{\left( A \{ Y \leq q_{1,\xi} \} - F_1 \{ q_{1,\xi}; S(\theta^*) \} \right) + (1 - A) \{ I \{ Y \leq q_{0,\xi} \} - F_0 \{ q_{0,\xi}; S(\theta^*) \} \}}{f_1(q_{1,\xi}) \{ e(X; \alpha^*) \}^2} \right) \frac{\partial e(X; \alpha^*)}{\partial \alpha} \]

\[ \gamma_{42} = -E \left[ \frac{A - e(X; \alpha^*)}{1 - e(X; \alpha^*)} \right] \frac{\partial F_0 \{ q_{0,\xi}; S(\theta^*) \}}{f_0(q_{0,\xi})} \frac{\partial \beta_0}{\partial \beta_0} \]

\[ \gamma_{43} = -E \left[ \frac{A - e(X; \alpha^*)}{e(X; \alpha)} \right] \frac{\partial F_1 \{ q_{1,\xi}; S(\theta^*) \}}{f_1(q_{1,\xi})} \frac{\partial \beta_1}{\partial \beta_1} \]

If Assumptions 3 and 4 hold, we have \( e(X; \alpha^*) = e(X) \) and \( \mu_a(X; \beta_a^*) = \mu_a(X) \) for \( a = 0, 1 \). Then \( \gamma_k \) for \( k = 1, \ldots, 4 \) can be simplified.

**Remark 2** We discuss the impact of estimating the nuisance parameters on the matching estimators. To fixed ideas, we focus on estimating the ATE \( \tau \). Abadie and Imbens (2016) showed that for \( \tau \), matching on the estimated propensity score always improves the estimation efficiency compared to matching on the true propensity score. This improvement is due to the correlation of the matching estimator and the score function for the parameters in the propensity score. In our context, comparing the asymptotic variances in Theorems 4 and 5, the difference between \( V_\tau,\text{adj} \) and \( V_\tau, \gamma_1^T \Sigma_U^{-1} \gamma_1 + \gamma_2^T \Sigma_{\theta^*} \gamma_2 \), can be either positive, zero, or negative; i.e., matching on the estimated double score can either increase or decrease the estimation efficiency compared to matching on the true double score. To explain the difference, we note that the variance reduction term \( -\gamma_1^T \Sigma_U^{-1} \gamma_1 \) is still due to the correlation of the matching estimator and the score function for the parameters in the double score, while the variance inflation term \( \gamma_2^T \Sigma_{\theta^*} \gamma_2 \) is because if either the prognostic score model or the propensity score model is misspecified, \( \tau \) may depend on the nuisance parameters through

\[ \tau = E \left[ \frac{A \{ Y - \mu_1(X; \beta_1^*) \}}{e(X; \alpha^*)} \right] - \frac{(1 - A) \{ Y - \mu_0(X; \beta_0^*) \}}{1 - e(X; \alpha^*)} + \{ \mu_1(X; \beta_1^*) - \mu_0(X; \beta_0^*) \} \right] , \]
which contributes to the variance inflation term. On the other hand, Abadie and Imbens (2016) focused on the setting when the propensity score model is the only nuisance model and is correctly specified. In this case, $\tau$ does not depend on $\alpha^*$, $\gamma_2$ is zero, and therefore the variance inflation term is zero. Similar discussion applies to the double score matching estimator for the QTE.

5 Variance estimation and inference

Theorem 3 enables us to derive variance estimators for the double score matching estimators that can take all sources of variability into account. However, such variance estimators rely heavily on the asymptotic results. We consider variance estimation based on replication methods (Efron, 1979; Wolter, 2007), which may have better finite sample performance compared to asymptotic variance estimation. Lack of smoothness makes the standard replication methods invalid for the predictive mean matching estimator. If the number of matches increases with the sample size, such as in kernel matching and local linear matching Heckman et al. (1997b), the matching estimators are asymptotically smooth, which enable the conventional replication methods for inference. When the number of matches remains fixed, Abadie and Imbens (2008) demonstrated the failure of the bootstrap for matching estimators. This is because the non-parametric bootstrap cannot preserve the distribution of the number of times that each unit is used as a match. In this case, Otsu and Rai (2017) proposed a wild bootstrap procedure for the matching estimator when matching is directly based on the covariates.

Given the two-stage estimation procedure for the double score matching estimators, the variability of the matching estimators results from two sources: estimation of the double score function and matching. To faithfully take into account all sources of variability, we propose a parallel two-stage replication variance estimation procedure. First, we construct replicates of the nuisance parameter estimators in the double score function. Second, based on the asymptotic linearization of the matching estimators, we construct replicates of the matching estimators directly based on the linear terms with the replicated nuisance parameters. In this way, the distribution of the number of times that each unit is used as a match can be retained.

Specifically, the replication variance estimation algorithm proceeds as follows.

**VE-Step 1.** Obtain a bootstrap sample, or equivalently the bootstrap replication weights $\omega_{i}^* = n^{-1}m_{i}^*$ with $(m_{1}^*, \ldots, m_{n}^*)$ is a multinomial random vector with $n$ draws on $n$ equal probability cells. Obtain a bootstrap replicate of $\hat{\theta}$, $\hat{\theta}^* = (\hat{\alpha}^*, \hat{\eta}^*)$, by solving the estimating equation $n^{-1/2} \sum_{i=1}^{n} \{\omega_{i}^* U(A_i, X_i, Y_i; \theta)\} = 0$. For each unit $i$, calculate $S_{i}(\hat{\theta}^*) = \{\logit(e(X_i; \hat{\alpha}^*), \Psi(X_i; \hat{\eta}^*))\}^\top$.

For variance estimation of $\bar{\tau}_{dsm}(\bar{\theta})$, VE-Steps 2 and 3 proceed as follows:
VE-Step 2. Obtain a bootstrap replicate of $\tau_{dsm}(\hat{\theta})$,

$$
\hat{\tau}_{dsm}^*(\hat{\theta}) = n^{-1} \sum_{i=1}^{n} \omega_i^* \left[ \hat{\mu}_1 \{ S_i(\hat{\theta}^*) \} - \hat{\mu}_0 \{ S_i(\hat{\theta}^*) \} \right] 
+ n^{-1} \sum_{i=1}^{n} \omega_i^* \left( 2A_i - 1 \right) \left[ 1 + M^{-1} K_{S_i(\hat{\theta}),i} \right] \left[ Y_i - \hat{\mu}_{A_i} \{ S_i(\hat{\theta}^*) \} \right].
$$

VE-Step 3. Repeat VE-Steps 1 and 2 for a large number of times. Calculate the bootstrap variance estimator of $\hat{\tau}_{dsm}(\hat{\theta})$ as the empirical variance of $\hat{\tau}_{dsm}^*(\hat{\theta})$ over a large number of bootstrap replicates.

For variance estimation of $\hat{\Delta}_{\xi,dsm}(\hat{\theta})$, Steps 2 and 3 proceed as follows:

VE-Step 2'. For $a = 0, 1$, obtain a bootstrap replicate of $\hat{q}_{a,\xi,dsm}(\hat{\theta})$, $\hat{q}_{a,\xi,dsm}^*(\hat{\theta})$, by solving

$$
\tilde{F}_{a,dsm}^*(q) = n^{-1} \sum_{i=1}^{n} \omega_i^* \tilde{F}_a \{ q; S_i(\hat{\theta}^*) \}
+ n^{-1} \sum_{i=1}^{n} \omega_i^* I(A_i = a) \left[ 1 + M^{-1} K_{S_i(\hat{\theta}),i} \right] \left[ I(Y_i \leq q) - \tilde{F}_a \{ q; S_i(\hat{\theta}^*) \} \right] = \xi,
$$

for $q$. Then a bootstrap replicate of $\hat{\Delta}_{\xi,dsm}(\hat{\theta})$ is $\hat{\Delta}_{\xi,dsm}^*(\hat{\theta}) = \hat{q}_{1,\xi,dsm}^*(\hat{\theta}) - \hat{q}_{0,\xi,dsm}^*(\hat{\theta})$.

VE-Step 3'. Repeat VE-Steps 1 and 2' for a large number of times. Calculate the bootstrap variance estimator of $\hat{\Delta}_{\xi,dsm}(\hat{\theta})$ as the empirical variance of $\hat{\Delta}_{\xi,dsm}^*(\hat{\theta})$ over a large number of bootstrap replicates.

