Module X: Probabilistic Blocking

Rebecca C. Steorts

Agenda

- Data Cleaning Pipeline
- Blocking
- Probabilistic Blocking
- Locality Sensitive Hashing (LSH)
- Jaccard Similarity
- Shingling
- Hash functions
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- Characteristic Matrix
- Minhash (Jaccard Similarity Approximation)
- Back to LSH

Load R packages

```
## Loading required package: DBI

## Loading required package: RSQLite

## Loading required package: ff

## Loading required package: bit

##
## Attaching package: 'bit'

## The following object is masked from 'package:base':
##
##     xor

## Attaching package ff

## - getOption("fftempdir")=="/var/folders/bv/xhclmwh90zg08

## - getOption("ffextension")=="ff"

## - getOption("ffdrop")==TRUE
```

Data Cleaning Pipeline

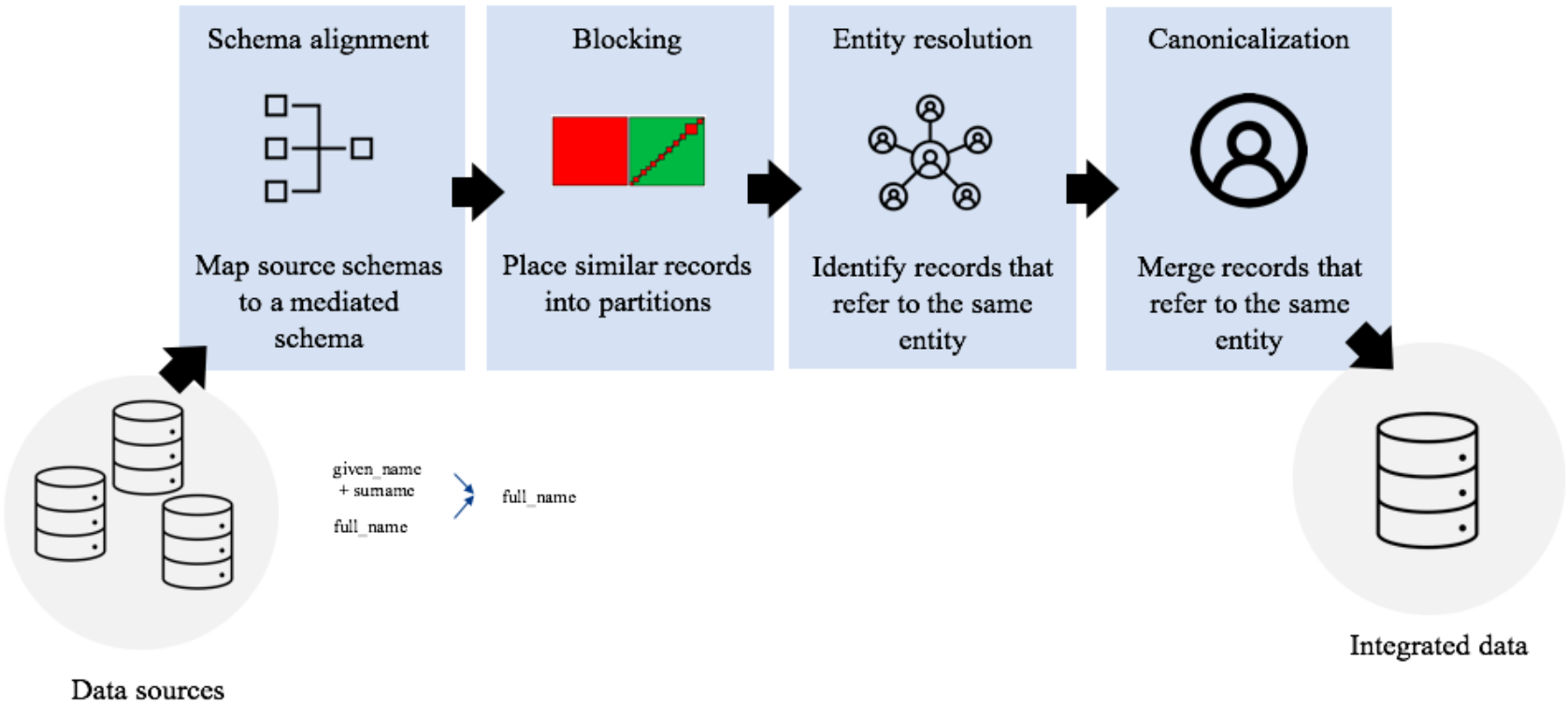


Figure 1: Data cleaning pipeline.

