

El Salvador Linkage Analysis

El Salvador Data: ParlR vs Sadinle17

I've attempted to reproduce the results from Sadinle's 2017 paper, which has been a little bit of a mixed bag. The code that Beka gave me does not seem to be the same that is used in the actual 2017 paper. I think this for two reasons:

- Code involves three datasets (ER, CHDES, and UNTC), while paper only links two (ER and CHDES)
- There is code for priors for "truncation points" which are used in Sadinle's 2014 model.

Nevertheless, I proceeded. For a first run-through, I tried to build the comparison vectors in the exact same way that Sadinle did. He uses 4 levels for many fields, which I'll discuss more later. Also, his paper calls for three agreement levels for location of death (exact municipality, adjacent municipality, nonmatch), but the code I have doesn't do that, and that would be pretty difficult to implement. So I just use binary comparisons.

My results are close, but not identical to what's provided in the Sadinle paper.

- After data cleaning, my ER dataset has 1323 records, while the paper says there should be 1324.
- The paper has a Bayes estimate with 187 links, but my implementation (with BRL) finds 180. This might be because the paper detects adjacent municipalities, while I do not.
- Distribution of m parameters for given name is a bit different from what's in the paper.

I can go more into details about these things, but for the moment, I'm more concerned with comparing the results of BRL and `parlR` in my own implementation, rather than reproducing Sadinle17 exactly.

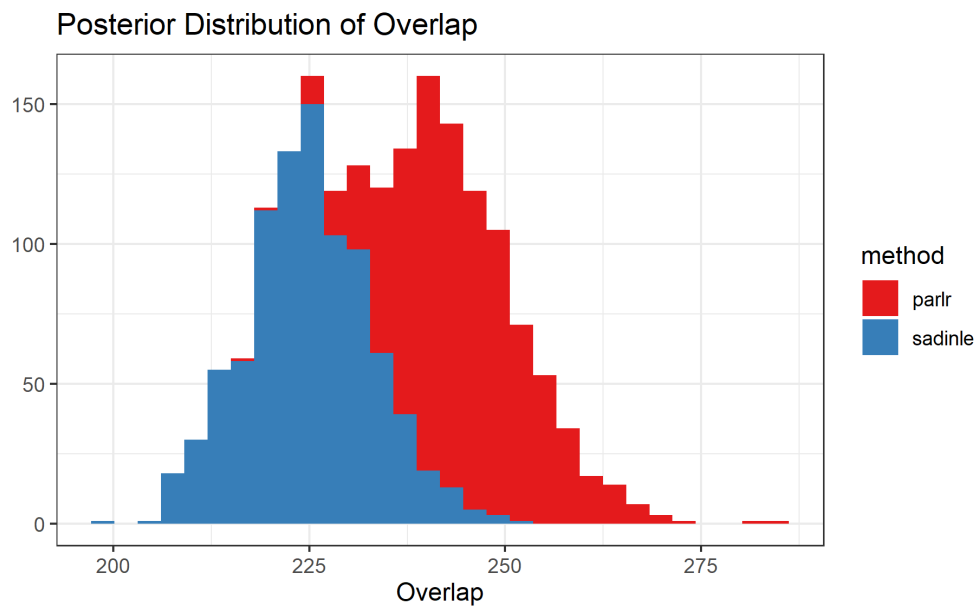
Using Sadinle's Levels

The table below shows the amount of overlap detected by each method, as well as the time it took for the linkage to run. Interestingly, since Sadinle uses so many levels per field, we have $4^5 \times 2^2 = 4096$ possible unique patterns, so I was worried that `parlR` wouldn't give the desired speedups. However, only 352 patterns are actually realized, so `parlR` goes pretty fast!

Linkage Results with $P = 4096$ patterns

	Overlap	time
parlr	193	405.72
parlr_resolved	180	405.72
sadinle	179	597.03

Below is the posterior distribution of the overlap between the files. We see that `parlr` typically matches me, which is to be expected; at minimum, there are the 13 matches that `parlr` made that violated one-to-one matching which Sadinle avoids. For two reasons, I do not consider this to be a problem.