6 Simulation study

We conduct a simulation study to investigate the finite-sample performance of the proposed double score matching estimators. The sample size $n = 1000$. The confounders $X = (X_1, \ldots, X_{10})$ follow $X_j \overset{iid}{\sim} \text{Uniform}[1 - \sqrt{3}, 1 + \sqrt{3}]$ for $j = 1, \ldots, 10$. Let a nonlinear transformation of $X$ to be $Z = (Z_1, \ldots, Z_{10})$, where

$Z_1 = \exp(X_1/2)$, $Z_2 = \exp(X_2/3)$, $Z_3 = \log((X_3 + 1)^2)$, $Z_4 = \log((X_4 + 1)^2)$, $Z_5 = I(X_5 > 0.5)$, $Z_6 = I(X_6 > 0.75)$, $Z_7 = \sin(X_7 - X_8)$, $Z_8 = \cos(X_7 + X_8)$, $Z_9 = \sin(X_9)$, $Z_{10} = \cos(X_{10})$,

which are further scaled and centered such that $E(Z_j) = 1$ and $\text{var}(Z_j) = 1$ for all $j$. The potential outcomes are $Y(0) = \beta_0^T Z + \epsilon(0)$ and $Y(1) = Y(0) - \epsilon(0) + \epsilon(1)$, where $\beta_0^T = (1, 1, 1, 1, 1, -1, -1, -1, -1, -1)/2$,

$\epsilon(0) \sim N(0, 2^2)$ and $\epsilon(1) \sim N(3, 1)$. Under the data generative model, the ATE $\tau$ is 0 and the 75th QTE is $-0.45$. The treatment indicator $A$ follows Bernoulli{\{e(X)}}, where $\text{logit}\{e(X)\} = \alpha_0^T Z$, where $\alpha_0^T = (1, 1, 1, 1, 1, -1, -1, -1, -1, -1)/4$.

We compare the following estimators: naive, which is the simple difference of standard estimators from two treatment groups; the bias-corrected matching estimator based on $X$ (“m.x”; Abadie and Imbens [2011]) or propensity score (“m.ps”) or prognostic score (“m.prog”) or double score (“m.ds”). To assess the double
robustness property of the double score matching estimator, we consider two model specifications for the propensity score: a logistic regression model with the predictor \(Z\) (correct) and that with the predictor \(X\) (wrong); we also consider two model specifications for prognostic score: \(\beta_0^T Z\) (correct) and \(\beta_0^T X\) (wrong). The matching estimators are implemented based on the steps in Section 3: if matching directly on \(X\), start with Step 2 and replace \(S_i(\hat{\theta})\) with \(X_i\); if matching on the propensity score, start with Step 1 and replace \(S_i(\hat{\theta})\) with \(\logit(X_i; \hat{\alpha})\); if matching on the prognostic score, start with Step 1 and replace \(S_i(\hat{\theta})\) with \(\Psi(X_i; \hat{\eta})\). For all matching estimators, the conditional outcome mean functions are approximated using power series; and the conditional distribution functions are approximated based on the power series for the normal linear model Zhang et al. (2012).

We compare four model specification scenarios (S1)–(S4) in Figure 1. The naive estimator is biased for the 75th QTE and the ATE. Matching directly based on 10-dimensional \(X\) has biases for the QTE and the ATE across scenarios even with bias correction. The single score matching estimators are singly robust and rely on a correct specification of the underlying score model. The double score matching estimator is doubly robust in that it has small biases for the QTE and the ATE even if one of the scores is misspecified as demonstrated in (S2) and (S3).

Table 1 reports the simulation results for the coverage properties for the 75th QTE and the ATE using the naive nonparametric bootstrap and the proposed replication-based method. Under the double robustness condition (i.e., if either the propensity score model or the prognostic score model is correctly specified), for the nonparametric bootstrap, the coverage rates are close to the nominal coverage for the 75th QTE however are much over the nominal coverage for the ATE; for the proposed replication method, the coverage rates are close to the nominal coverage. If the propensity score model and the prognostic score model are misspecified, the coverage rates are off the nominal coverage for both methods.
Figure 1: Simulation result based on 5000 Monte Carlo simulated datasets under four scenarios for propensity score (PS) model and prognostic score (PROG) model: “75th” is the 75th QTE and “mean” is the ATE.

Table 1: Simulation results based on 5000 Monte Carlo simulated datasets for the coverage properties for the 75th QTE (“75th”) and the ATE (“mean”) under four scenarios for propensity score (PS) model and prognostic score (PROG) model: empirical coverage rate and (empirical coverage rate ± 2×Monte Carlo standard error)

| Scenario | 75th       | Mean       |
|----------|------------|------------|
| PS:correct/PROG:correct | Naive bootstrap | Proposed method | Naive bootstrap | Proposed method |
| (S1)     | 95.5 (94.9, 96.0) | 95.4 (94.8, 96.0) | 99.4 (99.2, 99.6) | 95.0 (94.4, 95.6) |
| (S2)     | 95.3 (94.7, 95.8) | 95.7 (95.3, 96.4) | 99.5 (99.3, 99.7) | 95.8 (95.1, 96.3) |
| (S3)     | 94.9 (94.3, 95.5) | 94.9 (94.3, 95.5) | 99.5 (99.3, 99.6) | 95.5 (94.9, 96.0) |
| (S4)     | 78.5 (77.3, 79.6) | 79.1 (78.0, 80.3) | 100.0 (100.0, 100.0) | 54.7 (53.3, 56.0) |
7 Real-data application

In this section, we apply the proposed double score matching method as well as other existing methods in Section 6 to the well-known National Supported Work (NSW) data (LaLonde; 1986; Dehejia and Wahba; 1999; Firpo; 2007). This dataset documented the effect of a job training program for the unemployed on future earnings. Following Dehejia and Wahba (1999), we include the comparison group from Westat’s Matched Current Population Survey-Social Security (CPS) Administration File. In our analysis, we include 185 treated units and 689 control units from the NSW, as well as 429 comparison units from the CPS-3, a subset of the CPS data (LaLonde; 1986; Dehejia and Wahba; 1999; Firpo; 2007). Seven baseline confounding covariates are used for this application: age, education, race, Hispanic, married, having no college degree, and real earnings in 1975. The outcome of interest is the real earnings in 1978.

Because the outcome distributions are highly skewed (see Figure 2), the average treatment effect may not provide a comprehensive evaluation of the job training program. Therefore, we estimate the ATT and QTTs. The propensity score is estimated based on a logistic regression model with all first-order terms of the covariates and second-order terms of numerical variables, following Dehejia and Wahba (1999). The prognostic score is estimated based on a linear regression of the earnings with the same predictors as in the propensity score model for the control group.

Matching admits a transparent assessment of covariate balance before and after matching. Table 2 presents the means of all covariates by treatment group and the standardized difference in means before and after double score matching. The standardized difference is calculated as the difference of the group means divided by the overall standard error in the original sample. Double score matching makes standardized differences fall between $-0.05$ to $0.05$ for all covariates, reducing the differences of the observed covariates in the treated and the control.

Table 3 shows the estimated ATTs and QTTs at the 0.1, 0.25, 0.3, 0.5, 0.75 and 0.9 quantiles, and 95% Wald confidence intervals from the four matching methods, as well as ATE and QTE estimated by naive method. All four matching estimators show that the job training program does not have a significant effect on the average earning for the treated. Figure 3 shows the QTT plot estimated by double score matching algorithm. A closer inspection of the QTT plot reveals that the effect is in fact significant around percentile of 0.3, which suggests that the program is beneficial for the lower middle class.
Table 2: Covariate balance check before and after double score matching

|               | Age | Educ | Black | Hisp | Married | Nodgr | Re75 |
|---------------|-----|------|-------|------|---------|-------|------|
| Before        | 24.63 | 10.38 | 0.80  | 0.09 | 0.17    | 0.73  | 3066 |
| Matching      | 26.25 | 10.21 | 0.50  | 0.13 | 0.34    | 0.70  | 2745 |
| Stand diff. in means | -0.19 | 0.08  | 0.61  | -0.10 | -0.37   | 0.06  | 0.07 |
| After         | 24.63 | 10.38 | 0.80  | 0.09 | 0.17    | 0.73  | 3066 |
| Matching      | 25.04 | 10.39 | 0.80  | 0.11 | 0.17    | 0.72  | 2898 |
| Stand diff. in means | -0.05 | 0.00  | 0.01  | -0.05 | -0.01   | 0.01  | 0.04 |

