

Efficient and Scalable Entity Resolution with Fast Beta Linkage (fabl)

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Abstract

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1 INTRODUCTION

Entity resolution (or 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.

In this paper, we propose an extension to the *Beta Record Linkage* (BRL) method proposed by (Sadinle, 2017) for this very end. We increase the speed of the BRL procedure through the 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 Section 4 describes strategies used for more efficient and scalable implementation. Then, Section 5 demonstrates the accuracy and speed of our method through two simulation studies, and Section 6 reveals interesting properties of the method through a case study of El Salvadoran casualty records. Lastly, our discussion 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 Γ , which contains similarity scores between each pair of records across datasets. We say γ_{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.

Sadinle's Method for Bipartite Matching BRL 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. However, accounting for these dependencies throughout the linkage process is computationally burdensome, leaving BRL only suitable for small to moderate linkage problems.

Other Approaches (Will probably remove) Outside of the Fellegi-Sunter framework, some researchers have developed methods that model the data directly, not a derived set of comparison vectors. As an early example, produced **blink**, which had the advantage of a computational complexity that grew linearly with the data (as opposed to quadratically within Fellegi Sunter), but was plagued with slow mixing times and was unable to incorporate text data. Later, Steorts et al 2020 improved on this method with **dblink**, which was able to simulate text data within its Gibbs sampler by drawing from an empirical distribution, and remedied its slow mixing through a probabilistic blocking approach. However, this method remains computationally intensive and requires distributed computing to manage even moderate linkage problems in acceptable time. Because these methods fall outside of the Fellegi-Sunter framework, we do not consider them further in this paper.

3 A SCALABLE MODEL FOR BAYESIAN RECORD LINKAGE

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 γ_{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 provides 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, first name and gender are two clearly dependent fields), 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 λ 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.

$$P(\Gamma | \mathbf{Z}, \mathbf{m}, \mathbf{u}, \lambda) = \prod_{j=1}^{n_B} \prod_{i=1}^{n_A} \mathbf{m}_{ij}^{\mathbf{1}_{z_j=i}} \mathbf{u}_{ij}^{\mathbf{1}_{z_j \neq i}}$$

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

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

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

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

The prior for Z_j has equal probability of matching to all records $i \in A$, and non-matching probability governed by λ . 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 explore the ramifications of this distinction with the El Salvador case study.

3.2 Posterior Sampling

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

$$p(\mathbf{Z}, \mathbf{m}, \mathbf{u}, \lambda | \Gamma) \propto p(\Gamma | \mathbf{Z}, \mathbf{m}, \mathbf{u}) p(\mathbf{Z} | \lambda) p(\mathbf{m}, \mathbf{u}) p(\lambda)$$

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 $\alpha_{fl}(\mathbf{Z}) = \sum_{i,j} \mathbf{1}_{obs(\gamma_{ij}^f)} \mathbf{1}_{\gamma_{ij}^f=l} \mathbf{1}_{z_j=i}$ and $\beta_{fl}(\mathbf{Z}) = \mathbf{1}_{obs(\gamma_{ij}^f)} \mathbf{1}_{\gamma_{ij}^f=l} \mathbf{1}_{z_j \neq i}$.

Sample $\lambda^{(s+1)} | \mathbf{Z}^{(s)}$: As a function of λ , 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

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

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 $\Gamma_{.j}$ denote the set of n_A comparison vectors with $j \in B$, and note that as a function of Z_j , the likelihood $p(\Gamma_{.j} | Z_j, \mathbf{m}, \mathbf{u}) = \mathcal{L}(Z_j | \Gamma_{.j}, \mathbf{m}, \mathbf{u})$ is a discrete distribution with probabilities proportional to

