Parlr: Parallelized Record Linkage in R

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Introduction

Record linkage is the task of identifying duplicate records across multiple data sources. This task is straightforward when provided unique identifiers or highly reliable information, but becomes difficult when data sources are plagued with error. Additionally, many record linkage tasks are large in nature, and many existing methods are too computational intensive to be used in practice. In this paper, we propose a Bayesian model for record linkage that is amenable to parallel computing, hashing techniques and efficient storage mechanisms, that is scalable to large linkage tasks.

The proposed method is inspired by the "Beta Record Linkage" method proposed by Mauricio Sadinle's 2017 "Bayesian Estimation of Bipartite Matching for Record Linkage". As such, we demonstrate our method through a comparison of our methods against Sadinle's on the simulation study he designed and the El Salvador homocide case study he utilized. We include one additional simulation study to demonstrate the power of our method on large datasets. 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, Sections 5 and 6 demonstrate the method through simulations and a case study. Lastly, our discussion highlights open questions in the record linkage liturature and motivates future work.

Related Work

Most record linkage techniques are derived from the seminal 1969 paper by Fellegi and Sunter: "A Theory for Record Linkage". The defining characteristic of their model 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 a $n_A n_B \times F$ 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 γ_{ij}^f providing their similarity score on the fth 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. It is common to use use binary 0-1 variables to indicate exact matching, and 0-1-2 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.

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, and Jaro devised an procedure to reduce a set of conflicting matches to the mostly likely set of one-to-one matchings. One key strength of Sadinle's `BRL` is that it is garunteed to produce a set of bipartite matchings that respect one-to-one assumptions–without the need for any post-hoc 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.

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, Steorts et al 2016 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.

Notation and Assumptions

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

To indicate matching status, we adopt the *linkage structure parameter* $\mathbf{Z} = (Z_1, \ldots, Z_{n_B})$ 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, $\mathbf{m}^f = (m^{f1}, \ldots, m^{fL_f})$ is the probability distribution governing field f for matching records, and $\mathbf{m}_{ij} = \prod_{f=1}^{F} \prod_{l=1}^{L_f} \left(m^{fl}\right)^{\mathbf{1}_{\gamma_{ij}^f = l}} = P(\gamma_{ij}|Z_j = i)$ 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.

Model Specification

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

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

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

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

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

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

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 $\lambda \sim \text{Beta}(1, \frac{1}{n_A})$ 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, thereby weakening the one-to-one requirement; our sampler does ensure that each record in B can be matched to at most one record in A, but allows for the possiblity 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. With this change, components of the $\mathbf{Z}$ vector can be computed in parallel, 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. This will be explained further in .

Posterior Sampling

We work with the following factorization of the joint distribution:

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

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

$$p(\lambda | \mathbf{Z}) \propto p(\mathbf{Z} | \lambda) p(\lambda)$$

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

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

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

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

$$p(\Gamma_{\cdot j}|Z_j = z_j, \mathbf{m}, \mathbf{u}) \propto \prod_{i=1}^{n_A} \mathbf{m}_{ij}^{\mathbf{1}_{z_j=i}} \mathbf{u}_{ij}^{\mathbf{1}_{z_j \neq i}}$$

$$\propto \prod_{i=1}^{n_A} \left(\frac{\mathbf{m}_{ij}}{\mathbf{u}_{ij}} \right)^{\mathbf{1}_{z_j=i}} \qquad \text{By dividing through by } \prod_{i=1}^{n_A} \mathbf{u}_{ij}$$

$$= \begin{cases} w_{ij} & z_j \leq n_A; \\ 1 & z_j = n_A + 1 \end{cases}$$

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

$$p(Z_j|\Gamma_{\cdot j}, \mathbf{m}, \mathbf{u}, \lambda) \propto p(\Gamma_{\cdot j}|Z_j, \mathbf{m}, \mathbf{u})P(Z_j|\lambda)$$

$$\propto \left(\sum_{i=1}^{n_A} w_{ij} \mathbf{1}_{z_j=i} + \mathbf{1}_{z_j=n_A+1} \right) \left(\lambda \sum_{i=1}^{n_A} \frac{1}{n_A} \mathbf{1}_{z_j=i} + (1-\lambda)\mathbf{1}_{z_j=n_A+1} \right)$$

$$= \frac{\lambda}{n_A} \sum_{i=1}^{n_A} w_{ij} \mathbf{1}_{z_j=i} + (1-\lambda)\mathbf{1}_{z_j=n_A+1}$$

$$\implies Z_j^{(s+1)}|\mathbf{m}, \mathbf{u}, \Gamma, \lambda \propto \begin{cases} \frac{\lambda}{n_A} w_{ij} & z_j \leq n_A; \\ 1-\lambda & z_j = n_A+1 \end{cases}$$

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:

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

Bayes Estimate

(Adapt from Sadinle)

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. Rigorous proof of this resolution procedure is deferred to future work.

