Semiparametric Estimation of Average Treatment Effect with Sieve Method

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Abstract

Correctly identifying treatment effects in observational studies is very difficult due to the fact that the outcome model or the treatment assignment model must be correctly specified. Taking advantages of semiparametric models in this article, we use single-index models to establish the outcome model and the treatment assignment model, which can allow the link function to be unbounded and have unbounded support. The link function is regarded as a point in an infinitely dimensional function space, and we can estimate the link function and the index parameter simultaneously. The sieve method is used to approximate the link function and obtain the estimator of the average treatment effect by the simple linear regression. We establish the asymptotic properties of the proposed estimator. The finite-sample performance of the proposed estimator is evaluated through simulation studies and an empirical example.

Keywords: Hermite polynomials, Observational studies, Propensity score, Sieve method, Single-index model

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1 Introduction

Correctly identifying the effect of a policy or treatment is an important issue in social and biomedical sciences (Imbens and Rubin, 2015). Randomised controlled trials (RCTs) are considered to be the “gold standard” for treatment effects where the mechanism of the treatment assignment is random. However, it is not always feasible to conduct RCTs due to political, financial or ethical concerns. For example, we cannot randomly send people to college to evaluate the impact of college education on income; we cannot expose people randomly to air pollution for evaluating the impact of PM2.5 on health. Thus, much empirical work about treatment effects in economics and biomedical studies need to rely on observational data, where the treatment assignment is not random or manipulated by investigators (Athey and Imbens, 2017).

With rapid development of science and technology, observational data containing fine-grained information about markets and humans and their behavior are becoming available, which brings a great opportunity to study causal effects (Künzel et al., 2019). However, it also brings a great challenge to correctly identify treatment effects due to the lack of randomization in observational studies. Without randomization in the treatment allocation, there usually exist differences in the distribution of the baseline covariates between the treated and control groups. If these differences cannot be reasonably adjusted, the estimator of treatment effects will be seriously biased. The propensity score proposed by Rosenbaum and Rubin (1983) is commonly used to balance the distribution of the baseline covariates in the sense that subjects with similar propensity scores will have similar distribution of the baseline covariates no matter which groups they are in. However, the propensity score is usually unknown in observational studies and commonly estimated by the logistic and Probit models in practice.

Since the work of Rosenbaum and Rubin (1983), propensity score methods including the matching, stratification, inverse probability weighting and covariate adjustment have been well studied by many authors (e.g., Lunceford and Davidian, 2004; Austin, 2011; Hade and Lu, 2014; Zou et al., 2016; Hernán and Robins, 2020). Robins et al. (1994) proposed an augmented inverse probability weighting estimator by combining the propensity score with the outcome regression model, which had been widely studied due to its double robustness. The properties of double robustness mean that the estimator will be consistent if either the outcome regression model or the propensity score is correctly specified (Bang and Robins, 2005).

Correctly specifying the propensity score or the outcome model may not be an easy task in practice, furthermore if both of the above two models are misspecified, the doubly robust
estimator will be seriously biased \citep{Kang2007}. \citet{Tsiatis2007} also pointed out that the doubly robust estimator would be volatile when the estimated propensity score is close to zero or one. How to combine the outcome model and the propensity score to reduce the bias caused by the misspecification of the two models is an important issue in causal inference. Recently, \citet{Lee2018} proposed a simple least squares estimator for treatment effects with the outcome regression model being set to a polynomial function of the propensity score that was estimated by a Probit model, and thus the outcome regression model is a special case of the single index model. \citet{Wu2021} proposed a semiparametric estimator for the average causal effect using a propensity score-based spline with the propensity score estimated by a logistic model.

Parametric models heavily depend on their assumptions, such as the linearity assumption in the least square regression, logistic regression and Probit regression. However, there usually exists complex confounding structures in the treatment assignment of observational data. In order to take the full use of advantages of semiparametric models, we use single-index models to establish the outcome model and the treatment assignment model and allow the link function is unbounded and has unbounded support in this article. The link function is regarded as a point in an infinitely dimensional function space, which allows us to estimate the link function and the index parameter simultaneously. The link function and the index parameter can be derived from an optimization problem with constraints for the identification condition for the index parameter. Then, the estimator of the average treatment effect can be obtained by the simple linear regression.

