

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

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Abstract. Within the field of record linkage, Bayesian methods have the crucial advantage of quantifying uncertainty from imperfect linkages. However, current implementations of Bayesian Fellegi-Sunter models are computationally intensive, making them challenging to use on larger-scale record linkage tasks. To address these computational considerations, we propose fast beta linkage (**fabl**), an extension to the Beta Record Linkage (BRL) method of [Sadinle \(2017\)](#). Specifically, we use independent prior distributions over the matching space, allowing us to use hashing techniques that reduce computational overhead. This also allows us to complete pairwise record comparisons over large data files through parallel computing and to reduce memory costs through a new technique called storage efficient indexing. Through simulations and two case studies, we show that **fabl** has markedly increased speed with minimal loss of accuracy when compared to BRL.

Keywords: Bayesian methods, distributed computing, entity resolution, hashing, record linkage.

1 Introduction

In many data analysis tasks, analysts seek to identify duplicate records across two data files. This is an increasingly important task in “data cleaning” and is used for inferential and predictive analyses in fields such as statistics, computer science, machine learning, political science, economics, precision medicine, official statistics, and others ([Christen, 2012](#); [Gutman et al., 2013](#); [Dalzell and Reiter, 2018](#); [Tang et al., 2020](#)). In this article, we consider bipartite record linkage, which merges two data files that contain duplications across, but not within, the respective data files.

Many statistical record linkage methods are extensions of the seminal work of [Fellegi and Sunter \(1969\)](#) and [Newcombe et al. \(1959\)](#). Specifically, [Fellegi and Sunter \(1969\)](#) created comparison vectors for each pair of records in the data files and independently classified each pair as a match or a non-match using a likelihood ratio test. Recent work in the statistical literature has extended this approach for a wide variety of applications ([Winkler and Thibaudeau, 1990](#); [Fair, 2004](#); [Wagner et al., 2014](#); [Gill and Goldacre, 2003](#); [Enamorado et al., 2019](#); [Aleshin-Guendel and Sadinle, 2022](#)). Additionally, some methods directly model the linkage variables ([Steorts et al., 2016](#); [Marchant et al., 2021](#); [Betancourt et al., 2022](#)), but in this paper, we build on the contributions to the comparison vector approach.

The independent pairwise matching assumption from [Fellegi and Sunter \(1969\)](#) is popular mainly for its mathematical simplicity, but can be unreasonable in practice. In many situations, we know that there are no duplications within a data file, meaning

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39 that each record in one file should be linked with at most one other record in the other
40 file. Thus, when the procedure results in many-to-one matches, some of these links must
41 be false. Many extensions to Fellegi and Sunter (1969) resolve these false matches as a
42 post-processing step (Jaro, 1989), but this model misspecification can still lead to poor
43 results (Sadinle, 2017).

44 Alternatively, one can embed one-to-one matching requirements into the model
45 specification itself (Gutman et al., 2013; Tancredi and Liseo, 2011), at an additional
46 computational cost. Larsen (2005) employed a Metropolis-Hastings algorithm to only
47 allow sampling matches that respected one-to-one assumptions, but such algorithms
48 exhibit slow mixing due to the combinatorial nature of the constrained matching space.
49 Fortunato (2010) used simulated annealing to target the space of matches permitted
50 under the one-to-one constraint, but the method is computationally intensive and, to
51 our knowledge, has not been applied on data files with more than 100 records. Sadinle
52 (2017) proposed the Beta Record Linkage model (BRL), using a prior distribution over
53 the space of bipartite matchings to strictly enforce one-to-one requirements throughout
54 a Gibbs sampler. Additionally, he introduced a class of loss functions that allows for a
55 flexible estimation of the linkage structure, such that the modeler can weigh the relative
56 importance of false positives and false negatives, and identify records pairings to be
57 decided through clerical review. BRL was shown to work on larger tasks than previous
58 one-to-one methods, but in our experience, it becomes slow when applied to files with
59 more than a few thousand records.

60 In this paper, we propose fast beta linkage (**fabl**), which extends the BRL model for
61 increased efficiency and scalability. Following the suggestion in Wortman (2019), we relax
62 the one-to-one matching requirement of BRL and use independent priors over the matching
63 space. This allows us to (1) employ hashing techniques that speed up calculations and
64 reduce computational costs, (2) compute the pairwise record comparisons over large data
65 files via parallel computing, and (3) reduce memory costs through what we call storage
66 efficient indexing. These contributions allow **fabl** to perform record linkage on much
67 larger data files than previous Bayesian Fellegi-Sunter models at significantly increased
68 speed with minimal loss of accuracy. In particular, computation time under BRL grows
69 quadratically, with the size of each data file, while computation time under **fabl** grows
70 linearly, only with the size of the smaller data file.

71 In what follows, Section 2 reviews the work of Fellegi and Sunter (1969) and Sadinle
72 (2017). Section 3 proposes the **fabl** model, provides the Gibbs sampler for posterior
73 inference, and shows the loss function used to calculate the Bayes estimate for the
74 bipartite matching. Section 4 introduces the hashing technique and storage efficient
75 indexing used to increase the speed of calculations and the scale of linkage tasks amenable
76 to **fabl**. Sections 5 and 6 demonstrate the speed and accuracy of **fabl** through simulation
77 studies and case studies of homicides from the El Salvadoran Civil War and the National
78 Long Term Care Study. Finally, Section 7 summarizes our contributions and highlights
79 areas for further research.

2 Review of Prior Work

Consider two data files A and B , consisting of records A_i and B_j respectively, where $i \in \{1, \dots, n_A\}$ and $j \in \{1, \dots, n_B\}$. Without loss of generality, denote files such that $n_A \geq n_B$. Under bipartite matching, the set of matches across data files can be represented in two equivalent ways. First, we may use a matrix $\Delta \in \{0, 1\}^{n_A \times n_B}$, where

$$\Delta_{ij} = \begin{cases} 1, & \text{if records } A_i \text{ and } B_j \text{ refer to the same entity;} \\ 0, & \text{otherwise.} \end{cases} \quad (1)$$

This sparse matrix representation can become cumbersome for large linkage tasks. More compactly, bipartite matching also can be viewed as a labeling $\mathbf{Z} = (Z_1, \dots, Z_{n_B})$ for the records in B such that

$$Z_j = \begin{cases} i, & \text{if records } A_i \text{ and } B_j \text{ refer to the same entity;} \\ n_A + j, & \text{if record } B_j \text{ does not have a match in } A. \end{cases} \quad (2)$$

We can go back and forth between the two using $\Delta_{ij} = I(Z_j = i)$, where $I(\cdot) = 1$ when the expression inside the parentheses is true, and $I(\cdot) = 0$ otherwise.

Denote the set of matches by $\mathbf{M} = \{(i, j) : \Delta_{ij} = 1\}$, and the set of non-matches by $\mathbf{U} = \{(i, j) : \Delta_{ij} = 0\}$. The record linkage task can be viewed as identifying \mathbf{M} and \mathbf{U} . We refer to record pairs that are estimated as matches as “links” and to record pairs that are estimated as non-matches as “non-links.”

Intuitively, matching records (those that refer to the same entity) should be similar; records that are non-matching should be dissimilar. Fellegi and Sunter (1969) proposed encoding this using a comparison vector γ_{ij} computed for each record pair (i, j) in $A \times B$. Denote the number of criteria for comparing records by F , such that $\gamma_{ij} = (\gamma_{ij}^1, \dots, \gamma_{ij}^F)$. We collect the vectors γ_{ij} as the comparison matrix $\Gamma \in \mathbb{R}^{n_A n_B \times F}$.

The simplest way to compare any particular feature for two records is to check for exact agreement, and this is commonly used for categorical features. For example, if zip code is linking feature f , we can set $\gamma_{ij}^f = 1$ when the zip codes for records A_i and B_j agree exactly, and set $\gamma_{ij}^f = 2$ when they do not. For numerical features, we can use absolute difference between the two feature values. For example, if age is linking field f , we can set $\gamma_{ij}^f = 1$ when the ages for records A_i and B_j match exactly, $\gamma_{ij}^f = 2$ when the ages for records A_i and B_j are within one year but not equal, and $\gamma_{ij}^f = 3$ when the ages are two or more years apart. For text features, such as names, we can use string distance metrics such as Levenstein or Jaro-Winkler distance (Cohen et al., 2003). We then set thresholds that allow us to represent comparisons through discrete levels of disagreement (Bilenko and Mooney, 2006; Elmagarmid et al., 2007).

More generally, let $\mathcal{S}_f(i, j)$ denote a similarity measure for feature f of records A_i and B_j , where the range of \mathcal{S}_f can be divided into L_f intervals denoted by I_{f1}, \dots, I_{fL_f} . Here, I_{f1} represents the highest level of agreement (including complete agreement) and I_{fL_f} represents the highest level of disagreement (including complete disagreement).

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Thus, we can construct comparison vectors such that $\gamma_{ij}^f = l$ if $\mathcal{S}_f(i, j) \in I_{fl}$. The choices of I_{fl} are application specific, as we discuss in the simulation and case studies.

In the construction of comparison vectors, it is common to encounter missing information in record A_i or B_j . As a result, the comparison vector γ_{ij} will have missing values. We assume that this missingness occurs completely at random (MCAR, per Little and Rubin (2002)). With the MCAR assumption, we can marginalize over the missing data, and do all computation simply using the observed data. To notate a missing value in any γ_{ij}^f , we use $I_{obs}(\gamma_{ij}^f) = 1$ when γ_{ij}^f is observed and $I_{obs}(\gamma_{ij}^f) = 0$ otherwise.

