



Max-Planck-Institut für demografische Forschung
Max Planck Institute for Demographic Research
Konrad-Zuse-Strasse 1 · D-18057 Rostock · GERMANY
Tel +49 (0) 3 81 20 81 - 0; Fax +49 (0) 3 81 20 81 - 202;
<http://www.demogr.mpg.de>

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Comparison of DemoDiff Releases 2.0 and 3.0

Rainer Walke (walke@demogr.mpg.de)

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This technical report has been approved for release by: Dirk Vieregg (vieregg@demogr.mpg.de),
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Comparison of DemoDiff Releases 2.0 and 3.0

Rainer Walke, MPIDF Rostock*

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Abstract

In this Technical Report, results of the program **compareFinRaw** are presented. **compareFinRaw** is a tool that is particularly useful for comparing large data sets. It is typically used to compare different releases of the same data. In this example, we compare two different releases of the project **DemoDiff**. To be more precise, we compare the five revised files of DemoDiff Release 3.0 with the older Release 2.0 files. It should provide users of the **DemoDiff** data a comprehensive overview on all manipulations of the data that have occurred from Release 2.0 to Release 3.0.

Keywords data analysis, data comparability, data evaluation, data processing, software

1. Introduction

In a Technical Report by Walke and Müller [TR-2012-003] we have described a procedure to compare two datasets with little conditions. Only the ID had to be the same in each row of both datasets. The program that compares the datasets had been named **compareFinRaw**. It compares each column (variable) from one set with each column from the second data set. It furthermore checks whether there are bijective mappings between variables of the two data sets. If there is no direct mapping it computes how much the levels of the variables have to be changed to get a bijective mapping.

In this report, we use **compareFinRaw** to compare two different releases of the project **DemoDiff**. We are comparing Release 2.0 [DemoDiff 2.0] and Release 3.0 [DemoDiff 3.0]. Both are available by GESIS (www.gesis.org). We compare the following data sets: `anchor1_DD.dta`, `anchor2_DD.dta`, `partner1_DD.dta`, `partner2_DD.dta` and `weights.dta`¹.

We are using the statistical package R [R 2.15] for all the computations and RStudio, knitR and MiKTeX for the documentation. The output of these programs is a readable list that reports the number and the names of variables that completely match between the two releases, i.e. have the same name and same content. The program also identifies all modified variables such as renamed variables, bijective recoded variables and variables with marked differences. Furthermore we get the names of all variables without variation at all. We hope, that this material helps users of **DemoDiff** to get a clear picture on what has been changed between the two releases. It should be noted that, depending on the number of variables **compareFinRaw** takes minutes or hours to compare the files.²

*MPIDF, Konrad-Zuse-Straße 1, D-18057 Rostock, Germany. E-Mail: walke@demogr.mpg.de

¹There are further files in the releases. However, they have been omitted because they are not suitable for comparison.

²In our case, it took 7 hours to run the program for the largest data set (`anchor2_DD.dta`)

2. Classification

The idea is to classify all variables in data set **A** in respect to their relations to variables from data set **B**.

A typical solution would be first to check whether a variable with the same name is available in data set **B**. If this is true we could distinguish between identical and non identical content. This way we would classify all variable from set **A** into one of three possible categories.

This would give only a rough picture of the differences between the data sets. To detect renamed and recoded variables as well we use a more sophisticated classification scheme.

classification tree

1. The selected variable from **A** does not have variation.
 - 1.1 [x] No variable with the same name is available in data set **B**.
 - 1.2 One variable with the same name is available in data set **B**.
 - 1.21 [n] Both variables are not identical.
 - 1.22 [ni] Both variables are identical.
2. The selected variable from **A** does have variation.
 - 2.1 There exists no bivariate mapping to one of the variables in data set **B**.
 - 2.11 [v] No variable with the same name is available in data set **B**.
 - 2.12 [vn] One variable with the same name is available in data set **B**.
 - 2.2 There exists at least one bivariate mapping to one of the variables in data set **B**.
 - 2.21 There are more than one bivariate mappings.
 - 2.211 All mapped variables from **B** do have a different name.
 - 2.2111 [vb] No mapped variable from **B** is identical.
 - 2.2112 [vbi] At least one mapped variable from **B** is identical.
 - 2.212 One mapped variable from **B** has the same name.
 - 2.2121 [vbn] The mapped variable from **B** is not identical.
 - 2.2122 [vbni] The mapped variable from **B** is identical.
 - 2.22 There exists exactly one bivariate mapping.
 - 2.221 The mapped variable from **B** has a different name.
 - 2.2211 [vb1] Both variables are not identical.
 - 2.2212 [vb1i] Both variables are identical.
 - 2.222 The mapped variable from **B** has the same name.
 - 2.2221 [vb1n] Both variables are not identical.
 - 2.2222 [vb1ni] Both variables are identical.

Every variable out of **A** will be assign to exactly one of these 13 classes.

3. Results and Summary

The appendix contains the documented code. For each of the five data sets the code follows the same logic.

1. Analyze all variables without variation
2. Analyze all variables with variation, but without a bijective mapping
3. Analyze all variables with variation and with a bijective mapping
4. Provide a comparison summary

As an example we display here the summary output that our program has produced for the data set `anchor2_DD.dta`.

class	Release 2	Release 3
x	8	0
n	15	37
ni	612	612
v	1	7
vn	369	359
vb	2	0
vbi	11	1
vbn	2	1
vbni	954	956
vb1	4	5
vb1i	3	2
vb1n	3	4
vb1ni	1262	1260
sum	3246	3244

The results may be interpreted as follows:

Most variables are unchanged (ni, vbni, vb1ni). 612 variables do not have variation and are identical. 954 + 1262 variables (vbni, vb1ni, Release 2) are unchanged, but have variation. There is a weak probability that 954 variables (vbni) show some redundancy.

8 constant variables (x, Release 2) have been dropped. One variable (v, Release 2) with variation has been dropped as well.

15 variables (n, Release 2) have been gained variation or have changed to another constant value.

2 variables (vb, Release 2) have been (less probably) renamed and recoded. 11 variables (vbi, Release 2) have been (less probably) renamed. 2 variables (vbn, Release 2) have been (probably) recoded.

4 variables (vb1, Release 2) have been (probably) renamed and recoded. 3 variables (vb1i, Release 2) have been (probably) renamed. 3 variables (vb1n, Release 2) have been (probably) recoded.

369 variables (vn, Release 2) had been changed between releases. They have the same name, but there exist no bijective mapping. The provided Levenshtein distance (appendix) gives a rough idea whether only some cases have been changed or not.

4. Acknowledgements

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A. anchor1

Here we compare the data set `anchor1_dd.dta` from DemoDiff Release 2.0 with the same data set from DemoDiff Release 3.0.

We have to load the produced data collection. Release 2.0 files are denoted with **R** and **Raw**, release 3.0 files with **F** and **Fin**, respectively.

```
rm(list = ls())
duplicStrict <- function(A) {
  return(duplicated(A) | duplicated(A, fromLast = TRUE))
}
load("../compareR2R3\\anchor1\\Results\\compareFinRaw.RData")
```

A.1. no variation

We compare the variables without variation first.

```
(R.x <- sum(!(RawNames[Rnv] %in% FinNames)))

## [1] 1

(F.x <- sum(!(FinNames[Fnv] %in% RawNames)))

## [1] 0

# added or lost variance
(R.nA <- sum(!(RawNames[Rnv] %in% FinNames[Fnv]))) - R.x

## [1] 0

(F.nA <- sum(!(FinNames[Fnv] %in% RawNames[Rnv]))) - F.x

## [1] 0

Rnv2 <- data.frame(Rnv.tab)
Fnv2 <- data.frame(Fnv.tab)
Rnv2$nm <- gsub("R$", "", row.names(Rnv2))
Fnv2$nm <- gsub("F$", "", row.names(Fnv2))
RFnv2 <- merge(Rnv2, Fnv2, by = c("nm"), all = TRUE)

(R.ni <- sum((RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 423

F.ni <- R.ni

# changed values
(R.nB <- sum(!(RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))
```

```
## [1] 0

F.nB <- R.nB

(R.n <- R.nA + R.nB)

## [1] 0

(F.n <- F.nA + F.nB)

## [1] 0

RawNames[Rnv][!(RawNames[Rnv] %in% FinNames)]

## [1] "k10age"

RFnv2[is.na(RFnv2$Fin.no.var), 1]

## [1] "k10age"

FinNames[Fnv][!(FinNames[Fnv] %in% RawNames)]

## character(0)

RFnv2[is.na(RFnv2$Raw.no.var), 1]

## character(0)
```

Release 2.0 For 1 variables without variation (k10age) exist no variables with the same name in the comparison data set. 423 variables without variation are identical in both data sets.

Release 3.0 423 variables without variation are identical in both data sets.

A.2. variation, but no bijective mapping

```
rb <- results.bijec
RL.bi <- RawNames[!Rnv] %in% gsub("R$", "", as.character(rb$Raw.c.nm))
FL.bi <- FinNames[!Fnv] %in% gsub("F$", "", as.character(rb$Fin.c.nm))
sum(!RL.bi)

## [1] 43

sum(!FL.bi)

## [1] 48
```

```

(R.v <- sum(!(RawNames[!Rnv][!RL.bi] %in% FinNames)))

## [1] 0

RawNames[!Rnv][!RL.bi][!(RawNames[!Rnv][!RL.bi] %in% FinNames)]

## character(0)

(R.vn <- sum(RawNames[!Rnv][!RL.bi] %in% FinNames))

## [1] 43

RawNames[!Rnv][!RL.bi][RawNames[!Rnv][!RL.bi] %in% FinNames]

## [1] "sex"      "dobm"      "sd4g"      "sdp1m"     "sdply"
## [6] "frt11v1i1" "frt11v1i2" "frt11v1i3" "frt11v1i4" "frt11v1i5"
## [11] "frt11v1i6" "frt11v1i7" "frt11v1i8" "frt11v2i1" "frt11v2i2"
## [16] "frt11v2i3" "frt11v2i4" "frt11v2i5" "frt11v2i6" "frt11v2i7"
## [21] "frt11v2i8" "flag1"      "flag18"    "sex_gen"    "psex_gen"
## [26] "dobm_gen"  "pdoby_gen" "pdobm_gen" "age"        "page"
## [31] "mage"      "fage"      "k1age"     "k2age"     "homosex"
## [36] "infertile" "pregnant"  "hhsizemrd" "othmrd"    "hhcomp"
## [41] "isei"      "siops"     "hhincgcee"

(F.v <- sum(!(FinNames[!Fnv][!FL.bi] %in% RawNames)))

## [1] 5

FinNames[!Fnv][!FL.bi][!(FinNames[!Fnv][!FL.bi] %in% RawNames)]

## [1] "ykage"      "ykid"      "flag_isco08_kldb2010"
## [4] "kldb2010"  "isco08"

(F.vn <- sum(FinNames[!Fnv][!FL.bi] %in% RawNames))

## [1] 43

FinNames[!Fnv][!FL.bi][FinNames[!Fnv][!FL.bi] %in% RawNames]

## [1] "sex"      "dobm"      "sd4g"      "sdp1m"     "sdply"
## [6] "frt11v1i1" "frt11v1i2" "frt11v1i3" "frt11v1i4" "frt11v1i5"
## [11] "frt11v1i6" "frt11v1i7" "frt11v1i8" "frt11v2i1" "frt11v2i2"
## [16] "frt11v2i3" "frt11v2i4" "frt11v2i5" "frt11v2i6" "frt11v2i7"
## [21] "frt11v2i8" "flag1"      "flag18"    "sex_gen"    "psex_gen"
## [26] "dobm_gen"  "pdoby_gen" "pdobm_gen" "age"        "page"
## [31] "mage"      "fage"      "k1age"     "k2age"     "homosex"
## [36] "infertile" "pregnant"  "hhsizemrd" "othmrd"    "hhcomp"
## [41] "isei"      "siops"     "hhincgcee"

```

Release 2.0 43 variables share the name with one of the variables in Release 3.0 at least.

Release 3.0 For 5 variables with variation but without any bijective mapping exist no variables with the same name in the Release 2.0 data. 43 variables share the name with one of the variables in Release 2.0 at least.

