Causal Inferences in Small Area Estimation

Setareh Ranjbar, Nicola Salvati and Barbara Pacini

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Abstract

When doing impact evaluation and making causal inferences, it is important to acknowledge the heterogeneity of the treatment effects for different domains (geographic, socio-demographic, or socio-economic). If the domain of interest is small with regards to its sample size (or even zero in some cases), then the evaluator has entered the small area estimation (SAE) dilemma. Based on the modification of the Inverse Propensity Weighting estimator and the traditional small area predictors, the paper proposes a new methodology to estimate area specific average treatment effects for unplanned domains. By means of these methods we can also provide a map of policy impacts, that can help to better target the treatment group(s). We develop analytical Mean Squared Error (MSE) estimators of the proposed predictors. An extensive simulation analysis, also based on real data, shows that the proposed techniques in most cases lead to more efficient estimators.

1 Introduction

In recent years, the thrust of planning process has shifted from the macro to the micro level. There is a demand from administrators and policy planners for reliable estimates of various parameters at the micro level (Chandra et al., 2011). In particular, policy makers and decision takers would like to know the impact of a given policy in certain unplanned geographic, socio-demographic, or socio-economic domains. At this micro level, direct estimates for evaluating the impact of the policy are not accurate because sample surveys are usually designed so that direct estimators for larger domains (states, regions - macro level) lead to reliable estimates. If the domain of interested for impact evaluation is small with regards to its sample size (or even zero in some domains), then the evaluator has entered the small area estimation (SAE) dilemma. Small area techniques provide official statistics using the survey samples and other sources of available information from which the estimators can borrow strength.

It is still surprising that no link has been established between the SAE literature and causal analysis that would allow for evaluating the impact of such a policy or decisions at a finer population level. There are exceptions but with different intentions. Chan (2018) attempts to combine the strength of the two fields, causal inferences and small area estimation, to provide more precise generalization of the randomized trials to the entire population. This paper uses model-based techniques borrowed from the SAE literature to get a better estimate of the average treatment effect in the sub-classification stratas, which are defined by the propensity scores, that have a sparse sample from the randomized experiment. There has been some statistical research on how to assess the generalizability of randomized trials to the target population in which it may be implemented (external validity). Stuart et al. (2001) propose the use of propensity-score-based metrics to quantify the similarity of the participants in a randomized trial and a target population. Stuart et al. (2015) provide a case study using one particular method, which weights the subjects in a randomized trial to match the population on a set of observed characteristics. Methods for assessing and enhancing external validity are
just beginning to be developed and much of the discussion around external validity underestimates treatment effect heterogeneity.

Both causal inferences and SAE have a rich body of literature that covers a vast range of technical and practical issues. Here we provide a concise summary of the two. However, to our best knowledge almost no research has been conducted to combine the two methodologies, despite the fact that this could be relevant for designing efficient and effective policies.

Causal inferences has a long history in biometrics/biostatistics and medicine, for obvious reasons with the focus on randomized controlled trials (having treatment, control and/or placebo groups). However, in social sciences the major challenge is that for the evaluation of a project or a policy intervention such a randomization of the treatment assignment is often not possible, either due to anti-discriminatory policies or due to the individual’s choices to accept or reject the treatment (non-compliance) (Frumento et al., 2012; Mealli and Pacini, 2013). Therefore, from the very beginning of the project, the randomization assumption is violated to such an extent that the evaluators face the problem of selection bias. In the past 25 years the literature on impact evaluation in social sciences has developed considerably, and a variety of methods based on observational (non-experimental) data are proposed to address these issues. The pioneer works in this line of research include the series of papers by Rubin (1974, 1973a,b, 1977, 1978). For a comprehensive review of the subject we refer to Pearl (2009) and Imbens and Rubin (2015).

The SAE techniques aim at producing reliable estimates for domains with small sample sizes by borrowing strength from data of other domains. The SAE techniques are generally based on model-based methods. One popular approach uses mixed (random) effects models for SAE. Area-level and unit-level linear mixed models have been studied in the literature to obtain empirical best linear unbiased predictors of small area means (Fay and Herriot, 1979; Battese et al., 1988). Empirical best estimation is useful for estimating the small area means efficiently when normality holds. Otherwise its properties can be deteriorated especially by the presence of outliers in the data. In recent years, Chambers and Tzavidis (2006) have addressed the issue of outlier robustness in SAE proposing to apply the M-quantile (hereafter, MQ) regression models to SAE with the aim of obtaining reliable and outlier robust estimators without recourse to parametric assumptions for the residuals distribution using M-estimation theory. More recently, Sinha and Rao (2009) have also tackled this issue from the perspective of linear mixed models. We refer to Rao and Molina (2015) for a general introduction and an overview of these models.

In this paper, we propose new methods to estimate the area specific average treatment effects for unplanned domains in observational studies. The main motivation behind this is that such methods allow for local rather than universal policy advices. Another advantage of our proposed method over existing ones is that in case there are no treated units within the sample the classical approach will provide no estimate of the effect whereas the small area techniques can be used to predict the effects even if the sample size of the treated or controlled group is zero in the area of interest. We adopt the nested error unit-level regression models (Battese et al., 1988) and the M-quantile models (Chambers and Tzavidis, 2006) to estimate propensity scores and the unobserved outcome for the population. Then to estimate the area specific average treatment effects for unplanned domains we propose a modification of the Double Robust Inverse Probability Weighting estimator based on the estimated propensity scores and predicted outcomes (Rosenbaum and Rubin, 1983; Hahn, 1998).

As case study to apply the proposed methodology, we consider the following substantive policy issue. Suppose policy makers are interested in evaluating the impact of temporary employment contracts on the economic insecurity of households, with potential consequences on consumption behaviour, life satisfaction and well-being in general. The increase in non-standard forms of employment in many countries appears to have contributed to rising in-work poverty (Eurofound and the International Labour Office, 2017; Crettaz, 2013). The development of forms of flexible employment may have both positive and negative consequences. On the one hand it is expected to increase employment and reduce unemployment. On the other hand, this is
often associated with greater economic insecurity and poorer working conditions. Relatively little research has been dedicated to the link between job instability and subjective poverty. According to some scholars, temporary as opposed to permanent employment contributes to lower general life satisfaction and well-being and a worse perceived household income situation. Scherer (2009) investigates the social consequences of insecure employment (fixed-term contracts), taking into account information on current family life, future family plans and general well-being. The analysis, for Western European countries, confirms that insecure employment is accompanied by more problematic social and family situations. These negative consequences are partly shaped by the specific institutional context (welfare state and labour market conditions). Filandri and Struffolino (2018), using the 2014 Italian wave module of the EU-SILC (EU Statistics on Income and Living Conditions) survey, find that subjective poverty is associated with instability of household members’ job contracts, with effects on other life domains, such as well-being, adequate level of consumption, social integration.

Differently from the previous literature, in this paper we adopt a causal perspective and consider the effect of temporary employment on the feeling about the household economic status (declaring the lowest monthly income to make ends meet). As discussed above, an overall negative effect of temporary employment is expected compared to permanent employment. The effects may be confounded by local institutional contexts (local welfare policies and labour market conditions), in addition to socio-demographics characteristics and information on the employment situation (work intensity and the skill level of the occupation). We use the 2015 Italian wave module of the EU-SILC survey to implement a design based simulation study. We expect the effect to be heterogeneous across Italian regions due to different quality, and cost, of living.

The paper is organised as follows. Section 2 is devoted to setting out the theoretical background and the assumptions of the casual inference which is then used to extend the small area predictors. We introduce the proposed extensions to the EBLUP and M-quantile-based predictors under casual inference. Their corresponding MSE estimators are presented in Section 4. Section 5 discusses benchmarking properties of the estimators. In Sections 6 and 7 the performances of these newly proposed predictors are empirically assessed, both in terms of point estimation performance and MSE estimation, by means of a model-based simulation study that considers a number of different scenarios as well as by a design-based simulation based on EU-SILC data. Finally, in Section 8 we summarise our main findings, and provide directions for future research.

2 Notation and assumptions

To explain the methodology that is developed in this paper we need to link the notations and the terminologies based on the conventions used both in small area estimation and in causal inference. Specifically, in SAE, we usually use small letters to indicate the outcome variable because we analyse a finite population, while in the new framework we switch to capital letters to take into account the probabilistic assignment mechanism of treatment. In what follows we use the bold cases to indicate vectors and matrices. The parameters of interest are shown using Greek letters , for example $\alpha$, and their estimates are distinct by carrying a ‘hat’, for example $\hat{\alpha}$.

Consider a (super) population $U$ of size $N$ that is partitioned into $m$ mutually disjoint sub-populations/domains $U_j$ of size $N_j$, $j = 1, \ldots, m$. In what follows we assume the availability of survey data on the outcome variable and explanatory variables, which can be used to model them. In addition, the methods assume the availability of micro-level census or administrative data on the same set of explanatory variables. Therefore, we assume that values of a (continuous) outcome variable of interest $Y_{ij}$ are available from a random sample $s$, which includes units from all target domains. We assume that a set of auxiliary information, denoted as a vector of covariates $x_{ij}$, is available for all the units in the population and that provides predictive power for the unobserved part of the population. It is also assumed that the vector $x_{ij}$ of dimension $p \times 1$ contains
the set of all confounders and some additional covariates that are useful in predicting the outcome. More generally, the vector of covariates may include both individual and area-level covariates.

We are interested in studying the impact of a binary treatment, $W_{ij}$, that takes the value 1 for treated and 0 for non-treated (control) units in the population. We focus on treatment assigned at the individual level and assume that the information on treatment status exists for all population units, for example from administrative sources. This is a plausible assumption in many applications, such as unemployment benefits, government subsidies, pensions and so on.

We denote the sample size, the sampled part of the population and the non-sampled part of the population in each domain by $n_j$, $s_j$ and $r_j$ respectively, with $U_j = s_j \cup r_j$. The total sample size is given by $n = \sum_{j=1}^{m} n_j$.

To link the two methodologies on small area estimation and causal inference, we adopt the framework of Rubin Causal Model (RCM) (Rubin, 1974), and use the approach of potential outcomes to properly define the causal estimands of interest. In small area estimation setting the aim is to provide estimates of the average effects for each small sub-population or domain (i.e., these are the unplanned domains in the survey) rather than for the entire population. This is particularly relevant when heterogeneous effects are expected among different domains. In these cases our proposal can provide a map of policy impacts at a small area level, helping to better understand the outcome of an intervention and to better target the treatment group(s).

The potential outcome approach is firstly developed under SUTVA (Stable Unit Value Assumption; Rubin, 1980), stating that the outcome of each unit is unaffected by the treatment assignment of any other unit and also that there are no different versions of each treatment level, which may lead to different potential outcomes. Within the simplest framework, each unit has only two potential outcomes, defined as $Y_{ij}^0$ and $Y_{ij}^1$ under control and under treatment, respectively. The former, $Y_{ij}^0$, denotes the outcome that would be realized by the individual if he or she is not treated and the latter, $Y_{ij}^1$, indicates the outcome that would be realized by the same individual if he or she is treated. The potential outcomes for each unit would be vector-valued instead of scalars, including all the possible combinations of treatment assignment for a set of units.

