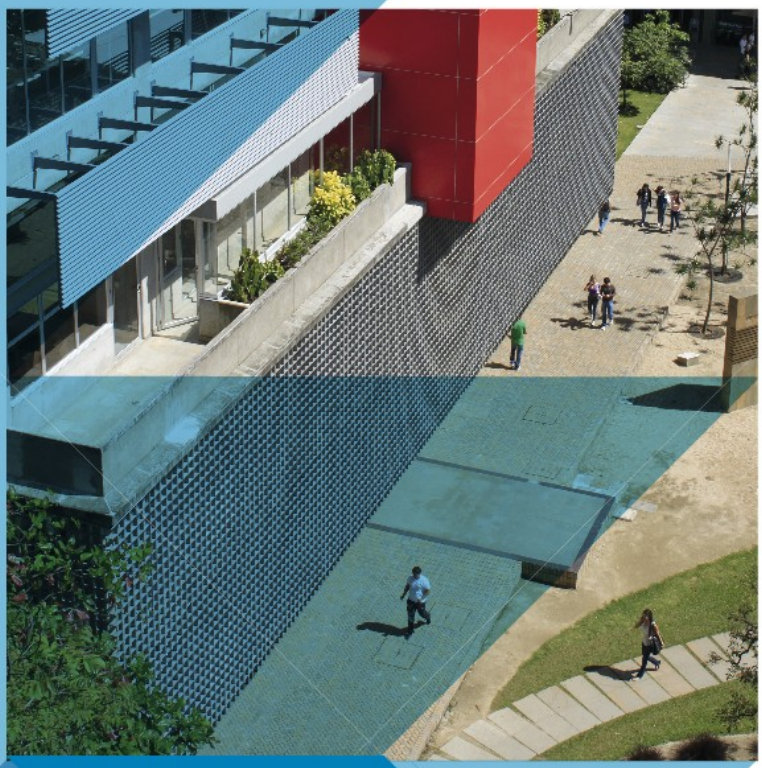

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Outliers in semi-parametric Estimation of Treatment Effects

Darwin Ugarte Ontiveros* , Gustavo Canavire-Bacarreza† and Luis Castro Peñarrieta‡

Abstract

Average treatment effects estimands can present significant bias under the presence of outliers. Moreover, outliers can be particularly hard to detect, creating bias and inconsistency in the semi-parametric ATE estimads. In this paper, we use Monte Carlo simulations to demonstrate that semi-parametric methods, such as matching, are biased in the presence of outliers. Bad and good leverage points outliers are considered. The bias arises because bad leverage points completely change the distribution of the metrics used to define counterfactuals. Whereas good leverage points increase the chance of breaking the common support condition and distort the balance of the covariates and which may push practitioners to misspecify the propensity score. We provide some clues to diagnose the presence of outliers and propose a reweighting estimator that is robust against outliers based on the Stahel-Donoho multivariate estimator of scale and location. An application of this estimator to LaLonde (1986) data allows us to explain the Dehejia and Wahba (2002) and Smith and Todd (2005) debate on the inability of matching estimators to deal with the evaluation problem.

JEL: C21, C14, C52, C13

Keywords: Treatment effects, Outliers, Propensity score, Mahalanobis distance

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1. Introduction

Parametric and nonparametric treatment effects techniques are the workhorse tool when examining the causal effects of interventions, i.e., whether the outcome for an observation is affected by the participation in a program or policy (treatment). Given the impossibility of observing the same observation under the two potential states (participation and non-participation), the use of counterfactual techniques is key when trying to better identify causal effects (Ashenfelter (1978); Ashenfelter and Card (1985); Heckman and Robb (1985); Heckman and Robb (1986)). As Bassi (1983), Bassi (1984) and Hausman and Wise (1985) argue, counterfactual estimates are precise when using randomized experiments. Yet, when looking at non-randomized experiments there are a number of assumptions, such as unconfoundedness, exogeneity, ignorability, or selection on observables, that should be considered before estimating the true effect, or to get close to that of a randomized experiment[1] Imbens (2004).

While there are several assumptions one needs to consider when identifying treatment effects (see King et al. (2017)), one that has been overlooked in the existing literature is the existence of outliers (both, on the outcome or on the covariates). We follow Jarrell (1994), Rasmussen (1988), and Stevens (1984) by defining outliers as those few observations that behave atypically from the bulk of the data, and are therefore much larger or smaller than the values of the remaining observations in the sample. One of the main problems caused by outliers is that they may bias or modify estimates of priority interest, and in our case, the treatment effect (see some discussion in Rasmussen (1988); Schwager and Margolin (1982); and Zimmerman (1994)). In addition, they may increase the variance and reduce in consequence the power of methods, especially those within the non-parametric family. If non-randomly distributed, they may reduce normality, violating in the multivariate analyses the assumption of sphericity and multivariate normality, as noted by Osborne and Overbay (2004).

To the best of our knowledge, the effects of outliers in the estimation of semiparametric treatment effects have not yet been analyzed in the literature. The only reference is Imbens (2004), who directly associates outlying values in the covariates to a lack of overlap. Imbens (2004) argues that outlier observations will present estimates of the probability of receiving treatment close to 0 or 1, and therefore, methods dealing with limited overlap can produce estimates approximately unchanged in bias and precision. As shown in this paper, this intuition is valid only for outliers what are considered good leverage points. Moreover, Imbens (2004) expresses that treated observations with outlying values may lead to biased covariate matching estimates since these observations would be matched to inappropriate controls. Control observations with outlying covariate values, on the other hand, will likely have little effect on the estimates of average treatment effect for the treated, since such observations are unlikely

[1] For a complete discussion and examples on the relationship between randomized and non-randomized experiments and their bias, see LaLonde (1986), Heckman et al. (1997a) and Heckman et al. (1997b).

to be used as matches. We provide evidence for this intuition.

Thus, in this paper, the relative performance of leading semi-parametric estimators of average treatment effects in the presence of outliers is examined. Three types of outliers are considered: bad leverage points, good leverage points and vertical outliers. The analysis considers outliers located in the treatment group, the control group, and in both groups. We focus on (i) the effect of these outliers in the estimation of the metric, propensity score and Mahalanobis distance, (ii) the effect of these contaminated (by outliers) metrics in the matching procedure when finding counterfactuals, and (iii) the effect of these matches in the estimation of the average treatment effect on the treated (TOT).

Using Monte Carlo simulations, we show that the semi-parametric estimators of average treatment effects produce biased estimations in the presence of outliers. A summary of our findings is as follows: First, bad leverage points bias estimations of average treatment effects. The bias emerges as this type of outlier completely changes the distribution of the metrics used to define good counterfactuals, and therefore changes the matches that had initially been undertaken, assigning as matches observations with very different characteristics. This effect is independent of the location of the outlier observation. Second, good leverage points in the treatment sample slightly bias estimations of average treatment effects, as they increase the chance of infringing the overlap condition. Third, good leverage points in the control sample do not affect the estimation of treatment effects, as they are unlikely to be used as matches. Fourth, these outliers distort the balance of the covariates criterion used to specify the propensity score. Fifth, vertical outliers in the outcome variable greatly bias estimations of average treatment effects. Sixth, good leverage points can be identified visually by looking at the overlap plot. Bad leverage points, however, are masked in the estimation of the metric and are, as a consequence, practically impossible to be identified unless a formal outlier identification method is implemented. Therefore, we suggest a re-weighting treatment effect estimator that is robust against outliers based on the Stahel (1981) and Donoho (1982) estimator of scale and location, proposed in the literature by Verardi et al. (2012). What we suggest is thus to identify all types of outliers in the data by this method, and again estimate treatment effects, down-weighting the importance of outliers; this is a one-step reweighted treatment effect estimator. Monte Carlo simulations support the utility of this tool to overcome the effects of outliers in the semi-parametric estimation of treatment effects.

An application of this estimator to LaLonde (1986) data allows us to understand the failure of Dehejia and Wahba (1999), Dehejia and Wahba (2002) matching estimations to overcome LaLonde's critique of non-experimental estimators. We show that the criticism by Smith and Todd (2005) about Dehejia and Wahba (1999), Dehejia and Wahba (2002) large bias when considering LaLonde's full sample can be explained by the presence of outliers in the data. When down-weighting the effect of these outliers, Dehejia and Wahba (1999), Dehejia and Wahba (2002) matching estimations approximate the experimental treatment effect of LaLonde's sample.

