

# 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 predicted ( $\hat{y} - \hat{y}$  matching; PMM A) and predicted to observed ( $\hat{y} - y$  matching; PMM B) values. We prove the consistency of two semi-parametric mass imputation estimators based on these approaches and derive their variance and estimators of variance. We underline the differences of our approach with the nearest neighbour approach proposed by Yang, Kim, and Hwang (2021) and prove consistency of the PMM A estimator under model mis-specification. 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 (for recent review see 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 (this is the  $\xi p$  framework as discussed by Wu (2022)).

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 of 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, the 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: matching either by predicted-predicted ( $\hat{y} - \hat{y}$ ) or predicted-observed ( $\hat{y} - y$ ) values. The first option is the standard PMM estimator, which is used in most of the existing studies, while the first one is less commonly discussed. The motivation for the  $\hat{y} - y$  is based on its performance when continuous variables are used and the model is correctly specified. Moreover, we discuss mixed matching that involves both cases.
2. We prove the consistency of these estimators under suitable assumptions where population size is either known or estimated. We provide proof for consistency of the  $\hat{y} - \hat{y}$  estimator under mis-specified model. The theorem can easily be extended to non-parametric models, such as Nadaraya–Watson kernel regression or even simple artificial neural networks. We also prove consistency when the model is mis-specified.
3. We derive analytic variance estimators and study their performance (along bootstrap estimators) 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 large non-probability sample behaviour of the variance estimator.

In the paper, we discuss the significant differences between the PMM estimator based on  $\hat{y} - \hat{y}$  matching and NN estimator. The two are identical only in one very special case, when the *assumed* model is linear and depends on a single covariate. Of particular importance is the fact that predictive mean matching approach resolves the curse of dimensionality and uses less restrictive assumptions than the NN estimator. Our rigorous approach to study properties of the two proposed PMM estimators is different from those in the Yang, Kim, and Hwang (2021).

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  $\mathbf{X}_i$  in the super-population) and the study variable  $y_i$  (a realisation of the random variable  $Y_i$  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  $\pi$  are available. Let  $\delta$  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  $d_i = 1/\pi_i$ . 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  $\mu_y$ . In this paper we do not consider modifications for the possibly occurring overlap.

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  $d$  denote a bivariate distance function on  $\mathbb{R}$  (a semi-metric). The estimators we are interested in are a result of the following algorithm:

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**Algorithm 1:** Two predictive mean matching imputation algorithms

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1 Estimate  $\beta$  in regression model  $\mathbb{E}[Y|\mathbf{X} = \mathbf{x}] = m(\mathbf{x}, \beta)$ .

2A ( $\hat{y} - \hat{y}$  imputation; PMM A) Impute  $\hat{y}_i = m(\mathbf{x}_i, \hat{\beta})$ ,  $\hat{y}_j = m(\mathbf{x}_j, \hat{\beta})$  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:

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

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

2B ( $\hat{y} - y$  imputation; PMM B) Impute  $\hat{y}_i = m(\mathbf{x}_i, \hat{\beta})$  for  $i \in S_B$  and map each  $i \in S_B$  to  $\hat{\nu}(i)$  where  $\hat{\nu}(i) = \arg \min_{j \in S_A} d(\hat{y}_i, y_j)$ .

If  $k > 1$  instead let:

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

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:

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


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We denote the  $k$  nearest neighbours for unit  $i$  by  $\hat{\nu}(i, t), t = 1 \dots, k$  to emphasise that it is a random variable with values in the index space.

Algorithm 1 (without step 2B) represents the standard  $\hat{y} - \hat{y}$  matching and throughout the paper this estimator is denoted as the  $\hat{y} - \hat{y}$  or as the PMM A estimator. The resulting estimator is given by the same expression (3) but the matching is done differently.

Algorithm 1 (without step 2A) 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) and throughout the paper this estimator is denoted as the  $\hat{y} - y$  or the PMM B estimator.

### 2.3 Comparison with the nearest neighbour imputation approach

If we let  $m(\mathbf{x}_i, \boldsymbol{\beta}) = m(x_i, \beta) = x_i\beta$  i.e. use only one covariate, the resulting estimator (3) for  $\hat{y} - \hat{y}$  matching is exactly the nearest neighbour estimator, since linear scaling preserves distances on  $\mathbb{R}_+$ . This is the only case in which these two coincide. When  $m$  is linear regression and  $d$  is a Euclidean distance the  $\hat{y} - \hat{y}$  matching could be thought of as a "pseudo-nearest neighbour" matching with a weighted (by estimated regression coefficients) distance function  $d' : (\mathbf{z}_i, \mathbf{z}_j) \mapsto \left| (\mathbf{z}_i - \mathbf{z}_j)^T \hat{\boldsymbol{\beta}} \right|$  which expands to (if we use  $\mathbb{X}$  to denote the matrix of covariates on  $S_A$  and  $\mathbf{Y}$  to denote the vector of response variables in  $S_A$ ):

$$d'(\mathbf{z}_i, \mathbf{z}_j) = \left| (\mathbf{z}_i - \mathbf{z}_j)^T \left( \sum_{t \in S_A} \mathbf{X}_t \mathbf{X}_t^T \right)^{-1} \sum_{t \in S_A} \mathbf{X}_t^T Y_t \right|,$$

which depends on  $y$  values from  $S_A$  and therefore one cannot simply assert that the  $\hat{y} - \hat{y}$  matching estimator inherits properties from the NN estimator since it requires the distance function to be deterministic. Similarly in general case of GLM regression with link function  $g$  the distance (in general not a metric) is given by:

$$d'(\mathbf{z}_i, \mathbf{z}_j) = \left| g^{-1} \left( \mathbf{z}_i^T \hat{\boldsymbol{\beta}} \right) - g^{-1} \left( \mathbf{z}_j^T \hat{\boldsymbol{\beta}} \right) \right|,$$

with  $\hat{\boldsymbol{\beta}}$  depending on the values of  $(Y, \mathbf{X})$  from  $S_A$ . In contrast the PMM B estimator based on the  $\hat{y} - y$  matching does not coincide with NN in any widely recognizable general setting.

In general despite similarity of PMM and NN in description of the algorithm there are more differences than similarities between properties of their corresponding imputations. One key difference is that PMM does not suffer from curse of dimensionality since our assumptions do

not place much restrictions on the number of covariates, if fact assumptions for  $\hat{y} - y$  matching are more readily attainable with higher number of covariates (cf. Yang and Kim (2020)). Moreover, we do not require positivity on contrary to the NN estimator and later on we show in simulation studies in Appendix C.4 that the PMM estimators works well under stochastic and deterministic under-coverage (with one exception).

**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 2 but may have comparatively poor finite sample properties in practice.*

## 2.4 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)  $\mathbb{E}[Y_i | \mathbf{X}_i] = m(\mathbf{X}_i, \beta_0)$  almost surely for some  $\beta_0 \in \mathbb{R}^p$  and continuous  $m$  (as a functional from  $\mathbb{R}^p \times \mathbb{R}^p$ ), with  $\hat{\beta}$  being a consistent estimator for  $\beta_0$ . In the Appendix A.1 we provide assumptions for this estimator.

(A2) We require that 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:

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

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  $\sigma$ -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) 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:

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

A necessary and sufficient condition for this assumption to hold is:

$$\mathbb{V} \left[ \sum_{i=1}^N (m(\mathbf{X}_i, \boldsymbol{\beta}_0) - Y_i) \right] = o(N^2), \text{ when: } N \rightarrow \infty.$$

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

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

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 the super population is such that:

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

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

Assumption (A3) describes a setting in which we explore consistency and is not important for finite sample performance.

## 2.5 Discussion regarding the assumptions

### 2.5.1 Distributions of covariates

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, one covariate  $x_j$  has support on the whole real line and  $m(\cdot, \boldsymbol{\beta})$  depends on this covariate and closure of the range of function  $x_j \mapsto m(\mathbf{x}, \boldsymbol{\beta})$  contains the support of  $Y$  such as in the case of logistic regression where closure of the range of:

$$x_j \mapsto (1 + \exp(-\beta_0 - \beta_1 x_1 - \dots - \beta_j x_j - \dots - \beta_p x_p))^{-1},$$

is  $[0, 1] \supseteq \{0, 1\}$ .

