sdcMicro GUI manual Documentation

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May 22, 2019

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This is documentation and guidance for *sdcApp*, a user interface for the *sdcMicro R* package, which provides tools for Statistical Disclosure Control (SDC) for microdata, also known as microdata anonymization.

CHAPTER

ONE

INTRODUCTION

1.1 What is sdcApp?

sdcApp is the Graphical User Interface (GUI) for the R package *sdcMicro* (see here). The *sdcApp* opens the functionality of *sdcMicro* to users not familiar with the statistical programming language *R*. *sdcMicro* is an add-on package for the statistical software *R* for Statistical Disclosure Control (SDC) of microdata and includes functions for risk measurement, anonymization and utility measurement for microdata. All functionality available in the *sdcMicro* package is also available in *sdcApp*.

1.2 Statistical Disclosure Control (SDC)

A large part of the data collected by statistical agencies cannot be published directly due to privacy and confidentiality concerns. These concerns are both of legal and ethical nature. SDC seeks to treat and alter the data so that the data can be published or released without revealing the confidential information it contains, while, at the same time, limit information loss due to the anonymization of the data. There are two strands of literature on SDC: 1) for microdata and 2) for tabular data. *sdcMicro* and *sdcApp* only provide the tools and methodology for protecting microdata.

1.3 What is the purpose of the manual?

This manual is designed to provide step-by-step guidance through the process of anonymizing a dataset with microdata. Both limited background information on methods and measures is provided as well as instructions on how to complete these steps in sdcApp. As *sdcApp* is a GUI for the *sdcMicro* package, users familiar with using *R* for statistical analysis may prefer to carry out the anonymization process using *R* from command-line. More information and guidance on using *sdcMicro* from command-line is available in the SDC Practice Guide available here. A theory guide is available here and provides more detailed background information on the SDC process, methods and measures.

1.4 Background literature on SDC for microdata

There is a broad scientific literature available on SDC for microdata. The theory guide contains many references to the appropriate literature. Two books written by practitioners in NSOs, which give a complete overview are especially worth mentioning:

Hundepool

Templ

1.5 Outline of this guide

This guide is divided into the following main sections:

1. the Section Installation and updating guides the user through the installation process of sdcApp, which includes the installation of R, RStudio as well as the required packages. It also discusses the need and process of regular updates of all software components.
2. the Section Introduction to sdcApp covers how to launch and close the application and provides a brief overview of structure of the application. of the structure of the application
3. the Section Loading and preparing data describes how to load microdata into the application. It also discusses the requirements to the
4. the Section Setup anonymization problem covers the variable selection and setup of an SDC problem.
5. the Section Risk measurement covers methods to measure the disclosure risk in the microdata.
6. the Section Anonymization methods covers anonymization methods for quantitative and qualitative variables.
7. the Section Utility measurement covers the measurement of information loss resulting from anonymization of the data
8. the Section Export data and reports describes how to export the anonymized dataset and generate reports.
9. the Section Reproducibility covers functionality that render the anonymization process reproducable.
10. the Section Case Studies presents two case studies illustrating the full SDC process in sdcApp.

CHAPTER

TWO

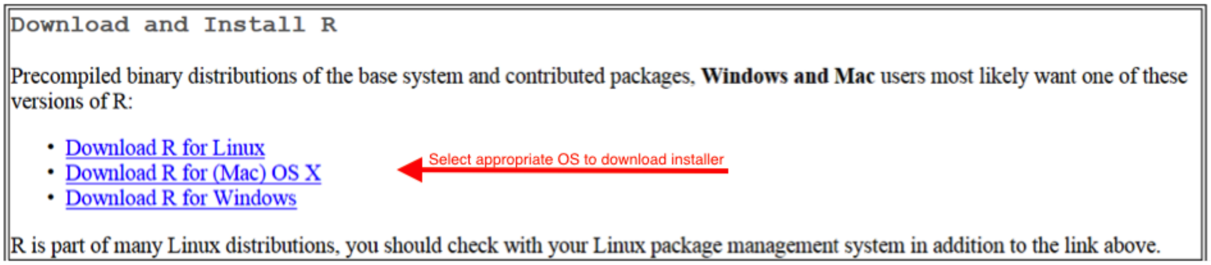
INSTALLATION AND UPDATING

This section will guide you through the steps you need to take to install *sdcApp*. *sdcApp* is a graphical user interface for the sdcMicro package. The *sdcMicro* package is an add-on package for the statistical software *R*. In order to start working with *sdcApp*, you need to install *R*, *RStudio*[1] as well as several add-on packages for R. All software is available free of charge and open-source. *R* and *RStudio* run on most platfroms, including Windows, Mac OS X and Linux. To use *sdcApp*, a webbrowser needs to be installed as well[2].

R, *RStudio*, the *sdcMicro* package as well as dependencies (other *R* packages that need to be installed for the *sdcMicro* package to work propoerly) are regularly updated. Therefore, it is recommended to regularly update to the latest version of the software. The Section *Updating R, RStudio and the sdcMicro package* shows how to check for updates and install updates.

2.1 Installing R and RStudio

The first step in the installation of *sdcApp* is the installation of *R* and *RStudio*. The free open source statistical software R can be downloaded from the CRAN website. By selecting your OS (cf. Fig. **??**), the installer will be dowloaded to your computer. In order to install *R*, open the installer and follow the installation steps.



Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- Download R for Linux
- Download R for (Mac) OS X
- Download R for Windows

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

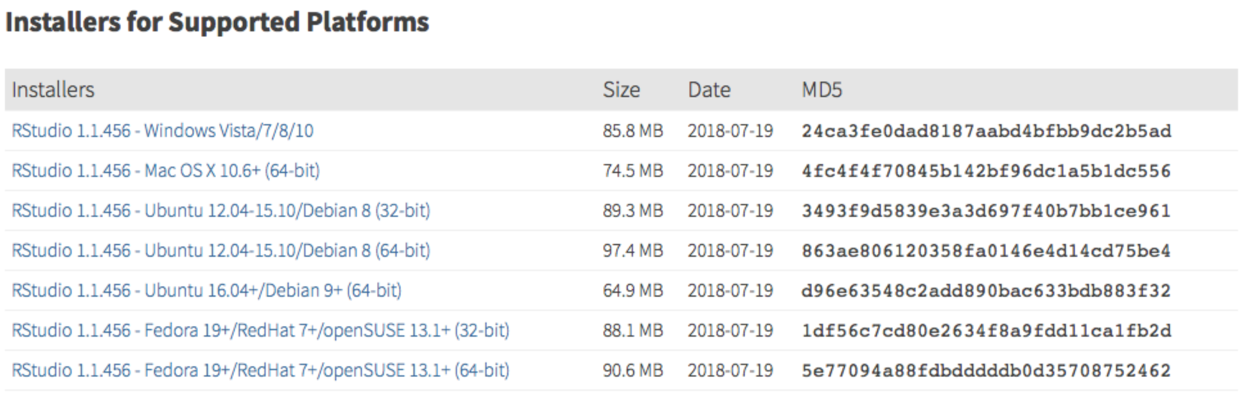
Fig. 2.1: Select OS to start downloading R

Once *R* is successfully installed, we can install *RStudio*. *RStudio* is an IDE (integrated development environment) for *R*. *RStudio* makes working with *R* much easier. *RStudio Desktop* and *RStudio Server* can be downloaded free of charge from the RStudio website. On this webpage, scroll down to the overview of different versions as shown in Fig. **??** and select the version corresponding to your OS to start downloading the installer. In order to install *RStudio*, open the installer and follow the installation steps.

Note: We recommend updating to the latest versions of R and RStudio if this software is already installed on your

[1] Technically speaking, *RStudio is not required to run *sdcApp*. Nevertheless, we recommend to install *RStudio* for a better user experience.

[2] *sdcApp* is a *Shiny* web application, which works best in a recent version of a webbrowser. Therefore, it is recommended to ensure that your webbrowser is updated regularly. Some webbrowsers may impede the proper functioning of *sdcApp*. If *sdcApp* doesn't work properly in your default web browser, please try to install Firefox or Google Chrome.



Installers for Supported Platforms

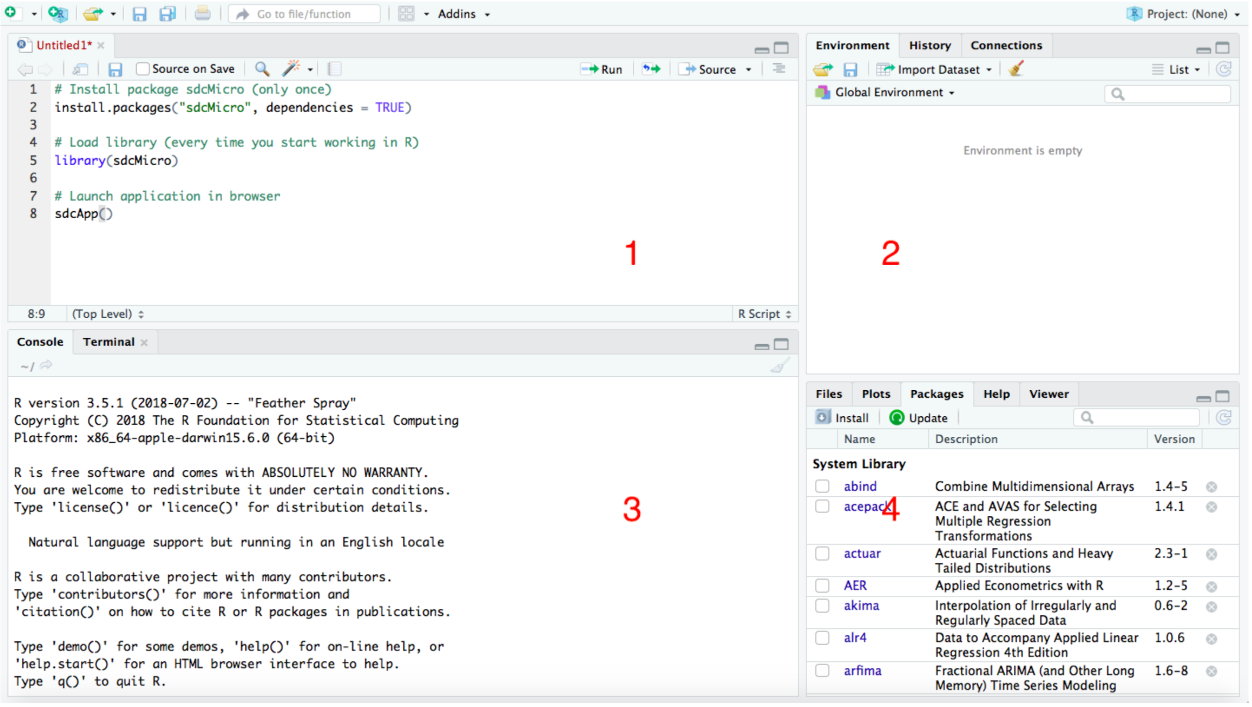
Installers	Size	Date	MD5
RStudio 1.1.456 - Windows Vista/7/8/10	85.8 MB	2018-07-19	24ca3fe0dad8187aabd4bfbb9dc2b5ad
RStudio 1.1.456 - Mac OS X 10.6+ (64-bit)	74.5 MB	2018-07-19	4fc4f4f70845b142bf96dc1a5b1dc556
RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (32-bit)	89.3 MB	2018-07-19	3493f9d5839e3a3d697f40b7bb1ce961
RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (64-bit)	97.4 MB	2018-07-19	863ae806120358fa0146e4d14cd75be4
RStudio 1.1.456 - Ubuntu 16.04+/Debian 9+ (64-bit)	64.9 MB	2018-07-19	d96e63548c2add890bac633bdb883f32
RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	88.1 MB	2018-07-19	1df56c7cd80e2634f8a9fdd11ca1fb2d
RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	90.6 MB	2018-07-19	5e77094a88fdbddddb0d35708752462

Fig. 2.2: Select version to start downloading RStudio

computer before moving on. See also the Sections *Updating R* and *Updating RStudio* for more information on updating the software.

Once *R* and *RStudio* are installed on your computer, open *RStudio*. The *RStudio* interface consists by default of four different panes as shown in Fig. **??**.

1. Script editor (by default left up)
2. Workspace and history (by default right up)
3. R console (by default left down)
4. Plots, files and help (by default right down)



```r
# Install package sdcMicro (only once)
install.packages("sdcMicro", dependencies = TRUE)

# Load library (every time you start working in R)
library(sdcMicro)

# Launch application in browser
sdcApp()
```

```
R version 3.5.1 (2018-07-02) -- "Feather Spray"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
```

	Name	Description	Version
	System Library		
□	abind	Combine Multidimensional Arrays	1.4-5
□	acepack	ACE and AVAS for Selecting Multiple Regression Transformations	1.4.1
□	actuar	Actuarial Functions and Heavy Tailed Distributions	2.3-1
□	AER	Applied Econometrics with R	1.2-5
□	akima	Interpolation of Irregularly and Regularly Spaced Data	0.6-2
□	alr4	Data to Accompany Applied Linear Regression 4th Edition	1.0.6
□	arfima	Fractional ARIMA (and Other Long Memory) Time Series Modeling	1.6-8

Fig. 2.3: Screenshot RStudio

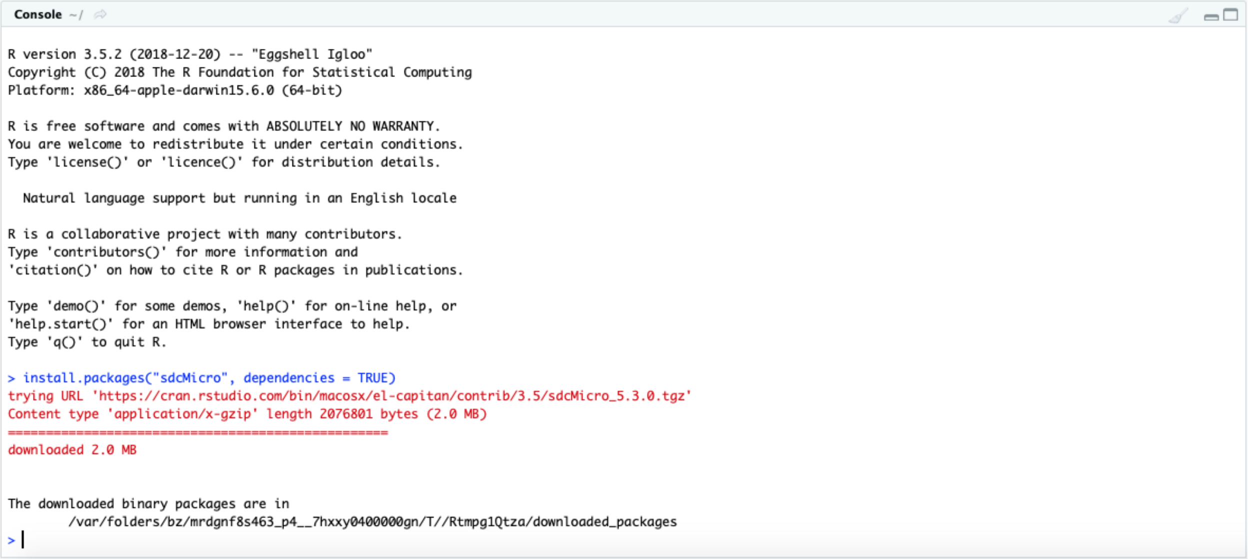
2.2 Installing sdcMicro package

sdcApp is included in the *R* package *sdcMicro*. Once *RStudio* is opened, *sdcMicro* can be installed by executing commands in the *R* console. *sdcMicro* and a set of other *R* packages that are required by the *sdcMicro* package are downloaded from the CRAN servers. Therefore, it is necessary to be connected to the internet during the installation process.[3]

In order to install the latest version of the *sdcMicro* package, type the command `install.packages("sdcMicro", dependencies = TRUE)` in the console and press enter to execute (cf. Fig. **??**). The first time you are installing R packages, a prompt will ask you to select a CRAN mirror (server) to install the package from. Since the packages on all mirrors are identical, you can choose any of the locations. The sdcMicro package itself uses functionality from a set of other R packages (e.g., *haven* for reading files in different formats). By specifying the dependencies argument to TRUE, these dependencies will automatically be installed too.

Listing 2.1: Installing sdcMicro package

```r
# install sdcMicro package
install.packages("sdcMicro", dependencies = TRUE)
```



```
R version 3.5.2 (2018-12-20) -- "Eggshell Igloo"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)

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Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> install.packages("sdcMicro", dependencies = TRUE)
trying URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.5/sdcMicro_5.3.0.tgz'
Content type 'application/x-gzip' length 2076801 bytes (2.0 MB)
==================================================
downloaded 2.0 MB


The downloaded binary packages are in
	/var/folders/bz/mrdgnf8s463_p4__7hxxy0400000gn/T//Rtmpg1Qtza/downloaded_packages
> 
```

Fig. 2.4: Installing sdcMicro package from *R* console

Note: Also dependencies will be installed and the installation may take some time. Dependencies are other add-on packages, of which the functionality is required to run the sdcMicro package.

Note: An internet connection is not required while using *sdcMicro* and *sdcApp* and the data are stored locally on your computer or server. The web browser uses a local host IP, which is not connected to the internet and the browser is only used to communicate with the running *R* session.

[3] It is possible to download *R*, *RStudio* and the packages and transfer the files to the computer with for example a USB drive in case the computer *sdcMicro* should be installed on cannot be connected to the internet for technical or confidentiality reasons.

2.3 Launching *sdcApp*

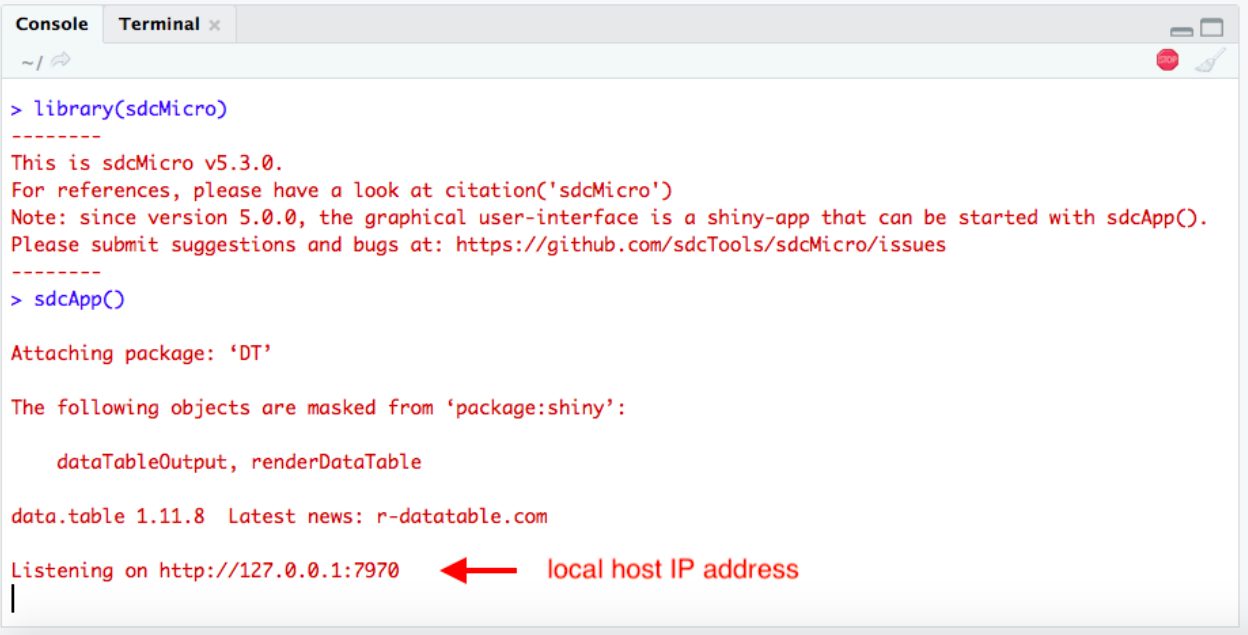
Once the *sdcMicro* package is successfully installed, the *sdcMicro* package needs to be loaded. Installing the package is only required once (except for updating), whereas loading the package is required every time a new *R* session is started.

You can load the *sdcMicro* package by typing `library(sdcMicro)` and launch the application by typing `sdcApp()`.

sdcApp opens in your system's default web browser through the local host IP `127.0.0.1:`. *sdcApp* works with recent versions of any webbrowser. Due to small issues encountered with some browsers, we recommend to use Google Chrome, Mozilla Firefox or Safari for the best performance. In case your default web browser is not one of the aforementioned browsers, you can simply open an alternative browser and copy paste the local host IP address in the new browser. *sdcApp* will open in the new browser.

Note: After launching *sdcApp* the *R* session is busy and cannot be used for other calculations.

Furthermore, it's important that your *R* session is enabled to use the installed webbrowser.



```
> library(sdcMicro)
--------
This is sdcMicro v5.3.0.
For references, please have a look at citation('sdcMicro')
Note: since version 5.0.0, the graphical user-interface is a shiny-app that can be started with sdcApp().
Please submit suggestions and bugs at: https://github.com/sdcTools/sdcMicro/issues
--------
> sdcApp()

Attaching package: ‘DT’

The following objects are masked from ‘package:shiny’:

    dataTableOutput, renderDataTable

data.table 1.11.8  Latest news: r-datatable.com

Listening on http://127.0.0.1:7970
```

Fig. 2.5: R console with local IP after launching *sdcApp*

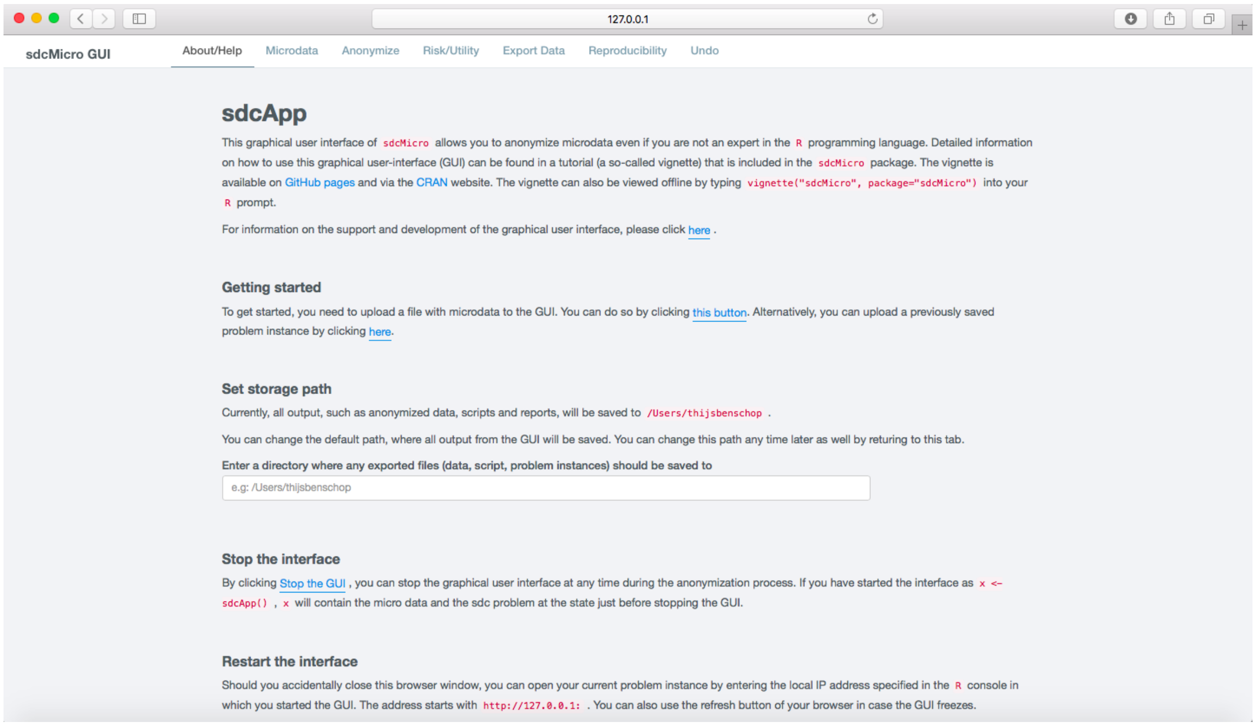
Listing 2.2: Loading sdcMicro package and launching *sdcApp*

```r
# Load sdcMicro package
library(sdcMicro)

# Launch sdcApp (opens in browser window)
sdcApp()
```

In rare cases, not all dependencies are correctly installed and the following error message appears in the R console upon loading the sdcMicro package.

Please install the package(s) indicated in the error message manually by using the command install.packages() with



sdcApp

This graphical user interface of `sdcMicro` allows you to anonymize microdata even if you are not an expert in the `R` programming language. Detailed information on how to use this graphical user-interface (GUI) can be found in a tutorial (a so-called vignette) that is included in the `sdcMicro` package. The vignette is available on GitHub pages and via the CRAN website. The vignette can also be viewed offline by typing `vignette("sdcMicro", package="sdcMicro")` into your `R` prompt.

For information on the support and development of the graphical user interface, please click here .

Getting started

To get started, you need to upload a file with microdata to the GUI. You can do so by clicking this button. Alternatively, you can upload a previously saved problem instance by clicking here.

Set storage path

Currently, all output, such as anonymized data, scripts and reports, will be saved to `/Users/thijsbenschop` .

You can change the default path, where all output from the GUI will be saved. You can change this path any time later as well by returing to this tab.

Enter a directory where any exported files (data, script, problem instances) should be saved to

e.g: /Users/thijsbenschop

Stop the interface

By clicking Stop the GUI , you can stop the graphical user interface at any time during the anonymization process. If you have started the interface as `x <- sdcApp()` , `x` will contain the micro data and the sdc problem at the state just before stopping the GUI.

Restart the interface

Should you accidentally close this browser window, you can open your current problem instance by entering the local IP address specified in the `R` console in which you started the GUI. The address starts with `http://127.0.0.1:` . You can also use the refresh button of your browser in case the GUI freezes.

Fig. 2.6: Start screen sdcApp in browser with local IP

the name of the package(s). In the example error message, this would be for the packages .

2.4 Updating R, RStudio and the sdcMicro package

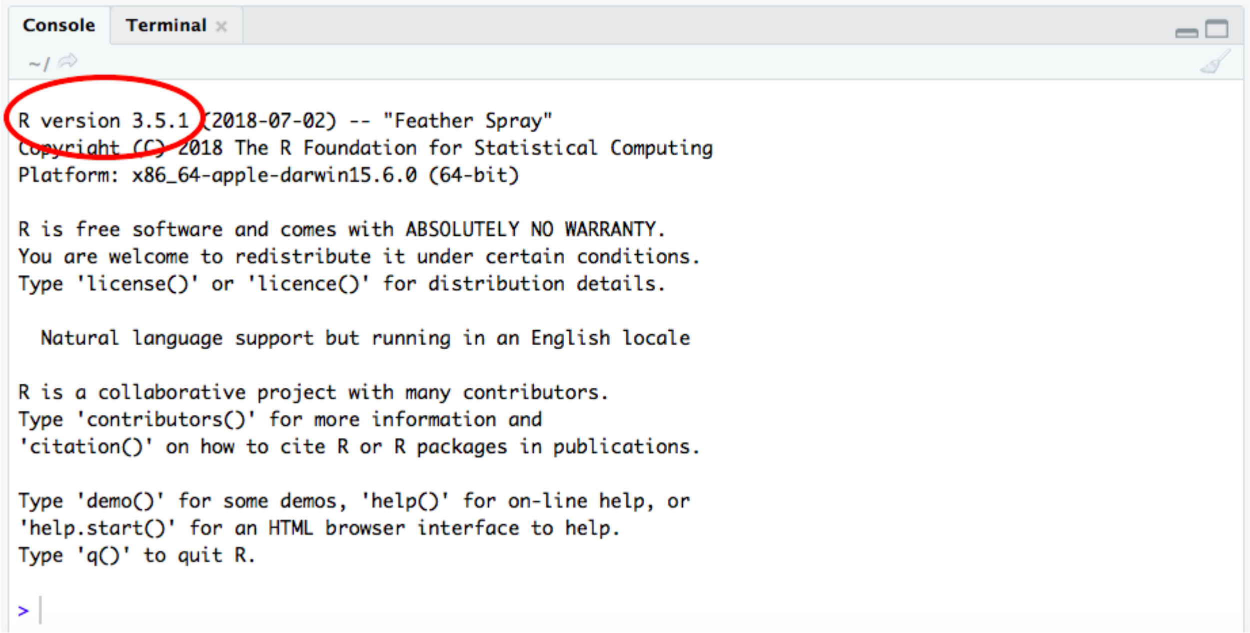
R, *RStudio*, the *dcMicro* package as well as dependencies are regularly updated. Updates include bug fixes as well as additional functionality. Therefore, it is recommended to regularly update to the latest version of the software.

2.4.1 Updating R

RStudio uses by default the most recent version of *R* available on your system. New versions of *R* packages, including the *sdcMicro* package, rely on the newest version of *R*. Therefore, it's important to regularly check for updates of *R*. The easiest way to do so is to visit regularly the CRAN website. If a new version of *R* is available, the same steps as for the installation of *R* need to be followed as described in the Section *Installing R and RStudio*. The version number of the *R* version installed on your computer appears in the R console upon launching *R* or *RStudio* (cf. `fig27`).

2.4.2 Updating RStudio

To check for updates in *RStudio*, go to Help -> Check for updates. If an update is available, the current version number and the newest version number are shown. In order to install the newer version, you need to visit the RStudio website and follow the steps as described in the Section *Installing R and RStudio*.



```
R version 3.5.1 (2018-07-02) -- "Feather Spray"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
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R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

Fig. 2.7: R console with version number

2.4.3 Updating R packages

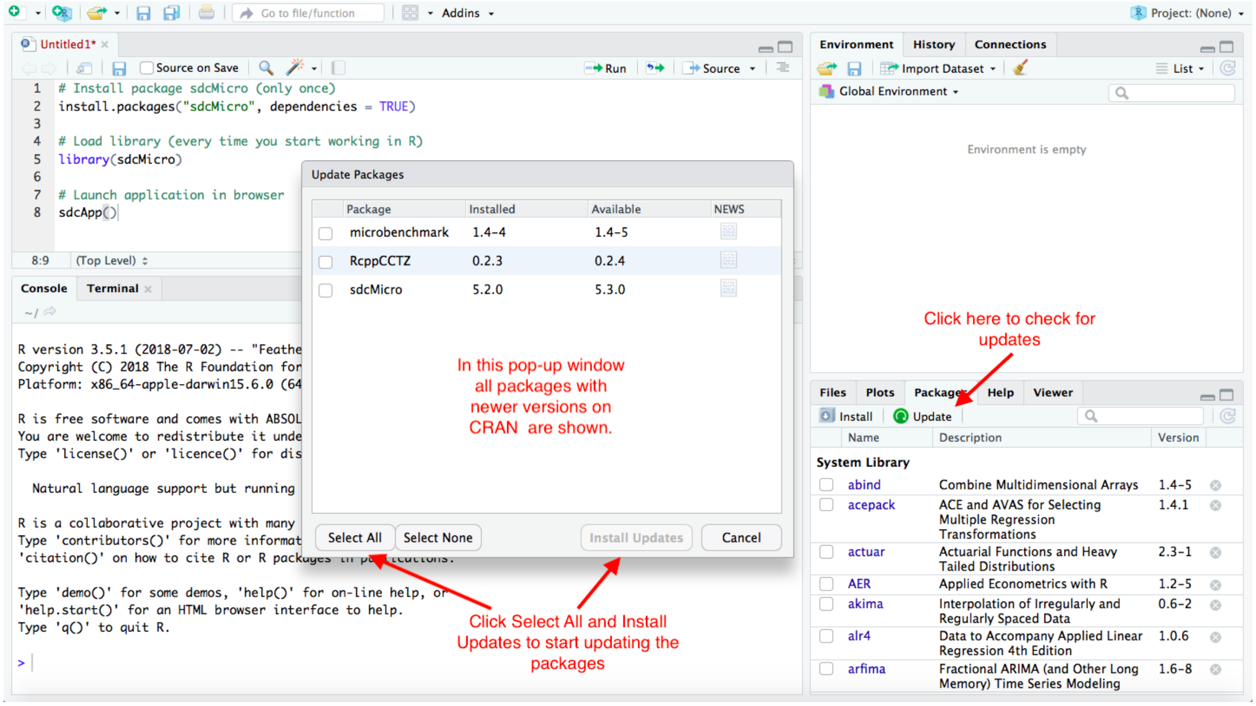
The *sdcMicro* package is regularly updated to fix bugs and add functionality. In order to check for newer versions, click on the Update button to get an overview of all packages that have newer versions available. By clicking Select all, these packages are all automatically updated.

Listing 2.3: Updating packages

```
# Update
install.packages()
```

2.5 Bug reporting on GitHub

The sdcMicro package is open source software and the source code can be easily viewed on the GitHub of the *sdcMicro* project. There you can also report alleged bugs and raise other issues.



```r
# Install package sdcMicro (only once)
install.packages("sdcMicro", dependencies = TRUE)

# Load library (every time you start working in R)
library(sdcMicro)

# Launch application in browser
sdcApp()
```

```
R version 3.5.1 (2018-07-02) -- "Feathe
Copyright (C) 2018 The R Foundation for
Platform: x86_64-apple-darwin15.6.0 (64

R is free software and comes with ABSOL
You are welcome to redistribute it unde
Type 'license()' or 'licence()' for dis

  Natural language support but running

R is a collaborative project with many
Type 'contributors()' for more informat
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 
```

Update Packages

	Package	Installed	Available	NEWS
□	microbenchmark	1.4–4	1.4–5	
□	RcppCCTZ	0.2.3	0.2.4	
□	sdcMicro	5.2.0	5.3.0	

In this pop-up window all packages with newer versions on CRAN are shown.

Click here to check for updates

Click Select All and Install Updates to start updating the packages

	Name	Description	Version
System Library			
□	abind	Combine Multidimensional Arrays	1.4–5
□	acepack	ACE and AVAS for Selecting Multiple Regression Transformations	1.4.1
□	actuar	Actuarial Functions and Heavy Tailed Distributions	2.3–1
□	AER	Applied Econometrics with R	1.2–5
□	akima	Interpolation of Irregularly and Regularly Spaced Data	0.6–2
□	alr4	Data to Accompany Applied Linear Regression 4th Edition	1.0.6
□	arfima	Fractional ARIMA (and Other Long Memory) Time Series Modeling	1.6–8

Fig. 2.8: Updating R packages in RStudio

CHAPTER

THREE

INTRODUCTION TO SDCAPP

sdcApp is a user-friendly application for microdata anonymization and is built on the Shiny technology. Shiny allows users to communicate through a GUI that runs in a webbrowser with a local *R* session. The local *R* session performs the necessary calculations. In the case of *sdcApp*, most functionality used in *R* is included in the sdcMicro package.

sdcApp has a tab structure and consists of seven tabs, which in turn consist of up to three panels. This structured is further explored below. The tabs and panels are used to navigate through the app.

3.1 Starting sdcApp

After succcesful installation (see the Section Installation and updating), *sdcApp* is ready for use. Every single time *sdcApp* is used, first the applications *R* or *RStudio* need to be opened. We recommend to use *RStudio* for ease of use. After launching *R* or *RStudio*, the *sdcMicro* package needs to be loaded and *sdcApp* needs to be launched. To load *sdcMicro* and launch *sdcApp*, enter the code as shown in Listing **??** in the *R* console. Press enter after each line to execute the line of code. Fig. **??** shows the output in the *R* console after successfully launching *sdcApp*.

Listing 3.1: Loading sdcMicro package and launching sdcApp

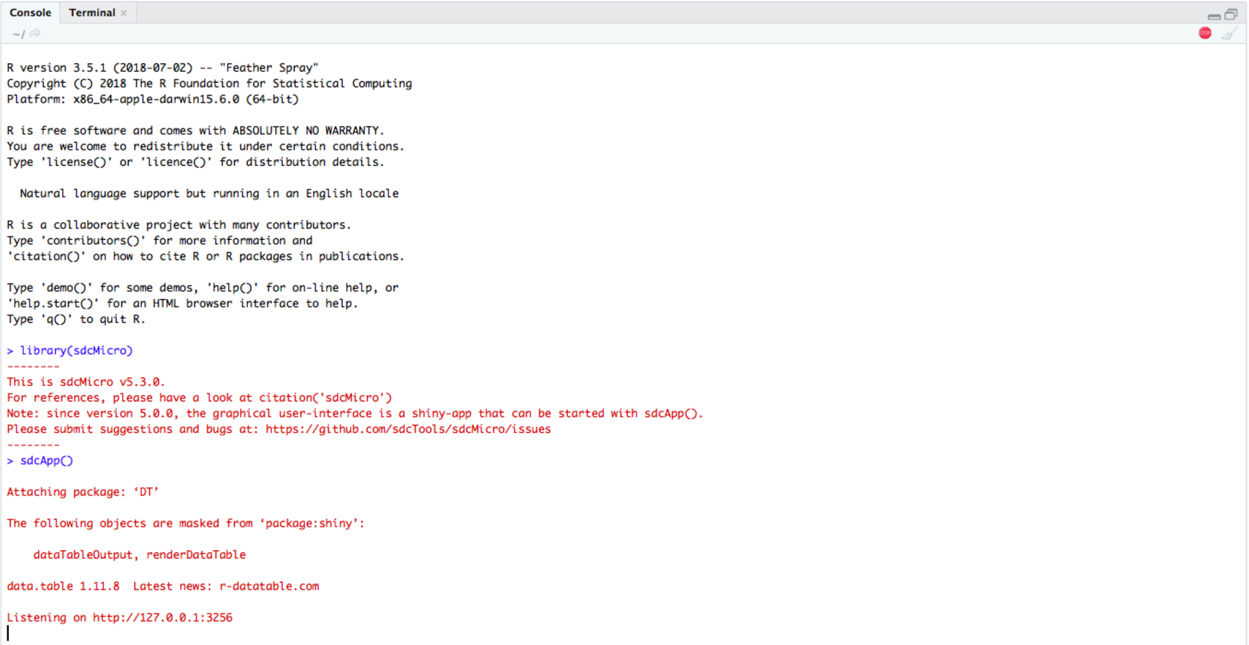
```
# Load sdcMicro package
library(sdcMicro)

# Launch sdcApp (opens in browser window)
sdcApp()
```

Note: You can omit the lines starting with a hash tag (#) as these are comment lines and ignored by the *R* interpreter.

The application opens in a new tab in your default web browser. In case you prefer to use an alternative web browser, you can simply copy the address of the localhost and paste it into a different browser on the same machine. The localhost address can be found in the output in the *R* console. The address starts with `http://127.0.0.1:` followed by a four digit number. In the example in Fig. **??**, the full localhost address is `http://127.0.0.1:3256`. The application opens on the **About/Help** tab (see Fig. **??**).

Note: Firewalls and other settings on your computer and browser may prevent *sdcApp* from opening in your webbrowser. As a first thing you could try to copy paste the localhost address into your webbrowser. If that is not successful, try changing the settings of your browser and firewall.