This paper is structured as follows. Section 2 briefly reviews the literature. Section 3 defines the balancing hypothesis, the semi-parametric estimators, the types of outliers considered, as well as the Stahel-Donoho estimation of location and scatter tool to detect outliers. In Section 4, the data generating process (DGP) is characterized. The analysis of the effects of outliers is presented in Section 5. An application to LaLonde's data is presented in Section 6. And in Section 7, we conclude.

2. A Brief Review of the Literature

Blundell and Costa Dias (2000) argue that the fundamental problem of causal inference arises because we can never observe both states (participation and non-participation) for the same observation at the same time, i.e., one of the states is counterfactual[2] . Thus, some assumptions are required to produce a more precise counterfactual and to estimate the actual causal effect. Within this framework, pure randomized controlled experiments are seen as desirable, especially for discovery and evidence for policy[3] . However, in the absence of experimental information, which is largely the case, alternative identification strategies for observational data are required[4] .

Many studies in the literature have shown that a comparison of the results of studies that used experimental data with those that used non-experimental data provide important advances to assess methods where it is impossible to work with experimental data. The results found in the experimental and non-experimental data were relatively close (seeLaLonde (1986); Heckman et al. (1997a); Heckman et al. (1997b); or Ferraro et al. (2015)).

In recent decades, there has been increasing interest in the econometric and statistical analysis of causal effects. Various methods for estimating average treatment effects for a binary treatment under different sets of assumptions have been suggested (Imbens and Wooldridge (2009)). One strand of this literature has developed statistical techniques for estimating treatment effects under the assumption that by adjusting treatment and control groups for differences in observed covariates, all biases in comparisons between treated and control observations are removed. The assumption is diversely referred to as unconfoundedness, exogeneity, ignorability, or selection on observables (see Imbens (2004) for a discussion). Under this assumption, nonparametric methods, such as matching, which have wide recognition for non-experimental statistical evaluation (see Heckman et al. (1997a)), have become a valued tool for recent evaluations of treatments in observational studies, as presented by Smith and Todd (2005) and Dehejia (2005). These methods select treated and comparison observations

[2] There are many references in literature that document this evaluation problem, including Ashenfelter (1978), Ashenfelter and Card (1985), Heckman and Robb (1985), and Heckman and Robb (1986).

[3] For a discussion on the goods and bads of experimentation see Deaton and Cartwright (2016).

[4] Some of the more relevant evaluation methods are the pure randomized social experiment, presented by Bassi (1983), Bassi (1984) and Hausman and Wise (1985), who based their contributions on previous statistical approaches presented by authors like Cochran and Rubin (1973) and Fisher (1951).

with similar characteristics in terms of covariates to predict the counterfactual outcome. This is done by defining similarity in terms of a metric: Mahalanobis distance values (Rubin (1980)) or propensity score values (Rosenbaum and Rubin (1983)). Some combination of both metrics has also been suggested (Zhao (2004)).

As argued earlier, an often overlooked, but important problem in econometric and statistical analysis is the existence of outliers. Outliers may bias and even modify point and distributional estimates, such as those produced when looking at treatment effects. Moreover, they increase the variance and reduce the power of the estimands, as argued by Rasmussen (1988), Schwager and Margolin (1982), Zimmerman (1994), and Osborne and Overbay (2004).

Various methods for identifying outliers have been proposed based on different methodologies, like statistical reasoning (Hadi et al. (2009)), distances (Angiulli and Pizzuti (2002); Knorr et al. (2000); and Orair et al. (2010)), or densities (Breunig et al. (2000)); (De Vries et al. (2010) and Keller et al. (2012)). But the issue is not completely solved, and in some methodologies, such as causal inference, this issue may become crucial. The problem increases as outliers often do not show up by simple visual inspection or by univariate analysis, and in the case several outliers are grouped close together in a region of the sample space, far away from the bulk of the data, they may mask one another (see Rousseeuw and Van Zomeren (1990)).

In regression analysis, Rousseeuw and Leroy (2005) define three types of outliers: *Good Leverage Points (GLP)* are observations (X_i, Y_i) whose X_i deviates from the majority in the X-dimension and follows the linear pattern of the majority. If, on the other hand, the observations do not follow this linear pattern and their X_i are outlying in the X-dimension, they are *Bad Leverage Points (BLP)*. Finally, if the observations deviate from the linear pattern but their $X_i$belong to the majority in the X-dimension they are called *Vertical Outliers (VO)*. Statistical estimations based on a sample including these extreme observations may dissent heavily from the true estimation (see Ruppert (1987), Hampel et al. (2011), Maronna et al. (2006), and Andersen (2008) for an assessment of estimation methods that are robust against outliers.

To illustrate the problem, in a labor market setting, as the one in Ashenfelter (1978) and Ashenfelter and Card (1985), consider a case in which the path of the data clearly shows that highly educated people attend a training program, while uneducated individuals do not. Now assume that there are a small number of individuals without schooling who are participating in the program, and a small number of educated individuals who are not in the training program, while having similar remaining characteristics. These peculiar individuals may constitute bad leverage points in the treatment and control sample, respectively. Enrolled individuals with an outstanding level of education may represent good leverage points. This small number of individuals, who may genuinely belong to the sample or may be errors from the data encoding process, may have a large influence on the treatment effect estimation and drive the conclusion about the impact of the training program for the entire sample, as pointed out by Khandker et al.

(2009) and Heckman and Vytlacil (2005). The problem considered in this paper is that as semi-parametric techniques, matching methods rely on a parametric estimation of the metrics (propensity score and Mahalanobis distance) used to define and compare observations with similar characteristics in terms of covariates, while the relationship between the outcome variables and the metric is nonparametric. Therefore, the presence of multivariate outliers in the dataset can strongly distort estimations of the metrics and lead to unreliable treatment effect estimations. According to information presented by Rousseeuw and Van Zomeren (1990), vertical outliers can also bias the nonparametric relationship between the metric and the outcome by distorting the average outcome in the observed or counterfactual group. Moreover, these distortions, by the presence of multivariate outliers in the dataset, can conflict the balance of the covariates when specifying the propensity score, as in Dehejia (2005). This has practical implications. When choosing the variables to specify the propensity score it may not be necessary to discard troublesome but relevant variables from a theoretical point of view or generate senseless interactions or nonlinearities. It might be sufficient to discard troublesome observations (outliers). That is, outliers can push practitioners to unnecessarily misspecify the propensity score.

3. Framework

(i) Matching methods: To lay out the setup, we rest on the traditional potential outcome approach developed by Rubin (1974), which views causal effects as comparisons of potential outcomes defined on the same unit. In the potential outcome framework, each observation $i = 1 \dots n$ has two potential responses (Y_i^0, Y_i^1) for a treatment. Y_i^1 is the outcome if observation i is treated (treatment group), and Y_i^0 is the outcome if observation i is not treated (control group). Each observation is exposed to a single treatment: $T_i = 0$ if the observation receives the control treatment and $T_i = 1$ if the observation receives the active treatment. In addition, each observation has a vector of characteristics X_i that are not affected by the treatment (usually referred to as covariates, pre-treatment variables or exogenous variables). For each observation, it is therefore observed the triplet $(Y_i; T_i \in \{0, 1\}; X_i)$, where Y_i is the realized outcome:$Y_i = T_i Y_i^1 + (1 - T_i) Y_i^0$. Unfortunately, we never observe both Y_i^0 and Y_i^1 simultaneously, so either Y_i^0 or Y_i^1 is missing for each observation. To estimate the average treatment effect, we thus need to estimate the unobserved potential outcome for each observation in the sample.

Non-parametric techniques, such as matching, impute the non-observable potential outcome (Y_i^0) by finding for each observation, other observations whose covariates are similar but who were not exposed to the treatment. To ensure that the matching estimators identify and consistently estimate the treatment effect of interest the following set of assumptions has been found useful: (i) that assignment to treatment is independent of the outcomes, conditional on the covariates, $(Y_i^0, Y_i^1) \perp T_i | X_i$, usually referred to as selection on observables, or unconfoundedness; and (ii) that the probability of

assignment is bounded away from zero and one, $\varsigma < P(X_i) \equiv P(T_i = 1|X_i) < 1 - \varsigma$, for some $\varsigma > 0$, also known as strict overlap assumption. See Imbens (2004) for a discussion of these assumptions. In this paper, we focus on the average treatment effect on the treated $\tau = E[Y_i^1 - Y_i^0|X_i, T_i = 1]$.