The rest of the article is organized as follows. In Section 2, we introduce the semiparametric models and statistical inference procedures. In Section 3, we establish the asymptotic properties of the proposed estimator. Simulation studies are conducted to evaluate the finite-sample performance of the proposed estimator in Section 4. A real dataset from Pennsylvania is analyzed to study the effect of maternal smoking on birth weight in Section 5. Some conclusions and remarks are presented in Section 6. The proofs are deferred to the Appendix.

\section{Semiparametric regression and inference procedures}

\subsection{Semiparametric regression model}

In order to simplify expressions, let \( Y \) denote the outcome of interest, a binary variable \( D \) denote the treatment assignment (\( D = 1 \) for treatment, \( D = 0 \) for control) and \( X = (X_1, \ldots, X_p)' \) denote a \( p \)-dimensional vector of the pre-treatment covariates. The observed
data \{(Y_i, D_i, X_i), i = 1, \ldots, n\} are assumed to be independent copies of \((Y, D, X)\). We consider the following semiparametric regression model

\[ Y = \alpha D + r(X) + \epsilon, \tag{2.1} \]

where \(\alpha\) denotes the treatment effect, \(r(X)\) is an unknown smoothed function and \(\epsilon\) is a mean-zero random error. The semiparametric model (2.1) had been widely studied in the literature of econometrics and statistics (e.g., Engle et al., 1986; Robinson, 1988; Stock, 1991). Robinson (1988) proposed an innovative method for estimating the parameter \(\alpha\) by rewriting model (2.1) as follows:

\[ Y - E[Y|X] = \alpha(D - E[D|X]) + \epsilon. \tag{2.2} \]

The estimator of \(\alpha\) obtained via the simple linear regression model (2.2) with \(E[Y|X]\) and \(E[D|X]\) estimated by the Nadaraya-Watson kernel method had been proved to be root-\(N\)-consistent by Robinson (1988).

Although Robinson’s estimator is root-\(N\)-consistent, there exist several limitations when applied to observational data to estimate the treatment effect. The performance of this semiparametric method heavily depends on the accuracy of the estimation of \(E[Y|X]\) and \(E[D|X]\). The nonparametric methods are limited due to the curse of dimensionality and the parametric model assumption may not capture the complicated relationship among the outcome, treatment assignment and baseline covariates in observational data. In order to avoid modeling \(E[Y|X]\) based on individual component of \(X\), Lee (2018) proposed to use the logistic regression to model the propensity score \(E[D|X]\) and then used the second or third order polynomials of \(X^T \hat{\beta}\) to model \(E[Y|X]\) with \(\hat{\beta}\) being the parametric estimator in the propensity score model.

In this article, we consider single-index models for \(E[Y|X]\) and \(E[D|X]\), respectively, which are given as follows:

\[ E[D|X] = \frac{\exp(g_{1,0}(X^T \beta_0))}{1 + \exp(g_{1,0}(X^T \beta_0))}, \tag{2.3} \]

and

\[ E[Y|X] = g_{2,0}(X^T \gamma_0), \tag{2.4} \]

where \(\beta_0 = (\beta_{0,1}, \ldots, \beta_{0,p})^T\) and \(\gamma_0 = (\gamma_{0,1}, \ldots, \gamma_{0,p})^T\) satisfy \(\|\beta_0\| = 1\) with \(\beta_{0,1} \geq 0\) and \(\|\gamma_0\| = 1\) with \(\gamma_{0,1} \geq 0\) for identifiability and the link functions \(g_{1,0}(\omega) \in L^2(\mathbb{R}, \pi(\omega))\) and \(g_{2,0}(\omega) \in L^2(\mathbb{R}, \pi(\omega))\) with \(\pi(\omega) = \exp(-\omega^2/2)\), where \(L^2(\mathbb{R}, \pi(\omega))\) denotes the Hilbert space.
The Hilbert space $L^2(\mathbb{R}, \pi(\omega))$ can cover many function classes, to name a few, all polynomials, all power functions and all bounded functions on $\mathbb{R}$ (Chen, 2007; Dong and Linton, 2018; Dong et al., 2019). Model (2.3) can cover the widely used logistic regression model and Probit model as its special cases. The method of Lee (2018) can be regarded as a special case of our proposed method.