For the sampled units (the set $s_j$) only one of the potential outcomes is observed for each individual; the other is necessarily missing and needs to be predicted, entering the so called fundamental problem of causal inference. We then observe the outcome variable $Y_{ij}$ where $Y_{ij} = W_{ij} Y_{ij}^1 + (1 - W_{ij}) Y_{ij}^0$, in this set. For the non-sampled units (the set $r_j$), however, neither of the potential outcomes are available and both are need to be predicted, implying that for the out of sample units $Y_{ij}$’s are never observed. In this respect, our problem resembles that studied widely in the literature of imputation for missing data in the context of small area estimation. See Haziza and Rao (2010), Cantoni and de Luna (2018) and Chen and Haziza (2019) for a comprehensive review of this topic. The main difference of this line of literature with our work is twofold: in our setting (i) causal inferences require additional assumptions and (ii) the percentage of missing values for which we need to predict the value is not negligible.

The individual treatment effect for the unit $i$ in area $j$ can be defined as a comparison of potential outcomes, such as the difference, denoted as:

$$
\tau_{ij} = Y_{ij}^1 - Y_{ij}^0.
$$

This parameter is not identifiable due to a lack of information for each unit, but several causal estimands can be defined as summaries of individual effects, which are identifiable and can be estimated out of the data under some additional assumptions. Here we distinguish between two sets of estimands that are essential for our analysis. The first includes the average treatment effect (SATE) for the sample units. The second set of estimands includes the ATE for the population, named PATE. Each of these estimands can be defined at the area (domain) level as follows:
The aim of our proposal is to provide reliable estimates of $\tau_{PATE_j}$ for different areas/domains, borrowing strength from small area estimation techniques.

Causal effects from observational data can be identified under a set of assumptions, guaranteeing that the treatment is effectively randomized within cells defined by the values of a set of observed covariates. Slight modifications are needed in some cases for the identification of heterogeneous effects among different domains.

Here, we assume SUTVA, which is implied in the notation above, together with strong ignorability assumptions:

**Assumption 1. Stable Unit Treatment Value**

The potential outcome for any unit does not vary with the treatments assigned to other units, and, for each unit, there are no different forms or versions of each treatment level. With multilevel data, this assumption may be questionable, especially for the units in the same area/domain. The implications of cluster structure, which may affect both the assignment to treatment and potential outcomes, have not been intensively studied, with a few exceptions (Arpino and Mealli, 2011; Li et al., 2013; Kim et al., 2017; Cafri et al., 2019). However in our study, it is reasonable to assume that the treatment administered at the unit level will not affect other units within the same area and that there are no expected movements and interference across domains. Therefore, SUTVA will be maintained assuming no interference within and between clusters.

**Assumption 2. Unconfoundedness based on propensity scores**

The assignment mechanism is unconfounded (with the potential outcomes, Rosenbaum and Rubin, 1983) if:

$$W_{ij} \perp (Y_{ij}^1, Y_{ij}^0) \mid X_{ij} = x_{ij}, \quad \forall i \in U_j,$$

or

$$W_{ij} \perp (Y_{ij}^1, Y_{ij}^0) \mid e(x_{ij}), \quad \forall i \in U_j,$$

where $e(x_{ij}) = Pr(W_{ij} = 1 | X_{ij} = x_{ij})$ is known as a propensity score. We assume that, conditional on a set of pre-treatment covariates or conditional solely on the propensity scores, the assignment mechanism is independent from the potential outcomes.

**Assumption 3. Common support (overlap)**

We assume that the unconfounded assignment mechanism is probabilistic, that is all the unit-level probabilities for receiving treatment are strictly between zero and one:

$$0 < e(x_{ij}) = Pr(W_{ij} = 1 | X_{ij} = x_{ij}) < 1 \quad \forall i \in U_j.$$

In other words, each unit in the defined population has a chance of being treated and a chance of not being treated (Rosenbaum and Rubin, 1983). We assume common support within area, based on the whole set of population auxiliary variables.
Treatment assignment mechanisms satisfying both overlap and unconfoundedness are called strongly ignorable, so that we assume strong ignorability within each area/domain.

Rubin et al. (2004) discuss the importance of using propensity scores to match the treatment and control units while using regression models in the complex survey settings. This approach can be also considered as a diagnostic tool to test the Assumption 3.

3 Small area estimators for causal inference

Our proposed estimators for $\tau_{PATE_{j}}$ are based on the inverse propensity score weighting (Rosenbaum and Rubin, 1983). The propensity scores are the probability that each individual will be treated by a program or affected by an intervention. This quantity is mainly unknown except for instance in complete randomized experiments. In this work we mainly focus and discuss the cases that are based on observational data which is more useful in practice; and therefore we estimate the unknown propensity scores. To develop our proposal we start with the setting where propensity scores are known. Then we can relax this assumption.

We first express the equation (1) as $\tau_{SATE_{j}} = E_j[Y_{1ij}] - E_j[Y_{0ij}]$, where the expectation is evaluated over the sub-sample of area $j$. Under unconfoundedness Assumption 2 Imbens and Wooldridge (2009) show that:

$$E_j[Y_{1ij}] = E_j \left[ \frac{W_{ij}Y_{ij}}{e(x_{ij})} \right],$$

and

$$E_j[Y_{0ij}] = E_j \left[ \frac{(1 - W_{ij})Y_{ij}}{1 - e(x_{ij})} \right],$$

where $e(\cdot)$ is the function that determines the units propensity scores based on their vector of confounding covariates, $x_{ij}$. The natural estimator for this parameter is:

$$\hat{\tau}_{SATE_{j}} = \frac{1}{n_j} \sum_{i=1}^{n_j} \left[ \frac{w_{ij}y_{ij}}{e(x_{ij})} - \frac{(1 - w_{ij})y_{ij}}{1 - e(x_{ij})} \right].$$ (3)

In the context of small area estimation we assume the unit level auxiliary information is available to predict the outcome for the out of sample units. Therefore, we extend equation (3) to the entire population, that is we provide an estimate for $\tau_{PATE_{j}}$ in the following:

$$\hat{\tau}_{PATE_{j}} = \frac{1}{N_j} \left( \sum_{i \in s_j} \left[ \frac{w_{ij}y_{ij}}{e(x_{ij})} - \frac{(1 - w_{ij})y_{ij}}{1 - e(x_{ij})} \right] + \sum_{i \in r_j} \left[ \frac{w_{ij}\hat{y}_{ij}}{\hat{e}(x_{ij})} - \frac{(1 - w_{ij})\hat{y}_{ij}}{1 - \hat{e}(x_{ij})} \right] \right).$$ (4)

If the propensity scores are unknown, the $e(x_{ij})$ values need to be replaced by their estimates. In this case the weights given to the observed outcome must be adjusted to sum up to 1 in each part of equations (5) and (6). Then the estimators are redefined as:

$$\hat{\tau}_{SATE_{j}} = \left( \sum_{i \in s_j} \frac{w_{ij}y_{ij}}{e(x_{ij})} \right)^{-1} \left( \sum_{i=1}^{n_j} \frac{w_{ij}}{e(x_{ij})} \right)^{-1} - \left( \sum_{i \in s_j} \left[ \frac{(1 - w_{ij})y_{ij}}{1 - e(x_{ij})} \right] \left( \sum_{i=1}^{n_j} \frac{1 - w_{ij}}{1 - e(x_{ij})} \right)^{-1} \right).$$ (5)

6
\[
\hat{\tau}_{PATE} = \left( \sum_{i \in s_j} \left[ \frac{w_{ij} \hat{y}_{ij}}{\hat{e}(x_{ij})} \right] + \sum_{i \in r_j} \left[ \frac{w_{ij} \hat{y}_{ij}}{\hat{e}(x_{ij})} \right] \right) \left( \sum_{i=1}^{N_j} \frac{w_{ij}}{\hat{e}(x_{ij})} \right)^{-1} - \left( \sum_{i \in s_j} \left[ \frac{(1 - w_{ij}) \hat{y}_{ij}}{1 - \hat{e}(x_{ij})} \right] + \sum_{i \in r_j} \left[ \frac{(1 - w_{ij}) \hat{y}_{ij}}{1 - \hat{e}(x_{ij})} \right] \right) \left( \sum_{i=1}^{N_j} \frac{1 - w_{ij}}{1 - \hat{e}(x_{ij})} \right)^{-1}.
\]

In what follows we refer to (5) as the IPW-Direct estimator, which is the classical IPW estimator proposed by Rosenbaum and Rubin (1983). Alternative direct estimators, that use the survey weights, have been proposed by Zanutto (2006) and by Miratrix et al. (2018). The estimator proposed in (6) can take two forms depending on the method we adopt to predict the unobserved \( y_{ij} \)'s and to estimate the propensity scores. In the first proposal we predict the unobserved outcomes using Empirical Best Linear Unbiased Prediction and use a generalized linear mixed model to estimate the propensities. This estimator is referred to as IPW-EBLUP hereafter and can also be seen as a modification of the EBLUP estimator for the area level mean. In the second proposal we use a robust approach based on M-quantile models proposed by Chambers and Tzavidis (2006) for the continuous outcome and by Chambers et al. (2016) for the binary case to predict the unobserved outcomes and estimate the propensity scores. The resulting estimator is labelled IPW-MQ hereafter. We explain in more detail the models and the estimating strategies used for IPW-EBLUP and IPW-MQ in Section 3.1.

The properties of IPW-Direct estimators are widely studied in the literature; see for instance Hirano et al. (2003) and Wooldridge (2007) for more details. However, when the area/domain sample sizes are small these estimates are no longer reliable, that is, they could vary significantly. Our proposed estimators IPW-EBLUP and IPW-MQ overcome this problem by borrowing strength from additional sources of information rather than merely using the sample data. The second estimator can also deal with data that is contaminated by outlying values. The large sample properties of IPW-EBLUP are studied in Appendix A.

### 3.1 Data generating processes and estimation strategies

To explain the data generating process and justify our estimation strategies for predicting the unobserved population outcomes and estimating the population propensity scores once again we use the potential outcome framework. Consider the two potential outcomes for individual \( i \) in area \( j \) to be related in the following way (Imbens and Rubin, 2015, p. 263):

\[
Y_{ij}^1 = Y_{ij}^0 + \tau_j,
\]

where \( \tau_j \) is the area specific causal effect of a policy intervention. Since our main objective is to acknowledge the heterogeneity of the average treatment effect over sub-populations (here small areas) we do not take into account the individual level heterogeneity.

To benefit from the hierarchical structure in the data, without loss of generality, we consider a nested error linear model (Battese et al., 1988) as the data generating process of the potential outcome in the absence of the treatment:

\[
y_{ij}^0 = X_{ij}^T \beta + u_j + \epsilon_{ij},
\]

where \( u_j \) is the area specific random effect and \( \epsilon_{ij} \) is the individual errors, the distributions of which are to be assumed (in general normal) if the model is fitted parametrically. This holds for the entire population as well as for the sample at hand in the absence of sample selection bias. Having \( w_{ij} \) as the individual treatment
status the outcome itself (observed in the sample and not observed for the population) is:

\[ y_{ij} = (w_{ij} y_{1ij} + (1-w_{ij}) y_{0ij}) = x_{ij}^T \beta + w_{ij} \tau_j + u_j + \epsilon_{ij}. \]  \hspace{1cm} (7)

In the context of small area estimation we need to fit this model to the sample data and predict the outcome for the entire population by using the estimated parameters of the model and the auxiliary information that is available for the entire population. There are many different techniques that are developed in the SAE literature; two sets of parametric models are discussed in this paper, but, of course, others can also be adopted if appropriate. It is also worth noting that, if we have the area level variables in the model then the interaction between these variables and the treatment variable must also be included in the random part of the model (Arpino and Mealli, 2011).

