

# Efficient and Scalable Bipartite Matching with Fast Beta Linkage (fabl)

Brian Kunding<sup>a</sup>      Jerome Reiter<sup>a</sup>      Rebecca C. Steorts<sup>b</sup>

<sup>a</sup> Department of Statistical Science, Duke University

<sup>b</sup> Department of Statistical Science and Computer Science, Duke University  
Principal Mathematical Statistician, United States Census Bureau

September 19, 2021

## **Abstract**

Abstract

*Keywords:* record linkage, Bayesian methods, parallellized computing, streaming algorithms

# 1 INTRODUCTION

Record linkage is the task of identifying duplicate records across multiple data sources. In many cases, this identification is itself the goal of an analysis, as in estimating human rights atrocities from disparate data sources, or linking voter information across election years. In others, we seek to perform some other statistical procedure, such as survival analysis or regression, using linked datasets, and one must propagate linkage uncertainty into the subsequent analysis.

Record linkage is straightforward when provided unique identifiers or highly reliable information, but becomes difficult when data sources are plagued with error. This motivates the use of probabilistic record linkage techniques that are able to model the reliability of the information and which are more robust to errors than are deterministic methods. Unfortunately, probabilistic record linkage is computationally intense, and many entity resolution tasks are large in nature, motivating the search for scalable and efficient record linkage techniques.

Most record linkage techniques are based the seminal (Fellegi and Sunter, 1969), which formalized the methods outlined by (Newcombe et al., 1959). This method creates comparison vectors for each pair of records in the data, and independently classifies those pairs as a match or a non-match. Though this independence is usually not reasonable, it is appealing for its mathematical simplicity and relative computational ease. Several authors have elaborated on this approach by including hierarchical structure on model parameters, aiding classification through regression to incorporate covariates, establishing joint models for linkage and analysis, and more (Larsen, 2005), (Hu Y., 2017), (Hof et al., 2017). Importantly, (Enamorado and Imai, 2019) modified the Fellegi-Sunter method with innovative hashing techniques, greatly expanding the scalability of the independent classification approach.

Despite the appeal of independent classification, it often leads to linkage decisions that do not enjoy transitive closure, and ignores that fact that we are often in scenarios where we know one record in one file has at most one match in another file. This setting is known as bipartite matching, and has received much less attention in the literature. (Sadinle, 2017) developed a prior distribution on the space of bipartite matchings such that his method,

known as Beta Record Linkage (BRL), resulted in one-to-one matchings without any need for post-processing. However, BRL was even more computationally intensive than the original Fellegi-Sunter method, making it infeasible for large linkage tasks.

In this paper, we propose an extension to the BRL method proposed by (Sadinle, 2017) for this very end. We increase the speed of the BRL procedure through a modification to the model specification that allows for parallel computing of the linkage parameter, and use hashing techniques to hasten calculations and reduce computational complexity. Additionally, we introduce storage efficient indexing (SEI), and a data partitioning approach to make the method amenable to large linkage tasks. To recognize the lineage from the original BRL method, we name our method *Fast Beta Linkage* (**fabl**, pronounced “fable”)

In what follows, Section 2 describes previous work in record linkage that lays the foundation for our method, Section 3 provides our model and the Gibbs sampler used for posterior inference, and Sections 4 and 5 describe strategies used for more efficient and scalable implementation. Then, Section 6 demonstrates the accuracy and speed of our method through two simulation studies, and Section ?? reveals interesting properties of the method through a case study of El Salvadoran casualty records. Lastly, Section ?? is a discussion that highlights open questions in the record linkage literature and motivates future work.

## 2 RELATED WORK

**Fellegi and Sunter Method** Most record linkage techniques are derived from the seminal (Fellegi and Sunter, 1969) paper “A Theory for Record Linkage”. The defining characteristic of their approach was to transform the sets of records, which often contain text data that is difficult to model, into sets of comparison vectors governed by parameters that can be more easily estimated. Concretely, if files  $A$  and  $B$  have  $n_A$  and  $n_B$  records respectively, and if the files share  $F$  fields in common upon which to base the linkage, the Fellegi and Sunter approach generates an  $n_A n_B \times F$  matrix  $\Gamma$ , which contains similarity scores between each pair of records across datasets. We say  $\gamma_{ij}$  is the comparison vector for record  $i \in A$  and record  $j \in B$ , with  $\gamma_{ij}^f \in \{1, \dots, L_f\}$  providing their similarity score on the  $f^{th}$  field. For

ease of modeling and computation, we restrict these similarity scores to be discrete, ordinal variables, and the construction of these is left to the modeler. We adopt the convention that  $\gamma_{ij}^f = 1$  corresponds to the highest level of agreement and  $\gamma_{ij}^f = L_f$  corresponds to the lowest. It is common to use binary 1-2 variables to indicate exact matching, and 1-2-3 variables to provide an option for partial matching. For text data, we calculate similarity based on Levenstein distance or some other text similarity score, and bin these scores to integers for use in the model. (Jaro, 1989) provided guidelines for appropriate binning for the comparison vectors, but details of implementation are generally context specific.

The likelihood in the original Fellegi Sunter model is a mixture model through which each record pair is independently classified as a match or nonmatch. This independent classification often leads to sets of matches that break expectations of transitivity, which is undesirable. Although (Jaro, 1995) devised an procedure to reduce a set of conflicting matches to the mostly likely set of one-to-one matchings, the abundance of false matches can bias the estimation of other parameters of the model, and ultimately leads to poor linkage performance.

(Sadinle, 2017) uses the same comparison vector approach as Fellegi and Sunter, but proposed a prior distribution for the set of matches that strictly enforced one-to-one matching without the need for any post-hoc processing procedures. Specifically, in each iteration of his Gibbs sampler, he considers each record  $j \in B$ , removes from consideration the records  $i \in A$  that have already been matched, and then samples a potential link. This leads to a sampler that is significantly more accurate than the standard Fellegi-Sunter approach. However, accounting for these dependencies throughout the linkage process is computationally burdensome, leaving BRL only suitable for small to moderate linkage problems.

### 3 A SCALABLE MODEL FOR BAYESIAN RECORD LINKAGE

In this section, we propose a statistical model suitable for efficient computation in large linkage tasks. Denote two files as  $A$  and  $B$ , with  $n_A$  and  $n_B$  records respectively, and

with records indexed as  $i \in \{1, \dots, n_A\}$  in  $A$  and  $j \in \{1, \dots, n_B\}$  in  $B$ . Without loss of generality, label the files such that  $n_A \geq n_B$ . We assume there are no duplicates within files, only across. For each record pair under consideration, we generate a comparison vector  $\gamma_{ij} = \{\gamma_{ij}^1, \dots, \gamma_{ij}^F\}$ , where  $F$  is the number of fields used in the linkage and each  $\gamma_{ij}^f$  takes on a value  $l \in \{1, \dots, L_f\}$  indicating the level agreement between the two records on a specified field.

To indicate matching status, we adopt the *linkage structure parameter*  $\mathbf{Z} = (Z_1, \dots, Z_{n_B})$  from Sadinle 2017, defined as

$$Z_j = \begin{cases} i, & \text{if records } i \in A \text{ and } j \in B \text{ refer to the same entity;} \\ n_A + 1, & \text{if record } j \in B \text{ does not have a match in file } A; \end{cases}$$

This parameter is vector of length  $n_B$ , providing more memory efficient storage for the linkage information than a  $n_A \times n_B$  sparse matrix of indicators.