```
R version 3.5.1 (2018-07-02) -- "Feather Spray"
Copyright (C) 2018 The R Foundation for Statistical Computing
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--------
This is sdcMicro v5.3.0.
For references, please have a look at citation('sdcMicro')
Note: since version 5.0.0, the graphical user-interface is a shiny-app that can be started with sdcApp().
Please submit suggestions and bugs at: https://github.com/sdcTools/sdcMicro/issues
--------
> sdcApp()

Attaching package: ‘DT’

The following objects are masked from ‘package:shiny’:

    dataTableOutput, renderDataTable

data.table 1.11.8  Latest news: r-datatable.com

Listening on http://127.0.0.1:3256
```
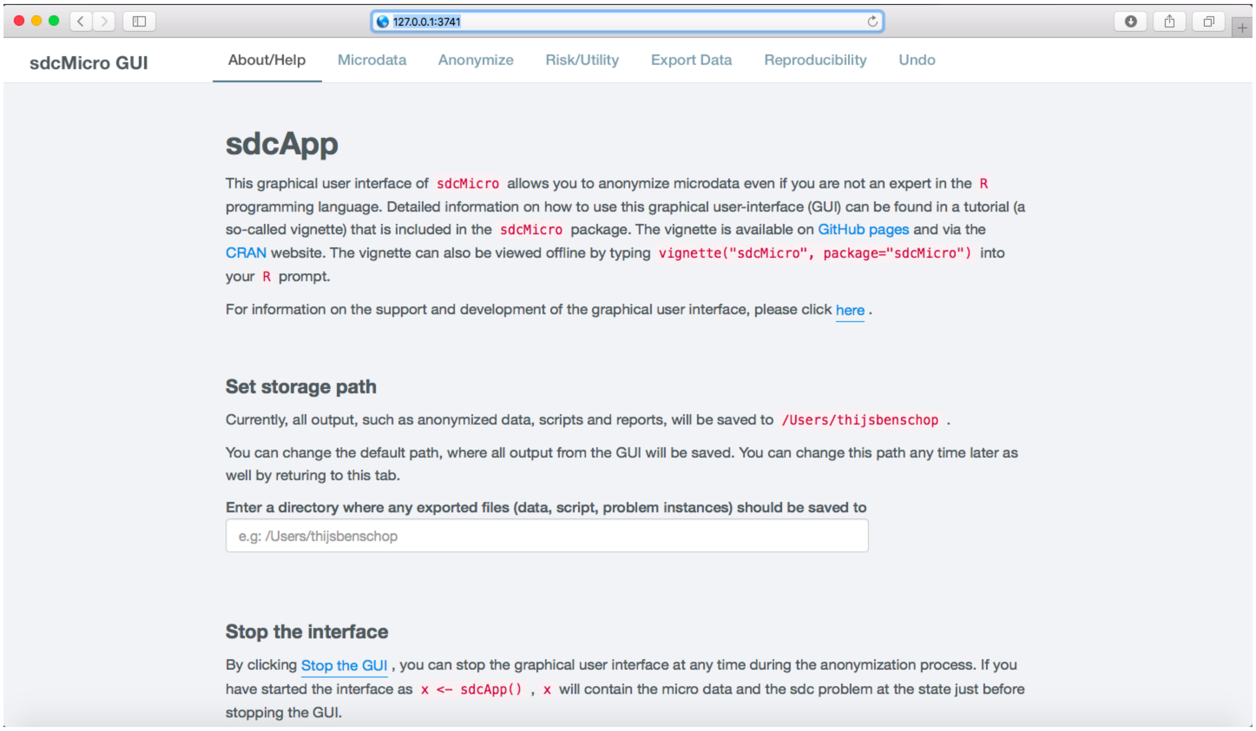

Fig. 3.1: R console after loading the *sdcMicro* package and launching *sdcApp*



sdcApp

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For information on the support and development of the graphical user interface, please click here .

Set storage path

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You can change the default path, where all output from the GUI will be saved. You can change this path any time later as well by returing to this tab.

Enter a directory where any exported files (data, script, problem instances) should be saved to

e.g: /Users/thijsbenschop

Stop the interface

By clicking Stop the GUI , you can stop the graphical user interface at any time during the anonymization process. If you have started the interface as `x <- sdcApp()` , `x` will contain the micro data and the sdc problem at the state just before stopping the GUI.

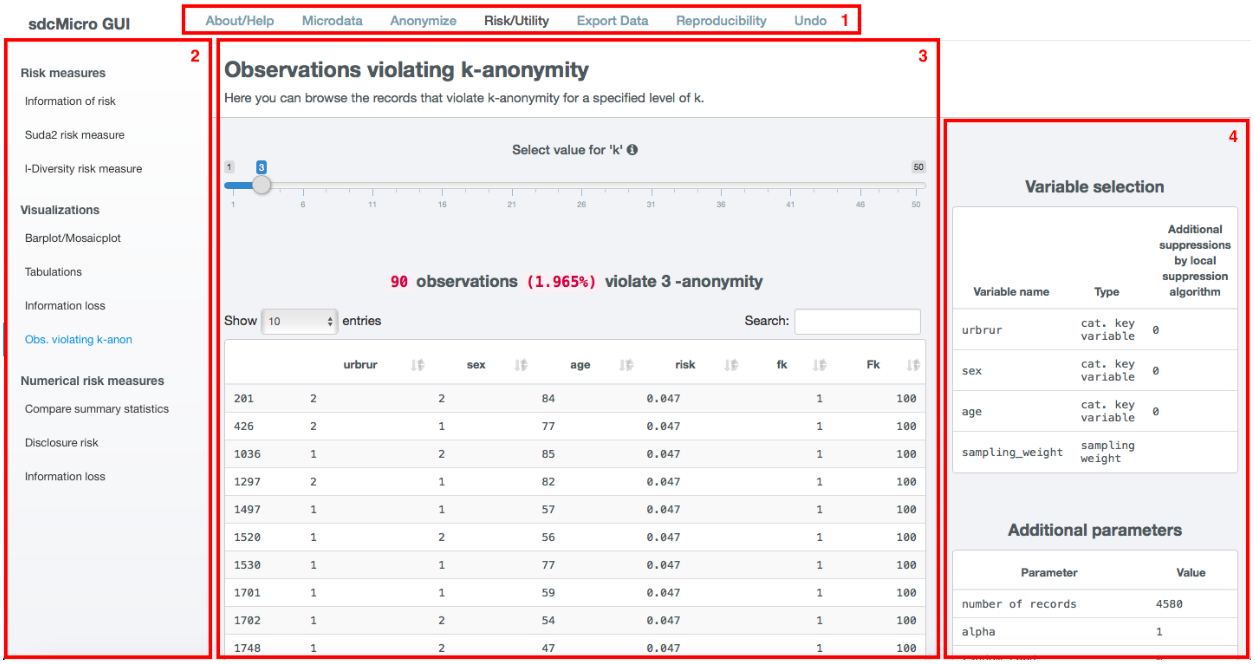
Fig. 3.2: **About/Help** tab in web browser after launching *sdcApp* with localhost address

3.2 Tab and panel structure

The sdcApp consists of seven different tabs that serve different parts of the SDC process. The tabs can be selected in the navigation bar at the top of the page (cf. the area indicated with 1 in Fig. **??**). The navigation bar is visible at all times. The content of each tab may change as function the specified SDC problem and the current state of the SDC process. For example, anonymization methods for continuous key variables are not shown on the **Anonymize** tab, if no continuous key variables are selected.

- **About/Help** Landing page to set storage path, quit and restart *sdcApp* as well as provide feedback to the developers
- **Microdata** Page to load, view, explore and prepare the microdata to be anonymized
- **Anonymize** Page to setup the anonymization problem (select variables, set parameters). Once the problem is defined, this page shows a summary of the anonymization problem and allows to apply anonymization methods
- **Risk/Utility** Page to evaluate disclosure risk and information loss (data utility)
- **Export Data** Page to export the anonymized data and reports on the anonymization process
- **Reproducibility** Page with functionality to guarantee the reproducibility of the process by exporting the *R* script or problem instance
- **Undo** Page to revert one or several steps in the anonymization process

Each tab consists of two panels: the left sidebar (cf. the area indicated with 2 in Fig. **??**) and the main panel (cf. the area indicated with 3 in Fig. **??**). The left panel allows the user to navigate between different function on the same tab, e.g., different risk measures. Some tabs have an additional right sidebar (cf. the area indicated with 4 in Fig. **??**), which provide summary information on the current SDC problem.



Observations violating k-anonymity

Here you can browse the records that violate k-anonymity for a specified level of k.

90 observations (1.965%) violate 3 -anonymity

	urbrur	sex	age	risk	fk	Fk
201	2	2	84	0.047	1	100
426	2	1	77	0.047	1	100
1036	1	2	85	0.047	1	100
1297	2	1	82	0.047	1	100
1497	1	1	57	0.047	1	100
1520	1	2	56	0.047	1	100
1530	1	1	77	0.047	1	100
1701	1	1	59	0.047	1	100
1702	1	2	54	0.047	1	100
1748	1	2	47	0.047	1	100

Variable selection

Variable name	Type	Additional suppressions by local suppression algorithm
urbrur	cat. key variable	0
sex	cat. key variable	0
age	cat. key variable	0
sampling_weight	sampling weight	

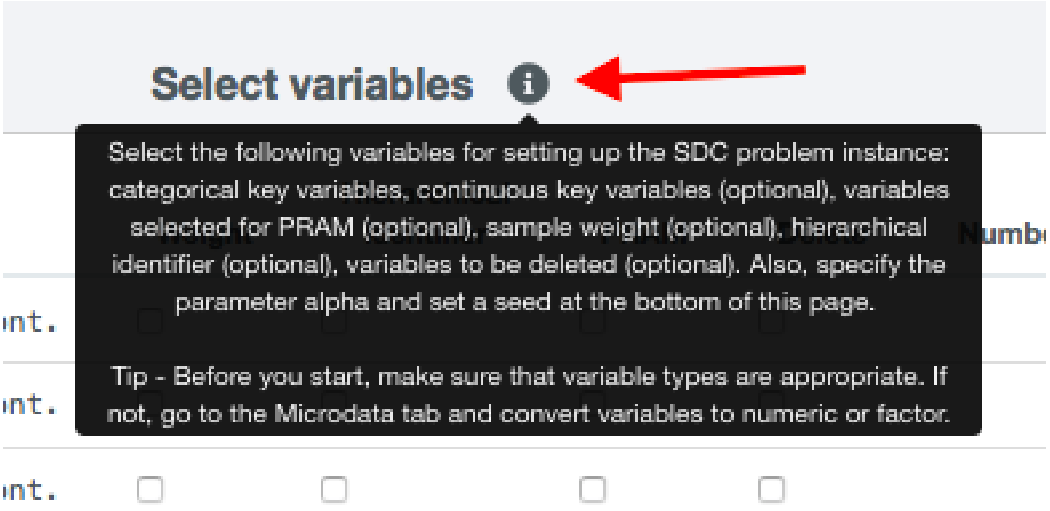
Additional parameters

Parameter	Value
number of records	4580
alpha	1

Fig. 3.3: Risk/Utility tab with navigation bar and panel structure

3.3 In-app help

By hovering with the mouse pointer over the ℹ icon in *sdcApp*, additional information on e.g., specific parameters and the interpretation of results is provided. The help information is mainly intended to provide a brief reminder and is not meant to replace a thorough study of the SDC literature on risk and utility measurement and anonymization methods. Fig. **??** shows the help pop-up for the variable selection table.



Select the following variables for setting up the SDC problem instance: categorical key variables, continuous key variables (optional), variables selected for PRAM (optional), sample weight (optional), hierarchical identifier (optional), variables to be deleted (optional). Also, specify the parameter alpha and set a seed at the bottom of this page.

Tip - Before you start, make sure that variable types are appropriate. If not, go to the Microdata tab and convert variables to numeric or factor.

Fig. 3.4: Help pop-up when moving with mouse cursor over *i* icon

3.4 Getting started

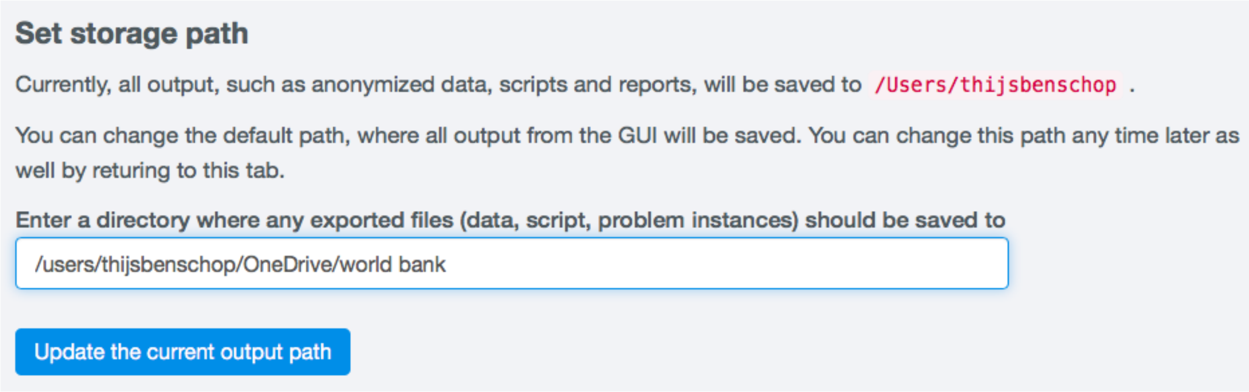
Use testdata dataset: all examples in this guide are illustrated with the testdata dataset.

3.5 Set storage path

All output exported from *sdcApp*, such as the anonymized dataset, reports and scripts will be saved in the directory shown under the header **Set storage path** on the **About/Help** tab (cf. Fig. **??**). Upon launching *sdcApp*, this directory is set to the *R* working directory. Change the working directory to a the folder in the project directory with the dataset to be anonymized by typing the path to this folder in the input box (cf. Fig. **??**). Once a valid path on your computer is entered, click the blue button **Update the current output path** to change the path. If the entered path is not a valid path on your system, a red button appears with the text **The specified directory does not exist, thus the path can't be updated**. It is recommended to create a new folder in the project directory for the *sdcApp* output. The file names of the output files contain a date and time stamp as well as a brief description, e.g., exportedData_sdcMicro_20181010_1211.dta for the anonymized microdata in STATA format on October 10, 2018 at 12:11 and exportedProblem_sdcMicro_20180304_1633.rdata for the saved problem instance as *R* datafile on March 4, 2018 ar 16:33.

Note: The storage path to the output folder needs to be specified every time *sdcApp* is launched.

Note: If an sdcProblem is saved and reloaded, the storage path is set to the path saved in the sdcProblem. If the problem is loaded on a different computer than it was saved at, the storage path may be invalid and needs to be updated in the same way as described above.



Set storage path

Currently, all output, such as anonymized data, scripts and reports, will be saved to `/Users/thijsbenschop` .

You can change the default path, where all output from the GUI will be saved. You can change this path any time later as well by returing to this tab.

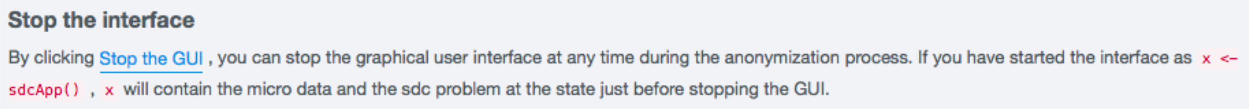
Enter a directory where any exported files (data, script, problem instances) should be saved to

/users/thijsbenschop/OneDrive/world bank

Fig. 3.5: View and set storage path for file export

3.6 Quiting sdcApp

To quit *sdcApp*, click on **Stop the GUI** under the header **Stop the interface** on the **About/Help** tab. It is recommended to quit *R* or *RStudio* after quitting *sdcApp* to ensure that nothing is left in the memory. This especially applies to a restart due to *sdcApp* not responding.



Stop the interface

By clicking Stop the GUI , you can stop the graphical user interface at any time during the anonymization process. If you have started the interface as `x <- sdcApp()` , `x` will contain the micro data and the sdc problem at the state just before stopping the GUI.

Fig. 3.6: Button to quit *sdcApp* on the **About/Help** tab

Save SDC problem to continue working later. Possible once the SDC problem is defined. See undo section

CHAPTER

FOUR

LOADING AND PREPARING DATA

This section discusses how to load microdata into *sdcApp* and prepare the data for the SDC process.

The first step in the SDC process is loading the dataset into *sdcApp*. *sdcApp* supports most common statistical data formats, such as *R*, *STATA*, *SPSS* and *SAS* files. First time users may also load one of the two practice datasets, which are included in *sdcApp*, to explore *sdcApp* and methods. Most examples in this guide are illustrated by using the practice dataset *testdata* and can be reproduced by using this dataset.

After loading the data, the user needs to prepare the data for the SDC process. Most preparation steps can be carried out in *sdcApp*, although users may find it more convenient to perform some of these actions in another statistical software before loading the data in *sdcApp*.

4.1 Loading data

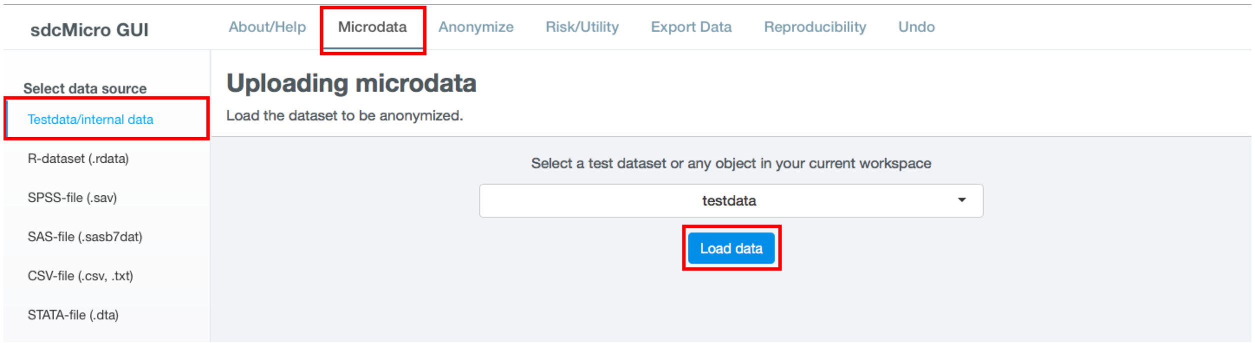
4.1.1 Testdata

sdcApp includes two practice datasets: *testdata* and *testdata2*. The dataset *testdata* is used to illustrate methods and examples in this guide. In order to replicate these examples, the user needs to load this dataset. In order to load the testdata dataset, navigate to the **Microdata tab** and select **Testdata/Internal data** in the left sidebar. Select the dataset from the dropdown menu and click the button **Load data**. This is illustrated in Fig. **??**.

Note: Any other datasets loaded in the current *R* session are also shown in the dropdown list with available datasets and can be loaded. **Add screenshot of dropdown menu with mymicrodata**

After loading the dataset, the data is displayed in the **Microdata** tab. The **Microdata** tab changes and the functionality for loading microdata is replaced with functionality to explore and prepare the dataset (cf. Fig. **??**). The left sidebar shows different options to explore and prepare the data for the anonymization process, as discussed in the next sections.

After loading the testdata dataset, the loaded dataset is displayed (cf. Fig. **??**). By default the first 20 records are displayed. With the dropdown menu in the topleft corner it is possible to display 20, 50, 100 or all records per page. It is not recommended to select *all* in case of larger datasets *sdcApp* will run very slow. In the right bottom it is possible to navigate to different pages, either by clicking *Next* or by clicking on a page number. The table with the data is both horizontally and vertically scrollable with the scrollbars on the right side and bottom of the table. To sort the data by a variable, click on the symbol with two arrows (↓↑ or ▲▼) next to the variable name in the header of the table. The data is searchable by using the search bar on the right top of the table. Only records with matches are displayed. The search is performed simultaneously on all variables.



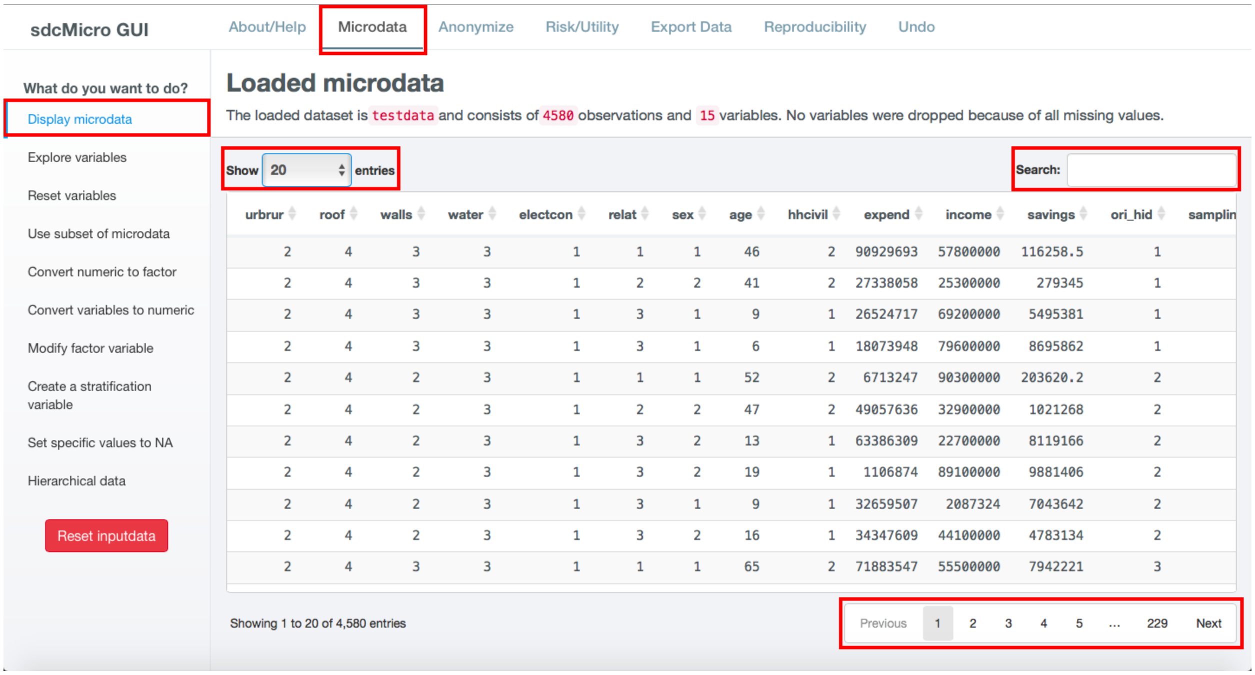
Uploading microdata

Load the dataset to be anonymized.

Select a test dataset or any object in your current workspace

testdata

Fig. 4.1: Load testdata on **Microdata** tab



Loaded microdata

The loaded dataset is testdata and consists of 4580 observations and 15 variables. No variables were dropped because of all missing values.

Show 20 entries

Search:

urbrur	roof	walls	water	electcon	relat	sex	age	hhcivil	expend	income	savings	ori_hid	samplin
2	4	3	3	1	1	1	46	2	90929693	57800000	116258.5	1	
2	4	3	3	1	2	2	41	2	27338058	25300000	279345	1	
2	4	3	3	1	3	1	9	1	26524717	69200000	5495381	1	
2	4	3	3	1	3	1	6	1	18073948	79600000	8695862	1	
2	4	2	3	1	1	1	52	2	6713247	90300000	203620.2	2	
2	4	2	3	1	2	2	47	2	49057636	32900000	1021268	2	
2	4	2	3	1	3	2	13	1	63386309	22700000	8119166	2	
2	4	2	3	1	3	2	19	1	1106874	89100000	9881406	2	
2	4	2	3	1	3	1	9	1	32659507	2087324	7043642	2	
2	4	2	3	1	3	2	16	1	34347609	44100000	4783134	2	
2	4	3	3	1	1	1	65	2	71883547	55500000	7942221	3	

Showing 1 to 20 of 4,580 entries

Fig. 4.2: Loaded dataset

4.1.2 Other microdata

sdcApp supports datasets in several foreign data formats (cf. Table **??**). If the microdata is not in one of these data formats, another software can be used to convert the data, such as *Stat/Transfer*. Also some statistical software allow to export the data in another data format.

Table 4.1: Data formats compatible with sdcApp

Software	File extension
R/RStudio	.rdata
SPSS	.sav
SAS	.sas7bdat
CSV	.csv, .txt
STATA	.dta

In order to load a dataset, select the corresponding data format from the left sidebar of the **Microdata** tab. For all formats the user can set two options:

1. **Convert string variables (character vectors) to factor variables?** If `TRUE` (default), variables of type string are automatically converted to categorical variables (type factor in *R*). Categorical variables need to be of type factor in *sdcApp*. Remove any textual variables, such as 'Specify other:' variables before loading the data. These variables are oftentimes not suitable for release and require long computation times to be transformed to factor. If `FALSE`,
2. **Drop variables with only missing values (NA)?** If `TRUE` (default), variables that contain only missing values (`NA` in *R*) are removed upon loading the data. This does not cause any loss of information, as these variabels do not contain information. However, variables with only missing values can cause issues in *sdcApp*. If `FALSE`, no variables are deleted.

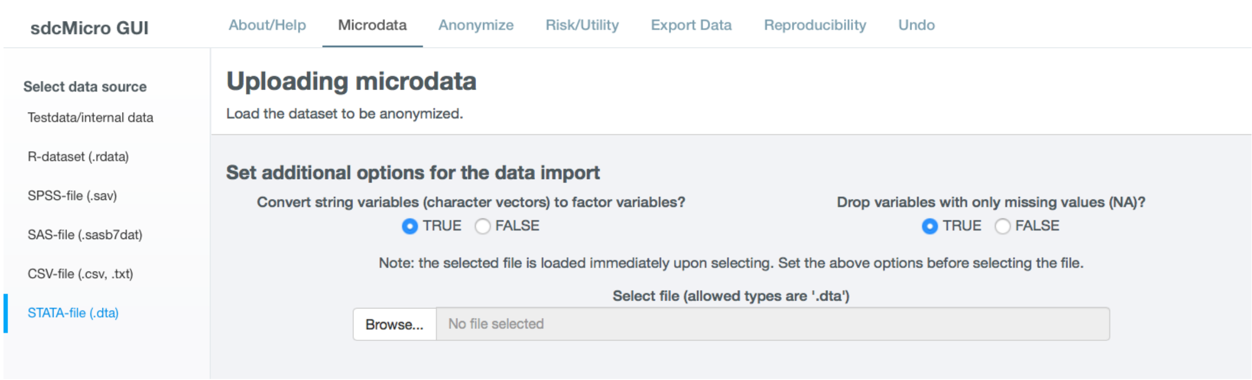
If the selected data format is a CSV-file, two additional options need to be specified:

1. **Does the first row contain the variable names?** If `TRUE`, the values in the first row are used as variable names. If `FALSE`, the variables names are set to V1, V2, V3, … in the order of appearance in the dataset.
2. **Field separator** The field separator in the csv file needs to be specified. Options are comma (,), semicolon (;) and tab.

After setting the options for the data upload, click on the button **Browse** to access the file system in your computer and select the microdata file. The file is upload immediately after selection. After loading the file, which may

Note: Set the additional options before selecting the datafile from your file system. Upon selection after clicking **Browse**, the file is immediately loaded and settings can no longer be changed. If the file was accidentally loaded before setting all parameters, the file needs to be reloaded after first restting the microdata by clicking **Reset microdata** in the left sidebar.

Note: The default maximum file size in *sdcApp* is 50 MB. In order to upload larger files, the maximum file size in MB needs to be specified upon launching *sdcApp*. This can be achieved by specifying the argument `maxRequestSize`:



Uploading microdata

Load the dataset to be anonymized.

Set additional options for the data import

Convert string variables (character vectors) to factor variables? ● TRUE ○ FALSE

Drop variables with only missing values (NA)? ● TRUE ○ FALSE

Note: the selected file is loaded immediately upon selecting. Set the above options before selecting the file.

Select file (allowed types are '.dta')

No file selected

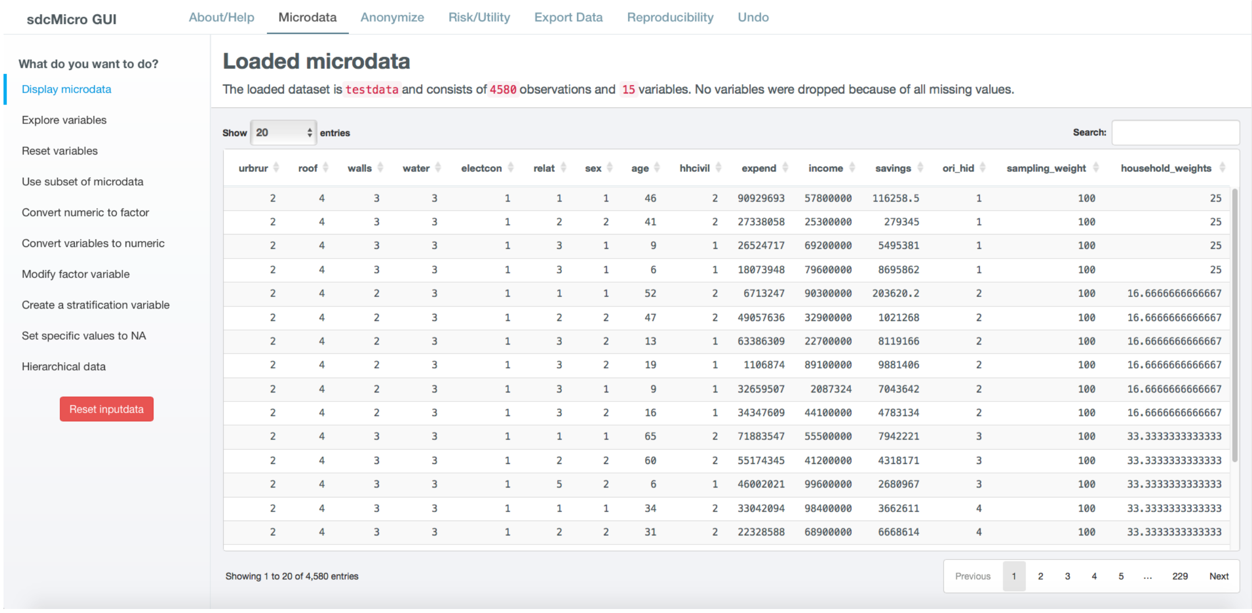
Fig. 4.3: Load data on Microdata tab - example STATA dataset

Listing 4.1: Launching *sdcApp* to load larger files

