Predictive mean matching imputation in survey sampling

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Abstract

Predictive mean matching imputation is popular for handling item nonresponse in survey sampling. In this article, we study the asymptotic properties of the predictive mean matching estimator of the population mean. For variance estimation, the conventional bootstrap inference for matching estimators with fixed matches has been shown to be invalid due to the nonsmoothness nature of the matching estimator. We propose asymptotically valid replication variance estimation. The key strategy is to construct replicates of the estimator directly based on linear terms of the estimator, instead of individual records of variables. Extension to nearest neighbor imputation is also discussed. A simulation study confirms that the new procedure provides valid variance estimation.

Key Words: Bootstrap; Jackknife variance estimation; Martingale central limit theorem; Missing at random.

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1 Introduction

Predictive mean matching imputation (Rubin, 1986) is popular for handling item nonresponse in survey sampling. Hot deck imputation within imputation cells is a special case, where the predictive mean function is constant within cells. On the other hand, predictive mean matching is a version of nearest neighbor imputation. In nearest neighbor imputation, the vector of the auxiliary variables $x$ is directly used in determining the nearest neighbor, while in predictive mean matching imputation, a scalar predictive mean function is used in determining the nearest neighbor. The nearest neighbor is then used as a donor for hot deck imputation.

Although these imputation methods have a long history of application, there are relatively few papers on investigating their asymptotic properties. Chen and Shao (2000, 2001) have developed a nice set of asymptotic theories for the nearest neighbor imputation estimator, but their approach is only applicable to the case with one scalar covariate. Kim et al. (2011) presented an application of the nearest neighbor imputation for the US census long form data. Vink et al. (2014) and Morris et al. (2014) investigated predictive mean matching as a tool for multiple imputation using extensive simulation studies. One notable exception is Abadie and Imbens (2006) in econometrics, where the matching estimator is investigated to estimate the average treatment effect from observational studies. Up to our best knowledge, there is no literature on theoretical investigation of predictive mean matching for mean estimation in survey sampling, which motivates this article.

Predictive mean matching is implemented in two steps. First, the predictive mean function is estimated. Second, for each nonrespondent, the nearest
neighbor is identified among the respondents based on the predictive mean function, and then the observed outcome value of the nearest neighbor is used for imputation. Because the predictive mean function is estimated prior to matching, it is necessary to account for the uncertainty due to parameter estimation. Traditionally, Taylor expansion techniques can be applied when the imputation estimator is a differentiable function of the estimated parameters \cite{Kim and Rao 2009}. However, this approach is not applicable for the predictive mean matching estimator, due to the inherent nondifferentiability of the matching estimator. Our derivation is based on the technique developed by \textit{Andreou and Werker} \cite{Andreou and Werker 2012}, which offers a general approach for deriving the limiting distribution of statistics that involve estimated nuisance parameters and does not require asymptotic smoothness conditions.

Lack of smoothness also makes the conventional replication methods invalid for variance estimation for the predictive mean matching estimator. We propose new replication variance estimation. Based on the linear representation of the predictive mean matching estimator, we construct replicates of the estimator directly based on its linear terms, instead of the individual record of variables. In this way, the distribution of the number of times each unit is used as a match can be preserved, which leads to a valid variance estimation. Furthermore, our replication variance method is flexible, which can accommodate bootstrap, jackknife, among others.

2 Basic Setup

Let $\mathcal{F}_N = \{(x_i, y_i, \delta_i) : i = 1, \ldots, N\}$ denote a finite population, where $x_i$ is always observed, $y_i$ has missing values, and $\delta_i$ is the response indicator of
$y_i$, i.e., $\delta_i = 1$ if $y_i$ is observed and 0 if it is missing. The $\delta_i$’s are defined throughout the finite population, as in Fay (1992), Shao and Steel (1999), and Kim et al. (2006). We assume that $F_N$ is a random sample from a superpopulation model $\zeta$, and $N$ is known. Our objective is to estimate the finite population mean $\mu = N^{-1}\sum_{i=1}^{N} y_i$. Let $A$ denote an index set of the sample selected by a probability sampling design. Let $I_i$ be the sampling indicator, i.e., $I_i = 1$ if unit $i$ is selected into the sample, and $I_i = 0$ otherwise. Suppose that $\pi_i$, the probability of selection of $i$, is positive and known throughout the sample. We make the following assumption for the missing data process.

**Assumption 1 (Missing at random and positivity)** The missing data process satisfies $\text{pr}(\delta = 1 \mid x, y) = \text{pr}(\delta = 1 \mid x)$, which is denoted by $p(x)$, and with probability 1, $p(x) > \epsilon$ for a constant $\epsilon > 0$.

In order to construct the imputed values, we assume that

$$E(y_i \mid x_i) = m(x_i; \beta^*), \tag{1}$$

holds for every unit in the population, where $m(\cdot)$ is a function of $x$ known up to $\beta^*$. Under Assumption 1, let the normalized estimating equation for $\beta$ be

$$S_N(\beta) = \frac{n^{1/2}}{N} \sum_{i \in A} \frac{1}{\pi_i} \delta_i g(x_i; \beta) \{y_i - m(x_i; \beta)\} = 0, \tag{2}$$

where $g(x; \beta)$ is any function with which the solution to (2) exists uniquely. Under certain regularity conditions (e.g. Fuller, 2009), $\hat{\beta}$ converges to $\beta^*$ in probability. Here, the probability distribution is the joint distribution of the sampling distribution and the superpopulation model (1). The sampling
weight $\pi^{-1}_i$ is used to obtain a consistent estimator of $\beta^*$ under informative sampling (Berg et al.; 2016).

Under the model (1), the predictive mean matching method can be described as follows:

**Step 1.** Obtain a consistent estimator of $\beta$, denoted by $\hat{\beta}$, by solving (2).

For each unit $i$ with $\delta_i = 0$, obtain a predicted value of $y_i$ as $\hat{y}_i = m(x_i; \hat{\beta})$. Find the nearest neighbor of unit $i$ from the respondents with the minimum distance between $y_j$ and $\hat{y}_i$. Let $i(1)$ be the index of the nearest neighbor of unit $i$, which satisfies $d(y_{i(1)}, \hat{y}_i) \leq d(y_j, \hat{y}_i)$, for any $j \in A_R = \{i \in A : \delta_i = 1\}$, where $d(y_i, y_j) = |y_i - y_j|$.