Table 3: Estimated ATT and QTTs at the 0.1, 0.25, 0.3, 0.5, 0.75 and 0.9 quantiles, and 95% Wald confidence intervals

| Estimand | m.x         | m.ps        | m.prog      | m.ds         | Naive(ATE&QTE) |
|----------|-------------|-------------|-------------|--------------|----------------|
| ATT      | 372 (-746,1489) | 918 (-222,2058) | -150 (-1215,914) | 1088 (-57,2233) | -65 (-957,827) |
| 0.1-QTT  | 0 (0,0)     | 0 (0,0)     | 0 (0,0)     | 0 (0,0)      | 0 (0,0)        |
| 0.25-QTT | 549 (-90,1189) | 549 (-55,1154) | 549 (-104,1202) | 549 (-76,1175) | 549 (-55,1153) |
| 0.3-QTT  | 935 (57,1813) | 1064 (268,1860) | 1039 (96,1982) | 1019 (134,1904) | 604 (-641,1170) |
| 0.5-QTT  | 524 (-1606,2654) | 889 (-741,2519) | 1296 (-252,2844) | 757 (-997,2511) | 69 (-1093,1230) |
| 0.75-QTT | -391 (-2752,1970) | 617 (-1451,2686) | 737 (-2070,3544) | 1763 (-656,4182) | -195 (-1441,1578) |
| 0.9-QTT  | -963 (-3482,1556) | 897 (-1750,3543) | -936 (-4770,1795) | 864 (-1395,3123) | -2326 (-2021,2158) |

8 Discussion

We establish the statistical properties of the double score matching estimators of the ATEs and the QTEs utilizing the double balancing property of the propensity score and the prognostic score. We also propose a double-resampling technique for variance estimation that takes into account the uncertainty due to the double score estimation prior to matching. R package dsmatch is available on github.

Several issues are worth discussing. As in propensity score matching, although the matching variables are well balanced, individual covariates may not for a given application. In this case, if the researchers

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1 https://github.com/Yunshu7/dsmatch
know important confounders based on substantive knowledge, they can augment the double score by adding those confounders to ensure balance for these confounders; however, adding too many variables will result in potential bias as demonstrated in our simulation. Alternatively, one can use regression adjustment for the matched sample Abadie and Spiess (2016), which can remove remaining confounding biases.

Although the literature has proposed flexible machine learning methods for estimating the propensity score function and the prognostic score function, our current development relies on parametric model assumptions, which enables to quantify the impact of double score estimation on the matching estimators and the subsequent inference. In the existing high-dimensional causal inference literature, the doubly robust weighting estimators have been shown to be robust to selection errors using penalization (Farrell, 2015) or approximation errors using machine learning (Chernozhukov et al., 2018), while still retaining the root-\(n\) consistency. In our future work, we will investigate this new role of double robustness in the double score matching framework.

We focus on a binary treatment. Yang et al. (2016) has developed the generalized propensity score matching for estimating the treatment effects for more than two treatments. Instead of creating a matched set to estimate the treatment contrast directly, Yang et al. (2016) proposed to create matched sets to estimate potential outcome means separately. This approach allows matching based on one scalar function, namely the generalized propensity score at a given treatment level, one at a time. It is also of interest to extend our double score matching algorithm to more than two treatment comparison.

It is important to highlight that as for all existing matching methods, the double score matching method
cannot account for unmeasured confounding. Following [Rosenbaum and Rubin (1983)](https://doi.org/10.1007/bf02290207) and [Robins et al. (2000)](https://doi.org/10.1007/bf02290207), we will develop sensitivity analyses to no unmeasured confounding in the matching framework.

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Supplementary material for “Double score matching estimators for average and quantile treatment effects”

S.1 Proof of Theorem 1

For simplicity of the presentation, we omit the dependence of $\theta^*$ for $S$ if there is no ambiguity.

Following Abadie and Imbens (2011) and Abadie and Imbens (2012), assuming that $\hat{B}_n = B_n + o_P(1)$ requiring additional regularity conditions on nonparametric estimation, $\hat{\tau}_{dsm}(\theta^*)$ has the following asymptotic linear form:

$$ n^{1/2} \{ \hat{\tau}_{dsm}(\theta^*) - \tau \} = n^{-1/2} \sum_{i=1}^{n} \{ \mu_1(S_i) - \mu_0(S_i) - \tau \} $$

$$ + n^{-1/2} \sum_{i=1}^{n} (2A_i - 1) \{ 1 + M^{-1} K_{S,i} \} \{ Y_i - \mu_{A_i}(S_i) \} + o_P(1). \quad (S.1) $$

If either Assumption 3 or Assumption 4 holds, $\mu_1(S_i) - \mu_0(S_i)$ is unbiased of $\tau$, and therefore $n^{1/2} \{ \hat{\tau}_{dsm}(\theta^*) - \tau \}$ converges to zero.

It is easy to verify that the covariance of the two terms in (S.1) is zero. Thus, the asymptotic variance of $n^{1/2} \{ \hat{\tau}_{dsm}(\theta^*) - \tau \}$ is

$$ \text{var} \left[ n^{-1/2} \sum_{i=1}^{n} \{ \mu_1(S_i) - \mu_0(S_i) - \tau \} \right] + \text{var} \left[ n^{-1/2} \sum_{i=1}^{n} (2A_i - 1) \{ 1 + M^{-1} K_{S,i} \} \{ Y_i - \mu_{A_i}(S_i) \} \right]. $$

The first term becomes $E \left[ (\mu_1(S) - \mu_0(S) - \tau)^2 \right].$ Following Abadie and Imbens (2006), the second term, as $n \to \infty$, becomes

$$ \text{plim} \left[ n^{-1} \sum_{i=1}^{n} (1 + M^{-1} K_{S,i})^2 \text{var}(Y_i \mid S_i) \right] = E \left( \sigma^2_1(S) \left[ \frac{1}{e(S)} + \frac{1}{2M} \left\{ \frac{1}{e(S)} - e(S) \right\} \right] \right) $$

$$ + E \left( \sigma^2_0(S) \left[ \frac{1}{1 - e(S)} + \frac{1}{2M} \left\{ \frac{1}{1 - e(S)} - 1 + e(S) \right\} \right] \right). $$

S.2 Derivation of $\hat{F}_{a,dsm}(q)$ in (6)

We obtain the following decomposition
\[ n^{1/2} \left\{ \hat{F}_{a,dsm}^{(0)}(q) - F_a(q) \right\} = n^{-1/2} \sum_{i=1}^{n} \{ I(A_i = a) (1 + M^{-1}K_{S,i}) I(Y_i \leq q) - F_a(q) \} = n^{-1/2} \sum_{i=1}^{n} I(A_i = a) (1 + M^{-1}K_{S,i}) \{ I(Y_i \leq q) - F_a(q; S_i) \} + n^{-1/2} \sum_{i=1}^{n} I(A_i = a) (1 + M^{-1}K_{S,i}) \{ F_a(q; S_i) - F_a(q) \} = n^{-1/2} \sum_{i=1}^{n} \{ F_a(q; S_i) - F_a(q) \} + n^{-1/2} \sum_{i=1}^{n} I(A_i = a) (1 + M^{-1}K_{S,i}) \{ I(Y_i \leq q) - F_a(q; S_i) \} - n^{-1/2} \sum_{i=1}^{n} I(A_i = 1 - a) M^{-1} \sum_{j \in J_{S,i}} \{ F_a(q; S_i) - F_a(q; S_j) \} \]

and denote
\[
D_{a,n}(q) = n^{-1/2} \sum_{i=1}^{n} \{ F_a(q; S_i) - F_a(q) \} + n^{-1/2} \sum_{i=1}^{n} I(A_i = a) (1 + M^{-1}K_{S,i}) \{ I(Y_i \leq q) - F_a(q; S_i) \},
\]
\[
B_{a,n}(q) = -n^{-1/2} \sum_{i=1}^{n} I(A_i = 1 - a) M^{-1} \sum_{j \in J_{S,i}} \{ F_a(q; S_i) - F_a(q; S_j) \}. \tag{S.2}
\]

Because of \([\text{1}]\) and \([\text{2}]\), \(E\{F_a(q; S_i)\} = F_a(q)\), so \(D_{a,n}(q)\) is unbiased. The difference \(F_a(q; S_i) - F_a(q; S_j)\) in \(\text{S.2}\) accounts for the matching discrepancy, and therefore \(B_{a,n}(q)\) contributes to the asymptotic bias of the matching estimator. To correct for the bias due to matching discrepancy, let \(\hat{F}_a(q; S)\) be a nonparametric estimator of \(F_a(q; S)\), for \(a = 0, 1\). We propose a de-biasing double score matching estimator \(\hat{F}_{a,dsm}(q)\) of \(F_a(q)\) in \([\text{2}]\).

