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ADMINISTRATIVE DATA LINKING AND STATISTICAL POWER PROBLEMS IN RANDOMIZED EXPERIMENTS

Sarah Tahamont
Zubin Jelveh
Aaron Chalfin
Shi Yan
Benjamin Hansen

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ABSTRACT

The increasing availability of administrative data has led to a particularly exciting innovation in public policy research, that of the "low-cost" randomized trial in which administrative data are used to measure outcomes in lieu of costly primary data collection. Linking data from an experimental intervention to administrative records that track outcomes of interest typically requires matching datasets without a common unique identifier. In order to minimize mistaken linkages, researchers will often use "exact matching" (retaining an individual only if all their demographic variables match exactly in two or more datasets) in order to ensure that speculative matches do not lead to errors in an analytic dataset. We argue that when this approach is used to detect the presence of a binary outcome, this seemingly conservative approach leads to attenuated estimates of treatment effects, and critically, to underpowered experiments. For marginally powered studies, which are common in empirical social science, exact matching is particularly problematic. In this paper, we derive an analytic result for the consequences of linking errors on statistical power and show how the problem varies across different combinations of relevant inputs, including the matching error rate, the outcome density and the sample size. We conclude on an optimistic note by showing that machine learning-based probabilistic matching algorithms allow researchers to recover a considerable share of the statistical power that is lost to errors in data linking.

Sarah Tahamont
University at Albany,SUNY
tahamont@umd.edu

Zubin Jelveh
University of Chicago
zjelveh@uchicago.edu

Aaron Chalfin
University of Pennsylvania
achalfin@sas.upenn.edu

Shi Yan
Arizona State University
shiyan@asu.edu

Benjamin Hansen
Department of Economics
1285 University of Oregon
Eugene, OR 97403
and NBER
bchansen@uoregon.edu

1 Introduction

Among the more exciting developments in social science research is the innovation of the increasingly ubiquitous "low-cost" randomized trial in which observations from an experimental intervention are matched to administrative data in order to minimize primary data collection and keep the costs of experimentation low. By linking together administrative datasets, researchers can leverage the richness of information in pre-existing administrative data sets and test the effect of an intervention of interest on a host of outcomes in domains as diverse as criminal justice, education and health (Kinner et al., 2013; Mueller-Smith, 2016; Petrou and Gray, 2011). Scholars are lauded for compiling and combining data from multiple sources but, despite considerable attention to issues attendant to linking data in the statistical literature (Fellegi and Sunter, 1969; Lahiri and Larsen, 2005; Neter et al., 1965; Newcombe et al., 1959; Scheuren and Winkler, 1993, 1997), in practice, there is typically little discussion of how data sources are actually linked together in applied research. It is not uncommon for researchers to have little information on the linking process itself, because it is often the case that administrative agencies to do the linking in order to maintain confidentiality. As a result, the description of the linking process that most research papers provide is often limited to a footnote — if that.[1]

When a unique identifier is available in all of the datasets that require linking and data quality is high, linking can, in some cases, be fairly trivial. These types of cross-system unique identifiers are frequently available in Scandinavian countries (e.g. Black et al., 2005; Dahl et al., 2014; Kuhn et al., 2011, among others). Unique identifiers in the United States are essentially restricted to particular administrative system, requiring linking across datasets which is typically both costly and results in some level of error. It is often the case that unique identifiers are system-specific and virtually unknown outside of the data (e.g. patient identifiers in hospital data or fingerprint numbers in arrest data). Even system-specific administrative identifiers that are known outside a database (e.g. social security number or student identification number) are not as reliable for linking datasets as we might wish them to be because of problems with recording and reporting. As a consequence, efforts to link data from an experimental intervention to administrative records that track outcomes of interest often require linking datasets that were not built

[1] For an exception, see Khwaja and Mian (2005) an example from the applied economics literature, which details the process for linking data and observes that matching errors will lead to attenuation in the coefficient estimates.

to be matched to one another and, which, often, lack a common unique identifier. In the absence of this identifier, demographic characteristics like name and date of birth are used to match data sets and, as a consequence, errors in data linkage are inevitable.

Matching errors can take on many forms depending on the record linkage problem at hand. In this paper, we identify a special case of record linkage that is very common but, unfortunately, is particularly difficult to deal with: the case in which the goal is to link datasets in an attempt to detect the presence of a binary outcome such as arrest or high school graduation. Although the case we present is specific, our findings could extend to a number of settings including program participation in Supplemental Nutritional Assistance Program (Courtemanche et al., 2018), employment prevalence measured through unemployment insurance wage records (Mas and Johnston, forthcoming), injuries measured through hospitalization data (Powell and Seabury, forthcoming), or financial health measured through bankruptcy or liens (Dobkin et al., 2018).

At first glance, it is not obvious why the form of the outcome variable should be a first order concern. To see why it is, we note that with a continuous outcome, when an individual in an experimental sample cannot be linked to an outcome dataset, there is a clear explanation of what has happened: the outcome data are missing. Consider, for example, an outcome like a student's score on a state standardized test. If Student A, a participant in a study, is linked to a student record in a state's education database, it is possible that matching error might occur if the student was linked to the wrong student's outcome. But if, after the linking process, Student A's record has not linked to a record in the state database, then it is clear that the data are missing (either because of bad matching or because the student did not take the exam).[2]. Ultimately, the primary question for the researcher, in this case, is whether the data are missing at random or if statistical adjustment is required to address the problem of non-random missing data. While this can be a thorny problem in applied research, there is a litany of formal guidance and many associated "rules of thumb" to help navigate this particular issue.

On the other hand, consider a different scenario in which a researcher is interested in evaluating whether a job training program for at-risk youth reduces the likelihood of arrest. In constructing an analytic dataset, individuals whose names link to the post-intervention arrest file are considered "arrested" and individuals whose names do not link to the arrest

[2] Note that, in this case, there might even be an indicator for whether or not the student took the exam, which might help differentiate between bad matching and missing data.

file are considered "not arrested." Notably though, those individuals who cannot be found in the arrest file did not necessarily have zero arrests — some of these individuals may not have been found due to errors in their names, dates of birth, or other identifying characteristics that were used to link the data. In this case, it is not clear what a non-linked record means: does this mean that the individual has not been re-arrested or that the individual's arrest record cannot be found in the outcome dataset? Not limited to arrest, this issue is applicable to any context in which the goal of the linking process is to determine the presence of an outcome and there is no prior prediction for how many records *should* match — for example, hospital utilization, college matriculation or program completion for an intervention.[3]

There are two important features of our arrest scenario — or any scenario in which the outcome of interest is binary — which bear further discussion. First, with a binary outcome variable, the rate of successful record linking becomes the outcome density in the analytic dataset. Because it is not clear *a priori* how many of the experimental records *should* link to the outcome data, there is no way to use the match rate between datasets to evaluate the quality of the match. Second, from a data-linking perspective, the most important thing is to link the experimental observations to the correct *outcome* as opposed to linking to the correct *individual* in the outcome data. That is, in this particular case, if Person A is mistakenly linked to Person B in the outcome data, the mismatch will only be empirically consequential if Person A and Person B have different outcomes (e.g., Person A is arrested and Person B is not arrested). This is not generally the case with a continuous outcome where the outcome can take on many possible values.[4] These points distinguish this linking case from other kinds of longitudinal record linking cases (Bailey et al., 2017; Feigenbaum, 2016) but, to our knowledge, this distinction has not been discussed in the prior literature on administrative data matching.

A good match is critical, because bad matches introduce noise that obscures the relationship between the outcome variable and the treatment variable. In the presence of noisy matching, even a perfectly-executed randomized controlled trial will fail to deliver an unbiased estimate of the effectiveness of an intervention. In this paper, we show ana-

[3] Consider that a low match rate in this context could either mean that there is a low re-arrest rate in the sample or that there was a high rate of matching error.

[4] It is important to note that this particular definition of matching error only applies when the experimental data is *only* being linked to the outcome data. If there are also additional variables in the administrative data in addition to the outcome, those could generate problematic linking errors if they do not share the demographic profile of the experimental observation to which they are linked.

lytically that matching errors of this form will attenuate estimates of the treatment effect in an RCT. Critically though, while attenuation is an unwanted outcome, by far the most insidious result of matching error is its effect on ex-ante statistical power and, therefore, on a researcher's ability to detect a true treatment effect when one exists (Type II errors). While modest matching errors will lead to modest attenuation, given that few experiments are *overly* well-powered, even small amounts of matching error can have outsize effects on Type II error rates. For rare outcomes (e.g. Gelber et al., 2016) and small sample sizes (e.g. Fischbacher et al., 2001), both of which are common and even typical in randomized experiments, matching errors are particularly problematic. For instance, medical studies, housing lotteries, or educational experiments all are examples of potential experiments where some of the most important outcomes are rare and could be measured with administrative data. Researchers who conduct ex-ante power analyses, and subsequently link to administrative data to detect the presence of their outcome of interest, will therefore overestimate their power to detect effects, often by a considerable margin. If null findings are less likely to be published, attenuation bias can have dire consequences not only for individual papers but also for entire literatures. Indeed, this form of publication bias (filing papers in the "desk drawer") may contribute to the "replication crisis" in empirical social science (Camerer et al., 2016; Gerber and Malhotra, 2008; Gilbert et al., 2016; Pashler and Wagenmakers, 2011; Vivalt, 2017).[5]

How do researchers handle the problem of imperfect data linkage? Despite the existence of a number of proposed linking methods (Lahiri and Larsen, 2005; Scheuren and Winkler, 1993, 1997), we observe that researchers, in practice, often use "exact matching", considering an individual to be a match only if his or her demographic identifiers (i.e., name and date of birth, etc.) match *exactly* in two or more datasets, in order to minimize incorrect linkages in the data (Whitaker, 2004). Researchers impose stringent matching criteria in order to ensure that speculative matches do not lead to errors in the dataset that will be used to evaluate the intervention. This has been a popular approach to administrative data linking (Gelber et al., 2016; Hser and Evans, 2008; Khwaja and Mian, 2005; Mueller-Smith, 2016), and is thought to be conservative, as it minimizes the probability that a bad match will make it into the analytic dataset, thus keeping the data as "pure" as possible.[6]

[5] Concerns over the misuse of researcher degrees of freedom and specification searching have likewise spurred recommendations which include the use of very small α levels (Benjamin et al., 2018), which increases the probability of Type II errors as a consequence of matching error even more.

[6] A large literature considers the implications that measurement error can have for econometric models

This "conservative" approach to data linking is seemingly logical as it will minimize false positive matches in which the wrong outcome data are linked to a given individual in the study sample.[7,8] However, creating stringent character match requirements will, by definition, increase false negative links. We argue that researchers should focus not on "bad matches" but on the sum of false positive and false negative error rates in the matching process. By allowing more false negatives in order to decrease false positive links, "exact matching" can lead to a more matching error and more pronounced attenuation bias. Instead, more flexible matching strategies can reduce the rate of "missed" good matches (even if they may slightly increase the rate of false positive links) and also decrease the sum of the error rates. We further show that matches performed using machine-learning algorithms (which draw on probabilistic matching techniques) can, in most cases, reduce the sum of false positive and false negative error rates considerably by allowing for some flexibility in the match. Finally, we demonstrate how specifically minimizing the sum of false positive and false negative error rates as the objective in a machine learning-based matching algorithm leads to the lowest attenuation bias in regression estimates.

