Analyzing linked data

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This Version: October 27, 2019

Abstract

This paper compares different methods for estimating parametric models with linked data, i.e. when x and y are observed in distinct datasets with imperfect identifiers. This setup requires that the researcher must attempt to identify which observations in the x- and y-datafiles refer to the same individual, prior to performing inference about the joint or conditional distributions of x and y. At a minimum, random errors in the matching step introduce measurement error that must be accounted for in subsequent inference; however, additional concerns about sample selection arise when these errors are correlated with unobservables that affect x or y.

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1 Introduction

When analyzing multiple data sources with overlapping units, automated record linkage procedures offer the least cost solution for merging data. These methods allow the researcher to specify a set of matching variables that are recorded across all of the datasets, and a decision rule for linking record pairs, in order to obtain a matched dataset in a matter of minutes. When the files to be linked are large, the time saved relative to manual linking or automated linking with clerical review is immense.

In the social sciences, interest in automated record linkage methods emerged in response to the increasing availability of administrative datasets, including recently digitized historical complete count population censuses. Although these techniques originated in other fields – primarily statistics, computer science, operations research, and epidemiology – social scientists have developed their own linking methods in response to concerns about the accuracy and representativeness of data that are matched using imperfect identifiers.

This new research agenda is driven by economic historians and historical demographers, who use data with identifiers that are prone to typographical, duplication, enumeration, and digitization error. Additionally, the identifiers may be misreported – for example, ages may be rounded to integers ending with a 0 or 5 – or repeated within a sample, as might happen if multiple Rachel Anderson's were born in the same year. Historical record linkage procedures primarily differ according to how they address these issues of data quality.

Examples of this literature include recent papers by Abramitzky et al. (2019) and Bailey et al. (2017), who compare the performance of popular historical record linkage methods to datasets matched by hand-linking or to simulated "ground truth" datasets. Although they implement different methods, both papers document a tradeoff between the false positive rate and the (true) match rate across procedures, and seem to agree that using more conservative algorithms leads to more representative data.

Other contributions to this literature include papers by Abramitzky et al. (2018) and Enamorado et al. (2019), who demonstrate how to apply probabilistic record linkage methods from statistics to match historical and large-scale survey data. These methods offer an advantage over the deterministic methods studied by Abramitzky et al. (2019) and Bailey et al. (2017), in that they can quantify the uncertainty about the matched data. Furthermore, this extra information can be used to correct for bias introduced by false matches in the OLS estimator, using methods proposed by Scheuren and Winkler (1993) and Lahiri and Larsen (2005).

The ability to use probabilistic record linkage to correct for bias in the OLS estimator illustrates how the *outputs* of different matching procedures determine which estimation methods are available for subsequent analysis. Similarly, Anderson et al. (2019) develop methods for consistently estimating GMM models using linked data that include multiple matches per observation. Unfortunately, none of these estimation methods is acknowledged in the survey papers by Abramitzky et al. (2019) and Bailey et al. (2017); however, it seems natural that the choice of which matching procedure to use should be informed by which estimation methods are available.

The goal of this paper is to build a bridge between the matching and estimation steps in the analysis of linked data. I compare the performance a comparison of different methods that incorporate different types of information, as well as extend the methods from Anderson et al. (2019) to incorporate probabilities as may be outputted from a record linkage procedure.

By comparing the estimation methods, this gives suggestion to which record linkage procedure should be used (or, better yet, which outputs of the record linkage procedure are necessary for optimal estimation). The main result is that unless probabilities can be estimated accurately, knowledge about them should not be incorporated in the estimation step.

My preliminary results support the following suggestions for analyzing linked data: if you use deterministic matching, you should allow for multiple matches and use the estimator in Anderson et al. (2019). If you use probabilistic record linkage, you should choose the match with the highest probability of being correct if it exceeds a certain threshold; otherwise you should use multiple matches because the estimated probabilities can be noisy, and can result in large weights on observations with small $\pi_{i\ell}$. When it doubt, implement all methods and compare the results!

In order to illustrate the techniques studied in this paper, Section 2 introduces a numerical example that is used to demonstrate the matching and estimation techniques described in Sections 3 and 4. Section 5 provides details about the implementation of the methods and data generating processes. Section 6 contains the results, and Section 7 concludes.

2 Setup

In this section, I describe a simplified version of the estimation problem described in Anderson et al. (2019). Whereas Anderson et al. (2019) study how to incorporate multiple matches in a GMM framework, this paper focuses on estimating β in the linear regression model,

$$y_i = x_i'\beta + \varepsilon_i,\ \ E[\varepsilon|x_i] = 0,\ \ E[\epsilon_i^2] = \sigma^2 \tag{1}$$

where x_i and y_i are recorded in different datasets, and must be linked using auxiliary variables that are contained in both data sources.

Formally, the data consist of observations $\{x_i, w_i\}_{i=1}^{N_x}$ in the x-datafile, and observations $\{y_j, w_j\}_{j=1}^{N_y}$ in the y-datafile. I assume that $N_y \geq N_x$, and that every x_i has a unique match in the y-datafile that satisfies the relationship in (1), but the index j that corresponds with the match is unknown. Some y_j may not correspond to any observation in the x dataset, nor satisfy the relationship in (1) for some unobserved x_j. Hence, estimating the model in

(1) requires identifying which (x_i, y_j) pairs refer to the same individuals by comparing w_i and w_j and designating matches according to some matching procedure.

Example 1. To fix ideas, consider the work of Aizer et al. (2016), who seek to estimate the impact of providing cash transfers to single mothers on the life expectancy of their children. The x-datafile consists of mothers' welfare program applications, where x_i includes a binary variable equal to 1 if person i's mother received a cash transfer, and other demographic variables. The y-datafile is a universal database of death records, which includes y_j, person j's age at death for all deaths reported to the Social Security Administration after 1965. Both of the x- and y-datafiles also contain identifiers w_i and w_j, which include first name, middle initial, last name, day, month, and year of birth, so that individuals with common names are not identified uniquely.

For the purposes of this paper, a matching procedure is defined as a set of rules used to construct a (potentially multi-valued) linking function, $\varphi : \{1, \ldots, N_x\} \to \{1, \ldots, N_y\} \cup \varnothing$, where $\varphi(i) = j$ if the ith observation in the x-datafile is matched to the jth observation in the y-datafile, and $\varphi(i) = \varnothing$ if i is not assigned a match. If w_i and w_j identify individuals uniquely and without error, then setting $\varphi(i) = j$ if and only if $w_i = w_j$, and $\varphi(i) = \varnothing$ otherwise, will correctly identify all true matches contained in the data. In most applications, however, w_i and w_j cannot be used to unambiguously differentiate true matches, so that assigning φ may include linking false matches or excluding true matches. In this case, φ may be constructed using estimates of π_{ij}, which denotes the probability that an (i, j) pair refers to a match.

Example 1 (cont'd). Aizer et al. (2016) construct φ using a deterministic linking method that allows for errors in strings and dates of birth. To account for changes in spelling and typographical errors, they convert all names into sounds using a phonetic algorithm, and measure the similarity between two individual's phonetically-spelled names using a string distance metric called SPEDIS. They assign as matches all pairs of individuals whose birthdates fall within a predetermined range and whose SPEDIS score falls below a threshold. Notably, their procedure does not enforce unique matches, so that some individuals are matched to multiple death records, and φ is a correspondence.

Although I will discuss a few of the most popular methods used to construct φ in later sections, this is not the focus of this paper. Like Anderson et al. (2019), I take φ and the matched dataset it produces as given. The matched dataset can be written in the general form

$$\mathcal{D}_n \equiv \left(x_i, w_i, \{y_{i\ell}\}_{\ell=1}^{L_i}, \{\pi_{i\ell}\}_{\ell=1}^{L_i}\right)_{i=1}^{N} \tag{2}$$

where x_i is a vector of covariates for a single observation in the x-datafile, and $\{y_{i\ell}\}_{\ell=1}^{L_i}$ are the outcomes from the y-datafile to which it is linked based on the identifying variables w_i. The variables $\{\pi_{i\ell}\}_{\ell=1}^{L_i}$ correspond to the conditional probability that a particular $y_{i\ell}$ refers to the correct match, so that $\sum_{\ell=1}^{L_i} \pi_{i\ell} = 1$. If φ was constructed without estimating $\pi_{i\ell}$, as in a deterministic matching procedure, I assume that $\pi_{i\ell} = \frac{1}{L_i}$.

Additionally, I assume that (i) the true match y_i is included among the possible matches $\{y_{i\ell}\}_{\ell=1}^{L_i}$ for all i, and that (ii) the observed x_i and $\{y_{i\ell}\}_{\ell=1}^{L_i}$ are i.i.d. draws from their marginal distributions conditional on the identifying variables w_i. Assumption (i) is necessary for identification, and Assumption (ii) is a selection on observables assumption, which requires that all individuals with the same identifying information are equally likely to be included in $\mathcal{D}_n$. I defer to later sections the discussion about when these assumptions are likely to fail in practice.

3 Estimation methods for linked data

In this section, I review two estimation methods designed to handle matched data of the form (2).

Other methods exist, however they are ad hoc or are not easily adapted to the setup in Section 2. For example, Bleakley and Ferrie (2016) generated "composite match" equal to the average of the linked observations. Nix and Qian (2015) construct bounds on the parameter of interest using different configurations of matched data. Abramitzky et al. (2012) use traditional estimation methods using only individuals who are uniquely matched, and then reweight on observables (not sure what this means?). In statistics, authors have suggested using probabilistic record linkage and multiple imputation to correct for bias introduced by errors in the matching process Scheuren and Winkler (1993); Lahiri and Larsen (2005); Goldstein et al. (2012). Multiple imputation is not useful here, as we do not consider missing data. The Lahiri methods require $N_x = N_y$ and so we are left with two methods.

3.1 Anderson et al. (2019)

The goal of Anderson et al. (2019) is to estimate θ_0 that satisfies the model

$$E_0 \left[m \left(y_i, x_i; \theta_0 \right) \right] = 0 \tag{3}$$

where y_i and x_i are vectors or scalars of data for an individual i, the function $m(\cdot)$ is known, and the expectation is taken with respect to the joint distribution $f_0(y, x)$. The data consist of observations $\left(x_i, w_i, \{y_{i\ell}\}_{\ell=1}^{L_i} \right)_{i=1}^{N}$, where the x_i and $y_{i\ell}$ are recorded in distinct datasets and matched according to the identifier w_i. They assume $L_i > 1$ for some i, so that the identity of the outcome that generates the relationship in (3) is unknown.

Under assumptions (i) and (ii) in Section 2, (3) can be rewritten,

$$E_0[m(y_i, x_i; \theta)] = E\left[\sum_{\ell=1}^{L_i} m(y_{i\ell}, x_i; \theta) \right] - E\left[(L_i - 1) g(w_i, L_i; x_i; \theta) \right]$$

$$g(w_i, L_i, x_i; \theta) = E\left[m(y_i, x_i; \theta) \right| w_i, L_i]$$

so if g is known or can be estimated consistently, a sample version of (3) can be constructed as follows,

$$\overline{m}_n(\theta, \hat{g}) = \frac{1}{N}\sum_{i=1}^{N}\sum_{\ell=1}^{L_i} m(y_{i\ell}, x_i; \theta) - \frac{1}{N}\sum_{i=1}^{N}(L_i - 1)\hat{g}(w_i, L_i, x_i; \theta) \tag{4}$$

which is in general a two-step procedure, where $\hat{g}$ is estimated using nonparametric methods such as k-Nearest Neighbors or local polynomial regression in the first step. The GMM estimator applied to (4) is consistent and asymptotically normal under the regularity conditions described in Anderson et al. (2019).

