

Data integration of non-probability and probability samples with predictive mean matching

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Abstract

In this paper we study predictive mean matching mass imputation estimators to integrate data from probability and non-probability samples. We consider two approaches: matching predicted to observed ($\hat{y}-y$ matching) or predicted to predicted ($\hat{y}-\hat{y}$ matching) values. We prove the consistency of two semi-parametric mass imputation estimators based on these approaches and derive their variance and estimators of variance. Our approach can be employed with non-parametric regression techniques, such as kernel regression, and the analytical expression for variance can also be applied in nearest neighbour matching for non-probability samples. We conduct extensive simulation studies in order to compare the properties of this estimator with existing approaches, discuss the selection of k -nearest neighbours, and study the effects of model mis-specification. The paper finishes with empirical study in integration of job vacancy survey and vacancies submitted to public employment offices (admin and online data). Open source software is available for the proposed approaches.

Keywords: mass imputation, non-probability surveys, variance estimation, bootstrap, job vacancy survey

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1 Introduction

With the availability of large sets of administrative data, voluntary internet panels, social media and big data, inference with non-probability samples is being heavily studied in the statistical literature (Beaumont, 2020; Beręsewicz, 2017; Citro, 2014; Elliott & Valliant, 2017). Because of their non-statistical character and unknown sampling mechanism, these sources cannot be used directly for estimating population characteristics.

Several inference approaches have been proposed in the literature with respect to data from non-probability samples, which either involve data integration with population level data or probability samples from the same population (see for recent review Wu, 2022). Main techniques for inference based on such data can broadly be classified into inverse probability weighting (IPW) estimators, prediction estimators (PE) and doubly robust (DR) estimators, which include both IPW and PE. In this paper we focus on mass imputation (MI) estimators, which are a variant of prediction estimators used for integrating probability and non-probability samples (cf. Elliott & Valliant, 2017). The general idea is to impute values of the target variable Y for all units in a probability sample based on values observed in non-probability samples.

In recent papers two distinct MI estimators have been proposed: (1) the nearest neighbour (NN; cf. Yang, Kim, and Hwang (2021)) imputation estimator and (2) the parametric (PAR) and non-parametric (NPAR) imputation estimator (cf. Chen, Yang, & Kim, 2022; Kim et al., 2021). The latter two consist in using a model for $\mathbb{E}[Y|\mathbf{X}]$ with parameters estimated from a non-probability sample and then using predictions from this model as imputed values for a probability sample. In contrast, NN imputation involves finding k nearest neighbours for each unit in a probability sample from a set of units from a non-probability sample (imputed values are observed values of Y from the non-probability sample).

In this paper we focus on the predictive mean matching (PMM) MI estimator in the context of data integration, which can be seen as a technique combining NN and parametric (or non-parametric) imputation estimators. PMM combined with multiple imputation was introduced by Little (1988) and Rubin (1986) for imputing missing data in surveys. Schenker and Taylor (1996) and Horton and Lipsitz (2001) advocated PMM imputation because of its robustness to model mis-specification. The asymptotic properties of the PMM estimator were recently discussed in the context of survey non-response by Yang and Kim (2020). Initial work on

multiply robust estimation was done by Chen, Haziza, and Stubblefield (2021). However, the PMM estimator has not yet been discussed or studied in the context of data integration involving non-probability and probability samples.

Our contribution can be summarized as follows:

1. We study properties of two variants of semi-parametric PMM estimators for the data integration problem in two settings: matching either by predicted-observed ($\hat{y} - y$) or predicted-predicted ($\hat{y} - \hat{y}$) values. The latter option is the standard PMM estimator, which is used in most of the existing studies, while the first one is less commonly discussed.
2. We prove the consistency of these estimators under suitable assumptions where population size is either known or estimated. The theorem can easily be extended to non-parametric models, such as kernel or local linear regression. We also discuss consistency when the model is mis-specified.
3. We derive analytical and bootstrap variance estimators and study their performance for finite populations. Furthermore, the proposed closed form expression for analytical variance can also be used for the NN estimator. We also prove a result analogous to Yang, Kim, and Hwang (2021) concerning asymptotic and large non-probability sample behaviour of the variance estimator.

The structure of the paper is as follows. In section 2 we provide basic notation, describe two PMM algorithms and discuss the assumptions underlying the PMM estimators. Section 3 provides proof of consistency of the PMM estimators and the exact variance and its estimators. Section 4 describes one of the simulation studies, whose results verify the proposed approach under simple random sampling where two linear and non-linear models are considered. Section 5 presents our empirical study. The article ends with conclusions and the Appendix including details concerning the proofs as well as additional simulation studies. All calculations in the article can be reproduced using R (R Core Team, 2023) and the `nonprobsvy` package (Chrostowski, Beręsewicz, & Chlebicki, 2023) developed by the authors. All codes are available at <https://github.com/ncn-foreigners/paper-nonprob-pmm>.

2 Basic setup

2.1 Notation and motivation

Let $U = \{1, \dots, N\}$ denote the target population consisting of N labelled units. Each unit i has an associated vector of auxiliary variables \mathbf{x}_i (a realisation of the random vector \mathbf{X} in the super-population) and the study variable y_i (a realisation of the random variable Y in the super-population). Let $\{(y_i, \mathbf{x}_i), i \in S_A\}$ be a dataset of a non-probability sample of size n_A and let $\{(\mathbf{x}_i, \pi_i), i \in S_B\}$ be a dataset of a probability sample of size n_B , where only information about variables \mathbf{X} and inclusion probabilities π are available. Let δ be an indicator of inclusion into non-probability sample. Each unit in the sample S_B has been assigned a design-based weight given by $d_i = 1/\pi_i$. There is no overlap between the two samples. The setting is summarised in Table 2.1.

Table 2.1: Two sample setting.

Sample	ID	Sample weight $d = \pi^{-1}$	Covariates \mathbf{x}	Study variable y
Non-probability sample (S_A)	1	?	✓	✓
	\vdots	?	\vdots	\vdots
	n_A	?	✓	✓
Probability sample (S_B)	1	✓	✓	?
	\vdots	\vdots	\vdots	?
	n_B	✓	✓	?

The goal is to estimate a finite population mean $\mu_y = \frac{1}{N} \sum_{i=1}^N y_i$ of the target variable y . As values of y_i are not observed in the probability sample, it cannot be used to estimate the target quantity. Instead, one could try combining the non-probability and probability samples to estimate μ_y .

In our paper we focus on prediction, which is an appealing solution as it allows us to make available micro-level data with fully imputed target variables and design specification. Moreover, we impute *observed* values of Y , which makes it easier to explain them to users of the micro-data (since observations are not generated from an *unknown* model).

2.2 Predictive mean matching algorithms

In this section we describe two general algorithms for semi-parametric PMM estimators. Let \hat{y}_i be a predicted value for unit i from the assumed regression model $m(\mathbf{x}_i, \hat{\boldsymbol{\beta}})$. Algorithm 1 (without step 2B) is a $\hat{y} - y$ matching imputation estimator, in which units from the probability sample S_B are matched based on \hat{y} to those from the non-probability sample S_A based on y . This estimator is given by (3) (throughout the paper this estimator is denoted as $\hat{y} - y$ or the PMM A estimator). Algorithm 1 (without step 2A) represents the standard $\hat{y} - \hat{y}$ matching (throughout the paper this estimator is denoted as $\hat{y} - \hat{y}$ or as the PMM B estimator). The resulting estimator is given by the same expression (3) but the matching is done differently.

Algorithm 1: Two predictive mean matching imputation algorithms

- 1 Estimate regression model $\mathbb{E}[Y|\mathbf{X} = \mathbf{x}] = m(\mathbf{x}, \boldsymbol{\beta})$.
- 2A ($\hat{y} - y$ imputation; PMM A) Impute $\hat{y}_i = m(\mathbf{x}_i, \hat{\boldsymbol{\beta}})$ for $i \in S_B$ and map each $i \in S_B$ to $\hat{\nu}(i)$ where: $\hat{\nu}(i) = \arg \min_{j \in S_A} \|\hat{y}_i - y_j\|$ or $\hat{\nu}(i) = \arg \min_{j \in S_A} d(\hat{y}_i, y_j)$ if d is not norm-induced.
If $k > 1$ instead let:

$$\hat{\nu}(i, z) = \arg \min_{j \in S_A \setminus \bigcup_{t=1}^{z-1} \{\hat{\nu}(i, t)\}} d(\hat{y}_i, y_j). \quad (1)$$
- 2B ($\hat{y} - \hat{y}$ imputation; PMM B) Impute $\hat{y}_i = m(\mathbf{x}_i, \hat{\boldsymbol{\beta}})$, $\hat{y}_j = m(\mathbf{x}_j, \hat{\boldsymbol{\beta}})$ for $i \in S_B, j \in S_A$ and map each $i \in S_B$ to $\hat{\nu}(i)$ where: $\hat{\nu}(i) = \arg \min_{j \in S_A} \|\hat{y}_i - \hat{y}_j\|$ or $\hat{\nu}(i) = \arg \min_{j \in S_A} d(\hat{y}_i, \hat{y}_j)$ if d is not norm-induced. If $k > 1$ let instead let:

$$\hat{\nu}(i, z) = \arg \min_{j \in S_A \setminus \bigcup_{t=1}^{z-1} \{\hat{\nu}(i, t)\}} d(\hat{y}_i, \hat{y}_j), \quad (2)$$

i.e. the $\hat{\nu}(i, z)$ is the z 'th nearest neighbour from the sample.

- 3 Use imputed value in estimation: $\hat{\mu} = \frac{1}{N} \sum_{i \in S_B} \frac{1}{\pi_i} y_{\hat{\nu}(i)}$, or if $k > 1$ then instead:

$$\hat{\mu} = \frac{1}{N} \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i, t)}. \quad (3)$$

Remark 1. (Regarding $\hat{y} - y$ matching) If the study variable Y is a binary variable, then $\hat{y} - y$ matching estimator (3) is just a modification of the GLM estimator, in which, instead of predicted values, we impute a classification for each $i \in S_B$. The resulting estimate may still be

consistent according to Theorem 1 but may have comparatively poor finite sample properties in practice.

Remark 2. (Regarding nearest neighbour) If we let $m(\mathbf{x}_i, \boldsymbol{\beta}) = \mathbf{x}_i^T \boldsymbol{\beta}$ and use only one covariate, the resulting estimate (3) for $\hat{y} - \hat{y}$ matching is exactly the nearest neighbour estimate, since linear scaling preserves partial linear order \leq on \mathbb{R}_+ .

When m is a linear regression and d is a Euclidean distance $\hat{y} - \hat{y}$ matching is a "pseudo-nearest neighbour" matching with a weighted (by estimated regression coefficients) distance function $d' : (\mathbf{x}_i, \mathbf{x}_j) \mapsto |(\mathbf{x}_i - \mathbf{x}_j)^T \hat{\boldsymbol{\beta}}|$. If the number of covariates is greater than one, the partial order generated by the distance function is not deterministic in the general case, since $\hat{\boldsymbol{\beta}}$ is a random variable, and therefore one cannot simply assert that the $\hat{y} - \hat{y}$ matching estimator inherits properties from the NN estimator.

2.3 Assumptions

We state the main assumptions used for studying properties of estimators defined in (3) with a distance function being the Euclidean metric. See Kim et al. (2021) and Yang and Kim (2020) for a comparison with assumptions for other mass imputation estimators.

