Unveiling parlr

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Overview

- Computational Speed-ups
- Next Step

parlr

- I have been playing around with calling my method "Parallelized Record Linkage in R", or parlr for short.
- Broadly speaking, I use two strategies for computational speedup:
  - Performing operations on the **unique aggreement patterns** rather than the individual record pairs. Rigorously, sums over the unique patterns are *sufficient statistics*.
  - Relaxation of one to one matching to allow for parallel sampling of Z

Together, these have made **huge** improvements on code

Identifying Unique Patterns

- Enamorado uses the following hashing function to identify unique aggreement patterns. I've also figured out how to do this efficiently in `dplyr`.

$$H(i,j) = \sum_{f=1}^{F} \mathbf{1}_{\gamma_f(i,j)>0} 2^{\gamma_f(i,j) + \mathbf{1}_{f>1} \times \sum_{a=1}^{f-1}(L_a - 1)}$$

- I identify the unique patterns, the number of each of of those patterns in the data as a whole, and the number of those patterns for each record $j \in B$.
- Define P to be the number of unique agreement patterns, and note it is bounded by $\prod_{f=1}^{F} L_f$. This *does not grow* with the size of the data.

Calculating FS weights

- Within a Gibbs iteration, all records with the same agreement pattern will have the same FS weight. So instead of calculating the weight for each of $n_A \times n_B$ records, I only need to do it for P unique patterns.
- This step is taken directly from `fastlink`.

Identifying Unique Patterns

- `fastlink` doesn't have posterior updates for Dirichlet distributions, so I came up with this step on my own.
- Each agreement pattern corresponds to a particular type of contribution to the posteriors of the m and u parameters.
- To update m, I used to sum over each variable for all N record pairs. Now, I simply identify the number of matchings in the Z vector corresponding to each of P patterns.
- The nonmatches are even easier: just substract this number from the total present in the data!

Breaking up the Z sampler

- Four observations
  - Sampling many objects with varying probabilities difficult
  - Sampling *fewer* objects with varying probabilities is easy
  - Sampling many objects with *uniform* probabilities is also easy
  - For a record $j \in B$, each record $i \in A$ with a given agreement pattern has the same probability of matching. That is, the unique patterns form *equivalence classes*, and within a class, each record is equally likely.

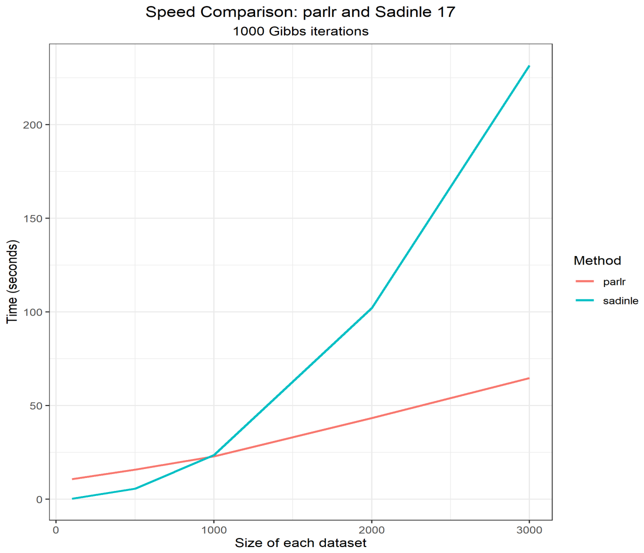
Breaking up the Z sampler

- Rather than sampling Z_j sequentially from N many records, I can sample it in parallel from P many equivalence classes of unique patterns, each one multiplied by its prevalance for record j.
- After sampling the unique pattern, I sample the record associated with that pattern uniformly at random.
- Since all calculations within the Gibbs Sampler depend only on the unique pattern, and since my model samples the Z_j independently, I can sample for the records *at the end of the entire Gibbs procedure*

Summary

- We have *almost entirely* removed dependence on N from our Gibbs procedure, and replaced them with steps that depend on P.
- Only major hurdle with N is calculating the comparison vectors, which is just unavoidable in the Fellegi Sunter Framework. However, whatever Ted does for `fastlink` would work here too.
- Filling in the Gibbs sampler post-hoc technically depends on N, but its a very inexpensive step that only has to be done once

Speed up



Speed Comparison: parlr and Sadinle 17
1000 Gibbs iterations
Time (seconds)
0
50
100
150
200
0
1000
2000
3000
Size of each dataset
Method
parlr
sadinle

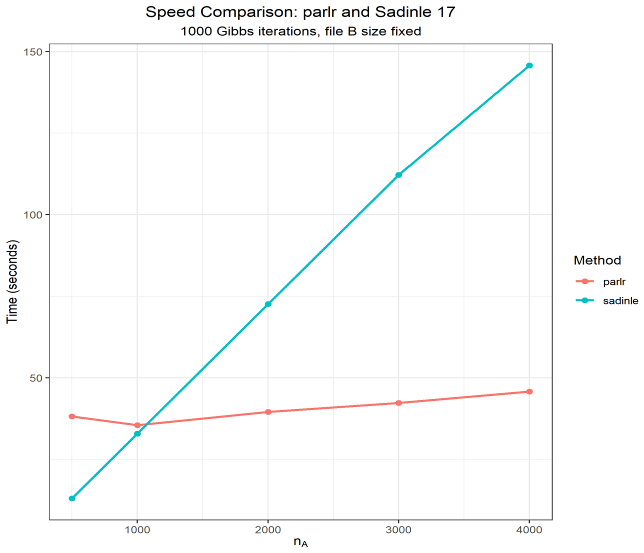
Speed up

- When n_A and n_B are small, the computational savings are minimal, and Sadinle's `BRL` runs faster just because its in C.
- As the datasets grow bigger, computation for `BRL` grows *quadratically*, while `parlr` seems to grow *linearly*
- The plot shown is with **no parallel computing**
- If my method was programmed in C, I would expect even greater computational savings