**Step 2.** The imputation estimator based on predictive mean matching is computed by

$$\hat{\mu}_{\text{PMM}} = \frac{1}{N} \sum_{i \in A} \frac{1}{\pi_i} \{\delta_i y_i + (1 - \delta_i) y_{i(1)}\}.$$  \hspace{1cm} (3)

In (3), the imputed values are real observations. The imputation model is used only for identifying the nearest neighbor, but not for creating the imputed value itself. Variance estimation of $\hat{\mu}_{\text{PMM}}$ is challenging because of the non-smoothness of the matching mechanism in Step 1. In the next section, we formally discuss the asymptotic properties of the predictive mean matching estimator.
3 Main result

3.1 Predictive mean matching

We introduce additional notation. Let $A = A_R \cup A_M$, where $A_R$ and $A_M$ are the sets of respondents and nonrespondents, respectively. Define $d_{ij} = 1$ if $y_{j(1)} = y_i$, i.e., unit $i$ is used as a donor for unit $j \in A_M$, and $d_{ij} = 0$ otherwise. We write $\hat{\mu}_{PMM} = \hat{\mu}_{PMM}(\hat{\beta})$, where

$$
\hat{\mu}_{PMM}(\beta) = \frac{1}{N} \sum_{i \in A} \frac{1}{\pi_i} \{ \delta_i y_i + (1 - \delta_i) y_{i(1)} \}
$$

$$
= \frac{1}{N} \left\{ \sum_{i \in A} \frac{1}{\pi_i} \delta_i y_i + \sum_{j \in A} \frac{1}{\pi_j} (1 - \delta_j) \sum_{i \in A} \delta_i d_{ij} y_i \right\} = \frac{1}{N} \sum_{i \in A} \frac{\delta_i}{\pi_i} (1 + k_{\beta,i}(\hat{\beta}))
$$

with

$$
k_{\beta,i} = \sum_{j \in A} \frac{\pi_i}{\pi_j} (1 - \delta_j) d_{ij}. \quad (5)
$$

Under simple random sampling, $k_{\beta,i} = \sum_{j \in A} (1 - \delta_j) d_{ij}$ is the number of times that unit $i$ is used as the nearest neighbor for the nonrespondents, where determination of the nearest neighbor is based on the predictive mean function $m(x_i; \beta)$.

We first consider the case when $\beta^*$, and hence $m(x_i) = m(x_i; \beta^*)$, is known. Suppose that the superpopulation model satisfies the following assumption.

**Assumption 2** (i) The matching variable $m(x)$ has a compact and convex support, with density bounded and bounded away from zero. Denote $m_i = m(x_i)$. Let $g_1(m_i)$ and $g_0(m_i)$ be the conditional density of $m_i$ given $\delta_i = 1$ and $\delta_i = 0$, respectively. Suppose that there exist constants $C_{1L}$ and $C_{1U}$ such that $C_{1L} \leq g_1(m_i)/g_0(m_i) \leq C_{1U}$; (ii) $m(x)$ is Lipschitz continuous in $x$; i.e.,
there exists a constant $C_2$ such that $|m(x) - m(x')| < C_2d(x, x')$, for any $x$ and $x'$, where $d(x, x')$ is a generic distance between $x$ and $x'$; (iii) there exists $\delta > 0$ such that $E(|y|^{2+\delta} \mid x)$ is uniformly bounded for any $x$.

Assumption 2 (i) a convenient regularity condition (Abadie and Imbens; 2006). Assumption 2 (ii) imposes a smoothness condition for $m(x)$, which is not restrictive (Chen and Shack; 2000). Assumption 2 (iii) is a moment condition for the central limit theorem.

Denote $E_p(\cdot)$ and $\text{var}_p(\cdot)$ to be the expectation and the variance under the sampling design, respectively. We impose the following regularity conditions on the sampling design.

Assumption 3 (i) There exist positive constants $C_1$ and $C_2$ such that $\pi_i N^{-1} \leq C_2$, for $i = 1, \ldots, N$; (ii) the sequence of the Hotvitz-Thompson estimators $\hat{\mu}_{HT} = N^{-1} \sum_{i \in A} \pi_i^{-1} y_i$ satisfies $\text{var}_p(\hat{\mu}_{HT}) = O(n^{-1})$, and

$$\{\text{var}_p(\hat{\mu}_{HT})\}^{-1/2} (\hat{\mu}_{HT} - \mu) \mid \mathcal{F}_N \to \mathcal{N}(0, 1)$$

in distribution, as $n \to \infty$.

Assumption 3 is widely accepted assumption in survey sampling (Fuller; 2009).

To study the asymptotic properties of the predictive mean matching estimator, we use the following decomposition:

$$n^{1/2}\{\hat{\mu}_{PMM}(\beta) - \mu\} = D_N(\beta) + B_N(\beta), \quad (6)$$

where

$$D_N(\beta) = \frac{n^{1/2}}{N} \left[ \sum_{i \in A} \frac{1}{\pi_i} \left\{ m(x_i; \beta) + \delta_i(1 + k_{\beta,i}) \{ y_i - m(x_i; \beta) \} - \sum_{i=1}^{N} y_i \right\} \right], \quad (7)$$
and
\[
B_N(\beta) = \frac{n^{1/2}}{N} \sum_{i \in A} \frac{1}{\pi_i} (1 - \delta_i) \{m(x_{i(1)}; \beta) - m(x_i; \beta)\}.
\] (8)

The difference \(m(x_{i(1)}; \beta) - m(x_i; \beta)\) accounts for the matching discrepancy, and \(B_N(\beta)\) contributes to the asymptotic bias of the matching estimator. In general, if the matching variable \(x\) is \(p\)-dimensional, Abadie and Imbens (2006) showed that \(d(x_{i(1)}, x_i) = O_p(n^{-1/p})\). Therefore, for nearest neighbor imputation with \(p \geq 2\), the bias \(B_N = O_p(n^{1/2-1/p}) \neq o_p(1)\) is not negligible; whereas, for predictive mean matching, the matching variable is a scalar function \(m(x)\), and hence \(B_N = O_p(n^{-1/2}) = o_p(1)\).

We establish the asymptotic distribution of \(\hat{\mu}_{\text{PMM}}(\beta^*)\).

**Theorem 1** Under Assumptions 1–3, suppose that \(m(x) = E(y \mid x) = m(x; \beta^*)\) and \(\sigma^2(x) = \text{var}(y \mid x)\). Then, \(n^{1/2}\{\hat{\mu}_{\text{PMM}}(\beta^*) - \mu\} \to \mathcal{N}(0, V_1)\) in distribution, as \(n \to \infty\), where
\[
V_1 = V^m + V^e
\] (9)

with
\[
V^m = \lim_{n \to \infty} nN^{-2}E[\text{var}_p\{\sum_{i \in A} \pi_i^{-1} m(x_i)\}],
\]
\[
V^e = \lim_{n \to \infty} nN^{-2}E[\sum_{i \in A} \{\pi_i^{-1} \delta_i(1 + k_{\beta,i}) - 1\}^2 \sigma^2(x_i)],
\]
and \(k_{\beta,i}\) is defined in (5).