Throughout the paper we assume that in the super-population model every Y variable has a finite variance, i.e. $\forall i : \mathbb{E}[Y_i^2] < \infty$.

(A1) $\mathbb{E}[Y|\mathbf{X}] = m(\mathbf{X}, \boldsymbol{\beta}_0)$ almost surely for some $\boldsymbol{\beta}_0 \in \mathbb{R}^p$ and continuous m (as a function from $\mathbb{R}^p \times \mathbb{R}^p$ to \mathbb{R}), with $\hat{\boldsymbol{\beta}}$ being a consistent estimator for $\boldsymbol{\beta}_0$.

(A2) $\mathbb{P}[Y \in dy|\mathbf{X}, \delta] = \mathbb{P}[Y \in dy|\mathbf{X}]$ almost surely, i.e. Y is independent of the sampling process for the non-probability sample conditional on \mathbf{X} , and for every event M_{j,i_1,\dots,i_k} event depending only on units j, i_1, \dots, i_k in the population, if $\mathbb{P}(M_{j,i_1,\dots,i_k}) > 0$ for infinitely many tuples (i_1, \dots, i_k) and we set j from the super-population then:

$$\lim_{n_A \rightarrow \infty} \mathbb{P}[1 \leq \#\{j, i_1, \dots, i_k \in S_A : M_{j,i_1,\dots,i_k}\} | j \in S_B] = 1.$$

In this case we consider event M to depend only on units j, i_1, \dots, i_k if and only if it belongs to σ -algebra generated by $\{\mathbb{1}_{\{i_1 \in S_A\}}, \mathbb{1}_{\{i_1 \in S_B\}}, \mathbf{x}_{i_1}, y_{i_1}, \dots, \mathbb{1}_{\{j \in S_A\}}, \mathbb{1}_{\{j \in S_B\}}, \mathbf{x}_j, y_j\}$.

(A3) The variable of interest is square-integrable (in the super-population model). We study the asymptotic properties of (3) in the setting of a sequence of populations such that:

$$\exists C_1, C_2 \forall i : C_1 \leq \frac{N\pi_i}{n_B} \leq C_2,$$

and each population in the sequence is a random sample from some the super-population and where $\lim_{n_A \rightarrow \infty} n_B = \infty$ a.s.

(A4) We require that:

$$\lim_{N \rightarrow \infty} \frac{1}{N} \sum_{j=1}^N (m(\mathbf{x}_i, \boldsymbol{\beta}_0) - y_j) = 0 \text{ in probability.}$$

Note that by virtue of (A1) the same holds after replacing $\boldsymbol{\beta}_0$ with $\hat{\boldsymbol{\beta}}$.

(A5) Matching between S_A and S_B is asymptotically weakly uniquely identifiable i.e. for each $i \in S_B$ asymptotically there exists at most 1 set of $y_{\hat{\nu}(i,1)}, \dots, y_{\hat{\nu}(i,k)}$, meaning there is only one choice for $\{\hat{\nu}(i,1), \dots, \hat{\nu}(i,k)\}$ or for every choice of $\{\hat{\nu}(i,1), \dots, \hat{\nu}(i,k)\}$ we get the same $y_{\hat{\nu}(i,1)}, \dots, y_{\hat{\nu}(i,k)}$. In other words, with probability 1 the following property holds:

$$\forall i \in S_B, j \in S_A : (d(y_i, y_{\hat{\nu}(i,k)}) = d(y_i, y_j) \implies y_j = y_{\hat{\nu}(i,k)}).$$

This assumption is met, for instance, if at least one covariate is continuous and with support on \mathbb{R} and the regression coefficient β associated with this variable is non-zero.

(B1) (For $\hat{y} - \hat{y}$ matching only) For any $\varepsilon > 0$ we assume that:

$$\lim_{n_A \rightarrow \infty} \mathbb{P} \left[\exists j_1, j_2, \dots, j_k \in S_A : \max_t \|\mathbf{x}_i - \mathbf{x}_{j_t}\| < \varepsilon \mid i \in S_B \right] = 1,$$

i.e. asymptotically we will cover at least k units that have similar \mathbf{X} values to $i \in S_B$.

(C1) (For $\hat{y} - y$ matching only) The support of \mathbf{X} in S_B (or equivalently in U) is such that:

$$\forall \varepsilon > 0, y : (\mathbb{P}[Y \in (y - \varepsilon, y + \varepsilon)] > 0 \implies \mathbb{P}[m(\mathbf{X}, \boldsymbol{\beta}) \in (y - \varepsilon, y + \varepsilon)] > 0),$$

for $\boldsymbol{\beta}$ in some arbitrarily small open neighbourhood of $\boldsymbol{\beta}_0$.

2.3.1 Discussion regarding the assumptions

Assumption (A3) describes a setting in which we explore consistency and is not important for finite sample performance. Assumptions (B1) and (C1) are not strictly necessary for reasonable performance in finite samples, but the PMM estimator will perform better if the non-probability sample is reasonably diverse, which is basically what (B1) and (C1) are getting at. Assumption (C1) is satisfied if, for example, at least one covariate has support on \mathbb{R} and $m(\cdot, \boldsymbol{\beta})$ depends on this covariate and Y is continuous under reasonable link functions, or if Y is discrete and $m(\mathbf{X}, \boldsymbol{\beta}) = \exp(\mathbf{X}^T \boldsymbol{\beta})$.

A reasonable question is whether assumption (A4) can be proved from other assumptions. The answer is negative since we can take Y to be independent from \mathbf{X} and $\forall t = 1, \dots, N : y_t \sim \mathcal{N}(0, t)$ independently, then $m \equiv 0$ and $\frac{1}{N} \sum_{j=1}^N y_j \sim \mathcal{N}\left(0, \frac{N+1}{2}\right)$ which does not converge to 0 in distribution (and therefore does not converge in probability). Nevertheless, it is trivially met by almost all regression models used in practice.

In proving consistency we do not assume positivity, contrary to Kim et al. (2021) or Yang, Kim, and Hwang (2021). Instead we have some very weak assumption as part of (A2) and assumption (B1)/ (C1) depending on the PMM estimator. (B1)/ (C1) is less restrictive and allows discrete \mathbf{x} , as in Kim et al. (2021). In the case of discrete \mathbf{X} (e.g. age, gender, etc.) we do not require that for all units $\mathbb{P}(\delta = 1 | \mathbf{X} = \mathbf{x}_i) > 0$, as may happen in quota sampling or Internet surveys, where certain units may be missing due to the lack of access to the Internet; instead, we only require that each level of \mathbf{X} will *eventually* be represented (with at least k units) as sample size increases to infinity. The case of continuous variables is analogous, i.e. if we set $i \in U$ and $\varepsilon > 0$ we require that eventually sample S_A will contain at least k units such that distance between a \mathbf{x}_i and \mathbf{x} corresponding to these k units will be no greater than ε . This convergence may in principal be arbitrarily slow (although this will have its impact on speed of convergence for $\hat{\mu}$).

3 Main results

3.1 Consistency

The proof strategy, which is somewhat similar to the proof of consistency presented in Kim et al. (2021), can essentially be reduced to first proving that (3) and the *hypothetical* Horvitz-Thompson (HT) estimator, i.e. what would be the HT estimator if we knew values of Y for units in S_B , have the same limit, and then inferring the consistency of (3) from the consistency of the *hypothetical* HT in the setting described in section 2.

Theorem 1. *Under assumptions (A1)-(A5) and (C1) for $\hat{y} - y$ matching and (B1) for $\hat{y} - \hat{y}$ matching, estimators in (3) are consistent. Additionally, the modified estimators with unknown population size:*

$$\hat{\mu} = \frac{1}{\sum_{r \in S_B} \pi_r^{-1}} \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}.$$

are also consistent.

Proof. To establish consistency first notice that for:

$$|\hat{\mu} - \mu| = \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \sum_{j=1}^N y_j \right| \quad (4)$$

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \sum_{j \in S_B} \frac{1}{\pi_j} y_j \right|, \quad (5)$$

both (4) and (5) have the same limit in probability almost surely, since by inverse triangle inequality:

$$\begin{aligned} & \left| \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \sum_{j=1}^N y_j \right| - \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \sum_{j \in S_B} \frac{1}{\pi_j} y_j \right| \right| \leq \\ & \left| \frac{1}{N} \left(\sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \sum_{j=1}^N y_j \right) - \frac{1}{N} \left(\sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \sum_{j \in S_B} \frac{1}{\pi_j} y_j \right) \right| = \\ & \left| -\frac{1}{N} \sum_{j=1}^N y_j + \frac{1}{N} \sum_{j \in S_B} \frac{1}{\pi_j} y_j \right|, \end{aligned}$$

and the HT estimator of the population mean is consistent in this setting, so it is sufficient to

check whether (3) is consistent for the *hypothetical* HT estimator. By the same argument for

$$|\hat{\mu} - \mu| = \left| \frac{1}{\sum_{r \in S_B} \pi_r^{-1}} \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \frac{1}{N} \sum_{j=1}^N y_j \right|$$

$$= \frac{1}{\sum_{r \in S_B} \pi_r^{-1}} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \sum_{j \in S_B} \frac{1}{\pi_j} y_j \right|,$$

an analogous property holds if N is unknown.

By inverse triangle inequality and (A4) for the expression in (5) the following occurs:

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - \sum_{j \in S_B} \frac{1}{\pi_j} y_j \right| \leq \quad (6)$$

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right) \right| + \underbrace{\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} (m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) - y_i) \right|}_{\xrightarrow{n_A \rightarrow \infty} 0 \text{ in probability}},$$

again we can replace $\frac{1}{N}$ by $\frac{1}{\sum_{r \in S_B} \pi_r^{-1}}$ and obtain an analogous property. Thus we have reduced the problem of proving the consistency of (3) to proving that:

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \left(\sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right) \right| \rightarrow 0 \text{ in probability.} \quad (7)$$

(Consistency of the PMM A estimator with $\hat{y} - y$) Notice that from the continuity of m we have the following implications:

$$\forall \varepsilon' > 0 : \mathbb{P}(|\mathbf{x}_i - \mathbf{X}| < \varepsilon' | \{i \in S_B\}) > 0, \quad (8)$$

$$\implies \forall \varepsilon > 0, \boldsymbol{\beta} : \mathbb{P}(|m(\mathbf{x}_i, \boldsymbol{\beta}) - m(\mathbf{X}, \boldsymbol{\beta})| < \varepsilon | \{i \in S_B\}) > 0.$$

and:

$$\forall \varepsilon > 0, \boldsymbol{\beta} : \{\exists j \in S_B : |y_j - m(\mathbf{x}_i, \boldsymbol{\beta})| < \varepsilon\} \cap \{i \in S_B\},$$

happens with positive probability. Notice for $\hat{y} - y$ matching $\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}})$ is exactly the minimized quantity from Algorithm 1. By virtue of the above reasoning and assumptions

(A2), (C1) we have:

$$\forall \varepsilon > 0, i : \lim_{n_A \rightarrow \infty} \mathbb{P} \left[k \leq \# \left\{ j \in S_A : \left| y_j - m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right) \right| < \varepsilon \right\} \mid \{i \in S_B\} \right] = 1, \quad (9)$$

from which one infers that:

$$\begin{aligned} \lim_{n_A \rightarrow \infty} \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \left(\sum_{t=1}^k y_{\hat{\nu}(i,t)} - m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right) \right) \right| \leq \\ \lim_{n_A \rightarrow \infty} \max_{i \in S_B} \left\{ \frac{n_B}{N \pi_i} \right\} \max_{i \in S_B} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right) \right| \leq \frac{\varepsilon}{C_1}, \end{aligned}$$

so the $\hat{y} - y$ matching estimator from Algorithm 1 is consistent.