### S.3 Proof of Theorem \([\text{2}]\)

Under Assumption \([\text{6}]\) we can write
\[
\hat{F}_{a,dsm}(\hat{q}_a,\hat{\xi},\text{ds}m) - F_a(q_a,\xi) = \hat{F}_{a,dsm}(\hat{q}_a,\xi) - F_a(q_a,\xi) + f_a(q_a,\xi)(\hat{q}_a,\xi,\text{ds}m - q_a,\xi) + o_P(n^{-1/2}). \tag{S.3}
\]

Then the Bahadur-type representation for \(\hat{q}_a,\xi,\text{ds}m\) in \([\text{10}]\) follows. Therefore, we have
\[
n^{1/2} \left\{ \hat{\Delta}_{\xi,\text{ds}m}(\theta^*) - \Delta \xi \right\} = n^{1/2} \left\{ -\hat{F}_{1,dsm}(q_1,\xi) f_1(q_1,\xi) + \hat{F}_{0,dsm}(q_0,\xi) f_0(q_0,\xi) - \Delta \xi \right\} + o_P(1) = n^{-1/2} \sum_{i=1}^{n} \left\{ -\frac{F_1(q_1,\xi; S_i)}{f_1(q_1,\xi)} + \frac{F_0(q_0,\xi; S_i)}{f_0(q_0,\xi)} - \Delta \xi \right\} - n^{-1/2} \sum_{i=1}^{n} (2A_i - 1) \left\{ 1 + M^{-1}K_{S,i} \right\} \left\{ \frac{I(Y_i \leq q_{A_i,\xi}) - F_{A_i}(q_{A_i,\xi}; S_i)}{f_{A_i}(q_{A_i,\xi})} \right\} + o_P(1).
\]

Following a similar derivation in the proof for Theorem \([\text{1}]\) the asymptotic variance of \(n^{1/2} \left\{ \hat{\Delta}_{\xi,\text{ds}m}(\theta^*) - \Delta \xi \right\}\) is given by \([\text{11}]\).
S.4 Proof of Remark 1

We prove Remark 1 for the ATEs. The same proof applies to the QTEs and is omitted. To compare the asymptotic variance of the matching estimators, we note that the derivation for the double score matching estimator in Section S.1 applies to the propensity score matching estimator and the prognostic score matching estimator by replacing $S$ with $e(X)$ and $\Psi(X)$, respectively.

If the prognostic score model is correctly specified, we have $\Psi(X; \eta^*) = \Psi(X)$ and

$$
\mu_a(S) = E\{Y(a) \mid S\} = E\{Y(a) \mid e(X; \alpha^*), \Psi(X)\} = E\{Y(a) \mid X\} = \mu_a(X).
$$

Then, for the double score matching estimator, $V_\tau$ in (9) becomes

$$
V_{\tau, dsm} = E \left[ (\mu_1(X) - \mu_0(X) - \tau)^2 \right] + E \left( \sigma^2_1(X) \left[ \frac{1}{e(S)} + \frac{1}{2M} \left\{ \frac{1}{e(S)} - e(S) \right\} \right] \right)
+ E \left( \sigma^2_0(X) \left[ \frac{1}{1 - e(S)} + \frac{1}{2M} \left\{ \frac{1}{1 - e(S)} - 1 + e(S) \right\} \right] \right).
$$

For the prognostic score matching estimator, it is easy to derive that the corresponding asymptotic variance is

$$
V_{\tau, prog} = E \left[ (\mu_1(X) - \mu_0(X) - \tau)^2 \right] + E \left( \sigma^2_1(X) \left( \frac{1}{e(\Psi(X))} + \frac{1}{2M} \left\{ \frac{1}{e(\Psi(X))} - e\{\Psi(X)\} \right\} \right) \right)
+ E \left( \sigma^2_0(X) \left( \frac{1}{1 - e\{\Psi(X)\}} + \frac{1}{2M} \left\{ \frac{1}{1 - e\{\Psi(X)\}} - 1 + e\{\Psi(X)\} \right\} \right) \right).
$$

By Jensen’s inequality, we have

$$
E \left\{ \frac{1}{e(S)} \mid \Psi(X) \right\} \geq \frac{1}{E\{e(S) \mid \Psi(X)\}} = \frac{1}{e\{\Psi(X)\}}.
$$

$$
E \left\{ \frac{1}{1 - e(S)} \mid \Psi(X) \right\} \geq \frac{1}{E\{1 - e(S) \mid \Psi(X)\}} = \frac{1}{1 - e\{\Psi(X)\}}.
$$

It follows that $V_{\tau, dsm} \geq V_{\tau, prog}$.

If the propensity score model is correctly specified, we have $e(X; \alpha^*) = e(X)$ and

$$
e(S) = P(A = 1 \mid S) = P\{A = 1 \mid e(X), \Psi(X; \eta^*)\} = e(X).
$$

Then, for the double score matching estimator, $V_\tau$ in (9) becomes

$$
V_{\tau, dsm} = E \left[ (\mu_1(S) - \mu_0(S) - \tau)^2 \right] + E \left( \sigma^2_1(S) \left[ \frac{1}{e(X)} + \frac{1}{2M} \left\{ \frac{1}{e(X)} - e(X) \right\} \right] \right)
+ E \left( \sigma^2_0(S) \left[ \frac{1}{1 - e(X)} + \frac{1}{2M} \left\{ \frac{1}{1 - e(X)} - 1 + e(X) \right\} \right] \right).
$$
For the propensity score matching estimator, it is easy to derive that the corresponding asymptotic variance is

$$V_{\tau, psm} = E\left(\left[\mu_1\{e(X)\} - \mu_0\{e(X)\} - \tau\right]^2\right) + E\left(\sigma^2_1\{e(X)\} \left[\frac{1}{e(X)} + \frac{1}{2M} \left\{\frac{1}{1 - e(X)} - 1 + e(X)\right\}\right]\right) + E\left(\sigma^2_0\{e(X)\} \left[\frac{1}{1 - e(X)} + \frac{1}{2M} \left\{\frac{1}{1 - e(X)} - 1 + e(X)\right\}\right]\right).$$

To compare $V_{\tau, dsm}$ and $V_{\tau, psm}$, we decompose

$$Y(a) = \mu_a\{e(X)\} + \epsilon_{a,S|e(X)} + \epsilon_a,$$

where $\epsilon_{a,S|e(X)}$ and $\epsilon_a$ have mean zero and satisfy that $\mu_a\{e(X)\} \perp \{\epsilon_{a,S|e(X)}, \epsilon_a\}$ and $\epsilon_{a,X|e(X)} \perp \epsilon_a$. With this decomposition, $\sigma^2_0\{e(X)\} = E\{\epsilon^2_{a,S|e(X)} \mid e(X)\} + E(\epsilon_a^2)$ and $\sigma^2_0(S) = E(\epsilon_a^2)$. Then, it follows that

$$V_{\tau, psm} - V_{\tau, dsm} = -E\left\{(\epsilon_{1,S|e(X)} - \epsilon_{0,S|e(X)})^2\right\} + E\left(\epsilon_{1,S|e(X)} \left[\frac{1}{e(X)} + \frac{1}{2M} \left\{\frac{1}{1 - e(X)} - 1 + e(X)\right\}\right]\right) + E\left(\epsilon_{0,S|e(X)} \left[\frac{1}{1 - e(X)} + \frac{1}{2M} \left\{\frac{1}{1 - e(X)} - 1 + e(X)\right\}\right]\right).$$

The last two terms are always non-negative; however, the sign of $-2E\left\{\epsilon_{1,S|e(X)}\epsilon_{0,S|e(X)}\right\}$ and therefore that of $V_{\tau, psm} - V_{\tau, dsm}$ can be either positive, zero, or negative. So for estimating $\tau$, it is not guaranteed that the double score matching estimator is more efficient than propensity score matching. For estimating $E\{Y(a)\}$, using the similar argument as above, $-2E\left\{\epsilon_{1,S|e(X)}\epsilon_{0,S|e(X)}\right\}$ is absent, so the double score matching estimator is more efficient than the propensity score matching estimator.