2.1 Fellegi-Sunter Models

The seminal Fellegi and Sunter (1969) model employs two independence assumptions: first, that comparison vectors are conditionally independent given their matching status, and second, that the matching status of the record pairs are independent. Using these assumptions, Winkler (1999); Jaro (1989); Larsen and Rubin (2001); Enamorado et al. (2019) and others model the comparison data through mixture models of the form

$$\Gamma_{ij} = \gamma_{ij} \mid \Delta_{ij} = 1 \stackrel{iid}{\sim} \mathcal{M}(\mathbf{m}), \quad (3a)$$

$$\Gamma_{ij} = \gamma_{ij} \mid \Delta_{ij} = 0 \stackrel{iid}{\sim} \mathcal{U}(\mathbf{u}), \quad (3b)$$

$$\Delta_{ij} \stackrel{iid}{\sim} \text{Bernoulli}(\lambda). \quad (3c)$$

Here, \mathcal{M} and \mathcal{U} are the distributions for matching and non-matching record pairs, \mathbf{m} and \mathbf{u} are their respective sets of parameters, and λ is the marginal probability that a record pair is a match. When using comparison vectors with discrete agreement levels, \mathcal{M} and \mathcal{U} are collections of independent multinomial distributions for each linkage feature. Accordingly, $\mathbf{m} = (\mathbf{m}_1, \dots, \mathbf{m}_F)$, where $\mathbf{m}_f = (m_{f1}, \dots, m_{fL_f})$ and $m_{fl} = P(\gamma_{ij}^f = l \mid \Delta_{ij} = 1)$ for all fields f and agreement levels l . The \mathbf{u} parameters are defined similarly, with $u_{fl} = P(\gamma_{ij}^f = l \mid \Delta_{ij} = 0)$.

Within this framework, record pairs are independently classified as matches and non-matches based on the estimated parameters. However, such independent classifications often leads to links that violate one-on-one matching assumptions, requiring post-processing to achieve desirable results. To address this issue, Jaro (1989) proposed an optimization technique using the estimated model parameters to produce a bipartite matching. Sadinle (2017) later showed that this method is equivalent to a maximum likelihood estimate.

To estimate a one-to-one matching without using a post-processing step, Sadinle (2017) incorporates this constraint directly into the model through a Bayesian framework. In addition to standard Dirichlet priors for the \mathbf{m}_f and \mathbf{u}_f parameters, he proposes the “beta distribution for bipartite matching” for the linkage parameter \mathbf{Z} . He assigns a prior distribution for the probability of the indicator that a record in B has a match in A , so that $I(Z_j \leq n_A) \sim \text{Bernoulli}(\pi)$, where π itself is taken to be distributed $\text{Beta}(\alpha_\pi, \beta_\pi)$. It follows that the number of records in B that have matches, denoted $n_{AB}(\mathbf{Z}) = \sum_{j=1}^{n_B} I(Z_j \leq n_A)$, is distributed according to a Beta-Binomial($n_B, \alpha_\pi, \beta_\pi$).

Conditioning on the set of records in B that have matches, formally denoted $\{I(Z_j \leq n_A)\}_{j=1}^{n_B}$, all $n_A!/(n_A - n_{AB}(\mathbf{Z}))!$ bipartite matchings are taken to be equally likely. Thus, the beta distribution for bipartite matching, is given by

$$P(\mathbf{Z}|\alpha_\pi, \beta_\pi) = \frac{(n_A - n_{AB}(\mathbf{Z}))!}{n_A!} \frac{B(n_{AB}(\mathbf{Z}) + \alpha_\pi, n_B - n_{AB}(\mathbf{Z}) + \beta_\pi)}{B(\alpha_\pi, \beta_\pi)}, \quad (4)$$

where $B(\cdot, \cdot)$ represents the Beta function. This prior strictly enforces one-to-one matching, inducing a Gibbs sampler that removes previously matched records from the set of candidate records when sampling each Z_j . This makes the sampler inherently serial, which can be slow when working on linkage tasks with more than a few thousand records.

3 Fast Beta Linkage

In contrast to the prior over the vector \mathbf{Z} from [Sadinle \(2017\)](#), we follow [Wortman \(2019\)](#) and use independent priors for each component Z_j . However, unlike [Wortman \(2019\)](#) who proposes a flat prior for Z_j , we use a proper prior. We denote the fast Beta prior as follows. For each Z_j , we have

$$p(Z_j = z_j|\pi) = \begin{cases} \frac{1}{n_A}\pi, & z_j \leq n_A; \\ 1 - \pi, & z_j = n_A + j; \end{cases} \quad (5)$$

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

We can interpret (5) as follows: record B_j has some match in A with probability π , and each record A_i is equally likely to be that match. The hyperparameters α_π and β_π encode prior beliefs about the proportion of records in B that have matches in A .

In the [Wortman \(2019\)](#) flat prior, each value $\{1, \dots, n_A, n_A + j\}$ is a priori equally likely for Z_j . This however amounts to a prior probability of $n_A/(n_A + 1)$ that record B_j has a match in A . In our preliminary studies, the flat prior results in poor precision; hence, we prefer (5). We also note that the flat prior is equivalent to a special case of the fast Beta prior with π fixed at the mean of a Beta $(1, 1/n_A)$ random variable.

Note that linkage with `fabl` is conducted at the record level, rather than at the record pair level, as in the Fellegi-Sunter model. That is, π under `fabl` estimates the proportion of records in B that have matches, whereas λ in the Fellegi-Sunter model estimates the proportion of record pairs that are matches. We find π to be more an interpretable parameter than λ in the bipartite case. In this setting, there are at most n_B matching pairs out of $n_A n_B$ total pairs, meaning that λ is bounded above by $\frac{1}{n_A}$ and tends towards 0 as the size of the linkage task grows. Additionally, while the Fellegi-Sunter model makes $n_A \times n_B$ independent matching decisions and BRL makes n_B dependent matching decisions, `fabl` strikes a middle ground between the two, making n_B independent matching decisions. As shown in Sections 5 and 6, this allows `fabl` to fit a Bayesian record linkage model like BRL while making computational efficiency gains possible by exploiting independence.

To obtain an estimate $\hat{\mathbf{Z}}$ of the linkage structure, we use the loss functions and Bayes estimate from [Sadinle \(2017\)](#). Since the prior does not strictly enforce one-to-one

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Symbol	Description
A, B	data files
$i \in 1, \dots, n_A$	index over records in A
$j \in 1, \dots, n_B$	index over records in B
$f \in 1, \dots, F$	index over fields used for comparisons
$l \in 1, \dots, L_f$	index over agreement levels for feature f
n_{AB}	number of entities in common between A and B
γ_{ij}	comparison vector for records A_i and B_j
$Z_j = i$	records A_i and B_j match
$Z_j = n_A + j$	record B_j has no match in A
m_{fl}	$P(\gamma_{ij}^f = l Z_j = i)$
u_{fl}	$P(\gamma_{ij}^f = l Z_j \neq i)$
π	probability that a record in B has a match in A

Table 1: Summary of model notation.

157 matching, it is possible for this Bayes estimate to link multiple records in B to one record
 158 in A . To achieve a Bayes estimate that fulfills the one-to-one matching requirement,
 159 we minimize the expected loss subject to the constraint that $\hat{Z}_j \neq \hat{Z}_{j'}$ for all $j \neq j'$.
 160 Details for the initial Bayes estimate and the post-processing procedure are provided in
 161 Appendix 8.1.

For clarity, we present our full model below. A summary of notation is provided in Table 1.

$$\mathcal{L}(\mathbf{Z}, \mathbf{m}, \mathbf{u} \mid \Gamma) = \prod_{i=1}^{n_A} \prod_{j=1}^{n_B} \prod_{f=1}^F \prod_{l=1}^{L_f} \left[m_{fl}^{I(Z_j=i)} u_{fl}^{I(Z_j \neq i)} \right]^{I(\gamma_{ij}^f=l) I_{obs}(\gamma_{ij}^f)}, \quad (6a)$$

$$\mathbf{m}_f \sim \text{Dirichlet}(\alpha_{f1}, \dots, \alpha_{fL_f}), \quad (6b)$$

$$\mathbf{u}_f \sim \text{Dirichlet}(\beta_{f1}, \dots, \beta_{fL_f}), \quad (6c)$$

$$p(Z_j = z_j \mid \pi) = \begin{cases} \frac{1}{n_A} \pi, & z_j \leq n_A; \\ 1 - \pi, & z_j = n_A + j; \end{cases} \quad (6d)$$

$$\pi \sim \text{Beta}(\alpha_\pi, \beta_\pi). \quad (6e)$$

162 3.1 Gibbs Sampler

We initialize \mathbf{m} and \mathbf{u} from random draws from their prior distributions, and initialize \mathbf{Z} to reflect no matches across data files; that is, $\mathbf{Z} = (n_A + 1, \dots, n_A + n_B)$. To take the $(s + 1)$ th sample of each \mathbf{m}_f and \mathbf{u}_f given \mathbf{Z}^s , we use the full conditionals,

$$\mathbf{m}_f^{(s+1)} \mid \Gamma, \mathbf{Z}^{(s)} \sim \text{Dirichlet}(\alpha_{f1}(\mathbf{Z}^{(s)}), \dots, \alpha_{fL_f}(\mathbf{Z}^{(s)})), \quad (7a)$$

$$\mathbf{u}_f^{(s+1)} \mid \Gamma, \mathbf{Z}^{(s)} \sim \text{Dirichlet}(\beta_{f1}(\mathbf{Z}^{(s)}), \dots, \beta_{fL_f}(\mathbf{Z}^{(s)})), \quad (7b)$$

163 where $\alpha_{fl}(\mathbf{Z}^{(s)}) = \alpha_{fl} + \sum_{i,j} I_{obs}(\gamma_{ij}^f) I(\gamma_{ij}^f = l) I(z_j^{(s)} = i)$, and $\beta_{fl}(\mathbf{Z}^{(s)}) =$
 164 $\beta_{fl} + \sum_{i,j} I_{obs}(\gamma_{ij}^f) I(\gamma_{ij}^f = l) I(z_j^{(s)} \neq i)$.

Next, we sample \mathbf{Z} componentwise from the full conditionals for each Z_j :

$$p\left(Z_j^{(s+1)} = z_j | \Gamma, \mathbf{m}^{(s+1)}, \mathbf{u}^{(s+1)}, \mathbf{Z}^{(s)}\right) \propto \begin{cases} w_{z_j, j}^{(s)}, & z_j \leq n_A; \\ n_A \frac{n_B - n_{AB}(\mathbf{Z}^{(s)}) + \beta_\pi}{n_{AB}(\mathbf{Z}^{(s)}) + \alpha_\pi}, & z_j = n_A + j, \end{cases} \quad (8)$$

where, for all $i \in \{1, \dots, n_A\}$,

$$w_{ij}^{(s)} = \prod_{f=1}^F \prod_{l=1}^{L_f} \left(\frac{m_{fl}^{(s)}}{u_{fl}^{(s)}} \right)^{I(\gamma_{ij}^f=l)I_{obs}(\gamma_{ij}^f)}. \quad (9)$$

Derivations for these full conditionals can be found in Appendix 8.2.