```
# Launch sdcApp with increased max. file size (200MB)
sdcApp(maxRequestSize = 200)
```

After loading the testdata dataset, the loaded dataset is displayed (cf. Fig. **??**). By default the first 20 records are displayed. With the dropdown menu in the topleft corner it is possible to display 20, 50, 100 or all records per page. It is not recommended to select *all* in case of larger datasets *sdcApp* will run very slow. In the right bottom it is possible to navigate to different pages, either by clicking *Next* or by clicking on a page number. The table with the data is both horizontally and vertically scrollable with the scrollbars on the right side and bottom of the table. To sort the data by a variable, click on the symbol with two arrows next to the variable name in the header of the table.

After loading the dataset, the data is shown in the **Microdata** tab. The **Microdata** tab changes and the functionality for loading microdata is replaced with functionality to explore and prepare the dataset (cf. Fig. **??**). The left sidebar shows different options to explore and prepare the data for the anonymization process, as discussed in the next sections.



Loaded microdata

The loaded dataset is testdata and consists of 4580 observations and 15 variables. No variables were dropped because of all missing values.

Show 20 entries

urbrur	roof	walls	water	electcon	relat	sex	age	hhcivil	expend	income	savings	ori_hid	sampling_weight	household_weights
2	4	3	3	1	1	1	46	2	90929693	57800000	116258.5	1	100	25
2	4	3	3	1	2	2	41	2	27338058	25300000	279345	1	100	25
2	4	3	3	1	3	1	9	1	26524717	69200000	5495381	1	100	25
2	4	3	3	1	3	1	6	1	18073948	79600000	8695862	1	100	25
2	4	2	3	1	1	1	52	2	6713247	90300000	203620.2	2	100	16.6666666666667
2	4	2	3	1	2	2	47	2	49057636	32900000	1021268	2	100	16.6666666666667
2	4	2	3	1	3	2	13	1	63386309	22700000	8119166	2	100	16.6666666666667
2	4	2	3	1	3	2	19	1	1106874	89100000	9881406	2	100	16.6666666666667
2	4	2	3	1	3	1	9	1	32659507	2087324	7043642	2	100	16.6666666666667
2	4	2	3	1	3	2	16	1	34347609	44100000	4783134	2	100	16.6666666666667
2	4	3	3	1	1	1	65	2	71883547	55500000	7942221	3	100	33.3333333333333
2	4	3	3	1	2	2	60	2	55174345	41200000	4318171	3	100	33.3333333333333
2	4	3	3	1	5	2	6	1	46002021	99600000	2680967	3	100	33.3333333333333
2	4	3	3	1	1	1	34	2	33042094	98400000	3662611	4	100	33.3333333333333
2	4	3	3	1	2	2	31	2	22328588	68900000	6668614	4	100	33.3333333333333

Showing 1 to 20 of 4,580 entries

Fig. 4.4: Microdata tab after loading dataset

maxrequestsize option for loading larger files

4.2 Inspect and explore data

After loading the dataset into *sdcApp*, the data is shown on the Microdata tab. At the top of the data viewer, the number of observations and variables is shown as well as the number of variables that were deleted as a result all missing values (cf. Fig. **??**).

Note: If *Drop variables with only missing values (NA)?* is set to TRUE, the number of variables shown may be lower than the number of variables in the loaded dataset.

It is important to check whether the data was imported completely and correctly by browsing the dataset in *sdcApp*. If, for example, records are missing or labels are corrupted, then these issues need to be fixed outside of *sdcApp* and the data need to be reimported.

By clicking **Explore variables** in the left sidebar, univariate and bivariate summary statistics appropriate for the variable type can displayed. If one variable is selected, univariate summary statistics are shown.

Note: The choice of summary statistics is based on the variable type specified in *R* (shown in brackets after the variable name, e.g., urbrur (integer)). Therefore, the representation may not be correct, if the variable type does not correspond with the variable content. By converting the variable (see *Convert variable type*), the correct summary statistics will be displayed.

4.3 Preparing data

Most datasets need to be prepared before the start of the anonymization process. Examples of data preparation are removing variables that are not suitable for release, etc. It is recommended to carry out the data preparation in a statistical software of choice, before loading the data in sdcApp. Data preparation includes

After loading the data in sdcApp, still some steps may need to be carried, which are specific to the needs of the sdcApp. These steps are discussed in the following subsections.

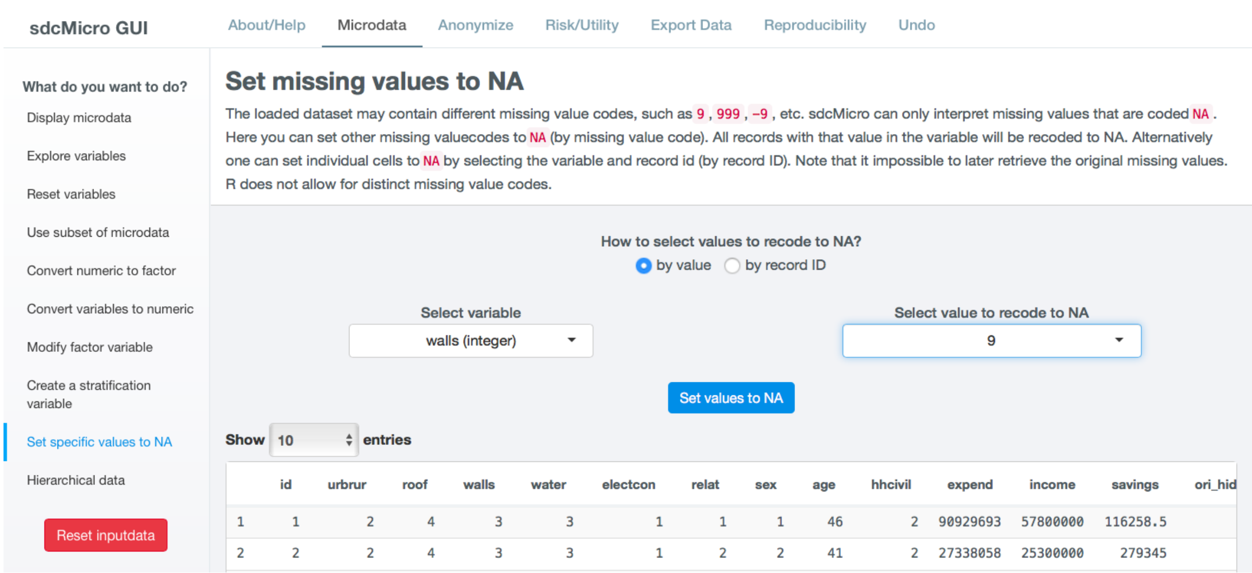
4.3.1 Convert variable type

numeric to factor

to numeric

4.3.2 Set specific values to NA

Missing values play an important role in anonymization of microdata. In particular when measuring disclosure risk of categorical key variables (see **‘Risk‘__**). sdcApp only considers the R missing value `NA` as missing. Therefore, it is important to recode other missing values, such as 9, 99, 998 or 999, “Missing”, “Not applicable” after loading the data to the R missing value `NA`, if appropriate. Many standard missing value codes in the data, such as `.` in STATA are automatically converted to NA upon loading the data into *sdcApp*.



Set missing values to NA

The loaded dataset may contain different missing value codes, such as `9`, `999`, `-9`, etc. sdcMicro can only interpret missing values that are coded `NA`. Here you can set other missing valuecodes to `NA` (by missing value code). All records with that value in the variable will be recoded to NA. Alternatively one can set individual cells to `NA` by selecting the variable and record id (by record ID). Note that it impossible to later retrieve the original missing values. R does not allow for distinct missing value codes.

How to select values to recode to NA?
● by value ○ by record ID

Select variable: walls (integer)

Select value to recode to NA: 9

Show 10 entries

	id	urbrur	roof	walls	water	electcon	relat	sex	age	hhcivil	expend	income	savings	ori_hid
1	1	2	4	3	3	1	1	1	46	2	90929693	57800000	116258.5	
2	2	2	4	3	3	1	2	2	41	2	27338058	25300000	279345	

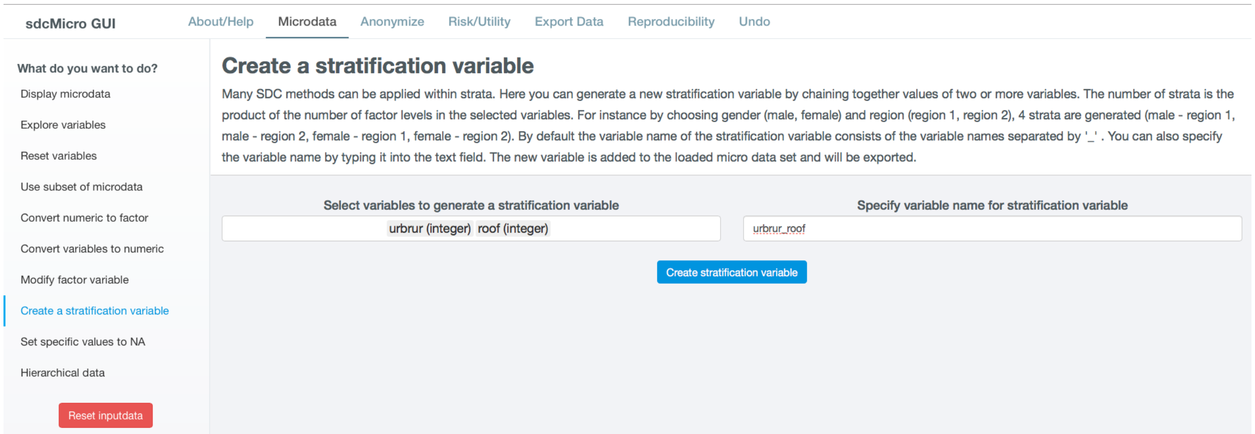
Fig. 4.5: Screen to set specific value in a variable to NA

4.3.3 Modify factor variable

Recoding (see Recoding)

Note: (this note may come in other places as well) *sdcApp* is an aid for completing the microdata anonymization process. However, sometimes it may be easier and quicker to use other statistical software packages for performing data preparation steps, such as recoding.

4.3.4 Create stratification variable



Create a stratification variable

Many SDC methods can be applied within strata. Here you can generate a new stratification variable by chaining together values of two or more variables. The number of strata is the product of the number of factor levels in the selected variables. For instance by choosing gender (male, female) and region (region 1, region 2), 4 strata are generated (male - region 1, male - region 2, female - region 1, female - region 2). By default the variable name of the stratification variable consists of the variable names separated by '_' . You can also specify the variable name by typing it into the text field. The new variable is added to the loaded micro data set and will be exported.

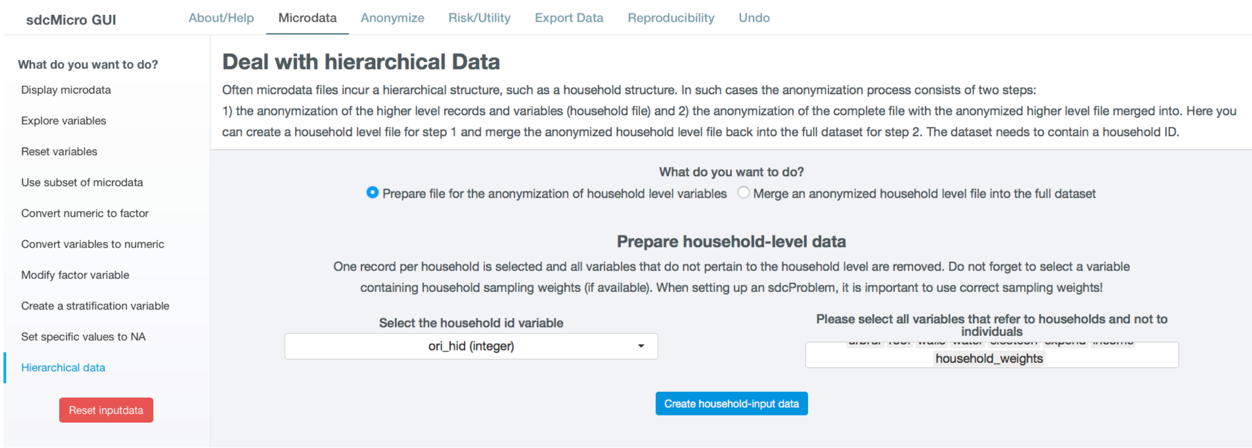
Select variables to generate a stratification variable: urbrur (integer) roof (integer)

Specify variable name for stratification variable: urbrur_roof

Fig. 4.6: Screen to create new stratification variable

4.3.5 Reset variables

4.3.6 Hierarchical data



Deal with hierarchical Data

Often microdata files incur a hierarchical structure, such as a household structure. In such cases the anonymization process consists of two steps: 1) the anonymization of the higher level records and variables (household file) and 2) the anonymization of the complete file with the anonymized higher level file merged into. Here you can create a household level file for step 1 and merge the anonymized household level file back into the full dataset for step 2. The dataset needs to contain a household ID.

What do you want to do?

● Prepare file for the anonymization of household level variables ○ Merge an anonymized household level file into the full dataset

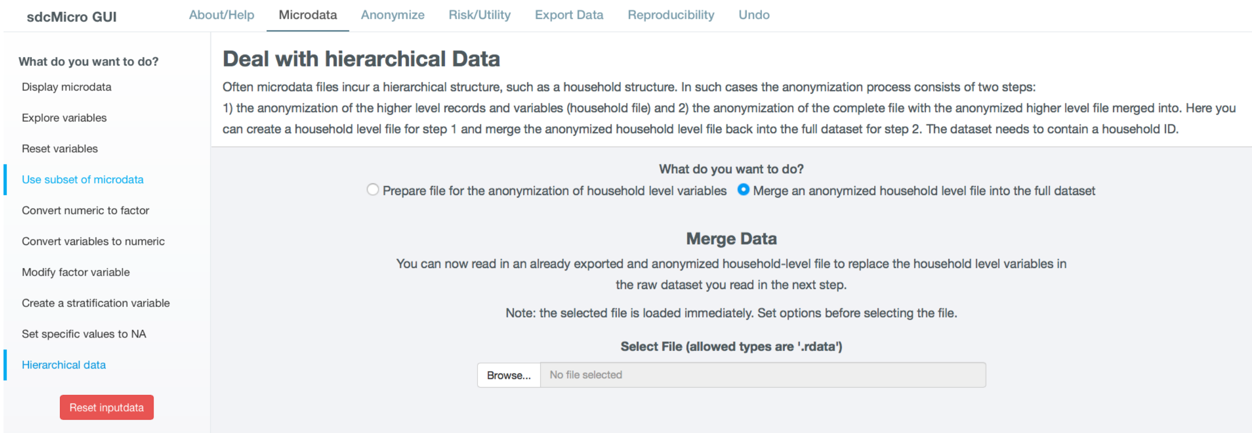
Prepare household-level data

One record per household is selected and all variables that do not pertain to the household level are removed. Do not forget to select a variable containing household sampling weights (if available). When setting up an sdcProblem, it is important to use correct sampling weights!

Select the household id variable: ori_hid (integer)

Please select all variables that refer to households and not to individuals: urbrur roof walls water electcon expend income household_weights

Fig. 4.7: Screen to create household level dataset



Deal with hierarchical Data

Often microdata files incur a hierarchical structure, such as a household structure. In such cases the anonymization process consists of two steps: 1) the anonymization of the higher level records and variables (household file) and 2) the anonymization of the complete file with the anonymized higher level file merged into. Here you can create a household level file for step 1 and merge the anonymized household level file back into the full dataset for step 2. The dataset needs to contain a household ID.

What do you want to do?

○ Prepare file for the anonymization of household level variables ● Merge an anonymized household level file into the full dataset

Merge Data

You can now read in an already exported and anonymized household-level file to replace the household level variables in the raw dataset you read in the next step.

Note: the selected file is loaded immediately. Set options before selecting the file.

Select File (allowed types are '.rdata'): No file selected

Fig. 4.8: Screen merge anonymized household level dataset with individual level dataset

4.3.7 Use subset of microdata

CHAPTER

FIVE

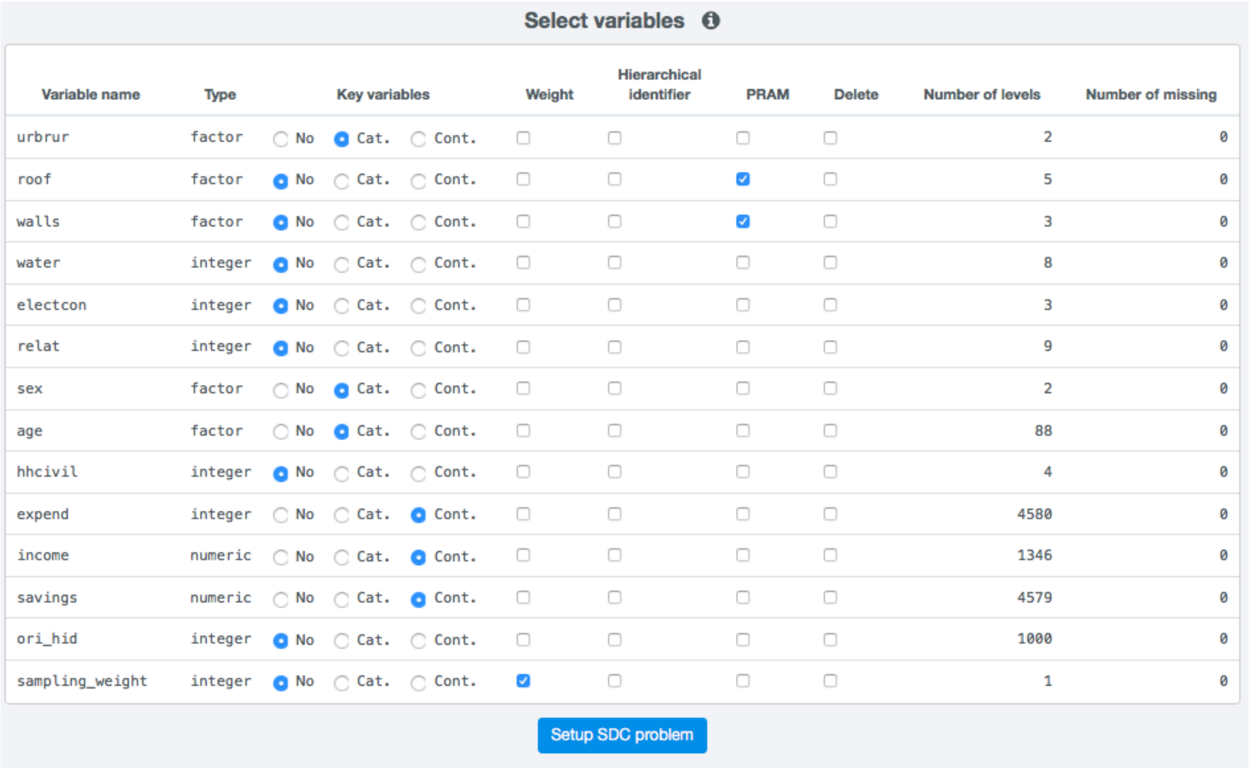
SETUP ANONYMIZATION PROBLEM

Based on the analysis of the disclosure scenarios (see), the user needs can make the variable selection in *sdcApp* and set some other parameters in order to define the so-called SDC problem. Once the data is loaded and prepared, the tab *Anonymize* shows a variable selection matrix in the main panel. The right sidebar shows several parameter settings and allows to have a quick summary view of each of the variables in the loaded dataset.

5.1 Variable selection

In order to setup an SDC problem the user needs to make a variable selection. The variable selection itself is the result of the analysis of diclosure scenarios and is beyond the scope of this manual. We refer to Chapter in for a thorough discussion of disclosure scenarios.

The matrix shown in Fig. **??** contain one row for each variable in the loaded dataset and nine different columns as described in Table **??**.



Select variables

Variable name	Type	Key variables	Weight	Hierarchical identifier	PRAM	Delete	Number of levels	Number of missing
urbrur	factor	○ No ● Cat. ○ Cont.	□	□	□	□	2	0
roof	factor	● No ○ Cat. ○ Cont.	□	□	☑	□	5	0
walls	factor	● No ○ Cat. ○ Cont.	□	□	☑	□	3	0
water	integer	● No ○ Cat. ○ Cont.	□	□	□	□	8	0
electcon	integer	● No ○ Cat. ○ Cont.	□	□	□	□	3	0
relat	integer	● No ○ Cat. ○ Cont.	□	□	□	□	9	0
sex	factor	○ No ● Cat. ○ Cont.	□	□	□	□	2	0
age	factor	○ No ● Cat. ○ Cont.	□	□	□	□	88	0
hhcivil	integer	● No ○ Cat. ○ Cont.	□	□	□	□	4	0
expend	integer	○ No ○ Cat. ● Cont.	□	□	□	□	4580	0
income	numeric	○ No ○ Cat. ● Cont.	□	□	□	□	1346	0
savings	numeric	○ No ○ Cat. ● Cont.	□	□	□	□	4579	0
ori_hid	integer	● No ○ Cat. ○ Cont.	□	□	□	□	1000	0
sampling_weight	integer	● No ○ Cat. ○ Cont.	☑	□	□	□	1	0

Fig. 5.1: Table on Anonymize tab for variable selection

Table 5.1: Columns in setup table

Column header	Description
Variable name	Name of variable in original dataset
Type	Variable type in *R* (factor, integer, numeric, character)
Key variables	Radio buttons to select variable as categorical or continuous key variable
Weight	Column to select variable as weight variable
Hierarchical identifier	Column to select variable as hierarchical identifier
PRAM	Column to select variable for PRAM method
Delete	Column to select variable to be deleted from released dataset
Number of levels	Number of different values (including NA/missing) in a categorical (type factor) variable
Number of missing	Number of records with missing value for this particular variable

The user can select for each variable the function it has in the SDC problem. No selection needs to be made for variables that are not relevant to the anonymization process and can be released without further treatment. Each of the columns is described in more detail:

1. **Variable name** This column specifies the variable name as provided in the original dataset. Variable names cannot be changed in *sdcApp*, as they are unique identifiers. If the anonymization process renders a variable name no longer appropriate, the variable must be renamed after exporting the dataset in a software of choice.

2. **Type** Each variable has a internal variable type in *R*. The different types include numeric, integer, factor and string. Each of the different functions in the SDC process requires a specific variable type, e.g., the weight needs to be numeric. If a variable is not of the appropriate type, the type of the variable needs to be changed before a selection is made (see the Section Convert variable type).

3. **Key variables** Variables that are determined as key variables in the disclosure scenario need to be selected with the radiobutton. Key variables can be either categorical (select *cat.*) or numeric(select *cont.*). The sets of categorical key variables and numeric key variables are treated independently in *sdcApp*. Categorical key variables can be of type integer or factor. Numeric key variables can be of type integer or numeric. If a variable is not a key variable, the default value *No* should be selected. At least one variable needs to be selected as categorcial key variable in order to create an SDC problem.

4. **Weight** The sampling weight is used to measure the disclosure risk. The weight variable needs to be of type numeric.

5. **Hierarchical identifier** If the data has a hierarchical structure, e.g., individuals in households, the variable that defines this hierarchy needs to be selected as hierarchical identifier (see also the Section *Risk*). This could be for instance a household ID. The hierarchical identifier needs to be unique for each hierarchical unit (e.g., household) in the complete dataset and the same for each member of the hierarchical unit (e.g., household member). The hierarchical identifier can be of any type, but it is recommended not to use a string variable. Only one variable can be selected as hierarchical identifier. If the unique hierachical indentifier is composed of several variabels, e.g., a geographical identifier, such as region, and a household ID which is unique within regions but not across, a unique hierarchical identifier needs to generated before importing the data into *sdcApp*. This can be done in a software of choice by concatenating the different components.

6. **PRAM** If some variables are considered for application of the PRAM method (see PRAM), they need to be specified at this stage. PRAM variables must be of type factor.

7. **Delete** Variables that need to be deleted from the dataset for release, such as direct identifiers, need to be selected here. Variables to be deleted can be of any type.

8. **Number of levels** This column shows the number of unique values in each variable. For instance a gender variable has typically two different levels. Note that if a variable contains missing values, this is also considered as a distinct value.

9. **Number of missing** This column indicates the number of missing values in each variable. If values were set to NA, the missing value code in R, these are counted here. Other missing value codes, such as 9, 99, 998 need to be set to NA (see also the Section Set missing values to NA).

Note: All variables need to be of the appropriate variable type. If the variable type of a variable is not suitable for the selected variable function, a popup window with an error message will appear. If necessary, the variable type needs to be changed before setting up the SDC problem.

Once a valid variable selection is made, a blue button will appear at the bottom of the setup table:

Fig. 5.2: Blue setup button appears below the setup table if the variable selection is valid

If a variable selection is invalid, the setup button will disappear and only reappears once all invalid choices are corrected. Popup windows as shown in Fig. **??**, will guide the user through the variables that need to be fixed. The most common invalid choices are the selection of more than one function for a variable and the selection of a function that does not correspond with the variable type.

Before clicking the blue button to setup the SDC problem, several parameters have to be set, as outlined in the next section.

Note: If an invalid variable choice is made, such as an invalid variable type or a variable is selected for more than one choice, a pop-up window with an informative error message is shown. An example is shown in Fig. **??**. The error message can be closed by clicking *Continue*. It is important to undo the invalid selection after clicking away the error message, as this doesn't happen automatically. Not correcting the selection will make it later difficult to trace back the invalid selections. The blue setup button disappears and reappears once the problem is fixed.

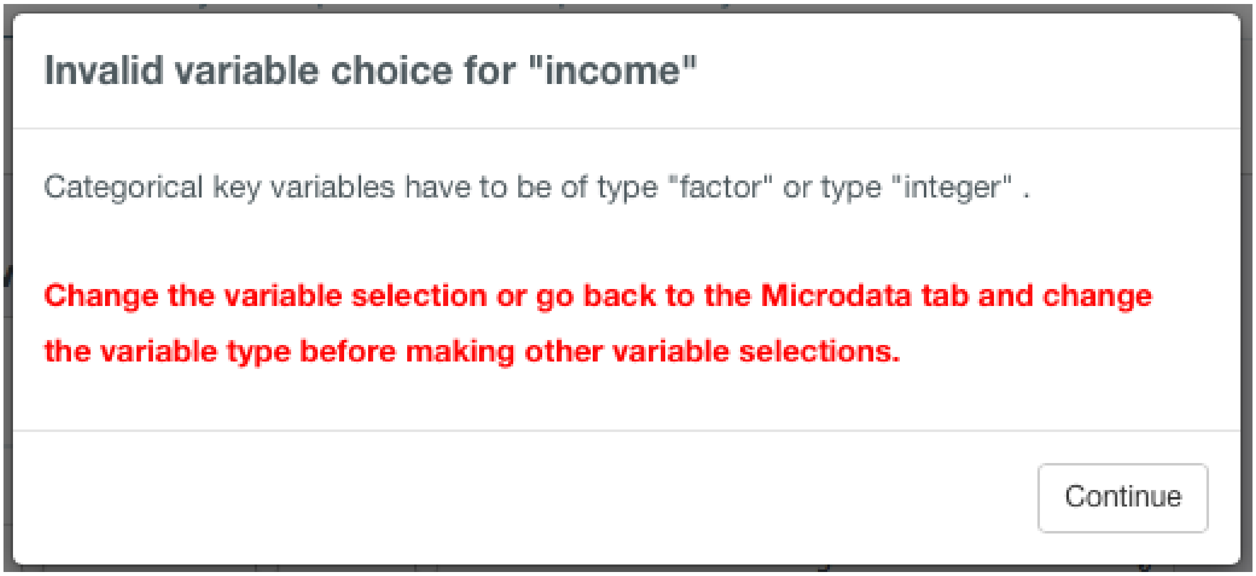
Note: The variable selection cannot be saved before setting up the SDC problem. If, for instance, a variable is not of the appropriate variable type for its use in the SDC problem, the variable type needs to be changed on the *Microdata* tab. By returning to the *Microdata* tab, all selections made on the *Anonymize* tab are lost and need to be reselected. Therefore, it is recommended to first check all variable types before starting the variable selection.

5.2 Settings

Besides the variable selection, there are two more parameters to be set before creating the SDC problem: alpha and seed. Both parameters can be set with sliders in the right sidepanel (see Fig. **??**).

5.2.1 Alpha

The parameter alpha is used to compute the frequencies of keys, which is used to compute risk measures for categorical key variables. Alpha is the weight with which a key that coincides based on a missing value (NA) contributes to these frequencies. The default value of the parameter alpha is 1, which means that two records that have the same key (combination of values in key variables), are considered to coincide completely.

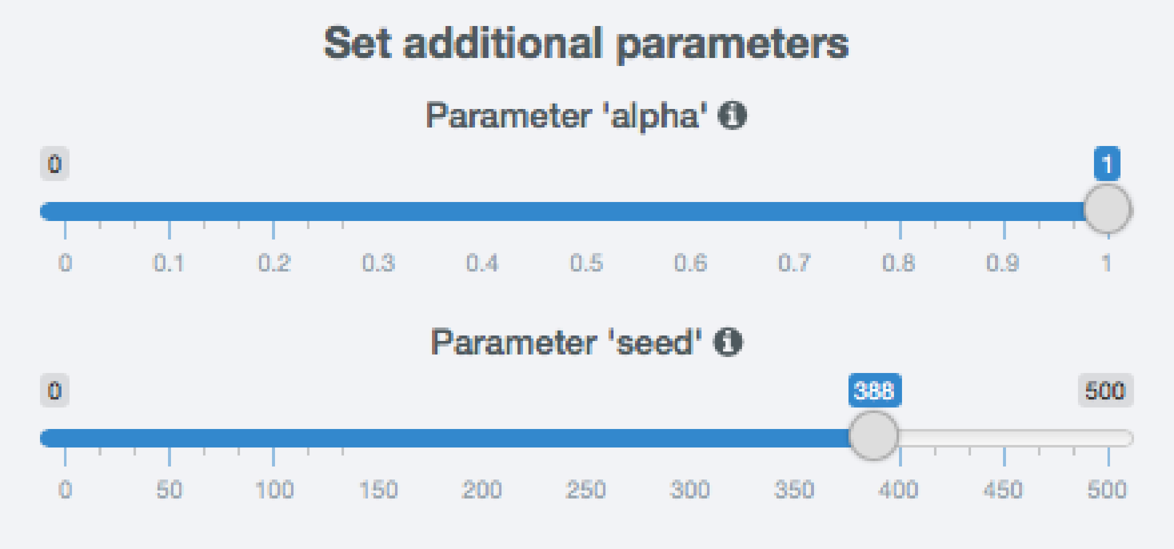


Invalid variable choice for "income"

Categorical key variables have to be of type "factor" or type "integer" .

Change the variable selection or go back to the Microdata tab and change the variable type before making other variable selections.

Fig. 5.3: Example of a popup window with an error message after an invalid variable choice



Set additional parameters

Parameter 'alpha'

1

Parameter 'seed'

388

Fig. 5.4: Sliders to set additional parameters for the SDC problem

5.2.2 Seed

Every time a probabilistic method is used, a different outcome is generated. For these methods it is often recommended that a seed be set for the random number generator if you want to produce replicable results. The seed is used to initialize the random number generator used for probabilistic methods. In *sdcApp*, the seed can be set to any integer value from 0 to 500. To select a value, you can click with the mouse pointer on the slider and use the arrow keys (left and right or up and down) to select an exact value. In Fig. **??** the seed is set at 388.

Note: In order to replicate exact results when using probabilistic methods, the order in which the methods are carried out influences the results. Therefore, besides the seed, also the order of the operations needs to be the same. The seed changes when used in the random number generator. When the undo button is used (see), the seed is not reset to the value prior to the reverted step.

5.3 Summary view

After setting up the SDC problem, the application jumps automatically to the summary view of the *Anonymize* tab. When an SDC problem is available, the *Anonymize* tab provides a summary of the SDC problem and allows to apply anonymization methods.

This tab first shows a Summary overview of the problem. The content of the summary page varies with the SDC problem. For example, if no numerical key variables were selected, the information on numeric key variables is omitted. Fig shows the summary page.

Note: Once the SDC problem is set up, it is possible and highly recommended to save the SDC problem. By saving the SDC problem, you can reload the problem including the preparation steps and variable selection in case of issues with sdcApp or to revert to this ‘clean’ state without any methods applied in order to compare several methods.

Note: If you would like to change the variable selection after setting up the SDC problem, click the red button [add png]. By doing so, you need to respecify the full variable selection.

CHAPTER

SIX

RISK MEASUREMENT

6.1 Summary view

6.1.1 Global risk measure

For categorical variables

6.1.2 k-anonymity

The risk measure k-anonymity is based on the principle that, in a safe dataset, the number of individuals sharing the same combination of values (keys) of categorical quasi-identifiers should be higher than a specified threshold k. k-anonymity is a risk measure based on the microdata to be released, since it only takes the sample into account. An individual violates k-anonymity if the sample frequency count f_k for the key k is smaller than the specified threshold k. For example, if an individual has the same combination of quasi-identifiers as two other individuals in the sample, these individuals satisfy 3-anonymity but violate 4-anonymity. In the dataset, six individuals satisfy 2-anonymity and four violate 2-anonymity. The individuals that violate 2-anonymity are sample uniques. The risk measure is the number of observations that violates k-anonymity for a certain value of *k*, which is

$$\sum_i I(f_k < k),$$

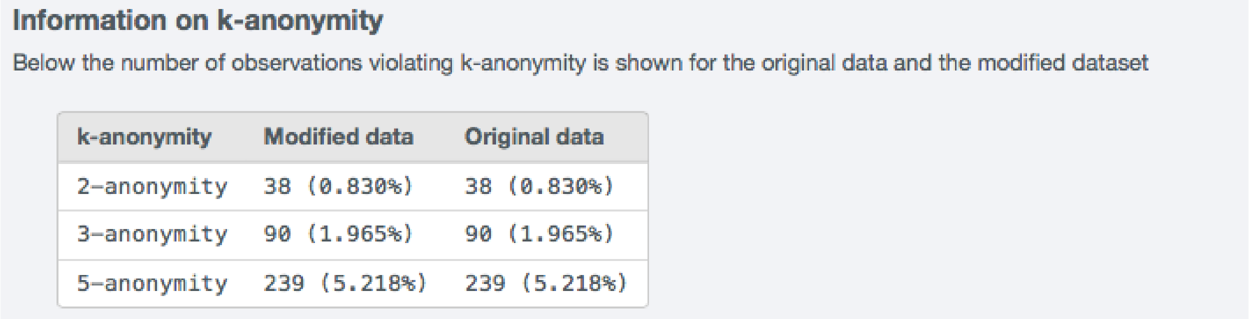
where I is the indicator function and i refers to the i^{th} record. This is simply a count of the number of individuals with a sample frequency of their key lower than k. The count is higher for larger k, since if a record satisfies k-anonimity, it also satisfies $(k+1)$-anonimity. The risk measure k-anonymity does not consider the sample weights, but it is important to consider the sample weights when determining the required level of k-anonymity. If the sample weights are large, one individual in the dataset represents more individuals in the target population, the probability of a correct match is smaller, and hence the required threshold can be lower. Large sample weights go together with smaller datasets. In a smaller dataset, the probability to find another record with the same key is smaller than in a larger dataset. This probability is related to the number of records in the population with a particular key through the sample weights.

