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Abstract

Matched sampling is a methodology used to estimate treatment effects. A caliper mechanism is used to achieve better similarity among matched pairs. We investigate finite sample properties of matching with calipers and propose a slight modification to the existing mechanism. The simulation study compares the performance of both methods and shows that a standard caliper performs well only in case of constant treatment or uniform propensity score distribution. Secondly, in a case of non-uniform distribution or non-uniform treatment the dynamic caliper method outperforms standard caliper matching.

Keywords:
propensity score matching, caliper, efficiency, Monte Carlo study, finite sample properties

JEL:
C14, C21, C52

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1. Introduction

Quasi-experimental methods are nowadays widely applied in evaluation studies. Their advantage, in comparison to fully controlled experimental design, is low cost. Matched sampling is a methodology for reducing bias due to observed covariates in comparative observational studies. However, even when matching on observable characteristics, it is necessary in order to estimate treatment effects to adjust for the difference in the distributions of those characteristics between treated and non-treated population. The most frequently used technique in application is pair matching, also called the nearest neighbour matching. The procedure seeks for each treated observation a non-treated counterpart with identical or very similar characteristics. In the adjustment process propensity score matching plays a fundamental role, since it reduces the course of dimensionality problem and allows for one-dimensional non-parametric regression (Rosenbaum and Rubin, 1983).

Caliper matching, introduced in a work by Cochran and Rubin (1973), is a modification of the nearest neighbour matching procedure that imposes a tolerance on the difference in characteristics between matched objects. Treated observations for which no matches can be found within a caliper are excluded from the analysis, which is one way of imposing a common support condition. A drawback of caliper matching is that it is difficult to know *a priori* what choice for tolerance level is reasonable (Todd, 2006).

In this paper we propose a slight modification of the caliper mechanism. We postulate that the size of the caliper should be retrieved from investigated data instead of choosing some *ad hoc* value. We call this procedure a dynamic caliper, as the size of the caliper depends solely on the estimated propensity score value. In other words, the size of the caliper is adjusted to the empirical data in the estimation process. A similar method was proposed by Rubin and Neal (2000) but with a considerably larger caliper value on covariates. Furthermore, one-to-one matching estimators are widely used in empirical studies, and it is important to understand their properties. Thus, we analyse the properties of the dynamic caliper in comparison with the standard procedure, and show its strengths and weaknesses. Our main result is that a standard caliper performs poorly when treatment is not the same for all units. Secondly, we show that in case of non-uniform distribution of the propensity score and non-constant treatment the dynamic caliper method has a lower bias and hence is better than standard matching with a caliper.

The article is divided into four sections. The following section briefly introduces matching estimators. In the next section we describe Monte Carlo simulations for different distributions of the propensity score and the outcome equations. In the subsequent section we present our main results, while the final section summarises and concludes.

2. The Caliper matching

The main problem in treatment effect literature is the estimation of the average treatment effect on the treated. We follow a standard notation. Let Y_{1i} be an outcome when individual *i* receives a treatment and Y_{0i} when he or she does not. The latter situation is called control treatment. Let $P_i \in \{0,1\}$ be an indicator of treatment status. The average treatment effect on the treated (ATT) is defined as

$$ATT = E[Y_1|P = 1] - E[Y_0|P = 1] \quad (1)$$

A typical matching estimator has the form (Smith and Todd, 2005)

$$\frac{1}{N}\sum_{i=1}^{N}\left[Y_{1i} - E\left(Y_{0i} \mid P_i = 1\right)\right] \quad (2)$$

where $E(Y_0 \mid P_i = 1) = \sum W(i,j) Y_{0i}$ is an estimator of the counterfactual state, ***W(i,j)*** is a matrix of distance between *i* and *j*, and *N* is a number of matched pairs. The fundamental problem of inference is that for each individual we can observe only one of these potential outcomes, because each unit will receive either treatment or control, not both. The estimation of causal effects can thus be thought of as a missing data problem (Rubin, 1973), where we are interested in predicting the unobserved potential outcomes.