A reasonable question is whether assumption (C2) can be proved from other assumptions. The answer is negative since we can take  $Y$  such that  $\forall i = 1, \dots, N : Y_i | \mathbf{X}_i \sim \mathcal{N}(m(\mathbf{X}_i, \boldsymbol{\beta}_0), N)$  independently given  $\mathbf{X}_1, \dots, \mathbf{X}_N$ . Then:

$$\frac{1}{N} \sum_{i=1}^N (Y_i - m(\mathbf{X}_i, \boldsymbol{\beta}_0)) \Bigg| \mathbf{X}_1, \dots, \mathbf{X}_N \sim \mathcal{N}(0, N),$$

and therefore  $\frac{1}{N} \sum_{i=1}^N (Y_i - m(\mathbf{X}_i, \boldsymbol{\beta}_0))$  does not converge to 0 in distribution nor in probability. Nevertheless is strictly necessary since we have the following Theorem (proof is given in the Appendix [A.2](#)):

**Theorem 1.** *If (A4) does not hold then there does not exists  $(\sigma(\mathbf{X}_1, \dots, \mathbf{X}_N))_{N \in \mathbb{N}}$  adapted sequence of random variables  $(\hat{\mu}_N)_{N \in \mathbb{N}}$  that converges to  $\mu$  in probability.*

Theorem 1 tells us that it is not possible to build a consistent estimator using only covariates. Moreover since a priori it may happen that  $\mathbb{E}[Y_i | Y_j, \mathbf{X}_i] = \mathbb{E}[Y_i | \mathbf{X}_i]$  and we cannot (a priori) know whether all *problem units* denoted by  $\Gamma$  i.e. those whose exclusion would cause

$$\frac{1}{N} \sum_{i \notin \Gamma} (Y_i - m(\mathbf{X}_i, \boldsymbol{\beta}_0)) \rightarrow 0 \text{ in probability,}$$

are in  $S_A$ . If we accept this heuristic argument then there is not potential estimate based on pure mass imputation that would be consistent. A potential remedy to violation of (C2) is to add more relevant covariates to the model.

### 2.5.2 Restrictions on non-probability sampling

In proving consistency we do not assume positivity, contrary to Kim et al. (2021) and Yang, Kim, and Hwang (2021). Instead a very weak assumption (A2) on the quality of non-probability sampling (which is much harder to violate than it is to satisfy) is required and less restrictive assumptions (B1)/(C1) depending on the PMM estimator.

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 or via dependence on some unobserved variables, 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 tends 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  $\mathbf{x}_j$  corresponding to these  $k$  units will be no greater than  $\varepsilon$ .

## 3 Main results

### 3.1 Consistency under correctly specified model

The proof strategy, which is a standard strategy for non-probability samples, can essentially be reduced to first proving that (3) and the Horvitz-Thompson (HT) estimator (which we cannot construct) 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 2.** *If (C1), (A2), (A3) hold and the model is correctly specified then mass imputation estimator:*

$$\hat{\mu}_{MI} = \sum_{i \in S_B} \frac{1}{\pi_i} m(\mathbf{X}_i, \hat{\boldsymbol{\beta}})$$

*consistent when and only when  $\hat{y} - y$  matching estimator in (3) is consistent. Moreover assumptions (A1), (A4) are sufficient for this consistency.*

*Proof.* Sufficiency of (A1) and (A4) is clear since:

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \left( m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) - Y_i \right) \right| \leq \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \left( m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) - m(\mathbf{X}_i, \boldsymbol{\beta}_0) \right) \right| \quad (4)$$

$$+ \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} (m(\mathbf{X}_i, \boldsymbol{\beta}_0) - Y_i) \right|, \quad (5)$$

where (5) converges to 0 by (A4) and (4) converges to 0 by (A1) since:

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} (m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) - m(\mathbf{X}_i, \boldsymbol{\beta}_0)) \right| \leq \max_{i \in S_B} \left( \frac{n_B}{N\pi_i} \right) \max_{i \in S_B} |m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) - m(\mathbf{X}_i, \boldsymbol{\beta}_0)|$$

which converges to 0 by consistency of  $\hat{\boldsymbol{\beta}}$ . Now to prove that consistency of  $\hat{\mu}_{\text{MI}}$  is sufficient notice that, by triangle inequality we have that:

$$\begin{aligned} \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)} - \sum_{i \in S_B} \frac{1}{\pi_i} Y_i \right| &\leq \\ \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \left( \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)} - m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) \right) \right| &+ \underbrace{\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} (m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) - Y_i) \right|}_{\xrightarrow{n_A \rightarrow \infty} 0 \text{ in probability}}. \end{aligned} \quad (6)$$

Notice that from the continuity of  $m$  we have the following implications:

$$\begin{aligned} \forall \varepsilon' > 0 : \mathbb{P}[|\mathbf{x}_i - \mathbf{X}| < \varepsilon' | \{i \in S_B\}] &> 0, \\ \implies \forall \varepsilon > 0, \boldsymbol{\beta} : \mathbb{P}[|m(\mathbf{x}_i, \boldsymbol{\beta}) - m(\mathbf{X}, \boldsymbol{\beta})| < \varepsilon | \{i \in S_B\}] &> 0. \end{aligned} \quad (7)$$

for  $\boldsymbol{\beta}$  in some neighbourhood of  $\boldsymbol{\beta}_0$ , therefore by (C1) with positive probability we have:

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

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 assumption (A2) we have:

$$\forall \varepsilon > 0, i : \lim_{n_A \rightarrow \infty} \mathbb{P} \left[ k \leq \# \left\{ j \in S_A : |Y_j - m(\mathbf{X}_i, \hat{\boldsymbol{\beta}})| < \varepsilon \right\} \mid \{i \in S_B\} \right] = 1, \quad (8)$$

from which one infers that:

$$\lim_{n_A \rightarrow \infty} \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k (Y_{\hat{\nu}(i,t)} - m(\mathbf{X}_i, \hat{\boldsymbol{\beta}})) \right| \leq$$

$$\lim_{n_A \rightarrow \infty} \max_{i \in S_B} \left\{ \frac{n_B}{N \pi_i} \right\} \max_{i \in S_B} \left| \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)} - m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) \right| \leq \frac{\varepsilon}{C_1}, \quad (9)$$

where  $C_1$  is the bound from (A3), so the  $\hat{y}-y$  matching estimator from Algorithm 1 is consistent. To prove that consistency of  $\hat{\mu}_{\text{MI}}$  is necessary see that (9) still stands and that if  $\hat{y}-y$  estimator is consistent we have:

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

which converges to 0.  $\square$

**Theorem 3.** *Under assumptions (A2), (A3) and (B1)  $\hat{y} - \hat{y}$  estimator in (3) under correctly specified regression model  $m$  is consistent when  $\hat{\mu}_{\text{MI}}$  is consistent. Assumptions (A1), (A4) are sufficient for this consistency.*

Proof of the Theorem 3 is given in Appendix B.1. Theorem 3 says nothing on necessity of consistency of  $\hat{\mu}_{\text{MI}}$  unlike in theorem 2. Additionally 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.

Since  $\hat{\mu}$  and the *hypothetical* HT estimator 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 estimator to be asymptotically normal with  $(\mu_{n_B}^{(HT)}, V_{n_B}^{(HT)})$ .

**Remark 2.** *(Regarding assumption (A1)) We may 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 or even neural networks, could potentially be used in (3) under suitable assumptions (to ensure their consistency), see e.g. Mielniczuk and Tyrcha (1993) for discussion of (stronger type) consistency for perceptrons.

In the Appendix we present simulation study that covers some examples. A question of whether convergence in  $\|\cdot\|_\infty$  can be replaced by convergence in weaker topology could be subject to further research.

### 3.2 Consistency under mis-specified model

Yang and Kim (2020) discussed robustness of the PMM estimator for imputation of item non-response in survey sampling. The following Theorem provides conditions when the PMM A estimator for data integration is consistent (proof is given in Appendix 4).