**S.5 Le Cam’s third Lemma**

Consider two sequences of probability measures $(Q^{(n)})_{n=1}^{\infty}$ and $(P^{(n)})_{n=1}^{\infty}$. Assume that under $P^{(n)}$, a statistic $T_n$ and the likelihood ratios $dQ^{(n)}/dP^{(n)}$ satisfy

$$\left(\frac{T_n}{\log(dQ^{(n)}/dP^{(n)})}\right) \rightarrow N\left\{\left(\begin{array}{c} 0 \\ -\sigma^2/2 \end{array}\right), \left(\begin{array}{cc} \tau^2 & c \\ c & \sigma^2 \end{array}\right)\right\}$$

in distribution, as $n \rightarrow \infty$. Then, under $Q^{(n)}$,

$$T_n \rightarrow N(c, \tau^2)$$

in distribution, as $n \rightarrow \infty$. See Le Cam and Yang (1990), Bickel et al. (1993) and van der Vaart (2000) for textbook discussions.
S.6 Proof for Theorem 3

We follow the technique in Andreou and Werker (2012) and Abadie and Imbens (2016). In Abadie and Imbens (2016), the propensity score matching estimators rely on the nuisance parameter estimator under a correct specification of propensity score model. In our setting, the nuisance parameters include both parameters in the propensity score model and the prognostic score model, and either one of the models may be misspecified. Let $P$ be the distribution of $(A_i, X_i, Y_i)$, for $i = 1, \ldots, n$. Consider $P = P^{\theta^*}$ to be indexed by $\theta^* = (\alpha^T, \beta_0^T, \beta_1^T)^T$, which satisfies

$$E\{U(A, X, Y; \theta^*)\} = E\left\{ \begin{pmatrix} U_1(A, X; \alpha^*) \\ U_2(A, X, Y; \beta_0^*) \\ U_3(A, X, Y; \beta_1^*) \end{pmatrix} \right\} = 0. \tag{S.6}$$

We invoke standard regularity conditions on Z-estimation or M-estimation (van der Vaart, 2000) as follows.

Assumption S.1 (i) Under $P^{\theta^*}$, $U_n(\theta^*) \rightarrow \mathcal{N}(0, \Sigma_U)$ in distribution, as $n \rightarrow \infty$, where $\Sigma_U = E\{U(A, X, Y; \theta^*)U(A, X, Y; \theta^*)^T\}$; (ii) $\Gamma_\theta = E\{\partial U(A, X, Y; \theta)/\partial \theta^T\}$ is nonsingular around $\theta^*$; and (iii) for any vector of constant $h$, $\exp\{n^{1/2}h^T\Gamma_\theta^*\Sigma_U^{-1}U_n(\theta^*)\}$ is uniformly integrable.

Under Assumption S.1

$$n^{1/2}(\hat{\theta} - \theta^*) = -\Gamma_\theta^{-1}U_n(\theta^*) + o_P(1) \rightarrow \mathcal{N}(0, \Sigma_{\theta^*}) \tag{S.7}$$

in distribution, as $n \rightarrow \infty$, where $\Sigma_{\theta^*} = \Gamma_{\theta^*}^{-1}\Sigma_U(\Gamma_{\theta^*}^{-1})^T$.

To derive the large sample distribution of $\hat{\tau}_{dsm}(\hat{\theta})$, following Abadie and Imbens (2016), we impose the following regularity conditions.

Assumption S.2 There exists a neighborhood of $\theta^*$, such that for any $\theta$ in this region, the following conditions hold: (i) the matching variable $S(\theta)$ has a compact and convex support $\mathcal{S}$, with a continuous density bounded and bounded away from zero; (ii) for $a = 0, 1$, $\mu_a\{S(\theta)\}$ and $\sigma_a^2\{S(\theta)\}$ satisfy the Lipschitz continuity condition; and (iii) for $a = 0, 1$, there exists $\delta > 0$ such that $E\{|Y(a)|^{2+\delta} | S(\theta)\}$ is uniformly bounded for any $S(\theta) \in \mathcal{S}$.

Following Andreou and Werker (2012), because we consider a semiparametric model for $\theta^*$, to invoke the Le Cam’s lemma, we specify an auxiliary parametric model $P^{\theta_n}$ defined locally though $\theta^*, \theta_n = \theta^* + n^{-1/2}h$, with a density

$$\frac{\exp\{n^{1/2}(\theta_n - \theta^*)^T\Gamma_{\theta^*}\Sigma_U^{-1}U_n(\theta^*) - 2^{-1}n(\theta_n - \theta^*)^T\Sigma_{\theta^*}^{-1}(\theta_n - \theta^*)\}}{E\left\{\exp\{n^{1/2}(\theta_n - \theta^*)^T\Gamma_{\theta^*}\Sigma_U^{-1}U_n(\theta^*) - 2^{-1}n(\theta_n - \theta^*)^T\Sigma_{\theta^*}^{-1}(\theta_n - \theta^*)\}\right\}}. \tag{S.8}$$
By Assumption S.1 (iii), \( \exp\{n^{1/2}(\theta_n - \theta^*)^T \Gamma_{\theta^*} \Sigma_U^{-1} U_n(\theta^*)\} \) is uniformly integrable, and thus model (S.8) is uniformly locally asymptotically normal. Because under \( P^{\theta^*}, U_n(\theta^*) \to \mathcal{N}(0, \Sigma_U) \) in distribution, the normalizing constant in the denominator converges to 1 as \( n \to \infty \). The Fisher information under the parametric model (S.8) is \( n \Sigma_{\theta^*}^{-1} \). Therefore, \( \hat{\theta} \) is efficient under model (S.8).

Now consider \( (A_i, X_i, Y_i) \), for \( i = 1, \ldots, n \), with the local shift \( P^{\theta_n} \) (Bickel et al., 1993). Under model (S.8), the likelihood ratio under \( P^{\theta_n} \) is

\[
\log(dP^{\theta^*}/dP^{\theta_n}) = -h^T \Gamma_{\theta^*} \Sigma_U^{-1} U_n(\theta^*) + \frac{1}{2} h^T \Sigma_{\theta^*}^{-1} h + o_P(1)
\]

\[
= -h^T \Gamma_{\theta^*} \Sigma_U^{-1} U_n(\theta_n) - \frac{1}{2} h^T \Sigma_{\theta^*}^{-1} h + o_P(1), \tag{S.9}
\]

where the second equality follows by the Taylor expansion of \( U_n(\theta^*) \) at \( \theta_n \). Moreover, under \( P^{\theta_n} \): \( U_n(\theta_n) \to \mathcal{N}(0, \Sigma_U) \) in distribution, as \( n \to \infty \), and

\[
n^{1/2}(\hat{\theta} - \theta_n) = \Gamma_{\theta^*}^{-1} U_n(\theta_n) + o_P(1). \tag{S.10}
\]

We also assume the following regularity condition:

**Assumption S.3** For all bounded continuous functions \( h(A, X, Y) \), the conditional expectation \( E_{\theta_n} \{h(A, X, Y)\} \) converges in distribution to \( E \{h(A, X, Y)\} \), where \( E_{\theta_n}(\cdot) \) is the expectation taken with respect to \( P^{\theta_n} \).

We derive the results in Theorem 3 in two steps.

In the first step, under \( P^{\theta_n} \), we write \( \tau = \tau(\theta_n) \) to reflect its dependence on \( \theta_n \); to be specific, we have

\[
\tau(\theta_n) = E \left[ \frac{A\{Y - \mu(X; \beta_{1,n})\}}{e(X; \alpha_n)} - \frac{(1 - A)\{Y - \mu_0(X; \beta_{0,n})\}}{1 - e(X; \alpha_n)} + \{\mu_1(X; \beta_{1,n}) - \mu_0(X; \beta_{0,n})\} \right].
\]