In the summary view

6.1.3 Risk measures for numerical key variables

6.1.4 Household risk

If household identifier is selected, household risk will automatically be displayed.



Information on k-anonymity

Below the number of observations violating k-anonymity is shown for the original data and the modified dataset

k-anonymity	Modified data	Original data
2-anonymity	38 (0.830%)	38 (0.830%)
3-anonymity	90 (1.965%)	90 (1.965%)
5-anonymity	239 (5.218%)	239 (5.218%)

Fig. 6.1: Information on k-anonymity violators in summary view

6.2 Detailed view

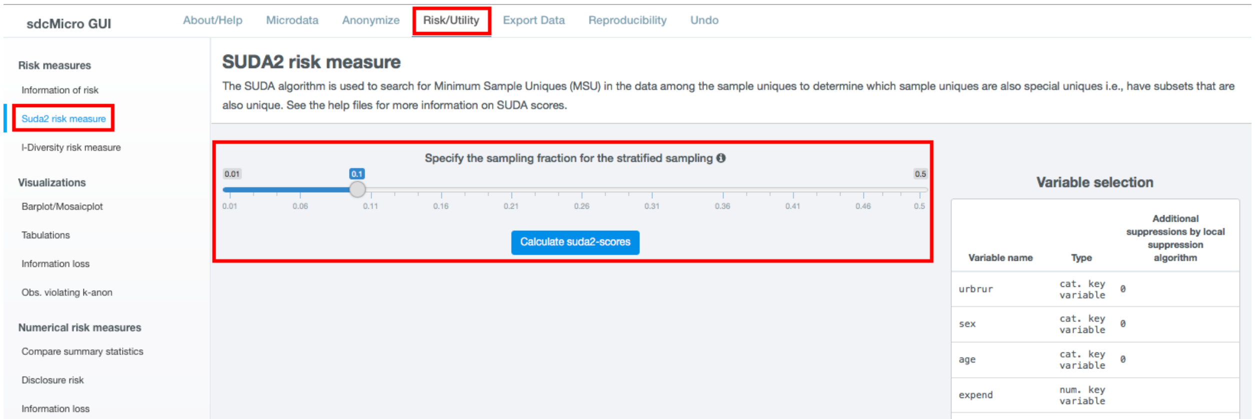
The Risk/Utility tab provides more detailed information on risk measures and records at (high) risk.

6.2.1 Risky observations

6.2.2 SUDA

The SUDA algorithm identifies all the MSUs in the sample, which in turn are used to assign a SUDA score to each record. This score indicates how "risky" a record is. The potential risk of the records is determined based on two observations:

- The smaller the size of the MSU within a record (i.e., the fewer variables are needed to reach uniqueness), the greater the risk of the record
- The larger the number of MSUs possessed by a record, the greater the risk of the record



SUDA2 risk measure

The SUDA algorithm is used to search for Minimum Sample Uniques (MSU) in the data among the sample uniques to determine which sample uniques are also special uniques i.e., have subsets that are also unique. See the help files for more information on SUDA scores.

Specify the sampling fraction for the stratified sampling

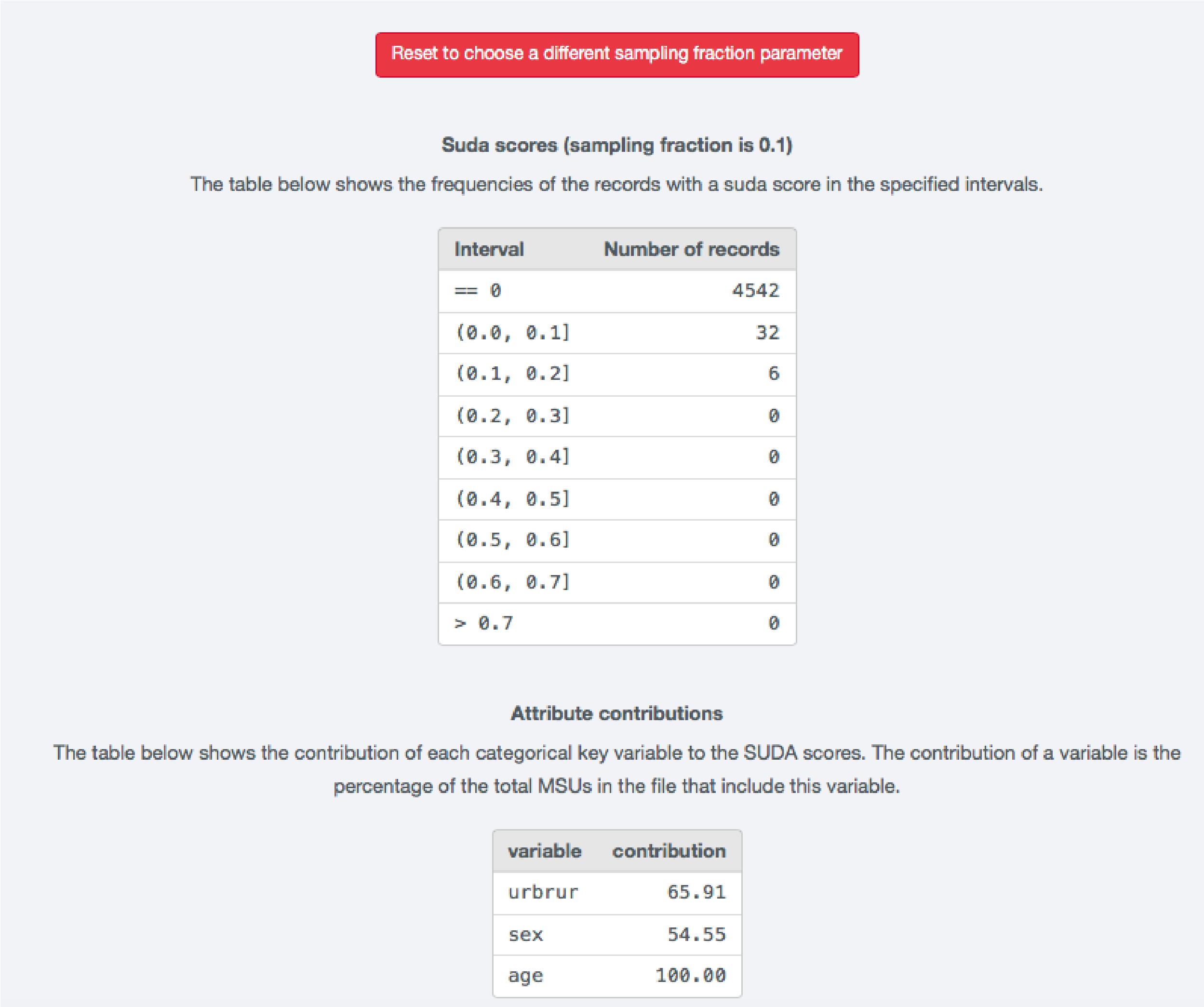
Variable selection

Variable name	Type	Additional suppressions by local suppression algorithm
urbrur	cat. key variable	0
sex	cat. key variable	0
age	cat. key variable	0
expend	num. key variable	

Fig. 6.2: Compute SUDA scores

6.2.3 l-diversity

A dataset satisfies l-diversity if for every key k there are at least l different values for each of the sensitive variables. In the example, the first two individuals satisfy only 1-diversity, individuals 4 and 6 satisfy 2-diversity. The required level of l-diversity depends on the number of possible values the sensitive variable can take. If the sensitive variable



Suda scores (sampling fraction is 0.1)

The table below shows the frequencies of the records with a suda score in the specified intervals.

Interval	Number of records
== 0	4542
(0.0, 0.1]	32
(0.1, 0.2]	6
(0.2, 0.3]	0
(0.3, 0.4]	0
(0.4, 0.5]	0
(0.5, 0.6]	0
(0.6, 0.7]	0
> 0.7	0

Attribute contributions

The table below shows the contribution of each categorical key variable to the SUDA scores. The contribution of a variable is the percentage of the total MSUs in the file that include this variable.

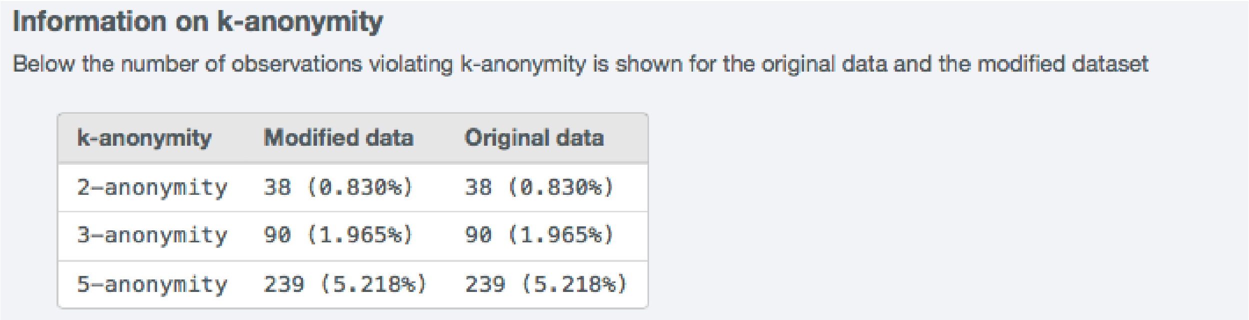
variable	contribution
urbrur	65.91
sex	54.55
age	100.00

Fig. 6.3: Result of SUDA calculation

is a binary variable, the highest level if l-diversity that can be achieved is 2. A sample unique will always only satisfy 1-diversity.

To compute l-diversity for sensitive variables in sdcApp

6.2.4 k-anonymity



Information on k-anonymity

Below the number of observations violating k-anonymity is shown for the original data and the modified dataset

k-anonymity	Modified data	Original data
2-anonymity	38 (0.830%)	38 (0.830%)
3-anonymity	90 (1.965%)	90 (1.965%)
5-anonymity	239 (5.218%)	239 (5.218%)

Fig. 6.4: Information on k-anonymity violators for any level of k

CHAPTER

SEVEN

ANONYMIZATION METHODS

Once the disclosure risk is evaluated and is too high for release, SDC methods need to be applied to the variables to reduce the risk. This process is iterative, i.e., after applying a certain method with a set of parameters, the disclosure risk needs to be reassessed and the information loss needs to be evaluated. If the result is not satisfactory, other methods can be applied to other variables. It is also possible to undo the method (see Undo) and reapply the same method with a different set of parameters.

In this section, we provide a brief description of common SDC methods for microdata and show how to use these in *sdcApp*. For more information on the choice of the appropriate method and more detailed information on the methods themselves, we refer to the respective section in the SDC theory guide (link).

7.1 Recoding

7.1.1 Global recoding

Global recoding combines several categories (levels) of a categorical variable or constructs intervals for continuous variables. This reduces the number of categories available in the data and potentially the disclosure risk, especially for categories with few observations, but also, importantly, it reduces the level of detail of information available to the analyst.

In order to perform global recoding in *sdcApp*, navigate to on the **Anonymize** tab and select **Recoding** from the left sidebar. First select the variable to be recoded. In the example in Fig. **??** the semi-continuous variable age is selected. Only variables selected as categorical key variables in the problem setup can be recoded here.

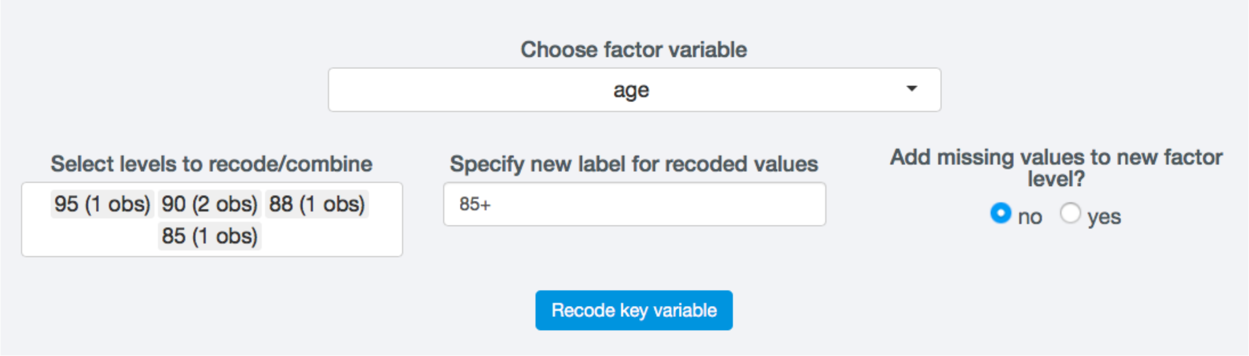
add: distribution is shown to determine breaks: refer to theory guide, also add in screenshot

Next select all the existing levels in the variable to be combined. In the example, we select all values of age equal or larger to 85. Behind each value the number of observations in the dataset with this value is displayed. The label of the variable to be created is by default the concatenation of the labels of all combined values (85_88_90_95), but can be changed to any string. In the example the new label is 85+.

In case the system missing value (:code:NA) should be included in the newly created level, set the option Add missing values to new factor level? to Yes. This could be for example useful if a new group is created combining other and not applicable. The default of this option is No.

After selecting the variable, levels and specifying a new label the variable is recoded by clicking Recode key variable. The risk measures are immediately updated once the method is applied.

Note: When exploring the recoded variable, the old levels still appear in the frequency table. They stay in the variable with 0 observations.



Choose factor variable: age

Select levels to recode/combine: 95 (1 obs) 90 (2 obs) 88 (1 obs) 85 (1 obs)

Specify new label for recoded values: 85+

Add missing values to new factor level? ● no ○ yes

Fig. 7.1: Settings for global recoding to recode the variable age

For each group (new level), this process needs to be repeated. If, for example, age should be recoded in 5-year age bands, these steps need to be carried out for each 5-year age group separately.

Tip: Global recoding for a variable with many different levels, such as age, can be a daunting task in *sdcApp*, as it involves many clicks and is prone to making mistakes. As an alternative, one could perform the recoding in another statistical software before loading the data in *sdcApp*. This would influence the initial risk levels.

add: Variables can already be recoded before on data tab

7.1.2 Top and bottom coding

Top and bottom coding are similar to global recoding, but instead of recoding all values, only the top and/or bottom values of the distribution or categories are recoded. This can be applied only to ordinal categorical variables and (semi-)continuous variables, since the values have to be at least ordered. Top and bottom coding is especially useful if the bulk of the values lies in the center of the distribution with the peripheral categories having only few observations (outliers). Examples are age and income; for these variables, there will often be only a few observations above certain thresholds, typically at the tails of the distribution. The fewer the observations within a category, the higher the identification risk. One solution could be grouping the values at the tails of the distribution into one category. This reduces the risk for those observations, and, importantly, does so without reducing the data utility for the other observations in the distribution.

In order to perform top or bottom coding in *sdcApp*, navigate to on the **Anonymize** tab and select **Top/bottom coding** from the left sidebar. First select the variable to be recoded. In the example in Fig. **??** the continuous variable income is selected. Only variables of type numeric can be top or bottom coded.

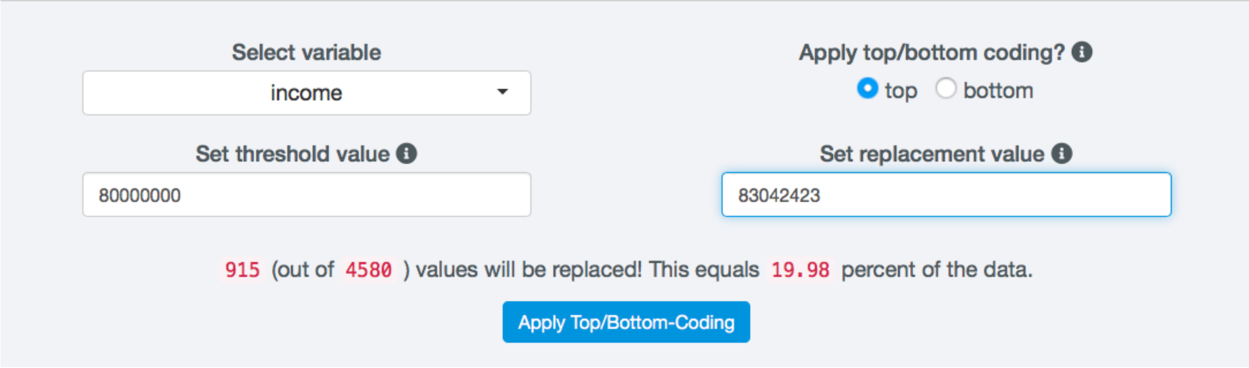
add: boxplot to check distribution

Note: Top and bottom coding ca only be applied to numeric variables. If age, as in our example, is converted to factor, the global recoding method needs to be used, in order to topcode age by grouping all values above the threshold.

Next select top or bottom coding. In case of top coding all values above the set threshold are replaced, in case of bottom coding all values below the set threshold are replaced. Set the threshold value and replacement value by entering these in the numeric fields. After entering the threshold and replacement values, the number of records with values below/above the threshold that are replaced is shown.

Note: It is advised to use a replacement value different than the threshold value, such as the weighted mean or median to reduce information loss. The replacement value needs to be computed in a different software and manually inserted in *sdcApp*.

After selecting the variable, type and specifying the threshold and replacement values, the variable is topcoded by clicking Apply Top/Bottom-Coding. The risk measures are automatically updated after the method is applied.



Select variable

income

Apply top/bottom coding?

● top ○ bottom

Set threshold value

80000000

Set replacement value

83042423

915 (out of 4580) values will be replaced! This equals 19.98 percent of the data.

Fig. 7.2: Settings for topcoding the variable income at 8 million

7.2 k-Anonymity / local suppression

It is common in surveys to encounter values for certain variables or combinations of quasi-identifiers (keys) that are shared by very few individuals. When this occurs, the risk of re-identification for those respondents is higher than the rest of the respondents. Often local suppression is used after reducing the number of keys in the data by recoding the appropriate variables. Recoding reduces the number of necessary suppressions as well as the computation time needed for computing the suppression pattern. Suppression of values means that values of a variable are replaced by a missing value (NA in R). The the Section k-anonymity discusses how missing values influence frequency counts and k-anonymity.

In order to perform local suppression to achieve k-anonymity in *sdcApp*, navigate to on the **Anonymize** tab and select **k-Anonimity** from the left sidebar. Local suppression is always performed on the complete set off selected categorical key variables.

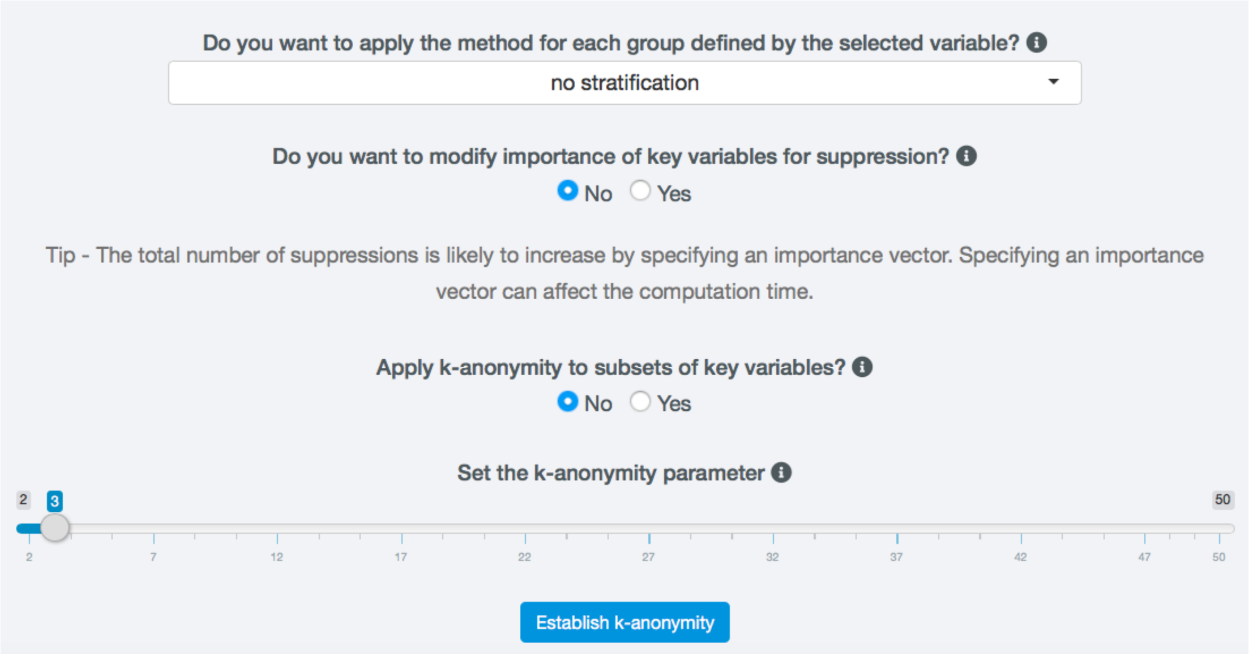
In order to apply the default local suppression algorithm, the user only needs to set the level of k to be achieved.

add: overview of suppressions /suppression patterns

7.2.1 Importance

By default the algorithm considers variables with many different levels first. Therefore, it is more likely that these variables will contain suppressed values. Sometimes variables with many different levels are important for the

7.2.2 Subsets



Do you want to apply the method for each group defined by the selected variable?

no stratification

Do you want to modify importance of key variables for suppression?

● No ○ Yes

Tip - The total number of suppressions is likely to increase by specifying an importance vector. Specifying an importance vector can affect the computation time.

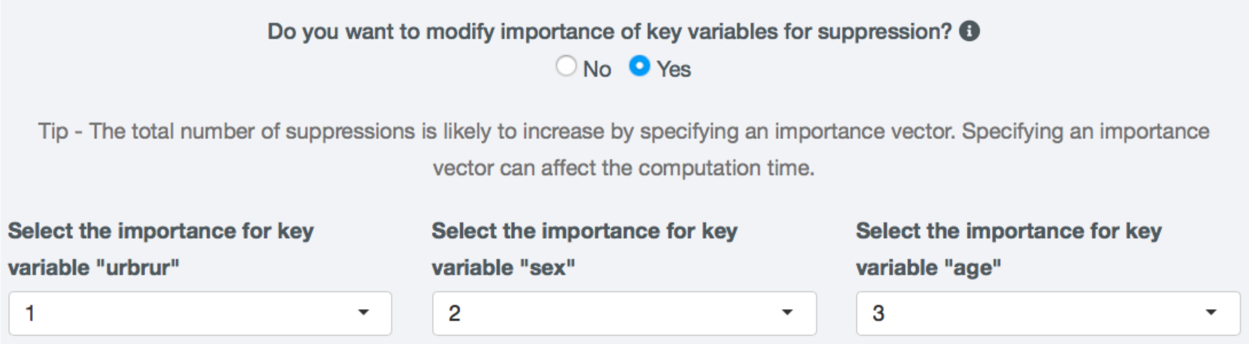
Apply k-anonymity to subsets of key variables?

● No ○ Yes

Set the k-anonymity parameter

3

Fig. 7.3: Settings for local suppression to achieve 3-anonimity



Do you want to modify importance of key variables for suppression?

○ No ● Yes

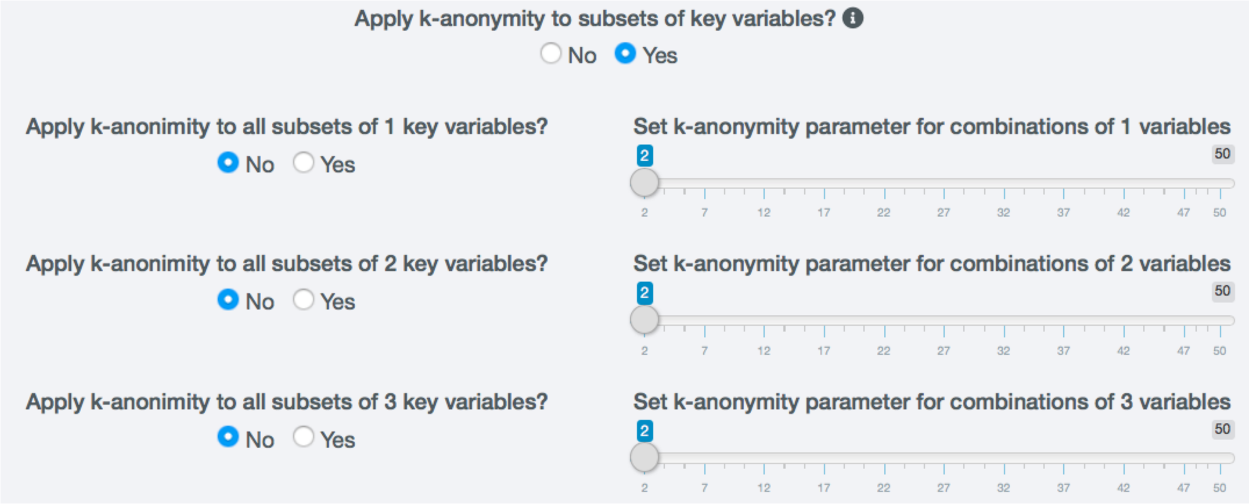
Tip - The total number of suppressions is likely to increase by specifying an importance vector. Specifying an importance vector can affect the computation time.

Select the importance for key variable "urbrur": 1

Select the importance for key variable "sex": 2

Select the importance for key variable "age": 3

Fig. 7.4: Importance settings for local suppression



Apply k-anonymity to subsets of key variables?

○ No ● Yes

Apply k-anonimity to all subsets of 1 key variables?

● No ○ Yes

Set k-anonymity parameter for combinations of 1 variables: 2

Apply k-anonimity to all subsets of 2 key variables?

● No ○ Yes

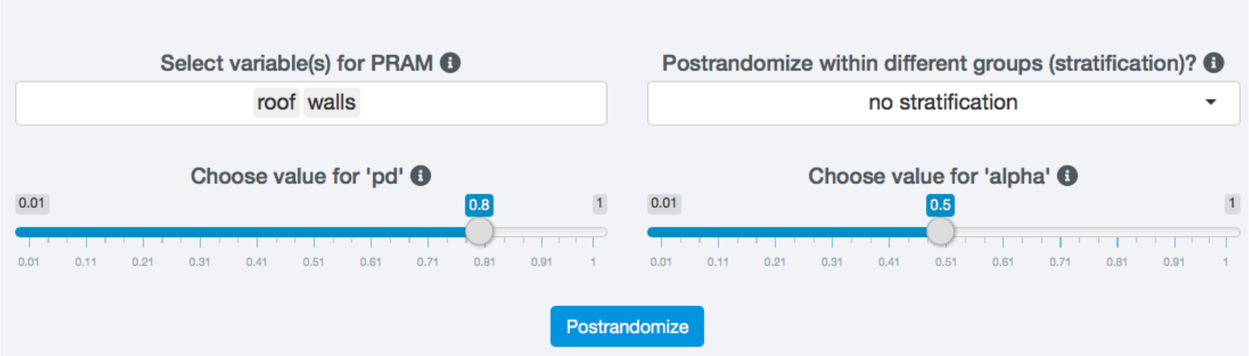
Set k-anonymity parameter for combinations of 2 variables: 2

Apply k-anonimity to all subsets of 3 key variables?

● No ○ Yes

Set k-anonymity parameter for combinations of 3 variables: 2

Fig. 7.5: Subset settings for local suppression



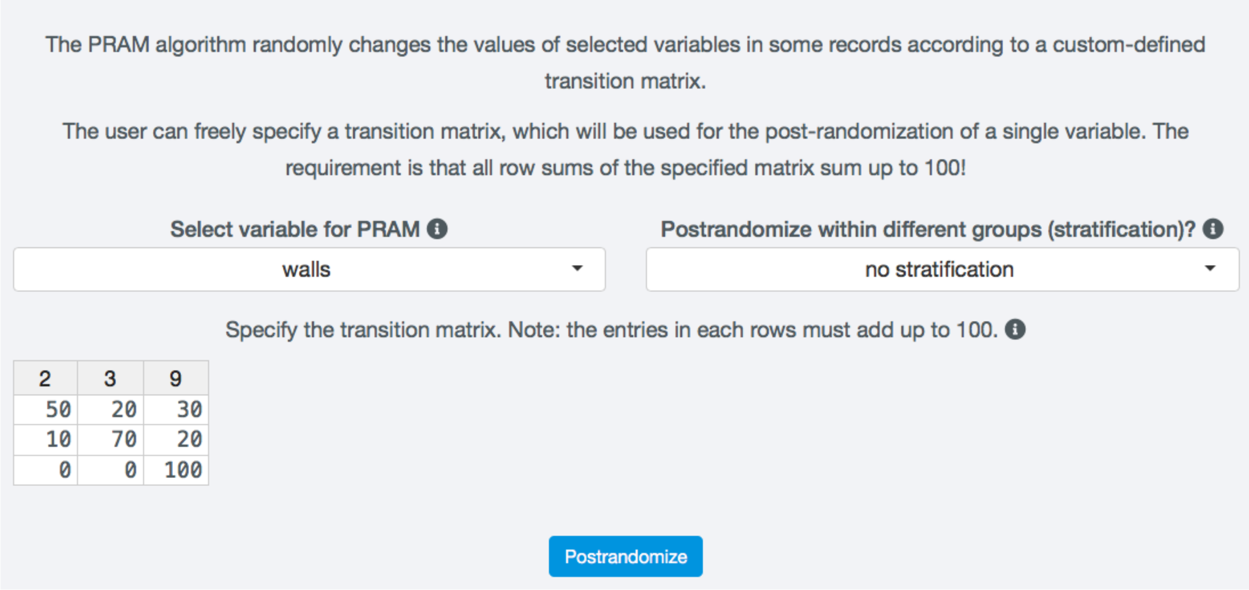
Select variable(s) for PRAM: roof walls

Postrandomize within different groups (stratification)? no stratification

Choose value for 'pd': 0.8

Choose value for 'alpha': 0.5

Fig. 7.6: Settings for PRAM



The PRAM algorithm randomly changes the values of selected variables in some records according to a custom-defined transition matrix.

The user can freely specify a transition matrix, which will be used for the post-randomization of a single variable. The requirement is that all row sums of the specified matrix sum up to 100!

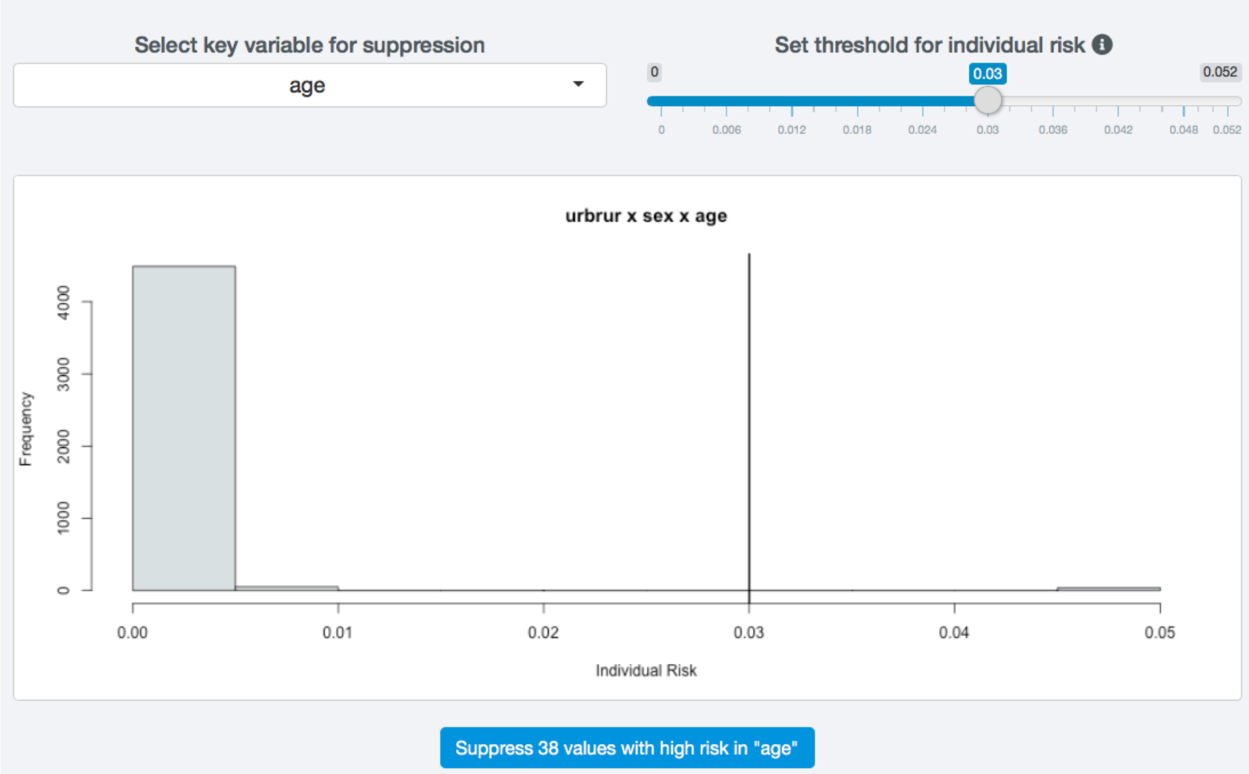
Select variable for PRAM: walls

Postrandomize within different groups (stratification)? no stratification

Specify the transition matrix. Note: the entries in each rows must add up to 100.

2	3	9
50	20	30
10	70	20
0	0	100

Fig. 7.7: Settings for PRAM with customized transition matrix



Select key variable for suppression

age

Set threshold for individual risk

0.03

Suppress 38 values with high risk in "age"

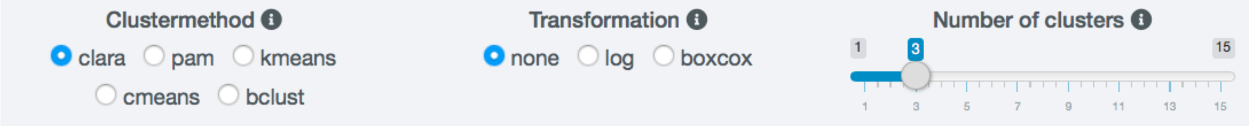
Fig. 7.8: Settings for suppressing values in records with high risk

7.3 PRAM

7.4 Suppress values with high risk

7.5 Top/Bottom coding

7.6 Microaggregation



Clustermethod

● clara ○ pam ○ kmeans

○ cmeans ○ bclust

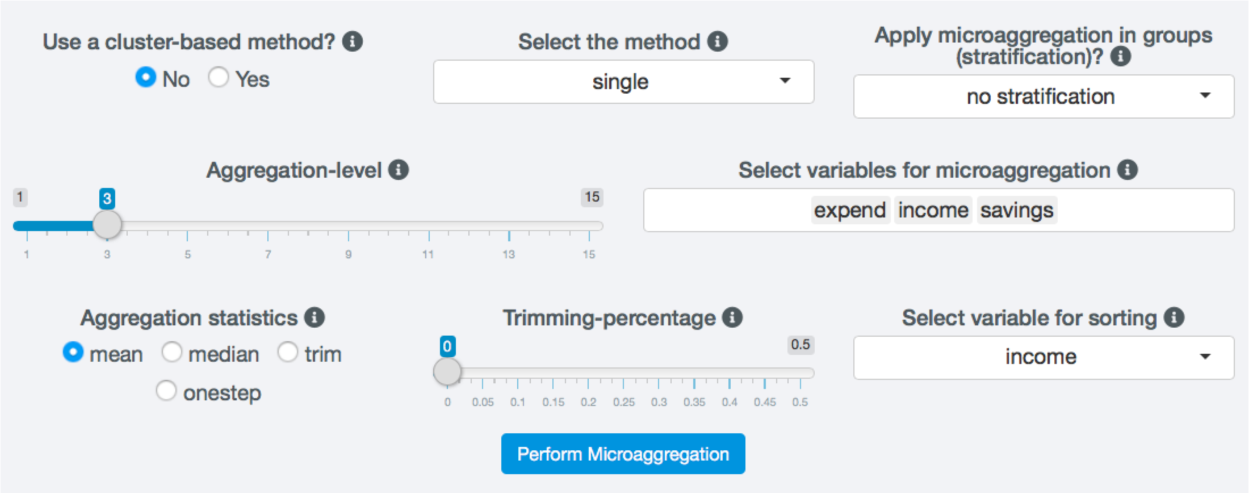
Transformation

● none ○ log ○ boxcox

Number of clusters

3

Fig. 7.9: Settings for microaggregation



Use a cluster-based method? ● No ○ Yes

Select the method: single

Apply microaggregation in groups (stratification)?: no stratification

Aggregation-level: 3

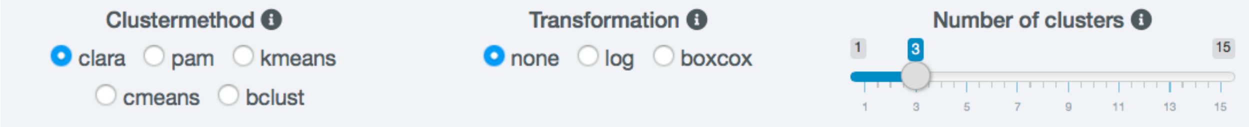
Select variables for microaggregation: expend income savings

Aggregation statistics: ● mean ○ median ○ trim ○ onestep

Trimming-percentage: 0

Select variable for sorting: income

Fig. 7.10: Additional settings for microaggregation



Clustermethod: ● clara ○ pam ○ kmeans ○ cmeans ○ bclust

Transformation: ● none ○ log ○ boxcox

Number of clusters: 3

Fig. 7.11: Cluster settings for microaggregation

7.7 Adding noise

7.8 Rank swapping

7.9 Undo

Finding an anonymization strategy for a microdata dataset is a trial-and-error process. The effect on risk and utility of different methods with different parameter settings can only be assessed by executing the methods on the actual dataset. Therefore, it is unlikely to find a satisfactory anonymization strategy at the first attempt. Before another method is applied, the previous method needs to be canceled. In *sdcApp* it is possible to undo the last method applied with one click. To test the effect of a combination of several methods, which is recommended, it is necessary to cancel several steps. To do so, the state of the SDC problem before applying the methods is saved to disk and can be reloaded afterwards. This is the same as canceling several steps. Both methods are described below.

7.9.1 Undo one step

In order to undo one step,

risk measures etc are also reset, script not, random seed not

7.9.2 Undo several steps

Recommended to

Save and reload

CHAPTER

EIGHT

UTILITY MEASUREMENT

8.1 General utility measures in *sdcApp*

8.1.1 Compare summary statistics

Categorical variables

Continuous variables

8.1.2 IL1s measure

8.2 Customized utility measures

As the statistical analyses based on the microdata depend, amongst others, on to the topic of the survey, the country and the definition of the variables, it is not feasible to include all these measures in *sdcApp*. Instead, it is recommended to compute the statistics and indicators and perform statistical an econometric analyses on the original and anonymized datasets and evaluate the differences in the results. If a publication based on the microdata is already published, it is recommended to recompute the statistics in these publications from the anonymized dataset.

The approach is to compare the indicators calculated on the untreated data and the data after anonymization with different methods. If the differences between the indicators are not too large, the anonymized dataset can be released for use by researchers. It should be taken into account that indicators calculated on samples are estimates with a certain variance and confidence interval. Therefore, for sample data, it is more informative to compare the overlap of confidence intervals and/or to evaluate whether the point estimate calculated after anonymization is contained within the confidence interval of the original estimate.

Note: Some analyses may no longer be possible or not possible in exactly the same way. E.g. regression on age if age is recoded in 5-year intervals.

In order to do so, it is posible to export the dataset at any point in *sdcApp*. See Export dataset. Several datasets can be exported after applying different methods with different parameters settings to compare the information loss resulting from the anonymization. This information can be used to select the anonymization methods as well as to inform the user about the implications of the anonymization on the validity of the dataset for analysis.

CHAPTER

NINE

EXPORT DATA AND REPORTS

9.1 Export anonymized dataset

sdcApp supports datasets in several foreign data formats. The file formats that are supported for loading microdata are also supported for export (cf. Table **??**).

In order to export the file, click on **Anonymized Data** in the left sidebar on the **Export Data** tab. The dataset shown is the file as it will be exported. Select the appropriate file format with the radiobuttons underneath the data.

In case the microdata is exported as csv or STATA file, additional options need to be specified. For a csv file, whether first row should include column names, the field separator as well as the decimal separator. For STATA files, the version of STATA needs to be specified. STATA cannot STATA files saved for a higher version.

Option to randomize the order of the records. Order may reveal values, e.g. ordered by region with suppressed region value Need to replace existing ID

In order to export the dataset, click on blue button **Save dataset**. The dataset is saved to the

By clicking on the blue button Save script to file at the top of the page, the script is saved as R script (extension .R) on disk to the selected storage path on the About/Help tab (see Introduction to sdcApp). The filename of the exported script starts with 'exportedScript_sdcMicro' followed by a date and time stamp, e.g., 'exportedScript_sdcMicro_20181010_1212.R'. , exported two with file name… Exported to

the microdata, select

Table 9.1: Data formats compatible with sdcApp

Software	File extension
R/RStudio	.rdata
SPSS	.sav
SAS	.sas7bdat
CSV	.csv, .txt
STATA	.dta

Also for intermediate export

..NOTE:: Categorical variables (type factor in *sdcApp*) that were had a value and a label in the input dataset are

labels (variable, value), coding 0,1 to 1,2 etc.

Extra for STATA input files: change variable labels for STATA files

9.2 Exporting reports

It is extremely important to document the SDC process of microdata both for internal use as well as for external use. The internal report should contain detailed descriptions of all steps carried out as well as reasoning for

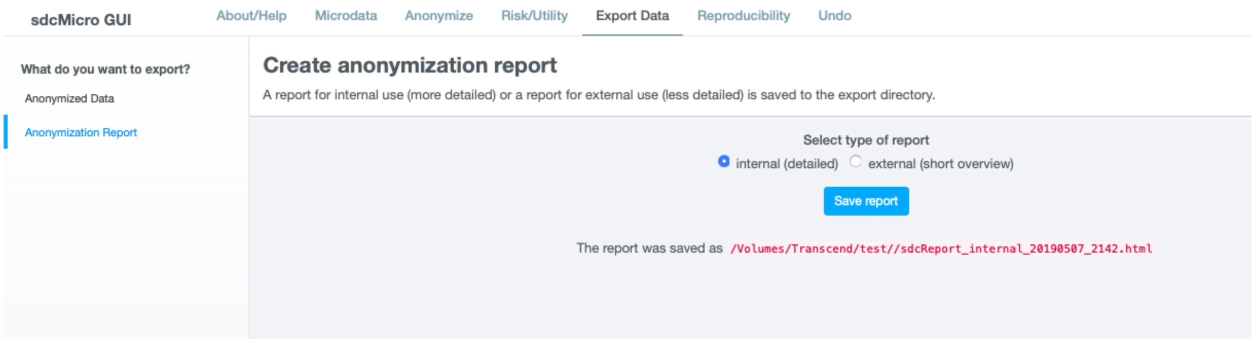
Generic drafts of both an

9.2.1 Internal report

An important step in the SDC process is reporting, both internal and external. Internal reporting contains the exact description of anonymization methods used, parameters but also the risk measures before and after anonymization. This allows replication of the anonymized dataset and is important for supervisory authorities/bodies to ensure the anonymization process is sufficient to guarantee anonymity according to the applicable legislation.

Report is just technical overview, not complete

file path, name of file



Create anonymization report

A report for internal use (more detailed) or a report for external use (less detailed) is saved to the export directory.

Select type of report

● internal (detailed) ○ external (short overview)

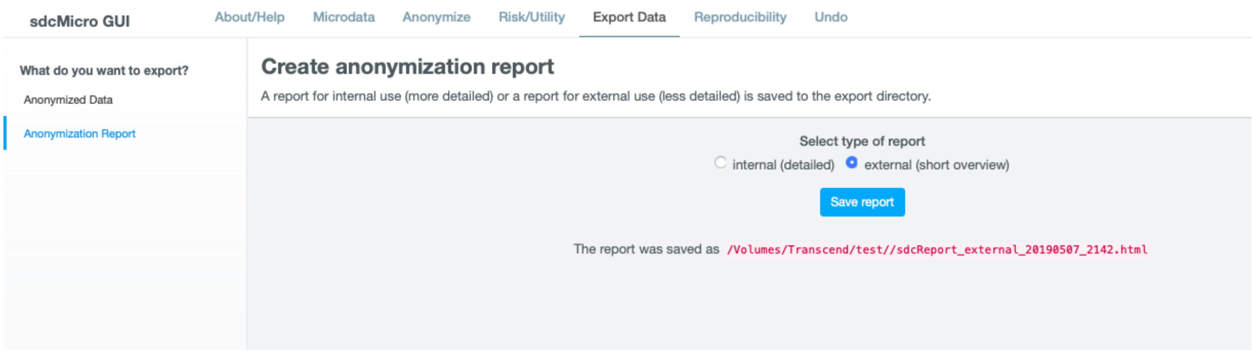
The report was saved as `/Volumes/Transcend/test//sdcReport_internal_20190507_2142.html`

Fig. 9.1: Exporting an internal report

9.2.2 External report

The external report informs the user that the data has been anonymized, provides information for valid analysis on the data and explains the limitations to the data as a result of the anonymization. A brief description of the methods used can be included. The release of anonymized microdata should be accompanied by the usual metadata of the survey (survey weight, strata, survey methodology) as well as information on the anonymization methods that allow researchers to do valid analysis (e.g., amount of noise added, transition matrix for PRAM).

file path, name of file



Create anonymization report

A report for internal use (more detailed) or a report for external use (less detailed) is saved to the export directory.

Select type of report

○ internal (detailed) ● external (short overview)

The report was saved as `/Volumes/Transcend/test//sdcReport_external_20190507_2142.html`

Fig. 9.2: Exporting an external report

CHAPTER

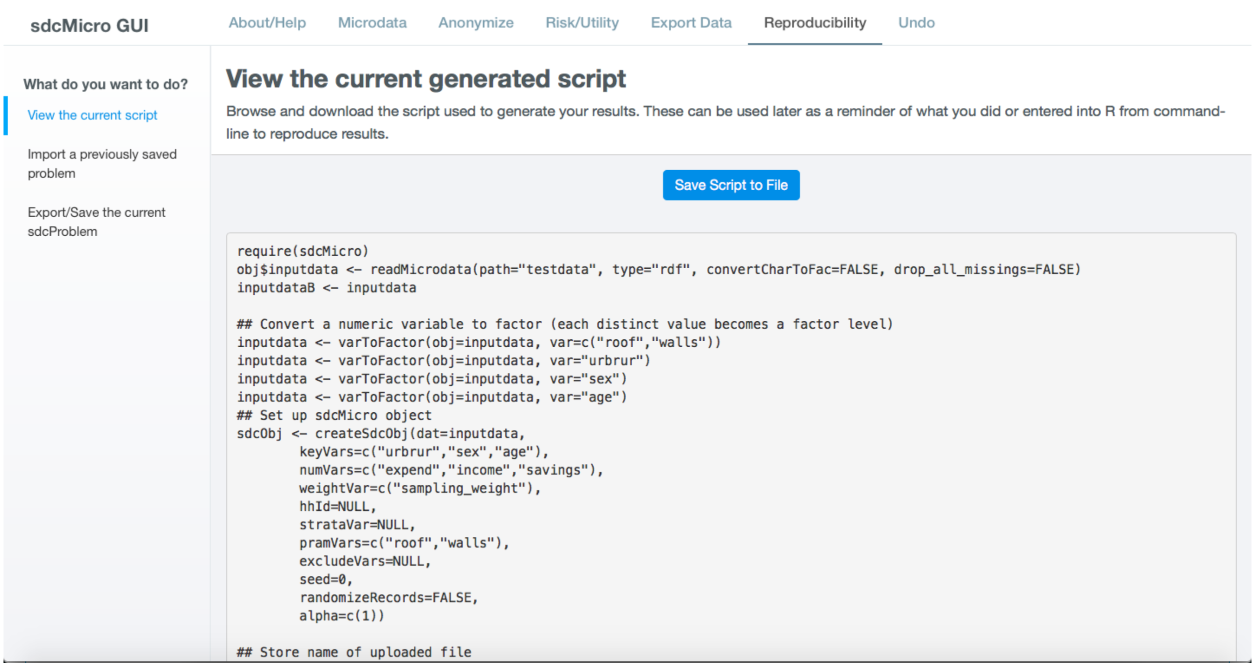
TEN

REPRODUCIBILITY

Reproducibility is key to the SDC process, as . . .

10.1 Exporting *R* script

sdcApp is a GUI for the *R* package *sdcMicro*. All steps executed in *sdcApp* are translated into *R* commands. Therefore, the full anonymization can also be performed from command-line in *R*. While carrying out the anonymization process, the code to perform the same action from command-line is generated. The code can be viewed and exported on the **Reproducibility** tab by selecting **View the current script** from the left sidebar (cf. Fig. **??**). The script also contains comments, which are the lines starting with the hash tag (#). These comments are meant to help with the interpretation of the code blocks.



View the current generated script

Browse and download the script used to generate your results. These can be used later as a reminder of what you did or entered into R from command-line to reproduce results.