(Consistency of the PMM B estimator with $\hat{y} - \hat{y}$ matching) In the case of $\hat{y} - \hat{y}$ matching by (A1), (A2), (B1) and (8) we have:

$$\forall \varepsilon > 0, i : \lim_{n_A \rightarrow \infty} \mathbb{P} \left[k \leq \# \left\{ j \in S_A : \left| m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right) - m \left(\mathbf{x}_j, \hat{\boldsymbol{\beta}} \right) \right| < \varepsilon \right\} \mid \{i \in S_B\} \right] = 1. \quad (10)$$

In other words, there will be at least k units in S_A that are "similar" to $i \in S_B$ and we can asymptotically replace $m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right)$ with $m \left(\mathbf{x}, \hat{\boldsymbol{\beta}} \right)$ value of any of those k -units.

Notice that the term in (7) has the same limit as:

$$\begin{aligned} \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k \left(m \left(\mathbf{x}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}} \right) - m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right) \right) \right| \leq \\ \max_{i \in S_B} \left\{ \frac{n_B}{N \pi_i} \right\} \max_{i \in S_B} \left| \frac{1}{k} \sum_{t=1}^k \left(m \left(\mathbf{x}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}} \right) - m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right) \right) \right|, \end{aligned} \quad (11)$$

since by inverse triangle inequality

$$\begin{aligned} \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right) \right| - \sum_{i \in S_B} \frac{1}{\pi_i} \left| \frac{1}{k} \sum_{t=1}^k m \left(\mathbf{x}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}} \right) - m \left(\mathbf{x}_i, \hat{\boldsymbol{\beta}} \right) \right| \right| \leq \\ \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k \left(y_{\hat{\nu}(i,t)} - m \left(\mathbf{x}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}} \right) \right) \right|, \end{aligned}$$

which tends to 0 in probability with $n_A \rightarrow \infty$ by the consistency of the Horvitz-Thompson

estimate for the random variable $\frac{1}{k} \sum_{t=1}^k \left(y_{\hat{\nu}(i,t)} - m(\mathbf{x}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}}) \right)$, whose mean is 0 since:

$$\begin{aligned} \mathbb{E} \left[\frac{1}{k} \sum_{t=1}^k \left(y_{\hat{\nu}(i,t)} - m(\mathbf{x}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}}) \right) \middle| \sigma(\{\hat{\nu}(i,t)\}_{i,t=1,\dots,0,k}) \right] &= 0 \text{ a.s.} \\ \implies \mathbb{E} \left[\frac{1}{k} \sum_{t=1}^k \left(y_{\hat{\nu}(i,t)} - m(\mathbf{x}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}}) \right) \right] &= 0 \end{aligned}$$

by (A1). By virtue of (10) we have:

$$\forall \varepsilon > 0 : \lim_{n_A \rightarrow \infty} \max_{i \in S_B} \left| \frac{1}{k} \sum_{t=1}^k m(\mathbf{x}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}}) - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right| < \varepsilon,$$

so by virtue of (11), $\hat{\mu}$ estimators from (3) are consistent. Additionally, for unknown N :

$$\frac{1}{\sum_{r \in S_B} \pi_r^{-1}} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right) \right| \leq \underbrace{\max_{i \in S_B} \left\{ \frac{n_B \pi_i^{-1}}{\sum_{r \in S_B} \pi_r^{-1}} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right| \right\}}_{\xrightarrow{n_A \rightarrow \infty} 0 \text{ in probability}},$$

since

$$\begin{aligned} & \max_{i \in S_B} \left\{ \left| \frac{n_B \pi_i^{-1}}{\sum_{r \in S_B} \pi_r^{-1}} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right| - \frac{n_B}{\pi_i N} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right| \right| \right\} \\ & \leq n_A \max_{i \in S_B} \left\{ \frac{1}{\pi_i} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right| \left| \frac{1}{\sum_{r \in S_B} \pi_r^{-1}} - \frac{1}{N} \right| \right\} \\ & \leq \max_{i \in S_B} \left\{ \frac{n_B}{N \pi_i} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right| \right\} \frac{1}{\sum_{r \in S_B} \pi_r^{-1}} \left| \sum_{r \in S_B} \pi_r^{-1} - N \right| \xrightarrow{n_A \rightarrow \infty} 0 \text{ in probability,} \end{aligned}$$

so if N is unknown and estimated by $\sum_{r \in S_B} \pi_r^{-1}$, corrected estimates for $\hat{\mu}$ from (3) are also consistent. \square

Since $\hat{\mu}$ and the *hypothetical* HT estimate have the same limit in order for (3) to be asymptotically normal with $(\mu_{n_B}^{(HT)}, V_{n_B}^{(HT)})$, it is both sufficient and necessary for the HT estimate to be asymptotically normal with $(\mu_{n_B}^{(HT)}, V_{n_B}^{(HT)})$.

Remark 3. (Regarding the proof of Theorem 1) If Y is multivariate we can, under analogous assumptions (though these assumptions may be somewhat less realistic in a multivariate case), replace $|\cdot|$ norm by the Euclidean norm $\|\cdot\|$ and get the consistency of the PMM estimators in a multivariate case.

Additionally, Proof 1 can be rewritten to accommodate distance functions other than the Euclidean metric (under reasonable restrictions) almost in an exactly analogous manner.

Remark 4. (Regarding robustness of $\hat{y} - \hat{y}$ matching) If the assumption that model $\mathbb{E}[Y|\mathbf{X}] = m(\mathbf{X}, \beta_0)$ is correctly specified is violated and instead we have chosen the $m'(\mathbf{X}, \cdot)$ model with m and m' being different, then in order for (3) to be consistent m' only needs to satisfy (A1) and:

$$\forall i \in S_B : \bigcup_{j=1}^k \{\hat{\nu}(i, j)\} = \bigcup_{j=1}^k \{\hat{\nu}'(i, j)\},$$

where:

$$\begin{aligned} \hat{\nu}(i, z) &= \arg \min_{\substack{z-1 \\ j \in S_A \setminus \bigcup_{t=1} \{\hat{\nu}(i, t)\}}} \left| m(\mathbf{x}_i, \hat{\beta}) - m(\mathbf{x}_j, \hat{\beta}) \right|, \\ \hat{\nu}'(i, z) &= \arg \min_{\substack{z-1 \\ j \in S_A \setminus \bigcup_{t=1} \{\hat{\nu}'(i, t)\}}} \left| m'(\mathbf{x}_i, \hat{\beta}') - m'(\mathbf{x}_j, \hat{\beta}') \right|. \end{aligned}$$

In other words, the linear order created by \hat{m} and \hat{m}' asymptotically agrees (at least approximately), which is realistically possible.

For example, Yang and Kim (2020) discussed robustness of the $\hat{y} - \hat{y}$ PMM estimator in cases when the regression model m has a Lipschitz property i.e. when:

$$\exists L \in \mathbb{R} \forall i, j : |m(\mathbf{x}_i, \beta) - m(\mathbf{x}_j, \beta)| \leq L \|\mathbf{x}_i - \mathbf{x}_j\|.$$

Remark 5. (Regarding assumption (A1)) We can relax assumption (A1) by assuming that for continuous m : $\mathbb{E}[Y|\mathbf{X}] = m(\mathbf{X})$ almost surely, i.e. a continuous function is a parameter, not just a vector in the Euclidean space. Then, under modified assumption (A1): \hat{m} is consistent

for m in the sense that:

$$\forall \varepsilon > 0 : \lim_{n_A \rightarrow \infty} \mathbb{P} [\|m - \hat{m}\|_\infty < \varepsilon] = \lim_{n_A \rightarrow \infty} \mathbb{P} \left[\sup_{\mathbf{x} \in \mathbb{R}^p} \|m(\mathbf{x}) - \hat{m}(\mathbf{x})\| < \varepsilon \right] = 1,$$

and almost surely continuous, we can establish the consistency of (3), where matching is done using \hat{m} with almost exactly the same argument.

This means that certain non-parametric regression techniques, such as kernel regression via the Nadaraya–Watson estimator or even local linear regression techniques, could potentially be used in (3) under suitable assumptions (to ensure their consistency).

In the Appendix we present simulation study that covers these examples. We have not determined whether convergence in $\|\cdot\|_\infty$ can be replaced by convergence in weaker topology.

3.2 Exact variance

Let us now study the variance of (3) choosing the case when Y is univariate for the sake of simplicity. The results can easily be generalized to multivariate Y by replacing products of scalars with outer products of vectors.

Theorem 2. *If the population size N is known, the variance of estimators (3) is given by*

$$\mathbb{V}[\hat{\mu}] = V_1 + V_2, \tag{12}$$

where

$$\begin{aligned} V_1 &= \frac{1}{N^2 k^2} \sum_{i=1}^N \frac{1}{\pi_i} \left(\frac{1}{\pi_i} - 1 \right) \mathbb{E} \left[\left(\sum_{t=1}^k y_{\hat{\nu}(i,t)} \right)^2 \right] \\ &\quad + \frac{1}{N^2 k^2} \sum_{\substack{i,j=1 \\ i \neq j}}^N \pi_i^{-1} \pi_j^{-1} \pi_{ij}^{-1} \mathbb{E} \left[\text{cov}(\mathbb{1}_{\{i \in S_B\}}, \mathbb{1}_{\{j \in S_B\}}) \sum_{t',t=1}^k y_{\hat{\nu}(i,t)} y_{\hat{\nu}(j,t')} \right] \\ &= \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \frac{\pi_{ij} - \pi_i \pi_j}{\pi_i \pi_j \pi_{ij}} \mathbb{E} \left[\left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right) \left(\frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right) \right], \end{aligned} \tag{13}$$

and

$$V_2 = \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \text{cov} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right) = \mathbb{V} \left[\frac{1}{N} \sum_{i=1}^N \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right]. \tag{14}$$

The proof of Theorem 2 is given in Appendix A. The V_1 term is just a variance of the HT estimator for the mean of imputed values via Algorithm 1 and the V_2 term can be seen as a compensation for inherent randomness (induced into S_A by unknown sampling, regression estimation etc.) resulting from PMM imputation.

Remark 6. (Regarding Theorem 2) When deriving the expression for $\mathbb{V}[\hat{\mu}]$ we conditioned variance on knowing values of y_i and $\hat{v}(i, t)$ for $i = 1, \dots, N$, $t = 1, \dots, k$. We can choose to do the same for nearest neighbour imputation (if we treat k as a random variable and not a hyper-parameter we additionally have to condition on k) in the spirit of Yang, Kim, and Hwang (2021). This gives us an exactly analogous expression for V_1, V_2 with matching variables $\hat{v}(i, t)$ being constructed by the k NN algorithm from which exact variance for k NN (conditional on k if it is a random variable) imputation can be obtained (a finite population correction V_2 was not considered in Yang, Kim, and Hwang (2021)).

