

Statistical Matching and Imputation of Survey Data with the Package StatMatch for the R Environment*

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1 Introduction

Statistical matching techniques aim at integrating two or more data sources, usually data from sample surveys carried out on the same target population. In the basic statistical matching framework, there are two data sources A and B sharing a set of variables X then the variable Y is available only in A while the variable Z is observed just in B . In practice the X variables are common to both the data sources, while the variables Y and Z are not jointly observed. The objective of statistical matching (hereafter denoted as SM) consists in integrating A and B in order to investigate the relationship between Y and Z . It is worth noting that the units in the two data sources come without an identifying code that permits to discover whether the same units has been observed in both the surveys; generally, in sample surveys, the chance the same units is included in both the surveys is close to zero.

The objective of SM can be achieved through a “micro” or a “macro” approach (D’Orazio *et al.*, 2006b). In the micro approach SM aims at creating a “synthetic” data source in which all the variables, X , Y and Z , are available (usually A filled in with the values of Z). In the macro approach the data sources are used to derive an estimate of the parameter of interest, e.g. the correlation coefficient between Y and Z or the contingency table $Y \times Z$. SM can be performed in a parametric or in a nonparametric framework. The parametric approach requires the explicit adoption of a model for (X, Y, Z) ; obviously if the model is misspecified then the results will not be reliable. The nonparametric approach is more flexible in handling complex situations (mixed type

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Table 1: Objectives and approaches to Statistical matching.

Objectives of Statistical matching	Approaches to statistical Matching		
	Parametric	Nonparametric	Mixed
MAcro	yes	yes	no
MIcro	yes	yes	yes

variables). The two approaches can be mixed: first a parametric model is assumed and its parameters are estimated then a completed synthetic data set is derived through a nonparametric micro approach. In this manner the advantages of both parametric and nonparametric approaches are maintained: the model is parsimonious while nonparametric techniques offer protection against model misspecification. An interesting comparison of some mixed methods that deal with continuous X , Y and Z variables is carried out by (Moriarity and Scheuren, 2001, 2003). A further comparison is available in (D’Orazio *et al.*, 2005). Table 1 provides a summary of the objectives and approaches to SM (D’Orazio *et al.*, 2008).

It is worth noting that in the traditional SM framework, when only A and B are available, all the SM methods (parametric, nonparametric and mixed) that use the set of common variables X to match A and B , implicitly assume the *conditional independence* (CI) of Y and Z given X :

$$f(x, y, z) = f(y|x) \times f(z|x) \times f(x)$$

This assumption is particularly strong and seldom holds in practice. In order to avoid the CI assumption the SM should incorporate some auxiliary information concerning the relationship between Y and Z (see Chap. 3 in D’Orazio *et al.* 2006b). The auxiliary information can be at micro level (a new data source in which Y and Z or X , Y and Z are jointly observed) or at macro level (e.g. an estimate of the correlation coefficient ρ_{XY} or an estimate of the contingency table $Y \times Z$, etc.) or simply consist of some logic constraints about the relationship between Y and Z (structural zeros, etc.; for further details see D’Orazio *et al.*, 2006a).

An alternative approach to SM consists in evaluating the *uncertainty* concerning an estimate of the parameter of interest. This uncertainty is due to the lack of joint information concerning Y and Z . For instance, let us consider a SM application whose target consists in estimating the correlation matrix of the trivariate normal distribution holding for (X, Y, Z) ; in the basic SM framework the available data allow to estimate all the components of the correlation matrix with the exception of ρ_{YZ} ; in this case, due to the properties of the correlation matrix (has to be semidefinite positive), it is possible to conclude that:

$$\rho_{XY}\rho_{XZ} - \sqrt{(1 - \rho_{YX}^2)(1 - \rho_{XZ}^2)} \leq \rho_{YZ} \leq \rho_{XY}\rho_{XZ} + \sqrt{(1 - \rho_{YX}^2)(1 - \rho_{XZ}^2)}$$

The higher is the correlation between X and Y and between X and Z , the shorter

will be the interval and consequently the lower will be the uncertainty. In practical applications, by substituting the unknown correlation coefficient with the corresponding estimates it is possible to derive a “range” of admissible values of the unknown ρ_{YZ} . The topic of the uncertainty will be covered in the Section 6.

Section 2 will be discuss some practical aspects concerning the preliminary steps necessary to apply SM techniques, with a particular emphasis on the choice of the matching variables; moreover some example data will be introduced in Section 2.1. In Section 3 some approaches to SM at micro level based on nonparametric methods will be shown. Section 4 is devoted to the mixed approaches to SM when dealing with continuous variables. Section 5 will discuss approaches to SM when dealing with data arising from complex sample surveys from finite populations.

2 Practical steps in an application of statistical matching

Before applying SM methods in order to integrate two or more data sources some decisions and preprocessing steps are required (Scanu, 2008). In practice, given two data sources A and B the following steps are necessary:

- Choice of the target variables Y and Z , i.e. of the variables observed distinctly in two sample surveys.
- Identification of all the common variables X shared by A and B . In this step some harmonization procedures may be required because of different definitions and/or classifications. Obviously, if two similar variables can not be harmonized they have to be discarded. The common variables should not present missing values and the observed values should be accurate (low or absent measurement error). It is worth noting that the common variables in the two data sources should have the same marginal/joint distribution, if A and B are representative samples of the same population.
- Potentially all the X variables can be used as matching variables but actually, not all them are used in the SM. Section 2.2 will provide more details concerning this topic.
- The choice of the matching variables is strictly related to the choice concerning the matching framework, i.e. micro or macro objective, parametric, nonparametric or a mixed approach etc.
- Once decided the framework, a SM technique is used to match the samples.
- Finally the results of the matching, whereas possible, should be evaluated.

2.1 Example data

The next Sections will provide a series of examples of application of some SM techniques in the R environment (R Development Core Team, 2011) by using the functions provided by the package **StatMatch** (D’Orazio, 2011). These examples will refer to data

derived from the data set `eusilcS` contained in the package **simPopulation** (Alfons and Kraft, 2011). This is an artificial data set generated from real Austrian EU-SILC (European Union Statistics on Income and Living Conditions) survey data containing 11 725 observations on 18 variables (see `eusilcS` help pages for details):

```
> library(simPopulation) #loads pkg simPopulation
> data(eusilcS)
> str(eusilcS)

'data.frame':      11725 obs. of  18 variables:
 $ db030      : int   1 1 2 3 4 4 4 5 5 5 ...
 $ hsize      : int   2 2 1 1 3 3 3 5 5 5 ...
 $ db040      : Factor w/ 9 levels "Burgenland","Carinthia",...: 4 4 7 5 7 7 7 4 4 4 ...
 $ age        : int   72 66 56 67 70 46 37 41 35 9 ...
 $ rb090      : Factor w/ 2 levels "male","female": 1 2 2 2 2 1 1 1 2 2 ...
 $ pl030      : Factor w/ 7 levels "1","2","3","4",...: 5 5 2 5 5 3 1 1 3 NA ...
 $ pb220a     : Factor w/ 3 levels "AT","EU","Other": 1 1 1 1 1 1 3 1 1 NA ...
 $ netIncome: num   22675 16999 19274 13319 14366 ...
 $ py010n     : num    0 0 19274 0 0 ...
 $ py050n     : num    0 0 0 0 0 ...
 $ py090n     : num    0 0 0 0 0 ...
 $ py100n     : num   22675 0 0 13319 14366 ...
 $ py110n     : num    0 0 0 0 0 0 0 0 0 NA ...
 $ py120n     : num    0 0 0 0 0 0 0 0 0 NA ...
 $ py130n     : num    0 16999 0 0 0 ...
 $ py140n     : num    0 0 0 0 0 0 0 0 0 NA ...
 $ db090      : num    7.82 7.82 8.79 8.11 7.51 ...
 $ rb050      : num    7.82 7.82 8.79 8.11 7.51 ...
```

In order to use these data to show how SM works, some manipulations are needed to discard not relevant units (obs. with `age<16`, whose income and personal economic status are missing), to categorize some variables, etc.

```
> # discard units with age<16
> silc.16 <- subset(eusilcS, age>15) # units
> nrow(silc.16)

[1] 9522

> #
> # categorize age
> silc.16$c.age <- cut(silc.16$age, c(16,24,49,64,100), include.lowest=T)
> #
> # truncate hsize
> aa <- as.numeric(silc.16$hsize)
```

```

> aa[aa>6] <- 6
> silc.16$hsize6 <- factor(aa, ordered=T)
> #
> # recode personal economic status
> aa <- as.numeric(silc.16$pl030)
> aa[aa<3] <- 1
> aa[aa>1] <- 2
> silc.16$work <- factor(aa, levels=1:2, labels=c("working","not working"))
> #
> # categorize personal net income
> silc.16$c.netI <- cut(silc.16$net/1000,
+                       breaks=c(-6,0,5,10,15,20,25,30,40,50,200))

```

In order to reproduce the basic SM framework, the data frame `silc.16` is split randomly in two data sets: `rec.A` consisting of 4000 observations and `don.B` with the remaining 5522 units. The two data frames `rec.A` and `don.B` share the variables `X.vars`; the person's economic status (`y.var`) is available only in `rec.A` while the net income (`z.var`) is available in `don.B`.

```

> set.seed(123456)
> obs.A <- sample(nrow(silc.16), 4000, replace=F)
> X.vars <- c("hsize", "hsize6", "db040", "age", "c.age",
+           "rb090", "pb220a", "rb050")
> y.var <- c("pl030", "work")
> z.var <- c("netIncome", "c.netI")
> rec.A <- silc.16[obs.A, c(X.vars, y.var)]
> don.B <- silc.16[-obs.A, c(X.vars, z.var)]
> #
> # determine a rough weighting
> # compute N, the est. size of pop(age>16)
> N <- round(sum(silc.16$rb050))
> N

[1] 67803

> #rescale origin weights
> rec.A$wwA <- rec.A$rb050/sum(rec.A$rb050)*N
> don.B$wwB <- don.B$rb050/sum(don.B$rb050)*N

```

2.2 The choice of the matching variables

In SM *A* and *B*, may share many common variables. In practice, not all the common variables are used in SM but just the most relevant ones. The selection of the common variables to be used in SM, usually called *matching variables*, should be performed

through opportune statistical methods (descriptive, inferential, etc.) and by consulting subject matter experts.

