# Example Session for Weight Based Deduplication

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This document shows an example session using the package *RecordLinkage*. A single data set is deduplicated using an EM algorithm for weight calculation. Conducting linkage of two data sets differs only in the step of generating record pairs.

## 1 Generating record pairs

The data to be deduplicated is expected to reside in a data frame or matrix, each row containing one record. Example data sets of 500 and 10000 records are included in the package as RLData500 and RLData10000.

```
> data(RLdata500)
> RLdata500[1:5, ]
```

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

For deduplication, compare.dedup is to be used. In this example, blocking is set to return only record pairs which agree in at least two components of the subdivided date of birth, resulting in 810 pairs. The argument identity preserves the true matching status for later evaluation.

```
> pairs = compare.dedup(RLdata500, identity = identity.RLdata500,
+ blockfld = list(c(5, 6), c(6, 7),
+ c(5, 7)))
> summary(pairs)

Deduplication Data Set

500 records
571 record pairs

49 matches
522 non-matches
0 pairs with unknown status
```

# 2 Weight calculation

Weights are calculated by means of an EM algorithm. This step is computationally intensive and might take a while. The histogram shows the resulting weight distribution.

```
> pairs = emWeights(pairs)
> hist(pairs$Wdata, plot = FALSE)
$breaks
 [1] -15 -10
             -5
                   0
                      5
                        10 15 20 25
                                         30 35
[12] 40 45
$counts
[1] 352
         13
              0
                  0
                      5 26 42 123
                                       9
                                          0
                                              0
[12]
      1
$intensities
 [1] 0.1232924694 0.0045534151 0.0000000000
 [4] 0.000000000 0.0017513135 0.0091068301
 [7] 0.0147110333 0.0430823117 0.0031523643
[10] 0.000000000 0.000000000 0.0003502627
$density
 [1] 0.1232924694 0.0045534151 0.0000000000
 [4] 0.0000000000 0.0017513135 0.0091068301
 [7] 0.0147110333 0.0430823117 0.0031523643
[10] 0.000000000 0.000000000 0.0003502627
$mids
 [1] -12.5 -7.5 -2.5
                        2.5
                              7.5 12.5 17.5
 [8] 22.5 27.5 32.5 37.5
                             42.5
$xname
[1] "pairs$Wdata"
$equidist
[1] TRUE
attr(,"class")
[1] "histogram"
```

#### 3 Classification

For determining thresholds, record pairs within a given range of weights can be printed using  $getPairs^1$ . In this case, 24 is set as upper and -7 as lower

<sup>&</sup>lt;sup>1</sup>The output of getPairs is shortened in this document.

threshold, dividing links, possible links and non-links. The summary shows the resulting contingency table and error measures.

```
> getPairs(pairs, 30, 20)
```

```
Weight id fname_c1 fname_c2 lname_c1
23 24.11923 106
                     ANDRE
                                <NA> MUELLER
            175
                     ANDRE
                                <NA>
                                      MUELLER
                    MONIKA
25 24.11923 370
                                <NA>
                                      MUELLER
26
            478
                    {\tt MONIKA}
                                <NA>
                                      MUELLER
27 24.08427 127
                                <NA>
                      KARL
                                        KLEIN
            142
                      KARL
                                <NA>
                                       KLEIBN
29 21.69109
             61
                     ANDRE
                                <NA>
                                      FISCHER
30
                  STEFANIE
                                <NA>
            254
                                      FISCHER
31 21.69109 353
                      INGE
                                <NA>
                                       SEIDEL
                     INGEU
                                <NA>
            355
                                       SEIDEL
33 21.69109 17 ALEXANDER
                                <NA>
                                      MUELLER
34
                                <NA> MUELLER
            193 CHRISTIAN
35 21.65612 389
                    URSULA
                                <NA> HOFFMANN
36
            449
                   CHRISTA
                                <NA> KRUEGER
              by bm bd
   lname_c2
23
                  2 25
       <NA> 1976
24
       <NA> 1976
                   1 25
       <NA> 2000
25
                  8 26
       <NA> 2000
26
                  5 26
       <NA> 2002
27
                   6 20
       <NA> 2002
28
                   6
                     29
29
       <NA> 1943
                  6 25
30
       <NA> 1943 11 25
       <NA> 1949
                  9
31
32
       <NA> 1949
       <NA> 1974
33
                   9
                      9
       <NA> 1974
34
                   8 9
       <NA> 1929
                   5 12
35
36
       <NA> 1929
                   5
> pairs = emClassify(pairs, threshold.upper = 24,
      threshold.lower = -7)
> summary(pairs)
Deduplication Data Set
500 records
571 record pairs
49 matches
522 non-matches
O pairs with unknown status
```

Weight distribution:

```
[-15, -10]
           (-10, -5]
                          (-5,0]
                                       (0,5]
                                                 (5,10]
      352
                   13
                               0
                                           0
  (10, 15]
             (15,20]
                         (20, 25]
                                    (25,30]
                                                (30,35]
                   42
                             123
                                           9
                                                       0
       26
  (35,40]
             (40,45]
        0
```

15 links detected 198 possible links detected 358 non-links detected

alpha error: 0.000000 beta error: 0.002786 accuracy: 0.997319

#### Classification table:

classification

true status N P L FALSE 358 163 1 TRUE 0 35 14

Review of the record pairs denoted as possible links is facilitated by getPairs, which can be forced to show only possible links via argument show. A list with the ids of linked pairs can be extracted from the output of getPairs with argument single.rows set to TRUE.

```
> possibles <- getPairs(pairs, show = "possible")
> possibles[1:6, ]
```

```
Weight id fname_c1 fname_c2 lname_c1
1 21.691086 61
                              <NA> FISCHER
                    ANDRE
2
            254
                 STEFANIE
                              <NA> FISCHER
3 21.691086 353
                     INGE
                              <NA>
                                     SEIDEL
            355
                    INGEU
                              <NA>
                                     SEIDEL
5 21.691086 17 ALEXANDER
                              <NA> MUELLER
                              <NA> MUELLER
6
            193 CHRISTIAN
  lname_c2
           by bm bd
      <NA> 1943 6 25
1
      <NA> 1943 11 25
2
3
      <NA> 1949 9
4
      <NA> 1949
                8
5
      <NA> 1974
                9
                    9
6
      <NA> 1974 8
> links = getPairs(pairs, show = "links",
      single.rows = TRUE)
> link_ids <- links[, c("id1", "id2")]</pre>
> link_ids
```