Classes for record linkage of big data sets

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As of version 0.3, the package RecordLinkage includes extensions to overcome the problem of high memory consumption that arises when processing a large number of records (i.e. building record pairs out of ≥ 1000 records without blocking). This is achieved by blockwise creation of comparison patterns instead of computing and storing the whole set of patterns at once, which was the only choice in the former version. In addition, an embedded SQLite database is used through package RSQLite to perform blocking, application of phonetic codes or string metrics and creation of comparison patterns. This allows to make use of the efficient data structures (e.g. indexing) implemented in the SQLite engine.

In order to facilitate a tidier design, S4 classes and methods were used to implement the extensions. In favor of backward compatibility and development time, plans of a complete transition to S4 were dismissed. Nevertheless, the existing functions were joined with their new counterparts, resulting in methods which dispatch on the new S4 as well as on the existing S3 classes. This approach combines two advantages: First, existing code using the package still works, second, the new classes and methods offer (nearly) the same interface, i.e. the necessary function calls for a linkage task differ only slightly. An exception is getPairs, whose arguments differ from the existing version (see man page).

1 Defining data and comparison parameters

The existing S3 class "RecLinkData" is supplemented by the S4 classes "RL-BigDataLinkage" and "RLBigDataDedup" for linking two datasets and deduplication of one dataset respectively. Both share the common abstract superclass "RLBigData".

- > library(RecordLinkage)
- > showClass("RLBigData")

Virtual Class "RLBigData" [package "RecordLinkage"]

Slots:

Name: frequencies blockFld excludeFld Class: numeric list numeric Name: strcmpFld strcmpFun phoneticFld Class: numeric character numeric

Name: phoneticFun drv con Class: character DBIDriver DBIConnection

Name: dbFile Class: character

Known Subclasses: "RLBigDataDedup", "RLBigDataLinkage"

> showClass("RLBigDataDedup")

Class "RLBigDataDedup" [package "RecordLinkage"]

Slots:

Name: data identity frequencies Class: data.frame factor numeric

Name: blockFld excludeFld strcmpFld Class: list numeric numeric

Name: strcmpFun phoneticFld phoneticFun Class: character numeric character

Name: drv con dbFile Class: DBIDriver DBIConnection character

Extends: "RLBigData"

> showClass("RLBigDataLinkage")

Class "RLBigDataLinkage" [package "RecordLinkage"]

Slots:

Name: data1 data2 identity1 Class: data.frame data.frame factor

Name: identity2 frequencies blockFld Class: factor numeric list

Name: excludeFld strcmpFld strcmpFun Class: numeric numeric character

Name: phoneticFld phoneticFun drv Class: numeric character DBIDriver

Name: con dbFile Class: DBIConnection character

Extends: "RLBigData"

For the two non-virtual classes, the constructor-like function RLBigDataDedup and RLBigDataLinkage exist, which correspond to compare.dedup and compare.linkage for the S3 classes and share most of their arguments. In contrast to the latter, these functions do not create the whole set of comparison patterns but only instantiate an object that holds all the information necessary to construct these pairs on demand.

The following example shows the basic usage of the constructors, for details consult their documentation.

```
> data(RLdata500)
> data(RLdata10000)
> rpairs1 <- RLBigDataDedup(RLdata500, identity = identity.RLdata500,
+ blockfld = list(1, 3), strcmp = 1:4)
> s1 <- 471:500
> s2 <- sample(1:10000, 300)
> identity2 <- c(identity.RLdata500[s1],
+ rep(NaN, length(s2)))
> dataset <- rbind(RLdata500[s1, ], RLdata10000[s2,
+ ])
> rpairs2 <- RLBigDataLinkage(RLdata500,
+ dataset, identity1 = identity.RLdata500,
+ identity2 = identity2, phonetic = 1:4,
+ exclude = "lname_c2")</pre>
```

In order to create comparison patterns, the following backend functions exist, which are usually not directly executed by the user:

begin Constructs an SQL statement to execute blocking, phonetic code, string comparison and building comparison patterns and sends this query to the underlying SQLite database. Takes as argument the object to process.

nextPairs Fetches a block of patterns after the query has been send. Takes as arguments the object from which to fetch and the maximum number of comparison patterns to return.

clear Clears the result set after comparison patterns have been fetched. Takes as argument the object to process.

```
> rpairs1 <- begin(rpairs1)
> nextPairs(rpairs1, 10)
```

```
id1 id2 fname_c1 fname_c2 lname_c1 lname_c2
1
     1
         8 0.0000000
                            NA 1.000000
                                              NA
2
       64 0.6190476
                           NA 1.000000
                                              NΑ
3
     1 141 0.5619048
                           NA 1.000000
                                              NA
     1 185 0.6190476
                           NA 1.000000
                                              NΑ
5
     1 217 0.6761905
                           NA 1.000000
                                              NA
     1 248 0.6761905
                           NA 1.000000
                                              NA
7
     1 268 0.6011905
                           NA 1.000000
                                              NA
8
     1 325 0.3952381
                           NA 1.000000
                                              NA
     1 428 0.5396825
                            NA 1.000000
                                               NA
    1 174 1.0000000
                           NA 0.447619
10
                                              NA
```

```
by bm bd is_match
   0 0
        0
2
   0
      1
        0
                 0
      0 0
4
   0 0 0
                 0
5
   0 0 0
                 0
6
   0 0 0
7
   0 0 0
8
   0 0 0
                 0
9
   0 0 0
                 0
10 0 0 0
                 0
```