In practice, \(\beta^*\) is unknown and therefore has to be estimated prior to matching. The following theorem presents the approximate asymptotic distribution of \(\hat{\mu}_{\text{PMM}}(\hat{\beta})\).
Theorem 2  Under Assumptions 1–3 and certain regularity conditions specified in the Supplementary Material, $n^{1/2}\{\hat{\mu}_{PMM}(\hat{\beta}) - \mu\} \to \mathcal{N}(0, V_2)$ in distribution, as $n \to \infty$, where $\hat{\beta}$ is the solution to the estimating equation (2) and

$$V_2 = V_1 - \gamma_1^T V_s^{-1} \gamma_1 + \gamma_2^T \left( \tau_{\beta^*}^{-1} V_s \tau_{\beta^*}^{-1} \right) \gamma_2,$$

(10)

$\gamma_1 = \lim_{n \to \infty} n N^{-2} E[\sum_{i=1}^N \{\pi_i^{-1}(1+k_{\beta^*,i})-1\} \delta_i g(x_i; \beta^*) \sigma^2(x_i)], \gamma_2 = E\{ \tilde{m}(x; \beta^*) \},$  $V_1$ is defined in (7), $V_s = \text{var}\{S_N(\beta^*)\}, \tau_{\beta^*} = E\{p(x)g(x; \beta)\tilde{m}(x; \beta)^T\}, p(x) = \Pr(\delta = 1 \mid x), \text{ and } \tilde{m}(x; \beta) = \partial m(x; \beta)/\partial \beta.$

The difference between $V_2$ and $V_1$, $-\gamma_1^T V_s^{-1} \gamma_1 + \gamma_2^T (\tau_{\beta^*}^{-1} V_s \tau_{\beta^*}^{-1}) \gamma_2$, can be positive or negative. Thus, ignoring the estimation error in the predictive mean function may lead to invalid inference. To demonstrate the implication of Theorem 2, we use simple random sampling as an example. Under simple random sampling with $g(x; \beta) = \sigma^{-2}(x)\tilde{m}(x; \beta)$ in (2), $\tau_{\beta^*} = V_s$ and $\tau_{\beta^*}^{-1} V_s \tau_{\beta^*}^{-1} = V_s^{-1}$. Also, if $n/N = o(1)$, $\gamma_1 = E\{\Pr(\delta = 1 \mid m)^{-1} p(x)\tilde{m}(x; \beta^*)\}$. If $m(x; \beta)$ does not reduce the dimension of $x$ in the sense that $\Pr(\delta = 1 \mid x) = \Pr(\delta = 1 \mid m)$, then $\gamma_1 = \gamma_2$ and the variance adjustment is zero. In this case, the predictive mean matching estimators with the estimated and true predictive mean function have the same asymptotic variance.

3.2 Nearest neighbor imputation

Nearest neighbor imputation can be described in the following steps:

Step 1. For each unit $i$ with $\delta_i = 0$, find the nearest neighbor from the respondents with the minimum distance between $x_j$ and $x_i$. Let $i(1)$ be the index set of its nearest neighbor, which satisfies $d(x_i(1), x_i) \leq$
\( d(x_j, x_i) \), for \( j \in A_R \), where \( d(x_i, x_j) \) is a distance function between \( x_i \) and \( x_j \). For example, \( d(x_i, x_j) = ||x_i - x_j|| \), where \( ||x|| = (x^T x)^{1/2} \).

**Step 2.** The nearest neighbor imputation estimator of \( \mu \) is computed by

\[
\hat{\mu}_{\text{NNI}} = \frac{1}{N} \sum_{i \in A} \frac{1}{\pi_i} \{ \delta_i y_i + (1 - \delta_i) y_{i(1)} \} = \frac{1}{N} \sum_{i \in A} \frac{1}{\pi_i} \delta_i (1 + k_i) y_i, \tag{11}
\]

where \( k_i \) is defined similarly as in (5), but with the matching variable \( x \).

Following (6), write \( n^{1/2}(\hat{\mu}_{\text{NNI}} - \mu) = D_N + B_N \), where

\[
D_N = n^{1/2} \left[ \frac{1}{N} \sum_{i \in A} \frac{1}{\pi_i} \{ m(x_i) + \delta_i (1 + k_i) \{ y_i - m(x_i) \} - \mu \} \right],
\]

and

\[
B_N = \frac{n^{1/2}}{N} \sum_{i \in A} \frac{1}{\pi_i} (1 - \delta_i) \{ m(x_{i(1)}) - m(x_i) \}. \tag{12}
\]

Because the matching is based on a \( p \)-vector matching variable, the bias term \( B_N = O_p(n^{1/2-1/p}) \) with \( p \geq 2 \) is not negligible. For bias correction, let \( \hat{m}(x) \) be a consistent estimator of \( m(x) = E(y \mid x) \). Then, we can estimate \( B_N \) by \( \hat{B}_N = n^{-1/2} N \sum_{i \in A} \pi_i^{-1} (1 - \delta_i) \{ \hat{m}(x_{i(1)}) - \hat{m}(x_i) \} \). A bias-corrected nearest neighbor imputation estimator of \( \mu \) is

\[
\tilde{\mu}_{\text{NNI}} = \frac{1}{N} \sum_{i \in A} \frac{1}{\pi_i} \{ \delta_i y_i + (1 - \delta_i) y_i^* \}, \tag{13}
\]

where \( y_i^* = \hat{m}(x_i) + y_{i(1)} - \hat{m}(x_{i(1)}) \). Under certain regularity conditions imposed on the nonparametric estimator \( \hat{m}(x) \), \( \hat{B}_N \) is consistent for \( B_N \), i.e., \( \hat{B}_N - B_N = o_p(1) \). This implies that the bias-corrected nearest neighbor imputation estimator is asymptotically equivalent to the predictive mean matching estimator with known \( \beta^* \).
4 Replication variance estimation

We consider replication variance estimation (Rust and Rao, 1996; Wolter, 2007) for the predictive mean matching estimator. Let \( \hat{\mu} \) be the Horvitz-Thompson estimator of \( \mu \). The replication variance estimator of \( \hat{\mu} \) takes the form of

\[
\hat{V}_{\text{rep}}(\hat{\mu}) = \sum_{k=1}^{L} c_k (\hat{\mu}^{(k)} - \hat{\mu})^2,
\]

where \( L \) is the number of replicates, \( c_k \) is the \( k \)th replication factor, and \( \hat{\mu}^{(k)} \) is the \( k \)th replicate of \( \hat{\mu} \). When \( \hat{\mu} = \sum_{i \in A} \omega_i y_i \), we can write the replicate of \( \hat{\mu} \) as \( \hat{\mu}^{(k)} = \sum_{i \in A} \omega_i^{(k)} y_i \) with some \( \omega_i^{(k)} \) for \( i \in A \). The replications are constructed such that

\[
E\{\hat{V}_{\text{rep}}(\hat{\mu})\} = \text{var}(\hat{\mu})\{1 + o(1)\}.
\]

