

Module 3: Pipeline and Deterministic ER

Rebecca C. Steorts

Reading

- ▶ Binette and Steorts (2020)
- ▶ Christen (2012), Chapters 1-3

Agenda

- ▶ Pipeline Approach
- ▶ Deterministic Record Linkage
- ▶ Exact Matching
- ▶ Scoring Functions
- ▶ Application to El Salvador

Load R packages

```
library(RecordLinkage)
```

Data Cleaning Pipeline



Figure 1: Data cleaning pipeline.

Deterministic Record Linkage

The most commonly used record linkage methods are based on a series of deterministic rules involving the comparison of record attributes.

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Exact matching (or extensions) are used when all the attributes are categorical as it tends to perform well, as opposed to when textual variables are introduced.

RLdata500

Consider the RLdata500 data set, removing any columns that contain missing values.

```
library(blink) # load RLdata500
data(RLdata500)
data <- RLdata500[-c(2,4)] # Remove missing values
head(data)
```

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

All pairs of records

Now let's consider all possible pairs of records.

```
# create all pairs of records  
pairs <- t(combn(1:nrow(RLdata500), 2))  
head(pairs)
```

```
##      [,1] [,2]  
## [1,]    1    2  
## [2,]    1    3  
## [3,]    1    4  
## [4,]    1    5  
## [5,]    1    6  
## [6,]    1    7
```

Pairwise features that disagree

For each pair of records, compute the number of features that disagree.¹

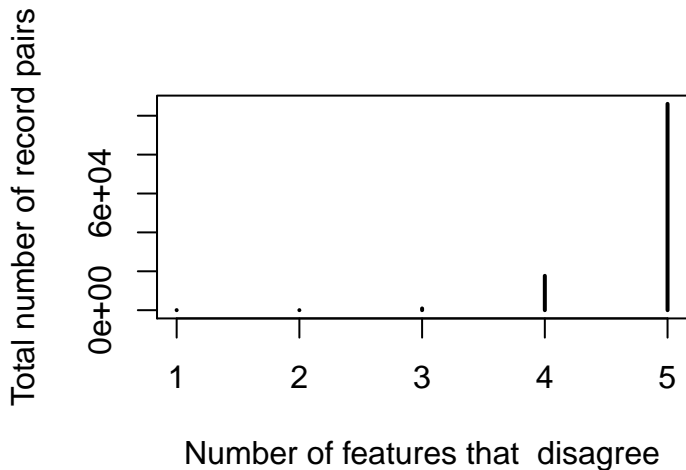
```
n_disagree = sapply(1:nrow(pairs), function(i) {  
  recordA = data[pairs[i,1],]  
  recordB = data[pairs[i,2],]  
  sum(recordA != recordB)  
})
```

¹This takes a few minute to compute in R. (There are more efficient ways to do this).

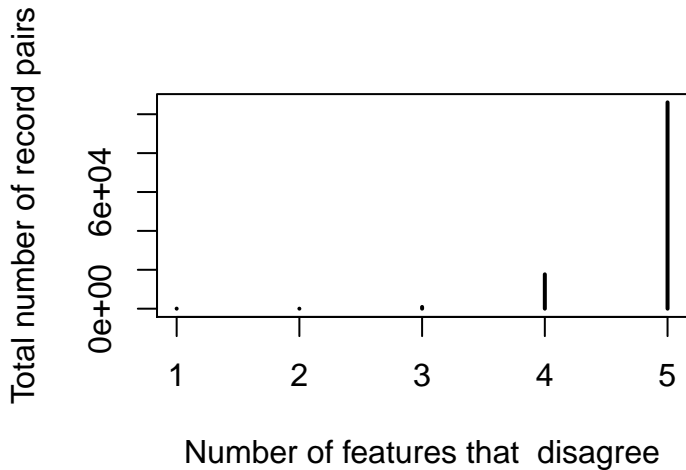
Distribution of Feature Disagreement Among Record Pairs

Let's plot the total number of record pair comparisons versus the number of features that disagree.

```
plot(table(n_disagree),  
      xlab="Number of features that disagree",  
      ylab="Total number of record pairs")
```



What do you observe?



Distribution of Feature Disagreement Among Record Pairs

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Is this intuitive?

Exact Matching, Etc

Now, let's investigate exact matching (and extensions) on the RLdata500 data set.

Exact Matching

Exact matching: Link record pairs that agree on all features.

```
sum(n_disagree == 0)
```

```
## [1] 0
```

No pairs are exact matches!

Off by one matching

Off by 1 matching: Link record pairs that disagree only in one feature.

```
# Links  
links = pairs[n_disagree <= 1, ]
```

```
# Number of estimated links  
nrow(links)
```

```
## [1] 46
```

```
# Number of correctly estimated links  
sum(sapply(1:nrow(links), function(i) {  
  identity.RLdata500[links[i,1]] ==  
    identity.RLdata500[links[i,2]]  
}))
```

```
## [1] 46
```

Off by two matching

How would you extend this to off by two matching?

What do you find?

Scoring Rules

We now turn to scoring rules and how these are used in entity resolution tasks.

Scoring Rules

- ▶ Record attributes are often distorted by noise. Why would this occur?
- ▶ Linkage rules should account for such noise, distortions, and errors through scoring rules or functions.
- ▶ Examples commonly used for westernized names are the Edit (Levenshtein), Jaro, and Jaro-Winkler distance functions.

Edit (Levenshtein) distance (1966)

The Edit distance calculates the minimum number of substitutions required to transform a string s_1 into a string s_2 .

Formally,

$$\text{Edit} = 1 - \frac{L}{\text{maxLength}(s_1, s_2)}.$$

Example

Consider the number of substitutions required to transform from **Adam** to **Alan**. Use the Edit distance formulate to find the similarity score that is between $[0, 1]$.

Solution

The number of substitutions required is $L = 2$.

This is normalized into a similarity function using the following:

$$\text{Edit} = 1 - \frac{L}{\text{maxLength}(s_1, s_2)} = 1 - 2/4 = 1 - 0.5 = 0.5$$

Solution

Let's verify this in R.

```
s1 <- "Adam"  
s2 <- "Alan"  
levenshteinSim("s1", "s2")
```

```
## [1] 0.5
```

Jaro-Winkler

- ▶ The Jaro distance (1989), called J , considered common characters and character transpositions.
- ▶ The Jaro-Winkler (1990) similarity measure, denoted JW is:

$$JW(A, B) = J(A, B) + 0.1p(1 - J(A, B))$$

where p is the # of the first four characters that agree exactly.

Example

Let's return to the example of comparing Adam and Alan.

- ▶ Here, $p = 1$.
- ▶ Given the complexity, we will calculate J and JW using R .

Example

```
## It seems Jaro is not supported in R  
jarowinkler(s1,s2)
```

```
## [1] 0.7
```

e.g. Adam vs Alan: $p=1$, $J=0.67$ and $JW=0.7$.

These work well on English names that are less than 7 characters.

Other distance functions

There are many other distance functions, such as the Jaccard, Hamming, and Cosine distances just to name a few.

Recap

You should now be familiar with the following:

- ▶ the pipeline approach
- ▶ deterministic record linkage methods
- ▶ exact matching and extensions
- ▶ scoring functions