Module 8: Bayesian Fellegi and Sunter

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BDD package

- Marchant, Rubinstein, and Steorts (2021) have provided a package for implementing Sadinle (2014), which is referred to as BDD (Bayesian Duplicated Detection).

RLdata500 data set

- We investigate it on the RLdata500 data set.

```r
library(magrittr)    # pipe operator (must be loaded before BDD)
library(comparator)  # normalized Levenshtein distance
library(clevr)       # evaluation functions
library(BDD)
RLdata500[['rec_id']] <- seq.int(length.out=nrow(RLdata500))
head(RLdata500)
```

```
##   fname_c1 fname_c2 lname_c1 lname_c2   by bm bd rec_id
## 1  CARSTEN     <NA>    MEIER     <NA> 1949  7 22      1
## 2     GERD     <NA>    BAUER     <NA> 1968  7 27      2
## 3   ROBERT     <NA> HARTMANN     <NA> 1930  4 30      3
## 4   STEFAN     <NA>    WOLFF     <NA> 1957  9  2      4
## 5     RALF     <NA>  KRUEGER     <NA> 1966  1 13      5
## 6  JUERGEN     <NA>   FRANKE     <NA> 1929  7  4      6
```

Distance functions

```r
scoring_fns <- list(
  fname_c1 = Levenshtein(normalize = TRUE),
  lname_c1 = Levenshtein(normalize = TRUE),
  by = function(x, y) abs(x - y),
  bm = function(x, y) abs(x - y),
  bd = function(x, y) abs(x - y)
)
```

Breaks

For each scoring function above, we provide a breaks vectors, which specifies the discrete levels of agreement (from ‘high’ agreement to ‘low’).

```r
scoring_breaks <- list(
  fname_c1 = c(-Inf,.05,.15,.3,Inf),
  lname_c1 = c(-Inf,.05,.15,.3,Inf),
  by = c(-Inf,0,1,3,Inf),
  bm = c(-Inf,0,1,3,Inf),
  bd = c(-Inf,0,2,7,Inf)
)
```

Comparison vectors

- Now we are ready to compute the attribute comparison scores for the record pairs.
- Since this is a small data set, we consider all pairs using the `pairs_all` function.
- For larger data sets, blocking/indexing is recommended using `pairs_hamming`, `pairs_fuzzyblock`, or a custom blocking function.

Comparison vectors

```r
pairs <- pairs_all(RLdata500$rec_id) %>%
  compute_scores(RLdata500, scoring_fns, id_col = 'rec_id'
  discretize_scores(scoring_breaks)
```

Speeding up inference

- To speed up inference, we only consider a subset of the pairs as candidate matches.
- Specifically, we consider pairs that have a strong agreement on name (accounting for missing names).

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```
pairs[['candidate']] <- (pairs$fname_c1 < 4) & (pairs$lname_c1 < 4) |
                            is.na(pairs$fname_c1) | is.na(pairs$lname_c1)
```

priors on *m* and *u* probabilities

- Next we specify the priors on the m* and u* probabilities for each attribute and agreement level.
- `lambda` contains the lower truncation points for the truncated Beta priors on the m* probabilities. `alpha1` and `beta1` are the shape parameters for the truncated Beta distributions to the `BDD` function below.
- The Beta priors on the u* probabilities are uniform by default but can be adjusted using the alpha0 and beta0 arguments.

priors on *m* and *u* probabilities