```
require(sdcMicro)
obj$inputdata <- readMicrodata(path="testdata", type="rdf", convertCharToFac=FALSE, drop_all_missings=FALSE)
inputdataB <- inputdata

## Convert a numeric variable to factor (each distinct value becomes a factor level)
inputdata <- varToFactor(obj=inputdata, var=c("roof","walls"))
inputdata <- varToFactor(obj=inputdata, var="urbrur")
inputdata <- varToFactor(obj=inputdata, var="sex")
inputdata <- varToFactor(obj=inputdata, var="age")
## Set up sdcMicro object
sdcObj <- createSdcObj(dat=inputdata,
        keyVars=c("urbrur","sex","age"),
        numVars=c("expend","income","savings"),
        weightVar=c("sampling_weight"),
        hhId=NULL,
        strataVar=NULL,
        pramVars=c("roof","walls"),
        excludeVars=NULL,
        seed=0,
        randomizeRecords=FALSE,
        alpha=c(1))

## Store name of uploaded file
```

Fig. 10.1: *R* script to reproduce anonymization process after setting up SDC problem

The goal of the *R* script is threefold: 1) To reproduce the steps taken in the anonymization process. This guarantees the reproducibility, since the all variabele selections and parameters are contained in the code and the order of the application of different methods is preserved in the code. 2) As a starting point to learn *R* and use *sdcMicro* from *R* command-line. Especially for users with some degree of familiarity with *R*, the script 3) To rerun the same methods with different parameter settings without the need to make all selections by mouseclick in the GUI. It's relatively easy to change the parameter settings in the *R* code and rerun the code. However, the code does not include commands to shw the results.

By clicking on the blue button **Save script to file** at the top of the page, the script is saved as *R* script (extension .R) on disk to the selected storage path on the **About/Help** tab (see Introduction to sdcApp). The filename of the exported script starts with ‘exportedScript_sdcMicro’ followed by a date and time stamp, e.g., ‘exportedScript_sdcMicro_20181010_1212.R’.

In order to run the script in *R*, open the saved script in *RStudio*. The only thing to do is to change the path of the input file to the actual file path on your computer. In the second line of the *R* script,

Note: In case a method was applied in *sdcApp* and subsequently reverted by using the **Undo** button, the method is not erased from the script, but rather the undo command is added. For example, if local suppression was applied and reverted, this appears as follows in the script:

```
## Local suppression to obtain k-anonymity
sdcObj <- kAnon(sdcObj, importance=c(1,2,3), combs=NULL, k=c(3))
sdcObj <- undolast(sdcObj)
```

This code preceding the :code:‘undoLast‘command and the :code:‘undoLast‘command can be deleted without changing the results.

CHAPTER

ELEVEN

UNDO

Microdata anonymization is a trial-and-error process. It is necessary to several methods, each with different parameter settings, to find optimal set of anonymization measures that minimize the information loss, while reducing the risk of disclosure to an acceptable level. Before applying an alternative method to the same variable or set of variables, it is important to undo the previously applied methods. Only in this way, it is possible to compare the effect on risk and information loss of a particular method or parameter setting. For instance to compare the effect of recoding the age variable in 5 or 10 year intervals, it is necessary to first undo the recoding in 5-year intervals before recoding in 10 year intervals.

In *sdcApp* it is possible to undo the last anonymization step. In order to undo several steps, it is required to save and reload the SDC problem. Both ways are explained below.

11.1 Undo one step

In order to undo one step, go to the **Undo** tab. The screen shows

risk measures etc are also reset, script not (completely), random seed not

11.2 Undo several steps

Save and reload

Recommended to save the SDC problem after each method to be able to reload. This is also practical if *sdcApp* or *R* crash. Also useful to continue working at a later point of transfer a problem to a different computer

11.2.1 Save a previously saved problem

11.2.2 Load a previously saved problem

Note: sdcApp exports four different file types Different file names for different files (data, sdcProblem)

CHAPTER

TWELVE

CASE STUDIES (ILLUSTRATING THE SDC PROCESS)

In order to evaluate the use of different SDC methods on different types of survey datasets, we compared the results of the different methods applied to 75 datasets from 52 countries representing six geographic regions: Latin America and the Caribbean (LAC), Sub-Saharan Africa (AFR), South Asia (SA), Europe and Central Asia (ECA), Middle East and North Africa (MENA) as well as East Asia and the Pacific (EAP). The datasets chosen were from a mix of datasets that are already publically available, as well as data made available to the World Bank. The surveys used included, amongst others, household, demographic, and health surveys. The variables from these surveys used for the experiments were selected based on their relevance for users (e.g., for indicators, MDGs), their sensitivity, and their classification with respect to the SDC process.

The following case studies draw from knowledge gained from these experiments and try to incorporate the lessons learned. The case studies use synthetic data that mimic the structure of the survey types we used in our experiments and present the anonymization of a dataset similar to many surveys designed to measure household income and consumption, labor force participation and general demographic characteristics. The first case study creates a SUF, whereas in the second case study we take this SUF and treat it further to create a PUF.

12.1 Case study 1- SUF

This case study shows an example of how the anonymization process might be approached, particularly for a dataset with many continuous variables. We also show how this can be achieved using *sdcApp*, the GUI for the open source and free *sdcMicro R* package.

Note: The choices of methods and parameters in this case study are based on this particular dataset and the results and choices might be different for other datasets.

The aim is to show the process, not to compare methods per se.

This example uses a dataset with a similar structure to that of a typical social survey with a focus on demographics, labor force participation and income and expenditure patterns. The dataset has been compiled using observations from several datasets from different countries. They are considered synthetic data and as such are used only for illustrative purposes. The source datasets were already treated for disclosure control by their producers. This does not matter, as our concern is to illustrate the process only. The data from which we compiled our case study file was from surveys that contain many variables, but pay particular attention to labor force variables as well as household income and household expenditure variables. The variables in the demo dataset have already been pre-selected from the total set of variables available in the datasets. See Appendix A for the complete overview of all variables.

This case study follows the steps of the SDC process outlined in the Section The SDC Process.

12.1.1 Step 1: Need for disclosure control

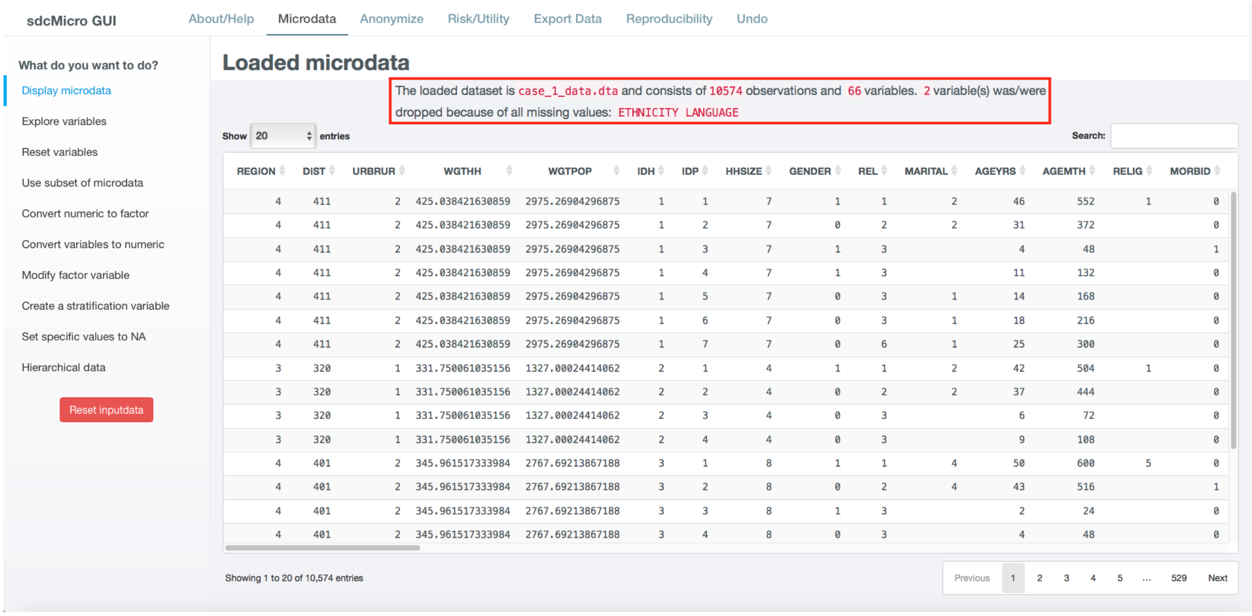
The statistical units in this dataset are individuals and households. The household structure provides a hierarchical structure in the data, which should be taken into account when measuring risk and selecting anonymization methods.

The data contains variables with demographic information, income, expenditures, education variables and variables relating to the labor status of the individual. These variables include sensitive and confidential variables. The dataset is an example of a social survey and, due to the nature of the statistical units and the variables, disclosure control is needed before release of the microdata. This is the case regardless of the legal framework, which is not specified here, as this is a hypothetical dataset.

12.1.2 Step 2: Data preparation and exploring data characteristics

The first step is to explore the data. First launch *sdcApp* and specify the output directory (see the Section **'Starting sdcApp <introsdcApp.html#Starting sdcApp'__**). To analyze the data in *sdcApp* we first have to load the dataset. In our case, the data is saved as a *STATA* file (.dta file). (see the Section Loading data on importing data in *sdcApp*). Load the dataset case_1_data.dta with the default options for string conversion and dropping variables with only missing values. After loading the dataset, the dataset is shown in the Microdata tab.

On top of the table we can check the name of the loaded dataset, the number of variables and the number of observation, as shown in Fig. **??**. Note that the variables ETHNICITY and LANGUAGE were dropped due to all missing values in these variables. The loaded dataset contains 10,574 observations and 66 variables.



Loaded microdata

The loaded dataset is case_1_data.dta and consists of 10574 observations and 66 variables. 2 variable(s) was/were dropped because of all missing values: ETHNICITY LANGUAGE

Show 20 entries

Search:

REGION	DIST	URBRUR	WGTHH	WGTPOP	IDH	IDP	HHSIZE	GENDER	REL	MARITAL	AGEYRS	AGEMTH	RELIG	MORBID
4	411	2	425.038421630859	2975.26904296875	1	1	7	1	1	2	46	552	1	0
4	411	2	425.038421630859	2975.26904296875	1	2	7	0	2	2	31	372		0
4	411	2	425.038421630859	2975.26904296875	1	3	7	1	3		4	48		1
4	411	2	425.038421630859	2975.26904296875	1	4	7	1	3		11	132		0
4	411	2	425.038421630859	2975.26904296875	1	5	7	0	3	1	14	168		0
4	411	2	425.038421630859	2975.26904296875	1	6	7	0	3	1	18	216		0
4	411	2	425.038421630859	2975.26904296875	1	7	7	0	6	1	25	300		0
3	320	1	331.750061035156	1327.00024414062	2	1	4	1	1	2	42	504	1	0
3	320	1	331.750061035156	1327.00024414062	2	2	4	0	2	2	37	444		0
3	320	1	331.750061035156	1327.00024414062	2	3	4	0	3		6	72		0
3	320	1	331.750061035156	1327.00024414062	2	4	4	0	3		9	108		0
4	401	2	345.961517333984	2767.69213867188	3	1	8	1	1	4	50	600	5	0
4	401	2	345.961517333984	2767.69213867188	3	2	8	0	2	4	43	516		1
4	401	2	345.961517333984	2767.69213867188	3	3	8	1	3		2	24		0
4	401	2	345.961517333984	2767.69213867188	3	4	8	0	3		4	48		0

Showing 1 to 20 of 10,574 entries

Fig. 12.1: Microdata tab after loading case study dataset

The dataset has 10,574 individuals in 2,000 households and contains 68 variables. The survey corresponds to a population of about 4.3 million individuals, which means that the sample is relatively small and the sample weights are high. This has an impact on the disclosure risk, as we will see in Steps 6a and 6b.

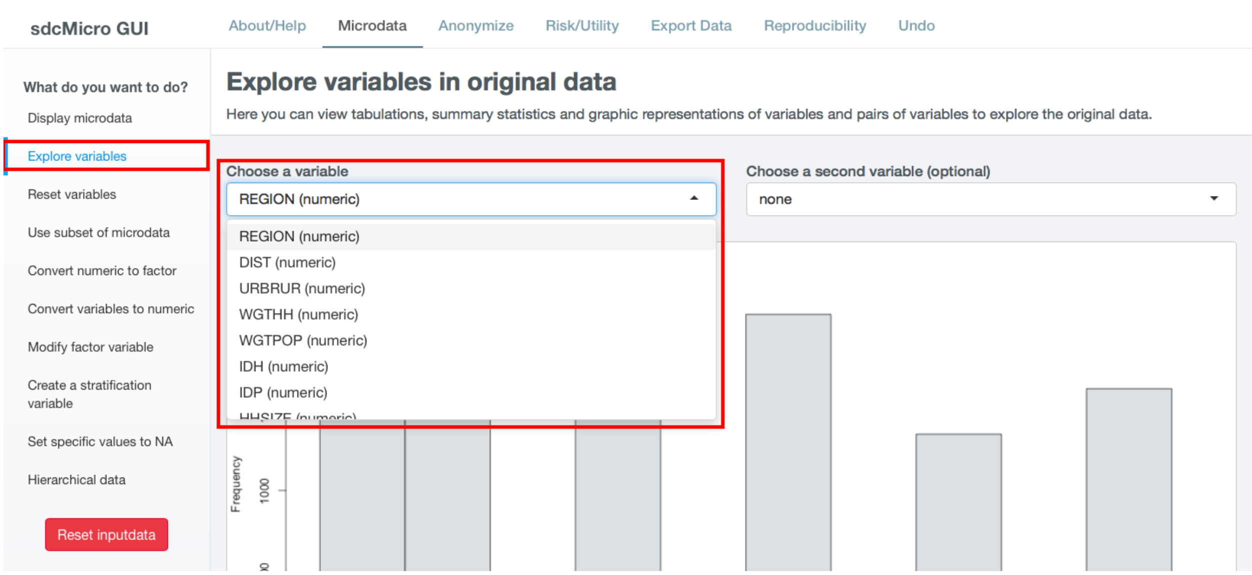
To get an overview of the values of the variables, we use tabulations and cross-tabulations for categorical variables and summary statistics for continuous variables. To include the number of missing values (NA or other), we use the option useNA = "ifany" in the table() function (see `code94`).

In Table **??** the variables in the dataset are listed along with concise descriptions of the variables, the level at which they are collected (individual (IND), household (HH)), the measurement type (continuous, semi-continuous, categorical) and value ranges. Note that the dataset contains a selection of 68 variables (cf. Appendix A) of a total of 112 variables in the survey dataset. The variables have been preselected based on their relevance for data users. This allows to reduce the total numbers of variables to consider in the anonymization process and makes the process easier. The numerical values for many of the categorical variables are codes that refer to values, e.g., in the variable URBRUR, 1 stands for rural and 2 for urban. More information on the meanings of coded values of the categorical variables is available in the *R* code for this case study.

We identified the following sensitive variables in the data: ETHNICITY, RELIGION, variables related to the labor force status of the individual and the variables containing information on income and expenditures of the household. Whether variables can be identified as sensitive may vary across countries and datasets.

The case study dataset does not have any direct identifiers that, if they were present, would need to be removed at this stage. Examples of direct identifiers would be names, telephone numbers, geographical location coordinates, etc.

Before exploring the data, the variable type of all variables needs to be checked and, if necessary, be adapted. Categorical key variables need to be of type *factor* and continuous key variables need to be of type *numeric*.



Explore variables in original data

Here you can view tabulations, summary statistics and graphic representations of variables and pairs of variables to explore the original data.

Choose a variable: REGION (numeric)

Choose a second variable (optional): none

Fig. 12.2: Check variable type

Table 12.1: Overview of variables in dataset

No.	Variable name	Description	Level	Measurement	Values
1	IDH	Household ID	HH	.	1-2,000
2	IDP	Individual ID	IND	.	1-33
3	REGION	Region	HH	categorical	1-6
4	DIST	District	HH	categorical	101-1105
5	URBRUR	Area of residence	HH	categorical	1, 2
6	WGTHH	Individual weighting coefficient	HH	weight	31.2-8495
7	WGTPOP	Population weighting coefficient	IND	weight	45.8-93452.2
8	HHSIZE	Household size	HH	semi-cont	1-33
9	GENDER	Gender	IND	categorical	0, 1
10	REL	Relationship to household head	IND	categorical	1-9
11	MARITAL	Marital status	IND	categorical	1-6
12	AGEYRS	Age in completed years	IND	semi-continuous	0-95 (under 1, 1/12 year increments)
13	AGEMTH	Age of child in completed years	IND	semi-continuous	1-1140

Continued on next page

Table 12.1 – continued from previous page

No.	Variable name	Description	Level	Measurement	Values
14	RELIG	Religion of household head	HH	categorical	1, 5-7, 9
15	ETHNICITY	Ethnicity of household head	HH	categorical	all missing values
16	LANGUAGE	Language of household head	HH	categorical	all missing values
17	MORBID	Morbidity last x weeks	IND	categorical	0, 1
18	MEASLES	Child immunized against measles	IND	categorical	0, 1, 9
19	MEDATT	Sought medical attention	IND	categorical	0, 1
20	CHWEIGHTKG	Weight of child (Kg)	IND	continuous	2 – 26.5
21	CHHEIGHTCM	Height of child (cms)	IND	continuous	7 - 140
22	ATSCHOOL	Currently enrolled in school	IND	categorical	0, 1
23	EDUCY	Highest level of education attended	IND	categorical	1-6
24	EDYRS	Years of education	IND	semi-continuous	0-18
25	EDYRSCURRAT	Years of education for currently enrolled	IND	semi-continuous	1-18
26	SCHTYP	Type of school attending	IND	categorical	1-3, 9
27	LITERACY	Literacy	IND	categorical	1-3
28	EMPTYP1	Type of employment	IND	categorical	1-9
29	UNEMP1	Unemployed	IND	categorical	0, 1
30	INDUSTRY1	Industry classification (1-digit)	IND	categorical	1-10
31	EMPCAT1	Employment categories	IND	categorical	11, 12, 13, 14, 2
32	WHOURSWEEK1	Hours worked last week	IND	continuous	0-154
33	OWNHOUSE	Ownership of dwelling	HH	categorical	0, 1
34	ROOF	Main material used for roof	IND	categorical	1-5, 9
35	TOILET	Main toilet facility	HH	categorical	1-4, 9
36	ELECTCON	Electricity	HH	categorical	0-3
37	FUELCOOK	Main cooking fuel	HH	categorical	1-5, 9
38	WATER	Main source of water	HH	categorical	1-9
39	OWNAGLAND	Ownership of agricultural land	HH	categorical	1-3
40	LANDSIZEHA	Land size owned by household (ha) (agric and non agric)	HH	continuous	0-1214
41	OWNMOTORCYCLE	Ownership of motorcycle	HH	categorical	0, 1
42	CAR	Ownership of car	HH	categorical	0, 1
43	TV	Ownership of television	HH	categorical	0, 1
44	LIVESTOCK	Number of large-sized livestock owned	HH	semi-continuous	0-25
45	INCRMT	Income – Remittances	HH	continuous	
46	INCWAGE	Income - Wages and salaries	HH	continuous	
47	INCBONSOCAL	Income - Bonuses and social allowances derived from wage jobs	HH	continuous	
48	INCFARMBSN	Income - Gross income from household farm businesses	HH	continuous	
49	INCNFARMBSN	Income - Gross income from household nonfarm businesses	HH	continuous	
50	INCRENT	Income - Rent	HH	continuous	
51	INCFIN	Income - Financial	HH	continuous	
52	INCPENSN	Income - Pensions/social assistance	HH	continuous	
53	INCOTHER	Income - Other	HH	continuous	
54	INCTOTGROSSHH	Income - Total	HH	continuous	
55	FARMEMP				
56	TFOODEXP	Total expenditure on food	HH	continuous	
57	TALCHEXP	Total expenditure on alcoholic beverages, tobacco and narcotics	HH	continuous	
58	TCLTHEXP	Total expenditure on clothing	HH	continuous	
59	THOUSEXP	Total expenditure on housing	HH	continuous	
60	TFURNEXP	Total expenditure on furnishing	HH	continuous	
61	THLTHEXP	Total expenditure on health	HH	continuous	
62	TTRANSEXP	Total expenditure on transport	HH	continuous	

Continued on next page

Table 12.1 – continued from previous page

No.	Variable name	Description	Level	Measurement	Values
63	TCOMMEXP	Total expenditure on communication	HH	continuous	
64	TRECEXP	Total expenditure on recreation	HH	continuous	
65	TEDUEXP	Total expenditure on education	HH	continuous	
66	TRESHOTEXP	Total expenditure on restaurants and hotels	HH	continuous	
67	TMISCEXP	Total expenditure on miscellaneous spending	HH	continuous	
68	TANHHEXP	Total annual nominal household expenditures	HH	continuous	

It is always important to ensure that the relationships between variables in the data are preserved during the anonymization process and to explore and take note of these relationships before beginning the anonymization. In the final step in the anonymization process, an audit should be conducted, using these initial results, to check that these relationships are maintained in the anonymized dataset.

In our demo dataset, we identify several relationships between variables that need to be preserved during the anonymization process. The variables TANHHEXP and INCTOTGROSSHH represent the total annual nominal household expenditure and the total gross annual household income, respectively, and these variables are aggregations of existing income and expenditure components in the dataset.

The variables related to education are available only for individuals in the appropriate age groups and missing for other individuals. We make a similar observation for variables relating to children, such as height, weight and age in months. In addition, the household-level variables (cf. fourth column of Table **??**) have the same values for all members in any particular household. The value of household size corresponds to the actual number of individuals belonging to that household in the dataset. As we proceed, we have to take care that these relationships and structures are preserved in the anonymization process.

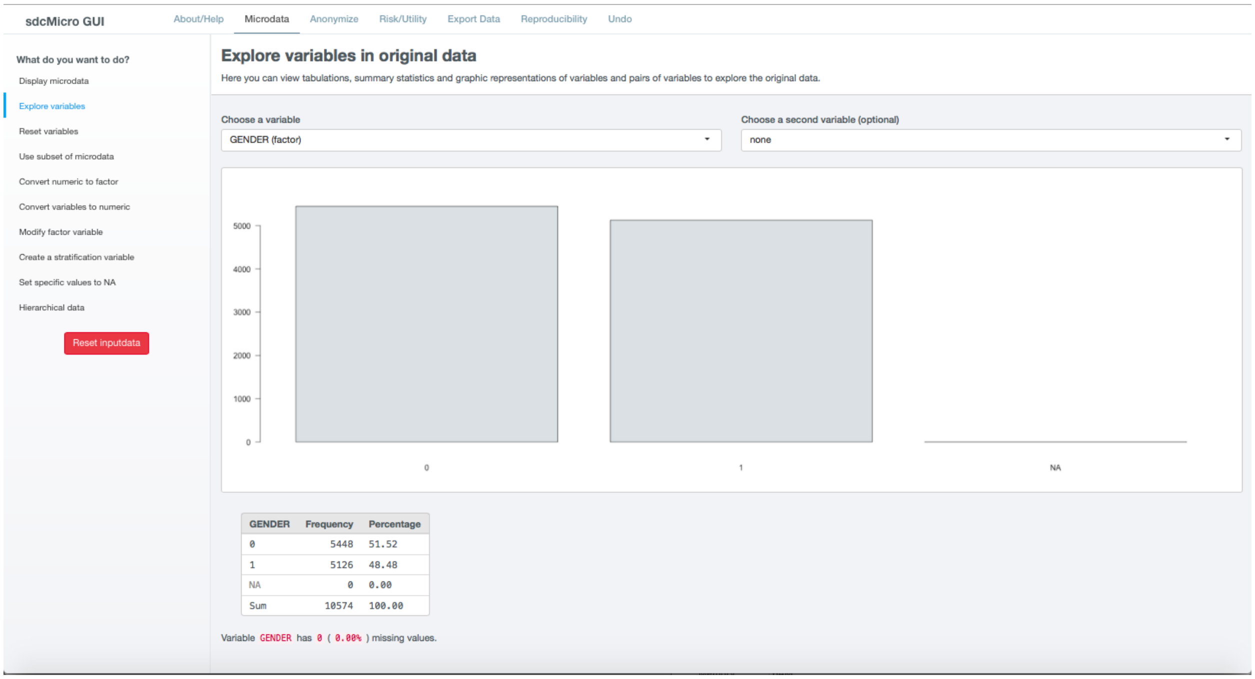
When tabulating the variables, we notice that the variables RELIG, EMPTYP1 and LIVESTOCK have missing value codes different from the *R* standard missing value code NA. Before proceeding, we need to recode these to NA so *R* interprets them correctly. The missing value codes are resp. 99999, 99 and 9999 for these three variables. These are genuine missing value codes and not caused by the variables being not applicable to the individual. Listing **??** shows how to make these changes.

Note: At the end of the anonymization process, and if desired for users, it is relatively easy to change these values back to their original missing value code.

Listing 12.1: Recoding missing value codes

```
# Set different NA codes to R missing value NA
file[,'RELIG'][file[,'RELIG'] == 99999]         <- NA
file[,'EMPTYP1'][file[,'EMPTYP1'] == 99]        <- NA
file[,'LIVESTOCK'][file[,'LIVESTOCK'] == 9999] <- NA
```

We also take note that the variables LANGUAGE and ETHNICITY have only missing values. Variables that contain only missing values should be removed from the dataset at this stage and excluded from the anonymization process. Removing these variables does not mean loss of data or reduction of the data utility, since these variables did not contain any information. It is, however, necessary to remove them, because keeping them can lead to errors in some of the anonymization methods in *R*. It is always possible to add these variables back into the dataset to be released at the end of the anonymization process. It is useful to reduce the dataset to those variables and records relevant for the anonymization process. This guarantees the best results in *R* and fewer errors. In Listing **??** we drop the variables that contain all missing values.



Explore variables in original data

Here you can view tabulations, summary statistics and graphic representations of variables and pairs of variables to explore the original data.

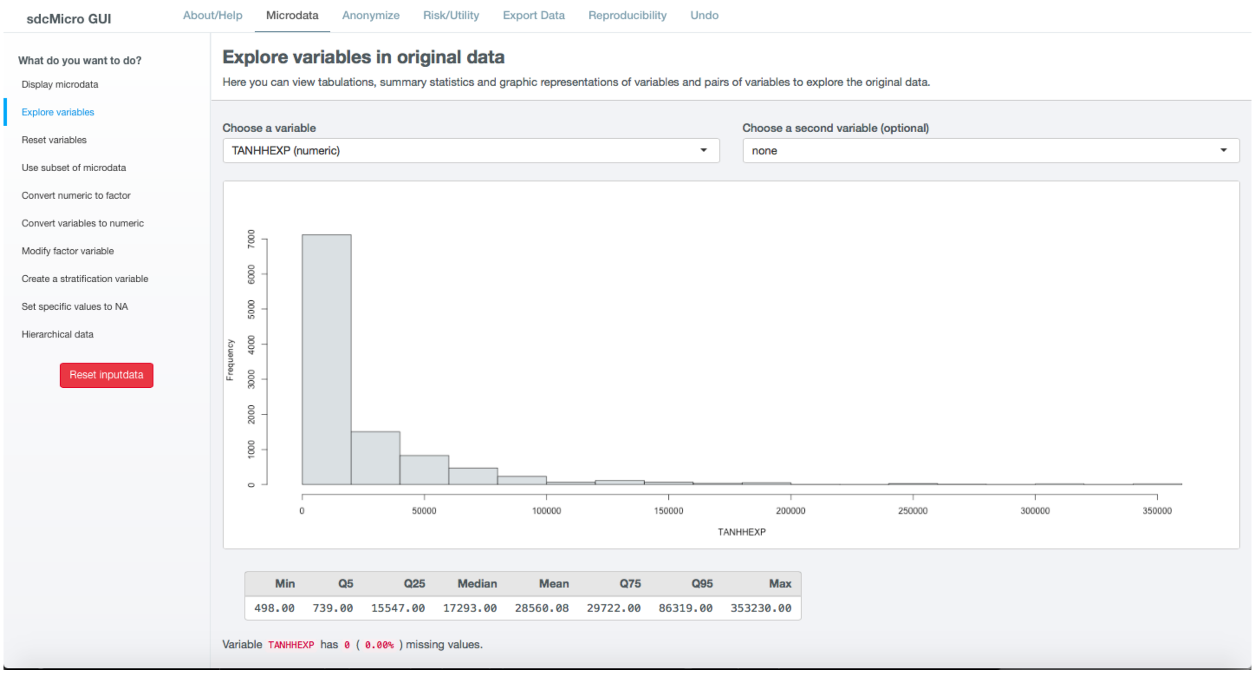
Choose a variable: GENDER (factor)

Choose a second variable (optional): none

GENDER	Frequency	Percentage
0	5448	51.52
1	5126	48.48
NA	0	0.00
Sum	10574	100.00

Variable GENDER has 0 (0.00%) missing values.

Fig. 12.3: Summary statistics for categorical variable, example variable ‘gender’



Explore variables in original data

Here you can view tabulations, summary statistics and graphic representations of variables and pairs of variables to explore the original data.

Choose a variable: TANHHEXP (numeric)

Choose a second variable (optional): none

Min	Q5	Q25	Median	Mean	Q75	Q95	Max
498.00	739.00	15547.00	17293.00	28560.08	29722.00	86319.00	353230.00

Variable TANHHEXP has 0 (0.00%) missing values.

Fig. 12.4: Summary statistics for continuous variable, example variable ‘total annual expenditures’

Listing 12.2: Dropping variables with only missing values