As a corollary of Theorem 2 we have the following approximation for (3) with unknown population size estimated via the usual $\hat{N} = \sum_{r \in S_B} \pi_r^{-1}$:

$$\begin{aligned} \mathbb{V} \left[\frac{N}{\sum_{r \in S_B} \pi_r^{-1}} \hat{\mu} \right] &\approx V_1 + V_2 + \mathbb{E}[\hat{\mu}]^2 \frac{\mathbb{V}[\hat{N}]}{N^2} - 2 \frac{\text{cov}(\hat{N}, \hat{\mu})}{N} \\ &= V_1 + V_2 + \frac{\mathbb{E}[\hat{\mu}]^2}{N^2} \sum_{i,j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_i \pi_j} - 2 \frac{1}{N^2} \sum_{i,j=1}^N \pi_i^{-1} \pi_j^{-1} \text{cov} \left(\mathbb{1}_{i \in S_B}, \mathbb{1}_{j \in S_B} \frac{1}{k} \sum_{t=1}^k y_{\hat{v}(j,t)} \right) \quad (15) \\ &= V_1 + V_2 + \frac{\mathbb{E}[\hat{\mu}]^2}{N^2} \sum_{i,j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_i \pi_j} - 2 \frac{1}{N^2} \sum_{i,j=1}^N \frac{\pi_{ij} - \pi_i \pi_j}{\pi_i \pi_j} \mathbb{E} \left[\frac{1}{k} \sum_{t=1}^k y_{\hat{v}(j,t)} \right] \end{aligned}$$

Since \hat{N} is unbiased for N we obtain (15) by Taylor series expansion.

3.3 Variance estimator

3.3.1 "Analytic" variance estimator

Theorem 3 provides a consistent estimator of the variance estimator provided in Theorem 2.

Theorem 3. If second order inclusion probabilities are known, assumptions of Theorem 1 are satisfied, the standard variance estimator of the "hypothetical" HT estimator is consistent and

$\left| \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}} \right|$ is bounded for all i, j , then:

$$\widehat{\mathbb{V}}[\hat{\mu}] = \hat{V}_1 = \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}} \frac{\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}}{\pi_i} \frac{\frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')}}{\pi_j}, \quad (16)$$

is a consistent estimator for $\mathbb{V}[\hat{\mu}]$.

The full proof of Theorem 3 is presented in Appendix B.

The result $\lim_{n_A \rightarrow \infty} V_2 = 0$, which is a corollary to Theorem 3, is intuitively expected since $\mathbb{V} \left[\frac{1}{N} \sum_{i=1}^N \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right]$ is an alternative expression for V_2 and under (B1) or (C1) asymptotically we will almost surely find k units that will not differ “too much” from each $i \in S_B$ and therefore in large samples $y_{\hat{\nu}(i,1)} \approx y_{\hat{\nu}(i,2)} \approx \dots \approx y_{\hat{\nu}(i,k)}$, which implies that $\forall i : \mathbb{V} \left[\frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(i,t')} \right] \approx 0$, therefore variance of the sum of $\frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')}$ will not grow faster than N^2 .

The first component \hat{V}_1 is the Horvitz-Thomson variance estimator for the mean computed via imputed values. Computation of the term \hat{V}_2 , which in the light of Theorem 3 can be seen as a finite sample correction, given by:

$$\hat{V}_2 = \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \pi_{ij}^{-1} \widehat{\text{COV}} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right),$$

is more challenging as it requires an estimator for covariance of imputed values. Fortunately, as we demonstrate in the simulation study we can omit the \hat{V}_2 term for large S_A samples.

If the population size N is unknown and estimated from the probability sample we can use the plug-in estimator for (15) given by

$$\begin{aligned} & \frac{1}{\hat{N}^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}} \frac{\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}}{\pi_i} \frac{\frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')}}{\pi_j} \\ & + \frac{1}{\hat{N}^2} \sum_{i \in S_B} \sum_{j \in S_B} \pi_{ij}^{-1} \widehat{\text{COV}} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right), \\ & + \frac{\hat{\mu}^2}{\hat{N}^2} \sum_{i,j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_i \pi_j} - 2 \frac{\hat{\mu}}{\hat{N}^2} \sum_{i,j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} \end{aligned}$$

where the first two lines refer to estimators for V_1 and V_2 under estimated population size and the last line is a correction for randomness of \hat{N} .

Unfortunately, the V_2 term cannot be estimated directly from samples S_A and S_B ; therefore we propose a simple "mini-bootstrap" to estimate $\text{cov} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right)$. The procedure is explained in Algorithm 2.

Algorithm 2: Non-parametric mini-bootstrap estimator for covariance terms

- 1 Sample n_A units from S_A with replacement to create S'_A (if pseudo-weights are present inclusion probabilities should be proportional to their inverses).
 - 2 Estimate regression model $\mathbb{E}[Y|\mathbf{X} = \mathbf{x}'] = m(\mathbf{x}', \boldsymbol{\beta})$ based on $j \in S'_A$ from step 1
 - 3 Compute $\hat{\nu}'(i, t)$ for $t = 1, \dots, k, i \in S_B$ using estimated $m(\mathbf{x}', \cdot)$ and $\{(y_j, \mathbf{x}_j) | j \in S'_A\}$
 - 4 Compute $\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}'(i)}$ using Y values from S'_A .
 - 5 Repeat steps 1-4 M times (we set $M = 50$ in our simulations)
 - 6 Estimate covariance between imputed values for each pair $i, j \in S_B$ using constructed pseudo-sample with values from 4.
-

The estimates from Algorithm 2 are satisfactory for $\hat{y} - y$ matching and a little pessimistic for $\hat{y} - \hat{y}$ matching judging by numerical simulations from section 4. But the performance of Algorithm 2 is not explained by any solid theoretical argument.

The intuitive reason as to why Algorithm 2 may be an appropriate bootstrap for \hat{V}_2 is that as per equation (14), V_2 is just the variance of the mean of imputed values for the whole population. Since imputation to the whole population can be done with just the S_A sample (if we know \mathbf{X} values for the entire population), the sampling for sample A is the only source of randomness that is relevant to V_2 . Therefore, we only need to account for sampling in S_A and use the probability sample S_B to estimate the $\frac{1}{N} \sum_{i=1}^N \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}$ by the usual weighted estimator and compute the variance of estimates obtained via Algorithm 2. This also explains why results from Algorithm 2 are a little pessimistic since we are essentially estimating

$$\mathbb{V} \left[\frac{1}{N} \sum_{i=1}^N \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right],$$

by an estimator for:

$$\mathbb{V} \left[\frac{1}{N} \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right],$$

which induces more randomness.

3.4 Bootstrap variance estimator

In this section we provide a bootstrap variance estimator for the mean. Since we estimate V_2 using the “mini-bootstrap” described by Algorithm 2, we need to estimate V_1 using the appropriate bootstrap approach for probability samples.

Algorithm 3: Bootstrap variance estimator

- 1 Sample with replacement n_A units from S_A to create S'_A (if pseudo-weights are present, inclusion probabilities should be proportional to their inverses).
- 2 Sample with replacement n_B units from S_B according to the sampling design to create S'_B .
- 3 Estimate regression model parameters $\mathbb{E}[Y|\mathbf{X} = \mathbf{x}'] = m(\mathbf{x}', \boldsymbol{\beta})$ based on $j \in S'_A$ from step 1
- 4 Follow steps 2A/2B-3 from Algorithm 1 depending on the imputation method ($\hat{y} - \hat{y}$ or $\hat{y} - y$) to compute $\hat{\mu}$ in current iteration.
- 5 Repeat steps 1-4 L times (we set $L = 500$ in our simulations).
- 6 Estimate V_2 term using Algorithm 2.

- 7 Estimate variance V_1 term as $\hat{V}_1 = \frac{1}{L-1} \sum_{i=1}^L (\hat{\mu}_i - \bar{\mu})^2$ where $\bar{\mu} = \frac{1}{L} \sum_{i=1}^L \hat{\mu}_i$ and final bootstrap variance as $\hat{V} = \hat{V}_1 + \hat{V}_2$
-

In the simulation study we compare the analytic and the bootstrap approach and show that both estimators have the assumed nominal coverage rate.

4 Simulation study

Our simulation study follows the procedure described in Kim et al. (2021). We generate a finite population of size $N = 10^5$, random variables $X \sim \mathcal{N}(2, 1)$ and $\varepsilon \sim \mathcal{N}(0, 1)$ and assume the following models: 1) $y_{1i} = 1 + 2x_i + \varepsilon_i$; 2) $y_{2i} = 3 + x_i + 2\varepsilon_i$; and 3) $y_{3i} = 2.5 + 0.5x_i^2 + \varepsilon_i$. We consider two sample sizes for the non-probability sample $n_A = 500$ and $n_A = 1,000$. Sample S_A is drawn from the population using simple random sampling within two strata created by $x_i \leq 2$ and $x_i > 2$ with the following sample sizes: $n_{strata1} = 0.7n_A$ and $n_{strata2} = 0.3n_A$, respectively. For the probability sample we assume a fixed sample size $n_B = 500$ and simple random sampling without replacement from the population. In each of 500 simulation runs and for every y we calculated

- The naive estimator (sample mean) from sample A given by $\hat{\mu} = n_A^{-1} \sum_{i \in S_A} y_i$,
- The mass imputation estimator using a linear regression model $\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i$, where $(\hat{\beta}_0, \hat{\beta}_1)$ are regression coefficients estimated from the non-probability sample. We denote

this estimator as MI-GLM.

- Two PMM mass imputation estimators given by (3) using $k = 1$ denoted as PMM1A for $\hat{y} - y$ and PMM1B for $\hat{y} - \hat{y}$ matching,
- Two PMM mass imputation estimators given by (3) using $k = 5$ denoted as PMM5A for $\hat{y} - y$ and PMM5B for $\hat{y} - \hat{y}$ matching.

Three results are reported in this section. Firstly, we report Monte Carlo bias (Bias), standard error (SE), relative mean square error (RMSE) and empirical coverage rate (CR) of 95% confidence intervals using the analytical variance estimator based on $R = 500$ simulations for each Y variables: $\text{Bias} = \bar{\hat{\mu}} - \mu$, $\text{SE} = \sqrt{\frac{\sum_{r=1}^R (\hat{\mu}^{(r)} - \bar{\hat{\mu}})^2}{R-1}}$ and $\text{RMSE} = \sqrt{\text{Bias}^2 + \text{SE}^2}$, where $\bar{\hat{\mu}} = \sum_{r=1}^R \hat{\mu}^{(r)} / R$ and $\hat{\mu}^{(r)}$ is an estimate of the mean in the r -th replication. Secondly, we compare how the CI's change if we drop \hat{V}_2 from the PMM variance estimator. Finally, we compare analytic and bootstrap estimators for the PMM estimators discussed in this section.

Table 4.1 presents the main results of the simulation study. For the first variable (Y_1), where the model is correctly specified, values of both the bias and the RMSE are similar to the MI-GLE estimator proposed by Kim et al. (2021). The main difference between the proposed PMM estimators is the standard error, which is larger for $\hat{y} - \hat{y}$ imputation compared to the standard $\hat{y} - y$ imputation. This relationship is particularly visible for the larger sample ($n = 1000$). In the case of Y_1 , there is no significant difference between the proposed PMM $\hat{y} - y$ and the MI-GLM estimator.