From a statistical point of view, the choice of the matching variables X_M ($X_M \subseteq X$) should be carried out in a “multivariate sense” in order to identify the subset of the X_M variables connected at the same time with Y and Z (Cohen, 1991); unfortunately this would require the availability of an auxiliary data source in which all the variables (X, Y, Z) are observed. In the basic SM framework the data in A permit to explore the relationship between Y and X , while the relationship between Z and X can be investigated in the file B . Then the results of the two separate analyses have to be combined in some manner; usually the subset of the matching variables is obtained as $X_M = X_Y \cup X_Z$, being X_Y the subset of the common variables that better explains Y ($X_Y \subseteq X$), while X_Z is the subset of the common variables that better explain Z ($X_Z \subseteq X$).

The simplest procedure to identify X_Y consists in fitting regression models to data available in A . The same procedure is carried out with data in B in order to identify the subset of the common variables X_Z that better explains Z .

The following R examples provide an idea of how to proceed. In particular, in the example data, the variable Y in A is a categorical binary variable (**work**), therefore a logistic regression model is fitted in order to identify X_Y .

```
> # analyses on A
> # logistic regression
> work.glm <- glm(work~hsize+db040+age+rb090+pb220a, data=rec.A,
+                 family=binomial(link = "logit"))
> summary(work.glm)
```

Call:

```
glm(formula = work ~ hsize + db040 + age + rb090 + pb220a, family = binomial(link = "logit",
data = rec.A)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.7327	-0.9511	-0.5405	0.9211	2.2492

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.105822	0.259524	-11.967	<2e-16 ***
hsize	0.010677	0.025941	0.412	0.6807
db040Carinthia	-0.065318	0.229838	-0.284	0.7763
db040Lower Austria	-0.207209	0.209499	-0.989	0.3226
db040Salzburg	-0.028442	0.236368	-0.120	0.9042
db040Styria	-0.102106	0.212338	-0.481	0.6306
db040Tyrol	-0.258700	0.225449	-1.147	0.2512
db040Upper Austria	-0.135302	0.210093	-0.644	0.5196

db040Vienna	-0.193611	0.214358	-0.903	0.3664	
db040Vorarlberg	0.008169	0.250389	0.033	0.9740	
age	0.055375	0.002434	22.750	<2e-16	***
rb090female	0.880804	0.072125	12.212	<2e-16	***
pb220aEU	-0.237560	0.239145	-0.993	0.3205	
pb220aOther	0.242078	0.141839	1.707	0.0879	.

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 5513.8 on 3999 degrees of freedom
Residual deviance: 4607.6 on 3986 degrees of freedom
AIC: 4635.6

Number of Fisher Scoring iterations: 3

In order to identify X_Y an automatic selection procedure can be used (forward, backward or stepwise selection):

```
> # stepwise selection
> new.work.glm <- step(work.glm, trace=0)
> summary(new.work.glm)
```

Call:

```
glm(formula = work ~ age + rb090 + pb220a, family = binomial(link = "logit"),
     data = rec.A)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.7394	-0.9536	-0.5341	0.9137	2.1955

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.198019	0.123036	-25.993	<2e-16 ***
age	0.055118	0.002277	24.212	<2e-16 ***
rb090female	0.879327	0.072009	12.211	<2e-16 ***
pb220aEU	-0.276207	0.236205	-1.169	0.2423
pb220aOther	0.244811	0.139171	1.759	0.0786 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 5513.8 on 3999 degrees of freedom
Residual deviance: 4612.5 on 3995 degrees of freedom
AIC: 4622.5
```

```
Number of Fisher Scoring iterations: 3
```

```
> # X_Y
> X.Y.glm <- c("age", "rb090", "pb220a")
```

According to the automatic selection procedure it comes out that X_Y is composed by the three variables "age", "rb090" and "pb220a".

In complex situations when a nonlinear relationship is supposed to exist, the selection of the subset X_Y can be demanded to nonparametric procedures such as *Classification And Regression Trees* (Breiman *et al.*, 1984). Instead of fitting a single tree it may be better to fit a *random forest* (Breiman, 2001) by using the functions available in the package **randomForest** (Liaw and Wiener, 2002). This technique provides a measure of importance for the predictors (that has to be used with caution). Alternatively *conditional inference trees* (Hothorn *et al.*, 2006) can be fitted; in this case the tree fitting is based on hypothesis testing and by considering explicitly the association between responses and covariates. In R these procedures are made available by the functions in the package **party** (Hothorn *et al.*, 2006).

The same analysis carried out in *A* should be carried out in *B*. In the example data, the target variable Z in *B* is the `netIncome` (better to consider its log).

```
> summary(don.B$netIncome)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-4373	6080	14130	14810	20810	185500

```
> don.B$lognetI <- log(don.B$netIncome+4373+1)
```

```
> summary(don.B$lognetI)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-0.2877	9.2550	9.8260	9.6520	10.1300	12.1500

```
> #regression
```

```
> lnetI.lm <- lm(lognetI~hsize+db040+age+rb090+pb220a, data=don.B)
```

```
> summary(lnetI.lm)
```

Call:

```
lm(formula = lognetI ~ hsize + db040 + age + rb090 + pb220a,
    data = don.B)
```

Residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

-9.7620 -0.3785 0.0878 0.4253 2.2285

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	9.7753007	0.0551851	177.137	< 2e-16 ***
hsize	-0.0596160	0.0062136	-9.594	< 2e-16 ***
db040Carinthia	0.0451692	0.0498676	0.906	0.36509
db040Lower Austria	0.0121853	0.0446170	0.273	0.78478
db040Salzburg	0.1303552	0.0520001	2.507	0.01221 *
db040Styria	0.0381493	0.0452166	0.844	0.39887
db040Tyrol	0.0701096	0.0486102	1.442	0.14928
db040Upper Austria	0.0844992	0.0446713	1.892	0.05860 .
db040Vienna	0.1364211	0.0455115	2.998	0.00273 **
db040Vorarlberg	0.0722760	0.0551028	1.312	0.18969
age	0.0060719	0.0005054	12.015	< 2e-16 ***
rb090female	-0.5218040	0.0169144	-30.850	< 2e-16 ***
pb220aEU	-0.0897179	0.0584009	-1.536	0.12454
pb220aOther	-0.2975103	0.0353512	-8.416	< 2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6268 on 5508 degrees of freedom
Multiple R-squared: 0.2029, Adjusted R-squared: 0.201
F-statistic: 107.9 on 13 and 5508 DF, p-value: < 2.2e-16

```
> # stepwise selection
> new.lnetI.lm <- step(lnetI.lm, trace=0)
> summary(new.lnetI.lm)
```

Call:

```
lm(formula = lognetI ~ hsize + db040 + age + rb090 + pb220a,
    data = don.B)
```

Residuals:

Min	1Q	Median	3Q	Max
-9.7620	-0.3785	0.0878	0.4253	2.2285

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	9.7753007	0.0551851	177.137	< 2e-16 ***
hsize	-0.0596160	0.0062136	-9.594	< 2e-16 ***
db040Carinthia	0.0451692	0.0498676	0.906	0.36509
db040Lower Austria	0.0121853	0.0446170	0.273	0.78478
db040Salzburg	0.1303552	0.0520001	2.507	0.01221 *

```

db040Styria      0.0381493  0.0452166   0.844  0.39887
db040Tyrol       0.0701096  0.0486102   1.442  0.14928
db040Upper Austria 0.0844992  0.0446713   1.892  0.05860 .
db040Vienna      0.1364211  0.0455115   2.998  0.00273 **
db040Vorarlberg  0.0722760  0.0551028   1.312  0.18969
age              0.0060719  0.0005054  12.015 < 2e-16 ***
rb090female      -0.5218040  0.0169144 -30.850 < 2e-16 ***
pb220aEU         -0.0897179  0.0584009  -1.536  0.12454
pb220aOther      -0.2975103  0.0353512  -8.416 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

Residual standard error: 0.6268 on 5508 degrees of freedom
Multiple R-squared:  0.2029,    Adjusted R-squared:  0.201
F-statistic: 107.9 on 13 and 5508 DF,  p-value: < 2.2e-16

```

```

> # X_Z
> X.Z.lm <- c("hsize", "db040", "age", "rb090", "pb220a")

```

This regression analysis ends with a model including all the available predictors. Then, according to the results of the two separate analyses on the example data, if it is decided that the matching variables are obtained as $X_M = X_Y \cup X_Z$, it comes out that all the available common variables should be used in the SM application.