We compare all variables pairs (with variation) which share the same name but are not connected with a bijective mapping. Those variables imply different information. DemoDiff data user should check whether they are using those variables for possible effects on their research. (The number of pairs may differ from 43 and 43).

```

results$same.name <-
  gsub("R$", "", as.character(results$Raw.c.nm)) == gsub("F$", "", as.character(results$Fin.c.nm))
sum(results$same.name & results$map.di>0)

## [1] 43

print(results[(results$same.name & results$map.di>0),c(2,3,5,6,7,8)],row.names=FALSE)

##      Fin.c.nm Fin.c.ls   Raw.c.nm Raw.c.ls map.di ed.di.sum
##      sexF      2      sexR      2      4      2
##      dobmF     12     dobmR     12     10     7
##      sd4gF      3      sd4gR      3      4      4
##      sdp1mF    17     sdp1mR    17     20     17
##      sdp1yF    45     sdp1yR    45     30     25
##      frt11v1i1F 10     frt11v1i1R 9      1      1
##      frt11v1i2F 10     frt11v1i2R 9      1      1
##      frt11v1i3F 10     frt11v1i3R 9      1      1
##      frt11v1i4F 10     frt11v1i4R 9      1      1
##      frt11v1i5F 10     frt11v1i5R 9      1      1
##      frt11v1i6F 10     frt11v1i6R 9      1      1
##      frt11v1i7F 9      frt11v1i7R 8      1      1
##      frt11v1i8F 10     frt11v1i8R 9      1      1
##      frt11v2i1F 6      frt11v2i1R 5      1      1
##      frt11v2i2F 6      frt11v2i2R 5      1      1
##      frt11v2i3F 6      frt11v2i3R 5      1      1
##      frt11v2i4F 6      frt11v2i4R 5      1      1
##      frt11v2i5F 6      frt11v2i5R 5      1      1
##      frt11v2i6F 6      frt11v2i6R 5      1      1
##      frt11v2i7F 6      frt11v2i7R 5      1      1
##      frt11v2i8F 6      frt11v2i8R 5      1      1
##      flag1F     2      flag1R     2      4      5
##      flag18F    3      flag18R    3      2      3
##      sex_genF   2      sex_genR   2      4      2
##      psex_genF  3      psex_genR  3      4      4
##      dobm_genF 12     dobm_genR 12     10     7
##      pdoby_genF 45     pdoby_genR 45     30     25
##      pdobm_genF 17     pdobm_genR 17     20     17
##      ageF       9      ageR       9      2      1
##      pageF     45     pageR     45     36     25
##      mageF     43     mageR     43     16     13
##      fageF     46     fageR     46     20     12
##      k1ageF    29     k1ageR    29     4      2
##      k2ageF    26     k2ageR    26     4      3
##      homosexF  3      homosexR  3      4      6

```



```
## infertileF      3 infertileR      3      2      2
## pregnantF     4 pregnantR      4      4      6
## hhsizemrdF    9 hhsizemrdR      9      2      1
## othmrdF       6 othmrdR        6      2      1
## hhcompF      15 hhcompR       15      2      1
## iseif        174 iseifR         60     462     2486
## siopsF       177 siopsR         57     478     2529
## hhincgeeF    330 hhincgeeR      331      1      7
```

A.3. variation and bijective mapping

```
# mark all identical cases
rb$ident <- (rb$ed.di.sum == 0)
# mark all not duplicated raw variables
rb$dup.Raw <- !duplicStrict(rb$Raw.c.nm)
# mark all not duplicated fin variables
rb$dup.Fin <- !duplicStrict(rb$Fin.c.nm)
# mark all equal name pairs
rb$same.name <- gsub("R$", "", as.character(rb$Raw.c.nm)) == gsub("F$", "",
  as.character(rb$Fin.c.nm))

rb$Raw.same.name <- (ave(rb$same.name, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.same.name <- (ave(rb$same.name, rb$Fin.c.nm, FUN = sum) > 0)

rb$Raw.ident <- (ave(rb$ident, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.ident <- (ave(rb$ident, rb$Fin.c.nm, FUN = sum) > 0)

(R.vb <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"])))

## [1] 0

(R.vbi <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"])))

## [1] 0

(R.vbn <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"])))

## [1] 0

(R.vbni <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"])))

## [1] 225

R.vb1 <- length(unique(rb[rb$dup.Raw & !rb$same.name & !rb$ident, "Raw.c.nm"]))
as.character(unique(rb[rb$dup.Raw & !rb$same.name & !rb$ident, "Raw.c.nm"]))

## [1] "kldbR" "iscoR"

R.vbli <- length(unique(rb[rb$dup.Raw & !rb$same.name & rb$ident, "Raw.c.nm"]))
as.character(unique(rb[rb$dup.Raw & !rb$same.name & rb$ident, "Raw.c.nm"]))
```

```

## [1] "flag_isco_kldbR"

(R.vb1n <- length(unique(rb[rb$dup.Raw & rb$same.name & !rb$ident, "Raw.c.nm"])))

## [1] 0

(R.vb1ni <- length(unique(rb[rb$dup.Raw & rb$same.name & rb$ident, "Raw.c.nm"])))

## [1] 703

(F.vb <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbi <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbn <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbni <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"])))

## [1] 225

F.vb1 <- length(unique(rb[rb$dup.Fin & !rb$same.name & !rb$ident, "Fin.c.nm"]))
as.character(unique(rb[rb$dup.Fin & !rb$same.name & !rb$ident, "Fin.c.nm"]))

## [1] "kldb1992F" "isco88F"

F.vb1i <- length(unique(rb[rb$dup.Fin & !rb$same.name & rb$ident, "Fin.c.nm"]))
as.character(unique(rb[rb$dup.Fin & !rb$same.name & rb$ident, "Fin.c.nm"]))

## [1] "flag_isco88_kldb1992F"

(F.vb1n <- length(unique(rb[rb$dup.Fin & rb$same.name & !rb$ident, "Fin.c.nm"])))

## [1] 0

(F.vb1ni <- length(unique(rb[rb$dup.Fin & rb$same.name & rb$ident, "Fin.c.nm"])))

## [1] 703

```

A.4. comparison summary for anchor1_DD.dta Release 2.0 and Release 3.0

class	Release 2	Release 3
x	1	0
n	0	0
ni	423	423
v	0	5
vn	43	43
vb	0	0
vbi	0	0
vbn	0	0
vbni	225	225
vb1	2	2
vb1i	1	1
vb1n	0	0
vb1ni	703	703
sum	1398	1402

Most variables are unchanged (ni, vbni, vb1ni). A small number (x, v) had been dropped or added. A number of variables (vb1, vb1i) had been (probably) renamed or recoded. A group of variables (vn) had been changed. This analysis provide no further hints for this group.

A.5. selected in-depth comparison

For illustrative purposes we present some detailed results.

```
D1 <- cbind(Raw$klbR, Fin$klb1992F)
D1[D1[, 1] != D1[, 2], ]

##      [,1] [,2]
## [1,] " -1" " -7"
## [2,] " -1" " -7"
```

Both variables share the same number of levels. The level '-1' has been recoded to '-7'. Changing '-1' to '-7' for two individuals takes 2 Levenshtein steps (see details in [TR-2012-003]).

```
D2 <- cbind(Raw$dobmR, Fin$dobmF)
D2[D2[, 1] != D2[, 2], ]

##      [,1] [,2]
## [1,] " 5" " 6"
## [2,] " 8" " 1"
## [3,] " 6" "12"
## [4,] "10" "11"
## [5,] "11" " 8"
```

Both variables share the same number of levels. $12 + 12 + 10 = 34$, $34/2 = 17$ mappings between the levels are in use. For a bijective mapping we need 5 mappings less. Coincidentally 5 individual show a changed level. It takes 7 Levenshtein steps to make the levels equal.

```
D3 <- cbind(Raw$pageR, Fin$pageF)
D3[D3[, 1] != D3[, 2], ]
```

```
##      [,1] [,2]
## [1,] "-7" "36"
## [2,] "21" "23"
## [3,] "25" "24"
## [4,] "21" "22"
## [5,] "-7" "46"
## [6,] "20" "30"
## [7,] "26" "27"
## [8,] "25" "24"
## [9,] "25" "26"
## [10,] "38" "37"
## [11,] "35" "37"
## [12,] "34" "33"
## [13,] "26" "27"
## [14,] "21" "22"
## [15,] "30" "33"
## [16,] "29" "28"
## [17,] "42" "41"
## [18,] "20" "19"
## [19,] "32" "33"
## [20,] "44" "45"
## [21,] "26" "27"
## [22,] "26" "24"
```

22 individuals have a new level for 'page'. It takes 25 Levenshtein steps to get them equal. There is no bijective mapping available.

```
D4 <- cbind(Raw$iseiR, Fin$iseiF)
dim(D4[D4[, 1] != D4[, 2], ])

## [1] 918  2

head(D4[D4[, 1] != D4[, 2], ])

##      [,1] [,2]
## [1,] " 23" "5153"
## [2,] " 53" " 37"
## [3,] " 38" " 51"
## [4,] " 48" "3435"
## [5,] " 51" " 53"
## [6,] " 51" "3344"
```

918 individuals do have a different level. There is no bijective mapping.

B. anchor2

Using the same tools we compare the data set `anchor2_dd.dta` from DemoDiff Release 2.0 with the same data set from DemoDiff Release 3.0.

At first we have to load the produced data collection. Release 2.0 files are denoted with **R** and **Raw**, release 3.0 files with **F** and **Fin**, respectively.

```
rm(list = ls())
duplicStrict <- function(A) {
  return(duplicated(A) | duplicated(A, fromLast = TRUE))
}
load("../compareR2R3/anchor2/Results/compareFinRaw.RData")
```

B.1. no variation

We compare the variables without variation first.

```
(R.x <- sum(!(RawNames[Rnv] %in% FinNames)))

## [1] 8

(F.x <- sum(!(FinNames[Fnv] %in% RawNames)))

## [1] 0

# added or lost variance
(R.nA <- sum(!(RawNames[Rnv] %in% FinNames[Fnv]))) - R.x

## [1] 15

(F.nA <- sum(!(FinNames[Fnv] %in% RawNames[Rnv]))) - F.x

## [1] 37

Rnv2 <- data.frame(Rnv.tab)
Fnv2 <- data.frame(Fnv.tab)
Rnv2$nm <- gsub("R$", "", row.names(Rnv2))
Fnv2$nm <- gsub("F$", "", row.names(Fnv2))
RFnv2 <- merge(Rnv2, Fnv2, by = c("nm"), all = TRUE)

(R.ni <- sum((RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 612

F.ni <- R.ni

# changed values
(R.nB <- sum(!(RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 0

F.nB <- R.nB

(R.n <- R.nA + R.nB)

## [1] 15
```

```

(F.n <- F.nA + F.nB)

## [1] 37

RawNames[Rnv][!(RawNames[Rnv] %in% FinNames)]

## [1] "d402" "d403" "d404" "d405" "d406" "d411" "d412" "d420"

RFnv2[is.na(RFnv2$Fin.no.var), 1]

## [1] "d402"      "d403"      "d404"      "d405"      "d406"
## [6] "d411"      "d412"      "d420"      "ehc27p4i1" "ehc27p4i2"
## [11] "ehc28p2m1" "ehc28p2m2" "ehc28p3m1" "ehc28p3m2" "ehc28p3m3"
## [16] "ehc4p2m10" "ehc4p2m11" "ehc4p2m12" "ehc4p2m13" "ehc4p2m14"
## [21] "ehc4p2m15" "ehc4p2m16" "ehc4p2m17"

FinNames[Fnv][!(FinNames[Fnv] %in% RawNames)]

## character(0)

RFnv2[is.na(RFnv2$Raw.no.var), 1]

## [1] "ehc10k5h2" "ehc10k6h2" "ehc10k7h2" "ehc10k8h2" "ehc10k9h2"
## [6] "ehc16m1"   "ehc16m2"   "ehc16m3"   "ehc17"      "ehc17m10"
## [11] "ehc17m11"  "ehc17m12"  "ehc17m13"  "ehc17m14"  "ehc17m15"
## [16] "ehc17m16"  "ehc17m17"  "ehc17m4"   "ehc17m5"   "ehc17m6"
## [21] "ehc17m7"   "ehc17m8"   "ehc17m9"   "ehc25p1h3" "ehc25p2h3"
## [26] "ehc25p3h3" "ehc25p4h3" "ehc25p5h2" "ehc25p5h3" "ehc25p6h2"
## [31] "ehc25p6h3" "ehc25p7h2" "ehc25p7h3" "ehc25p8h2" "ehc25p8h3"
## [36] "ehc26h3"   "flag25"

```

Release 2.0 For 8 variables without variation (d402, d403, d404, d405, d406, d411, d412, d420) exist no variables with the same name in the comparison data set. 612 variables without variation are identical in both data sets. 15 variables share the same name, but are not identical (got variance, changed value).