4 Efficient and Scalable Implementation

The scale of linkage tasks possible through BRL is limited by the memory costs of storing $n_A \times n_B$ comparison vectors for every pair of records across the two data files, and the speed of the linkage algorithm over those comparison vectors. One approach to reduce the number of comparisons is blocking, which places similar records into partitions, or “blocks” (Christen, 2019). In deterministic blocking, the modeler chooses fields thought to be highly reliable, and only compares records that agree on those fields. The record linkage method is applied independently across all blocks, which can be done in parallel for additional speed gains. Of note, blocking on an unreliable field can lead to missed matches, making this form of blocking undesirable in some situations (Steorts et al., 2014).

After computing all comparison vectors within a block, the modeller can further reduce the number of comparison vectors used in the linkage algorithm through indexing. 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 that exactly match on a specified number of fields. However, the impact of indexing on model parameters is not well understood; (Murray, 2016) reviewed this issue in the context of the frequentist Fellegi-Sunter model, leaving the effect of indexing on Bayesian record linkage models to future work.

With **fabl**, we introduce two techniques to further expand the scalability of probabilistic record linkage. First, we propose hashing methods that allow us to compute sufficient statistics that reduce the computational complexity of the Gibbs sampler. Second, we introduce storage efficient indexing, which reduces the memory costs associated with unlikely matches. For convenience, Table 4.3 summarizes the notation introduced throughout this section.

4.1 Data Representation, Hashing, and Storage

Since each component γ_{ij}^f is discrete, there are only finitely many possible realizations of the comparison vector γ_{ij} . Let P be the number of patterns realized in Γ and note that it

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Symbol	Description
P	number of agreement patterns exhibited in Γ
h_p	agreement pattern p
$\gamma_{ij} = h_p$	comparison vector between records A_i and $i \in B$ exhibits pattern p
r_{p_j}	list of records in A that share agreement pattern p with record B_j
N_{p_j}	number of records in A that share agreement pattern p with record B_j

Table 2: Summary of hashing notation.

is bounded above by $P^* = F + \prod_{f=1}^F L_f$, where we have noted the possibility of missing values. Note that this quantity is controlled by the modeller in their choices for F and L_f , and does not scale with n_A or n_B . To obtain a memory efficient representation of the data, we map the agreement pattern of each record pair to a unique integer. [Enamorado et al. \(2019\)](#) accomplished this through the hashing function

$$h^*(i, j) = \sum_{f=1}^F I(\gamma_{ij}^f > 0) 2^{\gamma_{ij}^f + I(f>1) \sum_{d=1}^{f-1} (L_d - 1)}. \quad (10)$$

We then map these integers to sequential integers $\{1, \dots, P\}$. We refer to each unique agreement pattern as h_p , and to the set of unique agreement patterns as $\mathcal{P} = \{h_1, \dots, h_P\}$. When the (i, j) record pair exhibits agreement pattern p , we say $\gamma_{ij} = h_p$.

With all record pairs converted to hashed values, we identify the records in A with comparison vectors corresponding to each pattern p for each record B_j . We denote this set $r_{p_j} = \{i | \gamma_{ij} = h_p\}$, and collect all such sets in the nested list $\mathcal{R} = \{r_{p_j} | p \in \{1, \dots, P\}, j \in \{1, \dots, n_B\}\}$. We then compute the number of records in A that share agreement pattern p with record B_j , given by

$$N_{p_j} = |r_{p_j}| = \sum_{i=1}^{n_A} I(\gamma_{ij} = h_p). \quad (11)$$

We collect these counts in $\mathcal{N} = \{N_{p_j} | p \in 1, \dots, P, j \in 1, \dots, n_B\}$. As we show in Section 4.3, $\tilde{\Gamma} = \{\mathcal{P}, \mathcal{R}, \mathcal{N}\}$ serves as a set of sufficient statistics and fully characterizes the comparison matrix Γ with no loss of information.

4.2 Scaling to Large Linkage Tasks

We next introduce storage efficient indexing (SEI), which allows us to compute \mathcal{N} for all $n_A \times n_B$ record pairs but greatly reduce the memory costs associated with unlikely matches. This allows all-to-all comparisons for substantially larger linkage tasks. All records A_i that share agreement pattern p with record B_j have the same w_{ij} . Therefore, these records have the same probability to be identified as the link for record B_j . Thus, we know that records $i \in r_{p_j}$ such that N_{p_j} is large are very unlikely to be sampled consistently enough to be deemed a match through the Bayes estimate. We know this regardless of the form of the agreement pattern itself, or its associated probabilities. Therefore, rather than store all of these record labels, we store only a small number S of

208 them in a new nested list \mathcal{R}^{SEI} . Instead of storing $n_A \times n_B$ record labels, with SEI we
 209 store at most $n_B \times P \times S$ labels, regardless of how large n_A might be.

210 In practice, we recommend $S = 10$, as this reduces the number of stored indices
 211 for highly unlikely record pairings, but is not likely to eliminate any of the indices for
 212 plausible matches. Choosing S too low, like $S = 1$ or $S = 2$, can concentrate undue mass
 213 on few matches and distort linkage results. All original record pairs still contribute to
 214 the likelihood through \mathcal{N} , and thus we can proceed with posterior inference through the
 215 memory reduced $\tilde{\Gamma}^{SEI} = \{\mathcal{P}, \mathcal{R}^{SEI}, \mathcal{N}\}$.

For linkage tasks with large amounts of records, we can partition the two data files A and B into A^* and B^* smaller disjoint chunks $\{A^a | a = 1, \dots, A^*\}$ and $\{B^b | b = 1, \dots, B^*\}$ for more manageable computations. For each data file A^a , we conduct all-to-all comparisons with each B^b to construct the comparison matrix Γ^{ab} . We then conduct hashing, obtain the compressed $\tilde{\Gamma}$ for later calculations, and delete the larger Γ^{ab} from memory before continuing with the next chunk of data. In detail, we calculate

$$r_{p_j}^{ab} = \{i \in |\gamma_{ij} = h_p, j \in B^b\}, \quad (12a)$$

$$N_{p_j}^{ab} = |r_{p_j}^{ab}|, \quad (12b)$$

These can be computed serially or in parallel. We reduce memory costs through SEI on each r_{p_j} , while retaining counts of each agreement pattern through $N_{p_j}^{ab}$. Summary statistics from each pairwise chunk comparison can be easily synthesized to recover sufficient statistics for the full comparison matrix Γ . Specifically, we combine information through

$$r_{p_j}^{SEI} = (r_{p_j}^{SEI,11}, \dots, r_{p_j}^{SEI,A^*B^*}) \text{ for } a = 1, \dots, A^* \text{ and } b = 1, \dots, B^*, \quad (13a)$$

$$N_{p_j} = \sum_{a=1}^{A^*} \sum_{b=1}^{B^*} N_{p_j}^{ab}, \quad (13b)$$

216 4.3 Efficient Posterior Inference

To ground the discussion of posterior inference, we first re-express the likelihood function from (6a) in terms of the agreement patterns and summary statistics in . Let $m(p) = p(\gamma_{ij} = h_p | Z_j = i)$ be probability that records A_i and B_j form agreement pattern p given that they are a match. Similarly define $u(p)$. These probabilities are simply products of relevant \mathbf{m} and \mathbf{u} parameters. Viewed through the perspective of patterns, the likelihood is

$$\mathcal{L}(\mathbf{Z}, \mathbf{m}, \mathbf{u} | \tilde{\Gamma}) = \prod_{j=1}^{n_B} \prod_{p=1}^P \prod_{i \in r_{p_j}} m(p)^{I(Z_j=i)} u(p)^{1-I(Z_j=i)}. \quad (14)$$

217 Should this first paragraph go at the end of Section 4.1? And should I be writing r^{SEI}
 218 each time it comes up?

In this form, we can see that the statistics collected in $\tilde{\Gamma}$ are sufficient for each of the model parameters in their respective conditional likelihoods and provide straightforward

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posterior updates. Conditioning on \mathbf{Z} , we can express the conditional likelihood for \mathbf{m} and \mathbf{u} as

$$\mathcal{L}(\mathbf{m}, \mathbf{u} \mid \mathbf{\Gamma}, \mathbf{Z}) = \prod_{p=1}^P m(p)^{N_p^m} u(p)^{N_p - N_p^m} \quad (15)$$

where $N_p^m = \sum_{j=1}^{n_B} I(\gamma_{Z_j, j} = h_p)$ is the number of matching record pairs with agreement pattern p , and $N_p = \sum_{j=1}^{n_B} N_{p_j}$ is the total occurrence of pattern p in the data across all record pairs. Note that the \mathbf{m} and \mathbf{u} parameters depend on the data only through the quantities calculated from \mathcal{N} and \mathcal{P} .

Additionally, let $\boldsymbol{\alpha}_0 = (\alpha_{11}, \dots, \alpha_{FL_F})$ be a concatenated vector of prior parameters for the \mathbf{m} distributions, and define $\boldsymbol{\beta}_0$ similarly for the \mathbf{u} distributions. Let $e(h_p)$ be a one hot encoding of agreement pattern p , as described in Appendix 8.3. Then the terms needed for the posterior updates for level l of field f of the \mathbf{m} and \mathbf{u} parameters are given by the appropriate components of the vectors

$$\boldsymbol{\alpha}(\mathbf{Z}) = \boldsymbol{\alpha}_0 + \sum_{p=1}^P N_p^m \times e(h_p), \quad (16a)$$

$$\boldsymbol{\beta}(\mathbf{Z}) = \boldsymbol{\beta}_0 + \sum_{p=1}^P (N_p - N_p^m) \times e(h_p). \quad (16b)$$

These quantities are identical those presented in (7a), and (7b), but are calculated through P multiplications of scalar quantities over the vectors h_p , and then vectorized summations. This is markedly more efficient than summing over $n_A n_B$ record pairs for each field and agreement level.