It is assumed that conditional on all factors that influence the potential outcome and the decision to participate, P is independent of $Y_{0.}$ This assumption is called unconfoundness, conditional independence, or overlap or selection on observables (Imbens, 2004). The counterfactual mean can be identified, provided that the support of X among the treated is contained in the support of X among the non-treated. This property is called common support condition. An additional assumption is the Stable Unit Treatment Value Assumption (SUTVA) (Rubin, 1980), which states that the outcomes of one individual are not affected by treatment assignment of any other individual.

The idea of matching is to compute a similarity measure and use the algorithm to match observations from the treatment group with their closest counterpart from the control group. The aim is a construction adequate comparison group that replaces missing data and allows to estimate $E(Y_{0i}|P_i = 1)$ without imposing additional *a priori* assumptions (Blundell and Costa-Dias, 2009). Objects are matched according to the estimated value of the similarity measure. The straightforward algorithm is to choose for each object in the treatment group an object with the same or very close value of the similarity measure *p* from the control group. Usually the propensity score, which is probability of receiving the treatment, is chosen for that purpose. Let us define set A_i such that only one comparison unit *i* belongs to A_i:

$$A_i = \left\{ j \mid j \in \{1 \ldots n\} : \min \left\| p_i - p_j \right\| \right\} \qquad (3)$$

where ||.|| is a metric. In case of the nearest neighbour matching set A_i can be treated as weighting matrix. The weight matrix ***P(i,j)*** is a square matrix with zeros and ones as elements. The value one is for the closest neighbour, and zeros for all remaining objects. This type of matching is called one-to-one matching. Each unit from the treatment group is linked with only one element in the control group.

The nearest neighbour matching estimator has good statistical properties if p_i and p_j are defined on a common set. The role of the evaluator is to decide how to treat poorly matched observations (Lee 2005, pp. 89). The total distance, the average distance, or the median distance between matched pairs p_i-p_j may be viewed as a measure of matching quality (Rosenbaum, 1985). The lower the measure the better the fit. For the ideal procedure all quality measures should equal 0. Relying on all matched pairs regardless of matching quality may affect the balance. The balance is a weaker condition than close matching within each pair, and since it is weaker it can often be attained when close matching within pairs is not possible. Rosenbaum and Rubin (1985) showed that balancing two samples on the propensity score is sufficient to equalise covariate distributions. On the other hand, if a large number of poorly matched pairs were left out, the size of the control group shrinks and for certain observations in the treatment group there cannot be an adequate comparison in the control group. As a result, they are dropped from the analysis. This would help with the balance but at the cost of efficiency, because some information is not used. The evaluator has to choose between the bias and the variance of the estimator.

One-to-one or one-to-many matching is characterised by the risk of having poorly matched pairs, that is, pairs that are distant in terms of the chosen similarity measure. The caliper matching (Cochran and Rubin, 1973) is a variation of the nearest neighbour matching that attempts to avoid "bad" matches (those for which p_j is far from p_i) by imposing a tolerance of the maximum distance $||p_i-p_j||$ allowed. The impact of the caliper may be

compared to the focus in a camera. When attention is paid to specific point, other distant points are not visible. The procedure simply drops objects without close match.

$$A_i = \left\{ j \mid j \in \{1 \ldots n\} : \min \left\| p_i - p_j \right\| < \delta \right\} \quad (4)$$

The set A_i is made of such objects *j*, that their distance from the nearest match is not greater than δ. That is, a match for person *i* is selected only if $||p_i - p_j|| < \delta$, where δ is pre-specified tolerance. Treated persons for whom no matches can be found within the caliper are excluded from the analysis, which is one way of imposing a common support condition. Implementation of caliper matching may lead to a smaller bias in regions where similar controls are sparse. An unresolved problem is choosing an *a priori* reasonable value for tolerance level.