```

> # the matching variables
> union(X.Y.glm, X.Z.lm)

[1] "age"      "rb090"    "pb220a"   "hsize"    "db040"

```

If a smaller subset of the matching variables is necessary, then by considering $X_M = X_Y \cap X_Z$, it would result a subset consisting of just three X variables:

```

> #the smallest subset of matching variables
> intersect(X.Y.glm, X.Z.lm)

[1] "age"      "rb090"    "pb220a"

```

The approach to SM based on the study of uncertainty offers the possibility of choosing the matching variables in a better way: by selecting just those common variables with the highest contribution to the reduction of the uncertainty. The function `Fbwidths.by.x` in **StatMatch** permits to explore the reduction of uncertainty when all the variables (X, Y, Z) are categorical. In particular, in the basic SM framework it is possible to show that

$$P_{j,k}^{(low)} \leq P(Y = j, Z = k) \leq P_{j,k}^{(up)},$$

being

$$P_{j,k}^{(low)} = \sum_i P(X = i) \max \{0; P(Y = j|X = i) + P(Z = k|X = i) - 1\}$$

$$P_{j,k}^{(up)} = \sum_i P(X = i) \min \{P(Y = j|X = i); P(Z = k|X = i)\}$$

for $j = 1, \dots, J$ and $k = 1, \dots, K$, being J and K the categories of Y and Z respectively.

The function `Fbwidths.by.x` estimates $[P_{j,k}^{(low)}, P_{j,k}^{(up)}]$ for each cell in the contingency table $Y \times Z$ in correspondence of all the possible combinations of the X variables; then the reduction of uncertainty is measured naively by considering the average widths of the intervals:

$$\bar{d} = \frac{1}{J \times K} \sum_{j=1}^J \sum_{k=1}^K (\hat{P}_{j,k}^{(up)} - \hat{P}_{j,k}^{(low)})$$

```
> xx <- xtabs(~db040+hsize6+c.age+rb090+pb220a, data=rec.A)
> xy <- xtabs(~db040+hsize6+c.age+rb090+pb220a+work, data=rec.A)
> xz <- xtabs(~db040+hsize6+c.age+rb090+pb220a+c.netI, data=don.B)
> #
> library(StatMatch) #loads StatMatch
> out.fbw <- Fbwidths.by.x(tab.x=xx, tab.xy=xy, tab.xz=xz)
> # average widths of uncertainty bounds
> out.fbw$av.widths
```

	n.vars	av.width
db040	1	0.10000000
hsize6	1	0.10000000
pb220a	1	0.10000000
rb090	1	0.10000000
c.age	1	0.08439346
hsize6+rb090	2	0.10000000
db040+rb090	2	0.10000000
rb090+pb220a	2	0.09997147
db040+hsize6	2	0.09985849
hsize6+pb220a	2	0.09977896
db040+pb220a	2	0.09970130
c.age+pb220a	2	0.08432518
db040+c.age	2	0.08374131
hsize6+c.age	2	0.08282457
c.age+rb090	2	0.07738444
hsize6+rb090+pb220a	3	0.09918992
db040+rb090+pb220a	3	0.09869455
db040+hsize6+pb220a	3	0.09768879

db040+hsize6+rb090	3	0.09688779
db040+c.age+pb220a	3	0.08171158
hsize6+c.age+pb220a	3	0.08137625
db040+hsize6+c.age	3	0.07711730
c.age+rb090+pb220a	3	0.07642623
hsize6+c.age+rb090	3	0.07623534
db040+c.age+rb090	3	0.07580610
db040+hsize6+rb090+pb220a	4	0.09232628
hsize6+c.age+rb090+pb220a	4	0.07360024
db040+hsize6+c.age+pb220a	4	0.07197990
db040+c.age+rb090+pb220a	4	0.07175106
db040+hsize6+c.age+rb090	4	0.06411282
db040+hsize6+c.age+rb090+pb220a	5	0.05775534

The results show that there is a marked reduction of the average width when passing from three to four common variables; the model with the matching variables "db040", "hsize6", "c.age" and "rb090" seems a good compromise among reduction of uncertainty and the necessity of not having too many matching variables. If there is the need of having less matching variables, in this example one should consider just two variables: "c.age" and "rb090"; in fact, the models with three matching variables do not provide a great decrease of average uncertainty with respect to the ones with just two.

The choice of the matching variables is a crucial phase in most of the SM applications. Choosing too many variables increases the complexity of the problem and may affect negatively the results of SM. In particular, in the micro approach it may introduce additional undesired variability and bias in estimating the joint (marginal) distribution of X_M and Z .

3 Nonparametric micro techniques

Nonparametric approach is very popular in SM when the objective is micro, i.e. the creation of a synthetic data set. Most of the nonparametric micro approaches consist in filling in the data set chosen as the *recipient* with the values of the variable which is available only in the other data set, the *donor* one. In this approach it is important to decide which data set plays the role of the recipient. Usually this is the data set which should be used as the basis for further statistical analysis; a natural choice would appear that of using the larger ones because it would provide more accurate results. Unfortunately, such a way of working may provide inaccurate SM results, especially when the sizes of the two data sources are very different. The reason is quite simple, the larger is the recipient with respect to the donor, the more times a unit in the latter could be selected as a donor; in this manner, there is a high risk that the distribution of the imputed variable does not reflect the original one (estimated from the donor data set).

In the following it will be assumed that A is the recipient while B is the donor, being $n_A \leq n_B$ (n_A and n_B are the sample sizes of A and B respectively). Hence the objective

of SM will be that of filling in A with values of Z (variable available only in B).

In **StatMatch** the following nonparametric micro techniques are available: *random hot deck*, *nearest neighbor hot deck* and *rank hot deck* (see Section 2.4 in D’Orazio *et al.*, 2006b; Singh *et al.*, 1993).

3.1 Nearest neighbor distance hot deck

The nearest neighbor distance hot deck techniques is implemented in the function `NND.hotdeck`. This function searches in `data.don` the nearest neighbor of each unit in `data.rec` according to a distance computed on the matching variables X_M specified with the argument `match.vars`. By default the Manhattan (city block) distance is considered (`dist.fun="Manhattan"`). In order to reduce the computation effort due to computation of distances it is preferable to define some donation classes (argument `don.class`): for a record in given imputation class it will be selected a donor in the same class (the distances are computed only among units belonging to the same class). Usually, the donation classes are defined according to one or more categorical common variables (geographic area, etc.). In the following, a simple example of usage of `NND.hotdeck` is reported.

```
> group.v <- c("rb090", "db040")
> X.mtc <- c("hsize", "age")
> out.nnd <- NND.hotdeck(data.rec=rec.A, data.don=don.B,
+                        match.vars=X.mtc, don.class=group.v,
+                        dist.fun="Manhattan")
```

```
Warning: The Manhattan distance is being used
All the categorical matching variables in rec and don
data.frames, if present are recoded into dummies
```

The function `NND.hotdeck` does not create the synthetic data set; for each unit in A the corresponding closest donor in B is identified according to the chosen distance function; the recipient-donor units’ identifiers are saved in the data.frame `mtc.ids` stored in the output list returned by `NND.hotdeck`. The output list provides also the distance between each couple recipient-donor (saved in the `dist.rd` component of the output list) and the number of available donors at the minimum distance for each recipient (component `noad`). Note that when there are more donors at the minimum distance then one of them is picked up at random.

```
> summary(out.nnd$dist.rd) # summary distances rec-don
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.0000	0.0000	0.0000	0.3278	0.0000	8.0000

```
> summary(out.nnd$noad) # summary available donors at min. dist.
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1.000	1.000	2.000	2.882	4.000	16.000

```
> table(out.nnd$noad)
```

1	2	3	4	5	6	7	8	9	10	11	12	13
1288	921	638	421	275	192	113	49	39	22	11	18	4
14	16											
6	3											

In order to derive the synthetic data set it is necessary to run the function `create.fused`:

```
> head(out.nnd$mtc.ids)
```

	rec.id	don.id
[1,]	"401"	"376"
[2,]	"71"	"118"
[3,]	"92"	"106"
[4,]	"225"	"253"
[5,]	"364"	"288"
[6,]	"370"	"380"

```
> fA.nnd.m <- create.fused(data.rec=rec.A, data.don=don.B,
+                           mtc.ids=out.nnd$mtc.ids,
+                           z.vars=c("netIncome", "c.netI"))
> head(fA.nnd.m) #first 6 obs.
```

	hsize	hsize6	db040	age	c.age	rb090	pb220a	rb050
401	5	5	Burgenland	45	(24,49]	male	AT	4.545916
71	2	2	Burgenland	65	(64,100]	male	AT	6.151409
92	2	2	Burgenland	81	(64,100]	male	AT	6.151409
225	3	3	Burgenland	51	(49,64]	male	AT	5.860364
364	4	4	Burgenland	18	[16,24]	male	AT	6.316554
370	5	5	Burgenland	50	(49,64]	male	AT	4.545916
	pl030	work	wwA	netIncome	c.netI			
401	1	working	10.85782	47159.21	(40,50]			
71	5	not working	14.69250	21316.32	(20,25]			
92	5	not working	14.69250	21667.53	(20,25]			
225	1	working	13.99734	34166.20	(30,40]			
364	1	working	15.08694	10228.02	(10,15]			
370	1	working	10.85782	9456.25	(5,10]			

As far as distances are concerned (argument `dist.fun`), all the distance functions in the package **proxy** (Meyer and Butchta, 2011) are available. Anyway, for some

particular distances it was decided to write specific R functions. In particular, when dealing with continuous matching variables it is possible to use the *maximum distance* (L^∞ norm) implemented in `maximum.dist`; this function works on the true observed values (continuous variables) or on transformed ranked values (argument `rank=TRUE`) as suggested in (Kovar *et al.*, 1988); the transformation (ranks divided by the number of units) removes the effect of different scales and the new values are distributed in the interval $[0, 1]$. The Mahalanobis distance can be computed by using `mahalanobis.dist` which allows an external estimate of the covariance matrix (argument `vc`). When dealing with mixed type matching variables, the *Gowers's dissimilarity* (Gower, 1981) can be computed (function `gower.dist`): it is an average of the distances computed on the single variables according to different rules, depending on the type of the variable. All the distances are scaled to range from 0 to 1, hence the overall distance can take a value in $[0, 1]$. It is worth noting that when dealing with mixed types matching variables it is still possible to use the distance functions for continuous variables but `NND.hotdeck` transforms factors into dummies (by means of the function `fact2dummy`).

```
> group.v <- c("rb090", "db040")
> X.mtc <- c("hsize", "age", "pb220a")
> out.nnd.g <- NND.hotdeck(data.rec=rec.A, data.don=don.B,
+                           match.vars=X.mtc, don.class=group.v,
+                           dist.fun="Gower")
> summary(out.nnd.g$dist.rd) # summary distances rec-don
```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	0.000000	0.000000	0.000000	0.005218	0.004329	0.148500

```
> fA.nnd.g <- create.fused(data.rec=rec.A, data.don=don.B,
+                           mtc.ids=out.nnd.g$mtc.ids,
+                           z.vars=c("netIncome", "c.netI"))
```

By default `NND.hotdeck` does not pose constraints on the “usage” of donors: a record in the donor data set can be selected many times as a donor. The multiple usage of a donor can be avoided by resorting to a *constrained hot deck* (argument `constrained=TRUE` in `NND.hotdeck`); in such a case, a donor can be used just once and all the donors are selected in order to minimize the overall matching distance (assuming that $n_A \leq n_B$). In practice, the donors are identified by solving a traveling salesperson problem; two alternative algorithms are available the classic one (argument `constr.alg="lpSolve"`) (Berkelaar *et al.*, 2011) and the RELAX-IV algorithm (Bertsekas and Tseng, 1994) (argument `constr.alg="relax"`). This latter one is much faster but there are some restrictions on its license.