**Theorem 4.** *If (A2), (A3), (A4), (B1) and  $\hat{y} - \hat{y}$  matching is done via  $m$  while:*

$$\mathbb{E}[Y|\mathbf{X}] = m'(\mathbf{X}, \beta_0)$$

where possibly  $m' \neq m$  and:

(D1)  $\beta^* = \lim \hat{\beta}$  in probability exists,

(D2)  $|\mathbb{E}[Y_i - Y_j | m(\mathbf{X}_i, \beta^*), m(\mathbf{X}_j, \beta^*)]| \leq C |m(\mathbf{X}_i, \beta^*) - m(\mathbf{X}_j, \beta^*)|$  almost surely,

then  $\hat{y} - \hat{y}$  matching estimator is consistent. Additionally if MI estimator based on model  $m'$  converges in  $L^1$  norm then  $\hat{y} - \hat{y}$  estimator also converges in  $L^1$  norm.

**Remark 3.** (Regarding the Theorems 2, 3, 4) 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, the proofs can be rewritten to accommodate distance functions other than the Euclidean metric (under reasonable restrictions) almost in an exactly analogous manner.

Yang and Kim (2020) in their approach for missing data assumed convex compact support for  $m(\mathbf{X}, \beta_0)$  with fixed  $\beta$  along with missing at random assumption, while we require (A4) to

hold. As we argued in the discussion in Section 2.4 the (A4) assumption is less restrictive.

### 3.3 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 5.** *If the population size  $N$  is known, the variance of estimators (3) is given by*

$$\mathbb{V}[\hat{\mu}] = V_1 + V_2, \quad (10)$$

where

$$\begin{aligned} V_1 &= \frac{1}{N^2 k^2} \sum_{i=1}^N \mathbb{E} \left[ \frac{1}{\pi_i} \left( \frac{1}{\pi_i} - 1 \right) \left( \sum_{t=1}^k Y_{\hat{\nu}(i,t)} \right)^2 \right] \\ &\quad + \frac{1}{N^2 k^2} \sum_{\substack{i,j=1 \\ i \neq j}}^N \mathbb{E} \left[ \pi_i^{-1} \pi_j^{-1} \text{cov}(\mathbb{1}_{\{i \in S_B\}}, \mathbb{1}_{\{j \in S_B\}}) \sum_{t',t=1}^k Y_{\hat{\nu}(i,t)} Y_{\hat{\nu}(j,t')} \right] \\ &= \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \frac{\pi_{ij} - \pi_i \pi_j}{\pi_i \pi_j \pi_{ij}} \mathbb{E} \left[ \left( \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)} \right) \left( \frac{1}{k} \sum_{t'=1}^k Y_{\hat{\nu}(j,t')} \right) \right], \end{aligned} \quad (11)$$

and

$$V_2 = \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \text{cov} \left( \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k Y_{\hat{\nu}(j,t')} \right) = \mathbb{V} \left[ \frac{1}{N} \sum_{i=1}^N \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)} \right]. \quad (12)$$

The proof of Theorem 5 is given in Appendix B.3. 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 4.** (Regarding Theorem 5) When deriving the expression for  $\mathbb{V}[\hat{\mu}]$  we conditioned variance on knowing values of  $y_i$  and  $\hat{\nu}(i, t)$  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  $\hat{\nu}(i, t)$  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 5 we have the following approximation for (3) with unknown population size estimated via the usual  $\hat{N} = \sum_{i \in S_B} \pi_i^{-1}$ :

$$\begin{aligned} \mathbb{V} \left[ \frac{N}{\sum_{r \in S_B} \pi_r^{-1}} \hat{\mu} \right] &\approx V_1 + V_2 + \mathbb{E} [\hat{\mu}]^2 \frac{\mathbb{V} [\hat{N}]}{N^2} - 2 \frac{\text{cov}(\hat{N}, \hat{\mu})}{N} \\ &= V_1 + V_2 + \frac{\mathbb{E} [\hat{\mu}]^2}{N^2} \sum_{i,j=1}^N \text{cov}(\mathbb{1}_{i \in S_B} \pi_i^{-1}, \mathbb{1}_{j \in S_B} \pi_j^{-1}) \\ &\quad - 2 \frac{1}{N^2} \sum_{i,j=1}^N \frac{1}{k} \sum_{t=1}^k \text{cov}(\mathbb{1}_{\{i \in S_B\}} \pi_i^{-1}, \pi_j^{-1} \mathbb{1}_{\{j \in S_B\}} Y_{\hat{\nu}(j,t)}) \end{aligned} \quad (13)$$

Since  $\hat{N}$  is unbiased for  $N$  we obtain (13) by Taylor series expansion of  $f(x, y) = x/y$ .

### 3.4 Variance estimator

#### 3.4.1 Partially analytic variance estimator

Theorem 6 provides a consistent estimator of the variance estimators (3). The full proof is presented in Appendix B.4.

**Theorem 6.** *If second order inclusion probabilities are known, assumptions of Theorems 2, 3, 4 respectively 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:*

$$\widehat{\mathbb{V}}[\hat{\mu}] = \hat{V}_1 = \frac{1}{N^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} \left( \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right) \left( \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right), \quad (14)$$

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

The result  $\lim_{n_A \rightarrow \infty} V_2 = 0$ , which is a corollary to Theorem 6, 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-Thompson variance estimator for the mean computed via imputed values. Computation of the term  $\hat{V}_2$ , which in the light of Theorem 6 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 (13) given by

$$\begin{aligned} \widehat{\mathbb{V}} \left[ \frac{N}{\sum_{r \in S_B} \pi_r^{-1}} \hat{\mu} \right] &= \frac{1}{\hat{N}^2} \sum_{i \in S_B} \sum_{j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j} \left( \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)} \right) \left( \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right) \\ &+ \frac{1}{\hat{N}^2} \sum_{i \in S_B} \sum_{j \in S_B} \pi_{ij}^{-1} \widehat{\text{cov}} \left( \frac{1}{k} \sum_{t=1}^k y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k y_{\hat{\nu}(j,t')} \right) \\ &+ \frac{\hat{\mu}^2}{\hat{N}^2} \sum_{i,j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_i \pi_j} - 2 \frac{\hat{\mu}}{\hat{N}^2} \sum_{i,j \in S_B} \frac{\pi_{ij} - \pi_i \pi_j}{\pi_{ij} \pi_i \pi_j}, \end{aligned} \quad (15)$$

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.

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 (12),  $V_2$  is just the variance of the mean of imputed values for the whole



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

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- 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  $\mathbb{E}[Y|\mathbf{X}] = m(\mathbf{X}, \boldsymbol{\beta})$  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.
- 

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.

### 3.5 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.

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

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**Algorithm 3:** Bootstrap variance estimator

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- 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  $\mathbb{E}[Y|\mathbf{X} = \mathbf{x}'] = m(\mathbf{x}', \beta)$  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  $\hat{V} = \hat{V}_1 + \hat{V}_2$
- 

## 4 Simulation study

We generate a finite population of size  $N = 10^5$ , three random variables  $X_1, X_2$  and  $X_3$  independently from the  $\mathcal{N}(2, 1)$  and  $\varepsilon \sim \mathcal{N}(0, 1)$  and assume the following models: 1)  $y_{1i} = 1 + 2x_{1i} + \varepsilon_i$ ; 2)  $y_{2i} = -1 + x_{1i} + x_{2i} + x_{3i} + \varepsilon_i$ ; and 3)  $y_{3i} = -10 + x_{1i}^2 + x_{2i}^2 + x_{3i}^2 + \varepsilon_i$ . 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 without replacement (SRSWOR) 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 SRSWOR from the population.

The goal of the study is to verify the performance of the proposed estimators with comparison to two existing alternatives for mass imputation: nearest neighbour (denoted as NN) and regression prediction (denoted as GLM). We verify the effect of the number of covariates as well as model mis-specification.

For all target variables we assume correctly specified model as defined above. In addition for  $Y_3$  use mis-specified model (i.e. linear regression with  $X_1$  and  $X_2$  only). 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 denoted as GLM.
- The NN mass imputation estimators. We studied the impact of  $k$  using  $k = 1$  and  $k = 5$  which is denoted as NN1 and NN5.