```
lambda <- list(
  fname_c1 = c(0.8,0.85,0.99),
  lname_c1 = c(0.8,0.85,0.99),
  by = c(0.8,0.85,0.99),
  bm = c(0.8,0.85,0.99),
  bd = c(0.8,0.85,0.99)
)
```

Intialization and Gibbs sampler

Finally we initialize the model and run inference using Markov chain Monte Carlo.

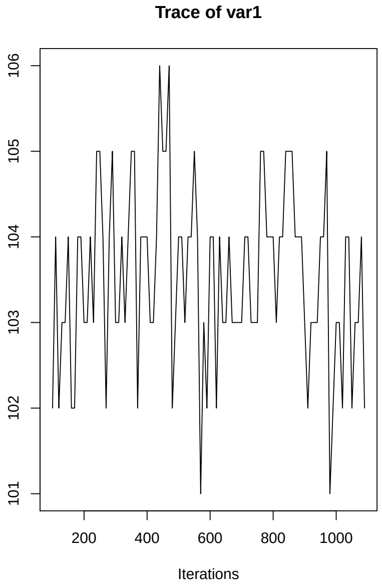
```
model <- BDD(pairs, lambda,
             id_cols = c("rec_id.x", "rec_id.y"),
             candidate_col = "candidate")
fit <- run_inference(model, 100,
                     thin_interval = 10,
                     burnin_interval = 100)
# Completed sampling in 0.7 seconds
```

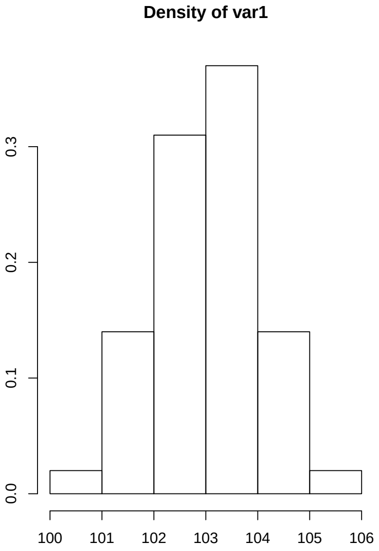
Posterior samples

- The posterior samples of the linkage structure can be accessed by calling `extract(fit, "links")`.
- However, these samples only cover the records that were considered as candidate pairs.
- We can obtain samples of the complete linkage structure (for all records) using the following function.

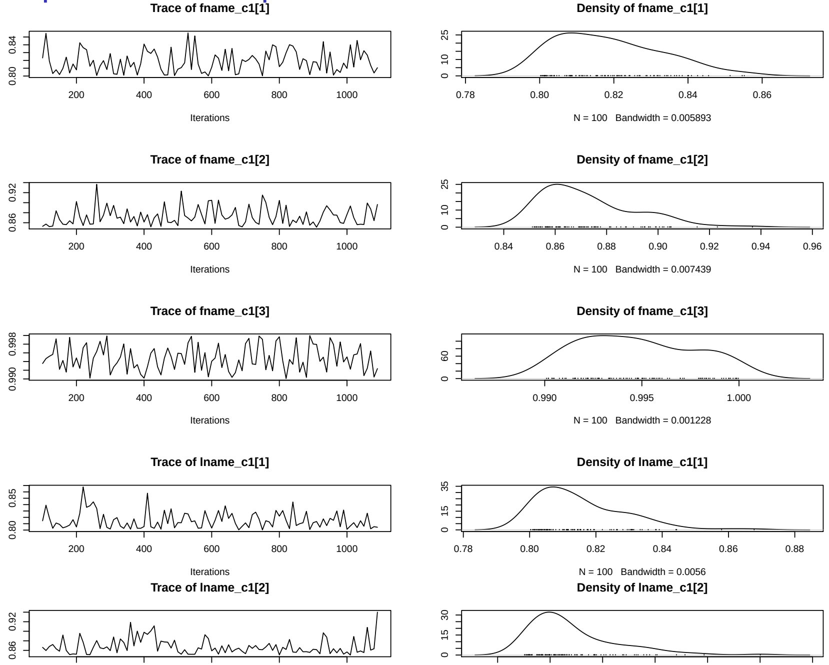
```r
links_samples <-
  complete_links_samples(fit, RLdata500$rec_id)
```

Traceplot of the cluster sizes

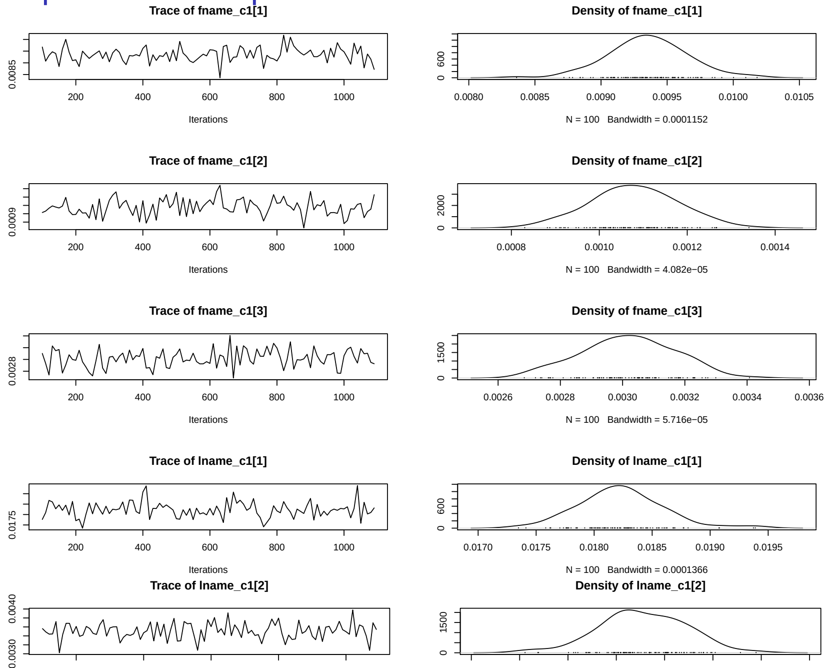




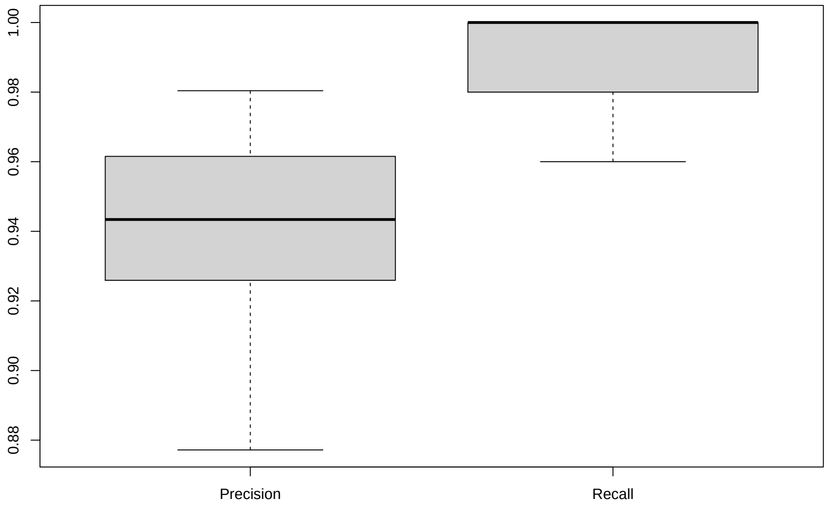
Traceplot of the m probabilities



Traceplot of the u probabilities



Pairwise Evaluation Metrics (Boxplots)



Your Turn and Discussions

- What other evaluation metrics would you look at?
- Work on these either with a partner or in your free time?
- What types of evaluations can we look at given the fact that this is an unsupervised problem?

Your Turn and Discussions

- You might think about how you would try and replicate the analysis that Sadinle did in his 2014 paper given this package.
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- Can you think of a simulation study to study the sensitivity of the method?
- If you like this method, go read Sadinle (2017) and Sadinle (2018)!