As mentioned above, matching estimators impute the missing potential outcome by using outcomes for observations with similar values for the covariates. However, when there are many covariates it is impractical to match them directly because of the curse of dimensionality. Therefore, it is necessary to map the multiple covariates into a balancing metric $m(X_i)$, a scalar, that can measure the closeness of two observations. This metric is defined by Rosenbaum and Rubin (1983) as a function of the observed covariates such that the conditional distribution of X_i given $m(X_i)$ is the same for the treated and comparison groups. The most often used metrics in the literature are the *Mahalanobis distance*, $D(X_i) \equiv ||X||_s = (X'SX)^{1/2}$, which is the vector norm with positive definite matrix S corresponding to the inverse of the sample covariance matrix of the covariates, and the *Propensity Score*, $P(X_i) \equiv P(T_i = 1|X_i)$, which is the predicted probability for $T_i = 1$ given the covariates X_i. Then, conditioning on covariates $D(X_i)$, or conditioning on the propensity score $P(X_i)$, will both make the distribution of the covariates in the treated group the same as the distribution of the covariates in the control group.[5] This is the balancing hypothesis, and it can be represented as $T_i \perp X_i|m(X_i)$. If it is achieved, observations with the same metric must have the same distribution of observable (and unobservable) characteristics, independent of treatment status. The achievement of a balanced model depends on the specification used to estimate the metric, see Dehejia and Wahba (2002) for a discussion on specification issues.

A variety of matching estimators has been proposed for estimating the counterfactual mean. Following the approach of Busso et al. (2009), the out-of-sample forecast for treated unit l based only on control units j can be represented as $\hat{Y_i^0} = \sum_j (1 - T_i) Y_j W_{l,j} / \sum_j (1 - T_j) W_{l,j}$, where $W_{l,j}$ provides the distance between observations l and j in terms of the metric $m(X_i) = \{D(X_i), P(X_i)\}$. The matching estimators differ in the weight $W_{l,j}$ used to estimate the counterfactual $\hat{Y_i^0}$.

In this paper, we will focus on those estimators that, supported by recent evidence, show good finite-sample performance and have established asymptotic properties (see Frölich (2004), Busso et al. (2009), and Busso et al. (2014)). We thus examine the effect of outliers on the following matching estimators: propensity score pair matching, propensity score local linear ridge matching, bias-corrected covariate matching, and reweighting based on propensity score. Busso et al. (2009) show that pair matching exhibits good performance in terms of bias, but with higher variance in small samples. Local linear ridge matching and reweighting perform well in terms of bias and variance once $n = 500$. In addition, Busso et al. (2014) showed that the bias-corrected covariate estimator is more effective in settings with poor overlap. Large sample properties

[5] See Rubin (1980), Rosenbaum and Rubin (1983), and recently Zhao (2004) for a comparison and data requirements for the implementation of these metrics.

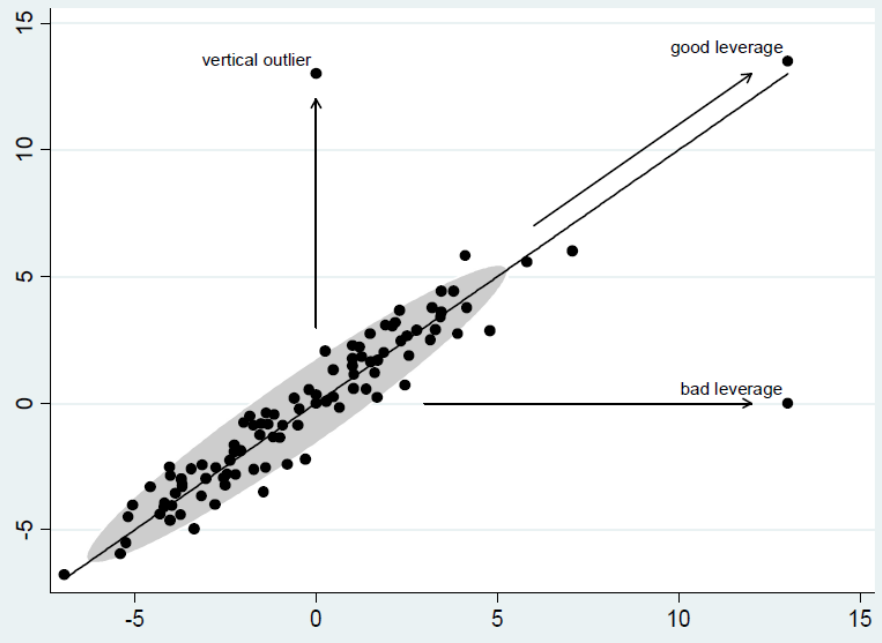
for these estimators have been approached by Heckman et al. (1997a), Hirano et al. (2003), and Abadie and Imbens (2006). Pair matching proceeds by finding for each treated observation a control observation with a very similar value of $m(X_i)$, that is, it sets $W_{l,j} = 1$ if the control observation j has the metric closest to that of treatment observation l, and sets $W_{l,j} = 0$ otherwise. Local linear ridge matching (Seifert and Gasser (2000)), is a variation of kernel matching based on a local linear regression estimator that adds a ridge term to the denominator of the weight $W_{l,j}$ in order to stabilize the local linear estimator. To estimate it we consider the Epanechnikov kernel. The bandwidth is selected by a simple leave-one-out cross-validation procedure with the search grid $h = 0.01\sqrt{1.2^{g-2}}$ for $g = 1, 2, \ldots, \infty$ following Frölich (2004). The bias-corrected covariate matching estimator attempts to remove the bias in the nearest neighbor covariate matching estimator coming from inexact matching in finite samples. It adjusts the difference within the matches for the differences in their covariate values. This adjustment is based on regression functions (see Abadie and Imbens (2011)) for details. Finally, in addition to these matching estimators, we consider the normalized reweighting estimator, where $W_{l,j} = P(X_j)/(1 - P(X_j))$ and the sum of the weights is 1.

(ii) Classification of outliers: Semi-parametric estimators of treatment effects may be very sensitive to outliers. As explained by Rousseeuw and Leroy (2005), in cross-section regression analysis, a source of bias may come from three kinds of contamination sources: in the error term (*vertical outliers*) and the explanatory variables (*two kinds of leverage points: good and bad*). Vertical outliers are those observations that are far away from the bulk of the data in the Y-dimension, i.e., outlying in the dependent variable, but present a behavior similar to the group in the X-dimension, i.e., are not outlying in the design space. Vertical outliers can affect the value of the coefficients in regression analysis and bias them downward or upward. Good leverage points (GLP) are observations that are far from the bulk of the data in the X-dimension, i.e., outlying in the regressors but are not located far from the regression line. Their existence in regression analysis does not affect the estimators but can affect the inference and induce the estimator to not be rejected as statistically significant. Finally, bad leverage points (BLP) are observations that are far from the bulk of the data in the X-dimension and are located far from the regression line. They affect the coefficients in regression analysis. A diagram to help distinguish these types of outliers can be found in Verardi and Croux (2009) (see figure 1).

(iii) A reweighted estimator: What we suggest for coping with the effect of these outliers is to identify all types of outliers in the data and down-weight their importance (a one-step reweighted treatment effect estimator). Here we suggest following Verardi et al. (2012) and use as an outlier identification tool the projection-based method of Stahel (1981) and Donoho (1982), hereafter called SD.

An interesting feature of this projection-based tool is that contrary to what occurs in other multivariate tools to identify outliers, like the minimum covariance determinant estimator (MCD) or the S-estimator of multivariate location and scatter (Smultiv),

Figure 1: Classification of outliers



Source: Verardi and Croux (2009).

dummies are not a problem. This feature is important as we are considering treatment effects and the main variable of interest is a dummy (T_i). Moreover, the presence of categorical explanatory variables in treatment effects empirical research is highly frequent. The advantage of the SD tool is its geometric approach: in regression analysis, even if one variable is always seen as dependent on others, geometrically there is no difference between explanatory and dependent variables and the data is thus a set of points (Y_i, T_i, X_i) in a $(p+1)$ dimensional space. Thus, an outlier can be seen as a point that lies far away from the bulk of the data in any direction. Note that the utility of this tool is not restricted to treatment effect models and it can be implemented to detect outliers in a broad range of models (see Verardi et al. (2012) for some applications).