3.1.1 IPW-EBLUP

We start by assuming that the area specific causal effects, \( \tau_j \)'s, are randomly distributed with \( \tau_j \sim N(\gamma_0, \sigma_\gamma^2) \). Then equation (7) can be rewritten as

\[ y_{ij} = \tilde{x}_{ij}^T \tilde{\beta} + w_{ij} \gamma_j + u_j + \epsilon_{ij}, \]  \hspace{1cm} (8)

where \( \tilde{x}_{ij} = (x_{ij}^T, w_{ij})^T \) is of dimension \((p+1) \times 1\), \( \tilde{\beta} = (\beta^T, \gamma_0)^T \) is the vector of fixed effects and we further assume that \( u_j \sim N(0, \sigma_u^2) \), and \( \epsilon_{ij} \sim N(0, \sigma_\epsilon) \). As a consequence of our assumption on the distribution of the area specific causal effects we have \( \gamma_j \sim N(0, \sigma_\gamma) \), that is the random slope associated with the treatment status. For obtaining the IPW-EBLUP, a mixed linear model (more specifically a random slope model) is fitted, using the maximum likelihood (ML) or restricted maximum likelihood (REML) method (McCulloch and Searle, 2001; Pinheiro and Bates, 2006), to predict the outcome \( \hat{y}_{ij} \) for \( i \in r_j \) under model (8). The assumption of normality of the random components are mainly in place to specify the form of ML or REML used for estimating the unknown parameters of the model, including the unknown parameters of the variance-covariance matrix. However, this assumption can easily be relaxed using other existing methods for fitting random effect models, such as quasi-likelihood methods or Generalized Estimating Equation (Liang and Zeger, 1986) under some other mild conditions.

**Proposition 1.** Under Assumption 2, unconfoundedness, the vector of random slopes \( \gamma \) and random intercepts \( u \) in equation (8) are independent, that is:

\[
\begin{bmatrix}
\gamma \\
u
\end{bmatrix} \overset{i.i.d}{\sim} \begin{pmatrix} 0, \Sigma_\omega \end{pmatrix},
\]

where \( \gamma = (\gamma_1, \cdots, \gamma_m)^T \), \( u = (u_1, \cdots, u_m) \), and \( \Sigma_\omega = \begin{pmatrix} \Sigma_\gamma & 0 \\ 0 & \Sigma_u \end{pmatrix} \).

**Proof.** Based on Assumption 2 the treatment assignment is independent from the potential outcomes conditional on the set of pre-treatment covariates (confounders). This assumption requires that conditional on observed covariates there are no unobserved factors that are associated both with the assignment mechanism and potential outcomes, that is, \( E[\gamma_j (u_j + \epsilon_{ij})] = 0 \). Because \( E[\gamma_j \epsilon_{ij}] = 0 \) it goes that \( E[\gamma_j u_j] = 0 \).

In equation (8) the average return to \( w_{ij} \) is captured by the fixed effect and the area specific heterogeneity of the return to \( w_{ij} \) is modeled through a random slope \( \gamma_j \), that needs to be predicted (Li et al., 2013). However, our estimators of the total causal effect do not merely depend on the estimation/prediction of
these two effects. In addition, we balance the characteristics of treated and control groups by weighting the outcomes based on the individual propensity scores. Therefore, these estimators have doubly robust properties (Bang and Robins, 2005), that is, having misspecified only one of the models for the prediction of the outcomes or for the estimation of the propensity scores, we can still provide a consistent estimator for the causal effects of each area. Further, the hierarchical structure of the data as it is defined in equation (8) for the outcome model should also be considered in the estimation model of the propensity scores, see Arpino and Mealli (2011); Arpino and Cannas (2016). Then, we consider the following model for the propensity scores:

\[ \eta_{ij} = \Lambda(e(x_{ij})) = x_{ij}^T \alpha + \nu_j, \]  

(9)

where \( \Lambda(\cdot) \) is a logit link function. Substituting the estimated values \( \hat{y}_{ij} = x_{ij}^T \hat{\beta} + w_{ij} \hat{\gamma}_j + \hat{u}_j \) and \( \hat{e}(x_{ij}) = \Lambda^{-1}(x_{ij}^T \hat{\alpha} + \hat{\nu}_j) \) in equation (6) provides the estimates of IPW-EBLUP. Asymptotic properties of the IPW-EBLUP are presented in Appendix A.

3.1.2 IPW-MQ

An alternative to mixed models and IPW-EBLUP is given by the M-quantile regression models for estimating the outcome variable and the propensity scores. If an outlying value can destabilize a population estimate based on a large survey sample, it can almost certainly destroy the validity of the corresponding direct estimate for the small area from which the outlier is sourced, since this estimate will be based on a much smaller sample size. This problem does not disapper when the small area estimator is a model based estimator such as EBLUP: large deviations from the expected response (outliers) are known to have a large influence on classical maximum likelihood inference based on generalized linear mixed models (GLMM). Chambers and Tzavidis (2006) and Sinha and Rao (2009) addressed the issue of outlier robustness in SAE proposing techniques that can be used to down-weigh any outliers when fitting the underlying model. In particular, Chambers and Tzavidis (2006) proposed to apply the M-quantile regression models to SAE with the aim of obtaining reliable and outlier robust estimators without recourse to parametric assumptions for the residuals distribution using M-estimation theory. For details on M-quantile regression see Breckling and Chambers (1988).

When using the M-quantile method the unobserved outcomes are predicted as follows:

\[ \hat{y}_{ij} = x_{ij}^T \hat{\beta}_{q_j} + w_{ij} \hat{\gamma}_{q_j}, \]  

(10)

where \( \hat{\beta}_{q_j} \) and \( \hat{\gamma}_{q_j} \) are the regression coefficients of the M-quantile model estimate at quantile \( q_j \), that is, the average of the estimated quantiles for the sample units in area \( j \). The Chambers and Tzavidis (2006) proposal is an alternative to the random effect models for characterizing the variability across the population not accounted for by the regressors based on the the M-quantile coefficients of the population units. The authors observed that if a hierarchical structure does explain part of the variability in the population data, units within areas defined by this hierarchy are expected to have similar M-quantile coefficients. For details on the computation of M-quantile coefficients see Chambers and Tzavidis (2006).

For estimating the propensity scores the M-quantile for binary data proposed by Chambers et al. (2016) is adopted. Modelling the M-quantiles of a binary outcome presents more challenges than modelling the M-quantiles of a count outcome. A detailed account of these challenges is provided in Chambers et al. (2016). The authors proposed a new semiparametric M-quantile approach to small area prediction for binary data that extends the ideas of Cantoni and Ronchetti (2001) and Chambers and Tzavidis (2006). This predictor can be viewed as an outlier robust alternative to the more commonly used conditional expectation predictor (9) for binary data that is based on a logit GLMM with Gaussian random effects. With the proposed
approach random effects are avoided and between-area variation in the response is characterized by variation in area-specific values of M-quantile indices. Furthermore, outlier robust inference is achieved in the presence of both misclassification and measurement error.

Under the M-quantile framework the propensity scores are estimated as:

\[ \hat{\eta}_{ij} = \Lambda(\hat{e}(x_{ij})) = x_{ij}^T \hat{\alpha}_{\hat{q}_j}, \]  

(11)

where the area level M-quantile coefficients are computed in different way with respect to the continuous outcome. See Chambers et al. (2016) for details. Substituting the \( \hat{y}_{ij} \) and \( \hat{e}(x_{ij}) \) in equation (6) provides the estimates of IPW-MQ.

4  MSE estimators in the finite population

In the context of randomized experiments Ding et al. (2019) proposed the decomposition of overall treatment effect variation into systematic and idiosyncratic components. In this paper we are in the framework of observational data and we are using the inverse propensity weighting; for this reason, we decompose the variation of the effect into the variation due to the estimation of the (i) outcome and the (ii) propensity scores. For the first component of variation we propose its estimation with an analytical derivation. In particular, for the IPW-EBLUP the proposal is based on the MSE estimation approach that is described in Prasad and Rao (1990) and represents an extension of the ideas in Opsomer et al. (2008). For IPW-MQ the MSE estimator is based on second order approximations to the variances of solutions of outlier robust estimating equations and represents an extension of the ideas in Chambers et al. (2014). The proposed analytical MSE estimators do not take into account the variability due to the estimation of the propensity scores. So to add this component of variability we suggest using re-sampling techniques. Miratrix et al. (2018) point out the importance of considering the extra variability that is introduced when estimating \( \tau_{PATE} \) using weights, which is a similar problem to ours. In particular, for IPW-EBLUP we suggest using a parametric bootstrap technique, such as that proposed by Gonzalez-Manteiga et al. (2008) or a non-parametric bootstrap procedure as in Opsomer et al. (2008). For IPW-MQ, we suggest applying an outlier robust bootstrap estimator that is the modified version of the block-bootstrap approach of Chambers and Chandra (2013). These bootstrap methods are explained in detail in Appendix B.

We show in simulation experiments (Section 6) how these approaches can be useful for estimating the MSE of various small area predictors that are considered in this paper.

To develop the analytical MSE estimators for small area predictors based on EBLUP and MQ approaches, we rewrite the estimator in equation (6) as a linear combination of observed and unobserved outcomes:

\[ \hat{\tau}_{PATE,j} = K_j^{-1} \left( \sum_{i \in s_j} \left[ \frac{w_{ij} y_{ij}}{\hat{e}(x_{ij})} \right] + \sum_{i \in r_j} \left[ \frac{w_{ij} \hat{y}_{ij}}{\hat{e}(x_{ij})} \right] \right) \]

\[ \quad - T_j^{-1} \left( \sum_{i \in s_j} \left[ \frac{(1 - w_{ij}) y_{ij}}{1 - \hat{e}(x_{ij})} \right] + \sum_{i \in r_j} \left[ \frac{(1 - w_{ij}) \hat{y}_{ij}}{1 - \hat{e}(x_{ij})} \right] \right) \]

\[ = \sum_{i \in s_j} D_{ij} y_{ij} + \sum_{i \in r_j} D_{ij} \hat{y}_{ij}, \]  

(12)
where \( K_j = \sum_{i=1}^{N_j} w_{ij}/\hat{\epsilon}(x_{ij}), T_j = \sum_{i=1}^{N_j}(1 - w_{ij})/(1 - \hat{\epsilon}(x_{ij})), \) and 
\[
D_{ij} = \left( \frac{K_j^{-1} w_{ij}}{\hat{\epsilon}(x_{ij})} - \frac{T_j^{-1} (1 - w_{ij})}{1 - \hat{\epsilon}(x_{ij})} \right).
\]

### 4.1 MSE of IPW-EBLUP

We start from equation (12) to derive the analytic formula of the MSE for IPW-EBLUP. We consider that the \( D_{ij} s \) are known for the entire population, so we do not account for their variations originating from the estimation of the propensity scores. If the proportion of observed outcomes, \( f_j = \frac{n_j}{N_j} \), is small(negligible) we can write:
\[
\hat{\tau}_{PATE,j} - \tau_j = D_j^T \hat{y}_j - D_j^T y_j = D_j^T (\hat{y}_j - y_j).
\]
where \( D_j, \hat{y}_j \) and \( y_j \) are the vectors of \( D_{ij} s, \) the response variable and predicted outcomes, respectively, for the population in area \( j \) (Prasad and Rao, 1990). The prediction of the outcome is obtained using the equation (8):
\[
\hat{y}_j = \hat{X}_j^T \hat{\beta} + \hat{W}_j \hat{\gamma} + Z_j \hat{u}, \tag{13}
\]
where \( \hat{X}_j \) is the matrix of auxiliary variables for area \( j \) of dimension \((p+1) \times n_j\), \( \hat{W}_j \) is a sparse matrix with the \( j \)th column being replaced by the treatment status of individuals in area \( j \), \( Z_j \) is a sparse matrix of area indicators with only the elements of column \( j \)th equal to one, so that \( var(y) = \Sigma = \hat{W} \Sigma \hat{W}^T + Z \Sigma Z^T + \Sigma \).