Blocking

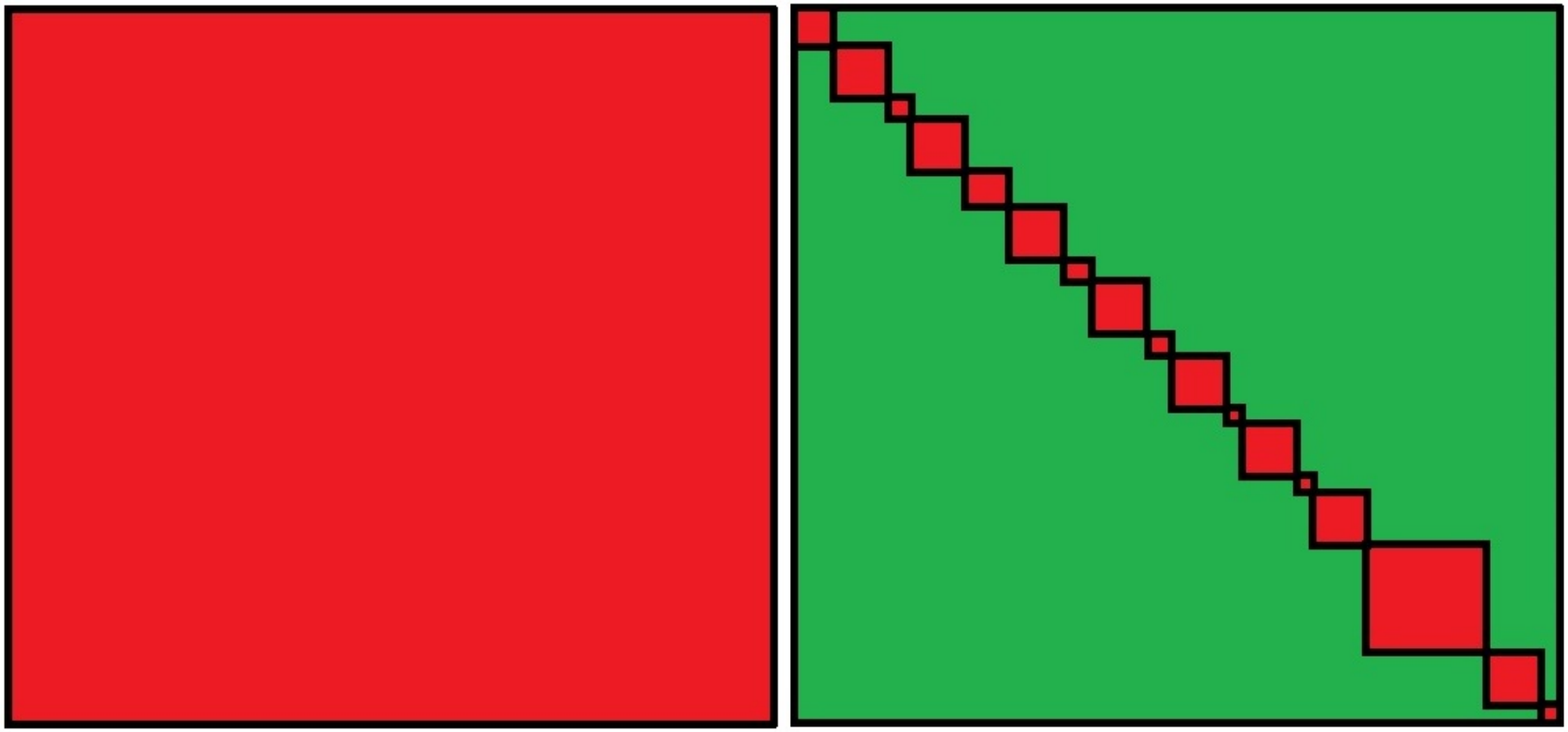


Figure 2: Left: All to all record comparison. Right: Example of resulting blocking partitions.