The Stahel (1981) and Donoho (1982) estimation of location and scatter (SD) consists of calculating the outlyingness of each point by projecting the data cloud unidimensionally in all possible directions and estimating the distance from each observation to the center of each projection. The degree of outlyingness is defined as the maximal distance that is obtained when considering all possible projections. Since this outlyingness distance (δ) is distributed as $\sqrt{\chi^2_p}$, we can choose a quantile above which we consider an observation as being outlying (we consider here the 95th percentile)[6] . For specific details about this method see Verardi et al. (2012), and Maronna et al. (2006).

Once the outliers have been identified, a one-step reweighted treatment effect estima-

[6] A Stata code to implement this tool is available upon request.

tor can be implemented. In this paper, we use the most drastic weighting scheme that consists of awarding a weight of zero to any outlying observation. Once the importance awarded to outliers is down-weighted, the bias coming from outliers will disappear.

4. Monte Carlo Setup

The data generating process (DGP) is as follows:

$$\begin{aligned} T_i &= 1(T_i^* > 0) \\ T_i^* &= f(X_i) + \mu_i \\ Y_i &= \tau T_i + \gamma X_i + \varepsilon_i \end{aligned}$$

Where $\mu_i \sim N(0,1)$ and $\varepsilon_i \sim N(0,1)$ are independent of $X_i \sim N(0,1)$ and of each other. The sample sizes are $n = \{500, 1500\}$ and the number of covariates $p = \{2, 10\}$. 2000 replications are performed. The experiment is designed to detect the effect of outliers on the performance of various estimators. A benchmark case is considered, which sidesteps important issues that may constitute a source of bias in the estimation, like poor overlap in the metrics between treatment and control units, misspecification of the metric, etc. The idea is to see how outliers can move us away from this benchmark case. The design of the Monte Carlo study consists of two parts, (i) the functional form and distribution of the metric in the treated and control groups, and (ii) the kind of outlier contaminating the data.

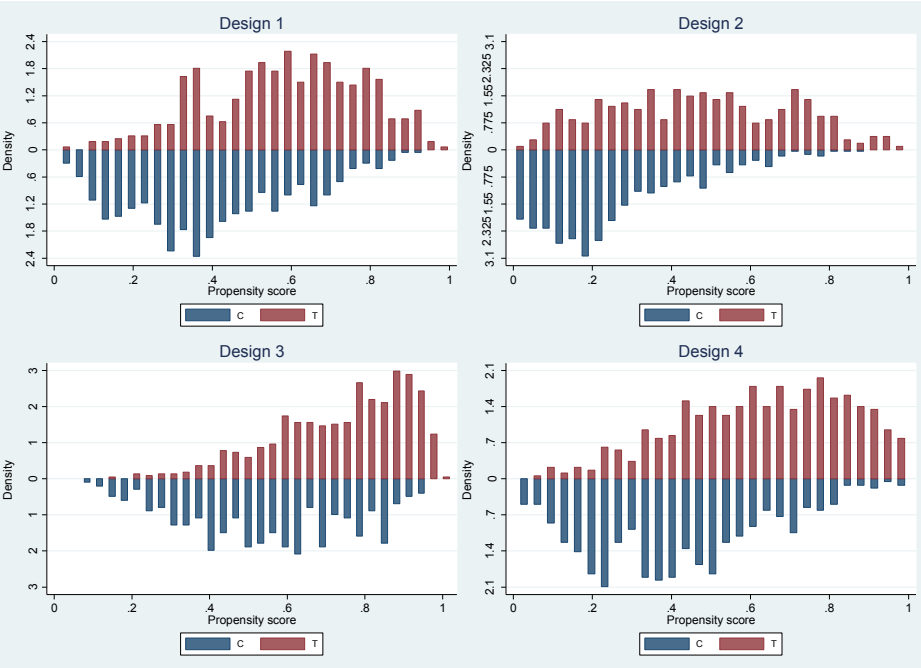
Initially, following Frölich (2004), the propensity score is specified as a linear function $f(X_i) = \alpha + \beta X_i$ and through the choice of different values for α, different ratios of control to treated observations are generated. The parameter α manages the average value of the propensity score and the number of treated relative to the number of controls in the sample. Then, in the first design (for $p = 2$), $f(X_i) = 0.5X_1 + 0.5X_2$ the population mean of the propensity score is 0.5. That is, the expected ratio of control to treated observations is $1:1$. In the second design, $f(X_i) = 0.65 + 0.5X_1 + 0.5X_2$ the ratio is $7:3$ (the pool of control observations is large), and in the third design, $f(X_i) = -0.65 + 0.5X_1 + 0.5X_2$, the ratio is $3:7$ (the treated greatly exceed the controls). We consider these designs, as during the estimation of the counterfactual mean, more precisely during the matching step. The effects of outliers in the treated or control groups could be offset by the number of observations in this group. The fourth design considers the equal size of the treatment and control groups, but a nonlinear specification of the propensity score on the covariate of interest: $f(X_i) = 0.5X_1 + 0.15X_1^2 + 0.5X_2$. In addition, $Y_i = 0.15 + T_i + 0.5X_1 + 0.5X_2$, that is, the true treatment effect is one. In the DGP we do not consider different functional forms for the conditional expectation function of Y_i given T_i. Results from Frölich (2004) suggest that when the matching estimator takes the average, the effects of these nonlinearities may disappear.

As mentioned before, the strict overlap assumption is always satisfied in these designs. Following Khan and Tamer (2010), this is a sufficient assumption for $\sqrt{n}$-

consistency of semi-parametric treatment effect estimators. Busso et al. (2009) show that with X_i and μ_i distributed standard normal for the linear specification of $f(X_i)$. This assumption is achieved when $|\beta| \leq 1$. The intuition behind this result is that when β approaches 1, an increasing mass of observations have propensity scores near 0 and 1. This leads to fewer and fewer comparable observations and an effective sample size smaller than n. This is important because it implies potentially poor finite sample properties of semi-parametric estimators in contexts where β is near 1. In our designs, we set $\beta = 0.5$ for the linear and nonlinear functions of $f(X_i)$. The overlap plots support the achievement of the strict overlap assumption for these cases, as they do not display mass near the corners. This can be observed in figure 2, where the conditional density of the propensity score given treatment status (overlap plot) for the four designs considered in the Monte Carlo simulations are displayed.

The second part of the design concerns the type of contamination in the sample. To grasp the influence of the outliers we will consider three contamination setups inspired by Croux and Haesbroeck (2003). The first is called clean with no contamination. In the second, called mild, 5% of X_1 are awarded a value $1.5\sqrt{p}$ units larger than what the DGP would suggest. The third is a setup called severe in which 5% of X_1 are awarded a value $5\sqrt{p}$ units larger than the DGP would suggest. Moreover, as mentioned above, three types of outliers are recognized in the literature: bad leverage points, good leverage points, and vertical outliers. Then, nine additional scenarios can be considered in the analysis depending on the localization of these outliers in the sample. That is, three types of outliers can be located in the treatment sample (T), in the control sample (C), and in both groups (T and C). Therefore, we assess the relative performance of the estimators described in last section in a total of seventy-two different contexts. These different contexts are characterized by combinations of four designs for $f(X_i)$, two types of contamination (mild and severe), and three types of outliers located in treatment, control and in both groups, respectively.

Figure 2: Overlap plots for the designs



Source: Authors calculations.

5. The effect of outliers in the estimation of treatment effects

This section analyses the effect of outliers in the estimation of treatment effects through the illustration of two simple cases, the effect of outliers in the estimation of the metrics used to define similarity, and the effect of these (spurious) metrics in the assignment of matches when finding counterfactuals, is described.

