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To cite this article: José R. Zubizarreta & Luke Keele (2017) Optimal Multilevel Matching in Clustered Observational Studies: A Case Study of the Effectiveness of Private Schools Under a Large-Scale Voucher System, Journal of the American Statistical Association, 112:518, 547-560, DOI: [10.1080/01621459.2016.1240683](https://doi.org/10.1080/01621459.2016.1240683)

To link to this article: <https://doi.org/10.1080/01621459.2016.1240683>



Published online: 13 Jul 2017.



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# Optimal Multilevel Matching in Clustered Observational Studies: A Case Study of the Effectiveness of Private Schools Under a Large-Scale Voucher System

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## ABSTRACT

A distinctive feature of a clustered observational study is its multilevel or nested data structure arising from the assignment of treatment, in a nonrandom manner, to groups or clusters of units or individuals. Examples are ubiquitous in the health and social sciences including patients in hospitals, employees in firms, and students in schools. What is the optimal matching strategy in a clustered observational study? At first thought, one might start by matching clusters of individuals and then, within matched clusters, continue by matching individuals. But as we discuss in this article, the optimal strategy is the opposite: in typical applications, where the intracluster correlation is not one, it is best to first match individuals and, once all possible combinations of matched individuals are known, then match clusters. In this article, we use dynamic and integer programming to implement this strategy and extend optimal matching methods to hierarchical and multilevel settings. Among other matched designs, our strategy can approximate a paired clustered randomized study by finding the largest sample of matched pairs of treated and control individuals within matched pairs of treated and control clusters that is balanced according to specifications given by the investigator. This strategy directly balances covariates both at the cluster and individual levels and does not require estimating the propensity score, although the propensity score can be balanced as an additional covariate. We illustrate our results with a case study of the comparative effectiveness of public versus private voucher schools in Chile, a question of intense policy debate in the country at the present.

## ARTICLE HISTORY

Received March 2015  
Revised August 2016

## KEYWORDS

Causal inference; Group randomization; Hierarchical/multilevel data; Observational study; Optimal matching

## 1. Introduction

### 1.1. Clustered Observational Studies with Multilevel Data

Clustered observational studies are ubiquitous in the health and social sciences. Examples include patients receiving similar treatments in hospitals, employees facing a policy change inside firms, and students following a particular learning program within schools. Clustered observational studies have a nested or multilevel data structure with observed and unobserved covariates both at the cluster and unit levels. In this context, research interest typically lies in the effect of the cluster level treatment on unit level outcomes, however this effect may be confounded by differences in the distributions of covariates across the treatment groups both at the cluster and unit levels. Therefore, an important question in clustered observational studies is: how to adjust for observed covariates taking into account the multilevel structure of the data? Ideally, these adjustments will balance covariates at the cluster and unit levels in a transparent manner, while mimicking a target clustered randomized experiment and facilitating sensitivity analyses to hidden biases due to unobserved covariates (Rosenbaum 2010).

Perhaps the most well-known multilevel data structure arises in educational settings, with unit level measures such as the student's score on a standardized test, and also cluster level covariates such as school enrollment (Lee and Bryk 1989). Both

covariates may act as confounders when evaluating, for instance, the impact of a study program or administration regime targeted at improving learning. A conventional approach to adjust for cluster and unit level covariates is hierarchical or multilevel regression modeling. Multilevel regression models can aid causal inference by accounting for the design of the data collection, and, under certain assumptions, by adjusting for unmeasured covariates and modeling variation in treatment effects (Feller and Gelman 2015).

Nonparametric alternatives to multilevel regression modeling often rely on propensity scores (Hong and Raudenbush 2006; Arpino and Mealli 2011; Li, Zaslavsky, and Landrum 2013). For example, Hong and Raudenbush (2006) stratified on a multilevel propensity score to approximate a two-stage experiment where schools and students are randomly assigned to treatment within blocks. Matching methods are extensively used in observational studies (Stuart 2010; Lu et al. 2011), however they do not typically account for multilevel data structures.

In this article, we develop an optimal matching strategy for clustered observational studies. Contrary to intuition and common practice, which first matches clusters and then matches units within matched clusters, our strategy does the opposite: it first matches pairs of units across all possible combinations of treated and control clusters, and, once all the possible combinations of pairs of units across pairs of clusters are known, it then

matches the clusters. As we discuss, our strategy is optimal in the sense that it minimizes the total sum of covariate distances between matched pairs of units (when implemented with optimal matching; Rosenbaum 1989), or that it maximizes size of the pair-matched sample that balances covariates as required by the investigator (when implemented with cardinality matching; Zubizarreta, Paredes, and Rosenbaum 2014). With cardinality matching, the investigator can directly balance not only the first moments of the observed covariates but also their entire distributions. Cardinality matching does not require estimating the propensity score, although the propensity score can be used as an additional balancing covariate. Even though we implement our matching strategy in a clustered observational study with two levels—students within schools—it can readily be extended to settings with three or more levels such as students within schools within districts. In particular, we illustrate this method on a case study of the comparative effectiveness of public versus private voucher schools in standardized tests in Chile. This is a question of intense policy debate in the country at the present, and we describe it subsequently.

## 1.2. Private and Public Schools Under a Voucher System in Chile

In Chile in the 1980s, the military dictatorship enacted a far-reaching educational reform as it implemented, among other policies, a universal voucher system. That system, which is still in force today, is based on a direct payment to each school as a function of daily attendance. As a result of this new system, a large number of private schools subsidized by the voucher emerged, and today students in Chile can choose between three major types of schools. First, students can attend public schools that are run by local government authorities. Second, they can attend private subsidized schools. For both of these types of schools, the school receives a fixed amount of voucher money for each student based on daily attendance. Private subsidized schools, however, tend to set admissions policies, design curriculum, and they can also charge additional tuition (copayment). These private subsidized schools are often referred to as voucher schools, even though public schools also operate under a general voucher system. Finally, there are private nonsubsidized schools, which do not accept voucher payments from the government and are entirely funded by student tuition. Today approximately 55% of the students attend private subsidized schools, 37% attend public schools, and the rest attend private nonsubsidized schools (MINEDUC 2015b).

An important open question today is whether private subsidized schools deliver a better education than public schools. Following the student movement of 2011 in Chile (The Economist 2011; The New York Times 2011), a number of initiatives have been proposed (such as prohibiting the selection of students, co-financing, and eliminating profits for private subsidized schools; Bachelet 2013; MINEDUC 2015a), which would likely result in closing many private subsidized schools and replacing them with public schools. Current evidence on the effectiveness of private subsidized schools relative to public schools is mixed. A number of studies have found that private voucher schools increase test scores by at least 15% to 20% of a standard deviation (Mizala and Romaguera 2001; Anand, Mizala, and Repetto

2009) though other studies have found larger effects (Sapelli and Vial 2002, 2005). Other work has found effects that are either not statistically detectable (McEwan 2001; Hsieh and Urquiola 2006) or are much smaller (Lara, Mizala, and Repetto 2011).

In this article, we conduct an observational study of the comparative effectiveness of private subsidized or voucher schools versus public schools in terms of standardized test scores. Our study seeks to understand the effect of closure of entire private schools and replacement by public schools in a sample of comparable students in comparable schools. As such, while students and their families decide to which schools to attend (within certain constraints), closing and replacing one type of school with another type of school is an intervention that happens at the school level and not at the student level. Such reforms are not as common as interventions that seek to change one aspect of a school, but these reforms are consistent with a movement in education known as whole school or comprehensive reform. Under whole school reform, reforms extend beyond curriculum to an overhaul of the entire school system (Editorial Projects in Education Research Center 2004). One such example of whole school reform in the U.S. is Success for All (e.g., Borman et al. 2007).

As we describe subsequently, our data have a multilevel structure in that we observe student level covariates such as gender and socio-economic status as well as school level covariates such as enrollment and whether the school is in an urban or rural area. Consistent with the hypothetical intervention as being applied to entire schools as well as the data structure, we seek to mimic a clustered randomized experiment in which similar clusters are assigned to treatment and control, and furthermore, we also seek to remove overt bias to guarantee comparability at the student level. In this manuscript, we develop a matching strategy, consistent with both the data structure and a clustered treatment assignment mechanism, that pairs similar students within the paired schools.

This article is organized as follows. Section 2 presents the notation and basic assumptions, as well as the longitudinal census data and the design that we use in our study. Section 3 reviews cardinality matching for finding the largest matched sample that is balanced, explains the multilevel matching strategy, and presents it in more generality. Section 4 evaluates the matched sample. Section 5 analyzes the comparative effectiveness of public and private voucher schools in Chile. Section 6 concludes with a summary and a discussion.