Release 3.0 612 variables without variation are identical in both data sets. 37 variables share the same name, but are not identical (lost variance, changed value).

B.2. variation, but no bijective mapping

```

rb <- results.bijec
RL.bi <- RawNames[!Rnv] %in% gsub("R$", "", as.character(rb$Raw.c.nm))
FL.bi <- FinNames[!Fnv] %in% gsub("F$", "", as.character(rb$Fin.c.nm))
sum(!RL.bi)

## [1] 370

```

```

sum(!FL.bi)

## [1] 366

(R.v <- sum(!(RawNames[!Rnv][!RL.bi] %in% FinNames)))

## [1] 1

RawNames[!Rnv][!RL.bi][!(RawNames[!Rnv][!RL.bi] %in% FinNames)]

## [1] "isco"

(R.vn <- sum(RawNames[!Rnv][!RL.bi] %in% FinNames))

## [1] 369

RawNames[!Rnv][!RL.bi][RawNames[!Rnv][!RL.bi] %in% FinNames]

## [1] "d4" "sex" "ehc1p1n" "ehc1p1g"
## [5] "ehc2p1" "ehc3p1" "ehc4p1" "ehc1p2n"
## [9] "ehc1p2g" "ehc2p2" "ehc3p2" "ehc4p2"
## [13] "ehc6p2" "ehc4p1m8" "ehc4p1m9" "ehc4p1m10"
## [17] "ehc4p1m11" "ehc4p1m12" "ehc4p1m13" "ehc4p1m14"
## [21] "ehc4p1m15" "ehc4p1m16" "ehc4p1m17" "ehc2p2m8"
## [25] "ehc2p2m9" "ehc2p2m10" "ehc2p2m11" "ehc2p2m12"
## [29] "ehc2p2m13" "ehc2p2m14" "ehc2p2m15" "ehc2p2m16"
## [33] "ehc2p2m17" "ehc3p2m8" "ehc3p2m9" "ehc3p2m10"
## [37] "ehc3p2m11" "ehc3p2m12" "ehc3p2m13" "ehc3p2m14"
## [41] "ehc3p2m15" "ehc3p2m16" "ehc3p2m17" "ehc27p1i2"
## [45] "ehc28p1" "ehc29p1" "ehc27p2i1" "ehc27p2i2"
## [49] "ehc28p2" "ehc29p2" "ehc27p3i1" "ehc27p3i2"
## [53] "ehc28p3" "ehc29p3" "ehc28p1m8" "ehc28p1m9"
## [57] "ehc28p1m10" "ehc28p1m11" "ehc28p1m12" "ehc28p1m13"
## [61] "ehc28p1m14" "ehc28p1m15" "ehc28p1m16" "ehc28p1m17"
## [65] "ehc28p2m3" "ehc28p2m4" "ehc28p2m5" "ehc28p2m6"
## [69] "ehc28p2m7" "ehc28p2m8" "ehc28p2m9" "ehc28p2m10"
## [73] "ehc28p2m11" "ehc28p2m12" "ehc28p2m13" "ehc28p2m14"
## [77] "ehc28p2m15" "ehc28p2m16" "ehc28p2m17" "ehc28p3m4"
## [81] "ehc28p3m5" "ehc28p3m6" "ehc28p3m7" "ehc28p3m8"
## [85] "ehc28p3m9" "ehc28p3m10" "ehc28p3m11" "ehc28p3m12"
## [89] "ehc28p3m13" "ehc28p3m14" "ehc28p3m15" "ehc28p3m16"
## [93] "ehc28p3m17" "ehc16m4" "ehc16m5" "ehc16m6"
## [97] "ehc16m7" "ehc16m8" "ehc16m9" "ehc16m10"
## [101] "ehc16m11" "ehc16m12" "ehc16m13" "ehc16m14"
## [105] "ehc16m15" "ehc16m16" "ehc16m17" "ehc17m5"
## [109] "ehc17m6" "ehc17m7" "ehc17m8" "ehc17m9"
## [113] "ehc17m10" "ehc17m11" "ehc17m12" "ehc17m13"
## [117] "ehc17m14" "ehc17m15" "ehc17m16" "ehc17m17"
## [121] "ehc16" "ehc17" "ehc22p1n" "ehc22p2n"
## [125] "ehc22p3n" "ehc22p4n" "ehc22p5n" "ehc23p1"
## [129] "ehc23p2" "ehc23p3" "ehc23p4" "ehc23p5"
## [133] "ehc24p1m" "ehc24p2m" "ehc24p3m" "ehc24p4m"
## [137] "ehc24p5m" "ehc24p6m" "ehc24p1y" "ehc24p2y"

```

```

## [141] "ehc24p3y"      "ehc24p4y"      "ehc24p5y"      "ehc24p6y"
## [145] "ehc25p1h1"     "ehc25p2h1"     "ehc25p3h1"     "ehc25p4h1"
## [149] "ehc25p5h1"     "ehc25p1h2"     "ehc25p2h2"     "ehc25p3h2"
## [153] "ehc25p4h2"     "ehc25p5h2"     "ehc25p7h2"     "ehc25p1h3"
## [157] "ehc25p2h3"     "ehc25p3h3"     "ehc25p4h3"     "ehc25p5h3"
## [161] "ehc25p7h3"     "ehc26h1"       "ehc26h2"       "ehc26h3"
## [165] "ehc10k1h1"     "ehc10k2h1"     "ehc10k3h1"     "ehc10k4h1"
## [169] "ehc10k5h1"     "ehc10k6h1"     "ehc10k7h1"     "ehc10k1h2"
## [173] "ehc10k2h2"     "ehc10k3h2"     "ehc10k4h2"     "hhnr"
## [177] "hh1nr"         "hh2nr"         "hh1a"          "hh2a"
## [181] "hh1l"         "hh2l"         "hh1t0"         "hh2t0"
## [185] "hp"           "hpnr"         "hpn"           "hpg"
## [189] "hp0"         "hpsep"        "hpmt"          "hpm"
## [193] "hpc"         "hps2"         "hp0nr"         "hp0n"
## [197] "hp0g"        "hp0ct0"       "hc6h1"         "hc6h2"
## [201] "job17"       "job18h"       "sat2"          "sin3i1"
## [205] "sin3i2"      "sin1"         "sin2"          "sin6i1"
## [209] "sin6i2"      "sin6i3"       "sin6i4"        "sin6i5"
## [213] "pa2m"        "pa30"         "pa3"           "sdp1d"
## [217] "sdp1m"       "sdp1y"        "sdp2i1"        "sdp2i2"
## [221] "sdp2i3"      "sdp2i4"       "sdp2i5"        "sdp2i6"
## [225] "sdp2i7"      "sdp2i8"       "sdp2i9"        "sdp2i10"
## [229] "sdp2i11"     "sdp2i12"      "sdp3"          "sdp6"
## [233] "sdp21"       "sdp22"        "sdp10i16"     "sdp10i17"
## [237] "sdp10i7"     "sdp10i18"    "sdp10i19"     "sdp10i9"
## [241] "sdp10i20"   "sdp10i21"    "sdp10i22"     "sdp10i1"
## [245] "sdp10i2"    "sdp10i3"     "sdp10i4"      "sdp10i5"
## [249] "sdp10i6"    "sdp10i13"    "sdp10i8"      "sdp10i10"
## [253] "sdp10i11"   "sdp10i12"    "sdp10i15"     "sdp10i14"
## [257] "sdp16"      "sdp17"       "sdp18"        "hcp1i1"
## [261] "hcp1i2"     "hcp2"        "hcp3h"        "hcp3m"
## [265] "hcp4h"      "hcp5"        "pa9"          "pa11"
## [269] "pa13"       "pa14i1"      "pa14i2"       "pa14i3"
## [273] "pa14i4"     "pa14i5"      "pa15"         "cps1"
## [277] "sat3"       "pa26"        "pa27"         "pa28"
## [281] "sep1i1"     "sep1i2"      "sep2"         "sep18"
## [285] "sep12"     "sep13"       "sep14"        "sep17i1"
## [289] "sep17i2"   "sep17i3"     "sep17i4"     "sep16"
## [293] "frt2"      "frt11v1i6"   "frt11v1i7"   "frt11v1i8"
## [297] "frt11v2i6" "frt11v2i7"   "frt11v2i8"   "crn22p1"
## [301] "crn33p1i1" "crn33p1i2"   "crn33p1i3"   "crn34p1"
## [305] "igr22"     "igr25"       "igr28"        "igr39p3"
## [309] "igr40p3"   "igr41p1"     "rtr43"        "inc24"
## [313] "inc26i2"   "inc26i3"     "inc27i2"     "inc27i3"
## [317] "int4i6"    "lmhh1"       "lmhh2"        "lvhh1"
## [321] "lvhh2"     "avhh1"       "hv1"          "tag_sex"
## [325] "tag_dobp"   "flag25"      "sex_gen"      "psex_gen"
## [329] "pdoby_gen"  "pdobm_gen"   "page"         "mage"
## [333] "klage"     "k2age"       "pcob"         "pnat1"
## [337] "marstat"   "np"          "ncoh"         "nmar"
## [341] "meetdur"   "reldur"     "cohabdur"     "mardur"
## [345] "homosex"   "infertile"   "pregnant"     "pnkidsbioalv"
## [349] "res2nd"    "hhsizemrd"   "mmrd"         "fmrdr"
## [353] "childmrd"  "othmrd"     "hhcomp"       "penrol"
## [357] "pschool"   "pvocat"     "piscd"        "piscd2"
## [361] "pcasmin"   "pyeduc"     "egp"          "isei"

