

Regression analysis with linked data

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This Version: October 2, 2019

Abstract

This paper studies what happens when the goal is to estimate a parametric model using observations (x, y) , but 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 .

1 Introduction

Consider estimating β in a linear regression model,

$$y_i = x_i' \beta + \varepsilon_i, \quad E[\varepsilon | x_i] = 0, \quad E[\varepsilon_i^2] = \sigma^2 \quad (1)$$

but, instead of observing (x, y) pairs directly, x and y are recorded in separate datasets. Additionally, both datasets contain a set of common variables w , that can be used to learn about the joint distribution of (x, y) .

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Perhaps the most straightforward way to estimate β in this setting involves first identifying which (x, y) pairs refer to the same underlying units, and then applying standard methods to estimate (1) using the matched pairs. Formally, for data $\{x_i, w_i\}_{i=1}^{N_x}$ and $\{y_j, w_j\}_{j=1}^{N_y}$, the matching step consists of estimating a function,

$$\varphi : \{1, \dots, N_x\} \rightarrow \{1, \dots, N_y\} \cup \emptyset \quad (2)$$

where $\varphi(i) = j$ if individual i in the x -datafile and individual j in the y -datafile refer to the same entity, and $\varphi(i) = \emptyset$ if i does not have a match in y -datafile. Note that if w identifies individuals uniquely and without error, then $\varphi(i) = j$ if and only if $w_i = w_j$, and $\varphi(i) = \emptyset$ otherwise. However, if w is not unique or recorded with error, then φ needs to be estimated, and inference about β may need to be adjusted accordingly.

To fix ideas, suppose that the goal is to estimate the effect of providing cash transfers to single mothers on the life expectancy of their children. Mathematically, the parameter of interest can be represented as β_1 in the regression model,

$$y_i = \beta_0 + x_{1i}\beta_1 + x'_{2i}\beta_2 + \varepsilon_i \quad (3)$$

where x_{1i} is a binary variable equal to 1 if person i 's mother received a cash transfer, and x_{2i} includes all other demographic variables that are recorded on the welfare program applications (the x -datafile). The outcome y_i is person i 's age at death, as reported in a universal database of death records (the y -datafile). The two data sources additionally contain a common set of variables w , including first and last name, and year of birth. Since no combination of these variables is necessarily unique, estimating φ in this setting would likely require distinguishing among multiple observations with identical w .

Although the previous example is motivated by a specific research question in Aizer et al. (2016), the “imperfect identifier problem” is by no means unique. In statistics, the task of

recovering φ is known as *record linkage*, but this problem also appears frequently in computer science, operations research, and epidemiology, under names such as data linkage, entity resolution, instance identification, de-duplication, merge/purge processing, and reconciliation. In economics, a strong interest in record linkage has emerged as the result of newly available, large administrative datasets; and, a number of recent papers compare the performance of popular matching techniques used in economic history on the representativeness and accuracy of the datasets that they produce (Abramitzky et al., 2019, 2018; Bailey et al., 2017).

These reviews illustrate how each step of the record linkage process introduces the possibility that a true match is overlooked (Type II error), or that a false match is designated as correct (Type I error); and, generally, there is a tradeoff between reducing either one of the two (Abramitzky et al., 2019; Doidge and Harron, 2018). However, the impact of data pre-processing choices on estimation is still not well understood. Furthermore, inference using linked data requires joint assumptions for the matching and estimation steps.

In particular, whether to allow for multiple matches? When using multiple matches, authors have generated a “composite match” equal to the average of the linked observations (Bleakley and Ferrie, 2016), constructed bounds on the parameter of interest using different configurations of matched data (Nix and Qian, 2015), or used methods that allow for multiple, equally likely outcomes by Anderson et al. (2019). This example also shows how the outputs of the matching process determine which estimation tools are available. Had the authors used probabilistic record linkage methods to link the data, they could have used the robust OLS estimators from Lahiri and Larsen (2005), or prior-informed imputation for missing records proposed by Goldstein et al. (2012).