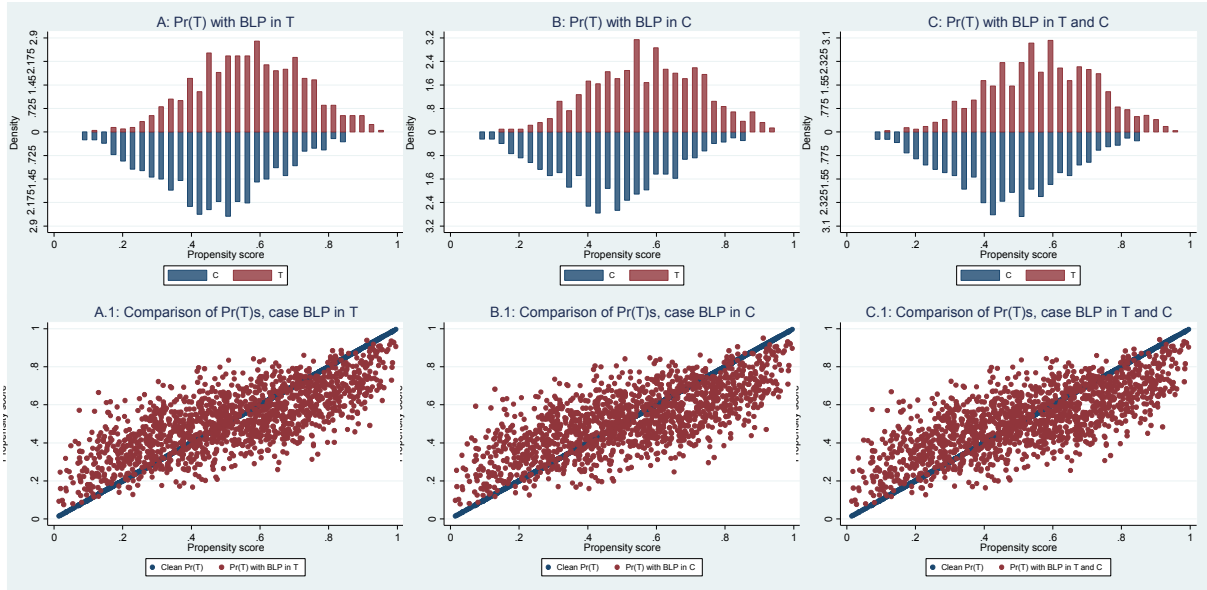
5.1 The effect of outliers in the metrics

a) The distribution of the Propensity Score in presence of outliers

Then, an artificial dataset is used to illustrate the effect of outliers in the distribution of the metrics in the presence of bad and good leverage points. 1500 observations were generated following the first design of our DGP. The original distribution of the propensity score by treatment status (overlap plot) corresponds to the top left graph of figure 2. The graphs on the top of figure 3 applies to the overlap plots for the same sample but with five percent of the data contaminated by *bad leverage points* in the treatment sample, in the control, and in both samples respectively. As can be seen, the propensity score is now clearly less spread out than the one obtained with the original data in both treatment and control groups. That is, the distribution of the propensity score changes completely. On the bottom of figure 3, the straight line

corresponds to the values of the original propensity score, whereas the cloud of points corresponds to the values of the propensity score in the presence of bad leverage points in the treatment sample, in the control, and in both samples respectively. They show huge differences in the values of the propensity score between the original and the contaminated sample. These changes in the distribution of the propensity score due to some outliers suggest, in addition, that the propensity score masks bad leverage points, as they cannot be distinguished in the data. Note that these effects are identical if we consider bad leverage points in the control sample, or in both treatment and control groups.

Figure 3: Effect of bad leverage points on the propensity score

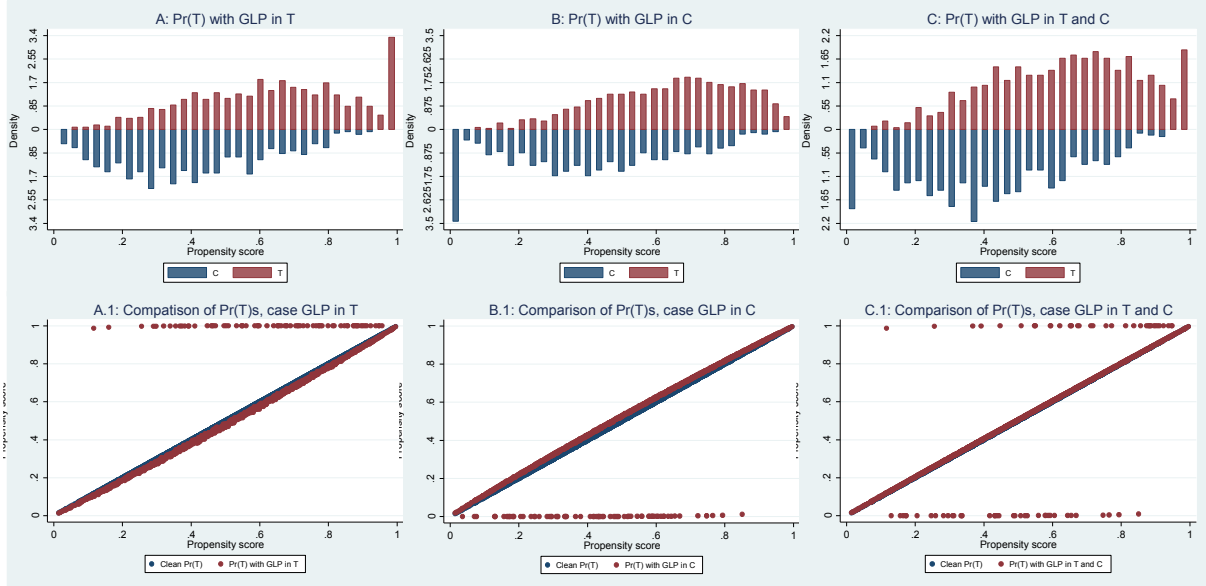


Source: Authors calculations.

On the top of figure 4, the distribution of the propensity score by treatment status in the presence of good leverage points in the treatment sample, in the control, and in both samples, is displayed. On the bottom of Figure 4, the straight line corresponds to the values of the original propensity score, whereas the cloud of points corresponds to the values of the propensity score in the presence of good leverage points. As can be observed, a difference of bad leverage points, the so called good leverage points do not change completely the distribution of the propensity score and can be identified visually.

A theoretical explanation for these results can be found in Croux et al. (2002), who showed that the non-robustness against outliers of the maximum likelihood estimator in binary models is characterized because *it does not explode to infinity as in ordinary linear regressions, but implodes to zero when bad leverage outliers are present in the data*

Figure 4: Effect of good leverage points on the propensity score



Source: Authors calculations.

set. That is, given the maximum likelihood estimator of a binary dependent variable,

$$\hat{\beta}_{ML} = \arg\max_{\beta} Log\ L(\beta; X_n)$$

where $Log\ L(\beta; X_n)$ is the log-likelihood function calculated in β. Croux et al. (2002) showed two important facts: (i) good leverage points (glp) do not perturb the fit obtained by the ML procedure, that is $\beta_{ML}^{glp} \to \beta_{ML}$. However, as displayed in figure 4, the fitted probabilities of these outlying observations will be close to zero or one. Here, it can lead to unstable estimates of the treatment effects as the support (or overlap) condition is not met. (ii) In presence of bad leverage points (blp), the ML-estimator never explodes, asymptotically it tends to zero. That is, $\beta_{ML}^{blp} \to 0$. In addition, following Frölich (2004) and Khan and Tamer (2010), coefficients close to zero in the estimation of the propensity score will then reduce the variability of the propensity score, as these coefficients (β) determine the spread of the propensity score. Therefore, the presence of bad leverage points in the data will always narrow the distribution of the propensity score, as found in figure 3. As is showed below, this tightness in the distribution of the propensity score may increase the chance of matching observations with very different characteristics.