```
# Drop variables containing only missings
file <- file[,!names(file) %in% c('LANGUAGE', 'ETHNICITY')]
```

We assume that the data are collected in a survey that uses simple sampling of households. The data contains two weight coefficients: WGTHH and WGTPOP. The relationship between the weights is WGTPOP = WGTHH * HHSIZE. WGTPOP is the sampling weight for the households and WGTHH is the sampling weight for the individuals to be used for disclosure risk calculations. WGTHH is used for computing individual-level indicators (such as education) and WGTPOP is used for population level indicators (such as income indicators). There are no strata variables available in the data. We will use WGTPOP for the anonymization of the household variables and WGTHH for the anonymization of the individual-level variables.

12.1.3 Step 3: Type of release

In this case study, we assume that data will be released as a SUF, which will be only available under license to accredited researchers with approved research proposals (see the Section Conditions for SUFs for more information of the release of a SUF). Therefore, the accepted risk level is higher and a broader set of variables can be released than would be the case when releasing a PUF. Since we do not have an overview of the requirements of all users, we restrict the utility measures to a selected number of data uses (see Step 5).

12.1.4 Step 4: Intruder scenarios and choice of key variables

Next, we analyze possible intruder scenarios and select quasi-identifiers or key variables based on these scenarios. Since the dataset used in this case study is a demo dataset that does not stem from an existing country (and hence we do not have information on external data sources available to possible intruders) and the original data has already been anonymized, it is not possible to define exact disclosure scenarios. Instead, we draft intruder scenarios for this demo dataset based on some hypothetical assumptions about availability of external data sources. We consider two types of disclosure scenarios: 1) matching to other publicly available datasets and 2) spontaneous recognition. The license under which the dataset will be distributed (SUF) prohibits matching to external resources. Still this can happen. However, the more important scenario is the one of spontaneous recognition. We describe both scenarios in the following two paragraphs.

For the sake of illustration, we assume that population registers are available with the demographic variables gender, age, place of residence (region, urban/rural), religion and other variables such as marital status and variables relating to education and professional status that are also present in our dataset. In addition, we assume that there is a publically available cadastral register on land ownership. Based on this analysis of available data sources, we select the variables REGION, URBRUR, HHSIZE, OWNAGLAND, RELIG, GENDER, REL (relationship to household head), MARITAL (marital status), AGEYRS, INDUSTRY1 and two variables relating to school attendance as categorical quasi-identifiers, the expenditure and income variables as well as LANDSIZEHA as continuous quasi-identifiers. According to our assessment, these variables might enable an intruder to re-identify an individual or household in the dataset by matching with other available datasets.

Table **??** gives an overview of the selected quasi-identifiers and their levels of measurement.

The decision to release the dataset as a SUF means the level of anonymization will be relatively low and consequently, the variables are more detailed and a scenario of spontaneous recognition is our main concern. Therefore, we should check for rare combinations or unusual patterns in the variables. Variables that may lead to spontaneous recognition in our sample are amongst others HHSIZE (household size), LANDSIZEHA as well as income and expenditure variables. Large households and large land ownership are easily identifiable. The same holds for extreme outliers in wealth and expenditure variables, especially when combined with other identifying variables such as region. There might be only one or a few households in a certain region with a high income, such as the local doctor. Variables that are easily observable and known by neighbors such as ROOF, TOILET, WATER, ELECTCON, FUELCOOK, OWNMOTORCYCLE, CAR, TV and LIVESTOCK may also need protection depending on what stands out in the community, since a researcher might be able to identify persons (s)he knows. This is called the nosy-neighbor scenario.

Table 12.2: List of selected quasi-identifiers

Name	Measurement
REGION (region)	Household, categorical
URBRUR (area of residence)	Household, categorical
HHSIZE (household size)	Household, categorical
OWNAGLAND (agricultural land ownership)	Household, categorical
RELIG (religion of household head)	Household, categorical
LANDSIZEHA (size of agr. and non-agr. land)	Household, continuous
TANHHEXP (total expenditures)	Household, continuous
TEXP (expenditures in category)	Household, continuous
INCTOTGROSSHH (total income)	Household, continuous
INC (income in category)	Household, continuous
GENDER (sex)	Individual, categorical
REL (relationship to household head)	Individual, categorical
MARITAL (marital status)	Individual, categorical
AGEYRS (age in completed years)	Individual, semi-continuous
EDYRSCURATT (years of education for currently enrolled)	Individual, semi-continuous
EDUCY (highest level of education completed)	Individual, categorical
ATSCHOOL (currently enrolled in school)	Individual, categorical
INDUSTRY1 (industry classification)	Individual, categorical

12.1.5 Step 5: Data key uses and selection of utility measures

In this case study, our aim is to create a SUF that provides sufficient information for accredited researchers. We know that the primary use of these data will be to evaluate indicators relating to income and inequality. Examples are the GINI coefficient and indicators on what share of income is spent on what type of expenditures. Furthermore, we focus on some education indicators. Table **??** gives an overview of the utility measures we selected. Besides these utility measures, which are specific to the data uses, we also do standard checks, such as comparing tabulations, cross-tabulations and summary statistics before and after anonymization.

Table 12.3: Overview of selected utility measures

Gini point estimates and confidence intervals for total expenditures	.
Lorenz curves for total expenditures	
Mean monthly per capita total expenditures by area of residence	
Average share of components for expenditures	
Mean monthly per capita total income by area of residence	
Average share of components for income	
Net enrollment in primary education by gender	

There are no published figures and statistics available that are calculated from this dataset because it is a demo. In general, the published figures should be re-computed based on the anonymized dataset and compared to the published figures in Step 11. Large differences would reduce the credibility of the anonymized dataset.

12.1.6 Hierarchical (household) structure

Our demo survey collects data on individuals in households. The household structure is important for data users and should be considered in the risk assessment. Since some variables are measured on the household level and thus have identical values for each household member, the values of the household variables should be treated in the same way for each household member (see the Section Anonymization of the quasi-identifier household size). Therefore, we first anonymize only the household variables. After this, we merge them with the individual-level variables and then anonymize the individual-level and household-level variables jointly.

Since the data has a hierarchical structure, Steps 6 through 10 are repeated twice: Steps 6a through 10a are for the household-level variables and Steps 6b through 10b for the combined dataset. In this way, we ensure that household-level variable values remain consistent across household members for each household and the household structure cannot be used to re-identify individuals. This is further explained in the Sections Levels of risk and Randomizing order and numbering of individuals or households .

Before continuing to Step 6a, we select the categorical key variables, continuous key variables and any variables selected for use in PRAM routines, as well as household-level sampling weights. We extract these selected household variables and the households from the dataset and save them as *fileHH*. The choice of PRAM variables is further explained in Step 8a. Listing **??** illustrates how these steps are done in *R* (see also the Section Household structure).

Note: In our dataset, some of the categorical variables when imported from the STATA file were not imported as factors. sdcMicro requires that these be converted to factors before proceeding.

Conversion of these variables to factors is also shown in Listing **??**.

Listing 12.3: Selecting the variables for the household-level anonymization

```r
### Select variables (household level)
# Key variables (household level)
selectedKeyVarsHH = c('URBRUR', 'REGION', 'HHSIZE', 'OWNHOUSE',
                      'OWNAGLAND', 'RELIG')

# Changing variables to class factor
file$URBRUR    <- as.factor(file$URBRUR)
file$REGION    <- as.factor(file$REGION)
file$OWNHOUSE  <- as.factor(file$OWNHOUSE)
file$OWNAGLAND <- as.factor(file$OWNAGLAND)
file$RELIG     <- as.factor(file$RELIG)

# Numerical variables
numVarsHH = c('LANDSIZEHA', 'TANHHEXP',   'TFOODEXP',       'TALCHEXP',
              'TCLTHEXP',   'THOUSEXP',   'TFURNEXP',       'THLTHEXP',
              'TTRANSEXP',  'TCOMMEXP',   'TRECEXP',        'TEDUEXP',
              'TRESHOTEXP', 'TMISCEXP',   'INCTOTGROSSHH', 'INCRMT',
              'INCWAGE',    'INCFARMBSN', 'INCNFARMBSN',    'INCRENT',
              'INCFIN',     'INCPENSN',   'INCOTHER')
# PRAM variables
pramVarsHH = c('ROOF', 'TOILET', 'WATER', 'ELECTCON',
               'FUELCOOK', 'OWNMOTORCYCLE', 'CAR', 'TV', 'LIVESTOCK')

# sample weight (WGTPOP) (household)
weightVarHH = c('WGTPOP')

# All household level variables
HHVars <- c('HID', selectedKeyVarsHH, pramVarsHH, numVarsHH, weightVarHH)
```

We then extract these variables from *file*, the dataframe in *R* that contains all variables. Every household has the same number of entries as it has members (e.g., a household of three will be repeated three times in *fileHH*). Before analyzing the household-level variables, we select only one entry per household, as illustrated in Listing **??**. This is further explained in the Section Household structure.

Listing 12.4: Taking a subset with only households

```
# Create subset of file with households and HH variables
fileHH <- file[,HHVars]

# Remove duplicated rows based on IDH, select uniques,
# one row per household in fileHH
fileHH <- fileHH[which(!duplicated(fileHH$IDH)),]

dim(fileHH)
## [1] 2000   39
```

The file *fileHH* contains 2,000 households and 39 variables. We are now ready to create our *sdcMicro* object with the corresponding variables we selected in Listing **??**. For our case study, we will create an *sdcMicro* object called *sdcHH* based on the data in *fileHH*, which we will use for steps 6a – 10a (see Listing **??**).

Note: When the sdcMicro object is created, the sdcMicro package automatically calculates and stores the risk measures for the data.

This leads us to Step 6a.

Listing 12.5: Creating a *sdcMicro* object for the household variables

```
# Create initial SDC object for household level variables
sdcHH <- createSdcObj(dat = fileHH, keyVars = selectedKeyVarsHH, pramVars = pramVarsHH,
                      weightVar = weightVarHH, numVars = numVarsHH)

numHH <- length(fileHH[,1]) # number of households
```

12.1.7 Step 6a: Assessing disclosure risk (household level)

As a first measure, we evaluate the number of households violating k-anonymity at the levels 2, 3 and 5.

Table **??** shows the number of violating households as well as the percentage of the total number of households. Listing **??** illustrates how to find these values with *sdcMicro*. The print() function in *sdcMicro* shows only the values for thresholds 2 and 3. Values for other thresholds can be calculated manually by summing up the frequencies smaller than the k-anonymity threshold, as shown in Listing **??**.

Table 12.4: Number and proportion of households violating k-anonymity

k-anonymity level	Number of HH violating	Percentage of total number of HH
2	103	5.15 %
3	229	11.45 %
5	489	24.45 %

Listing 12.6: Showing number of households violating k-anonymity for levels 2, 3 and 5

```
# Number of observations violating k-anonymity (thresholds 2 and 3)
print(sdcHH)
## Infos on 2/3-Anonymity:
##
```

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```
## Number of observations violating
##   - 2-anonymity: 103
##   - 3-anonymity: 229
##
## Percentage of observations violating
##   - 2-anonymity: 5.150 %
##   - 3-anonymity: 11.450 %
--------------------------------------------------------------------------

# Calculate sample frequencies and count number of obs. violating k(5) - anonymity
kAnon5 <- sum(sdcHH@risk$individual[,2] < 5)

kAnon5
## [1] 489

# As percentage of total
kAnon5 / numHH
## [1] 0.2445
```

It is often useful to view the values for the household(s) that violate k-anonymity. This might help clarify which variables cause the uniqueness of these households; this can then be used later when choosing appropriate SDC methods. Listing **??** shows how to assess the values of the households violating 3- and 5-anonymity. It seems that among the categorical key variables, the variable HHSIZE is responsible for many of the unique combinations and the origin of much of the risk. Having determined this, we can flag HHSIZE as a possible first variable to treat to obtain the required risk level. In practice, with a variable like HHSIZE, this will likely involve removing large households from the dataset to be released. As explained in the Section Anonymization of the quasi-identifier household size , recoding and local suppression are no valid options for the variable HHSIZE. The frequencies of household size in Table **??** show that there are few households with more than 13 household members. This makes these households easily identifiable based on the number of household members and at high risk of re-identification, also in the context of the nosy neighbor scenario.

Listing 12.7: Showing households that violate k-anonymity

```
# Show values of key variable of records that violate k-anonymity
fileHH[sdcHH@risk$individual[,2] < 3, selectedKeyVarsHH] # for 3-anonymity
fileHH[sdcHH@risk$individual[,2] < 5, selectedKeyVarsHH] # for 5-anonymity
```

We also assess the disclosure risk of the categorical variables with the individual and global risk measures as described in the Sections Individual risk and Global risk. In *fileHH* every entry represents a household. Therefore, we use the individual non-hierarchical risk here, where the individual refers in this case to a household. *fileHH* contains only households and has no hierarchical structure. In Step 6b, we evaluate the hierarchical risk in *file*, the dataset containing both households and individuals. The individual and global risk measures automatically take into consideration the household weights, which we defined in Listing **??**. In our file, the global risk measure calculated using the chosen key variables is 0.05%. This percentage is extremely low and corresponds to 1.03 expected re-identifications. The results are also shown in Listing **??**. This low figure can be explained by the relatively small sample size of 0.25% of the total population. Furthermore, one should keep in mind that this risk measure is based only on the categorical quasi-identifiers at the household level. Listing **??** illustrates how to print the global risk measure.

Listing 12.8: Printing global risk measures

```
print(sdcHH, "risk")

## Risk measures:
##
## Number of observations with higher risk than the main part of the data: 0
```

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```
## Expected number of re-identifications: 1.03 (0.05 %)
```

The global risk measure does not provide information about the spread of the individual risk measures. There might be a few households with relatively high risk, while the global (average) risk is low. It is therefore useful as a next step to inspect the observations with relatively high risk. The highest risk is 5.5% and only 14 households have risk larger than 1%. Listing **??** shows how to display those households with risk over a certain threshold. Here the threshold is 0.01 (1%).

Listing 12.9: Observations with individual risk higher than 1%

```
# Observations with risk above certain threshold (0.01)
fileHH[sdcHH@risk$individual[, "risk"] > 0.01,]
```

Since the selected key variables at the household level are both categorical and numerical, the individual and global risk measures based on frequency counts do not completely reflect the disclosure risk of the entire dataset. Both categorical and continuous key variables are important for the data users, thus options like recoding the continuous variables (e.g., by creating quantiles of income and expenditure variables) to make all of them categorical will likely not satisfy the data user's needs. We therefore avoid recoding continuous variables and assess the disclosure risk of the categorical and continuous variables separately. This approach can be partly justified by the fact that any potential matching to external data sources for the continuous and categorical variables are available from different external data sources and as such will not be used simultaneously for matching.

Continuous variables

To measure the risk of the continuous variables, we use an interval measure, which measures the number of anonymized values that are too close to their original values. See the Section Interval measure for more information on interval-based risk measures for continuous variables. This measure is an ex-post measure, meaning that the risk can be evaluated only after anonymization and measures whether the perturbation is sufficiently large. Since it is an ex-post measure, we can evaluate it only in Step 9a after the variables have been treated. Evaluating this measure based on the original data would lead to a risk of 100%; all values would be too close to the original values since they would coincide with the original values, no matter how small the chosen intervals would be.

We also look at the distribution of LANDSIZEHA. In the variable LANDSIZEHA high values are rare and can lead to re-identification. An example is a large landowner in a specific region. To evaluate the distribution of the variable LANDSIZEHA, we look at the percentiles. Every percentile represents approximately 20 households. In addition, we look at the values of the largest 50 plots. Listing **??** shows how to use *R* to display the quantiles and the largest landplots. Table **??** shows the 90th – 100th percentiles and Table **??** displays the largest 50 values for LANDSIZEHA. Based on these values, we conclude that values of LANDSIZEHA over 40 make the household very identifiable. These large households and households with large land plots need extra protection, as discussed in Step 8a.

Listing 12.10: Percentiles of LANDSIZE and listing the sizes of the largest 50 plots

```
# 1st - 100th percentiles of land size
quantile(fileHH$LANDSIZEHA, probs = (1:100)/100, na.rm= TRUE)

# Values of landsize for largest 50 plots
tail(sort(fileHH$LANDSIZEHA), n = 50)
```

Table 12.5: Percentiles 90-100 of the variable LANDSIZE

Percentile	90	91	92	93	94	95
Value	6.00	8.00	8.09	10.12	10.12	10.12
Percentile	96	97	98	99	100	
Value	12.14	20.23	33.83	121.41	1,214.08	

Table 12.6: 50 largest values of the variable LANDSIZE

12.14	15.00	15.37	15.78	16.19	20.00	20.23	20.23	20.23	20.23
20.23	20.23	20.23	20.23	20.23	20.23	20.23	20.23	20.23	20.23
20.23	20.23	20.50	30.35	32.38	40.47	40.47	40.47	40.47	40.47
40.47	40.47	80.93	80.93	80.93	80.93	121.41	121.41	161.88	161.88
161.88	182.11	246.86	263.05	283.29	404.69	404.69	607.04	809.39	1214.08

12.1.8 Step 7a: Assessing utility measures (household level)

The utility of the data does not only depend on the household level variables, but on the combination of household-level and individual-level variables. Therefore, it is not useful to evaluate all the utility measures selected in Step 5 at this stage, i.e., before anonymizing the individual level variables. We restrict the initial measurement of utility to those measures that are solely based on the household variables. In our dataset, these are the measures related to income and expenditure and their distributions. The results are presented in Step 10a, together with the results after anonymization, which allow direct comparison. If after the next anonymization step it appears that the data utility has been significantly decreased by the suppression of some household level variables, we can return to this step.

12.1.9 Step 8a: Choice and application of SDC methods (household variables)

This step is divided into the anonymization of the variable HHSIZE, as this is a special case, the anonymization of the other selected categorical quasi-identifiers and the anonymization of the selected continuous quasi-identifiers.

Variable HHSIZE

The variable HHSIZE poses a problem for the anonymization of the file, since suppressing it will not anonymize this variable: a simple headcount based on the household ID would allow the reconstruction of this variable. Table **??** shows the absolute frequencies of HHSIZE. The number of households for each size larger than 13 is 6 or fewer and can be considered outliers with a higher risk of re-identification, as discussed in Step 6a. One way to deal with this is to remove all households of size 14 or larger from the dataset[1]. Removing 29 households of size 14 or larger reduces the number of 2-anonymity violations by 18, of 3-anonymity violations by 26 and of 5-anonymity violations by 29. This means that all removed households violated 5-anonymity due to the value of the variable HHSIZE and many of them 2- or 3-anonymity. In addition, the average individual risk amongst the 29 households is 0.15%, which is almost three times higher than the average individual risk of all households. The impact on the global risk measure of removing these 29 households is, however, limited, due to the relatively small number of removed households in comparison to the total number of 2,000 households. Removing the households is primarily to protect these specific households, not to reduce the global risk.

Changes, such as removing records, cannot be done in the *sdcMicro* object. Listing **??** illustrates the way to remove households and recreate the *sdcMicro* object.

Table 12.7: Frequencies of variable HHSIZE (household size)

HHSIZE	1	2	3	4	5	6	7	8	9	10	11	12
Frequency	152	194	238	295	276	252	214	134	84	66	34	21
HHSIZE	13	14	15	16	17	18	19	20	21	22	33	
Frequency	11	6	6	5	4	2	1	2	1	1	1	

[1] Other methods and guidance on treating datasets where household size is a quasi-identifier are discussed in the Section Anonymization of the quasi-identifier household size.

Listing 12.11: Removing households with large (rare) household sizes

```
# Tabulation of variable HHSIZE
table(sdcHH@manipKeyVars$HHSIZE)

# Remove large households (14 or more household members) from file and fileHH
file <- file[!file[,'HHSIZE'] >= 14,]

fileHHnew <- fileHH[!fileHH[,'HHSIZE'] >= 14,]

# Create new sdcMicro object based on the file without the removed households
sdcHH <- createSdcObj(dat=fileHHnew, keyVars=selectedKeyVarsHH, pramVars=pramVarsHH,
                      weightVar=weightVarHH, numVars = numVarsHH)
```

Categorical variables

We are now ready to move on to the choice of SDC methods for the categorical variables on the household level in our dataset. As noted in our discussion of the methods, applying perturbative methods and local suppression may lead to large loss of utility. The common approach is to apply recoding to the largest possible extent as a first approach, to reach a prescribed level of risk and reduce the number of suppressions needed. Only after that should methods such as local suppression be applied. If this approach does not already achieve the desired result, we can consider perturbative methods.

Since the file is to be released as a SUF, we can keep a higher level of detail in the data. The selected categorical key variables at the household level are not suitable for recoding at this point. Due to the relatively low risk of re-identification based on the five selected categorical household level variables, it is possible in this case to use an option like local suppression to achieve our desired level of risk. Applying local suppression when initial risk is relatively low will likely only lead to suppression of few observations and thus limit the loss of utility. If, however, the data had been measured to have a relatively high risk, then applying local suppression without previous recoding would likely result in a large number of suppressions and greater information loss. Efforts such a recoding should be taken first before suppressing in cases where risk is initially measured as high. Recoding will reduce risk with little information loss and thus the number of suppressions, if local suppression is applied as an additional step. We apply local suppression to reach 2-anonymity. The choice of the low level of two is based on the overall low re-identification risk due to the high sample weights and the release as SUF. High sample weights mean, ceteris paribus, a low level of re-identification risk. Achieving 2-anonymity is the same as removing sample uniques. This leads to 42 suppressions in the variable HHSIZE and 4 suppressions in the variable REGION. As explained earlier, suppression of the value of the variable HHSIZE does not lead to actual suppression of this information. Therefore, we redo the local suppression, but this time we tell *sdcMicro* to, if possible, not suppress HHSIZE but one of the other variables.

In *sdcMicro* it is possible to tell the algorithm which variables are important and less important for making small changes (see also the Section Local suppression). To prevent HHSIZE being suppressed, we set the importance of HHSIZE in the importance vectors to the highest (i.e., 1). Listing **??** shows how to apply local suppression and put importance on the variable HHSIZE. The variable REGION is the type of variable that should not have any suppressions either. We also set the importance of REGION to 2 and the importance of RURURB to 3. This leads to an order of the variables to be considered for suppression by the algorithm. Instead of 42 suppressions in the variable HHSIZE, this leads one suppressed value in the variable HHSIZE, and to 6, 1, 48 and 16 suppressions respectively for the variables URBRUR, REGION, OWNAGLAND and RELIG (which we set as less important). The importance is clearly reflected in the number of suppression. The total number of suppressions is higher than without importance vector (71 vs. 46), but 2-anonymity is achieved in the dataset with fewer suppressions in the variables HHSIZE and REGION. We remove the one household with the suppressed value of HHSIZE (13) to protect this household.

Note: In Listing **??** we use the undolast() function in sdcMicro to go one step back after we had first applied local suppression with no importance vector.

The undolast() function restores the *sdcMicro* object back to the previous state (i.e., before we applied local suppression), which allows us to rerun the same command, but this time with an importance vector set. The undolast() function can only be used to go one step back.

Listing 12.12: Local suppression with and without importance vector

```
# Local suppression
sdcHH <- localSuppression(sdcHH, k=2, importance = NULL) # no importance vector

print(sdcHH, "ls")
## Local Suppression:
##      KeyVar | Suppressions (#) | Suppressions (%)
##      URBRUR |                0 |            0.000
##      REGION |                4 |            0.203
##      HHSIZE |               37 |            1.877
##   OWNAGLAND |                0 |            0.000
##       RELIG |                0 |            0.000

sdcHH <- undolast(sdcHH)

sdcHH <- localSuppression(sdcHH, k=2, importance = c(3, 2, 1, 5, 5))
# importance on HHSIZE (1), REGION (2) and URBRUR (3)

print(sdcHH, "ls")
## Local Suppression:
##      KeyVar | Suppressions (#) | Suppressions (%)
##      URBRUR |                6 |            0.304
##      REGION |                1 |            0.051
##      HHSIZE |                1 |            0.051
##   OWNAGLAND |               43 |            2.182
##       RELIG |               16 |            0.812
```

The variables ROOF, TOILET, WATER, ELECTCON, FUELCOOK, OWNMOTORCYCLE, CAR, TV and LIVESTOCK are not sensitive variables and were not selected as quasi-identifiers because we assumed that there are no external data sources containing this information that could be used for matching. Values can be easily observed or be known to neighbors, however, and therefore are important, together with other variables, for the spontaneous recognition scenario and nosy neighbor scenario. To anonymize these variables, we want to introduce a low level of uncertainty in them. Therefore, we decide to use invariant PRAM for the variables ROOF, TOILET, WATER, ELECTCON, FUELCOOK, OWNMOTORCYCLE, CAR, TV and LIVESTOCK, where we treat LIVESTOCK as a semi-continuous variable due to the low number of different values. The Section PRAM (Post RAndomization Method) provides more information on the PRAM method and its implementation in *sdcMicro*. Listing **??** illustrates how to apply PRAM. We choose the parameter *pd*, the lower bound for the probability that a value is not changed, to be relatively high at 0.8. We can choose a high value, because the variables themselves are not sensitive and we only want to introduce a low level of changes to minimize the utility loss. Because the distribution of many of the variables chosen for PRAM depends on the REGION, we decide to use the variable REGION as a strata variable. In this way the transition matrix is computed for each region separately. Because PRAM is a probabilistic method, we set a seed for the random number generator before applying PRAM to ensure reproducibility of the results.

Note: In practice, it is not advisable to set a seed of 12345, but rather a longer more complex and less easy to guess sequence.

The seed should not be released, since it allows for reconstructing the original values if combined with the transition matrix. The transition matrix can be released: this allows for consistent statistical inference by correcting the statistical methods used if the researcher has knowledge about the PRAM method (at this point *sdcMicro* does not allow the retrieval of the transition matrix).

Listing 12.13: Applying PRAM

```
# Pram
set.seed(12345)
sdcHH <- pram(sdcHH, strata_variables = "REGION", pd = 0.8)

## Number of changed observations:
## - - - - - - - - - - -
## ROOF != ROOF_pram : 98 (4.97%)
## TOILET != TOILET_pram : 151 (7.66%)
## WATER != WATER_pram : 167 (8.47%)
## ELECTCON != ELECTCON_pram : 90 (4.57%)
## FUELCOOK != FUELCOOK_pram : 113 (5.73%)
## OWNMOTORCYCLE != OWNMOTORCYCLE_pram : 41 (2.08%)
## CAR != CAR_pram : 172 (8.73%)
## TV != TV_pram : 137 (6.95%)
## LIVESTOCK != LIVESTOCK_pram : 149 (7.56%)
```

PRAM has changed values within the variables according to the invariant transition matrices. Since we used the invariant PRAM method (see the Section PRAM (Post RAndomization Method)), the absolute univariate frequencies remain unchanged. This is not the case for the multivariate frequencies. In Step 10a we compare the changes in the multivariate frequencies for the PRAMmed variables.

Continuous variables

We have selected income and expenditures variables and the variable LANDSIZEHA as numerical quasi-identifiers, as discussed in Step 4. In Step 5 we identified variables having high interest for the users of our data: many users use the data for measuring inequality and expenditure patterns.

Based on the risk evaluation in Step 6a, we decide to anonymize the variable LANDSIZEHA by top coding at the value 40 (cf. Table **??** and Table **??**) and round values smaller than 1 to one digit, and values larger than 1 to zero digits. Rounding the values prevents exact matching with the available cadastral register. Furthermore, we group the values between 5 and 40 in the groups 5 – 19 and 20 – 39. After these steps, no household has a unique plot size and the number of households in the sample with the same plot size was increased to at least 7. This is shown by the tabulation of the variable LANDSIZEHA after manipulation in the last line of Listing **??**. In addition, all outliers have been removed by top coding the values. This has reduced the risk of spontaneous recognition as discussed in Step 6. How to recode values in *R* is introduced in the Section Recoding and, for this particular case, shown in Listing **??**.

Listing 12.14: Anonymizing the variable LANDSIZEHA

```
# Rounding values of LANDSIZEHA to 1 digit for plots smaller than 1 and
# to 0 digits for plots larger than 1
sdcHH@manipNumVars$LANDSIZEHA[sdcHH@manipNumVars$LANDSIZEHA <= 1 &
                              !is.na(sdcHH@manipNumVars$LANDSIZEHA)] <-
             round(sdcHH@manipNumVars$LANDSIZEHA[sdcHH@manipNumVars$LANDSIZEHA <= 1 &
                                                  !is.na(sdcHH@manipNumVars
↪$LANDSIZEHA)],
                   digits = 1)

sdcHH@manipNumVars$LANDSIZEHA[sdcHH@manipNumVars$LANDSIZEHA > 1 &
                              !is.na(sdcHH@manipNumVars$LANDSIZEHA)] <-
             round(sdcHH@manipNumVars$LANDSIZEHA[sdcHH@manipNumVars$LANDSIZEHA > 1 &
                                                  !is.na(sdcHH@manipNumVars
↪$LANDSIZEHA)],
                   digits = 0)

# Grouping values of LANDSIZEHA into intervals 5-19, 20-39
```

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```
sdcHH@manipNumVars$LANDSIZEHA[sdcHH@manipNumVars$LANDSIZEHA >= 5 &
sdcHH@manipNumVars$LANDSIZEHA < 20 & !is.na(sdcHH@manipNumVars$LANDSIZEHA)] <- 13

sdcHH@manipNumVars$LANDSIZEHA[sdcHH@manipNumVars$LANDSIZEHA >= 20 &
sdcHH@manipNumVars$LANDSIZEHA < 40 &!is.na(sdcHH@manipNumVars$LANDSIZEHA)] <- 30

# Topcoding values of LANDSIZEHA larger than 40 (also recomputes risk after manual changes)
sdcHH <- topBotCoding(sdcHH, value = 40, replacement = 40, kind = 'top', column = 'LANDSIZEHA')

# Results for LANDSIZEHA
table(sdcHH@manipNumVars$LANDSIZEHA)
##    0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9   1   2   3   4  13  30  40
## 188 109  55  30  24  65  22   7  31  16 154 258  53  60 113  18  25
```

For the expenditure and income variables we compared, **based on the actual case study data**, several methods. As mentioned earlier, the main use of the data is to compute inequality measures, such as the Gini coefficient. Recoding these variables into percentiles creates difficulties computing these measures or changes these measures to a large extent and is hence not a suitable method. Often, income and expenditure variables that are released in a SUF are anonymized by top-coding. This protects the outliers, which are the values that are the most at risk. Top-coding, however, destroys the inequality information in the data, by removing high (and low) incomes. Therefore, we decide to use noise addition. To take into account the higher risk of outliers, we add a higher level of noise to those.

Adding noise can lead to a transformation of the shape of the distribution. Depending on the magnitude of the noise (see the Section Noise addition for the definition of the magnitude of noise), the values of income can also become negative. One way to solve this would be to cut off the values below zero and set them to zero. This would, however, destroy the properties conserved by noise addition (amongst others the value of the expected mean, see also the Section Noise addition) and we chose to keep the negative values.

As mentioned before, the aggregates of income and expenditures are the sums of the components. Adding noise to each of the components might lead to violation of this condition. Therefore, one solution is to add noise to the aggregates and remove the components. We prefer to keep the components in the data and apply noise addition to each component separately. This allows to apply a lower level of noise than when applying noise only to the aggregates. A noise level of 0.01 seems to be sufficient with extra noise of 0.05 added to the outliers. The outliers are defined by a robust Mahalanobis distance (see the Section Noise addition). After adding noise to the components, we recomputed the aggregates as the sum of the perturbed components.

Note: This result is only based on the actual case study dataset and is not necessarily true for other datasets.

The noise addition is shown in Listing **??**. Before applying probabilistic methods such as noise addition, we set a seed for the random number generator. This allows us to reproduce the results.

