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Guidelines for the Anonymization of Microdata Using R-package sdcMicro

(Version 1.0)

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1 About The Guidelines

These guidelines have the aim to give insights how to anonymise microdata using package `sdcMicro` [??]. This package includes a collection of methods but also a point-and-click interface is provided by the add-on package `sdcMicroGUI` [??]. These packages represent the standard and state-of-the-art library of statistical disclosure control methods for microdata anonymization, implemented in the statistical environment `R` [?].

The guidelines are written in a manner that they can be used by experts and subject matter specialists to anonymize their microdata as well as to provide tools that can easily be used. The style of the guidelines is therefore dedicated to subject matter specialists who are not necessarily experts in statistical disclosure control. We will try to point out the key-concepts that subject matter specialists should know when they intend to apply a specific method.

The software that is used in the guidelines provides easy-to-use functions that allow to apply complex statistical disclosure methods without the need of detailed programming skills of the users. Moreover, the application of the methods can be carried out by a point

and click interface [??] without having any knowledge in `R`.
In the guidelines, we will also list the name of the function of `sdcMicro` that can be used to apply a given method as well as we present the same application with the point and click interface of `sdcMicro`.

This guidelines are structured as follows.

In Section 2 we briefly introduce main concepts required to create anonymized microdata sets. These concepts include k-Anonymity (Section 3.2), concepts of measuring risk and data utility (Section 3), global recoding of variables (Section 4.3), local suppression (Section 4.4), post-randomization (Section 4.5), adding noise (Section 4.7) and microaggregation (Section 4.6). The methods are not mathematically defined and proven but explained in plain language so that profound mathematical knowledge is not required to catch the basic ideas of each concept. This will of course help subject matter specialists to learn about protecting microdata. For interested readers we also give references to papers in which specific methods are described in greater detail. General introductions are given, for example, in [????].

We continue to present the application of these concepts on real world data using `sdcMicro`. For this reason we use two different data sets that are decribed in Section 5.2. Detailed information of the FIES data that are used are listed in Section A.1, information about SES data are given in Section A.2. The practical application using the software is presented in Section 5. In this section we both show the code and the results required to achieve specific goals so that it is possible for everybody to reproduce the results and also to use this guidelines as a supportive paper when using `sdcMicro` to anonymize other microdata sets.

Finally, in Section 9 we give a short conclusion and summary.

The appendix contains additional information about the data used in this deliverable (Appendix A) and information about certain benchmarking indicators (Appendix B) used to evaluate the anonymised data.

2 Concepts to Proctect Microdata

A microdata file is defined as a data set of records/observations. For each observation or individual respondent a set of variables is available. In the following, these variables are splitted for the purpose of the application of statistical disclosure methods. For the application of those methods, a workflow characterise the possible usage on each stage of the process of anonymisation of microdata. After that, the software is described since we continuously showing the application of that software within the text. Subsequently, the concept of measuring the disclosure risk are discussed followed by describing the concepts to measure the information loss and data utility.

2.1 Categorization of Variables for SDC

It is possible to classify these variables into mainly 3 groups that are not neccessary disjunct.

- **Direct Identifiers:** Variables that definitely identify a statistical unit. An example would be the social insurance number.
- **key variables:** A set of variables that - when considered together - may be used to identify an individual unit. For example using gender, age, region, occupation together it may be very well possible to identify specific units. Other examples for (confidential) key variables could be income, health information or political preferences. For the description of the methods, it is advantageous to distinguish between categorical and continuous scaled key variables.
- **Non-confidential variables:** All variables that are not classified in any of the former two groups.

The goal of anonymizing a microdata set is to prevent that confidential information can be linked to a specific respondent.

2.2 Workflow

Figure 1 outlines the most common practice when applying a set and steps of actions to gain confidential data. These steps are motivated in the following:

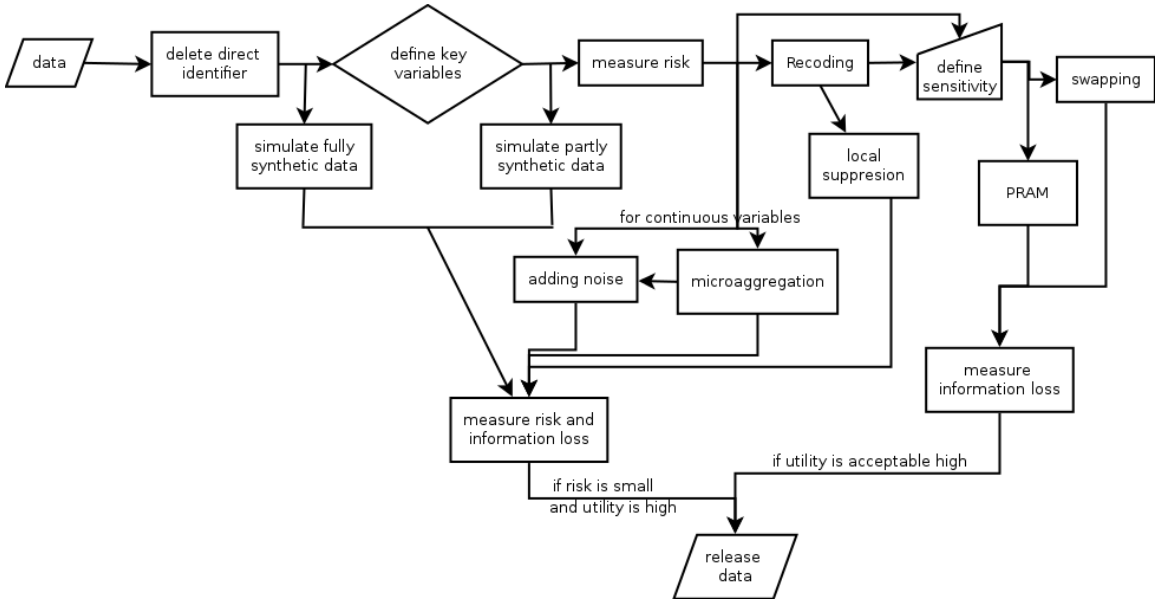


Figure 1: Workflow related to some of the possibilites for anonymising data using different techniques.

The following steps are included in Figure 1.

1. The first step must always be to remove all direct identification variables and variables that contain direct information on individuals (such as name, addresses or social insurance numbers) from the data set.

2. Secondly, the key variables have to be determined. Note that this decision is subjective and involves discussion with subject matter specialists as well as with the interpretation of the related (national) laws is often necessary. Please, see Section 5 for practical applications to define the key variables. Note that for the simulation of fully synthetic data, the choice of key variables is not necessary [**?**].

3. After the key variables have been selected, the disclosure risk have to be measured. This includes the analysis of the sample frequency counts as well as the application of probability methods to estimate the corresponding re-identification risk for each individual by taking the population frequencies into account, see Section 3 for details.

4. The observations with considerable high risk may then to be perturbed. For categorical key variables this can be done with recoding and local suppression, or with recoding and swapping or post randomization (pram). Note, that in principle, pram or swapping can also be applied without recoding the key variables but the swapping rate might be defined lower if recoding is applied first. The decision on the method is depended on the structure of the key variables. In general one can use recoding plus local suppression when the amount of unique combinations of the key variables is low, and pram when the number of key variables is large and the number of unique combinations is very high. For details, see Section 4.3, 4.5 and the practical application in Section 5.
   The values of continuous key variables has to be perturbed as well. Hereby, microaggragation is always a good choice (see Section 4.6).

5. After the data are perurbed, the information loss and the disclosure risk has to be estimated. The goal is to release a safe microdata set that has low risk of linking confidential information to individual respondents and that still has high data utility. If the risk is considerable low and the data utility is high, the anonymised data set is ready for release. If not, the whole process has to be repeated either with additional perturbations (when the risk is too high) or with actions that will increase the data utility. For details on issues related to the dependency of both the utility and the risk, see Section 4 and Figure 2 that is discussed afterwards.

2.2.1 Simulation of Synthetic Data

In addition, data can be also be simulated with the aim of producing synthetic close-to-reality data (see also Figure 1). Huge efforts are necessary to simulating synthetic data that are close-to-reality.

Simulation of population microdata is closely related to the field of *microsimulation* [e.g., **?**], which is a well-established methodology within the social sciences, although the aims are quite different. Microsimulation models attempt to reproduce the behavior of individual units such as persons, households or firms over the course of many years for policy analysis purposes. Hence they are highly complex and time-consuming. Survey statisticians, on the other hand, need synthetic populations as a basis for extensive simulation studies on the behavior of their statistical methods.

An alternative approach for the generation of synthetic data sets is discussed by **?**]. He addresses the confidentiality problem connected with the release of publicly available

microdata and proposes the generation of fully synthetic microdata sets (all variables are generated synthetically) using multiple imputation. **?**], **?**] and **?**] discuss this approach in more detail as well as the concept of simulating only the key variables (partly synthetic data).

The generation of synthetic microdata for selected surveys is described by **?**] and **?**], and is further developed by **?**]. Here, a very low number of basic categorical variables are generated at the first stage by random draws from the actual survey data, using the sample weights as probability weights. Additional categorical and continuous variables are estimated with models obtained from the actual survey data. In particular, the generation of continuous variables also involves random draws from certain probability distributions or adding random error terms. Since the sample weights are considered, on average m-anonymity (see the definition of k-anonymity in Section 3.2) is provided, where m denotes the smallest sampling weight. The disclosure risk is thereby very low, because m is usually high for household surveys [for details, see, **?**]. Even if re-identification were successful, the corresponding observations consist of synthetically generated values, thus rendering such a re-identification useless.

The drawback to simulate synthetic data is that it is highly ressource-intensive from highly specialised researchers and that researchers and users often feel not comfortable when they should deal with synthetic and not real data. Because of both disadvantages, these methods are not further discussed, but we mention the `simPopulation` [**?**] `R`-package that can be used to create synthetic data. We also note that the Structural Earnings Data that are used in this guidelines are created with this package. For the methods used, we refer to **?**].

2.2.2 Remote Access and Remote Execution

Remote access facilities provide a flexible way to limit disclosure, i.e., simulations with disclosive population data are performed on the data holders' server using a secure connection, but the data itself cannot be downloaded. However, this approach is not applicable in most countries due to legal restrictions. With *remote execution*, on the other hand, it is possible to carry out simulations without having direct access to the data, i.e., the user sends the code to the data holders, who apply it to the disclosive data. Confidential results are then returned to the user. This is not a preferable approach, though, since no model should be applied without any possibility to explore the raw data in detail first. In addition, such a procedure can be highly time-consuming for the data holders. Therefore, often close-to-reality synthetic data are produced so that the users of the data can fit their models on that synthetic data first, but for final computations, the developed code is run by the data holders stuff on the disclosive original data.

2.3 Risk Versus Data Utility

As mentioned before, the goal is to release a safe microdata set that has low risk of linking confidential information to individual respondents and that still has high data utility.

Figure 2 shows a typical situation. Here, data (the SES data in Section A.2) have been perturbed by using one specific method with different parameter values, going from 10 (small perturbation) to 100 (perturbation is ten times higher). By using 100, the disclosure risk is low (since the data are heavily perturbed), but the information loss is

very high, i.e. the data utiltiy is low. Having a low perturbation, the risk and the data utility is high. In any case, best is to have a method that gives you low risk and high data utility, that is the region in the lower left area of the figure.

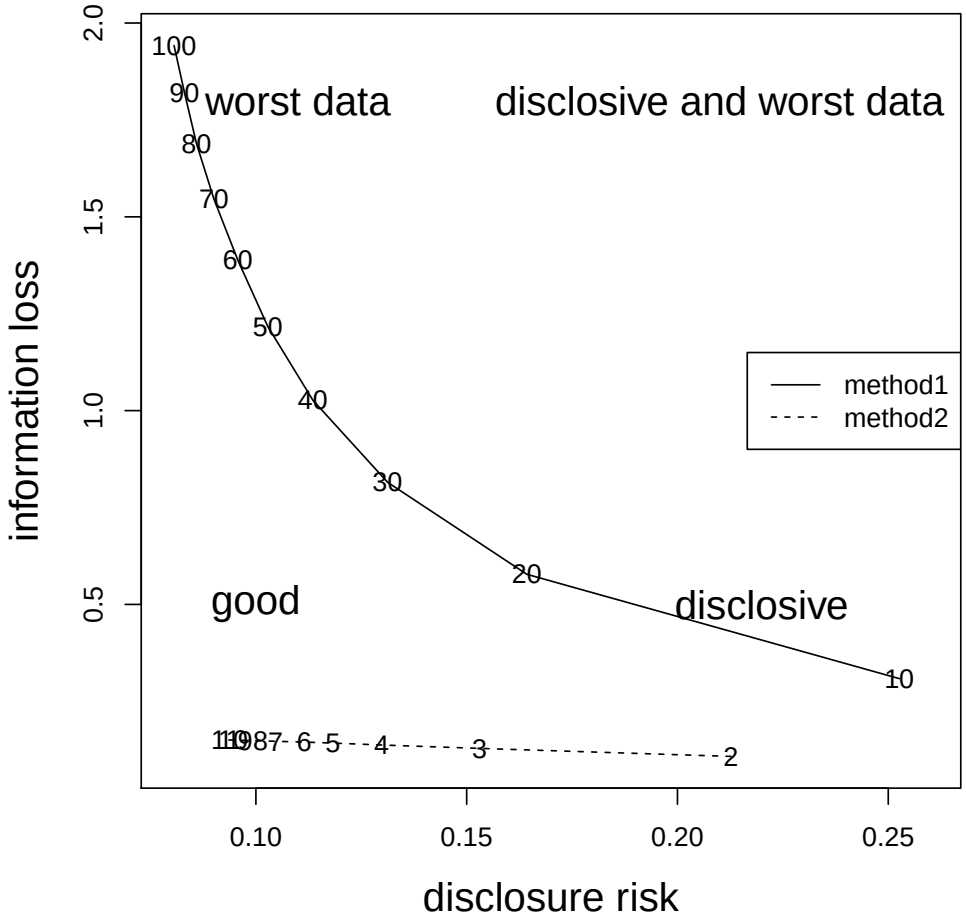


Figure 2: Risk versus information loss obtained for one specific perturbation method applied on the SES data.