Additionally, we can express the conditional likelihood for Z_j as

$$\mathcal{L}(Z_j \mid \mathbf{m}, \mathbf{u}, \tilde{\mathbf{\Gamma}}) = \prod_{p=1}^P u(p)^{N_{p_j}} \prod_{i \in r_{p_j}} w(p)^{I(Z_j=i)} \propto \prod_{p=1}^P \prod_{i \in r_{p_j}} w(p)^{I(Z_j=i)} \quad (17)$$

Should I include the proportionality step? where $w(p) = \frac{m(p)}{u(p)}$. Note that Z_j interacts with the data only through \mathcal{N} and \mathcal{R} . This likelihood also lends itself to markedly faster posterior computations. Although sampling Z_j from the full conditional provided in (8) is conceptually straightforward, it can become computationally expensive when n_A is large. This is because sampling a value from n_A options with unequal weights requires normalizing the weights to probabilities, which has a computational cost that scales with n_A . To speed up computation, we break this sampling step into two. We first sample among $P + 1$ options for the agreement pattern between B_j and its potential link, according to

$$P\left(\gamma_{Z_j^{(s+1)}, j} = h_p \mid \tilde{\mathbf{\Gamma}}, \mathbf{m}, \mathbf{u}, \mathbf{Z}^{(s)}\right) \propto \begin{cases} N_{p_j} \times w_p, & \gamma_{z_j, j} = h_p; \\ n_A \frac{n_B - n_{AB}(\mathbf{Z}^{(s)}) + \beta_\pi}{n_{AB}(\mathbf{Z}^{(s)}) + \alpha_\pi}, & \text{otherwise.} \end{cases} \quad (18)$$

Since all posterior updates are governed by the agreement patterns of the record pairs rather than the record labels themselves, we complete the entire Gibbs sampler first at the level of the P agreement patterns. Since all records in A sharing the same agreement pattern with B_j are equally likely, we then sample among candidate records uniformly using

$$P\left(Z_j^{(s+1)} = z_j \mid \gamma_{z_j^{(s+1)},j} = h_p\right) = \begin{cases} \frac{1}{N_{p_j}}, & z_j \in r_{p_j}; \\ 0, & \text{otherwise.} \end{cases} \quad (19)$$

227 These changes can greatly improve the speed of the sampler, and each can be paral-
 228 lelized if desired for additional computational speed-ups. We emphasize the computational
 229 gains of this split sampler through Lemma 1.

230 **Lemma 1.** *Recall that n_A and n_B are the number of records in A and B , respectively.*
 231 *Let F be the number of fields used for comparisons across records, and P be the number*
 232 *of patterns that comparison vectors exhibit in $A \times B$. We assume C cores available for*
 233 *parallelization and a Gibbs sampler with T iterations. Then, the overall computational*
 234 *complexity of **fabl** is $O(\frac{F}{C}n_An_B) + O(\frac{T}{C}n_BP)$.*

235 *Proof.* We consider two steps: constructing the comparison vectors and the Gibbs sampler.
 236 The computational complexity of all pairwise comparisons across A and B is $O(Fn_An_B)$.
 237 The hashing procedure for all pairwise comparisons is also $O(Fn_An_B)$. With B processors
 238 available, we can split these computations across B equally sized partitions and compute
 239 these comparisons in parallel, so the complexity becomes $O(\frac{F}{B}n_An_B)$. There are then
 240 trivial computational costs associated with synthesizing summary statistics across these
 241 partitions.

242 Without hashing, the computational complexity of updating the \mathbf{m} and \mathbf{u} parameters
 243 is $O(Fn_An_B)$. However, by doing calculations over the agreement patterns rather than
 244 the individual records, hashing reduces the overall complexity to $O(P)$. The complexity
 245 of updating \mathbf{Z} sequentially at the record level is $O(n_An_B)$. With hashing, we split
 246 this sampling into two steps. First, we sample the agreement pattern of the match
 247 with complexity $O(n_BP)$, and then we sample the record exhibiting that pattern with
 248 complexity $O(n_B)$. Thus, the complexity of sampling \mathbf{Z} in a single iteration is $O(n_BP)$.
 249 Since $P \ll n_A$ in most applications, we have reduced the complexity of sampling \mathbf{Z} from
 250 $O(Fn_An_B)$ under **BRL** to $O(n_BP)$ under **fabl**. With parallelization, this complexity is
 251 further reduced to $O(\frac{1}{C}n_BP)$, and so the entire Gibbs sampler has complexity $O(\frac{T}{C}n_BP)$.
 252 In summary, the total computational complexity is $O(\frac{F}{C}n_An_B) + O(\frac{T}{C}n_BP)$. \square

253 5 Simulation Studies

254 We demonstrate the speed and accuracy of **fabl** as compared to **BRL** through several
 255 simulation studies.

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	<i>m</i>		<i>u</i>	
	Agree	Disagree	Agree	Disagree
First Name	$\frac{19}{20}$	$\frac{1}{20}$	$\frac{1}{100}$	$\frac{99}{100}$
Last Name	$\frac{19}{20}$	$\frac{1}{20}$	$\frac{1}{100}$	$\frac{99}{100}$
Day	$\frac{20}{19}$	$\frac{1}{20}$	$\frac{1}{30}$	$\frac{29}{30}$
Month	$\frac{20}{19}$	$\frac{1}{20}$	$\frac{1}{12}$	$\frac{11}{12}$
Year	$\frac{20}{19}$	$\frac{1}{20}$	$\frac{1}{12}$	$\frac{11}{12}$

Table 3: Probabilities used for *m* and *u* distributions in simulation study in Section 5.1.

5.1 Speed

In our first simulation, we generate comparison vectors from pre-specified distributions so that we can easily increase the size of the linkage problem. We use $F = 5$ binary comparisons with probabilities for matching and non-matching pairs shown in Table 3. For each record in B , we simulate n_A comparison vectors, resulting in a comparison matrix $\Gamma \in \mathbb{R}^{n_A n_B \times F}$. For $n_B/2$ of these records, there is no match in A , so we simulate n_A comparison vectors from the *u* distribution. For the other $n_B/2$ of these records, there is one match in A , so we simulate 1 comparison vector from the *m* distribution, and $n_A - 1$ comparison vectors from the *u* distribution. We compare the run-time of *fabl* against BRL as we increase n_A and n_B . Since we have five binary comparison fields with no missingness, the number of unique patterns P is bounded above by $2^5 = 32$, a bound which is consistently attained in simulations with more records.

The Gibbs sampler in the implementation of BRL that we use is coded in C (Sadinle, 2017). In contrast, we use non-optimized code written only in R for *fabl*. While this complicates comparisons, and indeed disfavors *fabl*, the computational speed gains for *fabl* are still evident, especially for larger sample sizes. Additionally, although *fabl* is amenable to parallelization, this simulation is run on a single core. Implementing *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.

In Figure 1, where we increase both n_A and n_B , BRL is faster than *fabl* for low sample sizes, but *fabl* is significantly faster at handling larger sample sizes. In particular, run-time for BRL grows quadratically (or linearly with the size of both A and B) while run-time for *fabl* grows linearly (in the size of only B).

In Figure 2, where we fix $n_B = 500$, we see near linear growth for the run-time under BRL as n_A increases, and much more static run-time under *fabl*. The slight increases in run-time for *fabl* are due primarily to the hashing step, which again can be run in parallel for large data. To illustrate that these trends are generalizeable to other specifications of the comparison vectors, we have included the run-time results for an additional simulation study, under different comparison vector settings, in Appendix 8.6.

5.2 Accuracy

Computational speed-ups are only worthwhile if not accompanied by a notable loss of record linkage accuracy. Therefore, we examine the accuracy of *fabl* relative to BRL by

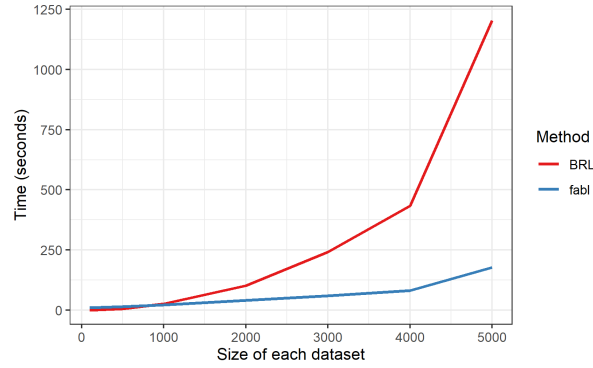


Figure 1: Run-time for BRL and `fabl` to run 1000 Gibbs iterations, including the hashing step for `fabl`, for increasing values of both n_A and n_B , as described in Section 5.1. We see near quadratic growth in run-time for BRL, and near linear growth for `fabl`.

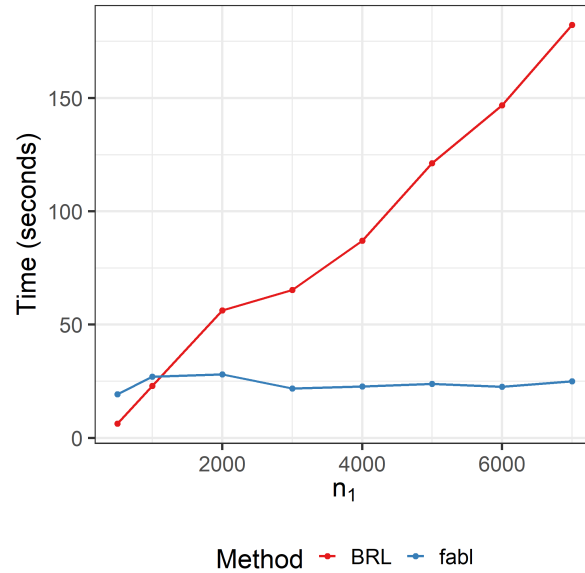


Figure 2: Run-time for BRL and `fabl` to run 1000 Gibbs iterations, including hashing step for `fabl`, with n_B fixed at 500, as described in Section 5.1. We see near linear growth in run-time for BRL, and near constant run-time for `fabl`.