$$\begin{aligned} p(\Gamma_{.j} | Z_j = z_j, \mathbf{m}, \mathbf{u}) &\propto \prod_{i=1}^{n_A} \mathbf{m}_{ij}^{\mathbf{1}_{z_j=i}} \mathbf{u}_{ij}^{\mathbf{1}_{z_j \neq i}} \\ &\propto \prod_{i=1}^{n_A} \left(\frac{\mathbf{m}_{ij}}{\mathbf{u}_{ij}} \right)^{\mathbf{1}_{z_j=i}} && \text{By dividing through by } \prod_{i=1}^{n_A} \mathbf{u}_{ij} \\ &= \begin{cases} w_{ij} & z_j \leq n_A; \\ 1 & z_j = n_A + 1 \end{cases} \end{aligned}$$

where $w_{ij} = \frac{\mathbf{m}_{ij}}{\mathbf{u}_{ij}} = \frac{P(\gamma_{ij}|Z_j=i)}{P(\gamma_{ij}|Z_j \neq i)}$. 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 λ 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, θ_R is the loss from not making a decision on the linkage status, θ_{10} is the loss from a false non-match, θ_{01} is the loss from a false match, and θ_{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 indepth 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. 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 γ_{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 . 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 were used by (Enamorado and Imai, 2019) to produce **fastlink** a fast a scalable implementation of the Fellegi-Sunter model, and others have been created here for our particular context.

4.1 Data Representation, Hashing, and Storage

The classic Fellegi Sunter method represents the γ_{ij} comparison vector as vector of length F , with each component γ_{ij}^f taking on values in $\{1, \dots, L_f\}$. To ease computations, we instead represent the comparison as a concatenation of F many binary indicator vectors of lengths L_f . 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 will ease calculations and posterior updates. This is also the form the data takes in the **BRL** package in **R**.

In the classic Fellegi Sunter framework, Γ 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 a hashed value 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 α 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 β 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,

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

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

Lastly, we recognize that all posterior updates are governed by the agreement patterns

$$\begin{aligned}\text{Recall} &= \frac{\text{Matches Correctly Identified}}{\text{True Matches in Data}} \\ \text{Precision} &= \frac{\text{Declared Matches}}{\text{True Matches in Data}} \\ \text{F-Measure} &= 2 \left(\frac{\text{Recall} \times \text{Precision}}{\text{Recall} + \text{Precision}} \right)\end{aligned}$$

Figure 1: Definitions of performance metrics

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.

6 SIMULATION STUDIES

In his 2017 paper, Sadinle demonstrated the accuracy of his method by running **BRL** on simulated pairs of files with differing levels of errors and overlap. Each file consists of first name, last name, gender, postal code, age, and occupation, and following Sadinle’s implementation, we use only four fields for the linkage process: both names, age, and occupation. Similarity scores for the names are binned into three levels according the default settings for the `compareRecords` function in the **BRL** package, and age and occupation similarity scores are binary for exact matching. We use flat priors for all \mathbf{m} and \mathbf{u} parameters, and run the Gibbs sampler for 1000 iterations, with the first 100 discarded as burn-in.

Comparing our method against **BRL** on these same simulated datasets, we find that our method only has weakened performance in the most extreme scenario of very high errors and very high overlap across files. We use the following measures of accuracy in our analysis: although using only recall and precision is common in the literature, we find it useful to have a single metric to gauge overall performance, and thus also include F measure.

To demonstrate speed, we generate comparison vectors from pre-specified distributions