> clear(rpairs1)

[1] TRUE

2 Supervised classification

The existing function classifySupv was transformed to a S4 method which handles the old S3 object ("RecLinkData") as well as the new classes. However, at the moment a classificator can only be trained with an object of class "RecLinkData".

```
> train <- getMinimalTrain(compare.dedup(RLdata500,
+     identity = identity.RLdata500, blockfld = list(1,
+         3)))
> rpairs1 <- RLBigDataDedup(RLdata500, identity = identity.RLdata500)
> classif <- trainSupv(train, "rpart", minsplit = 2)
> result <- classifySupv(classif, rpairs1)</pre>
```

The result is an object of class "RLResult" which contains the indices of links and optionally possible links.

```
> showClass("RLResult")
Class "RLResult" [package "RecordLinkage"]
Slots:
```

Name: data links possibleLinks Class: RLBigData matrix matrix

Name: nPairs Class: numeric

A contingency table can be viewed via getTable, various error measures are calculated by getErrorMeasures.

```
> getTable(result)
```

```
classification
true status
                N
                                L
      FALSE 124696
                         0
                                4
      TRUE
                               48
> getErrorMeasures(result)
$alpha
[1] 0.04
$beta
[1] 3.207698e-05
$accuracy
[1] 0.9999519
$precision
[1] 0.9230769
$sensitivity
[1] 0.96
$specificity
[1] 0.9999679
$ppv
[1] 0.9230769
$npv
[1] 0.999984
```

3 Weight-based classification

As with "RecLinkData" objects, weight-based classification with "RLBigData*" classes includes weight calculation and classification based on one or two thresholds, dividing links, non-links and, if desired, possible links. The following example applies classification with Epilink (see documentation of epiWeights for details):

By default, the weights for each individual record pair are stored in the associated database, which speeds up subsequent classification significantly. If the resulting disk usage is an issue, this behavior can be changed as follows:

- In the case of weight calculation with an EM algorithm by calling emWeights with argument save.weights = FALSE. This results in only 2#attributes per-pattern weights being stored.
- In the case of Epilink weights, epiWeights can be called directly. In this case, weights are calculated during classification but are not saved in memory.

4 Evaluation and results

In addition to getTable and getErrorMeasures, getPairs, which was redesigned as a versatile S4 method, is an important tool to inspect data and linkage results. For example, the following code extracts all links with weights greater or equal than 0.7 from the result set obtained in the last example:

```
> getPairs(result, min.weight = 0.7, filter.link = "link")
```

```
id fname_c1 fname_c2 lname_c1 lname_c2
                                               by bm
         HELGA ELFRIEDE
1 290
                            BERGER
                                        <NA> 1989
2 466
         HELGA ELFRIEDE
                                        <NA> 1989
                            BERGER
                                                   1
3
4 467
        ULRIKE
                  NICOLE
                            BECKRR
                                        <NA> 1982
5
 472
        ULRIKE
                  NICOLE
                            BECKER
                                        <NA> 1982
6
7 313
        URSULA
                  BIRGIT
                           MUELLRR
                                        <NA> 1940
                                                   6
8 457
        URSULA
                  BIRGIT
                           MUELLER
                                        <NA> 1940
  bd is_match Class
                        Weight
1 18
2 28
         TRUE
                   L 0.7786012
3
4
  4
5
   4
         TRUE
                   L 0.7293529
6
7 15
8 15
         TRUE
                   L 0.7293529
9
```

A frequent use case is to inspect misclassifed record pairs; for this purpose two shortcuts are included that call getPairs with appropriate arguments:

> getFalsePos(result)

```
id fname_c1 fname_c2 lname_c1 lname_c2
                                               by bm
1 388
        ANDREA
                    <NA>
                             WEBER.
                                       <NA> 1945
                                                   5
2 408
        ANDREA
                    <NA>
                          SCHMIDT
                                       <NA> 1945
3
  bd is_match Class
                        Weight
1 20
2
 20
        FALSE
                   L 0.5067013
3
```

> getFalseNeg(result)

	ic	d fi	name_c1	fname_c2	lname_c1	lname_c2	by
1	353	3	INGE	<na></na>	SEIDEL	<na></na>	1949
2	355	5	INGEU	<na></na>	SEIDEL	<na></na>	1949
3							
4	285	5	ERIKA	<na></na>	WEBER	<na></na>	1995
5	379		ERIKA	<na></na>	WEBER	<na></na>	1992
6							
7	127	7	KARL	<na></na>	KLEIN	<na></na>	2002
8	142	2	KARL	<na></na>	KLEIBN	<na></na>	2002
9							
10	37	7 H	ARTMHUT	<na></na>	HOFFMSNN	<na></na>	1929
11	72	2 I	HARTMUT	<na></na>	HOFFMANN	<na></na>	1929
12							
	bm	bd	is_matc	ch Class	Weight		
1	9	4					
2	8	4	TRU	JE N (0.4948059		
3							
4	2	1					
5	2	29	TRU	JE N (0.4782410		
6							
7	6	20					
8	6	29	TRU	JE N (0.4692532		
9							
10	12	29					
11	12	29	TRU	JE N (0.4081096		
12							