## 2. Notation, Data, and Study design

### 2.1. Notation and Assumptions

Here, we introduce the basic notation and assumptions. Before matching, we have a sample of treated and control students within treated and control schools. As we explain in more detail in Section 3, in our matched design we form pairs of treated and control students within pairs of treated and control schools. Following Hansen, Rosenbaum, and Small (2014), after matching there are  $K$  matched pairs of clusters,  $k = 1, \dots, K$ , with two schools,  $j = 1, 2$ , one treated and one control, so there are  $2K$  clusters in total. Each cluster  $kj$  contains  $n_{kj} > 1$  individuals,  $i = 1, \dots, n_{kj}$ , each with a vector of observed covariates

$\mathbf{x}_{kji}$ . Similarly,  $u_{kji}$  represents an unobserved covariate of individual unit  $i$  in cluster  $kj$ . The covariates  $(\mathbf{x}_{kji}, u_{kji})$  may consist of measurements of either the student  $kji$  or the school  $kj$  of this student. In our study, we assume that treatment assignment occurs at the school level as whole schools are either private subsidized (voucher) or public schools. If the  $j$ th school in pair  $k$  receives the treatment, we write  $Z_{kj} = 1$ , whereas if this school receives the control we write  $Z_{kj} = 0$ , so  $Z_{k1} + Z_{k2} = 1$  for each  $k$  as each pair contains one treated school and one control school.

Each student has two potential responses; one response that is observed under treatment  $Z_{kj} = 1$  and the other observed under control  $Z_{kj} = 0$  (Neyman 1923; Rubin 1974). We denote these responses as  $(y_{Tkji}, y_{Ckji})$ , where  $y_{Tkji}$  is observed from the  $i$ th subject in pair  $k$  under  $Z_{kj} = 1$ , and  $y_{Ckji}$  is observed from this subject under  $Z_{kj} = 0$ . In our application  $y_{Tkji}$  is the test score that student  $kji$  would exhibit if the student is enrolled in a private subsidized school and  $y_{Ckji}$  is the test score this same student would exhibit if that school were converted to a public school. Of course, we do not observe both potential outcomes, but we do observe the responses  $Y_{kji} = Z_{kj}y_{Tkji} + (1 - Z_{kj})y_{Ckji}$ . Under this framework, the observed response  $Y_{kji}$  varies with  $Z_{kj}$  but the potential outcomes do not vary with treatment assignment.

Note that our notation implicitly assumes that there is no interference among units across schools. This assumption is often referred to as one part of the stable unit treatment value assumption (SUTVA; Rubin 1986). In our application, this assumption implies that potential test scores of a student in one school do not depend on the treatment assignment of students in other schools. In this context,  $y_{Tkji}$  denotes the response of student  $kji$  if all students in school  $kj$  receive the treatment, while  $y_{Ckji}$  denotes the response of student  $kji$  if all students in school  $kj$  receive the control. Therefore, we do not assume that we would observe the same response from student  $kji$  if the treatment were assigned to some but not all of the students in school  $kj$ .

Our aim is to estimate the effect on test scores of attending a private voucher school as opposed to a public school for comparable matched students  $kji$  within matched schools  $kj$ . Therefore, this causal effect is defined for the population of students that are comparable in terms of their observed covariates and that are marginal in the sense that they may or not receive the treatment (Rosenbaum 2012b). In other words, this effect is not about the students that will never attend a private voucher school, or that will never attend a public school, but instead about students that may attend either type of school as a function of their observed covariates. As we explain in Section 4.3, this estimand acknowledges the fact that not all the students are comparable in terms of observed covariates and it depends on the sample data (Crump et al. 2009). It also makes explicit that inferences to other target populations will require further modeling assumptions. In Section 4.3, we discuss how the estimand may change when the treated and control students are not comparable, and describe the population of students to which the results from the matched sample in principle generalize.

To identify this effect, we assume that the school level treatment assignment is strongly ignorable (Rosenbaum and Rubin 1983). Formally, this assumption states that the cluster level

treatment assignment is unconfounded,

$$\begin{aligned} \Pr(Z_{kj} = 1 | \{(y_{Tkji}, y_{Ckji}, \mathbf{x}_{kji}, u_{kji}), i = 1, \dots, n_{kj}\}) \\ = \Pr(Z_{kj} = 1 | \{\mathbf{x}_{kji}, i = 1, \dots, n_{kj}\}), \end{aligned}$$

and probabilistic

$$0 < \Pr(Z_{kj} = 1 | \{(y_{Tkji}, y_{Ckji}, \mathbf{x}_{kji}, u_{kji}), i = 1, \dots, n_{kj}\}) < 1,$$

for each cluster  $kj$  (Imbens and Rubin 2015, sec. 3.4). Intuitively, this assumption implies that after matching for observed covariates there are no systematic, pretreatment differences in unobserved covariates between the treatment and control groups, and that every school has a nonzero probability of receiving treatment. In Section 5.3, we assess the sensitivity of our findings to departures from the assumption that treatment assignment is unconfounded.

In general, under strong ignorability, our matching approach estimates an average of  $E[y_{Tkji} - y_{Ckji} | \mathbf{x}_{kji}]$  over some distribution of  $\mathbf{x}_{kji}$ . In our work, the distribution of  $\mathbf{x}_{kji}$  describes similar students in similar schools, that is, students at the margin who might have attended the opposite school in a matched pair of schools. Within a given pair of schools, not all students are “marginal” in this sense, although there may be many such marginal students. To avoid strong modeling assumptions, we confine our analyses to those marginal or similar students that are in similar schools.

Our matched design is meant to replicate a paired group randomized controlled trial (RCT). In a group RCT, treatment assignment occurs at the cluster, here school, level, and all units within a cluster are assigned to receive treatment. In a paired group RCT, clusters are paired using baseline covariates prior to randomization. However, this is a limited parallel, since we pair not only clusters but also units within matched clusters. We do this to guarantee that paired clusters are balanced both in terms of covariates and sample size. Thus, our design is comparable to a paired group RCT, where before randomization both clusters and units within clusters are paired. One reason to favor such a design is that randomization of clusters may not balance unit level covariates. See Hansen and Bowers (2009) for an example where clustered allocation of treatment left imbalances in unit level covariates.

## 2.2. Longitudinal Census of Students and Schools

In 1988, Chile introduced a national student assessment system known as the Sistema Nacional de Medición de la Calidad de la Educación or SIMCE. The SIMCE is an “educational census.” That is, in the SIMCE, the Chilean Ministry of Education collects data of all the students in fourth, eighth, tenth, and eleventh grades to evaluate their performance in language, mathematics, and sciences. The SIMCE data are collected roughly every 2 years from four different sources. First, data are collected from students, which includes test scores that are complemented with other student covariates such as gender. Second, both parents and teachers complete questionnaires. Finally, for schools, student test scores are aggregated, and a few additional covariates are collected. Students are given unique identifiers, which allows us to form a true panel over a 2 year period. Student records can also be linked to teacher, parent, and school level covariates.



In our study, we use SIMCE data from years 2003, 2004, and 2006. From year 2003, we use school-level measurements of secondary-only schools before the hypothesized treatment intervention. From 2004, we use student-level data for students in primary-only public schools when they were in eighth grade. Finally, from 2006 we use student test scores on language and mathematics administered when students were in the tenth grade as our outcome measures.

### 2.3. Data Structure and Study Design

In our study, the data structure and study design are intricately linked. We now outline how we constructed the match to fit the data structure. One advantage of our approach is that we can tailor the covariate adjustments to explicitly use the multilevel structure of the data, which is important since we have student, parent, teacher, and school level data. We match at two levels that correspond to students and schools. Next, we describe the covariates used in the student level match.

For each student with test scores observed in 2006, we match on student, parent, teacher, and primary school covariates from the SIMCE data collection in 2004. For the student match, we first list student level covariates. The key covariate here is student test scores from the 8th grade. In 8th grade, students are tested on four topics: language, mathematics, social sciences, and natural sciences. The student level data also measure gender. For the student match, we also include three covariates from parents: income measured in six categories, father's education, and mother's education. We also link students to primary school level measures, and we match on primary school covariates in the student level match. At the primary school level, we match on a five category socio-economic status indicator for each school that is created by the Chilean Ministry of Education. This five category indicator is constructed from questions based on parental education, family incomes in the school, and an index of school vulnerability. We also use school level measures that are aggregates of data observed at other levels. As such, we match on average test scores for each primary school, the number of teachers, and the number of enrolled students. Finally, in the teacher survey, teachers are asked what level of education they expect the majority of their students to achieve. Teachers responded using a five category scale that records responses from 8th grade to a college degree. We aggregate this measure and recorded the median for each primary school and use it in the student level match.

The school match is based on secondary school data from 2003. Since the SIMCE forms a panel, we can match on characteristics of the secondary schools before any student is exposed to the treatment. That is, we match on the schools the students will attend using data from before they attend that school. For the school match, we match on enrollment, school level math and language test score averages, the proportion of female students in the school, average student income, urban versus rural status, and the same five category socio-economic status indicator for each school that is recorded for primary schools.<sup>1</sup> Some

of these covariates are aggregates that we created from either student, teacher, or parent level data in 2003.