Single-index models have been well studied in the literature of statistics and econometrics. The non-parametric kernel method and spline method are two commonly used methods to estimate single-index models (Xia, 2006; Yu and Ruppert, 2002; Ma and Song, 2015). However, those methods need to assume the boundedness of the link function or its support. Alternatively, sieve methods can provide good approximations to unknown functions and are convenient to calculate (Chen, 2007). In this article, we use the Hermite orthogonal polynomials to approximate the link function in single-index models, which do not need to assume the link function is bounded and has bounded support.

2.2 Inference procedures

The Hermite polynomials form a complete orthogonal system in the Hilbert space $L^2(\mathbb{R}, \pi(\omega))$ with $\pi(\omega) = \exp(-\omega^2/2)$ and its bases are

$$H_m(\omega) = (-1)^m \exp(\omega^2/2) \frac{d^m}{dw^m} \exp(-\omega^2/2), \quad m = 0, 1, 2, \ldots,$$

which satisfy $\int H_m(\omega)H_n(\omega)\pi(\omega)d\omega = m!\sqrt{2\pi}\delta_{mn}$ with $\delta_{mn}$ being the Kronecker delta. Furthermore, define $h_m(\omega) = (\sqrt{2\pi m!})^{-1/2}H_m(\omega)$, then $\{h_m(\omega), m = 0, 1, 2, \ldots\}$ becomes the standard orthogonal basis and satisfies $\int h_m(\omega)h_n(\omega)\pi(\omega)d\omega = \delta_{mn}$ in the Hilbert space $L^2(\mathbb{R}, \pi(\omega))$. For any function $g(\omega) \in L^2(\mathbb{R}, \pi(\omega))$, it has an orthogonal series expansion in terms of $\{h_m(\omega), m = 0, 1, 2, \ldots\}$ given as follows

$$g(\omega) = \sum_{m=0}^{\infty} c_m h_m(\omega) \quad \text{with} \quad c_m = \int g(\omega)h_m(\omega)\pi(\omega)d\omega. \quad (2.5)$$

In the Hilbert space $L^2(\mathbb{R}, \pi(\omega))$, the norm $\| \cdot \|_{L^2}$ is defined as

$$\|g\|_{L^2} = \left\{ \int |g(\omega)|^2\pi(\omega)d\omega \right\}^{1/2},$$

which is equal to $\sqrt{\sum_{m=0}^{\infty} c_m^2}$ by Parseval’s equality. Therefore, the function $g(\omega)$ can be identified by the associated coefficients $\{c_m, m = 0, 1, 2, \ldots\}$. For any truncation parameter $k \geq 1$, the orthogonal series expansions can be split into two parts:

$$g(\omega) = g_k(\omega) + \delta_k(\omega), \quad (2.6)$$
where \( g_k(\omega) = \sum_{m=0}^{k-1} c_m h_m(\omega) \) and \( \delta_k(\omega) = \sum_{m=k}^{\infty} c_m h_m(\omega) \). Under some regularity conditions, it is well known that \( g_k(\omega) \to g(\omega) \) or \( \delta_k(\omega) \to 0 \) as \( k \to \infty \). The term \( g_k(\omega) \)

\( \Omega_k(\theta) \) = \( \mathcal{H}(\omega)^T C_k \) with \( \mathcal{H}(\omega) = (h_0(\omega), h_1(\omega), \ldots, h_{k-1}(\omega))^T \) and \( C_k = (c_0, c_1, \ldots, c_{k-1})^T \).

Due to the expansion (2.6), the non-parametric function \( g(\cdot) \) can be parameterized with \( \{c_m, m = 0, 1, \ldots\} \). To simply notations, we use \( \theta \) for \( \beta \) or \( \gamma \) and \( \theta_0 \) for \( \beta_0 \) or \( \gamma_0 \), respectively. The non-parametric function \( g(\cdot) \) and the unknown parametric \( \theta_0 \) can be reviewed as a point in an infinite-dimensional Euclidean space, which is the two-fold Cartesian product space by \( L^2(\mathbb{R}, \pi(\omega)) \) and \( \mathbb{R}^p \) and is equipped with the norm \( \| \cdot \| \) being

\[
\| (\theta, g) \| = \left( \sum_{m=0}^{\infty} c_m^2 + \| \theta \|^2 \right)^{1/2}
\]