We propose a new replication variance estimation for the predictive mean matching estimator. We first consider \( \hat{\mu}_{\text{PMM}}(\beta^*) \) with a known \( \beta^* \) given in (4). For simplicity, we suppress the dependence of quantities on \( \beta^* \), and let \( \omega_i = N^{-1} \pi_i^{-1} \). Write \( \hat{\mu}_{\text{PMM}} - \mu = (\hat{\mu}_{\text{PMM}} - \hat{\psi}_{\text{HT}}) + (\hat{\psi}_{\text{HT}} - \mu_\psi) + (\mu_\psi - \mu) \), where

\[
\hat{\psi}_{\text{HT}} = \sum_{i \in A} \omega_i \psi_i, \quad \psi_i = m(x_i) + \delta_i (1 + k_i) \{y_i - m(x_i)\}, \quad \mu_\psi = N^{-1} \sum_{i=1}^{N} \psi_i.
\]

Because \( \mu_{\text{PMM}} - \hat{\psi}_{\text{HT}} = o_p(n^{-1/2}) \) by Theorem 4 and \( \mu_\psi - \mu = O_p(N^{-1/2}) \), we have \( \hat{\mu}_{\text{PMM}} - \mu = \hat{\psi}_{\text{HT}} - \mu_\psi + o_p(n^{-1/2}) \), if \( nN^{-1} = o(1) \). Therefore, it is sufficient to estimate the variance of \( \hat{\psi}_{\text{HT}} - \mu_\psi \). Because \( E(\hat{\psi}_{\text{HT}} - \mu_\psi \mid \mathcal{F}_N) = 0 \), we have \( \text{var}(\hat{\psi}_{\text{HT}} - \mu_\psi) = E\{\text{var}(\hat{\psi}_{\text{HT}} - \mu_\psi \mid \mathcal{F}_N)\} \), which is essentially the sampling variance of \( \hat{\psi}_{\text{HT}} \). This suggests that we treat \( \{\psi_i : i \in A\} \) as pseudo observations in applying replication variance estimator. Otsu and Rai (2016) used a similar idea to develop a wild bootstrap technique for a matching estimator. To be specific, we construct replicates of \( \hat{\psi}_{\text{HT}} \) as follows:

\[
\hat{\psi}_{\text{HT}}^{(k)} = \sum_{i \in A} \omega_i^{(k)} \psi_i, \quad \text{where} \quad \omega_i^{(k)} \quad \text{is the replication weight that account for}
\]


complex sampling design. The replication variance estimator of $\hat{\psi}_{HT}$ is obtained by applying $\hat{V}_{rep}(\cdot)$ in (14) for the above replicates $\hat{\psi}^{(k)}_{HT}$. It follows that $E\{\hat{V}_{rep}(\hat{\psi}_{HT})\} = \text{var}(\hat{\psi}_{HT} - \mu_\psi)\{1 + o(1)\} = \text{var}(\hat{\mu}_{PMM} - \mu)\{1 + o(1)\}$.

We now consider $\hat{\mu}_{PMM}(\hat{\beta})$, which can be expressed as

$$\hat{\mu}_{PMM}(\hat{\beta}) = \sum_{i \in A} \omega_i [m(x_i; \hat{\beta}) + \delta_i (1 + k_{\hat{\beta},i}) \{y_i - m(x_i; \hat{\beta})\}] + o_p(n^{-1/2}).$$

We propose two steps for each replication $k$:

**Step 1.** Obtain the $k$th replicate of $\hat{\beta}$, denoted as $\hat{\beta}^{(k)}$, by solving $S^{(k)}(\hat{\beta}) = \sum_{i \in A} \omega_i^{(k)} \delta_i g(x_i; \hat{\beta}) \{y_i - m(x_i; \hat{\beta})\} = 0$, and calculate $m(x_i; \hat{\beta}^{(k)})$ for $i \in A$.

**Step 2.** Calculate the $k$th replicate as

$$\hat{\mu}_{PMM}^{(k)}(\hat{\beta}^{(k)}) = \sum_{i \in A} \omega_i^{(k)} [m(x_i; \hat{\beta}^{(k)}) + \delta_i (1 + k_{\hat{\beta},i}) \{y_i - m(x_i; \hat{\beta}^{(k)})\}] \quad (15)$$

If $\beta^*$ is known, we do not need to reflect the effect of estimating $\beta^*$, and the above procedure is the one we proposed for the case when $\beta^*$ is known. On the other hand, when $\beta^*$ is estimated, Step 1 is necessary, because as shown in Theorem 2 the predictive mean matching estimators by matching on the true and estimated predictive mean function may have different asymptotic distributions. The asymptotic consistency of the replication variance estimator is presented in the following theorem.

**Theorem 3** Under the assumptions in Theorem 2, suppose that $\hat{V}_{rep}(\hat{\mu})$ in (14) is consistent for $\text{var}_p(\hat{\mu})$. Then, if $nN^{-1} = o(1)$, the replication variance estimators for $\hat{\mu}_{PMM}(\hat{\beta})$ is consistent, i.e., $n\hat{V}_{rep}\{\hat{\mu}_{PMM}(\hat{\beta})\}/V_2 \to 1$ in probability, as $n \to \infty$, where $\hat{V}_{rep}(\cdot)$ is given in (14), the replicates of $\hat{\mu}_{PMM}(\hat{\beta})$ are given in (15), and $V_2$ is given in (10).
Table 1: Simulation results: Bias ($\times 10^2$) and S.E. ($\times 10^2$) of the point estimator, Relative Bias of jackknife variance estimates ($\times 10^2$) and Coverage Rate (%) of 95% confidence intervals.