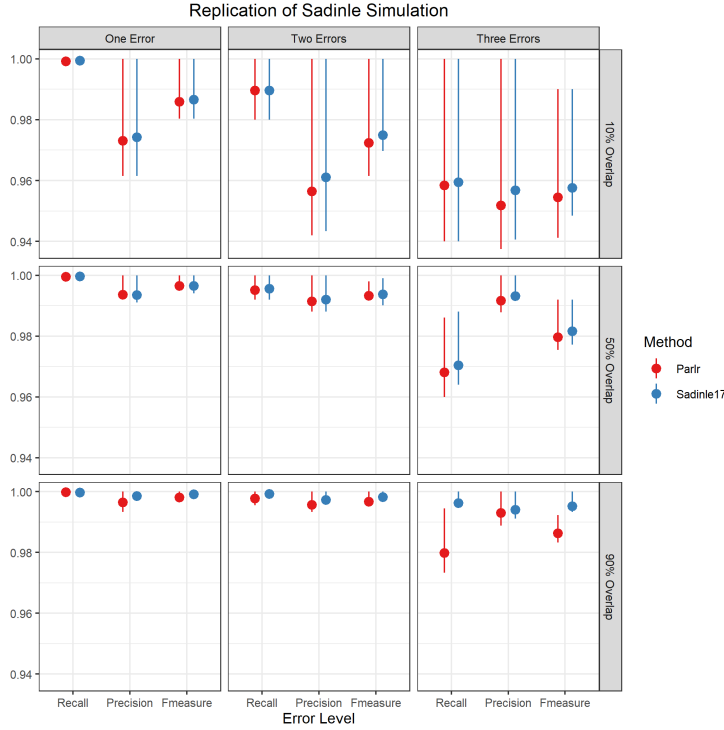


Figure 2: Posterior means and credible intervals for accuracy metrics under the replication of simulation study from Sadinle 2017. For each level of overlap and each level of error, we have 100 paired sets of 500 records.

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 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,

	m	u
fname	(0.95, 0.05)	(0.01, 0.99)
lname	(0.95, 0.05)	(0.01, 0.99)
day	(0.95, 0.05)	(0.03, 0.97)
month	(0.95, 0.05)	(0.08, 0.92)
year	(0.95, 0.05)	(0.07, 0.93)

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

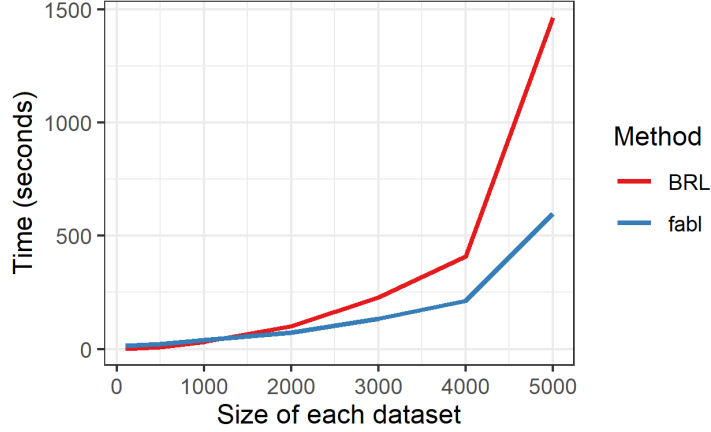


Figure 3: Run-time for BRL and fabl to run 1000 Gibbs iterations, including hashing step for fabl, for increasing values of both n_A and n_B

fixing $n_B = 500$, we see linear growth for the run-time under BRL as n_A increases, with 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.