288 replicating a simulation study from [Sadinle \(2017\)](#). The simulations employ a collection
 289 of synthetic data files with varying amounts of error and overlap (the number of records

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Fields	Similarity	Level of Disagreement			
		1	2	3	4
First and Last Name	Levenstein	0	(0, .25]	(.25, .5]	(.5, .1]
Age and Occupation	Binary	Agree	Disagree		

Table 4: Construction of comparison vectors for accuracy study with simulated data files of Section 5.2.

in common across files). Following methods proposed by Christen and Pudjijono (2009) and Christen and Vatsalan (2013), clean records are first simulated from frequency tables for first name, last name, age, and occupation in Australia. Fields are then chosen for distortion uniformly at random. Names are subject to string insertions, deletions and substitutions, as well as common keyboard, phonetic, and optical recognition errors. Age and occupation are distorted through keyboard errors and missingness. These synthetic data files are available in the supplement to Sadinle (2017).

We create comparison vectors according to the default settings of the `compareRecords` function from the `BRL` package, shown in Table 4. Each simulation identifies matched individuals between two data files, 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 data files. Under each of these settings, we have 100 pairs of simulated data files in order to obtain uncertainty quantification on our performance metrics. We use uniform priors for all \mathbf{m} and \mathbf{u} parameters, with $\alpha_{fl} = \beta_{fl} = 1$ for all f and l . We run the Gibbs sampler for 1000 iterations, and discard the first 100 as burn-in. We calculate Bayes estimates $\hat{\mathbf{Z}}$ of the linkage structure using the loss function and post-processing procedure described in Appendix 8.1. Traceplots for parameters of interest for one example simulation are provided in Appendix 8.5; they show no obvious concern over MCMC convergence. We also replicate this simulation allowing `fabl` to leave some components of the linkage structure undetermined and left for clerical review; these results are in Appendix 8.4.

We compare `fabl` to `BRL` in terms of recall, precision and F-measure, as defined in Christen (2012). Recall is the proportion of true matches found by the model, that is, $\sum_{j=1}^{n_B} I(\hat{Z}_j = Z_j, Z_j \leq n_A) / \sum_{j=1}^{n_B} I(Z_j \leq n_A)$. Precision is the proportion of links found by the model that are true matches, that is, $\sum_{j=1}^{n_B} I(\hat{Z}_j = Z_j, Z_j \leq n_A) / \sum_{j=1}^{n_B} I(\hat{Z}_j \leq n_A)$. The F-measure balances the two metrics to provide an overall measure of accuracy, and is defined as $2 \times (\text{Recall} + \text{Precision}) / (\text{Recall} \times \text{Precision})$. In Figure 3, we see that the two methods have comparable performance at all levels of error and overlap. In the specific case of high error and low overlap, widely regarded as the most difficult linkage scenario, we see that `fabl` performs slightly worse than `BRL` on average; however, the overall accuracy level remains high.

6 Case Studies

In our first case study, we revisit data from the El Salvadoran Civil War analyzed by Sadinle (2017). Though the data files used in this case study are small, it shows how

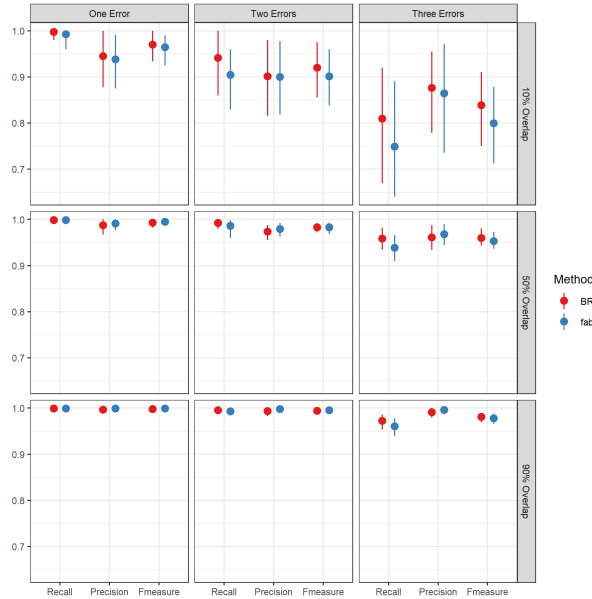


Figure 3: Posterior means and credible intervals for accuracy metrics under the replication of simulation study from [Sadinle \(2017\)](#). For each level of overlap and each level of error, we have 100 paired sets of 500 records. Thus this table summarizes results for 900 data files. We see comparable performance for all levels of error and overlap.

the computational complexity of `fabl` depends on the number of unique agreement patterns found in the data, and how significant computational gains can be achieved by simplifying the construction of the comparison vectors. In the second case study, we apply `fabl` to link records from the National Long Term Care Study, a larger linkage task that is not feasible in reasonable time under BRL with typical computing setups.

6.1 Civilian Casualties from the El Salvadoran Civil War

The country of El Salvador was immersed in civil war from 1980 to 1991, and we are interested in estimating the total number of casualties from the war. We utilize lists of casualties from the war, one collected by El Rescate - Tutela Regal (ERTL) and another from the Salvadoran Human Rights Commission (CDHES, by its acronym in Spanish).¹ The ERTL dataset comprises digitized denunciations published throughout the conflict, and the CDHES dataset comprises casualties reported directly to the organization ([Howland, 2008](#); [Ball, 2000](#)). The ERTL required additional investigation before recording denunciations as human rights abuses, and reports to the CHDES were made shortly after the events occurred; thus, both data files are thought to be fairly

¹We thank the Human Rights Data Analysis Group (HRDAG) for granting access to these data.

Fields	Similarity	Level of Disagreement			
		1	2	3	4
First and Last Name	Modified Levenstein	0	(0, .25]	(.25, .5]	(.5, 1]
Year of Death	Absolute Difference	0	1	2	3+
Month of Death	Absolute Difference	0	1	2-3	4+
Day of Death	Absolute Difference	0	1-2	3-7	8+
Municipality	Binary	Agree	Disagree		

Table 5: Construction of comparison vectors for El Salvador data resembling original implementation from [Sadinle \(2017\)](#). This setup leads to 2048 possible agreement patterns in total.

reliable. 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. Instead, record linkage techniques must be used to merge data files before analyzing the data ([Lum et al., 2013](#)).

There are several challenges with these data. First, both data files have been automatically digitized, which inherently leads to some degree of typographical error. Second, 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.

Following [Sadinle \(2017\)](#), we utilize records that have non-missing entries for given and last name, which results in $n_A = 4420$ records in CHDES and $n_B = 1323$ records in ERTL. We standardize names to account for common misspellings and use a modified Levenstein distance when comparing names to account for the fact that second names are often omitted in Spanish. Place of death is recorded by municipality and department within that municipality; however, since department is missing in 95% of records in CHDES and 80% of records in ERTL, we exclude department from our analysis. Thus, we conduct record linkage using given name, last name, municipality, and day, month, and year of death. We use uniform priors for the \mathbf{m} and \mathbf{u} parameters.

We initially followed the comparison vector constructions set by [Sadinle \(2017\)](#), using four levels of agreement for each field, according to the thresholds provided in Table 5. This results in $4^5 \times 2 = 2048$ possible agreement patterns, with 1173 patterns realized in the data. However, we noticed that the posterior distributions of several levels of the \mathbf{m} and \mathbf{u} parameters were nearly identical in an initial run of BRL, suggesting that these levels were unnecessary.

Therefore, we perform our analysis with the agreement levels for each field according to Table 6. Among the 216 possible agreement patterns, 159 are realized in the data. With this revised comparison specification, **fabl** runs in 61 seconds, approximately 4 times faster than the BRL run time of 239 seconds. The estimates of the \mathbf{m} parameters under each method are similar, as shown in Figure 5. Estimates of \mathbf{u} are indistinguishable, and thus omitted. Traceplots for parameters of interest are provided in Appendix 8.7.

For completeness, we note that linkage with the more detailed comparison vectors requires 240 seconds for BRL, and 261 seconds for **fabl**. Apparently, the number of

Fields	Similarity	Level of Disagreement		
		1	2	3
First and Last Name	Modified Levenstein	0	(0, .25]	(.25, 1]
Year of Death	Binary	Agree	Disagree	
Month of Death	Binary	Agree	Disagree	
Day of Death	Absolute Difference	0	1	2+
Municipality	Binary	Agree	Disagree	

Table 6: Construction of comparison vectors for El Salvador data for increased speed under **fabl**. This setup leads to 216 possible agreement patterns in total.

Fields	Similarity	Level of Disagreement		
		1	2	3
Sex	Binary	Agree	Disagree	
Year of Birth	Binary	Agree	Disagree	
Month of Birth	Binary	Agree	Disagree	
Day of Birth	Binary	Agree	Disagree	
Location	Custom	Same State and Office	Same State	Otherwise

Table 7: Construction of comparison vectors for NTLCS data.

patterns is sufficiently many that the computational savings from **fabl** does not overcome the inherent speed differences of C as opposed to R.

Through **fabl**, we arrive at a Bayes estimate of 179 individuals recorded in both data files. We calculate posterior samples of the size of the overlap across files by finding the number of links in each iteration of the Gibbs sampler, and subtracting the number of matches that violate one-to-one matching. The posterior 95% credible interval for the overlap across files is (206, 238), indicating that the Bayes estimate identifies fewer matches than the Gibbs sampler identifies on average. This is because a large number of records in ERTL have multiple plausible matches in CDHES; **fabl** recognizes that a match exists among the several options, but is unable to definitely declare a specific pair as a match in the Bayes estimate. We see similar results under **BRL**, with a Bayes estimate of 181 individuals recorded in both data files, and a posterior 95% credible interval of (211, 244). See Figure 4 for a visual comparison of the Bayes estimates and posterior credible intervals for the two methods. We note that Bayes estimates falling outside of posterior credible intervals has been observed previously in the record linkage literature (Sadinle, 2017; Steorts et al., 2016), and remains a topic for future research.