This is not always possible and therefore the data anonymisation specialist have to make some decisions:

1. What is the legal situation regarding data privacy?
2. How sensitive is the information of the data and who will get the anonymised data file?
3. Which method is suitable for which purpose?

ad 1) Laws on privacy varying between countries. Some countries have quite restricitive laws on data privacy, some not. Laws in one country are often different for different kind of data (business statistics, labour force statistics, social statistics, mediacal data, etc.).

ad 2) Usually, laws consider two different kind of data users: users form universities and other research organisations or general users - the public. In the first case, often special contracts are signed between the data users and the data holders. Usually, these contracts explicitely forbits the use of the data outside a reasearch project and with the condition to save the data on a save place. For these kind of users, the anonymised data are called *scientific use file*, whereas data for the public are typically named *public use file*. Of course, the disclosure risk of a public use file should be very low, and lower as for scientific use files, whereas for scientific use files the data utility is typically higher than for public use files.
Another aspect is how sensitive is the information. Data on medical treatment of people might be more sensitiv than turnover and number of employees from establishments. If the data include very sensitive information, the data should also be protected more than data having low benefits by dislosure the information.

ad 3) The application of some specific methods result in low disclosure risk and large information loss, other methods may provide data with reasonable high disclosure risk. Other methods, like swapping or post randomisation, may provide high or low dislosure risk and data utility, depending on the parameter choice. However, defining a swapping rate might be fixed by a data lawyer, because the definition of disclosure risk when swapping values from, for example, every 7th observation can hereby only be fixed by an expertise in data privacy laws and might be heavly depend on the data, on national laws on privacy and the target user group.

2.4 The sdcMicro Package

For each method explained we additionally show it's usage in software for both, via command line and via point and click interface. Therefore, a small introduction to the package is given before the methods are explained.

In the last years, the statistical software environment `R` [**?**] (for short: `R`) gets more and more popular. Nowadays `R` has more users than any other statistical software[1], and `R` has got the standard statistical software for data analysis and graphics. For statisticians it has become the major programming language in its field.

The first version, version 1.0.0 of the `sdcMicro` package was realeased in 2007 on the comprehensive `R` archive network (CRAN, http://cran.r-project.org). The current release, version 3.0.0, is a huge step forward. Almost all methods have been written in `C` or do call `C++` code, so the performace in terms of computational speed is fine. For the latter one, the International Household Survey Network (IHSN) provided code for that, which is now integrated in `sdcMicro`.

Integrating IHSN `C++` code into `R` have several benefits, some of which are listed below:

- code written by IHSN can be used within a free and open-source statistical software environment.

[1] See, for example, http://www.tiobe.com/index.php/content/paperinfo/tpci/index.html, where `R` entered the top 20 of all programming software in January 2012. `SAS` is ranked on place 32.

- The methods are provided within the most popular statistical software
- The integration of C++ code allows fast computations in R.
- sdcMicro is a collection of microdata protection methods and thereby easily called.

After installing and starting R, the index of methods that are available in the package sdcMicro can be called by using the **help** function as shown in Listing 2. The package description shows a summary information about the package, see also Listing 1.

```
1 packageDescription("sdcMicro")
```

Listing 1: Accessing the index file to list the available methods in sdcMicro.

```
Package: sdcMicro
Type: Package
Title: Statistical Disclosure Control methods for the generation of
        public- and scientific-use files.
Version: 3.0.0
Date: 2012-01-30
Author: Matthias Templ, Alexander Kowarik, Bernhard Meindl
Maintainer: Matthias Templ <matthias.templ@gmail.com>
Description: Data from statistical agencies and other institutions are
        mostly confidential. This package can be used for the
        generation of anonymized (micro)data, i.e. for the generation
        of public- and scientific-use files. The package includes also
        a graphical user interface.
Depends: R (>= 2.10), robustbase, Rcpp, car, cluster, MASS, e1071,tcltk
Imports: car, robustbase, cluster, MASS, e1071, Rcpp
License: GPL-2
Packaged: 2012-01-27 16:46:04 UTC; alex
Repository: CRAN
Date/Publication: 2012-01-28 09:12:58
Built: R 2.15.0; universal-apple-darwin9.8.0; 2012-02-14 23:39:28 UTC;
        unix

-- File: /Library/Frameworks/R.framework/Versions/2.15/Resources/library/sdcMicro/Meta
```

One should also note that for each of the methods that has been implemented in sdcMicro, a help file is available that not only describes all possible parameters that can be changed but that also features a simple, working example that can directly be copied into R. The help files for a given function can be accessed by calling an R-function with a ? directly before the function name. An example is given in Listing 2.

```
1 help(package=sdcMicro)    ## index of methods
2 ?microaggregation         ## same as help("microaggregation")
```

Listing 2: Accessing the index of methods and the help file for function 'microaggregation' of sdcMicro.

sdcMicro also features a so called vignette - a manual that is available in pdf-format. Such vignettes give a good overview of the capabilities of the software package. The vignettes contained in R package sdcMicro can be opened using the code listed in Lising 3. The first vignette contains a earlier report on sdcMicro. The second one represents always the newest version of these guidelines. In the third vignette some information about the integration of the IHSN C++ code in sdcMicro and testing of methods in terms of computational speed is integrated. The latter two vignettes are included in sdcMicro from version 3.1.2 onwards.

```
vignette("sdcMicroPaper")
vignette("sdcMicroGuideSDC")
vignette("sdcMicroTesting")
```

Listing 3: Accessing the package vignettes of sdcMicro.

2.5 The Point and Click Graphical User Interface of sdcMicro

Almost all calculations can also be done using the graphical user interface (GUI) of sdcMicro - available at CRAN as the sdcMicroGUI R-package [??]. The development of the new version of this GUI was funded by Google and by IHSN.

This GUI serves as an easy-to-handle tool for users who want to use the sdcMicro package for statistical disclosure control but are not familiar with the native R command line interface. In addition to that, interactions between objects that result from the anonymization process are provided within this GUI. This allows an automated recalculation and display of frequency counts, individual risk, information loss and data utility after each anonymization step. Furthermore, the code of every anonymization step carried out within the GUI is saved in a script, which can easily be modified and re-used. Therefore, the GUI also allows reproducibility of any result.

The GUI can be installed within R and called by

```
install.packages("sdcMicroGUI")
library(sdcMicroGUI)
```

Listing 4: The graphical user interface of sdcMicro.

The GUI provides full functionality of the main functions of sdcMicro and offers some more features to the users, for example:

- comprehensive overview of the main functions and their output
- facilities to rename and regroup categories and to change values of a variable
- automated recalculation of frequencies and individual risk after each step
- display of the output of the frequency and risk estimation interactively within the GUI
- recording of the code and the selected values after each step
- possibility to save/load/edit a script for later re-use (reprocuible results!)

- (R specific) no need to manually re-assign computed data to a data frame
- simplified load / save data option

For the basic description of the GUI, please have a look at the publication, which is available online for free, see **?**]. Note, that the current version of the GUI includes more methods and the interaction with the data is revisited.

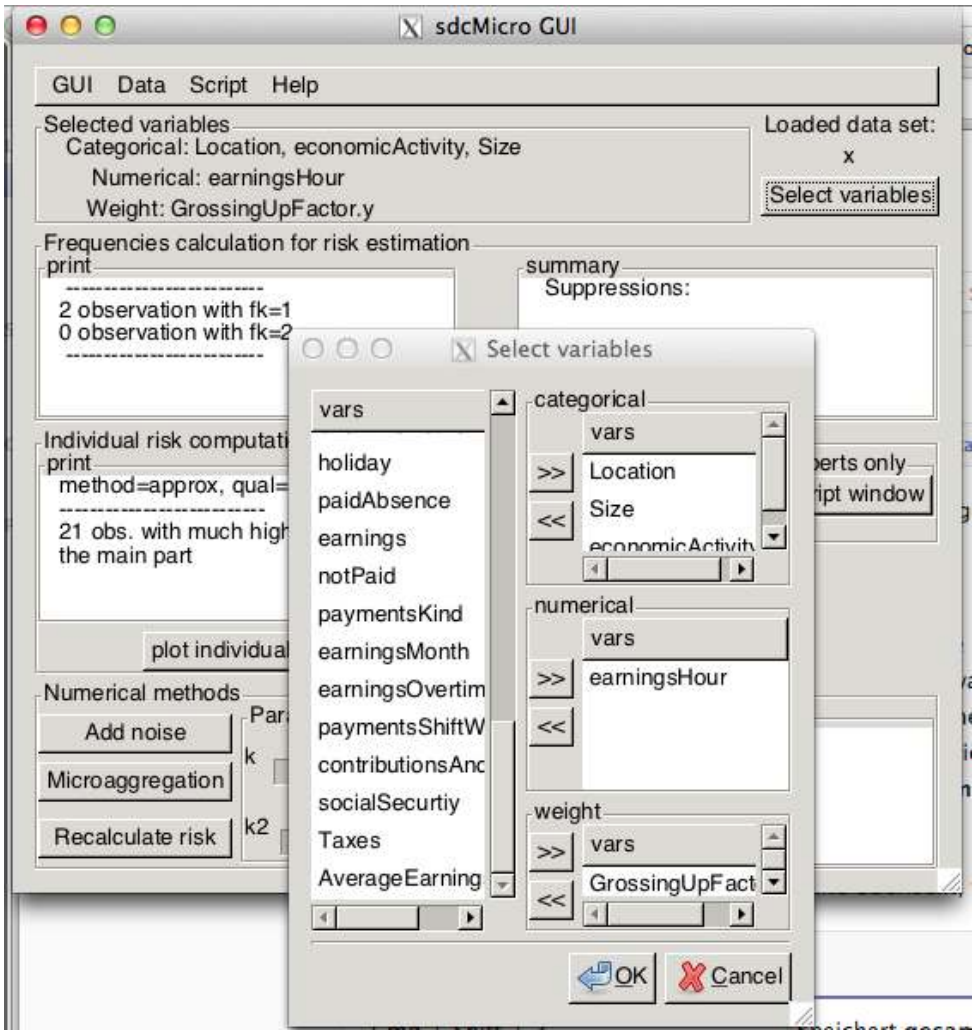


Figure 3: NEUER SCREENSCHOT! The variable selection menu of the GUI. Here, some variables for the SES data are selected.

Figure 3 shows a screenshot of the GUI and it's variable selection menu.

3 Measuring disclosure risk

Measuring risk in an microdata set is of course of great concern when having to decide on wheter a microdata set is safe to be released. To be able to assess the disclosure risk it is required to make realistic assumptions on the information data users might have at hand

to match against the microdata set. This assumptions are called 'disclosure risk scenarios'. Based on a disclosure risk scenario one must define a set of identifying variables (key variables) that can be used as input for the risk evaluation procedure.

Typically risk evaluation is based on the concept of "rareness/uniqueness" in the sample and/or in the population. The interest is on units/individuals/observations that possess rare combinations of key variables. Those can be assumed to be identified easier and thus have higher risk. It is possible to cross tabulate all identifying variables and have a look at its cast. Patterns[2] with only very few individuals are in this sense considered risky. It is also by definition that all units with the same values in the key variables have the same risk-value.

3.1 Frequencies Counts

Let us define the frequency counts also in a mathematical notation. Consider a random sample of size n drawn from a finite population of size N. Let $\pi_j, j = 1, \ldots, N$ be the (first order) inclusion probabilities, i.e. the probability that the element u_j of a population of the size N is chosen in a sample of the size n.