We derive that under \( P^{\theta_n} \),

\[
\left( \frac{n^{1/2}(\hat{\tau}_{\text{dsm}}(\theta_n) - \tau(\theta_n))}{n^{1/2}(\hat{\theta} - \theta_n)} \right) \to \mathcal{N} \left\{ \begin{pmatrix} 0 \\ 0 \\ -\frac{1}{2} h^T \Sigma_{\theta^*}^{-1} h \end{pmatrix}, \begin{pmatrix} V_r & \gamma^T_{1} \Gamma_{\theta^*}^{-1} - \gamma^T_{1} \Sigma_{\theta^*}^{-1} \Gamma_{\theta^*} h \\ \Gamma_{\theta^*}^{-1} \gamma_{1} & -h^T \Sigma_{\theta^*}^{-1} h \\ -h^T \Gamma_{\theta^*} \Sigma_U^{-1} \gamma_{1} & h^T \Sigma_{\theta^*}^{-1} h \end{pmatrix} \right\} \tag{S.11}
\]

in distribution, as \( n \to \infty \). We then express \( \tau(\theta_n) = \tau(\theta^*) + \gamma_2 (n^{-1/2} h) + o(n^{-1/2}) \), where \( \gamma_2 = \partial \tau(\theta) / \partial \theta \bigg|_{\theta = \theta^*} \), and use the shorthand \( \tau \) for \( \tau(\theta^*) \). Then by Le Cam’s third lemma, under \( P^{\theta^*} \),

\[
\left( \frac{n^{1/2}(\hat{\tau}_{\text{dsm}}(\theta^* + n^{-1/2} h) - \tau)}{n^{1/2}(\hat{\theta} - \theta^*)} \right) \to \mathcal{N} \left\{ \begin{pmatrix} 0 \\ 0 \\ -\frac{1}{2} h^T \Sigma_{\theta^*}^{-1} h \end{pmatrix}, \begin{pmatrix} V_r & \gamma^T_{1} \Gamma_{\theta^*}^{-1} - \gamma^T_{1} \Sigma_{\theta^*}^{-1} \Gamma_{\theta^*} h \\ \Gamma_{\theta^*}^{-1} \gamma_{1} & -h^T \Sigma_{\theta^*}^{-1} h \\ -h^T \Gamma_{\theta^*} \Sigma_U^{-1} \gamma_{1} & h^T \Sigma_{\theta^*}^{-1} h \end{pmatrix} \right\} \tag{S.12}
\]

in distribution, as \( n \to \infty \). Replacing \( \theta_n \) by \( \theta^* + n^{-1/2} h \) yields that under \( P^{\theta^*} \),

\[
\left( \frac{n^{1/2}(\hat{\tau}_{\text{dsm}}(\theta^* + n^{-1/2} h) - \tau)}{n^{1/2}(\hat{\theta} - \theta^*)} \right) \to \mathcal{N} \left\{ \begin{pmatrix} 0 \\ 0 \\ -\frac{1}{2} h^T \Sigma_{\theta^*}^{-1} h \end{pmatrix}, \begin{pmatrix} V_r & \gamma^T_{1} \Gamma_{\theta^*}^{-1} - \gamma^T_{1} \Sigma_{\theta^*}^{-1} \Gamma_{\theta^*} h \\ \Gamma_{\theta^*}^{-1} \gamma_{1} & -h^T \Sigma_{\theta^*}^{-1} h \\ -h^T \Gamma_{\theta^*} \Sigma_U^{-1} \gamma_{1} & h^T \Sigma_{\theta^*}^{-1} h \end{pmatrix} \right\} \tag{S.12}
\]
in distribution, as \( n \to \infty \).

In the second step, we provide a heuristic derivation for (S.12) to imply the approximate distribution (12). If the normal distribution were exact, then

\[
 n^{1/2} \{\hat{\tau}_{\text{dsms}}(\theta^* + n^{-1/2}h) - \tau\} \mid n^{1/2}(\hat{\theta} - \theta^*) = h \sim N\left(-\gamma_1^T h, V_{\tau} - \gamma_1^T \Sigma_U^{-1} \gamma_1\right). \tag{S.13}
\]

Given that \( n^{1/2}(\hat{\theta} - \theta^*) = h \), we have \( \theta^* + n^{-1/2}h = \hat{\theta} \), and hence \( \hat{\tau}_{\text{dsms}}(\theta^* + n^{-1/2}h) = \hat{\tau}_{\text{dsms}}(\hat{\theta}) \). Marginalizing (S.13) over the asymptotic distribution of \( n^{1/2}(\hat{\theta} - \theta^*) \), we derive (12). The formal technique to derive (12) can be found in Andreou and Werker (2012) and Abadie and Imbens (2016). To avoid repetition, we omit this step.

In the following, we provide the proof to (S.11) in the first step of the proof. Asymptotic normality of \( n^{1/2}\{\hat{\tau}_{\text{dsms}}(\theta_n) - \tau(\theta_n)\} \) under \( P^{\theta_0} \) follows from Theorem 1 and the uniform local asymptotic normality of model (S.9). Asymptotic joint normality of \( \log(dP^{\theta^*}/dP^{\theta_0}) \) and \( n^{1/2}(\hat{\theta} - \theta_n) \) follows from (S.9) and (S.10). Also, \( n^{1/2}\{\hat{\tau}_{\text{dsms}}(\theta_n) - \tau(\theta_n)\} = D_n(\theta_n) + o_P(1) \), where

\[
 D_n(\theta_n) = n^{-1/2} \sum_{i=1}^n \left[ \mu_1\{S_i(\theta_n)\} - \mu_0\{S_i(\theta_n)\} - \tau(\theta_n) \right] 
 + n^{-1/2} \sum_{i=1}^n (2A_i - 1) \left\{ 1 + M^{-1}K_{S_i(\theta_n)} \right\} \left\{ Y_i - \mu A_i\{S_i(\theta_n)\} \right\} + o_P(1).
\]

Therefore, the remaining is to show that, under \( P^{\theta_0} \):

\[
 \begin{pmatrix} D_n(\theta_n) \\ U_n(\theta_n) \end{pmatrix} \to N \left\{ \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} V_{\tau} & \gamma_1^T \\ \gamma_1 & \Sigma_U \end{pmatrix} \right\} \tag{S.14}
\]

in distribution, as \( n \to \infty \). To prove (S.14), consider the linear combination

\[
 T_n = c_0 D_n(\theta_n) + c^T U_n(\theta_n) 
 = c_0 n^{-1/2} \sum_{i=1}^n \left[ \mu_1\{S_i(\theta_n)\} - \mu_0\{S_i(\theta_n)\} - \tau(\theta_n) \right] 
 + c_0 n^{-1/2} \sum_{i=1}^n (2A_i - 1) \left\{ 1 + M^{-1}K_{S_i(\theta_n)} \right\} \left\{ Y_i - \mu A_i\{S_i(\theta_n)\} \right\} 
 + c_1 T_1 n^{-1/2} \sum_{i=1}^n \frac{\partial e(X_i; \alpha_n)}{\partial \alpha} A_i - e(X_i; \alpha_n) 
 + c_1 T_2 n^{-1/2} \sum_{i=1}^n (1 - A_i) \frac{\partial \mu_0(X_i; \beta_{0,n})}{\partial \beta_0} \left\{ Y_i - \mu_0(X_i; \beta_{0,n}) \right\} 
 + c_2 T_2 n^{-1/2} \sum_{i=1}^n A_i \frac{\partial \mu_1(X_i; \beta_{1,n})}{\partial \beta_1} \left\{ Y_i - \mu_1(X_i; \beta_{1,n}) \right\} + o_P(1),
\]
where $c = (c_1^T, c_2^T, c_3^T)^T$. We analyze $T_n$ using the martingale theory. We rewrite $T_n = \sum_{k=1}^{2n} \xi_{n,k}$, where

$$
\xi_{n,k} = \begin{cases}  
\sum_{j=1}^{8} \xi_{n,k}^{(j)}, & 1 \leq k \leq n, \\
\sum_{j=9}^{11} \xi_{n,k}^{(j)}, & n + 1 \leq k \leq 2n,
\end{cases}
$$