6.2 National Long Term Care Study

The National Long Term Care Study (NLTCS) is a longitudinal study tracking the health outcomes of Medicare recipients (Steorts et al., 2016). The initial survey began in 1982, with follow-up surveys taken approximately every five years. As such, patients are surveyed at most once in a given year, and many patients are surveyed across multiple years. In addition, patients can either drop out of the study, pass away, or enter as new patients. Hence, the assumptions of our model hold for this study. We seek to link

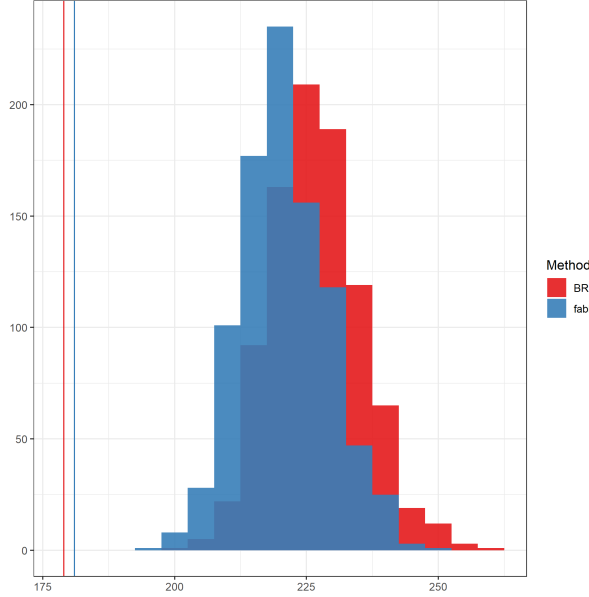


Figure 4: Posterior distribution and Bayes estimate of overlap across the two files. We note they are quite similar under both methods.

records over the $n_A = 20485$ individuals from 1982 to the $n_B = 17466$ individuals from 1989. The NLTCs data have longitudinal links, so that in reality one does not need to conduct record linkage. However, following the strategy in [Guha et al. \(2022\)](#), we break the longitudinal links and treat the data from 1982 and 1989 as stand-alone data files.

We link records using sex, date of birth, and location using the thresholds shown in Table 7. Storing three comparison scores for each of $20485 \times 17466 \approx 400,000,000$ record pairs would require approximately 8GB of memory. Standard settings on a 16GB personal computer do not allow storage of an object of this size, and thus BRL is unable to perform this linkage task on such a machine. However, through the `fabl` framework, we compute comparisons over 30 smaller comparison tasks, hash results, and compress information through storage efficient indexing. The resulting data object is just 10 MB, approximately 0.1% of what is required for the raw comparisons. Constructing the comparisons sequentially took approximately 40 minutes, which could be reduced considerably through parallel computing.

We run a Gibbs sampler for 1000 iterations, taking about 235 seconds. As shown in Figure 6, the Bayes estimate of the linkage structure consists of 9634 matches, with a 95% credible interval of (9581, 9740). Since we have access to the true linkage structure, we can calculate recall to be 0.89 and precision to be 0.98, resulting in an F-measure of 0.94. Traceplots do not suggest convergence issues, and are similar to those seen in Appendix 8.5 and 8.7

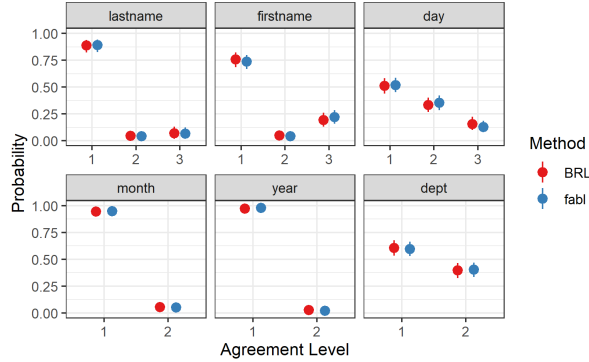


Figure 5: Posterior estimates of \mathbf{m} parameters with 95% credible intervals for the El Salvador case study. They are quite similar across the two methods.

7 Conclusion

In this paper, we have proposed **fabl**, a Bayesian record linkage method that extends the work of [Sadinle \(2017\)](#) to scale to large data sets. We have proven that the proposed hashing method and model assumptions allow for a linkage procedure whose computational complexity does not scale with the size of the larger data file. This makes **fabl** computationally advantageous in many linkage scenarios, particularly when one data file is substantially smaller than the other. We have also shown that storage efficient indexing, in tandem with hashing, greatly reduces the memory costs required for all-to-all comparisons, giving practitioners an option for larger record linkage tasks potentially even without the use of blocking or indexing. We have demonstrated the speed and accuracy of **fabl** by replicating a simulation study and a case study in [Sadinle \(2017\)](#), and through an additional case study that is computationally impractical under BRL.

Although the **fabl** method greatly reduces the memory costs for all-to-all comparisons, computing all $n_A \times n_B$ record pairs still can be prohibitive for larger linkage tasks. Indeed, constructing the comparison vectors for the NLTCs linkage task involving around 40,000 records in Section 6.2 took around 40 minutes. Due to the quadratic nature of the comparison space, this computation time would grow quickly with the size of the linkage task, and would be infeasibly slow when dealing with millions of records. Although it is common to use deterministic blocking to reduce the comparison space and then apply probabilistic record linkage within each block, issues arise when sizes of blocks vary across the linkage task. In future work, we seek to extend **fabl** to account for such deterministic blocking, making the framework amenable to arbitrarily large linkage tasks.

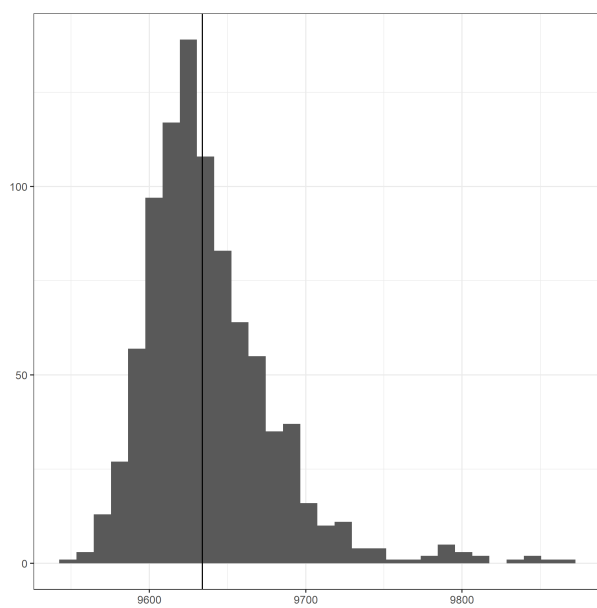


Figure 6: Posterior distribution and Bayes estimate of overlap across years 1982 and 1989 of NLCS data.

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8 Appendix

8.1 Bayes Estimate

We calculate a Bayes estimate \hat{Z} for the linkage parameter 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 $\hat{Z}_j \in \{1, \dots, n_A, n_A + j, R\}$, with R representing the option to leave the matching undetermined by the model. Specifically, we have

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

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.

In general, we set $(\theta_{10}, \theta_{01}, \theta_{11}, \theta_R) = (1, 1, 2, \infty)$ inducing the decision rule

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

Since **fabl** does not strictly enforce one-to-one matching, it is possible for this Bayes estimate to link multiple records in \mathbf{X}_2 to one record in \mathbf{X}_1 . In the event that we have two records B_j and $B_{j'}$ such that both $P(\hat{Z}_j = i | \Gamma) > \frac{1}{2}$ and $P(\hat{Z}_{j'} = i | \Gamma) > \frac{1}{2}$, we accept the match with the higher posterior probability, and declare the other to have no match. Since each Z_j is independent, this is equivalent to minimizing the expected loss subject to the constraint that $\hat{Z}_j \neq \hat{Z}_{j'}$ for all $j \neq j'$. A similar approach appears in the most probable maximal matching sets used by [Steorts et al. \(2016\)](#) to match records to latent entities.

When we seek a partial estimate of the linkage structure, leaving a portion of record pairs to be classified manually in clerical review, we adopt losses $(\theta_{10}, \theta_{01}, \theta_{11}, \theta_R) = (1, 1, 2, .1)$. For a more in-depth explanation of this function and the induced Bayes estimate, see [Sadinle \(2017\)](#).

8.2 Derivations of Full Conditionals

We provide detailed derivations of the full-conditionals provided in Section 3.1. The \mathbf{m} and \mathbf{u} parameters are updated through standard multinomial-Dirichlet distributions. For a particular m_{fl} , we have

$$p(m_{fl} | \Gamma, \mathbf{Z}) \propto \prod_{i=1}^{n_A} \prod_{j=1}^{n_B} m_{fl}^{I(Z_j=i)I(\gamma_{ij}^f=l)I_{obs}(\gamma_{ij}^f)} \times m_{fl}^{\alpha_{fl}-1}$$

$$= m_{fl}^{\alpha_{fl}(\mathbf{Z})-1},$$

556 where $\alpha_{fl}(\mathbf{Z}) = \alpha_{fl} + \sum_{i,j} I_{obs}(\gamma_{ij}^f) I(\gamma_{ij}^f = l) I(z_j = i)$. Analogous procedures lead to the
 557 posterior distribution $p(u_{fl} | \Gamma, \mathbf{Z}) \propto u_{fl}^{\beta_{fl}(\mathbf{Z})-1}$, where $\beta_{fl}(\mathbf{Z}) = \beta_{fl} + \sum_{i,j} I_{obs}(\gamma_{ij}^f) I(\gamma_{ij}^f =$
 558 $l) I(z_j \neq i)$. Thus for the vectors of parameters \mathbf{m}_f and \mathbf{u}_f , we have

$$\begin{aligned} \mathbf{m}_f | \mathbf{Z}, \Gamma &\sim \text{Dirichlet}(\alpha_{f1}(\mathbf{Z}), \dots, \alpha_{fL_f}(\mathbf{Z})), \\ \mathbf{u}_f | \mathbf{Z}, \Gamma &\sim \text{Dirichlet}(\beta_{f1}(\mathbf{Z}), \dots, \beta_{fL_f}(\mathbf{Z})). \end{aligned}$$

In order to define the full conditional for \mathbf{Z} , we must provide the posterior distribution for π , and provide a more tractable expression for the portion of the likelihood relevant to a particular record B_j . Since π encodes the rate of matching across the two data files, the posterior distribution $p(\pi | \Gamma, \mathbf{Z}, \mathbf{m}, \mathbf{u}, \alpha_\pi, \beta_\pi)$ depends only on the number of links $n_{AB}(\mathbf{Z}) = \sum_{i=1}^{n_B} I(z_j < n_A + j)$ encoded by \mathbf{Z} (and hyperparameters). Thus, we use $p(\pi | \mathbf{Z}, \alpha_\pi, \beta_\pi)$ and have

$$\begin{aligned} p(\pi | \mathbf{Z}, \alpha_\pi, \beta_\pi) &\propto p(\mathbf{Z} | \pi) p(\pi) \\ &\propto \pi^{n_{AB}(\mathbf{Z})} (1 - \pi)^{n_B - n_{AB}(\mathbf{Z})} \pi^{\alpha_\pi - 1} (1 - \pi)^{\beta_\pi - 1} \\ &\propto \pi^{n_{AB}(\mathbf{Z}) + \alpha_\pi - 1} (1 - \pi)^{n_A - n_{AB}(\mathbf{Z}) + \beta_\pi - 1}. \end{aligned}$$

559 Thus $\pi^{(s+1)} | \mathbf{Z}^{(s+1)}, \alpha_\pi, \beta_\pi$ has a $\text{Beta}(n_{AB}(\mathbf{Z}) + \alpha_\pi, n_B - n_{AB}(\mathbf{Z}) + \beta_\pi)$ distribution.