```
> group.v <- c("rb090", "db040")
> X.mtc <- c("hsize", "age")
> out.nnd.mc <- NND.hotdeck(data.rec=rec.A, data.don=don.B,
+                           match.vars=X.mtc, don.class=group.v,
```

```
+                               dist.fun="Manhattan", constrained=T,
+                               constr.alg="lpSolve")
```

Warning: The Manhattan distance is being used
All the categorical matching variables in rec and don
data.frames, if present are recoded into dummies

```
> fA.nnd.mc <- create.fused(data.rec=rec.A, data.don=don.B,
+                           mtc.ids=out.nnd.mc$mtc.ids,
+                           z.vars=c("netIncome", "c.netI"))
```

The constrained matching requires a higher computational effort but preserves better the marginal distribution of the variable imputed in the synthetic data set. Obviously the overall matching distance tends to be greater than the one in the unconstrained case.

```
> # comparing marginal distribution of C.netI
> tt.0 <- prop.table(xtabs(~c.netI, data=don.B))
> tt.m <- prop.table(xtabs(~c.netI, data=fA.nnd.m))
> tt.g <- prop.table(xtabs(~c.netI, data=fA.nnd.g))
> tt.mc <- prop.table(xtabs(~c.netI, data=fA.nnd.mc))
> tt <- cbind(origin=c(tt.0), m4.unc=c(tt.m),
+             g5.unc=c(tt.g), m4.constr=c(tt.mc))
> round(tt*100, 2)
```

	origin	m4.unc	g5.unc	m4.constr
(-6,0]	12.89	13.18	12.38	12.78
(0,5]	9.25	9.18	9.10	9.50
(5,10]	14.03	13.80	13.85	13.95
(10,15]	17.35	17.38	17.40	17.15
(15,20]	18.60	18.68	18.95	18.65
(20,25]	13.27	12.68	12.62	13.25
(25,30]	6.61	7.00	7.50	6.53
(30,40]	5.11	5.22	4.98	5.22
(40,50]	1.32	1.25	1.52	1.38
(50,200]	1.56	1.65	1.70	1.60

```
> # distance wrt to the origin distr.
> 1/2*colSums(abs(tt-tt[,1]))
```

	origin	m4.unc	g5.unc	m4.constr
	0.000000000	0.009848243	0.016385639	0.005115357

```
> #overall matching distances
> sum(out.nnd$dist.rd) #unconstrained
```

```
[1] 1311
```

```
> sum(out.nnd.mc$dist.rd) #constrained
```

```
[1] 2906
```


3.2 Random hot deck

The function `RANDwNND.hotdeck` carries out the random selection of each donor from a suitable subset of all the available donors. This subset can be formed in different ways, e.g. by considering all the donors sharing the same characteristics of the recipient (defined according to some X_M variables, such as geographic region, etc.) or simply the closest donors according to a particular rule. The traditional *random hot deck* within imputation classes (Singh *et al.*, 1993) is performed by simply specifying the donation classes via the argument `don.class` (the classes are formed by crossing the categories of the categorical variables being considered). For each record in the recipient data set in a given donation class, a donor is picked up completely at random within the same donation class.

```
> group.v <- c("db040", "rb090")
> rnd.1 <- RANDwNND.hotdeck(data.rec=rec.A, data.don=don.B,
+                           match.vars=NULL, don.class=group.v)
> fA.rnd <- create.fused(data.rec=rec.A, data.don=don.B,
+                       mtc.ids=rnd.1$mtc.ids,
+                       z.vars=c("netIncome", "c.netI"))
```

As for `NND.hotdeck`, the function `RANDwNND.hotdeck` does not create the synthetic data set; the recipient-donor units' identifiers are saved in the component `mtc.ids` of the list returned in output by `RANDwNND.hotdeck`. The number of donors available in each donation class are saved in the component `noad`.

It is worth noting that the donors can also be selected with probability proportional to a weight (specified with the argument `weight.don`); an example will be provided in Section 5.

`RANDwNND.hotdeck` implements various alternative methods to restrict the subset of the potential donors. These methods are based essentially on a distance measure computed on the matching variables provided via the argument `match.vars`. In practice, when `cut.don="k.dist"` only the donors whose distance from the recipient is less or equal to threshold k are considered (see Andridge and Little, 2010). By setting `cut.don="exact"` the k ($0 < k \leq n_D$) closest donors are retained (n_D is the number of available donors for a given recipient). With `cut.don="span"` a proportion k ($0 < k \leq 1$) of the closest available donors it is considered while with `cut.don="rot"` only the subset reduces to the $\lceil \sqrt{n_D} \rceil$ closest donors. Finally, when `cut.don="min"` only the donors at the minimum distance from the recipient are retained.

```
> # random choiches of a donor among the closest k=20 wrt age
> group.v <- c("db040", "rb090")
> X.mtc <- "age"
> rnd.2 <- RANDwNND.hotdeck(data.rec=rec.A, data.don=don.B,
+                           match.vars=X.mtc, don.class=group.v,
+                           dist.fun="Manhattan",
+                           cut.don="exact", k=20)
```

Warning: The Manhattan distance is being used
 All the categorical matching variables in rec and don data.frames,
 if present, are recoded into dummies

```
> fA.knnd <- create.fused(data.rec=rec.A, data.don=don.B,
+                           mtc.ids=rnd.2$mtc.ids,
+                           z.vars=c("netIncome", "c.netI"))
```

When distances are computed on the matching variables, then the output of `RAND-wNND.hotdeck` provides some information concerning the distances of the possible available donors for each recipient observation in the data.frame.

```
> head(rnd.2$sum.dist)
```

	min	max	sd	cut	dist.rd
[1,]	0	47	11.02087	5	3
[2,]	0	49	14.54555	4	1
[3,]	0	65	19.01027	9	2
[4,]	1	41	10.09283	6	5
[5,]	1	74	19.53088	11	2
[6,]	0	42	10.16749	5	2

In particular, "min", "max" and "sd" columns report respectively the minimum, the maximum and the standard deviation of the distances (all the available donors are considered), while "cut" refers to the distance of the kth closest donor; "dist.rd" is distance existing among the recipient and the randomly chosen donor.

```
> tt.0 <- prop.table(xtabs(~c.netI, data=don.B))
> tt.rnd <- prop.table(xtabs(~c.netI, data=fA.rnd))
> tt.knnd <- prop.table(xtabs(~c.netI, data=fA.knnd))
> tt <- cbind(origin=c(tt.0), rnd=c(tt.rnd), k.nnd=c(tt.knnd))
> round(tt*100, 2)
```

	origin	rnd	k.nnd
(-6,0]	12.89	13.53	13.70
(0,5]	9.25	9.72	9.47
(5,10]	14.03	13.58	13.53
(10,15]	17.35	16.35	17.80
(15,20]	18.60	18.35	18.50
(20,25]	13.27	13.15	12.47
(25,30]	6.61	6.78	6.90
(30,40]	5.11	5.83	4.88
(40,50]	1.32	1.43	1.38
(50,200]	1.56	1.30	1.38

```
> # distance wrt to the origin distr.
> 1/2*colSums(abs(tt-tt[,1]))
```

```
      origin      rnd      k.nnd
0.00000000 0.02088473 0.01821532
```

When selecting a donor among those available in the subset identified by `cut.don` and `k` it is possible to use a weighted selection by specifying a weighting variable via `weight.don` argument. The aspects related to the usage of weights will be covered in Section 5.

3.3 Rank hot deck

The *rank hot deck distance* method has been introduced by Singh *et al.* (1993). It searches for the donor at a minimum distance from the given recipient record but, in this case, the distance is computed on the percentage points of the empirical cumulative distribution function of the unique (continuous) common variable X_M being considered. The empirical cumulative distribution function is estimated by:

$$\hat{F}(x_k) = \frac{1}{n} \sum_{i=1}^n I(x_i \leq x_k)$$

being $I() = 1$ if $x_i \leq x_k$ and 0 otherwise. This transformation provides values uniformly distributed in the interval $[0, 1]$; moreover, it can be useful when the values of X_M can not be directly compared because of measurement errors which however do not affect the “position” of a unit in the whole distribution (D’Orazio *et al.*, 2006b). This method is implemented in the function `rankNND.hotdeck`. In the following just a simple example of usage is reported.

```
> rnk.1 <- rankNND.hotdeck(data.rec=rec.A, data.don=don.B,
+                          var.rec="age", var.don="age")
> #create the synthetic data set
> fA.rnk <- create.fused(data.rec=rec.A, data.don=don.B,
+                       mtc.ids=rnk.1$mtc.ids,
+                       z.vars=c("netIncome", "c.netI"),
+                       dup.x=TRUE, match.vars="age")
> head(fA.rnk)
```

	hsize	hsize6	db040	age	c.age	rb090	pb220a
4547	2	2	Carinthia	45	(24,49]	male	AT
9819	4	4	Salzburg	35	(24,49]	female	AT
4461	2	2	Carinthia	57	(49,64]	male	AT
10222	2	2	Tyrol	69	(64,100]	female	AT
8228	4	4	Upper Austria	25	(24,49]	female	AT
3361	3	3	Vienna	22	[16,24]	male	Other

	rb050	pl030	work	wwA	age.don	netIncome
4547	6.863162	1	working	16.39250	45	14337.87
9819	6.089967	1	working	14.54575	35	9350.56
4461	6.863162	1	working	16.39250	58	4331.63
10222	6.857877	5	not working	16.37988	70	16343.10
8228	6.945309	4	not working	16.58871	25	13167.76
3361	8.374000	1	working	20.00110	22	11626.29
	c.netI					
4547	(10,15]					
9819	(5,10]					
4461	(0,5]					
10222	(15,20]					
8228	(10,15]					
3361	(10,15]					

The function `rankNND.hotdeck` allows defining some donation classes with the argument `don.class`; in this case the empirical cumulative distribution is estimated separately class by class.