For the linear regression model in (1), the AHL estimator can be computed by applying OLS to the transformed regression model,

$$\sum_{\ell=1}^{L_i} y_{i\ell} - (L_i - 1)\hat{g}(w_i, L_i) = x_i'\beta + u_i \tag{5}$$

where $\hat{g}(w_i, L_i)$ is a (possibly nonparametric) estimator of $E[y_{i\ell}|w_i, L_i]$, $u_i = \varepsilon_i + \sum_{\ell=1}^{L_i} \nu_{i\ell}$, and $\nu_{i\ell} = y_{i\ell} - \hat{g}(w_i, L_i)$. If, additionally, $E[\varepsilon_i^2|x_i, w_i, L_i] = \sigma_\varepsilon^2$ and $E[\nu_{i\ell}^2|x_i, w_i, L_i] = \sigma_\nu^2$ then the efficient estimator is weighted least squares,

$$\hat{\beta}^{WLS} = \left(\sum_{i=1}^{N}\frac{x_i x_i'}{\sigma(X_i)}\right)^{-1}\left(\sum_{i=1}^{N}\frac{x_i}{\sigma(X_i)}\left(\sum_{\ell=1}^{L_i} y_{i\ell} - (L_i - 1)g(w_i, L_i)\right)\right) \tag{6}$$

where $\sigma(X_i) = \sigma_\varepsilon^2 + (L_i - 1)\sigma_\nu^2$.

Unfortunately, the performance of the AHL estimator depends on the accuracy of $\hat{g}(w_i, L_i)$, which depends on a potentially high-dimensional vector w_i containing a combination of string and numeric variables. One way to circumvent this issue that I explore in this paper is based on noting that if $E[m(y_i, x_i; \theta)|L_i = \ell] = E[m(y_i, x_i; \theta)]$, then

$$E[m(y_i, x_i; \theta)] = E\left[\sum_{\ell=1}^{L_i} m(y_{i\ell}, x_i; \theta)\middle| L_i = 2\right] - E\left[\sum_{\ell=1}^{L_i} m(y_{i\ell}, x_i; \theta)\middle| L_i = 3\right] \tag{7}$$

and

$$E[m(y_i, x_i; \theta)] = E[m(y_{i\ell}, x_i; \theta)|L_i = 1] \tag{8}$$

which suggests we can use (7) and (8) as moment conditions. Applying this to the model of interest in (1), this version of the AHL estimator amounts to using the following moments in a standard GMM model:

$$\begin{bmatrix} \frac{2}{N_{L_2}} \sum_{i=1}^{N_{L_2}} (y_{i1} + y_{i2} - x_i'\beta)x_i - \frac{1}{N_{L_3}} \sum_{i=1}^{N_{L_3}} (y_{i1} + y_{i2} + y_{i3} - x_i'\beta)x_i \\ \frac{1}{N_{L_1}} \sum_{i=1}^{N_{L_1}} (y_i - x_i'\beta)x_i \end{bmatrix} = 0 \tag{9}$$

where N_{L_ℓ} is the number of observations matched to ℓ observations.

The precision of the first moment is limited by the number of observations with two and three matches, respectively.

3.2 Scheuren and Winkler (1993)

Scheuren and Winkler (1993) develop methods for linked data where each x_i observation is linked to a single outcome, so that $L_i = 1$ for all i. They label these observations (x_i, z_i) for $i = 1, \ldots, N$, where z_i may or may not correspond to the true y_i. Specifically,

$$z_i = \begin{cases} y_i & \text{with probability } q_{ii} \\ y_j & \text{with probability } q_{ij} \text{ for } j \neq i,\ j = 1, \ldots, N_y \end{cases}$$

and $\sum_{j=1}^{N_y} q_{ij} = 1,\ i = 1, \ldots, N$, where N_y is the size of the y-datafile and N is the size of the matched dataset. Estimating (1) using z_i as the dependent variable yields the naive least squares estimator,

$$\hat{\beta}_N = (X'X)^{-1}X'z \tag{10}$$

which is biased, because $E[z_i] = E\left[q_{ii}y_i + \sum_{j\neq i} q_{ij}y_j\right] \neq E[y_i]$ if $q_{ii} \neq 1$ for some i. Denoting $q_i = (q_{i1}, \ldots, q_{iN_y})'$, we can write the bias of $\hat{\beta}_N$ conditional on the observed values of y as,

$$\text{bias}(\hat{\beta}_N|y) = E[(\hat{\beta}_N - \beta)|y] = (X'X)^{-1}X'B \tag{11}$$

where $B = (B_1, \ldots, B_n)'$ and $B_i = (q_{ii} - 1)y_i + \sum_{j\neq i} q_{ij}y_j = q_i'y - y_i$, which is the difference between a weighted average of responses from all observations and the true response y_i.

Observing (11), Scheuren and Winkler (1993) proposed estimating $\hat{B}$ to correct for the bias of $\hat{\beta}_N$. To reduce the computational burden of constructing $\hat{B}$, they suggest using the first and second highest elements of the vector q_{ij_1} and q_{ij_2} and their corresponding values y_{ij_1} and y_{ij_2} to compute $\hat{B}_i^{TR} = (q_{ij_1} - 1)y_{ij_1} + q_{ij_2}y_{ij_2}$, and then calculating

$$\hat{\beta}_{SW} = \hat{\beta}_N - (X'X)^{-1}X'\hat{B}^{TR} \tag{12}$$

Although $\hat{B}^{TR}$ can incorporate an arbitrary number of elements of q_i, Scheuren and Winkler (1993) note that if the probability is high that the best candidate link is the true link, then the truncation with two links results in a very small bias.

The downside of the Scheuren and Winkler (1993) method is that it requires knowledge of q_{ij}, as well as the second most likely value of y for each observation of x. This information is not typically available when using deterministic matching procedures such as those developed by Abramitzky et al. (2012). However, even if estimates of q_{ij} are available (as may be the case when using probabilistic record linkage), the bias may persist if the estimates $\widehat{q_{ij}}$ are correlated with x or y, as this would introduce endogeneity.

The endogeneity problem arises because $\widehat{q_{ij}}$ are typically calculated by plugging in estimates of the parameters $\psi \equiv \{p_M, P(\boldsymbol{\gamma}_{\mathbf{ij}}|M),\ P(\boldsymbol{\gamma}_{\mathbf{ij}}|U)\}$ into equation (26). Thus, $\widehat{q_{ij}}$ will be correlated with x or y if errors in the matching variables, which determine the distribution of $\hat{\psi}$, are correlated with x or y. This is likely to be a problem in economics applications, such as in Nix and Qian (2015), where y measures whether a person's recorded ethnicity changes between Census years, but changes in names (the matching variables) are also strongly correlated with y.

One possible solution to the challenges described above is to use the estimator from Anderson et al. (2019), which is unbiased if the errors in estimating the conditional expectation of y be independent of the x_i, which holds if x_i and y_i are random samples conditional on the matching variables[1]. Specifically, for the model in (1),

Like the Scheuren and Winkler (1993) estimator, the AHL estimator requires that the true match for x_i is included among the matches $\{y_{i\ell}\}_{\ell=1}^{L_i}$ for all ℓ. The simulations in Section 7 suggest that this is a reasonable assumption when multiple matches are allowed. When $L_i = 1$ for all i, the AHL estimator reduces to the OLS estimator $\hat{\beta}_N$, so it is only meaningful to compute for linked datasets with some $L_i > 1$.

The AHL estimator also requires that x and y are random samples conditional on the matching variables. Practically speaking, this means thats all individuals with the same identifying information (such as name, age, Census block) have equal probability of appearing in the sample. This assumption would be violated if, for example, higher income individuals have a greater probability of appearing in the sample (unless individuals are matched by income); but the OLS estimator using perfectly linked data would also be biased because of unobserved sample selection.

Other approaches for regression analysis using linked data have been proposed by Lahiri and Larsen (2005) and Neter et al. (1965), however neither is appropriate for the setup de-

[1] Technically, the result in Anderson et al. (2019) is proven for GMM, so the necessary condition is that errors in estimating a conditional moment condition are independent of x_i

scribed in Section 2. The methods in Lahiri and Larsen (2005) assume that each observation appearing y-datafile is generated according to the DGP in (1), and that its corresponding value of x appears in the x-datafile. This is a problem both conceptually and for implementation when entries in the x-datafile represent a strict subset of observations in the y-datafile. The methods in Neter et al. (1965) are simplified versions of those in Scheuren and Winkler (1993), and hence face the same implementation issues described above.

By contrast, the AHL estimator is agnostic about whether the incorrectly linked y_j are generated by (1) or by some other data generating process. The AHL estimator has additional robustness properties due to the fact that it weights multiple matches equally and does not require estimating match probabilities, which are explored in the following section.

4 Incorporating probabilities

Consider the problem of estimating the mean of a random variable $X \sim F_X(\mu; \sigma^2)$ using two observations X_1 and X_2. With probability π, X_1 is drawn from the true distribution F_X and X_2 is noise drawn from the distribution $F_Y(\kappa, \omega^2)$. With probability $1-\pi$, X_2 is drawn from the correct distribution and X_1 is noise. Under this specification, exactly one of X_1 or X_2 is drawn from the distribution of interest at all times.

Observe that if π is known, we can construct an unbiased estimator using only X_1,

$$\hat{\mu}_1 = \frac{X_1}{\pi} - \frac{1-\pi}{\pi}\kappa \tag{13}$$

and, similarly, we can construct an unbiased estimator using only X_2,

$$\hat{\mu_2} = \frac{X_2}{1-\pi} - \frac{\pi}{1-\pi}\kappa \tag{14}$$

Any unbiased linear estimator of μ that uses X_1 and X_2 can be written as a combination of $\hat{\mu}_1$

and $\hat{\mu}_2{}^2$, so finding the minimum variance, unbiased linear estimator $\hat{\mu}$ requires minimizing

$$\min_d \ \mathrm{Var}\left(d\hat{\mu}_1 + (1-d)\hat{\mu}_2\right)$$

which is solved by

$$d^* = \frac{\mathrm{Var}\left(\hat{\mu}_2\right) - \mathrm{Cov}(\hat{\mu}_1, \hat{\mu}_2)}{\mathrm{Var}\left(\hat{\mu}_1\right) + \mathrm{Var}\left(\hat{\mu}_2\right) - 2\mathrm{Cov}(\hat{\mu}_1, \hat{\mu}_2)} \tag{15}$$

where[3]

$$\mathrm{Var}\left(\hat{\mu}_1\right) = \frac{\mathrm{Var}(X_1)}{\pi^2} = \frac{1}{\pi^2}\left(\pi\sigma^2 + (1-\pi)\omega^2 + \pi(1-\pi)(\mu-\kappa)^2\right) \tag{16}$$

$$\mathrm{Var}\left(\hat{\mu}_2\right) = \frac{\mathrm{Var}\left(X_2\right)}{(1-\pi)^2} = \frac{1}{(1-\pi)^2}\left((1-\pi)\sigma^2 + \pi\omega^2 + \pi(1-\pi)(\mu-\kappa)^2\right) \tag{17}$$

$$\mathrm{Cov}(\hat{\mu}_1, \hat{\mu}_2) = \frac{\mathrm{Cov}(X_1, X_2)}{\pi(1-\pi)} = \frac{1}{\pi(1-\pi)}\left((1-\pi^2-(1-\pi)^2)\mu\kappa - \pi(1-\pi)(\mu^2+\kappa^2)\right) \tag{18}$$

Thus, the minimum variance unbiased estimator is

$$\hat{\mu}^* = d^*\hat{\mu}_1 + (1-d^*)\hat{\mu}_2 \tag{19}$$

where d^* is defined as in (15). Notably, d^* is strictly increasing in π, but at a rate that depends on σ^2, ω^2, μ, and κ, as illustrated in Figure 1.