- 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 CR change if we drop  $\hat{V}_2$  from the NN and 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 GLM estimator proposed by Kim et al. (2021). As expected the results for the NN and the PMM estimator are exactly the same. 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 GLM estimator.

As regards the second variable  $Y_2$ , a similar pattern can be observed as for  $Y_1$  with one exception. The larger the number of nearest neighbours, the higher bias is observed for the NN estimator. For the PMM B estimator increasing the number of nearest neighbours has no significant effect on the bias or the standard error. The empirical coverage rates for all estimators are close to the nominal 95%.

The main differences can be observed for the last variable  $Y_3$  (non-linear). If we use correctly specified transformations and linear regression for all estimators the bias is negligible for the GLM and PMM estimators but not for the NN estimator. The PMM A with  $\hat{y} - \hat{y}$  fitting and the GLM are now characterised by the lowest bias and a CR close to the nominal 95%. This is in line with Remark 4 regarding robustness of  $\hat{y} - \hat{y}$  matching.

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	-64.08	4.86	64.26	—	-31.48	5.98	32.04	—	-127.15	20.92	128.86	—
<i>correctly specified</i>												
GLM	0.30	9.90	9.90	94.20	0.18	8.64	8.64	94.60	0.11	33.36	33.36	94.00
NN1	0.21	11.07	11.07	94.60	-1.32	9.74	9.83	94.60	-19.86	32.09	37.74	90.40
NN5	0.18	10.24	10.24	94.40	-2.48	8.30	8.66	94.80	-38.09	30.76	48.96	74.20
PMM1A	0.21	11.07	11.07	94.80	0.09	10.09	10.09	95.80	-0.80	33.99	34.00	94.40
PMM1B	0.28	9.89	9.90	95.00	0.16	8.64	8.64	94.20	-0.64	33.33	33.34	94.00
PMM5A	0.18	10.24	10.24	94.60	-0.11	8.92	8.92	95.00	-2.06	33.31	33.37	93.80
PMM5B	0.19	9.86	9.86	94.60	0.10	8.63	8.63	94.40	-2.07	33.12	33.18	94.00
<i>mis-specified</i>												
GLM	—	—	—	—	—	—	—	—	-10.83	28.72	30.69	93.20
NN1	—	—	—	—	—	—	—	—	-5.58	37.13	37.55	94.20
NN5	—	—	—	—	—	—	—	—	-14.14	31.90	34.89	91.20
PMM1A	—	—	—	—	—	—	—	—	-1.25	38.05	38.07	97.40
PMM1B	—	—	—	—	—	—	—	—	-10.41	28.66	30.49	93.80
PMM5A	—	—	—	—	—	—	—	—	-3.99	31.19	31.45	96.60
PMM5B	—	—	—	—	—	—	—	—	-10.21	28.64	30.40	93.80
$n_A = 1,000$												
Naive	-64.48	7.09	64.87	—	-32.14	8.53	33.25	—	-129.02	30.86	132.66	—
<i>correctly specified</i>												
GLM	0.05	10.46	10.46	95.80	-0.10	9.40	9.40	95.00	-0.18	33.68	33.68	94.40
NN1	-0.12	11.77	11.77	94.40	-2.13	10.26	10.48	94.80	-29.91	32.43	44.12	83.80
NN5	-0.41	10.69	10.70	95.60	-3.93	9.04	9.86	91.20	-54.85	30.26	62.65	55.80
PMM1A	-0.12	11.77	11.77	94.60	-0.22	10.96	10.96	94.60	-1.48	34.15	34.18	94.60
PMM1B	-0.01	10.45	10.45	95.20	-0.15	9.40	9.40	95.20	-1.61	33.49	33.53	94.40
PMM5A	-0.41	10.69	10.70	96.00	-0.45	9.64	9.65	94.80	-4.11	33.09	33.35	94.20
PMM5B	-0.25	10.40	10.40	95.40	-0.26	9.37	9.37	95.00	-4.36	33.12	33.41	94.60
<i>mis-specified</i>												
GLM	—	—	—	—	—	—	—	—	-10.98	33.06	34.83	92.60
NN1	—	—	—	—	—	—	—	—	-10.36	39.93	41.25	95.60
NN5	—	—	—	—	—	—	—	—	-23.61	34.04	41.43	88.60
PMM1A	—	—	—	—	—	—	—	—	-4.32	42.73	42.95	96.60
PMM1B	—	—	—	—	—	—	—	—	-10.39	33.01	34.60	93.00
PMM5A	—	—	—	—	—	—	—	—	-7.23	35.85	36.58	94.40
PMM5B	—	—	—	—	—	—	—	—	-10.16	32.94	34.47	92.80

As expected, when the model is mis-specified (rows under *mis-specified*), i.e. we use linear regression with  $x_1$  and  $x_2$  only, all estimators are characterised with bias. However, the bias is the lowest for the PMM A estimator. Interestingly, increasing  $k$  for the NN leads to an increase of bias. On the other hand, the PMM B estimators are characterised with the lowest variance and thus lowest RMSE (along with PMM5A). All estimators have CR close to the nominal 95%.

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 for NN and PMM estimators. The NN estimator for the  $Y_3$  variable is characterised with the lowest CR in both scenarios. The second part suggests that the proposed analytical and bootstrap variance estimation approaches yield the same results for all study variables and sample sizes.

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						
	$V_1$	$V_1 + V_2$	$V_1$	$V_1 + V_2$	$V_1$	$V_1 + V_2$
$n_A = 500$						
NN1	88.20	94.40	89.00	94.80	81.00	83.80
NN5	90.40	95.60	83.00	91.20	46.20	55.80
PMM1A	88.20	94.60	89.00	94.60	93.80	94.60
PMM1B	89.00	95.20	93.80	95.20	89.60	94.40
PMM5A	90.40	96.00	89.60	94.80	93.20	94.20
PMM5B	89.00	95.40	88.80	95.00	93.40	94.60
$n_A = 1,000$						
NN1	91.20	94.60	89.20	94.60	87.00	90.40
NN5	89.80	94.40	90.00	94.80	71.80	74.20
PMM1A	91.20	94.80	92.80	95.80	93.60	94.40
PMM1B	89.80	95.00	91.80	94.20	94.40	94.00
PMM5A	89.80	94.60	92.00	95.00	94.40	93.80
PMM5B	89.80	94.60	91.80	94.40	94.20	94.00
Comparison of analytic and bootstrap variance estimators						
	Analytic	Bootstrap	Analytic	Bootstrap	Analytic	Bootstrap
$n_A = 500$						
NN1	94.40	95.20	94.80	95.80	83.80	84.20
NN5	95.60	96.00	91.20	93.00	55.80	56.40
PMM1A	94.60	94.80	94.60	97.20	94.60	94.60
PMM1B	95.20	95.00	95.20	94.60	94.40	94.80
PMM5A	96.00	96.00	94.80	95.60	94.20	94.80
PMM5B	95.40	95.00	95.00	94.60	94.60	94.60
$n_A = 1,000$						
NN1	94.60	95.00	94.60	94.80	90.40	90.80
NN5	94.40	95.40	94.80	94.80	74.20	74.00
PMM1A	94.80	95.60	95.80	96.80	94.40	95.00
PMM1B	95.00	94.60	94.20	94.20	94.00	93.80
PMM5A	94.60	94.80	95.00	96.00	93.80	93.80
PMM5B	94.60	94.00	94.40	94.20	94.00	93.80

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, see section C.1); 2) variable selection for the 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 (see section C.2); 3) non-parametric regression using a local linear model can be employed, although in practice better

non-parametric methods ought to be considered (see section C.3); 4) the proposed estimators perform similarly to the GLM estimator when the positivity assumption is violated with some exceptions when a non-linear model is considered (see section C.4); 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, see section C.5). 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),  $\log(\text{RE})$ ,  $\log(\text{vac})$  (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: GLM (Kim et al., 2021), NN1 ( $\log(\text{RE})$  and  $\log(\text{vac})$  only), NN2, 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.

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 and NN1 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 (except for the NN estimators), with the lowest values for mass imputation estimators. Results for GLM, PMM A and PMM B in this empirical study are not distinguishable.