```
> rnk.2 <- rankNND.hotdeck(data.rec=rec.A, data.don=don.B, var.rec="age",
+                           var.don="age", don.class="db040")
> fA.grnk <- create.fused(data.rec=rec.A, data.don=don.B,
+                          mtc.ids=rnk.2$mtc.ids,
+                          z.vars=c("netIncome", "c.netI"),
+                          dup.x=TRUE, match.vars="age")
> head(fA.grnk)
```

	hsize	hsize6	db040	age	c.age	rb090	pb220a	rb050
401	5	5	Burgenland	45	(24,49]	male	AT	4.545916
245	3	3	Burgenland	64	(49,64]	female	AT	5.860364
71	2	2	Burgenland	65	(64,100]	male	AT	6.151409
92	2	2	Burgenland	81	(64,100]	male	AT	6.151409
86	2	2	Burgenland	27	(24,49]	female	AT	6.151409
113	2	2	Burgenland	58	(49,64]	female	AT	6.151409
	pl030		work	wwA	age.don	netIncome	c.netI	
401	1		working	10.85782	39	15308.91	(15,20]	
245	5		not working	13.99734	63	21639.69	(20,25]	
71	5		not working	14.69250	64	8988.24	(5,10]	
92	5		not working	14.69250	77	15648.92	(15,20]	
86	2		working	14.69250	26	16607.60	(15,20]	
113	1		working	14.69250	55	21745.87	(20,25]	

In estimating the empirical cumulative distribution it is possible to consider the weights of the observations (arguments `weight.rec` and `weight.don`). This topic will be covered in Section 5.

3.4 Using functions in StatMatch to impute missing values in a survey

All the functions in **StatMatch** that implement the hot deck imputation techniques can be used to impute missing values in a single data set. In this case it is necessary to separate the observations in two data sets: the file *A* plays the role of recipient and will contain the units with missing values on the target variable while the file *B* is the donor and will contain all the available donors (units with non missing values for the target variable). In the following a simple example with the `iris` data.frame is reported.

```
> # introduce missing values in iris
> set.seed(1324)
> miss <- rbinom(150, 1, 0.30) #generates randomly missing
> iris.miss <- iris
> iris.miss$Petal.Length[miss==1] <- NA
> summary(iris.miss$Petal.L)

    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
    1.1    1.6    4.3    3.8    5.1    6.9   46.0

> # separate units in two data sets
> rec <- subset(iris.miss, is.na(Petal.Length), select=-Petal.Length)
> don <- subset(iris.miss, !is.na(Petal.Length))
```

Once the starting data set has been split in two (recipient and donor) a nonparametric imputation technique can be used to search for a donor for each observation in the recipient data set. In the following example the nearest neighbor hotdeck is considered.

```
> # search for closest donors
> X.mtc <- c("Sepal.Length", "Sepal.Width", "Petal.Width")
> nnd <- NND.hotdeck(data.rec=rec, data.don=don,
+                   match.vars=X.mtc, don.class="Species",
+                   dist.fun="Manhattan")
```

Warning: The Manhattan distance is being used
All the categorical matching variables in rec and don
data.frames, if present are recoded into dummies

At this point the function `create.fused` is used to fill in the target variable ("`Petal.Length`" in the example) in the recipient data set. Then the filled recipient and the donor one can be concatenated to obtain the origin dataset with imputed values.

```
> # fills rec
> imp.rec <- create.fused(data.rec=rec, data.don=don,
+                       mtc.ids=nnd$mtc.ids, z.vars="Petal.Length")
> imp.rec$imp.PL <- 1 # flag for imputed
> #
```

```

> # re-aggregate data sets
> don$imp.PL <- 0
> imp.iris <- rbind(imp.rec, don)
> summary(imp.iris)

  Sepal.Length  Sepal.Width  Petal.Width      Species
Min.   :4.300   Min.   :2.000   Min.   :0.100   setosa      :50
1st Qu.:5.100   1st Qu.:2.800   1st Qu.:0.300   versicolor:50
Median :5.800   Median :3.000   Median :1.300   virginica  :50
Mean   :5.843   Mean   :3.057   Mean   :1.199
3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:1.800
Max.   :7.900   Max.   :4.400   Max.   :2.500
  Petal.Length      imp.PL
Min.   :1.100   Min.   :0.0000
1st Qu.:1.500   1st Qu.:0.0000
Median :4.250   Median :0.0000
Mean   :3.736   Mean   :0.3067
3rd Qu.:5.100   3rd Qu.:1.0000
Max.   :6.900   Max.   :1.0000

> #summary stat of imputed and non imputed Petal.Length
> tapply(imp.iris$Petal.Length, imp.iris$imp.PL, summary)

$`0`
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.1    1.6    4.3    3.8    5.1    6.9

$`1`
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 1.300  1.425  4.200  3.591  5.100  6.700

```

4 Mixed methods

A SM mixed method consists of two steps: (1) a model is fitted and all its parameters are estimated, then (2) a nonparametric approach is used to create the synthetic data set. The model is more parsimonious while the nonparametric approach offers “protection” against model misspecification. The proposed mixed approaches for SM are based essentially on *predictive mean matching* imputation methods (see D’Orazio *et al.* 2006b, Section 2.5 and 3.6). The function `mixed.mtc` in **StatMatch** implements two similar mixed methods that deal with variables (X_M, Y, Z) following the multivariate normal distribution. The main difference consists in the estimation of the parameters of the two regressions Y vs. X_M and Z vs. X_M . By default the parameters are estimated through maximum likelihood (argument `method="ML"`); in alternative a method proposed by Moriarity and Scheuren (2001, 2003) (argument `method="MS"`) is available. D’Orazio *et al.*

(2005) compared these methods in an extensive simulation study: in general ML tends to perform better, moreover it permits to avoid some incoherencies in the estimation of the parameters that are possible with the Moriarity and Scheuren approach.

At the end of the first step, after the estimation of the parameters of the two regression models, the data set A is filled in with the “intermediate” values $\tilde{z}_a = \hat{z}_a + e_a$ ($a = 1, \dots, n_A$) obtained by adding a random residual term e_a to the predicted values \hat{z}_a . The same happens in B which is filled in with the values $\tilde{y}_b = \hat{y}_b + e_b$ ($b = 1, \dots, n_B$). Finally, in the step (2) each record in A is filled in with the value of Z observed on the donor found in B according to a constrained distance hot deck; the Mahalanobis distance is computed by considering the intermediate and live values: couples (y_a, \tilde{z}_a) in A and (\tilde{y}_b, z_b) in B .

Such a two steps procedure offers various advantages: it offers protection against model misspecification and also reduces the risk of bias in the marginal distribution of the imputed variable because the distances are computed on intermediate and truly observed values of the target variables, Y and Z , instead of the matching variables X_M . In fact when computing the distances by considering all the matching variables, variables with low predictive power on the target variable may influence negatively the distances.

In the following example the `iris` data set is used just to show how `mixed.mtc` works.

```
> # uses iris data set
> iris.A <- iris[101:150, 1:3]
> iris.B <- iris[1:100, c(1:2,4)]
> X.mtc <- c("Sepal.Length", "Sepal.Width") # matching variables
> # parameters estimated using ML
> mix.1 <- mixed.mtc(data.rec=iris.A, data.don=iris.B, match.vars=X.mtc,
+                   y.rec="Petal.Length", z.don="Petal.Width",
+                   method="ML", rho.yz=0,
+                   micro=TRUE, constr.alg="lpSolve")
> mix.1$mu #estimated means
```

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
5.843333	3.057333	4.996706	1.037109

```
> mix.1$cor #estimated cor. matrix
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
Sepal.Length	1.0000000	-0.1175698	0.9131794	0.8490516
Sepal.Width	-0.1175698	1.0000000	-0.0992586	-0.4415012
Petal.Length	0.9131794	-0.0992586	1.0000000	0.7725288
Petal.Width	0.8490516	-0.4415012	0.7725288	1.0000000

```
> head(mix.1$filled.rec) # A filled in with Z
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
101	6.3	3.3	6.0	1.0

102	5.8	2.7	5.1	1.3
103	7.1	3.0	5.9	1.5
104	6.3	2.9	5.6	1.0
105	6.5	3.0	5.8	1.5
106	7.6	3.0	6.6	1.6

```
> cor(mix.1$filled.rec)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
Sepal.Length	1.0000000	0.4572278	0.8642247	0.5049387
Sepal.Width	0.4572278	1.0000000	0.4010446	0.1100799
Petal.Length	0.8642247	0.4010446	1.0000000	0.4052548
Petal.Width	0.5049387	0.1100799	0.4052548	1.0000000

When using `mixed.mtc` the synthetic data set is provided in output as the component `filled.rec` of the list returned by calling it with the argument `micro=TRUE`. When `micro=FALSE` the function `mixed.mtc` returns just the estimates of the parameters (parametric macro approach).