Table 4.1: Simulated Bias, SE, RMSE (multiplied by 100) and CI of 5 estimators

Estimator	Y_1				Y_2				Y_3			
	Bias	SE	RMSE	CR	Bias	SE	RMSE	CR	Bias	SE	RMSE	CR
$n_A = 500$												
Naive	-64.36	6.83	64.73		-32.29	8.81	33.47		-64.33	6.54	64.66	
MI-GLM	-0.52	10.33	10.34	94.20	-0.56	10.21	10.22	95.60	-6.34	10.44	12.22	89.60
PMM1A	-0.59	10.32	10.34	95.00	-0.56	10.20	10.22	96.20	-6.07	10.43	12.06	89.00
PMM1B	-0.60	12.21	12.22	93.00	-0.46	16.66	16.67	92.80	-0.97	12.51	12.54	93.00
PMM5A	-0.82	10.25	10.28	95.00	-0.57	10.20	10.22	95.80	-5.90	10.40	11.95	89.60
PMM5B	-1.11	10.81	10.87	94.60	-1.02	12.13	12.18	95.00	-2.37	11.09	11.34	94.60
$n_A = 1,000$												
Naive	-64.01	5.21	64.22		-31.89	6.88	32.62		-64.01	4.97	64.20	
MI-GLM	-0.32	9.88	9.89	94.80	-0.14	8.27	8.28	93.80	-6.01	9.50	11.24	88.20
PMM1A	-0.34	9.87	9.87	95.00	-0.14	8.28	8.28	94.40	-5.83	9.48	11.13	88.80
PMM1B	-0.66	11.25	11.27	95.60	-0.74	13.34	13.36	96.00	-0.79	11.70	11.73	95.60
PMM5A	-0.43	9.84	9.85	94.80	-0.14	8.27	8.27	93.40	-5.66	9.45	11.01	88.80
PMM5B	-0.59	10.11	10.13	95.00	-0.37	9.49	9.50	96.20	-1.19	10.54	10.61	94.80

As regards the second variable Y_2 , a similar pattern can be observed as for Y_2 with one exception. The larger the number of nearest neighbours, the smaller the bias and the standard

error for the $\hat{y} - \hat{y}$ matching PMM estimator. In the case of $\hat{y} - y$ matching PMM, increasing the number of nearest neighbours has no significant effect on the bias or the standard error. The empirical coverage rates are close to the nominal 95%.

The main differences can be observed for the last variable Y_3 , which includes the non-linear part (i.e. x_i^2). The PMM B with $\hat{y} - \hat{y}$ fitting is now characterised by the lowest bias of all estimators under consideration and a CR close to the nominal 95%. This is in line with Remark 4 regarding robustness of $\hat{y} - \hat{y}$ matching. MI-GLM and the PMM with $\hat{y} - y$ are characterised with similar bias, SE, RMSE and CR.

Table 4.2: Empirical coverage rate intervals for two cases: the effect of V_2 on the variance estimator and analytic and bootstrap variance estimators.

	Y_1		Y_2		Y_3	
Effect of V_2 on the variance estimator and its empirical coverage rate						
	V_1	$V_1 + V_2$	V_1	$V_1 + V_2$	V_1	$V_1 + V_2$
$n_A = 500$						
PMM1A	90.80	95.00	58.60	96.20	81.00	89.00
PMM1B	89.40	93.00	78.20	92.80	89.60	93.00
PMM5A	90.60	95.00	58.80	95.80	80.80	89.60
PMM5B	91.20	94.60	71.00	95.00	90.20	94.60
$n_A = 1,000$						
PMM1A	94.40	95.00	76.20	94.40	85.00	88.80
PMM1B	93.80	95.60	87.20	96.00	93.80	95.60
PMM5A	94.40	94.80	76.00	93.40	85.20	88.80
PMM5B	94.00	95.00	83.20	96.20	92.60	94.80
Comparison of analytic and bootstrap variance estimators						
	Analytic	Bootstrap	Analytic	Bootstrap	Analytic	Bootstrap
$n_A = 500$						
PMM1A	95.00	94.40	96.20	95.80	89.00	89.40
PMM1B	93.00	93.60	92.80	96.00	93.00	93.40
PMM5A	95.00	94.80	95.80	96.00	89.60	89.80
PMM5B	94.60	94.60	95.00	96.20	94.60	94.40
$n_A = 1,000$						
PMM1A	95.00	94.60	94.40	94.00	88.80	89.20
PMM1B	95.60	95.20	96.00	97.80	95.60	95.80
PMM5A	94.80	95.40	93.40	93.60	88.80	88.80
PMM5B	95.00	95.80	96.20	97.80	94.80	95.00

Table 4.2 shows two results. The first part of the table shows the effect of the second component V_2 on the variance estimator of the mean. The second compares the analytic and bootstrap variance estimators as discussed in the previous section. As suggested by theory, the proportion of variance assigned to the V_2 component decreases with sample size. Moreover,

only for the Y_2 variable the impact of V_2 is not negligible, the CR based only on the probability part (V_1) is significantly smaller than the expected 95%, with values around 60% for $\hat{y} - y$ and 80-70% for $\hat{y} - \hat{y}$ matching. The second part suggests that the proposed analytical and bootstrap variance estimation approaches yield the same results for all study variables and sample sizes. As expected, the number of nearest neighbours does not affect the CR as only small differences are observed.

In the Appendix we provide additional results: 1) choosing k number of nearest neighbours does not improve coverage but lowers MSE (as was also shown by Yang, Kim, and Hwang (2021) for the NN estimator); 2) variable selection for the MI-GLM and PMM estimators using the SCAD penalty (as in Yang, Kim, and Song (2020)) improves estimates and the coverage rate and should be considered in applications; 3) non-parametric regression using a local linear model can be employed, although in practice better non-parametric methods ought to be considered; 4) the proposed estimators perform similarly to the MI-GLM estimator when the positivity assumption is violated with some exceptions when a non-linear model is considered; and finally 5) the initial result on the multiply robust procedure proposed by Chen, Haziza, and Stubblefield (2021) seems to work well but provides comparable results to standard PMM B matching (i.e. without the property of being multiply robust). This, however, requires further studies as no theory has been developed for the multiply robust PMM estimator.

5 Empirical study

In this section we present an attempt to integrate administrative and survey data about job vacancies for the end of 2022Q2 in Poland. The aim was to estimate the share of vacancies aimed at Ukrainian workers. We defined our target variable as follows: Y indicates *whether the vacancy has been translated into Ukrainian*. As the survey only provides information about the number of vacancies and not specific vacancies, our models were based on the independent variable y defined as the share of vacancies translated into Ukrainian calculated separately for each unit. We present a brief description of the datasets, but we encourage readers to read the full description of the dataset and the relationships between the target and auxiliary variables as described in Beręsewicz and Szymkowiak (2024).

The first source we used is the Job Vacancy Survey (JVS, also known as the Labour Demand

Survey), which is a stratified sample of 100,000 units, with a response rate of about 60% (S_B). The survey population consists of companies and their local units with 1 or more employees. The sampling frame includes information about NACE (19 levels), region (16 levels), sector (2 levels), size (3 levels) and the number of employees according to administrative data integrated by Statistics Poland (RE). The JVS sample contains 304 strata created separately for enterprises with up to 9 employees and those with more than 10 employees (cf. Statistics Poland, 2021). Of the 60,000 responding units, around 7,000 reported at least one vacancy. Our target population included units with at least one vacancy; according to the survey, there were between 38,000 and 43,000 of such units at the end of 2022Q2.

The second source is the Central Job Offers Database (CBOP), which is a register of all vacancies submitted to Public Employment Offices (PEOs – S_A). CBOP is available online and can be accessed via API. CBOP includes all types of contracts and jobs outside Poland, so data cleaning was carried out to align the definition of a vacancy with that used in the JVS. CBOP data collected via API include information about whether a vacancy is outdated (e.g. 17% of vacancies were outdated when downloaded at the end of 2022Q2). CBOP also contains information about unit identifiers (REGON and NIP), so we were able to link units to the sampling frame to obtain auxiliary variables with the same definitions as those used in the survey (24% of records contained no identifier because the employer has the right to withhold this information). The final CBOP dataset contained about 8,500 units included in the sampling frame.

The following variables were considered: Region (16 levels), NACE (19 levels), Sector (2 levels), Size (3 levels), $\log(\text{RE})$, $\log(\# \text{ vacancies})$ (the number of vacancies), $I(\# \text{ vacancies} = 1)$ (whether employer seeks only one person). We considered 5 estimators in the empirical study (for all models linear regression is assumed)

- Mass imputation (MI) estimators: MI-GLM (Kim et al., 2021), PMM A, PMM B ,
- Inverse probability weighting (IPW) estimator with calibration constraints (cf. Chen, Li, & Wu, 2020),
- Doubly robust (DR) estimator with IPW defined above (cf. Chen, Li, & Wu, 2020).

Variance was estimated using the following bootstrap approach: 1) JVS sample was re-

sampled using a stratified bootstrap approach, 2) CBOP was resampled using simple random sampling with replacement. This procedure was repeated $B = 500$ times. Table 5.1 shows point estimates (denoted as Point), bootstrap standard errors (denoted as SE), the coefficients of variation (CV) and 95% confidence intervals.

Table 5.1: Estimates of the share of job vacancies aimed at Ukrainians at the end of 2022Q2 in Poland

Estimator	Point	SE	CV	2.5%	97.5%
Naïve	20.51	–	–	–	–
IPW	21.79	0.60	2.75	20.57	22.96
MI-GLM	22.72	0.57	2.51	21.49	23.79
PMM A	22.79	0.57	2.51	21.58	23.84
PMM B	22.79	0.57	2.51	21.58	23.84
DR	21.79	0.60	2.75	20.57	22.96

As can be seen in Table 5.1, the point estimates produced by all the estimators in the study are at a similar level and fluctuate around 22%, with the exception of the Naïve estimator, for which the estimated share of job vacancies aimed at Ukrainians is lower and amounts to 20.51%. CV values for the discussed estimators are similar, with the lowest values for mass imputation estimators. Results for MI-GLM, PMM A and PMM B in this empirical study are not distinguishable.

6 Conclusions

We have discussed the asymptotic properties of two PMM estimators that can be used to integrate data from non-probability and probability samples. We have proved their consistency and derived analytical variance estimators. The results obtained in the study hold not only for parametric but also for non-parametric models used for matching. The variance estimators can be applied to the NN estimator for non-probability samples.

In the simulation study, we have shown that the PMM estimator based on $\hat{y} - \hat{y}$ matching is robust to model mis-specification and has a lower bias than existing alternatives. This is in line with results on PMM estimators for survey non-response or statistical matching. However, this gain is achieved at the expense of an increase in variance, but only for linear models. In additional simulation studies presented in the appendix, we verified the use of PMM estimators for different settings.

A natural extension of the study is that we can maintain consistency if the design weights d_i are replaced with calibration weights, which is often the case when working with survey sample datasets. The next interesting question regards the choice of k hyper-parameters, and some suggestions are given in the appendix. Another problem worth investigating is whether we can replace probability convergence in $\|\cdot\|_\infty$ with weaker convergence for estimators of \hat{m} from **Remark 5**. In finite dimensional spaces all norms and topologies induced by them are equivalent, so it only matters for non-parametric regression models. Further studies may focus on the best method for estimating V_2 , for which we have proposed a "mini" bootstrap.

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Contribution: Piotr Chlebicki is the main author responsible for deriving properties of the MI PMM estimators and proving Theorems 1-3. Łukasz Chrostowski was responsible for implementing these and other methods for non-probability samples in the `nonprobsvy` package in the R language. Maciej Beręsewicz was responsible for the initial idea, selected simulation studies and the empirical study and prepared the final version of the manuscript.