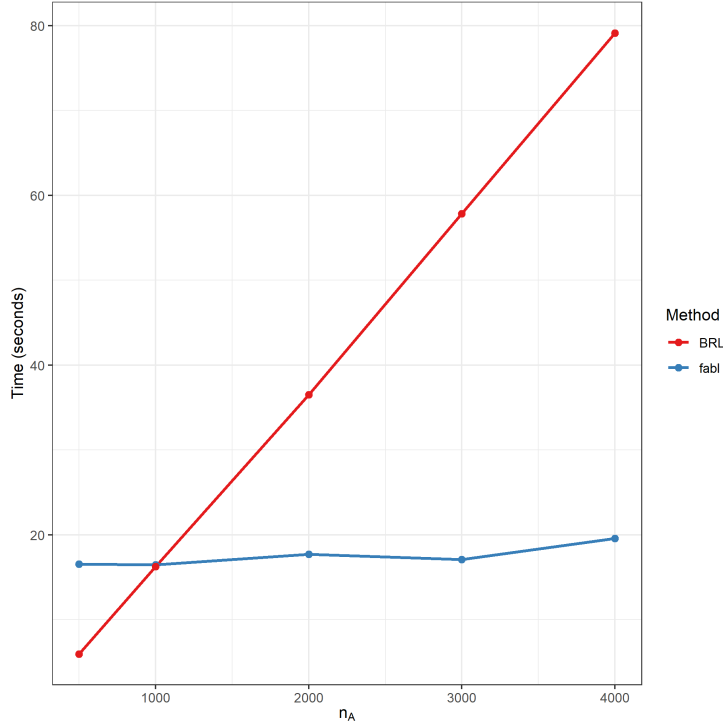


Figure 4: Run-time for BRL and fabl to run 1000 Gibbs iterations, including hashing step for fabl, with increasing n_A , and n_B fixed at 500

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** 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.

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 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

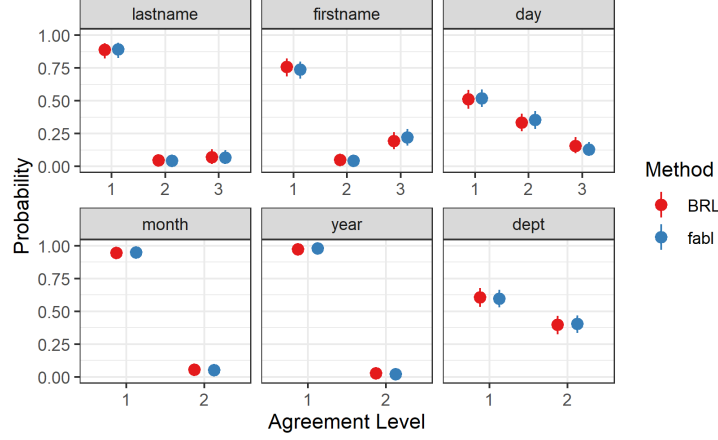


Figure 5: Posterior estimates of m parameters with 95% credible intervals

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 5.

Violations of One-to-One Matching Figure 6 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

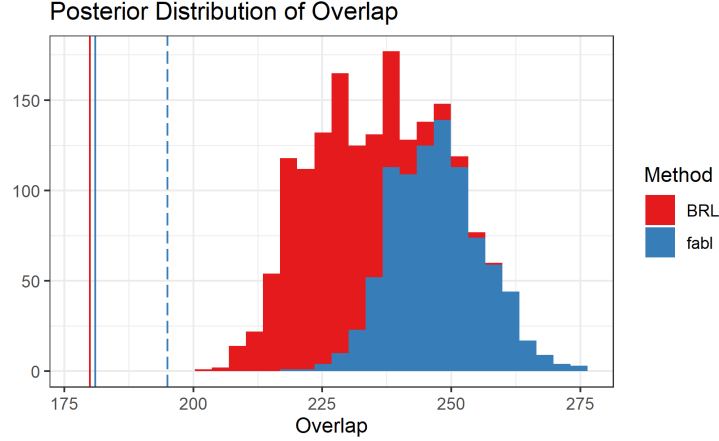


Figure 6: Posterior distribution of overlap across the two files. The solid lines show the Bayes estimate for the amount of overlap, and the dashed line is the Bayes estimate under `fabl` before resolving violations of one-to-one matching

	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 7: Example of linkage situation with multiple plausible matches

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 7 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