The paper proceeds as follows. First, we briefly review the literature on matching errors in empirical social science. Next, we derive an analytic result for the consequences of the matching error on treatment effect estimation and show that the sum of false positive and false negative error rates is what matters, not either of these error rates in isolation. Next, we present numerical estimates to demonstrate how the attenuation of treatment effects and the corresponding erosion of statistical power varies across different combinations of relevant inputs including the 1) the sum of false positive and false negative error rates, 2) the outcome density, and 3) the sample size. Results suggest that, in most empirical applications, the problem of bad data matching is not trivial — in a relatively large experiment ($n = 750$) with a relatively non-dense outcome ($\bar{Y} = 0.5$), power would be 20% lower (0.6 instead of 0.8) in the presence of a realistic amount of matching error. We proceed with an empirical example

but, to our knowledge, there is considerably less formal guidance with respect to how bad data matching can confound randomized experiments. It is also worth noting that when scholars need to match datasets without a common identifier there is no "ground truth" to assess the quality of the match. Likewise, there is often no prior about what the match rate should be, rendering it difficult to diagnose whether the matching procedure employed is sufficient or not.

[7] We emphasize, again, that, in this case, that the "right" match in the special case that we discuss does not depend on linking an observation to its own record, per se, but rather to a record with the same value of the outcome.

[8] It is important to note that the definition of matching error, as well as the implications for how matching error will affect coefficient estimates varies by matching context. For example, Moore et al. (2014) show that when estimating relative risk ratios, minimizing false positive links *is* the best approach to data linkage.

that shows the difference between conservative exact matching strategies and linking using a simple machine learning algorithm, which incorporates probabilistic linking components. We conclude on an optimistic note by showing that, in most cases, we can mitigate the consequences of matching error using data linkages derived using a simple machine learning algorithm.

2 Motivation and Context

Scholarly consideration of the implications of data linkage dates back to the early days of computerized record linkage itself (Fellegi and Sunter, 1969; Neter et al., 1965; Newcombe et al., 1959). However, despite multi-disciplinary recognition that linking errors have implications for subsequent analyses (Aigner, 1973; Campbell, 2009; Khwaja and Mian, 2005; Lahiri and Larsen, 2005; Neter et al., 1965; Scheuren and Winkler, 1993, 1997), it appears that, until recently, by and large, scholars working with empirical applications have devoted relatively little attention to describing the techniques used to link data, evaluating the quality of the matches in linked data, or to determining how their study conclusions might have varied based on the use of different data linking strategies.[9]

In this section we provide a high-level conceptual overview of the essentials of data linking in the social sciences. The purpose of this discussion is not to weigh in on best practice in administrative data linking but instead to provide a framework to think about how data linking can affect downstream estimates of a treatment effect of interest. In this study, we use a very simple probabilistic matching algorithm in order to demonstrate that even a basic implementation of probabilistic matching techniques can yield substantial reductions in the bias introduced by linking errors and correspondingly large increases in ex ante statistical power. Accordingly, we do not discuss the particulars of algorithm building here but note, for interested readers, that excellent reviews can be found in Christen (2012) and Winkler (2006).

Record linkage refers broadly to the practice of identifying records from different datasets that correspond to the same individual.[10] In some circumstances, linkages can be generated

[9] For a notable exception, see the extensive work of Winkler and colleagues who have been tackling related issues for decades with Census data (Scheuren and Winkler, 1993, 1997; Winkler, 2006).

[10] For narrative clarity, we limit our discussion to the linkage of data containing records on persons. This discussion would extend to groups or firms, but the characteristics available for linking might be different.

using biometric indicators, such as fingerprints, or other truly unique identifiers.[11] While biometric data can lead to misidentification in certain circumstances, linking using biometric indicators is generally considered more accurate than the traditional types of text-based identifiers that we discuss in this paper (Watson et al., 2014) and may be sufficiently accurate to dramatically narrow the scope of matching errors and their resultant effects on empirical research. However, databases used to evaluate experimental interventions often do not share a common unique identifier, and even less often share common biometric identifiers, so researchers have to rely on demographic information in order to identify individuals in the data linkage process. Frequently-used demographic variables include an individual's name (including first and last names, and sometimes a middle name or middle initial), date of birth, social security number, gender, race, and ethnicity (for simplicity, hereinafter, we refer to this set of information as a "demographic profile"). When researchers use demographic profiles to link individuals across datasets, the linking enterprise is necessarily imperfect for a variety of reasons, including typographical errors, changes in names, geographic mobility and sometimes due to the intentional provision of inaccurate information (e.g., an arrestee providing a false identify to a police officer).

Given that there is underlying uncertainty about the rate of errors in the data, researchers need to develop a set of rules that govern whether two demographic profiles will be treated as though they belong to the same observation. This process is inherently subjective and while there are long established models for data linkage (Fellegi and Sunter, 1969), there has been little discussion about linking choices and processes in the applied literature (Connelly et al., 2016; Goerge and Lee, 2001). We can organize approaches to data linkage into several broad categories: manual review, deterministic linkage, probabilistic linkage and hybrid linking approaches.

Borrowing techniques from archival matching of historical records, scholars with a small number of cases to link can, and sometimes do, conduct a manual review of profile disagreements and decide whether or not two profiles should be considered to be a match.[12] Problems arise when there is limited information to work with and instead of being able to

[11] For example, in the criminal justice domain, individuals are often tracked using unique fingerprint-based identifiers in criminal case processing data managed by multiple law enforcement agencies such as police agencies, courts and prisons. For an application that uses this type of matching, (see Freudenberg et al., 1998).

[12] In this instance we define "manual review" as the comparison of two records by an individual as compared to a computer, this is distinct from the kind of archival review referenced in Bailey et al. (2017) during which trained reviewers use information from multiple sources to identify matches.

triangulate using contextual factors, the raters are simply guessing based on a fixed set of characteristics. In these cases, there is little reason to believe that manual review of cases leads to higher accuracy when only demographic information is provided.[13] For example, if two records share the same birthday, is Michael Smith a match for a record for Michael Smyth, Mike Smith, or Mikey Smith? These might be typographical errors or nicknames, but these might also be different individuals. The scenario is further complicated when the two records do not exactly share a birthday or an address. Likewise, studies in which the pool of potential matches is large — for instance, a study of 200 students within a school system with 50,000 students — it is impractical to conduct a thorough manual review, even presuming that such a review could potentially produce more accurate matches.

When manual reviews are not possible, or even desirable, there are two approaches to developing a set of rules that govern profile linking (Mason and Tu, 2008; Winkler, 2006). The first, deterministic matching, refers to the practice of developing a set of criteria *a priori*, and considering two demographic profiles to be the same individual if and only if the original criteria are met. The strictest approach of this kind is "exact matching," under which a match is recognized only if all matching variables are identical across the two profiles. Less stringent deterministic matching rules require only a subset of letters or digits to match, such as the first three or four letters of names, or the month and date digits of dates of birth. Importantly, profiles only link when they meet all of the similarity criteria.

A second approach is probabilistic matching. Instead of making rules based on the number of agreeing letters and digits, probabilistic matching seeks to estimate the probability that two profiles belong to the same individual.[14] Probabilistic linking typically leverages techniques that can calculate the similarity of names based on phonetic computation (e.g., Soundex, Double Metaphone, etc.). The more refined algorithms can also take into account nicknames and the rarity of names in population (see for an example, Campbell et al., 2007). A fully probabilistic linking approach was proposed by Lahiri and Larsen (2005) who advocated using the matching weights in subsequent data analyses, re-weighting the data using the matching probabilities, in order to account for the uncertainty in the linking process.[15]

[13] In fact, there is some reason to suspect that manual review of matches might lead to lower levels of consistency due to reviewer fatigue, learning, or issues with inter-rater reliability.

[14] According to our reading of the applied literature, "probabilistic matching" is used as a catch-all term for any linkage method that incorporates a probabilistic technique, but, in practice, the term "probabilistic matching" can refer to a number of different approaches some of which are conceptually very different from one another.

[15] Lahiri and Larsen (2005) builds on the work of Scheuren and Winkler (1993) who advocate for a similar

Carrying the matching probabilities into the analysis is the only pure form of probabilistic data linking. However, in order to fully incorporate the probabilistic approach, a full set of match weights is necessary. We were unable to find an example of pure probabilistic linking in the applied literature. This is perhaps because it is a computationally intensive strategy, which may be intractable with large data sets.

In practice, the most common probabilistic data linking approach is actually a hybrid method that combines probabilistic methods used to identify candidate links and then sets a deterministic threshold to classify links, nonlinks (and, in some cases, potential links).[16] To our knowledge, references to probabilistic matching in the applied literature generally include a deterministic component even if a linking threshold is not mentioned explicitly. Although these approaches may be most accurately characterized as "hybrid probabilistic-deterministic," in order to be consistent with the bulk of the extant applied literature, we will refer to probabilistic matching with a deterministic linking threshold as "probabilistic matching" throughout the rest of the manuscript. Some researchers have used probabilistic matching algorithms with deterministic thresholds, often in the form of commercial linking packages (Gold et al., 2010; Heller, 2014; Kariminia et al., 2007). There are also studies in which a third party, rather than the researchers, conducts the linking. In those cases, the algorithm is determined by the linking agency and is often proprietary and therefore unavailable to be interrogated by referees or other scholars in the field (Binswanger et al., 2007; Chowdry et al., 2013; Jiang et al., 2011; Zauber et al., 2012).

Different approaches to matching can lead to considerable variation in match accuracy based on how the approaches handle disagreements between profiles. There are two types of matching errors: 1) false positives and 2) false negatives, and different approaches to matching will result in different combinations of these matching errors since there is an inherent trade-off between false positives and false negative matches (Christen and Goiser, 2007). To see why this will be the case, consider that raising the stringency of the criteria that are used to identify a match will reduce the number of false positive matches at the expense of increasing the number of false negative matches. On the other hand, less stringent

strategy, but with a blocked matrix of probabilities (as opposed to a fully defined matrix of probabilities), Lahiri and Larsen (2005) demonstrate that there are substantial gains to be made from fully defining the matrix of match probabilities. However, their method presumes that it is tractable to fully define this matrix, which may not be feasible when linking large administrative databases.

[16] The goal of the Fellegi and Sunter (1969) model is to minimize the number of ambiguous candidate links that require additional review.

deterministic rules and hybrid probabilistic matching will result in a greater number of false positive matches and fewer false negative matches (Zingmond et al., 2004). In general, comparisons of matching algorithms have found that probabilistic matching algorithms have higher overall accuracy rates than deterministic rules (Campbell, 2009; Campbell et al., 2008; Gomatam et al., 2002; Tromp et al., 2011), or, at a minimum, have similar accuracy rates to deterministic rules (Clark and Hahn, 1995).

Several studies have examined the effects of matching errors on coefficient estimates when linking two separate files (Cryer et al., 2001; Lahiri and Larsen, 2005; Neter et al., 1965; Scheuren and Winkler, 1993). At the inception of computerized data linkage, the key conclusion from Neter and colleagues was that "the consequences of even small mismatch rates can be considerable" (Neter et al., 1965, p. 1021). Moreover, researchers have recognized that classification errors, as a special case of classical measurement error, can lead to downward bias in effect size estimates (Aigner, 1973; Campbell, 2009; Khwaja and Mian, 2005). For example, Khwaja and Mian (2005, p. 1379, emphasis original) cautioned the readers that "when [their] algorithm matches a firm to a politician, but the match is incorrect ... estimates of political corruption are likely to be *underestimates* of the true effect."

While downward bias may not be a first order concern when the biased estimates are still statistically significant, the bias can be very problematic when researchers are unable to detect real relationships between an intervention and an outcome of interest, a problem which may be greatly exacerbated by the difficulty of publishing findings that are not statistically significant at conventional levels of confidence. In the presence of publication bias, statistical power problems generated by matching errors can have negative consequences not only for individual papers but also, potentially, for entire literatures. We proceed by deriving an analytic result that shows how matching errors attenuate coefficient estimates and how they affect estimated standard errors. We then note the implications for statistical power empirically demonstrate that probabilistic matching can be extremely helpful in most circumstances.[17]

[17] This result builds on Aigner (1973).