All possible combinations of categories in the key variables $X_1, \ldots, X_m$ can be calculated by cross tabulation of these categorical variables. Let $f_i, i = 1, \ldots, n$ be the frequency counts obtained by cross tabulation and let F_i be the frequency counts of the population which belong to the same category. If $f_i = 1$ applies the corresponding observation is unique in the sample. If $F_i = 1$ applies then the observation is unique in the population. Note that F_i is usually unknown since in statistics usually information on samples is collected and only few information about the population is known from registers and/or external sources - we will outline how to deal with population frequency counts in Section 3.5 but show the basic estimation now in the example in Listing 5. Here, a small example data set is loaded and the basic function for calculating sample frequencies - **freqCalc**() - is applied. One can easily see, that observation 1 and 8 are equal and the sample frequency count is two. The estimated population frequencies are obtained by summing up the sample weights for equal observations. Here, the values of observation 1 and 8 are equal in the underlying key variables, for example. Thus the sample frequency counts are $f_1 = 2$ and $f_8 = 2$. The frequency in the population $\hat{F}_1$ and $\hat{F}_8$ can be estimated with the sum of their sampling weights, w_1 and w_8, which equals to 110. Hence, two observations with the pattern $(1, 2, 5, 1)$ exist in the sample and 110 observations with these entities can be expected to exist in the population.

```
require(sdcMicro)
data(francdat)
x <- francdat[,c(2,4,5,6,8)]
ff <- freqCalc(x, keyVars=1:4, w=5)
print(cbind(x, ff$fk, ff$Fk))
  Key1 Key2 Key3 Key4     w ff$fk ff$Fk
1    1    2    5    1  18.0     2 110.0
```

[2] a pattern is defined as a specific combination of values of all key variables

```
2   1   2   1   1   45.5   2   84.5
3   1   2   1   1   39.0   2   84.5
4   3   3   1   5   17.0   1   17.0
5   4   3   1   4  541.0   1  541.0
6   4   3   1   1    8.0   1    8.0
7   6   2   1   5    5.0   1    5.0
8   1   2   5   1   92.0   2  110.0
```

Listing 5: Example for sample and estimated population frequency counts.

freqCalc() includes basically three parameters which could be displayed in `R` either using

```
args(freqCalc)
  function (x, keyVars = 1:3, w = 4, ...)
```

Listing 6: Displaying the arguments of function `freqCalc()`.

or typing `?freqCalc` which displays the whole help file. `x` is an object of class data.frame or matrix, `keyVars` is a vector specifying the column index of the key variables and `w` defines the column index of the weight variable. The resulting output of the function are the frequency counts of the sample and the estimated frequency counts of the population. Note that by using the point and click interface of `sdcMicro`, the `sdcMicroGUI`, the frequencies are calculated automatically at every step of the anonymisation process.

3.2 The k-Anonymity Concept

Based on a set of key variables a desired characteristic of a protected microdata set might be to achieve the concept of k-anonymity [**??**]. This means that each possible combination of the values of the key variables features at least k units in the microdata, meaning that all $f_i \geq 3$, $i = 1, ..., n$. A typical value is $k = 3$.

k-anonymity is typically achieved by recoding categorical key variables (see Section 4.3) and by additionally suppressing specific values in the key variables of individual units (Section 4.4).

For local suppression, function **localSuppression**() to accomplish k-anonymity can be used. Hereby, a heuristic algorithm is called to suppress as few values as possible. Provided as a function argument, it is possible to specify a desired ordering of key variables which the algorithm takes into account when performing the local suppression. One could even specify key variables that are considered of such importance that almost no values in these variables are suppressed. All functions can also be used by point and click in the `sdcMicroGUI`.

3.3 l-Diversity

An extension of k-anonymity is l-diversity [**?**]. Consider for one group of observations with the same pattern in the key variables and let the group fulfil k-anonymity. A possible data intruder can therefore not identify an individual in this group. However, if all

observations have the same entries in a sensitive variable (such as *cancer* in the variable *medical diagnosis*) then the attack is successful anyway. For example, with the knowledge that one individual is in the group - say the individual's name is Carl Carlson - then you know that Carl has cancer with certainty if all members in that group have cancer. The distribution of the target sensitive variable is refered to as l-diversity.

```
x <- data.frame(key1=c(1,1,1,1,2,2), key2=c(1,1,1,2,2,2), sens1=
    c(50,50,42,42,62,62))
ff <- freqCalc(x, keyVars=1:2, w=NULL)
div <- measure_risk(x, keyVars=c("key1","key2"), ldiv_index="
    sens1")
cbind(x, ff$fk, div$ldiv[,1])
  key1 key2 sens1 ff$fk sens1_Distinct_Ldiversity
1    1    1    50     3                        2
2    1    1    50     3                        2
3    1    1    42     3                        2
4    1    2    42     1                        1
5    2    2    62     2                        1
6    2    2    62     2                        1
```

Listing 7: k-anonymity and l-diversity.

In Listing 7 we consider a small example data set that should highlight the calculations related to get the l-diversity. It also points out the (slight) difference to k-anonymity. In the first two columns the categorical key variables are present. The third column of `x` defines a variable containing sensitive information. The sample frequency counts have been calculated and present in the fourth column. They are equal 3 for the first three observations, the fourth observation is unique and for the last two observations, the frequency counts are 2. Only observation four violates 2-anonymity. When having a closer look at the first three observations we see that only two different values are present in the sensitive variable, so the l-(distinct)-diversity is just 2. For the last two observations, k-anonymity is achieved but still the intruder knows the exact information of the sensitive variable . However, the l-diversity is 1 indicating that the sensitive information can be disclosed, since all values are equal in the sensitive variable ($= 62$).

The difference in values in the sensitive variable can be measured in different ways - here we presented only the distinct diversity that measures how many different observations are present in a group. Other methods are implemented for l-diversity in `sdcMicro` (entropy, recursive, multi-recursive) as well, see the help manual of the package for further information.

3.4 Considering Sample Frequencies on Subsets: SUDA

SUDA (**S**pecial **U**niques **D**etection **A**lgorithm) estimates a disclosure risk for each individual. SUDA2 [see, e.g., **?**] is a recursive algorithm for finding Minimal Sample Uniques. The algorithm generates all possible variable subsets of defined categorical key variables and scans them for unique patterns in the subsets of variables. The risk of an observation is then dependend on two aspects.

(a) The lower the amount of variables needed to receive uniqueness, the higher the risk (and the higher the *suda score*) of the corresponding observation.

(b) The larger the number of minimal sample uniquenes contained within an observation, the higher the risk of the observation.

(a) is calculated for each observation i by $l_i = \prod_{k=MSUmin_i}^{m-1}(m-k) \quad , i = 1, ..., n$, for m the *depth* (the maximum size of variable subsets of the key variables), $MSUmin_i$ the number of minimal uniques of observation i and n the number of observations of the data set. Since each observation is treated independently, the l_i that belongs to one pattern are summed up to result in a common suda score for each of the observation belonging to this pattern (this summation is the contriubtion of (b)).

To result in the final SUDA score, the suda score are normalized due division by $p!$, with p being the number of key variables.

To receive the so called DIS score, loosely speaking, an iterative algorithm based on sampling of the data and matching of subsets of the sampled data with the orginal data is applied, whereas the probilities of correct matches given unique matches are calculated. In fact, it is out of scope to exactly describe the algorithm but we refer to **?**] for details. The DIS suda score is then calculated from the suda and the DIS scores (in `sdcMicro` `disScore`).

Note that this method does also not consider population frequencies in general but consider sample frequencies on subsets. The dis sudo scores somehow approximately consider based on the sample information - population uniqueness by simulation, but - to our knowledge - in generally it do not consider sampling weights and biased estimates may therefore result.

```
1  data(francdat)
2  x <- francdat[,c(2,4,5,6,8)]
3  ff <- freqCalc(x, keyVars=1:4, w=5)
4  s <- suda2(francdat, variables=1:4)
5  cbind(x[,1:4], ff$fk, s$score, s$disScore)
6    Key1 Key2 Key3 Key4 ff$fk s$score  s$disScore
7  1    1    2    5    1     2    0.00 0.000000000
8  2    1    2    1    1     2    0.00 0.000000000
9  3    1    2    1    1     2    0.00 0.000000000
10 4    3    3    1    5     1    3.50 0.016380722
11 5    4    3    1    4     1    0.00 0.000000000
12 6    4    3    1    1     1    0.00 0.000000000
13 7    6    2    1    5     1    1.75 0.007196697
14 8    1    2    5    1     2    0.00 0.000000000
```

Listing 8: Example showing how to estimate suda scores.

In Listing 8 again the example data set already used in Section 3.1 is used and the frequency counts but also the suda and dis suda scores are calculated. The suda scores are largest for observation 4 since also subsets of observation four are unique, while for observation five and six, not any subset is unique.

Suda, in fact suda2 [SUDA2, **?**], is implemented in `sdcMicro` (function **suda2**()) based on `C++` code from the IHSN.

Additional output, like the contribution percentage of each variable to the score, is also valued as function output. The contribution to the suda score is simple calculated by looking how often a category of a key variable contributes to the score.

3.5 Considering Population Frequencies - The Individual Risk Approach

To define if an individual unit is at risk, typically a threshold approach is used. If the invidual risk of reidentification for an individual is above a certain threshold value, the unit is said to be at risk. To calculate the individual risks it is neccessary to estimate the frequency of a given key in the population. In the previous section, Section 3.1, the population frequencies are already estimated. However, one can show that these estimates almost always overestimate small population frequency counts [**?**, details can be found in] and should not be used to estimate the disclosure risk.

A better approach is to use so called superpopulation models (the population frequency counts are modelled by a certain distribution). The whole estimation procedure of sample counts given the population counts can be modeled, for example, by using a Negative Binomial distribution [see, e.g., **?**] and is implemented in `sdcMicro` in function measure_risk() [for details, see **?**], and, of course, it can be called within the point and click GUI.

In Listing 9 all concepts are applied once again - the frequency count estimation on sample and population level (sum of the weights for each group), the l-diversity, the suda algorithm and the individual risk estimation. One can see that the individual risk is low for observation five, for example, since the sampling weight is quite high and therefore one may expect no population uniqueness. On the other hand, the individual risk is especially high for sample uniqueness in combination with small sampling weights, i.e. the inclusion probability of each individual is respected when estimating the individual risk.

```
1  data(francdat)
2  x <- francdat[,c(2,4,5,6,1,8)]
3  ff <- freqCalc(x, keyVars=1:4, w=6) # frequencies
4  div <- measure_risk(x, keyVars=1:4, ldiv_index=5,w=6)
5  s <- suda2(francdat, variables=1:4) # suda
6  cbind(x, freqS=ff$fk, freqP=ff$Fk, ldiv=div$ldiv[,1], suda=s$
       score, indivR=round(indivRisk(ff)$rk,3))
7    Key1 Key2 Key3 Key4 Num1     w freqS freqP ldiv suda indivR
8  1    1    2    5    1 0.30  18.0     2 110.0    0 0.00  0.017
9  2    1    2    1    1 0.12  45.5     2  84.5    0 0.00  0.022
10 3    1    2    1    1 0.18  39.0     2  84.5    0 0.00  0.022
11 4    3    3    1    5 1.90  17.0     1  17.0    0 3.50  0.177
12 5    4    3    1    4 1.00 541.0     1 541.0    0 0.00  0.011
13 6    4    3    1    1 1.00   8.0     1   8.0    0 0.00  0.297
14 7    6    2    1    5 0.10   5.0     1   5.0    0 1.75  0.402
15 8    1    2    5    1 0.15  92.0     2 110.0    0 0.00  0.017
```

Listing 9: Estimating the risk.

3.6 Measuring the Global Risk

Although the individiual risk have to be respected since a data intruder should not be able to identify individuals, often also a measure of the global risk is estimated in order to have one number that expresses the risk of the whole data set.

3.6.1 Measuring the Global Risk Based on the Individual Risks

The first approach is to determine a threshold for the individiual risk and to calculate the percentage of individuals that have larger individual risk than this threshold. The output can be seen in Listing 11.

```
data(francdat)
x <- francdat[,c(2,4,5,6,1,8)]
ff <- freqCalc(x, keyVars=1:4, w=6) # frequencies
(measure_risk(x, keyVars=1:4, w=6, max_global_risk = 0.1))

3 obs. with much higher risk than the main part
Expected no. of re-identifications:
 0.97 ( 12.08 %)
Threshold: 0.18
 (for maximal global risk 0.1 )
```

Listing 10: Estimating the global risk.

3.6.2 Measuring the Risk Using Log-Linear Models

The sample frequencies, considered for each of M patterns m, f_m , $m = 1, ..., M$ can be modeled by a Poisson distribution, and the global risk may be defined as [see **?**]

$$\tau_1 = \sum_{m=1}^{M} \exp\left(-\frac{\mu_m(1-\pi_m)}{\pi_m}\right) \quad \mu_m = \pi_m \lambda_m \quad . \tag{1}$$

For simplicity, the inclusion probabilities are assumed to be equal, $\pi_m = \pi$, $m = 1, ..., M$. τ_1 can be estimated by log-linear models including the main effects and possible interactions. The model is

$$\log(\pi_m \lambda_m) = \log(\mu_m) = \mathbf{x}_m \beta \quad .$$

To estimate the μ_m's, the regression coefficients β have to be estimated, for example by the iterative proportional fitting approach that is used in function **LLmodGlobalRisk**().

4 Measuring data utility

Of couse it is also of great interest to measure the data utility of the microdata set after disclosure limitation methods have been applied.

4.1 General Applicable Methods

Anonymized data should have the same structure of the original data and should allow any analysis with high precision.

To evaluate the precision, the estimation of different classical estimates like means and covariances are in focus. Using **dUtility**() it is possible to calculate several different measures on continuous scaled variables that are based on classical or robust distances. These estimates are computed for the original data and the perturbed data and they are finaly compared with the estimates on the original data.

