Parlr: Parallelized Record Linkage in R
Technical Appendix

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Notation and Assumptions

Denote two files as A and B, with n_A and n_B records respectively, 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. 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. With notation $\gamma_{ij}^f \in \{0, \ldots, L_f - 1\}$ for the number of possible agreement levels for field f, we 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.

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 the product 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 $\mathbf{Z}$.

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

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

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

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

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

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

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

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

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

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

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:

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

Bayes Estimate

Our Gibbs sampler provides posterior samples of $\mathbf{Z}$ which we use to make our final decisions about the linkage structure. In the case where we false matches and missed matches contribute the same loss, we declare (i, j) to be a match whenever $P(Z_j = i) > \frac{1}{2}$ according to these posterior samples. We can create more elaborate decisions by attributing different loss values to different kinds of error, and allowing pairings with middling posterior probabilities to be left unlabeled by the algorithm so that the modeler can address those manually. For further discussion, see Sadinle 2017.

Since our Gibbs procedure does not strictly enforce one-to-one matching, it is possible for the final Bayes estimate to link multiple records in B to one record in A. The modeler can either report both such matches (with their respective posterior match probabilities), or resolve these conflicts by accepting only the match with highest posterior probability. 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. We index these agreement patterns by $p \in \{1, \ldots, P\}$, and say $(i, j) \in h_p$ when the (i, j) pair exhibits the pth agreement pattern. Wherever possible, we conduct calculations over these P agreement patterns rather than the $n_A \times n_B$ record pairs.

Data Representation and Hashing

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 the a hashed value corresponding to the agreement pattern of the (i, j) pair. Enamorado et al (2019) provided the hashing function

$$\sum_{f=1}^{F} \mathbf{1}_{\gamma_{(i,j)}^f > 0} 2^{\gamma_{(i,j)}^f + \mathbf{1}_{f>1} \times \sum_{e=1}^{f-1}(L_e - 1)}$$

to map each agreement pattern to a unique value, but packages like `dplyr` in `R` are capable of this as well.

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.

Lastly, 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.

Gibbs Sampling

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

$\alpha(\mathbf{Z}) = \alpha_0 + \sum_{p=1}^{P} H_p^m \times h_p$. Then, we can easily calculate H_p^u, the number of nonmatching record pairs of agreement pattern p, by subtracting the number of matching pairs from the total present in the data; that is $H_p^u = H_p - H_p^m$. From this, we can update our β parameter through $\beta(\mathbf{Z}) = \beta_0 + \sum_{p=1}^{P} H_p^u \times h_p$. Note that these constitute P many summations over n_B quantities, and thus avoid the $n_A \times n_B$ summation from the original method.

Sadinle uses a prior for $\mathbf{Z}$ that induces the a full conditional for Z_j 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*. By weakening the one-to-one requirement, our full conditional for Z does not depend on the rest of the $\mathbf{Z}_{-j}$ vector, and thus can be computed in parallel. 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. This boosts computation time far greater than parallelization.

To do this, we calculate the Fellegi Sunter weight w_{h_p} for each unique pattern, sample the agreement pattern between j and its potential match, and then sample the record label uniformly among viable records. 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,

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

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 $\tilde{\Gamma}$.