3 Derivation of Estimated Treatment Effects, Standard Errors and Statistical Power

In this section we derive the effects of matching errors on the estimated treatment effect, $\hat{\tau}$, as well as its standard error, $se(\hat{\tau})$, in a randomized experiment with a binary treatment condition. We show that the effects of matching errors on both quantities have a closed form solution. The estimated $\hat{\tau}$ will be attenuated and the degree of attenuation will be proportional to the sum of the false positive and false negative matching error rates. The effect of matching errors on $se(\hat{\tau})$ is more complicated and may result in an increase or decrease in the estimate of the standard error relative to the no matching error scenario. In general, relative to the effect on coefficient estimates, standard errors are not very sensitive to matching errors and, as a result, matching errors will *always* lead to a higher rate of failing to reject a false null hypothesis, and in so doing, lead to a higher likelihood of failing to detect a true treatment effect of a randomized intervention under study. As we show, matching errors can be very detrimental to statistical power in all but the largest randomized experiments.

3.1 Estimated Treatment Effect

We begin by showing that, in a randomized experiment, matching errors lead to attenuated estimates of an average causal effect in absolute terms. Consider a randomized control trial with a study sample of n units of which a fraction, p, are assigned to treatment and the remaining $(1-p)$ are assigned to a control condition. Information on this experimental sample is stored in a dataset, E. We are interested in estimating the average treatment effect of our intervention on an outcome, y. In this case, the outcome measure is stored in an administrative dataset, D, where the number of individuals in D is much larger than n. In order to estimate the average treatment effect, we need to match our experimental sample to the outcomes stored in administrative dataset. If a record in E links to a record in D then observed $y=1$ and otherwise observed $y=0$. The realized outcome for an individual in E is given by the potential outcomes corresponding to the treatment condition:

$$y_i(T_i)\begin{cases} y_i(0) & \text{if } T_i = 0, \\ y_i(1) & \text{if } T_i = 1 \end{cases} \tag{1}$$

As such, the average treatment effect of the intervention, τ can be computed as:

$$\tau = \mathbb{E}[y_i(1) - y_i(0)] = P(y_i = 1|T_i = 1) - P(y_i = 1|T_i = 0) \tag{2}$$

where T is a treatment indicator. The process of matching the experimental data to the outcome data can lead to two types of errors:

- False positive link (FP): An instance in which an individual i has the true outcome $y_i^* = 0$, but was incorrectly linked to some other individual's record in D with $y_j^* = 1$ where $i \neq j$, such that in this case, the observed value of y after the linking process is equal to 1.

- False negative link (FN): An instance in which an individual i has the true outcome $y_i^* = 1$, but was not linked to a record in D. In this case, the observed value after the linking process is $y = 0$.

It is important to note that since we are trying to match observations in E to a given outcome in D, matching errors are only driven by whether the correct outcome is observed, and not that the link refers to the same person in both datasets. Specifically, this means that it would not be considered an error with respect to measuring the outcome if a record in E is linked to the wrong person in D, provided the linked record had the same outcome value as the true match. When records are matched to erroneous outcomes this will lead to the following biased estimate of τ:

$$\hat{\tau} = P(y_i = 1|T_i = 1) - P(y_i = 1|T_i = 0) \tag{3}$$

To further characterize the nature of the bias in τ we introduce the following four definitions:

- True Positive Rate (TPR): $P(y_i = 1|y_i^* = 1)$, or the probability that an individual with outcome $y = 1$ will be linked to an individual in D yielding an observed outcome $y^* = y = 1$.

- True Negative Rate (TNR): $P(y_i = 0|y_i^* = 0)$, or the probability that an individual with outcome $y = 0$ will not be linked to an individual in D yielding an observed outcome $y^* = y = 0$.

- False Negative Rate (FNR): $P(y_i = 0|y_i^* = 1)$, or the probability that an individual with outcome $y^* = 1$ will not be linked to an individual in D, yielding an observed outcome $y^* \neq y$. FNR is equivalent to 1 - TPR.
- False Positive Rate (FPR): $P(y_i = 1|y_i^* = 0)$, or the probability that an individual with outcome $y^* = 0$ will be incorrectly linked to an individual in D, resulting in an observed outcome $y^* \neq y$. FPR is equivalent to 1 - TNR.

Then the observed, and potentially biased, treatment effect can be written as:

$$\begin{aligned}
\hat{\tau} &= P(y_i = 1|T_i = 1) - P(y_i = 1|T_i = 0) \\
&= \sum_{j \in \{0,1\}} P(y_i = 1, y_i^* = j|T_i = 1) - \sum_{j \in \{0,1\}} P(y_i = 1, y_i^* = j|T_i = 0) \\
&= \sum_{j \in \{0,1\}} P(y_i = 1|y_i^* = j, T_i = 1) P(y_i^* = j|T_i = 1) \\
&- \sum_{j \in \{0,1\}} P(y_i = 1|y_i^* = j, T_i = 0) P(y_i^* = j|T_i = 0) \\
&= TPR_T \; P(y_i^* = 1|T_i = 1) \; - \; TPR_C \; P(y_i^* = 1|T_i = 0) \\
&+ FPR_T \; P(y_i^* = 0|T_i = 1) \; - \; FPR_C \; P(y_i^* = 0|T_i = 0) \qquad (4)
\end{aligned}$$

TPR_T and TPR_C are the true positive rates for the treatment and control groups, respectively. Similarly, the false positive rate for the treatment and control groups are FPR_T and FPR_C. In the case where matching error rates are equivalent for both treatment and control groups, as is expected under random assignment, we let $TPR_T = TPR_C$ and $FPR_T = FPR_C$. We can then re-write the expression more compactly:

$$\begin{aligned}
\hat{\tau} &= TPR \, [P(y_i^* = 1|T_i = 1) - P(y_i^* = 1|T_i = 0)] \\
&+ FPR \, [P(y_i^* = 0|T_i = 1) - P(y_i^* = 0|T_i = 0)] \qquad (5)
\end{aligned}$$

which can, in turn, be written as:

$$\begin{aligned}
\hat{\tau} &= TPR \, [P(y_i^* = 1|T_i = 1) - P(y_i^* = 1|T_i = 0)] \\
&- FPR \, [P(y_i^* = 1|T_i = 1) - P(y_i^* = 1|T_i = 0)] \qquad (6)
\end{aligned}$$

The bracketed term in (6) is simply τ, the true treatment effect, which leads to the following final form in the case of equivalent matching error across treatment and control:

$$\hat{\tau} = (TPR - FPR) \; \tau \qquad (7)$$

We note that if the error rates were known, the true treatment effect could be recaptured:

$$\tau = \frac{\hat{\tau}}{TPR - FPR} \tag{8}$$

Non-zero matching error will always attenuate the absolute value of the true treatment effect.[18] Finally, we can re-write the denominator as $1 - (FNR + FPR)$ and generate two critical insights. First, bias will be proportional to the total matching error rate. The finding that the sum of false positive and false negative error rates drives the bias is particularly important given the tendency toward "exact matching," which is thought to minimize error, but, in fact, reduces the number of false positive links while increasing the number of false negative links. Second, under reasonable assumptions on the magnitude of the error rates (i.e. when $FNR + FPR < 1$), $\hat{\tau}$ will be attenuated towards zero — that is, the estimated treatment effect will be too small.

3.2 Estimated Standard Errors

In Section 3.1 we showed that matching error leads to an attenuated estimate of the average treatment effect and we further posited that bias introduced by matching errors will reduce statistical power. However, in order to draw conclusions about the effect of matching errors on statistical power, we must also consider the effect of matching error on estimated standard errors. To see how matching error affects σ_τ, note that the variance of τ is given by:

$$\sigma_\tau^2 = \frac{1}{p(1-p)} \frac{\sigma^2}{N} \tag{9}$$

where p is the proportion of the study sample enrolled in treatment, N is the sample size, and σ^2 is the residual outcome variance from a regression of y on the treatment indicator, T. Taking the square root of the quantity on the right-hand side of in (9) yields the estimated standard error around τ.

The only remaining step is to estimate the residual variance. We note that in the case of linear regression, σ^2 can be defined via the residual sum of squares, and, with a binary outcome and a binary treatment, results in the following form where y_T and y_C are the

[18] If $TPR = FPR$ then the previous equation is undefined and the observed treatment effect will equal zero, but that situation is unlikely to occur in practice as it implies a random match.

number of individuals in the experimental group linked to records in the administrative data for the treatment and control group, respectively (see derivation in Appendix B).

$$\sum_i (y_i - \hat{y}_i)^2 = y_T \left(1 - \frac{y_T}{N_T}\right) + y_C \left(1 - \frac{y_C}{N_C}\right) \tag{10}$$

While attenuation in the treatment effect depends only on the the sum of false positive and false negative error rates, matching error affects the standard errors through the control group mean, the treatment effect, and the distribution of false positive and false negative links. To see how the distribution of matching error types affects the standard errors, consider a scenario where there is no treatment effect. When the false positive rate is greater than the false negative rate, the number of instances where $y = 1$ will increase and the outcome density will also increase. Conversely, when the false negative rate is higher the number of instances where $y = 0$ will increase and the outcome density will decrease. The outcome density that maximizes the variance is $\bar{y} = 0.5$.[19] Whether the standard errors increase or decrease depends on the extent to which the errors move the outcome density toward or away from 0.5. For example, if the overall mean is 0.4, but the matching algorithm produces more false negatives than false positives, then the observed treatment group mean will be less than 0.4 and the resulting standard error will shrink. The situation is slightly more complicated when there is a treatment effect, but we show in Appendix C that Equation 10 is maximized when the control group mean plus the treatment effect equal 0.5.

The interplay between these factors means that there will be scenarios in which matching error will produce *smaller* standard errors when compared with the no error case. But in the next section we show that even in these situations, matching error compromises a researcher's ability to detect a true treatment effect.

3.3 Implications for Statistical Power

While attenuation of coefficients can be troublesome, the effect of matching errors on statistical power is a far greater concern. Due to resource constraints, few randomized experiments are overpowered, so modest matching errors can have an outsize effect on statistical

[19] To see this, consider the scenario where there an equal number of individuals in the treatment and control groups, then Equation 10 simplifies to 2 $y_C \left(1 - \frac{y_C}{N_C}\right)$. It is straightforward to show that this quantity is maximized when $y_C = \frac{N_C}{2}$.

power.[20] We begin by noting that since there is a closed form solution for the effect of matching errors on the estimated average treatment effect and its standard error, there is also a closed form solution for the effect of matching errors on statistical power $(1-\beta)$. To see this, consider that, for a given Type I error rate (α) and a standard error around the average treatment effect, the probability of a Type II error is given by:

$$\beta = \Phi\Bigg[-\ \Phi^{-1}\Big(\frac{\alpha}{2}\Big) - \frac{\tau_h}{\sigma_{\tau_h}}\Bigg] \tag{11}$$

where τ_h is the hypothesized treatment effect, σ_{τ_h} is the standard error, and Φ is the cumulative distribution function for the normal distribution.[21] One minus this quantity is statistical power. If the following condition holds, then power will always be lower under matching error:

$$\frac{\tau_h}{\sigma_{\tau_h}} > \frac{\hat{\tau}}{\sigma_{\hat{\tau}}} \tag{12}$$

Since the true treatment effect will be adjusted according to $1-(FNR+FPR)$, Equation 12 can be re-written as:

$$\begin{aligned} \frac{\tau_h}{\sigma_{\tau_h}} &> \frac{\big[1-(FNR+FPR)\big]\tau_h}{\sigma_{\hat{\tau}}} \\ \sigma_{\hat{\tau}} &> \big[1-(FNR+FPR)\big]\ \sigma_{\tau_h} \end{aligned}$$

As we discussed in the previous section, there will be situations in which $\sigma_{\hat{\tau}} < \sigma_{\tau_h}$, but in the Appendix we show that even in these situations the shrinkage in the standard errors is never enough to offset the consequences of coefficient attenuation, and, therefore, statistical power *always* decreases under matching error.