We describe the matching algorithm in greater detail in [Section 3](#). The algorithm is based on integer programming, which allows us to enforce different forms of balance for different covariates (Zubizarreta 2012; Zubizarreta, Paredes, and Rosenbaum 2014). This is relevant since we tailored the constraints for each covariate. Here, we describe the different balance constraints we applied to each covariate. For the student level covariates, we applied a mean balance constraint to limit the maximum absolute difference in the means of primary school test score measures, primary school enrollment, the number of teachers in the primary school, the average expected level of educational attainment, and the proportion of female students in the primary school. For student level test score measures, we enforced a constraint on the entire distribution via the Kolmogorov–Smirnov test statistic, which is the maximum discrepancy in the empirical cumulative distribution functions. For the school level match, we enforced a mean balance constraint on secondary school test scores, missingness indicators for test scores, secondary school enrollment, income category, SES category, urban or rural status, and the proportion of female students in the secondary school.<sup>2</sup>

For nominal student- and school-level covariates considered to be strong predictors of the outcome, we used an approximate fine balance constraint. Fine balance is a constraint on a nominal covariate that perfectly balances its marginal distribution. However, unlike exact matching, fine balance does not require units to be matched within each of the categories of the covariate, so when applied to several covariates simultaneously, it is a considerably less stringent requirement than exact matching. Approximate fine balance allows small deviations from fine balance. We applied approximate fine balance to student sex, father and mother's education level, parental income categories, and primary school SES categories. See Rosenbaum, Ross, and Silber (2007) for a discussion of fine balance and Rosenbaum (2010, Part II) for a discussion of different forms of covariate balance. In the following section, we describe our approach to multilevel matching.

### 3. Dynamic and Integer Programming for Multilevel Matching

As implemented in our case study, the goal of our multilevel matching approach is to find the largest sample of matched pairs of treated and control units within matched pairs of treated and control clusters that is balanced on the observed covariates. For assessing the sensitivity of results to the influence of unobserved covariates we use a sensitivity analysis proposed by Rosenbaum (1987, 2002) and tailored to clustered treatment assignments by Hansen, Rosenbaum, and Small (2014; see sec. 5.3 therein). In our case study, units are students and clusters are schools, and, importantly, because results can be confounded both by student and school level covariates, we match pairs of students and schools to balance covariates at both levels. The basic tool that we use in the implementation of our multilevel

<sup>1</sup> For student in secondary schools, the SIMCE only collects test scores on language and math. At the primary school level, we have test scores for language, mathematics, social sciences, and natural sciences.

<sup>2</sup> To be precise, we required the absolute differences in means in these covariates to differ at most by 0.1 standard deviations. Please see [Table 3](#).

matching strategy is cardinality matching that we describe subsequently.

### 3.1. Review of Cardinality Matching

Common matching methods attempt to achieve covariate balance indirectly, by finding treated and control units that are close on a summary measure of the covariates such as the Mahalanobis distance or the propensity score (see Stuart 2010; Lu et al. 2011 for reviews). Unlike these matching methods, cardinality matching uses the original covariates to match units and directly balance their covariate distributions (Zubizarreta, Paredes, and Rosenbaum 2014). Specifically, by solving an integer programming problem, cardinality matching finds the *largest* matched sample that satisfies the investigator's specifications for covariate balance. Following Zubizarreta (2012), these specifications for covariate balance may not only require balancing the means of the covariates, but perhaps also balancing entire distributions via fine balance (Rosenbaum, Ross, and Silber 2007),  $x$ -fine balance (Zubizarreta et al. 2011), and strength- $k$  balance (Hsu et al. 2015). For example, cardinality matching will find the largest sample of matched pairs in which all the covariates have differences in means smaller than one-tenth of a standard deviation and the marginal distributions of nominal covariates of greater prognostic importance are perfectly balanced (fine balance). In this manner, with cardinality matching subject matter knowledge about the research question at hand comes into the matching problem through the specifications for covariate balance, finding the largest matched sample that satisfies them.

Cardinality matching is well suited for studying unit-level interventions but it is unclear how to use it for cluster-level interventions with any optimality guarantees (a consideration that also applies to other matching methods such as optimal matching). As we describe in Section 3.2, our multilevel matching strategy uses cardinality matching to match treated and control students across all the possible combinations of treated and control schools, and then uses a modified version of cardinality matching to match schools with the largest number of matched students. As we discuss, our multilevel matching strategy can be used with other matching methods such as optimal matching to minimize the total sum of covariate distances between matched students within matched schools.

### 3.2. A Multistage Decision Strategy for Multilevel Matching

Let  $k_t \in \mathcal{K}_t = \{1, \dots, K_t\}$  index the treated clusters and  $k_c \in \mathcal{K}_c = \{1, \dots, K_c\}$  denote the control clusters. Let  $i_{k_t}$  be treated unit  $i$  in treated cluster  $k_t$ , with  $i_{k_t} \in \mathcal{I}_{k_t} = \{1, \dots, I_{k_t}\}$ , and  $i_{k_c}$  stand for control unit  $i$  in control cluster  $k_c$  with  $i_{k_c} \in \mathcal{I}_{k_c} = \{1, \dots, I_{k_c}\}$ . Put  $\mathbf{x}_{k_t}$  for the vector of observed covariates of treated cluster  $k_t$ , and similarly write  $\mathbf{x}_{i_{k_t}}$  for the observed covariates of treated unit  $i_{k_t}$ ; analogous notation applies for control clusters and units. Based on the unit-level covariates, calculate a distance  $\delta_{i_{k_t}, i_{k_c}}$  between treated unit  $i_{k_t}$  and control unit  $i_{k_c}$  (for instance, this distance may be the robust Mahalanobis distance specified in sec. 8.3 of Rosenbaum 2010). Define  $\mathcal{A}$  and  $\mathcal{B}_a$  as the sets of feasible solutions for the cluster- and unit-level matches within matched clusters (hence the subindex  $a$  in

$\mathcal{B}_a$ ). In practice,  $\mathcal{A}$  and  $\mathcal{B}_a$  are defined by linear inequality constraints in an integer program and they enforce the investigator's requirements for covariate balance and matching structures at the cluster and unit levels, respectively (for instance,  $\mathcal{A}$  may require the means of the cluster covariates to be balanced and the matched groups to form pairs of clusters, and  $\mathcal{B}_a$  may require the marginal distributions of the unit covariates to be balanced and the matched groups to form pairs of units). Importantly, since the requirements in  $\mathcal{A}$  refer to clusters and those in  $\mathcal{B}_a$  refer to units,  $\mathcal{A}$  and  $\mathcal{B}_a$  are disjoint. Let  $\mathcal{I}_{k_t}^{(m)}$  be the set of treated units matched in treated cluster  $k_t$  and  $\mathcal{I}_t^{(m)} = \bigcup_{k_t \in \mathcal{K}_t} \mathcal{I}_{k_t}^{(m)}$  be the set of treated units matched across all treated clusters. Finally, let  $\mathcal{K}_t^{(m)}$  be the set of matched treated clusters.

Building upon the framework of Rosenbaum (2012a), an optimal cardinality matching of units within clusters can be characterized by the quadruple  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta)$  of assignments of clusters  $\alpha: \mathcal{K}_t^{(m)} \rightarrow \mathcal{K}_c$  and units  $\beta: \mathcal{I}_t^{(m)} \rightarrow \mathcal{I}_{k_c}$  that maximize the cardinality of the set of matched units within matched clusters subject to the constraints in  $\mathcal{A}$  and  $\mathcal{B}_a$ , respectively. If there are two cardinality matchings that satisfy the requirements in  $\mathcal{A}$  and  $\mathcal{B}_a$ , then we prefer one matching over the other if it has a larger cardinality, or, alternatively, if they both have the same cardinality, if it has a smaller sum of total distances between matched units. Formally, we prefer the cardinality matching  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta)$  to  $(\tilde{\mathcal{K}}_t^{(m)}, \tilde{\alpha}, \tilde{\mathcal{I}}_t^{(m)}, \tilde{\beta})$ , denoted by  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta) \succ (\tilde{\mathcal{K}}_t^{(m)}, \tilde{\alpha}, \tilde{\mathcal{I}}_t^{(m)}, \tilde{\beta})$ , if  $|\mathcal{I}_t^{(m)}| > |\tilde{\mathcal{I}}_t^{(m)}|$ , or alternatively if  $|\mathcal{I}_t^{(m)}| = |\tilde{\mathcal{I}}_t^{(m)}|$  and  $\sum_{i_{k_t} \in \mathcal{I}_t^{(m)}} \delta_{i_{k_t}, \beta(i_{k_t})} < \sum_{i_{k_t} \in \tilde{\mathcal{I}}_t^{(m)}} \delta_{i_{k_t}, \tilde{\beta}(i_{k_t})}$ . If  $|\mathcal{I}_t^{(m)}| = |\tilde{\mathcal{I}}_t^{(m)}|$  and  $\sum_{i_{k_t} \in \mathcal{I}_t^{(m)}} \delta_{i_{k_t}, \beta(i_{k_t})} = \sum_{i_{k_t} \in \tilde{\mathcal{I}}_t^{(m)}} \delta_{i_{k_t}, \tilde{\beta}(i_{k_t})}$ , then we are indifferent between the two cardinality matchings and write  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta) \sim (\tilde{\mathcal{K}}_t^{(m)}, \tilde{\alpha}, \tilde{\mathcal{I}}_t^{(m)}, \tilde{\beta})$ . If we have either  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta) \succ (\tilde{\mathcal{K}}_t^{(m)}, \tilde{\alpha}, \tilde{\mathcal{I}}_t^{(m)}, \tilde{\beta})$  or  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta) \sim (\tilde{\mathcal{K}}_t^{(m)}, \tilde{\alpha}, \tilde{\mathcal{I}}_t^{(m)}, \tilde{\beta})$ , we write  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta) \succeq (\tilde{\mathcal{K}}_t^{(m)}, \tilde{\alpha}, \tilde{\mathcal{I}}_t^{(m)}, \tilde{\beta})$ . Our optimal multilevel matching problem is the following.