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
GLM	22.72	0.57	2.51	21.49	23.79
NN1	25.88	6.41	24.78	13.31	38.45
NN2	23.38	1.91	8.18	19.63	27.13
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

## 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.

A possible application of  $\hat{y} - y$  matching outside of just being more efficient under heavy assumptions is that we can consider mixed matching with respect to the distance function:

$$d(i, j) = \frac{1}{a_N} \left| y_i - m(\mathbf{x}_j, \hat{\beta}) \right| + \left| m(\mathbf{x}_i, \hat{\beta}) - m(\mathbf{x}_j, \hat{\beta}) \right|,$$

or:

$$d(i, j) = \left| \frac{1}{a_N} \left( y_i - m(\mathbf{x}_j, \hat{\beta}) \right) + m(\mathbf{x}_i, \hat{\beta}) - m(\mathbf{x}_j, \hat{\beta}) \right|,$$

where  $a_N \rightarrow \infty$  as  $N \rightarrow \infty$  but slowly so that the new estimator retains asymptotic properties of  $\hat{y} - \hat{y}$  matching but is closer to  $\hat{y} - y$  matching in finite samples. Some initial simulations gave very optimistic results. The performance of such estimators and the optimal choice of a sequence  $a_n$  will be subject to further research.

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.

Simulation in the Appendix shows C.1 initial results on a dynamic selection of  $k$  hyperparameter. The results are promising but one should be aware that minimizing the estimated variance way of choosing  $k$  though the variance should then be adjusted due to randomness in  $k$  via:

$$\mathbb{V}[\hat{\mu}] = \mathbb{E}[\mathbb{V}[\hat{\mu}|k]] + \mathbb{V}[\mathbb{E}[\hat{\mu}|k]] = \sum_{t=1}^{\infty} (V_1(t) + V_2(t))\mathbb{P}[k=t] + \mathbb{V}[\mathbb{E}[\hat{\mu} - \mu|k]],$$

which could be very difficult and could be the subject of further research. Sensitivity analysis via CV is always a viable alternative.

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. 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 1-6. 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, the empirical study and prepared the final version of the manuscript.

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# Appendix

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# A Assumptions

## A.1 Regarding consistency of regression

We do not strictly require that  $\mathbb{P}[Y \in dy|\mathbf{X}, \delta] = \mathbb{P}[Y \in dy|\mathbf{X}]$  almost surely but in practice checking the consistency of regression may require checking this condition, as one reliable way of assessing consistency of  $\hat{\boldsymbol{\beta}}$  (see e.g. the discussion in Kim et al. (2021)) is checking whether:

(A1.1)  $\mathbb{P}[Y \in dy|\mathbf{X}, \delta] = \mathbb{P}[Y \in dy|\mathbf{X}]$  holds and

(A1.2)  $\hat{\boldsymbol{\beta}}$  is a unique solution to score equations:

$$\frac{1}{n_A} \sum_{i \in S_A} \left( y_i - m(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) \right) \mathbf{h}(\mathbf{x}_i, \hat{\boldsymbol{\beta}}) = \mathbf{0},$$

for some  $\mathbf{h} : \mathbb{R}^p \times \mathbb{R}^p \rightarrow \mathbb{R}^p$  chosen in such a way that some more technical assumptions (cf. Tsiatis, 2006) are met, namely for  $\boldsymbol{\beta}$  is some neighbourhood of  $\boldsymbol{\beta}_0$ :

1.  $\mathbb{E}_{\boldsymbol{\beta}} [(Y - m(\mathbf{X}, \boldsymbol{\beta})) \mathbf{h}(\mathbf{X}, \boldsymbol{\beta})] = \mathbf{0}$  when the distribution is such that  $\boldsymbol{\beta}$  is the true regression parameter,
2.  $\mathbb{E}_{\boldsymbol{\beta}} \left[ (Y - m(\mathbf{X}, \boldsymbol{\beta}))^2 \mathbf{h}(\mathbf{X}, \boldsymbol{\beta})^T \mathbf{h}(\mathbf{X}, \boldsymbol{\beta}) \right] < \infty$ ,
3.  $\mathbb{E}_{\boldsymbol{\beta}} \left[ (Y - m(\mathbf{X}, \boldsymbol{\beta}))^2 \mathbf{h}(\mathbf{X}, \boldsymbol{\beta}) \mathbf{h}(\mathbf{X}, \boldsymbol{\beta})^T \right]$  is positive define,
4.  $\mathbb{E}_{\boldsymbol{\beta}} \left[ \frac{\partial}{\partial \boldsymbol{\beta}^T} (Y - m(\mathbf{X}, \boldsymbol{\beta})) \mathbf{h}(\mathbf{X}, \boldsymbol{\beta}) \right]$  is non singular,
5.  $\frac{1}{n_A} \sum_{i \in S_A} \frac{\partial}{\partial \boldsymbol{\beta}^T} (Y_i - m(\mathbf{X}_i, \boldsymbol{\beta})) \mathbf{h}(\mathbf{X}_i, \boldsymbol{\beta}) \longrightarrow \mathbb{E}_{\boldsymbol{\beta}_0} \left[ \frac{\partial}{\partial \boldsymbol{\beta}^T} (Y - m(\mathbf{X}, \boldsymbol{\beta})) \mathbf{h}(\mathbf{X}, \boldsymbol{\beta}) \right]$  in probability, uniformly in  $\boldsymbol{\beta}$ , when sampling is done from distribution where true regression parameter is  $\boldsymbol{\beta}_0$ .

We do not however require all covariates which are significant for regression on  $Y$  to be observed. Indeed consider the following toy model (the previously discussed regularity conditions are known to hold for linear regression if covariates are not too pathological):

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \epsilon$$

$$\delta = (1 - \exp(X_1 + \eta))^{-1},$$

where  $\beta_0, \beta_1, \beta_2, \beta_1 \neq 0$  are constants, random errors  $\epsilon, \eta$  are independent and independent of  $X_2$ , then the estimators for  $\beta'_0, \beta_1$  in model:

$$Y = \beta'_0 + \beta_1 X_1 + \epsilon',$$

where  $\beta'_0 = \beta_0 + \beta_2 \mathbb{E}[X_2]$ ,  $\epsilon' = \epsilon + \beta_2(X_2 - \mathbb{E}[X_2])$  are consistent since  $Y$  and  $\delta$  are independent given  $X_1$  and assumptions for  $\hat{y} - \hat{y}$  estimator are satisfied if the distribution of  $X_1$  is not too pathological. If in addition  $X_1$  has continuous distribution with support  $\mathbb{R}$  and all  $X_1, X_2, \epsilon$  have finite variance for all units in the population then assumptions for  $\hat{y} - y$  are also satisfied.

Notice that analogous model  $Y = \beta''_0 + \beta_2 X_2 + \epsilon''$  would not satisfy (A1.1).

## A.2 Proof of Theorem 1

*Proof.* By linearity we have that  $\mathbb{E}[\mu | \mathbf{X}_1, \dots, \mathbf{X}_N] = \frac{1}{N} \sum_{i=1}^N m(\mathbf{X}_i, \beta_0)$ , moreover by definition of conditional expectation this estimator is unbiased and optimal in terms of mean squared error and therefore since, by assumption of falsity for (A4):

$$\exists C > 0 \forall N : \mathbb{V} \left[ \mu - \frac{1}{N} \sum_{i=1}^N m(\mathbf{X}_i, \beta_0) \right] \geq C,$$

so we have that for every  $\sigma(\mathbf{X}_1, \dots, \mathbf{X}_N)$  measurable  $\hat{\mu}_N$ :

$$\mathbb{V}[\mu - \hat{\mu}_N] + \mathbb{E}[\mu - \hat{\mu}_N]^2 = \mathbb{E}[(\mu - \hat{\mu}_N)^2] \geq \mathbb{E} \left[ \left( \mu - \frac{1}{N} \sum_{i=1}^N m(\mathbf{X}_i, \beta_0) \right)^2 \right] \geq C,$$

so  $\mu - \hat{\mu}_N$  cannot converge to 0, it is either asymptotically biased or not convergent to any constant. □