In the next section we show that even with modest matching errors, there can be large declines in statistical power. Since, in the context of a randomized experiment, researchers tend to set $1-\beta$ on the basis of their relative tolerance for the risk of an underpowered finding, the result is that researchers will undertake randomized experiments that are underpowered relative to their desired power thresholds.

[20] Ioannidis et al. (2017) show that the median statistical power for a large body of studies in economics, most of them observational, is just 18%.

[21] For smaller samples, Φ would be replaced by the cumulative distribution function for the t distribution.

4 Analytic Results

In order to provide a sense for the degree to which matching errors lead to attenuation in experimental estimates, incorrect standard errors, and corresponding declines in statistical power, we compute the Type II error rate over a range of reasonable parameter values. We focus specifically on the outcome density for the control group $\bar{y_C}$, the hypothesized treatment effect τ_h, the sample size N and the matching error rates. Our goal here is to demonstrate the dynamics of this problem and the contexts in applied research for which it is likely to be especially pernicious.

4.1 Setup

In order to explore the effect of matching errors under a range of different parameterizations, using the analytic results in Section 3, we derive closed form solutions for τ, $se(\tau)$ and, ultimately, the Type II error rate, β, in two potential scenarios: one in which there are no matching errors and another in which matching errors are present. While it is the sum of false positive and false negative error rates (FPR+FNR) that dictates the degree of attenuation in $\hat{\tau}$, as we have shown, the extent to which matching errors affect the standard error around this estimate and, relatedly statistical power, will also depend on the ratio of false positive to false negative match rates. We motivate our setup using a dichotomous outcome, y and a binary treatment, T where, as before, p is the proportion of the sample that is treated and the remaining $1 - p$ are untreated.[22]

4.2 Main Results

Figure 1 contains four panels that report ex ante power calculations with and without matching errors, corresponding to four control mean-effect size combinations ($\bar{y}^* = 0.3$, 0.5 and $\tau_h = 15\%$, 25%) that are typical of power calculations in planning a randomized experiment. In each panel, the total matching error rate — that is the sum of the false negative and false positive match rates — is plotted on the X-axis while the Type II error rate (β) is plotted on the Y-axis. The lines plot Type II error rates for a given sample size, N.

We begin our discussion with Panel (a) which corresponds with $\bar{y}^* = 0.5$ and $\tau = 25\%$,

[22] The computational details of this exercise are described in the computational appendix to this paper.

the parameterization which is best powered for a given sample size. Consider, for example, a very large experiment in which $N = 2{,}000$. In such an experiment, a Type II error will be extraordinarily rare — approximately zero — in the absence of matching errors. Even when the matching error rate is as high as 30%, the probability of a Type II error will be approximately 3%, meaning that such an experiment will have a 97% probability of detecting a treatment effect of 25%. This is sensible as matching errors have little effect on statistical power when an experiment is extremely overpowered. However, due to resource constraints, overpowered experiments are rare. A more realistic scenario is an experiment in which $N = 500$. This sample size corresponds with the solid, red line in Panel (a). In the absence of matching errors, this study has a Type II error rate of approximately 20% which is considered by many researchers to be a reasonable default rule in conducting ex ante statistical power calculations (Moher et al., 1994). Under even a relatively modest matching error rate of 10%, Type II error rates rise to approximately 28%; with a 20% matching error rate, the probability of a Type II error nearly doubles to 39%.

Another way to understand the impact of matching errors is to consider how much larger the study would have to be to maintain a given Type II error rate, β. This too can be seen in Figure 1. Referring to Panel (a), consider a study of size, $N = 500$ which has a Type II error rate of approximately 20% in the absence of matching errors but a 38% Type II error rate under 20% matching error. Here, it would take a 50% increase in the size of the study (from $N = 500$ to 750) to return to the desired Type II error rate of 20%. As resource constraints are often binding, increasing the size of a study by 50% is most often infeasible.

The effects of matching error on statistical power are even more dramatic with a less dense outcome and a smaller treatment effect of interest. In Panel (b), $\bar{y}^*$ is fixed at 0.5 but now we are interested in being able to detect a smaller treatment effect, $\tau = 15\%$. Now, even in the absence of matching error, we will need a larger sample size to detect a treatment effect of this magnitude (e.g. for $N = 500$, the Type II error rate at zero matching error is greater than 60%). Focusing on the sample size ($N = 1{,}500$) that roughly yields the default Type II error rate of 20% in the absence of matching errors. In this case, we see that when the sum of false positive and false negative errors is at a reasonable level (15%) Type II error rates will increase by approximately 50%, from 20% to around 30%. We see a similar relationship when the treatment effect of interest is 25% but the outcome is less dense (Panel c). Finally, we turn to Panel (d) in which we have both a less dense outcome $\bar{y}^* = 0.3$ and a smaller treatment effect of interest 15%. Here, even a very large experiment will sometimes fail to detect a true treatment effect as the Type II error rate for a study of size $N = 3{,}000$ is approximately 25% in the absence of matching errors. In this case, a reasonable matching error rate of 15%, takes the Type II error rate to 40%.

4.3 Extensions

Next, we consider two extensions of the simple model outlined in 4.1. Specifically, we allow for the presence of a covariate that is correlated with the outcome and we consider the implications of matching errors for tests of treatment heterogeneity.

4.3.1 Allowing for Covariates

The results reported in Section 4.2 presume that researchers do not have access to or, at least, do not use pre-test covariates in estimating $\hat{\tau}$. While a healthy debate exists about the wisdom of controlling for covariates in a finite sample, it is common empirical practice in analyzing randomized experiments to condition on covariates and estimate an average treatment effect by regressing y on both T and a vector of covariates, X (Angrist and Pischke, 2009; Duflo et al., 2007). The wisdom behind controlling for covariates is straightforward. Given that the treatment is randomized, X will be unrelated to T but may be helpful in explaining y. The result is that residual variation will shrink and so too will estimated standard errors. Thus, controlling for covariates will increase a researcher's power to detect treatment effects and, in expectation, will not bias the estimated treatment effect. Given that the primary purpose of controlling for covariates in an experimental setup is to increase statistical power, a natural question is whether doing so has implications for the effect of matching errors on statistical power.

In order to answer this question, we generate a covariate, X, that is correlated with y^* but which, by construction, is uncorrelated with T. For simplicity, we generate a dichotomous X which is found in equal proportions in the treatment and control groups (though all of the analytic results will also hold in the case in which X is continuous). The setup is the same as before with the exception that we specify an imbalance parameter, r, which governs the strength of the relationship between y^* and X. Specifically, r is difference in the proportion of the sample for which $y^* = 1$ when $X = 0$ and when $X = 1$. In other words, r represents the amount of imbalance in the outcome density between individuals who possess characteristic X and those who do not. For example, if $\bar{y}^*$ is 0.5, when $r = 0.1$, $\bar{y}^* = 0.4$ for the $X = 1$ group and 0.6 for $X = 0$ group, or vice versa. When r is large, y^* and X will be highly correlated and standard errors shrink by a relatively large amount. In the demonstration below, we fix r =0.1. However, the choice of r does not have a first order effect on the extent to which matching errors lead to Type II errors.[23] We present findings in Figure 2 in which Panels (a)-(d) correspond with the same parameterizations shown in Figure 1. Referring to Panel (a) in which $\bar{y}^* = 0.5$ and $\tau = 25\%$, we see that, compared to Figure 1, the y-intercept has shifted downwards reducing the probability of Type II error when a covariate is added to the model. Without matching error, a sample of $N = 500$ yielded a Type II error rate of approximately 20% in the absence of a covariate, conditioning on a reasonably predictive covariate reduces the Type II error rate to just over 15%. In the case of this marginally powered sample ($N = 500$), a reasonable error rate of 15% doubles the Type II error. Referring to Panel (b) where the researcher would like to detect a treatment effect of 15%, we see that the consequences of matching errors continue to be severe in the presence of a covariate with Type II error rates typically increasing by between 50% and 75% with a relatively modest matching error rate of 15%. The key takeaway is that despite the statistical power gains from covariate adjustment, matching error remains a concern for experiments with marginally palatable Type II error rates.

4.3.2 Treatment Heterogeneity

A final issue which is worth discussing concerns the task of testing for treatment heterogeneity in an experiment. Naturally tests for treatment heterogeneity will always be underpowered relative to tests for the average treatment effect. How though will these tests be affected by the presence of matching errors? We extend the setup in (4.3.1) and consider a researcher who is interested in testing whether the effect of treatment differs according to a dichotomous covariate, G which, to be concrete, we will assume is gender. In order to

[23] The parameter r captures the strength of the relationship between X and y^*. Therefore, as r increases in magnitude, statistical power increases, both in the absence and the presence of matching errors. However, the *relative* gain statistical power is slightly larger when we do not condition on X. Across the parameterizations we examine, in the absence of a covariate, the average loss of power under matching errors is 8.4%. When $r = 0.1$, the loss of power is 8.8% when X is conditioned on. When $r = 0.3$, the average loss of power under matching errors is 11.9% when X is conditioned on. Hence while a larger r is uniformly power enhancing, it does mean that controlling for a covariate will be slightly less helpful in maximizing statistical power than it otherwise would be.

determine whether the effect of treatment is different for men and women, the researcher will specify the following regression model:

$$y_i = \alpha + \tau T_i + \pi G_i + \rho T_i G_i + \varepsilon_i \tag{13}$$

Letting $G = 1$ denote the male group, in this model the treatment effect for men will be $\tau + \rho$ and the treatment effect for women will be simply τ. Hence ρ represents the difference in treatment effects between men and women.

In the presence of matching errors, when estimating (13), τ will be incorrectly estimated. However, the extent to which matching errors affect the estimate of ρ depends on whether the matching errors are orthogonal to G. In the case in which men and women are equally likely to be incorrectly linked, the estimate of ρ will be unbiased; the estimate of the average treatment effect for men and women will be attenuated by an equal amount. However, if the groups have different error rates in the match, then the estimate of ρ will be biased. This is likely to be a common problem. In the case of men and women, a number of papers indicate that link rates are expected to be lower for women than for men because women often change their names upon getting married (Bohensky et al., 2010; Maizlish and Herrera, 2005). The capacity to estimate heterogeneous treatment effects is called into question if match rates differ by the category in question.

In the event that matching errors vary by group, the estimate of ρ will be biased upward in the case that the G=1 group has more matching errors and will be biased downward when the G=0 group has more matching errors. Thus, while matching errors are guaranteed to lead to an attenuated estimate of the overall average treatment effect, when the matching errors vary by group, the direction of the bias in tests for treatment heterogeneity will be ambiguous and will depend on the group specific matching error rates.

5 Empirical Example

Having established that matching errors can lead to a considerable number of Type II errors in empirical applications, we next consider how to mitigate this problem. In Section 3, we established that it is the sum of false positive and false negative error rates (rather than either the false positive or false negative match rates individually) that controls the degree of attenuation of parameter estimates and therefore, statistical power. While "exact matching" will reduce the number of false positive links, it will, in general, not minimize the *sum* of false positive and false negative error rates since the number of false negative links grows because of the stringency of the matching criteria. There is, therefore, promise in testing the performance of more flexible matching strategies as an alternative to exact matching.