|                  | PMM Bias | S.E. | NNI Bias | S.E. | SRI Bias | S.E. | RB  | CR  | RB  | CR  | RB  | CR  |
|------------------|----------|------|----------|------|----------|------|-----|-----|-----|-----|-----|-----|
| Simple Random Sampling |          |      |          |      |          |      |     |     |     |     |     |     |
| (P1)             | -0.15    | 6.46 | -0.21    | 6.54 | -0.23    | 6.44 | 5   | 95.1| 3   | 95.1| 5   | 95.8|
| (P2)             | -0.22    | 6.54 | -0.25    | 6.55 | -0.37    | 6.46 | 5   | 95.4| 3   | 95.3| 5   | 95.6|
| (P3)             | 1.90     | 11.85| 18.59    | 11.06| 0.11     | 11.17| 4   | 95.2| 4   | 63.8| 4   | 95.5|

|                  | PMM RB  | CR  | NNI RB  | CR  | SRI RB  | CR  |     |     |     |     |     |
|------------------|----------|-----|----------|-----|----------|-----|-----|-----|-----|-----|-----|
| Probability Proportional to Size Sampling |          |     |          |     |          |     |     |     |     |     |     |
| (P1)             | 0.05     | 6.46| 0.13     | 6.37| 0.18     | 6.53| 2   | 95.5| 3   | 94.8| 2   | 94.9|
| (P2)             | 0.30     | 6.52| 0.12     | 6.47| 0.16     | 6.60| 1   | 95.4| 0   | 95.3| 3   | 94.9|
| (P3)             | 1.33     | 10.99| 17.53   | 10.70| 0.40     | 11.10| 7   | 95.8| 3   | 65.5| -3  | 95.6|

PMM: predictive mean matching; NNI: nearest neighbor imputation; SRI: stochastic regression imputation.

5 Simulation study

In this simulation study, we assess the performance of the proposed replication variance estimator. For generating finite populations of size $N = 50,000$: first, let $x_{1i}$, $x_{2i}$ and $x_{3i}$ be generated independently from Uniform[0,1], and $x_{4i}$, $x_{5i}$, $x_{6i}$ and $e_i$ be generated independently from $\mathcal{N}(0, 1)$; then, let $y_i$ be generated as (P1) $y_i = -1 + x_{1i} + x_{2i} + e_i$, (P2) $y_i = -1.167 + x_{1i} + x_{2i} + (x_{1i} - 0.5)^2 + (x_{2i} - 0.5)^2 + e_i$, and (P3) $y_i = -1.5 + x_{1i} + \cdots + x_{6i} + e_i$. The covariates are fully observed, but $y_i$ is not. The response indicator of $y_i$, $\delta_i$, is generated from Bernoulli($p_i$) with logit$\{p(x_i)\} = 0.2 + x_{1i} + x_{2i}$. This results in the average response rate about 75%. The parameter of interest is $\mu = \frac{1}{N} \sum_{i=1}^{N} y_i$. To generate samples, we consider two sampling designs: (S1) simple random sampling (SRS) with $n = 400$; (S2) probability proportional to size sampling. In (S2), for each unit in the population, we generate a size variable $s_i$ as $\log(|y_i + \nu_i| + 4)$, where $\nu_i \sim \mathcal{N}(0,1)$. The
selection probability is specified as $\pi_i = 400s_i/\sum_{i=1}^{N} s_i$. Therefore, (S2) is informative, where units with larger $y_i$ values have larger probabilities to be selected into the sample.

For estimation, we consider predictive mean matching imputation, nearest neighbor imputation, and stochastic regression imputation. In stochastic regression imputation, for units with $\delta_i = 0$, the imputation of $y_i$ is obtained as $y_i^* = \hat{y}_i + \hat{\epsilon}_i^*$, where $\hat{y}_i = m(x_i; \hat{\beta})$ and $\hat{\epsilon}_i^*$ is randomly selected from the observed residuals $\{\hat{\epsilon}_i = y_i - \hat{y}_i : \delta_i = 1\}$. For (P1) and (P2), we specify the mean function to be $m(x; \beta) = \beta_0 + \beta_1 x_1 + \beta_2 x_2$. Note that for (P1), $m(x; \beta)$ is correctly specified; whereas for (P2), $m(x; \beta)$ is misspecified. For (P3), we specify the mean function to be $m(x; \beta) = \beta_0 + \beta^T x$, where $x = (x_1, \ldots, x_6)$.

We construct 95% confidence intervals using $(\hat{\mu}_I - z_{0.975} \hat{V}_I^{1/2}, \hat{\mu}_I + z_{0.975} \hat{V}_I^{1/2})$, where $\hat{\mu}_I$ is the point estimate and $\hat{V}_I$ is the variance estimate obtained by the proposed jackknife variance estimation. For the jackknife replication method under (S2), in the $k$th replicate, the replication weights are $\omega_i^{(k)} = n\omega_i/(n-1)$ for all $i \neq k$, and $\omega_k^{(k)} = 0$. For stochastic regression imputation, the $k$th replicate of $\mu$ is given by $\hat{\mu}_{\text{REG}}^{(k)}(\hat{\beta}^{(k)}) = \sum_{i \in A} \omega_i^{(k)} \{m(x_i; \hat{\beta}^{(k)}) + \delta_i (1 + k_i) \{y_i - m(x_i; \hat{\beta}^{(k)})\}\}$, where $\hat{\beta}^{(k)}$ is obtained from the estimating equation of $\beta$ based on the replication weights, and $k_i$ is the number of times that $\hat{\epsilon}_i$ is selected to impute the missing values of $y$ based on the original data.

Table I presents the simulation results based on 2,000 Monte Carlo samples. When the covariate is 2-dimensional, all three imputation estimators have small biases, even when the mean function is misspecified. In addition, the proposed jackknife method provides accurate coverage of confidence intervals for the predictive mean matching and stochastic regression impu-
tation estimators in all scenarios. This suggests that the proposed replication method can be used widely even for stochastic regression imputation. When the covariate is 6-dimensional, nearest neighbor imputation presents large biases in some scenarios. In addition, the jackknife variance estimator works well when the covariate has a low dimension, whereas it tends to under-estimate the true variance when the covariate has a relatively high dimension in some scenarios. This is expected because the jackknife variance estimator assumes that the bias of nearest neighbor imputation is negligible, which however is not the case for a relatively high dimension of covariate.

6 Discussion

Instead of choosing the nearest neighbor as a donor for missing items, we can consider fractional imputation (Kim and Fuller; 2004; Yang and Kim; 2016) using $K$ ($K > 1$) nearest neighbors. Such extension remains an interesting avenue for future research.

Supplementary Material

Supplementary material includes proofs of Theorems 1–3.