LSH

Locality sensitive hashing (LSH) is a fast method of blocking for record linkage that orginates from the computer science literature.

Finding similar records

Our goal is to find *similar* records, where the records are assumed to be strings

How do we define *similar*?

Jaccard similarity

We will work with the *Jaccard similarity*:

$$Jac(S, T) = \frac{|\, S \cap T \,|}{|\, S \cup T \,|}.$$

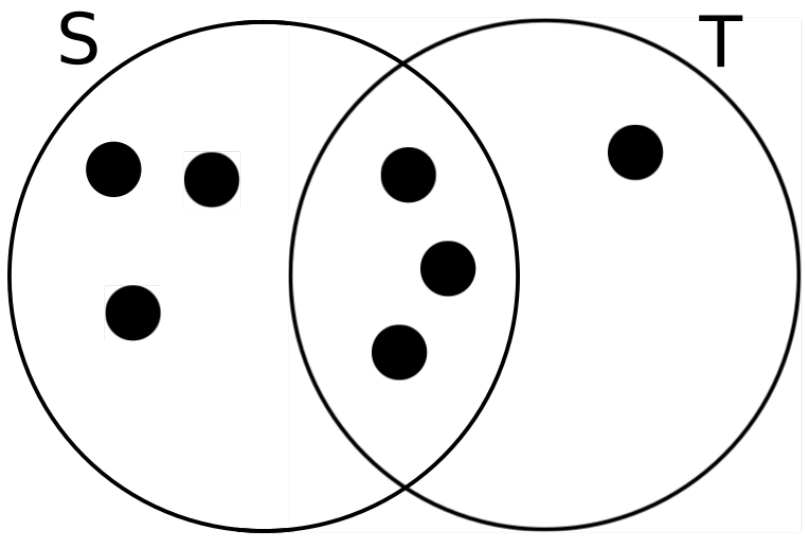


Figure 3: Two sets S and T with Jaccard similarity 3/7. The two sets share 3 elements in common, and there are 7 elements in total.

How to represent data as sets?

We want to talk about the similarity of our data (records)$\Rightarrow$ we need to compare sets of records!

- We can construct a set of **short strings** from the data
- This is useful because similar datasets will have many common elements (common short strings)
- We can do construct these short strings using *shingling*

k-shingling (how-to)

1. Think of the data set as a string of characters

2. A k-shingle (k-gram) is any sub-string (word) of length k found within the a record of the data set

3. Associate with each data set the set of k-shingles that appear one or more times

Let's try

Suppose our data set is the string "Hello world", then

- the set of 2-shingles is {he, el, ll, lo, ow, wo, or, rl, ld}
- the set of 3-shingles is {hel, ell, llo, low, owo, wor, orl, rld}

Your turn

We have the following two records:

```
# load RL data
data("RLdata500")

# select only 2 records
records <- RLdata500[129:130, c(1,3)]
names(records) <- c("First name", "Last name")

# inspect records
kable(records)
```

	First name	Last name
129	MICHAEL	VOGEL
130	MICHAEL	MEYER

Your turn (continued)

1. Compute the 2-shingles for each record

2. Using Jaccard similarity, how similar are they?

3. What do you learn from this exercise?

Your turn solution

1. The 2-shingles for the first record are {mi, ic, ch, ha, ae, el, lv, vo, og, ge, el} and for the second are {mi, ic, ch, ha, ae, el, lm, me, ey, ye, er}

2. There are 6 items in common {mi, ic, ch, ha, ae, el} and 15 items total
{mi, ic, ch, ha, ae, el, lv, vo, og, ge, lm, me, ey, ye, er}, so the Jaccard similarity is $\frac{6}{15} = \frac{2}{5} = 0.4$

3. You should have learned that this is very tedious to do by hand!

Useful packages/functions in R

(Obviously) We don't want to do this by hand most times.