This paper adds to this literature by comparing how different *combinations* of matching and estimation techniques affect parameter estimates and their confidence intervals in standard econometric models. It also makes practical suggestions for choosing which methods best suit a given setting. 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 Empirical Example

The purpose of this section is to introduce a synthetic dataset that will be referenced throughout this paper. The benefits of using a synthetic dataset are threefold: first, I can control which variables in (1) are correlated with errors in the identifiers w ; second, I can compare the performance of the matching algorithms and estimation techniques to a “ground truth” dataset containing all of the true matches; third, I can control the degree of overlap and similarity among observations, which is important for manipulating the number of possible matches if multiple matches are desired. To make the data as real as possible, I choose the identifiers and their corresponding transcription error rates to mimic those reported in the 1940 Census data, as reported by Abramitzky et al. (2019).

The “ground truth” dataset consists of 1000 observations of $(x_{1i}, x_{2i}, y_i, w_i)$, where x_{1i} and x_{2i} are mutually independent, $x_{1i} \stackrel{i.i.d}{\sim} \text{Bernoulli}(0.5)$, and $x_{2i} \stackrel{i.i.d}{\sim} \mathcal{N}(0, 2)$. The y_i values are generated according to the linear relationship,

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \varepsilon_i, \quad \varepsilon_i \mid x_{1i}, x_{2i} \stackrel{i.i.d}{\sim} \mathcal{N}(0, \sigma^2) \quad (4)$$

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 also assigned the identifiers, w_i , which include include a first and last name drawn at random from a list of first and last names¹, and a random birthday between January 1, 1900, and December 31,

¹The first and last name lists contain 41 and 24 names, respectively, and can be found in the replication

1925. The resulting dataset looks like the observations in the top panel of Figure 1.

Figure 1: 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
				\vdots		
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
				\vdots		
1000	y_{500}	$x_{1,500}$	$x_{2,500}$	Vicky	Anderson	1915-04-14



x -Datafile				y -Datafile			
ID	x	Name	Birthday	ID	y	Name	Birthday
2	$(x_{1,2}, x_{2,2})$	Branden Christenson	1905-06-27	1	y_1	Tyler Ashenfelter	1915-05-13
		...		2	y_2	Brandon Christensen	1904-06-27
195	$(x_{1,195}, x_{2,195})$	Samantha Anderson	1914-08-21			...	
198	$(x_{1,198}, x_{2,198})$	Jon Smyth	1918-12-20	195	$y_{1,195}$	Samantha Anderson	1914-08-18
		
1000	$(x_{1,1000}, x_{2,1000})$	Vic Andersn	1915-04-14	1000	y_{1000}	Vicky Anderson	1915-04-14

Next, I split the ground truth dataset into an x - and y -datafile, which contain (x_1, x_2, w) and (y, w) values respectively. To construct the x -datafile, I select 400 observations at random from the ground truth dataset, and introduce random errors in their corresponding identifiers. 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 1 illustrates how the x - and y -datafiles are split visually.

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.

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 .

3 Record Linkage Methods

Recall that the data consist of an x -datafile, denoted $X \equiv \{(x_i, w_i) : i = 1, \dots, N_x\}$, and a y -datafile, denoted $Y \equiv \{(y_j, w_j) : j = 1, \dots, N_y\}$, and the goal of record linkage is to use w_i and w_j to determine which $i \in \{1, \dots, N_x\}$ and $j \in \{1, \dots, N_y\}$ 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.²

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

²By contrast, Bailey et al. (2017) categorize record linkage procedures according to the set of assumptions that motivate their use.

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) 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.

3.1 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 ± 1 year of reported birth year, and if this is unsuccessful, it looks for matches within ± 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.