```



```

## [365] "siops"          "hhincgee"      "pcasprim"     "pcassec"
## [369] "plfs"

(F.v <- sum(!(FinNames[!Fnv][!FL.bi] %in% RawNames)))

## [1] 7

FinNames[!Fnv][!FL.bi][!(FinNames[!Fnv][!FL.bi] %in% RawNames)]

## [1] "flag_isco88_kldb1992" "flag_isco08_kldb2010" "ykage"
## [4] "ykid"                  "kldb2010"           "isco88"
## [7] "isco08"

(F.vn <- sum(FinNames[!Fnv][!FL.bi] %in% RawNames))

## [1] 359

FinNames[!Fnv][!FL.bi][FinNames[!Fnv][!FL.bi] %in% RawNames]

## [1] "d4"          "sex"          "ehc1p1n"     "ehc1p1g"
## [5] "ehc2p1"     "ehc3p1"      "ehc4p1"      "ehc1p2n"
## [9] "ehc1p2g"    "ehc2p2"      "ehc3p2"      "ehc4p2"
## [13] "ehc6p2"     "ehc4p1m8"    "ehc4p1m9"    "ehc4p1m10"
## [17] "ehc4p1m11" "ehc4p1m12"   "ehc4p1m13"   "ehc4p1m14"
## [21] "ehc4p1m15" "ehc4p1m16"   "ehc4p1m17"   "ehc2p2m8"
## [25] "ehc2p2m9"   "ehc2p2m10"   "ehc2p2m11"   "ehc2p2m12"
## [29] "ehc2p2m13" "ehc2p2m14"   "ehc2p2m15"   "ehc2p2m16"
## [33] "ehc2p2m17" "ehc3p2m8"    "ehc3p2m9"    "ehc3p2m10"
## [37] "ehc3p2m11" "ehc3p2m12"   "ehc3p2m13"   "ehc3p2m14"
## [41] "ehc3p2m15" "ehc3p2m16"   "ehc3p2m17"   "ehc4p2m8"
## [45] "ehc4p2m9"   "ehc4p2m10"   "ehc4p2m11"   "ehc4p2m12"
## [49] "ehc4p2m13" "ehc4p2m14"   "ehc4p2m15"   "ehc4p2m16"
## [53] "ehc4p2m17" "ehc27p1i2"   "ehc28p1"     "ehc29p1"
## [57] "ehc27p2i1" "ehc27p2i2"   "ehc28p2"     "ehc29p2"
## [61] "ehc27p3i1" "ehc27p3i2"   "ehc28p3"     "ehc29p3"
## [65] "ehc27p4i1" "ehc27p4i2"   "ehc28p1m8"   "ehc28p1m9"
## [69] "ehc28p1m10" "ehc28p1m11" "ehc28p1m12" "ehc28p1m13"
## [73] "ehc28p1m14" "ehc28p1m15" "ehc28p1m16" "ehc28p1m17"
## [77] "ehc28p2m1" "ehc28p2m2"   "ehc28p2m3"   "ehc28p2m4"
## [81] "ehc28p2m5" "ehc28p2m6"   "ehc28p2m7"   "ehc28p2m8"
## [85] "ehc28p2m9" "ehc28p2m10" "ehc28p2m11" "ehc28p2m12"
## [89] "ehc28p2m13" "ehc28p2m14" "ehc28p2m15" "ehc28p2m16"
## [93] "ehc28p2m17" "ehc28p3m1"   "ehc28p3m2"   "ehc28p3m3"
## [97] "ehc28p3m4" "ehc28p3m5"   "ehc28p3m6"   "ehc28p3m7"
## [101] "ehc28p3m8" "ehc28p3m9"   "ehc28p3m10"  "ehc28p3m11"
## [105] "ehc28p3m12" "ehc28p3m13" "ehc28p3m14"  "ehc28p3m15"
## [109] "ehc28p3m16" "ehc28p3m17" "ehc16m5"     "ehc16m6"
## [113] "ehc16m7"    "ehc16m8"     "ehc16m9"     "ehc16m10"
## [117] "ehc16m11"   "ehc16m12"    "ehc16m13"    "ehc16m14"
## [121] "ehc16m15"   "ehc16m16"    "ehc16m17"    "ehc16"
## [125] "ehc22p1n"   "ehc22p2n"    "ehc22p3n"    "ehc22p4n"
## [129] "ehc22p5n"   "ehc23p1"     "ehc23p2"     "ehc23p3"
## [133] "ehc23p4"    "ehc23p5"     "ehc24p1m"    "ehc24p2m"

```

## [137]	"ehc24p3m"	"ehc24p4m"	"ehc24p5m"	"ehc24p7m"
## [141]	"ehc24p1y"	"ehc24p2y"	"ehc24p3y"	"ehc24p4y"
## [145]	"ehc24p5y"	"ehc24p7y"	"ehc25p1h1"	"ehc25p2h1"
## [149]	"ehc25p3h1"	"ehc25p4h1"	"ehc25p5h1"	"ehc25p7h1"
## [153]	"ehc25p1h2"	"ehc25p2h2"	"ehc25p3h2"	"ehc26h1"
## [157]	"ehc26h2"	"ehc10k1h1"	"ehc10k2h1"	"ehc10k3h1"
## [161]	"ehc10k4h1"	"ehc10k5h1"	"ehc10k6h1"	"ehc10k7h1"
## [165]	"ehc10k1h2"	"ehc10k2h2"	"ehc10k3h2"	"ehc10k4h2"
## [169]	"hhnr"	"hh1nr"	"hh2nr"	"hh1a"
## [173]	"hh2a"	"hh1l"	"hh2l"	"hh1t0"
## [177]	"hh2t0"	"hp"	"hpnr"	"hpn"
## [181]	"hpg"	"hp0"	"hpsep"	"hpmt"
## [185]	"hpm"	"hpc"	"hps2"	"hp0nr"
## [189]	"hp0n"	"hp0g"	"hp0ct0"	"hc6h1"
## [193]	"hc6h2"	"job17"	"job18h"	"sat2"
## [197]	"sin3i1"	"sin3i2"	"sin1"	"sin2"
## [201]	"sin6i1"	"sin6i2"	"sin6i3"	"sin6i4"
## [205]	"sin6i5"	"pa2m"	"pa30"	"pa3"
## [209]	"sdp1d"	"sdp1m"	"sdp1y"	"sdp2i1"
## [213]	"sdp2i2"	"sdp2i3"	"sdp2i4"	"sdp2i5"
## [217]	"sdp2i6"	"sdp2i7"	"sdp2i8"	"sdp2i9"
## [221]	"sdp2i10"	"sdp2i11"	"sdp2i12"	"sdp3"
## [225]	"sdp6"	"sdp21"	"sdp22"	"sdp10i16"
## [229]	"sdp10i17"	"sdp10i7"	"sdp10i18"	"sdp10i19"
## [233]	"sdp10i9"	"sdp10i20"	"sdp10i21"	"sdp10i22"
## [237]	"sdp10i1"	"sdp10i2"	"sdp10i3"	"sdp10i4"
## [241]	"sdp10i5"	"sdp10i6"	"sdp10i13"	"sdp10i8"
## [245]	"sdp10i10"	"sdp10i11"	"sdp10i12"	"sdp10i15"
## [249]	"sdp10i14"	"sdp16"	"sdp17"	"sdp18"
## [253]	"hcp1i1"	"hcp1i2"	"hcp2"	"hcp3h"
## [257]	"hcp3m"	"hcp5"	"pa9"	"pa11"
## [261]	"pa13"	"pa14i1"	"pa14i2"	"pa14i3"
## [265]	"pa14i4"	"pa14i5"	"pa15"	"cps1"
## [269]	"sat3"	"pa26"	"pa27"	"pa28"
## [273]	"sep1i1"	"sep1i2"	"sep2"	"sep18"
## [277]	"sep12"	"sep13"	"sep14"	"sep17i1"
## [281]	"sep17i2"	"sep17i3"	"sep17i4"	"sep16"
## [285]	"frt2"	"frt11v1i6"	"frt11v1i7"	"frt11v1i8"
## [289]	"frt11v2i6"	"frt11v2i7"	"frt11v2i8"	"crn22p1"
## [293]	"crn33p1i1"	"crn33p1i2"	"crn33p1i3"	"crn34p1"
## [297]	"igr22"	"igr25"	"igr28"	"igr39p3"
## [301]	"igr40p3"	"igr41p1"	"rtr43"	"inc24"
## [305]	"inc26i2"	"inc26i3"	"inc27i2"	"inc27i3"
## [309]	"int4i6"	"lmhh1"	"lmhh2"	"lvhh1"
## [313]	"lvhh2"	"hv1"	"tag_sex"	"tag_dobp"
## [317]	"sex_gen"	"psex_gen"	"pdoby_gen"	"pdobm_gen"
## [321]	"page"	"mage"	"k1age"	"k2age"
## [325]	"pcob"	"pnat1"	"marstat"	"np"
## [329]	"ncoh"	"nmar"	"meetdur"	"reldur"
## [333]	"cohabdur"	"mardur"	"homosex"	"infertile"
## [337]	"pregnant"	"pnkidsbioalv"	"res2nd"	"hhsizemrd"
## [341]	"mmrd"	"fmrdr"	"childmrd"	"othmrd"
## [345]	"hhcomp"	"penrol"	"pschool"	"pvocat"
## [349]	"piscd"	"piscd2"	"pcasmin"	"pyeduc"
## [353]	"egp"	"isei"	"siops"	"hhincgcee"
## [357]	"pcasprim"	"pcassec"	"plfs"	

Release 2.0 For 1 variables with variation but without any bijective mapping exist no variables with the same name in the Release 3.0 data. 369 variables share the name with one of the variables in Release 3.0 at least.

Release 3.0 For 7 variables with variation but without any bijective mapping exist no variables with the same name in the Release 2.0 data. 359 variables share the name with one of the variables in Release 2.0 at least.

We compare all variables pairs (with variation) which share the same name but are not connected with a bijective mapping. Those variables imply different information. DemoDiff data user should check whether they are using those variables for possible effects on their research. The number of pairs may differ from 369 and 359.

```
results$same.name <-
  gsub("R$", "", as.character(results$Raw.c.nm)) == gsub("F$", "", as.character(results$Fin.c.nm))
sum(results$same.name & results$map.di>0)

## [1] 351

print(results[(results$same.name & results$map.di>0),c(2,3,5,6,7,8)],row.names=FALSE)

##      Fin.c.nm Fin.c.ls      Raw.c.nm Raw.c.ls map.di ed.di.sum
##      d4F      2      d4R      2      2      1
##      sexF      2      sexR      2      2      1
##      ehc1p1nF  3      ehc1p1nR  3      2      16
##      ehc1p1gF  3      ehc1p1gR  3      4      14
##      ehc2p1F   3      ehc2p1R   3      2      24
##      ehc3p1F   3      ehc3p1R   3      2      22
##      ehc4p1F   3      ehc4p1R   3      4      21
##      ehc1p2nF  2      ehc1p2nR  2      2      2
##      ehc1p2gF  3      ehc1p2gR  3      2      2
##      ehc2p2F   3      ehc2p2R   3      2      2
##      ehc3p2F   3      ehc3p2R   3      2      2
##      ehc4p2F   2      ehc4p2R   2      2      2
##      ehc6p2F   2      ehc6p2R   2      2      2
##      ehc4p1m8F  3      ehc4p1m8R  3      2      1
##      ehc4p1m9F  3      ehc4p1m9R  3      2      1
##      ehc4p1m10F 2      ehc4p1m10R 2      2      1
##      ehc4p1m11F 2      ehc4p1m11R 2      2      1
##      ehc4p1m12F 2      ehc4p1m12R 2      2      1
##      ehc4p1m13F 2      ehc4p1m13R 2      2      1
##      ehc4p1m14F 2      ehc4p1m14R 2      2      1
##      ehc4p1m15F 2      ehc4p1m15R 2      2      1
##      ehc4p1m16F 2      ehc4p1m16R 2      2      1
##      ehc4p1m17F 2      ehc4p1m17R 2      2      1
##      ehc2p2m8F  3      ehc2p2m8R  3      2      2
##      ehc2p2m9F  3      ehc2p2m9R  3      2      2
##      ehc2p2m10F 3      ehc2p2m10R 2      1     1174
##      ehc2p2m11F 3      ehc2p2m11R 2      1     1174
##      ehc2p2m12F 3      ehc2p2m12R 2      1     1174
##      ehc2p2m13F 3      ehc2p2m13R 2      1     1174
##      ehc2p2m14F 3      ehc2p2m14R 2      1     1174
##      ehc2p2m15F 3      ehc2p2m15R 2      1     1174
##      ehc2p2m16F 3      ehc2p2m16R 2      1     1174
##      ehc2p2m17F 3      ehc2p2m17R 2      1     1174
```