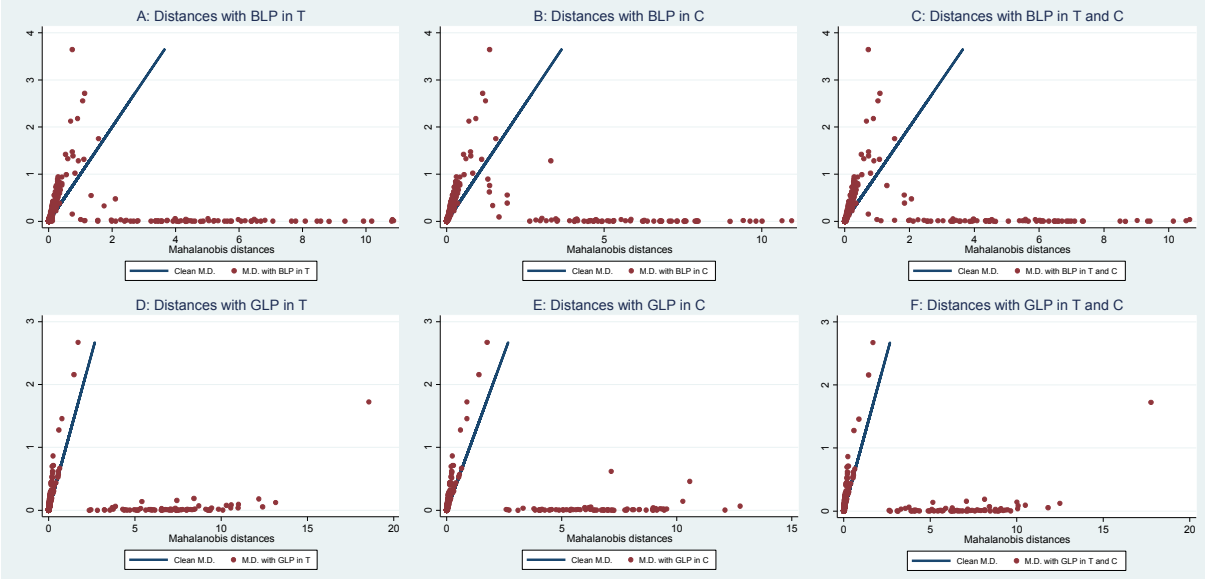
The effect of these distortions in the density of the propensity score in the matching process and in the treatment effect estimation is discussed in next sections.

b) The distribution of the Mahalanobis distance in presence of outliers

In figure 5, the straight line corresponds to the values of the Mahalanobis distance computed with the original data, whereas the cloud of points corresponds to the values

of this metric in the presence of bad and good leverage points in the treatment sample, in the control, and in both samples, respectively. Three remarks can arise from these graphs. First, bad and good leverage points present an atypical behavior in the sense that they display larger distances. Since Mahalanobis distances are computed individually for each observation, bad and good leverage points present bigger values, whereas remaining observations stay relatively stable. This behavior is independent of the location of the outlier. Second, bad and good leverage points slightly change the distribution of the distances, the stability of the not contaminated observations is relative in the sense that all distances are standardized by the sample covariance matrix of the covariates (S^{-1}), which is in turn based on biased measures (by the outliers) of the averages and variances in the sample. Third, concluding that observations with large distances can directly be called outliers may be fallacious, just in the sense that to be called outliers these distances need to be estimated by a procedure that is robust against outliers in order to provide reliable measures for the recognition of outliers. This is the masking effect, see Rousseeuw and Van Zomeren (1990). Single extreme observations or groups of observations, departing from the main data structure, can have a severe influence on this distance measure because the covariance (S^{-1}) is estimated in a non-robust manner; that is, it is biased.

Figure 5: Effect of bad and good leverage points on the Mahalanobis distance



Source: Authors calculations.

5.2 A description of the matching process in the presence of outliers

In this section, a small, artificial dataset is used to illustrate the effect of outliers in the assignment of matches when finding counterfactuals. Fifteen normally distributed

observations for the first design of our DGP are generated. These variables are presented in the first four columns of table 1. The exercises consist of substituting the value of one observation in one covariate, seeing in detail its effect on the matches assigned. One bad and one good leverage point is generated by moving the value of the last observation of X_1 by $+2.5\sqrt{2}$ and by $-2.5\sqrt{2}$, respectively. Columns five to seven of table 1 present the propensity score estimated with the original and contaminated data, respectively. As observed, the distribution of the propensity score with bad leverage points completely changes. Observations 5 and 9, for example, change their probability of participating in the program from 0.19 to 0.5 and from 0.85 to 0.54, respectively. The distribution of the propensity score with good leverage points holds the same path, but the probability of the outlier observation jumps from 0.3 to 0.99. Columns eight to ten show the consequent effect of the variation in this metric on the matches assigned to generate the counterfactuals (by using the nearest neighbor criteria)[7] . Consider observation 13, for example. Initially, it is presented as a counterfactual observation 1, but due to the presence of the bad leverage point, the nearest observation now corresponds with observation 4. The matches assigned in the presence of good leverage points are the same (with the exception of the observation with an outlier). Columns eleven to thirteen show the behavior of the Mahalanobis distance. As can be observed, the effect of the bad and good leverage point on this metric is similar. In both cases, the distribution changes slightly and the distances of the outlier observations increase abruptly. In the last three columns, we can see the effect on the assignation of counterfactuals. Observation 12, for example, is originally matched to observation 1. But in presence of the outlier it is matched to observation 2.

Table 1: Effect of a bad leverage point on the matching assignment

	Original data				Propensity score			Propensity score matches (ID)			Mahalanobis distance			Covariate matches (ID)		
ID	Y	X1	X2	T	P(T)o	P(T)blp	P(T)glp	mo	mblp	mglp	MDo	MDblp	MDglp	mo	mblp	mglp
1	0.57	-0.04	0.07	0	0.388	0.433	0.342	11	11	11	0.031	0.031	0.031	11	11	11
2	0.82	-0.70	0.75	0	0.280	0.474	0.224	13	11	13	0.652	0.404	0.450	11	11	12
3	-0.58	-0.79	-2.18	0	0.019	0.176	0.023	13	15	13	3.872	3.110	2.167	13	13	13
4	0.00	-1.85	0.13	0	0.024	0.339	0.019	13	13	13	4.472	1.753	1.985	11	15	11
5	0.66	-1.25	1.25	0	0.193	0.500	0.141	13	12	13	2.365	1.363	1.448	11	12	12
6	-0.22	-0.19	-0.96	0	0.178	0.312	0.171	13	15	13	0.407	0.214	0.192	13	13	13
7	0.61	-0.79	-0.26	0	0.124	0.355	0.108	13	14	13	1.156	0.841	0.576	11	11	11
8	0.33	1.08	-1.81	0	0.452	0.291	0.463	11	15	12	0.531	0.536	0.442	14	14	14
9	1.23	1.17	0.44	0	0.853	0.547	0.809	10	12	10	0.586	0.423	0.513	10	10	10
10	2.43	0.65	1.04	1	0.801	0.586	0.733	9	9	9	0.586	0.423	0.513	9	9	9
11	1.63	-0.07	0.24	1	0.411	0.452	0.358	1	1	1	0.031	0.031	0.031	1	1	1
12	2.55	0.15	0.75	1	0.590	0.524	0.515	8	9	8	0.590	0.538	0.450	1	2	2
13	1.48	0.36	-1.02	1	0.336	0.336	0.324	1	4	1	0.407	0.214	0.192	6	6	6
14	1.35	1.24	-1.15	1	0.637	0.369	0.624	8	7	8	0.531	0.536	0.442	8	8	8
15	1.76	0.09	0.58	1	0.533	0.302	0.999	8	6	9	0.320	1.753	3.760	1	4	9

Source: Authors calculations.

For a proper estimation of the unobserved potential outcomes, we want to compare treated and control groups that are as similar as possible. These simple illustrations explain that extreme values can easily distort the metrics used to define similarity and thus may bias the estimation of treatment effects by making the groups very different.

[7] Note that although we searched for the single closest match, as will be shown below, the illustration discussed above holds for different matching methods.

That is, the prediction of $\hat{Y}_l^0$ for the treated group is made using information from observations that are different from themselves. In the next section, we present evidence about the effects on the treatment effect estimations.

5.3 Monte Carlo Results

In this section the results of the Monte Carlo simulations are examined. The aim is to analyze the effect of outliers in the estimation of treatment effects in different scenarios.

Table 2 examines the performance in the estimation of the average treatment effect on the treated of the four selected estimators for the first design of our DGP. It presents the bias and mean squared error, scaled by 1000, from 2000 replications. The sample size (n) is 1500 and the number of covariates $p = 2$. The severe and mild contamination setups are considered in panel A and panel B, respectively. Columns correspond to the type of outlier and rows to the estimators. Column one, called clean, involves the no-contamination scenario. Columns two to four contain bad leverage points in the treatment, control, and both groups simultaneously, respectively. Similarly, columns five to seven consider good leverage points, whereas columns eight to ten correspond to vertical outliers in the treatment, control, and in both samples, respectively.