Following the Fellegi Sunter framework, we define  $m^{fl} := P(\gamma_{ij}^f = l | Z_j = i)$  to be the probability of observing agreement level  $l$  in field  $f$  for records  $i$  and  $j$  given that the records are a match, and similarly define  $u^{fl} := P(\gamma_{ij}^f = l | Z_j \neq i)$ , for non-matches. We also adopt Fellegi and Sunter's conditionally independent fields assumption that the level of agreement on one field is independent of the level of agreement on another. Though this assumption is often not reasonable (for example, two individuals of a different genders are more likely to have different names than two individuals of the same gender), but it is common within the record linkage literature and generally leads to models that perform well in practice; see discussion for further remarks. Lastly, we define  $\lambda$  to be the (marginal) probability that some record  $j \in B$  has a match in  $A$ .

Wherever possible, we reserve superscripts for denoting field and level, while reserving subscripts for record indices. For example,  $\mathbf{m}^f = (m^{f1}, \dots, m^{fL_f})$  is the probability distribution governing field  $f$  for matching records, and  $\mathbf{m}_{ij} = \prod_{f=1}^F \prod_{l=1}^{L_f} (m^{fl})^{\mathbf{1}_{\gamma_{ij}^f=l}} = P(\gamma_{ij} | Z_j = i)$  is product of the relevant of the appropriate  $\mathbf{m}$  parameters for record pair  $(i, j)$ . We hope that these conventions avoid overloaded notation in the likelihood and subsequent derivations.

### 3.1 Model Specification

For fields  $f \in \{1, \dots, F\}$  and levels  $l \in \{1, \dots, L_f\}$  we adopt the following likelihood and prior distributions.

$$P(\Gamma|\mathbf{Z}, \mathbf{m}, \mathbf{u}) = \prod_{j=1}^{n_B} \prod_{i=1}^{n_A} \left[ \prod_{f=1}^F \prod_{l=1}^{L_f} m_{fl}^{I(Z_j=i)} u_{fl}^{I(Z_j \neq i)} \right]^{I(\gamma_{ij}^f=l)}$$

$$\mathbf{m}^f \sim \text{Dirichlet}(\alpha^{f1}, \dots, \alpha^{fL_f})$$

$$\mathbf{u}^f \sim \text{Dirichlet}(\beta^{f1}, \dots, \beta^{fL_f})$$

$$Z_j|\lambda = \begin{cases} \frac{1}{n_A}\lambda & z_j \leq n_A; \\ 1 - \lambda & z_j = n_A + 1 \end{cases}$$

$$\lambda \sim \text{Beta}(\alpha_\lambda, \beta_\lambda)$$

The prior for  $Z_j$  has equal probability of matching to all records  $i \in A$ , and non-matching probability governed by  $\lambda$ . Therefore a  $\lambda \sim \text{Beta}(1, 1)$  corresponds to a prior belief that nonmatches and matches are equally likely, and a  $\lambda \sim \text{Beta}\left(1, \frac{1}{n_A}\right)$  prior corresponds to a uniform prior on the labeling of  $\mathbf{Z}$ .

Here the reader should the relationship between our proposed model and that of Sadinle 2017. In his model, Sadinle constructs a prior distribution on the entire  $\mathbf{Z}$  vector, which induces a Gibbs sampler that strictly enforces one-to-one matching. In particular, this sampler removes previously matches records from the set of candidate records when sampling  $Z_j$ , creating a dependency that makes the sampler *inherently serial*. We however use independent priors for each  $Z_j$ , creating a sampler that is *perfectly parallelizable*, allowing for significant computational gains. More importantly, since only the agreement pattern of  $Z_j$  is used for calculations within the Gibbs sampler, and not the particular record label, we can conduct this sampling only at the level of the unique agreement patterns, offering even more computational savings. In doing so however, we thereby weaken the one-to-one requirement from BRL; our sampler does ensure that each record in  $B$  can be matched to at most one record in  $A$ , but allows for the possibility that multiple records in  $B$  match

to the same record in  $A$ . We then resolve these contradictions through a straightforward post-processing step. We explore the ramifications of this distinction with the El Salvador case study.

## 3.2 Gibbs Sampler

We work with the following factorization of the joint posterior distribution:

$$\begin{aligned}
p(\mathbf{Z}, \mathbf{m}, \mathbf{u}, \lambda | \Gamma) &\propto p(\Gamma | \mathbf{Z}, \mathbf{m}, \mathbf{u}) p(\mathbf{Z} | \lambda) p(\mathbf{m}, \mathbf{u}) p(\lambda) \\
&\propto \prod_{j=1}^{n_B} \prod_{i=1}^{n_A} \left[ \prod_{f=1}^F \prod_{l=1}^{L_f} m_{fl}^{I(Z_j=i)} u_{fl}^{I(Z_j \neq i)} \right] \\
&\times \prod_{f=1}^F \prod_{l=1}^{L_f} m_{fl}^{\alpha_{fl}-1} \times \prod_{f=1}^F \prod_{l=1}^{L_f} u_{fl}^{\beta_{fl}-1} \\
&\times \prod_{j=1}^{n_B} \left[ I(Z_j \leq n_A) \frac{1}{n_A} \lambda + I(Z_j = n_A + 1) (1 - \lambda) \right]
\end{aligned}$$

This factorization leads to following Gibbs Sampler:

Sample  $\mathbf{m}^{(s+1)}$   $\mathbf{u}^{(s+1)} | \Gamma, \mathbf{Z}^{(s)}$ : The  $\mathbf{m}$  and  $\mathbf{u}$  parameters are updated through standard multinomial-dirichlet mechanics. Thus we have

$$\mathbf{m}_f | \mathbf{Z}, \Gamma \sim \text{Dirichlet}(\alpha_{f1}(\mathbf{Z}), \dots, \alpha_{fL_f}(\mathbf{Z}))$$

$$\mathbf{u}_f | \mathbf{Z}, \Gamma \sim \text{Dirichlet}(\beta_{f1}(\mathbf{Z}), \dots, \beta_{fL_f}(\mathbf{Z}))$$

where  $\alpha_{fl}(\mathbf{Z}) = \alpha_{fl} + \sum_{i,j} I(\gamma_{ij}^f = l) I(z_j = i)$  and  $\beta_{fl}(\mathbf{Z}) = \beta_{fl} + I(\gamma_{ij}^f = l) I(z_j \neq i)$ .