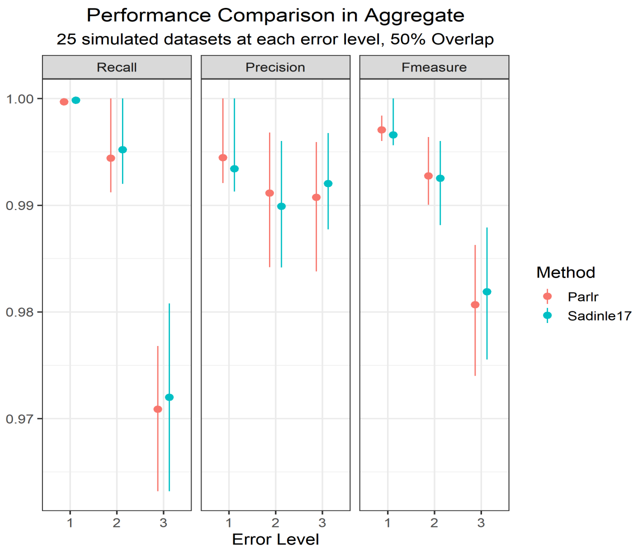
More on Speed Up

- Within the Gibbs sampler, calculations only depend on n_B (the number samples I need to take to fill a Z vector), and P (the number of unique patterns). n_A only influences the scale of the counts for the unique patterns.
- n_A only comes to play in forming the comparison vectors and in back-filling the samples of Z at the end of the sampler.
- This suggests that the sampler should be *almost constant* in n_A (ie, the Gibbs sampling for a 4000×500 problem should not be substantially longer than for a 500×500 problem)
- Particularly useful for linking a smaller dataset to a much larger dataset. One example would be the DNC data in BRACS!

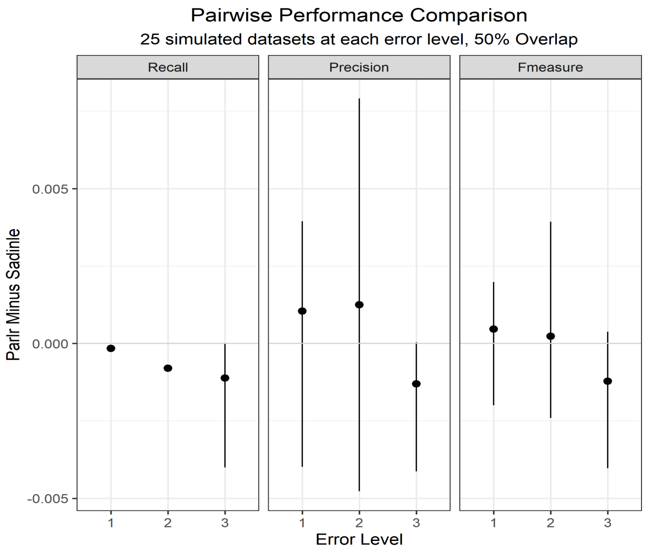
More on Speed Up



Accuracy


Performance Comparison in Aggregate
25 simulated datasets at each error level, 50% Overlap
Recall
Precision
Fmeasure
1.00
0.99
0.98
0.97
1
2
3
Error Level
Method
Parlr
Sadinle17

Accuracy



Pairwise Performance Comparison
25 simulated datasets at each error level, 50% Overlap
Recall
Precision
Fmeasure
Parlr Minus Sadinle
0.005
0.000
-0.005
1
2
3
Error Level

Accuracy

- Overal, the `parlr` method peforms comparably to Sadinle17. There is slight evidence that recall is systematically lower for `parlr` at high error levels, but it is *very* slight. I'll need to run this at different level of overlap to explore more.

Limitations

- The original FS method is $O(n_A \times n_B)$ hard. With hashing methods, `fastlink` makes the problem only $O(P)$ hard, since record pairs are considered indepenently and classification is based *only* on the unique pattern.
- Hashing methods in my model make the problem $O(n_B \times P)$ hard. No matter what, I need to sample n_B many times to fill a linkage vector Z. In this sense, `fastlink` is inherently faster than this method
- However, method takes into consider much more of the dependency structure in the data, making this computational burden worthwhile
- Note: If this line of thinking is useful for the paper, I'll need some help making this rigorous!

Next Steps

- I have not yet implemented any parallelization. We will cover this soon is Shawns class. The steps above however provide *the vast majority* of the computational speed up.
- Later on, I'll be able to use this same hashing function for linkage clusters by replacing 2 with the k^{th} prime number for the k^{th} linkage cluster. (For Jody's paper, I'll present just the standard method)

Next Steps

- This model and these computational savings really inform everything everything I'm doing. Apart from the BRACS paper with Jody, I'm really going to focus on getting this done
- Larger versions of the simulations above, with different levels of overlap.
- Question: What other kinds of simulations or evaluations would I need?
- Question: Is this still a good fit for Bayesian Analysis? Or should it go to a journal more concerned with computation and scalability?