Let $\Gamma_{.j}$ denote the set of n_A comparison vectors with B_j . We have

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

where

$$w_{ij} = \prod_{f=1}^F \prod_{l=1}^{L_f} \left(\frac{m_{fl}}{u_{fl}} \right)^{I(\gamma_{ij}^f=l) I_{obs}(\gamma_{ij}^f)}.$$

560 With the likelihood in this form, we derive an expression for the posterior distribution
 561 of \mathbf{Z} . Because we sample each Z_j independently of all other $Z_{j'}$, we use only the full
 562 conditional for an individual Z_j :

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

For more direct comparability with the method from [Sadinle \(2017\)](#), we avoid sampling π directly, and instead integrate over it in the final full conditional for Z_j .

$$\begin{aligned}
& p\left(Z_j^{(s+1)} = z_j | \Gamma, \mathbf{m}, \mathbf{u}, \mathbf{Z}^{(s)}\right) \\
& = \int_{\pi} p\left(Z_j^{(s+1)} | \Gamma, \mathbf{m}, \mathbf{u}, \mathbf{Z}^{(s)}, \pi\right) p\left(\pi | \mathbf{Z}^{(s)}\right) d\pi \\
& = \int_{\pi} \left[\frac{\pi}{n_A} w_{z_j, j} I(z_j \leq n_A) + (1 - \pi) I(z_j = n_A + j) \right] p\left(\pi | \mathbf{Z}^{(s)}\right) d\pi \\
& = \frac{\int_{\pi} \pi p\left(\pi | \mathbf{Z}^{(s)}\right) d\pi}{n_A} w_{z_j, j} I(z_j \leq n_A) + \left(1 - \int_{\pi} \pi p\left(\pi | \mathbf{Z}^{(s)}\right) d\pi \right) I(z_j = n_A + j) \\
& = \frac{n_{AB}(\mathbf{Z}) + \alpha_{\pi}}{n_A(n_B + \alpha_{\pi} + \beta_{\pi})} w_{z_j, j} I(z_j \leq n_A) + \frac{n_B - n_{AB}(\mathbf{Z}) + \beta_{\pi}}{n_B + \alpha_{\pi} + \beta_{\pi}} I(z_j = n_A + j) \\
& \propto w_{z_j, j} I(z_j \leq n_A) + n_A \frac{n_B - n_{AB}(\mathbf{Z}) + \beta_{\pi}}{n_{AB}(\mathbf{Z}) + \alpha_{\pi}} I(z_j = n_A + j) \\
& = \begin{cases} w_{z_j, j} & z_j \leq n_A; \\ n_A \frac{n_B - n_{AB}(\mathbf{Z}) + \beta_{\pi}}{n_{AB}(\mathbf{Z}) + \alpha_{\pi}} & z_j = n_A + j. \end{cases}
\end{aligned}$$

8.3 One Hot Encoding Transformation

As described in Section 4, **fabl** makes use of one-hot encodings to aid in vectorized computations. For γ_{ij}^f with L_f levels, define e_{ij}^f to be an $L_f \times 1$ vector. When $\gamma_{ij}^f = l$, we set the l^{th} element of e_{ij}^f to be 1, and set the other $L_f - 1$ elements of e_{ij}^f to be 0. We then concatenate the e_{ij}^f for all $f \in \{1, \dots, F\}$, resulting in the one-hot encoded comparison vector e_{ij} of length $\sum_{f=1}^F L_f$.

For example, consider comparing the toy records shown in Table 8 with $L = (3, 3, 2, 2)$ levels of agreement for last name, first name, DOB, and city respectively. Since the first name differs by only one letter, a reasonable comparison vector for this pair would be $\gamma_{ij} = (1, 2, 1, 2)$. The one hot encoding representation of this vector is $e_{ij} = (1, 0, 0, 0, 1, 0, 1, 0, 0, 1)$.

Last Name	First Name	DOB	City
Smith	Taylor	01/01/2000	Durham
Smith	Tayler	01/01/2000	Raleigh

Table 8: Example records for one hot encoding.

8.4 Accuracy under Partial Estimates

In this section, we repeat the simulation study in Section 5.2 of the main text, allowing for clerical review rather than forcing all records to have or not have links. Specifically, by leaving $\theta_{10} = \theta_{01} = 1$ and $\theta_{11} = 2$, but setting $\theta_R = 0.1$, we allow the model to decline to decide a match for certain records, with nonassignment being 10% as costly as a false match. In this context, we are no longer focused on finding all true matches, but rather protecting against false matches. Thus, instead of recall, we use the negative predictive value (NPV), defined as the proportion of non-links that are actual non-matches. Mathematically, $\text{NPV} = \sum_{j=1}^{n_B} I(\hat{Z}_j = Z_j = n_A + j) / \sum_{j=1}^{n_B} I(\hat{Z}_j = n_A + j)$. We continue to use the precision, which is renamed the positive predictive value (PPV) in this context. Lastly, we also examine the rejection rate (RR), or how often the model declines to make a linkage decision, defined as $\text{RR} = \sum_{j=1}^{n_B} I(\hat{Z}_j = R) / n_B$. To convey this information alongside NPV and PPV, for which values close to 1 indicate strong performance, we report the decision rate (DR), defined as $\text{DR} = 1 - \text{RR}$.

In Figure 7, we see that **fabl** maintains equivalently strong PPV as **BRL** across all linkage settings. However, with high amounts of error, and thus fewer accurate and discerning fields of information, the rejection rate under **fabl** rises, leading to a decrease in NPV. Since **fabl** does not remove previously matched records from consideration for a new record, posterior probabilities of matches at times can be split across more records; in contrast, **BRL** is able to maintain higher confidence in matches in this setting. If one wishes to use partial estimates, **fabl** will possibly leave more linkages for the modeller to match by hand than would be left under **BRL**, but the decisions made by each method will have nearly equal accuracy.

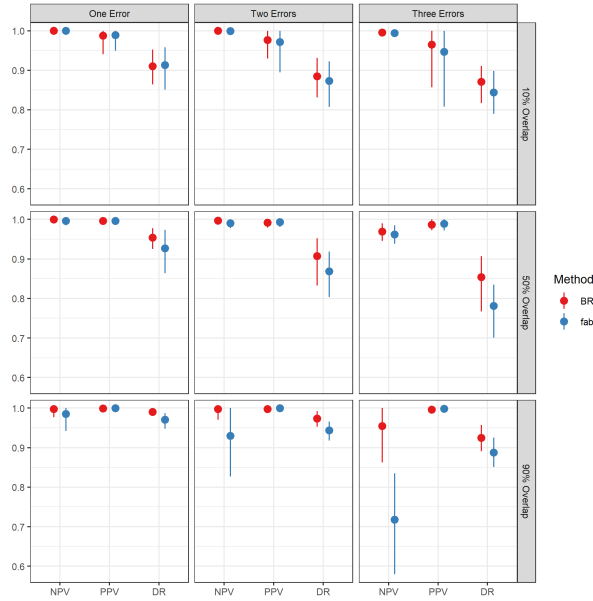


Figure 7: Negative predictive value (NPV), positive predictive value (PPV), and decision rate (DR) on data files in the simulation in Appendix 8.4. We see poorer performance for `fabl` only in situations with high overlap.

8.5 Traceplots for Simulation Study

Below are traceplots for one of the 900 linkage tasks that comprise the simulation in Section 5.2. It is set up with one error across the linkage fields and 50 duplicates across files. Traceplots across other settings exhibit similar behavior. Note that traceplots for \mathbf{u} parameters show very little variation because the overwhelming majority of record pairs are nonmatching.

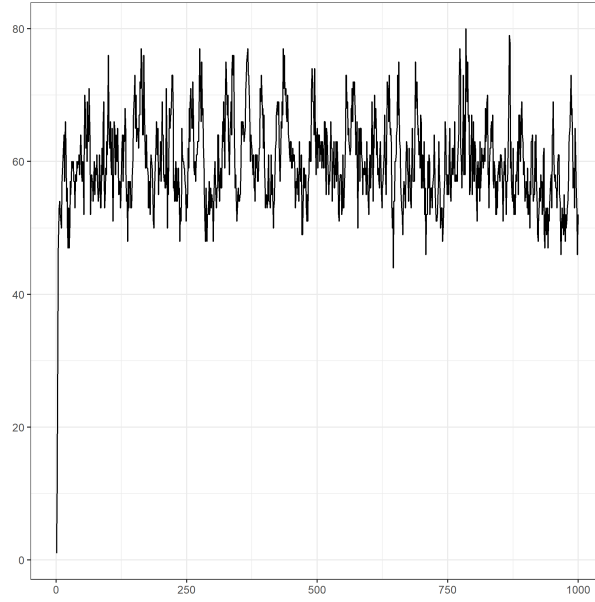


Figure 8: Representative traceplot of overlap between files from simulation study in Section 5.2.