If the variances of the random components are known, standard results from BLUP theory (McCulloch and Searle, 2001, Chapter 9) guarantee that, given the model specifications (8) and Preposition 1, the generalized least squares estimator
\[
\hat{\beta} = \left( \hat{X}^T \Sigma^{-1} \hat{X} \right)^{-1} \hat{X}^T \Sigma^{-1} Y
\]
and the predictors
\[
\hat{\gamma} = \Sigma_{\omega} \hat{W}^T \Sigma^{-1} \left( Y - \hat{X} \hat{\beta} \right) \quad \hat{\gamma}_\Sigma = \Sigma_{\omega} \Sigma_{\omega} Z^T \Sigma^{-1} \left( Y - \hat{X} \hat{\beta} \right)
\]
are optimal among linear estimators and predictors, respectively. Replacing \( \hat{y}_j \) with (13) we can write
\[
\hat{\tau}_{PATE,j} - \tau_j = D_j^T (\hat{y}_j - y_j) = D_j^T c_j (\hat{\beta} - \bar{\beta}) + D_j^T \hat{Z}_j \left[ \Sigma_{\omega} \hat{Z}^T \Sigma^{-1} \left( Y - \hat{X} \hat{\beta} \right) - \omega \right], \tag{14}
\]
where \( c_j = \hat{X}_j^T - \left( \hat{Z}_j \Sigma_{\omega} \hat{Z}^T \hat{V}^{-1} \hat{X} \right), \hat{Z}_j = (\hat{W}_j, Z_j), \hat{Z} = (\hat{W}, Z), \) and \( \omega = (\gamma^T, u^T)^T, \) \( \Sigma_{\gamma} = \sigma_{\gamma} I_m, \) \( \Sigma_{\omega} = \sigma_{\omega} I_m. \) If both the random slopes and the area specific intercepts are treated as true random effects in the underlying model (8), the mean prediction error is 0 and the covariance between the two terms in equation (14) is also 0, so that the MSE of the prediction errors is
\[
E \left[ \left( \hat{\tau}_{PATE,j} - \tau_j \right)^2 \right] = D_j^T \hat{Z}_j \Sigma_{\omega} \left( I - \hat{Z}^T \hat{V}^{-1} Z \Sigma_{\omega} \right) \hat{Z}_j^T D_j + D_j^T c_j (\hat{X}^T \Sigma^{-1} \hat{X}) c_j^T D_j. \tag{15}
\]
To extend these results for IPW-EBLUP, that is, where \( V \) is unknown, the variation that comes from the estimation of variance components has to be added. The resulting EBLUP version of equation (14) is
\[
D_j^T c_j (\hat{\beta} - \bar{\beta}) + D_j^T \hat{Z}_j \left[ \Sigma_{\omega} \hat{Z}^T \hat{V}^{-1} \left( Y - \hat{X} \hat{\beta} \right) - \omega \right], \tag{16}
\]
with \( \hat{c}_j = \hat{X}_j^T - (\hat{Z}_j \hat{\Sigma}_w \hat{Z}_j^T \hat{V}^{-1} \hat{X}) \) using restricted maximum likelihood estimators for the unknown variance components in \( V \) and \( \Sigma_w \). To derive a second-order approximation for the MSE as well as an estimator for the MSE that is correct up to the second order we follow the method proposed by Opsomer et al. (2008). The vector of unknown components of the variance-covariance matrix is \( \theta = (\sigma^2_{\gamma}, \sigma^2_{\omega}, \sigma^2_{\epsilon}) \) and we define

\[
S_t = D_j^T \hat{Z}_j \left( \frac{\partial \Sigma_w}{\partial (\theta)_{c}} \hat{Z}_j^T \hat{V}^{-1} + \Sigma_w \hat{Z}_j^T \frac{\partial V^{-1}}{\partial (\theta)_{c}} \right), \quad t = 1, 2, 3.
\]

Further, let us define the \( 3 \times 3 \) matrix \( I \), the Fisher information matrix with respect to the variance components \( \theta \), then, the MSE of the IPW-EBLUP predictor is given by

\[
MSE(\hat{\tau}_{EBLUP}^{PATE}) = E \left[ (\hat{\tau}_{EBLUP}^{PATE} - \tau_j)^2 \right] + tr \left( S \Sigma \Sigma^T I^{-1} \right) + o(m^{-1}),
\]

and its estimator can be obtained as

\[
mse(\hat{\tau}_{EBLUP}^{PATE}) = D_j^T \hat{Z}_j \hat{\Sigma}_w \left( I - \hat{Z}_j \hat{V}^{-1} \hat{Z} \hat{\Sigma}_w \right) \hat{Z}_j^T D_j + D_j^T \hat{c}_j (\hat{X}^T \hat{V}^{-1} \hat{X}) \hat{c}_j^T D_j
\]

\[
+ 2 \left( Y - \hat{X} \hat{\beta} \right)^T \hat{V} \hat{S}^T I^{-1} \hat{S} \left( Y - \hat{X} \hat{\beta} \right),
\]

substituting \( \theta \) by the restricted maximum likelihood estimates in \( S \) and \( I \).

### 4.2 MSE of IPW-MQ

In this section we propose an analytical derivation of the MSE for the IPW-MQ type estimator. This is based on the linearization ideas that are set out in Booth and Hobert (1998) and that are used by Chambers et al. (2014) to propose a new estimator of the MSE of a small area estimator that is defined by the solution of a set of robust estimating equations. The MSE is a sum of a prediction variance and a squared bias term. The theoretical development, as in Chambers et al. (2014), is based on approximations that correspond to assuming that \( max(n_j) = O(1) \), so that, as the number of small areas tends to infinity, the prediction variance and the squared bias are \( O(1) \). We also make the standard assumption that a consistent estimator of the MSE of a linear approximation to the small area estimator of interest can be used as its MSE estimator. As noted by Harville and Jeske (1992), such an approach will not generally be consistent, and the resulting MSE estimator can be downward biased. However, in small sample problems, this is not generally an issue.

Note that we assume that the \( \hat{q}_j \) values are known. The prediction error of the IPW-MQ estimator is then:

\[
\hat{\tau}_{MQ}^{PATE} - \tau_j = \sum_{i \in r_j} D_{ij} \hat{y}_{ij} - \sum_{i \in r_j} D_{ij} \tau_{ij},
\]

where \( \hat{y}_{ij} = x_{ij}^T \hat{\beta}_{\hat{q}_j} + w_{ij} \hat{\gamma}_{\hat{q}_j} \). Following Chambers et al. (2014) the prediction variance of IPW-MQ estimator is:

\[
Var(\hat{\tau}_{MQ}^{PATE} - \tau_j|\hat{q}_j) = \sum_{i \in r_j} \left\{ D_{ij}^2 \left( x_{ij} \quad w_{ij} \right)^T Var \left( \begin{array}{c} \hat{\beta}_{\hat{q}_j} \\ \hat{\gamma}_{\hat{q}_j} \end{array} \right) \left( x_{ij} \quad w_{ij} \right) \right\} + \sum_{i \in r_j} D_{ij}^2 Var(y_{ij}).
\]

A first order approximation to \( Var(\hat{\beta}_{\hat{q}_j}, \hat{\gamma}_{\hat{q}_j}) \) is obtained following Chambers et al. (2014) and Bianchi and
These approximated expressions lead to the following sandwich estimator:

\[
\hat{\text{Var}} \left( \frac{\bar{\beta}_{\tilde{q}_j}}{\hat{\gamma}_{\tilde{q}_j}} \right) = n(n-p-1)^{-1} \sum_{j=1}^{\bar{m}} \sum_{s_j} \psi^2 \left( \omega_{ij}^{-1} (y_{ij} - \hat{x}_{ij}^T \hat{\beta}_{\tilde{q}_j} - w_{ij} \hat{\gamma}_{\tilde{q}_j}) \right) \left( \begin{array}{cc} \bar{X} & \bar{W} \end{array} \right)^T \left( \begin{array}{cc} \bar{X} & \bar{W} \end{array} \right)^{-1},
\]

where \( \omega_{ij} \) is a robust estimator of the scale of the residual \( y_{ij} - \hat{x}_{ij}^T \hat{\beta}_{\tilde{q}_j} - w_{ij} \hat{\gamma}_{\tilde{q}_j} \) in area \( j \). An estimator of the first-order approximation (20) is then

\[
\hat{\text{Var}}(\hat{\tau}_{PATE}^{MQ}, | \tilde{q}_j) = \sum_{i \in r_j} D_{ij}^2 \left( x_{ij} \quad w_{ij} \right)^T \hat{\text{Var}} \left( \frac{\bar{\beta}_{\tilde{q}_j}}{\hat{\gamma}_{\tilde{q}_j}} \right) \left( x_{ij} \quad w_{ij} \right) + \hat{\text{Var}}(y_{ij}) \sum_{i \in r_j} D_{ij}^2,
\]

(22)

where \( \hat{\text{Var}}(y_{ij}) = (n-1)^{-1} \sum_{j=1}^{\bar{m}} \sum_{i \in s_j} (y_{ij} - \hat{x}_{ij}^T \hat{\beta}_{\tilde{q}_j} - w_{ij} \hat{\gamma}_{\tilde{q}_j})^2 \).

A corresponding estimator of the area-specific bias of the IPW-MQ estimator is

\[
\hat{B}(\hat{\tau}_{PATE}^{MQ}, | \tilde{q}_j) = \sum_{k=1}^{\bar{m}} \sum_{i \in s_k} c_{ij} (x_{ij}^T \hat{\beta}_{\tilde{q}_k} + w_{ik} \hat{\gamma}_{\tilde{q}_k}) - \sum_{i \in U_j} D_{ij} \left( x_{ij}^T \hat{\beta}_{\tilde{q}_j} + w_{ij} \hat{\gamma}_{\tilde{q}_j} \right),
\]

(23)

where \( c_{ij} = b_{ij} + D_{ij} I(i \in j) \) and

\[
b_j = (b_{ij} = \left( \sum_{i \in r_j} D_{ij} \left( x_{ij} \quad w_{ij} \right) \right) W_{MQ} \left( \begin{array}{cc} \bar{X} & \bar{W} \end{array} \right) \left( \begin{array}{cc} \bar{X} & \bar{W} \end{array} \right)^T W_{MQ} \left( \begin{array}{cc} \bar{X} & \bar{W} \end{array} \right)^{-1}.
\]

The final expression for the estimator of the MSE of IPW-MQ is just the sum of equation (22) and the square of equation (23):

\[
\hat{\text{MSE}}(\hat{\tau}_{PATE}^{MQ}, | \tilde{q}_j) = \hat{\text{Var}}(\hat{\tau}_{PATE}^{MQ}, | \tilde{q}_j) + \hat{B}^2(\hat{\tau}_{PATE}^{MQ}, | \tilde{q}_j).
\]

(24)

Following the approach of Bianchi and Salvati (2015), a further adjustment to the approximation of the MSE is needed to account for the variation due to the estimation of the area M-quantile coefficient \( \tilde{q}_j \) in the equation (24). Therefore,

\[
\hat{\text{Var}}(\hat{\tilde{q}}_j) = \left( \begin{array}{cc} \hat{X}_j & \hat{W}_j \end{array} \right) G_{\tilde{q}_j}^T G_{\tilde{q}_j} \left( \begin{array}{cc} \hat{X}_j & \hat{W}_j \end{array} \right)^T \hat{v}_{\tilde{q}_j}^2,
\]

(25)

where \( G_{\tilde{q}_j} = n^{-1} \sum_{j=1}^{\bar{m}} \left( H_{j}^{-1} \{ \partial_q \hat{L}_{j\tilde{q}_j} - \partial_q \hat{H}_{j\tilde{q}_j}, H_{j\tilde{q}_j}^{-1} L_{j\tilde{q}_j} \} \right) \) with \( H_{j\tilde{q}_j} = \hat{X}_j^T W_{\tilde{q}_j}^M \hat{X}_j, L_{j\tilde{q}_j} = \hat{X}_j^T W_{\tilde{q}_j}^M \hat{W}_j, \partial_q \hat{X}_j \partial_q \hat{X}_j, \partial_q \hat{W}_j \partial_q \hat{W}_j, \partial_q \hat{X}_j \partial_q \hat{W}_j, \partial_q \hat{W}_j \partial_q \hat{X}_j, \partial_q \hat{W}_j \partial_q \hat{W}_j = 2 \Omega_j^{-1} \psi \left( H_{j\tilde{q}_j}^{-1} \{ \hat{y}_j \beta_{\tilde{q}_j} \} \right) \left( \hat{y}_j \beta_{\tilde{q}_j} \right)^{-1} \Omega_j = diag(\omega_{ij}), \right.