Figure 1 plots the optimal d^* for $\pi \in [0, 0.5]$, since the solution is symmetric in π. When $\pi = 0.5$, $\mathrm{Var}\left(\mu_1\right) = \mathrm{Var}\left(\mu_2\right)$ so that $d^* = 0.5$, regardless of the other parameter values. When the variance of both the correct and incorrect distributions are the same (i.e.,

[2] see Lemma 1 in the Appendix

[3] $\mathrm{Var}\left(X_1\right)$ and $\mathrm{Var}\left(X_2\right)$ are calculated using the law of total variance, using the random variable $D = 1$ if X_1 is drawn from the correct distribution (and X_2 is drawn from the incorrect distribution), and $D = 0$ otherwise:

$$\begin{aligned}\mathrm{Var}\left(X_1\right) &= E[\mathrm{Var}\left(X_1|D\right)] + \mathrm{Var}\left(E[X_1|D]\right)\\ &= P(D=1)\sigma^2 + P(D=0)\omega^2 + \mathrm{Var}\left(\mu D + \kappa(1-D)\right)\\ &= \pi\sigma^2 + (1-\pi)\omega^2 + \pi(1-\pi)(\mu-\kappa)^2\end{aligned}$$

The same trick can be applied to calculate $\mathrm{Var}\left(X_2\right)$

$\sigma^2 = \omega^2$), then $\text{Var}(X_1) = \text{Var}(X_2)$, and differences in d^* reflect only changes in π. When $\sigma^2 \neq \omega^2$, the optimal d^* puts additional weight (relative to the equal variance case) on the estimator based on the X_i that is more likely to come from the lower variance distribution. The curve with $\sigma^2 = 1$ and $\omega^2 = 10$ is the extreme version of this scenario, and represents what may happen if κ is estimated imprecisely. The resulting d^* assigns very low weight to the observation that is more likely drawn from the incorrect distribution.

More generally, the estimator $\hat{\mu}^*$ can be computed for sample of observations $(X_{i1}, X_{i2})_{i=1}^N$, where X_{i1} is drawn from F_X with probability π_i, and X_{i2} is drawn from F_X with probability $1 - \pi_i$. In this case, d^* is calculated according to (15) using,

$$\hat{\mu}_1 = \sum_{i=1}^N \frac{X_{i1}}{\pi_i} - \frac{1-\pi_i}{\pi_i}\kappa \qquad \text{Var}(\hat{\mu}_1) = \frac{1}{N^2}\sum_{i=1}^N \frac{g(\pi_i;\theta)}{\pi_i^2}$$

$$\hat{\mu}_2 = \sum_{i=1}^N \frac{X_{i2}}{1-\pi_i} - \frac{\pi_i}{1-\pi_i}\kappa \qquad \text{Var}(\hat{\mu}_2) = \frac{1}{N^2}\sum_{i=1}^N \frac{g(1-\pi_i;\theta)}{(1-\pi_i)^2}$$

$$\text{Cov}(\hat{\mu}_1, \hat{\mu}_2) = \frac{1}{N^2}\sum_{i=1}^N \frac{\text{Cov}(X_{1i}, X_{2i})}{\pi_i(1-\pi_i)}$$

where $g(x;\theta) = x\sigma^2 + (1-x)\omega^2 + x(1-x)(\mu-\kappa)^2$ is the variance of $X_{i\ell}$, for $\ell \in \{1,2\}$, that has probability x of being drawn from the correct distribution.

4.1 Errors in $\hat{\pi}$

The construction of $\hat{\mu}^*$ was based on the assumption that π was known; this section studies the performance of $\hat{\mu}^*$ when only an estimate $\hat{\pi}$ is available.

Suppose that we have an i.i.d. sample of observations $(X_{i1}, X_{i2})_{i=1}^N$, where X_{i1} is drawn from F_X with probability π, and X_{i2} is drawn from F_X with probability $1-\pi$. In the context of record linkage, X_{i1} and X_{i2} may refer to two possible matches for an observation, and π is the probability that X_{i1} is the true match. The estimated probabilities $\hat{\pi}$ may be obtained from a probabilistic record linkage procedure or reflect prior knowledge about the matching application[4].

As observed in Anderson et al. (2019), when π is unknown, it is possible to construct an unbiased linear estimator of $\hat{\mu}$ by weighting all observations equally,

$$\hat{\mu}^{AHL} = \frac{1}{N}\sum_{i=1}^{N} X_{i1} + \frac{1}{N}\sum_{i=1}^{N} X_{i2} - \kappa \tag{20}$$

The variance of this estimator is

$$\mathrm{Var}\left(\hat{\mu}^{AHL}\right) = \frac{\mathrm{Var}\left(X_{1i} + X_{2i}\right)}{N} \tag{21}$$

Note that $\mathrm{Var}\left(\hat{\mu}^{AHL}\right)$ can be achieved by setting $d^* = \pi$, so that $\mathrm{Var}\left(\hat{\mu}^{AHL}\right) \geq \mathrm{Var}\left(\hat{\mu}^*\right)$ if π is known, with equality holding if and only if $\pi = 0.5$.

Since $\hat{\mu}^{AHL}$ is always available, it is therefore interesting to study the tradeoff in efficiency when choosing whether to incorporate possibly incorrect beliefs about π. Unless $\hat{\pi} = 0.5$, if $\hat{\pi} \neq \pi$, then the estimator $\hat{\mu}^*$ that incorporates the incorrect beliefs $\hat{\pi}$ is biased. For example, if $(\mu, \sigma^2, \kappa, \omega^2) = (0, 1, 1, 2)$ and $\pi = 0.6$, but the econometrician believes $\hat{\pi} = 0.9$, then

$$\hat{\mu}_1 = \frac{1}{N}\sum_{i=1}^{N}\frac{X_{i1}}{\hat{\pi}} - \frac{1-\hat{\pi}}{\hat{\pi}} = \frac{1}{N}\sum_{i=1}^{N}\frac{10}{9}X_1 - \frac{1}{9}$$
$$\hat{\mu}_2 = \frac{1}{N}\sum_{i=1}^{N}\frac{X_2}{1-\hat{\pi}} - \frac{\hat{\pi}}{1-\hat{\pi}} = \frac{1}{N}\sum_{i=1}^{N} 10X_2 - 9$$

each of which are biased, because $E[\hat{\mu}_1] = \frac{1}{3}$ and $E[\hat{\mu}_2] = -3$. Similarly, using $\hat{\pi}$ instead of π in (16)-(18) to calculate $\mathrm{Var}\left(\hat{\mu}_1\right)$, $\mathrm{Var}\left(\hat{\mu}_2\right)$, and $\mathrm{Cov}(\hat{\mu}_1, \hat{\mu}_2)$ results in $d^* = 0.987$, and $\mathrm{Bias}(\hat{\mu}^*) = 0.292$ and $\mathrm{Var}\left(\hat{\mu}^*\right) = \frac{1.94}{N}$.

[4]For example, $\hat{\pi}$ may reflect the econometrician's belief that "Alicia" is more likely than "Alex" to refer to the true match of an individual named "Ali".

By comparison, Bias($\hat{\mu}^{AHL}$) $= 0$ and Var $\left(\hat{\mu}^{AHL}\right) = \frac{3}{N}$, so we can solve for N such that $MSE_n(\hat{\mu}^{AHL}) < MSE_n(\hat{\mu}^*)$ for all $n \geq N$:

$$0.292^2 + \frac{1.94}{N} = \frac{3}{N} \implies N = 12.43$$

This example suggests that for fixed $\theta = (\mu, \sigma^2, \kappa, \omega^2)$ and N, we can compare the ratio of $MSE_n(\hat{\mu}^*; \theta)/MSE_n(\hat{\mu}^{AHL}; \theta)$ for different values of Bias($\hat{\pi}$). Alternatively, for a fixed value of Bias($\hat{\pi}$), we can calculate the minimum sample size N such that it is more efficient to use $\hat{\mu}^{AHL}$.

Before performing this exercise, I plot the bias and variance of $\hat{\mu}^*$ as a function of the mis-specified beliefs $\hat{\pi}$ in Figures 2 and 3. The bias is quadratic in $|\hat{\pi} - \pi|$, with zero bias at $\hat{\pi} = \pi$ and $\hat{\pi} = 0.5$. The variance of $\hat{\mu}^*$ is not minimized at $\hat{\pi} = \pi$, but at some value determined by σ^2, ω^2, $(\mu - \kappa)^2$, and Bias($\hat{\pi}$). The variance term is less interesting, because it is dominated by the bias as $N \to \infty$.

Tables 1-3 compare the ratio of the $MSE_N(\hat{\mu}^{AHL}; \theta)/MSE_N(\hat{\mu}^*; \theta)$, where $\hat{\mu^*}$ is calculated for different values of $\hat{\pi}$. Each table displays this ratio for different values of N and $\theta = (\mu, \sigma^2, \kappa, \omega^2)$. One combination is referred to in the text for values of $N = 10, 100$, and 1,000, but more parameter combinations are included in the Appendix.

For $N = 1,000$, $\hat{\mu}^*$ only performs better when $\hat{\pi} = \pi$, and the benefits decrease as the true π approaches 0.5. For $N = 100$, the ratio is close to 1 for Bias($\hat{\pi}$) $= 0.1$, so that the efficiency gain from incorporating knowledge about π is reduced for $N > 100$. This suggests that for small samples, you may want to incorporate knowledge about probabilities; but for samples of a large size, it's best to ignore them and weight multiple matches equally.

4.2 Applying argument to OLS

Suppose we have two matches $\{y_{i1}, y_{i2}\}_{i=1}^{N}$ for each observation. We get the same conditions for unbiasedness of the OLS estimator if we consider using a linear combination of the y's, as in the model:

$$a_1 y_{i1} + a_2 y_{i2} - \kappa = x_i'\beta + \varepsilon_i \tag{22}$$

Then the OLS estimator is

$$\hat{\beta} = \left(\frac{1}{N}\sum_{i=1}^{N} x_i x_i'\right)^{-1} \left(\frac{1}{N}\sum_{i=1}^{N} x_i'(a_1 y_{i1} + a_2 y_{i2} - \kappa)\right)$$

and

$$\begin{aligned} E\left[\hat{\beta}\right] &= E[x_i x_i']^{-1} E[x_i'(a_1 y_{i1} + a_2 y_{i2} - \kappa] \\ &= \beta(a_1\pi + a_2(1-\pi)) + E[x_i x_i']^{-1} E[x_i](a_2\pi + (1-\pi)a_1 - a_3)\kappa \end{aligned}$$

Unbiasedness requires the same conditions on a_1, a_2, and a_3 as derived in Lemma 1, i.e.

$$\begin{aligned} a_2(a_1) &= \frac{1-\pi a_1}{1-\pi} \\ a_3(a_1) &= \frac{\pi}{1-\pi} + \frac{a_1 - 2\pi a_1}{1-\pi} \end{aligned}$$

which means that any unbiased linear estimator $\hat{\beta}$ can be written as a linear combination of unbiased estimators that use only y_{i1} or y_{i2},

$$\begin{aligned} \hat{\beta}_1 &= \frac{1}{N}\sum_{i=1}^{N} \frac{x_i y_{i1}}{\pi} - \frac{1-\pi}{\pi}\kappa \\ \hat{\beta}_2 &= \frac{1}{N}\sum_{i=1}^{N} \frac{x_i y_{i2}}{1-\pi} - \frac{\pi}{1-\pi}\kappa \end{aligned}$$

and so the minimum variance estimator is $\hat{\beta}^* = d^* \hat{\beta}_1 + (1 - d^*)\hat{\beta}_2$, where

$$d^* = \frac{\text{Var}\left(\hat{\beta}_2\right) - \text{Cov}\left(\hat{\beta}_1, \hat{\beta}_2\right)}{\text{Var}\left(\hat{\beta}_1\right) + \text{Var}\left(\hat{\beta}_2\right) - 2\text{Cov}\left(\hat{\beta}_1, \hat{\beta}_2\right)} \tag{23}$$

and we can repeat the exercise in the previous sections, comparing variance and bias for misspecified beliefs $\hat{\pi}$ and different parameter combinations. The choice of the weights d^* that give the optimal $\hat{\beta}^*$ is now complicated by the fact that it depends on the second moments of X_i, so this is best performed by simulation.

5 Numerical Example

Now I study how these methods work in practice. This section introduces a numerical example, that illustrates what I do in the Monte Carlo below.