3.2 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*,

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

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 $\boldsymbol{\gamma}_{ij}$ can be modeled as arising from the mixture distribution:

$$P(\boldsymbol{\gamma}_{ij}) = P(\boldsymbol{\gamma}_{ij}|M)p_M + P(\boldsymbol{\gamma}_{ij}|U)p_U \quad (5)$$

where $P(\boldsymbol{\gamma}_{ij}|M)$ and $P(\boldsymbol{\gamma}_{ij}|U)$ are the probabilities of observing the pattern $\boldsymbol{\gamma}_{ij}$ 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 $\boldsymbol{\gamma}_{ij}$,

$$P(M|\boldsymbol{\gamma}_{ij}) = \frac{p_M P(\boldsymbol{\gamma}_{ij}|M)}{P(\boldsymbol{\gamma}_{ij})} \quad (6)$$

Thus, if we can estimate p_M , $P(\boldsymbol{\gamma}_{ij}|M)$ and $P(\boldsymbol{\gamma}_{ij}|U)$, then we can estimate the probability that any two records refer to the same entity using (6). 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 γ_{ij} ³. While in principle we could model $P(\gamma_{ij}|M)$ and $P(\gamma_{ij}|U)$ as

$$\begin{aligned}(\gamma_{ij}^1, \dots, \gamma_{ij}^K) \mid M &\sim \text{Dirichlet}(\delta_{\mathbf{M}}) \\ (\gamma_{ij}^1, \dots, \gamma_{ij}^K) \mid U &\sim \text{Dirichlet}(\delta_{\mathbf{U}})\end{aligned}$$

but the parameters $\delta_{\mathbf{M}}$ and $\delta_{\mathbf{U}}$ 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:

$$P(\gamma_{ij}|C) = \prod_{k=1}^K P(\gamma_{ij}^k|C)^{\gamma_{ij}^k} (1 - Pr(\gamma_{ij}^k|C))^{1-\gamma_{ij}^k} \quad C \in \{M, U\} \quad (7)$$

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 $P(\gamma_{ij}|M)$ and $P(\gamma_{ij}|U)$. The parameters can be estimated using the expectation-maximization (EM), first applied to record linkage by Larsen and Rubin (2001). For this paper, I use the **fastLink** algorithm developed by Enamorado et al. (2019).

³There are more, if any of the comparison criteria are non-binary

4 Estimation Methods

This section provides an overview of the estimation methods I compare for analyzing the matched datasets.

4.1 OLS Bias Correction

Scheuren and Winkler (1993) and Lahiri and Larsen (2005) propose techniques for correcting the bias from mismatched pairs in linear regression. They assume that the matching procedure produces n pairs (x_i, z_i) , where z_i may or may not correspond to y_i , yet the true y_i is included among the matches. Hence,

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

and $\sum_{j=1}^n q_{ij} = 1$, $i = 1, \dots, n$. Estimating (1) using z_i as the dependent variable yields the naive least squares estimator,

$$\hat{\beta}_N = (X'X)^{-1}X'z \quad (8)$$

which is biased. Denoting $q_i = (q_{i1}, \dots, q_{in})'$ and $Q = (q_1, \dots, q_n)'$, we can write the bias of $\hat{\beta}_N$ as

$$\text{bias}(\hat{\beta}_N) = [(X'X)^{-1}X'QX - I]\beta$$

since $E[z_i] = E[q_i'y] = q_i'X\beta = \sum_{j=1}^n q_{ij}x_j'\beta$.

To reduce the bias of $\hat{\beta}_N$, Scheuren and Winkler (1993) observed that

$$\text{bias}(\hat{\beta}_N|y) = E[(\hat{\beta}_N - \beta)|y] = (X'X)^{-1}X'B \quad (9)$$

where $B = (B_1, \dots, B_n)'$ 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 actual response y_i . The authors suggest estimating (9) using the first and second highest elements of the vector q_i , so that $\hat{B}_i^{TR} = (q_{ij_1} - 1)z_{j_1} + q_{ij_2}z_{j_2}$, and

$$\hat{\beta}_{SW} = \hat{\beta}_N - (X'X)^{-1}X'\hat{B}^{TR} \quad (10)$$

The estimator can incorporate any number of elements of q_i , but, if the probability is high that the best candidate link is the true link, then the truncation results in a very small bias.