S7 Proof for Theorem 1

Based on the decomposition in (6), write

$$n^{1/2}\{\hat{\mu}_{\text{PMM}}(\beta^*) - \mu\} = D_N(\beta^*) + B_N(\beta^*),$$

(S1)

where $D_N(\beta)$ and $B_N(\beta)$ are defined in (7) and (8), respectively. Under Assumption 2, for the predictive mean matching estimator, $m(x_{i(1)}) - m(x_i) =$
\(O_p(1)\). Together with Assumption 3, we derive the order of \(B_N(\beta^*)\) as
\[
B_N(\beta^*) = \frac{n^{1/2}}{N} \sum_{i \in A} \frac{1}{\pi_i} (1 - \delta_i) \{ m(x_{i(1)}; \beta^*) - m(x_i; \beta^*) \} = O_p(n^{-1/2}) = o_p(1).
\]
Therefore, (S1) reduces to
\[
n^{1/2} \{ \hat{\mu}_{\text{PMM}}(\beta^*) - \mu \} = D_N(\beta^*) + o_p(1).
\]
Then, to study the asymptotic properties of \(n^{1/2} \{ \hat{\mu}_{\text{PMM}}(\beta^*) - \mu \}\), we only need to study the asymptotic properties of \(D_N(\beta^*)\). For simplicity, we introduce the following notation: \(m_i = m(x_i; \beta^*)\) and \(e_i = y_i - m_i\). We express
\[
D_N(\beta^*) = \frac{n^{1/2}}{N} \sum_{i \in A} \frac{1}{\pi_i} \{ m_i + \delta_i(1 + k_{\beta^*,i}) e_i \} - \frac{N}{n} \sum_{i=1}^N y_i
\]
and we can verify that the covariance of the two terms in (S2) is zero. Thus,
\[
\text{var} \{ D_N(\beta^*) \} = \text{var} \left( \frac{n^{1/2}}{N} \sum_{i=1}^N \left( \frac{I_i}{\pi_i} - 1 \right) m_i \right) + \text{var} \left( \frac{n^{1/2}}{N} \sum_{i=1}^N \left( \frac{I_i}{\pi_i} \delta_i(1 + k_{\beta^*,i}) - 1 \right) e_i \right).
\]
The first term, as \(n \to \infty\), becomes
\[
V^m = \lim_{n \to \infty} \frac{n}{N^2} E \left( \text{var}_p \left( \sum_{i \in A} m_i / \pi_i \right) \right),
\]
and the second term, as \(n \to \infty\), becomes
\[
V^e = \text{plim} \frac{n}{N^2} \sum_{i=1}^N \left( \frac{I_i}{\pi_i} \delta_i(1 + k_{\beta^*,i}) - 1 \right)^2 \text{var}(e_i | x_i).
\]
The remaining is to show that \(V^e = O(1)\). To do this, the key is to show that the moments of \(k_{\beta^*,i}\) are bounded. Under Assumption 3, it is easy to verify that
\[
\underline{\omega} k_{\beta^*,i} \leq k_{\beta^*,i} \leq \overline{\omega} k_{\beta^*,i}, \quad (S3)
\]
for some constants $\omega$ and $\bar{\omega}$, where $\tilde{k}_{\beta^*,i} = \sum_{j=1}^{n}(1 - \delta_j)d_{ij}$ is the number of unit $i$ used as a match for the nonrespondents. Under Assumption 2, $\tilde{k}_{\beta^*,i} = O_p(1)$ and $E(\tilde{k}_{\beta^*,i})$ and $E(\tilde{k}_{\beta^*,i}^2)$ are uniformly bounded over $n$ (Abadie and Imbens, 2006, Lemma 3); therefore, together with (S3), we have $k_{\beta^*,i} = O_p(1)$ and $E(k_{\beta^*,i})$ and $E(k_{\beta^*,i}^2)$ are uniformly bounded over $n$. Therefore, a simple algebra yields $V_e = O(1)$.

Combining all results, the asymptotic variance of $n^{1/2}\{\hat{\mu}_{PMM}(\beta^*) - \mu\}$ is $V^m + V^e$. By the central limit theorem, the result in Theorem 1 follows.

S8 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 $P^{(N)}$, some statistic $T_N$ and the likelihood ratios $dQ^{(N)}/dP^{(N)}$ satisfy

$$\left( \frac{T_N}{\log(dQ^{(N)}/dP^{(N)})} \right) \to \mathcal{N} \left\{ \begin{pmatrix} 0 \\ \tau^2/2 \end{pmatrix}, \begin{pmatrix} \sigma^2 & c \\ c & \sigma^2 \end{pmatrix} \right\}$$

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

$$T_N \to \mathcal{N}(c, \tau^2)$$

in distribution, as $N \to \infty$. See Le Cam and Yang (1990), Bickel et al. (1993) and van der Vaart (2000) for textbook discussions.

S9 Proof for Theorem 2

To discuss the asymptotic properties of $\hat{\mu}_{PMM}(\hat{\beta})$, consider sequences that are local to $\beta^*$, $\beta_N = \beta^* + n^{-1/2}h$, indexed by $N$. In our context, we have the
population size $N$ goes to infinity with sample size $n$. Denote the distribution of $(x, y, \delta, I)$ given by the local shift $P^{\beta_N}$ (Bickel et al.; 1993). Consider $z_{N,i} = \{x_{N,i}, y_{N,i}, \delta_{N,i}, I_{N,i}\}$ with distribution $P^{\beta_N}$. We can treat the consistent estimator $\hat{\beta}$ as the solution to the estimating equation

$$S_N(\beta) = \frac{n^{1/2}}{N} \sum_{i=1}^{N} \frac{I_{N,i}}{\pi_{N,i}} \delta_{N,i} g(x_{N,i}; \beta) \{y_{N,i} - m(x_{N,i}; \beta)\} = 0. \quad (S4)$$

Let

$$\tau_\beta = E_p \{p(x)g(x; \beta)\hat{m}(x; \beta)^T\}. \quad (S5)$$

We make the following regularity assumptions:

**Assumption S4** (i) The superpopulation model is regular (Bickel et al.; 1993, pp 12–13); (ii) under $P^{\beta_N}$: $S_N(\beta_N) \to \mathcal{N}(0, V_s)$ in distribution, as $n \to \infty$; (iii) $\tau_\beta$ in (S5) is nonsingular around $\beta^*$, and $n^{1/2}(\hat{\beta} - \beta_N) = \tau_\beta^{-1} S_N(\beta_N) + o_p(1)$; (iv) for all bounded continuous functions $h(x, y, \delta, I)$, the conditional expectation $E_{\beta_N} \{h(x, y, \delta, I) \mid x, \delta = 1\}$ converges in distribution to $E \{h(x, y, \delta, I) \mid x, \delta = 1\}$, where $E_{\beta_N}$ is the expectation with respect to $P^{\beta_N}$.

To establish the asymptotic distribution of $n^{1/2}\{\hat{\mu}_{PMM}(\hat{\beta}) - \mu\}$, we rely on Le Cam’s third lemma. We give a sketch proof.

Because

$$n^{1/2}(\hat{\beta} - \beta_N) = \tau_\beta^{-1} S_N(\beta_N) + o_p(1),$$

we specify the central sequence under $P^{\beta_N}$ as

$$\log(dP^{\beta^*}/dP^{\beta_N}) = -h^T S_N(\beta_N) - \frac{1}{2} h^T V_s h + o_p(1).$$

We can derive that under $P^{\beta_N}$,
in distribution, as \( n \to \infty \), where \( \Lambda = \tau_{\beta}^{-1}V_s\tau_{\beta}^{-1} \). Note that here, we write \( \mu = \mu(\beta_N) \) to reflect its dependence on \( \beta_N \).