The purpose of this section is to introduce a numerical example that will be used to illustrate the different matching techniques discussed in this paper. The benefits of using synthetic data are that I can control the degree of similarity among identifying variables, and overlap between datasets, all while knowing the true match status of each (x_i, y_j) record pair. As a result, I can compare how sensitive my results are to data quality, and compare how the various matching and estimation procedures perform relative to the correctly specified model applied to a dataset containing only correct links.

I begin by constructing a "ground truth" dataset with 1000 observations of $(x_{1i}, x_{2i}, y_i, w_i)$, where x_{1i} and x_{2i} are mutually independent, $x_{1i} \overset{i.i.d}{\sim} \text{Bernoulli}(0.5)$, and $x_{2i} \overset{i.i.d}{\sim} \mathcal{N}(0, 2)$. The y_i values are generated according to the linear relationship,

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \varepsilon_i, \quad \varepsilon_i \mid x_{1i}, x_{2i} \overset{i.i.d}{\sim} \mathcal{N}(0, \sigma^2) \tag{24}$$

with $(\beta_0, \beta_1, \beta_2, \sigma^2) = (2, 0.5, 1, 2)$, so that estimating the correctly specified linear regression model yields an R^2 value of approximately 0.50. Each observation is assigned a vector of identifying variables, w_i, which includes a first and last name drawn at random from a list of first and last names[5], and a random birthday between January 1, 1900, and December 31, 1925. The resulting dataset looks like the observations in the top panel of Figure 4.

Next, I split the ground truth dataset into the x- and y-datafile, which contain the (x_1, x_2, w) and (y, w) values respectively. To construct the x-datafile, I select 500 observations at random from the ground truth dataset, and introduce random errors in their corresponding identifiers. To make the synthetic data resemble a real application, I set the probabilities of introducing transcription errors equal to those reported for the 1940 Census data in Abramitzky et al. (2019). These errors include deleting characters (e.g., "Anderson" becomes "Andersn"), exchanging vowels (e.g., "Rachel" becomes "Rachal"), and swapping English phonetic equivalents (e.g. "Ellie" becomes "Elie"). I also add normally distributed errors to the birth day, month, and year. The probabilities of introducing an error are set to match the transcription error rates reported in the 1940 Census by Abramitzky et al. (2019); for example, 7% of observations have misreported first names and 17% of observations have misreported last names. The bottom panel of Figure 4 illustrates how the x- and y-datafiles are split visually.

The y-datafile includes all 1,000 values from the ground truth data, and does not contain any errors in the identifiers w. As a result, it will be likely that some x will be matched to multiple y. In later sections, I will consider versions of this synthetic dataset, where errors in w are correlated with x_1 or y.

[5] The first and last name lists contain 41 and 24 names, respectively, and can be found in the replication files. Note that the number of possible names is smaller than the number of observations to ensure that there are multiple observations with the same name.

6 Record Linkage Methods

Recall that the data consist of an x-datafile, denoted $X \equiv \{(x_i, w_i) : i = 1, \ldots, N_x\}$, and a y-datafile, denoted $Y \equiv \{(y_j, w_j) : j = 1, \ldots, N_y\}$, and the goal of record linkage is to use w_i and w_j to determine which $i \in \{1, \ldots, N_x\}$ and $j \in \{1, \ldots, N_y\}$ refer to the same individual.

For the purposes of this paper, I define a record linkage procedure as a set of decisions about (i) selecting and standardizing the identifying variables in w_i and w_j, (ii) choosing which (i, j) pairs to consider as potential matches, (iii) defining which patterns of (w_i, w_j) constitute (partial) agreements, and (iv) designating (i, j) pairs as matches.[6]

Step (i) addresses the fact that differences may arise in w_i and w_j because of transcription error or misreporting, even when observations i and j refer to the same individual. In practice, this step consists of removing spaces and non-alphabetic characters from string variables and processing names with phonetic algorithms to account for potential misspellings; common nicknames may also be replaced with full names.

Step (ii) reduces the computational burden of a matching procedure when $N_x \times N_y$ is large by partitioning $X \times Y$ into "blocks." Only records within the same block are attempted to be matched, while records in different blocks are assumed to be non-matches. Blocking variables should be recorded with minimal error, otherwise blocking may adversely affect the Type II error rate.

Step (iii) defines a metric for quantifying the similarity between non-numeric variables, such as Jaro-Winkler distances for strings. For more details, see Abramitzky et al. (2018).

Finally, Step (iv) is where record linkage procedures differ in the most meaningful ways; hence, this step will be the focus of my analysis. Consider the following (deterministic)

[6] By contrast, Bailey et al. (2017) categorize record linkage procedures according to the set of assumptions that motivate their use.

record linkage procedure as an example:

(i) Use a phonetic algorithm to standardize the first and last names in both datasets;

(ii) Consider as potential matches all (i, j) pairs whose phonetically standardized names begin with the same letter, and whose birth years are within ± 2 years;

(iii) Measure the distance between any two names using Jaro-Winkler string distance, and the distance between any two birth dates as a difference in months;

(iv) Designate as matches all (i, j) pairs with Jaro-Winkler scores exceeding a pre-determined cut-off; and, if a record i has multiple possible matches that exceed the cut-off, then choose the corresponding j with the highest score (or pick one match at random if there is a tie).

Another record linkage procedure could be defined using the same steps (i)-(iii), but replacing (iv) with a probabilistic matching rule that does not enforce one-to-one matching:

(iv*) Use the Expectation-Maximization algorithm to compute "match weights" for each (i, j) pair; then, designate as matches all pairs with match weights exceeding a threshold that is set to reflect specific tolerances for Type I and Type II error.

Except in rare cases, the estimated matching functions obtained by switching (iv) and (iv*) will differ, if only because the former method matches each x with at most one y, the latter potentially matches the same x with multiple y. This example also illustrates the difference between deterministic and probabilistic record linkage methods: while (iv) uses pre-determined rules to designate pairs as matches, (iv*) uses statistical theory to inform the selection of the decision rule. Probabilistic record linkage also involves the estimation of match weights, which can be incorporated in subsequent estimation steps.

Below I will discuss two record linkage methods – one deterministic and one probabilistic – that I will use in my analysis. Each method will be implemented twice: first, requiring unique matches, and then allowing for multiple matches. While these methods are by no means exhaustive, they are intended to be representative of the most commonly used methods in economics. For a detailed survey of record linkage techniques, please refer to books by Harron et al. (2015); Christen (2012) or Herzog et al. (2007), or any of the references in this paper.

6.1 Deterministic

The deterministic matching algorithm described herein is based upon methods developed by Abramitzky et al. (2012). It consists of the following steps.

1. Clean names in the x- and y- datafiles to remove any non-alphabetic characters and account for common mis-spellings and nicknames (e.g., so that Ben and Benjamin would be considered the same name).

2. Restrict the sample to people in the x-datafile with unique first name, last name, and birth year combinations

3. For each record in the x-datafile, look for records in the y-datafile that match on first name, last name, place of birth, and exact birth year. At this point there are three possibilities

   (a) If there is a *unique* match, this pair of observations is considered a match.

   (b) If there are multiple potential matches in the y-datafile with the same year of birth, the observation is discarded.

   (c) If there are no matches by exact year of birth, the algorithm searches for matches within $\pm$ 1 year of reported birth year, and if this is unsuccessful, it looks for matches within $\pm$ 2 years. In each of these steps, only unique matches are accepted. If none of these attempts produces a unique match, the observation is discarded.

4. Repeat Step 3 for each record in the y-datafile, searching for matches in the x-datafile; then designate as matches all record pairs in the intersection of the two matched samples.

An interesting quirk of this algorithm is that an individual with multiple matches is dropped from the sample only if those matches occur before a unique match is found in Step 3. That is, a person with a unique, same-year match, and multiple matches with birth years within one year, will not be dropped from the sample. If the same-year match were not included in the dataset, then that same individual would be dropped. This has significant implications for bootstrapping standard errors; notably, the nonparametric bootstrap will fail.

Note that this quirk only occurs when the algorithm enforces unique matches. When allowing for multiple matches, I designate as a match any pair that satisfies any of the categories in Step 3.

6.2 Probabilistic Record Linkage

The probabilistic record linkage technique implemented in this paper is based on the canonical model by Fellegi and Sunter (1969), which views record linkage as a classification problem, where every record pair belongs either to the set of *matches* (M) or *non-matches* (U):

$$M = \{(i, j) \in X \times Y : j \in \varphi(i)\}$$

$$U = \{(i, j) \in X \times Y : j \notin \varphi(i)\}$$

To determine whether a record pair (i, j) belongs to M or U, the pair is evaluated according to K different comparison criteria. These comparisons are represented in a *comparison vector*,

$$\boldsymbol{\gamma}_{\mathbf{ij}} = (\gamma_{ij}^{1}, \ldots, \gamma_{ij}^{k}, \ldots, \gamma_{ij}^{K})$$

where each comparison field γ_{ij}^{k} may be binary-valued, as in "i and j have the same birthday" and "i and j have the same last name," or use ordinal values to indicate partial agreement between strings.

The probability of observing a particular configuration of $\boldsymbol{\gamma}_{\mathbf{ij}}$ can be modeled as arising from the mixture distribution:

$$P(\boldsymbol{\gamma}_{\mathbf{ij}}) = P(\boldsymbol{\gamma}_{\mathbf{ij}}|M)p_M + P(\boldsymbol{\gamma}_{\mathbf{ij}}|U)p_U \tag{25}$$

where $P(\boldsymbol{\gamma}_{\mathbf{ij}}|M)$ and $P(\boldsymbol{\gamma}_{\mathbf{ij}}|U)$ are the probabilities of observing the pattern $\boldsymbol{\gamma}_{\mathbf{ij}}$ conditional on the record pair (i, j) belonging to M or U, respectively. The proportions p_M and $p_U = 1 - p_M$ are the marginal probabilities of observing a matched or unmatched pair. Applying Bayes' Rule, we obtain the probability of $(i, j) \in M$ conditional on observing $\boldsymbol{\gamma}_{\mathbf{ij}}$,

$$P(M|\boldsymbol{\gamma}_{\mathbf{ij}}) = \frac{p_M P(\boldsymbol{\gamma}_{\mathbf{ij}}|M)}{P(\boldsymbol{\gamma}_{\mathbf{ij}})} \tag{26}$$

Thus, if we can estimate p_M, $P(\boldsymbol{\gamma}_{\mathbf{ij}}|M)$ and $P(\boldsymbol{\gamma}_{\mathbf{ij}}|U)$, then we can estimate the probability that any two records refer to the same entity using (26). These probabilities can then be used to designate pairs as matches, or to estimate the false positive rate associated with a particular match configuration using the formulas in Fellegi and Sunter (1969).

One difficulty arises from the fact that there are at least $2^K - 1$ possible configurations of $\boldsymbol{\gamma}_{\mathbf{ij}}$[7]. While in principle we could model $P(\boldsymbol{\gamma}_{\mathbf{ij}}|M)$ and $P(\boldsymbol{\gamma}_{\mathbf{ij}}|U)$ as

$$(\gamma_{ij}^1, \ldots, \gamma_{ij}^K) \mid M \sim \text{Dirichlet}(\boldsymbol{\delta}_{\mathbf{M}})$$
$$(\gamma_{ij}^1, \ldots, \gamma_{ij}^K) \mid U \sim \text{Dirichlet}(\boldsymbol{\delta}_{\mathbf{U}})$$

but the parameters $\boldsymbol{\delta}_{\mathbf{M}}$ and $\boldsymbol{\delta}_{\mathbf{U}}$ may be high-dimensional. However, if the comparison fields γ_{ij}^k are independent across k conditional on match status, then the number of parameters used to describe each mixture class can be reduced to K by factoring:

$$P(\gamma_{ij}|C) = \prod_{k=1}^{K} P(\gamma_{ij}^k|C)^{\gamma_{ij}^k}(1 - Pr(\gamma_{ij}^k|C))^{1-\gamma_{ij}^k} \qquad C \in \{M, U\} \tag{27}$$

Alternatively, dependence between fields can be modeled using log-linear models; however, I will assume conditional independence to ease computation, and because the matching variables in the synthetic dataset are generated independently of each other.