Efficient Computation

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 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 $h_1, \ldots, h_P$. When the (i, j) pair exhibits the pth 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.

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 $\{0, \ldots, L_f - 1\}$. 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 $\gamma_{ij} = (1, 0, 2)$ 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.

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. We however 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 pth component of the jth 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.

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, collect results, 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. Storing this hashed information still becomes burdensome for large data, but this hashing method greatly expands the capabilities of the Fellegi-Sunter framework.

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 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 random indexing, 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_j}, H_p^m, and H_p^u. 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. Coupled with the partitioning strategy for creating comparison vectors, this greatly expands the size of the linkage tasks we can undertake.

Gibbs Sampling

Updating **m** and **u**: After receiving matching statuses from **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 **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_{h_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,

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

Lastly, we recognize that all posterior updates are governed by the agreement patterns of the record pairs rather than the record labels themselves. Thuse We complete the entire Gibbs procedure at the level of the P agreement patterns. After, we can back-fill the records corresponding to the agreement patterns by sampling uniformly at random among candidate records stored in $\tilde{\Gamma}$. Sampling uniformly is computational simple even for large sets of candidate records, but this step can also be parallelized when working with large data.

Simulation Study 1 - Accuracy

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 the gauge overall performance, and thus also include F measure.

$$
\text{Recall} = \frac{\text{Matches Correctly Identified}}{\text{True Matches in Data}}
$$

$$
\text{Precision} = \frac{\text{Declared Matches}}{\text{True Matches in Data}}
$$

$$
\text{F-Measure} = 2\left(\frac{\text{Recall} \times \text{Precision}}{\text{Recall} + \text{Precision}}\right)
$$

Replication of Sadinle Simulation
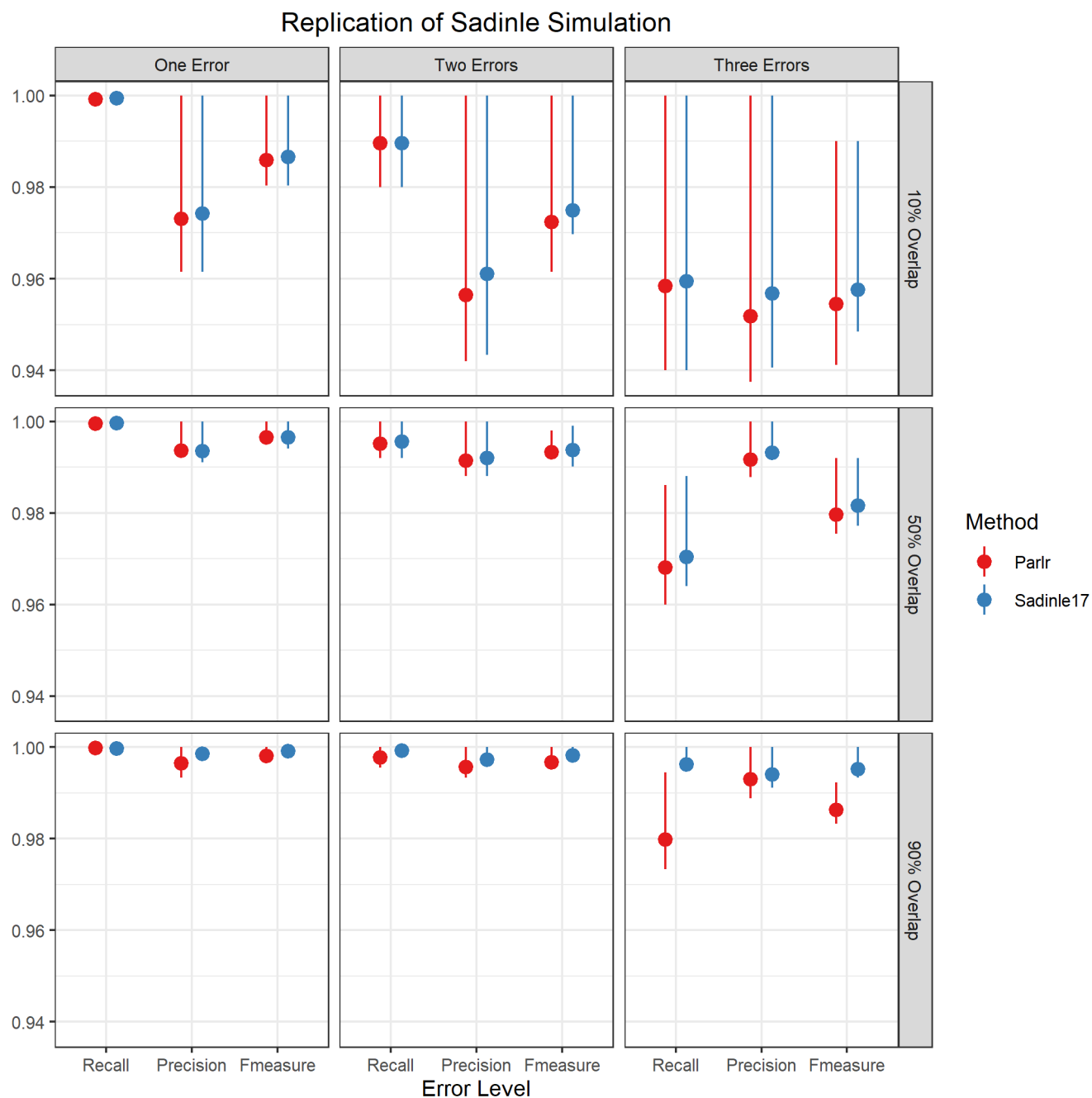
Simulation Study 2 - Speed