Table 2: Simulated bias and MSE of treatment effect estimations in the presence of outliers

Panel A: Severe contamination		**Bad Leverage Points**			**Good Leverage Points**			**Vertical outliers in Y**		
Estimators:	**Clean**	**in T**	**in C**	**in T and C**	**in T**	**in C**	**in T and C**	**in T**	**in C**	**in T and C**
BIAS										
Pair Matching	**6,7**	388,8	387,6	388,6	124,6	6,4	58,4	723,6	705,3	16,0
Ridge M. Epan	**7,2**	391,8	389,4	390,7	117,2	2,7	58,1	724,3	712,8	7,0
IPW	**4,2**	387,2	383,0	385,4	41,3	8,3	2,2	722,3	715,3	5,0
Covariate M. BC	**1,0**	358,7	1,3	182,1	358,5	0,8	181,6	717,2	716,8	1,6
MSE										
Pair Matching	**0,8**	152,6	151,7	152,4	18,2	0,9	4,9	524,7	525,3	16,7
Ridge M. Epan	**0,6**	154,1	152,3	153,3	15,5	0,6	4,4	525,4	523,9	10,0
IPW	**3,9**	150,6	147,4	149,3	3,8	2,6	3,2	524,9	529,3	13,1
Covariate M. BC	**0,6**	130,0	0,7	33,8	131,5	0,7	34,3	515,3	538,0	14,2
Rejection Balance of Cov	**10,0%**	99,6%	90,0%	18,4%	41,2%	49,8%	50,8%			
Panel B: Mild contamination										
BIAS										
Pair Matching	**6,7**	132,4	201,3	173,6	89,6	8,6	50,1	222,0	206,5	8,3
Ridge M. Epan	**7,2**	132,9	203,3	178,1	85,6	9,7	48,2	222,5	207,4	9,6
IPW	**4,2**	173,2	161,0	169,4	43,7	23,8	41,1	214,2	214,9	1,9
Covariate M. BC	**1,0**	108,9	152,2	146,8	106,0	11,9	59,7	216,3	214,1	4,1
MSE										
Pair Matching	**0,8**	18,4	41,6	31,1	9,3	0,9	3,5	50,0	46,1	2,3
Ridge M. Epan	**0,6**	18,2	41,9	32,3	8,2	0,6	3,0	50,0	45,2	1,4
IPW	**3,9**	31,3	27,5	30,2	7,2	2,0	7,2	49,8	51,3	4,5
Covariate M. BC	**0,6**	12,4	24,2	22,4	12,1	0,7	4,2	47,4	48,6	1,6
Rejection Balance of Cov	**11,8%**	85,4%	75,6%	50,0%	27,2%	12,4%	14,0%			

Source: Authors calculations.

The results suggest several important conclusions. First, in the absence of outliers

all the estimators we considered perform well, which is in accordance with recent evidence provided by Busso et al. (2009), and Busso et al. (2014). The bias-corrected covariate matching of Abadie and Imbens (2011) has the smallest bias, followed by the local linear ridge propensity score matching and the reweighting estimator based on the propensity score. Second, in the presence of bad leverage points, all the estimators present a considerable bias. For the propensity score matching methods, the size of the bias is generally the same, independent of the location of the outlier. This is expected since, as explained in the last section, the complete distribution of the metrics changes when bad leverage points exist in the data. The spread of the metrics decreases and observations that initially presented larger (lower) values of the metric may now match with observations that initially had lower (larger) values. Therefore, for pair matching the spurious metric will match inappropriate controls. For local linear ridge matching the weights $W_{l,j}$, which are a function (kernel) of the differences in the propensity score, will decrease notably. And in the case of the reweighted estimator, some control observations will receive higher weights as their propensity score values are higher than those values from the original data, and some will receive lower weights (as the weights are normalized to sum up to one). For the covariate matching estimator, treatment observations with bad leverage points bias the treatment effect estimation as the distribution of the distances changes completely. Moreover, outlier observations present larger values for the metric and are matched to inappropriate controls. Bad leverage points in the control sample have little effect on the estimates of average treatment effect for the treated as the distribution of the distances changes completely, but outlier observations are less likely to be considered as counterfactuals.

Third, good leverage points in the treatment sample also bias the treatment effect estimations of the propensity score matching estimators. Good leverage points in the treatment sample have estimates of the probability of receiving treatment close to 1. These treated observations with outlying values lack suitable controls against which to compare them. This violates the overlap assumption and therefore increases the likelihood of biasing the matching estimations. In the case of the reweighted estimator, the unbiasedness is explained as just the outliers receive higher weights, while remaining observations present almost the same weight (slightly modified by a normalization procedure). Moreover, good leverage points in the treatment group greatly bias the covariate matching estimator. This effect, which is similar to those coming from bad leverage points, is explained as these outlying observations have larger values for the metric and are therefore matched to inappropriate controls.

Fourth, good leverage points in the control sample do not affect matching methods. For the propensity score matching estimators, the values of the propensity score for the outliers are close to 0 and these observations would cause little difficulty because they are unlikely to be used as matches. For the reweighted estimator, these outlying observations would get close to zero weight. For the covariate matching estimators, good leverage points in the control sample have little effect on the estimations, as such observations are less likely to be considered as counterfactuals. Fifth, when good

leverage points are presented in both samples, treatment effect estimations are biased. This bias probably comes from the outliers in the treatment group.

Sixth, vertical outliers bias the treatment effect estimations. This bias is easy to understand since extreme values in the outcomes, Y_i^1 or Y_i^0, will move the average values toward them in their respective groups, independent of the estimator used to match the observations. Seventh, the immediate effect of outliers is to reject the balancing hypothesis.

Finally, table 3 analyses the effectiveness of the reweighted treatment effect estimator based on the projection-based identification of outliers' tool (SD). The aim of this set of simulations is to check how the outlier identification tool we propose and the subsequent reweighted estimator behaves with these models. The structure of table 3 is similar to that of table 1. The results suggest two main conclusions. First, the SD algorithm performs well in a scenario without outliers. That is, applying the SD algorithm does not influence the estimation of treatment effects in case no outliers are present in the data. Similar results were obtained when applying this tool to other estimators (see Verardi et al. (2012)). Second, as expected, the reweighted estimators we propose resist the presence of outliers and lead to estimations that are similar to those obtained with the clean sample in all contamination scenarios.

It is worth mentioning that the general conclusions obtained with designs two to four are very similar, although the effect of outliers is slightly smaller in design four. Similarly, the results obtained when considering $n = 500$, or when using ten covariates ($p = 10$) are practically identical to those presented above. These results are available upon request.

Table 3: Simulated bias and MSE of the reweighted treatment effect estimations based on the SD method

Panel A: Severe contamination		Bad Leverage Points			Good Leverage Points			Vertical outliers in Y		
Estimators:	**Clean**	**in T**	**in C**	**in T and C**	**in T**	**in C**	**in T and C**	**in T**	**in C**	**in T and C**
BIAS										
Pair Matching	**6,4**	6,2	8,3	7,6	6,3	8,3	7,7	2,3	1,0	0,6
Ridge M. Epan	**7,3**	8,9	8,4	9,0	8,9	8,5	9,0	0,0	0,1	0,3
IPW	**21,5**	27,1	23,4	26,4	27,1	23,8	26,6	13,6	12,5	14,2
Covariate M. BC	**1,3**	1,1	0,6	0,6	1,1	0,6	0,6	5,9	5,9	5,7
MSE										
Pair Matching	**0,8**	0,8	0,9	0,8	0,8	0,9	0,8	0,8	0,9	0,9
Ridge M. Epan	**0,6**	0,6	0,6	0,6	0,6	0,6	0,6	0,5	0,6	0,6
IPW	**1,8**	2,0	2,0	2,1	2,0	2,1	2,1	1,9	2,0	2,0
Covariate M. BC	**0,6**	0,7	0,7	0,7	0,7	0,7	0,7	0,7	0,8	0,7
Rejection Balance of Cov	**4,2%**	8,6%	7,4%	8,2%	8,4%	7,4%	8,2%			
Panel B: Mild contamination										
BIAS										
Pair Matching	**6,4**	43,0	41,7	57,2	19,4	5,0	4,7	17,0	19,8	17,9
Ridge M. Epan	**7,3**	44,0	40,3	58,3	18,0	4,3	4,0	19,2	19,0	19,3
IPW	**21,5**	50,4	47,7	51,0	18,5	10,7	12,0	27,0	18,9	19,1
Covariate M. BC	**1,3**	32,7	30,6	46,8	29,8	3,7	14,2	13,3	19,9	18,0
MSE										
Pair Matching	**0,8**	2,9	3,2	4,5	1,4	0,9	0,9	1,8	2,1	1,8
Ridge M. Epan	**0,6**	2,6	3,5	4,3	1,0	0,6	0,6	1,7	1,8	2,1
IPW	**1,8**	5,4	3,4	4,5	1,7	1,8	1,8	3,3	1,9	1,6
Covariate M. BC	**0,6**	1,8	2,1	3,1	1,7	0,6	0,8	1,5	2,0	2,6
Rejection Balance of Cov	**4,4%**	40,2%	16,2%	13,8%	9,8%	9,2%	7,6%			

Source: Authors calculations.