Since membership to M or U is not actually observed, a convenient way of simultaneously estimating p_M, p_U and classifying record pairs as matches or non-matches is via mixture modeling, with mixture distributions $P(\boldsymbol{\gamma}_{\mathbf{ij}}|M)$ and $P(\boldsymbol{\gamma}_{\mathbf{ij}}|U)$. The parameters can be estimated using the expectation-maximization (EM), first applied to record linakge by Larsen and Rubin (2001). For this paper, I use the `fastLink` algorithm developed by Enamorado et al. (2019).

7 Monte Carlo Study

Following the same procedure for simulating the empirical example described in Section 2, I generate 1,000 random x- and y- dataset pairs. I implement four types of matching procedures using each dataset pair: (i) deterministic matching with unique matches (ABE

[7]There are more, if any of the comparison criteria are non-binary

Single), (ii) deterministic matching with multiple matches (ABE Multi), (iii) probabilistic matching with unique matches (PRL Single), and (iv) probabilistic matching with multiple matches (PRL Multi). Allowing for multiple matches means that a single observation in the x- datafile may be matched to multiple observations in the y-datafile.

Each matching method produces a distinct matched dataset, so that the matching step produces a total of 4,000 linked datasets. Using each of the linked datasets, I then compute (i) naive OLS estimator (using all observations and also with observations assigned ($L_i = 1$), (ii) the Scheuren and Winkler (1993) bias-corrected estimator, and (iii) the AHL estimator that assigns equal weights to multiple matches. As a benchmark, I also compute the OLS estimator that uses only the correctly matched pairs produced by the matching algorithm, and the OLS estimator applied to all 500 correctly linked record pairs. Details on the implementation of these algorithms and estimation procedures can be found in the appendix.

7.1 Matching results

To evaluate the matching procedures, I compute the following statistics for each linked dataset, reported in Table 4:

- the proportion of observations in the x-datafile that are linked to at least one observation in the y-datafile (match rate),
- the total number of links made by the matching algorithm,
- the proportion of links that are incorrect (Type I error rate),
- the proportion of correct (x, y) links that are not found by the matching algorithm (Type II error rate),
- the proportion of observations whose links include the true match

For the linked datasets that contain multiple matches per observation, I report also the average number of links per observation, and how often those links include the true match (Table 5).

As seen in Table 4, the average match rates range between 71 and 79 percent across the various matching procedures, but plotting the distribution of match rates in Figure 5shows that ABE Multi consistently matches more observations than any other procedure. PRL Single and PRL Multi have about the same match rate, which suggests that allowing for multiple matches adds additional matches per observations rather than matching new individuals (however, this may be an artifact of how my PRL implementation). ABE Multi, on the other hand, seems to increase match rates by matching new observations relative to ABE Single.

When comparing Type I error rates, it is important to note that multiple-match methods will produce more false links by construction. Therefore, it is best to compare multi-match methods by measuring the proportion of observations whose matches contain the true link. In this metric, both ABE Multi and PRL Multi perform very well. Furthermore, we can compute these values for each value of L_i, as in Table 5, which shows that allowing multiple matches improves the accuracy of the ABE algorithm. Table 5 also shows that ABE Multi and PRL Multi rarely assign more than three matches to any given observation.

Comparing ABE Single and PRL Single in Table 4, demonstrates the usual tradeoff between Type I and Type II errors. ABE Single is more conservative, produces incorrect matches only 3 percent of the time, but failing to identify 26 percent of all matches. PRL Single is less conservative, missing only 15 percent of matches, but at the cost of matching false links 11 percent of the time.

Based on these results, ABE Multi seems to perform well if multiple matches are desired. The linked datasets produced by ABE Multi are very likely to include the true match, which is required for all of the estimation methods described in this paper. It is also easier in terms of computation, because it does not require linear sum assignment programs or thresholds to determine which record pairs should be designated as matches.

7.2 Estimation Results

I compare the estimators according to median absolute deviation, and plot histograms of the estimated values in Figures 6-10. In implementing the AHL (2019) estimator, I set $\hat{g}(w_i, L_i) = \sum_{j=1}^{N_y} y_j$, the mean of all y observations, to reduce the computational burden and because I have generated y such that it is independent of the identifiers w_i. The AHL estimator will probably perform better in scenarios where w_i has predictive power in estimating the conditional mean of y_i.

8 Discussion/Conclusion

To what extent my results generalize beyond the simulated data is unclear, as I made many arbitrary choices while generating the synthetic data – such as the dictionary of names and the structure of the typographical errors that I introduce in the x-datafile – that may impact my results in important ways. However, my theoretical results suggest that (i) using the match that is most likely to be correct, and bias correcting based on the probability that it is correct is optimal, (ii) if weights are estimated imprecisely, or if no match has a high probability of being correct, then the it is better to assign equal weights to multiple matches. This result needs to be studied using more general models, and ideally applied to real data.

9 Appendix: Implementation Notes

9.1 Proofs

Lemma1. Consider,

$$\hat{\mu} = a_1 X_1 + a_2 X_2 - a_3 \kappa \tag{28}$$

which has the following expectation,

$$E[\hat{\mu}] = (a_1\pi + a_2(1-\pi))\mu + (a_1(1-\pi) + a_2\pi - a_3)\kappa$$

so that unbiased, requires

$$a_1\pi + a_2(1-\pi) = 1 \implies a_2(a_1) = \frac{1}{1-\pi} - \frac{a_1\pi}{1-\pi} \tag{29}$$

$$a_1(1-\pi) + a_2\pi = a_3 \implies a_3(a_1) = \frac{\pi}{1-\pi} + \frac{a_1 - 2a_1\pi}{1-\pi} \tag{30}$$

Hence we can write $\hat{\mu}$ as a function of a_1,

$$\hat{\mu}(a_1) = a_1 X_1 + \left(\frac{1}{1-\pi} - \frac{a_1\pi}{1-\pi}\right) X_2 - \left(\frac{\pi}{1-\pi} + \frac{a_1 - 2a_1\pi}{1-\pi}\right)\kappa$$

When $a_1 = \frac{1}{\pi}$, then $\hat{\mu} = \hat{\mu}_1$; and if $a_1 = 0$ then $\hat{\mu} = \hat{\mu}_2$.

We can write:

$$\begin{aligned}
\hat{\mu} &= (a_1\pi)\hat{\mu}_1 + (1 - a_1\pi)\hat{\mu}_2 + a_1(1-\pi)\kappa + \frac{\pi}{1-\pi}(1-a_1)\kappa - \left(\frac{\pi}{1-\pi} + \frac{a_1 - 2a_1\pi}{1-\pi}\right)\kappa \\
&= (a_1\pi)\hat{\mu}_1 + (1 - a_1\pi)\hat{\mu}_2 - (a_1\pi)\kappa
\end{aligned}$$

Hence any unbiased estimator $\hat{\mu}$ that uses X_1 and X_2 can be written as a linear combination of estimators using only X_1 or X_2.

9.2 implementation notes

Let's talk about what I need to include here. Here are some ideas:

Formulas for SE of SW estimator.

Details about implementation of fastLink algorithm. Also

- what threshold level I use for the fastLink algorithm (0.6)
- what nonparametric technique I use for AHL (nearest neighbor)
- how I choose z in LL when there are multiple matches (randomly)
- how I calculate standard errors for all of the estimators (using formulas for now)
- how I standardize the variables for matching (nysiis function in R)
- I change Step 2 in the ABE algorithm to restrict the all observations with unique first name, last name, date of birth, and (x_1, x_2) combinations.
- When allowing for multiple matches, I count as matches all record pairs with the same name, and the difference in recorded birth years is within two (or five) years. That is, I designate all potential matches that arise in Step 3 as matches.

10 More MSE Tables

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Figure 1: Optimal d^* as a function of π and $\sigma^2, \omega^2, \mu, \kappa$