The function `mixed.mtc` by default performs mixed SM under the CI assumption ($\rho_{YZ|X_M} = 0$ argument `rho.yz=0`). When some additional auxiliary information about the correlation between Y and Z is available (estimates from previous surveys or from external sources) then it can be exploited in SM by specifying a value ($\neq 0$) for the argument `rho.yz`; it represents guess for $\rho_{YZ|X_M}$ when using the ML estimation or a guess for ρ_{YZ} when estimating the parameters by using the Moriarity and Scheuren method.

```
> # parameters estimated using ML and rho_YZ/X=0.85
> mix.2 <- mixed.mtc(data.rec=iris.A, data.don=iris.B, match.vars=X.mtc,
+                   y.rec="Petal.Length", z.don="Petal.Width",
+                   method="ML", rho.yz=0.85,
+                   micro=TRUE, constr.alg="lpSolve")
> mix.2$cor
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
Sepal.Length	1.0000000	-0.1175698	0.9131794	0.8490516
Sepal.Width	-0.1175698	1.0000000	-0.0992586	-0.4415012
Petal.Length	0.9131794	-0.0992586	1.0000000	0.9113867
Petal.Width	0.8490516	-0.4415012	0.9113867	1.0000000

```
> head(mix.2$filled.rec)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
101	6.3	3.3	6.0	1.5
102	5.8	2.7	5.1	1.3
103	7.1	3.0	5.9	1.6

104	6.3	2.9	5.6	1.4
105	6.5	3.0	5.8	1.5
106	7.6	3.0	6.6	1.5

Special attention is required when specifying a guess for ρ_{YZ} under the Moriarity and Scheuren estimation approach (`method="MS"`); in particular it may happen that the specified value for ρ_{YZ} is not compatible with the given SM framework (remember that the correlation matrix must be positive semidefinite). If this is the case, then the `mixed.mtc` substitutes the input value `rho.yz` by its closest admissible value, as shown in the following example.

```
> mix.3 <- mixed.mtc(data.rec=iris.A, data.don=iris.B, match.vars=X.mtc,
+                   y.rec="Petal.Length", z.don="Petal.Width",
+                   method="MS", rho.yz=0.75,
+                   micro=TRUE, constr.alg="lpSolve")

input value for rho.yz is 0.75
low(rho.yz)= -0.1662
up(rho.yz)= 0.5565
Warning: value for rho.yz is not admissible: a new value is chosen for it
The new value for rho.yz is 0.5465

> mix.3$rho.yz

      start low.lim up.lim   used
0.7500 -0.1662  0.5565  0.5465
```

5 Statistical matching of data from complex sample surveys

The SM techniques presented in the previous Sections implicitly or explicitly assume that the observed values in A and B are i.i.d. Unfortunately, when dealing with samples selected from a finite population by means of complex sampling designs (with stratification, clustering, etc.) it is difficult to maintain the i.i.d. assumption (it would mean that the sampling design can be ignored) and the sampling design and the weights assigned to the units (usually design weights corrected for unit nonresponse, frame errors, etc.) have to be considered when making inferences (see Särndal *et al.*, 1992, Section 13.6).

When matching data from complex samples surveys, two different alternatives ways can be followed: *naive* approaches which essentially consist in using SM methods developed for i.i.d. samples or *ad hoc* approaches that explicitly take into account the sampling design and the corresponding sampling weights. In this latter case, three different SM methods are available: Renssen's approach based on weights' *calibrations* (Renssen, 1998); Rubin's *file concatenation* (Rubin, 1986) and the approach based on the *empirical likelihood* proposed by Wu (2004). A comparison among these approaches can be found in D'Orazio (2010).

5.1 Naive approaches

Most of these approaches consists in applying SM nonparametric micro methods (nearest neighbour distance, random or rank hotdeck) without considering the design nor the units weights. Once obtained the synthetic dataset (recipient filled in with the missing variables) the successive statistical analyses are carried out by considering the sampling design underlying the recipient data set and the corresponding survey weights. In the following a simple SM example based on nearest neighbor hotdeck is reported.

```
> # summary info on the weights
> sum(rec.A$wwA) # estimated pop size from A

[1] 67803

> sum(don.B$wwB) # estimated pop size from B

[1] 67803

> summary(rec.A$wwA)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 8.538 14.470 16.510 16.950 19.370 29.920

> summary(don.B$wwB)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 6.149 10.580 11.890 12.280 13.950 21.550

> # NND unconstrained hotdeck
> group.v <- c("rb090", "db040")
> X.mtc <- c("hsize", "age")
> out.nnd <- NND.hotdeck(data.rec=rec.A, data.don=don.B,
+                        match.vars=X.mtc, don.class=group.v,
+                        dist.fun="Manhattan")

Warning: The Manhattan distance is being used
All the categorical matching variables in rec and don
data.frames, if present are recoded into dummies

> fA.nnd.m <- create.fused(data.rec=rec.A, data.don=don.B,
+                          mtc.ids=out.nnd$mtc.ids,
+                          z.vars=c("netIncome", "c.netI"))
> # estimating average net income
> weighted.mean(fA.nnd.m$netIncome, fA.nnd.m$wwA) # imputed in A

[1] 15190.13
```

```
> weighted.mean(don.B$netIncome, don.B$wwB) # ref. estimate in B
```

```
[1] 15073.95
```

```
> # comparing marginal distribution of C.netI using weights
> tt.0w <- prop.table(xtabs(wwB~c.netI, data=don.B))
> tt.fw <- prop.table(xtabs(wwA~c.netI, data=fA.nnd.m))
> tt <- cbind(origin=c(tt.0w), nnd.naive=c(tt.fw))
> round(tt*100, 2)
```

	origin	nnd.naive
(-6,0]	11.95	12.91
(0,5]	9.04	8.53
(5,10]	14.10	13.94
(10,15]	17.52	17.63
(15,20]	18.97	18.68
(20,25]	13.54	12.41
(25,30]	6.75	7.10
(30,40]	5.17	5.39
(40,50]	1.33	1.49
(50,200]	1.63	1.92

```
> # distance wrt to the origin distr.
> 1/2*colSums(abs(tt-tt[,1]))
```

origin	nnd.naive
0.00000000	0.02085371

As far as imputation of missing values is concerned, a way of taking into account the sampling design can consist in forming the donation classes by using the design variables (stratification and/or clustering variables) jointly with the most relevant common variables (Andridge and Little, 2010). Unfortunately this operation can increase the complexity of SM or may be unfeasible because the design variables may not be available (or partly available). In particular, when the two sample surveys have quite different designs it is common that the design variables characterizing one survey are not available in the other one and vice versa.

When imputing missing values in a survey, another possibility consists in using sampling weights (design weights) to form the donation classes (Andridge and Little, 2010). But again, in SM applications the problem can be slightly more complex even because the sets of weights can be quite different from one survey to the other (usually the available weights are the design weights corrected to compensate for unit nonresponse, to satisfy some given constraints etc.). The same Authors (Andridge and Little, 2010) indicate that in the imputation framework, the selection of the donors can be carried out with probability proportional to weights associated to the donors (*weighted random*

hot deck). Andridge and Little (2009) found that such a usage of the the sample weights can give poor results.

The properties of the weighted random hot deck in the SM applications have not been investigated, nevertheless the function `RANDwNDD.hotdeck` permits to select the donors with probability proportional to weights specified via the `weight.don` argument.

```
> rnd.2 <- RANDwNDD.hotdeck(data.rec=rec.A, data.don=don.B,
+                             match.vars=NULL, don.class=group.v,
+                             weight.don="wwB")
> fA.wrnd <- create.fused(data.rec=rec.A, data.don=don.B,
+                          mtc.ids=rnd.2$mtc.ids,
+                          z.vars=c("netIncome", "c.netI"))
> head(fA.wrnd)
```

	hsize	hsize6	db040	age	c.age	rb090	pb220a	rb050
401	5	5	Burgenland	45	(24,49]	male	AT	4.545916
71	2	2	Burgenland	65	(64,100]	male	AT	6.151409
92	2	2	Burgenland	81	(64,100]	male	AT	6.151409
225	3	3	Burgenland	51	(49,64]	male	AT	5.860364
364	4	4	Burgenland	18	[16,24]	male	AT	6.316554
370	5	5	Burgenland	50	(49,64]	male	AT	4.545916
	pl030	work	wwA	netIncome	c.netI			
401	1	working	10.85782	24069.74	(20,25]			
71	5	not working	14.69250	12850.50	(10,15]			
92	5	not working	14.69250	15430.68	(15,20]			
225	1	working	13.99734	11346.32	(10,15]			
364	1	working	15.08694	0.00	(-6,0]			
370	1	working	10.85782	24069.74	(20,25]			

```
> weighted.mean(fA.wrnd$netIncome, fA.wrnd$wwA) # imputed in A
```

```
[1] 15060
```

```
> weighted.mean(don.B$netIncome, don.B$wwB) # ref. estimate in B
```

```
[1] 15073.95
```

```
> # comparing marginal distribution of C.netI using weights
> tt.0w <- prop.table(xtabs(wwB~c.netI, data=don.B))
> tt.fw <- prop.table(xtabs(wwA~c.netI, data=fA.wrnd))
> tt <- cbind(origin=c(tt.0w), nnd.naive=c(tt.fw))
> round(tt*100, 2)
```

	origin	nnd.naive
(-6,0]	11.95	12.73

(0,5]	9.04	8.18
(5,10]	14.10	14.20
(10,15]	17.52	18.32
(15,20]	18.97	19.20
(20,25]	13.54	12.33
(25,30]	6.75	6.95
(30,40]	5.17	4.60
(40,50]	1.33	1.76
(50,200]	1.63	1.74

```
> # distance wrt to the origin distr.
> 1/2*colSums(abs(tt-tt[,1]))
```

```
origin nnd.naive
0.0000000 0.0264548
```