In this section, we show how a machine learning approach for probabilistic matching can reduce the likelihood of Type II errors. There are two primary reasons to augment traditional probabilistic matching techniques with machine learning methods. First, we deal with a large dataset of over one million records. Probabilistic techniques involve computing similarity metrics across a number of identifying characteristics such as name and date of birth. It becomes prohibitively, computationally expensive to perform these calculations for each potential record pair as the dataset size grows. Ideally, we would only perform these computations for records for which we had some prior belief referred to the same person. Techniques such as approximate nearest neighbors allow for fast detection of likely matches that drastically reduce the number of comparisons that need to be made in the linking process.[24] Second, the adaptivity of machine learning models for learning non-linear functions and the practice of assessing performance on out-of-sample data lead to predictive accuracy that outperforms linear models such as logistic regression. While not limited to machine learning approaches, we augment our algorithm below by explicitly having it minimize the right objective function for reducing the attenuation bias. The end result is that we can trade off false positive and false negative matches to minimize the attenuation due to matching error.

In order to explore the potential gains from probabilistic matching with machine learning, we need an empirical example. The reason for this is that while we can solve for the bias that accrues from a given error rate, sample size and effect size, the extent to which we can reduce bias via a given matching strategy requires empirical data — names, dates of birth and addresses, etc. which can be used to generate candidate matches. With empirical data and a simulated randomized experiment in which a ground truth treatment effect is known, we can compare bias under exact matching and probabilistic matching with machine learning. We can therefore assess the extent to which probabilistic matching reduces bias relative to exact matching for a given sample size and effect size.

[24] Although, Lahiri and Larsen (2005) show that a fully saturated matrix of comparisons yields the most accurate probabilistic matching result, it has become increasingly common to observe matching cases that render an unblocked linking procedure intractable.

We pause here to describe what the ideal empirical application will look like, noting that the perfect application is not easily found. We will need two datasets: an "input" dataset which contains information on a universe of research subjects including their treatment indicators (our experimental dataset, E) and an "outcome" dataset with the universe of candidate matches and their outcomes (our administrative dataset, D). The ideal application must contain individually identified data that can be used to generate candidate matches and should contain a "ground truth" identifier that allows us to estimate a ground truth treatment effect in the absence of matching errors. We have identified empirical data on individuals from the State of Oregon that meet each of these criteria (Hansen and Waddell, 2018). We use the data to assign a placebo treatment indicator in order to simulate a randomized experiment. Since we have a ground truth unique identifier and a known data generating process, we can understand the consequences of using either exact matching or probabilistic matching on our estimates.

5.1 Empirical Simulation

For this study we use identified administrative records on 3 million charges filed in Oregon courts during the 1990-2012 window, maintained in the Oregon Judicial Information Network (OJIN). These data have been used previously to show how legal access to alcohol affects criminality. Hansen and Waddell (2018) measured recidivism by recording whether individuals appeared in dataset multiple times using exact matching. The individual records in the OJIN data contain the following relevant variables: name, date of birth, race, incident date, and a unique identification number that links the same individuals across rows in the dataset.[25]

In order to simulate the linking scenario described above, we first randomly sample 80% of the data as input training data for our matching algorithm. These data represent our administrative dataset, which we refer to as D. The remaining records are split equally between a sample of records which we will use to optimize our matching algorithm, referred to as E_1, and a holdout sample from which we will derive our error rates for the algorithm, E_2. While D is at the record level, meaning a person can appear multiple times, we convert

[25] There are situations where the two rows in the dataset will match on all relevant variables save for the unique identifier. As it is ambiguous whether these rows refer to different individuals or if there is an error in the unique identifier, we drop these records from the empirical simulation. This reduces the number of records to about one million.

both E_1 and E_2 to be at the person level by dropping duplicate rows with the same unique identifier. Our algorithm works by identifying instances in the training data where two records are known to either refer to, or not refer to, the same person. We then compute similarity measures a between these known pairs for the following fields: first name, last name, date of birth, race, and indictment date. A random forest model Breiman (2001) run on these data produces probabilities for whether two records refer to the same person. Further details of the algorithm appear in Jelveh and McNeill (2018). We use a cutoff threshold p_c and we consider record pairs with predicted probabilities above p_c to be links.

Recall that our objective is to minimize the quantity $1 - (FPR + FNR)$ and that it is computed at the individual level, not the record level. Additionally, our measure of false positives is a function of whether a link was made to the administrative data, not that correct links are made at the individual level. Therefore, with E_1 we simulate the scenario we have described in this paper. To do so, for each person in E_1, we generate probabilities for whether they are linked to individuals in D. We then estimate our objective for a range of values for p_c and choose the one that minimizes $1 - (FPR + FNR)$. To estimate out-of-sample error rates, we then predict links between E_2 and D using the optimal p_c and report false positive and false negatives rates.

Table 1 compares the performance of the machine learning algorithm against exact matching by name and date of birth when linking E_2 to D. As expected, the true positive rate for exact matching is lower than that achieved by probabilistic matching. On the other hand, exact matching is significantly more likely to introduce false negatives. Most importantly, as Table 1 shows, we substantially reduce sum of false positive and false negative error rates by using a machine-learning strategy.

5.2 Empirical Simulation Results

To simulate matching error bias we follow the same procedure as in Section 4, this time using actual linkage rates from exact and machine learning matching of our empirical data. We explore the comparative performance of exact matching versus probabilistic matching in Figure 3 which plots, for a given $\bar{y}^*$, τ and n combination, the share of linking errors in the empirical data that are abated by using probabilistic matching as opposed to exact matching. For example, referring to the figure, when $\bar{y}^* = 0.5$, $\tau = 15\%$ and $n = 500$, nearly 60 percent of linking errors that exist under exact matching are overturned when we deploy a probabilistic matching algorithm. Across all parameterizations, probabilistic matching with machine learning typically overturns half of the errors that exist under exact matching. While our example here is limited to the performance of one probabilistic algorithm, given our analytic results, we expect that the gains from using probabilistic matching techniques will by and large outperform the stringency of “exact matching.”

6 Conclusion

We have shown that matching errors, even when introduced at random, have consequences for our evidence base in empirical social science — in particular, by creating potentially enormous challenges for developing evidence from randomized experiments, which remain the gold standard for generating causal inferences about the social world. Our reading of the prior literature is that scholars sometimes favor stringent matching criteria (i.e., exact matching) in an effort to minimize false positive matches with the goal of generating an analytic dataset with as few errors as possible. However, a key insight from this research is that the the sum of false positive and false negative error rates is the parameter that drives the attenuation bias from matching errors, which means that stringent matching criteria will increase, rather than minimize matching error bias. This is because while stringent criteria minimize false positive matches, they substantially increase false negative matches. As matching error affects coefficient estimates, there are descriptive as well as inferential consequences.

In the presence of matching errors, for any sample size, coefficients will be underestimated, with degree of attenuation being proportional to the error rate in the match.[26] While attenuation is unwelcome, matching errors have far more destructive consequences for statistical inference. This is because researchers who plan randomized experiments rarely have more statistical power than they need to detect an effect. The result is that a small degree of attenuation can easily make an effect size that was thought a priori to be detectable, undetectable. As we show, this problem can be especially severe in experiments with small samples or with larger samples and small effect sizes. Taken study by study, this issue might be dismissed as trivial, but because studies with “null results” are plausibly less likely to be submitted and accepted for publication, as “low-cost randomized trials” gain traction,

[26] It is worthwhile to note that the descriptive consequences of matching error cannot be resolved by increasing sample size.

this problem stands to erode the quality of the social scientific evidence base — perhaps substantially. While our analytical results apply specifically to randomized control trials, similar patterns could also emerge for quasi-experimental settings. Likewise, although we specifically focus on binary outcomes, continuous variables measuring outcomes like program utilization, earnings, or duration could all suffer from similar problems when derived from administrative data. In fact, it might even be more problematic if the lack of a match is a recorded as a zero, a common mass point in those types of continuous variables.

On an optimistic note, we find that probabilistic matching via machine learning algorithms vastly outperforms exact matching and, in fact, in many scenarios approximates a zero error scenario. We argue that these results provide compelling evidence that exact matching should be abandoned in favor of probabilistic matching and that applied researchers should pay greater attention to the way in which data linking is done more generally.

Appendices

A Computational Details

In this appendix we provide additional details for how statistical power can be computed under two possible states of the world: 1) in the absence of matching errors and 2) in the presence of matching errors. We use the derivations in this appendix to empirically demonstrate the effect of matching errors on statistical power in a hypothetical experiment in Section 5 of the paper.

We motivate the derivation by introducing a framework — a confusion matrix — that governs the incidence of matching errors in a generic dataset. Each row of the confusion matrix represents the incidence of an actual class while each column represents the instances in a predicted class. The matrix thus allows an analyst to understand the extent to which the algorithm is successful in classifying observations. In our context, we use a confusion matrix to see how a matching algorithm has performed in correctly determining the presence of an individual in a dataset.

In the following confusion matrix, y^* represents the true state of the world and y represents the observed state of the world after matching. The cells provide counts of the number of true negatives, false negatives, false positives and true positives, respectively in linking the data.

True state of the world

	$y^* = 0$	$y^* = 1$
$y = 0$	TN	FN
$y = 1$	FP	TP

The diagonal entries of the matrix correspond to an alignment of the true and observed states of the world — observations for which $y^* = y = 0$ are true negatives and observations for which $y^* = y = 1$ are true positives. The off-diagonal entries provide us with the number of matching errors. In particular, the 2,1 element of the matrix provides the number of false positive matches — this is the number of times in which an observation which is truly y^* $= 1$ is mistakenly linked to $y = 0$.[27] Similarly, the 1,2 element of the matrix provides the

[27] For consistency, we describe this as a mistaken link, when in practice, it is often the case that these records would be non-links that are then assumed to have the value $y = 0$.

number of false negative matches where an observation that is truly $y^* = 0$ is mistakenly linked to a record for which $y = 1$.

The table allows us to compute several quantities that are instrumental in deriving the impact of matching errors on statistical power. We begin by noting that the matrix allows us to compute four different rates which allow us to measure the success of a given linking strategy:

$$\begin{aligned} TPR &= \frac{TP}{TP + FN} \\ TNR &= \frac{TN}{TN + FP} \\ FPR &= 1 - TNR \\ FNR &= 1 - TPR \end{aligned}$$

The true positive rate (TPR) is defined as the number of linked positives divided by the number of true positives (TP+FN). Likewise the true negative rate (TNR) is the number of linked negatives divided by the number of true negatives (TN+FP). The corresponding false positive and false negative match rates are obtained by subtracting each of these quantities from 1. As we show in Section 3 of the paper, estimated treatment effects will be attenuated under matching errors and the attenuation will be proportional to 1-FPR-FNR. So long as FPR+FNR < 1, this will be strict attenuation towards zero but if FPR+FNR exceeds 1 then there can be a change in the sign of the bias.

Overall, there are $TP + FN$ actual failures and $TP + FP$ observed failures. This aspect of the table motivates our first step in deriving a statistical power computation. In particular, we can write down an expression for the number of failures in the control group in the absence and presence of matching errors as follows:

$$\begin{aligned} y^*_{T=0} &= (TP + FN) \times (1 - p) \\ y_{T=0} &= (TP + FP) \times (1 - p) \end{aligned}$$

$y^*_{T=0}$ is the true number of failures in the control group and $y_{T=0}$ is the observed number of failures where p is the proportion of the sample that receives the treatment.