**Problem 1.** For given sets of cluster-level constraints  $\mathcal{A}$  and unit-level constraints  $\mathcal{B}_a$ , find a matching  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta)$  that satisfies  $\mathcal{A}$  and  $\mathcal{B}_a$  such that, for any other matching  $(\tilde{\mathcal{K}}_t^{(m)}, \tilde{\alpha}, \tilde{\mathcal{I}}_t^{(m)}, \tilde{\beta})$  that also satisfies  $\mathcal{A}$  and  $\mathcal{B}_a$ ,  $(\mathcal{K}_t^{(m)}, \alpha, \mathcal{I}_t^{(m)}, \beta) \succeq (\tilde{\mathcal{K}}_t^{(m)}, \tilde{\alpha}, \tilde{\mathcal{I}}_t^{(m)}, \tilde{\beta})$ .

Intuition may suggest that the best way to solve Problem 1 and match with multilevel data is first to match clusters and then within matched clusters to match units. In our case study, this would require first pairing schools and then, within pairs of schools, pairing students. However, this strategy will not always find the largest matched sample that is balanced as two schools that are paired on their school level characteristics may have different student compositions so that when their students are paired it may result in a smaller sample size than optimal. For this reason, the optimal matching strategy needs to contemplate what is optimal both at the student and school levels simultaneously. Applying Bellman's (1957) principle of optimality, the optimal matching strategy is first to match units across all the possible combinations of pairs of treated and control clusters, and, once all possible combinations of matched units are known, then to match clusters.

In abstract terms, the following algorithm and proposition state this. To implement the optimal assignments  $\alpha$  and  $\beta$ , let  $a_{k_t, k_c} = 1$  if treated cluster  $k_t$  is paired to control cluster  $k_c$  and  $a_{k_t, k_c} = 0$  otherwise; similarly let  $b_{i_{k_t}, i_{k_c}} = 1$  if treated unit  $i$  in treated cluster  $k_t$  is paired to control unit  $i$  in control cluster  $k_c$ , and  $b_{i_{k_t}, i_{k_c}} = 0$  otherwise.

**Algorithm 1.** For each of the possible  $K_t \times K_c$  pairs of treated and control clusters, find the optimal cardinality matching of units that satisfies  $\mathcal{B}_a$ . This is, for each  $k_t \in \mathcal{K}_t$  and each  $k_c \in \mathcal{K}_c$  find  $m_{k_t, k_c} = \max_{\mathbf{b}} \sum_{i_{k_t} \in \mathcal{I}_{k_t}} \sum_{i_{k_c} \in \mathcal{I}_{k_c}} b_{i_{k_t}, i_{k_c}}$  subject to  $\mathbf{b} \in \mathcal{B}_a$ . Then find the optimal cardinality cluster matching that solves  $\max_{\mathbf{a}} \sum_{k_t \in \mathcal{K}_t} \sum_{k_c \in \mathcal{K}_c} m_{k_t, k_c} a_{k_t, k_c}$  subject to  $\mathbf{a} \in \mathcal{A}$ .

**Proposition 1.** Algorithm 1 solves the optimal multilevel cardinality matching problem 1.

*Proof.* Let  $f(\mathbf{a}, \mathbf{b})$  be the total number of pairs of treated and control units matched by  $\mathbf{b}$  within pairs of treated and clusters matched by  $\mathbf{a}$ . In the abstract, in Problem 1 we want to maximize the function  $f(\mathbf{a}, \mathbf{b})$  subject to the constraints  $\mathcal{A}$  and  $\mathcal{B}_a$ . This is, find  $\mathbf{a}$  and  $\mathbf{b}$  to solve

$$\max_{\mathbf{a}, \mathbf{b}} f(\mathbf{a}, \mathbf{b}) \text{ subject to } \mathbf{a} \in \mathcal{A}, \mathbf{b} \in \mathcal{B}_a. \quad (1)$$

In a trivial way, we may solve (1) by first solving

$$g(\mathbf{a}) = \max_{\mathbf{b}} f(\mathbf{a}, \mathbf{b}) \text{ subject to } \mathbf{b} \in \mathcal{B}_a \quad (2)$$

for each  $\mathbf{a} \in \mathcal{A}$ , and then solving

$$\max_{\mathbf{a}} g(\mathbf{a}) \text{ subject to } \mathbf{a} \in \mathcal{A}. \quad (3)$$

While (2) seems hard in general (because there are many possible choices of  $\mathbf{b}$ ), the nested structure of the units-in-clusters problem makes it easier because  $f(\mathbf{a}, \mathbf{b})$  separates into a sum of parts for cluster pairs because the constraint sets  $\mathcal{A}$  and  $\mathcal{B}_a$  are disjoint. Algorithm 1 does exactly this.  $\square$

In our case study, for each pairing of schools  $\mathbf{a}$ , we find the best pairing of students  $\mathbf{b}$  within those schools (2), and then pick the best pairing of schools with the associated best pairing of students for that pairing of schools (3). Again, while (2) seems hard in general (because there are many possible student matches  $\mathbf{b}$  across schools), the nested structure of the students-in-schools problem makes it easier because  $f(\mathbf{a}, \mathbf{b})$  separates into a sum of parts for school pairs. For example, if treated school  $k_t$  is paired to control school  $k_c$ , then the contribution of schools  $k_t$  and  $k_c$  is the same of number of pairs regardless of how the other schools are paired.

With Algorithm 1, the multilevel cardinality matching problem can be solved optimally by breaking it into simpler matching subproblems and recursively finding the optimal match. This is an application of dynamic programming to matching in observational studies that takes advantage of the multilevel structure of the data (see, e.g., Bertsekas 2005 for an extensive exposition of dynamic programming).

### 3.3. Illustrative Example

We present a simple example to fix ideas. In this example, there are three treated schools and five control schools indexed

by  $k_t \in \mathcal{K}_t = \{1, \dots, 3\}$  and  $k_c \in \mathcal{K}_c = \{1, \dots, 5\}$ , respectively. The first step in our multilevel matching strategy as implemented with cardinality matching is to find the student pair-matches across all the possible combinations of pairs of treated and control schools. Here, since there are three treated schools and five control schools, we must first solve  $3 \times 5 = 15$  student matching problems.<sup>3</sup> For each of these 15 combinations of pairs of treated and control schools, we use cardinality matching and record the cardinality of the pair-matched students,  $m_{k_t, k_c}$  (so  $m_{1,1}$  is the number of students that were pair-matched between treated school and control school 1,  $m_{1,2}$  is the number of pair-matched students between treated school 1 and control school 2, and so on). The size of the cardinalities  $m_{k_t, k_c}$  will depend on the student covariate balance constraints, denoted  $\mathcal{B}_a$ , and the cardinality may be zero if the balance constraints cannot be met. Once we obtain all the  $m_{k_t, k_c}$ 's, the second step is to solve the school level matching problem, which maximizes the total number of pair-matched students within pair-matched schools subject to school level balance constraints,  $\mathcal{A}$ . This problem is  $\max_{\mathbf{a}} \sum_{k_t \in \mathcal{K}_t} \sum_{k_c \in \mathcal{K}_c} m_{k_t, k_c} a_{k_t, k_c}$  subject to  $\mathbf{a} \in \mathcal{A}$ . Solving the problem backward—from the students to the schools, instead of the opposite—ensures that we find the overall optimum number of student matches. If we were to do the opposite (this is, first match schools and then within matched schools match students), then we would likely find a suboptimal solution as we show in the comparison study in Section 4.2.

### 3.4. Additional Considerations

Note that if we had three or more levels (such as students within schools within districts), then our multilevel matching strategy would extend naturally. With  $l$  levels, the strategy would require first matching the lowest level  $l$  under the assumptions that levels  $l-1, l-2, \dots, 1$  have been matched optimally, to then (once the matches at level  $l$  are completed) matching level  $l-1$  under the assumptions that levels  $l-2, l-3, \dots, 1$  have been matched optimally, and so on.