Sample  $\lambda^{(s+1)} | \mathbf{Z}^{(s)}$ : As a function of  $\lambda$ , the linkage structure parameter  $\mathbf{Z}$  is sequence of successes (when  $z_j < n_A + 1$ ) and failures (when  $z_j = n_A + 1$ ), and therefore  $p(\mathbf{Z} | \lambda) = \mathcal{L}(\lambda | \mathbf{Z})$  is determined only by the number of duplicates  $D = \sum_{i=1}^{n_B} \mathbf{1}_{z_j < n_A + 1}$  encoded by  $\mathbf{Z}$ . Thus we have

$$\begin{aligned}
p(\lambda | \mathbf{Z}) &\propto p(\mathbf{Z} | \lambda) p(\lambda) \\
&\propto \lambda^D (1 - \lambda)^{n_B - D} \lambda^{\alpha_\lambda - 1} (1 - \lambda)^{\beta_\lambda - 1}
\end{aligned}$$

$$\propto \lambda^{D+\alpha_\lambda-1}(1-\lambda)^{n_B-D+\beta_\lambda-1}$$

$$\implies \lambda^{(s+1)}|\mathbf{Z}^{(s+1)} \sim \text{Beta}(D + \alpha_\lambda, n_B - D + \beta_\lambda)$$

Sample  $\mathbf{Z}^{(s+1)}|\Gamma, \mathbf{m}^{(s+1)}, \mathbf{u}^{(s+1)}, \lambda^{(s+1)}$ : Because we sample  $Z_j$  independently of all other  $Z_{j'}$ , we use only the full conditional for an individual  $Z_j$ . Let  $\Gamma_{\cdot j}$  denote the set of  $n_A$  comparison vectors with  $j \in B$ , and note that as a function of  $Z_j$ , the likelihood  $p(\Gamma_{\cdot j}|Z_j, \mathbf{m}, \mathbf{u}) = \mathcal{L}(Z_j|\Gamma_{\cdot j}, \mathbf{m}, \mathbf{u})$  is a discrete distribution with probabilities proportional to

$$\begin{aligned} p(\Gamma_{\cdot j}|Z_j = z_j, \mathbf{m}, \mathbf{u}) &\propto \prod_{i=1}^{n_A} \left[ \prod_{f=1}^F \prod_{l=1}^{L_f} m_{fl}^{I(Z_j=i)} u_{fl}^{I(Z_j \neq i)} \right]^{I(\gamma_{ij}^f=l)} \\ &\propto \prod_{i=1}^{n_A} \left( \prod_{f=1}^F \prod_{l=1}^{L_f} \frac{m_{fl}}{u_{fl}} \right)^{I(z_j=i, \gamma_{ij}^f=l)} \\ &= \begin{cases} w_{ij} & z_j \leq n_A; \\ 1 & z_j = n_A + 1 \end{cases} \end{aligned}$$

where  $w_{ij} = \left( \frac{\prod_{f=1}^F \prod_{l=1}^{L_f} m_{fl}}{\prod_{f=1}^F \prod_{l=1}^{L_f} u_{fl}} \right)^{I(\gamma_{ij}^f=l)} = \frac{P(\gamma_{ij}|Z_j=i)}{P(\gamma_{ij}|Z_j \neq i)}$ . The interested reader should note that these are precisely the likelihood ratios used in the Fellegi-Sunter model to classify matches and non-matches, and we therefore refer to  $w_{ij}$  as the *Fellegi Sunter weights*.

With the likelihood in this form, we can derive the full conditional

$$\begin{aligned} p(Z_j|\Gamma_{\cdot j}, \mathbf{m}, \mathbf{u}, \lambda) &\propto p(\Gamma_{\cdot j}|Z_j, \mathbf{m}, \mathbf{u})P(Z_j|\lambda) \\ &\propto \left( \sum_{i=1}^{n_A} w_{ij} \mathbf{1}_{z_j=i} + \mathbf{1}_{z_j=n_A+1} \right) \left( \lambda \sum_{i=1}^{n_A} \frac{1}{n_A} \mathbf{1}_{z_j=i} + (1-\lambda) \mathbf{1}_{z_j=n_A+1} \right) \\ &= \frac{\lambda}{n_A} \sum_{i=1}^{n_A} w_{ij} \mathbf{1}_{z_j=i} + (1-\lambda) \mathbf{1}_{z_j=n_A+1} \\ &\implies Z_j^{(s+1)}|\mathbf{m}, \mathbf{u}, \Gamma, \lambda \propto \begin{cases} \frac{\lambda}{n_A} w_{ij} & z_j \leq n_A; \\ 1-\lambda & z_j = n_A + 1 \end{cases} \end{aligned}$$



In order to make fair comparisons against the (Sadinle, 2017) model, we integrate over the posterior of  $\lambda$  and rearrange terms to produce the final full conditional:

$$p\left(Z_j^{(s+1)} = i | \mathbf{m}, \mathbf{u}, \mathbf{Z}^{(s)}\right) \propto \begin{cases} w_{ij} & i \leq n_A; \\ n_A \frac{n_B - D + \beta_\lambda}{D + \alpha_\lambda} & i = n_A + 1 \end{cases}$$

### 3.3 Bayes Estimate

We calculate a Bayes estimate  $\hat{\mathbf{Z}}$  for the linkage parameter  $\mathbf{Z}$  by assigning different positive losses to different types of errors, and minimizing posterior expected loss. We adopt the loss function proposed in Sadinle 2017, in which  $\hat{Z}_j \in \{1, \dots, n_A + 1, R\}$ , with  $R$  representing the option to leave the matching undetermined by the model. Specifically, we minimize the quantity  $L(\hat{\mathbf{Z}}, \mathbf{Z}) = \sum_{j=1}^{n_B} L(\hat{Z}_j, Z_j)$  where

$$L(\hat{Z}_j, Z_j) = \begin{cases} 0 & \text{if } Z_j = \hat{Z}_j; \\ \theta_R, & \text{if } \hat{Z}_j = R; \\ \theta_{10}, & \text{if } Z_j \leq n_A, \hat{Z}_j = n_A + 1; \\ \theta_{01}, & \text{if } Z_j = n_A + 1, \hat{Z}_j \leq n_A; \\ \theta_{11}, & \text{if } Z_j, \hat{Z}_j \leq n_A, Z_j \neq \hat{Z}_j; \end{cases}$$

Here,  $\theta_R$  is the loss from not making a decision on the linkage status,  $\theta_{10}$  is the loss from a false non-match,  $\theta_{01}$  is the loss from a false match, and  $\theta_{11}$  is the loss from the special case of a false match in which the record has a true match other than the one estimated by the model. This loss function leads to closed form decision rules for minimizing posterior expected loss. In this paper, we adopt losses  $\theta_R = \infty, \theta_{10} = 1, \theta_{01} = 1, \theta_{11} = 2$ , inducing the intuitive decision rule

$$\hat{Z}_j = \begin{cases} i, & \text{if } P(Z_j = i | \Gamma) > \frac{1}{2}; \\ 0, & \text{otherwise;} \end{cases}$$

For a more in-depth explanation of this function and the induced Bayes estimate, see (Sadinle, 2017).

Since our Gibbs procedure does not strictly enforce one-to-one matching, it is possible for the final Bayes estimate to link multiple records in  $B$  to one record in  $A$ . The modeler can either report both such matches (with their respective posterior match probabilities), or resolve these conflicts by accepting only the match with highest posterior probability. A similar approach can be seen in the most probable maximal matching sets used by (Steorts and Fienberg, 2014) to match records to latent entities. Such a resolution procedure indeed is equivalent to minimizing posterior risk under the restriction of one-to-one matching, and as thus theoretically justified within the Bayesian framework.