Rosenbaum and Rubin (1985) discuss the choice of the caliper size, generalizing the results from Table 2.3.1 of Cochran and Rubin (1973). When variance of the linear propensity score in the treatment group is twice as large as that in the control group, a caliper of 0.2 standard deviations removes 98% of the bias in a normally distributed covariate. Rosenbaum and Rubin generally suggest a caliper of 0.25 standard deviation of the linear propensity score. However, in the analysis they considered matching on the Mahalanobis distance, not on the propensity score.

Unfortunately, there is no single optimal value for the caliper. The literature suggests small numbers such as 0.005 or 0.001 (Austin, 2009). The caliper reduces the bias of the average treatment effect estimator at the cost of an increased variance (Heckman et al., 1997). In a special case, when the propensity score distribution is the same in the treatment and the control group, the caliper cuts off the worst matched pairs and lowers the bias without significant increase in estimator variance. The caliper also lowers the value of matching quality measures. The cost is lower number of successfully matched pairs. As a consequence the variance of the average treatment effect may increase. However, this is not a major concern as long as one is interested in precise estimation of the ATT (Smith and Todd, 2005). On the other hand, Smith and Todd (2005) point out that the potential problem with a caliper is a lack of *a priori* knowledge about its optimal value. It is common practice to set the value by trial and error.

We postulate to use as matching procedure a slightly modified caliper mechanism

$$A_i = \left\{ j \mid j \in \{1 \ldots n\} : \min \left\| p_i - p_j \right\| < \delta p_i \right\} \quad (5)$$

In this setting the caliper value is directly linked with estimated propensity score. For the observations with low treatment probability, the modified mechanism requires better matches from the control group in order to be included in computation of the ATT estimator value. In practice, there are a few such observations, but on the other hand, it is very likely that there is a good counterfactual in the control group for them. A large number of matched pairs with low treatment probability could cause the ATT estimator to be biased. Therefore, in our opinion influence of observation with low value of the propensity score should be limited, even though for those observations it is relatively easy to find a good counterfactual observation. In a situation where probability of participation approaches 1 a dynamic caliper will have no major differences from the standard one. As a result, we expect that a greater number of matched pairs is left aside in the computation, those with low participation probability.

3. Monte Carlo Study

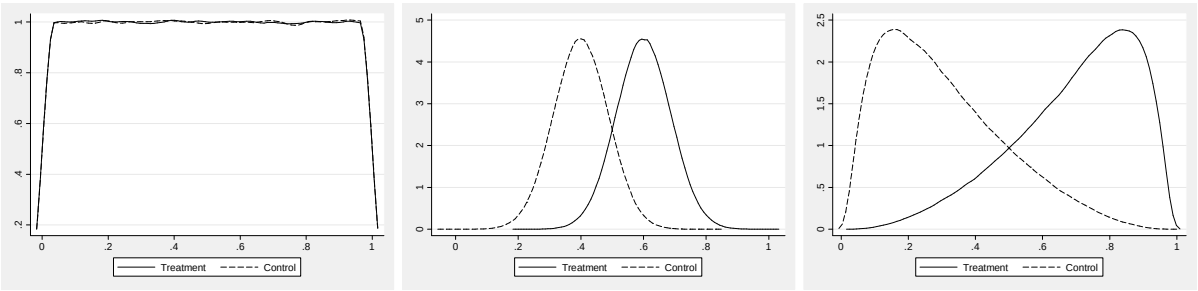
In this section we describe the Monte Carlo simulation conducted to examine the properties of the propensity score matching with a dynamic caliper in comparison with the

standard matching with caliper procedure. Since the propensity score is unknown in general, it is assumed, that is, estimated in a semi-parametric way.