##	ehc3p2m8F	2	ehc3p2m8R	3	1	2
##	ehc3p2m9F	3	ehc3p2m9R	3	2	2
##	ehc3p2m10F	3	ehc3p2m10R	2	1	1174
##	ehc3p2m11F	3	ehc3p2m11R	2	1	1174
##	ehc3p2m12F	3	ehc3p2m12R	2	1	1174
##	ehc3p2m13F	3	ehc3p2m13R	2	1	1174
##	ehc3p2m14F	3	ehc3p2m14R	2	1	1174
##	ehc3p2m15F	3	ehc3p2m15R	2	1	1174
##	ehc3p2m16F	3	ehc3p2m16R	2	1	1174
##	ehc3p2m17F	3	ehc3p2m17R	2	1	1174
##	ehc4p2m8F	2	ehc4p2m8R	2	2	2
##	ehc4p2m9F	2	ehc4p2m9R	2	2	2
##	ehc27p1i2F	9	ehc27p1i2R	8	1	2
##	ehc28p1F	2	ehc28p1R	2	2	12
##	ehc29p1F	3	ehc29p1R	3	4	19
##	ehc27p2i1F	3	ehc27p2i1R	2	3	33
##	ehc27p2i2F	16	ehc27p2i2R	15	11	34
##	ehc28p2F	4	ehc28p2R	3	5	33
##	ehc29p2F	4	ehc29p2R	3	1	8
##	ehc27p3i1F	3	ehc27p3i1R	2	1	4
##	ehc27p3i2F	6	ehc27p3i2R	5	1	4
##	ehc28p3F	4	ehc28p3R	3	1	4
##	ehc29p3F	3	ehc29p3R	2	1	3
##	ehc28p1m8F	3	ehc28p1m8R	3	2	1
##	ehc28p1m9F	3	ehc28p1m9R	3	2	2
##	ehc28p1m10F	2	ehc28p1m10R	2	2	4
##	ehc28p1m11F	2	ehc28p1m11R	2	2	4
##	ehc28p1m12F	2	ehc28p1m12R	2	2	5
##	ehc28p1m13F	2	ehc28p1m13R	2	2	9
##	ehc28p1m14F	2	ehc28p1m14R	2	2	10
##	ehc28p1m15F	2	ehc28p1m15R	2	2	10
##	ehc28p1m16F	2	ehc28p1m16R	2	2	11
##	ehc28p1m17F	2	ehc28p1m17R	2	2	12
##	ehc28p2m3F	3	ehc28p2m3R	2	1	3
##	ehc28p2m4F	4	ehc28p2m4R	3	3	5
##	ehc28p2m5F	4	ehc28p2m5R	3	3	16
##	ehc28p2m6F	4	ehc28p2m6R	3	3	16
##	ehc28p2m7F	4	ehc28p2m7R	3	3	22
##	ehc28p2m8F	4	ehc28p2m8R	3	5	28
##	ehc28p2m9F	4	ehc28p2m9R	3	5	33
##	ehc28p2m10F	4	ehc28p2m10R	3	5	33
##	ehc28p2m11F	4	ehc28p2m11R	3	5	33
##	ehc28p2m12F	4	ehc28p2m12R	3	5	33
##	ehc28p2m13F	4	ehc28p2m13R	3	5	33
##	ehc28p2m14F	4	ehc28p2m14R	3	5	33
##	ehc28p2m15F	4	ehc28p2m15R	3	5	33
##	ehc28p2m16F	4	ehc28p2m16R	3	5	33
##	ehc28p2m17F	4	ehc28p2m17R	3	5	33
##	ehc28p3m4F	3	ehc28p3m4R	2	1	2
##	ehc28p3m5F	3	ehc28p3m5R	2	1	3
##	ehc28p3m6F	3	ehc28p3m6R	2	1	4
##	ehc28p3m7F	4	ehc28p3m7R	3	1	4
##	ehc28p3m8F	4	ehc28p3m8R	3	1	4
##	ehc28p3m9F	4	ehc28p3m9R	3	1	4
##	ehc28p3m10F	4	ehc28p3m10R	3	1	4
##	ehc28p3m11F	4	ehc28p3m11R	3	1	4

##	ehc28p3m12F	4	ehc28p3m12R	3	1	4
##	ehc28p3m13F	4	ehc28p3m13R	3	1	4
##	ehc28p3m14F	4	ehc28p3m14R	3	1	4
##	ehc28p3m15F	4	ehc28p3m15R	3	1	4
##	ehc28p3m16F	4	ehc28p3m16R	3	1	4
##	ehc28p3m17F	4	ehc28p3m17R	3	1	4
##	ehc16m4F	3	ehc16m4R	3	2	308
##	ehc16m5F	3	ehc16m5R	3	2	660
##	ehc16m6F	3	ehc16m6R	3	4	1000
##	ehc16m7F	4	ehc16m7R	4	4	1412
##	ehc16m8F	4	ehc16m8R	4	4	1822
##	ehc16m9F	4	ehc16m9R	4	4	2276
##	ehc16m10F	4	ehc16m10R	4	4	2280
##	ehc16m11F	3	ehc16m11R	3	4	2280
##	ehc16m12F	3	ehc16m12R	3	4	2282
##	ehc16m13F	3	ehc16m13R	4	5	2281
##	ehc16m14F	4	ehc16m14R	4	6	2282
##	ehc16m15F	3	ehc16m15R	4	5	2280
##	ehc16m16F	3	ehc16m16R	4	5	2285
##	ehc16m17F	3	ehc16m17R	4	5	2284
##	ehc16F	3	ehc16R	4	5	2284
##	ehc22p1nF	5	ehc22p1nR	4	5	63
##	ehc22p2nF	4	ehc22p2nR	5	7	69
##	ehc22p3nF	4	ehc22p3nR	4	6	35
##	ehc22p4nF	4	ehc22p4nR	3	5	13
##	ehc22p5nF	3	ehc22p5nR	3	4	5
##	ehc22p7nF	2	ehc22p7nR	3	1	1
##	ehc23p1F	12	ehc23p1R	12	30	71
##	ehc23p2F	12	ehc23p2R	14	26	74
##	ehc23p3F	12	ehc23p3R	13	23	40
##	ehc23p4F	8	ehc23p4R	8	10	16
##	ehc23p5F	4	ehc23p5R	4	2	4
##	ehc24p1mF	15	ehc24p1mR	14	13	48
##	ehc24p2mF	15	ehc24p2mR	14	15	49
##	ehc24p3mF	14	ehc24p3mR	13	9	28
##	ehc24p4mF	8	ehc24p4mR	8	4	10
##	ehc24p5mF	5	ehc24p5mR	5	2	2
##	ehc24p6mF	4	ehc24p6mR	3	1	1
##	ehc24p7mF	3	ehc24p7mR	2	1	1
##	ehc24p1yF	45	ehc24p1yR	44	13	62
##	ehc24p2yF	42	ehc24p2yR	43	11	64
##	ehc24p3yF	24	ehc24p3yR	24	8	32
##	ehc24p4yF	11	ehc24p4yR	11	4	12
##	ehc24p5yF	6	ehc24p5yR	6	2	2
##	ehc24p6yF	4	ehc24p6yR	3	1	1
##	ehc24p7yF	3	ehc24p7yR	2	1	1
##	ehc25p1h1F	5	ehc25p1h1R	4	5	68
##	ehc25p2h1F	5	ehc25p2h1R	4	7	81
##	ehc25p3h1F	5	ehc25p3h1R	4	3	44
##	ehc25p4h1F	5	ehc25p4h1R	4	5	14
##	ehc25p5h1F	4	ehc25p5h1R	4	2	6
##	ehc25p7h1F	3	ehc25p7h1R	4	1	2
##	ehc25p1h2F	3	ehc25p1h2R	4	3	316
##	ehc25p2h2F	3	ehc25p2h2R	4	3	286
##	ehc25p3h2F	2	ehc25p3h2R	4	2	114
##	ehc25p4h2F	2	ehc25p4h2R	4	2	30

##	ehc26h1F	3	ehc26h1R	3	6	261
##	ehc26h2F	3	ehc26h2R	3	4	1796
##	ehc10k1h1F	3	ehc10k1h1R	3	6	188
##	ehc10k2h1F	3	ehc10k2h1R	3	4	75
##	ehc10k3h1F	3	ehc10k3h1R	3	4	35
##	ehc10k4h1F	3	ehc10k4h1R	3	4	12
##	ehc10k5h1F	2	ehc10k5h1R	3	3	6
##	ehc10k6h1F	2	ehc10k6h1R	3	1	6
##	ehc10k7h1F	2	ehc10k7h1R	3	1	2
##	ehc10k1h2F	3	ehc10k1h2R	3	4	1448
##	ehc10k2h2F	3	ehc10k2h2R	3	4	836
##	ehc10k3h2F	3	ehc10k3h2R	3	2	244
##	ehc10k4h2F	3	ehc10k4h2R	3	2	84
##	hhnrF	3	hhnrR	3	4	1177
##	hh1nrF	4	hh1nrR	5	9	1197
##	hh2nrF	4	hh2nrR	3	3	3
##	hh1aF	3	hh1aR	2	3	8
##	hh2aF	3	hh2aR	2	3	5
##	hh1lF	13	hh1lR	13	6	9
##	hh2lF	12	hh2lR	11	5	4
##	hh1tOF	2	hh1tOR	2	4	4
##	hh2tOF	3	hh2tOR	3	4	4
##	hpF	2	hpR	2	4	2
##	hpnrF	3	hpnrR	3	4	4
##	hpnF	2	hpnR	2	4	4
##	hpgF	3	hpgR	3	6	5
##	hpOF	2	hpOR	2	2	3
##	hpsepF	2	hpsepR	2	4	2
##	hpmtF	2	hpmtR	2	2	1
##	hpmF	3	hpmR	3	4	4
##	hpcF	3	hpcR	3	2	4
##	hps2F	2	hps2R	2	4	2
##	hp0nrF	2	hp0nrR	2	2	2
##	hp0nF	2	hp0nR	2	4	4
##	hp0gF	3	hp0gR	3	2	2
##	hp0ctOF	3	hp0ctOR	3	4	4
##	hc6h1F	7	hc6h1R	6	1	2
##	hc6h2F	8	hc6h2R	7	1	1
##	job17F	9	job17R	8	1	2
##	job18hF	6	job18hR	5	1	2
##	sat2F	14	sat2R	13	3	2
##	sin3i1F	8	sin3i1R	7	3	2
##	sin3i2F	8	sin3i2R	7	3	2
##	sin1F	6	sin1R	5	3	3
##	sin2F	6	sin2R	5	3	3
##	sin6i1F	9	sin6i1R	8	1	1
##	sin6i2F	9	sin6i2R	8	1	1
##	sin6i3F	9	sin6i3R	8	1	2
##	sin6i4F	9	sin6i4R	8	1	2
##	sin6i5F	9	sin6i5R	8	1	2
##	pa2mF	19	pa2mR	18	1	2
##	pa30F	3	pa30R	3	2	2
##	pa3F	11	pa3R	10	1	1
##	sdp1dF	5	sdp1dR	4	1	2
##	sdp1mF	16	sdp1mR	15	3	15
##	sdp1yF	29	sdp1yR	28	3	23

##	sdp2i1F	4	sdp2i1R	3	1	2
##	sdp2i2F	3	sdp2i2R	2	1	2
##	sdp2i3F	3	sdp2i3R	2	1	2
##	sdp2i4F	3	sdp2i4R	2	1	2
##	sdp2i5F	3	sdp2i5R	2	1	2
##	sdp2i6F	3	sdp2i6R	2	1	2
##	sdp2i7F	3	sdp2i7R	2	1	2
##	sdp2i8F	3	sdp2i8R	2	1	2
##	sdp2i9F	3	sdp2i9R	2	1	2
##	sdp2i10F	3	sdp2i10R	2	1	2
##	sdp2i11F	3	sdp2i11R	2	1	2
##	sdp2i12F	4	sdp2i12R	3	1	2
##	sdp3F	3	sdp3R	2	1	2
##	sdp6F	5	sdp6R	4	1	2
##	sdp21F	7	sdp21R	6	1	2
##	sdp22F	18	sdp22R	18	4	2
##	sdp10i16F	6	sdp10i16R	6	4	2
##	sdp10i17F	6	sdp10i17R	6	4	2
##	sdp10i7F	6	sdp10i7R	6	4	2
##	sdp10i18F	6	sdp10i18R	6	4	2
##	sdp10i19F	6	sdp10i19R	6	4	2
##	sdp10i9F	6	sdp10i9R	6	4	2
##	sdp10i20F	6	sdp10i20R	6	4	2
##	sdp10i21F	6	sdp10i21R	6	4	2
##	sdp10i22F	5	sdp10i22R	5	4	2
##	sdp10i1F	6	sdp10i1R	6	4	2
##	sdp10i2F	6	sdp10i2R	6	4	2
##	sdp10i3F	6	sdp10i3R	6	4	2
##	sdp10i4F	6	sdp10i4R	6	4	2
##	sdp10i5F	6	sdp10i5R	6	4	2
##	sdp10i6F	6	sdp10i6R	6	4	2
##	sdp10i13F	6	sdp10i13R	6	4	2
##	sdp10i8F	6	sdp10i8R	6	4	2
##	sdp10i10F	5	sdp10i10R	5	4	2
##	sdp10i11F	6	sdp10i11R	6	4	2
##	sdp10i12F	6	sdp10i12R	6	4	2
##	sdp10i15F	6	sdp10i15R	6	4	2
##	sdp10i14F	6	sdp10i14R	6	4	2
##	sdp16F	5	sdp16R	4	3	3
##	sdp17F	5	sdp17R	4	1	2
##	sdp18F	6	sdp18R	6	4	2
##	hcp1i1F	5	hcp1i1R	6	1	2
##	hcp1i2F	17	hcp1i2R	18	1	2
##	hcp2F	8	hcp2R	9	1	2
##	hcp3hF	15	hcp3hR	16	1	2
##	hcp3mF	18	hcp3mR	19	1	2
##	hcp4hF	5	hcp4hR	4	1	2
##	hcp5F	6	hcp5R	6	4	2
##	pa9F	7	pa9R	8	1	2
##	pa11F	9	pa11R	8	1	1
##	pa13F	5	pa13R	5	2	1
##	pa14i1F	9	pa14i1R	9	2	2
##	pa14i2F	8	pa14i2R	8	2	2
##	pa14i3F	10	pa14i3R	10	2	2
##	pa14i4F	9	pa14i4R	9	2	2
##	pa14i5F	8	pa14i5R	7	1	1