Simulation Studies

In his 2017 paper, Sadinle demonstrated the strength of his method by running `BRL` on simulated pairs of files with differing levels of errors and overlap. Comparing our method against `BRL` on these same simulated datasets, we find that our method only has weakened performance in the 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
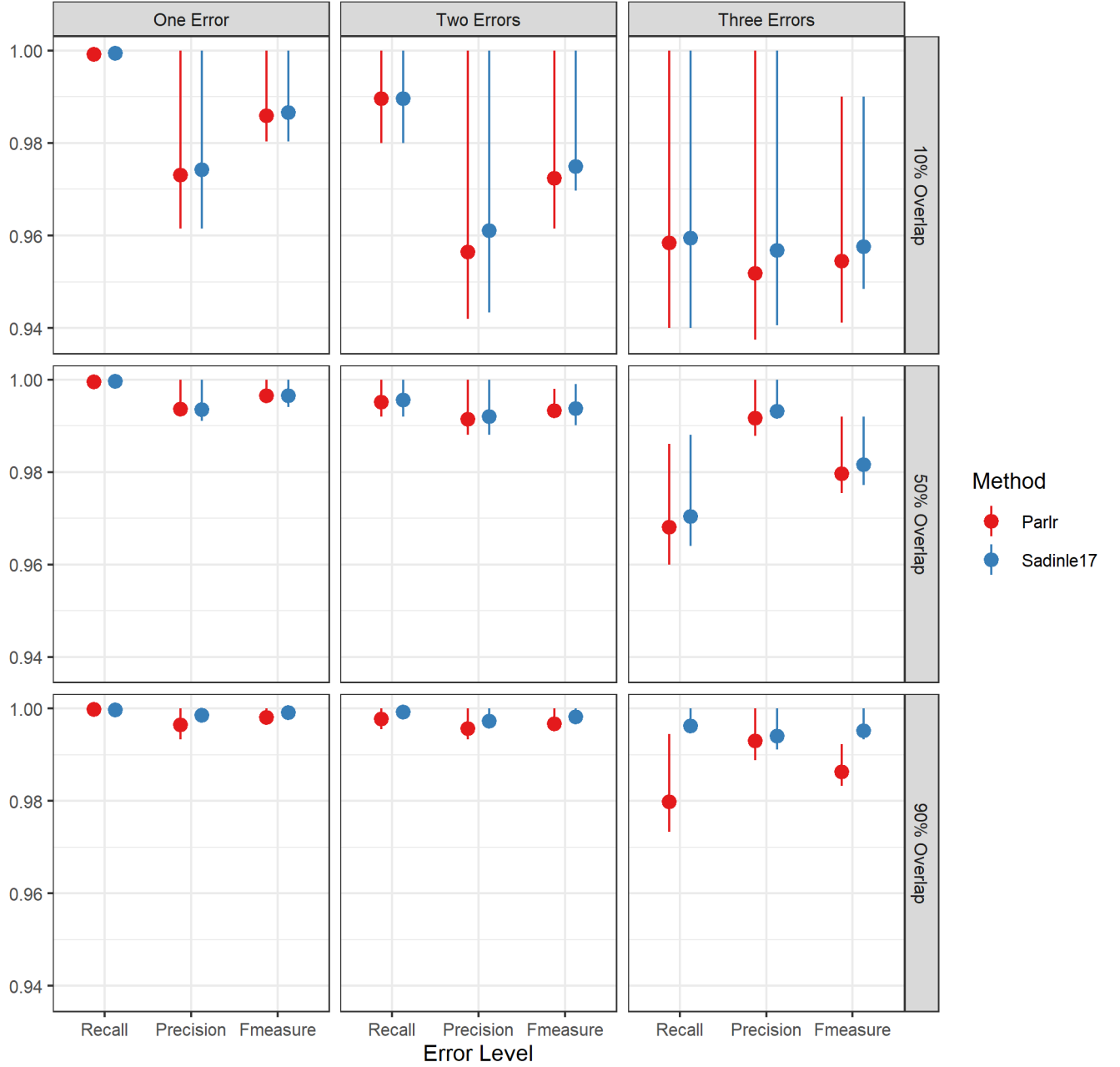
To demonstrate speed, we generate comparison vectors from pre-specified distributions so that we can easily increase the size of the linkage problem. Distributions are meant to emulate the behavior of similarity scores across first name, last name, and day, month, and and year of birth, with 1 indicating 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 runtime of parlr against BRL. We see that at low data size, BRL outperforms, but that parlr

is significantly faster at handling larger data.

In particular, runtime for BRL seems to grow quadratically while runtime for parlr seems to grow linearly.