## B Main results

### B.1 Proof of Theorem 3

*Proof.* The objective expression for proving sufficiency of consistency of  $\hat{\mu}_{\text{MI}}$ :

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)} - \sum_{i \in S_B} \frac{1}{\pi_i} Y_i \right|,$$

can be subdivided into three parts:

$$\begin{aligned} & \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k (Y_{\hat{\nu}(i,t)} - Y_i) \right| \leq \\ & \frac{1}{N} \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k \left| m(\mathbf{X}_i, \hat{\beta}) - m(\mathbf{X}_{\hat{\nu}(i,t)}, \hat{\beta}) \right| + \end{aligned} \quad (16)$$

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} (Y_i - m(\mathbf{X}_i, \hat{\beta})) \right| + \quad (17)$$

$$\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k (Y_{\hat{\nu}(i,t)} - m(\mathbf{X}_{\hat{\nu}(i,t)}, \hat{\beta})) \right|, \quad (18)$$

notice that (17) tends to 0 by assumption. By (A2), (B1) and (7) we have:

$$\forall \varepsilon > 0, i : \lim_{n_A \rightarrow \infty} \mathbb{P} \left[ k \leq \# \left\{ j \in S_A : \left| m(\mathbf{X}_i, \hat{\beta}) - m(\mathbf{X}_j, \hat{\beta}) \right| < \varepsilon \right\} \mid \{i \in S_B\} \right] = 1. \quad (19)$$

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

Therefore expression in (16) is satisfies:

$$\begin{aligned} & \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} \frac{1}{k} \sum_{t=1}^k (m(\mathbf{X}_{\hat{\nu}(i,t)}, \hat{\beta}) - m(\mathbf{X}_i, \hat{\beta})) \right| \leq \\ & \max_{i \in S_B} \left\{ \frac{n_B}{N\pi_i} \right\} \max_{i \in S_B} \left| \frac{1}{k} \sum_{t=1}^k (m(\mathbf{X}_{\hat{\nu}(i,t)}, \hat{\beta}) - m(\mathbf{X}_i, \hat{\beta})) \right|, \end{aligned} \quad (20)$$

and, by virtue of (19) and (A2) we have:

$$\forall \varepsilon > 0 : \lim_{n_A \rightarrow \infty} \max_{i \in S_B} \left\{ \frac{n_B}{N\pi_i} \right\} \max_{i \in S_B} \left| \frac{1}{k} \sum_{t=1}^k m(\mathbf{X}_{\hat{\nu}(i,t)}, \hat{\beta}) - m(\mathbf{X}_i, \hat{\beta}) \right| < \frac{\varepsilon}{C_1},$$

so (16) tends to 0 in probability. Similarly since by law of total probability:

$$\mathbb{P} \left[ \left| Y_{\hat{\nu}(i,t)} - m \left( \mathbf{X}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}} \right) \right| > \varepsilon \right] = \sum_{j=1}^N \mathbb{P} \left[ \left| Y_j - m \left( \mathbf{X}_j, \hat{\boldsymbol{\beta}} \right) \right| > \varepsilon \right] \mathbb{P} [\hat{\nu}(i,t) = j],$$

$m \left( \mathbf{X}_{\hat{\nu}(i,t)}, \hat{\boldsymbol{\beta}} \right)$  is (asymptotically) an optimal estimator for  $Y_{\hat{\nu}(i,t)}$  so by consistency of  $\hat{\mu}_{\text{MI}}$  we have that that (18) tends to 0 in probability, so  $\hat{y} - \hat{y}$  estimator from (3) is consistent.  $\square$

## B.2 Proof of Theorem 4

*Proof.* Set  $\varepsilon > 0$  and recall from (19) that for each  $i \in S_B$  with probability one asymptotically we will have at least  $k$  units in  $S_A$  such that:

$$\left| m \left( \mathbf{X}_i, \hat{\boldsymbol{\beta}} \right) - m \left( \mathbf{X}_j, \hat{\boldsymbol{\beta}} \right) \right| < \varepsilon,$$

but since:

$$\begin{aligned} |m(\mathbf{X}_i, \boldsymbol{\beta}^*) - m(\mathbf{X}_j, \boldsymbol{\beta}^*)| &\leq \left| m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) - m(\mathbf{X}_j, \hat{\boldsymbol{\beta}}) \right| + \\ &\left| m(\mathbf{X}_j, \hat{\boldsymbol{\beta}}) - m(\mathbf{X}_j, \boldsymbol{\beta}^*) \right| + \left| m(\mathbf{X}_i, \hat{\boldsymbol{\beta}}) - m(\mathbf{X}_i, \boldsymbol{\beta}^*) \right|, \end{aligned}$$

we have that these same  $k$  units in  $S_A$  will satisfy:

$$|m(\mathbf{X}_i, \boldsymbol{\beta}^*) - m(\mathbf{X}_j, \boldsymbol{\beta}^*)| < 3\varepsilon,$$

and we therefore have:

$$\begin{aligned} \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{k\pi_i} \sum_{t=1}^k (Y_i - Y_{\hat{\nu}(i,t)}) \right| &\leq \underbrace{\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i} (Y_i - m'(\mathbf{X}_i, \boldsymbol{\beta}_0)) \right|}_{n_A \rightarrow 0 \text{ in probability by (A4)}} + \\ &\underbrace{\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{k\pi_i} \sum_{t=1}^k (Y_{\hat{\nu}(i,t)} - m'(\mathbf{X}_{\hat{\nu}(i,t)}, \boldsymbol{\beta}_0)) \right|}_{n_A \rightarrow 0 \text{ in probability by (A4)}} + \\ &\frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i k} \sum_{t=1}^k (m'(\mathbf{X}_i, \boldsymbol{\beta}_0) - m'(\mathbf{X}_{\hat{\nu}(i,t)}, \boldsymbol{\beta}_0)) \right|, \end{aligned} \tag{21}$$



where the last term converges to 0 in  $L^1$  norm since:

$$\begin{aligned}
& \mathbb{E} \left[ \frac{1}{N} \left| \sum_{i \in S_B} \frac{1}{\pi_i k} \sum_{t=1}^k (m'(\mathbf{X}_i, \boldsymbol{\beta}_0) - m'(\mathbf{X}_{\hat{\nu}(i,t)}, \boldsymbol{\beta}_0)) \right| \right] \leq \\
& \frac{1}{C_1} \max_{i \in S_B} \mathbb{E} \left[ \frac{1}{k} \left| \sum_{t=1}^k (m'(\mathbf{X}_i, \boldsymbol{\beta}_0) - m'(\mathbf{X}_{\hat{\nu}(i,t)}, \boldsymbol{\beta}_0)) \right| \right] \leq \\
& \frac{1}{C_1} \max_{i \in S_B} \mathbb{E} \left[ \mathbb{E} \left[ \frac{1}{k} \sum_{t=1}^k |m'(\mathbf{X}_i, \boldsymbol{\beta}_0) - m'(\mathbf{X}_{\hat{\nu}(i,t)}, \boldsymbol{\beta}_0)| \left| m(\mathbf{X}_i, \boldsymbol{\beta}^*), m(\mathbf{X}_{\hat{\nu}(i,t)}, \boldsymbol{\beta}^*) \right| \right] \right] \leq \\
& \frac{C}{C_1} \max_{\substack{i \in S_B \\ t=1, \dots, k}} \mathbb{E} [m(\mathbf{X}_i, \boldsymbol{\beta}^*) - m(\mathbf{X}_{\hat{\nu}(i,t)}, \boldsymbol{\beta}^*)] < 3 \frac{C}{C_1} \varepsilon.
\end{aligned}$$

The last remark about convergence in  $L^1$  is clear since we may just replace convergence in probability with  $L^1$  convergence in inequality (21).  $\square$