For evaluating the multivariate structure of perturbed data, comparisons based on eigenvalues and robust eigenvalues can be also made with function **dUtility**().

4.2 Specific Tools

In practice it is not possible to create an anonymized file that have exactly the same structure as the orginal file in every sense. However, the difference between estimations with anonymized and original data of the **most important statistics** should be very small or even zero. This approach is therefore to measure the data utility based on benchmarking indicators [**??**] and is a more serious approach than applying general tools.

The first step in assessing quality is to decide on a set of benchmarking indicators. In order to do so, one has to evaluate what the users of the underlying data are analysing and report on the most important estimates. These estimators are often called *benchmarking indicators* [see, e.g., **??**]. Special emphasis should be put on benchmarking indicators with respect to the most important variables but also to the most sensible variables within the micro data set.

The general procedure is quite simple and can be described in the following steps:

- Selection of a set of benchmarking indicators
- Choice of a set of criteria on how to compare indicators
- Calculation of all benchmarking indicators on the original, unmodified micro data set
- Calculation of the benchmarking indicators on the protected micro data set
- Comparison of statistical properties such as point estimates, variances or overlaps in confidence intervals for each benchmarking indicator
- Assessment if the data utility of the protected micro data set is good enough to be used by researchers

If the quality assessment in the last step of the sketched algorithm is positive, the anonymized micro data set may be published. If the deviations of the main indicators calculated from the original and the protected data are too large one should restart the anonymization procedure and either modify selected parameters or completely change the anonymization process.

Usually the evaluation is focused on the properties of numeric variables given unmodified and modified micro data. However, it is of course also possible to have a look at the impact of local suppression or recoding that has been conducted to reduce individual reidentification risks.

Another possibility to evaluate the data utility of numerical variables is to define a model that is fitted on the original, unmodified microdata. The main idea is to predict important, sensitive variables using this model both for the original and the protected micro data set in a first step. In a second step, statistical properties of the model results, such as the differences in point-estimates or variances are compared for the predictions given original and modified micro data, are compared and the resulting quality is assessed. If the deviations are small enough one may go on to publish the safe and protected micro data set. Otherweise adjustments in the protection procedure need to be done.

Also, it is interesting to evaluate the set of benchmarking indicators not only for the entire data set but also for some domains. In this case the data set is partitioned into a set of h groups. The evaulation of benchmarking indicators is then performed for each of the h groups and results are evaluated by looking at differences between indicators for original and modified data in each group.

In this report, Appendix B gives a detailed description on the benchmarking indicators for the data used in this report. For the detailed application to real data and discussion theirein, see Section 7.

4.3 Recoding

Recoding is a non-perturbative method that can be applied to both categorical and continous variables. If global recoding is applied to a categorical variable the main idea is to combine several categories into a new, less informative category. When the method is applied to a continous variable it means to discretize the variable. The main idea is in both cases to reduce the total number of possible outcomes of the variable under consideration. Typically, recoding is applied to categorical variables where it is possible to reduce the number of categories with a small number of observations (extreme categories).

A special case of global recoding is 'top and bottom coding' which can be applied to ordinal and categorical variables. The main idea for this approach is to combine all values above (top-coding) and/or below (bottom-coding) pre-specified threshold values into a new category.

Function **globalRecode**() can be applied in `sdcMicro` to perform global recoding and also top/bottom coding. The help file with some examples is accessible using ? **globalRecode**. Note, that a more user-friendly version of global recoding can be applied using the graphical user interface of `sdcMicro`.

4.4 Local Suppression

Local suppression is a non-perturbative method that is typically applied to categorical variables. The key-idea is to suppress certain values of one or more variables. Typically the input variables are part of the defined set of key variables that are used for risk-

calculations as it was described in 3. Individual values are suppressed in a way that the set of variables aggreeing on a specific combination of values of key variables are increased. Local suppression is often used to achieve the goal of k-Anonymity as described in Section 3.2.

Using function **localSupp**() of `sdcMicro` it is possible to suppress the values of a key-variable for all those individual units for which the calculated individual risk of reidentification given a disclosure risk scenario is above a threshold. This is somehow a manual method.

For automatically suppress a minimum amount of values in the key variables to achieve k-anonymity, function **localSuppression**() can be used.

```
data(francdat)
## Local Suppression
localS <- localSuppression(francdat, keyVar=c(4,5,6))
localS
 ----------------------------------
[1] "Total Suppressions in the key variables -2"
[1] "Number of suppressions in the key variables "

 0 0 2
 ----------------
[1] "2-anonymity == TRUE"
 ----------------------------------
```

Listing 11: Local Suppression to achieve k-anonymity.

Note that the importance of variables can be specified as a parameter in function **localSuppression**(), aiming that some variables might be prefered for suppression while in some variables should only a minimum of suppression been done to achieve k-anonymity for all key variables.

4.5 Post-Randomization

Post-Randomization (equivalently referred to as PRAM) [**?**] is a perturbative, probabilistic method that can be applied to categorical variables. The key idea is that the values of a categorical variable in the original microdata file are changed into other categories with respect to a pre-defined transition probabilities. This process is usually modeled using a known transition matrix in which for each possible category of a categorical variable a probabilty for each transition to another category is specified. A simplified example would be to have a varibles with three categories/classes, A1, A2 and A3. The transition of a value from category A1 to category is, for example, fixed at 0.15, meaning with probability $p_1 = 0.85$ a value is not changed from A1 to A2. A value changed to A2 is fixed with probability $p_2 = 0.1$ and changed to A3 with $p_3 = 0.05$. Also probabilites to change values from class A2 to the other classes and for A3, respectively, have to be fixed. This is stored in a matrix of such transition probability which is the main input to function **pram**() in `sdcMicro`. This above mentioned example is used in Listing 12 whereas the default parameters of **pram**() are used. One can see that one value changed the category.

```
set.seed(1234)
A <- as.factor(rep(c("A1","A2","A3"), each=5))
A
 [1] A1 A1 A1 A1 A1 A2 A2 A2 A2 A2 A3 A3 A3 A3 A3
Levels: A1 A2 A3
Apramed <- pram(A)
Apramed
...
 Parameters for PRAM:
 alpha =  0.5
 minimum diagonal element =  0.8

summary(Apramed)
 ------------------------------
 original frequencies:
A1 A2 A3
 5  5  5
 ------------------------------
 frequencies after perturbation:
A1 A2 A3
 6  4  5
 ------------------------------
 transitions:
  transition Frequency
1     1 --> 1         5
2     2 --> 1         1
3     2 --> 2         4
4     3 --> 3         5
```

Listing 12: Example for pram.

PRAM is applied to each observation independently and the procedure is random, meaning that without setting a seed, different solutions are obtained for every call of **pram**() or **pram**_strat().One should note that the method is quite flexible since the transition matrix can be specified freely as a function parameter.

Two implementations are available in `sdcMicro`: **pram**() and **pram**_strat(), the corresponding help files can be accessed with ?**pram** or ?**pram**_strat. With the latter one includes a stratified version of pram.

4.6 Microaggregation

Microaggregation is a perturbative method that is typically applied to continous variables. The main idea is that records are partitioned into groups. Within each group values of each variable are aggregated (typically the mean is used). The individual values of the records for each variables are finally replaced by the group aggregation, see e.g. Listing 13 where always two values that are most similar are replaced by their columnwise means.

```
data(francdat)
x <- francdat[,c(1,3,7)]
m <- microaggregation(x, aggr=2)
mx <- m$mx
colnames(mx) <- c("MicNum1","MicNum2","MicNum2")
cbind(x, mx)
  Num1 Num2 Num3 MicNum1 MicNum2 MicNum2
1 0.30 0.40    4   0.240   0.600     6.0
2 0.12 0.22   22   0.560   0.760    17.5
3 0.18 0.80    8   0.240   0.600     6.0
4 1.90 9.00   91   1.450   5.200    52.5
5 1.00 1.30   13   0.560   0.760    17.5
6 1.00 1.40   14   1.450   5.200    52.5
7 0.10 0.01    1   0.125   0.255     3.0
8 0.15 0.50    5   0.125   0.255     3.0
```

Listing 13: Example for microaggregation.

In function **microaggregation**() parameters for the method used, the aggregation level (how many observations are combined) and the statistics that is used to calculate the aggregation statistics (default = arithmetic mean).

All of the above settings (and many more) can be applied in `sdcMicro` using function **microaggregation**(). The corresponding help file can be viewed with command ?**microaggregation**. A plot method is available, just type **plot**(m), where m is an object of class "micro".

4.7 Adding noise

Adding noise is a perturbative microdata protection method that is typically applied to continous variables. The main idea is to add statistical noise to a given continous variable. This approach protects data against exact matching with external files if information on specific variables is available e.g. from registers.

While this approach sounds simple in principle, a lot of different algorithms can be used to add (stochastic) noise. It is possible to add uncorrelated random noise where the noise is typically normally distributed with the variance of the noise term is proportional to the variance of the original data vector. Adding uncorrelated noise preserves means but variances and correlation coefficients between variables are not preserved while this is respected for the correlated noise method(s). For the correlated noise method [**?**] the noise term derived from a distribution with a covariance matrix that is proportional to the covariance matrix of the original microdata set. In the case of correlated noise addition, correlation coefficients are preserved and at least the covariance matrix can be consistently estimated from the perturbed data. However, the data structure may differ a lot if the assumption of normality is violated. Since this is virtually always the case when working with real-world data, a robust version of the correlated noise method is included in `sdcMicro` (more details can be found in the help file of the package by calling

?addNoise and in ?]) that allows departures from model assumptions.

In sdcMicro several other algorithms are available that can be used to add noise to continous variables. For example it is possible to add noise only to outlying observations for which the assumtion is that such observations possess higher risk than non-outlying observations or to make sure that the amount of noise that should be added takes account the underlying sample sizes.

Noise can be added to variables in sdcMicro using function **addNoise**(). The help file can be shown by typing ?**addNoise**.

Listing 14 shows how this function can be applied with sdcMicro.

```
1 a <- addNoise(x, method="correlated2")$xm
```

Listing 14: Example for adding correlated noise to continuous variables.

5 Practical Application

In this section we show how to apply the concepts and methods introduced in Section 2 using sdcMicro.

5.1 Pre-processing steps

The first step is to start R, install sdcMicro from CRAN and load the package as it is shown in Listing 15.

```
1 install.packages('sdcMicro')
2 library(sdcMicro)
```

Listing 15: Installing and loading sdcMicro.

Once the package is loaded, we can use all the functions and methods that the package provides. For an overview the user is advised to have a look at the manual which can be accessed by typing **help**(**package**=sdcMicro) into the R console.

The first step in creating safe microdata is of course a very accurate analysis of the raw data set to get an idea about key-characteristics and possible use of the data. Furthermore it is also neccessary to take into account legal considerations. Especially it is important to define which properties are required from a microdata set that it can be considered safe. Since legal regulations vary from country to country it is not possible to define general rules. These judgements have to be made by subject matter experts.

5.2 Data sets under consideration

In this Section we show how to apply the disclosure limitation techniques discussed in Section 2 to two different data sets. It is worth mentioning that the anonymization methods applied on data that are saved in flat files.

We will now give an overview about the microdata sets under consideration and refer to Annex A to a more detailed overview of the data.

5.2.1 FIES

The *Family Income and Expenditure Survey* (FIES) from 2006 data has been provided by the National Statistics Office of the Philippines. It is a household survey to gather information on family income and expeditures and it is also been used to measure inequality.

5.2.2 SES

The Structural Earnings Survey (SES) is conducted in almost all European countries and it includes variables on earnings of employees and other variables on employees and employment level (e.g. region, size of the enterprise, economic activities of the enterprise, gender and age of the employees, ...).

5.3 General approach

To create safe microdata files for both the FIES and the SES data set, we will take the following approach.

1. define a set of key variables and thus a disclosure risk scenario
2. assess the disclosure risk of the unmodified data
3. possibly perform recoding of variables
4. achieve k-anonymity within the key variables by local suppression
5. reassess disclosure risk after local suppression
6. protect numeric variables using suitable methods
7. remove additional information from microdata set if it is neccessary

In Section 5.4 and 5.5 we will now show how to transform a microdata set into a safe microdata file that could be published. It must be noted however that the purpose of this document is to create guidelines and not to actually create a safe microdata set.

5.4 Application to FIES data

The first step consists in loading the data into R. In this case the microdata are already available as a R-data file and can easily be loaded as shown in Listing 16.

```
1 data <- load('FIES06V2.RData')
```

Listing 16: Loading microdata into R.

We observe that in the data set no direct identifiers such as names or adresses exist. Thus it is not required to remove any variables from the data set now. Looking at the data and its metadata[3] we learn that the statistical units are households and the microdata set is the result of a survey. It is therefore important to take survey weights into account if we want to asses the disclosure risk. The variable holding sampling weights is called "rfact".

The next step consists of deciding on a set of key variables that attacker could use to identify households. In this case we arbitrarily[4] choose the following variables to be key variables.