Next, we consider how many successes there will be in the treatment group, with and without matching errors. In order to compute these quantities we introduce a treatment effect, τ which, for simplicity, is expressed in percent (rather than percentage point) terms. For our purposes, τ will be negative but this choice is trivial. The number of failures in the treatment group will then be given by:

$$\begin{aligned} y^*_{T=1} &= (TP+FN)(1-\tau)\times p \\ y_{T=1} &= (TP+FP)\left[1-[\tau(1-FPR-FNR)]\right]\times p \end{aligned}$$

In the absence of matching errors, the number of observed failures will be equal to the number of actual failures in the data multiplied by the proportion treated and one minus the treatment effect. When matching errors are present, the treatment effect will be multiplied by $1-FPR-FNR$ to account for attenuation.

To appreciate how this works, consider a dataset of size $N=900$, fix $P=0.5$ and $\tau=0.1$ (10%) and use the following confusion matrix:

	$y^*=0$	$y^*=1$
$y=0$	TN=280	FN=100
$y=1$	FP=20	TP=500

In this dataset, the FPR $= 1-\frac{500}{500+100} = 0.167$ and the FNR $= 1-\frac{280}{280+20} = 0.067$. Accordingly, we will have the following numbers of failures in the treatment and control groups in each of our two states of the world:

$$\begin{aligned} y^*_{T=0} &= (TP+FN)\times(1-p) = 300 \\ y^*_{T=1} &= (TP+FN)(1-\tau)\times p = 270 \\ y_{T=0} &= (TP+FP)\times(1-p) = 260 \\ y_{T=1} &= (TP+FP)\left[1-[\tau(1-FPR-FNR)]\right]\times p = 240 \end{aligned}$$

In the true state of the world, there are 300 failures in the control group and 270 in the treatment group, reflecting the fact that $\tau=0.1$. With matching errors, the observed number of failures in the control group is 260 and in the treatment group is 240. The observed treatment effect is smaller than 10%.

In order to compute statistical power to detect a given potential treatment effect, we need to compute a standard error which is computed according to:

$$var(\hat{\tau}) = \frac{1}{p(1-p)} \frac{\sigma^2}{N} \tag{14}$$

The square root of this quantity is the standard error around the estimated treatment effect. N and p are simply the sample size and the proportion treated but we will need to compute σ^2 which is the mean square error from a regression of either y^* or y on D, depending on which state of the world we are in. We show how to compute σ^2 in absence and presence of matching errors in Appendix B.

We can then compute statistical power according to:

$$\beta = \Phi\left[\Phi^{-1}\left(\frac{\alpha}{2} - \frac{\tau_h}{se(\tau_h)}\right)\right]$$

Carrying through the numerical example from our confusion table, power to detect a treatment effect of 10% in these data are 90 percent in the true state of the world and just 67 percent in the state of the world with matching errors. What would have been an exceedingly well-powered experiment is no longer well-powered in the presence of modest matching errors.

B Deriving Outcome Variance

In this section we show how to compute the residual sum of squares with a binary outcome and binary treatment in order to compute the σ^2. Let $\bar{y}_C$ equal the control group mean and τ the treatment effect:

$$\sum_i (y_i - \hat{y}_i)^2 = \sum_i (y_i - \bar{y}_C - \tau T_i)^2$$

We can decompose the above equation into four mutually exclusive groups determined by whether an individual is in the treatment or control group, and whether their associated outcome is $y = 0$ or $y = 1$.

$$\sum_{i \in \{i|y_i=0,T_i=0\}} (-\bar{y}_C)^2 + \sum_{i \in \{i|y_i=1,T_i=0\}} (1 - \bar{y}_C)^2 + \sum_{i \in \{i|y_i=0,T_i=1\}} (-\bar{y}_C - \tau)^2 + \sum_{i \in \{i|y_i=1,T_i=1\}} (1 - \bar{y}_C - \tau)^2$$
$$= n_{C,0}\ \bar{y}_C^2 + n_{C,1} + n_{C,1}\ \bar{y}_C^2 - n_{C,1}\ 2\bar{y}_C + n_{T,0}\bar{y}_T^2 + n_{T,1} + n_{T,1}\ \bar{y}_T^2 - n_{T,1}\ 2\bar{y}_T$$
$$= n_C\ \bar{y}_C^2 + n_{C,1} - n_{C,1}\ 2\bar{y}_C + n_T\bar{y}_T^2 + n_{T,1} - n_{T,1}\ 2\bar{y}_T$$
$$= n_{C,1}\ \bar{y}_C + n_{C,1} - n_{C,1}\ 2\bar{y}_C + n_{T,1}\bar{y}_T + n_{T,1} - n_{T,1}\ 2\bar{y}_T$$
$$= n_{C,1}(\bar{y}_C + 1 - 2\bar{y}_C) + n_{T,1}(\bar{y}_T + 1 - 2\bar{y}_T)$$
$$= n_{C,1}(1 - \bar{y}_C) + n_{T,1}(1 - \bar{y}_T)$$

C Maximizing RSS

We now show why Equation 10 is maximized when the control group mean, $\bar{y}_C$, plus the treatment effect, τ, equal 0.5. Let $N_{T,1}$ equal the number of individuals in the treatment group with $y = 1$ and $N_{T,0}$ equal the number of individuals in the treatment group with $y = 0$. Note that $N_{T,1} = (\bar{y}_C + \tau)N_T$ and $N_{T,0} = N_T(1 - (\bar{y}_C + \tau))$.

$$\sum_i (y_i - \hat{y}_i)^2 = \sum_i (y_i - (\bar{y}_C + \tau T_i))^2$$

For a given control group mean we will take derivatives with respect to τ, which means we will only consider individuals in the treatment group. We can decompose the previous equation into:

$$\begin{aligned}
\sum_{i \in T} (y_i - \hat{y}_i)^2 &= N_{T,0}(-\bar{y}_C - \tau)^2 + N_{T,1}(1 - \bar{y}_C - \tau)^2 \\
&= N_T(1 - (\bar{y}_C + \tau))(-\bar{y}_C - \tau)^2 + N_T(\bar{y}_C + \tau)(1 - \bar{y}_C - \tau)^2 \\
&= N_T(1 - \bar{y}_C - \tau)(\bar{y}_C + \tau)^2 + N_T(\bar{y}_C + \tau)(1 - \bar{y}_C - \tau)^2 \\
&= N_T(1 - \bar{y}_C - \tau)(\bar{y}_C + \tau)(\bar{y}_C + \tau + 1 - \alpha - \tau) \\
&= N_T(1 - \bar{y}_C - \tau)(\bar{y}_C + \tau)
\end{aligned}$$

Let $\kappa(\tau) = N_T(1 - \bar{y}_C - \tau)(\bar{y}_C + \tau)$, then taking derivatives with respect to τ:

$$\frac{d\kappa}{d\tau} = N_T(-2\bar{y}_C - 2\tau)$$

Setting the previous equation to zero and solving for τ leads to

$$\bar{y}_C + \tau = 0.5$$

D Proof for Power Attenuation

In this section we show that even when the standard error estimated under matching error is smaller than the standard error estimated under no error, statistical power will still be larger for the latter scenario. Let κ be True Positive Rate and ω be the False Positive Rate.

$$\begin{aligned}
\frac{\tau_h}{\sigma_{\tau_h}} &> \frac{\hat{\tau}}{\sigma_{\hat{\tau}}} \\
\frac{\tau_h}{\sigma_{\tau_h}} &> \frac{(\kappa-\omega)\tau_h}{\sigma_{\hat{\tau}}} \\
\sigma_{\hat{\tau}} &> (\kappa-\omega)\sigma_{\tau_h} \\
\sigma_{\hat{\tau}} - (\kappa-\omega)\sigma_{\tau_h} &> 0
\end{aligned}$$

We can replace $\sigma_{\hat{\tau}}$ and σ_{τ_h} with just the residual sum of squares components since all other terms in their respective computations cancel out. Here $N^*_{j,1}$ represents the number of observations for which the true value of y, $y^* = 1$ and $N^*_{j,0}$ represents the number of observations for which the true value of y, $y^* = 0$. This allows us to write the last inequality above as

$$\begin{aligned}
\sum_{j\in\{T,C\}} (\kappa\ N^*_{j,1} + \omega\ N^*_{j,0}) \left(1 - \frac{\kappa\ N^*_{j,1} + \omega\ N^*_{j,0}}{N^*_j}\right) - (\kappa-\omega)N^*_{j,1}\left(1 - \frac{N^*_{j,1}}{N^*_j}\right) &> 0 \\
\sum_{j\in\{T,C\}} (\kappa\ N^*_{j,1} + \omega\ N^*_{j,0}) \left(\frac{(1-\kappa)N^*_{j,1} + (1-\omega)N^*_{j,0}}{N^*_{j,1} + N^*_{j,0}}\right) - (\kappa-\omega)\left(\frac{N_{j,1^*}\ N^*_{j,0}}{N^*_{j,1} + N^*_{j,0}}\right) &> 0 \\
\sum_{j\in\{T,C\}} \kappa(1-\kappa)N^{*2}_{j,1} + \omega(1-\omega)N^{*2}_{j,0} + N^*_{j,1}N^*_{j,0}2\omega(1-\kappa) &> 0
\end{aligned}$$

All terms in the last inequality are greater than zero, satisfying the condition.

References

Aigner, D. J. (1973). Regression with a binary independent variable subject to errors of observation. *Journal of Econometrics 1*(1), 49–59.

Angrist, J. D. and J.-S. Pischke (2009). *Mostly harmless econometrics.* Princeton, NJ: Princeton University Press.

Bailey, M., C. Cole, M. Henderson, and C. Massey (2017, November). How well do automated methods perform in historical samples? Evidence from new ground truth. Working Paper 24019, National Bureau of Economic Research.

Benjamin, D. J., J. O. Berger, M. Johannesson, B. A. Nosek, E. J. Wagenmakers, R. Berk, K. A. Bollen, B. Brembs, L. Brown, C. Camerer, D. Cesarini, C. D. Chambers, M. Clyde, T. D. Cook, P. De Boeck, Z. Dienes, A. Dreber, K. Easwaran, C. Efferson, E. Fehr, F. Fidler, A. P. Field, M. Forster, E. I. George, R. Gonzalez, S. Goodman, E. Green, D. P. Green, A. G. Greenwald, J. D. Hadfield, L. V. Hedges, L. Held, T. Hua Ho, H. Hoijtink, D. J. Hruschka, K. Imai, G. Imbens, J. P. A. Ioannidis, M. Jeon, J. H. Jones, M. Kirchler, D. Laibson, J. List, R. Little, A. Lupia, E. Machery, S. E. Maxwell, M. McCarthy, D. A. Moore, S. L. Morgan, M. Munafó, S. Nakagawa, B. Nyhan, T. H. Parker, L. Pericchi, M. Perugini, J. Rouder, J. Rousseau, V. Savalei, F. D. Schönbrodt, T. Sellke, B. Sinclair, D. Tingley, T. Van Zandt, S. Vazire, D. J. Watts, C. Winship, R. L. Wolpert, Y. Xie, C. Young, J. Zinman, and V. E. Johnson (2018). Redefine statistical significance. *Nature Human Behaviour 2*(1), 6–10.

Binswanger, I. A., M. F. Stern, R. A. Deyo, P. J. Heagerty, A. Cheadle, J. G. Elmore, and T. D. Koepsell (2007). Release from prison: A high risk of death for former inmates. *The New England Journal of Medicine 356*(2), 157–165.

Black, S. E., P. J. Devereux, and K. G. Salvanes (2005). Why the apple doesn't fall far: Understanding intergenerational transmission of human capital. *American Economic Review 95*(1), 437–449.

Bohensky, M. A., D. Jolley, V. Sundararajan, S. Evans, D. V. Pilcher, I. Scott, and C. A. Brand (2010). Data linkage: a powerful research tool with potential problems. *BMC Health Services Research 10*(1), 346.