##	pa15F	9	pa15R	9	2	2
##	cps1F	4	cps1R	4	4	2
##	sat3F	14	sat3R	14	4	2
##	pa26F	6	pa26R	6	4	2
##	pa27F	6	pa27R	6	4	2
##	pa28F	6	pa28R	6	4	2
##	sep1i1F	8	sep1i1R	8	2	1
##	sep1i2F	8	sep1i2R	8	2	1
##	sep2F	7	sep2R	7	2	1
##	sep18F	5	sep18R	5	2	1
##	sep12F	6	sep12R	6	2	1
##	sep13F	4	sep13R	4	2	1
##	sep14F	6	sep14R	6	2	1
##	sep17i1F	7	sep17i1R	6	3	3
##	sep17i2F	7	sep17i2R	6	3	3
##	sep17i3F	7	sep17i3R	6	3	3
##	sep17i4F	7	sep17i4R	6	3	3
##	sep16F	6	sep16R	6	2	3
##	frt2F	8	frt2R	8	4	2
##	frt11v1i6F	10	frt11v1i6R	10	4	2
##	frt11v1i7F	9	frt11v1i7R	9	4	2
##	frt11v1i8F	9	frt11v1i8R	9	4	2
##	frt11v2i6F	6	frt11v2i6R	6	4	2
##	frt11v2i7F	6	frt11v2i7R	6	4	2
##	frt11v2i8F	6	frt11v2i8R	6	4	2
##	crn22p1F	11	crn22p1R	11	2	2
##	crn33p1i1F	7	crn33p1i1R	7	2	2
##	crn33p1i2F	6	crn33p1i2R	5	1	2
##	crn33p1i3F	8	crn33p1i3R	8	2	2
##	crn34p1F	7	crn34p1R	7	2	2
##	igr22F	5	igr22R	4	1	14
##	igr25F	5	igr25R	4	3	13
##	igr28F	5	igr28R	4	1	2
##	igr39p3F	10	igr39p3R	9	1	2
##	igr40p3F	9	igr40p3R	8	1	1
##	igr41p1F	10	igr41p1R	9	5	14
##	rtr43F	5	rtr43R	5	2	1
##	inc24F	38	inc24R	37	1	7
##	inc26i2F	7	inc26i2R	6	11	20
##	inc26i3F	7	inc26i3R	6	9	20
##	inc27i2F	8	inc27i2R	7	1	9
##	inc27i3F	8	inc27i3R	7	1	9
##	int4i6F	4	int4i6R	4	4	2
##	lmhh1F	2	lmhh1R	2	2	4
##	lmhh2F	2	lmhh2R	2	2	3
##	lvhh1F	2	lvhh1R	2	4	4
##	lvhh2F	2	lvhh2R	2	2	3
##	avhh1F	2	avhh1R	2	2	1
##	hv1F	4	hv1R	3	1	2
##	tag_sexF	2	tag_sexR	2	2	1
##	tag_dobpF	2	tag_dobpR	2	4	25
##	sex_genF	2	sex_genR	2	2	1
##	psex_genF	3	psex_genR	4	5	5
##	pdoby_genF	43	pdoby_genR	44	15	15
##	pdobm_genF	14	pdobm_genR	15	9	9
##	pageF	44	pageR	44	16	11

##	mageF	40	mageR	40	4	3
##	k1ageF	28	k1ageR	28	2	1
##	k2ageF	26	k2ageR	26	4	2
##	pcobF	18	pcobR	19	3	4
##	pnat1F	15	pnat1R	16	3	3
##	marstatF	5	marstatR	5	2	1
##	npF	10	npR	10	20	23
##	ncohF	7	ncohR	7	10	17
##	nmarF	3	nmarR	3	6	12
##	meetdurF	279	meetdurR	278	13	18
##	reldurF	265	reldurR	262	37	94
##	cohabdurF	242	cohabdurR	249	187	134
##	mardurF	191	mardurR	192	13	14
##	homosexF	3	homosexR	3	4	2
##	infertileF	3	infertileR	3	4	4
##	pregnantF	4	pregnantR	4	6	4
##	pnkidsbioalvF	7	pnkidsbioalvR	7	12	64
##	res2ndF	3	res2ndR	2	3	1175
##	hhsizemrdF	13	hhsizemrdR	13	16	17
##	mmrdF	2	mmrdR	2	2	4
##	fmrdf	2	fmrdfR	3	3	4
##	childmrdF	9	childmrdR	8	7	8
##	othmrdF	5	othmrdR	5	2	1
##	hhcompF	14	hhcompR	15	21	29
##	penrolF	11	penrolR	11	2	1
##	pschoolF	10	pschoolR	10	6	5
##	pvocatF	11	pvocatR	11	4	2
##	piscedF	11	piscedR	11	6	3
##	pisced2F	11	pisced2R	11	6	3
##	pcasminF	13	pcasminR	13	4	2
##	pyeducF	20	pyeducR	20	6	3
##	egpF	129	egpR	11	264	3514
##	iseiF	73	iseiR	56	451	1720
##	siopsF	55	siopsR	54	431	1331
##	hhincgeeF	413	hhincgeeR	414	21	118
##	pcasprimF	22	pcasprimR	22	4	3
##	pcassecF	17	pcassecR	17	2	1
##	plfsF	14	plfsR	14	4	3

B.3. variation and bijective mapping

```

# mark all identical cases
rb$ident <- (rb$ed.di.sum == 0)
# mark all not duplicated raw variables
rb$dup.Raw <- !duplicStrict(rb$Raw.c.nm)
# mark all not duplicated fin variables
rb$dup.Fin <- !duplicStrict(rb$Fin.c.nm)
# mark all equal name pairs
rb$same.name <- gsub("R$", "", as.character(rb$Raw.c.nm)) == gsub("F$", "",
  as.character(rb$Fin.c.nm))

```

```

rb$Raw.same.name <- (ave(rb$same.name, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.same.name <- (ave(rb$same.name, rb$Fin.c.nm, FUN = sum) > 0)

```

```

rb$Raw.ident <- (ave(rb$ident, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.ident <- (ave(rb$ident, rb$Fin.c.nm, FUN = sum) > 0)

R.vb <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"]))
as.character(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"]))

## [1] "ehc24p7yR" "ehc25p7h1R"

R.vbi <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"]))
as.character(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"]))

## [1] "ehc16m1R" "ehc16m2R" "ehc16m3R" "ehc4p2m8R" "ehc4p2m9R"
## [6] "ehc10k6h2R" "ehc10k9h2R" "ehc24p7mR" "ehc25p8h2R" "ehc25p8h3R"
## [11] "ehc10k8h2R"

R.vbn <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"]))
as.character(unique(rb[!rb$dup.Raw & rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"]))

## [1] "dpidR" "hcp4mR"

(R.vbni <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"])))

## [1] 954

R.vb1 <- length(unique(rb[rb$dup.Raw & !rb$same.name & !rb$ident, "Raw.c.nm"]))
as.character(unique(rb[rb$dup.Raw & !rb$same.name & !rb$ident, "Raw.c.nm"]))

## [1] "ehc17m4R" "ehc22p7nR" "ehc25p6h2R" "ehc25p6h3R"

R.vbli <- length(unique(rb[rb$dup.Raw & !rb$same.name & rb$ident, "Raw.c.nm"]))
as.character(unique(rb[rb$dup.Raw & !rb$same.name & rb$ident, "Raw.c.nm"]))

## [1] "ehc10k5h2R" "ehc10k7h2R" "kldbR"

R.vbn <- length(unique(rb[rb$dup.Raw & rb$same.name & !rb$ident, "Raw.c.nm"]))
as.character(unique(rb[rb$dup.Raw & rb$same.name & !rb$ident, "Raw.c.nm"]))

## [1] "ehc21h1R" "job18mR" "pa2yR"

(R.vbn1ni <- length(unique(rb[rb$dup.Raw & rb$same.name & rb$ident, "Raw.c.nm"])))

## [1] 1262

(F.vb <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

F.vbi <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"]))
as.character(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"]))

```

```
## [1] "ehc25p4h2F"

F.vbn <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"]))
as.character(unique(rb[!rb$dup.Fin & rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"]))

## [1] "dpidF"

(F.vbni <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"])))

## [1] 956

F.vb1 <- length(unique(rb[rb$dup.Fin & !rb$same.name & !rb$ident, "Fin.c.nm"]))
as.character(unique(rb[rb$dup.Fin & !rb$same.name & !rb$ident, "Fin.c.nm"]))

## [1] "ehc16m4F" "ehc22p7nF" "ehc24p6mF" "ehc24p6yF" "hcp4hF"

F.vb1i <- length(unique(rb[rb$dup.Fin & !rb$same.name & rb$ident, "Fin.c.nm"]))
as.character(unique(rb[rb$dup.Fin & !rb$same.name & rb$ident, "Fin.c.nm"]))

## [1] "avhh1F" "kldb1992F"

F.vb1n <- length(unique(rb[rb$dup.Fin & rb$same.name & !rb$ident, "Fin.c.nm"]))
as.character(unique(rb[rb$dup.Fin & rb$same.name & !rb$ident, "Fin.c.nm"]))

## [1] "ehc21h1F" "job18mF" "pa2yF" "hcp4mF"

(F.vb1ni <- length(unique(rb[rb$dup.Fin & rb$same.name & rb$ident, "Fin.c.nm"])))

## [1] 1260
```

B.4. comparison summary for anchor2_DD.dta Release 2.0 and Release 3.0

class	Release 2	Release 3
x	8	0
n	15	37
ni	612	612
v	1	7
vn	369	359
vb	2	0
vbi	11	1
vbn	2	1
vbni	954	956
vb1	4	5
vb1i	3	2
vb1n	3	4
vb1ni	1262	1260
sum	3246	3244

Most variables are unchanged (ni, vbni, vb1ni). A small number (x, v) had been dropped or added. Some variables (n) had lost or gained variation or changed to another constant value. A number of variables (vb,

vbi, vbn, vb1, vb1i, vb1n) had been (probably) renamed or recoded. A huge group of variables (vn) had been changed.