- **w_regn**: region with 17 characteristics
- **z2011_h_sex**: sex with 2 characteristics
- **z2021_h_age**: age with 86 characteristics
- **z2041_h_educ**: educational attainment with 21 characteristics

We now assess the disclosure risk given our choice of key variables. In Listing 17 it is shown how to set up the disclosure scenario.

```
1 kVars <- c('w_regn','z2011_h_sex','z2021_h_age','z2041_h_educ')
2 keyVars <- match(kVars, colnames(dat))
3 weightVar <- match('rfact', colnames(dat))
4 (fk <- freqCalc(dat, keyVars, weightVar))
```

Listing 17: Performing frequency calculations

First the key variables are defined and its position in the dataset is calculated (lines 1 and 2). Since we are dealing with sample data it is also required to define the variable holding sample weights and to calculate its position within the microdata set which is done in line 3. In line 4 the actual calculation of frequencies at survey and population level within possible keys is performed and the results of the frequencies at population level are printed in code listing 18.

```
4506 observation with fk=1
3562 observation with fk=2
```

Listing 18: Results of first frequency calculation

We see that a total of 4506 keys is unique in the sample (fk=1) and additionally 3562 combinations of characteristics of key variables are occupied only by two units (fk=2). Note, that the corresponding estimates for population frequencies are stored in the object `fk`. They are estimated with help of the sampling weights and therefore not suitable for risk estimation [for details have a look at **?**]. Therefore a theoretical distribution for the frequency counts of the population with respect to the frequency counts in the sample is usually chosen and theoretical values of this superpopulation distribution are used for

[3] available in xml-file format.

[4] since we do not have any knowledge which information might be available to attackers in the Philippines from registers or other data sources.

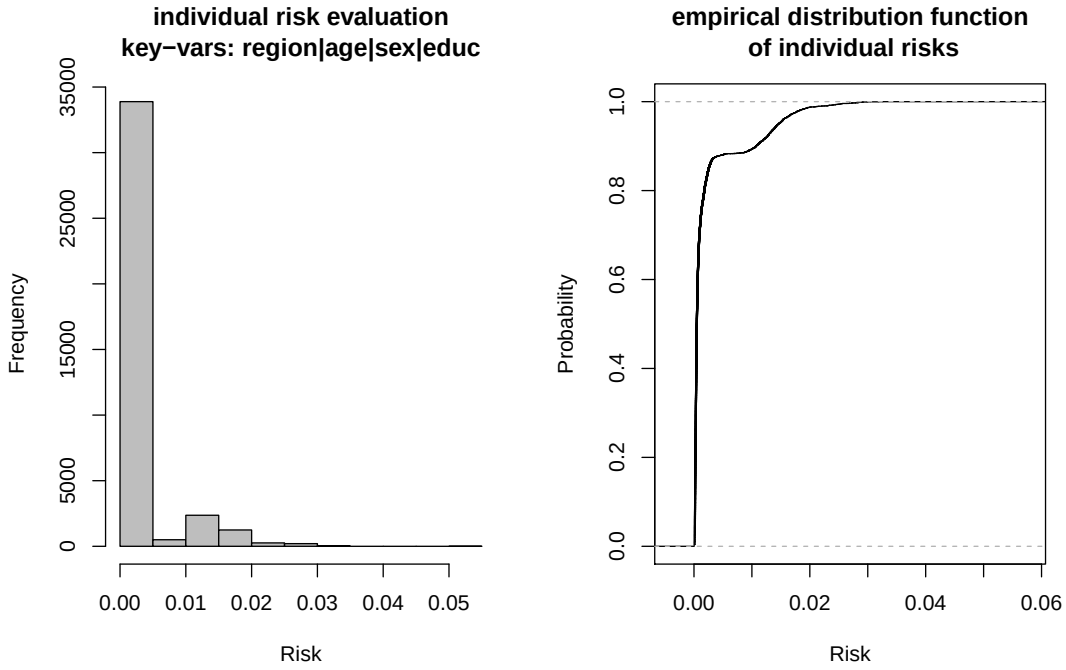


Figure 4: Risk evaluation of unmodified data given key variables 'region', 'sex', 'age' and 'attained education'.

risk estimation [for details, see **?**]. Listing 19 shows how to assess the disclosure risk of the unmodified microdata set in practice.

```
rk <- indivRisk(fk, survey=TRUE)
plot(rk)
```

Listing 19: Assessing disclosure risk of unmodified microdata

Function **indivRisk**() is called with two parameters. The first input parameter is an object of class "freqCalc" derived by using function **freqCalc**(). The second parameter survey has to be set to "TRUE" if one deals with survey data as it is the case here. Figure 4 (produced by simple calling plot() on the object `rk`, see Listing 19) shows the distribution of the risks.

It is easy to see that some observations have high risk of disclosure, i.e. we observe that some units are clearly at risk to be identified with respect to the chosen set of key variables when choosing the maximum individual risk at 5%, for example.

It is now our goal to achieve 3-anonymity which means that at least 3 units need to contribute to each key. To accomplish this goal we have several possibilities. One possibility is to recode key variables in order to reduce the number of keys. Having a look at the key variables we choose it makes sense to reduce the number of characteristics for variables age and attained education since these variable have a lot of characteristics. Listing 20 shows how to recode variable 'z2021_h_age' into 10-year age categories and reducing information in variable 'z2041_h_educ' by combining categories.

```
a <- dat$z2021_h_age; v <- dat$z2041_h_educ
```

```
2
3  # recode age
4  a <- globalRecode(a, seq(9,99,10), 1:9)
5
6  # recode education
7  v[v %in% c(6,53,58)] <- 0
8  v[v %in% 60:69] <- 6
9  v[v %in% 70:79] <- 7
10
11 dat$z2021_h_age <- a; dat$z2041_h_educ <- v
12
13 fk <- freqCalc(dat, keyVars, weightVar)
14 rk <- indivRisk(fk, survey=TRUE)
```

Listing 20: Recoding of key variables

In lines 1 and 2 of Listing 20 we create local copies of the variables 'z2021_h_age' and 'z2041_h_educ'. Line 4 shows how to apply function **globalRecode**() to create 10-year age categories from an integer scaled variable. In this case the first age group is 10-19 years, the second group ranges from 20-29 years. In lines 7 to 9 it is shown how to recode the educational status. In line 5, characteristics 6, 53 and 58 for which no formal description is given are combined with characteristic 0 (no grade completed). In line 8, characteristics 60 to 69 which all represent some kind of bachelor degree are combined into a new category (6). A similar approach is taken in line 9 where characteristics 70 to 79 which represent some kind of post graduation are combined into a new single category (7). In line 11, the original variables in the microdata set are finally replaced with the recoded variables "a" and "v", respectively while in lines 12 and 13 the frequency and risk-calculations based on the recoded key variables is done.

The recoding greatly reduces the number of possible combinations of the key variables. We can observe that the number of key that are occupied by one or two households is much lower as it is shown in Listing 21.

```
print(fk)
231 observation with fk=1
270 observation with fk=2
```

Listing 21: Results of frequency calculation after recoding

Having a look at Figure 5 we learn that also the individual risk have been reduced through recoding. However, the goal of 3-anonymity is not yet reached. Therefore it is required to suppress values of certain units in the key variables to obtain a dataset in which at least 3 units contribute to every possible key. Using `sdcMicro` this can easily be achieved by using function **localSupp**() which is shown in Listing 22.

```
1 # local Suppression for key-variable 'z2041_h_educ'
2 lSupp <- localSupp(fk, keyVars[4], rk$rk, threshold=0.004)
3 fk <- freqCalc(lSupp$freqCalc, keyVars, weightVar)
4 rk <- indivRisk(fk, survey=TRUE)
```

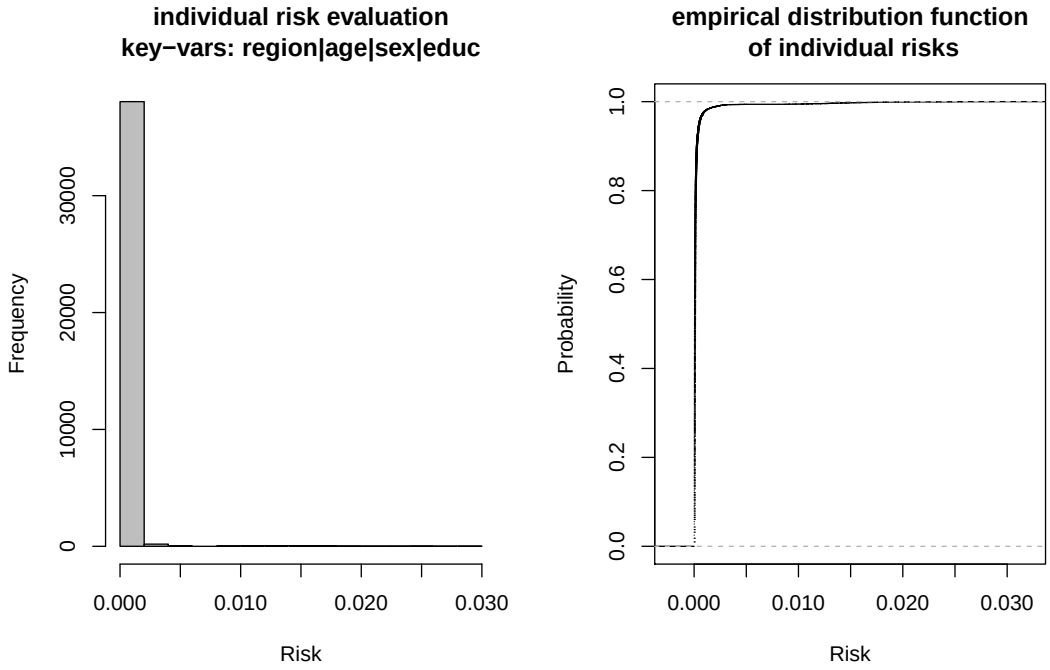


Figure 5: Risk evaluation of data given key variables 'region', 'sex', 'age' and 'attained education' after reducing categories through recoding.

```
5
6 # use same approach for other key variables!
```

Listing 22: Achieving 3-anonymity

With respect to Listing 22 we start dealing with key-variable 'z2041_h_educ'. In lines 2 we suppress the values of all units that have an individual risk that is larger than 0.004. The threshold of 0.004 is motivated from the histogram and the empirical cummulative distribution plot in the right graphic of Figure 5. In such a plot one can see the distribution of the risk and it is resonable to set a threshold that separates the main bulk of the data with the risky data. Note, that their exists no general definition of the threshold, and also legal aspects could play a role to determine the threshold, i.e. for highly sensitive data a lower threshold might be chosen than for data which seems to include no highly confidential information.

In line 3 we re-calculate the frequencies based on the data set with suppressions and calculate the corresponding individual reidentification risks in line 4.

The same approch is repeated for the other key variables with the only difference being the value of the threshold that should be used for suppressing values. We note that the individual risks for each unit can be accessed from objects calculated with function **indivRisk**() and the value of the threshold can again be specified explorative at a plot showing the empirical cummulative distriubtion function as in the right graphic of Figure 5. After suppressing values for each of the four key variables, we observe that we have

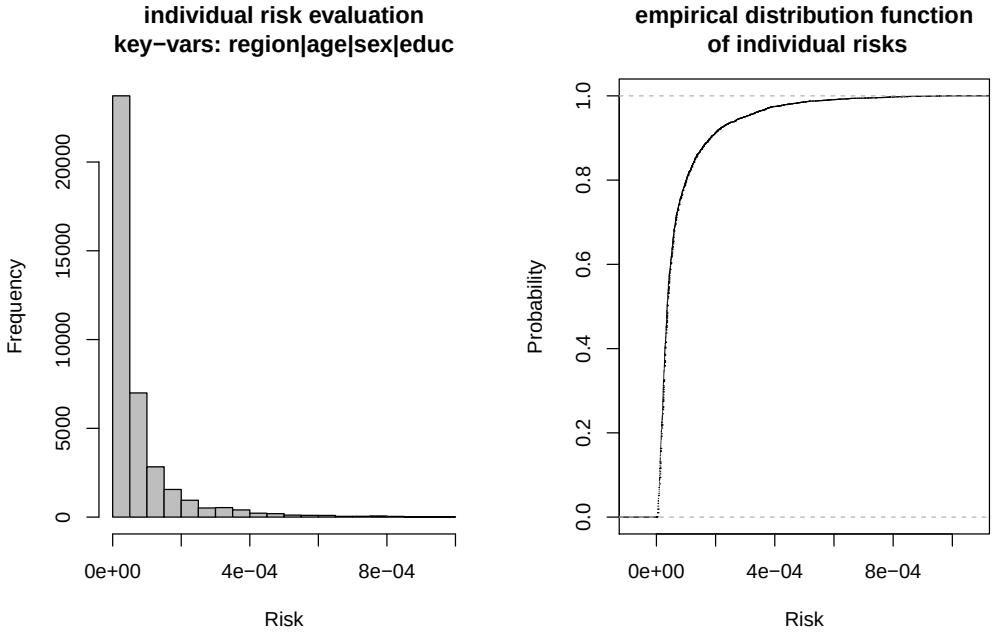


Figure 6: Risk evaluation of data given key variables 'region', 'sex', 'age' and 'attained education' after recoding and local suppression.

reached our goal of k-Anonymity as it is shown in Section 23.

```
0 observation with fk=1
0 observation with fk=2
```

Listing 23: Results of frequency calculation after local suppression

We now have reached 3-anonymity within the selected subset of key variables but we had to suppress values. A total of 251 values were suppressed in variable z2041_h_educ, 117 values have been suppressed in z2021_h_age, 93 values in z2011_h_sex and 4 values had to be removed in w_regn. We note that `sdcMicro` also provides a function that allow to reach k-Anonymity automatically. For a detailed information the interested reader is suggested to have a look at the corresponding help file ?**localSupp2Wrapper**.