The design of the experiment involves several assumptions and pre-set parameters values. At the beginning we decided to work with moderate sample sizes, and we established this parameter at 500. A number of that range is very common in this type of simulation found in the literature. The next pre-set parameter value is a ratio of treated observations to control observations. Frölich (2004) has shown that the mean squared error of matching is lower and hence the quality of matching procedure is higher when control to treated ratio is higher than one-to-one and is low in cases where there are more treated observations than those in the control group. Relying on those results we decided to set a constant relation between the number of treated observation and the number of controls, and set this parameter to 1:2. The precise number is each simulation is determined stochastically. For each observation we draw a random number from standard uniform distribution and we include the observation in the treated group if this random number is below 1/3. Otherwise, this particular observation is located in the control group. In this way, we receive on average 165 treated observations and 335 control observations. The following step involves setting the distribution of propensity score values. We considered three different distributions: uniform, normal, and Johnson S_B distribution. In a case of the latter two distributions, the distribution in the treatment group is concentrated on the right tail, while in the control group it is on the left tail (see Figure 1).

The uniform distribution of the propensity score vector, presented on the left panel of Figure 1, is just used as a benchmark. The normal distributions, presented on the middle panel of Figure 1, are a picture of a rather ideal case in which most of the characteristics follow a normal distribution. The normal distribution of several personal characteristics is a common assumption in social science. On the right panel the propensity scores follow a Johnson S_B distribution. This is a very flexible distribution, described by four parameters, and has a closed form. These properties mean that this distribution is frequently used in simulation based studies. The distributions are parameterised in such a way that propensity score values belong to the (0,1) interval.

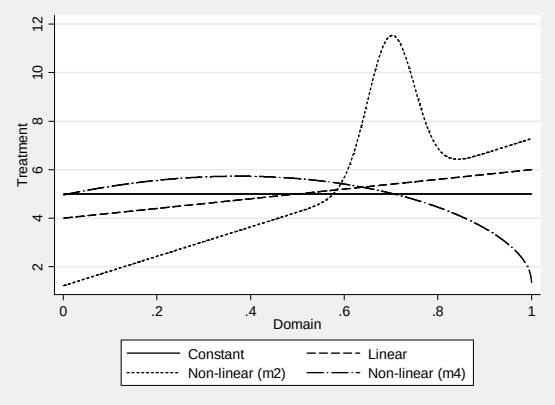
Figure 1. Propensity score distributions



Legend: Solid line represent distribution in treated groups, dashed in controls ones.
Source: Own computations.

Another parameter that we control in simulation is a shape of the outcome in the treated population conditional on the propensity score value. We consider four different distributions; they are presented in Figure 2, and in Table 1.

Figure 2. Distribution of treatment effect



Source: Own computations.

The uniform distribution mirrors the ideal case, when the value of the treatment is the same for all objects. This distribution will be also used as a benchmark. The linear distribution reflects the situation in which objects that are more likely to take part in a program will benefit more. For instance, this is very common in social support programs. Two other nonlinear curves are adapted from Frölich (2004). The nonlinear m2 curve might represent a situation where the outcome depends discontinuously on an object characteristic that is strongly related to the propensity score. The nonlinear m4 curve could be thought of as a reversal of linear curve. The program pays the most for those participants that are less likely to participate. Consider job training programs and education as a key determinant of the propensity score. Usually, well-educated persons do not need such programs and are able to find a job without external help.

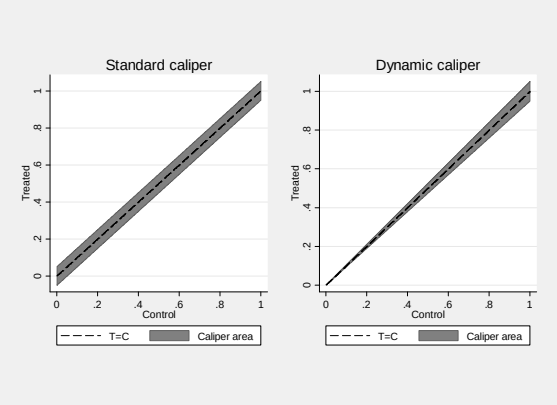
Table 1. Outcome equations for treated population

Distribution	Outcome equation for treated group
Constant	$y = 5 + e$, $e \sim U(0,.01)$
Linear	$y = 4 + 2*P + e$, $e \sim U(0,.01)$
Nonlinear m2	$y = 0.1 + 0.5*P + 1/2*(\exp(-200*(P-0.7)^2)) + e$, $e \sim U(0,.01)$
Nonlinear m4	$y = 0.2 + (1 - P)^{0.5} - 0.6*(0.9 - P)^2 + e$, $e \sim U(0,.01)$

Please note that curves are adjusted by linear transformation to have mean value of 5.