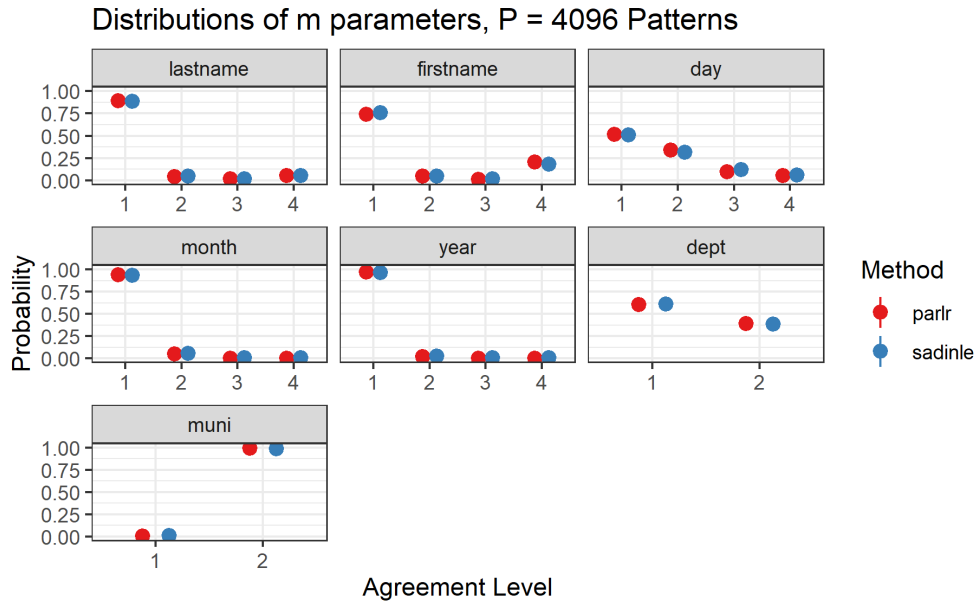


- Within the Sadinle framework, it is typical that Gibbs iterations have more matches than the eventual Bayes estimate. This is because many of the matches are due to randomness, and they only make it

through to the Bayes estimate if that same matching occurs consistently 50% of the time. In Sadinle’s paper, the overlap has a mean of 241, and a 90% credible interval of [227, 256], but a Bayes estimate of only 187.

- Severe overmatching within the Gibbs iterations can possibly lead to biased posteriors for the m parameters. There is an interesting conversation to be had here. When Enamorado compared **fastlink** to BRL, he notes that the first estimate under **fastlink** has way too many matches, but that **fastlink** produces similar results to BRL after resolving all the matches that violate one-to-one. While this is true, the overmatching within his EM algorithm lead to biases in the m parameters, and these can not be cleaned up posthoc. In the Sadinle paper, he notes that the FS method leads to nonsensical estimates of the m parameters, and I believe it is for this reason.

This led to me worry that parameter estimates under **parlr** would be similarly biased. However, good news, they are not! This is because the overmatching under **parlr** is very slight compared to **fastlink**.



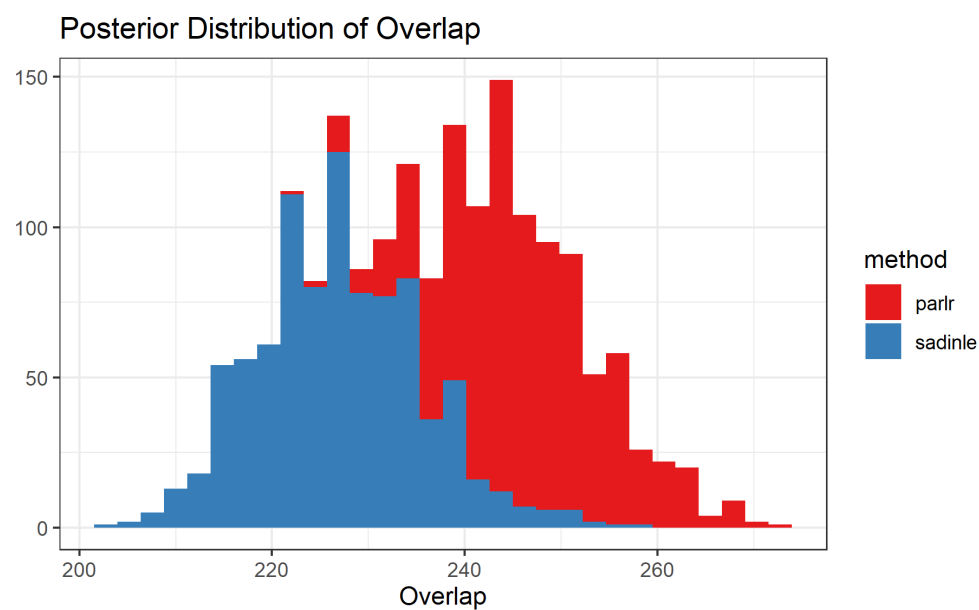
Looking at these m parameters, we see that many levels are redundant. Also, since less than 10% of the possible patterns are realized, it really does seem like that many levels are unnecessary. So now we’re going to run **parlr** with fewer levels and see how things change.