The multilevel matching problem above is formulated to maximize the size of the matched sample in terms of students, but it can be easily modified to maximize a weighted combination of students and clusters, namely,

$$\max_{\mathbf{a}} \sum_{k_t \in \mathcal{K}_t} \sum_{k_c \in \mathcal{K}_c} m_{k_t, k_c} a_{k_t, k_c} + \lambda \sum_{k_t \in \mathcal{K}_t} \sum_{k_c \in \mathcal{K}_c} a_{k_t, k_c} \text{ subject to } \mathbf{a} \in \mathcal{A} \quad (4)$$

for a suitable scalar  $\lambda$ . Also, the multilevel matching problem can be formulated to minimize a covariate distance between students by using optimal matching to solve each of the component problems. In all these cases, the optimal matching strategy will be to match backward, by first matching the units and then matching the clusters.

We have discussed the optimality of our multilevel matching strategy using arguments from mathematical programming. From a statistical standpoint, this matching approach as implemented with cardinality matching gives priority to reducing bias over increasing precision, and is optimal in the sense that given a matching structure (e.g., pair matching) and degree of bias

<sup>3</sup> We match the students within treated school 1 and control schools  $\{1, \dots, 5\}$ , treated school 2 and control schools  $\{1, \dots, 5\}$ , and so on.



**Table 1.** Mean balance for student-level covariates after matching. All the covariates are measured in 2004.

Covariate	Mean		Std. dif.
	Private	Public	
Language score	244.84	244.75	0.00
Mathematics score	245.71	244.92	0.02
Natural science score	248.74	248.57	0.00
Social science score	244.38	244.49	−0.00
School language score	238.84	238.42	0.02
School mathematics score	239.89	239.32	0.03
School female proportion	0.51	0.51	−0.01
School number of students	84.23	84.17	0.00
School teacher to student ratio	8.22	8.14	0.04
Urban area	0.85	0.85	−0.00
Socioeconomic status A	0.13	0.13	−0.01
Socioeconomic status B	0.57	0.56	0.01
Socioeconomic status C	0.28	0.29	−0.01
Socioeconomic status D	0.02	0.01	0.02
Expected education: primary	0.01	0.01	−0.00
Expected education: secondary, technical-professional	0.72	0.69	0.05
Expected education: secondary, scientific-humanities	0.16	0.17	−0.04
Expected education: technical-professional	0.10	0.10	−0.01
Expected education: college	0.01	0.02	−0.05

NOTE: The last column shows standardized differences in means.

reduction (these are the covariate balancing requirements) it maximizes the accuracy of the study (by maximizing the size of the matched sample). More precisely, extending the argument in Kilcioglu and Zubizarreta (2016), under an homoscedastic constant additive treatment effect model, Algorithm 1 with (4) minimizes the variance of a difference-in-means effect estimator. In general, the statistical optimality of matching methods is an important area that remains to be further studied within a formal statistical framework.

## 4. Evaluation of the Matched Sample

### 4.1. Covariate Balance and Sample Size

After applying basic exclusion criteria, there are 64,245 students in 517 schools, 150 private subsidized, and 367 public schools (henceforth treated and control schools, respectively). Out of the 64,245 students, 15,682 students are from treated schools and 48,563 are from control schools. Using the multilevel matching approach above, we matched in two stages within similar groups regions of the country (namely, regions I–III, IV–V, VI–VII, VIII, IX, X–XII, and the Metropolitan region).

At the student level, we used cardinality matching to find the largest balanced sample of pairs of students across all the possible combinations of pairs of schools within the groups of regions. In each of these matches we balanced the means of 19 covariates (including student test scores, school test scores, and indicators for socioeconomic status and expected educational achievement; see Table 1 for details),<sup>4</sup> approximately fine balanced the marginal distribution of four nominal covariates (sex, mother and father education, and household income; see Table 2) and balanced the marginal distribution of two continuous covariates (the sum of the test scores in language and mathematics

**Table 2.** Approximate fine balance for student-level covariates after matching.

Covariate	School type	
	Private	Public
Sex		
Male	4634	4638
Female	4168	4164
Mother education		
Primary school	4016	4026
Secondary school	2578	2577
Technical	176	173
College or higher	73	75
Missing	1959	1951
Father education		
Primary school	3538	3552
Secondary school	2732	2724
Technical	196	195
College or higher	130	131
Missing	2206	2200
Household income category (in 1000 pesos)		
[0, 100]	251	248
[100, 200]	3356	3373
(200, 400]	3346	3346
(400, 600]	974	971
(600, 1400]	289	291
> 1400	206	203
Missing	380	370

NOTES: All the covariates are measured in 2004. The tabulated values are counts of the number of students in each category of the covariates. In addition, matching was exact for groups of counties (not shown here).

at baseline). Figure 1 shows that the marginal distributions are very closely balanced after matching, and so are the joint distributions. As a matter of fact, the 95% bivariate normal density contours are almost indistinguishable after matching.

At the school level, we used the modified version of cardinality matching, outline above, in the second stage of Algorithm 1 and mean balanced 16 other covariates: percentage female, total enrollment, language and math scores (plus indicators for missing values), urban area, parental income categories (1–5), and socioeconomic groups (A–D). Again, covariates were exact matched for the seven region groups (for this, we basically solved different matching problems for each of these region groups). We balanced all covariates with and without weighting for the size of the school; see Table 3. Note that after matching all the differences in means are smaller than 0.05 standard deviations. In this way, we matched 8802 students in 4401 pairs, and 280 schools in 140 pairs. In this match, all the available regions of the country are represented in both the treatment and control groups.

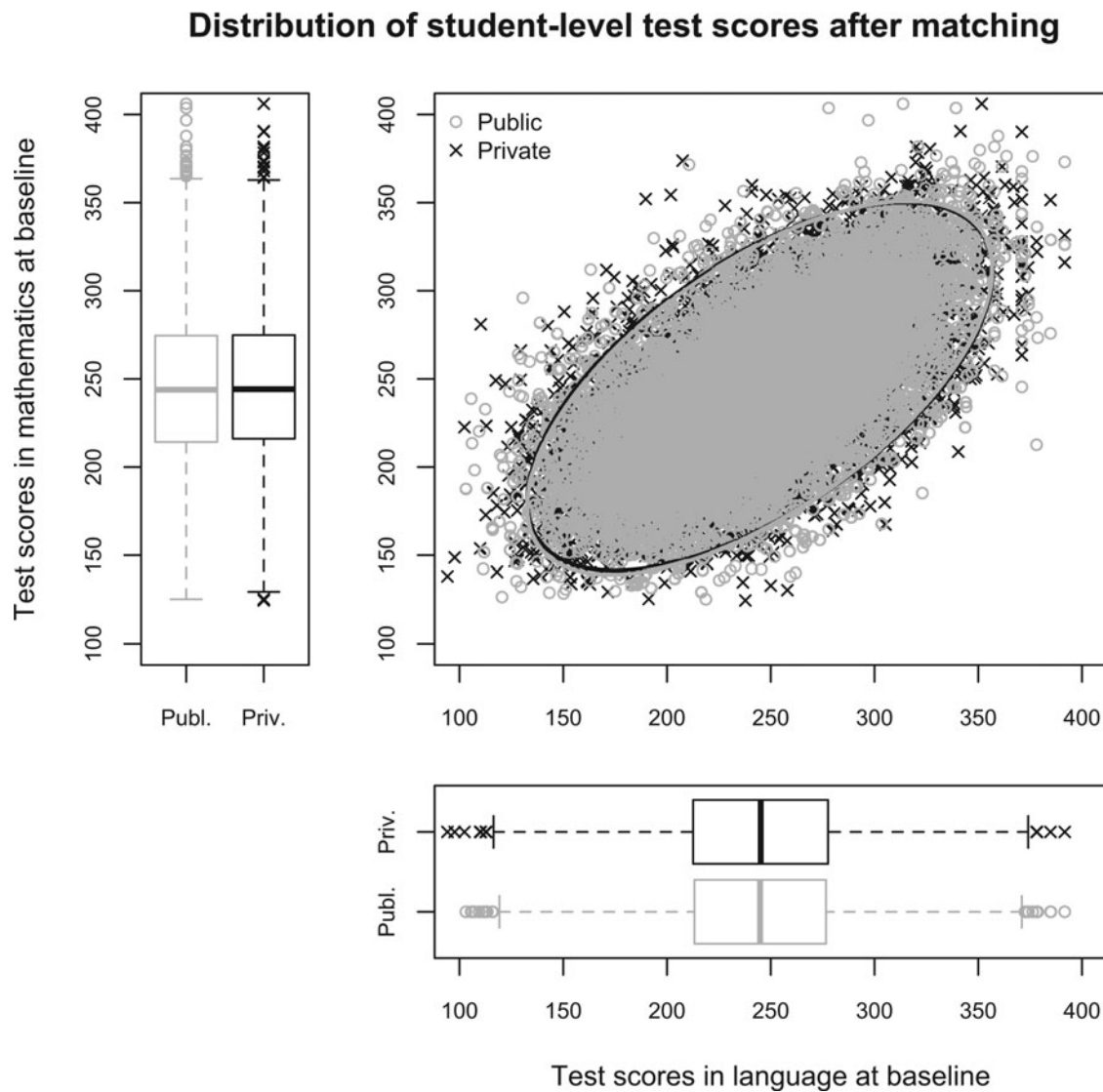
### 4.2. Comparison to Myopic Matching

We now compare the performance of our dynamic matching strategy to an alternative strategy, which first matches schools followed by matching students within these matched schools. We implement this alternative matching strategy using two different methods: optimal matching (using a robust Mahalanobis distance matrix with calipers for violations on the propensity score; see Rosenbaum and Rubin 1985 and sec. 8.3 of Rosenbaum 2010) and cardinality matching, using the approximation scheme in Zubizarreta and Kilcioglu (2016).<sup>5</sup> We call these two

<sup>4</sup> To be precise, we required the absolute differences in means in these covariates to differ at most by 0.1 standard deviations. The matched sample that we found did not only satisfy these mean balance constraints but achieved absolute differences in means smaller than 0.05 standard deviations. Please see Table 1.