The last assumption involves the outcome value in the non-treated population and it is set to 0 for simplicity. Knowing the propensity score value and the outcome for all observations we were able to compare the result of standard caliper matching with our proposition of dynamic caliper matching. The construction of the caliper mechanism is different in both methods, as shown in equations (4) and (5). For the same numerical value of caliper parameter the standard method seeks comparison units in a larger area. The shape of the area for allowed matches is rectangular in case of the standard method, and triangular for a dynamic caliper (see Figure 3). Thus, with the same parameter value in both mechanisms the size of the area for possible matches using a dynamic caliper is half of that in the standard method. To overcome this difference in simulation, the caliper size in dynamic setting is going to be twice of that for a standard caliper. The simulation is carried out for all distributions of the propensity score vector and the functional forms for outcome equation with 10,000 replications.

Figure 3. Effect of caliper



Source: Own computations.

Before moving to the results it is worth noting that the numerical experiment is designed in such a way that "true" value of the average treatment effect should be 5 regardless of the distribution of the propensity score vector and the functional form of the outcome equation. The small error added to the outcome equation implies that a deviation from a value of 5 no greater than 0.01 should be regarded as purely random. Conversely, larger deviations would be an indication of bias of a particular estimation technique. We also run simulations with larger errors but it has no impact on the final results.

4. Empirical Results

The main results of our numerical experiment are presented in three separate tables. Each table consist of outcomes for only one distribution of the propensity score and all possible combinations of other parameters are considered. The values in the caliper size column refer to the size of the caliper in the standard approach. In case of the dynamic caliper they are simply doubled.

The results presented in Table 2 are a kind of benchmark for further results. They are obtained under assumption of identical distribution of the propensity score in the treatment and the control group. In this case the dynamic caliper method should be no better or worse than standard caliper matching. In case of the constant impact of treatment, in fact, there is no difference. However, when the impact of treatment is not uniform and depends on the value of the propensity score, the results show a different pattern. With linear outcome equation a standard caliper technique still gives unbiased results, while the results from a dynamic caliper method are positively biased. Nevertheless, as the size of the caliper increases the bias is smaller, due to greater number of successfully matched pairs (see Table 5). The sizes of standard errors for both methods are on the same level. Similar results are observed for both nonlinear specifications. Standard methods provide unbiased estimates, while results of estimation with the dynamic caliper mechanism are biased and the bias disappears as the caliper size increases.

Table 2. The ATT estimated with uniform distribution of propensity score

Treatment	constant		linear		m2		m4	
Caliper size	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper
0.001	5.000	5.000	5.000	5.265	5.010	6.082	4.997	4.750
	0.000	0.001	0.064	0.057	0.307	0.295	0.099	0.119
0.005	5.000	5.000	5.000	5.123	5.011	5.508	4.998	4.941
	0.000	0.000	0.046	0.044	0.219	0.224	0.071	0.080
0.010	5.000	5.000	5.000	5.069	5.010	5.278	4.997	4.981
	0.000	0.000	0.045	0.044	0.215	0.218	0.069	0.075
0.020	5.000	5.000	5.000	5.036	5.010	5.148	4.997	4.994
	0.000	0.000	0.045	0.044	0.215	0.216	0.069	0.072
0.025	5.000	5.000	5.000	5.029	5.010	5.121	4.997	4.995
	0.000	0.000	0.045	0.044	0.215	0.215	0.069	0.072
0.050	5.000	5.000	5.000	5.015	5.010	5.066	4.997	4.997
	0.000	0.000	0.045	0.045	0.215	0.215	0.069	0.070

Please note that in for each caliper size the number in top row is an estimate of ATT and in bottom row its standard error.
Source: Own computations.