## 4 EFFICIENT AND SCALABLE IMPLEMENTATION

Broadly speaking, we increase our computational efficiency by recognizing that record pairs contribute to posterior calculations only through the agreement pattern of the  $\gamma_{ij}$  vector. Let  $\mathcal{H}$  be the set of unique agreement patterns in the data, let  $P = |\mathcal{H}|$  denote the total number of unique agreement patterns. Note that  $P$  is bounded above by  $\prod_{f=1}^F L_f$ , and that this bound does not scale with  $n_A$  or  $n_B$ . Prior to processing the data, we identify all  $P$  patterns in  $\mathcal{H}$  and enumerate them  $h_1, \dots, h_P$ , and map record pairs to this hashed value. When the  $(i, j)$  pair exhibits the  $p^{th}$  agreement pattern, we say  $(i, j) \in h_p$ . Wherever possible, we conduct calculations over these  $P$  agreement patterns rather than the  $n_A \times n_B$  record pairs. Some of these techniques are similar to those used by (Enamorado and Imai, 2019) to produce **fastlink**, a fast and scalable implementation of the Fellegi-Sunter model, and others have been created here for our particular context.

### 4.1 Data Representation, Hashing, and Storage

We first hash record pairs of the same agreement pattern to unique integer values. (Enamorado and Imai, 2019) accomplished this efficiently through the hashing function

$$\tilde{\gamma}_{ij} = \sum_{f=1}^F I(\gamma_{ij}^f > 0) 2^{\gamma_{ij}^f + I(k>1) \sum_{e=1}^{k-1} (L_e - 1)}$$

This function maps each agreement pattern to a unique integer, allowing us to store a scalar quantity instead of an entire vector for each record pair. For computational ease, we then

map these integers to sequential integers from 1 to  $P$ .

The classic Fellegi Sunter method represents the  $\gamma_{ij}$  comparison as a vector of length  $F$ , with each component  $\gamma_{ij}^f$  taking on values in  $\{1, \dots, L_f\}$ . To ease computations, we instead use a one hot encoding of the comparison vector. For example, if  $L_1 = L_2 = 2$  and  $L_3 = 3$ , then  $\gamma_{ij} = (2, 1, 3)$  under the classical framework becomes  $\gamma_{ij} = (0, 1, 1, 0, 0, 0, 1)$  under our framework. This is a bijective transformation that does not change the meaning of the data, but this representation eases calculations and posterior updates. This is also the form the data takes in the BRL package in R.

In the classic Fellegi Sunter framework,  $\Gamma$  is a  $n_A n_B \times F$  matrix, with each row providing the comparison vector for a different  $(i, j)$  pair. In contrast, we do not store these comparison vectors themselves, but instead only the hashed value  $h_p$  corresponding to the agreement pattern of the  $(i, j)$  pair. We store this information in a nested list  $\tilde{\Gamma}$  where the  $p^{th}$  component of the  $j^{th}$  list contains a vector of records in  $A$  that share agreement pattern  $p$  with record  $j \in B$ . For each  $p$ , we also calculate  $H_p = \sum_{i=1}^{n_A} \sum_{j=1}^{n_B} \mathbf{1}_{(i,j) \in h_p}$ , the total instances of agreement pattern  $p$  throughout the data, and also for each  $j$ , we calculate  $H_{p_j} = \sum_{i=1}^{n_A} \mathbf{1}_{(i,j) \in h_p}$  the instances of agreement pattern  $p$  among the comparison vectors between record  $j \in B$  and each of the  $n_A$  records in  $A$ .

The hashing procedure described above considerably reduces the memory needed to store the comparison information: instead of storing  $n_A \times n_B$  comparison vectors, which are relatively long under either the Fellegi Sunter or our modified framework, we only store the  $P$  unique vectors, and then  $n_A \times n_B$  scalar quantities relating record pairs to those vectors. However, even storing these  $n_A \times n_B$  scalar labels can become burdensome with large data. Worse, the overwhelming majority of these labels relate to record pairs that are clear non-matches.

To address this, we propose a new strategy called *storage efficient indexing* (SEI). In standard indexing, the modeler decides a certain criteria that they expect all true matching pairs to satisfy, and a priori label any record pairs that do not meet that criteria as non-matching. For example, one might only consider pairs with a certain similarity score on a field deemed to be important (like first name), or only pairs with exact matching on a

specified number of fields. While generally chosen to be quite loose, establishing these criteria requires knowledge of the problem and invites room for human error. We propose a method of reducing the comparison space (and reducing storage requirements) without these drawbacks. Note that all records of the same agreement pattern have the same probability when sampling  $Z_j$ . Therefore we know that records belonging to an  $h_p$  such that  $H_{p_j}$  is large are very unlikely to be sampled consistently enough to be deemed a match through the Bayes estimate, even without considering the form of the agreement pattern itself.

In SEI, rather than store all of these unlikely record labels, we choose to store only a small number  $R$  of them. Posterior calculations still attribute the appropriate weight to all records through the summary statistics  $H_p$ , and  $H_{p_j}$ . Rather than storing  $n_A \times n_B$  record labels, SEI allows us to store at most  $n_B \times P \times R$  labels, regardless of how large  $n_A$  is.

Lastly, for large data, we can partition the two datasets  $A$  and  $B$  into smaller blocks  $\{A_m\}$  and  $\{B_m\}$  for more manageable computations. On a single machine, we can read-in data sequentially, conduct hashing, compress information through SEI, and delete the original data from memory before continuing with the next chunk of data. With multiple cores or multiple machines, this can be done in parallel. Thus the combination of hashing, SEI, and partitioning allows us to conduct linkage tasks over much larger datasets.

## 5 EFFICIENT POSTERIOR INFERENCE

Updating  $\mathbf{m}$  and  $\mathbf{u}$ : After receiving matching statuses from  $\mathbf{Z}$ , the Sadinle method calculates  $\alpha_{fl}(\mathbf{Z})$  and  $\beta_{fl}(\mathbf{Z})$  for each field and level. This constitutes  $2 \times \sum L_f$  many summations over  $n_A \times n_B$  quantities, and becomes computationally burdensome with large data. In contrast, we recognize that each unique agreement pattern contributes to the posterior  $\alpha(\mathbf{Z})$  and  $\beta(\mathbf{Z})$  vectors in the same way. In fact, if we denote  $H_p^m = \sum_{j=1}^{n_B} \mathbf{1}_{(Z_j, j) \in h_p}$  to be the number of matching record pairs with agreement pattern  $p$ , then the contribution of pairs of pattern  $p$  to the  $\alpha(\mathbf{Z})$  vector is simply  $H_p^m \times h_p$ . Thus our posterior update for the  $\alpha$  vector is simply  $\alpha(\mathbf{Z}) = \alpha_0 + \sum_{p=1}^P H_p^m \times h_p$ . Then, we can easily calculate  $H_p^u$ , the number of nonmatching record pairs of agreement pattern  $p$ , by subtracting the number of matching pairs from the total present in the data; that is  $H_p^u = H_p - H_p^m$ . From this, we can update

our  $\beta$  parameter through  $\beta(\mathbf{Z}) = \beta_0 + \sum_{p=1}^P H_p^u \times h_p$ . Note that these constitute  $P$  many summations over  $n_B$  quantities, and thus avoid the  $n_A \times n_B$  summation from the original method.