Alternatively, Lahiri and Larsen (2005) use the fact that $E(z_i) = w_i'\beta$, where $w_i = q_i'X_i\beta$, to construct the unbiased estimator:

$$\hat{\beta}_U = (W'W)^{-1}W'z$$

where $W = (w_1, \dots, w_N)'$. To construct $\hat{\beta}_U$ in practice, they also recommend using a truncated version of W , with $w_i^{TR} = q_{ij_1}x_{j_1} + q_{ij_2}x_{j_2}$.

For both methods, the values q_{ij} are typically calculated using (6) and parameter values $\psi = \{p_M, P(\gamma_{ij}|M), \text{ and } P(\gamma_{ij}|U)\}$. Thus, we can write the estimators $\hat{\beta}_{SW} = \hat{\beta}_{SW}(\psi)$ and $\hat{\beta}_U = \hat{\beta}_U(\psi)$. In practice, ψ is unknown, and a reasonable estimator $\hat{\psi}$ must be used. Details on how to estimate $\hat{\psi}$ are provided in the next section. Importantly, $\hat{\beta}_U(\hat{\psi})$ is unbiased whenever $\hat{\psi}$ is independent of z , which occurs if errors in the matching variables (which determine the distribution of $\hat{\psi}$ are independent of the response variable y . Unfortunately, this assumption is unlikely to hold in many economic applications, such as Nix and Qian (2015), where y indicates whether a person's recorded ethnicity changes between survey years, but data quality significantly differs for individuals with different values of y .

4.2 Multiple match WLS

Anderson et al. (2019) propose a GMM estimator that uses data where each observation x_i is linked to L_i equally likely, potential outcomes, denoted $\{y_{i\ell}\}_{\ell=1}^{L_i}$. Importantly, their methods require that (i) the true outcome is included among the set of possible matches, (ii) each of the possible matches is equally likely to be the true match, and (iii) that the observations x_i and $\{y_{i\ell}\}_{\ell=1}^{L_i}$ are random samples from their marginal distributions conditional on (w_i, L_i) .

Under these assumptions, the authors show how to construct an unbiased and consistent estimator $\hat{\beta}$ by considering the smoothed regression:

$$\sum_{\ell=1}^{L_i} y_{i\ell} - (L_i - 1)g(w_i, L_i) = x_i' \beta + u_i \quad (11)$$

where $g(w_i, L_i) = E[y_{i\ell}|w_i, L_i]$, $u_i = \varepsilon_i + \sum_{\ell=1}^{L_i} \nu_{i\ell}$, and $\nu_{i\ell} = y_{i\ell} - E[y_{i\ell}|w_i, L_i]$.

If, additionally, $E[\varepsilon_i^2|w_i, L_i] = \sigma_\varepsilon^2$ and $E[\nu_{i\ell}^2|z_i, L_i] = \sigma_\nu^2$ then $\hat{\beta}$ can be estimated efficiently using weighted least squares, with $\sigma(X_i) = \sigma_\varepsilon^2 + (L_i - 1)\sigma_\nu^2$, and

$$\hat{\beta}^{WLS} = \left(\sum_{i=1}^N \frac{x_i x_i'}{\sigma(X_i)} \right)^{-1} \left(\sum_{i=1}^N \frac{x_i}{\sigma(X_i)} \left(\sum_{\ell=1}^{L_i} y_{i\ell} - (L_i - 1)g(w_i, L_i) \right) \right) \quad (12)$$

which can be estimated in two-steps, where the first step involves estimating $\hat{g}(\cdot)$ and $\hat{\sigma}(X_i)$. The resulting estimator is consistent and asymptotically normal under the regularity conditions described in Anderson et al. (2019).

Assumption (iii) rules out the possibility of unobserved sample selection, in the sense that all individuals with the same identifying information 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 w_i includes income). However,

unlike the OLS bias correction estimators, the methods here explicitly correct for any dependence between the outcome variable and the matching variables w_i and the parameters of the matching procedure, insofar as they are captured by L_i .

[This suggests that the AHL (2019) estimator may be more robust when L_i is correlated with $x_{i..}$]

5 Implementation Notes

Here I will talk about all the nit-picky stuff, like

- 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.