with \( \| \theta \| = \sqrt{\theta_0^2 + \cdots + \theta_d^2} \). Suppose \( \Theta \) is a compact set of \( \mathbb{R}^p \) with \( \theta_0 \) being its interior point and \( G \) is a subset of \( L^2(\mathbb{R}, \pi(\omega)) \) with \( \sup_{g \in G} \| g \|_{L^2} < M \) with \( M \) being a large constant, \( g_1, 0 \in G \) and \( g_2, 0 \in G \). Define \( G_k = G \cap \text{span}\{h_0(\omega), h_1(\omega), \ldots, h_{k-1}(\omega)\} \) with \( k \) being the truncation parameter. Because the treatment assignment in model (2.3) is a binary variable, we define

\[
L_n(\beta, g) = -n^{-1} \sum_{i=1}^{n} \left\{ D_i (\mathcal{H}(X_i^T \beta)^T C_k) - \log \left( 1 + \exp(\mathcal{H}(X_i^T \beta)^T C_k) \right) \right\}.
\]

Because the outcome in model (2.4) is a continuous variable, we define

\[
L_n(\gamma, g) = n^{-1} \sum_{i=1}^{n} \left[ y_i - \mathcal{H}(X_i^T \gamma)^T C_k \right]^2.
\]

Then, the estimators of \( \theta_0 \) and \( C_{0,k} \) can be obtained by solving the following constrained minimization problem

\[
(\hat{\theta}, \hat{C}_k) = \arg \min_{\Omega_k, \lambda} W_n(\theta, g) = \arg \min_{\Omega_k, \lambda} \left[ L_n(\theta, g) + \lambda(\| \theta \|^2 - 1) \right], 
\]

(2.7)

where \( \Omega_k = \{ (\theta, C_k) : \theta \in \Theta, \| C_k \|_2 \leq M \} \subseteq \mathbb{R}^{d+k} \) with \( C_k = (c_0, \ldots, c_{k-1})^T \). The estimator for the average treatment effect is given as follows

\[
\hat{\alpha}_n = \frac{\sum_{i=1}^{n} \left[ y_i - \hat{g}_{2,k}(X_i^T \gamma) \right] \left[ D_i - \frac{\exp(\hat{g}_{1,k}(X_i^T \beta))}{1 + \exp(\hat{g}_{1,k}(X_i^T \beta))} \right]}{\sum_{i=1}^{n} \left[ D_i - \frac{\exp(\hat{g}_{1,k}(X_i^T \beta))}{1 + \exp(\hat{g}_{1,k}(X_i^T \beta))} \right]^2}, 
\]

(2.8)

where \( \hat{g}_{1,k}(X^T \beta) = \hat{C}_{1,k}^T \mathcal{H}(X^T \beta) \) and \( \hat{g}_{2,k}(X^T \gamma) = \hat{C}_{2,k}^T \mathcal{H}(X^T \gamma) \).
3 Asymptotic properties

In order to establish the asymptotic properties of the proposed estimators, we assume the following conditions hold.

C1 $\Theta \subset \mathbb{R}^p$ is a convex and compact set and $\beta_0$ and $\gamma_0$ are two interior points of $\Theta$. $G \subset L^2(\mathbb{R}, \pi(\omega))$ with $\sup_{g \in G} \|g\|_{L^2} < M$ with $g_{1,0} \in G$, $g_{2,0} \in G$ and $M$ being a large constant.

C2 Define $\Sigma_1(\theta_0, C_{0,k}) = E \left[(\mathcal{H}(X^T \theta_0)^T C_{0,k})^2 X X^T \right]$ and $\Sigma_2(\theta_0) = E \left[\mathcal{H}(X^T \theta_0) \mathcal{H}(X^T \theta_0)^T \right]$, we have $\varepsilon_1 \leq \lambda_{\text{min}}(\Sigma_1(\theta_0, C_{0,k})) \leq \lambda_{\text{max}}(\Sigma_1(\theta_0, C_{0,k})) \leq M_1$ and $\varepsilon_2 \leq \lambda_{\text{min}}(\Sigma_2(\theta_0)) \leq \lambda_{\text{max}}(\Sigma_2(\theta_0)) \leq M_2$, where $\varepsilon_1$, $\varepsilon_2$, $M_1$ and $M_2$ are positive constants, $\lambda_{\text{max}}(\Sigma)$ and $\lambda_{\text{min}}(\Sigma)$ denote the maximum and minimum eigenvalues of matrix $\Sigma$.