\begin{align*}
\xi_{n,k}^{(1)} &= c_0 n^{-1/2} \left[ \mu_1 \{ S_k(\theta_n) \} - \mu_0 \{ S_k(\theta_n) \} - \tau(\theta_n) \right], \\
\xi_{n,k}^{(2)} &= c_0 n^{-1/2} \left( 2A_k - 1 \right) \left\{ 1 + M^{-1} K_{S(\theta_n), k} \right\} \left[ \mu_{A_k} (X_k) - \mu_{A_k} \{ S_k(\theta_n) \} \right], \\
\xi_{n,k}^{(3)} &= c_1 T_n^{-1/2} \frac{\partial e(X_k; \alpha_n)}{\partial \alpha} \frac{e(X_k) - e(X_k; \alpha_n)}{e(X_k; \alpha_n) \{ 1 - e(X_k; \alpha_n) \}}, \\
\xi_{n,k}^{(4)} &= c_2 T_n^{-1/2} \left( 1 - e(X_k) \right) \frac{\partial \mu_0 (X_k; \beta_0, n)}{\partial \beta_0} \left\{ \mu_0 (X_k) - \mu_0 (X_k; \beta_0, n) \right\}, \\
\xi_{n,k}^{(5)} &= -c_3 n^{-1/2} e(X_k) \frac{\partial \mu_1 (X_k; \beta_1, n)}{\partial \beta_1} \left\{ \mu_1 (X_k) - \mu_1 (X_k; \beta_1, n) \right\}, \\
\xi_{n,k}^{(6)} &= c_1 T_n^{-1/2} \frac{\partial e(X_k; \alpha_n)}{\partial \alpha} \left( A_k - e(X_k) \right), \\
\xi_{n,k}^{(7)} &= -c_2 n^{-1/2} \left( A_k - e(X_k) \right) \frac{\partial \mu_0 (X_k; \beta_0, n)}{\partial \beta_0} \left\{ \mu_0 (X_k) - \mu_0 (X_k; \beta_0, n) \right\}, \\
\xi_{n,k}^{(8)} &= c_3 n^{-1/2} \left( A_k - e(X_k) \right) \frac{\partial \mu_1 (X_k; \beta_1, n)}{\partial \beta_1} \left\{ \mu_1 (X_k) - \mu_1 (X_k; \beta_1, n) \right\}, \\
\xi_{n,k}^{(9)} &= c_0 n^{-1/2} \left( 2A_k - 1 \right) \left\{ 1 + M^{-1} K_{S(\theta_n), k} \right\} \left\{ Y_{k-n} - \mu_{A_k-n} (X_{k-n}) \right\}, \\
\xi_{n,k}^{(10)} &= c_2 T_n^{-1/2} \left( 1 - A_k-n \right) \frac{\partial \mu_0 (X_k-n; \beta_0, n)}{\partial \beta_0} \left\{ Y_{k-n} - \mu_0 (X_{k-n}) \right\}, \\
\xi_{n,k}^{(11)} &= c_3 n^{-1/2} \left( 1 - A_k-n \right) \frac{\partial \mu_1 (X_k-n; \beta_1, n)}{\partial \beta_1} \left\{ Y_{k-n} - \mu_1 (X_{k-n}) \right\}.
\end{align*}

Consider the \( \sigma \)-fields

$$
\mathcal{F}_{n,k} = \begin{cases}  
\sigma(A_1, \ldots, A_k, X_1, \ldots, X_k), & 1 \leq k \leq n, \\
\sigma(A_1, \ldots, A_n, X_1, \ldots, X_n, Y_{k-1}, \ldots, Y_{k-n}), & 2n + 1 \leq k \leq 3n.
\end{cases}
$$

Then, we have \( \left\{ \sum_{k=1}^{i} \xi_{n,k}, \mathcal{F}_{n,i}, 1 \leq i \leq 2n \right\} \) is a martingale for each \( n \geq 1 \), which follows by the following reasons:

(i) because \( S_k(\theta_n) \) is a double balancing score,

$$
E_{\theta_n} \left( \xi_{n,k}^{(1)} \mid \mathcal{F}_{n,k-1} \right) = E \left( c_0 n^{-1/2} \left[ \mu_1 \{ S_k(\theta_n) \} - \mu_0 \{ S_k(\theta_n) \} - \tau(\theta_n) \right] \mid \mathcal{F}_{n,k-1} \right) = 0;
$$

(ii) let \( \mathcal{F}_{n,k}^0 = \sigma \{ A_1, \ldots, A_k, S_1(\theta_n), \ldots, S_k(\theta_n) \} \) for \( 1 \leq k \leq n \), then

$$
E_{\theta_n} \left( \xi_{n,k}^{(2)} \mid \mathcal{F}_{n,k-1} \right) = E_{\theta_n} \left( \xi_{n,k}^{(2)} \mid \mathcal{F}_{n,k-1}^0 \right) \mid \mathcal{F}_{n,k-1} = c_0 n^{-1/2} E_{\theta_n} \left[ \left( 2A_k - 1 \right) \left\{ 1 + M^{-1} K_{S(\theta_n), k} \right\} \right] \times E_{\theta_n} \left[ \mu_{A_k} (X_k) - \mu_{A_k} \{ S_k(\theta_n) \} \mid \mathcal{F}_{n,k-1}^0 \mid \mathcal{F}_{n,k-1} \right] \mathcal{F}_{n,k-1}) = c_0 n^{-1/2} E_{\theta_n} \left[ \left( 2A_k - 1 \right) \left\{ 1 + M^{-1} K_{S(\theta_n), k} \right\} \times 0 \mid \mathcal{F}_{n,k-1} \right] = 0;
$$
(iii) \( \mathbb{E}_n(\xi_{n,k}^3 \mid F_{n,k-1}) = \mathbb{E}_n(\xi_{n,k}^4 \mid F_{n,k-1}) = \mathbb{E}_n(\xi_{n,k}^5 \mid F_{n,k-1}) = 0 \) because \( \mathbb{E}_n\{U(\theta_n)\} = 0 \);

(iv) by the conditioning argument,

\[
\mathbb{E}_n\left( \xi_{n,k}^6 \mid F_{n,k-1} \right) = \mathbb{E}_n \left[ e_{n-1/2} \frac{\partial \xi_{n,k}(X_k; \alpha_n)}{\partial \alpha} \mathbb{E} \left\{ \frac{A_k - e(X_k)}{e(X_k; \alpha) \{1 - e(X_k; \alpha_n)\}} \mid F_{n,k-1} \right\} \right] = 0;
\]

(v) \( \mathbb{E}_n(\xi_{n,k}^7 \mid F_{n,k-1}) = 0 \) and \( \mathbb{E}_n(\xi_{n,k}^8 \mid F_{n,k-1}) = 0 \) due to that fact that \( A_k - e(X_k) \) is unbiased conditional on \( X_k \);

(vi) \( \mathbb{E}_n(\xi_{n,k}^9 \mid F_{n,k-1}) = 0 \) because \( (1 - A_k - n)\{Y_k - n - \mu_0(X_k - n)\} \) is unbiased given \( F_{n,k-1} \);

(vii) \( \mathbb{E}_n(\xi_{n,k}^{10} \mid F_{n,k-1}) = 0 \) because \( A_k - n\{Y_k - n - \mu_1(X_k - n)\} \) is unbiased given \( F_{n,k-1} \).

Therefore, we can apply the martingale central limit theorem \cite{Billingsley1995} to derive the limiting distribution of \( T_n \). Under Assumption S.2 we can verify the conditions for the martingale central limit theorem hold. It follows that under \( P^{\theta_n} \), \( T_n \rightarrow \mathcal{N}(0, \sigma^2) \) in distribution, as \( n \rightarrow \infty \), where \( \sigma^2 = \text{plim} \sum_{k=1}^{2n} \mathbb{E}_n(\xi_{n,k}^2 \mid F_{n,k-1}) \). Under Assumption S.3 we thus derive the expression of \( \sigma^2 \) and specify the components in S.14, where \( \gamma_1 \) is given in Theorem 1.

To derive (13), the key is to write

\[
\hat{q}_{i, \text{dsm}} - \hat{q}_{0, \text{dsm}} - \Delta_\xi(\theta^*) = \frac{\hat{F}_{1\text{,dsm}}(q_{1,\xi}) - F_1(q_{1,\xi})}{f_1(q_{1,\xi})} + \frac{\hat{F}_{0\text{,dsm}}(q_{0,\xi}) - F_0(q_{0,\xi})}{f_0(q_{0,\xi})} + o_P(n^{-1/2}),
\]

where

\[
\hat{F}_{a\text{,dsm}}(q_{a,\xi}) = n^{-1} \sum_{i=1}^{n} \left\{ F_a(q_{a,\xi}; S(\theta^*)) - \xi \right\} + n^{-1} \sum_{i=1}^{n} I(A_i = a) \left( \frac{(A_i - 1) K_{S_i}}{f_1(q_{1,\xi}) - f_0(q_{0,\xi})} \right) \left( I(Y_i \leq q_{a,\xi}) - F_a(q_{a,\xi}; S(\theta^*)) \right),
\]

\[
\Delta_\xi(\theta^*) = E \left[ \frac{A}{e(X; \alpha)} \left\{ I(Y \leq q_{1,\xi}) - F_1(q_{1,\xi}; S(\theta^*)) \right\} - \frac{1 - A}{1 - e(X; \alpha)} \left\{ I(Y \leq q_{0,\xi}) - F_0(q_{0,\xi}; S(\theta^*)) \right\} \right] + E \left[ \frac{F_1(q_{1,\xi}; S(\theta^*))}{f_1(q_{1,\xi})} - \frac{F_0(q_{0,\xi}; S(\theta^*))}{f_0(q_{0,\xi})} \right],
\]

and repeat a similar analysis with the following changes to \( \xi_{n,k}^{(1)}, \xi_{n,k}^{(2)} \) and \( \xi_{n,k}^{(9)} \):

\[
\xi_{n,k}^{(1)} = c_0 n^{-1/2} \left[ f_1(q_{1,\xi})^{-1} F_1(q_{1,\xi}; S_k(\theta_n)) - f_0(q_{0,\xi})^{-1} F_0(q_{0,\xi}; S_k(\theta_n)) - \Delta_\xi(\theta_n) \right],
\]

\[
\xi_{n,k}^{(2)} = c_0 n^{-1/2} (2A_k - 1) \left( 1 + M^{-1} K_{S(\theta_n),k} \right) f_{A_k}(q_{A_k,\xi})^{-1} \left\{ F_{A_k}(q_{A_k,\xi}; X_k) - F_{A_k}(q_{A_k,\xi}; S_k(\theta_n)) \right\},
\]

\[
\xi_{n,k}^{(9)} = c_0 n^{-1/2} (2A_k - 1) \left( 1 + M^{-1} K_{S(\theta_n),k-n} \right) f_{A_{k-n}}(q_{A_{k-n},\xi})^{-1} \left\{ I(Y_{k-n} \leq q_{A_{k-n},\xi}) - F_{A_{k-n}}(q_{A_{k-n},\xi}; X_{k-n}) \right\}.
\]