Table 3. The ATT estimated with normal distribution of propensity score

Treatment	constant		linear		m2		m4	
Caliper size	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper
0.001	5.000	5.000	4.065	4.072	3.462	3.518	5.211	5.202
	0.001	0.001	0.014	0.014	0.098	0.103	0.015	0.015
0.005	5.000	5.000	4.107	4.113	3.796	3.869	5.159	5.150
	0.001	0.001	0.010	0.010	0.097	0.101	0.013	0.013
0.010	5.000	5.000	4.124	4.129	3.996	4.083	5.135	5.126
	0.001	0.001	0.010	0.010	0.104	0.108	0.013	0.013
0.020	5.000	5.000	4.138	4.145	4.224	4.335	5.112	5.101
	0.001	0.001	0.010	0.010	0.113	0.119	0.013	0.013
0.025	5.000	5.000	4.143	4.150	4.307	4.430	5.104	5.092
	0.001	0.001	0.010	0.010	0.118	0.125	0.013	0.014
0.050	5.000	5.000	4.160	4.170	4.611	4.781	5.074	5.055
	0.001	0.001	0.010	0.010	0.137	0.146	0.014	0.016

Please note that in for each caliper size the number in top row is an estimate of ATT and in bottom row its standard error.
Source: Own computations.

In a situation in which distribution of the propensity score in the treatment group differs from those in the control group the results are different. Table 3 shows the situation when propensity score follows a normal distribution in both groups but with different mean value. As the size of the treatment is the same for all objects both methods, that is, caliper and dynamic caliper, provide identical and unbiased results. In a situation with linear dependence between treatment value and propensity score value both methods result in downward biased estimates, and again results from both methods do not differ statistically from one another. In simulations with nonlinear outcome equations both methods perform rather poorly and it is hard to decide which one is better. However, the results of the dynamic caliper mechanism are closer to the "true value" of 5 than those obtained from the standard method.

The last set of simulations deals with propensity score that follows Johnson S_B distribution. Again, when the treatment is a simple constant value there are no significant differences between the two methods of estimation. In a case of linear distribution of the

propensity score the ATT estimates obtained via the dynamic caliper method are closer to the "true values" than those from a standard caliper method. On the other hand, the differences are within one standard error with the exception of the smallest caliper value where they are larger. Under nonlinear outcome equation the picture is somewhat blurred. For the m2 equation all but two results for dynamic caliper are closer to the "true" value than from the standard method. Similar results are observed for the m4 equation: in most cases the dynamic caliper performs better than its standard counterpart. However, the estimates are significantly and positively biased.

The last element of the simulation is to check the influence of the caliper method and its size on the number of successfully matched pairs, that is the number of those objects in the treated group for which there is a pair within a caliper distance in the control group.

Table 4. ATT estimated with Johnson S_B distribution of propensity score

Treatment	constant		linear		m2		m4	
Caliper size	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper
0.001	5.000	5.000	4.694	4.777	4.197	4.604	5.686	5.582
	0.000	0.000	0.052	0.048	0.322	0.315	0.073	0.079
0.005	5.000	5.000	4.809	4.851	4.796	4.952	5.523	5.439
	0.001	0.001	0.032	0.030	0.213	0.197	0.055	0.056
0.010	5.000	5.000	4.863	4.897	5.018	5.076	5.418	5.336
	0.001	0.001	0.029	0.028	0.189	0.174	0.054	0.055
0.020	5.000	5.000	4.906	4.935	5.099	5.099	5.314	5.231
	0.001	0.001	0.027	0.027	0.170	0.158	0.054	0.056
0.025	5.000	5.000	4.918	4.947	5.103	5.097	5.281	5.197
	0.001	0.001	0.027	0.027	0.165	0.153	0.055	0.058
0.050	5.000	5.000	4.952	4.983	5.094	5.089	5.180	5.074
	0.001	0.001	0.026	0.026	0.151	0.141	0.058	0.064

Please note that in for each caliper size the number in top row is an estimate of ATT and in bottom row its standard error.
Source: Own computations.