	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

Speed Comparison: Parlr and Sadinle17
1000 Gibbs iterations
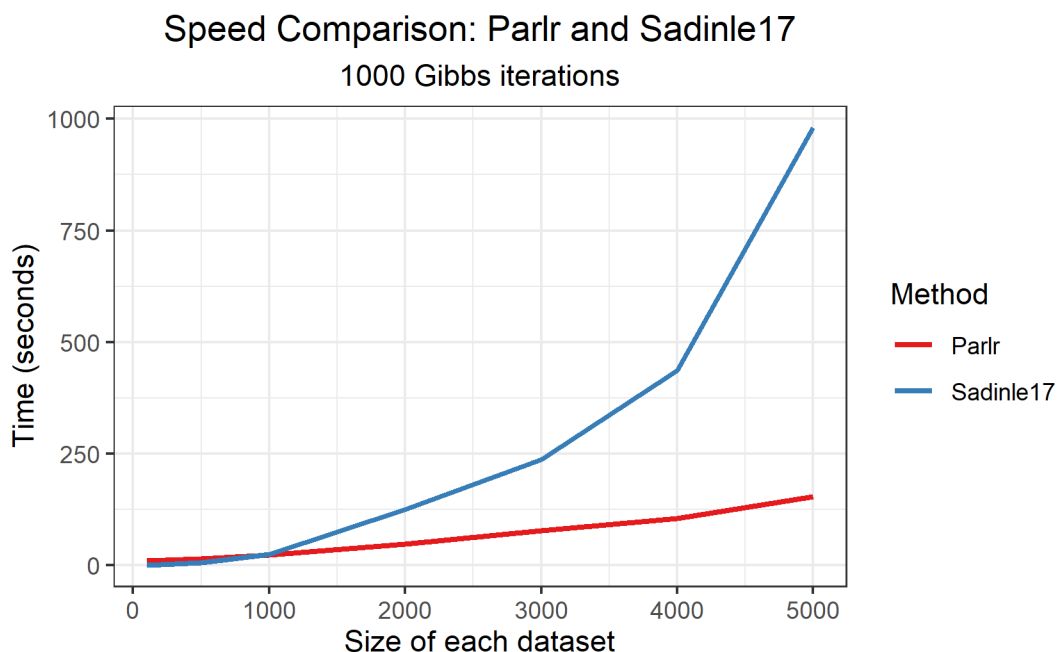
The above discussion suggests that for fixed n_B, computation time should remain mostly constant with growing n_A. Shockingly, this seems to be true. In the plot below, fixing $n_B = 500$, we see linear growth for the runtime under BRL as n_A increases, with much more static runtime under parlr. The slight increases in runtime 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
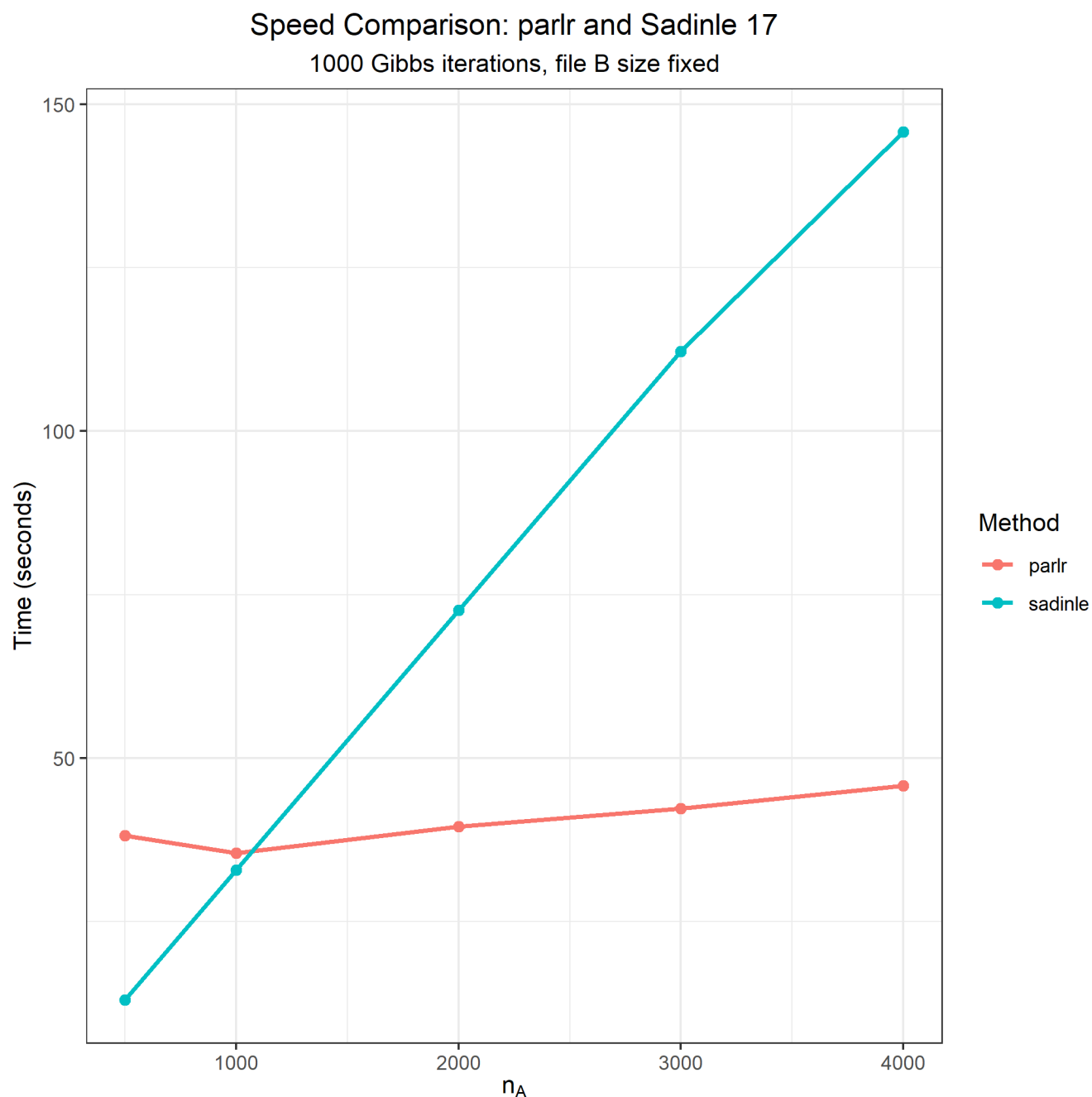
We note here that BRL is coded in C, which makes for unfair comparison against parlr, currently only built in R. Additionally, although parlr is amenable to parallezation, this simulation was run on a single core. Running parlr in C++ with paralellization for the hashing step and sampling the matching status of the record pairs should lead to even more drastic results.