Listing 12.15: Anonymizing continuous variables

```
# Add noise to income and expenditure variables by category

# Anonymize components
compExp <- c("TFOODEXP", "TALCHEXP", "TCLTHEXP", "THOUSEXP",
             "TFURNEXP", "THLTHEXP", "TTRANSEXP", "TCOMMEXP", "TRECEXP", "TEDUEXP",
             "TRESHOTEXP", "TMISCEXP")
set.seed(123)

# Add noise to expenditure variables
```

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```
sdcHH <- addNoise(noise = 0.01, obj = sdcHH, variables = compExp, method = "additive")

# Add noise to outliers
sdcHH <- addNoise(noise = 0.05, obj = sdcHH, variables = compExp, method = "outdect")

# Sum over expenditure categories to obtain consistent totals
sdcHH@manipNumVars[,'TANHHEXP'] <- rowSums(sdcHH@manipNumVars[,compExp])
compInc <- c('INCRMT', 'INCWAGE', 'INCFARMBSN', 'INCNFARMBSN',
             'INCRENT', 'INCFIN', 'INCPENSN', 'INCOTHER')

# Add noise to income variables
sdcHH <- addNoise(noise = 0.01, obj = sdcHH, variables = compInc, method = "additive")

# Add noise to outliers
sdcHH <- addNoise(noise = 0.05, obj = sdcHH, variables = compInc, method = "outdect")

# Sum over income categories to obtain consistent totals
sdcHH@manipNumVars[,'INCTOTGROSSHH'] <- rowSums(sdcHH@manipNumVars[,compInc])

# recalculate risks after manually changing values in sdcMicro object
calcRisks(sdcHH)
```

12.1.10 Step 9a: Re-measure risk

For the categorical variables, we conclude that we have achieved 2-anonymity in the data with local suppression. Only 104 households, or about 5% of the total number, violate 3-anonymity. Table **??** gives an overview of these risk measures. The global risk is reduced to 0.02% (expected number of re-identifications 0.36), which is extremely low. Therefore, we conclude that based on the categorical variables, the data has been sufficiently anonymized. No household has a risk of re-identification higher than 0.01 (1%). By removing households with rare values (or outliers) of the variable HHSIZE, we have reduced the risk of spontaneous recognition of these households. This reasoning can also be applied to the result of the risk of recoding the variable LANDSIZEHA and PRAMming the variables identified to be important in the nosy neighbor scenario. An intruder cannot know with certainty whether a household that he recognizes in the data is the correct household, due to the noise.

Table 12.8: Number and proportion of households violating k-anonymity after anonymization

k-anonymity	Number HH violating	Percentage
2	0	0 %
3	104	5.28 %
5	374	18.70 %

These measures refer only to the categorical variables. To evaluate the risk of the continuous variables we could use an interval measure or closest neighbor algorithm. These risk measures are discussed in the Section Risk measures for continuous variables. We chose to use an interval measure, since exact value matching is not our largest concern based on the assumed scenarios and external data sources. Instead, datasets with similar values but not the exact same values could be used for matching. Here the main concern is that the values are sufficiently far from the original values, which is measured with an interval measure.

Listing **??** shows how to evaluate the interval measure for each of the expenditure variables, which are contained in the vector *compExp*[2]. The different values of the parameter k in the function dRisk() define the size of the interval around the original value, as explained in the Section Interval measure. The larger k, the larger the intervals, the higher

[2] For illustrative purposes, we only show this evaluation for the expenditure variables. It can be easily copied for the income variables. The results are similar.

the probability that a perturbed value is in the interval around the original value and the higher the risk measure. The result is satisfactory with relatively small intervals (k = 0.01), but not when increasing the size of the intervals. In our case, k = 0.01 is sufficiently large, since we are looking at the components, not the aggregates. We have to pay special attention to the outliers. Here the value 0.01 for k is too small to assume that they are protected when outside this small interval. It would be necessary to check outliers and their perturbed values and there might be a need for a higher level of perturbation for outliers. We conclude that, from a risk perspective and based on the interval measure, the chosen levels of noise are acceptable. In the next step, we will look at the impact on the data utility of the noise addition.

Listing 12.16: Measuring risk of re-identification of continuous variables

```
dRisk(sdcHH@origData[,compExp], xm = sdcHH@manipNumVars[,compExp], k = 0.01)
[1] 0.0608828

dRisk(sdcHH@origData[,compExp], xm = sdcHH@manipNumVars[,compExp], k = 0.02)
[1] 0.9025875

dRisk(sdcHH@origData[,compExp], xm = sdcHH@manipNumVars[,compExp], k = 0.05)
[1] 1
```

12.1.11 Step 10a: Re-measure utility

None of the variables has been recoded and the original level of detail in the data is kept, except for the variable LANDSIZEHA. As described in Step 8a, local suppression has only removed a few values in the other variables, which has not greatly reduced the validity of the data.

The univariate frequency distributions of the variables ROOF, TOILET, WATER, ELECTCON, FUELCOOK, OWNMOTORCYCLE, CAR, TV and LIVESTOCK did not, by definition of the invariant PRAM method (see the Section PRAM (Post RAndomization Method)), change to a large extent. The tabulations are presented in Table **??** (the values 1 – 9 and NA in the first row are the values of the variables and .m after the variable name refers to the values after anonymization).

Note: Although the frequencies are almost the same, this does not mean that the values of particular households did not change.

Values have been swapped between households. This becomes apparent when looking at the multivariate frequencies of the WATER with the variable URBRUR in Table **??**. The multivariate frequencies of the PRAMmed with the variable URBRUR could be of interest for users, but these are not preserved. Since we applied PRAM within the regions, the multivariate frequencies of the PRAMmed variables with REGION are preserved.

Table 12.9: Univariate frequencies of the PRAMmed variable before and after anonymization

.	0	1	2	3	4	5	6	7	8	9	NA
ROOF		27	1	914	307	711				10	1
ROOF.m		25	1	907	319	712				6	1
TOILET		76	594	817	481					3	
TOILET.m		71	597	816	483					4	
WATER		128	323	304	383	562	197	18	21	35	
WATER.m		134	319	308	378	573	188	16	21	34	
ELECTCON	768	216	8	2							977
ELECTCON.m	761	218	8	3							981
FUELCOOK		1289	21	376	55	36				139	55
FUELCOOK.m		1284	22	383	50	39				143	50
OWNMOTORCYCLE	1883	86									2
OWNMOTORCYCLE.m	1882	86									2
CAR	963	31									977
CAR.m	966	25									
TV	1216	264									491
TV.m	1203	272									496

Table 12.10: Multivariate frequencies of the variables WATER with RURURB before and after anonymization

.	1	2	3	4	5	6	7	8	9
WATER/URB	11	49	270	306	432	183	12	15	21
WATER/RUR	114	274	32	76	130	14	6	6	14
WATER/URB.m	79	220	203	229	402	125	10	12	19
WATER/RUR.m	54	98	105	147	169	63	6	9	15

For conciseness, we restrict ourselves to the analysis of the expenditure variables. The analysis of the income variables can be done in the same way and leads to similar results.

We look at the effect of anonymization on some indicators as discussed in Step 5. Table **??** presents the point estimates and bootstrapped confidence interval of the GINI coefficient[3] for the sum of the expenditure components. The calculation of the GINI coefficient and the confidence interval are based on the positive expenditure values. We observe very small changes in the Gini coefficient, that are statistically negligible. We use a visualization to illustrate the impact on utility of the anonymization. Visualizations are discussed in the Section Assessing data utility with the help of data visualizations (in R) and the specific *R* code for this case study is available in the *R* script. The change in the inequality measures is illustrated in Fig. **??**, which shows the Lorenz curves based on the positive expenditure values before and after anonymization.

Table 12.11: GINI point estimates and bootstrapped confidence intervals for sum of expenditure components

.	before	after
Point estimate	0.510	0.508
Left bound of CI	0.476	0.476
Right bound of CI	0.539	0.538

We compare the mean monthly expenditures (MME) and mean monthly income (MMI) for rural, urban and total

[3] To compute the GINI coefficient, bootstrap to construct the confidence intervals and plot the Lorenz curve we used the *R* packages *laeken, reldist, bootstrap* and *ineq*.

Fig. 12.5: Lorenz curve based on positive total expenditures values

population. The results are shown in Table **??**. We observe that the chosen levels of noise add only small distortions to the MME and slightly larger changes to the MMI.

Table 12.12: Mean monthly expenditure and mean monthly income per capita by rural/urban

.	before	after
MME rural	400.5	398.5
MME urban	457.3	459.9
MME total	412.6	412.6
MMI rural	397.1	402.2
MMI urban	747.6	767.8
MMI total	472.1	478.5

Table **??** shows the share of each of the components of the expenditure variables before and after anonymization.

Table 12.13: Shares of expenditures components

.	TFOODEXP	TALCHEXP	TCLTHEXP	THOUSEXP	TFURNEXP	THLTHEXP
before	0.58	0.01	0.03	0.09	0.02	0.03
after	0.59	0.01	0.03	0.09	0.02	0.03
.	TTRANSEXP	TCOMMEXP	TRECEXP	TEDUEXP	TRESHOTEXP	TMISCEXP
before	0.04	0.02	0.00	0.08	0.03	0.05
after	0.04	0.02	0.00	0.08	0.03	0.05

Anonymization for the creation of a SUF will inevitably lead to some degree of utility loss. It is important to describe this loss in the external report, so that users are aware of the changes in the data. This is described in Step 11 and presented in Appendix C. Appendix C also shows summary statistics and tabulations of the household level variables before and after anonymization.

Merging the household- and individual-level variables

The next step is to merge the treated household variables with the untreated individual variables for the anonymization of the individual level variables. Listing **??** shows the steps to merge these files. This also includes the selection of variables used in the anonymization of the individual-level variables. We create the *sdcMicro* object for the anonymization of the individual variables in the same way as for the household variable in Listing **??**. Subsequently, we repeat Steps 6-10 for the individual-level variables.

Listing 12.17: Merging the files with household and individual-level variables and creating an *sdcMicro* object for the anonymization of the individual-level variables

```
### Select variables (individual level)
# Key variables (individual level)
selectedKeyVarsIND = c('GENDER', 'REL', 'MARITAL', 'AGEYRS',
```

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```
                       'EDUCY', 'ATSCHOOL', 'INDUSTRY1') # list of selected key␣
↪variables

# Sample weight (WGTHH, individual weight)
selectedWeightVarIND = c('WGTHH')

# Household ID
selectedHouseholdID = c('IDH')

# No strata

# Recombining anonymized HH datasets and individual level variables
indVars <- c("IDH", "IDP", selectedKeyVarsIND, "WGTHH") # HID and all non HH variables
fileInd <- file[indVars] # subset of file without HHVars

HHmanip <- extractManipData(sdcHH) # manipulated variables HH
HHmanip <- HHmanip[HHmanip[,'IDH'] != 1782,]

fileCombined <- merge(HHmanip, fileInd, by.x= c('IDH'))

fileCombined <- fileCombined[order(fileCombined[,'IDH'],
fileCombined[,'IDP']),]

dim(fileCombined)

# SDC objects with all variables and treated HH vars for
# anonymization of individual level variables
sdcCombined <- createSdcObj(dat = fileCombined, keyVars = selectedKeyVarsIND,
                            weightVar = selectedWeightVarIND, hhId =␣
↪selectedHouseholdID)
```

12.1.12 Step 6b: Assessing disclosure risk (individual level)

All key variables at the individual level are categorical. Therefore, we can use k-anonymity and the individual and global risk measures (see the Sections Individual risk and Global risk). The hierarchical risk is now of interest, given the household structure in the dataset *fileCombined*, which includes both household- and individual-level variables. The number of individuals (absolute and relative) that violate k-anonymity at the levels 2, 3 and 5 are shown in Table **??**.

Note: k-anonymity does not consider the household structure and therefore underestimates the risk. Therefore, we are more interested in the individual and global hierarchical risk measures.

Table 12.14: k-anonymity violations

k-anonymity	Number HH violating	Percentage
2	998	9.91%
3	1,384	13.75%
5	2,194	21.79%

The global risk measures can be found using *R* as illustrated in Listing **??**. The global risk is 0.24%, which corresponds to 24 expected re-identifications. Accounting for the hierarchical structure, this rises to 1.26%, or 127 expected re-identifications. The global risk measures are low compared to the number of k-anonymity violators due to the low sampling weights. The high number of k-anonymity violators is mainly due to the very detailed age variable. The risk measures are based only on the individual level variables, since we assume that the individual and household level variables are be used simultaneously by an intruder. If we would consider an intruder scenario where these variables are used simultaneously by an intruder to re-identify individuals, the household level variables should also be taken into account here. This would results in a high number of key variables.

Listing 12.18: Global risk of the individual-level variables

```
print(sdcCombined, 'risk')
## Risk measures:
##
## Number of observations with higher risk than the main part of the data: 0
## Expected number of re-identifications: 23.98 (0.24 %)
##
## Information on hierarchical risk:
## Expected number of re-identifications: 127.12 (1.26 %)
```

12.1.13 Step 7b: Assessing utility (individual level)

We evaluate the utility measures selected in Step 5 besides some general utility measures. The values computed from the raw data are presented in step 10b to allow for direct comparison with the values computed from the anonymized data.

12.1.14 Step 8b: Choice and application of SDC methods (individual level)

We use the same approach for the anonymization of the individual-level categorical key variables as for the household level categorical variables described earlier: first use global recoding to limit the necessary number of suppressions, then apply local suppressions and finally, if necessary, use of perturbative methods.

The variable AGEYRS (i.e., age in years) has many different values (age in months for children 0 – 1 years and age in years for individuals over 1 year). This level of detail leads to a high level of re-identification risk, given external datasets with exact age as well as knowledge of the exact age of close relatives. We have to reduce the level of detail in the age variables by recoding the age values (see the Section Recoding). First, we recode the values from 15 to 65 in ten-year intervals. Since some indicators related to education are computed from the survey dataset, our first approach is not to recode the age range 0 – 15 years. For children under the age of 1 year, we reduce the level of detail and recode these to 0 years. These recodes are shown in Listing **??**. We also top-code age at the age of 65 years. This protects individuals with high (rare) age values.

Listing 12.19: Recoding age in 10-year intervals in the range 15 – 65 and top code age over 65 years

```
# Recoding age and top coding age (top code 65), below that 10 year age
# groups, children aged under 1 are recoded 0 (previously in months)

sdcCombined@manipKeyVars$AGEYRS[sdcCombined@manipKeyVars$AGEYRS >= 0 &
sdcCombined@manipKeyVars$AGEYRS < 1] <- 0

sdcCombined@manipKeyVars$AGEYRS[sdcCombined@manipKeyVars$AGEYRS >= 15 &
sdcCombined@manipKeyVars$AGEYRS < 25] <- 20

...

sdcCombined@manipKeyVars$AGEYRS[sdcCombined@manipKeyVars$AGEYRS >= 55 &
sdcCombined@manipKeyVars$AGEYRS < 66] <- 60

```

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```
# topBotCoding also recalculates risk based on manual recoding above
sdcCombined <- **topBotCoding(obj = sdcCombined, value = 65,
replacement = 65, kind = 'top', column = 'AGEYRS')

table(sdcCombined@manipKeyVars$AGEYRS) # check results
##    0    1    2    3    4    5    6    7    8    9   10   11   12   13   14
##  311  367  340  332  260  334  344  297  344  281  336  297  326  299  263
##   20   30   40   50   60   65
## 1847 1220  889  554  314  325
```

These recodes already reduce the risk to 531 individuals violating 3-anonymity. We could recode the values of age in the lower range according to the age categories users require (e.g., 8 – 11 for education). There are many different categories for different indicators, however, including education indicators. This would reduce the utility of the data for some users. Therefore, we decide to look first at the number of suppressions needed in local suppression after this limited recoding. If the number of suppressions is too high, we can go back and recode age in the range 1 – 14 years.

In Listing **??** we demonstrate how one might experiment with local suppression to find the best option. We use local suppression to achieve 3-anonymity (see the Section Local suppression . On the first attempt, we do not specify any importance vector; this leads to many suppressions in the variable AGEYRS (see Table **??** below, first row), however. This is undesirable from a utility point of view. Therefore, we decide to specify an importance vector to prevent suppressions in the variable AGEYRS. Suppressing the variable GENDER is also undesirable from the utility point of view. The variable GENDER is a type of variable that should not have suppressions. We set GENDER as variable with the second highest importance. After specifying the importance vector to prevent suppressions of the age variable, there are no age suppressions (see Table **??**, second row). The total number of suppressions in the other variables increased, however, from 253 to 323 because of the importance vector. This is to be expected because the algorithm without the importance vector minimizes the total number of suppressions by first suppressing values in variables with many categories – in this case, age and gender. Specifying an importance vector prevents reaching this optimality and hence leads to a higher total number of suppressions. There is a trade-off between which variables are suppressed and the total number of suppressions. After specifying an importance vector, the variable REL has many suppressions (see Table **??**, second row). We choose this second option.

Listing 12.20: Experimenting with different options in local suppression

```
# Copy of sdcMicro object to later undo steps
sdcCopy <- sdcCombined

# Importance vectors for local suppression (depending on utility measures)
impVec1 <- NULL # for optimal suppression
impVec2 <- rep(length(selectedKeyVarsIND), length(selectedKeyVarsIND))
impVec2[match('AGEYRS', selectedKeyVarsIND)] <- 1 # AGEYRS
impVec2[match('GENDER', selectedKeyVarsIND)] <- 2 # GENDER

# Local suppression without importance vector
sdcCombined <- localSuppression(sdcCombined, k = 2, importance = impVec1)

# Number of suppressions per variable
print(sdcCombined, "ls")

## Local Suppression:
##        KeyVar | Suppressions (#) | Suppressions (%)
##        GENDER |                0 |            0.000
##           REL |               34 |            0.338
##       MARITAL |                0 |            0.000
##        AGEYRS |              195 |            1.937
##         EDUCY |                0 |            0.000
```

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```
##   EDYRSCURRAT |                    3 |              0.030
##      ATSCHOOL |                    0 |              0.000
##     INDUSTRY1 |                   21 |              0.209

# Number of suppressions per variable for each value of AGEYRS
table(sdcCopy@manipKeyVars$AGEYRS) - table(sdcCombined@manipKeyVars$AGEYRS)

##   0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 20 30 40 50 60 65
##   0  0  0  0  0  0  2  0  2  1  0  1  4  1  5 25 53 37 36 15 13

# Undo local suppression
sdcCombined <- undolast(sdcCombined)

# Local suppression with importance vector on AGEYRS and GENDER
sdcCombined <- localSuppression(sdcCombined, k = 2, importance = impVec2)

# Number of suppressions per variable
print(sdcCombined, "ls")
## Local Suppression:
##        KeyVar | Suppressions (#) | Suppressions (%)
##        GENDER |                0 |              0.000
##           REL |              323 |              3.208
##       MARITAL |                0 |              0.000
##        AGEYRS |                0 |              0.000
##         EDUCY |                0 |              0.000
##   EDYRSCURRAT |                0 |              0.000
##      ATSCHOOL |                0 |              0.000
##     INDUSTRY1 |                0 |              0.000

# Number of suppressions for each value of the variable AGEYRS
table(sdcCopy@manipKeyVars$AGEYRS) - table(sdcCombined@manipKeyVars$AGEYRS)
##   0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 20 30 40 50 60 65
##   0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
```

Table 12.15: Number of suppressions by variable for different variations of local suppression

Local suppression options	GENDER	REL	MARITAL	AGEYRS	EDUCY	EDYRSCURATT	ATSCHOOL	INDUSTRY1
k = 2, no imp	0	34	0	195	0	3	0	21
k = 2, imp on AGEYRS	0	323	0	0	0	0	0	0

12.1.15 Step 9b: Re-measure risk (individual level)

We re-evaluate the risk measures selected in Step 6b. Table **??** shows that local suppression, not surprisingly, has reduced the number of individuals violating 2-anonymity to 0.

Table 12.16: k-anonymity violations

k-anonymity	Number HH violating	Percentage
2	0	0.00 %
3	197	1.96 %
5	518	5.15 %

The hierarchical global risk was reduced to 0.11%, which corresponds to 11.3 expected re-identifications. The highest individual hierarchical re-identification risk is 1.21%. These risk levels would seem acceptable for a SUF.

12.1.16 Step 10b: Re-measure utility (individual level)

We selected two utility measures for the individual variables: primary and secondary education enrollment, both also by gender. These two measures are sensitive to changes in the variables gender (GENDER), age (AGEYRS) and education (EDUCY and EDYRSATCURR), and therefore give a good overview of the impact of the anonymization. As shown in Table **??** the anonymization did not change the results. The results of the tabulations in Appendix C confirm these results.

Table 12.17: Net enrollment in primary and secondary education by gender

.	Primary education			Secondary education		
Before	72.6%	74.2%	70.9%	42.0%	44.8%	39.1%
After	72.6%	74.2%	70.9%	42.0%	44.8%	39.1%

12.1.17 Step 11: Audit and reporting

In the audit step, we check whether the data allow for reproduction of published figures from the original dataset and relationships between variables and other data characteristics are preserved in the anonymization process. In short, we check whether the dataset is valid for analytical purposes. There are no figures available that were published from the dataset and need to be reproducible from the anonymized data.

In Step 2, we explored the data characteristics and relationships between variables. These data characteristics and relationships have been mainly preserved, since we took them into account when choosing the appropriate anonymization methods. The variables TANHHEXP and INCTOTGROSSHH are the sums of the individual components, because we added noise to the components and reconstructed the aggregates by summing over the components. Initially, the income variables were all positive. This characteristic has been violated, as a result of noise addition. Since values of the variable AGEYRS were not perturbed, but only recoded and suppressed, we did not introduce unlikely combinations, such as a 60-year-old individual enrolled in primary education. Also, by separating the anonymization process into two parts, one for household-level variables and one for individual-level variables, the values of variables measured at the household level agree for all members of each household.

Furthermore, we drafted two reports, internal and external, on the anonymization of the case study dataset. The internal report includes the methods used, the risk before and after anonymization as well as the reasons for the selected methods and their parameters. The external report focuses on the changes in the data and the loss in utility. Focus here should be on the number of suppressions as well as the perturbative methods (PRAM). This is described in the previous steps.

Note: When creating a SUF, it is inevitable that there will be a loss of information and it is very important for the users to be aware of these changes and release them in a report that accompanies the data.

Appendix C provides examples of an internal and external report of the anonymization process of this dataset. Depending on the users and readers of the reports, the content may differ. The code to this case study shows how to obtain the information for the reports. Some measures are also available in the standard reports generated with the report() function. This is shown in Listing **??**. The report() function will only use the data available in the *sdcMicro* object, which does not contain all households for sdcHH.

Listing 12.21: Using the report() function for internal and external reports

```
# Create reports with sdcMicro report() function
report(sdcHH, internal = F) # external (brief) report
report(sdcHH, internal = T) # internal (extended) report

# Create reports with sdcMicro report() function
report(sdcCombined, internal = F) # external (brief) report
report(sdcCombined, internal = T) # internal (extended) report
```

12.1.18 Step 12: Data release

The final step is the release of the anonymized dataset together with the external report. Listing **??** shows how to collect the data from the *sdcMicro* object with the extractManipData() function. Before releasing the file, we add an individual ID to the file (line number in household). We export the anonymized dataset in as *STATA* file. The Section Read functions in R presents functions for exporting files in other data formats.

Listing 12.22: Exporting the anonymized dataset

```
# Anonymized dataset
# Household variables and individual variables
# extracts all variables, not just the manipulated ones
dataAnon <- extractManipData(sdcCombined, ignoreKeyVars = F, ignorePramVars = F,
                             ignoreNumVars = F, ignoreStrataVar = F)

# Create STATA file
write.dta(dataframe = dataAnon, file= 'Case1DataAnon.dta', convert.dates=TRUE)
```

12.2 Case study 2 - PUF

This case study is a continuation of case study 1 in the Section *Case study 1- SUF* . Case study 1 produces a SUF file. In this case study we use this SUF file to produce a PUF file of the same dataset, which can be freely distributed. The structure of the SUF and PUF releases will be the same. However, the PUF will contain fewer variables and less (detailed) information than the SUF. We refer to the Section *Case study 1- SUF* for a description of the dataset.

Note: It is also possible to directly produce a PUF from a dataset without first creating a SUF.

As in case study 1, we show how the creation of a PUF can be achieved using the open source and free *sdcMicro* package and *R*. A ready-to-run *R* script for this case study and the dataset are also available to reproduce the results and allow the user to adapt the code (see http://ihsn.org/home/projects/sdc-practice). Extracts of this code are presented in this section to illustrate several steps of the anonymization process.

Note: The choices of methods and parameters in this case study are based on this particular dataset and the results and choices might be different for other datasets.

This case study follows the steps of the SDC process outlined in The SDC Process.

12.2.1 Step 1: Need for disclosure control

The same reasoning as in case study 1 applies: the SUF dataset produced in case study 1 contains data on individuals and households and some variables are confidential and/or sensitive. The decisions made in case study 1 are based on the disclosure scenarios for a SUF release. The anonymization applied for the SUF does not provide sufficient protection for the release as PUF and the SUF file cannot be released as PUF without further treatment. Therefore, we have to repeat the SDC process with a different set of disclosure scenarios based on the characteristics of a PUF release (see Step 4). This leads to different risk measures, lower accepted risk levels and different SDC methods.

12.2.2 Step 2: Data preparation and exploring data characteristics

In order to guarantee consistency between the released PUF and SUF files, which is required to prevent intruders from using the datasets together (SUF users have also access to the PUF file), we have to use the anonymized SUF file to create the PUF file (see also the Section Step 3: Type of release). In this way all information in the PUF file is also contained in the SUF, and the PUF does not provide additional information to an intruder with access to the SUF. We load the required packages to read the data (*foreign* package for *STATA* files) and load the SUF dataset into "file" as illustrated in Listing **??**. We also load the original data file (raw data) as "fileOrig". We need the raw data to undo perturbative methods used in case study 1 (see Step 8) and to compare data utility measures (see Step 5). To evaluate the utility loss in the PUF, we have to compare the information in the anonymized PUF file with the information in the raw data. For an overview of the data characteristics and a description of the variables in both files, we refer to Step 2 of *Case study 1- SUF* .

Listing 12.23: Loading required packages and datasets

```r
# Load required packages
library(foreign)  # for read/write function for STATA
library(sdcMicro) # sdcMicro package

# Set working directory - set to the path on your machine
setwd("/Users/CaseStudy2")

# Specify file name of SUF file from case study 1
fname <- "CaseDataAnon.dta"

# Specify file name of original dataset (raw data)
fnameOrig <- "CaseA.dta"

# Read-in files
file     <- read.dta(fname, convert.factors = TRUE) # SUF file case study 1
fileOrig <- read.dta(fnameOrig, convert.factors = TRUE) # original data
```

We check the number of variables and number of observations of both files and the variable names of the SUF file, as shown in Listing **??**. The PUF file has fewer records and fewer variables than the original data file, since we removed large households and several variables to generate the SUF file.

Listing 12.24: Number of individuals and variables and variable names

```r
# Dimensions of file (observations, variables)
dim(file)
## [1] 10068    49

dim(fileOrig)
## [1] 10574    68

colnames(file) # Variable names
```

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```
##  [1] "IDH"         "URBRUR"       "REGION"      "HHSIZE"
##  [5] "OWNAGLAND"   "RELIG"        "ROOF"        "TOILET"
##  [9] "WATER"       "ELECTCON"     "FUELCOOK"    "OWNMOTORCYCLE"
## [13] "CAR"         "TV"           "LIVESTOCK"   "LANDSIZEHA"
## [17] "TANHHEXP"    "TFOODEXP"     "TALCHEXP"    "TCLTHEXP"
## [21] "THOUSEXP"    "TFURNEXP"     "THLTHEXP"    "TTRANSEXP"
## [25] "TCOMMEXP"    "TRECEXP"      "TEDUEXP"     "TRESTHOTEXP"
## [29] "TMISCEXP"    "INCTOTGROSSHH" "INCRMT"     "INCWAGE"
## [33] "INCFARMBSN"  "INCNFARMBSN"  "INCRENT"     "INCFIN"
## [37] "INCPENSN"    "INCOTHER"     "WGTPOP"      "IDP"
## [41] "GENDER"      "REL"          "MARITAL"     "AGEYRS"
## [45] "EDUCY"       "EDYRSCURRAT"  "ATSCHOOL"    "INDUSTRY1"
## [49] "WGTHH"
```

To get an overview of the values of the variables, we use tabulations and cross-tabulations for categorical variables and summary statistics for continuous variables. To include the number of missing values (‘NA’ or other), we use the option useNA = “ifany” in the table() function. For some variables, these tabulations differ from the tabulations of the raw data, due to the anonymization of the SUF file.

In Table **??** the variables in the dataset “file” are listed along with concise descriptions of the variables, the level at which they are collected (individual level (IND) or household level (HH)), the measurement type (continuous, semi-continuous or categorical) and value ranges. Note that the dataset contains a selection of 49 variables of the 68 variable selected for the SUF release. The variables have been preselected based on their relevance for data users and some variables were removed while creating a SUF file. The numerical values for many of the categorical variables are codes that refer to values, e.g., in the variable “URBRUR”, 1 stands for ‘rural’ and 2 for ‘urban’. More information on the meanings of coded values of the categorical variables is available in the *R* code for this case study.

Any data cleaning, such as recoding missing value codes and removing empty variables, was already done in case study 1. The same holds for removing any direct identifiers. Direct identifiers are not released in the SUF file.

We identified the following sensitive variables in the dataset: variables related to schooling and labor force status as well as income and expenditure related variables. These variables need protection. Whether a variable is considered sensitive may depend on the release type, country and the dataset itself.

Table 12.18: Overview of the variables in the dataset

No.	Variable name	Description	Level	Measurement	Values
1	IDH	Household ID	HH	.	1-2,000
2	IDP	Individual ID	IND	.	1-13
3	REGION	Region	HH	categorical	1-6
4	URBRUR	Area of residence	HH	categorical	1, 2
5	WGTHH	Individual weighting coefficient	HH	weight	31.2-8495.7
6	WGTPOP	Population weighting coefficient	IND	weight	45.8-93452.2
7	HHSIZE	Household size	HH	semi-continuous	1-33
8	GENDER	Gender	IND	categorical	0, 1
9	REL	Relationship to household head	IND	categorical	1-9
10	MARITAL	Marital status	IND	categorical	1-6
11	AGEYRS	Age in completed years	IND	semi-continuous	0-65
12	RELIG	Religion of household head	HH	categorical	1, 5-7, 9
13	ATSCHOOL	Currently enrolled in school	IND	categorical	0, 1
14	EDUCY	Highest level of education attended	IND	categorical	1-6
15	EDYRSCUR AT	Years of education for currently enrolled	IND	semi-continuous	1-18
16	INDUSTRY	Industry classification (1-digit)	IND	categorical	1-10
17	ROOF	Main material used for roof	IND	categorical	1-5, 9

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Table 12.18 – continued from previous page

No.	Variable name	Description	Level	Measurement	Values
18	TOILET	Main toilet facility	HH	categorical	1-4, 9
19	ELECTCON	Electricity	HH	categorical	0-3
20	FUELCOOK	Main cooking fuel	HH	categorical	1-5, 9
21	WATER	Main source of water	HH	categorical	1-9
22	OWNAGLAN	Ownership of agricultural land	HH	categorical	1-3
23	LANDSIZE	Land size owned by household (ha) (agric and non agric)	HH	continuous	0-40
24	OWNMOTORYCLE	Ownership of motorcycle	HH	categorical	0, 1
25	CAR	Ownership of car	HH	categorical	0, 1
26	TV	Ownership of television	HH	categorical	0, 1
27	LIVESTOC	Number of large-sized livestock owned	HH	semi-continuous	0-25
28	INCRMT	Income – Remittances	HH	continuous	
29	INCWAGE	Income - Wages and salaries	HH	continuous	
30	INCFARMBSN	Income - Gross income from household farm businesses	HH	continuous	
31	INCNFARMBSN	Income - Gross income from household nonfarm businesses	HH	continuous	
32	INCRENT	Income - Rent	HH	continuous	
33	INCFIN	Income - Financial	HH	continuous	
34	INCPENSN	Income - Pensions/social assistance	HH	continuous	
35	INCOTHER	Income - Other	HH	continuous	
36	INCTOTGROSHH	Income - Total	HH	continuous	
37	FARMEMP				
38	TFOODEXP	Total expenditure on food	HH	continuous	
39	TALCHEXP	Total expenditure on alcoholic beverages, tobacco and narcotics	HH	continuous	
40	TCLTHEXP	Total expenditure on clothing	HH	continuous	
41	THOUSEXP	Total expenditure on housing	HH	continuous	
42	TFURNEXP	Total expenditure on furnishing	HH	continuous	
43	THLTHEXP	Total expenditure on health	HH	continuous	
43	TTRANSEXP	Total expenditure on transport	HH	continuous	
44	TCOMMEXP	Total expenditure on communication	HH	continuous	
45	TRECEXP	Total expenditure on recreation	HH	continuous	
46	TEDUEXP	Total expenditure on education	HH	continuous	
47	TRESHOTEXP	Total expenditure on restaurants and hotels	HH	continuous	
48	TMISCEXP	Total expenditure on miscellaneous spending	HH	continuous	
49	TANHHEXP	Total annual nominal household expenditures	HH	continuous	

It is always important to ensure that the relationships between variables in the data are preserved during the anonymization process and to explore and take note of these relationships before beginning the anonymization. At the end of the anonymization process before the release of the data, an audit should be conducted, using these initial results, to check that these relationships are maintained in the anonymized dataset (see Step 11).

In our dataset, we identify several relationships between variables that need to be preserved during the anonymization process. The variables “TANHHEXP” and “INCTOTGROSSHH” represent the total annual nominal household expenditure and the total gross annual household income, respectively, and these variables are aggregations of existing income and expenditure components in the dataset.

The variables related to education are available only for individuals in the appropriate age groups and missing for other individuals. In addition, the household-level variables (cf. fourth column of Table **??**) have the same values for all members in any particular household. The value of household size corresponds to the actual number of individuals belonging to that household in the dataset. As we proceed, we have to take care that these relationships and structures are preserved in the anonymization process.

We assume that the data are collected in a survey that uses simple sampling of households. The data contains two weight coefficients: “WGTHH” and “WGTPOP”. The relationship between the weights is $WGTPOP = WGTHH*$

$HHSIZE$. “WGTPOP” is the sampling weight for the households and “WGTHH” is the sampling weight for the individuals to be used for disclosure risk calculations. “WGTHH” is used for computing individual-level indicators (such as education) and “WGTPOP” is used for population level indicators (such as income indicators). There are no strata variables available in the data. We will use “WGTPOP” for the anonymization of the household variables and “WGTHH” for the anonymization of the individual-level variables.

12.2.3 Step 3: Type of release

In this case study, we assume that the file will be released as a PUF, which will be freely available to anyone interested in the data (see the Section Conditions for PUFs for the conditions and more information on the release of PUFs). The PUF release is intended for users with lower information requirements (e.g., students) and researchers interested in the structure of the data and willing to do preliminary research. The PUF file can give an idea to the researcher whether it is worthwhile for their research to apply for access to the SUF file. Researchers willing to do more in-depth research will most likely apply for SUF access. Generally, users of a PUF file are not restricted by an agreement that prevents them from using the data to re-identify individuals and hence the accepted risk level is much lower than in the case of the SUF and the set of released variables is limited.

12.2.4 Step 4: Intruder scenarios and choice of key variables

Next, based on the release type, we reformulate the intruder scenarios for the PUF release. This leads to the selection of a set of quasi-identifiers. Since this case study is based on a demo dataset, we do not have a real context and we cannot define exact disclosure scenarios. Therefore, we make hypothetical assumptions on possible disclosure scenarios. We consider two types of disclosure scenarios: 1) matching with other publically available datasets and 2) spontaneous recognition. Since the dataset will be distributed as PUF, there are de facto no restrictions on the use of the dataset by intruders.

For the sake of illustration, we assume that population registers are available with the demographic variables gender, age, place of residence (region, urban/rural), religion and other variables such as marital status and variables relating to education and professional status that are also present in our dataset. In addition, we assume that there is a publically available cadastral register on land ownership. Based on this analysis of available data sources, we have selected in case study 1 the variables “REGION”, “URBRUR”, “HHSIZE”, “OWNAGLAND”, “RELIG”, “GENDER”, “REL” (relationship to household head), “MARITAL” (marital status), “AGEYRS”, “INDUSTRY1” and two variables relating to school attendance as categorical quasi-identifiers, the expenditure and income variables as well as LANDSIZEHA as continuous quasi-identifiers. According to our assessment, these variables might enable an intruder to re-identify an individual or household in the dataset by matching with other available datasets. The key variables for PUF release generally coincide with the key variables for the SUF release. Possibly, more variables could be added, since the user has more possibilities to match the data extensively and is not bound by any contract, as is in the case of the SUF file. Equally, some key variables in the SUF file may not be released in the PUF file and, as a consequence, these variables are removed from the list of key variables.

Upon further consideration, this initial set of identifying variables is too large for a PUF release, as the number of possible combinations (keys) is very high and hence many respondents could be identified based on these variables. Therefore, we decide to limit the set of key variables, by excluding variables from the dataset for PUF release. The choice of variables to be removed is led by the needs of the intended PUF users. Assuming the typical users are mainly interested in aggregate income and expenditure data, we can therefore remove from the initial set of key variables “OWNAGLAND”, “RELIG” and “LANDSIZEHA” at the household level and “EDYRSCURRAT” and “ATSCHOOL” at the individual level.

Note: These variables will not be released in the PUF file.

We also remove the income and expenditure components from the list of key variables, since we reduce their information content by building proportions (see Step 8a). The list of the remaining key variables is presented in Table

??.

Table 12.19: Overview of selected key variables for PUF file

Variable name	Variable description	Measurement level
REGION	region	Household, categorical
URBRUR	area of residence	Household, categorical
HHSIZE	household size	Household, categorical
TANHHEXP	total expenditure	Household, continuous
INCTOTGROSSHH	total income	Household, continuous
GENDER	gender	Individual, categorical
REL	relationship to household head	Individual, categorical
MARITAL	marital status	Individual, categorical
AGEYRS	age in completed years	Individual, semi-continuous/categorical
EDUCY	highest level of education completed	Individual, categorical
INDUSTRY1	industry classification	Individual, categorical

The decision to release the dataset as a PUF means the level of anonymization will be relatively high and consequently, the variables are less detailed (e.g., after recoding) and a scenario of spontaneous recognition is less likely. Nevertheless, we should check for rare combinations or unusual patterns in the variables. Variables that may lead to spontaneous recognition in our sample are amongst others “HHSIZE” (household size) as well as “INCTOTGROSSHH” (aggregate income) and “TANHHEXP” (total expenditure). Large households and households with high income are easily identifiable, especially when combined with other identifying variables such as a geographical identifier (“REGION”). There might be only one or a few households/individuals in a certain region with a high income, such as the local doctor. Variables that are easily observable and known by neighbors such as “ROOF”, “TOILET”, “WATER”, “ELECTCON”, “FUELCOOK”, “OWNMOTORCYCLE”, “CAR”, “TV” and “LIVESTOCK” may also need protection depending on what stands out in the community, since a user might be able to identify persons (s)he knows. This is called the nosy-neighbor scenario.

12.2.5 Step 5: Data key uses and selection of utility measures

A PUF file contains less information and the file is generally used by students as a teaching file, by researchers to get an idea about the data structure, and for simple analyses. The users have generally lower requirements than for a SUF file and the results of analysis may be less precise. The researcher interested in a more detailed dataset, would have to apply for access to the SUF file. Therefore, we select more aggregate utility measures for the PUF file that reflect the intended use of a PUF file. Data intensive measures, such as the Gini coefficient, cannot be computed from the PUF file. Besides the standard utility measures, such as tabulations, we evaluate the decile dispersion ratio and a regression with the income deciles as regressand.

To measure the information loss, we should compare the initial data file before any anonymization (including the anonymization for the SUF) with the file after the anonymization for the PUF. Comparing the files directly before and after the PUF anonymization would underestimate the information loss, as this would omit the information loss due to SUF anonymization. Therefore, in Step 2, we also loaded the raw dataset.

Hierarchical (household) structure

As noted in case study 1, the data has a household structure. For the SUF release, we protected large households by removing these from the dataset. Since some variables are measured on the household level and thus have identical values for each household member, the values of the household variables should be treated in the same way for each household member (see the Section Anonymization of the quasi-identifier household size). Therefore, we first anonymize only the household variables. After this, we merge them with the individual-level variables and then anonymize the individual-level and household-level variables jointly.

Since the data has a hierarchical structure, Steps 6 through 10 are repeated twice: Steps 6a through 10a are for the household-level variables and Steps 6b through 10b for the combined dataset. In this way, we ensure that household-level variable values remain consistent across household members for each household and the household structure cannot be used to re-identify individuals. This is further explained in the Sections Levels of risk and Household structure.

Before continuing to Step 6a, we select the categorical key variables, continuous key variables and any variables selected for use in PRAM routines, as well as household-level sampling weights in *R*. We also collect the variable names of the variables that will not be released. The PRAM variables are variables select for the PRAM routine, which we discuss further in Step 8a. We extract these selected household variables from the SUF dataset and save them as "fileHH". The choice of PRAM variables is further explained in Step 8a. Listing **??** illustrates how these steps are done in *R* (see also the Section Household structure).

Listing 12.25: Selecting the variables for the household-level anonymization