As the number of matched pairs depends only on the distribution of propensity score, the table is common for all outcome equation specifications. With the uniform distribution of the propensity score, the caliper value equal to or larger than 0.01 has no impact on the number of matched pairs. The dynamic version of caliper is, as expected, more conservative and prevents a greater number of poor matches.

Table 5. Number of successfully matched pairs

	Propensity score distribution					
	uniform		normal		Johnson S_B	
Caliper size	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper
0.001	81	74	52	55	83	78
0.005	159	140	96	101	93	105
0.010	165	153	112	117	115	127
0.020	165	159	126	131	132	143
0.025	165	160	130	136	136	147
0.050	165	163	143	150	149	159

Source: Own computations.

With the normal distribution of the propensity score the dynamic version of caliper allows for about 5% more possible matches in comparison with the standard procedure. However, as the caliper size increases the difference between two methods in terms of the number of matched pairs becomes smaller. When propensity score follows a Johnson S_B distribution the situation is very similar to those for normal distribution, except that in each cell there is a greater number of successfully matched pairs.

The comparison of Root Mean Squared Error (RMSE) for both estimation methods confirms our results. To conserve space we show in Table 5 results for caliper of 0.005 only; other results are similar to those presented. When propensity scores follow uniform distribution or treatment is constant, the standard caliper procedure provides unbiased results with low variance. If the value of treatment depends on the value of propensity score, a dynamic mechanism that adjusts caliper to the data has lower RMSE. The difference between the two methods is significant in the case of nonlinear outcome equation.

Table 6. Root Mean Squared Error

Treatment	constant		linear		m2		m4	
Distribution	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper	standard caliper	dynamic caliper
uniform	0.000378	0.000398	0.046571	0.131745	0.223129	0.558589	0.072525	0.100656
normal	0.000659	0.000673	0.893121	0.887302	1.223241	1.157174	0.160712	0.152604
Johnson S_B	0.000571	0.000585	0.195951	0.155794	0.334864	0.244080	0.531482	0.452099

RMSE computed for caliper size of 0.005
Source: Own computations.

5. Conclusions

The influence of the caliper mechanism on the estimation of the Average Treatment Effect on the Treated is not well recognised in the literature. On the other hand, the caliper is frequently used in applications to control for the balance between treated and non-treated population. In this paper we tried to shed some light on impact of the caliper on the properties of the ATT estimator. We have also proposed a modification of the caliper mechanism and conducted a comparative study. We call our method the dynamic caliper. The name is rooted in the fact that we postulate that the size of the caliper should be retrieved empirically from available data.

We show that standard caliper matching provides unbiased estimates in specific situations. Namely, when the treatment is constant, that is, in a situation in which the influence of the treatment is the same for every treated subject, or the probability of being treated is the same for all objects. With a propensity score distribution that is closer to the real empirical data our simulations indicate that the estimates of the ATT are biased and the RMSEs are quite large. Also we observe that the smaller caliper size comes with the higher bias. This means usually there is a trade-off between achieving balance between the treated and the control group, and unbiased estimates of the ATT.

The dynamic caliper is characterised by lower bias and lower variance. On the other hand, the dynamic caliper method performs poorly when the propensity score follows uniform distribution. The estimates are severely biased and have significantly larger RMSE in most cases. In simulations in which we assumed propensity score distribution that is close to the real data realizations, in most cases the dynamic caliper is better, in the sense that using that technique causes a lower bias and mean squared error. This result shows that the likelihood of obtaining a closer estimate to the true value is larger when using the dynamic caliper.

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