<sup>5</sup> This approximation scheme solves a linear program relaxation of the integer programming problem in cardinality matching and then rounds the solution by solving a linear program again or using a more specialized network algorithm. This





**Figure 1.** Distribution of student test scores at baseline after matching. The baseline test scores are measured in 2004. The ellipses trace the 95% bivariate normal density contours of the joint distributions of test scores for the matched treated and control units. The contours are almost identical showing that not only marginal distributions of the test scores are very closely balanced but also their joint distribution.

more standard strategies “myopic” because they make locally optimal matching decisions at the school and student stages separately rather than collectively in view of the global optimum. The results from this comparison are summarized in Table 4.

By construction, myopic optimal matching uses all the available observations, but results in substantial imbalances at both the school and student level. In fact, out of the 17 school-level covariates, 4 of them have differences in means greater than 0.1 standard deviations after matching, and the total variation distance (defined as the sum of the treated-minus-control absolute value differences in percentage points across all categories of nominal covariates; Pimentel et al. 2015) for the marginal distributions of the covariates in Table 2 is more than 10 times larger with optimal matching than with the cardinality matching methods. Myopic cardinality matching achieves good covariate balance both at the school and student levels, but

**Table 3.** Covariate balance at the school level after matching.

Covariate	Mean		Std. dif.
	Private	Public	
Female proportion	0.46	0.49	− 0.09
Number of students	193.38	193.38	0.00
Language score	241.92	239.99	0.10
Mathematics score	231.21	228.92	0.09
Language score missing	0.02	0.02	− 0.05
Mathematics score missing	0.02	0.02	− 0.05
Urban area	0.92	0.94	− 0.09
Income category 1	0.20	0.24	− 0.08
Income category 2	0.67	0.66	0.02
Income category 3	0.12	0.10	0.05
Income category 4	0.01	0.00	0.08
Income category 5	0.00	0.00	0.00
Socioeconomic status A	0.30	0.35	− 0.10
Socioeconomic status B	0.55	0.54	0.03
Socioeconomic status C	0.15	0.12	0.09
Socioeconomic status D	0.00	0.00	0.00

NOTES: Both means and standardized differences are weighted by the number of students in each school. The last column shows standardized differences in means.

approximation may violate to some extent some of the balancing constraints but it runs quickly (in polynomial time), and in many applications the violations to the balancing constraints are not substantial.

**Table 4.** Comparison of matching methods.

Method	Matches		Imbalances		Speed	
	Schools	Students	Means schools	TV students	Problems solved	Time (min)
Myopic optimal matching	149	9643	4	0.179	149	0.48
Myopic cardinality matching <sup>†</sup>	143	4913	0	0.016	143	1.37
Dynamic cardinality matching <sup>†</sup>	140	8802	0	0.011	10,261	148.43

NOTES 1: For optimal matching, we used a robust Mahalanobis distance matrix (Rosenbaum 2010) with calipers for violations on the propensity score (Rosenbaum and Rubin 1985). For cardinality matching (†) we used the approximation scheme by Zubizarreta and Kilioglu (2016). In both cases, we used the R package *designmatch*. 2: Under “Imbalances,” the first column (“Means schools”) shows the number of covariates that have imbalance in means at the school level (there are 17 school covariates in total). In the second column, “TV” denotes the total variation distance for the marginal distributions of key covariates at the student level (Pimentel et al. 2015). 3: Under “Speed,” the first column shows the total number of student matching problems solved, and the second column shows the total time in minutes they took without parallelizing. On average, with the three matching methods each student matching problem took less than a second to be solved.

matches considerably fewer students: 4913 students instead of the 8802 students matched by our strategy, which illustrates why working backward from the optimal solutions is better than working forward in a greedy sense. This demonstrates that our dynamic strategy to multilevel matching reduces imbalances and uses a larger portion of the sample.

In terms of speed, the dynamic matching method takes longer. On a standard desktop computer (with a 3.4 GHz Intel Core i5 processor, 16 GB 1600 MHz DDR3 of memory, and the OS X 10.10.4 operating system), the dynamic method takes nearly two and a half hours, as opposed to the 0.48 and 1.17 min needed for the two myopic methods. The dynamic method requires more computing time, since it is considering all the possible combinations of pairs of treated and control schools within groups of regions; in other words, it is solving 10,261 student matching problems as opposed to 149 and 143 with the other methods. On average, with the dynamic method, as well as with the other matching methods, each student matching problem takes less than 1 sec to be solved. Again, the difference in time is driven by the number of student matching problems that each method is considering. To further reduce the computing time required for the dynamic matching, one could find the student level matches in parallel by separating all the possible pairs of treated and control schools into smaller mutually exclusive but exhaustive pairs of treated and control schools.

### 4.3. Limited Overlap and the Estimand

In observational studies, a common limitation encountered in practice is limited overlap or lack of common support of the covariate distributions across the treatment samples. As Crump et al. (2009) noted, lack of common support can lead to estimates that are highly biased, too variable, and overly sensitive to model misspecification. When faced with limited overlap, investigators often “trim” the samples and restrict their analyses to subsamples that have common support. For example, Dehejia and Wahba (1999) discarded the control units with an estimated

propensity score smaller (greater) than the minimum (maximum) one of the treated units. Formal methods for trimming are proposed by Crump et al. (2009) and Rosenbaum (2012b). However, most of these methods address the problem of limited overlap using the propensity score or another summary of the covariates such as the Mahalanobis distance. In contrast, with our multilevel matching strategy, cardinality matching addresses the common support problem without resorting to a summary of the covariates, as it directly finds the largest subsamples of treated and control units that meet the common support or balance constraints set by the investigator.

With all these methods, restricting the analysis to the samples of treated and control units that overlap (or, ultimately, that are balanced) changes the estimand such that it only applies to the population of comparable or marginal units, which may or may not receive the treatment (Rosenbaum 2012b). More specifically, the estimands that result from trimming units will be more local versions of commonly used estimands such as the average treatment effect or average treatment effect on the treated, and will depend on the sample data. Changing the estimand in this way acknowledges the inherent limitations imposed by the data. It also makes explicit that inferences to other target populations will require further modeling assumptions (Crump et al. 2009). In other words, this approach places greater importance on internal as opposed to external validity (Shadish, Cook, and Campbell 2002).

In our study, we estimate the effect of a cluster-level treatment on a sample of comparable units within comparable clusters. Specifically, we estimate the effect of attending private subsidized (voucher) schools instead of public schools on a sample of students by selecting both comparable students and schools. If we only selected schools to ensure common support and covariate balance, our estimand would be the effect of a school-level intervention on the students of a sample of comparable schools. However, since we also selected students (to ensure comparability of the students within the schools), our estimand is the effect of a school-level intervention on a sample of comparable students within comparable schools.