C3 The link function $g_0(u)$ is $m$-order differentiable on $\mathbb{R}$ and $g_0^{(j)}(u) \in L^2(\mathbb{R}, \pi(u))$, $j = 0, 1, \ldots, m$, for some positive integer $m$.

C4 The truncation parameter $k$ is divergent with $n$ such that $kn^{-1} \to 0$ and $nk^{-m} \to 0$ as $n \to \infty$, where $m$ is defined in Condition C3.

C5 $E[\epsilon|D, X] = 0$ and $E[\epsilon^2|D, X] = \sigma^2$, where $\sigma^2$ is a positive constant.

C6 $\sup_{(\theta, u) \in \Theta \times \mathbb{R}} \exp(u^2/2)f_\theta(u) \leq M$, where $f_\theta(u)$ is the probability density function of $u = X^T \theta$ and $\sup_{(\theta, u) \in \Theta \times \mathbb{R}} E\|XX^T\{g^{(1)}(x^T \theta)\}\| \leq M$.

Remark 1 Condition C1 is commonly needed for extremum estimation [Chen, 2007]. Conditions C2 is commonly used in the literature of single-index models [Yu and Ruppert, 2002]. Condition C3 imposes some smoothness on the link function to ensure the negligibility of the truncation residuals. Condition C4 ensures the truncation residuals can be smoothed out when we establish the asymptotic normality. Condition C5 shows the error is exogenous and homogeneous, which can be extended to heteroscedastic error. Condition C6 excludes heavy-tailed distributions due to the fact the link function may be unbounded.

Theorem 1 Under Conditions C1-C4, we have $\| (\hat{\beta}, \hat{g}_{1,k}) - (\beta_0, g_{1,0}) \| \to_P 0$ as $n$ goes to infinity.

We defer the proof of Theorem 1 to the supplemental materials.

Theorem 2 Under Conditions C1-C6, we have $\| (\hat{\gamma}, \hat{g}_{2,k}) - (\gamma_0, g_{2,0}) \| \to_P 0$ as $n$ goes to infinity.
The proof of Theorem 2 is given in the supplemental materials.

**Theorem 3** Under Conditions C1-C6, $\sqrt{n}(\hat{\alpha}_n - \alpha)$ converges in distribution to a zero-mean normal distribution with variance $\sigma^2\Psi^{-1}$, where $\Psi = E[D - E[D|X]]^2$ and $\sigma^2$ is defined in Condition C5.

The proof of Theorem 3 is presented in the supplemental materials.

**Remark 2** Theorem 3 shows the estimation errors of $\hat{E}[D|X] - E[D|X]$ and $\hat{E}[Y|X] - E[Y|X]$ can be ignored when we establish the asymptotic properties of the proposed estimator for treatment effects, which coincides with the conclusion of (Robinson, 1988).

## 4 Simulation study

In this section, we conduct simulation studies to study the finite-sample performance of the proposed method. We consider three scenarios to mimic the real world for casual effects in observational studies.

**Simulation I:** The response is generated by the linear regression model

$$Y = \alpha D + \gamma_1 X_1 + \gamma_2 X_2 + \gamma_3 X_3 + \epsilon,$$

where $D$ denotes the treatment assignment, $X_1$, $X_2$ and $X_3$ follow the standard normal distribution, the error term $\epsilon$ follows the standard normal distribution, $(\gamma_1, \gamma_2, \gamma_3) = (0.4, 0, 0.917)$ and $\alpha$ is equal to 0 or 0.5. The treatment assignment model is

$$P(D = 1|X_1, X_2, X_3) = \frac{\exp(\beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3)}{1 + \exp(\beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3)},$$

where $(\beta_1, \beta_2, \beta_3) = (0.8, 0, -0.6)$. It is obvious that the response model and the treatment assignment model are simple single-index models.

**Simulation II:** We consider the situation where the response model and the treatment assignment model are more complex single-index models. The response is generated by the following partially single-index model:

$$Y = \alpha D + \exp(\gamma_1 X_1 + \gamma_2 X_2 + \gamma_3 X_3) + \epsilon.$$

The treatment assignment model is

$$P(D = 1|X_1, X_2, X_3) = \frac{\exp((\beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3)^3 - 2(\beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3))}{1 + \exp((\beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3)^3 - 2(\beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3))},$$
The parameter settings are the same as in Simulation I.