To demonstrate speed, we generate comparison vectors from pre-specified distributions so that we can easily increase the size of the linkage problem. Distributions are meant to emulate the behavior of similarity scores across first name, last name, and day, month, and and year of birth, with 1 indicating an exact match on a particular field and 0 indicating a nonmatch. We simulate these data for different values of n_A and n_B, and compare the

run-time of `parlr` 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 `parlr` 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 `parlr` seems to grow linearly (in the size of B).

	m	u
fname_0	0.05	0.99
fname_1	0.95	0.01
lname_0	0.05	0.99
lname_1	0.95	0.01
day_0	0.05	0.97
day_1	0.95	0.03
month_0	0.05	0.92
month_1	0.95	0.08
year_0	0.05	0.93
year_1	0.95	0.07
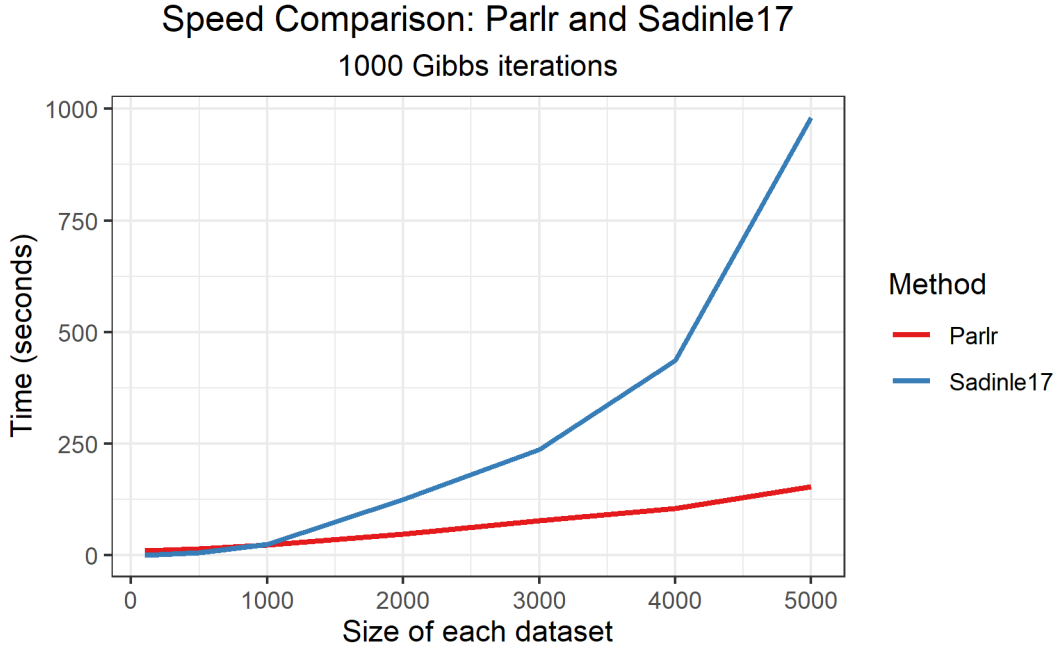
The above discussion suggests that for fixed n_B, computation time should remain mostly constant with growing n_A. Simulation study suggests that this is true. In the plot below, fixing $n_B = 500$, we see linear growth for the run-time under `BRL` as n_A increases, with much more static run-time under `parlr`. 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.