B.5. selected in-depth comparison

For illustrative purposes we present some detailed results.

```
D1 <- cbind(Raw$pyeducR, Fin$pyeducF)
D1[D1[, 1] != D1[, 2], ]

##      [,1] [,2]
## [1,] "-3.0" "-7.0"
## [2,] "14.5" "11.5"
## [3,] "-7.0" "-3.0"
```

Both variables share the same number of levels. The level '-3.0' has been recoded to '-7.0', the level '14.5' to '11.5' and the level '-7.0' to '-30'. This takes 3 Levenshtein steps (see details in [TR-2012-003]).

```
D2 <- cbind(Raw$nmarr, Fin$nmarr)
D2[D2[, 1] != D2[, 2], ]

##      [,1] [,2]
## [1,] "0" "1"
## [2,] "0" "1"
## [3,] "0" "1"
## [4,] "0" "1"
## [5,] "0" "1"
## [6,] "1" "0"
## [7,] "1" "0"
## [8,] "0" "1"
## [9,] "0" "1"
## [10,] "0" "1"
## [11,] "0" "1"
## [12,] "1" "2"
```

Both variables share the same number of levels. $3 + 3 + 6 = 12$, $12/2 = 6$ mappings between the levels are in use. For a bijective mapping we need 3 mappings less. 12 individuals show a changed level. It takes 12 Levenshtein steps to make the levels equal.

```
D3 <- cbind(Raw$pageR, Fin$pageF)
D3[D3[, 1] != D3[, 2], ]

##      [,1] [,2]
## [1,] "-7" "37"
## [2,] "26" "25"
## [3,] "-3" "25"
## [4,] "36" "38"
## [5,] "30" "29"
## [6,] "29" "30"
## [7,] "44" "46"
## [8,] "-7" "-3"
```

8 individuals have a new level for 'page'. It takes 11 Levenshtein steps to get them equal. There is no bijective mapping available.

```

D4 <- cbind(Raw$iseiR, Fin$iseiF)
dim(D4[D4[, 1] != D4[, 2], ])

## [1] 1128    2

head(D4[D4[, 1] != D4[, 2], ])

##      [,1] [,2]
## [1,] "23" "22"
## [2,] "32" "33"
## [3,] "53" "31"
## [4,] "38" "56"
## [5,] "48" "50"
## [6,] "51" "48"

```

1128 individuals do have a different level. There is no bijective mapping.

C. partner1

As usual we have first to load the produced data collection.

```

rm(list = ls())
duplicStrict <- function(A) {
  return(duplicated(A) | duplicated(A, fromLast = TRUE))
}
load("../compareR2R3\\partner1\\Results\\compareFinRaw.RData")

```

C.1. no variation

We compare the variables without variation first.

```

(R.x <- sum(!(RawNames[Rnv] %in% FinNames)))

## [1] 0

(F.x <- sum(!(FinNames[Fnv] %in% RawNames)))

## [1] 0

# added or lost variance
(R.nA <- sum(!(RawNames[Rnv] %in% FinNames[Fnv]))) - R.x

## [1] 0

(F.nA <- sum(!(FinNames[Fnv] %in% RawNames[Rnv]))) - F.x

## [1] 0

```

```

Rnv2 <- data.frame(Rnv.tab)
Fnv2 <- data.frame(Fnv.tab)
Rnv2$nm <- gsub("R$", "", row.names(Rnv2))
Fnv2$nm <- gsub("F$", "", row.names(Fnv2))
RFnv2 <- merge(Rnv2, Fnv2, by = c("nm"), all = TRUE)

(R.ni <- sum((RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 89

F.ni <- R.ni

# changed values
(R.nB <- sum(!(RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 0

F.nB <- R.nB

(R.n <- R.nA + R.nB)

## [1] 0

(F.n <- F.nA + F.nB)

## [1] 0

RawNames[Rnv][!(RawNames[Rnv] %in% FinNames)]

## character(0)

RFnv2[is.na(RFnv2$Fin.no.var), 1]

## character(0)

FinNames[Fnv][!(FinNames[Fnv] %in% RawNames)]

## character(0)

RFnv2[is.na(RFnv2$Raw.no.var), 1]

## character(0)

```

Release 2.0 89 variables without variation are identical in both data sets.

Release 3.0 89 variables without variation are identical in both data sets.

C.2. variation, but no bijective mapping

```

rb <- results.bijec
RL.bi <- RawNames[!Rnv] %in% gsub("R$", "", as.character(rb$Raw.c.nm))
FL.bi <- FinNames[!Fnv] %in% gsub("F$", "", as.character(rb$Fin.c.nm))
sum(!RL.bi)

## [1] 2

sum(!FL.bi)

## [1] 2

(R.v <- sum(!(RawNames[!Rnv][!RL.bi] %in% FinNames)))

## [1] 0

(R.vn <- sum(RawNames[!Rnv][!RL.bi] %in% FinNames))

## [1] 2

RawNames[!Rnv][!RL.bi][RawNames[!Rnv][!RL.bi] %in% FinNames]

## [1] "pdobm" "pdoby"

(F.v <- sum(!(FinNames[!Fnv][!FL.bi] %in% RawNames)))

## [1] 0

(F.vn <- sum(FinNames[!Fnv][!FL.bi] %in% RawNames))

## [1] 2

FinNames[!Fnv][!FL.bi][FinNames[!Fnv][!FL.bi] %in% RawNames]

## [1] "pdobm" "pdoby"

```

Release 2.0 2 variables share the name with one of the variables in Release 3.0 at least.

Release 3.0 2 variables share the name with one of the variables in Release 2.0 at least.

We compare all variables pairs (with variation) which share the same name but are not connected with a bijective mapping.

```

results$same.name <-
  gsub("R$", "", as.character(results$Raw.c.nm)) == gsub("F$", "", as.character(results$Fin.c.nm))
sum(results$same.name & results$map.di>0)

```

```
## [1] 2

print(results[(results$same.name & results$map.di>0),c(2,3,5,6,7,8)],row.names=FALSE)

##   Fin.c.nm Fin.c.ls Raw.c.nm Raw.c.ls map.di ed.di.sum
##   pdobmF      13  pdobmR      13      8      12
##   pdobyF      38  pdobyR      38     14      36
```

C.3. variation and bijective mapping

```
# mark all identical cases
rb$ident <- (rb$ed.di.sum == 0)
# mark all not duplicated raw variables
rb$dup.Raw <- !duplicStrict(rb$Raw.c.nm)
# mark all not duplicated fin variables
rb$dup.Fin <- !duplicStrict(rb$Fin.c.nm)
# mark all equal name pairs
rb$same.name <- gsub("R$", "", as.character(rb$Raw.c.nm)) == gsub("F$", "",
  as.character(rb$Fin.c.nm))

rb$Raw.same.name <- (ave(rb$same.name, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.same.name <- (ave(rb$same.name, rb$Fin.c.nm, FUN = sum) > 0)

rb$Raw.ident <- (ave(rb$ident, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.ident <- (ave(rb$ident, rb$Fin.c.nm, FUN = sum) > 0)

(R.vb <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"])))

## [1] 0

(R.vbi <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"])))

## [1] 0

R.vbn <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"]))
as.character(unique(rb[!rb$dup.Raw & rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"]))

## [1] "idR"

R.vbni <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"]))
as.character(unique(rb[!rb$dup.Raw & rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"]))

## [1] "pidR"

(R.vb1 <- length(unique(rb[rb$dup.Raw & !rb$same.name & !rb$ident, "Raw.c.nm"])))

## [1] 0

(R.vb1i <- length(unique(rb[rb$dup.Raw & !rb$same.name & rb$ident, "Raw.c.nm"])))
```



```

## [1] 0

R.vb1n <- length(unique(rb[rb$dup.Raw & rb$same.name & !rb$ident, "Raw.c.nm"]))
as.character(unique(rb[rb$dup.Raw & rb$same.name & !rb$ident, "Raw.c.nm"]))

## [1] "psd10R"

(R.vb1ni <- length(unique(rb[rb$dup.Raw & rb$same.name & rb$ident, "Raw.c.nm"])))

## [1] 137

(F.vb <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbi <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

F.vbn <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"]))
as.character(unique(rb[!rb$dup.Fin & rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"]))

## [1] "idF"

F.vbni <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"]))
as.character(unique(rb[!rb$dup.Fin & rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"]))

## [1] "pidF"

(F.vb1 <- length(unique(rb[rb$dup.Fin & !rb$same.name & !rb$ident, "Fin.c.nm"])))

## [1] 0

(F.vb1i <- length(unique(rb[rb$dup.Fin & !rb$same.name & rb$ident, "Fin.c.nm"])))

## [1] 0

F.vb1n <- length(unique(rb[rb$dup.Fin & rb$same.name & !rb$ident, "Fin.c.nm"]))
as.character(unique(rb[rb$dup.Fin & rb$same.name & !rb$ident, "Fin.c.nm"]))

## [1] "psd10F"

(F.vb1ni <- length(unique(rb[rb$dup.Fin & rb$same.name & rb$ident, "Fin.c.nm"])))

## [1] 137

```

C.4. comparison summary for partner1_DD.dta Release 2.0 and Release 3.0

class	Release 2	Release 3
x	0	0
n	0	0
ni	89	89
v	0	0
vn	2	2
vb	0	0
vbi	0	0
vbn	1	1
vbni	1	1
vb1	0	0
vb1i	0	0
vb1n	1	1
vb1ni	137	137
sum	231	231

Most variables are unchanged (ni, vbni, vb1ni). A small number of variables (vbn, vb1n) had been (probably) renamed or recoded. A small group of variables (vn) had been changed.

D. partner2

As usual we have first to load the produced data collection.

```
rm(list = ls())
duplicStrict <- function(A) {
  return(duplicated(A) | duplicated(A, fromLast = TRUE))
}
load("../compareR2R3\\partner2\\Results\\compareFinRaw.RData")
```

D.1. no variation

We compare the variables without variation first.

```
(R.x <- sum(!(RowNames[Rnv] %in% FinNames)))
## [1] 0

(F.x <- sum(!(FinNames[Fnv] %in% RowNames)))
## [1] 0

# added or lost variance
(R.nA <- sum(!(RowNames[Rnv] %in% FinNames[Fnv]))) - R.x
## [1] 0

(F.nA <- sum(!(FinNames[Fnv] %in% RowNames[Rnv]))) - F.x
## [1] 0
```

```

Rnv2 <- data.frame(Rnv.tab)
Fnv2 <- data.frame(Fnv.tab)
Rnv2$nm <- gsub("R$", "", row.names(Rnv2))
Fnv2$nm <- gsub("F$", "", row.names(Fnv2))
RFnv2 <- merge(Rnv2, Fnv2, by = c("nm"), all = TRUE)

(R.ni <- sum((RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 96

F.ni <- R.ni

# changed values
(R.nB <- sum(!(RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 0

F.nB <- R.nB

(R.n <- R.nA + R.nB)

## [1] 0

(F.n <- F.nA + F.nB)

## [1] 0

RawNames[Rnv][!(RawNames[Rnv] %in% FinNames)]

## character(0)

RFnv2[is.na(RFnv2$Fin.no.var), 1]

## character(0)

FinNames[Fnv][!(FinNames[Fnv] %in% RawNames)]

## character(0)

RFnv2[is.na(RFnv2$Raw.no.var), 1]

## character(0)

```

Release 2.0 96 variables without variation are identical in both data sets.

Release 3.0 96 variables without variation are identical in both data sets.

D.2. variation, but no bijective mapping

```

rb <- results.bijec
RL.bi <- RawNames[!Rnv] %in% gsub("R$", "", as.character(rb$Raw.c.nm))
FL.bi <- FinNames[!Fnv] %in% gsub("F$", "", as.character(rb$Fin.c.nm))
sum(!RL.bi)

## [1] 2

sum(!FL.bi)

## [1] 2

(R.v <- sum(!(RawNames[!Rnv][!RL.bi] %in% FinNames)))

## [1] 0

(R.vn <- sum(RawNames[!Rnv][!RL.bi] %in% FinNames))

## [1] 2

RawNames[!Rnv][!RL.bi][RawNames[!Rnv][!RL.bi] %in% FinNames]

## [1] "pdobm" "pdoby"

(F.v <- sum(!(FinNames[!Fnv][!FL.bi] %in% RawNames)))

## [1] 0

(F.vn <- sum(FinNames[!Fnv][!FL.bi] %in% RawNames))

## [1] 2

FinNames[!Fnv][!FL.bi][FinNames[!Fnv][!FL.bi] %in% RawNames]

## [1] "pdobm" "pdoby"

```

Release 2.0 2 variables share the name with one of the variables in Release 3.0 at least.

Release 3.0 2 variables share the name with one of the variables in Release 2.0 at least.