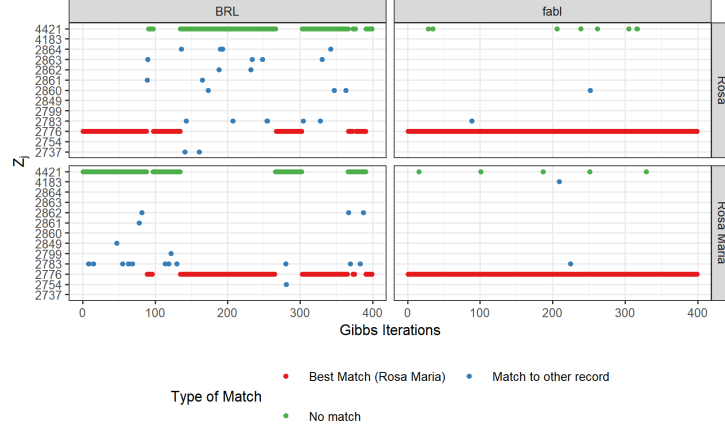


Figure 8: Gibbs sampling in situation with multiple plausible matches.

records are nearly identical. Additionally, using the modified Levenshtein distance from Sadinle 2017, the comparison vectors $\gamma_{2776,825}$ and $\gamma_{2776,826}$ are exactly identical.

Figure 8 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.

7.2 National Long Term Care Survey

The National Long Term Care Survey is a longitudinal study to track changes in health among Medicare recipients. It was conducted approximately every five years, and we concern ourselves here with linking records from years 1982 and 1989. The data only contains day, month, and year of birth, sex, state the individual lives in, and regional office. State and

regional office have been anonymized, presented as numbers instead of their actual values. We construct the comparison vectors using only binary exact matching for each field, since there is no straightforward way to incorporate partial matching in this context. The 1982 file contains $n_A = 20485$ records, 1989 file contains $n_B = 17466$ files, and the six linkage fields induces $2^6 = 64$ possible unique agreement patterns. We note that linkage quality is bound to be quite weak for many potential matches with such a large number of records and such limited identifying information.

With such large files, performing all-to-all comparisons under the original Fellegi-Sunter framework is infeasible. Indeed, this would require nearly 400 million comparison vectors, each containing 6 integer comparisons; the resulting data object would contain over 2 billion integers, and would require approximately 16 GBs of memory to hold. Instead, we take the partitioning approach reviewed in 4.1, and split each dataset into 10 smaller datasets. We use parallel computing on cluster service create the comparison vectors for each pair of data chunks, hash the results, and compress in size through storage efficient indexing. We then aggregate the results, creating a data object of just 87 MB, and proceed with the Gibbs Sampler.

Were a personal computer able to hold the 16 GB data object required by the direct approach, the Gibbs sampler under BRL would be tortuously slow, with computational complexity $O(n_A \times n_B \times F)$ where $n_A = 20485$. However, under `fabl` the sampler has complexity $O(P \times n_B \times F)$ where $P = 64$, so 1000 iterations of the Gibbs sampler are completed in just XX seconds. Posterior analysis yields an initial estimate of 9991 individuals linked across the the two datasets, and 8895 individuals linked once conflicts are resolved to ensure one-to-one matching.

Lastly, we comment on the significance of conducting this linkage without the use of deterministic blocking. With previous methods, one could link these two records by blocking on a certain field, and running separate Gibbs samplers on each of the separate blocks. This strategy drastically improves computation since it significantly reduces the number of comparison vectors that need to be formed and uses smaller data objects throughout the sampler. However, this computational savings comes at the cost of missing potential links,

specifically in cases where the blocking variable is recorded in error. In this case, 62 of the matched pairs exhibit a disagreement in sex, 17 exhibit a disagreement in state, and 39 exhibit a disagreement in regional office. We have no way to verify that the matches found under **fabl** are indeed correct, so it is possible that matches found with such disagreements are false positives. Even if not, the modeler may conclude that, for example, 17 missed matches are a small price to pay to be able to block on state and run 50 smaller, independent linkage procedures. However, **fabl** allows the modeler to make this choice for themselves, rather than being forced to do so for computational reasons. Additionally, by running on the Gibbs sampler the entirety of both files, we achieve m and u parameters that are interpretable for the entire study, rather than separate parameters for each block. Although these m and u 's are often regarded as nuisance parameters in the record linkage literature, **fabl** allows for study of these parameters that has been possible before.

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.

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