\( i \in s_j \) and \( v_{\tilde{q}_j}^2 = n^{-1} \sum_{i=1}^{s_j} (\tilde{q}_{ij} - \hat{\tilde{q}}_{ij})^2 \) where \( \tilde{q}_{ij} \) are the M-quantile coefficients at unit level.

This expression (25) can be estimated by

\[
\hat{\text{Var}}(\hat{\tilde{q}}_j) = \left( \begin{array}{cc} \hat{X}_j & \hat{W}_j \end{array} \right) G_{\tilde{q}_j}^T G_{\tilde{q}_j} \left( \begin{array}{cc} \hat{X}_j & \hat{W}_j \end{array} \right)^T \hat{v}_{\tilde{q}_j}^2,
\]

(26)

The final form of the MSE estimator of \( \hat{\tau}_{PATE}^{MQ} \) is then

\[
mse(\hat{\tau}_{PATE}^{MQ}) = \hat{\text{Var}}(\hat{\tau}_{PATE}^{MQ}) + \hat{B}^2(\hat{\tau}_{PATE}^{MQ}) + \hat{\text{Var}}(\hat{\tilde{q}}_j).
\]

(27)
5 Benchmarking properties of the small area estimators

Model-based methods may not satisfy coherence properties, that may be relevant to final users of small area estimates. In this section we focus on the benchmarking property of the proposed small area predictors. Let the small areas be a partition of a larger area. A set of estimates is said to be benchmarking if the estimated average of the treatment effect for the small areas sum to the average estimated for the larger area (typically using design unbiased or design consistent methods).

The IPW-EBLUP and IPW-MQ do not satisfy the benchmarking property. The estimator of the average treatment effect of the entire population is $\hat{\tau}_{PATE}$, and this may be written as the weighted average of the small area predictors $\hat{\tau}_{PATE_j}$. This property is desirable for all small area estimators, and it is, in this case, an alternative statement of the benchmarking property. In this section the weights that guarantee the benchmarked properties of the proposed estimators are obtained.

At population level the $\hat{\tau}_{PATE}$ can be written as follow:

$$\hat{\tau}_{PATE} = \sum_{j=1}^{m} \sum_{i \in s_j} \mathcal{D}_{ij} y_{ij} + \sum_{j=1}^{m} \sum_{i \in r_j} \mathcal{D}_{ij} \hat{y}_{ij},$$  

(28)

where $\mathcal{D}_{ij} = \frac{(\mathcal{X}^{-1} w_{ij} - \mathcal{T}^{-1}(1-w_{ij}))}{\mathcal{X}(x_{ij})}$, $\mathcal{X} = \sum_{i=1}^{m} \sum_{i=1}^{N_j} w_{ij}/\hat{\epsilon}(x_{ij}) = \sum_{j=1}^{m} K_j$ and $\mathcal{T} = \sum_{i=1}^{m} \sum_{i=1}^{N_j} (1 - w_{ij})/(1 - \hat{\epsilon}(x_{ij})) = \sum_{j=1}^{m} T_j$. The benchmarking equation can be written as $\hat{\tau}_{PATE} = \sum_{j=1}^{m} A_j \hat{\tau}_{PATE_j}$, where $A_j$s are the weights indicating the contribution of the average treatment effect of area $j$ to the average treatment effect of the entire population. Therefore, it follows that:

$$\hat{\tau}_{PATE} = \sum_{j=1}^{m} A_j \hat{\tau}_{PATE_j},$$

$$= \sum_{j=1}^{m} A_j \left( \sum_{i \in s_j} D_{ij} y_{ij} + \sum_{i \in r_j} D_{ij} \hat{y}_{ij} \right),$$

$$= \sum_{j=1}^{m} \sum_{i \in s_j} A_j D_{ij} y_{ij} + \sum_{j=1}^{m} \sum_{i \in r_j} A_j D_{ij} \hat{y}_{ij}.$$

Then the weight for area $j$ is

$$A_j = \frac{D_{ij}}{D_{ij}} \quad \forall i \in U_j,$$

(29)

where $A_j$ is a unique solution $\iff A_j = K_j/\mathcal{X} = T_j/\mathcal{T}$. This means that to guarantee the benchmarking property the weighted percentage of treated and controlled outcomes(weighted by their propensities) in each area to the total population of treated and controlled outcomes, respectively, must be equal to the proportion of the sub-population size in that area to the total population size.

An alternative solution to satisfy the benchmarking property for the proposed estimators is to consider weighing the two parts of equation (6) differently. In this case we define the average treatment effect of the
entire population as:

\[ \hat{\tau}_{PATE} = \sum_{j=1}^{m} B_j \left( \sum_{i \in \mathcal{E}_j} \left[ \frac{w_{ij}y_{ij}}{\hat{e}(x_{ij})} \right] + \sum_{i \in \mathcal{T}_j} \left[ w_{ij}\hat{y}_{ij} \right] \right) \left( \frac{N_j}{\sum_{i=1}^{N_j} \frac{w_{ij}}{\hat{e}(x_{ij})}} \right)^{-1} - \right. 

\left. \sum_{j=1}^{m} C_j \left( \sum_{i \in \mathcal{E}_j} \left[ (1 - w_{ij})y_{ij} \right] + \sum_{i \in \mathcal{T}_j} \left[ (1 - w_{ij})\hat{y}_{ij} \right] \right) \left( \frac{N_j}{\sum_{i=1}^{N_j} 1 - \hat{e}(x_{ij})} \right)^{-1}, \right. 

where \( B_j = K_i / \mathcal{X} \) and \( C_j = T_j / \mathcal{T} \).

6 Model-based simulations

The validity of model-based inference depends on the validity of the model assumed. In this section we empirically evaluate the properties of small area predictors and corresponding MSE estimators. In particular, we use Monte Carlo simulation to evaluate the performance of the proposed small area estimators in comparison with the performance of the IPW-Direct estimator at small area level. Our simulations are model-based, in the sense that population data are first generated under a model assumption or scenario, with a sample selected from each simulated population. Estimates of small area effects and corresponding MSEs are computed by using the data from these samples. Population data are generated for \( m = 50 \) small areas, with samples selected by simple random sampling without replacement within each area. The population and sample sizes are the same for all areas and are fixed at either \( N_i = 100 \) and \( n_i = 5 \) or \( N_i = 300 \) and \( n_i = 15 \). The auxiliary information, the values of the covariates and the treatment status are known for all the units in the population. The response variable \( (y_{ij}) \) and the propensity score (the probability of being treated, \( e(x_{ij}) \)) have been generated as

\[ y_{ij} = 100 + 2x_{1ij} + x_{2ij} + \tau_j w_{ij} + u_j + \epsilon_{ij}, \quad (30) \]

\[ e(x_{ij}) = \frac{\exp(-1 + 0.5x_{2ij} + \nu_j)}{1 + \exp(-1 + 0.5x_{2ij} + \nu_j)}, \quad (31) \]

where \( x_{1ij} \sim \text{LogNormal}(1, 0.5) \), \( x_{2ij} \sim \text{Uniform}(0, 1) \), \( x_{ij} = (x_{1ij}, x_{2ij}) \), and \( w_{ij} \sim \text{Bernoulli}(e(x_{ij})) \). The random-area and individual effects are independently generated according to four scenarios:

1. no outliers, no misclassification: \( u_j \sim \mathcal{N}(0, 3) \), \( \epsilon_{ij} \sim \mathcal{N}(0, 6) \) and \( \nu_j \sim \mathcal{N}(0, 0.25) \) is the baseline. The other scenarios are modified upon this setting;

2. outliers in both area and individual effects: \( u_j \sim \mathcal{N}(0, 3) \) for areas \( 1-39 \) and \( u_j \sim \mathcal{N}(9, 20) \) for areas \( 40-50 \), that is, random effects for areas \( 1-39 \) are drawn from a ‘well-behaved’ \( \mathcal{N}(0, 3) \) distribution, with those for areas \( 40-50 \) drawn from an outlier \( \mathcal{N}(9, 20) \) distribution; \( \epsilon_{ij} \sim \delta_1 \mathcal{N}(0, 6) + (1 - \delta_1)\mathcal{N}(20, 150) \) where \( \delta_1 \) is an independently generated Bernoulli random variable with \( Pr(\delta_1) = 0.97 \), that is, the individual effects are independent draws from a mixture of two normal distributions, with 97% on average drawn from a ‘well-behaved’ \( \mathcal{N}(0, 6) \) distribution and 3% on average drawn from an outlier \( \mathcal{N}(20, 150) \) distribution;

3. misclassification in treatment status: \( w_{ij} = w_{ij}'\delta_2 + (1 - w_{ij}' )(1 - \delta_2) \), where \( w_{ij}' \sim \text{Bernoulli}(e(x_{ij})) \) and \( \delta_2 \) is an independently generated Bernoulli random variable with \( Pr(\delta_2) = 0.98 \);

4. outliers in both area and individual effects and misclassification in treatment status: \( u_j \sim \mathcal{N}(0, 3) \) for areas \( 1-39 \) and \( u_j \sim \mathcal{N}(9, 20) \) for areas \( 40-50 \), \( \epsilon_{ij} \sim \delta_1 \mathcal{N}(0, 6) + (1 - \delta_1)\mathcal{N}(20, 150) \) and \( w_{ij} = w_{ij}'\delta_2 + (1 - w_{ij}' )(1 - \delta_2) \).
Each scenario includes two sub-scenarios that introduce a different degree of heterogeneity in the effects among areas: a) $\tau_{ij} \sim \mathcal{N}(10, 1)$ and b) $\tau_{ij} \sim \mathcal{N}(10, 3)$. Each scenario is independently simulated $S = 1000$ times. Table 1 summarises the scenarios of the simulation experiments.

| Scenarios | Presence of outliers | Misclassification |
|-----------|----------------------|-------------------|
| $1 - b$   | ✓                    | ✓                 |
| $1 - c$   | ✓                    | ✓                 |
| $2 - a$   | ✓                    | ✓                 |
| $2 - b$   | ✓                    | ✓                 |
| $3 - a$   | ✓                    | ✓                 |
| $3 - b$   | ✓                    | ✓                 |
| $4 - a$   | ✓                    | ✓                 |
| $4 - b$   | ✓                    | ✓                 |

Three different estimators are compared: IPW-Direct (5); IPW-EBLUP (6) using equations (8) and (9) to predict the outcomes and to estimate the propensity scores, respectively; IPW-MQ (6) with equations (10) and (11) for computing outcomes and propensity scores, respectively.