**S.7 Extension to the causal effects on the treated**

In this extension, we estimate the average causal effect on the treated \( \tau_{\text{ATT}} \) and the quantile treatment effect on the treated \( \Delta_{\text{ATT},\xi} = q_{1,\xi}|A=1 - q_{0,\xi}|A=1 \), where \( q_{a,\xi}|A=1 = \inf_q[P(Y(a) \leq q) \geq \xi | A = 1], a = 0, 1 \). Here,
because \( f\{Y(1) \mid A = 1\} = f(Y \mid A = 1) \), the outcome distribution for the treated is identifiable. Therefore, \( E\{Y(1) \mid A = 1\} = E(Y \mid A = 1) \) and \( q_{1,\xi|A=1} = \inf_q \{P(Y \leq q \mid A = 1) \geq \xi\} \).

To identify the outcome distribution for the control, Assumptions 1 and 2 can be relaxed (Heckman et al. 1997b).

**Assumption S.4** \( Y(0) \perp \perp A \mid X \).

**Assumption S.5** There exists a constant \( c \) such that \( e(X) \leq c < 1 \) almost surely.

For the causal effects on the treated, the prognostic score \( \Psi_0(X) \) is a sufficient statistic for \( Y(0) \) in the sense that \( Y(0) \perp \perp X \mid \Psi_0(X) \) according to Hansen (2008). Then, under Assumptions S.4 and S.5,

\[
\tau_{\text{ATT}} = E[E(Y \mid A = 1) - E(Y \mid A = 0, e(X)) \mid A = 1]
\]

and

\[
q_{0,\xi|A=1} = \inf_{q} (E[P\{Y \leq q \mid A = 0, e(X)\} \mid A = 1] \geq \xi)
\]

encoding the double balancing properties of \( S = \{e(X), \Psi_0(X)\} \).

The double score matching estimators for \( \tau_{\text{ATT}} \) and \( \Delta_{\text{ATT},\xi} \) follow similar steps as for \( \tau \) and \( \Delta_\xi \). We describe the differences below.

In the matching step, for each unit \( i \) with treatment \( A_i = 1 \), find \( M \) nearest neighbors from the control group \( A_i = 0 \) based on the matching variable \( S_i = S_i(\hat{\theta}) \). Let these matched units for unit \( i \) be indexed by \( J_{S(\hat{\theta}),i} \).

The initial and de-biasing double score matching estimators of \( \tau_{\text{ATT}} \) are

\[
\hat{\tau}_{\text{ATT,ds}}^{(0)} = n_1^{-1} \sum_{i=1}^{n} A_i\{Y_i - \bar{Y}_i(0)\}, \quad \hat{\tau}_{\text{ATT,ds}} = \tau_{\text{ATT,ds}}^{(0)} - n_1^{-1} \sum_{i=1}^{n} A_i\{\hat{\mu}_0(S_i) - M^{-1} \sum_{j \in J_{S,\hat{S},i}} \hat{\mu}_0(S_j)\}.
\]

Let the estimator of \( F_1(q \mid A = 1) = P\{Y(1) < q \mid A = 1\} \) be

\[
\hat{F}_1(q \mid A = 1) = n_1^{-1} \sum_{i=1}^{n} A_i I(Y_i \leq q).
\]

Then, we estimate \( q_{1,\xi|A=1} \) by

\[
\hat{q}_{1,\xi|A=1} = \inf_q \{\hat{F}_1(q \mid A = 1) \geq \xi\}.
\]
The initial and de-biasing double score matching estimators of $F_0(q | A = 1) = P\{Y(0) < q | A = 1\}$ are

\[
\hat{F}_{0,dsm}^{(0)}(q | A = 1) = n_1^{-1} \sum_{i=1}^{n} A_i M^{-1} \sum_{j \in J_{S,i}} (1 - A_j) I(Y_j \leq q) = n_1^{-1} \sum_{i=1}^{n} (1 - A_i) M^{-1} K_{S,i} I(Y_i \leq q),
\]

\[
\hat{F}_{0,dsm}(q | A = 1) = \hat{F}_{0,dsm}^{(0)}(q | A = 1) - n_1^{-1/2} \hat{B}_{0,n}(q),
\]

\[
\hat{B}_{0,n}(q) = -n_1^{-1/2} \sum_{i=1}^{n} A_i M^{-1} \sum_{j \in J_{S,i}} \left\{ \hat{F}_0(q; S_i) - \hat{F}_0(q; S_j) \right\}.
\]

Then, we estimate $q_{0,\xi|A=1}$ by

\[
\hat{q}_{0,\xi|A=1,dsm} = \inf_{\hat{q}} \{ \hat{F}_{0,dsm}(q | A = 1) \geq \xi \}.
\]

Lastly, the double score matching estimator of $\Delta_{ATT}$ is $\hat{\Delta}_{ATT,\xi,dsm} = \hat{q}_{1,\xi|A=1} - \hat{q}_{0,\xi|A=1,dsm}$.

For variance estimation, we replace the VE-Step 2 and VE-Step 2' for $\tau$ and $\Delta_{\xi}$ by the following steps:

**ATT-VE-Step 2.** Obtain a bootstrap replicate of $\hat{\tau}_{ATT,dsm}(\hat{\theta})$,

\[
\hat{\tau}_{ATT,dsm}^*(\hat{\theta}^*) = n_1^{-1} \sum_{i=1}^{n} \omega_i A_i \left[ \hat{\mu}_1 \{ S_i(\hat{\theta}^*) \} - \hat{\mu}_0 \{ S_i(\hat{\theta}^*) \} \right] + n_1^{-1} \sum_{i=1}^{n} \omega_i \left\{ A_i - (1 - A_i) M^{-1} K_{S,i} A \right\} \left[ Y_i - \hat{\mu}_A \{ S_i(\hat{\theta}^*) \} \right].
\]

**QTT-VE-Step 2'.** For $a = 1$, obtain a bootstrap replicate of $\hat{q}_{1,\xi|A=1}(\hat{\theta})$, $\hat{q}_{1,\xi|A=1}^*(\hat{\theta}^*)$, by solving

\[
\hat{F}_1^*(q | A = 1) = n_1^{-1} \sum_{i=1}^{n} \omega_i A_i I(Y_i \leq q) = \xi.
\]

For $a = 0$, obtain a bootstrap replicate of $\hat{q}_{0,\xi|A=1,dsm}(\hat{\theta})$, $\hat{q}_{0,\xi|A=1,dsm}^*(\hat{\theta}^*)$, by solving

\[
\hat{F}_{0,dsm}^*(q | A = 1) = n_1^{-1} \sum_{i=1}^{n} \omega_i A_i \hat{F}_0(q; S_i(\hat{\theta}^*)) + n_1^{-1} \sum_{i=1}^{n} \omega_i I(A_i = 0) M^{-1} K_{S,i} A \left[ I(Y_i \leq q) - \hat{F}_0(q; S_i(\hat{\theta}^*)) \right] = \xi,
\]

for $q$. Then a bootstrap replicate of $\hat{\Delta}_{ATT,\xi,dsm}(\hat{\theta})$ is $\hat{\Delta}_{ATT,\xi,dsm}^*(\hat{\theta}^*) = \hat{q}_{1,\xi|A=1}^*(\hat{\theta}^*) - \hat{q}_{0,\xi|A=1,dsm}^*(\hat{\theta}^*)$. 

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