Speed Comparison: parlr and Sadinle 17

1000 Gibbs iterations, file B size fixed
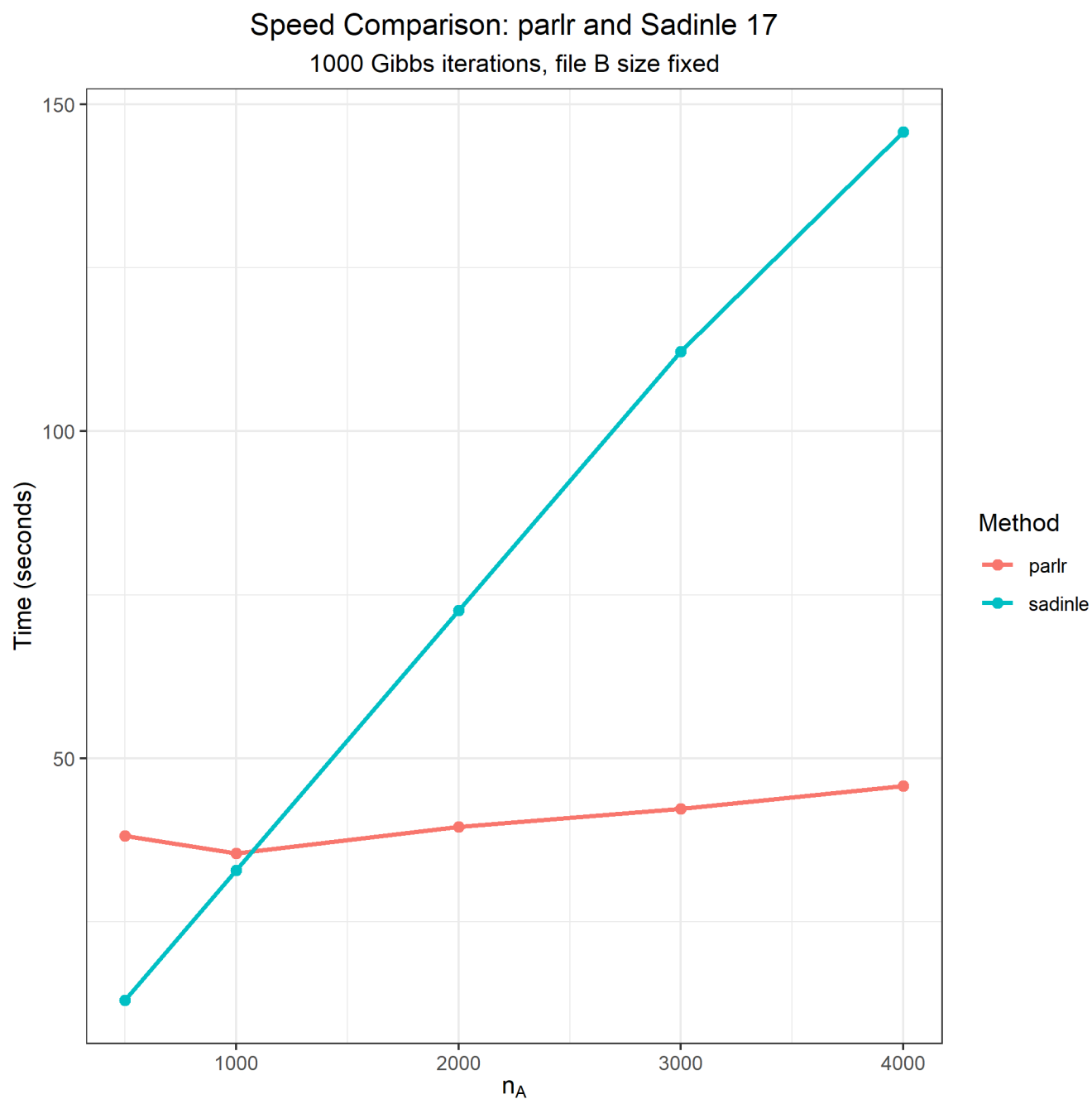
We note here that BRL is coded in C, which makes for unfair comparison against `parlr`, currently only built in R. Additionally, although `parlr` is amenable to parallelization, this simulation was run on a single core. Running `parlr` in C++ with paralellization for the hashing step and sampling the matching status of the record pairs should lead to even more drastic results.

Data Analysis

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 casualities, one cannot simply sum the numbers recorded by each organization, as it is likely that the same individuals are recorded in multiple casuality 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 above 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 ommited. 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 **m** and **u** parameters, but use 2000 Gibbs iterations with 200 discarded as burn-in to mirror the implementation in Sadinle 2017.

Discussion