### B.3 Proof of Theorem 5

*Proof.* Using law of total variance we have:

$$\mathbb{V}[\hat{\mu}] = \frac{1}{N^2 k^2} \mathbb{E} \left[ \mathbb{V} \left[ \sum_{i \in S_B} \frac{1}{\pi_i} \sum_{t=1}^k Y_{\hat{\nu}(i,t)} \middle| \sigma(\{Y_i, \mathbf{X}_i, \hat{\nu}(i,t)\}_{i \in U, t \in \{1, \dots, k\}}) \right] \right] \quad (22)$$

$$+ \frac{1}{N^2 k^2} \mathbb{V} \left[ \mathbb{E} \left[ \sum_{i \in S_B} \frac{1}{\pi_i} \sum_{t=1}^k Y_{\hat{\nu}(i,t)} \middle| \sigma(\{Y_i, \mathbf{X}_i, \hat{\nu}(i,t)\}_{i \in U, t \in \{1, \dots, k\}}) \right] \right]. \quad (23)$$

by Cauchy product (23) can be expressed as:

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

$$\begin{aligned}
&= \frac{1}{N^2 k^2} \sum_{i=1}^N \sum_{j=1}^N \sum_{t'=1}^k \sum_{t=1}^k \mathbb{E} [Y_{\hat{\nu}(i,t)} Y_{\hat{\nu}(j,t')}] \\
&\quad - \frac{1}{N^2 k^2} \left( \sum_{i=1}^N \sum_{j=1}^N \sum_{t=1}^k \sum_{t'=1}^k \mathbb{E} [Y_{\hat{\nu}(i,t)}] \mathbb{E} [Y_{\hat{\nu}(j,t')}] \right) \\
&= \frac{1}{N^2 k^2} \sum_{i=1}^N \sum_{j=1}^N \sum_{t'=1}^k \sum_{t=1}^k (\mathbb{E} [Y_{\hat{\nu}(i,t)} Y_{\hat{\nu}(j,t')}] - \mathbb{E} [Y_{\hat{\nu}(i,t)}] \mathbb{E} [Y_{\hat{\nu}(j,t')}] ) \\
&= \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \text{cov} \left( \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k Y_{\hat{\nu}(j,t')} \right),
\end{aligned}$$

which can be estimated by:

$$\frac{1}{N^2} \sum_{i=1}^{n_B} \sum_{j=1}^{n_B} \frac{1}{\pi_{ij}} \widehat{\text{cov}} \left( \frac{1}{k} \sum_{t=1}^k Y_{\hat{\nu}(i,t)}, \frac{1}{k} \sum_{t'=1}^k Y_{\hat{\nu}(j,t')} \right), \quad (24)$$

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 (22) on the other hand is:

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

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.4 Proof of Theorem 6

*Proof.* Let  $\hat{\mu}_{HT}$  denote the hypothetical Horvitz-Thompson estimate of  $\mu$ . Since by virtue of Theorems 2, 3  $|\hat{\mu} - \hat{\mu}_{HT}| \rightarrow 0$  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 Theorems 2, 3. 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:

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

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

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

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  $\frac{1}{N} \sum_{i=1}^N |Y_i|$ :

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

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

In all simulations, for the PMM and the NN estimators we estimated  $V_2$  component using the proposed mini-bootstrap.

### 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  $\mathbf{Z}_k \sim \mathcal{N}_5 \left( \left( 1 \quad 1 \quad 1 \quad 1 \quad 1 \right)^T, \Sigma \right)$  ( $\mathbf{Z}_k$  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  $\epsilon$ '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

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

where  $\epsilon_t$  is an empirical quantile of  $\epsilon$  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 four estimators discussed in the paper: GLM, NN, PMM A ( $\hat{y} - \hat{y}$  matching) and PMM B ( $\hat{y} - y$  matching). The NN and PMM estimators are 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 NN and PMM A estimator. Average  $k$  for the NN estimator is large about 25 while for the PMM A is 6 and PMM B around 1. This the reason for the lowest value of RMSE for the NN estimator.

Table C.1: Results for the simulation study on choosing of  $k$  hyper-parameter (all measures but  $\bar{k}$  are multiplied by 100)

Variable	Estimator	$k$ -selection	Bias	SE	RMSE	CR	$\bar{k}$
Y1	GLM	–	0.3328	2.8252	2.8448	97.40	–
	NN	Dynamic	0.5264	3.4232	3.4634	94.60	25.03
		Fixed	0.8701	5.0826	5.1565	98.80	–
	PMM A	Dynamic	0.3380	4.9198	4.9314	99.20	6.22
		Fixed	0.3209	5.2870	5.2967	98.80	–
	PMM B	Dynamic	0.3330	2.8258	2.8453	97.40	1.67
		Fixed	0.3321	2.8258	2.8452	97.40	–
Y2	GLM	–	-20.2908	7.3478	21.5803	22.80	–
	NN	Dynamic	-1.6257	8.1058	8.2672	94.20	15.11
		Fixed	-0.3436	8.7902	8.7969	98.20	–
	PMM A	Dynamic	-1.1050	8.2210	8.2949	98.40	6.32
		Fixed	-1.0242	8.4001	8.4623	98.20	–
	PMM B	Dynamic	-20.2884	7.3466	21.5775	23.00	1.70
		Fixed	-20.2851	7.3451	21.5740	22.80	–

In the case of the highly non-linear variable  $Y_2$ , both GLM and PMM B estimators are

significantly biased, while the NN and PMM A with either dynamic or fixed  $k$  is characterised by negligible bias. In addition, PMM A with dynamic selection of  $k$  is characterised by a smaller RMSE. Results regarding the average  $k$  are almost the same as for  $Y_1$  variable.



## 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  $\pi_B$  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:

$$\begin{aligned}
 & - \text{logit}(\pi_{B,i}) = \boldsymbol{\alpha}_0^T \mathbf{X}_i, \text{ where } \boldsymbol{\alpha}_0 = \begin{pmatrix} -2 & 1 & 1 & 1 & 1 & 0 & 0 & \dots & 0 \end{pmatrix}^T \text{ (model PSM I)} \\
 & - \text{logit}(\pi_{B,i}) = 3.5 + \boldsymbol{\alpha}_0^T \log(\mathbf{X}_i^2) - \sin(X_{3,i} + X_{4,i}) - X_{5,i} - X_{6,i}, \\
 & \text{ where } \boldsymbol{\alpha}_0 = \begin{pmatrix} 0 & 0 & 0 & 3 & 3 & 3 & 3 & 0 & \dots & 0 \end{pmatrix}^T \text{ (model PSM II)}
 \end{aligned}$$

- to generate a continuous outcome variable  $Y_i$ , we consider both linear and non-linear outcome models with  $\boldsymbol{\beta}_0 = \begin{pmatrix} 1 & 0 & 0 & 1 & 1 & 1 & 1 & 0 & \dots & 0 \end{pmatrix}^T$ 
  - $Y_i = \boldsymbol{\beta}_0^T \mathbf{X}_i + \epsilon_i, \epsilon_i \sim \mathcal{N}(0, 1)$  i.i.d (model OM I, denoted as  $Y_{11}$ ),
  - $Y_i = 1 + \exp(3 \sin(\boldsymbol{\beta}_0^T \mathbf{X}_i)) + X_{5,i} + X_{6,i} + \epsilon_i, \epsilon_i \sim \mathcal{N}(0, 1)$  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  $\boldsymbol{\beta}_0 = \begin{pmatrix} 1 & 0 & 0 & 3 & 3 & 3 & 3 & 0 & \dots & 0 \end{pmatrix}^T$  :
  - $Y_i \sim \text{Bernoulli}(\pi_Y(\mathbf{X}_i))$  with  $\text{logit}(\pi_Y(\mathbf{X}_i)) = \boldsymbol{\beta}_0^T \mathbf{X}_i$  (model OM III, denoted as  $Y_{21}$ ),
  - $Y_i \sim \text{Bernoulli}(\pi_Y(\mathbf{X}_i))$  with  $\text{logit}(\pi_Y(\mathbf{X}_i)) = 2 - \log((\boldsymbol{\beta}_0^T \mathbf{X}_i)^2) + 2X_{5,i} + 2X_{6,i}$  (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), GLM, PMM A and PMM B (except for OM III) are almost unbiased with coverage close to the nominal rate. The NN estimator without variable selection for the OM I and OM III scenarios is significantly biased and the bias decreases with the variable selection. The PMM B ( $\hat{y} - y$  matching) estimator is characterised by greater bias for both linear and non-linear selection mechanisms with comparable levels as the NN estimator. 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.