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Part I

Appendix

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A Proof of Theorem 2

Proof. Using law of total variance we have:

$$\mathbb{V}[\hat{\mu}] = \frac{1}{N^2 k^2} \mathbb{E} \left[\mathbb{V} \left[\sum_{i \in S_B} \frac{1}{\pi_i} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \middle| \sigma(\{y_i, \hat{\nu}(i,t)\}_{i \in U, t \in \{1, \dots, k\}}) \right] \right] \quad (17)$$

$$+ \frac{1}{N^2 k^2} \mathbb{V} \left[\mathbb{E} \left[\sum_{i \in S_B} \frac{1}{\pi_i} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \middle| \sigma(\{y_i, \hat{\nu}(i,t)\}_{i \in U, t \in \{1, \dots, k\}}) \right] \right]. \quad (18)$$

by Cauchy product (18) can be expressed as:

$$\begin{aligned} & \frac{1}{N^2 k^2} \mathbb{V} \left[\mathbb{E} \left[\sum_{i=1}^N \frac{1}{\pi_i} \mathbb{1}_{\{i \in S_B\}} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \middle| \sigma(\{y_i, \hat{\nu}(i,t)\}_{i \in U, t \in \{1, \dots, k\}}) \right] \right] = \frac{1}{N^2 k^2} \mathbb{V} \left[\sum_{i=1}^N \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right] \\ &= \frac{1}{N^2 k^2} \mathbb{E} \left[\left(\sum_{i=1}^N \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right)^2 \right] - \frac{1}{N^2 k^2} \left(\mathbb{E} \left[\sum_{i=1}^N \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right] \right)^2 \\ &= \frac{1}{N^2 k^2} \mathbb{E} \left[\left(\sum_{i=1}^N \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right) \left(\sum_{j=1}^N \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right) \right] \\ &= \frac{1}{N^2 k^2} \left(\sum_{i=1}^N \mathbb{E} \left[\sum_{t=1}^k y_{\hat{\nu}(i,t)} \right] \right) \left(\sum_{j=1}^N \mathbb{E} \left[\sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right] \right) \\ &= \frac{1}{N^2 k^2} \mathbb{E} \left[\sum_{i=1}^N \sum_{j=1}^N \sum_{t=1}^k \sum_{t'=1}^k y_{\hat{\nu}(i,t)} y_{\hat{\nu}(j,t')} \right] \\ &= \frac{1}{N^2 k^2} \left(\sum_{i=1}^N \sum_{j=1}^N \mathbb{E} \left[\sum_{t=1}^k y_{\hat{\nu}(i,t)} \right] \mathbb{E} \left[\sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right] \right) \\ &= \frac{1}{N^2 k^2} \sum_{i=1}^N \sum_{j=1}^N \sum_{t=1}^k \sum_{t'=1}^k \mathbb{E} [y_{\hat{\nu}(i,t)} y_{\hat{\nu}(j,t')}] \\ &= \frac{1}{N^2 k^2} \left(\sum_{i=1}^N \sum_{j=1}^N \sum_{t=1}^k \sum_{t'=1}^k \mathbb{E} [y_{\hat{\nu}(i,t)}] \mathbb{E} [y_{\hat{\nu}(j,t')}] \right) \\ &= \frac{1}{N^2 k^2} \sum_{i=1}^N \sum_{j=1}^N \sum_{t=1}^k \sum_{t'=1}^k (\mathbb{E} [y_{\hat{\nu}(i,t)} y_{\hat{\nu}(j,t')}] - \mathbb{E} [y_{\hat{\nu}(i,t)}] \mathbb{E} [y_{\hat{\nu}(j,t')}]) \\ &= \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \text{cov} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right) \\ &= \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \text{cov} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right), \end{aligned}$$

which can be estimated by:

$$\frac{1}{N^2} \sum_{i=1}^{n_B} \sum_{j=1}^{n_B} \frac{1}{\pi_{ij}} \widehat{\text{cov}} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right), \quad (19)$$

assuming we have an estimate for:

$$\text{cov} \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right).$$

The remaining term in (17) on the other hand is:

$$\begin{aligned} & \frac{1}{N^2 k^2} \mathbb{E} \left[\mathbb{V} \left[\sum_{i \in S_B} \frac{1}{\pi_i} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \middle| \sigma(\{y_i, \hat{\nu}(i, t)\}_{i \in U, t \in \{1, \dots, k\}}) \right] \right] = \\ & \frac{1}{N^2 k^2} \mathbb{E} \left[\mathbb{V} \left[\sum_{i=1}^N \mathbb{1}_{\{i \in S_B\}} \frac{1}{\pi_i} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \middle| \sigma(\{y_i, \hat{\nu}(i, t)\}_{i \in U, t \in \{1, \dots, k\}}) \right] \right] = \\ & \frac{1}{N^2 k^2} \sum_{i=1}^N \frac{1}{\pi_i^2} \mathbb{E} \left[\sum_{t=1}^k y_{\hat{\nu}(i,t)} \mathbb{V} [\mathbb{1}_{\{i \in S_A\}} \middle| \sigma(\{y_i, \hat{\nu}(i, t)\}_{i \in U, t \in \{1, \dots, k\}})] \right] + \\ & \frac{1}{N^2 k^2} \sum_{\substack{i,j=1 \\ i \neq j}}^N \frac{1}{\pi_i \pi_j} \mathbb{E} \left[\sum_{t', t=1}^k y_{\hat{\nu}(i,t)} y_{\hat{\nu}(j,t')} \text{cov} [\mathbb{1}_{\{i \in S_A\}}, \mathbb{1}_{\{j \in S_A\}} \middle| \sigma(\{y_i, \hat{\nu}(i, t)\}_{i \in U, t \in \{1, \dots, k\}})] \right] = \\ & \frac{1}{N^2 k^2} \sum_{i=1}^N \frac{1}{\pi_i^2} \mathbb{E} \left[\left(\sum_{t=1}^k y_{\hat{\nu}(i,t)} \right)^2 \pi_i (1 - \pi_i) \right] + \\ & \frac{1}{N^2 k^2} \sum_{\substack{i,j=1 \\ i \neq j}}^N \frac{1}{\pi_i \pi_j} \text{cov}(\mathbb{1}_{\{i \in S_A\}}, \mathbb{1}_{\{j \in S_A\}}) \mathbb{E} \left[\sum_{t', t=1}^k y_{\hat{\nu}(i,t)} y_{\hat{\nu}(j,t')} \right] = \\ & \frac{1}{N^2 k^2} \sum_{i=1}^N \frac{1 - \pi_i}{\pi_i} \mathbb{E} \left[\left(\sum_{t=1}^k y_{\hat{\nu}(i,t)} \right)^2 \right] + \\ & \frac{1}{N^2 k^2} \sum_{\substack{i,j=1 \\ i \neq j}}^N \frac{1}{\pi_i \pi_j} \text{cov}(\mathbb{1}_{\{i \in S_B\}}, \mathbb{1}_{\{j \in S_B\}}) \mathbb{E} \left[\sum_{t', t=1}^k y_{\hat{\nu}(i,t)} y_{\hat{\nu}(j,t')} \right], \end{aligned}$$

which (if second order inclusion probabilities are known) can be estimated by:

$$\frac{1}{N^2} \sum_{i \in S_B} (1 - \pi_i) \frac{\left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right)^2}{\pi_i^2} + \frac{1}{N^2} \sum_{i \in S_B} \sum_{\substack{j \in S_B \\ j \neq i}} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}} \frac{\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}}{\pi_i} \frac{\frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')}}{\pi_j}.$$

□

B Proof of Theorem 3

Proof. Let $\hat{\mu}_{HT}$ denote the hypothetical Horvitz-Thompson estimate of μ . Since by virtue of Theorem 1 $|\hat{\mu} - \hat{\mu}_{HT}| \rightarrow 0$ in probability, it also follows that $\hat{\mu} \rightarrow \hat{\mu}_{HT}$ in distribution and therefore:

$$\lim |\mathbb{V}[\hat{\mu}] - \mathbb{V}[\hat{\mu}_{HT}]| = \lim |V_1 + V_2 - \mathbb{V}[\hat{\mu}_{HT}]| = 0$$

in the sequence of samples described in the assumptions underlying Theorem 1. Furthermore:

$$\begin{aligned} \left| \hat{V}_1 - \widehat{\mathbb{V}[\hat{\mu}_{HT}]} \right| &\leq \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_i y_j \right| \\ &\leq \frac{n_B^2}{N^2} \max_{i,j \in S_B} \left\{ \frac{1}{\pi_i \pi_j} \left| 1 - \frac{\pi_i \pi_j}{\pi_{ij}} \right| \right\} \max_{i,j \in S_B} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_i y_j \right| \\ &\leq \frac{n_B^2}{N^2} \max_{i,j \in S_B} \{ \pi_{ij}^{-1} \} \max_{i,j \in S_B} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_i y_j \right| \end{aligned}$$

By elementary inequalities:

$$\begin{aligned} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_i y_j \right| &= \\ \left| \left(\frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i \right) \left(\frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right) - 2y_i y_j + y_i \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} + y_j \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right| &\leq \\ \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i \right| \left| \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right| + \left| y_i \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} + y_j \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - 2y_i y_j \right| & \end{aligned}$$

continuing this sequence:

$$\left| y_i \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} + y_j \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - 2y_i y_j \right| \leq$$

$$\left| y_i \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_i y_j \right| + \left| y_j \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i y_j \right| \leq |y_i| \left| \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right| + |y_j| \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i \right|$$

so if $\max_{i,j \in S_B} \left\{ \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}} \right\}$ is bounded:

$$\begin{aligned} & \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_i y_j \right| \leq \\ & \underbrace{\frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i \right| \left| \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right|}_{\xrightarrow{n_A \rightarrow \infty} 0} + \\ & \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} |y_i| \left| \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right| + \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} |y_j| \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i \right| \end{aligned}$$

the second line follows from:

$$\begin{aligned} & \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i \right| \left| \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right| \leq \\ & \max_{i,j \in S_B} \left\{ \left| \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}} \right| \right\} \frac{1}{N} \sum_{i \in S_B} \frac{1}{N} \frac{1}{\pi_i} \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i \right| \sum_{j \in S_B} \frac{1}{\pi_j} \left| \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right| \end{aligned}$$

which is a product of a essentially bounded random variable and two random variables converging to 0 in probability. By consistency of (3) and consistency of HT estimator for $\frac{1}{N} \sum_{i=1}^N |y_i|$:

$$\begin{aligned} & \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} |y_i| \left| \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right| + \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} |y_j| \left| \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} - y_i \right| \leq \\ & 2 \max_{i,j \in S_B} \left\{ \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij}} \right\} \underbrace{\frac{1}{N} \sum_{i \in S_B} \frac{|y_i|}{\pi_i}}_{\xrightarrow{n_A \rightarrow \infty} \frac{1}{N} \sum_{i=1}^N |y_i|} \underbrace{\frac{1}{N} \sum_{j \in S_B} \frac{1}{\pi_j} \left| \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} - y_j \right|}_{\xrightarrow{n_A \rightarrow \infty} 0} \end{aligned}$$

since by assumption $\widehat{\mathbb{V}}[\widehat{\mu}_{HT}] \rightarrow \mathbb{V}[\hat{\mu}_{HT}]$, $|V_1 + V_2 - \mathbb{V}[\hat{\mu}_{HT}]| \rightarrow 0$ and by inequalities above $|\hat{V}_1 - \widehat{\mathbb{V}}[\widehat{\mu}_{HT}]| \rightarrow 0$ it follows that $|V_1 + V_2 - \hat{V}_1| \rightarrow 0$. \square