Updating  $\mathbf{Z}$ : Although sampling  $Z_j$  from a the full conditional provided earlier is conceptually straightforward, it becomes computational burdensome when  $n_A$  is larger. The reader can confirm that sampling a value from a large set of unequal probabilities becomes difficult in most programming languages. To speed up computation, we break this sampling step into two simpler steps. First, we calculate the Fellegi Sunter weight  $w_p$  associated with each unique pattern and sample the agreement pattern between  $j$  and its potential match. Second, we sample the record label uniformly among records associated with that agreement pattern for that particular  $j \in B$ . More concretely, define  $h(Z_j)$  to be the agreement pattern between  $j$  and its potential match, and say  $h(Z_j) = h_{P+1}$  when  $Z_j = n_A + 1$ . Then,

$$P\left(h\left(Z_j^{(s+1)}\right) = p | \mathbf{m}, \mathbf{u}, \mathbf{Z}^{(s)}\right) \propto \begin{cases} w_p \times H_{p_j} & p \leq P; \\ n_A \frac{n_B - D + \beta_\lambda}{D + \alpha_\lambda} & p = P + 1 \end{cases}$$

$$P\left(Z_j^{(s+1)} = i \mid h\left(Z_j^{(s+1)}\right) = p\right) = \begin{cases} \frac{1}{H_{p_j}} & (i, j) \in h_p \\ 0 & \text{otherwise} \end{cases}$$

Lastly, we recognize that all posterior updates are governed by the agreement patterns of the record pairs rather than the record labels themselves. Thus we complete the entire Gibbs procedure first at the level of the  $P$  agreement patterns with the first equation above. After, we can back-fill the records corresponding to the agreement patterns through the second equation. Sampling uniformly is computationally simple even for large sets of candidate records, but this step can also be parallelized when working with large data.

To aid the reader, we provide summary of the `fabl` method through pseudocode:

## 6 SIMULATION STUDIES

We first compare `fabl` against `BRL` on several simulated datasets with varying amounts of error and overlap. We use first name, last name, age, and occupation for this linkage,

---

**Algorithm 1** Summary of fabl algorithm

---

1: **procedure** HASHING AND PREPROCESSING

2:   Partition files  $A$  and  $B$  into chunks  $\{A_I\}, \{B_J\}$

3:   **for** each  $I, J$  **do**

4:     Create comparison vectors between  $A_I$  and  $B_J$

5:     Hash results and calculate summary statistics

6:     Use SEI to reduce memory usage

7:   **end for**

8:   Synthesize results across pairings

9: **end procedure**

10: **procedure** GIBBS SAMPLING

11:   Initialize  $m$ ,  $u$ , and  $Z$  parameters

12:   **for**  $t \in \{1, \dots, T\}$  **do**

13:     Sample  $m^{t+1}|Z^t, \Gamma$  and  $u^{t+1}|Z^t, \Gamma$

14:     Sample  $H(Z^{t+1})|m^{t+1}, u^{t+1}, \Gamma$                     $\triangleright$  Sample agreement pattern, not record

15:   **end for**

16:   Sample  $Z|H(Z), \Gamma$     $\triangleright$  Fills in record label based on agreement pattern

17: **end procedure**

---

and create comparison vectors according to the default settings of the `compareRecords` function from the `BRL` package. Each simulation identifies duplicated individuals between two datasets, each with 500 records. We conduct linkage when matching records exhibit 1, 2, and 3 errors across the four fields, and when there are 50, 250, and 450 individuals in common across datasets. We use flat priors for all  $m$  and  $u$  parameters, run the Gibbs Sampler for 1000 iterations, and discard the first 100 as burn-in. This is a near exact replication of the simulation study provided by (Sadinle, 2017).

In cases when there are only one or two errors in matching records, and in cases with low to moderate duplication across records, we see that `fabl` provides approximately equivalent accuracy as `BRL`. We find that our method only has weakened performance in the most extreme scenario of very high errors and very high overlap across files. In these situations, `BRL` is removing large numbers of records from consideration throughout the Gibbs Sampler, making its implementation most different from `fabl`. We note however that such extreme linkage tasks, which such high amounts of errors and overlap, are extremely rare in practice.

To demonstrate speed, we generate comparison vectors from pre-specified distributions so that we can easily increase the size of the linkage problem. Distributions are meant to emulate the behavior of similarity scores across first name, last name, and day, month. For example,  $u^{\text{month}, 1} = P(\text{Records have same birth-month} \mid \text{Nonmatch}) = \frac{1}{12}$ . For simplicity, we consider only exact matching, so a vector  $(1, 0)$  corresponds to agreement and  $(0, 1)$  to disagreement. We simulate these data for different values of  $n_A$  and  $n_B$ , and compare the run-time of `fabl` against `BRL`. Note that the number of unique patterns  $P$  is bounded above by  $2^5 = 32$ , a bound which is consistently attained in the larger simulations.

We see that at low data size, `BRL` outperforms, but that `fabl` is significantly faster at handling larger data. In particular, run-time for `BRL` seems to grow quadratically (or linearly with the size of both  $A$  and  $B$ ) while run-time for `fabl` seems to grow linearly (in the size of  $B$ ).

The above discussion suggests that for fixed  $n_B$ , computation time should remain mostly constant with growing  $n_A$ . Simulation study suggests that this is true. In the plot below, fixing  $n_B = 500$ , we see linear growth for the run-time under `BRL` as  $n_A$  increases, with

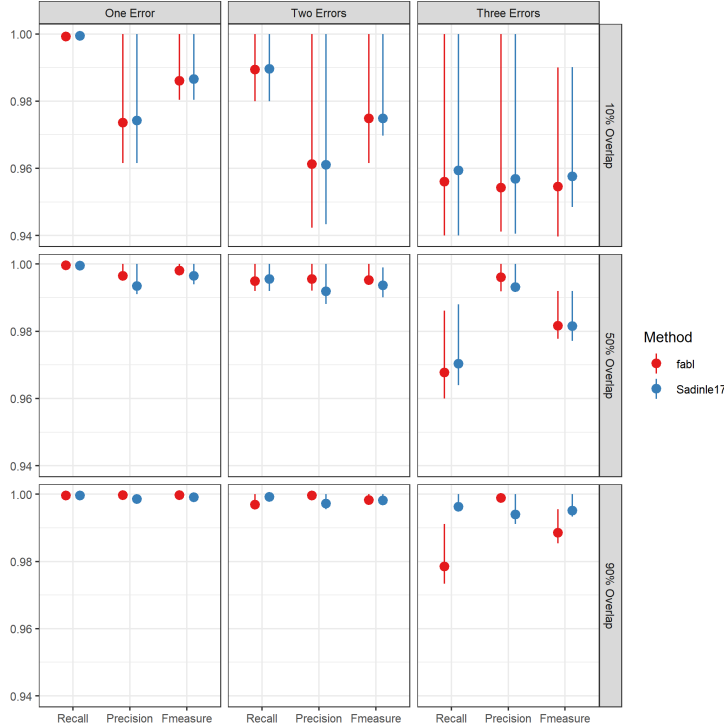


Figure 1: Posterior means and credible intervals for accuracy metrics under the replication of simulation study from Sadinle 2017. For each level of overlap and each level of error, we have 100 paired sets of 500 records.

much more static run-time under `fabl`. The slight increases in run-time that we do see are due primarily to the hashing step, which again can be run in parallel for large data.