Perhaps, a better usage of the units weights is achieved in the rank hot deck SM where the the weights, w_i , of the units in A and in B can be used in estimating the percentage points of the the empirical cumulative distribution function by means of the expression:

$$\hat{F}(x_k) = \frac{\sum_{i=1}^n w_i I(x_i \leq x_k)}{\sum_{i=1}^n w_i}$$

Such a procedure can provide quite good results in terms of preservation of the marginal distribution of the imputed variables in the synthetic data set. In the following it is reported an very simple example.

```
> rnk.w <- rankNND.hotdeck(data.rec=rec.A, data.don=don.B,
+                           don.class="db040", var.rec="age",
+                           var.don="age", weight.rec="wwA",
+                           weight.don="wwB")
> #
> #create the synthetic data set
> fA.wrnk <- create.fused(data.rec=rec.A, data.don=don.B,
+                         mtc.ids=rnk.w$mtc.ids,
+                         z.vars=c("netIncome", "c.netI"),
+                         dup.x=TRUE, match.vars="age")
> #
> weighted.mean(fA.wrnk$netIncome, fA.wrnk$wwA) # imputed in A

[1] 15047.15

> weighted.mean(don.B$netIncome, don.B$wwB) # ref. estimate in B

[1] 15073.95
```

```

> # comparing marginal distribution of C.netI using weights
> tt.0w <- prop.table(xtabs(wWB~c.netI, data=don.B))
> tt.fw <- prop.table(xtabs(wWA~c.netI, data=fA.wrnk))
> tt <- cbind(origin=c(tt.0w), nnd.naive=c(tt.fw))
> round(tt*100, 2)

```

	origin	nnd.naive
(-6,0]	11.95	12.40
(0,5]	9.04	9.23
(5,10]	14.10	13.21
(10,15]	17.52	16.93
(15,20]	18.97	20.33
(20,25]	13.54	13.49
(25,30]	6.75	6.40
(30,40]	5.17	4.87
(40,50]	1.33	1.29
(50,200]	1.63	1.85

```

> # distance wrt to the origin distr.
> 1/2*colSums(abs(tt-tt[,1]))

```

	origin	nnd.naive
	0.00000000	0.02225742

5.2 Renssen's statistical matching through weights calibrations

This approach consists in a series of calibration steps of the survey weights of A and B in order to achieve consistency between estimates (mainly totals) computed separately from them. Calibration is a technique very common in sample surveys for deriving new survey weights, as close as possible to the starting ones, which fulfill a series of constraints concerning totals for a set of auxiliary variables (for further details on calibration see Särndal, 2005). The Renssen's approach works well when dealing with categorical variables or in a mixed case in which the number of continuous variables is very limited. In the following it will be assumed that all the variables (X_M, Y, Z) are categorical. The procedure and the functions developed in **StatMatch** permit to handle one or more continuous variables (better just one) in the subset of the matching variables X_M , while Y and Z are assumed to be categorical (when this is not the case it is necessary to categorize the continuous variables).

The first step in the Renssen's procedure consists in calibrating weights in A and in B such that the new weights when applied to the set of the matching variables X_M allow to reproduce some known (or estimated) population totals. In **StatMatch** the harmonization step can be performed by using **harmonize.x**. This function performs weights calibration (or post-stratification) by means of functions available in the R package **survey** (Lumley, 2011). When the population totals are already known then they have to be passed to **harmonize.x** via the argument **x.tot**; on the contrary, when they

are unknown (`x.tot=NULL`) they are estimated by a weighted average of the totals estimated on the two surveys before the harmonization step:

$$\tilde{t}_{X_M} = \lambda \hat{t}_{X_M}^{(A)} + (1 - \lambda) \hat{t}_{X_M}^{(B)}$$

being $\lambda = n_A / (n_A + n_B)$ (n_A and n_B are the sample sizes of A and B respectively) (Korn and Graubard, 1999, pp. 281–284).

The following example shows how to harmonize the joint distribution of the gender and classes of age with the data from the previous example, assuming that the joint distribution of age and gender is not known.

```
> tt.A <- xtabs(wwA~rb090+c.age, data=rec.A)
> tt.B <- xtabs(wwB~rb090+c.age, data=don.B)
> (prop.table(tt.A)-prop.table(tt.B))*100
```

	c.age			
rb090	[16,24]	(24,49]	(49,64]	(64,100]
male	0.3661141	1.0995148	-0.9456418	-0.6383618
female	0.0891681	-0.4970682	1.0772175	-0.5509426

```
> library(survey) # loads survey
> # creates svydesign objects
> svy.rec.A <- svydesign(~1, weights=~wwA, data=rec.A)
> svy.don.B <- svydesign(~1, weights=~wwB, data=don.B)
> #
> # harmonizes wrt to joint distr. of gender vs. c.age
> out.hz <- harmonize.x(svy.A=svy.rec.A, svy.B=svy.don.B,
+                       form.x=~c.age:rb090-1)
> #
> summary(out.hz$weights.A) # new calibrated weights for A
```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	8.647	14.390	16.570	16.950	19.030	31.470

```
> summary(out.hz$weights.B) # new calibrated weights for B
```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	6.279	10.540	11.840	12.280	13.910	22.400

```
> tt.A <- xtabs(out.hz$weights.A~rb090+c.age, data=rec.A)
> tt.B <- xtabs(out.hz$weights.B~rb090+c.age, data=don.B)
> (prop.table(tt.A)-prop.table(tt.B))*100
```

	c.age			
rb090	[16,24]	(24,49]	(49,64]	(64,100]
male	0.000000e+00	-2.775558e-15	-1.387779e-15	-1.387779e-15
female	0.000000e+00	0.000000e+00	0.000000e+00	0.000000e+00

After the harmonization, the second step in the Renssen's procedure consists in estimating the two way contingency table $Y \times Z$. In absence of auxiliary information it is estimated under the CI assumption by means of:

$$\hat{P}^{(CIA)}(Y, Z) = \hat{P}^{(A)}(Y|X_M) \hat{P}^{(B)}(Z|X_M) \hat{P}(X_M)$$

In practice, $\hat{P}^{(A)}(Y|X_M)$ is computed from A ; $\hat{P}^{(B)}(Z|X_M)$ is computed from data in B while $P(X_M)$ can be estimated indifferently from A or B (the data set are harmonized with respect to the X_M distribution). In **StatMatch** an estimate of the table $Y \times Z$ under the CIA is provided by the function `comb.samples`.

```
> # estimating c.pl030 vs. c.netI under the CI assumption
> out <- comb.samples(svy.A=out.hz$cal.A, svy.B=out.hz$cal.B,
+                     svy.C=NULL, y.lab="work", z.lab="c.netI",
+                     form.x=~c.age:rb090-1)
> #
> addmargins(t(out$yz.CIA)) # table estimated under the CIA
```

	working	not working	Sum
(-6,0]	4203.9273	3929.4698	8133.3971
(0,5]	3212.7539	2941.5722	6154.3261
(5,10]	4436.4472	5108.0075	9544.4547
(10,15]	5648.5383	6199.2373	11847.7756
(15,20]	7129.6193	5716.1572	12845.7765
(20,25]	5391.3879	3802.7509	9194.1388
(25,30]	2877.6585	1696.1470	4573.8055
(30,40]	2249.5066	1256.9719	3506.4786
(40,50]	555.7829	345.2169	900.9998
(50,200]	688.8992	412.9481	1101.8473
Sum	36394.5210	31408.4790	67803.0000

When some auxiliary information represented by third data source C , containing all the variables (X_M, Y, Z) or just (Y, Z) , is available Renssen's approach permits to exploit it in estimating $Y \times Z$. Two alternative methods are available: (a) *incomplete two way stratification*; and (b) *synthetic two way stratification*. In practice, both the methods estimate $Y \times Z$ from C after some further calibration steps (for further details see Renssen, 1998). The function `comb.samples` implements both the methods. In practice, the synthetic two way stratification (argument `estimation="synthetic"`) can be applied only when C contains all the variables of interest (X_M, Y, Z) ; on the contrary, when the data source C observes just Y and Z , only the incomplete two way stratification method can be applied (argument `estimation="incomplete"`). In the following a simple example is reported based on the artificial EU-SILC data introduced in Section 2.1; here a small sample C ($n_C = 200$) with all the variables of interest (X_M, Y, Z) is artificially created.

```
> # generating artificial sample C
> set.seed(43210)
```



```

> obs.C <- sample(nrow(silc.16), 200, replace=F)
> #
> X.vars <- c("hsize", "hsize6", "db040", "age", "c.age",
+           "rb090", "pb220a", "rb050")
> y.var <- c("pl030", "work")
> z.var <- c("netIncome", "c.netI")
> #
> aux.C <- silc.16[obs.C, c(X.vars, y.var, z.var)]
> aux.C$wwC <- aux.C$rb050/sum(aux.C$rb050)*round(sum(silc.16$rb050)) # rough w
> svy.aux.C <- svydesign(~1, weights=~wwC, data=aux.C)
> #
> # incomplete two-way estimation
> out.inc <- comb.samples(svy.A=out.hz$cal.A, svy.B=out.hz$cal.B,
+           svy.C=svy.aux.C, y.lab="work", z.lab="c.netI",
+           form.x=~c.age:rb090-1, estimation="incomplete")
> #
> addmargins(t(out.inc$yz.est))

```

	working	not working	Sum
(-6,0]	318.3646	7815.0325	8133.3971
(0,5]	3155.6684	2998.6577	6154.3261
(5,10]	3960.8064	5583.6483	9544.4547
(10,15]	4736.0014	7111.7742	11847.7756
(15,20]	9302.3226	3543.4539	12845.7765
(20,25]	6318.9931	2875.1457	9194.1388
(25,30]	4011.6435	562.1620	4573.8055
(30,40]	2587.8739	918.6047	3506.4786
(40,50]	900.9998	0.0000	900.9998
(50,200]	1101.8473	0.0000	1101.8473
Sum	36394.5210	31408.4790	67803.0000

```

> new.wwC <- weights(out.inc$cal.C) #new cal. weights for C
> #
> # marginal distributions of work
> m.work.cA <- xtabs(out.hz$weights.A~work, data=rec.A)
> m.work.cC <- xtabs(new.wwC~work, data=aux.C)
> m.work.cA-m.work.cC

```

work	working	not working
	0	0

```

> #
> # marginal distributions of c.netI
> m.cnetI.cB <- xtabs(out.hz$weights.B~c.netI, data=don.B)