To obtain a basic understanding of how the matched sample differs from the larger population, we describe the samples of matched treated and control students and compared them to the full samples of students (Silber et al. 2015). Table 5 compares the means of the covariates in the samples of students before matching (“All”) and in the unmatched and matched samples. For the students in private schools, there are a number of significant differences between the matched and unmatched samples (not denoted in the table for clarity in the exposition). The largest differences are in urban area, with a lower proportion of the unmatched students living in urban areas, and in socio-economic status, with the unmatched students having a higher socio-economic status on average. These differences are less marked when comparing the matched and complete (“All”) samples of students in private schools. In principle, our results could be generalized to a population of students with characteristics similar to the ones of the matched samples, which do not differ much from the original sample of students under the private subsidized school treatment. However, such generalizations from the sample to a larger population would

**Table 5.** Description of the samples of students before and after matching.

Covariate	Private			Public		
	All	Unmatched	Matched	Matched	Unmatched	All
Language score	244.26	243.51	244.84	244.75	247.67	247.14
Mathematics score	245.04	244.19	245.71	244.92	247.28	246.85
Natural science score	248.19	247.47	248.74	248.57	250.73	250.34
Social science score	244.06	243.64	244.38	244.49	246.69	246.29
School language score	239.39	240.09	238.84	238.42	240.59	240.19
School mathematics score	240.46	241.20	239.89	239.32	241.94	241.47
School female proportion	0.52	0.52	0.51	0.51	0.53	0.53
School number of students	83.49	82.54	84.23	84.17	82.01	82.40
School teacher to student ratio	8.18	8.14	8.22	8.14	7.96	7.99
Urban area	0.82	0.79	0.85	0.85	0.81	0.82
Socioeconomic status A	0.15	0.17	0.13	0.13	0.16	0.16
Socioeconomic status B	0.55	0.52	0.57	0.56	0.51	0.52
Socioeconomic status C	0.28	0.27	0.28	0.29	0.31	0.31
Socioeconomic status D	0.03	0.04	0.02	0.01	0.02	0.02
Expected education: primary	0.01	0.02	0.01	0.01	0.01	0.01
Expected education: secondary, technical-professional	0.69	0.66	0.72	0.69	0.61	0.62
Expected education: secondary, scientific-humanities	0.17	0.19	0.16	0.17	0.23	0.22
Expected education: technical-professional	0.11	0.11	0.10	0.10	0.13	0.12
Expected education: college	0.02	0.02	0.01	0.02	0.02	0.02

require additional assumptions and methods (Stuart et al. 2011; Hartman et al. 2015).

## 5. Outcome Analyses

Having found the matched sample, we now estimate the effect of attending a private voucher school, test its significance, and assess the robustness of the findings to biases due to unobserved covariates. We first assume that treatment is as-if randomly assigned to clusters conditional on the matched pairs (Small, Have, and Rosenbaum 2008) and explore whether our results would differ if we relax this assumption using a sensitivity analysis for clustered observational studies developed by Hansen, Rosenbaum, and Small (2014).

### 5.1. Randomization Inference When Treatment is Assigned at the School Level

Following Small, Have, and Rosenbaum (2008), we collect in the set  $\Omega$  the  $2^K$  possible treatment assignments for the  $2K$  matched clusters,  $\mathbf{Z} = (Z_{11}, Z_{12}, \dots, Z_{K2})^T$ . If the probability of receiving treatment is equal for each school in each matched pair, then the conditional distribution of  $\mathbf{Z}$  given that there is exactly one treated school in each pair equals the randomization distribution with  $\Pr(Z_{kj} = 1 | y_{Tkji}, y_{Ckji}, \mathbf{x}_{kji}, u_{kji}, \Omega) = 1/2$  for each school  $j$  in pair  $k$ . Write  $\mathbf{Y} = (Y_{111}, \dots, Y_{K2n_{k2}})^T$  for the  $N = \sum_{k,j} n_{kj}$  dimensional vector of observed responses with the same notation for  $\mathbf{y}_c$ , which are the potential responses under control.

We denote  $T = t(\mathbf{Z}, \mathbf{Y})$  as our test statistic. Under the sharp null hypothesis of no treatment effect,  $\mathbf{Y} = \mathbf{y}_c$ , and therefore  $T = t(\mathbf{Z}, \mathbf{y}_c)$ . If treatment were randomly assigned within matched pairs, then  $\Pr\{t(\mathbf{Z}, \mathbf{Y}) \geq v | y_{Tkji}, y_{Ckji}, \mathbf{x}_{kji}, u_{kji}, \Omega\} = \Pr\{t(\mathbf{Z}, \mathbf{y}_c) \geq v | y_{Tkji}, y_{Ckji}, \mathbf{x}_{kji}, u_{kji}, \Omega\}$  with  $\Pr(\mathbf{Z} = \mathbf{z} | y_{Tkji}, y_{Ckji}, \mathbf{x}_{kji}, u_{kji}, \Omega) = 1/|\Omega|$  for some cutoff value  $v$ .

For  $T$ , we use a test statistic by Hansen, Rosenbaum, and Small (2014). This test statistic is a function of the score or rank

of each  $Y_{kji}$ , denoted by  $q_{kji}$ , so that under the null hypothesis,  $q_{kji}$  depends on  $y_{Ckji}$  and  $\mathbf{x}_{kji}$ , and it does not vary with  $Z_{kj}$ . To make  $q_{kji}$  resistant to outliers, we use the ranks of the residuals when  $Y_{kji}$  is regressed on the student level covariates using Huber's method of  $m$ -estimation (see Small, Have, and Rosenbaum 2008). The test statistic  $T$  is

$$T = \sum_{k=1}^K B_k Q_k,$$

where

$$B_k = 2Z_{k1} - 1 = \pm 1, \quad Q_k = \frac{w_k}{n_{k1}} \sum_{i=1}^{n_{k1}} q_{k1i} - \frac{w_k}{n_{k2}} \sum_{i=1}^{n_{k2}} q_{k2i}.$$

Hansen, Rosenbaum, and Small (2014) showed that  $T$  is the sum of  $k$  independent random variables each taking the value  $\pm Q_k$  with probability  $1/2$ , so  $E[T] = 0$  and  $\text{var}[T] = \sum_{k=1}^K Q_k^2$ . By the central limit theorem, as  $K \rightarrow \infty$ ,  $T/\sqrt{\text{Var}[T]}$  converges in distribution to the standard Normal distribution. In the above equation,  $w_k$  defines the weights that are a function of  $n_{kj}$ . Hansen, Rosenbaum, and Small (2014) discussed possible choices for  $w_k$ . We use constant weights,  $w_k \propto 1$ .<sup>6</sup>

If we test the hypothesis of a shift effect instead of the hypothesis of no effect, we can apply the method by Hodges and Lehmann (1963) to estimate the private school effect. The Hodges–Lehmann (HL) estimate of  $\tau$  is the value of  $\tau_0$  that when subtracted from  $Y_{kji}$  makes  $T$  as close as possible to its expectation under the null. Intuitively, the point estimate  $\hat{\tau}$  is the value of  $\tau_0$  such that  $T_{\tau_0}$  equals 0 when  $T_{\tau_0}$  is computed from  $Y_{kji} - Z_{kj}\tau_0$ . Using constant effects is convenient, but this assumption can be relaxed (see Rosenbaum 2003). If the treatment has an additive effect,  $Y_{kji} = y_{Ckji} + \tau$  then a 95% confidence interval for the additive treatment effect is formed

<sup>6</sup> Another possibility is to use weights that are proportional to the total number of students in a matched cluster pair:  $w_k \propto n_{k1} + n_{k2}$  or  $w_k = (n_{k1} + n_{k2}) / \sum_{\ell=1}^K (n_{\ell 1} + n_{\ell 2})$ . An analysis, with these weights did not alter the results.

by testing a series of hypotheses  $H_0 : \tau = \tau_0$  and retaining the set of values of  $\tau_0$  not rejected at the 5% level.

In this framework, the randomization distribution explicitly takes into account that the treatment is assigned at the cluster level, and that all the units in a school either receive the treatment, or all receive the control. Moreover, these methods allow for arbitrary patterns of dependence within schools, but not across them (Small and Rosenbaum 2008; Hansen, Rosenbaum, and Small 2014). In our case study, it is unlikely that students in different schools affect the test scores of one and other, but surely there may be dependence in the test scores of the students within the same school.

## 5.2. Comparative Effectiveness of Public Versus Private Subsidized Schools

We now test the hypothesis of no effect for private subsidized schools on test scores. We measure test scores using an additive measure of language and mathematics scores. The approximate one-sided  $p$ -value for the test of the sharp null hypothesis is 0.207. If there are no hidden confounders, the point estimate of the private subsidized treatment effect is  $\hat{\tau} = 2.55$  with a 95% confidence interval of  $-3.78$  and  $8.72$ . Thus, we cannot reject the hypothesis that attending a private subsidized school has no effect on test scores. In the education literature, an effect size of 0.2 of a standard deviation is considered to be an educationally meaningful effect (Lipsey 1990). Our estimated treatment effect is only 0.027 of a standard deviation. Therefore, our estimated treatment effect is well below the threshold for a meaningful effect. We next analyze the likelihood that bias from a hidden confounder masks a true treatment effect.

## 5.3. Test of Equivalence and Sensitivity Analysis

In an observational study, one concern is that bias from a hidden covariate can give the impression that a treatment effect exists when in fact no effect is present. Bias from hidden confounders can also mask an actual treatment effect leaving the investigator to conclude there is no effect when in fact such an effect exists. We explore this possibility using a test of equivalence and a sensitivity analysis (Rosenbaum 2008; Rosenbaum and Silber 2009; Rosenbaum 2010).