The performances of these different small area estimators for area $j$ were evaluated with respect to two criteria: the percentage of Relative Bias (RB) and the percentage of Relative Root Mean Square Errors (RRMSE):

$$RB_j = \frac{1}{S} \sum_{s=1}^{S} (\hat{\tau}_j^s - \tau_j^s) \times 100,$$

$$RRMSE_j = \frac{1}{S} \sum_{s=1}^{S} (\hat{\tau}_j^s - \tau_j^s)^2 \times 100,$$

where $\bar{\tau}_j = \frac{1}{S} \sum_{s=1}^{S} \tau_j^s$. The median values of RB and RRMSE over the $m$ small areas are set out by boxplots in Figures 1 and 2, where we see that claims in the literature (Chambers and Tzavidis, 2006) about the superior outlier robustness of the M-quantile predictor compared with the IPW-Direct and the IPW-EBLUP certainly hold true in these simulations.

The relative bias results confirm our expectations regarding the behaviour of the estimators: the IPW-Direct is less biased than the model-based predictors IPW-EBLUP and IPW-MQ. In particular, the increase in bias is most pronounced in IPW-MQ when there are misclassification and outliers in the area and individual effects, which is not unexpected since IPW-MQ is a robust estimator and area means are most affected by outliers in the population data (Chambers et al., 2014). To reduce the bias a predictive estimator could be developed adding a bias correction part in line with that proposed by Chambers et al. (2014). A predictive IPW-MQ is an avenue for future research.

Turning to the median RRMSE results, the superior outlier robustness of IPW-MQ compared with the IPW-EBLUP certainly hold true — provided that the outliers are in individual and in area effects (scenarios 2 and 4). However, the gap between these two estimators narrows considerably when only misclassification is present (scenarios 3 – a and 3 – b). Nevertheless, the proposed small area predictors, IPW-EBLUP and IPW-MQ, are much more efficient than the IPW-Direct and this suggests that it may be good to use these predictors to estimate the average treatment effect when sample size in each area becomes small. These results are confirmed when $N_j = 300$ and $n_j = 15$ with lower values of RB and RRMSE for all estimators. For reasons of space, they are not reported here, but are available from the authors upon request.
Figure 1: Relative bias in percentage for different estimators in the setting with \( N_j = 100 \) and \( n_j = 5 \). Each box plot represents the percentage of relative bias in estimating the average treatment effect.
Relative root mean square errors in percentage for different estimators in the setting with $N_j = 100$ and $n_j = 5$. Each box plot represents the percentage of RRMSE in estimating the average treatment effect.

To evaluate the performance of the analytic MSE estimators of the IPW-EBLUP and IPW-MQ proposed in Section 4 (see equations (18) and (27)) we used the data generated for scenarios 1 and 4 with sample size $n_j = 5$. Scenario 1 is shown because it represents the situation under which the MSE estimator for IPW-EBLUP has been developed. Instead scenario 4 has been chosen to assess the robust properties of the MSE estimators of both predictors. The results for the other scenarios are available for interested readers from the authors upon request. The performance of the MSE estimators has been evaluated by median values of Relative Bias of root MSE over the $m$ small areas and the median of the empirical coverage rate (CR) for nominal 95% confidence intervals. They are defined by the small area estimates plus or minus twice the values of the estimated root MSE. Examination of the results in Table 2 shows that the MSE estimators (27) tend to be biased towards low values, except for the case $4 - a$. This confirms the results obtained by Chambers et al. (2014). The MSE estimators (18) show good performance in terms of bias under all scenarios. In terms of CR the two MSE estimators show poor results with rates around 85 – 90%. However, this use of the estimated MSE to construct confidence intervals, though widespread, has been criticised. Chatterjee et al. (2008) discuss the use of bootstrap methods for constructing confidence intervals for small area parameters, arguing that there is no guarantee that the asymptotic behaviour underpinning normal theory confidence intervals applies in the context of the small samples that characterise small area estimation. Further research on using bootstrap and/or jackknife techniques to construct confidence intervals under the mixed effects and M-quantile models is left for the future.
Table 2: Median Relative Bias and Coverage Rate (%) for the root MSE estimators of IPW-EBLUP and IPW-MQ under scenarios 1 and 4 with $N_j = 100$, $n_j = 5$.

| Scenario | IPW-EBLUP | IPW-MQ |
|----------|-----------|--------|
|          | RB% | CR (95%) | RB% | CR (95%) |
| 1-a      | -0.83 | 88 | -4.84 | 89 |
| 1-b      | -4.73 | 91 | -33.64 | 75 |
| 4-a      | -1.38 | 89 | 3.88 | 93 |
| 4-b      | -8.59 | 86 | -16.47 | 86 |

7 A design-based simulation based on real data

In this section, we apply the proposed methods to estimate the effects of permanent versus temporary contracts on the economic insecurity of households in different regions of Italy. As indicated previously, such an impact has potential consequences on consumption behaviour, life satisfaction and well-being in general. The increase in non-standard forms of employment in many countries appears to have contributed to rising in-work poverty (Eurofound and the International Labour Office, 2017; Crettaz, 2013). We expect the effect to be heterogeneous across Italian regions, due to different quality and cost of living. To study the performance of IPW-EBLUP and IPW-MQ in a real-data example, we implement a design-based simulation study using the 2015 Italian module of the EU-SILC survey.

As a starting point of our analysis, we show in Figure 3 the graphical representation of the causal model that is considered as the data generating process. This is a simplified framework, far from being exhaustive with regards to the phenomenon under study. However, we have included a selection of variables that we believe make our assumptions and inference reasonable, conditional on the available data.

![Figure 3: Direct Acyclic Graph (DAG) explaining the causal path from job stability (permanent job) to subjective poverty (feeling of the head of the household about the household economic status). The top part includes the individual characteristics and the bottom part contains the household characteristics.](image-url)
In this setting the units of the analysis are the Italian households and the treatment. Job stability, is a dichotomous variable that gets the value 1 if the head of the household (or the household respondent) has a temporary job and 0 if she/he has a permanent job at the time of the interview. We assume the existence of a causal path from this variable to the lowest monthly income to make ends meet, which is a subjective measure of the household economic status. This is one of the EU-SILC target variables in the domain of social exclusion/non-monetary household deprivation indicators. Respondents are asked to provide their own assessed indication of the very lowest net monthly income that the household would have to get in order to make ends meet, that is, to pay its usual necessary expenses. We use this continuous outcome as a proxy variable for subjective poverty in the following analysis. For the outcome model, as it is common for highly right skewed outcome distributions, we use the log transformation and then we consider the transformed values per individual in the household by dividing the total value by the equivalised household size. We consider two sets of plausible confounders and predictors at the individual and household level. The individual characteristics concerns the head or the responsible person in the household. Figure 3 shows the set of confounding covariates $X = \{\text{Age}, \text{Gender}, \text{Education}, \text{Marital status}, \text{Tenure}, \text{Family type}\}$. Conditioned on this set of covariates is necessary for the unconfoundedness assumption to hold. In addition, the number of rooms in the house, the dwelling type, the existence of problems related to crime, violence and vandalism (Crime) in the local area from the point of view of the respondents, and the household disposable income are used as additional predictors of the outcome.

To implement a design-based simulation study, we consider as a pseudo-population the sub-sample of the workforce, aged between 25 and 80, in the 20 administrative regions of Italy, based on the 2015 Italian module of the EU-SILC survey. Due to sample size requirements Abruzzo and Molise were aggregated, leading to 19 areas. After accounting for common support within all areas 11011 units are left, from which 1254 units belong to the treated and the rest to the control group. Figure 7 in Appendix C shows the overall common support of the propensity scores among treated and control groups.

The original estimates of the impacts are considered as the true $\tau_j$ parameters to be estimated at the population level. This pseudo-population (population hereafter) is then kept fixed over the Monte Carlo simulations. Table 3 shows the full sample parameters. The heterogeneity of the area-specific effects is illustrated in Figure 4.
Table 3: Parameters of the full sample, to be considered as population parameters.

| NUTS2               | Original sample size | Percentage of treated | Original estimate (True) |
|---------------------|----------------------|-----------------------|--------------------------|
| Piemonte            | 665                  | 0.07                  | -0.37                    |
| Valle-d’Aosta       | 152                  | 0.13                  | -0.43                    |
| Lombardia           | 1329                 | 0.04                  | -0.13                    |
| Bolzano-Trento      | 444                  | 0.14                  | -0.48                    |
| Veneto              | 927                  | 0.08                  | -0.16                    |
| Friuli-Venezia-Giulia| 735                 | 0.10                  | -0.31                    |
| Liguria             | 598                  | 0.08                  | 0.37                     |
| Emilia-Romagna      | 842                  | 0.13                  | -0.24                    |
| Toscana             | 707                  | 0.08                  | -0.55                    |
| Umbria              | 310                  | 0.12                  | -0.59                    |
| Marche              | 586                  | 0.14                  | -0.16                    |
| Lazio               | 934                  | 0.12                  | 0.10                     |
| Abruzzo-Molise      | 363                  | 0.10                  | 0.21                     |
| Campania            | 594                  | 0.29                  | -0.13                    |
| Puglia              | 481                  | 0.25                  | 0.37                     |
| Basilicata          | 200                  | 0.31                  | 0.11                     |
| Calabria            | 398                  | 0.44                  | 0.23                     |
| Sicilia             | 475                  | 0.18                  | -0.13                    |
| Sardegna            | 271                  | 0.19                  | 0.06                     |
| Italy               | 11011                | 0.13                  | -0.14                    |

Figure 4: Distribution of area-specific population average treatment effect, showing the heterogeneity of the effects.

Balancing the covariates within each area has been verified by running t-tests on the difference in the average value of the propensity scores by treatment status. Table 6 in Appendix C shows that all covariates are balanced in the original sample (pseudo-population) for all 19 areas.
Table 4: 95% simulation confidence intervals - 1000 replications for 19 regions in Italy

| NUTS2                 | True  | IPW-Direct | IPW-EBLUP | IPW-MQ  |
|-----------------------|-------|------------|-----------|---------|
| Piemonte              | -0.37 | -1.91      | 1.77      | -0.39   |
| Valle-d’Aosta         | -0.43 | -2.77      | 2.57      | -0.54   |
| Lombardia             | -0.13 | -1.45      | 2.04      | -0.30   |
| Bolzano-Trento        | -0.48 | -1.99      | 0.91      | -0.68   |
| Veneto                | -0.16 | -1.33      | 1.16      | -0.29   |
| Friuli-Venezia-Giulia | -0.31 | -1.56      | 1.37      | -0.54   |
| Liguria               | 0.37  | -1.34      | 1.89      | 0.14    |
| Emilia-Romagna        | -0.24 | -1.24      | 0.93      | -0.40   |
| Toscana               | -0.55 | -1.66      | 1.21      | -0.65   |
| Umbria                | -0.59 | -2.00      | 2.07      | -0.73   |
| Marche                | -0.16 | -1.33      | 1.13      | -0.31   |
| Lazio                 | 0.10  | -1.15      | 1.66      | -0.10   |
| Abruzzo-Molise        | 0.21  | -1.55      | 2.82      | 0.11    |
| Campania              | -0.13 | -1.14      | 0.99      | -0.36   |
| Puglia                | 0.37  | -0.77      | 1.74      | 0.16    |
| Basilicata            | 0.11  | -1.39      | 1.91      | 0.03    |
| Calabria              | 0.23  | -0.86      | 1.34      | 0.08    |
| Sicilia               | -0.13 | -1.41      | 1.49      | -0.36   |
| Sardegna              | 0.06  | -1.39      | 2.14      | -0.03   |

1000 independent random samples without replacement are taken from the balanced population with regional common support, by randomly selecting individuals in the 19 regions with sample sizes in these areas set to 10% of the population (resulting in a proportional stratified sampling). The sample size is 1101 observations from the 19 regions and the area sample sizes range from 15 to 132 with a median of 58. The sample from each region is drawn not considering the treatment status. This means that the sample of a specific region might include both treated and control units, or it might only contain the observations from one of the two groups. This is one of the reasons for using our proposed method, because, as previously stated, it can be used even if the sample size of the treated or controlled group is zero in the domain of interest.