Simulation III: We consider the situation where the response model and the treatment assignment model are no longer single-index models. The response is generated by the following model:

$$Y = \alpha D + (\gamma_1 X_1 + \gamma_2 X_2 + \gamma_3 X_3)^2 + X_2 X_3 + \epsilon.$$ 

The treatment assignment model is

$$P(D = 1|X_1, X_2, X_3) = \frac{\exp(\beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + X_1^2)}{1 + \exp(\beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + X_1^2)}.$$ 

The parameter settings are the same as in Simulation I.

We generate 1000 simulated data sets with the total sample size $n$ being 300 or 600. The sample mean and sample standard deviation of 1000 estimators are given in the columns “Mean” and “SD”, respectively. The column “ESD” shows the estimated standard deviation and “CI” gives the nominal 95% confidence interval coverage rate using the estimated standard deviation. We compare the proposed estimator $\hat{\alpha}_P$ with two estimators: $\hat{\alpha}_R$, which is the estimator based on the covariate adjustment by propensity score (Vansteelandt and Daniel, 2014; Zou et al., 2016); $\hat{\alpha}_L$, which is the estimator based on the propensity score residuals (Lee, 2018). The parameter $k$ related to the proposed estimator $\hat{\alpha}_P$ is chosen by mean square error. The simulation results are summarized in Table 1.

Table 1 about here

From Table 1, we have the following observations. In Simulation I, the scenario is a relatively simple case. The three estimators $\hat{\alpha}_R$, $\hat{\alpha}_L$ and $\hat{\alpha}_P$ are all approximately unbiased. The average of the standard error estimators of all three estimators are close to their respective sample standard deviation and the confidence interval coverages are close to the nominal 95% level.

Simulation II considers more complex single index models. In this scenario, the three estimators $\hat{\alpha}_R$, $\hat{\alpha}_L$ and $\hat{\alpha}_P$ are all approximately unbiased. The average of the standard error estimators and the confidence intervals of the above three estimators are close to the sample standard deviation and attain coverage rate close to the nominal 95% level, respectively. The proposed estimator $\hat{\alpha}_P$ is more efficient than $\hat{\alpha}_R$ and $\hat{\alpha}_L$.

When the response model and the treatment assignment model are no longer single-index models in Simulation III, both $\hat{\alpha}_R$ and $\hat{\alpha}_L$ are seriously biased and consequently the 95% confidence interval coverages are much below the nominal level. The proposed estimator $\hat{\alpha}_P$ is approximately unbiased. The average of the standard error estimator of $\hat{\alpha}_P$ is close to the sample standard deviation and the 95% confidence interval coverage rate is close to the nominal level.
5 An empirical application

Low birth weight is one major determinant of infant morbidity and mortality and had been shown to be associated with prolonged negative effects on health and educational or labor market outcomes throughout life by many studies (Currie and Almond, 2011). Kramer (1987) showed that maternal smoking was the most important preventable negative cause of low birth weight. In this section, we use the dataset from Pennsylvania to study the effect of maternal smoking on birth weight by the proposed method.

Pennsylvania dataset contains observations of white mothers in Pennsylvania. We focus on observations of non-Hispanic white mothers and the total sample size is 3,754. The outcome of interest \( Y \) is infant birth weight, which is measured in grams. The treatment assignment \( D \) is a binary variable indicating whether the mother smokes. The baseline covariates \( X \) includes three quantitative variables (mother’s age, mother’s educational attainment and number of prenatal care visits) and four qualitative variables (indicator for alcohol consumption during pregnancy, indicator for the first baby, indicator for the first prenatal visit in the first trimester, and indicator for a previous birth where the newborn died).

We consider three estimators \( \hat{\alpha}_R, \hat{\alpha}_L \) and \( \hat{\alpha}_P \) that we considered in the simulation studies to study the effect of maternal smoking on birth weight. The estimators, standard errors, and \( p \) value of \( \hat{\alpha}_R, \hat{\alpha}_L \) and \( \hat{\alpha}_P \) are \((-271.657, 23.596, 0.000), (-270.728, 23.267, 0.000) \) and \((-289.990, 22.656, 0.000) \), respectively. All the estimators confirm the maternal smoking has a significant impact on low birth weight.