Breiman, L. (2001). Random forests. *Machine Learning 45*(1), 5–32.

Camerer, C. F., A. Dreber, E. Forsell, T.-H. Ho, J. Huber, M. Johannesson, M. Kirchler, J. Almenberg, A. Altmejd, T. Chan, E. Heikensten, F. Holzmeister, T. Imai, S. Isaksson, G. Nave, T. Pfeiffer, M. Razen, and H. Wu (2016). Evaluating replicability of laboratory experiments in economics. *Science 351*(6280), 1433–1436.

Campbell, K. M. (2009). Impact of record-linkage methodology on performance indicators and multivariate relationships. *Journal of Substance Abuse Treatment 36*(1), 110–117.

Campbell, K. M., D. Deck, A. Cox, and C. Broederick (2007). *The link king user manual: Version v5.2.3.*

Campbell, K. M., D. Deck, and A. Krupski (2008). Record linkage software in the public domain: a comparison of link plus, the link king, and a 'basic' deterministic algorithm. *Health Informatics Journal 14*(1), 5–15.

Chowdry, H., C. Crawford, L. Dearden, A. Goodman, and A. Vignoles (2013). Widening participation in higher education: analysis using linked administrative data. *Journal of the Royal Statistical Society: Series A (Statistics in Society) 176*(2), 431–457.

Christen, P. (2012). *Data matching: Concepts and techniques for record linkage, entity resolution, and duplicate detection.* New York, NY: Springer.

Christen, P. and K. Goiser (2007). Quality and complexity measures for data linkage and deduplication. In F. J. Guillet and H. J. Hamilton (Eds.), *Quality measures in data mining*, pp. 127–151. Berlin, Germany: Springer.

Clark, D. E. and D. R. Hahn (1995). Comparison of probabilistic and deterministic record linkage in the development of a statewide trauma registry. *Proceedings of the Annual Symposium on Computer Application in Medical Care 1995*, 397–401.

Connelly, R., C. J. Playford, V. Gayle, and C. Dibben (2016). The role of administrative data in the big data revolution in social science research. *Social Science Research 59*, 1–12.

Courtemanche, C. J., A. Denteh, and R. Tchernis (2018). Estimating the associations between snap and food insecurity, obesity, and food purchases with imperfect administrative measures of participation. Technical report, National Bureau of Economic Research.

Cryer, P. C., S. Westrup, A. C. Cook, V. Ashwell, P. Bridger, and C. Clarke (2001). Investigation of bias after data linkage of hospital admissions data to police road traffic crash reports. *Injury Prevention 7*(3), 234–241.

Dahl, G. B., A. R. Kostøl, and M. Mogstad (2014). Family welfare cultures. *The Quarterly Journal of Economics 129*(4), 1711–1752.

Dobkin, C., A. Finkelstein, R. Kluender, and M. J. Notowidigdo (2018). The economic consequences of hospital admissions. *American Economic Review 108*(2), 308–352.

Duflo, E., R. Glennerster, and M. Kremer (2007). Using randomization in development economics research: A toolkit. In T. P. Schultz and J. A. Strauss (Eds.), *Handbook of development economics*, Volume 4 of *Handbook of Development Economics*, pp. 3895–3962. Amsterdam, the Netherlands: North-Holland.

Feigenbaum, J. J. (2016). Automated census record linking: A machine learning approach. *Working Paper*.

Fellegi, I. P. and A. B. Sunter (1969). A theory for record linkage. *Journal of the American Statistical Association 64*(328), 1183–1210.

Fischbacher, U., S. Gächter, and F. Ernst (2001). Are people conditionally cooperative? evidence from a public goods experiment. *Economics Letters 71*(3), 397–404.

Freudenberg, N., I. Wilets, M. B. Greene, and B. E. Richet (1998). Linking women in jail to community services: Factors associated with rearrest and retention of drug-using women following release from jail. *Journal of the American Medical Women's Association 53*(2), 89–93.

Gelber, A., A. Isen, and J. B. Kessler (2016). The effects of youth employment: Evidence from new york city lotteries. *The Quarterly Journal of Economics 131*(1), 423–460.

Gerber, A. S. and N. Malhotra (2008). Do statistical reporting standards affect what is published? publication bias in two leading political science journals. *Quarterly Journal of Political Science 3*(3), 313–326.

Gilbert, D. T., G. King, S. Pettigrew, and T. D. Wilson (2016). Comment on "Estimating the reproducibility of psychological science". *Science 351*(6277), 1037.

Goerge, R. M. and B. J. Lee (2001). Matching and cleaning administrative data. In M. Ver Ploeg, R. A. Moffitt, and C. F. Citro (Eds.), *Studies of welfare populations: Data collection and research issues*, pp. 197–219. Washington, DC: National Academy Press.

Gold, M., S. Dugdale, R. J. Woodman, and K. A. McCaul (2010). Use of the Australian Childhood Immunisation Register for vaccine safety data linkage. *Vaccine 28*(26), 4308–4311.

Gomatam, S., R. Carter, M. Ariet, and G. Mitchell (2002). An empirical comparison of record linkage procedures. *Statistics in Medicine 21*(10), 1485–1496.

Hansen, B. and G. R. Waddell (2018). Legal access to alcohol and criminality. *Journal of Health Economics 57*, 277–289.

Heller, S. B. (2014). Summer jobs reduce violence among disadvantaged youth. *Science 346*(6214), 1219–1223.

Hser, Y. I. and E. Evans (2008). Cross-system data linkage for treatment outcome evaluation: lessons learned from the california treatment outcome project. *Evaluation and Program Planning 31*(2), 125–135.

Ioannidis, J. P., T. D. Stanley, and H. Doucouliagos (2017). The power of bias in economics research. *The Economic Journal 127*(605), F236–F265.

Jelveh, Z. and M. McNeill (2018). Downstream impact of probabilistic matching quality on prediction performance. *In Progress*.

Jiang, D., M. Walsh, and L. K. Augimeri (2011). The linkage between childhood bullying behaviour and future offending. *Criminal Behaviour and Mental Health 21*(2), 128–135.

Kariminia, A., T. Butler, S. Corben, M. Levy, L. Grant, J. Kaldor, and M. Law (2007). Extreme cause-specific mortality in a cohort of adult prisoners–1988 to 2002: A data-linkage study. *International Journal of Epidemiology 36*(2), 310–316.

Khwaja, A. I. and A. Mian (2005). Do lenders favor politically connected firms? rent provision in an emerging financial market. *The Quarterly Journal of Economics 120*(4), 1371–1411.

Kinner, S. A., S. Forsyth, and G. M. Williams (2013). Systematic review of record linkage studies of mortality in ex-prisoners: why (good) methods matter. *Addiction 108*(1), 38–49.

Kuhn, P., P. Kooreman, A. Soetevent, and A. Kapteyn (2011). The effects of lottery prizes on winners and their neighbors: Evidence from the Dutch postcode lottery. *American Economic Review 101*(5), 2226–2247.

Lahiri, P. and M. D. Larsen (2005). Regression analysis with linked data. *Journal of the American Statistical Association 100*(469), 222–230.

Maizlish, N. A. and L. Herrera (2005). A record linkage protocol for a diabetes registry at ethnically diverse community health centers. *Journal of the American Medical Informatics Association 12*(3), 331–337.

Mas, A. and A. Johnston (forthcoming). Potential unemployment insurance duration and labor supply: The individual and market-level response to a benefit cut. *Journal of Political Economy*.

Mason, C. A. and S. Tu (2008). Data linkage using probabilistic decision rules: a primer. *Birth Defects Research (Part A) 82*(11), 812–821.

Moher, D., C. S. Dulberg, and G. A. Wells (1994). Statistical power, sample size, and their reporting in randomized controlled trials. *JAMA 272*(2), 122–124.

Moore, C. L., J. Amin, H. F. Gidding, and M. G. Law (2014). A new method for assessing how sensitivity and specificity of linkage studies affects estimation. *PloS ONE 9*(7), e103690.

Mueller-Smith, M. (2016). The criminal and labor market impacts of incarceration. *Working paper*.

Neter, J., E. S. Maynes, and R. Ramanathan (1965). The effect of mismatching on the measurement of response errors. *Journal of the American Statistical Association 60*(312), 1005–1027.

Newcombe, H. B., J. M. Kennedy, S. Axford, and A. P. James (1959). Automatic linkage of vital records. *Science 330*(3381), 954–959.

Pashler, H. and E.-J. Wagenmakers (2011). Editors' introduction to the special section on replicability in psychological science: A crisis of confidence? *Perspectives on Psychological Science 7*(6), 528–530.

Petrou, S. and A. Gray (2011). Economic evaluation alongside randomised controlled trials: design, conduct, analysis, and reporting. *BMJ 342*, d1548.

Powell, D. and S. Seabury (forthcoming). Medical care spending and labor market outcomes: Evidence from workers' compensation reforms. *American Economic Review*.

Scheuren, F. and W. E. Winkler (1993). Regression analysis of data files that are computer matched, part i. *Survey Methodology 19*(1), 39–58.

Scheuren, F. and W. E. Winkler (1997). Regression analysis of data files that are computer matched, part ii. *Survey Methodology 23*(2), 157–165.

Tromp, M., A. C. Ravelli, G. J. Bonsel, A. Hasman, and J. B. Reitsma (2011). Results from simulated data sets: probabilistic record linkage outperforms deterministic record linkage. *Journal of Clinical Epidemiology 64*(5), 565–572.

Vivalt, E. (2017). The trajectory of specification searching and publication bias across methods and disciplines. *Working paper*.

Watson, C. I., G. P. Fiumara, E. Tabassi, W. J. Salamon, and P. A. Flanagan (2014). Fingerprint vendor technology evaluation. Report, NIST.