The different estimators are computed for each selected sample. Confidence intervals are reported in Table 4 (each interval is based on 1000 replications). We can note that the confidence intervals for IPW-EBLUP and IPW-MQ mostly contain the true value and have the correct sign, while intervals computed for the IPW-Direct estimator always include the zero due to the large values in the variance of the estimator.

Figure 5 illustrates the behaviour of relative bias and root mean square error, confirming the characteristics of the different estimators already highlighted in the simulation studies presented in the previous section. Figure 6 shows that IPW-MQ and IPW-EBLUP outperform the IPW-Direct in capturing the heterogeneity of the average treatment effects and they are in the reasonable range. The estimates obtained through the IPW-Direct method show a large variation and the values of area-specific ATE can be very far from the true range.
Figure 5: Relative bias and root mean square error - 1000 replications. Each box plot represents the results for 19 regions in Italy.

Figure 6: Performance of different estimators in capturing the heterogeneity of the effects across areas.

The relative efficiencies of the proposed estimators with respect to IPW-Direct are computed as the ratio of the average MSE for each area to the average MSE of the IPW-Direct. Table 5 presents the summary statistics over the 19 regions in the study. A value less than 100 for this ratio indicates that the MSE of the model-based estimate is smaller than that of the direct estimate. The results reported in Table 5 indicate that the best method for this application appears to be the robust version of the proposed estimator (IPW-MQ). These results are consistent for all the areas in the study.

Table 5: The efficiency of each estimator compared to IPW-Direct. Summary statistics over 19 regions in the study.

| Method    | Min. | 1st Qu. | Median | 3rd Qu. | Max. |
|-----------|------|---------|--------|---------|------|
| IPW-EBLUP | 25.73| 40.09   | 47.25  | 52.11   | 61.39|
| IPW-MQ    | 24.03| 39.22   | 44.92  | 50.31   | 59.01|
8 Conclusion

Small area techniques provide the official statistics for politicians and decision makers using sample surveys and other sources of information. However, to the extent of our knowledge there is no link between this literature and that on causal inference, even though sometimes the statements in the former literature are interpreted in a causal way.

In this paper we propose a methodological framework that links the two streams of literature and emphasise the relevance of such methods in many applications to real data. Our proposed methods take account of the heterogeneity of the effects across areas even at a very fine level (small area level). This allows policy makers and decision takers to know the impact of a given policy for a finer geographic, socio-demographic, or socio-economic grid and, consequently, to plan better local-targeted interventions.

Some of the usual assumptions for making causal inferences with observational data are revisited and modified to be consistent with the context of small area estimations. The proposed methods IPW-EBLUP and IPW-MQ are mainly based on weighting with propensity scores. These estimators inherit the properties of a doubly robust estimators, since both a model to estimate the scores and another model to predict the outcome are used for the part of the population that is not observed. This means that if one of these two models is misspecified the estimator is still consistent.

For each of the proposed estimators, IPW-EBLUP and IPW-MQ, we developed an analytical MSE estimator under the assumption that the propensity score is known. We also suggest a correction for the bias in the analytical MSE, that can occur due to the estimation of the propensity score, by proposing two different bootstrap methods, defined as a parametric bootstrap and modified random effect block bootstrap, for IPW-EBLUP and IPW-MQ, respectively. The performance of the MSE estimators are studied via simulations.

Monte Carlo model based simulations are used to evaluate the performance of the proposed estimators in comparison with the performance of the IPW-Direct at small area levels. The results show that the proposed small area predictors, IPW-EBLUP and IPW-MQ, are much more efficient than the IPW-Direct and this suggests that it may be best to use these predictors to estimate the average treatment effect when the sample size in each area becomes small. However, as expected, these methods manifest higher bias than the direct estimator.

The application to real data, conducted as a design-based simulation analysis, has shown the potential of the proposed method in reconstructing the detail of the impact at the regional level, albeit with differences in the performance of the estimators. Job stability affects the perception of economic insecurity, but not in a homogeneous way in the different regions. The effect is negative in most cases with even significant differences, which we can attribute to the different levels of quality and cost of living, as well as to a different social context in general. Once again, this highlights the importance of adopting local policies to support families and combat poverty.

As future lines of research, we plan to extend our results for other robust estimators, such as REBLUP (Sinha and Rao, 2009). Moreover, due to the presence of bias in IPW-EBLUP and IPW-MQ, observed in our simulation experiment, we would like to investigate bias calibration methods to make the approach predictive rather than projective. Finally, we aim to exploit the use of matching and Instrumental Variable (IV) estimators in small area estimation.

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Appendix A  Asymptotic properties of the IPW-EBLUP

In this Section we show the asymptotic properties of the proposed IPW-EBLUP estimator when $m \to \infty$ and $n \to \infty$ yet, $m/n \to 0$. Consider the following regularity conditions (Datta and Lahiri, 2000):

A.1 The propensity scores are known, that is, $D_{ij}$ values are known.
A.2 The number of areas $m \to \infty$ and $\max(n_j) = O(1)$
A.3 The elements of $\tilde{X}$ and $\tilde{Z}$ as in (14) are uniformly bounded so that $\tilde{X}_T\hat{V}^{-1}\tilde{X} = [O(m)]_{(p+1)(p+1)}$ and $\tilde{Z}_T\hat{V}^{-1}\tilde{Z} = [O(m)]_{(2m)(2m)}$.
A.4 The elements of $\hat{S}_T\hat{I}^{-1}\hat{S}$ must be uniformly bounded.
A.5 Using ML or REML to estimate the variance components results in the estimators of these parameters that is even and translation invariant.
A.6 The distributions of the random effects, $(u_j, \gamma_j)$, and the individual errors $\epsilon_{ij}$ are symmetric and centered around zero.

Assumption A.1 can be justified since information on the treatment status and auxiliary variables is available for the entire population. Assumption A.6 is verified, because the normality of the random effects, $(u_j, \gamma_j)$, and the sampling errors $\epsilon_{ij}$ as stated in Section 3.1.1, is assumed. The following theorem presents the distribution of the proposed IPW-EBLUP.

Proposition 2. Provided conditions A.1-A.6 are satisfied,

$$\sqrt{N_j}m(\hat{\tau}_{EBLUP}^{PATE} - \tau_j) \sim N(0, \gamma'(\theta)).$$

Proof. Under the aforementioned assumptions the IPW-EBLUP estimator of $\tau_j$ is unbiased. Since $\hat{y}_{ij}$ is an unbiased empirical predictor of the $y_{ij}$, fitted using ML or REML and $D_{ij}$ are assumed to be deterministic, it is straightforward that:

$$E \left[ \hat{\tau}_{EBLUP}^{PATE} - \tau_j \right] = \sum_{i \in r_j} D_{ij}(E[\hat{y}_{ij}] - E[y_{ij}]) = 0$$

Considering equations (15) and (17):

$$MSE(\hat{\tau}_{EBLUP}^{PATE}) = D_j^T\tilde{Z}_j\Sigma_{\omega}\left(1 - \tilde{Z}_T\hat{V}^{-1}\tilde{Z}\right)\tilde{Z}_j^TD_j + D_j^Tc_j(\tilde{X}_T\hat{V}^{-1}\tilde{X})c_j^TD_j + tr\left(SV\hat{S}^T\hat{I}^{-1}\right) + o(m^{-1}).$$

Under the assumptions A.3 to A.5 Datta and Lahiri (2000) have shown the order of magnitude for the EBLUP estimator, that also corresponds to our IPW-EBLUP proposal. The central limit theorem (CLT) follows directly then to achieve the asymptotic normality of the estimator. Since the $\hat{\tau}_{EBLUP}^{PATE}$ is unbiased the second-order correct estimator of the variance, $\hat{\gamma}(\theta) = mse(\hat{\tau}_{EBLUP}^{PATE})$ from equation (18).

Appendix B  Bias corrected MSE via bootstrap procedure

The proposed analytical MSE estimators (Section 4) do not take into account the variability due to the estimation of the propensity scores. For adding this component of variability re-sampling techniques are
proposed. In particular, for IPW-EBLUP we suggest using a parametric bootstrap technique, such as that proposed by Gonzalez-Manteiga et al. (2008), or a non-parametric bootstrap procedure as in Opsomer et al. (2008). For IPW-MQ, we suggest applying an outlier robust bootstrap approach that is a modified version of the block-bootstrap approach of Chambers and Chandra (2013).

### Parametric bootstrap for IPW-EBLUP

The use of a parametric bootstrap to get an estimate of the MSE is very common in SAE Hall and Maiti (2006). In this section modifications of existing techniques will allow us to capture part of the variation in the IPW-EBLUP that is due to the estimation of the propensity scores. The underlying assumption is that the error terms (area-specific and individual) are normally distributed.

The steps of this extended parametric bootstrap are as follows:

**Step 1** Fit model (8) to the initial data obtaining estimated value \((\hat{\beta}, \hat{\alpha})\) for the fixed part and \((\hat{\sigma}_e^2, \hat{\sigma}_y^2, \hat{\sigma}_u^2, \hat{\sigma}_v^2)\) for the random components.

**Step 2** Construct the bootstrap vectors \(\epsilon^*, u^*, \gamma^*\) and \(\nu^*\) whose elements are independent copies of \(N(0, \hat{\sigma}_e^2)\), \(N(0, \hat{\sigma}_y^2)\), \(N(0, \hat{\sigma}_u^2)\), and \(N(0, \hat{\sigma}_v^2)\), respectively, for the entire population.

**Step 3** Construct the bootstrap population data \((y_{ij}^*, x_{ij}, w_{ij}^*)\) from the model

\[
y_{ij}^* = \tilde{x}_{ij}^T \tilde{\beta} + w_{ij}^* \gamma_j^* + u_j^* + \epsilon_{ij}^*,
\]

where \(w_{ij}^* \sim \text{Bernoulli}(p_{ij}^*)\) and \(p_{ij}^* = \Lambda^{-1}(x_{ij}^T \alpha + \nu_j^*)\).

**Step 4** Draw a sample from the bootstrap population of size \(n_j\) for each area using the stratified random sampling and fit the models (8), (9). Then calculate the bootstrap estimated outcomes \(\hat{y}_{ij}^*\) and propensity score \(\hat{p}_{ij}^*\).

**Step 5** Calculate the bootstrap errors \(\hat{\tau}_j^* - \tau_j^*\), for each \(j = 1, \cdots, m\). The value \(\hat{\tau}_j^*\) is the true bootstrap value obtained by replacing \(\hat{y}_{ij}^*\) and \(\hat{p}_{ij}^*\) in equation (6) and the \(\hat{\tau}_j^*\) is the bootstrap estimate and it is derived by replacing the \(\hat{y}_{ij}^*\) and \(\hat{p}_{ij}^*\) in the same equations.