C Additional simulations

C.1 Simple procedure for choosing k hyper-parameter

In this simulation study we provide evidence for choosing the k hyper-parameter. We consider the following study design:

- Population size: $N = 100,000$,
- Probability sample size: $n_B = 500$,
- Expected non-probability sample size: $\mathbb{E}[n_A/N] \approx 0.20$,
- X_1 was generated from the multivariate normal distribution transformed to 1d vector (the reason for that was to introduce correlation between observations):

$\left(\mathbf{Z}_1^T \quad \mathbf{Z}_2^T \quad \dots \quad \mathbf{Z}_{N/5}^T \right)$ where $\mathbf{Z}_k \sim \mathcal{N}_5 \left(\left(\begin{pmatrix} 1 & 1 & 1 & 1 & 1 \end{pmatrix}^T, \Sigma \right) \right)$ (\mathbf{Z}_k being i.i.d) with

$$\Sigma = \begin{pmatrix} 1 & U_{12} & U_{13} & U_{14} & U_{15} \\ U_{12} & 1 & U_{23} & U_{24} & U_{25} \\ U_{13} & U_{23} & 1 & U_{34} & U_{35} \\ U_{14} & U_{24} & U_{34} & 1 & U_{45} \\ U_{15} & U_{25} & U_{35} & U_{45} & 1 \end{pmatrix}$$

in setting where $U_{12}, \dots \sim \mathcal{U} \left(-\frac{1}{2}, \frac{1}{2} \right)$ i.i.d.,

- $X_2 \sim \text{Exp}(1)$ i.i.d,
- Vector of ϵ 's analogously to x_1 being $\left(\mathbf{R}_1^T \quad \mathbf{R}_2^T \quad \dots \quad \mathbf{R}_{N/5}^T \right)^T$ where $\mathbf{R}_k \sim \mathcal{N}_5(\mathbf{0}, \Sigma)$ and $U_{12}, \dots \sim \mathcal{U}(-0.7, 1)$ i.i.d.,
- We generated two vector of probabilities for selection into the non-probability sample $p_1 = \frac{\exp(x_2)}{1 + \exp(x_2)}$ and $p_2 = \frac{\exp(x_1)}{1 + \exp(x_1)}$,
- The inclusion into non-probability sample S_A was generated as

$$\delta = \min \left\{ \text{Bernoulli}(p_1), \text{Bernoulli}(p_2), \mathbb{1}_{\{\epsilon > \epsilon_{.8}\}} + \mathbb{1}_{\{\epsilon < \epsilon_{.2}\}} \right\}$$

where ϵ_t is an empirical quantile of ϵ of order t .

- Two target variables were generated according to the following formulas:

$$Y_1 = 1 + \frac{1}{2}x_1 + \frac{35}{100}x_2 + \epsilon$$

$$Y_2 = 1.2 + (x_1 - 0.5)^2 + \arctan(x_2)^{3+\sin(x_1+x_2)} + \sin(x_1) \cos(x_2) + \epsilon$$

and k being chosen by minimising $\widehat{\mathbb{V}}[\hat{\mu}]$ in each simulation iteration.

We consider three estimators discussed in the paper: MI-GLM, PMM A ($\hat{y} - y$ matching) and PMM B ($\hat{y} - \hat{y}$ matching) with fixed $k = 5$ and dynamic selection of k .

Table C.1 shows the results of the simulation study. As regards the first variable (Y_1), slight differences are observed between the estimators under consideration. The dynamic selection is characterised by a smaller bias and a slightly better RMSE for the PMM A estimator. In the case of the highly non-linear variable Y_2 , both MI-GLM and PMM A estimators are significantly biased, while PMM B with either dynamic or fixed k is characterised by negligible bias. In addition, PMM B with dynamic selection of k is characterised by a smaller RMSE.

Table C.1: Results for the simulation study on choosing of k hyper-parameter (all measures multiplied by 100)

Variable	Estimator	k -selection	Bias	SE	RMSE	CR
Y1	MI-GLM	–	0.2132	3.1015	3.1088	95.40
	PMM A	Dynamic	0.2117	3.1022	3.1094	90.80
	PMM A	Fixed	0.2133	3.1018	3.1092	95.40
	PMM B	Dynamic	0.4676	5.2867	5.3073	99.60
	PMM B	Fixed	0.5688	5.2856	5.3161	99.40
Y2	MI-GLM	–	-20.2760	8.0450	21.8137	26.00
	PMM A	Dynamic	-20.2724	8.0422	21.8094	26.20
	PMM A	Fixed	-20.2698	8.0420	21.8069	26.20
	PMM B	Dynamic	-0.7583	9.3356	9.3664	96.20
	PMM B	Fixed	-0.7613	9.4749	9.5054	97.20

C.2 Simulation with variable selection

In this case our study designs follows that proposed by Yang, Kim, and Song (2020):

- finite population size was set to $N = 10000$,
- for each unit we generate $X_i = \begin{pmatrix} 1 & X_{1,i} & \dots & X_{p-1,i} \end{pmatrix}^T$ where $p = 50$ and $X_{i,t} \sim \mathcal{N}(0, 1)$ i.i.d for each i and $t = 0, \dots, p-1$,
- from the finite population, we select a non-probability sample \mathcal{A} of size $n_A \approx 2000$, according to the selection indicator $I_{A,i} \sim \text{Bernoulli}(\pi_{A,i})$,
- we select a probability sample \mathcal{A} of the average size $n_B = 500$ under Poisson sampling with $\pi_{B,i} \propto (0.25 + |X_{1,i}| + 0.03 |Y_i|)$ (we have 4 set of π_B as we have 4 Y variables defined below),
- for the non-probability sample inclusion probability, we consider both linear and non-linear sampling score models:

$$\begin{aligned}
 & - \text{logit}(\pi_{B,i}) = \alpha_0^T X_i, \text{ where } \alpha_0 = \begin{pmatrix} -2 & 1 & 1 & 1 & 1 & 0 & 0 & \dots & 0 \end{pmatrix}^T \text{ (model PSM I)} \\
 & - \text{logit}(\pi_{B,i}) = 3.5 + \alpha_0^T \log(X_i^2) - \sin(X_{3,i} + X_{4,i}) - X_{5,i} - X_{6,i}, \\
 & \quad \text{where } \alpha_0 = \begin{pmatrix} 0 & 0 & 0 & 3 & 3 & 3 & 3 & 0 & \dots & 0 \end{pmatrix}^T \text{ (model PSM II)}
 \end{aligned}$$

- to generate a continuous outcome variable Y_i , we consider both linear and non-linear outcome models with $\beta_0 = \begin{pmatrix} 1 & 0 & 0 & 1 & 1 & 1 & 1 & 0 & \dots & 0 \end{pmatrix}^T$
 - $Y_i = \beta_0^T X_i + \epsilon_i, \epsilon_i \sim \mathcal{N}(0, 1)$ i.i.d (model OM I, denoted as Y_{11}),
 - $Y_i = 1 + \exp(3 \sin(\beta_0^T X_i)) + X_{5,i} + X_{6,i} + \epsilon_i, \epsilon_i \sim \mathcal{N}(0, 1)$ i.i.d (model OM II, denoted as Y_{12}),
- to generate a binary outcome variable Y_i , we consider both linear and non-linear outcome models with $\beta_0 = \begin{pmatrix} 1 & 0 & 0 & 3 & 3 & 3 & 3 & 0 & \dots & 0 \end{pmatrix}^T$:
 - $Y_i \sim \text{Bernoulli}(\pi_Y(X))$ with $\text{logit}(\pi_Y(X)) = \beta_0^T X$ (model OM III, denoted as Y_{21}),
 - $Y_i \sim \text{Bernoulli}(\pi_Y(X))$ with $\text{logit}(\pi_Y(X)) = 2 - \log((\beta_0^T X)^2) + 2X_{5,i} + 2X_{6,i}$ (model OM IV, denoted as Y_{22}).

- variable selection was done using SCAD penalty.

Table C.2 shows the results of the simulation study with variable selection. As expected, when the model is linear (OM I and OM III), MI-GLM and PMM B ($\hat{y} - \hat{y}$ matching) are almost unbiased with coverage close to the nominal rate. The only difference is the PMM A ($\hat{y} - y$ matching) estimator, which is characterised by greater bias for both linear and non-linear selection mechanisms. Variable selection reduces the bias and slightly reduces the standard error for the estimators discussed. As a result, the RMSE for OM I and OM III is slightly lower than without variable selection.

Table C.2: Results of the simulation with variable selection (all numbers multiplied by 100)

Estimator	Selection	Linear PS (PSM I)				Non-linear PS (PSM II)			
		Bias	SE	RMSE	CR	Bias	SE	RMSE	CR
Y ₁₁ (OM I)									
MI-GLM	No	-0.24	10.18	10.18	95.00	-0.61	9.75	9.77	96.20
	Yes	-1.03	9.97	10.02	95.60	-0.80	9.78	9.81	96.20
PMM A	No	0.03	10.12	10.12	93.80	-0.61	9.75	9.77	95.20
	Yes	-0.74	9.93	9.96	94.60	-0.79	9.77	9.80	95.60
PMM B	No	0.55	10.22	10.24	93.40	-0.92	10.04	10.08	95.20
	Yes	-0.11	9.91	9.92	94.40	-0.77	10.11	10.14	94.80
Y ₁₂ (OM II)									
MI-GLM	No	82.55	23.62	85.87	8.40	-122.37	11.40	122.90	0.00
	Yes	87.80	20.49	90.16	2.20	-119.18	10.25	119.62	0.00
PMM A	No	82.55	23.63	85.86	0.00	-122.38	11.40	122.91	0.00
	Yes	87.69	20.56	90.07	0.00	-119.21	10.27	119.65	0.00
PMM B	No	84.41	29.09	89.28	4.40	-121.89	20.25	123.56	0.00
	Yes	88.87	27.74	93.10	2.40	-111.56	20.14	113.36	0.00
Y ₂₁ (OM III)									
MI-GLM	No	0.27	1.97	1.99	96.60	0.29	1.54	1.57	97.00
	Yes	0.38	1.75	1.79	96.60	0.33	1.52	1.55	97.40
PMM A	No	4.60	2.91	5.44	52.20	4.76	2.40	5.33	52.00
	Yes	5.19	2.73	5.87	43.40	5.47	2.40	5.97	38.60
PMM B	No	0.20	2.18	2.18	89.80	0.53	1.78	1.86	93.40
	Yes	0.45	1.96	2.01	92.60	0.64	1.76	1.87	92.20
Y ₂₂ (OM IV)									
MI-GLM	No	0.84	2.06	2.23	94.20	-7.39	1.67	7.57	2.40
	Yes	1.47	1.94	2.44	87.80	-7.42	1.65	7.60	1.40
PMM A	No	3.36	2.66	4.28	69.60	-5.52	2.57	6.09	44.60
	Yes	4.18	2.52	4.88	55.60	-5.32	2.60	5.92	48.00
PMM B	No	0.82	2.20	2.35	89.00	-8.16	1.85	8.36	0.40
	Yes	1.45	2.10	2.56	83.20	-8.23	1.93	8.45	1.40

In the case of non-linear OM II and OM IV, all the proposed estimators are characterised by large bias and variance. Furthermore, in this case variable selection leads to inconclusive results.

