Introduction to Bayesian record linkage

Brenda Betancourt and Andee Kaplan

Duke University
Department of Statistical Science

February 8, 2018

Slides available at `http://bit.ly/cimat-bayes`

What is "Bayesian"?

1. Setting up a *full probability model* – a joint probability distribution for all observable and unobservable quantities

$$p(\boldsymbol{x}|\boldsymbol{\theta}) - \text{ likelihood}$$
$$p(\boldsymbol{\theta}) - \text{ prior}$$

2. Conditioning on observed data – calculating and interpreting the appropriate *posterior distribution*

$$p(\boldsymbol{\theta}|\boldsymbol{x}) = \frac{p(\boldsymbol{x}, \boldsymbol{\theta})}{p(\boldsymbol{x})} = \frac{p(\boldsymbol{x}|\boldsymbol{\theta})p(\boldsymbol{\theta})}{p(\boldsymbol{x})} \propto p(\boldsymbol{x}|\boldsymbol{\theta})p(\boldsymbol{\theta})$$

Why Bayes?

Common approaches

Felligi-Sutner
Clustering
Beka's

Empirical Bayes graphical model for record linkage

`blink` package

`R` package that removes duplicate entries from multiple databses using the empirical Bayes graphical method:

```
install.packages("blink")
```

- Formatting data for use with `blink`
- Tuning parameters
- Running the Gibbs sampler (estimate model parameters)
- Output

RLdata500 data

We will continue with the RLdata500 dataset in the RecordLinkage package consisting of 500 records with 10% duplication.

```
library(blink) # load blink library
library(RecordLinkage) # load data library
data("RLdata500") # load data
head(RLdata500) # take a look
```

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

Formatting the data

```
# categorical variables
X.c <- as.matrix(RLdata500[, c("by","bm","bd")])
p.c <- ncol(X.c)

# string variables
X.s <- as.matrix(RLdata500[, c("fname_c1", "lname_c1")])
p.s <- ncol(X.s)
```

`X.c` and `X.s` include all files stacked on top of each other, for categorical and string variables respectively

```
# keep track of which rows of are in which files
file.num <- rep(c(1, 2, 3), c(200, 150, 150))
```

Tuning parameters

Hyperparameters

```
# Subjective choices for distortion probability prior
# parameters of a Beta(a,b)
a <- 1
b <- 999
```

Distortion

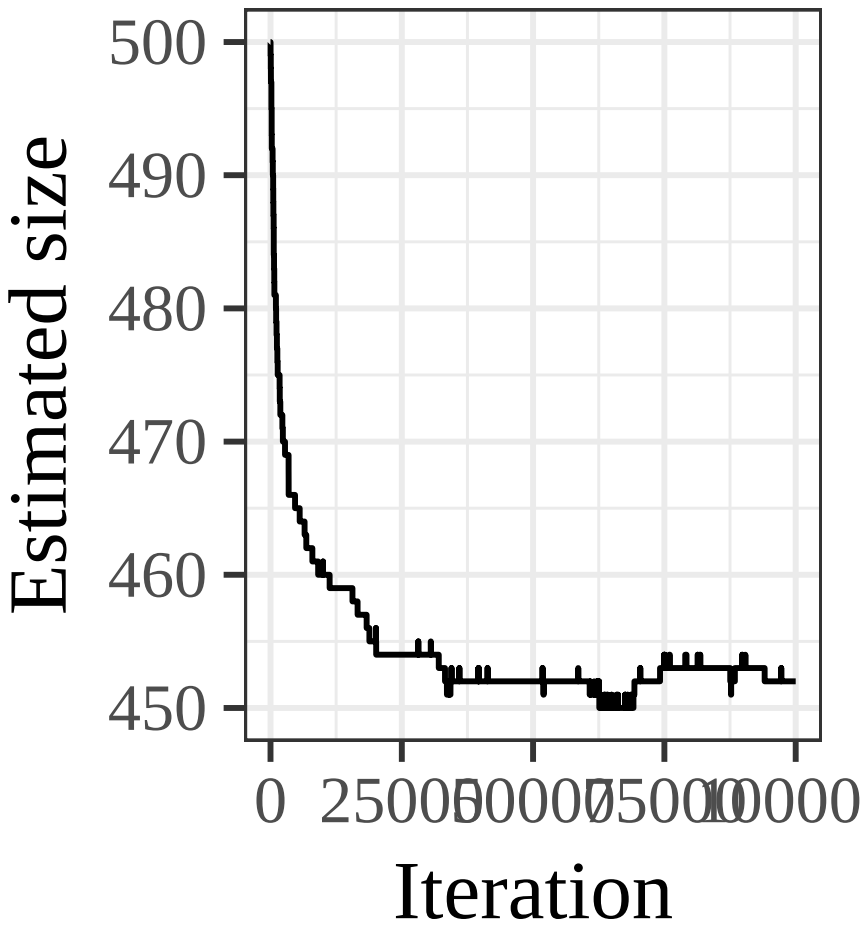
```
# string distance function example
d <- function(s1, s2) {
  adist(s1, s2) # approximate string distance
}

# steepness parameter
c <- 1
```