```

```

> m.cnetI.cC <- xtabs(new.wwC~c.netI, data=aux.C)
> m.cnetI.cB-m.cnetI.cC

c.netI
      (-6,0]      (0,5]      (5,10]      (10,15]
7.275958e-12 -9.094947e-13  0.000000e+00  0.000000e+00
      (15,20]      (20,25]      (25,30]      (30,40]
0.000000e+00  0.000000e+00  9.094947e-13 -4.547474e-13
      (40,50]      (50,200]
1.136868e-13  2.273737e-13

> # joint distribution of the matching variables
> tt.A <- xtabs(out.hz$weights.A~rb090+c.age, data=rec.A)
> tt.B <- xtabs(out.hz$weights.B~rb090+c.age, data=don.B)
> tt.C <- xtabs(new.wwC~rb090+c.age, data=aux.C)
> (prop.table(tt.A)-prop.table(tt.B))*100

      c.age
rb090      [16,24]      (24,49]      (49,64]      (64,100]
male      0.000000e+00 -2.775558e-15 -1.387779e-15 -1.387779e-15
female    0.000000e+00  0.000000e+00  0.000000e+00  0.000000e+00

> (prop.table(tt.A)-prop.table(tt.C))*100

      c.age
rb090      [16,24]      (24,49]      (49,64]      (64,100]
male     -3.5559464 -0.6181224  1.4472383 -0.8255670
female    0.4223229  2.1410662 -0.3271726  1.3161809

> #distance tt.A-tt.C
> 1/2*sum(abs(prop.table(tt.A)-prop.table(tt.C)))

[1] 0.05326808

```

The incomplete two way stratification method estimates the table $Y \times Z$ from C by preserving the marginal distribution of Y and of Z estimated respectively from A and from B after the initial harmonization step; on the contrary, the joint distribution of the matching variables X_M (which is the basis of the harmonization step) is not preserved.

```

> # synthetic two-way estimation
> out.synt <- comb.samples(svy.A=out.hz$cal.A, svy.B=out.hz$cal.B,
+                          svy.C=svy.aux.C, y.lab="work", z.lab="c.netI",
+                          form.x=~c.age:rb090-1, estimation="synthetic")
> #
> addmargins(t(out.synt$yz.est))

```

	working	not working	Sum
(-6,0]	351.6488	7781.7483	8133.3971
(0,5]	3610.2537	2544.0724	6154.3261
(5,10]	4052.7261	5491.7286	9544.4547
(10,15]	5384.8795	6462.8961	11847.7756
(15,20]	8542.0337	4303.7428	12845.7765
(20,25]	5971.5562	3222.5826	9194.1388
(25,30]	3781.3214	792.4840	4573.8055
(30,40]	2697.2545	809.2241	3506.4786
(40,50]	900.9998	0.0000	900.9998
(50,200]	1101.8473	0.0000	1101.8473
Sum	36394.5210	31408.4790	67803.0000

```
> new.wwC <- weights(out.synt$cal.C) #new cal. weights for C
> #
> # marginal distributions of work
> m.work.cA <- xtabs(out.hz$weights.A~work, data=rec.A)
> m.work.cC <- xtabs(new.wwC~work, data=aux.C)
> m.work.cA-m.work.cC
```

```
work
      working  not working
5.093170e-11 1.818989e-11
```

```
> # marginal distributions of c.netI
> m.cnetI.cB <- xtabs(out.hz$weights.B~c.netI, data=don.B)
> m.cnetI.cC <- xtabs(new.wwC~c.netI, data=aux.C)
> m.cnetI.cB-m.cnetI.cC
```

```
c.netI
      (-6,0]      (0,5]      (5,10]      (10,15]      (15,20]
1.000444e-11 6.366463e-12 9.094947e-12 1.091394e-11 1.455192e-11
      (20,25]      (25,30]      (30,40]      (40,50]      (50,200]
1.091394e-11 4.547474e-12 3.183231e-12 1.477929e-12 1.136868e-12
```

```
> # joint distribution of the matching variables
> tt.A <- xtabs(out.hz$weights.A~rb090+c.age, data=rec.A)
> tt.B <- xtabs(out.hz$weights.B~rb090+c.age, data=don.B)
> tt.C <- xtabs(new.wwC~rb090+c.age, data=aux.C)
> (prop.table(tt.A)-prop.table(tt.B))*100
```

```
      c.age
rb090  [16,24]      (24,49]      (49,64]      (64,100]
male    0.000000e+00 -2.775558e-15 -1.387779e-15 -1.387779e-15
female  0.000000e+00  0.000000e+00  0.000000e+00  0.000000e+00
```

```

> (prop.table(tt.A)-prop.table(tt.C))*100

      c.age
rb090  [16,24]  (24,49]  (49,64]  (64,100]
  male  -3.5960278  0.4416849  1.8174918 -0.4384661
 female  0.4739651  0.0017933 -0.4987798  1.7983386

> #distance tt.A-tt.C
> 1/2*sum(abs(prop.table(tt.A)-prop.table(tt.C)))

[1] 0.04533274

```

6 Exploring uncertainty due to the statistical matching framework

When the objective of SM consists in estimating a parameter (macro approach) it is possible to tackle the problem in an alternative way consisting in the “exploration” of the uncertainty on the model chosen for (X_M, Y, Z) , due to the lack of knowledge typical of the basic SM framework (no auxiliary information is available). This approach does not end with a unique estimate of the unknown parameter characterizing the joint p.d.f. for (X_M, Y, Z) ; on the contrary it identifies an interval of plausible values for it. When dealing with categorical variables, the estimation of the intervals of plausible values for the probabilities in the table $Y \times Z$ are provided by the Fréchet bounds:

$$\max\{0; P(Y = j) + P(Z = k) - 1\} \leq P(Y = j, Z = k) \leq \min\{P(Y = j); P(Z = k)\}$$

for $j = 1, \dots, J$ and $k = 1, \dots, K$, being J and K the categories of Y and Z respectively.

If the X_M variables are introduced, by conditioning on them, it is possible to derive the following result (D’Orazio *et al.*, 2006a):

$$P_{j,k}^{(low)} \leq P(Y = j, Z = k) \leq P_{j,k}^{(up)}$$

with

$$\begin{aligned}
P_{j,k}^{(low)} &= \sum_i P(X_M = i) \max\{0; P(Y = j|X_M = i) + P(Z = k|X_M = i) - 1\} \\
P_{j,k}^{(up)} &= \sum_i P(X_M = i) \min\{P(Y = j|X_M = i); P(Z = k|X_M = i)\}
\end{aligned}$$

for $j = 1, \dots, J$ and $k = 1, \dots, K$.

In the SM basic framework, the probabilities $P(Y = j|X_M = i)$ are estimated from A , the $P(Z = k|X_M = i)$ are estimated from B while the marginal distribution $P(X_M = i)$ can be estimated indifferently on A or on B , assuming that both the samples, being

representative samples of the same population, provide not significantly different estimates of $P(X_M = i)$. If this is not the case, before computing the bounds it would be preferable to harmonize the distribution of the X_M variables in A and in B by using the function `harmonize.x`.

In **StatMatch** the Fréchet bounds for $P(Y = j, Z = k)$ ($j = 1, \dots, J$ and $k = 1, \dots, K$), conditioning or not on the X_M variables, are provided by `Frechet.bounds.cat`.

```
> #comparing joint distribution of the X_M variables in A and in B
> t.xA <- xtabs(wwA~c.age+rb090, data=rec.A)
> t.xB <- xtabs(wwB~c.age+rb090, data=don.B)
> prop.table(t.xA)-prop.table(t.xB)
```

	rb090		
c.age	male	female	
[16,24]	0.003661141	0.000891681	
(24,49]	0.010995148	-0.004970682	
(49,64]	-0.009456418	0.010772175	
(64,100]	-0.006383618	-0.005509426	

```
> #
> #computing tables needed by Frechet.bounds.cat
> t.xy <- xtabs(wwA~c.age+rb090+work, data=rec.A)
> t.xz <- xtabs(wwB~c.age+rb090+c.netI, data=don.B)
> out.fb <- Frechet.bounds.cat(tab.x=t.xA, tab.xy=t.xy, tab.xz=t.xz,
+                               print.f="data.frame")
> out.fb
```

	work	c.netI	low.u	low.cx	CIA
1	working	(-6,0]	0	0.0000000000	0.062451939
2	not working	(-6,0]	0	0.0130833912	0.058088772
3	working	(0,5]	0	0.0000000000	0.047854165
4	not working	(0,5]	0	0.0100349443	0.043450884
5	working	(5,10]	0	0.0000000000	0.065841680
6	not working	(5,10]	0	0.0325145796	0.074582323
7	working	(10,15]	0	0.0044505872	0.083877816
8	not working	(10,15]	0	0.0409858756	0.090285053
9	working	(15,20]	0	0.0315476801	0.106111106
10	not working	(15,20]	0	0.0330428837	0.083072522
11	working	(20,25]	0	0.0271769197	0.080524320
12	not working	(20,25]	0	0.0221981534	0.055298451
13	working	(25,30]	0	0.0035480015	0.042818593
14	not working	(25,30]	0	0.0058632580	0.024631748
15	working	(30,40]	0	0.0000000000	0.033456492
16	not working	(30,40]	0	0.0032094037	0.018254479
17	working	(40,50]	0	0.0000000000	0.008213067

18	not working	(40,50]	0	0.0001182705	0.005004024
19	working	(50,200]	0	0.0000000000	0.010221237
20	not working	(50,200]	0	0.0002598896	0.005961328
	up.cx	up.u			
1	0.10745732	0.11953297			
2	0.12054071	0.11953297			
3	0.08127010	0.09037855			
4	0.09130505	0.09037855			
5	0.10790942	0.14101622			
6	0.14042400	0.14101622			
7	0.13317699	0.17515499			
8	0.16971228	0.17515499			
9	0.15614074	0.18965562			
10	0.15763595	0.18965562			
11	0.11362462	0.13543995			
12	0.10864585	0.13543995			
13	0.06158708	0.06746229			
14	0.06390234	0.06746229			
15	0.04850157	0.05171910			
16	0.05171097	0.05171910			
17	0.01309882	0.01334022			
18	0.01321709	0.01334022			
19	0.01592268	0.01630008			
20	0.01618257	0.01630008			

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