**Step 6** Repeat steps 2 – 5 \(B\) times. In the \(b\)th bootstrap replication, let \(\tau_j^{*(b)}\) be the quantity of interest for area \(j\) and \(\hat{\tau}_j^{*(b)}\) its bootstrap estimate. A bootstrap estimator of area \(j\) for the variability contribution of the estimates of propensity scores to the MSE of IPW-EBLUP can be calculated as

\[
\text{Var}(\hat{\tau}_j) = \frac{1}{B} \sum_{b=1}^{B} (\hat{\tau}_j^{*(b)} - \tau_j^{*(b)})^2. \tag{32}
\]

This value has to be added to the estimator of the MSE in equation (18).

### Modified random effect block bootstrap method for IPW-MQ

In this section we propose an M-quantile ensemble modelling approach to recreate the hierarchical population variability in the original population, combining it with a modified version of the block bootstrap method proposed by Chambers and Chandra (2013) for the estimation of the variability contribution of the estimates of propensity scores to the MSE of the IPW-MQ predictor. The advantage of this method is that there are no assumptions on the underlying distributions of the error terms.
Step 1 Compute the robust estimate $$\hat{\beta}_{0.5}$$ for the fixed effects vector defining the linear regression M-quantile of order $$q = 0.5$$ and calculate the marginal residuals defined as $$\hat{r}_{ij} = y_{ij} - x_{ij}^T \hat{\beta}_{0.5} - w_{ij} \gamma_{0.5}$$.

Step 2 Calculate the level two and level one empirical residuals generated by the fitted linear quantile regression of order $$q = 0.5$$ as:

\[
\hat{\gamma}_j = \frac{\sum_{i=1}^{n_j} (w_{ij} - w_j)(\hat{r}_{ij} - \hat{r}_j)}{\sum_{i=1}^{n_j} (w_{ij} - w_j)^2},
\]

\[
\hat{u}_j = \hat{r}_j - \hat{\gamma}_j w_j,
\]

\[
\hat{e}_{ij} = \hat{r}_{ij} - \hat{u}_j - w_{ij} \hat{\gamma}_j,
\]

where $$w_j = \frac{1}{n_j} \sum_{i=1}^{n_j} w_{ij}$$ and $$\hat{r}_j = \frac{1}{n_j} \sum_{i=1}^{n_j} \hat{r}_{ij}$$.

Step 3 Calculate the moment-based estimates $$\hat{\theta} = (\hat{\sigma}_c^2, \hat{\sigma}_u^2, \hat{\sigma}_\epsilon^2)$$ of the between area and within area variance components defined by the hierarchical linear model (7) (e.g., using the mbest package within R) and then center around zero and re-scale the empirical residuals and random effects calculated in the previous step to achieve consistency:

\[
\hat{\gamma}_{cs} = \hat{\sigma}_c \hat{\gamma}_j \left( \frac{1}{m} \sum_{h=1}^{m} (\hat{\gamma}_{ch})^2 \right)^{-1/2},
\]

\[
\hat{u}_{cs} = \hat{\sigma}_u \hat{u}_j \left( \frac{1}{m} \sum_{h=1}^{m} (\hat{u}_{ch})^2 \right)^{-1/2},
\]

\[
\hat{e}_{cs} = \hat{\sigma}_\epsilon \hat{e}_{ij} \left( \frac{1}{n} \sum_{h=1}^{n_h} \sum_{k=1}^{n_k} (\hat{e}_{kh})^2 \right)^{-1/2},
\]

where $$\hat{\gamma}_j = \hat{\gamma}_j - \frac{1}{m} \sum_{h=1}^{m} \hat{\gamma}_h$$, $$\hat{u}_j = \hat{u}_j - \frac{1}{m} \sum_{h=1}^{m} \hat{u}_h$$ and $$\hat{e}_{ij} = \hat{e}_{ij} - \frac{1}{n} \sum_{k=1}^{n_k} \hat{e}_{kh}$$.

Step 4 At this step we propose a re-sampling scheme that is mainly plausible if the mutual independence between the random components hold, that is, $$u_j, \gamma_j$$ and $$\epsilon_{ij}$$ are mutually independent. Therefore, in the estimation procedure the model is fit by imposing the restriction that covariance between random slopes and random intercepts is zero. That can avoid the over-parametrisation of the model. That is, for each bootstrap iteration $$b$$,

(a) Generate the random slopes values for the $$m$$ areas by drawing a simple random sample of size $$m$$ with replacement (srswr) from the vector $$\hat{\gamma}^* = (\hat{\gamma}_{1c}, \ldots, \hat{\gamma}_{mc})$$. Denote this sample by $$\gamma^*$$.

(b) Similarly, generate a vector of random intercepts $$\hat{u}^*$$ for $$m$$ areas by independently drawing simple random samples of size $$m$$ with replacement from the vector $$\hat{u}^{sc} = (\hat{u}_{1c}, \ldots, \hat{u}_{mc})$$.

(c) Generate level one errors within each area $$j$$ by independently drawing simple random samples of size $$N_j$$ with replacement from $$\hat{e}_{h(j)}^{sc}$$ where $$h(j)$$ is a random drawn from $$1, \ldots, m$$. Denote this sample by $$\epsilon^*_j$$.

Step 5 Calculate the vector of pseudo-random effects $$\hat{g}_j = \bar{\bar{x}}_j (\hat{\alpha}^*_j - \hat{\alpha}_{0.5})$$ from the M-quantile model for binary data, where $$\bar{\bar{x}}_j$$ is the vector of average values for the covariates in area $$j$$. Then center around zero and re-scale the empirical pseudo-random effects. Define the new vector as $$\hat{g}^{cs} = (\hat{g}_{1c}^{cs}, \ldots, \hat{g}_{mc}^{cs})$$. 

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Step 6 Generate a vector of random intercepts \( \hat{g}^* \) for \( m \) areas by independently drawing simple random samples of size \( m \) with replacement from the vector \( \hat{g}^{cs} \).

Step 7 Simulate bootstrap population data \( (y_{ij}^*, x_{ij}, w_{ij}^*) \):

\[
y_{ij}^* = x_{ij}^T \hat{\beta}_{0.5} + w_{ij}^* \hat{\gamma}_{0.5} + w_{ij}^* \gamma_{ij}^* + u_{ij}^* + \epsilon_{ij}^*,
\]

where \( w_{ij}^* \sim \text{Bernoulli}(p_{ij}^*) \) and \( p_{ij}^* = \Lambda^{-1}(x_{ij}^T \hat{\alpha}_{0.5} + g_{ij}^*) \).

Step 8 Draw a bootstrap sample from the bootstrap population using the sampling method used to obtain the original sample.

Step 9 Fit the models in the equations (10), (11) and predict for the non-sampled part of the bootstrap population. Then calculate the bootstrap estimated outcomes \( \hat{y}_{ij}^* \) and propensity score \( \hat{p}_{ij}^* \).

Step 10 Calculate the bootstrap errors \( \hat{\tau}_{ij}^* - \tau_{ij}^* \), for each \( j = 1, \cdots, m \). The value \( \tau_{ij}^* \) is the true bootstrap value obtained by replacing \( \hat{y}_{ij}^* \) and \( p_{ij}^* \) in equation (6) and the \( \hat{\tau}_{ij}^* \) is the bootstrap estimate and it is derived by replacing the \( \hat{y}_{ij}^* \) and \( \hat{p}_{ij}^* \) in the same equations.

Step 11 Repeat steps 4 – 9 \( B \) times. In the \( b \)th bootstrap replication, let \( \tau_{ij}^{*(b)} \) be the quantity of interest for area \( j \) and \( \hat{\tau}_{ij}^{*(b)} \) its bootstrap estimate. A bootstrap estimator of area \( j \) for the variability contribution of the estimates of propensity scores to the MSE of IPW-MQ can be calculated as

\[
\text{Var} (\hat{\tau}_j) = \frac{1}{B} \sum_{b=1}^{B} (\hat{\tau}_{j}^{*(b)} - \tau_{j}^{*(b)})^2. \tag{36}
\]

This value has to be added to the estimator of the MSE in equation (27).

The problem of no treated unit in the sample and the infinite slope
While fitting a line on the marginal residuals it might happen that \( \hat{\gamma}_j \) as in (33) is infinite. This is the case if for instance there are no treated units in the sample. In such cases, the classical methods that will only use the sample for inferences are incapable of providing an estimate of average treatment for such areas. However, our proposal can still provide an estimate in such cases by using the information on the entire sample. To solve this problem in our proposed bootstrap procedure in the area \( j \)-th where there is no treated unit in the sample, we restrict the \( \hat{\gamma}_j = 0 \) and then automatically \( \hat{u}_j = \hat{r}_j \). This makes sense since the sample data are not informative about the area specific effect of the treatment.

Appendix C  Common support and balancing in real data example

We assume the availability of the auxiliary data on the treatment status and the confounding covariates via other sources of information. This allows us to check the assumption of common support at the sub-population level for each area and correct for the unmatched items. In order to reach the complete overlap of the propensity scores between the treated and control unit within each area, we dismissed 1349 in the overall pseudo-population, ending up with 11011 units for the analysis.
We check the balancing property in the set of covariates using the propensity scores for the entire pseudo-population. The NULL hypothesis ($H_0$) is that the distribution of the covariates is balanced in the control and treated group within area $j$.

Consider, $l(x_{ij})$, the linearized propensity score or the odds of being treated, is defined as follows:

$$ l(x_{ij}) = \ln \left( \frac{e(x_{ij})}{1 - e(x_{ij})} \right) $$

where $e(x_{ij})$ is the true propensity score. Now we define the $\bar{l}_c$ and the $\bar{l}_t$ as the average value of linearized propensity score for the control and treated group in area $j$, respectively.

The following test statistic can be used to verify if weighting with these scores provides the balance required between the treated and control in each region. It follows then a Student’s $t$ distribution:

$$ \hat{\Delta}_j = \frac{\bar{l}_t - \bar{l}_c}{\sqrt{(s^2_{l_c} + s^2_{l_t})/2}} \sim t_\nu. $$

The number of degrees of freedom, $\nu$, is calculated as:

$$ \nu = \frac{(s^2_{l_c}/N^c_j + s^2_{l_t}/N^t_j)^2}{(s^2_{l_c}/N^c_j)^2/(N^c_j - 1) + (s^2_{l_t}/N^t_j)^2/(N^t_j - 1)}, $$

where $N^c_j$ and $N^t_j$ are the sizes of treated and control sub-populations in area $j$.

Table 6 reports the results of this test within each area, showing that $H_0$ cannot be rejected for any area $j$, $j = 1, \cdots, m$. 

Figure 7: The overall common support based on propensity scores.
Table 6: Testing the balance of covariates within each area using the linearized propensity scores

| NUTS2            | Test statistic | p-value |
|------------------|----------------|---------|
| Piemonte         | 0.77           | 0.44    |
| Valle-d’Aosta    | 0.58           | 0.57    |
| Lombardia        | 0.73           | 0.47    |
| Bolzano-Trento   | 0.56           | 0.58    |
| Veneto           | 0.82           | 0.41    |
| Friuli-Venezia-Giulia | 0.84     | 0.40    |
| Liguria          | 0.97           | 0.34    |
| Emilia-Romagna   | 0.63           | 0.53    |
| Toscana          | 0.56           | 0.57    |
| Umbria           | 0.60           | 0.55    |
| Marche           | 0.81           | 0.42    |
| Lazio            | 0.80           | 0.43    |
| Abruzzo-Molise   | 0.49           | 0.63    |
| Campania         | 0.92           | 0.36    |
| Puglia           | 0.91           | 0.36    |
| Basilicata       | 0.48           | 0.63    |
| Calabria         | 0.88           | 0.38    |
| Sicilia          | 0.55           | 0.58    |
| Sardegna         | 0.91           | 0.36    |