We then express \( \mu(\beta_N) = \mu(\beta^*) + \gamma_2^T(n^{-1/2}h) + o(n^{-1/2}) \), and use the shorthand \( \mu \) for \( \mu(\beta^*) \). By Le Cam’s third lemma, under \( P^{\beta^*} \), we have

\[
\left( \frac{n^{1/2}\{\hat{\mu}_{\text{PMM}}(\beta_N) - \mu(\beta_N)\}}{n^{1/2}(\hat{\beta} - \beta_N)} \right) \to \mathcal{N} \left\{ \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} V_1 & \gamma_1^T\tau_{\beta^*}^{-1} \\ -h^T\gamma_1 & \Lambda - h^TV_s\tau_{\beta}^{-1} \end{pmatrix} \right\}
\]

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

\[
\left( \frac{n^{1/2}\{\hat{\mu}_{\text{PMM}}(\beta^* + n^{-1/2}h) - \mu\}}{n^{1/2}(\hat{\beta} - \beta^*)} \right) \to \mathcal{N} \left\{ \begin{pmatrix} -\gamma_1^T h - \gamma_2^T h \\ -\tau_{\beta^*}^{-1}V_s h \end{pmatrix}, \begin{pmatrix} V_1 & \gamma_1^T\tau_{\beta^*}^{-1} \\ -h^T\gamma_1 & \Lambda - h^TV_s\tau_{\beta^*}^{-1} \end{pmatrix} \right\}
\]

in distribution, as \( n \to \infty \).

Heuristically, if the normal distribution was exact, then

\[
n^{1/2}\{\hat{\mu}_{\text{PMM}}(\beta^* + n^{-1/2}h) - \mu\} | n^{1/2}(\hat{\beta} - \beta^*) = h \sim \mathcal{N} \left( \begin{pmatrix} -\gamma_1^T h - \gamma_2^T h \\ -\tau_{\beta^*}^{-1}V_s h \end{pmatrix}, \begin{pmatrix} V_1 & \gamma_1^T\tau_{\beta^*}^{-1} \\ -h^T\gamma_1 & \Lambda - h^TV_s\tau_{\beta^*}^{-1} \end{pmatrix} \right) \]

in distribution, as \( n \to \infty \).

Given \( n^{1/2}(\hat{\beta} - \beta^*) = h \), we have \( \beta^* + n^{-1/2}h = \hat{\beta} \), and hence \( \hat{\mu}_{\text{PMM}}(\beta^* + n^{-1/2}h) = \hat{\mu}_{\text{PMM}}(\hat{\beta}) \). Integrating (S7) over the asymptotic distribution of \( n^{1/2}(\hat{\beta} - \beta^*) \), we derive

\[
n^{1/2}\{\hat{\mu}_{\text{PMM}}(\hat{\beta}) - \mu\} \sim \mathcal{N} \left( 0, V_1 - \gamma_1^T\gamma_1^{-1} + \gamma_2^T\Lambda\gamma_2 \right).
\]

The formal technique to derive (S8) can be found in Andreou and Werker (2012). (S8) gives the result in Theorem 2.
In the following, we provide the proof to (S6). Asymptotic normality of 
\( n^{1/2} \{ \hat{\mu}_{PMM}(\beta_N) - \mu \} \) under \( P^{\beta_N} \) follows from Theorem 1. Asymptotic joint normality of 
\( n^{1/2} (\hat{\beta} - \beta_N) \) and \( \log( dP^{\beta^*} / dP^{\beta_N}) \) follows from Assumption S4.

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

\[
\begin{pmatrix}
D_N(\beta_N) \\
S_N(\beta_N)
\end{pmatrix} \xrightarrow{\mathcal{N}} 
\begin{bmatrix}
0 \\
V_1 \gamma_1^T
\end{bmatrix}
\begin{bmatrix}
\gamma_1 \\
V_s
\end{bmatrix}
\]  

(S9)

in distribution, as \( n \to \infty \). To prove (S9), consider the following linear combination:

\[
C_N = c_1 D_N(\beta_N) + c_2 S_N(\beta_N) = c_1 n^{1/2} \sum_{i=1}^{N} \left( \frac{I_{N,i}}{\pi_{N,i}} - 1 \right) m(x_{N,i})
\]

\[
+ c_1 \frac{n^{1/2}}{N} \sum_{i=1}^{N} \left\{ \frac{I_{N,i}}{\pi_{N,i}} \delta_{N,i}(1 + k_{\beta_{N,i}}) - 1 \right\} \{y_{N,i} - m(x_{N,i}; \beta_N)\}
\]

\[
+ c_2 \frac{n^{1/2}}{N} \sum_{i=1}^{N} \left( \frac{I_{N,i}}{\pi_{N,i}} \delta_{N,i} g(x_{N,i}; \beta_N) \{y_{N,i} - m(x_{N,i}; \beta_N)\} \right)
\]

We analyze \( C_N \) using the martingale theory. First, we rewrite

\[
C_N = \sum_{k=1}^{2N} \xi_{N,k},
\]

where

\[
\xi_{N,k} = c_1 \frac{n^{1/2}}{N} \left( \frac{I_{N,k}}{\pi_{N,k}} - 1 \right) m(x_{N,k}; \beta_N), \quad 1 \leq k \leq N,
\]

and

\[
\xi_{N,k} = c_1 \frac{n^{1/2}}{N} \left\{ \frac{I_{N,k-N}}{\pi_{N,k-N}} \delta_{N,k-N}(1 + k_{\beta_{N,k-N}}) - 1 \right\} \{y_{N,k-N} - m(x_{N,k-N}; \beta_N)\}
\]

\[
+ c_2 \frac{n^{1/2}}{N} \frac{I_{N,k-N}}{\pi_{N,k-N}} \delta_{N,k-N} g(x_{N,k-N}; \beta_N) \{y_{N,k-N} - m(x_{N,k-N}; \beta_N)\}, \quad N+1 \leq k \leq 2N.
\]