Above we were unable to reject the null hypothesis that  $\tau = 0$  for all students. Next, we apply a test of equivalence to test the hypotheses that  $\tau$  is not small. In a test of equivalence, we test the null hypothesis  $H_{\neq}^{(\delta)} : |\tau| > \delta$ . Rejecting  $H_{\neq}^{(\delta)}$  provides a basis for asserting with confidence that  $|\tau| < \delta$ .  $H_{\neq}^{(\delta)}$  is the union of two exclusive hypotheses:  $\bar{H}_0^{(\delta)} : \tau \leq -\delta$  and  $\bar{H}_0^{(\delta)} : \tau \geq \delta$ , and  $H_{\neq}^{(\delta)}$  is rejected if both  $\bar{H}_0^{(\delta)}$  and  $\bar{H}_0^{(\delta)}$  are rejected (Rosenbaum and Silber 2009). We can apply the two tests without correction for multiple testing since we test two mutually exclusive hypotheses.

With a test of equivalence, it is not possible to demonstrate a total absence of effect, but if this were a randomized trial, we could test that our estimated effect is not as large as  $\delta$  by rejecting  $H_{\neq}^{(\delta)} : |\tau| > \delta$ . Since the treatment was not randomly assigned, it may be the case that we reject the null hypothesis of equivalence due to hidden confounding. However, using a sensitivity analysis

we may find evidence that the test of equivalence is insensitive to biases from nonrandom treatment assignment.

Thus far we have assumed that within matched pairs, receipt of the treatment is effectively random conditional on the matches. We consider how sensitive our conclusions are to violations of this assumption using the model of sensitivity analysis discussed by Rosenbaum (2002, chap. 4). In our study, matching on observed covariates  $\mathbf{x}_{kji}$  made students more similar in their chances of being exposed to the treatment. However, we may have failed to match on an important unobserved covariate  $u_{kji}$  such that  $\mathbf{x}_{kji} = \mathbf{x}_{kji'} \forall k, j, i, i'$ , but possibly  $u_{kji} \neq u_{kji'}$ . If true, the probability of being exposed to treatment may not be constant within matched school pairs. To explore this possibility, we use a sensitivity analysis. First, define  $\pi_k$  as the probability that student  $i$  in pair  $k$  was treated. For two matched students in pair  $k$ , say  $i$  and  $i'$ , because they have the same observed covariates  $\mathbf{x}_{kji} = \mathbf{x}_{kji'}$ , it may be true that  $\pi_k = \pi_{k'}$ . However, if these two students differ in an unobserved covariate,  $u_{kji} \neq u_{kji'}$ , then these two students may differ in their odds of being exposed to the private school treatment by at most a factor of  $\Gamma \geq 1$  such that

$$\frac{1}{\Gamma} \leq \frac{\pi_k / (1 - \pi_{k'})}{\pi_{k'} / (1 - \pi_k)} \leq \Gamma, \quad \forall k, k', \text{ with } \mathbf{x}_{kji} = \mathbf{x}_{kji'} \forall j, i, i'. \quad (5)$$

If  $\Gamma = 1$ , then  $\pi_k = \pi_{k'}$ , and the randomization distribution for  $T$  is valid. If  $\Gamma > 1$ , then quantities such as  $p$ -values and point estimates are unknown but are bounded by a known interval. In a sensitivity analysis, we observe at which value of  $\Gamma$  the upper bound on the  $p$ -value exceeds 0.05. If the value of  $\Gamma$  is large, we can be confident that it would take a large bias from a hidden confounder to reverse the conclusions of the study. The derivation for the sensitivity analysis as applied to our test statistic  $T$  can be found in the article by Hansen, Rosenbaum, and Small (2014).

Under a test of equivalence, we may be able to reject  $H_{\neq}^{(\delta)} : |\tau| > \delta$  if the  $p$ -value from the test is low. Rejecting this null, allows us to infer that the estimated treatment effect is not as large as  $\delta$ . We then apply the sensitivity analysis to understand whether this inference is sensitive to biases from nonrandom treatment assignment. In the analysis, we observe at what value of  $\Gamma$  the  $p$ -value exceeds the conventional 0.05 threshold for each test. If this  $\Gamma$  value is relatively large, we can be confident that the test of equivalence is not sensitive to hidden bias from nonrandom treatment assignment.<sup>7</sup>

## 5.4. How Much Bias Would Need to be Present to Mask a Positive Effect of Private Subsidized Schools?

In a test of equivalence, the null hypothesis asserts  $H_{\neq}^{(\delta)} : |\tau| > \delta$  for some specified  $\delta > 0$ . Rejection of this null hypothesis provides evidence that the effect of attending a private voucher school on test scores is less than  $\delta$ . What values should we select for  $\delta$ ? In education research, an effect of 0.2 standard deviations

<sup>7</sup> Hansen, Rosenbaum, and Small (2014) noted that sensitivity to hidden bias may vary with the choice of weights  $w_k$ . To understand whether different weights lead to different sensitivities to hidden confounders, we can conduct a different sensitivity analysis for each set of weights and correct these tests using a multiple testing correction (Rosenbaum 2012b). We then report a single corrected  $p$ -value for a value of  $\Gamma$ .



is often considered to be a meaningful effect size (Lipsey 1990). However, recent guidelines emphasize benchmarking against effect sizes from other studies on the same intervention (Lipsey et al. 2012). The smallest effect size in the extant literature on the effect of private voucher schools is 0.15 of a standard deviation (Sapelli and Vial 2002). However, among low income students the effects may be as large as 0.5 of a standard deviation, and Sapelli and Vial (2005) found an effect size of 0.6 standard deviations. To that end, we consider four values for  $\delta$  given by  $\delta_1 = 0.1$ ,  $\delta_2 = 0.2$ ,  $\delta_3 = 0.4$ , and  $\delta_4 = 0.6$  standard deviations. This range of effect sizes both brackets the range of effect sizes in the literature, but also tests against what is often considered to be a meaningful effect in test scores.

When conducting the equivalence test and sensitivity analysis on the matched sample, we are unable to reject  $H_{\neq}^{(\delta_1)}$  as we obtain a  $p$ -value of 0.159 when  $\Gamma = 1$ . Therefore, we are unable to reject the null hypothesis that the estimated treatment effect is equivalent to an effect size smaller than the smallest effect in the extant literature. For what is conceived to be an educationally meaningful effect size of 0.2 standard deviations, we can easily reject  $H_{\neq}^{(\delta_2)}$  when  $\Gamma = 1$  ( $p = 0.005$ ), and we find that when  $\Gamma = 1.49$  the  $p$ -value is 0.049. A bias of magnitude  $\Gamma = 1.49$  means that two students matched for their observed covariates  $\mathbf{x}_{kji}$  could differ in their odds of attending a private voucher school by almost 50% before materially altering our conclusions. Next, for an effect size of 0.4 standard deviations, we reject  $H_{\neq}^{(\delta_3)}$  when  $\Gamma = 1$  ( $p < 0.001$ ), and we find that when  $\Gamma = 4.98$  the  $p$ -value is 0.049. In this instance, an unobserved confounder would have to make the odds of treatment more than five times higher within a matched pair to alter our conclusions. Finally, for the largest effect size of 0.6 standard deviations, we find that when  $\Gamma = 9.8$ , the  $p$ -value is 0.049. In summary, a fairly modest bias could mask the difference between our estimated effect size and that of an educationally meaningful effect size. However, it would take a very large bias to mask differences between larger effect sizes.

## 6. Summary and Discussion

Clustered observational studies with hierarchical or multilevel data are very common in the health and social sciences. In these settings, we have shown that the optimal matching strategy is, under the assumption that clusters have been matched optimally, first to match units and then, considering these optimal unit-level matches, to match clusters. We emphasized that this strategy explicitly uses the nested structure of the data by breaking the multilevel matching problem into simpler, smaller matching subproblems that are solved only once and that can be solved in parallel to yield an optimal global solution. We implemented this strategy using and extending cardinality matching to find the largest matched sample of pairs of treated and control units within pairs of treated and control clusters that is balanced according to specifications given by the investigator. We noted that this strategy can also be implemented with other matching methods such as optimal matching to minimize the total sum of covariate distances between matched units. Unlike other matching methods for multilevel data, the cardinality matching implementation is optimal in the sense that it maximizes the

size of the matched sample, and it does not require estimating the propensity score (because it directly balances covariates as specified by the investigator). As we outlined, these specifications for covariate balance are not restricted to mean balance, but extend to other forms of distributional balance such as fine balance,  $x$ -fine balance, and strength- $k$  balance. This multilevel matching approach also facilitates sensitivity analyses to hidden biases due to unobserved covariates, and it readily extends to clustered observational studies with three or more levels of data.

The proposed multilevel matching strategy is optimal when the matching criterion is a sum of components that correspond to matched units within matched clusters, such as the total number of matched units (as in our case study), or, for example, the total sum of covariate distances between matched units. To our knowledge, this is the first application of dynamic and integer programming ideas to observational studies.

## Acknowledgments

For comments and suggestions, the authors thank three anonymous reviewers, an associate editor, and Joseph Ibrahim. The authors also thank Magdalena Bennett, Jake Bowers, Nicolás Grau, Cinar Kilcioglu, Winston Lin, Sam Pimentel, and Paul Rosenbaum, and seminar participants at Johns Hopkins University and the University of Pennsylvania.

## Funding

This work was supported by a grant from the Alfred P. Sloan Foundation.

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