Here are some useful packages in R that can help us!

```
library(textreuse) # text reuse/document similarity
library(tokenizers) # shingles
```

```
##
## Attaching package: 'tokenizers'

## The following objects are masked from 'package:textreuse
##
##     tokenize_ngrams, tokenize_sentences, tokenize_skip_n
##     tokenize_words
```

Shingling

We can use the following functions to create k-shingles and calculate Jaccard similarity for our data

```
# get k-shingles
tokenize_character_shingles(x, n)

# calculate jaccard similarity for two sets
jaccard_similarity(a, b)
```

Citation Data Set

Research paper headers and citations, with information on authors, title, institutions, venue, date, page numbers and several other fields

```
library(devtools)
```

```
## Loading required package: usethis
```

```
install_github("resteorts/cora")
```

```
## Skipping install of 'cora' from a github remote, the SHA1 (70e32d5d) has not changed since last instal
##   Use `force = TRUE` to force installation
```

```
library(cora)
library(ggplot2)
data(cora) # load the cora data set
str(cora) # structure of cora
```

```
## 'data.frame':    1879 obs. of  16 variables:
##  $ id          : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ title       : 'noquote' chr  "Inganas and M.R" NA NA NA ...
##  $ book_title  : 'noquote' chr  NA NA NA NA ...
##  $ authors     : 'noquote' chr  "M. Ahlskog, J. Paloheimo, H. Stubb, P. Dyreklev, M. Fahlman, O" "M. Ahl
##  $ address     : 'noquote' chr  NA NA NA NA ...
##  $ date        : 'noquote' chr  "1994" "1994" "1994" "1994" ...
##  $ year        : 'noquote' chr  NA NA NA NA ...
##  $ editor      : 'noquote' chr  NA NA NA NA ...
##  $ journal     : 'noquote' chr  "Andersson, J Appl. Phys." "JAppl. Phys." "J Appl. Phys." "J Appl.Phys."
##  $ volume      : 'noquote' chr  "76" "76" "76" "76" ...
##  $ pages       : 'noquote' chr  "893" "893" "893" "893" ...
##  $ publisher   : 'noquote' chr  NA NA NA NA ...
##  $ institution: 'noquote' chr  NA NA NA NA ...
##  $ type        : 'noquote' chr  NA NA NA NA ...
##  $ tech        : 'noquote' chr  NA NA NA NA ...
##  $ note        : 'noquote' chr  NA NA NA NA ...
```