6 Concluding remarks

Correctly identifying treatment effects in observational studies is very difficult due to the fact that the outcome model or the treatment assignment model must be correctly specified. To take advantages of the semiparametric model, the single-index models are used to model the relationship of the outcome and the treatment assignment between the baseline covariates. We do not assume the link function is bounded and has bounded support and use the sieve method to approximate the link function. By the sieve method, the link function is regarded as a point in an infinitely dimensional function space, which allows us to estimate the link function and the index parameter simultaneously. Then, the average treatment effect can be estimated by the simple linear regression. We establish the asymptotic properties of the proposed estimator. The finite-sample performance of the proposed estimator is evaluated through simulation studies. Simulation results show the proposed estimator outperforms
other commonly used competitor estimators.

In this article, we consider single-index models to estimate the treatment effect. It will be of interest to investigate using the Hilbert reproducible kernel space or deep learning methods to estimate the treatment effect in future work.

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Table 1: Simulation results in three scenarios

| Scenario | n  | Method | Mean | SD  | SE  | CI   | Mean | SD  | SE  | CI   |
|----------|----|--------|------|-----|-----|------|------|-----|-----|------|
| I        | 300| \(\hat{\alpha}_R\) | -0.000 | 0.013 | 0.013 | 0.946 | 0.500 | 0.013 | 0.013 | 0.946 |
|          |    | \(\hat{\alpha}_L\)  | -0.000 | 0.013 | 0.013 | 0.939 | 0.500 | 0.013 | 0.013 | 0.940 |
|          |    | \(\hat{\alpha}_P\)  | -0.000 | 0.013 | 0.021 | 0.954 | 0.500 | 0.013 | 0.019 | 0.954 |
|          | 600| \(\hat{\alpha}_R\)  | -0.000 | 0.009 | 0.009 | 0.941 | 0.500 | 0.009 | 0.009 | 0.941 |
|          |    | \(\hat{\alpha}_L\)  | -0.000 | 0.009 | 0.009 | 0.932 | 0.500 | 0.009 | 0.009 | 0.937 |
|          |    | \(\hat{\alpha}_P\)  | -0.000 | 0.009 | 0.015 | 0.956 | 0.499 | 0.009 | 0.013 | 0.950 |
| II       | 300| \(\hat{\alpha}_R\)  | 0.001  | 0.193 | 0.190 | 0.956 | 0.501 | 0.193 | 0.190 | 0.956 |
|          |    | \(\hat{\alpha}_L\)  | -0.001 | 0.185 | 0.188 | 0.962 | 0.499 | 0.185 | 0.188 | 0.962 |
|          |    | \(\hat{\alpha}_P\)  | 0.002  | 0.144 | 0.149 | 0.954 | 0.500 | 0.144 | 0.148 | 0.955 |
|          | 600| \(\hat{\alpha}_R\)  | 0.002  | 0.144 | 0.137 | 0.946 | 0.502 | 0.144 | 0.137 | 0.946 |
|          |    | \(\hat{\alpha}_L\)  | 0.001  | 0.137 | 0.135 | 0.958 | 0.501 | 0.137 | 0.135 | 0.958 |
|          |    | \(\hat{\alpha}_P\)  | -0.001 | 0.103 | 0.106 | 0.955 | 0.497 | 0.103 | 0.107 | 0.954 |
| III      | 300| \(\hat{\alpha}_R\)  | 0.195  | 0.240 | 0.234 | 0.868 | 0.695 | 0.240 | 0.234 | 0.868 |
|          |    | \(\hat{\alpha}_L\)  | 0.147  | 0.241 | 0.238 | 0.899 | 0.647 | 0.241 | 0.238 | 0.899 |
|          |    | \(\hat{\alpha}_P\)  | 0.055  | 0.179 | 0.174 | 0.947 | 0.531 | 0.174 | 0.170 | 0.953 |
|          | 600| \(\hat{\alpha}_R\)  | 0.201  | 0.166 | 0.167 | 0.781 | 0.701 | 0.166 | 0.167 | 0.781 |
|          |    | \(\hat{\alpha}_L\)  | 0.142  | 0.172 | 0.169 | 0.861 | 0.642 | 0.172 | 0.169 | 0.861 |
|          |    | \(\hat{\alpha}_P\)  | 0.052  | 0.128 | 0.125 | 0.928 | 0.535 | 0.127 | 0.120 | 0.929 |

Notation: \(\hat{\alpha}_R\) denotes the estimator based on propensity score regression, \(\hat{\alpha}_L\) denotes the estimator based on propensity score residuals, \(\hat{\alpha}_R\) denotes our proposed estimator.