For example, for the linear PSM I and OM II, variable selection increases the bias, but for some models it reduces the standard error. For the non-linear PSM II, bias and standard error are slightly reduced. In the case of binary (OM IV) and linear selection (PSM I), the MI-GLM and PMM B estimators have a coverage close to nominal, but variable selection increases bias while decreasing standard error. For this combination, the RMSE is larger for the estimators with variable selection. For non-linear selection (PSM II), all estimators are significantly biased and the coverage is close to zero, except for the PMM A estimator.

C.3 Non-parametric regression methods

In this section we check the performance of the PMM estimators with non-parametric regression through LOESS via `stats::loess` function in R with the following specification to boost performance:

- `loess.control(surface="interpolate")` – surface approximation using a KD-tree ,
- `loess.control(trace.hat="interpolate")` – approximated trace of the smoother matrix,
- span set to 0.2.

We adapt the same setting as in section C.1 and define additional target variable $Y_3 = x_1x_2\epsilon$. Table C.3 shows the results of this simulation study. As expected, the proposed PMM estimators based on non-parametric regression are characterised by negligible bias, but the variance is significantly larger than that of the MI-GLM estimator for Y_1 . As expected, the bias and variance for MI-GLM are large compared to the non-parametric PMM estimators for non-linear variables (Y_2 and Y_3). Note that the PMM B ($\hat{y} - \hat{y}$ matching) estimator is almost unbiased even when the target variables are highly non-linear. Owing to large standard errors for the last variable, the coverage is close to 100%.

Table C.3: Results for the simulation study with non-parametric predictive mean matching models (all numbers multiplied by 100)

Y	Estimator	Non-parametric?	Bias	SE	RMSE	CR
Y1	MI-GLM	No	0.31	2.93	2.95	97.60
	PMM A	No	0.31	2.93	2.95	97.23
		Yes	-0.36	3.08	3.10	97.23
	PMM B	No	0.46	5.18	5.20	99.82
		Yes	0.32	5.19	5.20	99.63
Y2	MI-GLM	No	-19.93	7.61	21.33	25.65
	PMM A	No	-19.93	7.61	21.33	25.28
		Yes	2.41	8.64	8.97	94.10
	PMM B	No	-1.05	9.02	9.08	97.97
		Yes	-1.57	9.15	9.28	97.05
Y3	MI-GLM	No	59.41	7.61	59.90	100.00
	PMM A	No	0.83	1.28	1.52	100.00
		Yes	-2.24	5.08	5.55	99.45
	PMM B	No	1.22	9.61	9.69	99.82
		Yes	1.51	9.93	10.04	99.63

C.4 Violation of the positivity assumption

In this section we check the performance of the proposed estimators when the positivity assumption is violated. We consider the same settings as in section C.1 with additional X_3 variable and effects connected with this variable.

- $X_3 \sim \text{NegBin}(\mu = 10, r = 4)$ and then numbers over 40 were grouped into one category "40",

- we created two target variables:

$$\begin{aligned} - Y_1 &= -7 + 6X_1 - 5X_2 + X_3^T \gamma + 15\epsilon, \\ - Y_2 &= -2 + 0.37 \cdot (X_1 - 0.5)^2 + X_2^2 + X_3^T \gamma + 5\epsilon, \end{aligned}$$

where $\gamma \sim \mathcal{U}(-6, 10)$ are coefficients associated with each level of X_3 variable (40 possible levels),

- we consider two scenarios for under-coverage:
 - *Stochastic*: where the samplable sub-population is generated from $\text{Binomial}(\pi_u)$ where $\text{logit}(\pi_u) = X_3^T \lambda$ and $\lambda = \begin{pmatrix} 0.75 & 0.72 & \dots & 0.10 \end{pmatrix}^T$, so the larger the X_3 the less likely to be observed in the sub-population.
 - *Deterministic*: where the samplable sub-population is generated in the following process:
 - * target variable π_u is defined as $\text{logit}(\pi_u) = 0.84 + 0.32X_1 + 0.68X_2 + X_3^T \lambda$ where λ is defined above,
 - * inclusion indicator was generated as $\mathbb{1}_{\{\pi_u > Q_{\pi_u, 0.25}\}}$, where $Q_{\pi_u, 0.25}$ is the 25% percentile of π_u .
- probabilities of inclusion in the non-probability sample from the under-represented populations were defined as follows:
 - *Stochastic*: $\text{logit}(p_i) = X_2 - X_1 - 2$, so the expected size is about 17% of the population.
 - *Deterministic*: $\text{logit}(p_i) = 0.6X_1 - X_2 - 2$, so the expected size is about 20% of the population.

Table C.4 shows the results of the simulation study when the positivity assumption is violated. For the linear Y_1 all the estimators yield the same results with slightly lower bias for the PMM B ($\hat{y} - \hat{y}$ fit). However, the PMM B suffers from larger standard errors and, as a result, the standard error and RMSE are larger for deterministic and stochastic results and the CR is close to 100%. For the non-linear Y_2 , the main difference exists for deterministic under-coverage. The bias of PMM B is lower than that of the MI-GLM and PMM A estimators and the standard error is comparable. Under this scenario, coverage is the highest (about 67%), but still does not reach the nominal level of 95%. In the case of stochastic under-coverage, the proposed estimators are comparable to the MI-GLM estimator, with a slightly smaller bias for the PMM B estimator.

Table C.4: Results of the simulation study when the positivity assumption is violated (results multiplied by 100)

Variable	Under-coverage	Estimator	Bias	SE	RMSE	CR
Y1	Deterministic	MI-GLM	0.36	43.17	43.17	96.20
		PMM A	0.36	43.17	43.17	96.20
		PMM B	2.44	62.25	62.30	99.20
	Stochastic	MI-GLM	1.96	43.36	43.40	96.40
		PMM A	1.96	43.36	43.40	96.40
		PMM B	2.92	60.49	60.56	98.80
Y2	Deterministic	MI-GLM	-84.66	32.60	90.72	29.40
		PMM A	-84.66	32.60	90.72	29.40
		PMM B	-60.20	33.37	68.83	71.20
	Stochastic	MI-GLM	11.21	30.93	32.90	94.20
		PMM A	11.21	30.93	32.90	94.00
		PMM	5.89	31.54	32.09	98.20

The deterministic case is supposed to mirror online sampling (or sampling via telephone connection) where a unit can only be sampled if it has the internet connection (a telephone number). Such cases usually depend on age, mirrored by X_3 , and, to a smaller extent, on social status, which may be correlated with covariates. Note that despite the violation of the positivity assumption in the deterministic case $\mathbb{P}[\delta = 1 | \mathbf{X}, Y] = \mathbb{P}[\delta = 1 | \mathbf{X}]$ a.s is maintained. In the case of stochastic under-coverage, the selection of units to the non-probability sample can be viewed as a two-stage sampling process; in this case, positivity is not violated, which explains good results of the MI-GLM estimator.

C.5 Multiply robust imputation

In this section we test whether the approach proposed by Chen, Haziza, and Stubblefield (2021) is suitable for non-probability samples. They proposed multiply robust imputation using predictive mean matching, where predictions from multiple models are used as independent variables. In this section we follow the same design as that described in section C.1 but we create two target variables as follows:

- $Y_1 = 1 + \frac{1}{5}x_1 + 5x_2 + \epsilon$,
- $Y_2 = -2 + 5(x_1 - 0.5)^5 + x_2^3 + \epsilon$.

For both models we consider two regression models:

- Model 1: linear regression with x_1 and x_2 ,
- Model 2: linear regression with $(x_1 - 0.5)^5$ and x_2^3 ,

so that for each model, one of the models considered is correctly specified. For both PMM estimators without the multirobust property, we used a linear model with x_1 and x_2 .

Table C.5: Results for the simulation study with multiply robust predictive mean matching

Variable	Estimator	MultiRobust	Bias	SE	RMSE	CR
Y_1	MI-GLM	–	0.00	0.23	0.23	93.60
	PMM A	No	0.00	0.23	0.23	93.60
		Yes	0.00	0.23	0.23	93.60
	PMM B	No	0.00	0.23	0.23	94.00
		Yes	0.00	0.23	0.23	94.40
	MI-GLM	–	-17.40	6.37	18.53	22.60
Y_2	PMM A	No	-17.30	6.36	18.43	23.60
		Yes	0.40	9.49	9.50	92.20
	PMM B	No	-1.33	8.77	8.87	90.80
		Yes	0.40	9.49	9.50	92.20
	MI-GLM	–	-17.40	6.37	18.53	22.60
	PMM A	No	-17.30	6.36	18.43	23.60

Table C.5 contains the results for multiply robust predictive mean matching. All linear estimators are characterised by the same bias, SE, RMSE and CR. Differences can be observed for the non-linear Y_2 . MI-GLM and the standard PMM A are characterised with the same bias and RMSE, while the addition of multiplicative robustness to the PMM A estimator significantly reduces its bias. For the PMM B estimator, it does not matter whether the fitting is done with a linear model with x_1 and x_2 or with predictions from the two models considered.

In this limited simulation study none of the models for Y_2 reached the nominal coverage rate of 95%.

D Implementation in the R language

The proposed methods are implemented in the R language in the `nonprobsvy` package. One should install the package from the github repository using the following code:

```
install.packages("remotes")
remotes::install_github("ncn-foreigners/nonprobsvy")
```

Below we present functions for the PMM estimator under specific settings. In general, the user should change the following arguments:

- `method_outcome = "pmm"` – specification that the PMM estimator is used
- `controlOut` – controls for MI estimator
 - `k` – number of nearest neighbours,
 - `predictive_match` – whether $\hat{y} - y$ ($=1$; PMM A) or $\hat{y} - \hat{y}$ ($=2$; PMM B) matching should be used.
- `controlInf` – controls for inference (variance estimation)
 - `pmm_exact_se` – whether \hat{V}_2 should be estimated using "mini" bootstrap ($=\text{TRUE}$) or not ($=\text{FALSE}$).

Example codes are shown below.

- Predictive mean matching with $\hat{y} - y$ matching (PMM A) with \hat{V}_2 estimated using "mini"-bootstrap presented in Section 3.

```
PMM_A <- nonprob(  
  outcome = y1 ~ x1 + x2,  
  data = sample_nonprob,  
  svydesign = sample_prob,  
  method_outcome = "pmm",  
  family_outcome = "gaussian",  
  control_outcome = controlOut(k = 5,  
                                predictive_match = 1),  
  control_inference = controlInf(pmm_exact_se = TRUE)  
)
```

- Predictive mean matching with $\hat{y} - \hat{y}$ matching (PMM B) with \hat{V}_2 estimated using "mini"-bootstrap presented in Section 3.

```
PMM_B <- nonprob(  
  outcome = y1 ~ x1 + x2,  
  data = sample_nonprob,  
  svydesign = sample_prob,  
  method_outcome = "pmm",  
  family_outcome = "gaussian",  
  control_outcome = controlOut(k = 5,  
                                predictive_match = 2),  
  control_inference = controlInf(pmm_exact_se = TRUE)  
)
```

- Predictive mean matching with $\hat{y} - \hat{y}$ matching with local linear regression (PMM B) with \hat{V}_2 estimated using "mini"-bootstrap presented in Section 3.

```

PMM_B <- nonprob(
  outcome = y1 ~ x1 + x2,
  data = sample_nonprob,
  svydesign = sample_prob,
  method_outcome = "pmm",
  family_outcome = "gaussian",
  control_outcome = controlOut(k = 5,
                                predictive_match = 2,
                                pmm_reg_engine = "loess"),
  control_inference = controlInf(pmm_exact_se = TRUE)
)

```