We compare all variables pairs (with variation) which share the same name but are not connected with a bijective mapping.

```

results$same.name <-
  gsub("R$", "", as.character(results$Raw.c.nm)) == gsub("F$", "", as.character(results$Fin.c.nm))
sum(results$same.name & results$map.di>0)

```

```
## [1] 2

print(results[(results$same.name & results$map.di>0),c(2,3,5,6,7,8)],row.names=FALSE)

##   Fin.c.nm Fin.c.ls Raw.c.nm Raw.c.ls map.di ed.di.sum
##   pdobmF      13  pdobmR      13      4      3
##   pdobyF      38  pdobyR      38      4      2
```

D.3. variation and bijective mapping

```
# mark all identical cases
rb$ident <- (rb$ed.di.sum == 0)
# mark all not duplicated raw variables
rb$dup.Raw <- !duplicStrict(rb$Raw.c.nm)
# mark all not duplicated fin variables
rb$dup.Fin <- !duplicStrict(rb$Fin.c.nm)
# mark all equal name pairs
rb$same.name <- gsub("R$", "", as.character(rb$Raw.c.nm)) == gsub("F$", "",
  as.character(rb$Fin.c.nm))

rb$Raw.same.name <- (ave(rb$same.name, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.same.name <- (ave(rb$same.name, rb$Fin.c.nm, FUN = sum) > 0)

rb$Raw.ident <- (ave(rb$ident, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.ident <- (ave(rb$ident, rb$Fin.c.nm, FUN = sum) > 0)

(R.vb <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"])))

## [1] 0

(R.vbi <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"])))

## [1] 0

(R.vbn <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"])))

## [1] 0

R.vbni <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"]))
as.character(unique(rb[!rb$dup.Raw & rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"]))

## [1] "idR" "pidR"

(R.vb1 <- length(unique(rb[rb$dup.Raw & !rb$same.name & !rb$ident, "Raw.c.nm"])))

## [1] 0

(R.vb1i <- length(unique(rb[rb$dup.Raw & !rb$same.name & rb$ident, "Raw.c.nm"])))
```

```

## [1] 0

(R.vb1n <- length(unique(rb[rb$dup.Raw & rb$same.name & !rb$ident, "Raw.c.nm"])))

## [1] 0

(R.vb1ni <- length(unique(rb[rb$dup.Raw & rb$same.name & rb$ident, "Raw.c.nm"])))

## [1] 180

(F.vb <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbi <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbn <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

F.vbni <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"]))
as.character(unique(rb[!rb$dup.Fin & rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"]))

## [1] "idF" "pidF"

(F.vb1 <- length(unique(rb[rb$dup.Fin & !rb$same.name & !rb$ident, "Fin.c.nm"])))

## [1] 0

(F.vb1i <- length(unique(rb[rb$dup.Fin & !rb$same.name & rb$ident, "Fin.c.nm"])))

## [1] 0

(F.vb1n <- length(unique(rb[rb$dup.Fin & rb$same.name & !rb$ident, "Fin.c.nm"])))

## [1] 0

(F.vb1ni <- length(unique(rb[rb$dup.Fin & rb$same.name & rb$ident, "Fin.c.nm"])))

## [1] 180

```

D.4. comparison summary for partner2_DD.dta Release 2.0 and Release 3.0

class	Release 2	Release 3
x	0	0
n	0	0
ni	96	96
v	0	0
vn	2	2
vb	0	0
vbi	0	0
vbn	0	0
vbni	2	2
vb1	0	0
vb1i	0	0
vb1n	0	0
vb1ni	180	180
sum	280	280

Most variables are unchanged (ni, vbni, vb1ni). A small group of variables (vn) had been changed.

E. weights

As usual we have first to load the produced data collection.

```
rm(list = ls())
duplicStrict <- function(A) {
  return(duplicated(A) | duplicated(A, fromLast = TRUE))
}
load("../compareR2R3\\weights\\Results\\compareFinRaw.RData")
```

E.1. no variation

We compare the variables without variation first.

```
(R.x <- sum(!(RawNames[Rnv] %in% FinNames)))

## [1] 0

(F.x <- sum(!(FinNames[Fnv] %in% RawNames)))

## [1] 0

# added or lost variance
(R.nA <- sum(!(RawNames[Rnv] %in% FinNames[Fnv])) - R.x)

## [1] 0

(F.nA <- sum(!(FinNames[Fnv] %in% RawNames[Rnv])) - F.x)

## [1] 0
```

```

Rnv2 <- data.frame(Rnv.tab)
Fnv2 <- data.frame(Fnv.tab)
Rnv2$nm <- gsub("R$", "", row.names(Rnv2))
Fnv2$nm <- gsub("F$", "", row.names(Fnv2))
RFnv2 <- merge(Rnv2, Fnv2, by = c("nm"), all = TRUE)

(R.ni <- sum((RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 0

F.ni <- R.ni

# changed values
(R.nB <- sum(!(RFnv2$Raw.no.var == RFnv2$Fin.no.var), na.rm = TRUE))

## [1] 0

F.nB <- R.nB

(R.n <- R.nA + R.nB)

## [1] 0

(F.n <- F.nA + F.nB)

## [1] 0

RawNames[Rnv][!(RawNames[Rnv] %in% FinNames)]

## character(0)

RFnv2[is.na(RFnv2$Fin.no.var), 1]

## character(0)

FinNames[Fnv][!(FinNames[Fnv] %in% RawNames)]

## character(0)

RFnv2[is.na(RFnv2$Raw.no.var), 1]

## character(0)

```

Release 2.0 No change for variables without variation.

Release 3.0 No change for variables without variation.

E.2. variation, but no bijective mapping

```

rb <- results.bijec
RL.bi <- RawNames[!Rnv] %in% gsub("R$", "", as.character(rb$Raw.c.nm))
FL.bi <- FinNames[!Fnv] %in% gsub("F$", "", as.character(rb$Fin.c.nm))
sum(!RL.bi)

## [1] 0

sum(!FL.bi)

## [1] 2

(R.v <- sum(!(RawNames[!Rnv][!RL.bi] %in% FinNames)))

## [1] 0

(R.vn <- sum(RawNames[!Rnv][!RL.bi] %in% FinNames))

## [1] 0

(F.v <- sum(!(FinNames[!Fnv][!FL.bi] %in% RawNames)))

## [1] 2

FinNames[!Fnv][!FL.bi][!(FinNames[!Fnv][!FL.bi] %in% RawNames)]

## [1] "lweightDD4" "lweightPF4"

(F.vn <- sum(FinNames[!Fnv][!FL.bi] %in% RawNames))

## [1] 0

```

Release 2.0 No changed variables with variation but without any bijective mapping.

Release 3.0 For 2 variables with variation but without any bijective mapping exist no variables with the same name in the Release 2.0 data.

See the comparison table as an illustration.

```

results$same.name <-
  gsub("R$", "", as.character(results$Raw.c.nm)) == gsub("F$", "", as.character(results$Fin.c.nm))
print(results[(results$same.name), c(2,3,5,6,7,8)], row.names=FALSE)

##      Fin.c.nm Fin.c.cls      Raw.c.nm Raw.c.cls map.di ed.di.sum
##      idF      13891      idR      13891      0      0
##      pairfamF      2      pairfamR      2      0      0
##      caweightF      535      caweightR      535      0      0

```

```
##      westF      2      westR      2      0      0
##    calweightF 1470 calweightR 1470      0      0
##    ddweightF   3    ddweightR   3      0      0
##   ddcaweightF 581 ddcaweightR 581      0      0
##    dlweightF   6    dlweightR   6      0      0
##  dlcalweightF 2380 dlcalweightR 2380      0      0
##   lweightDD3F  3   lweightDD3R   3      0      0
##   lweightPF2F  7   lweightPF2R   7      0      0
##   lweightPF3F  7   lweightPF3R   7      0      0
```

E.3. variation and bijective mapping

```
# mark all identical cases
rb$ident <- (rb$ed.di.sum == 0)
# mark all not duplicated raw variables
rb$dup.Raw <- !duplicStrict(rb$Raw.c.nm)
# mark all not duplicated fin variables
rb$dup.Fin <- !duplicStrict(rb$Fin.c.nm)
# mark all equal name pairs
rb$same.name <- gsub("R$", "", as.character(rb$Raw.c.nm)) == gsub("F$", "",
  as.character(rb$Fin.c.nm))

rb$Raw.same.name <- (ave(rb$same.name, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.same.name <- (ave(rb$same.name, rb$Fin.c.nm, FUN = sum) > 0)

rb$Raw.ident <- (ave(rb$ident, rb$Raw.c.nm, FUN = sum) > 0)
rb$Fin.ident <- (ave(rb$ident, rb$Fin.c.nm, FUN = sum) > 0)

(R.vb <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"])))
## [1] 0

(R.vbi <- length(unique(rb[!rb$dup.Raw & !rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"])))
## [1] 0

(R.vbn <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & !rb$Raw.ident, "Raw.c.nm"])))
## [1] 0

(R.vbni <- length(unique(rb[!rb$dup.Raw & rb$Raw.same.name & rb$Raw.ident, "Raw.c.nm"])))
## [1] 0

(R.vb1 <- length(unique(rb[rb$dup.Raw & !rb$same.name & !rb$ident, "Raw.c.nm"])))
## [1] 0

(R.vb1i <- length(unique(rb[rb$dup.Raw & !rb$same.name & rb$ident, "Raw.c.nm"])))
```

```

## [1] 0

(R.vb1n <- length(unique(rb[rb$dup.Raw & rb$same.name & !rb$ident, "Raw.c.nm"])))

## [1] 0

R.vb1ni <- length(unique(rb[rb$dup.Raw & rb$same.name & rb$ident, "Raw.c.nm"]))
as.character(unique(rb[rb$dup.Raw & rb$same.name & rb$ident, "Raw.c.nm"]))

## [1] "idR"          "pairfamR"      "caweightR"    "westR"
## [5] "calweightR"    "ddweightR"    "ddcaweightR"  "dlweightR"
## [9] "d1calweightR" "lweightDD3R"  "lweightPF2R"  "lweightPF3R"

(F.vb <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbi <- length(unique(rb[!rb$dup.Fin & !rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbn <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & !rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vbni <- length(unique(rb[!rb$dup.Fin & rb$Fin.same.name & rb$Fin.ident, "Fin.c.nm"])))

## [1] 0

(F.vb1 <- length(unique(rb[rb$dup.Fin & !rb$same.name & !rb$ident, "Fin.c.nm"])))

## [1] 0

(F.vb1i <- length(unique(rb[rb$dup.Fin & !rb$same.name & rb$ident, "Fin.c.nm"])))

## [1] 0

(F.vb1n <- length(unique(rb[rb$dup.Fin & rb$same.name & !rb$ident, "Fin.c.nm"])))

## [1] 0

F.vb1ni <- length(unique(rb[rb$dup.Fin & rb$same.name & rb$ident, "Fin.c.nm"]))
as.character(unique(rb[rb$dup.Fin & rb$same.name & rb$ident, "Fin.c.nm"]))

## [1] "idF"          "pairfamF"      "caweightF"    "westF"
## [5] "calweightF"    "ddweightF"    "ddcaweightF"  "dlweightF"
## [9] "d1calweightF" "lweightDD3F"  "lweightPF2F"  "lweightPF3F"

```

E.4. comparison summary for weights_DD.dta Release 2.0 and Release 3.0

class	Release 2	Release 3
x	0	0
n	0	0
ni	0	0
v	0	2
vn	0	0
vb	0	0
vbi	0	0
vbn	0	0
vbni	0	0
vb1	0	0
vb1i	0	0
vb1n	0	0
vb1ni	12	12
sum	12	14

All old variables are unchanged (vb1ni). A small number (v) had been added.

Literatur

- [DemoDiff 2.0] Kreyenfeld, Michaela; Goldstein, Joshua; Walke, Rainer; Trappe, Heike; Huinink, Johannes (2013): Demographic Differences in Life Course Dynamics in Eastern and Western Germany (DemoDiff). GESIS Datenarchiv, Köln. ZA5684 Datenfile Version 2.0.0, <http://dx.doi.org/doi:10.4232/demodiff.5684.2.0.0>
- [DemoDiff 3.0] Kreyenfeld, Michaela; Goldstein, Joshua; Walke, Rainer; Trappe, Heike; Huinink, Johannes (2013): Demographic Differences in Life Course Dynamics in Eastern and Western Germany (DemoDiff). GESIS Data Archive, Cologne. ZA5684 Data file Version 3.0.0, <http://dx.doi.org/doi:10.4232/demodiff.5684.3.0.0>
- [TR-2012-003] Walke, Rainer; Müller, Andreas (2012): compareFinRaw.r - an R program to measure the difference between datasets. MPIDR Technical Report TR-2012-003.
- [R 2.15] R Core Team (2012). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL <http://www.R-project.org/>.