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 GLM and PMM A 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 NN and PMM B estimator. Interestingly, the CR for the NN estimator for the OM IV and PSM II is close to the nominal rate which requires further studies.

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 <sub>11</sub> (OM I)									
GLM	No	0.61	10.18	10.20	96.00	0.08	9.87	9.87	94.80
	Yes	-0.06	9.94	9.94	95.40	-0.18	9.84	9.84	95.20
NN	No	76.29	7.81	76.69	0.00	-19.86	9.25	21.91	71.00
	Yes	17.36	11.53	20.84	59.60	-3.45	11.46	11.97	94.20
PMM A	No	1.34	10.34	10.42	96.80	-0.23	10.07	10.07	96.80
	Yes	0.83	10.25	10.28	95.60	-0.16	9.87	9.87	96.80
PMM B	No	0.85	10.14	10.18	95.80	0.08	9.87	9.87	94.80
	Yes	0.16	9.90	9.90	95.40	-0.20	9.84	9.84	95.60
Y <sub>12</sub> (OM II)									
GLM	No	83.26	23.49	86.51	7.60	-120.96	11.99	121.55	0.00
	Yes	87.91	20.62	90.30	2.00	-118.37	10.75	118.85	0.00
NN	No	113.46	29.61	117.26	6.40	-101.99	23.61	104.69	11.20
	Yes	107.31	33.63	112.46	10.40	-125.14	24.95	127.60	4.00
PMM A	No	84.06	29.99	89.25	37.00	-121.02	20.03	122.66	0.40
	Yes	87.66	26.04	91.45	23.60	-109.93	19.63	111.66	1.00
PMM B	No	83.25	23.49	86.50	7.80	-120.98	11.99	121.57	0.00
	Yes	87.93	20.60	90.31	2.00	-118.34	10.77	118.83	0.00
Y <sub>21</sub> (OM III)									
GLM	No	0.34	1.95	1.98	96.00	0.33	1.60	1.63	98.00
	Yes	0.46	1.73	1.79	94.80	0.40	1.58	1.63	96.80
NN	No	12.30	1.83	12.44	0.00	-3.17	1.68	3.59	85.60
	Yes	3.65	2.39	4.36	62.20	-2.35	2.19	3.21	89.20
PMM A	No	0.33	2.16	2.18	98.00	0.62	1.89	1.99	98.60
	Yes	0.47	1.98	2.03	96.60	0.78	1.83	1.99	97.80
PMM B	No	4.58	2.98	5.46	72.80	4.73	2.46	5.33	64.80
	Yes	5.31	2.60	5.92	56.60	5.55	2.43	6.06	50.00
Y <sub>22</sub> (OM IV)									
GLM	No	0.43	2.15	2.19	93.40	-7.60	1.75	7.80	2.40
	Yes	1.10	2.07	2.35	89.80	-7.66	1.70	7.85	2.00
NN	No	-3.36	2.10	3.96	75.20	-1.71	1.67	2.39	97.60
	Yes	0.88	2.11	2.29	92.80	-3.46	2.15	4.07	73.80
PMM A	No	0.42	2.30	2.34	95.60	-8.28	2.05	8.53	4.80
	Yes	1.08	2.23	2.47	92.80	-8.44	1.97	8.67	3.40
PMM B	No	2.95	2.92	4.15	81.20	-5.81	2.68	6.39	54.60
	Yes	3.78	2.76	4.68	65.60	-5.62	2.59	6.19	51.40

### 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  $Y_3 = x_1x_2\epsilon$  (with  $\mathbb{E}(Y_3) = 0$ ). 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 GLM estimator for  $Y_1$ . The NN estimator is characterised with significantly larger variance than the proposed estimators.

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	GLM	No	0.29	3.02	3.04	95.80
	NN	Yes	-0.01	10.22	10.22	96.80
	PMM A	No	0.20	4.97	4.97	99.40
		Yes	-0.01	4.88	4.88	100.00
	PMM B	No	0.29	3.02	3.04	96.00
		Yes	-0.49	3.20	3.24	96.40
Y2	GLM	No	-19.87	7.66	21.30	25.00
	NN	Yes	-0.59	12.79	12.81	96.80
	PMM A	No	-0.44	8.84	8.85	98.00
		Yes	-0.68	9.40	9.43	97.00
	PMM B	No	-19.87	7.66	21.30	24.80
		Yes	3.13	8.83	9.37	93.00
Y3	GLM	No	59.46	7.66	59.96	99.80
	NN	Yes	78.75	12.79	79.78	97.80
	PMM A	No	1.50	8.94	9.07	100.00
		Yes	2.20	8.90	9.17	100.00
	PMM B	No	0.94	1.22	1.54	99.80
		Yes	-2.27	4.76	5.27	99.00

As expected, the bias and variance for GLM are large compared to the non-parametric PMM estimators for non-linear variables ( $Y_2$  and  $Y_3$ ). Note that the PMM A ( $\hat{y} - \hat{y}$  matching)

estimator is almost unbiased even when the target variables are highly non-linear. Owing to  $\mathbb{E}(Y_3) = 0$  for the last variable, the coverage is close to 100%.

## 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  $\pi_u$  is defined as  $\text{logit}(\pi_u) = 0.84 + 0.32X_1 + 0.68X_2 + X_3^T \lambda$  where  $\lambda$  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  $\pi_u$ .
- 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	GLM	4.42	44.75	44.97	95.60
		NN	44.47	103.77	112.90	97.40
		PMM A	8.20	58.83	59.40	99.40
		PMM B	4.42	44.75	44.97	95.60
	Stochastic	GLM	6.05	43.94	44.35	95.80
		NN	3.15	61.14	61.22	97.60
		PMM A	7.13	60.50	60.92	99.40
		PMM B	6.05	43.94	44.35	95.60
Y2	Deterministic	GLM	-86.11	32.38	92.00	30.80
		NN	14.66	44.82	47.15	96.00
		PMM A	-61.56	32.54	69.63	70.80
		PMM B	-86.11	32.38	92.00	30.60
	Stochastic	GLM	9.68	30.15	31.67	95.40
		NN	-7.38	32.36	33.19	96.60
		PMM A	3.71	32.04	32.26	98.20
		PMM B	9.68	30.15	31.67	95.40

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 multiple robust 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
$Y_1$	GLM	–	0.00	0.23	0.23	93.60
	NN	–	0.00	0.23	0.23	94.00
	PMM A	No	0.00	0.23	0.23	93.80
		Yes	0.00	0.23	0.23	93.80
	PMM B	No	0.00	0.23	0.23	93.60
		Yes	0.00	0.23	0.23	93.60
$Y_2$	GLM	–	-17.93	6.67	19.13	21.40
	NN	–	0.18	9.55	9.55	92.20
	PMM A	No	-1.31	9.35	9.44	89.60
		Yes	0.11	9.91	9.91	91.20
	PMM B	No	-17.81	6.66	19.01	21.60
		Yes	0.11	9.91	9.91	91.20

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  $Y_2$ . GLM and the standard PMM A are characterised with the same bias and RMSE, while the addition of multiplicative robustness to the PMM B estimator significantly reduces its bias. For the PMM A 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%. For  $Y_2$  the NN estimator is characterised with the lowest RMSE and highest CR.

## D Implementation in the R language

The proposed methods are implemented in the R language in the `nonprobsvy` package. The 0.1.0 version is available on CRAN but in this paper we used the development version. One should install the package from the github repository using the following code:

```
install.packages("remotes")  
remotes::install_github("ncn-foreigners/nonprobsvy@dev") ## as of 17.06.2024
```

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  $\hat{y} - \hat{y}$  (=1; PMM A) or  $\hat{y} - y$  (=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 (=TRUE) or not (=FALSE).

Example codes are shown below.

- Predictive mean matching with  $\hat{y}-\hat{y}$  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  $\hat{y}-y$  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 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,
                                pmm_reg_engine = "loess"),
  control_inference = controlInf(pmm_exact_se = TRUE)
)

```

Furthermore, we would like to acknowledge the authors of the following packages that were utilized in this paper: `data.table`, `sampling`, `doSNOW`, `progress`, `foreach`, and `xtable`.