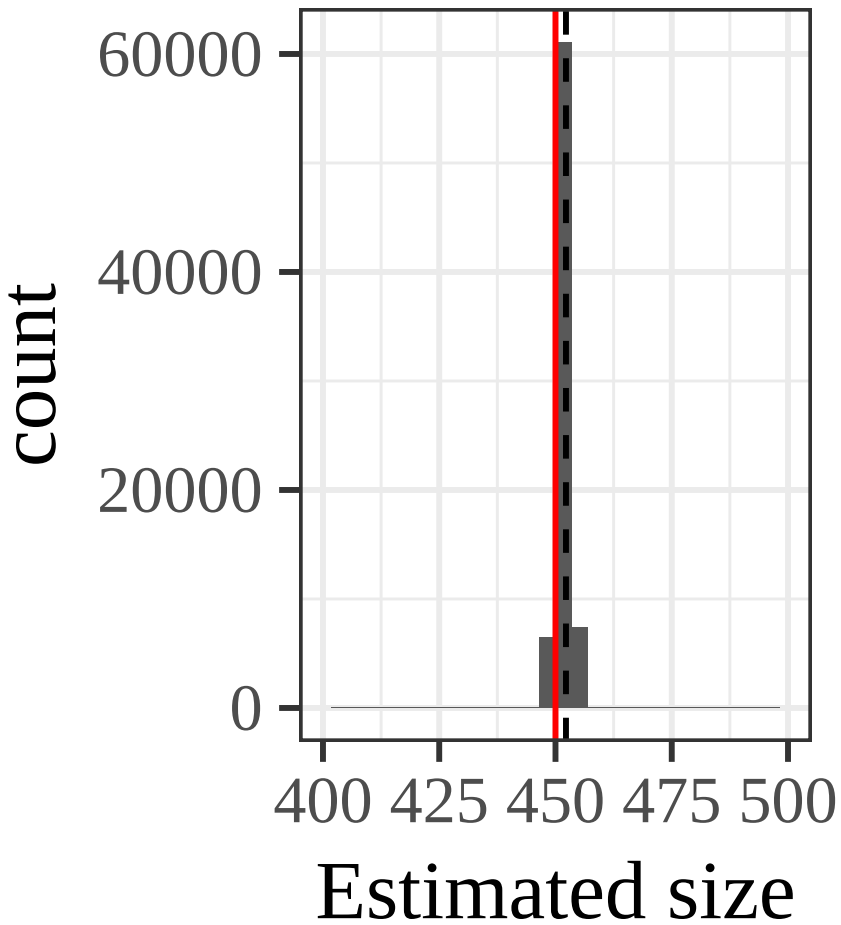
Running the Gibbs sampler

```
lam.gs <- rl.gibbs(file.num = file.num, # file
                   X.s = X.s, X.c = X.c, # data
                   num.gs = 100000, # iterations
                   a = a, b = b, # prior params
                   c = c, d = d, # distortion
                   M = 500) # max # latents
```

Output

```
# count how many unique latent individuals
size_est <- apply(lam.gs, 1, function(x) {
  length(unique(x))
  })
```





Evaluation

```
# estimated pairwise links
est_links_pair <- pairwise(links(lam.gs[-(1:25000), ]))

# true pairwise links
true_links_pair <- pairwise(links(matrix(identity.RLdata500, nrow = 1)))

#comparison
comparison <- links.compare(est_links_pair, true_links_pair, counts.only = TRUE

# false positive rate
fpr <- comparison$incorrect/comparison$correct

# false negative rate
fnr <- comparison$missing/comparison$correct

# false discovery rate
fdr <- comparison$incorrect/(comparison$correct + comparison$incorrect)

# results
c(fpr, fnr, fdr)
```

```
## [1] 0.00000000 0.04166667 0.00000000
```

Your turn