6. An outlier analysis of the Dehejia-Wahba (2002) and Smith-Todd (2005) debate

A debate has arisen, starting with LaLonde (1986), which evaluates the performance of non-experimental estimators using experimental data as a benchmark. Dehejia and Wahba (1999) and Dehejia and Wahba (2002) findings of low bias from applying propensity score matching toLaLonde (1986) data contributed strongly to the popularity and implementation of this method in the empirical literature - suggesting it as a good way to deal with the selection problem. Smith and Todd (2005) (hereafter called ST), using the same data and model specification as Dehejia and Wahba (hereafter called DW), suggest that the low bias estimates presented in DW are quite sensitive to the sample and the propensity score specification, thus claiming that matching methods do not solve the evaluation problem when applied to LaLonde's data.[8]

In this section, we suggest that the DW propensity score model's inability to ap-

[8] DW applied propensity score matching estimators to a subsample of the same experimental data from the National Supported Work (NSW) Demonstration, and the same non-experimental data from the Current Population Survey (CPS) and the Panel Study of Income Dynamics (PSID), analyzed by LaLonde (1986). ST re-estimated DW's model to three samples: LaLonde's full sample, DW's sub-sample, and a third sub-sample (ST-sample). See Dehejia and Wahba (1999), Dehejia and Wahba (2002), and Smith and Todd (2005), for details.

proximate the experimental treatment effect when applied to LaLonde's full sample is managed by the existence of outliers in the data. When down-weighting the effect of these outliers the DW propensity score model presents low bias. Note that we do not interpret these results as proof that propensity score matching solves the selection problem since the third subsample (ST sample) continues reporting biased matching estimates after down-weighting the effect of outliers. Moreover, this data allows us to highlight the role of outliers when performing the balance of the covariate checking in the specification of the propensity score. Dehejia (2005), in a reply to ST, argues that a different specification should be selected for each treatment group - comparison group combination, and that ST misapplied the specifications that DW selected for their samples to samples for which the specifications were not necessarily appropriate "as covariates are not balanced". Dehejia (2005) states that with suitable specifications selected for these alternative samples, with covariates well balanced, accurate estimates can be obtained. Remember that in estimating the propensity score the specification is determined by the need to condition fully on the observable characteristics that make up the assignment mechanism. That is, that the distribution of the covariates should be approximately the same across the treated and comparison groups once the propensity score is controlled for. Then the covariates can be defined as well-balanced when the differences in propensity score for treated and comparison observations are insignificant (see the appendix in Dehejia and Wahba (2002)).

ST suggests that matching fails to overcome LaLonde's critique of non-experimental estimators, as it presents large bias when applied to LaLonde's full sample, while Dehejia (2005) states that this failing comes from the use of a wrong specification of the propensity score for that sample (as the covariates are not balanced). In this section, we suggest that matching has low bias when applied to LaLonde's full sample and that the specification of the propensity score employed was not wrong, it was that the sample was contaminated with outliers. These outliers initially distorted the balance of the covariates, leading Dehejia (2005) to conclude that the specification was not right, and also biased the estimation of the treatment effect, causing ST to conclude that matching does not approximate the experimental treatment effect when applied to LaLonde's full sample. These conclusions can be found in table 4, which shows the propensity score nearest neighbor treatment effect estimations (TOT) for DW's subsample and LaLonde's full sample.[9] The dependent variable is real income in 1978. Columns one and two describe the sample, that is, the comparison and treatment groups, respectively. Column three reports the experimental treatment effect for each sample. Column four presents the treatment effect estimations for each sample. The specification of the propensity score corresponds to that used by Dehejia and Wahba (1999), Dehejia and Wahba (2002), and Smith and Todd (2005).[10] Column five reports the treatment effect estimations for each sample by using the same specification as in column four and

[9] I would like to thank professor Smith for kindly sharing his data with us.

[10] The specification for the PSID comparison group is: age, age squared, schooling, schooling squared, no high school degree, married, black, Hispanic, real earnings in 1974, real earnings in 1974 squared, real earnings in 1975, real earnings in 1975 squared, dummy zero earning in 1974, dummy zero earning

down-weighting the effect of outliers identified by the Stahel-Donoho method described in section 2. Three remarks arise from table 4. First, the treatment effect estimations for LaLonde's sample (in column four) are highly biased compared with the true effects (column three), as shown by DW. Second, once the outliers are identified and their importance down-weighted, the treatment effect estimations improve meaningfully in terms of bias, and the matching estimations approximate the experimental treatment effect when considering LaLonde's full sample. And third, once the effect of outliers is down-weighted, the propensity score specifications now balance the covariates successfully. This has practical implications, as when choosing the variables to specify the propensity score it might not be necessary to discard troublesome variables that may be relevant from a theoretical point of view, or to generate senseless interactions or non-linearities. It might be sufficient to discard troublesome observations (outliers). That is, outliers can push practitioners to unnecessarily misspecify the propensity score.

Table 4: Treatment effect estimations of the LaLonde and DW samples

Comparison group	**Treatment group**	**Experimental TOT**	**Estimated TOT**	**Estimated SD-TOT**
PSID [2490 obs]	LaLonde [297 obs]	886	-28 (1070)	670 (964)
PSID [2490 obs]	Dehejia-Wahba [185 obs]	1794	2317 (1266)	1203(1299)
CPS [15992 obs]	LaLonde [297 obs]	886	-351 (810)	736 (889)
CPS [15992 obs]	Dehejia-Wahba [185 obs]	1794	731 (882)	1587 (854)

Source: Authors calculations.

7. Conclusions

Assessing the impact of any intervention requires making an inference about the outcomes that would have been observed for program participants had they not participated. Matching estimators impute the missing outcome by finding other observations in the data whose covariates are similar but who were exposed to the other treatment. The criteria used to define similar observations, the metrics, is parametrically estimated by using the predicted probability of treatment (propensity score), or the standardized distance on the covariates (Mahalanobis distance).

Moreover, it is known that in statistical analysis the values of a few observations (outliers) often behave atypically from the bulk of the data. These atypical few observations can easily drive the estimations in empirical research.

In this paper, the relative performance of leading semi-parametric estimators of average treatment effects in the presence of outliers is examined. It is found that: (i)

in 1975, Hispanic* dummy zero earning in 1974. The specification for the CPS group is: age, age squared, age cubed, schooling, schooling squared, no high school degree, married, black, Hispanic, real earnings in 1974, real earnings in 1975, dummy zero earning in 1974, dummy zero earning in 1975, schooling* real earnings in 1974.

bad leverage points bias estimations of average treatment effects. This type of outlier changes completely the distribution of the metrics used to define good counterfactuals and, therefore, changes the matches that had initially been undertaken, assigning as matches observations with very different characteristics. (ii) Good leverage points in the treatment sample slightly bias estimations of average treatment effects and they increase the chance of infringing the overlap condition. (iii) Good leverage points in the control sample do not affect the estimation of treatment effects as they are unlikely to be used as matches. (iv) These outliers break the balancing criterion used to specify the propensity score. (v) Vertical outliers in the outcome variable greatly bias estimations of average treatment effects. (vi) Good leverage points can be identified visually by looking at the overlap plot. Bad leverage points, however, are masked in the estimation of the metric and are difficult to identify. (vii) The Stahel (1981) and Donoho (1982) estimator of scale and location, proposed by Verardi et al. (2012) as a tool to identify outliers is effective for this purpose. The proposed reweighted estimator produces unbiased matching estimators in the presence of outliers. (vii) An application of this estimator to LaLonde (1986) data allows us to understand the failure of Dehejia and Wahba (1999), and Dehejia and Wahba (2002) matching estimations to produce unbiased estimations when considering LaLonde's full sample. This failure can be explained by the presence of outliers in the data.

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