We note here that `BRL` is coded in C, which makes for unfair comparison against `fabl`, currently only built in R. Additionally, although `fabl` is amenable to parallelization, this simulation was run on a single core. Running `fabl` in C++ with parallelization for the hashing step and sampling the matching status of the record pairs should lead to even more computational gains.

## 7 CASE STUDIES

We now demonstrate the power of our method through two case studies. The first is a study of documented identifiable deaths (DID) from the El Salvadoran Civil War. Though the data files used here are small, this study shows how the computational complexity of `fabl`



	m	u
fname	$(\frac{19}{20}, \frac{1}{20})$	$(\frac{1}{100}, \frac{99}{100})$
lname	$(\frac{19}{20}, \frac{1}{20})$	$(\frac{1}{100}, \frac{99}{100})$
day	$(\frac{19}{20}, \frac{1}{20})$	$(\frac{1}{30}, \frac{29}{30})$
month	$(\frac{19}{20}, \frac{1}{20})$	$(\frac{1}{12}, \frac{11}{12})$
year	$(\frac{19}{20}, \frac{1}{20})$	$(\frac{1}{12}, \frac{11}{12})$

Table 1: Distributions used for  $m$  and  $u$  probabilities in simulation studies

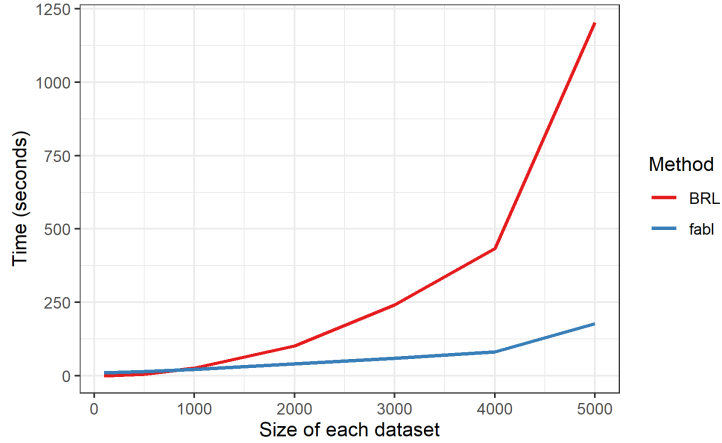


Figure 2: Run-time for BRL and fabl to run 1000 Gibbs iterations, including hashing step for fabl, for increasing values of both  $n_A$  and  $n_B$ . We see near quadratic growth in runtime for BRL, and near linear growth for fabl.

depends on the number of unique agreement patterns, and how significant computational gains can be achieved by simplifying the construction of the comparison vectors. Secondly, the case study reveals the impact of independently sampling  $Z_j$  rather than strictly enforcing one-to-one matching as done by BRL. The second case study is the National Long Term Care Survey (NLTCS), a much larger linkage tasks which BRL is unable to complete but which we complete with **fabl** with relative ease.

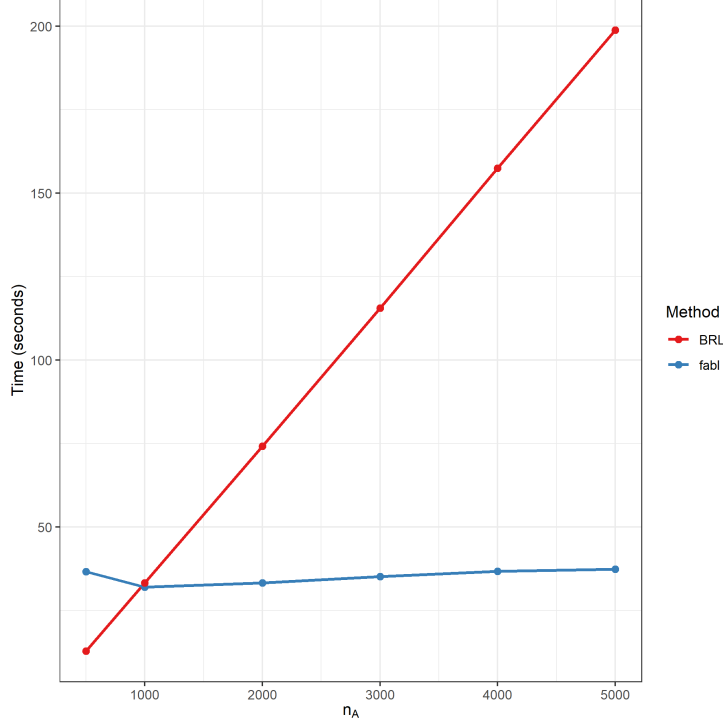


Figure 3: Run-time for BRL and fabl to run 1000 Gibbs iterations, including hashing step for fabl, with increasing  $n_A$ , and  $n_B$  fixed at 500. We see linear growth in runtime for BRL, and near constant runtime for fabl.

## 7.1 El Salvadoran Civil War

The country of El Salvador was immersed in civil war from 1980 to 1991, and throughout the time, several organizations attempted to document casualties of the conflict. When estimating the total number of casualties, one cannot simply sum the numbers recorded by each organization, as it is likely that the same individuals are recorded in multiple casualty lists. To obtain a more accurate estimate of the casualties then, we follow Sadinle’s 2017 paper and link records of El Salvadoran civilian casualties from two sources: El Rescate - Tutela Regal (ERTL) and the Salvadoran Human Rights Commission (CDHES, by its acronym in Spanish). The ERTL dataset consists of digitized reports that had been published throughout the conflict. The CDHES dataset consists of casualties that had been reported directly to the organization, and later digitized.

There are several challenges with working with such data. Firstly, both datasets have

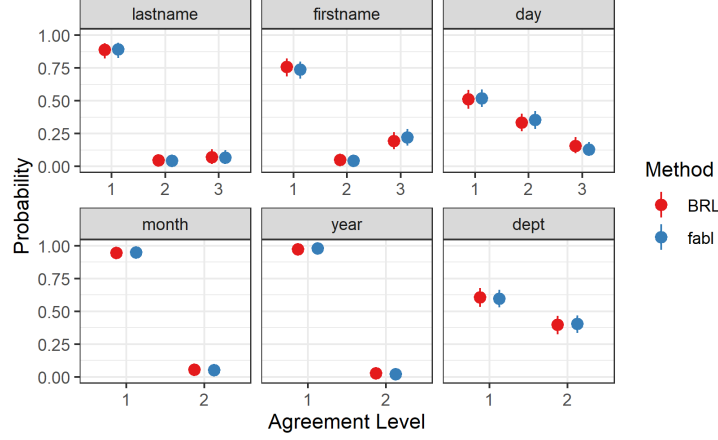


Figure 4: Posterior estimates of  $m$  parameters with 95% credible intervals

been automatically digitized, which inherently leads to some degree of typographical error. Secondly, the CDHES records are all second hand accounts reported by individuals, which can result in additional errors. Lastly, the only fields recorded are given name, last name, date of death, and place of death; it is relatively common for a parent and child to share the same given name, resulting in indistinguishable records for two different individuals. This last point nearly breaks the earlier mentioned assumption that there are no duplicates within files, and reveals a key difference between BRL and our proposed method.