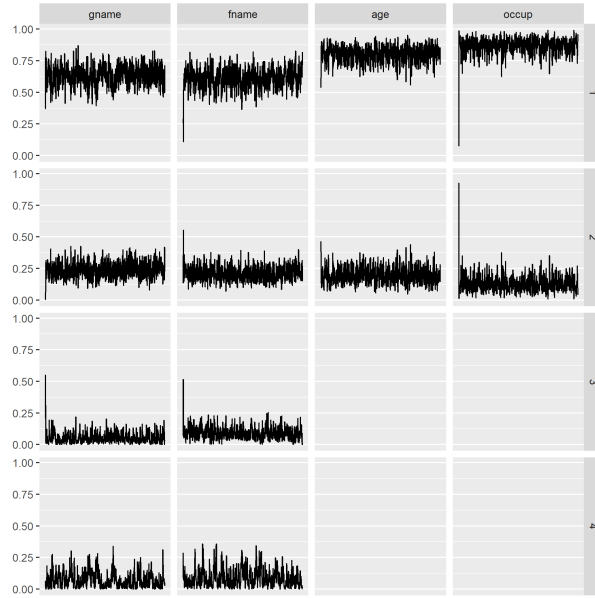


Figure 9: Representative traceplot of m parameter from simulation study in Section 5.2.

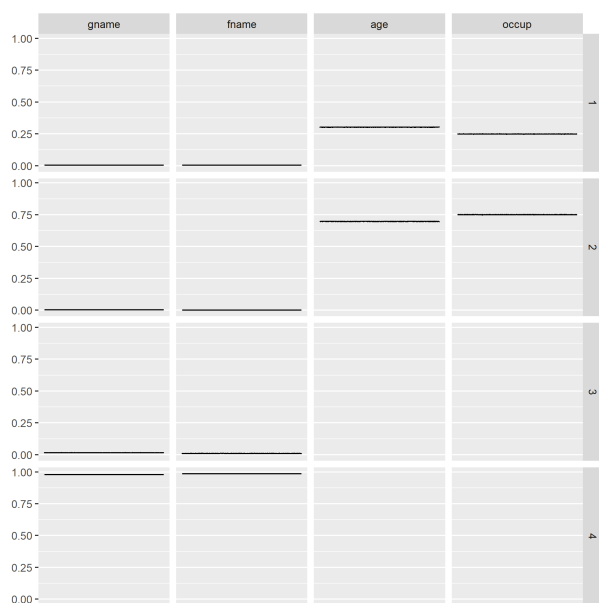


Figure 10: Representative traceplot of u parameters from simulation study in Section [5.2](#).

	\mathbf{m}			\mathbf{u}		
	Agree	Partial	Disagree	Agree	Partial	Disagree
Feature 1	$\frac{9}{10}$	$\frac{9}{100}$	$\frac{1}{100}$	$\frac{1}{100}$	$\frac{3}{100}$	$\frac{96}{100}$
Feature 2	$\frac{9}{10}$	$\frac{9}{100}$	$\frac{1}{100}$	$\frac{1}{100}$	$\frac{3}{100}$	$\frac{96}{100}$
Feature 3	$\frac{9}{10}$	$\frac{9}{100}$	$\frac{1}{100}$	$\frac{1}{100}$	$\frac{3}{100}$	$\frac{96}{100}$
Feature 4	$\frac{9}{10}$	$\frac{9}{100}$	$\frac{1}{100}$	$\frac{1}{100}$	$\frac{3}{100}$	$\frac{96}{100}$

Table 9: Probabilities used for \mathbf{m} and \mathbf{u} distributions in simulation study in Appendix 8.6.

8.6 Additional Speed Simulation Study

To illustrate that different constructions of the comparison vectors lead to similar speed gains, we replicate the speed study of Section 5.1 under different settings. Here, we use four fields of comparison, each with three possible levels of agreement, resulting in $3^4 = 81$ possible patterns. The \mathbf{m} and \mathbf{u} parameters for this simulation are shown Table 9.

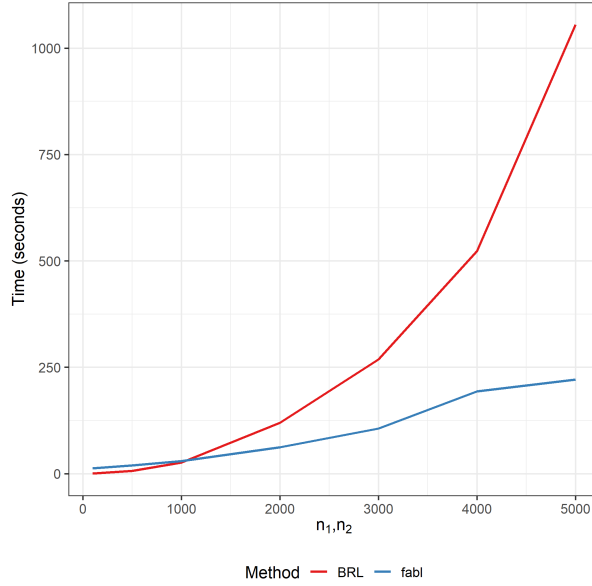


Figure 11: Run-time for BRL and `fabl` to run 1000 Gibbs iterations in simulation study in Appendix 8.6, including hashing step for `fabl`, for increasing values of both n_A and n_B . We see near quadratic growth in run-time for BRL, and near linear growth for `fabl`.

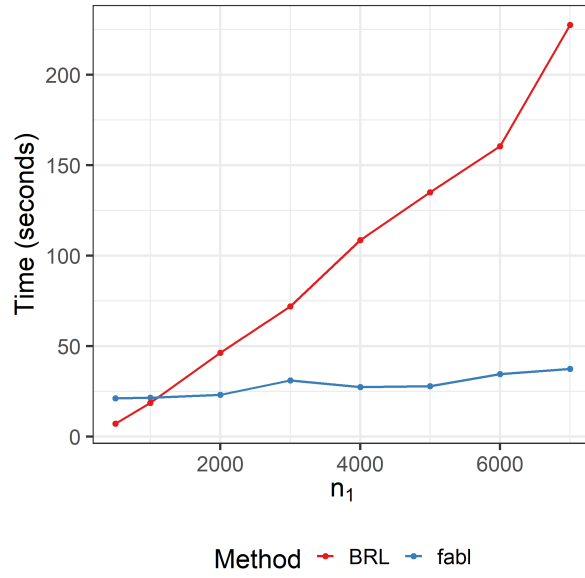


Figure 12: Run-time for BRL and `fabl` to run 1000 Gibbs iterations in simulation study in Appendix 8.6, including hashing step for `fabl`, with increasing n_A and n_B fixed at 500. We see linear growth in run-time for BRL, and near constant run-time for `fabl`.

8.7 Traceplots for El Salvador Case Study

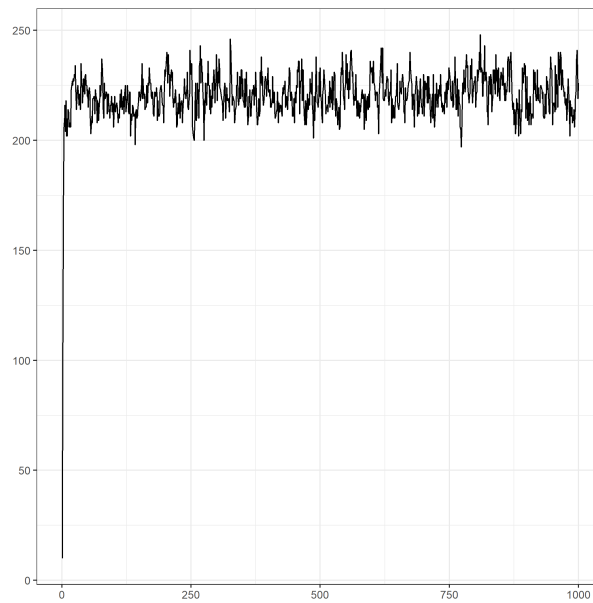


Figure 13: Traceplot for number of matches found across data files in El Salvador case study.

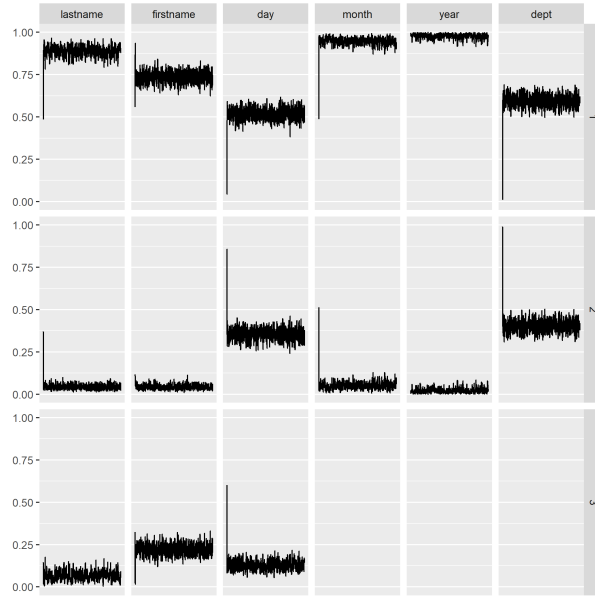


Figure 14: Traceplot for m parameter in El Salvador case study.

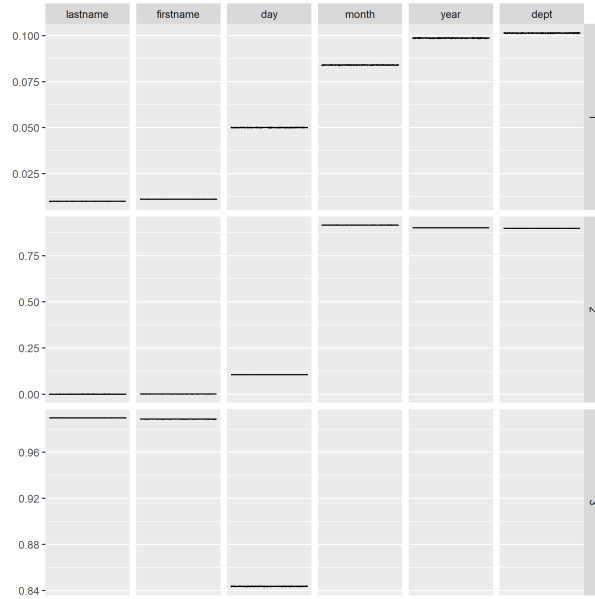


Figure 15: Traceplot for u parameter in El Salvador case study.