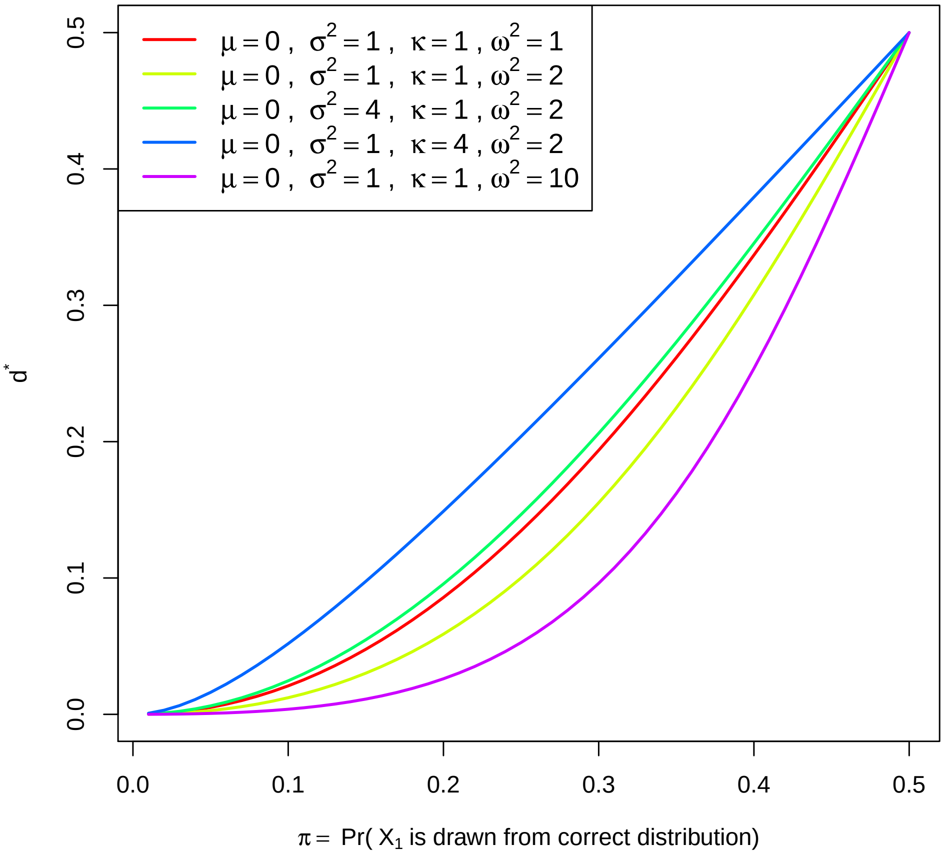


Figure 2: Bias of $\hat{\mu}^*$ as a function of $\hat{\pi}$

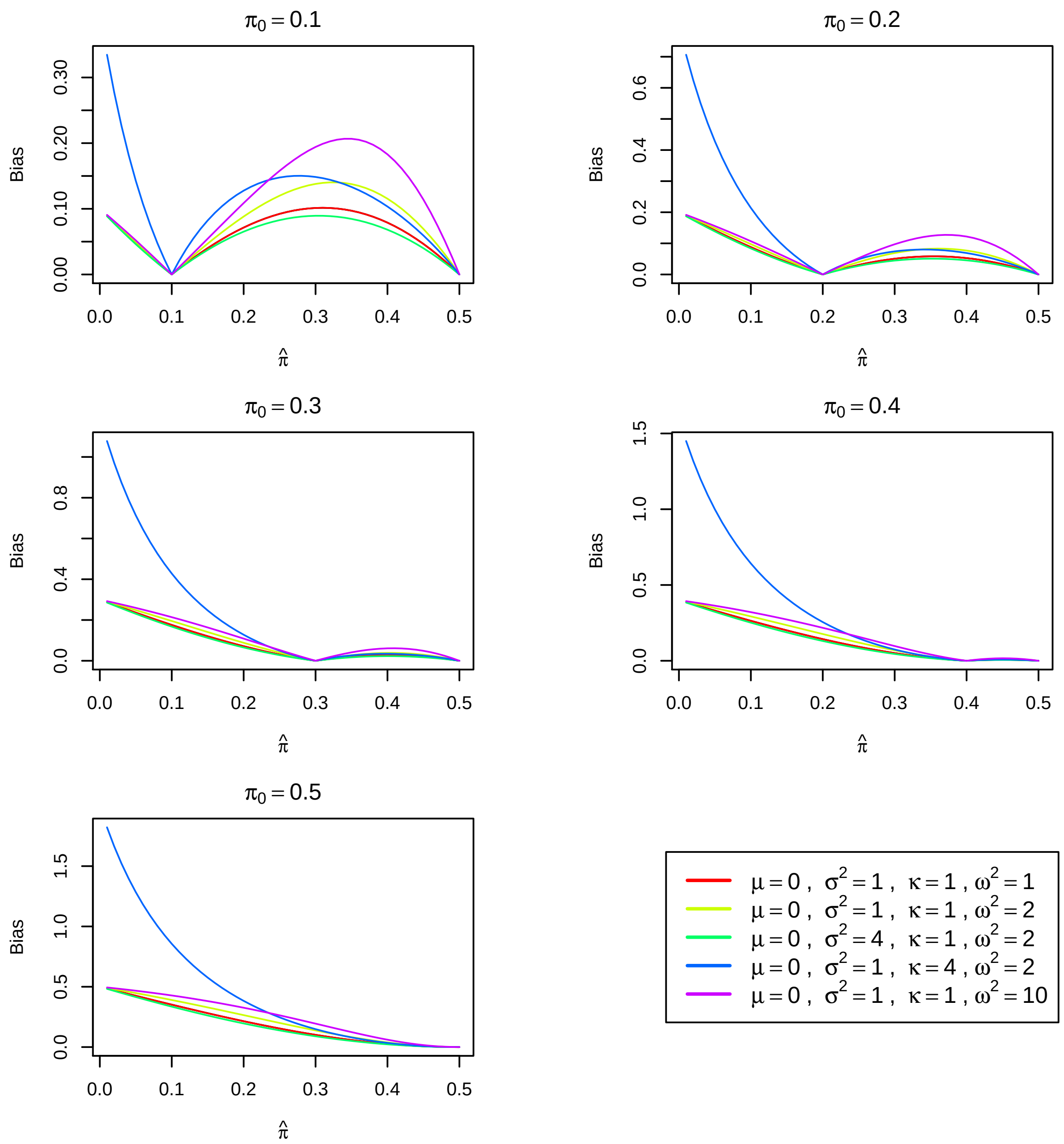


Figure 3: Variance of $\hat{\mu}^*$ as a function of $\hat{\pi}$ with $N = 1$

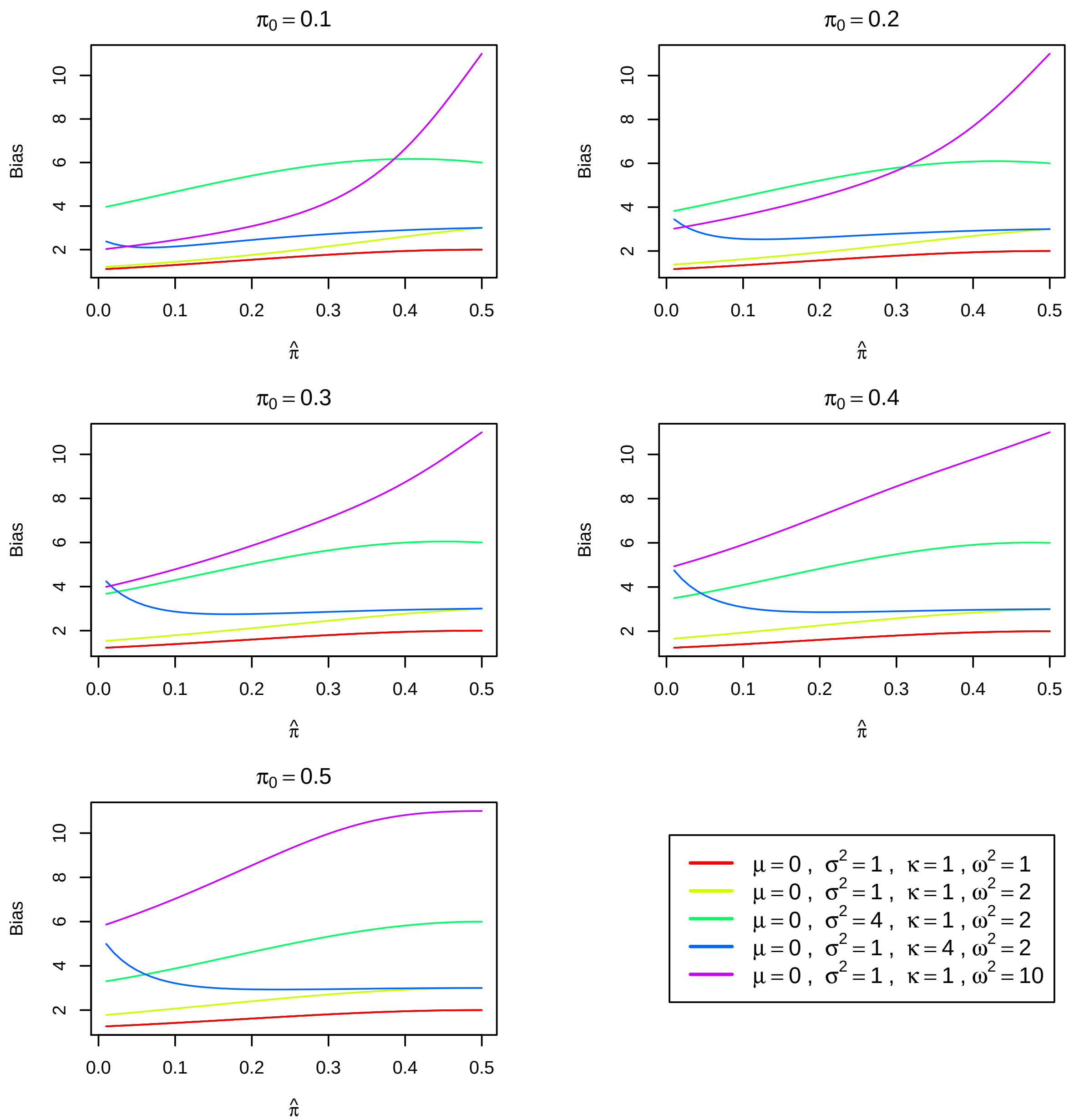


Figure 4: Creation of Synthetic Datasets

ID	y	x_1	x_2	First Name	Last Name	Birthday
1	y_1	$x_{1,1}$	$x_{2,1}$	Tyler	Ashenfelter	1915-05-13
2	y_2	$x_{1,2}$	$x_{2,2}$	Brandon	Christensen	1904-06-27
				⋮		
195	y_{195}	$x_{1,195}$	$x_{2,195}$	Samantha	Andersen	1914-08-18
196	y_{196}	$x_{1,196}$	$x_{2,196}$	Victoria	Andersen	1918-11-25
				⋮		
1000	y_{500}	$x_{1,500}$	$x_{2,500}$	Vicky	Anderson	1915-04-14

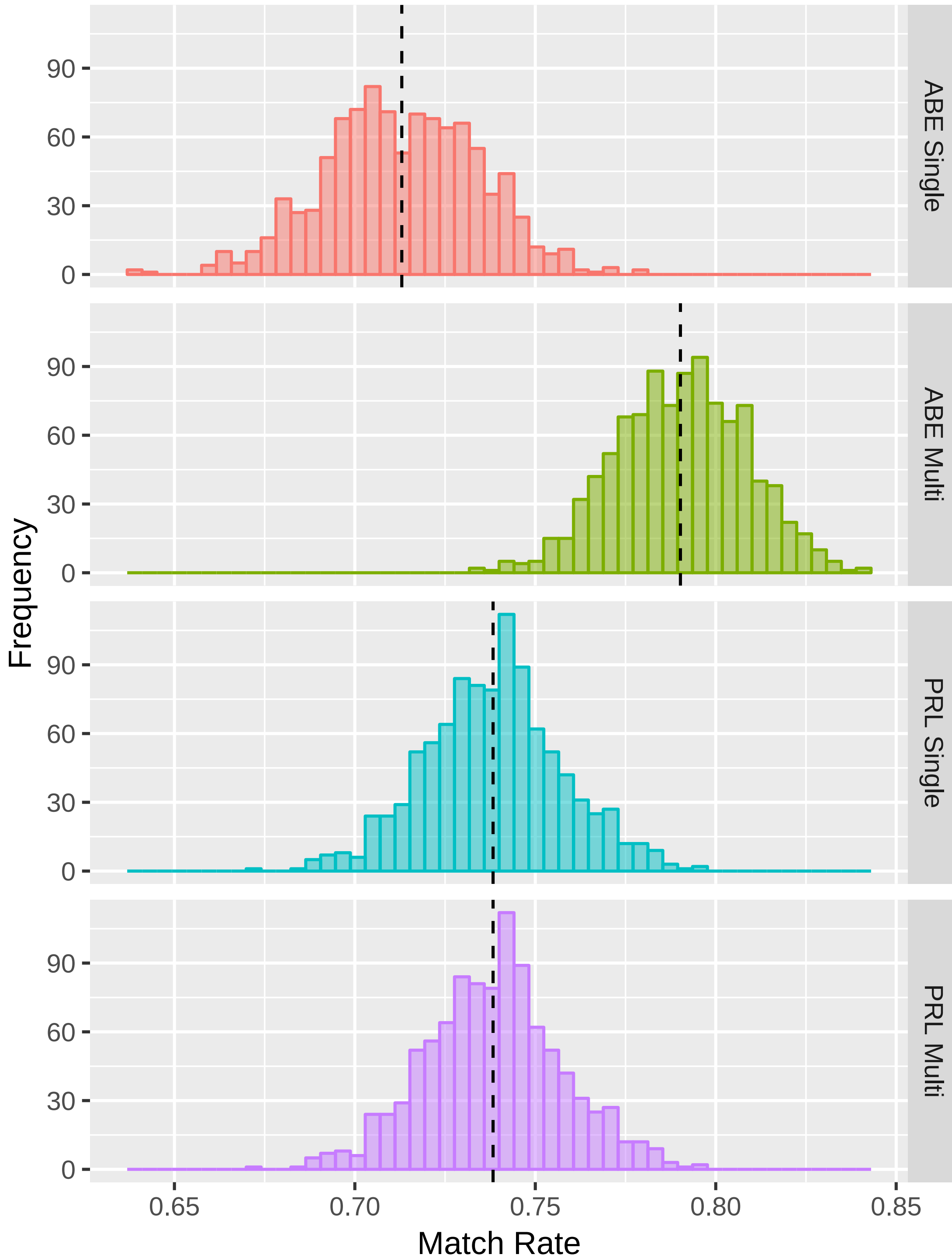
x-Datafile

ID	x	Name	Birthday
2	$(x_{1,2}, x_{2,2})$	Branden Christenson	1905-06-27
		...	
195	$(x_{1,195}, x_{2,195})$	Samantha Anderson	1914-08-21
198	$(x_{1,198}, x_{2,198})$	Jon Smyth	1918-12-20
		...	
1000	$(x_{1,1000}, x_{2,1000})$	Vic Andersn	1915-04-14