We only utilized records with nonmissing entries for given and last name, results in  $n_A = 4420$  files in CHDES and  $n_B = 1323$  files in ERTL. The names were standardized to account for common misspellings in the Spanish language, and then compared using a modified Levenstein distance to account for the fact that second names are often omitted. Place of birth is recorded by municipality and department within that municipality; however, since department was missing in 95% of records in CHDES and 80% of records in ERTL, we excluded it from our linkage process. Thus we conduct linkage using given name, last name, municipality, and day, month, and year of death. We again use flat priors for the  $\mathbf{m}$  and  $\mathbf{u}$  parameters.

To mirror the original implementation, we constructed the comparison vectors using 4 levels of agreement for each field, according to the thresholds provided in Figure XX. This took 422 seconds for our proposed method and 240 for BRL. However, we observed that

posterior distributions of several levels of the  $\mathbf{m}$  and  $\mathbf{u}$  parameters were nearly identical, and that of the  $4^5 \times 2 = 2048$  possible agreement patterns, only 1173 are realized in the data. This leads us to believe that such high number of agreement levels creates unnecessary distinctions in the data and makes the comparison vectors less interpretable. Therefore we re-ran our analysis with fewer agreement levels for each field (see Figure XX), and obtained analogous results. With 216 possible agreement patterns, 159 were realized in the data, and our proposed method became much faster, finishing in 124 seconds. Meanwhile BRL took 239 seconds, relatively unchanged from the first implementation. This demonstrates the way that the computational complexity of our method depends on the number of unique agreement patterns, and how significant computational gains can be made by simplifying the construction of the comparison vectors. We also note that estimates of the  $\mathbf{m}$  and  $\mathbf{u}$  parameters under each method are very similar, as shown in Figure 4.

**Violations of One-to-One Matching** Figure 5 shows the posterior distribution for  $D$ , the number of duplicates found across file for both `fabl` and BRL. We see that `fabl` consistently overmatches within each Gibbs iteration when compared to BRL, which is to be expected because BRL explicitly prevents matches that violate one-to-one matching throughout the entire sampler. Most of such matchings are due to the randomness in the sampling procedure, and they occur sporadically throughout the sampler in such a way that does not measurably influence the eventual Bayes estimate.

Overall, both methods presented similar results. `fabl` yielded an initial Bayes estimate of 195 matches found across files, and after resolving matches that violated one-to-one requirements, yielded 180 matches across files. This is acceptably close to the 181 matches found by BRL. The main reason for this discrepancy is the difference in how each model handles situations in which one file in  $B$  has multiple plausible matches in  $A$ .

The records shown in Figure 6 provide one such instance. Note these records present a near violation of our assumption that there are no duplications within files; we continue to assume that records 825 and 826 in ERTL correspond to different individuals, but their records are nearly identical. Additionally, using the modified Levenstein distance from Sadinle 2017, the comparison vectors  $\gamma_{2776,825}$  and  $\gamma_{2776,826}$  are exactly identical.

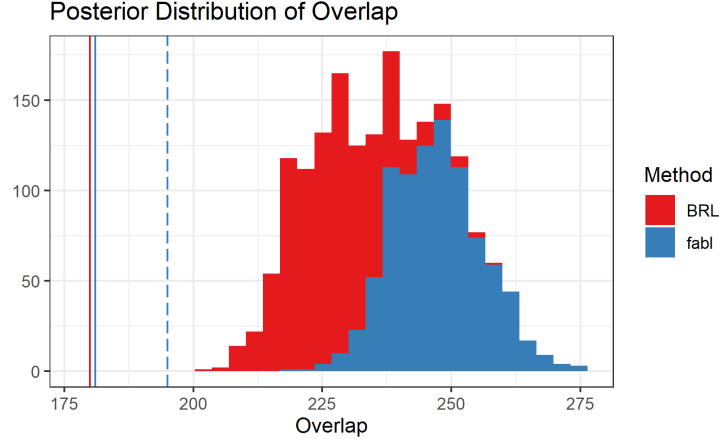


Figure 5: Posterior distribution of overlap across the two files. The solid lines show the Bayes estimate for the amount of overlap, and the dashed line is the Bayes estimate under `fabl` before resolving violations of one-to-one matching

	lastname	firstname	dataset	day	month	year	dept	muni
825	PINEDA	ROSA	CDHES	6	4	1984	NA	NA
826	PINEDA	ROSAMARIA	CDHES	6	4	1984	NA	NA
2776	PINEDA	ROSAMARIA	ER-TL	4	4	1984	CUSCATLAN	NA

Figure 6: Example of linkage situation with multiple plausible matches

Figure 7 shows the values that  $Z_{825}$  and  $Z_{826}$  take on throughout the Gibbs sampler, and demonstrates how each method handles this situation. Under `fabl`, both records in  $B$  match to the same record in  $A$  throughout the Gibbs process, creating consistent violations of one-to-one matching. Under `BRL`, the Gibbs process creates one matching configuration stays there for a while. However, if one pair “unmatches,” then the other record has a chance to latch on. Then, the Gibbs process is stuck with that matching status for a while, resulting in a Gibbs process with poor mixing. Additionally, `fabl` allows the modeler to inspect records with multiple plausible matches, and if they desire, to then choose the record pairing with the highest posterior probability. `BRL` in contrast, in strictly enforcing one-to-one matching throughout the sampler, can lead to situations where none of the plausible matches reach the threshold to be identified through the Bayes estimate.

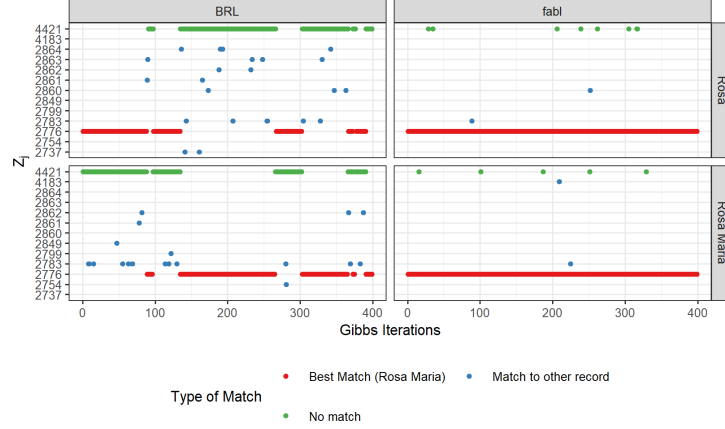


Figure 7: Gibbs sampling in situation with multiple plausible matches.

## 8 DISCUSSION

We have presented a method for Bayesian record linkage that is feasible for large datasets. In particular, our hashing procedure and model assumptions allow for a linkage procedure whose computational complexity does not scale with the size of the larger dataset, making this method particularly powerful in linking records when one datafile is substantially smaller than the other.

In our case study, we included an exploration of how to conduct record linkage when modeling assumptions are not met in practice. We explored “one-to-many” scenarios in which one record in  $A$  has multiple plausible matches in  $B$ , and showed how both **fabl** and **BRL** demonstrated undesirable qualities. Other issues arise under “many-to-one” scenarios, where one record in  $B$  has multiple plausible matches in  $A$ , and “many-to-many” scenarios in which there is duplication both across and within datasets. Tuning **fabl** for use in these scenarios is one potential avenue for future work.