Figure 6 clearly shows the reduced risk of reidentification of households compared to Figure 4 after performing both global recoding and local suppression to achieve 3-anonymity.

We now continue and work to protect confidential numerical variables. In this micro-data set, we decide that all variables containing information on income should be deemed confidential and thus be additionally protected while numerical variables containing information on expenditures are not confidential. To protect numerical confidential variables one could use function **microaggregation**() as shown in Listing 24.

```
1 mInd <- c(654:670, 671:681, 693:714)
2 m <- dat[,mInd]
3 mDat <- microaggregation(m, method = "mdav", aggr = 3)
```

```
4 dat[,mVars] <- mDat$mx
```

Listing 24: Microaggregation for confidential numerical variables

In the first line of Listing 24 we define the columns that contain variables dealing with any kind of income. In the second line we create a subset of the microdata set that only contains these confidential variables. In line 3 we apply function **microaggregation**() using method 'mdav' which forms the proximity using a multivariate distance method and calls a C++ implementation written by the International Household Survey Network (IHSN). Parameter aggr=3 is set to 3 so that proximities of size 3 are generated. Note that from size 3 automatically 3-anonymity is created, i.e. always three observations have the same values in the mircoaggregated variables. More protection is guaranteed if the aggregation level is increased but the data utility will be decreased at the same time. In the last line we map the microaggregated data set back to the original microdata set by simply replacing the non-microaggregated variables by their microaggregated counterparts.

It is now of course possible to add another layer of uncertainty to the data set by stochastically changing characteristics of some (categorical) variables using post-randomization with function **pram**() as it is shown in Listing 25.

```
1 vInd <- match('z2031_h_ms', colnames(dat))
2 pr <- pram(dat[,vInd], pd=0.85)
3 dat[,vInd] <- pr$xpramed
```

Listing 25: Post randomization for a categorical variable

In the first line of Listing 25 the column index of the variable 'z2031_h_ms' containing maritial status is calculated. In the second line the actual post randomization is performed. The parameter 'pd' is set to 0.85 which means that on average around 85% of the variable characteristics should not change. Decreasing this parameter value more values are changed to other categories and the data utility decreases as well as the disclosure risk. Again, this parameter should be specified on legal basis, i.e. the need for changing more values than 0.15 %, for example, should be argued by lawyers that can decide how many changes are sufficient so that an intruder is (enough) unsure if the value is true or not.

The transition matrix itself is internally calculated. The resulting output object 'pr' contains besides the transition matrix and the original input vector also the modified, post-randomized vector. In the third line we replace the original characteristics of variable 'z2031_h_ms' by its post-randomized version.

We can now state that we have created a microdata set that features 3-anonymity within the selected set of key variables that has low individual reidentification risks and that has been microaggregated in all variables that contain information on any sort of income which we defined as confidential. Additionally we have post-randomized another categorical variable. After performing these steps it would be the task of the subject matter specialists or people responsible to decide if the modified microdata set is safe to be published. If this is the case, the file could be published. If not, additional disclosure limitation techiques such as adding noise (using **addNoise**()) should be done or the

information of the microdata set could be even more reduced by suppression, recoding, post-randomization or any other method.

5.5 Application to SES data

First, the original microdata have to be loaded into R as shown in Listing 26.

```
load("ses.RData")
```

Listing 26: Loading the SES data.

The result of this step is an object 'x' that exists in the current workspace of R that contains the original, unmodified SES data.

5.5.1 Key Variables for Re-Identification

Again no direct identifiers are included in the data. The identification of an enterprise may leads to information about their employees.

For the categorical key variables at employment level the following variables are selected [see also **?**]:

- **Size**: size of the enterprise
- **age**: age in years
- **Location**: geographic location with 3 categories
- **economicActivity**: the economic branche of the corresponding work centre given as NACE Rev. 2 - Statistical classification of economic activities

As continuous key variables at employment level the following variables are selected:

- **earnings**: gross earnings
- **hourly earnings**: generated from earnings and hours paid in Listing 27.

5.5.2 Pre-processing Steps

Some important variables have to be constructed first. The variable that contains information on gender is recoded, the earnings per hour are constructed from earnings and hours paid, and the variable 'age' has to be calculated from the year of birth. Listing 27 shows how to perform these steps:

```
x$Sex <- factor(ifelse(x$Sex=='Male','male','female'))
x$earningsHour <- x$earningsMonth / x$hoursPaid
x$age <- 2006 - x$birth
```

Listing 27: Pre-processing of the SES data to generate new variables.

5.5.3 Risk Estimation

Now we are ready to estimate the disclosure risk of our data corresponding to the key variables that have been defined. In Listing 17 it is shown how to set up the disclosure scenario for the SES data. In this code we calculate the column-indices of the key-variables (variable 'keyEC') and the variable containing sampling weights (variable 'wVar').

```
## categorical key-variables
keyVars <- c('Size', 'age', 'Location', 'economicActivity')
keyEC <- match(keyVars, colnames(x))
wVar <- match('GrossingUpFactor.y', colnames(x))
fr2 <- freqCalc(x, keyVars=keyEC, w=wVar)
fr2
  ----------------------------------
4979 observation with fk=1
6312 observation with fk=2
  ----------------------------------
rk <- indivRisk(fr2)
rk

method=approx, qual=1
  ----------------------------------
37697 obs. with much higher risk than the main part
```

Listing 28: Frequency and risk estimation of the raw SES data.

It is easy to see the large number of unique combinations from cross-tabulating the categorical key variables (`fk`= 1 in Listing 28). Also a huge number of observations have a considerable higher risk (esitmated at population level) than the main part of the data.

5.5.4 Recoding and Local Suppression

It is therefore necessary to recode some categories of the key variables to receive a lower number of uniqueness. This is done in Listing 29. Here, the NACE classification is changed from 2-digit codes to 1-digit codes, whereas the aggregation of the classifications are based on expert knowledge, i.e. those categories are combined where the economic branches are similar. Next, the categories of the size of the enterprises is reduced. Finally, the age of the employees are categorized in six age classes.

```
## recode economic activity
library(stringr)
a <- as.character(x$economicActivity)
ecoANew <- rep('Q-ExtraTerr', nrow(x))
ecoANew[a %in% str_c('R', 10:14)] <- 'C-Mining'
ecoANew[a %in% str_c('R', 15:37)] <- 'D-Manufacturing'
ecoANew[a %in% str_c('R', 38:44)] <- 'E-Electricity'
ecoANew[a %in% str_c('R', 45:49)] <- 'F-Construction'
ecoANew[a %in% str_c('R', 50:54)] <- 'G-Trade'
ecoANew[a %in% str_c('R', 55:59)] <- 'H-Hotels'
```

```
ecoANew[a %in% str_c('R', 60:64)] <- 'I-Transport'
ecoANew[a %in% str_c('R', 65:69)] <- 'J-FinancialIntermediation'
ecoANew[a %in% str_c('R', 70:74)] <- 'K-RealEstate'
ecoANew[a %in% str_c('R', 75:79)] <- 'L-Public'
ecoANew[a %in% str_c('R', 80:84)] <- 'M-Education'
ecoANew[a %in% str_c('R', 85:89)] <- 'N-Health'
ecoANew[a %in% str_c('R', 90:94)] <- 'O-Other'
ecoANew[a %in% str_c('R', 95:98)] <- 'P-Households'
x$economicActivity <- ecoANew; rm(ecoANew,a)

## recode size classes:
levels(x$Size) <- list(E10_49=c('E10_49'), E50_249='E50_49',
    E250plus=c('E250_499','E500_999','E1000'))

## recode age
x$age <- cut(x$age, breaks=c(0,19,29,39,49,59,120))
```

Listing 29: Recoding economic activity, size and age.

After performing the recoding of key variables we can calculate the new frequencies as it is shown in Listing 30.

```
### Disclosure Scenario 2 (after recoding of key-variables)
fr2After <- freqCalc(x, keyVars=keyEC, w=wVar)
  ----------------------------------
0 observation with fk=1
0 observation with fk=2
  ----------------------------------
rk <- indivRisk(fr2After)
max(rk$rk)
[1] 0.0006009207
```

Listing 30: Frequency calculation based on the recoded variables.

In general there are at least four possiblities to archieve k-anonymity. The first possibility is to randomized the values of a categorical variable with the help of function **pram**(), as shown in Section 4.5. An alternative way could be to delete some values randomly and impute those values in a proceeding step.

Another possibility is to apply further recodings, for example, to allow fewer categories for the economic activity. The last possiblity is to apply local suppression as it was already shown in Listing 22. In this case however it is not required to take any further steps since we learn from the output of function **freqCalc**() that 3-anonymity has already been reached with the recoding that has already been done since the number of observations with 'fk' being one or two is zero. We also see that the maximal risk for re-identification is very low.

However, for the sake of completeness we list the three functions of `sdcMicro` that can used to perform local suppression. Function **localSupp**() can be used to suppress all values for a given key variable for all units which have a risk that is higer a specified threshold value. This value can be set when calling the function.

The other functions are **localSupp2**() and **localSupp2Wrapper**() that work slightly different. Both functions provide a heuristic algorithm that performs local suppression repeatedly until k-anonymity is reached. It is also possible to specify an importance vector that is taken into account when suppressing values in the key variables. It is therefore even possible to specify the importance of key variables in a way that no information is removed for these variables.

5.5.5 Perturbing the Continuous Scaled Variables

A bunch of methods are available to perturb continuously scaled (key) variables.

In the Listing 31 it is shown how to apply microaggregation as well as adding (correlated) stochastic noise to continuously scaled variables. In this example the *mdav* method for microaggregation is used. The parameter `aggr` determines how many observations are always considered together when performing the aggregation.

```
numVars <- c('earningsHour', 'earnings')
cInd <- match(numVars, colnames(x))

## perform microaggregation
x[,cInd] <- microaggregation(x[,cInd], method='mdav', aggr=3)

## add correlated noise
x[,cInd] <- addNoise(x[,cInd], method='correlated')
```

Listing 31: Microaggregation and addition of stochastic noise applied to continuous key variables of the SES data.

In Listing 31 we show how to use function **addNoise**() to add correlated noise to numerical key variables. In this case it is required to set parameter `method='correlated'` when calling the function. We note that quite a few different methods for noise-addition - even methods that takes the structure of outlying observations into account - can be selected in function **addNoise**().

6 Anonymised Data and Measuring the Risk

The data has been anonymised by recoding, suppression, by pram and by microaggragatin and adding noise. For details, have a look in the third deliverable of the project [**?**].

The risk measurement can only be done for recoding and local suppression (by using the the k-anonymisty approach and/or the risk framework of **?**] or **?**]) and methods that perturbe continous variables (using the function drisk() in R [**??**] package **sdcMicro**). Rank swapping or pram change values randomly and the risk of re-identification have to be evaluated by eperts on laws, i.e. a threshold, how many swapped values are enough so that an intruder have an uncertainty if a re-idenfication is wrong or not, has to be fixed.

In Section 8 we evaluate anonymised data that fulfills k-anonymity, and using the default parameters of **sdcMicro** for **pram** and rank swapping.

7 Utility Measures

After performing the task of anonymizing micro data it is alway neccessary to assess the quality of the resulting micro data set.

As mentioned in Section 4 anonymised data are usually evaluated using very generally defined utility measures such as differences in means or covariances. We also mentioned there that the evaluation of the data utility of anonymised data should better be based on those (benchmarking) statistics/indicators that are most important to estimate from the data.

For FIES and SES, this includes that famous indicators like the GINI coefficient (see Equation 4), but also model-based estimations that are typically applied on the data should be precise as possible. In addition, in the following we also evalute the methods based on overlaps in confidence intervals which has - to our knowledge - never been done in literature, but it seems to be very reasonable to look also if the variances of the estimates are preserved. And there is another reason to do that. When considering the variances of the estimates obtained from original data and anonymised data allows to take the sample size into account.

We now continue to describe how one can achieve the goal of evaluating the quality of the results. It should be also noted that it may be neccessary to perform the quality assessment multiple times to be able to compare different anonymization methods. This allows the SDC specialist to decide on an anonymization technique that not only leads to protected micro data but also to data that still feature high data quality.

The utility measures chosen, which are in the calculated on the benchmarking indicators defined in Appendix B, are the following

- about the difference in the estimation of the Gender Pay Gap (GPG) and the GINI coefficient from the original and perturbed data defined for h domains:

$$ARB = \frac{|\frac{1}{h}\sum_{i=1}^{h}(\hat{\theta}_i - \theta_i)|}{\theta_i} \quad . \tag{2}$$

- Additionally, one model is predicted (see Appendix B.3) and from the predicted values the indicator of interest (e.g. the GINI) is estimated.

- Moreover, the variances are estimated and the **overlap of the confidence intervals** of the perturbed and original data is evaluated and reported in percentages (of overlap).