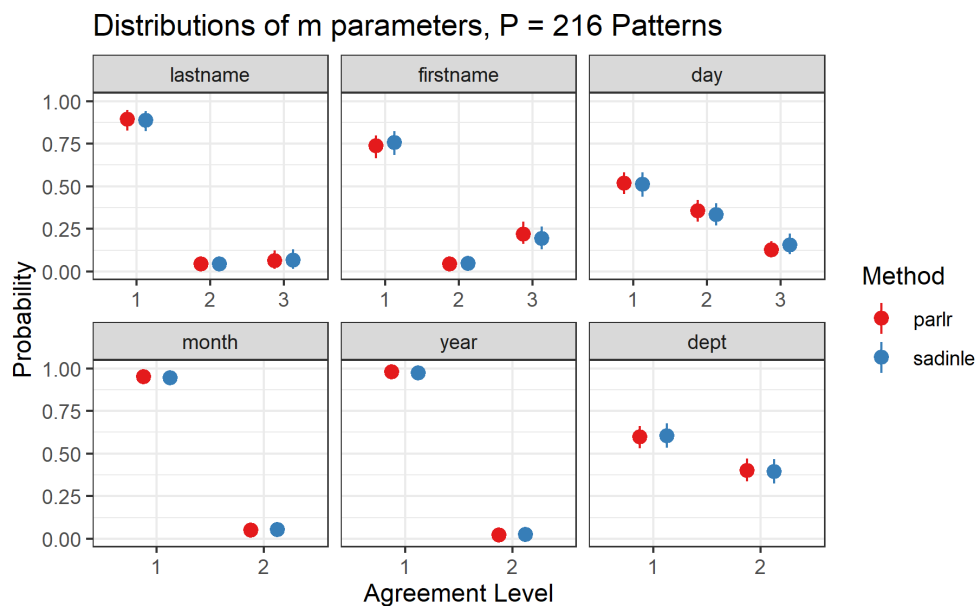
Using Less Patterns

I reran everything with only 3 levels for first name, last name, and day, and only 2 levels for everything else. I probably could use just two levels for the names since the code puts so much work into standardizing names and using a modified Levenshtein distance, but for now, I’ll stick with 3 levels. Here P is bounded by 216, and only 159 unique patterns are realized. Results stay basically the same, but see significant speed up for **parlr**.