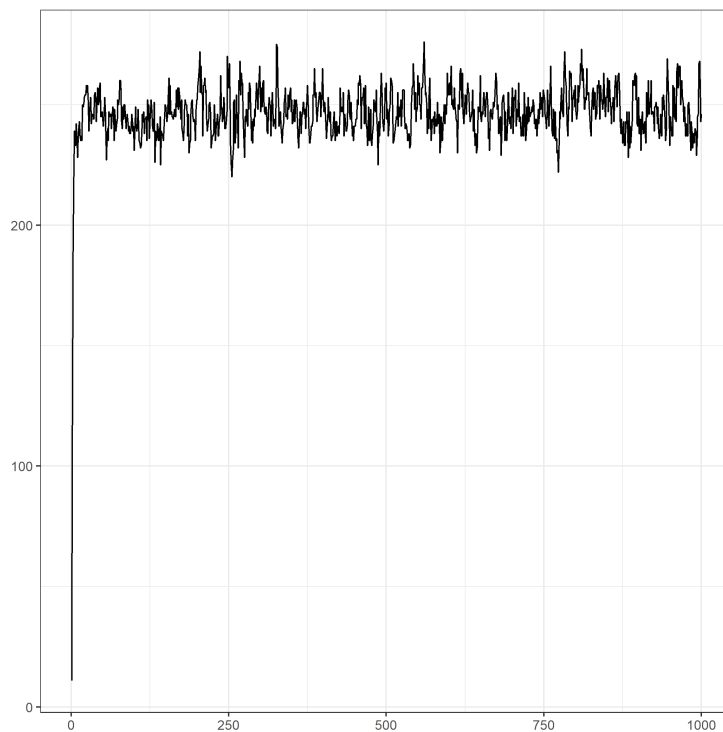


Figure 8: Traceplot for number of matches found across datasets in El Salvador case study

## 9 APPENDIX

### REFERENCES

- Enamorado, T. and Imai, K. “Validating self-reported turnout by linking public opinion surveys with administrative records.” *Public Opinion Quarterly*, 83(4):723–748 (2019).
- Fellegi, I. and Sunter, A. “A theory for record linkage.” *Journal of the American Statistical Association*, 64:1183–1210 (1969).
- Hof, M. H., Ravelli, A. C., and Zwinderman, A. H. “A Probabilistic Record Linkage Model for Survival Data.” *Journal of the American Statistical Association*, 112(520):1504–1515 (2017).
- Hu Y., V. D. C. P., Wang Q. “Improving Temporal Record Linkage Using Regression Classification.” *Advances in Knowledge Discovery and Data Mining* (2017).
- Jaro, M. “Advances in record-linkage methodology as applied to matching the 1985 census of Tampa, Florida.” *Journal of the American Statistical Association*, 84:414–420 (1989).

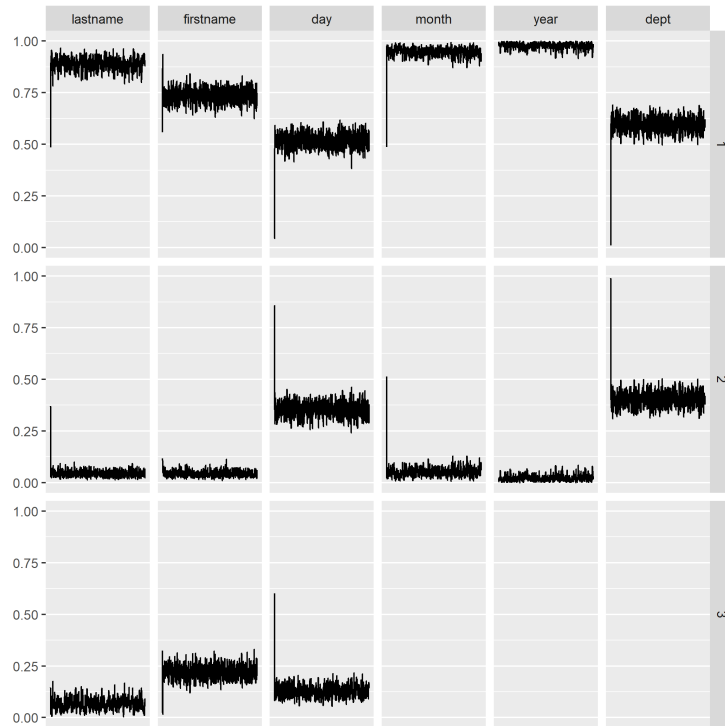


Figure 9: Traceplot for  $m$  parameter in El Salvador case study

—. “Probabilistic linkage of large public health data files.” *Statistics in Medicine*, 14:491–498 (1995).

Larsen, M. “Advances in record linkage theory: Hierarchical Bayesian record linkage theory.” In *Proceedings of the Section on Survey Research Methods*, 3277–3284. Alexandria, VA: American Statistical Association (2005).

Newcombe, H., Kennedy, J., Axford, S., and James, A. “Automatic linkage of vital records.” *Science*, 130:954–959 (1959).

Sadinle, M. “Bayesian estimation of bipartite matchings for record linkage.” *Journal of the American Statistical Association*, 112(518):600–612 (2017).

Steorts, H. R., R. and Fienberg, S. “A Bayesian Approach to Graphical Record Linkage and De-duplication.” *In Revision* (2014).



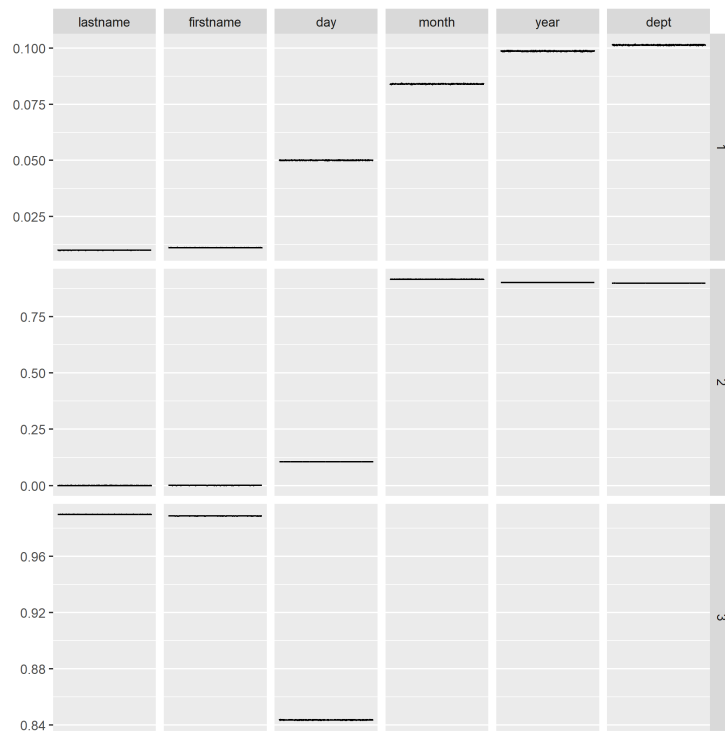


Figure 10: Traceplot for u parameter in El Salvador case study