In Section 8 we show how to assess data utility for some important indicators for the SES data set.

8 Results

8.1 ARB

Table 1 shows the ARB whereas the overall estimate is shown and the mean over the domain (sex × age class) estimates. It is easy to see that microaggregation ('ma'; here

method 'mdav' from package **sdcMicro ??**] was chosen) provides much better results than the correlated noise method **?**] using the default parameters of **sdcMicro**. The ARB estimates are the same for recoding, pram or swapped variables since the GPG is estimated only from the microaggregated hourly earnings. However, recoding, swapping and pram influences the model estimates since the age is categorized or swapped. Hereby, recoding provides better results than pram and swapping (see also Table 2 for similar results on the Gini coefficient). It can also be seen that the ARB is small when recoding and microaggregation were applied to anonymise the data. The model-based estimates become worst when swapping techniques like numerical rank swapping or pram are additionally applied.

Table 1: Comparison of different methods using the absolute Relative Bias (ARB) in gender pag gap. The .m indicates that the estimates based on models (see Appendix B.3), the h. indicates that the estimates is based on domain level.

	ARB	ARB.m	h.ARB	h.ARB.m
recode+noise	46.73		126.02	
recode+ma	0.02	0.30	0.03	6.11
recode+pram+ma	0.02	22.13	0.03	14.46
recode+swap+ma	0.02	12.84	0.03	6.44
pram+ma	0.02	14.60	0.03	10.77
swap+ma	0.02	11.76	0.03	8.56

Table 2: Comparison of different methods using the absolute Relative Bias (ARB) of the Gini coefficient. The .m indicates that the estimates based on models (see Appendix B.3), the h. indicates that the estimates is based on domain level.

	ARB	ARB.m	h.ARB	h.ARB.m
recode+noise	1.12		16.37	
recode+ma	0.02	0.07	0.07	6.11
recode+pram+ma	0.02	41.95	0.07	14.46
recode+swap+ma	0.02	34.16	0.07	6.44
pram+ma	0.02	35.69	0.07	10.77
swap+ma	0.02	34.22	0.07	8.56

8.2 Overlap in Confidence Intervals

By estimating the confidence interavals (for the gender pay gap, for example) one can also have look at the overlap of the confidence interval of a parameter estimated from the perturbed and the original data.

This can be done using the following lines of code shown in Listing 32. First the Gini coefficient and its variance (for more details on variane estimation see Appendix B) is estimated from both, the original data and the anonymised data. The confidence intervals

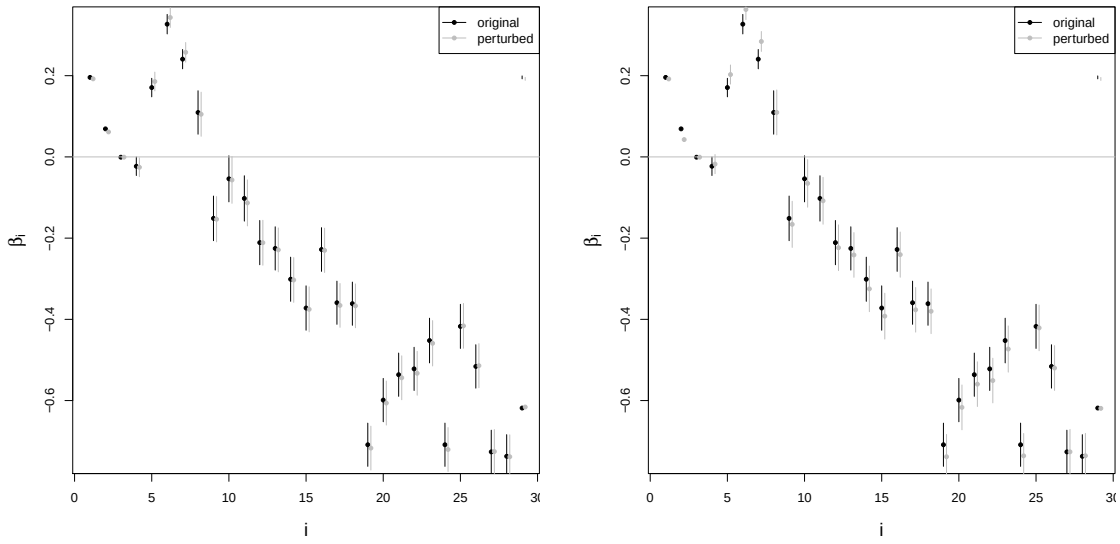
are very similar and almost completely overlaps. This is also true when displaying the confidence intervals by stratum (this is saved in object `v1` and `v1a`).

```
library(laeken)
# we take one stratum (for computational speed) and full time employees
x <- x[x$economicActivity=="R14" && x$FullPart=="FT",]
dim(x)
[1] 1554   43  ## number of observations and variables used

## gini from original data
g1 <- gini(inc="earningsHour", weigths="GrossingUpFactor.y", breakdown="education", data=x)

## gini from perturbed data
g1a <- gini(inc="earningsHourM", weigths="GrossingUpFactor.y", breakdown="education", data=x)

## corresponding variances
v1 <- variance("earningsHour", weights="GrossingUpFactor.y", data=x,
                  indicator=g1, X=calibVars(x$Location), breakdown="education", seed=123)
v1a <- variance("earningsHourM", weights="GrossingUpFactor.y", data=x,
                  indicator=g1a, X=calibVars(x$Location), breakdown="education", seed=123)
v1$ci
   lower    upper
15.31177 19.16410
v1a$ci
   lower    upper
15.32402 19.15750
```

Listing 32: Overlap in confidence intervals from estimates based on perturbed and original data.

But also the differences of the regression coefficients are of interest. Whereas it is not or hardly be possible to compare the coefficients obtained from a model based on original data with the coefficients obtained by recoded data (fewer categories includes other/fewer regression coefficients) it is possible to see the effect of numerical rank swapping or pram on the regression coefficients.

This is highlighted in Figure 7 whereas the overlap of confidence intervals is clearly feasible.



(a) Rank swapping.

(b) Pram using the default parameters.

Figure 7: Confidence intervals for the regression coefficients obtained from the model based on original data (black lines) and perturbed data (grey lines).

9 Conclusions

In this guidelines we have shown basic concepts of how microdata may be modified in order to generate confidential data that can be released. We also showed how to practically implement these concepts using the free and open source R package **sdcMicro**. For this reason these guidelines may prove helpful to subject matter experts that have to deal with the task of preparing safe micro data.

Additional methods are available and described in detail in the R package **sdcMicro**, such as the suda2 algorithm to find unique observations on subsets, further recoding facilities as well as a GUI, implemented in **sdcMicroGUI** [**?**].

In general, the following recommendations are given:

Recommendation 1: Carefully choose the set of variables that are disclosive using knowledge of both subject matter experts and disclosure control experts.

Recommendation 2: Always perform a frequency- and risk estimation in order to evaluate how many observations have a high risk of dislosure.

Recommendation 3: Apply recodings to reduce uniqueness given the set of categorical key variables. This approach should be done in an explorative manner. However, recodings on a variable should also be based on expert knowledge to combine categories that are reasonable to combine. Alternatively, swapping procedures may be applied on the categorical key variables so that data intruders can not be certain anymore if an observation has or has not been perturbed.

Recommendation 4: If recoding was applied, suppress the last remaining values to obtain k-anonymity.

Recommendation 5: Apply microaggregation to continuously scaled key variables. This automatically provides k-anonymity within those variables.

Recommendation 6: Quantify the data utility not only on typical estimates (like quantiles or correlations) but also on the most important data-specific benchmarking indicators.

The results show that recoding and microaggregation works well to obtain non-confidential data with high data quality. While the disclosure risk cannot be expressed in statistics for swapping methods like rank swapping or pram, these methods would have its advantages when a high number of key variables are chosen, since a high number of key variables leads to a high number of unique cominations that cannot be significantly reduced by recoding.

In general, the inclusion of `C++` code from the OECD leads to significant performance in computatational speed of the implementation [see **?**]. In addition, the package can be used for free without paying licences of a statisitical software such as SPSS or STATA.

References

A Detailed data description

A.1 FIES

The first microdata set that we use to apply popular microdata limitation techniques using `sdcMicro` is the *Family Income and Expenditure Survey* (FIES) from 2006 that has been conducted by the National Statistics Office of the Philippines. It is a nationwide survey of households that is the main source of information of data on family income and expenditures.

A.1.1 Objectives of FIES

The objectives of the survey are - among others - to gather information on family income and expenditures and related information that affects income and expenditure levels and patterns. It is also of great interest to collect information about different sources of income, levels of living and spending patterns and also about the degree of inequality among families.

For the FIES in 2006, households have been sampled according to a complex sampling design. With respect to the goal of this work which is to draft practical guidelines for creating protected microdata files it is not required to go into details about the sampling procedure. It is however important to note that sampling weights are available and should be taken into account.

The questionnaire was split into four main parts that are listed below:

- Identification and other Information
- Expenditures
- Income
- Entrepreneurial Activities

The required interviews have been conducted face to face by trained interviewers. The reporting unit was the family. The dataset features a total of 38483 units for which 721 variables have been measured.

More metadata on the FIES2006 data are available from www.census.gov.ph/nsoda, including variable description.

A.2 The Structural Statistics on Earnings Survey (SES)

A.2.1 General Information about SES

The Structural Earnings Survey (SES) is conducted in almost all European countries, and the most important figures are reported to Eurostat. Moreover, also anonymised microdata are sent from most European Union membership countries to Eurostat.

SES is a complex survey of Enterprises and Establishments with more than 10 employees (11600 enterprises in Austria in year 2006), NACE C-O, including a large sample of employees (Austria: 207.000). In many countries, a two-stage design is used whereas in the first stage a stratified sample of enterprises and establishments on NACE 1-digit level, NUTS 1 and employment size range is drawn with large enterprises commonly having higher inclusion probabilities. In stage 2, systematic sampling or simple random sampling is applied in each enterprise. Often, unequal inclusion probabilities regarding employment size range categories are used. Of course, calibration is applied to represent some population characteristics corresponding to NUTS 1 and NACE 1-digit level, but also calibration is carried out for gender (amount of men and womens in the population).

SES includes information from different perspectives and sources. In the Austrian case this belongs to:

Information on enterprise level: Question batteries are asked to enterprises like if an enterprise is private or public or if an enterprise has a collective bargaining agreement (both binary variables). As a multinomial variable, the kind of collective agreement is included in the questionnaire.

Information on individual employment level: The following questions to employees comes with the standard questionnaire: social security number, date of being employed, weekly working time, kind of work agreement, occupation, time for holidays, place of work, gross earning, earning for overtime and amount of overtime.

Information from registers: All other information may come from registers like information about age, size of enterprise, occupation, education, amount of employees, NACE and NUTS classifications.

A detailed information on the SES variables can be found in the appendix.

A.2.2 Applications and Statistics based on SES

Every four years the standard publication from national statistical offices is disseminated after the survey is conducted. In addition, special publications about low incomes, non-common occupation employment and gender-specific reports are published by some member states [see, e.g., **??**]. Many other national publications from statistical agencies or researchers are available in almost every country [for some summaries about publications until 1999, see **?????**].

It is interesting to note that anonymised SES 2002 and 2006 data [**?**] from 23 countries can be can be accessed for research purposes (by means of research contracts) through the safe centre or anonymised CD-ROM at the premises of Eurostat (http://epp.eurostat.ec.europa.eu/porta
The output of the users are checked by Eurostat on confidentiality and quality [**?**].
SES Microdata from Czech Republic, Hungary, Ireland, Italy, Latvia, Lithuania, Netherlands, Norway, Portugal, Slovakia and Spain can also be analysed via the Piep Lissy remote access system. The user can run `Stata` code on the Piep-Lissy server, whereas some commands (12 commands in summary) are blocked by the system to prevent listing of individuals. This is, of course not enough to prevent re-identification of individuals [see, e.g., **?**]. The Lissy servers has been intensively used within the EU project on *Linked Employer-Employee Data* (LEED) that studied the potential of linked employer-employee and panel data sets for analysis of European labour market policy. Moreover, this data set was used within the dynamic wage network that was funded by the European Central Bank.

Generally such linked employer-employee data are used to identify the determinants/differentials of earnings but also some indicators are directly derived from the hourly earnings like the gender pay gap or the Gini coefficient [**?**]. The most classical example is the income inequality between genders as discussed in **?**], for example.

A correct identification of factors influencing the earnings could lead to relevant evidence-based policy decisions. The research studies are usually focused on examining the determinants of disparities in earnings. Earnings comparisons among different industries or regions are frequently performed [see, e.g., **????????**]. Sometimes the socio-educational factors are investigated as possible explanatory variables of income, for example in **?**]. The overview of the analyses performed using SES data highlighted that, generally, the hourly log-earnings are modelled. The explanatory variables correspond to the employer activity (related to the enterprise), his/her experience (education, length of stay in service, qualification, etc.) and working hours. It was also observed that linear models are extensively used. Anova analysis, linear mixed-effects models and multi-level models are other examples of statistical tools that have been applied. However, a lot of similar models are applied in literature to model the log hourly earnings.

For a detailed overview on the usage of the SES data, have a look at **?**].