Linkage Results with P = 216 patterns

	Overlap	time (sec)
parlr	193	230.20
parlr_resolved	180	230.20
sadinle	181	556.63





Mixing and Multiple Possible Matches

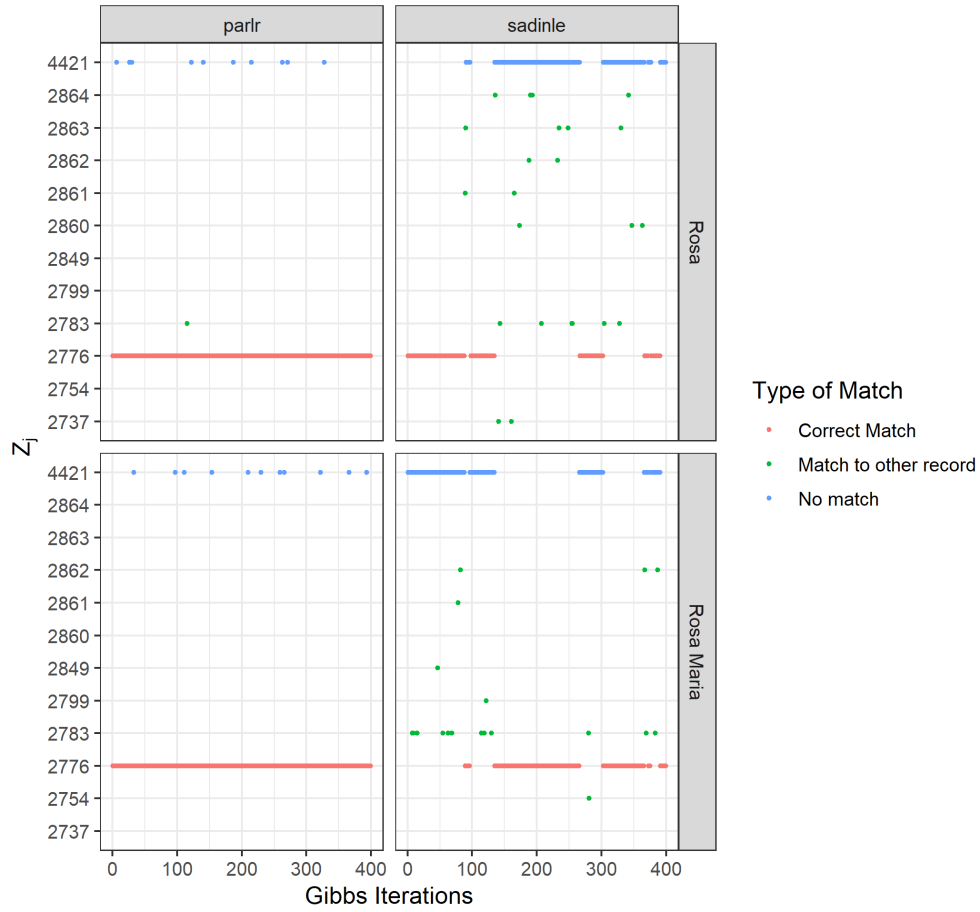
Something interesting about this comparison is that this dataset is specifically an example where `parlr` and `Sadinle` would differ the most. In cases where there were multiple plausible matches, each method produces undesirable behavior. For example, examine the records of Rosa and Rosa Maria in the CDHES dataset.

	lastname	firstname	dataset	day	month	year	dept	muni
825	PINEDA	ROSA	CDHES	6	4	1984	NA	NA
826	PINEDA	ROSA MARIA	CDHES	6	4	1984	NA	NA
2776	PINEDA	ROSA MARIA	ER-TL	4	4	1984	CUSCATLAN	NA

- In `parlr` both records in B match to the same record in A throughout the Gibbs process, creating consistent violations of one-to-one matching.
- In `Sadinle`, the Gibbs process creates one matching status and stays there for a while, but if one pair “unmatches,” then the other record has a chance to latch on. Then the Gibbs process is stuck with that matching status for a while. This seems to be poor mixing.

Near Matches under Parlr and Sadinle

Both have undesirable behavior



As a result, **parlr** provides an initial Bayes Estimate (without conflict resolution) with two matches, each with high posterior probability (90% +) The modeller can algorithmically take the one with highest posterior, or examine the records manually. Sadinle provides only one match (consistent with 1-1 matching), with low posterior probability (a bit above 50%).

I used to think this behavior made the El Salvador data a bad option for my case study, but I think its actually instructive to examine this closely. Let me know your thoughts on this!

(PS, it took me forever to figure out how to represent this visually!)

Questions

Is still a good case study to choose? The first thing that worries is that I have't been able to 100% replicate Sadinle's results. Let me know if you think this is an issue.

The second thing that worries me is this dataset is precisely one where Sadinle and **parlr** would have the largest discrepancy; the material discussed in the section above.