6 Results

In total, I will test three DGPs (two now; more in Monte Carlo). The first is exactly as described in Section 2. The second allows for correlation between x_1 and the probability of

an error. The third will allow for correlation between y and the probability of an error.

The y are generated according to the same DGP described above; that is the true $\beta_0 = (2, 0.5, 1)$. I compare my results to an oracle linkage method (“first best”), which would successfully link all 400 x observations to their correct y . This produces $\hat{\beta}_{FB}$, which is shown in the table below:

Table 1: Match rate for matching algorithms

method	nMatches	pCorrect	nUniqueX
ABE (Single)	327	0.95	327
ABE (Multi)	454	0.78	360
PRL (Single)	311	0.85	311
PRL (Multi)	373	0.79	311

Figure 2: Distribution of number of matches produced by multi-matching algorithms

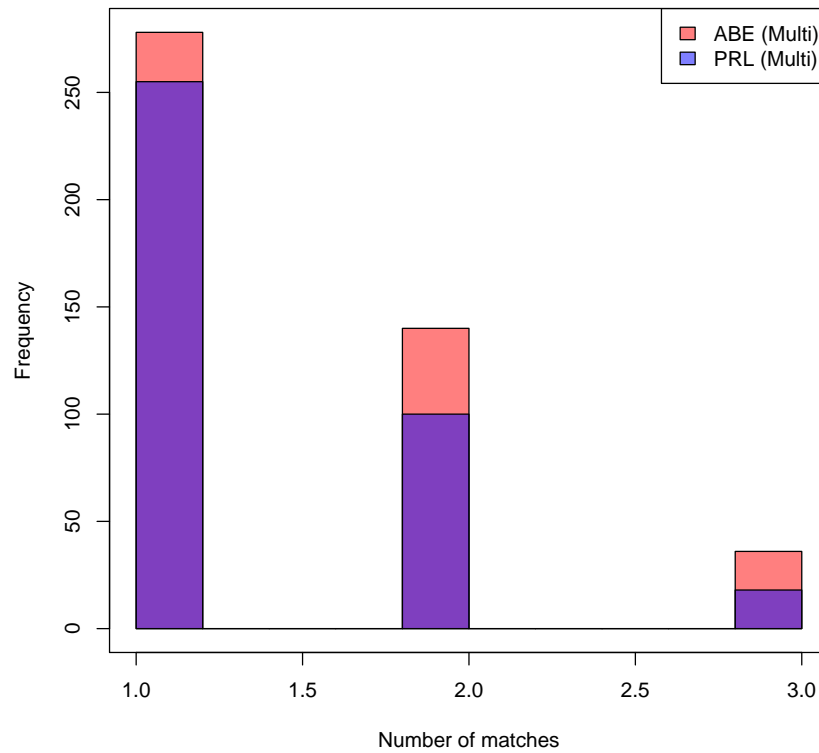


Figure 3: default

Table 2: Naive OLS for all of the matchings

	<i>Dependent variable:</i>				
	First Best	ABE (Single)	^y ABE (Multi)	PRL (Single)	PRL (Multi)
β_0	2.079*** (0.102)	2.106*** (0.125)	2.100*** (0.109)	1.932*** (0.131)	2.091*** (0.122)
β_1	0.408*** (0.143)	0.413** (0.172)	0.369** (0.153)	0.587*** (0.180)	0.357** (0.168)
β_2	1.096*** (0.052)	1.010*** (0.062)	0.905*** (0.056)	0.975*** (0.065)	0.930*** (0.062)
Observations	400	327	454	311	373
R ²	0.534	0.455	0.367	0.429	0.384

Note:

*p<0.1; **p<0.05; ***p<0.01

6.1 Matching step

Table 3:

	method	nMatches	pCorrect	nUniqueX
1	abe_single	338	0.96	338
2	abe_multi	479	0.77	375
3	prl_single	335	0.87	335
4	prl_multi	397	0.79	335