y-Datafile

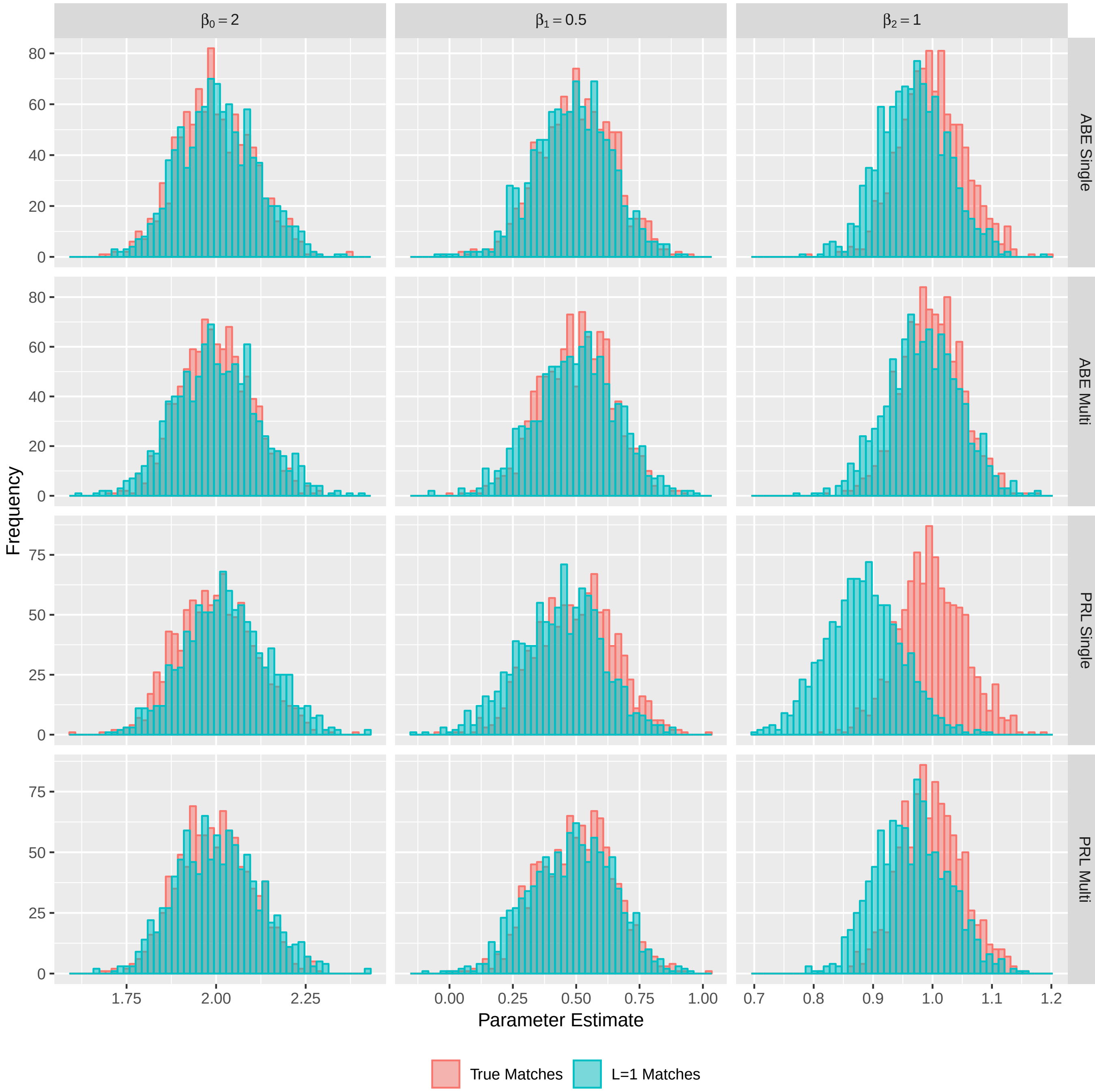
ID	y	Name	Birthday
1	y_1	Tyler Ashenfelter	1915-05-13
2	y_2	Brandon Christensen	1904-06-27
		...	
195	$y_{1,195}$	Samantha Anderson	1914-08-18
		...	
1000	y_{1000}	Vicky Anderson	1915-04-14

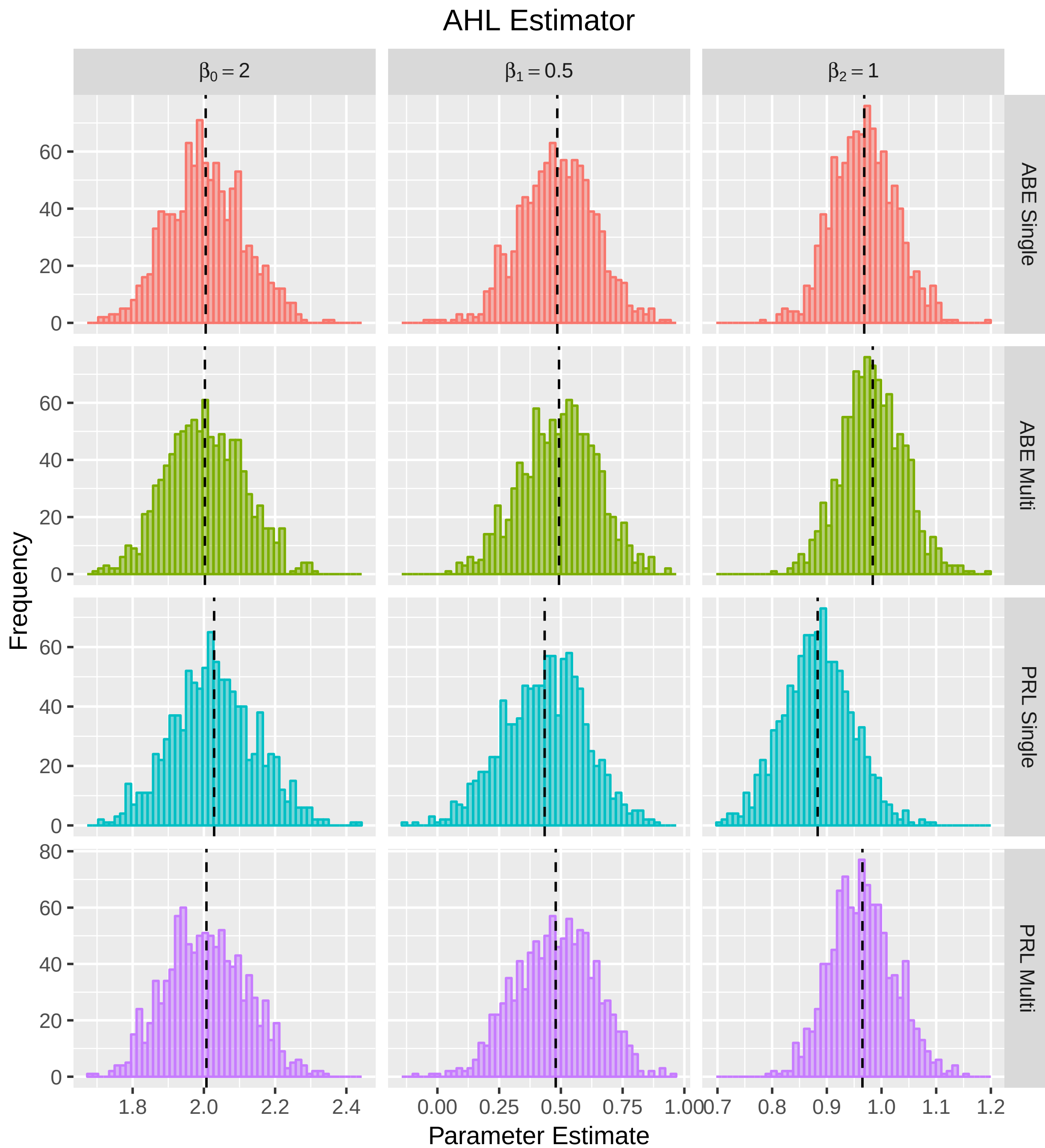
Figure 5: Match Rates by Linking Procedure



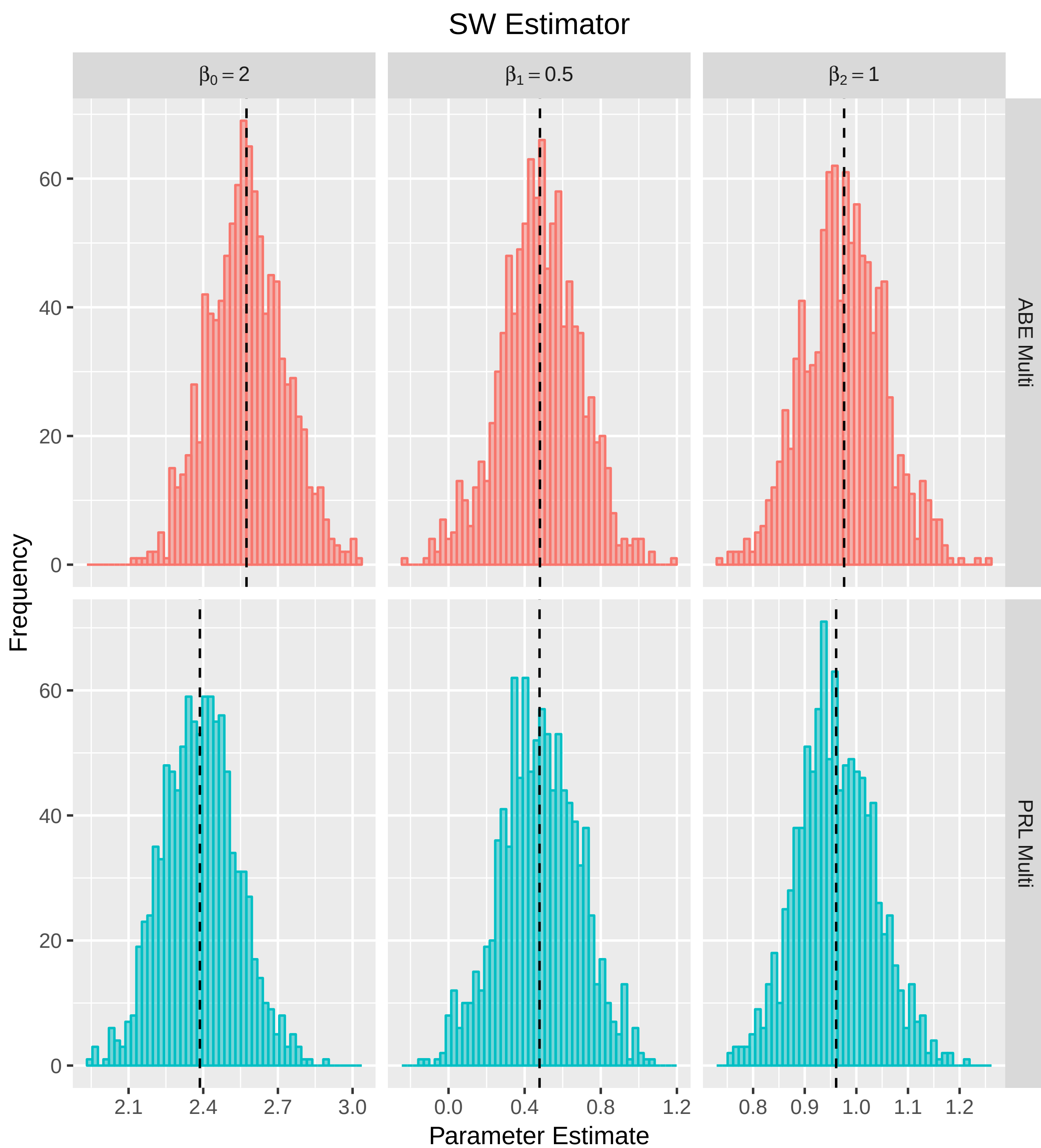
*Based on 1,000 simulations. Vertical line indicates the sample mean.