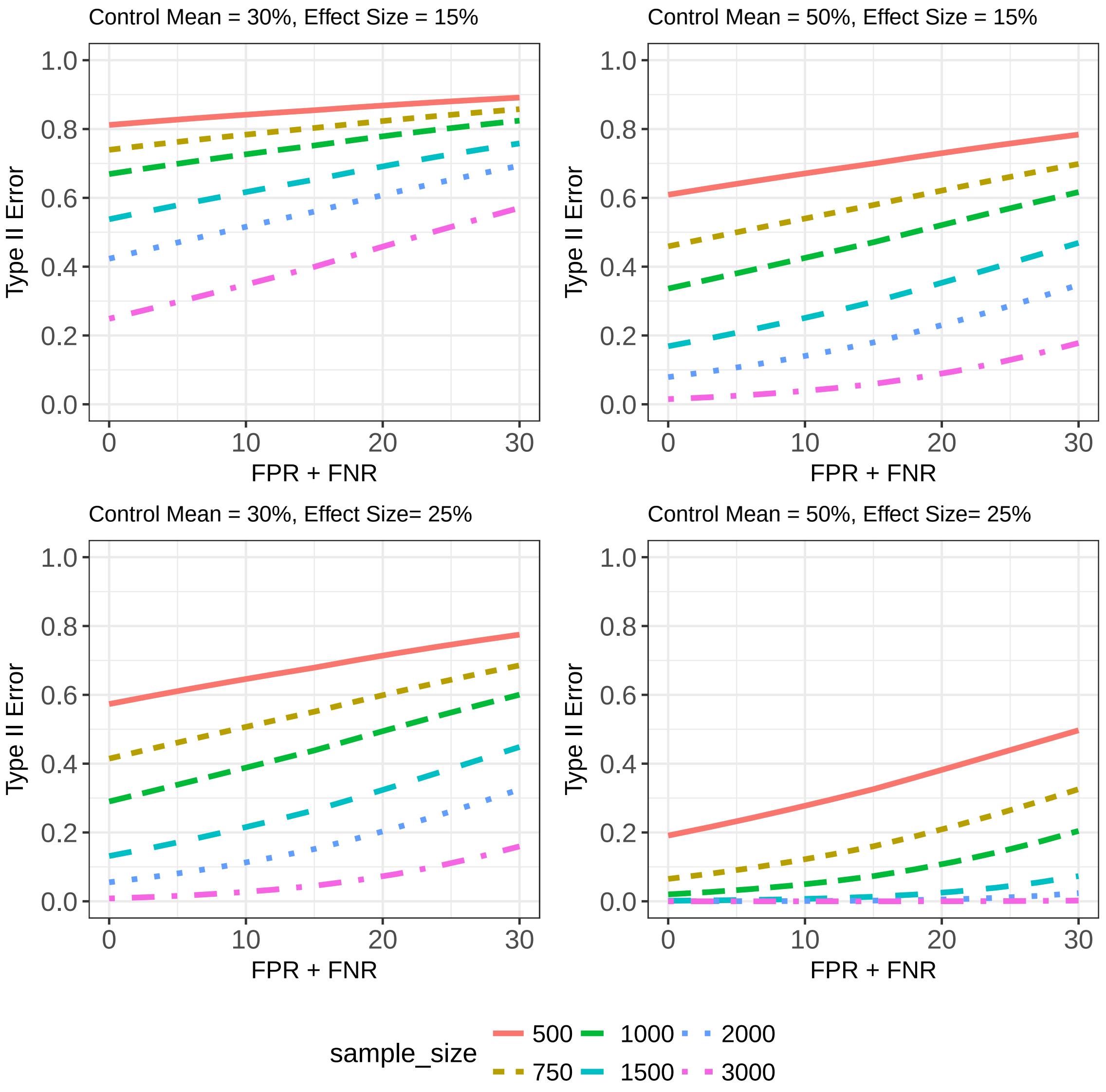
Whitaker, R. C. (2004). Predicting preschooler obesity at birth: The role of maternal obesity in early pregnancy. *Pediatrics 114*(1), e29–e36.

Winkler, W. E. (2006). Overview of record linkage and current research directions. Report, U.S. Census Bureau.

Zauber, A. G., S. J. Winawer, M. J. O'Brien, I. Lansdorp-Vogelaar, M. van Ballegooijen, B. F. Hankey, W. Shi, J. H. Bond, M. Schapiro, J. F. Panish, E. T. Stewart, and J. D. Waye (2012). Colonoscopic polypectomy and long-term prevention of colorectal-cancer deaths. *The New England Journal of Medicine 366*, 687–696.

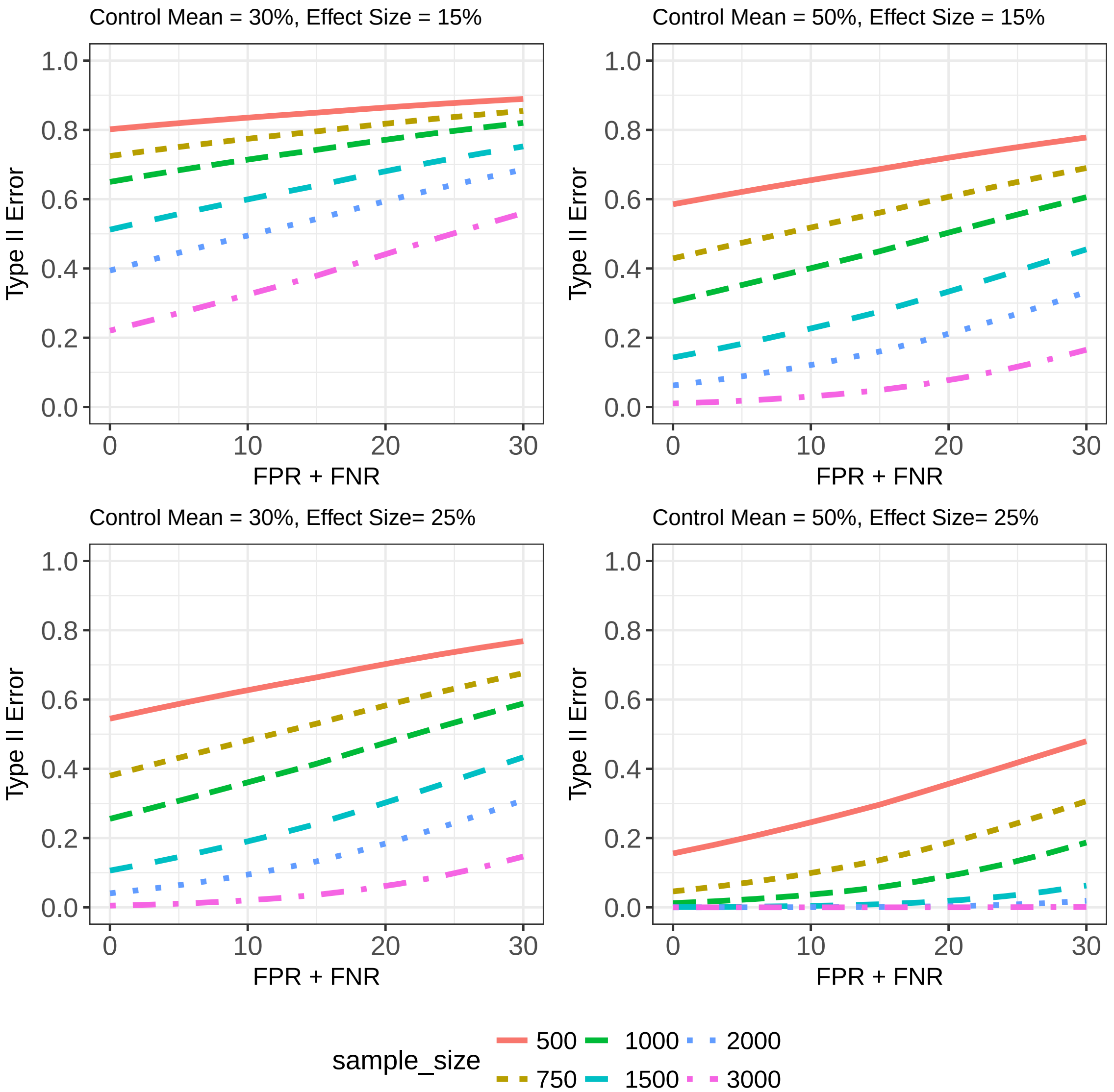
Zingmond, D. S., Z. Ye, S. L. Ettner, and H. Liu (2004). Linking hospital discharge and death records—accuracy and sources of bias. *Journal of Clinical Epidemiology 57*(1), 21–29.

Figure 1: Matching Error and Type II Error Rates By Outcome Density and Treatment Effect Size



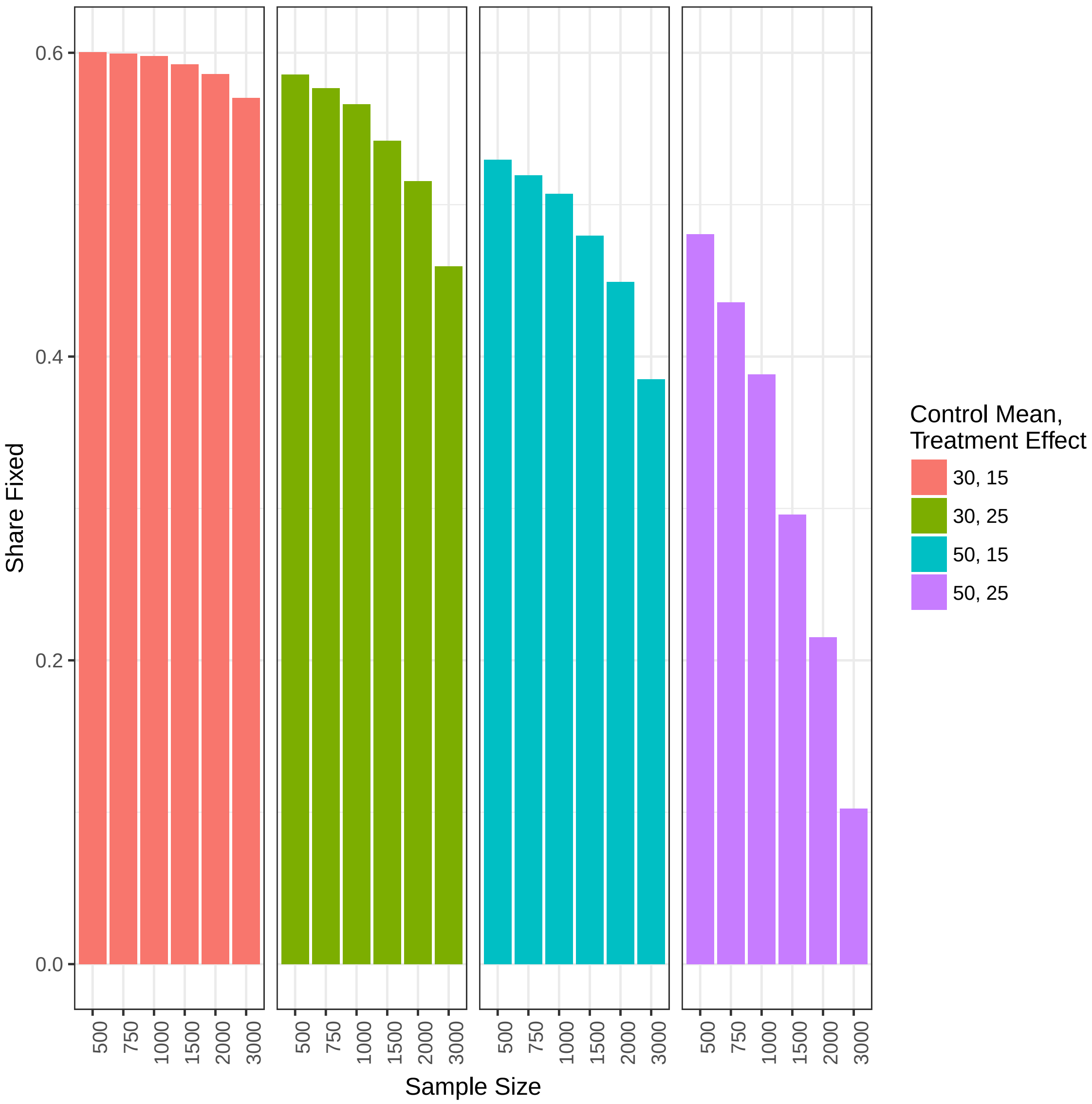
Note: Figures plot the Type II error rate (β) as a function of the total matching error rate for a given hypothesized effect size and control mean. In each plot, Type II error rates are plotted for sample sizes that range from $N = 500$ to $N = 3{,}000$.

Figure 2: Matching Error and Type II Error Rates w/ Covariate Adjustment By Outcome Density and Treatment Effect Size



Note: Figures plot the Type II error rate (β) as a function of the total matching error rate for a given hypothesized effect size, control mean, and correlated covariate. In each plot, Type II error rates are plotted for sample sizes that range from $N = 500$ to $N = 3{,}000$.

Figure 3: Percent of Exact Matching Errors Overturned



Note: Figures plot the share of errors under exact matching that are overturned when a probabilistic matching algorithm is employed. Each panel represents a different control mean and treatment effect combination.

Table 1: Performance metrics across matching schemes

	Exact Matching	Probabilistic Matching
False Negative Rate	14.0%	0.8%
False Positive Rate	0.0%	6.2%
$FNR + FPR$ Rate	14.0%	7.0%

Note: Average error rates from empirical matches of OJIN data.