Your turn

Using the `title`, `authors`, and `journal` fields in the `cora` dataset,

1. Get the 3-shingles for each record (**hint:** use `tokenize_character_shingles`)

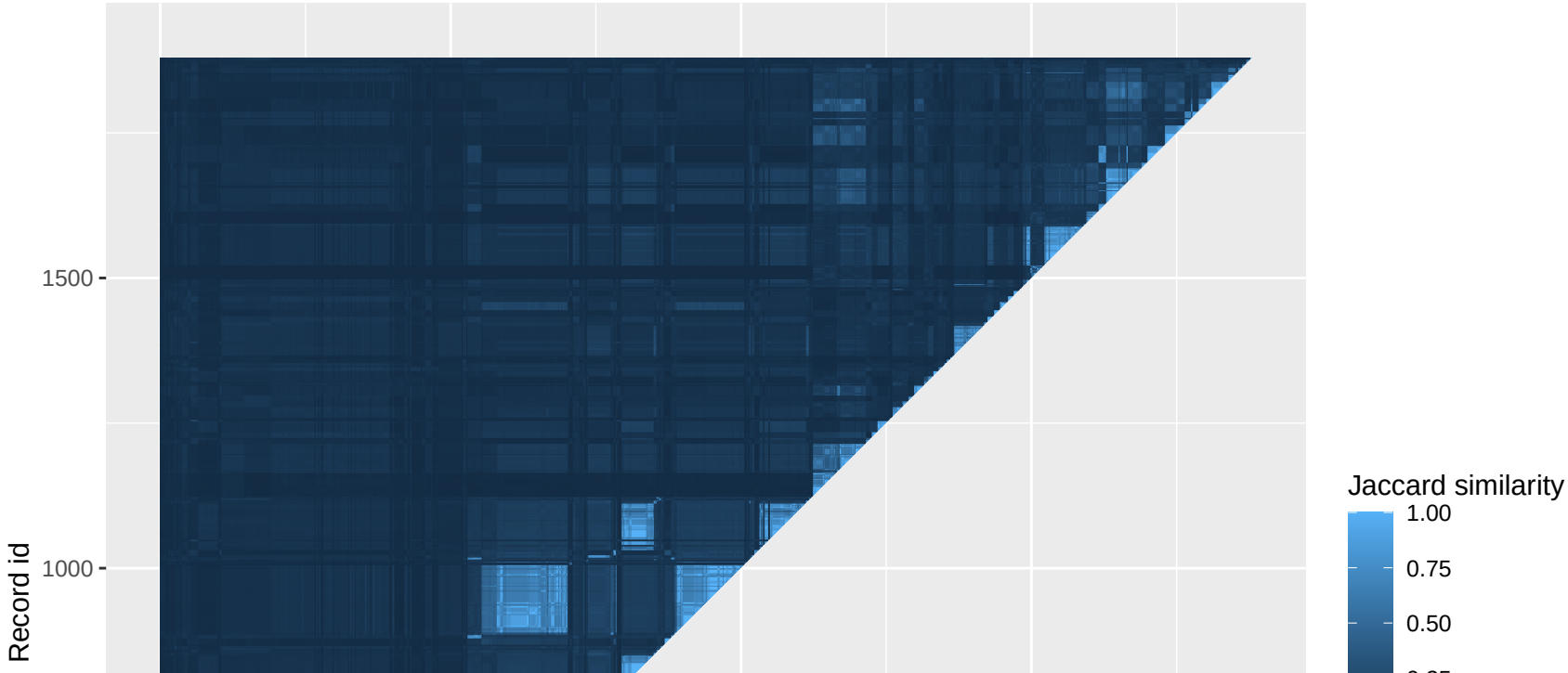
2. Obtain the Jaccard similarity between each pair of records (**hint:** use `jaccard_similarity`)

Your turn (solution)

```r
# get only the columns we want
n <- nrow(cora) # number of records
dat <- data.frame(id = seq_len(n)) # create id column
dat <- cbind(dat, cora[, c("title", "authors", "journal")]) # get colum

# 1. paste the columns together and tokenize for each record
shingles <- apply(dat, 1, function(x) {
  # tokenize strings
  tokenize_character_shingles(paste(x[-1], collapse=" "), n = 3)[[1]]
})

# 2. Jaccard similarity between pairs
jaccard <- expand.grid(record1 = seq_len(n), # empty holder for similar
                       record2 = seq_len(n))

# don't need to compare the same things twice
jaccard <- jaccard[jaccard$record1 < jaccard$record2,]

time <- Sys.time() # for timing comparison
jaccard$similarity <- apply(jaccard, 1, function(pair) {
  jaccard_similarity(shingles[[pair[1]]], shingles[[pair[2]]]) # get ja
})
time <- difftime(Sys.time(), time, units = "secs") # timing
```

Your turn (solution, cont'd)

```
# plot the jaccard similarities for each pair of records
ggplot(jaccard) +
  geom_raster(aes(x = record1, y = record2,
                  fill=similarity)) +
  theme(aspect.ratio = 1) +
  scale_fill_gradient("Jaccard similarity") +
  xlab("Record id") + ylab("Record id")
```



Your turn (solution, cont'd)