Consider the \( \sigma \)-fields \( \mathcal{F}_{N,k} = \sigma\{x_{N,1}, \ldots, x_{N,N}, I_{N,1}, \ldots, I_{N,k}\} \) for \( 1 \leq k \leq N \),

and \( \mathcal{F}_{N,k} = \sigma\{x_{N,1}, \ldots, x_{N,N}, I_{N,1}, \ldots, I_{N,N}, \delta_{N,1}, \ldots, \delta_{N,N}, y_{N,1}, \ldots, y_{N,k-N}\} \)
for $N + 1 \leq k \leq 2N$. Then, \( \{ \sum_{k=1}^{2N} \xi_{N,k}, \mathcal{F}_{N,i}, 1 \leq i \leq 2N \} \) is a martingale for each $N \geq 1$. Therefore, the limiting distribution of $C_N$ can be studied using the martingale central limit theorem (Theorem 35.12, Billingsley, 1995). Under Assumption 2, and the fact that $k_{\beta_{N,k}}$ has uniformly bounded moments, it follows that $\sum_{k=1}^{2N} E_{\beta_N}(\xi_{N,k}^2) \to 0$ for some $\delta > 0$. It then follows that Lindeberg’s condition in Billingsley’s theorem holds. As a result, we obtain that under $P_{\beta_N}$, $C_N \to \mathcal{N}(0, \sigma_1^2 + \sigma_2^2)$ in distribution, as $n \to \infty$, where $\sigma_1^2 = \text{plim} \sum_{k=1}^{N} E_{\beta_N}(\xi_{N,k}^2 \mid \mathcal{F}_{N,k-1})$ and $\sigma_2^2 = \text{plim} \sum_{k=N+1}^{2N} E_{\beta_N}(\xi_{N,k}^2 \mid \mathcal{F}_{N,k-1})$. Assumption S4 further implies the following expressions:

\[
\sigma_1^2 = \text{plim} \sum_{k=1}^{N} E_{\beta_N}(\xi_{N,k}^2 \mid \mathcal{F}_{N,k-1}) = c_1^2 \text{plim} \frac{n}{N^2} \sum_{k=1}^{N} E_{\beta_N} \left[ \left\{ \left( \frac{I_{N,k}}{\pi_{N,k}} - 1 \right) m(x_{N,k}) \right\}^2 \mid \mathcal{F}_{N,k-1} \right] = c_1^2 V^m,
\]

and

\[
\sigma_2^2 = \text{plim} \sum_{k=N+1}^{2N} E_{\beta_N}(\xi_{N,k}^2 \mid \mathcal{F}_{N,k-1}) = c_1^2 \text{plim} \frac{n}{N^2} \sum_{k=N+1}^{2N} \left\{ \frac{I_{N,k-N}}{\pi_{N,k-N}} \delta_{N,k-N}(1 + k_{\beta_{N,k-N}}) - 1 \right\}^2 \sigma^2(x_{N,k-N})
\]

\[
+ 2c_1^2 \text{plim} \frac{n}{N^2} \sum_{k=N+1}^{2N} \left\{ \frac{I_{N,k-N}}{\pi_{N,k-N}} \delta_{N,k-N}(1 + k_{\beta_{N,k-N}}) - 1 \right\} \times \frac{I_{N,k-N}}{\pi_{N,k-N}} \delta_{N,k-N} g(x_{N,k-N}; \beta_N) \sigma^2(x_{N,k-N}) c_1
\]

\[
+ c_1^2 \text{plim} \frac{n}{N^2} \sum_{k=N+1}^{2N} \frac{I_{N,k-N}}{\pi_{N,k-N}} \delta_{N,k-N} g(x_{N,k-N}; \beta_N) g(x_{N,k-N}; \beta_N)^T \sigma^2(x_{N,k-N}) c_2
\]

\[
= c_1^2 V^e + 2c_1^2 \gamma_1 c_1 + c_1^2 V c_2.
\]
Therefore, \( \sigma_1^2 + \sigma_2^2 = c_1^2 V_1 + c_2^2 V_2 + 2c_2^2 \gamma_1 c_1 \), and by the martingale central limit theorem, under \( P^\beta_N \), (S9) follows.

**S10 Proof for Theorem 3**

Note that in the derivation of the asymptotic distribution of \( \hat{\mu}_{\text{PMM}}(\hat{\beta}) \), we use the martingale representation. Now, to show that \( \hat{\mu}_{\text{PMM}}(\hat{\beta}) \) is consistent to \( \text{var}\{\hat{\mu}_{\text{PMM}}(\hat{\beta})\} \), we show that the jackknife replicates of the martingale representation of \( \hat{\mu}_{\text{PMM}}(\hat{\beta}) \) produces consistent estimation of the variability of the martingale representation.

From the proof in §S9, the asymptotic variance of \( \hat{\mu}_{\text{PMM}}(\hat{\beta}) \) can be derived from the unnormalized martingale representation under \( P^\beta_N \):

\[
\tilde{\psi}_n = c_1 \sum_{i \in A} \omega_i \left[ m(x_i; \beta_N) + \delta_i (1 + k_{\beta_N,i}) \{ y_i - m(x_i; \beta_N) \} - \mu \right]
+ c_2^T \sum_{i \in A} \omega_i \delta_i g(x_i; \beta_N) \{ y_i - m(x_i; \beta_N) \},
\]

where \( c_1 \) and \( c_2 \) are arbitrary constants. To ease our notation, let \( \psi_i = c_1 \left[ m(x_i; \beta_N) + \delta_i (1 + k_{\beta_N,i}) \{ y_i - m(x_i; \beta_N) \} - \mu \right] + c_2^T \delta_i g(x_i; \beta_N) \{ y_i - m(x_i; \beta_N) \} \). Then, \( \tilde{\psi}_n = \sum_{i \in A} \omega_i \psi_i \). The variance of \( \tilde{\psi}_n \) can be calculated as

\[
\text{var}(\tilde{\psi}_n) = E \{ \text{var}(\tilde{\psi}_n \mid \mathcal{F}_N) \} + \text{var} \left\{ E(\tilde{\psi}_n \mid \mathcal{F}_N) \right\} = E \{ \text{var}(\tilde{\psi}_n \mid \mathcal{F}_N) \}.
\]

Based on the two-step method in §4, the proposed jackknife replicate \( \check{\hat{\mu}}_{\text{PMM}}(\check{\hat{\beta}}(k)) \) perturbs the martingale representation \( \tilde{\psi}_n \) as \( \tilde{\psi}_n^{(k)} = \sum_{i \in A} \omega_i^{(k)} \psi_i \). The replication variance estimator of \( \tilde{\psi}_n \) is obtained by applying \( \check{V}_{\text{rep}}(\cdot) \) in (14) for the above replicates \( \tilde{\psi}_n^{(k)} \). It follows that \( \check{V}_{\text{rep}}(\tilde{\psi}_n)/\text{var}(\tilde{\psi}_n) \to 1 \), as \( n \to \infty \). This proves the consistency of the replication variance estimator for \( \text{var}\{\check{\hat{\mu}}_{\text{PMM}}(\check{\hat{\beta}})\} \).
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