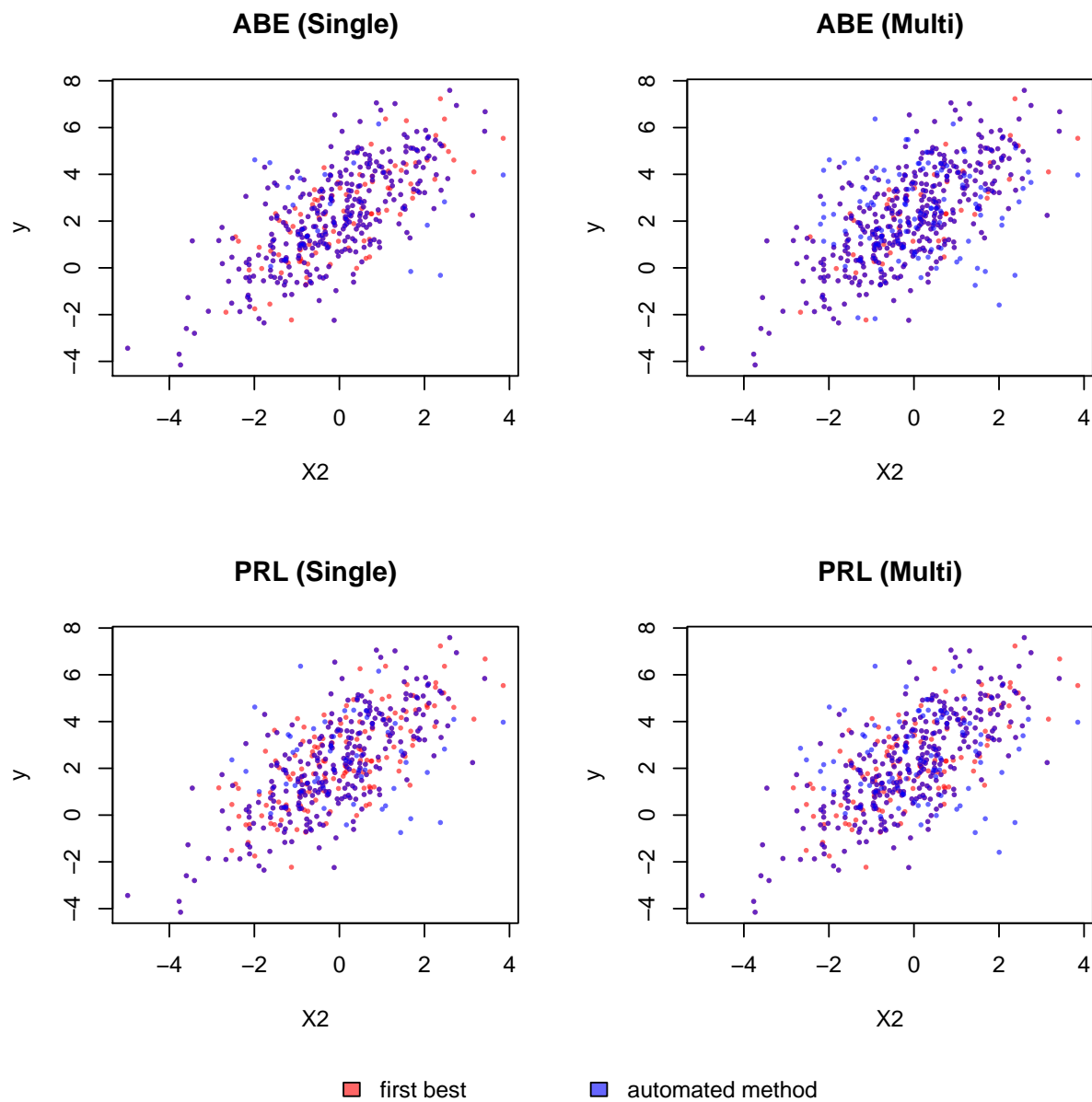
6.2 Estimation Results

Table 4: Parameter estimates for different matched datasets and estimation procedures

7 Conclusion

Borrow from the Bayesian Record Linkage.

Figure 4: (x, y) pairs produced by different matching algorithms



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