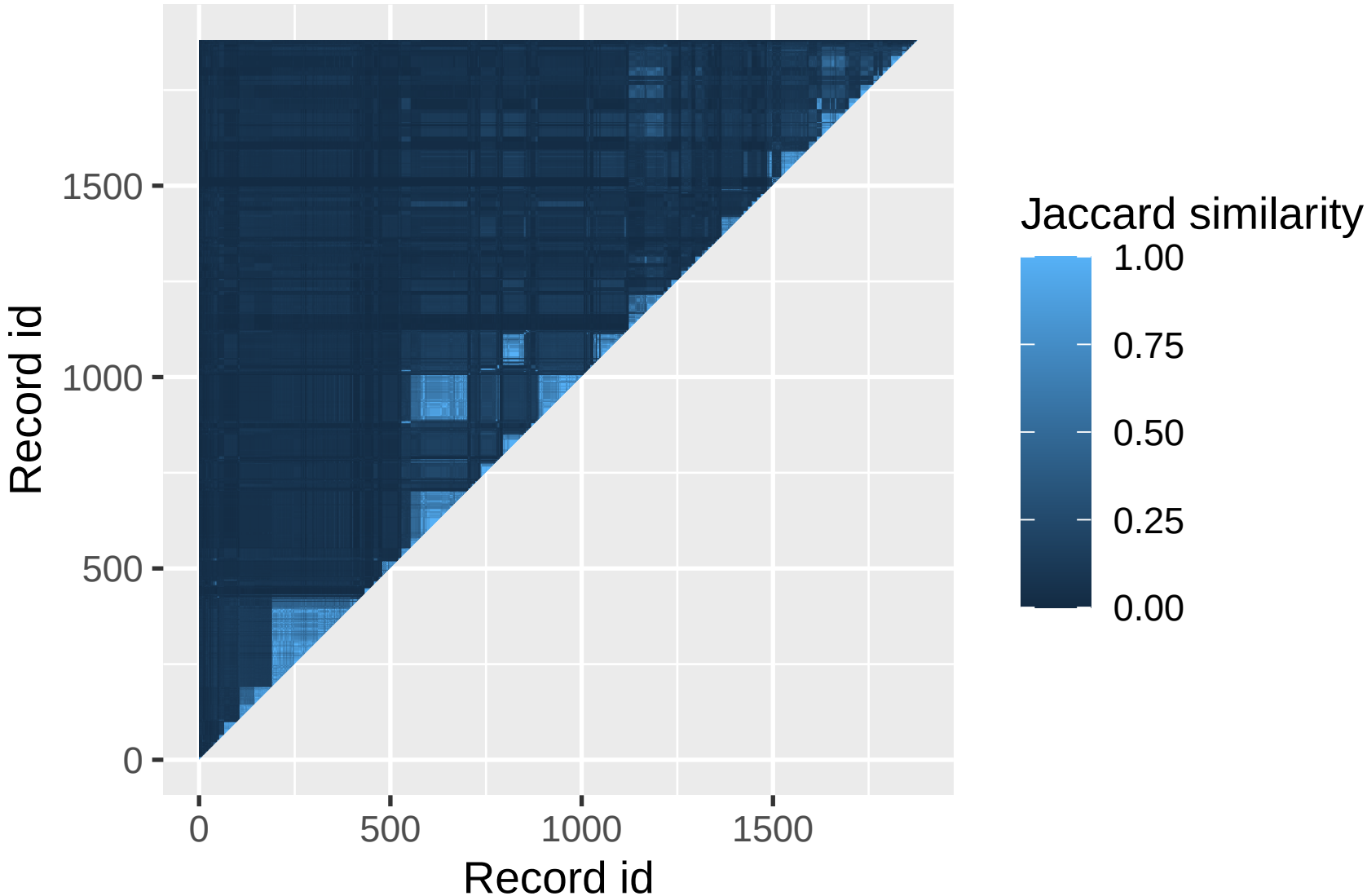


Figure 5: Jaccard similarity for each pair of records. Light blue indicates the two records are more similar and dark blue indicates less similar.

Summary

For a dataset of size n, the number of comparisons we must compute is

$$\frac{n(n-1)}{2}.$$

For our set of records, we needed to compute $1,764,381$ comparisons/

For very large data sets, we need something faster (where we filter out records that are not similar).

A better approach for datasets of any realistic size is to use *hashing*, which we will look at next time.