A.2.3 The Synthetic SES Data

In this contribution we use a synthetic close-to-reality SES data set that has been simulated partly within this project and partly by **?**]. In **?**] it is shown that these synthetic data fulfils the following properties:

- Actual sizes of regions and strata have to be reflected.

- Marginal distributions and interactions between variables are realistic and very close to the original ones. The distribution and conditional distributions of variables are realistic.
- Heterogeneities between subgroups, especially regional aspects, are present.
- All important estimates provide high quality, i.e. are be very close to the original ones.
- Mosaicplots, distrubution plots and all other explorative methods show very much the same as the original ones.

The synthetic data set was simulated with the help of R package **simPopulation** [?].

A.3 Details on SES variables

A.3.1 Variables on Enterprise Level

The most important variables are briefly described in the following:

1. `Location`: The geographical location of the local is cut into three areas based on NUTS 1-digit level. The three areas are AT1 (eastern Austria), AT2 (southern Austria) and AT3 (western Austria).
2. `NACE1`: The economic activity on NACE 2-digit level. The classes are shown in table 3.
3. `Size`: The employment size range. (6 categories, see Table 3
4. `payAgreement`: The form of collective pay agreement consists of seven levels.
5. `EconomicFinanc`: The form of economic and financial control has two levels: A (public control) and B (private control).

A.3.2 Variables on Employees Level

A.3.3 Categorical Variables

The most important variables are as follows:

1. `Sex`: The gender of the sampled person. (Table 4)
2. `Occupation`: This variable is coded according to the International Standard Classification of Occupations, 1988 version (ISCO-88(COM))at the two-digit level. Table 4 shows these levels.
3. `education`: Six categories of the highest successfully completed level of education and training are coded according to the International Standard Classification of Education, 1997 version (ISCED 97). (Table 4).
4. `FullPart`: The variable `FullPart` indicates if the employee is a full-time worker or a part-time worker.
5. `contract`: The categories of the type of employment contract are listed in Table 4.

Table 3: Variables on Enterprises Level

Variables of Enterprises		
variable name	**description**	**categories**
Location	Geographical location of the local unit	AT1: eastern austria AT2: southern austria AT3: western austria
NACE1	Principal economic activity of the local unit	C-Mining D-Manufactoring E-Electricity F-Construction G-Trade H-Hotels I-Transport J-FinancialIntermediation K-RealEstate M-Education N-Health
Size	Size of the enterprise number of employees	E10_49: 10-49 employees E50_249: 50-249 employees E250_499: 250-499 employees E500_999: 500-999 employees E1000: 1000 or more employees
EconomicFinanc	form of economic and financial control	A public control B private control
payAgreement	collective pay agreement	A national level or interconfederal agreement B industry agreement C agreement of individual industries in idividual regions D enterprise or single employer agreement E agreement applying only to workers in the local unit F any other typ of agreement N no collective agreement exists

Table 4: Categorical Variables on Employees Level

variable name	description	categories
Sex	Sex	female male
Occupation	Occupation in the reference month	11 Legislators and seniors officials 12 Corporate managers 13 Managers of small enterprises 21 Physical, mathematical and engineering science professionals 22 Life science and health professionals 23 Teaching professionals 24 Other professionals 31 Physical and engineering science associate professionals 32 Life science and health associate professionals 33 Teaching associate professionals 34 Other associate professionals 41 Office clerks 42 Customer services clerks 51 Personal and protective services workers 52 Models, salespersons and demonstrators 61 Skilled agricultural and fishery workers 71 Extraction and building trades workers 72 Metal, machinery and related trades workers 73 Precision, handicraft, craft printing and related trades workers 74 Other craft and related trades workers 81 Stationary plant and related operators 82 Machine operators and assemblers 83 Drivers and mobile plant operators 91 Sales and services elementary occupations 92 Agricultural, fishery and related labourers 93 Labourers in mining, construction, manufacturing and transport
education	Highest successfully completed level of education and training	1 ISCED 0 and 1 2 ISCED 2 3 ISCED 3 and 4 4 ISCED 5B 5 ISCED 5A 6 ISCED 6
FullPart	Contractual working time	FT full-time employee PT part-time employee
contract	Type of employment contract	A indefinite duration B temporary fixed duration C apprentice

A.3.4 Continuous Variables on Employees Level

1. `birth`: The year of birth.
2. `Length`: The total length of service in the enterprises in the reference month is be based on the number of completed years of service.
3. `ShareNormalHours`: The share of a full timer's normal hours. The hours contractually worked of a part-time employee should be expressed as a percentage of the number of normal hours worked by a full-time employee in the local unit.
4. `weeks`: Here the number of weeks in the reference year to which the gross annual earnings relate is mentioned. That is the employee's working time actually paid during the year and should correspond to the actual gross annual earnings. (2 decimal places).
5. `hoursPaid`: The number of hours paid in the reference month which means these hours actually paid including all normal and overtime hours worked and remunerated by the employee during the month.
6. `overtimeHours`: The variable `overtimeHours` contains the number of overtime hours paid in the reference month. Overtime hours are those worked in addition to those of the normal working month.
7. `holiday`: The annual days of holiday leave (in full days).
8. `earnings`: Let `earnings` be gross annual earnings in the reference year. The actual gross earnings for the calender year are supplied and not the gross annual salary featured in the contract.
9. `notPaid`: Examples of annual bonuses and allowances are Christmas and holiday bonuses, 13th and 14th month payments and productivity bonuses, hence any periodic , irregular and exceptional bonuses and other payments that do not feature every pay period. Besides the main difference between annual earnings and monthly earnings is the inclusion of payments that do not regularly occur in each pay period.
10. `earningsMonth`: The gross earnings in the reference month covers renumeration in cash paid during the reference month before any tax deductions and social security deductions and social security contributions payable by wage earners and retained by the employer.
11. `earningsOvertime`: It is also necessary to refer to earnings related to overtime. The amount of overtime earnings paid for overtime hours is required.
12. `paymentsShiftWork`: These special payments for shift work are premium payments during the reference month for shirt work, night work or weekend work where they are not treated as overtime.

B Benchmarking Indicators for SES and FIES

In the following, the user needs, i.e. the most important indicators are described in full detail. First, the (unadjusted) gender wage gap is introduced since it is one of the most important indicator obtained from SES data, before the GINI coefficient is described that is estimated from FIES data.

The GINI coefficient is chosen because, it is extremely sensitive to changes in the upper and lower tail of the distribution. So, if this estimator is not affected from anonymisation, we can be quite sure that the data have high data utility, since it is most difficult to preserve the structure of the data in the upper tail of the distribution.

Lastly, a model-based estimation on microdata level is described, representative for all model-based estimations. Note that this choice of indicators and models is subjective, but it can be expected that differences in estimations from anonymised and original data according to that models deduce differences in similar models as well.

Concluding that, the chosen indicators and models are representative for many other indicators and models estimated from this data set. Especially, because most of the chosen indicators are very sensitive to differences in the lower and upper tail of the distribution. To evaluate the effect of anonymisation on models, the chosen model should reflect these effects, representative for (almost) any other models used in statistical agencies, at Eurostat or research institutions.

B.1 The Gender Wage/Pay Gap

Probably the most important indicator derived from the SES data is the *gender pay gap / gender wage gap*.

The calculation of the gender pay gap is based on each person's hourly earnings. The hourly earnings equals to the gross monthly earnings from job divided by the number of hours usually worked per week in job during 4.33 weeks, see [**??**].

B.1.1 Definition Gender Pay Gap

The gender pay gap in unadjusted form is defined on population level as the difference between average gross earnings of male paid employees and of female paid employees divided by the earnings of mail paid employees [**?**].

B.1.2 Estimation of the Gender Pay Gap

Since the gender wage gap is usually estimated by survey information, the estimation has to consider sampling weights in order to ensure sample represantivity.

For the following definitions, let $\boldsymbol{x} := (x_1, \ldots, x_n)'$ be the hourly earnings with $x_1 \leq \ldots \leq x_n$ and let $\boldsymbol{w} := (w_i, \ldots, w_n)'$ be the corresponding personal sample weights, where n denotes the number of observations.

Let

$$J^{(M)} := \{j \in \{1, \ldots, n\} \mid \text{worked as least 1 hour per week} \wedge (16 \leq \text{age} \leq 65) \wedge \text{person is male}\} \quad ,$$

and $J^{(F)}$ those index set which differs from $J^{(M)}$ in the fact that it includes all females instead of males.

With these index sets the gender pay gap in unadjusted form is estimated by

$$GPG_{(mean)} = \frac{\frac{\sum_{i \in J^{(M)}} w_i x_i}{\sum_{i \in J^{(M)}} w_i} - \frac{\sum_{i \in J^{(F)}} w_i x_i}{\sum_{i \in J^{(F)}} w_i}}{\frac{\sum_{i \in J^{(M)}} w_i x_i}{\sum_{i \in J^{(M)}} w_i}} \quad . \tag{3}$$

The gender pay gap is usually estimated at domain level like economic branch, education and age groups [**?**].

B.2 The GINI Coefficient

The Gini coefficient [**?**] and the Quintile Share Ratio (QSR) are well known measure of inequality of a distribution and they are widely applied in many fields of research. They are often used to measure inequality of income or earnings as an economic indicator. For the SES data, the GINI and the QSR may be estimated for each enterprise, economic branch or for each country. The GINI and especially the QSR are sensitive to changes in values in the upper and lower tail of the distribution. Since large earnings have to be perturbed in a greater extend in the anonymisation process than the majority of the data, these indicators are ideally suited to evaluate protection methods on continuous variables.

The Gini coefficient according to **??**] is estimated by

$$\widehat{Gini} := 100 \left[\frac{2 \sum_{i=1}^{n} \left(w_i x_i \sum_{j=1}^{i} w_j \right) - \sum_{i=1}^{n} {w_i}^2 x_i}{\left(\sum_{i=1}^{n} w_i \right) \sum_{i=1}^{n} \left(w_i x_i \right)} - 1 \right]. \tag{4}$$

The Gini coefficient is closely related to the Lorenz curve [**?**], which plots the cumulative proportion of the total income against the corresponding proportion of the population.

The Gini coefficient is typically - among other domains - estimated with breakdown by age and gender or age, gender and region.

B.3 Model-based Predictions on Microdata Level

Respectively for all model-based estimations at employment level we choose a model described in **?**] applied within the PiEP Lissy project and which is also used in **?**]. They fit OLS regression models where they modeled the gross hourly earnings of workers in enterprises using age, age^2, sex, education and occupation as predictors.

Similar models are also fitted within the *wage dynamics network* of the Eurpean Central Bank [**??**] and within the *EU Linked Employer-Employee Project* [see, e.g., **?**].

The log hourly earnings for each country are predicted with the following predictors:

$$log(\texttt{earnings}) \sim \texttt{sex}\ (2) + \texttt{age} + \texttt{age}^2 + \texttt{education}\ (6) + \texttt{occupation}\ (23) + \text{error term} \quad .$$

The numbers in brackets correspond to the number of categories for binary or categorical variables.

In addition, the variance of that estimations are important to estimate since they reflect the statistical uncertainty.

B.3.1 Variance Estimation

We implemented a calibrated bootstrap to estimate the variances [**?**] for the gender pay gap but also for all other indicators defined in this contribution. The calibrated bootstrap is applied internally by calling function `variance()` in package **laeken** [**?**]. Note that a calibrated bootstrap is preferable over all other resampling methods [**??**].

Let $\boldsymbol{X}$ denote a survey sample with n observations and p variables. Then the *calibrated bootstrap algorithm* for estimating the variance and confidence interval of an indicator can be summarized as follows:

1. Draw R independent bootstrap samples $\boldsymbol{X}_1^*, \ldots, \boldsymbol{X}_R^*$ from $\boldsymbol{X}$.

2. Calibrate the sample weights for each bootstrap sample $\boldsymbol{X}_r^*$, $r = 1, \ldots, R$. Generalized raking procedures are thereby used for calibration: either a multiplicative method known as *raking*, an additive method or a logit method [see **??**].

3. Compute the bootstrap replicate estimates $\hat{\theta}_r^* := \hat{\theta}(\boldsymbol{X}_r^*)$ for each bootstrap sample $\boldsymbol{X}_r^*$, $r = 1, \ldots, R$, where $\hat{\theta}$ denotes an estimator for a certain indicator of interest. Of course the sample weights always need to be considered for the computation of the bootstrap replicate estimates.

4. Estimate the variance $V(\hat{\theta})$ by the variance of the R bootstrap replicate estimates:

$$\hat{V}(\hat{\theta}) := \frac{1}{R-1} \sum_{r=1}^{R} \left(\hat{\theta}_r^* - \frac{1}{R} \sum_{s=1}^{R} \hat{\theta}_s^* \right)^2 . \tag{5}$$

5. Estimate the confidence interval at confidence level $1 - \alpha$ by the percentile method: $\left[\hat{\theta}^*_{((R+1)\frac{\alpha}{2})}, \hat{\theta}^*_{((R+1)(1-\frac{\alpha}{2}))} \right]$, as suggested by **?**]. $\hat{\theta}^*_{(1)} \leq \ldots \leq \hat{\theta}^*_{(R)}$ denote the order statistics of the bootstrap replicate estimates.