Figure 6: Comparing OLS with true matches produced by matching algorithm vs. matches with L=1

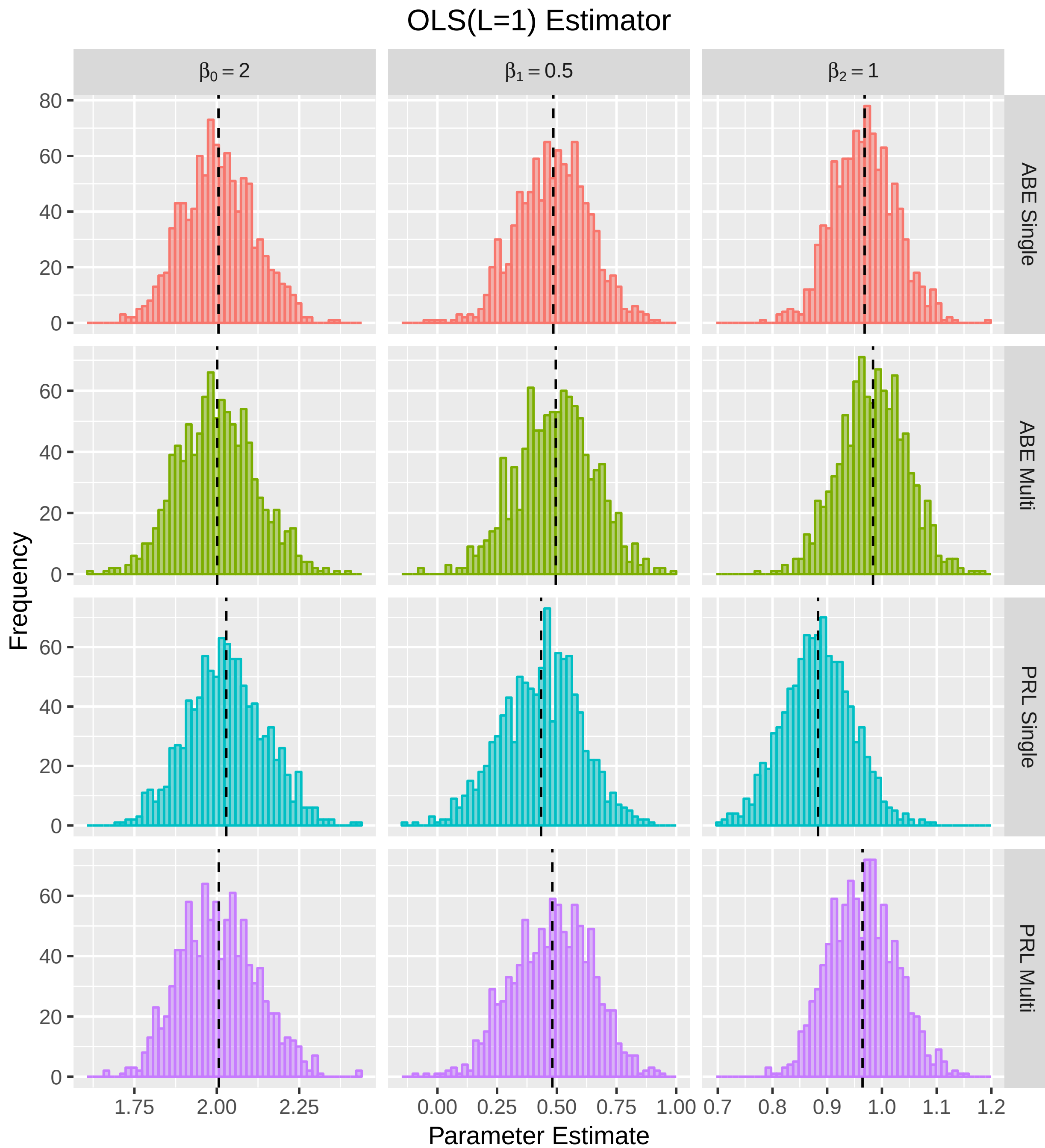




*Based on 1,000 simulations. Vertical line indicates the sample mean.



*Based on 1,000 simulations. Vertical line indicates the sample mean.



*Based on 1,000 simulations. Vertical line indicates the sample mean.

Table 1: MSE ratio for $\hat{\mu}^*$ and $\hat{\mu}^{AHL}$ for $N = 10$ and $(\mu, \sigma^2, \kappa, \omega^2) = (0,1,1,2)$

	$\hat{\pi}$				
π	0.1	0.2	0.3	0.4	0.5
0.1	2.085	1.635	1.280	1.097	1
0.2	1.744	1.545	1.275	1.093	1
0.3	1.381	1.371	1.225	1.078	1
0.4	1.073	1.165	1.141	1.054	1
0.5	0.836	0.967	1.036	1.022	1
0.6	0.658	0.796	0.924	0.983	1
0.7	0.527	0.656	0.814	0.938	1
0.8	0.428	0.543	0.713	0.891	1
0.9	0.354	0.454	0.623	0.842	1

Table 2: MSE ratio for $\hat{\mu}^*$ and $\hat{\mu}^{AHL}$ for $N = 100$ and $(\mu, \sigma^2, \kappa, \omega^2) = (0,1,1,2)$

	$\hat{\pi}$				
π	0.1	0.2	0.3	0.4	0.5
0.1	2.085	1.183	0.740	0.763	1
0.2	1.164	1.545	1.079	0.915	1
0.3	0.536	1.039	1.225	1.029	1
0.4	0.286	0.558	0.981	1.054	1
0.5	0.173	0.319	0.651	0.977	1
0.6	0.116	0.200	0.423	0.837	1
0.7	0.082	0.136	0.285	0.683	1
0.8	0.061	0.098	0.201	0.546	1
0.9	0.047	0.073	0.148	0.435	1

Table 3: MSE ratio for $\hat{\mu}^*$ and $\hat{\mu}^{AHL}$ for $N = 1000$ and $(\mu, \sigma^2, \kappa, \omega^2) = (0,1,1,2)$

	$\hat{\pi}$				
π	0.1	0.2	0.3	0.4	0.5
0.1	2.085	0.314	0.142	0.188	1
0.2	0.269	1.545	0.425	0.349	1
0.3	0.075	0.303	1.225	0.706	1
0.4	0.034	0.090	0.409	1.054	1
0.5	0.019	0.041	0.138	0.682	1
0.6	0.012	0.024	0.066	0.337	1
0.7	0.009	0.015	0.038	0.183	1
0.8	0.006	0.011	0.025	0.112	1
0.9	0.005	0.008	0.017	0.075	1

Table 4: Summary of matching algorithm performance

Method	Match Rate	# Matches	Type I	Type II	P(Contains True)
ABE (Single)	0.71 (0.02)	356.50 (10.60)	0.03 (0.01)	0.26 (0.02)	0.97 (0.01)
ABE (Multi)	0.79 (0.02)	505.08 (17.30)	0.23 (0.02)	0.20 (0.02)	0.99 (0.01)
PRL (Single)	0.74 (0.02)	369.15 (9.65)	0.11 (0.02)	0.15 (0.03)	0.89 (0.02)
PRL (Multi)	0.74 (0.02)	435.65 (14.94)	0.18 (0.02)	0.23 (0.02)	0.97 (0.01)

Note: Based on 1,000 simulations. Standard deviations are reported in parentheses.

Table 5: Performance of multiple match methods by value of L_i

L	1	2	3	4	5	6+
ABE Multi						
Pr(Contains True)	0.99 (0.01)	0.99 (0.01)	0.99 (0.02)	0.99 (0.07)	0.99 (0.10)	1.00 (0.00)
Pr(L=ℓ)	0.52 (0.15)	0.35 (0.16)	0.11 (0.11)	0.03 (0.03)	0.02 (0.03)	0.02 (0.01)
PRL Multi						
Pr(Contains True)	0.97 (0.01)	0.98 (0.02)	0.98 (0.06)	0.98 (0.12)	0.99 (0.05)	1.00 (0.00)
Pr(L=ℓ)	0.59 (0.21)	0.33 (0.22)	0.07 (0.11)	0.02 (0.05)	0.03 (0.06)	0.01 (0.01)

Note: Based on 1,000 simulations. Standard deviations are reported in parentheses.

Table 6: Median Absolute Deviations for Estimators

Parameter	AHL	SW	NaiveOLS	OLSTrue	OLS(L=1)
ABE Single					
β_0	0.113	0.113	0.113	0.109	0.113
β_1	0.150	0.150	0.150	0.152	0.150
β_2	0.057	0.057	0.057	0.054	0.057
ABE Multi					
β_0	0.115	0.155	0.103	0.100	0.120
β_1	0.155	0.201	0.149	0.148	0.159
β_2	0.055	0.077	0.064	0.050	0.061
PRL Single					
β_0	0.115	0.115	0.115	0.112	0.115
β_1	0.163	0.163	0.163	0.162	0.163
β_2	0.063	0.063	0.063	0.056	0.063
PRL Multi					
β_0	0.116	0.150	0.112	0.106	0.123
β_1	0.168	0.204	0.165	0.158	0.175
β_2	0.058	0.074	0.062	0.055	0.064

Table 7: MSE ratio for $\hat{\mu}^*$ and $\hat{\mu}^{AHL}$ for $N = 1,000$ and $(\mu, \sigma^2, \kappa, \omega^2)$ = (0,1,1,1)

	$\hat{\pi}$				
π	0.1	0.2	0.3	0.4	0.5
0.1	1.542	0.301	0.166	0.245	1
0.2	0.220	1.273	0.460	0.424	1
0.3	0.062	0.299	1.113	0.758	1
0.4	0.028	0.091	0.458	1.027	1
0.5	0.016	0.042	0.166	0.757	1
0.6	0.010	0.024	0.080	0.424	1
0.7	0.007	0.015	0.047	0.245	1
0.8	0.005	0.011	0.030	0.154	1
0.9	0.004	0.008	0.021	0.104	1

Table 8: MSE ratio for $\hat{\mu}^{*}$ and $\hat{\mu}^{AHL}$ for $N = 1,000$ and $(\mu, \sigma^2, \kappa, \omega^2) = (0,1,1,2)$

	$\hat{\pi}$				
π	0.1	0.2	0.3	0.4	0.5
0.1	2.085	0.314	0.142	0.188	1
0.2	0.269	1.545	0.425	0.349	1
0.3	0.075	0.303	1.225	0.706	1
0.4	0.034	0.090	0.409	1.054	1
0.5	0.019	0.041	0.138	0.682	1
0.6	0.012	0.024	0.066	0.337	1
0.7	0.009	0.015	0.038	0.183	1
0.8	0.006	0.011	0.025	0.112	1
0.9	0.005	0.008	0.017	0.075	1

Table 9: MSE ratio for $\hat{\mu}^*$ and $\hat{\mu}^{AHL}$ for $N = 1,000$ and $(\mu, \sigma^2, \kappa, \omega^2)$ = (0,4,1,2)

	$\hat{\pi}$				
π	0.1	0.2	0.3	0.4	0.5
0.1	1.288	0.622	0.431	0.555	1
0.2	0.522	1.150	0.770	0.736	1
0.3	0.185	0.646	1.063	0.921	1
0.4	0.089	0.275	0.802	1.015	1
0.5	0.052	0.140	0.451	0.947	1
0.6	0.034	0.083	0.259	0.769	1
0.7	0.023	0.054	0.162	0.583	1
0.8	0.017	0.038	0.110	0.434	1
0.9	0.013	0.028	0.078	0.327	1

Table 10: MSE ratio for $\hat{\mu}^*$ and $\hat{\mu}^{AHL}$ for $N = 1,000$ and $(\mu, \sigma^2, \kappa, \omega^2) = $ (0,1,4,2)

	$\hat{\pi}$				
π	0.1	0.2	0.3	0.4	0.5
0.1	1.399	0.160	0.121	0.221	1
0.2	0.062	1.146	0.361	0.391	1
0.3	0.016	0.157	1.052	0.726	1
0.4	0.007	0.044	0.356	1.012	1
0.5	0.004	0.020	0.120	0.719	1
0.6	0.003	0.011	0.057	0.387	1
0.7	0.002	0.007	0.033	0.219	1
0.8	0.001	0.005	0.021	0.136	1
0.9	0.001	0.004	0.015	0.092	1

Table 11: MSE ratio for $\hat{\mu}^*$ and $\hat{\mu}^{AHL}$ for $N = 1,000$ and $(\mu, \sigma^2, \kappa, \omega^2)$ = (0,1,1,10)

	$\hat{\pi}$				
π	0.1	0.2	0.3	0.4	0.5
0.1	4.501	0.739	0.263	0.274	1
0.2	0.730	2.456	0.729	0.488	1
0.3	0.218	0.623	1.546	0.883	1
0.4	0.101	0.202	0.612	1.125	1
0.5	0.058	0.096	0.231	0.757	1
0.6	0.037	0.055	0.114	0.412	1
0.7	0.026	0.036	0.067	0.237	1
0.8	0.019	0.025	0.044	0.150	1
0.9	0.015	0.019	0.031	0.102	1