```r
# Categorical key variables at household level
selectedKeyVarsHH <- c('URBRUR', 'REGION', 'HHSIZE')

# Continuous key variables
numVarsHH <- c('TANHHEXP', 'INCTOTGROSSHH')

# PRAM variables
pramVarsHH <- c('ROOF', 'TOILET', 'WATER', 'ELECTCON',
                'FUELCOOK', 'OWNMOTORCYCLE', 'CAR', 'TV', 'LIVESTOCK')

# Household weight
weightVarHH <- c('WGTPOP')

# Variables not suitable for release in PUF (HH level)
varsNotToBeReleasedHH <- c("OWNAGLAND", "RELIG", "LANDSIZEHA")

# Vector with names of all HH level variables
HHVars <- c('IDH', selectedKeyVarsHH, pramVarsHH, numVarsHH, weightVarHH)

# Create subset of file with only HH level variables
fileHH <- file[,HHVars]
```

Every household has the same number of entries as it has members (e.g., a household of three will be repeated three times in "fileHH"). Before analyzing the household-level variables, we select only one entry per household, as illustrated in Listing **??**. This is further explained in the Section Household structure. In the same way we extract "fileOrigHH" from "fileOrig". "fileOrigHH" contains all variables from the raw data, but contains every household only once. We need "fileOrigHH" in Steps 8a and 10a for undoing some perturbative methods used in the SUF file and computing utility measures from the raw data respectively.

Listing 12.26: Taking a subset with only households

```r
# Remove duplicated rows based on IDH, one row per household in fileHH
fileHH <- fileHH[which(!duplicated(fileHH$IDH)),] # SUF file
fileOrigHH <- fileOrig[which(!duplicated(fileOrig$IDH)),] # original dataset

# Dimensions of fileHH
dim(fileHH)
## [1] 1970   16

dim(fileOrigHH)
## [1] 2000   68
```

The file "fileHH" contains 1,970 households and 16 variables. We are now ready to create our *sdcMicro* object with the corresponding variables we selected in Listing **??**. For our case study, we will create an *sdcMicro* object called "sdcHH" based on the data in "fileHH", which we will use for steps 6a – 10a (see Listing **??**).

Note: When the sdcMicro object is created, the sdcMicro package automatically calculates and stores the risk measures for the data.

This leads us to Step 6a.

Listing 12.27: Creating a *sdcMicro* object for the household variables

```
# Create initial sdcMicro object for household level variables
sdcHH <- createSdcObj(dat = fileHH, keyVars = selectedKeyVarsHH,
                      pramVars = pramVarsHH, weightVar = weightVarHH, numVars =␣
↪numVarsHH)
numHH <- length(fileHH[,1]) # number of households
```

12.2.6 Step 6a: Assessing disclosure risk (household level)

Based on the key variables selected in the disclosure scenarios, we can evaluate the risk at the household level. The PUF risk measures show a lower risk level than in the SUF file after anonymization in case study 1. The reason is that the set of key variables is smaller, since some variables will not be released in the PUF file. Removing (key) variables reduces the risk, and it is one of the most straightforward SDC methods.

As a first measure, we evaluate the number of households violating k-anonymity at the levels 2, 3 and 5. Table **??** shows the number of violating households as well as the percentage of the total number of households. Listing **??** illustrates how to find these values with *sdcMicro*. The print() function in *sdcMicro* shows only the values for thresholds 2 and 3. Values for other thresholds can be calculated manually by summing up the frequencies smaller than the k-anonymity threshold, as shown in Listing **??**. The number of violators is already at a low level, due to the prior anonymization of the SUF file and the reduced set of key variables.

Table 12.20: Number and proportion of households violating k-anonymity

k-anonymity level	Number of HH violating	Percentage of total number of HH
2	0	0.0%
3	18	0.9%
5	92	4.7%

Listing 12.28: Showing number of households violating k-anonymity for levels 2, 3 and 5

```
# Number of observations violating k-anonymity (thresholds 2 and 3)
print(sdcHH)
## Infos on 2/3-Anonymity:
##
## Number of observations violating
##   - 2-anonymity: 0
##   - 3-anonymity: 18
##
## Percentage of observations violating
##   - 2-anonymity: 0.000 %
##   - 3-anonymity: 0.914 %
-------------------------------------------------------------------------

```

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```r
# Calculate sample frequencies and count number of obs. violating k(5) - anonymity
kAnon5 <- sum(sdcHH@risk$individual[,2] < 5)
kAnon5
## [1] 92

# As percentage of total
kAnon5 / numHH
## [1] 0.04670051
```

It is often useful to view the records of the household(s) that violate k-anonymity. This might help to find which variables cause the uniqueness of these households; this can then be used later when choosing appropriate SDC methods. Listing **??** shows how to access the values of the households violating 3 and 5-anonymity. Not surprisingly, the variable "HHSIZE" is responsible for many of the unique combinations and the origin of much of the risk. This is even the case after removing large households for the SUF release.

Listing 12.29: Showing records of households that violate k-anonymity

```r
# Show values of key variable of records that violate k-anonymity
fileHH[sdcHH@risk$individual[,2] < 3, selectedKeyVarsHH] # for 3-anonymity
fileHH[sdcHH@risk$individual[,2] < 5, selectedKeyVarsHH] # for 5-anonymity
```

We also assess the disclosure risk of the categorical variables with the individual and global risk measures as described in the Sections Individual risk and Global risk. In "fileHH" every entry represents a household. Therefore, we use the individual non-hierarchical risk here, where the individual refers in this case to a household. "fileHH" is a subset of the complete dataset and contains only households and has, contrary to the complete dataset, no hierarchical structure. In Step 6b, we evaluate the hierarchical risk in the dataset "file", the dataset containing both households and individuals. The individual and global risk measures automatically take into consideration the household weights, which we defined in Listing **??**. In our file, the global risk measure calculated using the chosen key variables is lower than 0.01% (the smallest reported value is 0.01%, in fact the global risk is 0.0000642 %). This percentage is extremely low and corresponds to 0.13 expected re-identifications. The results are also shown in Listing **??**. This low figure can be explained by the relatively small sample size of 0.25% of the total population (see case study 1). Furthermore, one should keep in mind that this risk measure is based only on the categorical quasi-identifiers at the household level.

Listing 12.30: Printing global risk measures

```r
print(sdcHH, "risk")
## Risk measures:
##
## Number of observations with higher risk than the main part of the data: 0
## Expected number of re-identifications: 0.13 (0.01 %)
```

The global risk measure does not provide information about the spread of the individual risk measures. There might be a few households with relatively high risk, while the global (average) risk is low. Therefore we check the highest individual risk as shown in Listing **??**. The individual risk of the household with the highest risk is 0.1 %, which is still very low.

Listing 12.31: Determining the highest individual risk

```r
# Highest individual risk
max(sdcHH@risk$individual[, "risk"])
## [1] 0.001011633
```

Since the selected key variables at the household level are both categorical and numerical, the individual and global risk measures based on frequency counts do not completely reflect the disclosure risk of the entire dataset. When generating the SUF file, we concluded that recoding of continuous variables to make them all categorical would likely not satisfy the needs of the SUF users. For the PUF file it is acceptable to recode continuous variables, such as income and expenditures since PUF content is typically less detailed. In Step 8a we will recode these variables into deciles and convert them into categorical variables. Therefore, we exclude these variables from the risk calculations now We take these variables into account while remeasuring risk after anonymization.

12.2.7 Step 7a: Assessing utility measures (household level)

The utility of the data does not only depend on the household level variables, but on the combination of household-level and individual-level variables. Therefore, it is not useful to evaluate all the utility measures selected in Step 5 at this stage, i.e., before anonymizing the individual level variables. We restrict the initial measurement of utility to those measures that are solely based on the household variables. In our dataset, these are the measures related to income and expenditure and their distributions. The results are presented in Step 10a, together with the results after anonymization, which allow direct comparison. If after the next anonymization step it appears that the data utility has been significantly decreased by the suppression of some household level variables, we can return to this step.

Note: To analyze the utility loss, the utility measures before anonymization have to be calculated from the raw data and not from the anonymized SUF file.

Not all measures from case study 1 can be computed from the PUF file, since the information content is lower. The set of utility measures we use to evaluate the information loss in the PUF file consists of measures that need less detailed variables. This reflects the lower requirements a PUF user has on the dataset.

12.2.8 Step 8a: Choice and application of SDC methods (household level)

This step is divided into the anonymization of the categorical key variables and the continuous key variables, since different methods are used for both sets of variables. As already discussed in Step 4, we do not release all variables in the PUF file. At the household level “RELIG” (religion of household head), “OWNAGLAND” (land ownership) and “LANDSIZEHA” (plot size in ha) are not released in addition to the variables removed for the SUF release. For the sake of illustration, we assume that the variable “RELIG” is too sensitive and the variables “OWNAGLAND” and “LANDSIZEHA” are too identifying.

Categorical variables

We are now ready to move on to the choice of SDC methods for the categorical variables on the household level in our dataset. In the SUF file we already recoded some of the key variables and used local suppression. We only have three categorical key variables at the household level; “URBRUR”, “REGION” and “HHSIZE”. The selected categorical key variables at the household level are not suitable for recoding at this point, since the values cannot be grouped further. “URBRUR” has only two distinct categories and “REGION” has only six non-combinable regions. As noted before, the variable “HHSIZE” can be reconstructed by a headcount per household. Therefore, recoding of this variable alone does not lead to disclosure control.

Due to the relatively low risk of re-identification based on the three selected categorical household level variables, it is possible in this case to use an option like local suppression to achieve our desired level of risk. Applying local suppression when initial risk is relatively low will likely only lead to suppression of few observations and thus limit the loss of utility. If, however, the data had been measured to have a relatively high risk, then applying local suppression without previous recoding would likely result in a large number of suppressions and greater information loss. Efforts such a recoding should be taken first before suppressing values in cases where risk is initially measured as high. Recoding will reduce risk with little information loss and thus the number of suppressions, if local suppression is applied as an additional step.

We apply local suppression to reach 5-anonymity. The chosen level of five is higher than in the SUF release and is based on the release type as PUF. This leads to a total of 39 suppressions, all in the variable “HHSIZE”. As explained earlier, suppression of the value of the variable “HHSIZE” does not lead to actual suppression of this information.

Therefore, we redo the local suppression, but this time we tell *sdcMicro* to, if possible, not suppress “HHSIZE” but one of the other variables. Alternatively, we could remove households with suppressed values of the variable “HHSIZE”, remove large households or split households.

In *sdcMicro* it is possible to tell the algorithm which variables are important and less important for making small changes (see also the Section Local suppression). To prevent values of the variable “HHSIZE” being suppressed, we set the importance of “HHSIZE” in the importance vectors to the highest (i.e., 1). We try two different importance vectors: the first where “REGION” is more important than “URBRUR” and the second with the importance of “REGION” and “URBRUR” swapped. Listing **??** shows how to apply local suppression and put importance on the variable “HHSIZE”.

Note: In Listing **??** we use the undolast() function in sdcMicro to go one step back after we had first applied local suppression with no importance vector.

The undolast() function restores the *sdcMicro* object back to the previous state (i.e., before we applied local suppression), which allows us to rerun the same command, but this time with an importance vector set. The undolast() function can only be used to go one step back.

The suppression patterns of the three different options are shown in Table **??**. The importance is clearly reflected in the number of suppressions per variable. The total number of suppressions is with an importance vector higher than without an importance vector (44/73 vs. 39), but 5-anonymity is achieved in the dataset with no suppressions in the variable “HHSIZE”. This means that we do not have to remove or split households. The variable “REGION” is the type of variable that should not have any suppressions either. From that perspective we chose the third option. This leads to more suppressions, but no suppressions in “HHSIZE” and as few as possible in “REGION”.

Table 12.21: Number of suppressions by variable after local suppression with and without importance vector

Key variable	Number of suppressions and proportion of total		
.	No importance vector	Importance HHSIZE, URBRUR, REGION	Importance HHSIZE, REGION, URBRUR
URBRUR	0 (0.0 %)	2 (0.1 %)	61 (3.1 %)
REGION	0 (0.0 %)	42 (2.1 %)	12 (0.6 %)
HHSIZE	39 (2.0 %)	0 (0.0 %)	0 (0.0 %)

Listing 12.32: Local suppression with and without importance vector

```
# Local suppression to achieve 5-anonimity
sdcHH <- localSuppression(sdcHH, k = 5, importance = NULL) # no importance vector
print(sdcHH, "ls")
## Local Suppression:
##  KeyVar | Suppressions (#) | Suppressions (%)
##  URBRUR |                0 |            0.000
##  REGION |                0 |            0.000
##  HHSIZE |               39 |            1.980
## ----------------------------------------------------------------------------

# Undo suppressions to see the effect of an importance vector
sdcHH <- undolast(sdcHH)

# Redo local suppression minimizing the number of suppressions in HHSIZE
sdcHH <- localSuppression(sdcHH, k = 5, importance = c(2, 3, 1))

print(sdcHH, "ls")
## Local Suppression:
```

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```
##   KeyVar | Suppressions (#) | Suppressions (%)
##   URBRUR |                2 |            0.102
##   REGION |               42 |            2.132
##   HHSIZE |                0 |            0.000
## ----------------------------------------------------------------------------

# Undo suppressions to see the effect of a different importance vector
sdcHH <- undolast(sdcHH)

# Redo local suppression minimizing the number of suppressions in HHSIZE
sdcHH <- localSuppression*(sdcHH, k = 5, importance = c(3, 2, 1))

print(sdcHH, "ls")
## Local Suppression:
##   KeyVar | Suppressions (#) | Suppressions (%)
##   URBRUR |               61 |            3.096
##   REGION |               12 |            0.609
##   HHSIZE |                0 |            0.000
## ----------------------------------------------------------------------------
```

In case study 1 we applied invariant PRAM to the variables "ROOF", "TOILET", "WATER", "ELECTCON", "FUELCOOK", "OWNMOTORCYCLE", "CAR", "TV" and "LIVESTOCK", since these variables are not sensitive and were not selected as quasi-identifiers because we assumed that there are no external data sources containing this information that could be used for matching. Values can be easily observed or be known to neighbors, however, and therefore are important, together with other variables, for the nosy neighbor scenario. For the PUF release we would like to level of uncertainty by increasing the number of changes. Therefore, we redo PRAM with a different transition matrix. As discussed in the Section PRAM (Post RAndomization Method), the invariant PRAM method has the property that the univariate distributions do not change. To maintain this property, we reapply PRAM to the raw data, rather than to the already PRAMmed variables in the SUF file.

Listing **??** illustrates how to apply PRAM. We use the original values to apply PRAM and replace the values in the *sdcMicro* object with these values. We choose the parameter 'pd', the lower bound for the probability that a value is not changed, to be relatively low at 0.6. This is a lower value than the 0.8 used in the SUF file and will lead to a higher number of changes (cf. Listing **??**). This is acceptable for a PUF file and introduces more uncertainty as required for a PUF release. Listing **??** also shows the number of changed records per variables. Because PRAM is a probabilistic method, we set a seed for the random number generator before applying PRAM to ensure reproducibility of the results.

Note: In some cases the choice of the seed matters. The choice of seed changes the results.

The seed should not be released, since it allows for reconstructing the original values if combined with the transition matrix. The transition matrix can be released: this allows for consistent statistical inference by correcting the statistical methods used if the researcher has knowledge about the PRAM method (at this point *sdcMicro* does not allow to retrieve the transition matrix).

Listing 12.33: Applying PRAM

```
# PRAM
set.seed(10987)

# Replace PRAM variables in sdcMicro object sdcHH with the original raw values
sdcHH@origData[,pramVarsHH] <- fileHH[match(fileHH$IDH, fileOrigHH$IDH), pramVarsHH]
sdcHH@manipPramVars <- fileHH[match(fileHH$IDH, fileOrigHH$IDH), pramVarsHH]

sdcHH <- pram(obj = sdcHH, pd = 0.6)
```

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```
## Number of changed observations:
## - - - - - - - - - - - -
## ROOF != ROOF_pram : 305 (15.48%)
## TOILET != TOILET_pram : 260 (13.2%)
## WATER != WATER_pram : 293 (14.87%)
## ELECTCON != ELECTCON_pram : 210 (10.66%)
## FUELCOOK != FUELCOOK_pram : 315 (15.99%)
## OWNMOTORCYCLE != OWNMOTORCYCLE_pram : 95 (4.82%)
## CAR != CAR_pram : 255 (12.94%)
## TV != TV_pram : 275 (13.96%)
## LIVESTOCK != LIVESTOCK_pram : 109 (5.53%)
```

PRAM has changed values within the variables according to the invariant transition matrices. Since we used the invariant PRAM method (see the Section PRAM (Post RAndomization Method)), the absolute univariate frequencies remain approximately unchanged. This is not the case for the multivariate frequencies. In Step 10a we compare the multivariate frequencies before and after anonymization for the PRAMmed variables.

Continuous variables

We have selected the variables “INCTOTGROSSHH” (total income) and “TANHHEXP” (total expenditure) as numerical quasi-identifiers, as discussed in Step 4. In Step 5 we identified variables having high interest for the users of our data: many users use the data for measuring inequality and expenditure patterns. The noise addition in the SUF file does not protect these variables sufficiently, especially, because outliers are not protected. Therefore, we decide to recode total income and total expenditure into deciles.

As with PRAM, we want to compute the deciles from the raw data rather than from the perturbed values in the SUF file. We compute the deciles directly from the raw data and overwrite these values in the *sdcMicro* object. Subsequently, we compute the mean of each decile from the raw data and replace the values for total income and total expenditures with the mean of the respective decile. In this way the mean of both variables does not change. This approach can be interpreted as univariate microaggregation with very large groups (group size n/10) with the mean as replacement value (see the Section Microaggregation).

The information in the income and expenditure variables by component is too sensitive to release as PUF, and, summing those variables would allow an intruder to reconstruct the totals. PUF users might however be interested in the shares. Therefore, we decide to keep the income and expenditure components as proportions of the raw totals, rounded to two digits. The anonymization of the income and expenditure variables is shown in Listing **??**.

Listing 12.34: Anonymization of income and expenditure variables

```
# Create bands (deciles) for income and expenditure variables
(aggregates) based on the original data
decExp <- as.numeric(cut(fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH), "TANHHEXP"],
                         quantile(fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH),
↪"TANHHEXP"],
                                  (0:10)/10, na.rm = T),
                         include.lowest = TRUE, labels = c(1, 2, 3, 4, 5, 6, 7, 8, 9,␣
↪10)))
 decInc <- as.numeric(cut(fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH), "INCTOTGROSSHH
↪"],
                          quantile(fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH),
↪"INCTOTGROSSHH"],
                                   (0:10)/10, na.rm = T),
                          include.lowest = TRUE, labels  = c(1, 2, 3, 4, 5, 6, 7, 8,␣
↪9, 10)))

# Mean values of deciles
decExpMean <- round(sapply(split(fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH),
↪"TANHHEXP"],
```

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```
                                 decExp), mean))
decIncMean <- round(sapply(split(fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH), "INCTOTGROSSHH"],
                                decInc), mean))

# Replace with mean value of decile
sdcHH@manipNumVars$TANHHEXP <- decExpMean[match(decExp,names(decExpMean))]
sdcHH@manipNumVars$INCTOTGROSSHH <- decIncMean[\ match(decInc, names(decIncMean))]

# Recalculate risks after manually changing values in sdcMicro object calcRisks(sdcHH)
calcRisks(sdcHH)

# Extract data from sdcHH
HHmanip <- extractManipData(sdcHH) # manipulated variables HH

# Keep components of expenditure and income as share of total,
# use original data since previous data was perturbed
compExp <- c('TFOODEXP', 'TALCHEXP', 'TCLTHEXP', 'THOUSEXP',
             'TFURNEXP', 'THLTHEXP', 'TTRANSEXP', 'TCOMMEXP',
             'TRECEXP', 'TEDUEXP', 'TRESTHOTEXP', 'TMISCEXP')
compInc <- c('INCRMT',  'INCWAGE', 'INCFARMBSN', 'INCNFARMBSN',
             'INCRENT', 'INCFIN',  'INCPENSN',   'INCOTHER')
HHmanip <- cbind(HHmanip, round(fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH), compExp] /
                                fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH),
                                           "TANHHEXP"], 2))
HHmanip <- cbind(HHmanip, round(fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH), compInc] /
                                fileOrigHH[match(fileHH$IDH, fileOrigHH$IDH),
                                           "INCTOTGROSSHH"], 2))
```

12.2.9 Step 9a: Re-measure risk (household level)

For the categorical variables, we conclude that we have achieved 5-anonymity in the data with local suppression. 5-anonymity also implies 2- and 3-anonymity. The global risk stayed close to zero (as the expected number of re-identifications), which is very low. Therefore, we conclude that based on the categorical variables, the data has been sufficiently anonymized. One should keep in mind that the anonymization methods applied are complementing the ones used for the SUF.

Note: The methods selected methods in this case study alone would not be sufficient to protect the data set for a PUF release.

We have reduced the risk of spontaneous recognition of households, by removing the variable “LANDSIZEHA” and PRAMming the variables identified to be important in the nosy neighbor scenario. An intruder cannot know with certainty whether a household that (s)he recognizes in the data is the correct household, due to the noise in these variables.

These measures refer only to the categorical variables. To evaluate the risk of the continuous variables we could use an interval measure or closest neighbor algorithm. These risk measures are discussed in the Section Risk measures for continuous variables. We chose to use an interval measure, since exact value matching is not our largest concern based on the assumed scenarios and external data sources. Instead, datasets with similar values but not the exact same values could be used for matching. Here the main concern is that the values are sufficiently far from the original values, which is measured with an interval measure.

Listing **??** shows how to evaluate the interval measure for the variables “INCTOTGROSSHH” and “TANHHEXP” (total income and expenditure). The different values of the parameter k in the function dRisk() define the size of the interval around the original value as a function of the standard deviation, as explained in the Section Interval measure . The larger k, the larger the intervals, the higher the probability that a perturbed value is in the interval around the original value and the higher the risk measure. The results are satisfactory, especially when keeping in mind that there are only 10 distinct values in the dataset (the means of each of the deciles). All outliers have been recoded. Looking at the proportions of the components, we do not detect any outliers (households with an unusual high or low spending pattern in one component).

Listing 12.35: Measuring risk of re-identification of continuous variables

```
# Risk evaluation continuous variables
dRisk(sdcHH@origData[,c("TANHHEXP", "INCTOTGROSSHH")],
      xm = sdcHH@manipNumVars[,c("TANHHEXP", "INCTOTGROSSHH")], k = 0.01)
## [1] 0.4619289

dRisk(sdcHH@origData[,c("TANHHEXP", "INCTOTGROSSHH")],
      xm = sdcHH@manipNumVars[,c("TANHHEXP", "INCTOTGROSSHH")], k = 0.02)
## [1] 0.642132

dRisk(sdcHH@origData[,c("TANHHEXP", "INCTOTGROSSHH")],
      xm = sdcHH@manipNumVars[,c("TANHHEXP", "INCTOTGROSSHH")], k = 0.05)
## [1] 0.8258883
```

12.2.10 Step 10a Re-measure utility (household level)

The utility in the data has decreased compared to the raw data, mainly because variables were completely removed. Many of the utility measures used in case study 1 are not applicable to the PUF file. However, by replacing the deciles with their means, we can still use the income and expenditure variables for arithmetic operations. Also the shares of the income and expenditure components can still be used, since they are based on the raw data.

We select two additional utility measures: the decile dispersion ratio and the share of total consumption by the poorest decile. The decile dispersion ratio is the ratio of the average income of the top decile and the average income of the bottom decile. Listing **??** shows how to compute these from the raw data and the household variables after anonymization. Table **??** presents the estimated values. The differences are small and mainly due to the removed households.

Table 12.22: Comparison of utility measures

.	Raw data	PUF file
Decile dispersion ratio	24.12	23.54
Share of consumption by the poorest decile	0.0034	0.0035

Listing 12.36: Computation of decile dispersion ratio and share of total consumption by the poorest decile

```
# Decile dispersion ratio
# raw data
mean(tail(sort(fileOrigHH$INCTOTGROSSHH), n = 200)) /
  mean(head(sort(fileOrigHH$INCTOTGROSSHH), n = 200))
## [1] 24.12152

mean(tail(sort(HHmanip$INCTOTGROSSHH), n = 197)) /
  mean(head(sort(HHmanip$INCTOTGROSSHH), n = 197))
## [1] 23.54179
```

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```

# Share of total consumption by the poorest decile households
sum(head(sort(fileOrigHH$TANHHEXP), n = 200)) / sum(fileOrigHH$TANHHEXP)
## [1] 0.003411664

sum(head(sort(HHmanip$TANHHEXP), n = 197)) / sum(HHmanip$TANHHEXP)
## [1] 0.003530457
```

Merging the household- and individual-level variables

The next step is to merge the treated household variables with the untreated individual variables for the anonymization of the individual level variables. Listing **??** shows the steps to merge these files. This also includes the selection of variables used in the anonymization of the individual-level variables. We create the *sdcMicro* object for the anonymization of the individual variables in the same way as for the household variable in Listing **??**. Generally, at this stage, the household level and individual level variables should be combined and quasi-identifiers at both levels be used (see the Section Levels of risk). Unfortunately, in our dataset, this leads to long computation times. Therefore, we create two *sdcMicro* objects, one with all key variables (“sdcCombinedAll”) and one with only the individual level key variables (“sdcCombined”). In Step 6b we compare the risk measures for both cases and in Step 8b we discuss alternative approaches to keeping the complete set of variables. We now repeat Steps 6-10 for the individual-level variables.

Listing 12.37: Merging the files with household and individual-level variables and creating an *sdcMicro* object for the anonymization of the individual-level variables

```
### Select variables (individual level)
selectedKeyVarsIND = c('GENDER', 'REL', 'MARITAL',
                       'AGEYRS', 'EDUCY', 'INDUSTRY1') # list of selected key␣
↪variables

# sample weight (WGTHH, individual weight)
selectedWeightVarIND = c('WGTHH')

# Household ID
selectedHouseholdID = c('IDH')

# Variables not suitable for release in PUF (IND level)
varsNotToBeReleasedIND <- c("ATSCHOOL", "EDYRSCURRAT")

# All individual level variables
INDVars <- c(selectedKeyVarsIND)

# Recombining anonymized HH data sets and individual level variables
indVars <- c("IDH", "IDP", selectedKeyVarsIND, "WGTHH") # HID and all non HH vars
fileInd <- file[indVars] # subset of file without HHVars
fileCombined <- merge(HHmanip, fileInd, by.x = c('IDH'))
fileCombined <- fileCombined[order(fileCombined[,'IDH'],  fileCombined[,'IDP']),]

dim(fileCombined)
## [1] 10068    44

# SDC objects with only IND level variables
sdcCombined <- createSdcObj(dat = fileCombined, keyVars = c(selectedKeyVarsIND),
                            weightVar = selectedWeightVarIND, hhId =␣
↪selectedHouseholdID)

# SDC objects with both HH and IND level variables
```

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```
sdcCombinedAll <- createSdcObj(dat = fileCombined,
                               keyVars = c(selectedKeyVarsIND, selectedKeyVarsHH ),
                               weightVar = selectedWeightVarIND, hhId =␣
↪selectedHouseholdID)
```

12.2.11 Step 6b: Assessing disclosure risk (individual level)

As first measure, we evaluate the number of records violating k-anonymity at the levels 2, 3 and 5. Table **??** shows the number of violating individuals as well as the percentage of the total number of households. The second and third column refer to “sdcCombined” and the fourth and fifth column to “sdcCombinedAll”. We see that combining the individual level and household level variables leads to a large increase in the number of k-anonymity violators. The choice not to include the household level variables is pragmatically driven by the computation time and can be justified by the different type of variables on the household level and individual level. One could assume that these variables are not available in the same dataset and can therefore not simultaneously be used by an intruder to re-identify individuals.

Table 12.23: Number of records violating k-anonimity

.	sdcCombined		sdcCombinedAll	
k-anonymity	Number of records violating	Percentage of total records	Number of records violating	Percentage of total records
2	0	0.0 %	4,048	40.2 %
3	167	1.7 %	6,107	60.7 %
5	463	4.6 %	8,292	82.4 %

The global hierarchical risk measure is 0.095%, which corresponds to approximately 10 expected re-identifications. We use here the hierarchical risk measure, since the re-identification of a single household member would lead to the re-identification of the other members of the same household too. This number is low compared to the number of k-anonymity violations, due to the high sample weights, which protect the data already to a large extent. Only 24 observations have an individual hierarchical risk higher than 1%, with a maximum of 1.17%. This is mainly because of the lower sample weights of these records. Listing **??** shows how to retrieve these measures in *R*.

Listing 12.38: Risk measures before anonymization

```
numIND <- length(fileCombined[,1]) # number of households

# Number of observations violating k-anonymity
print(sdcCombined)
## Infos on 2/3-Anonymity:
##
## Number of observations violating
##   - 2-anonymity: 0
##   - 3-anonymity: 167
##
## Percentage of observations violating
##   - 2-anonymity: 0.000 %
##   - 3-anonymity: 1.659 %
## ---------------------------------------------------------------------------

# Calculate sample frequencies and count number of obs. violating k(3,5) - anonymity
kAnon5 <- sum(sdcCombined@risk$individual[,2] 5)
kAnon5
## [1] 463

```

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```
# As percentage of total
kAnon5 / numIND
## [1] 0.04598729

# Global risk on individual level
print(sdcCombined, 'risk')
## Risk measures:
##
## Number of observations with higher risk than the main part of the data: 0
## Expected number of re-identifications: 1.69 (0.02 %)
##
## Information on hierarchical risk:
## Expected number of re-identifications: 9.57 (0.10 %)
## --------------------------------------------------------------------------

# Number of observation with relatively high risk
dim(fileCombined[sdcCombined@risk$individual[, "hier_risk"] > 0.01,])
## [1] 24 44

# Highest individual risk
max(sdcCombined@risk$individual[, "hier_risk"])
## [1] 0.01169091
```

12.2.12 Step 7b: Assessing utility measures (individual level)

We evaluate the utility measures as discussed in Step 5 based on the raw data (before applying any anonymization measures). The results are presented in Step 10b together with the values after anonymization to allow for direct comparison.

12.2.13 Step 8b: Choice and application of SDC methods (individual level)

In this step, we discuss four different techniques used for anonymization: 1) removing variables from the dataset to be released, 2) recoding of categorical variables to reduce the level of detail, 3) local suppression to achieve the required level of k-anonymity, 4) randomization of the order of the records in the file. Finally, we discuss some alternative options for treating the household structure in the dataset.

Removing variables

Additional to the variables removed from the dataset for the SUF release (see case study 1), we further reduce the number of variables in the dataset to be released. This is normal practice for PUF releases. Sensitive or identifying variables are removed, which allows to release other variables at a more detailed level. In a PUF release, the set of key variables should be limited.

In our case, we decide to remove at the individual level the variables "EDYRSCURRAT", as this variable is too identifying (identifies whether there are school-going children in the household). We keep the variable "EDUCY" (highest level of education attended) for information on education.

Note: As an alternative to removing the variables from the dataset, one could also set all values to missing. This would allow the user to see the structure and variables contained in the SUF file.

Recoding

As noted before, PUF users require a lower level of information and therefore we can recode the key variables even further to reduce the disclosure risk. The recoding of variables in case study 1 is not sufficient for a PUF release. Therefore, we recode most of the categorical key variables from Table **??** to reduce the risk and number of necessary suppressions by local suppression. Table **??** gives an overview of the recodes made. All new categories are formed with the needs of the data user in mind. Listing **??** shows how to do this in *R* and also shows value labels and the univariate tabulations of these variables before and after recoding.

Table 12.24: Overview of recodes of categorical variables at individual level

Variable	Recoding
REL (relation to household head)	recode 'Father/Mother', ' Grandchild', 'Son/Daughter in law', 'Other relative' to 'Other relative' and recode 'Domestic help' and 'Non-relative' to 'Other'
MARITAL (marital status)	recode 'Married monogamous', 'Married polygamous', 'Common law, union coutumiere, union libre, living together' to 'Married/living together' and 'Divorced/Separated' and 'Widowed' to 'Divorced/Separated/Widowed'
AGEYRS (age in completed years)	recode values under 15 to 7 (other values have been recoded for SUF)
EDUCY (highest level of education completed)	recode 'Completed lower secondary (or post-primary vocational education) but less than completed upper secondary', 'Completed upper secondary (or extended vocational/technical education)', 'Post secondary technical' and 'University and higher' to 'Completed lower secondary or higher'
INDUSTRY1	recode to 'primary', 'secondary' and 'tertiary'

Listing 12.39: Recoding the categorical and continuous variables

```
# Recode REL (relation to household head)
table(sdcCombined@manipKeyVars$REL, useNA = "ifany")
##
##    1    2    3    4    5    6    7    8    9 <NA>
## 1698 1319 4933   52  765   54  817   40   63  327

# 1 - Head, 2 - Spouse, 3 - Child, 4 - Father/Mother, 5 - Grandchild, 6 - Son/
↪Daughter in law
# 7 - Other relative, 8 - Domestic help, 9 - Non-relative
sdcCombined <- groupVars(sdcCombined, var = "REL", before = c("4", "5", "6", "7"),
                         after = c("7", "7", "7", "7")) # other relative
sdcCombined <- groupVars(sdcCombined, var = "REL", before = c("8", "9"),
                         after = c("9", "9")) # other

table(sdcCombined@manipKeyVars$REL, useNA = "ifany")
##
##    1    2    3    7    9 <NA>
## 1698 1319 4933 1688  103  327

# Recode MARITAL (marital status)
table(sdcCombined@manipKeyVars$MARITAL, useNA = "ifany")

##
##    1    2    3    4    5    6 <NA>
## 3542 2141  415  295  330  329 3016

# 1 - Never married, 2 - Married monogamous, 3 - Married polygamous,
# 4 - Common law, union coutumiere, union libre, living together, 5 - Divorced/
↪Separated,
```

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```
# 6 - Widowed
sdcCombined <- groupVars(sdcCombined, var = "MARITAL", before = c("2", "3", "4"),
                         after = c("2", "2", "2")) # married/living together
sdcCombined <- groupVars(sdcCombined, var = "MARITAL", before = c("5", "6"),
                         after = c("9", "9")) # divorced/seperated/widowed*

table(sdcCombined@manipKeyVars$MARITAL, useNA = "ifany")
##
##    1    2    9 <NA>
## 3542 2851  659 3016

# Recode AGEYRS (0-15 years)
table(sdcCombined@manipKeyVars$AGEYRS, useNA = "ifany")
##
##    0    1    2    3    4    5    6    7    8    9   10   11   12   13   14
##  311  367  340  332  260  334  344  297  344  281  336  297  326  299  263
##   20   30   40   50   60   65 <NA>
## 1847 1220  889  554  314  325  188

sdcCombined <- groupVars(sdcCombined, var = "AGEYRS",
                         before = c("0", "1", "2", "3", "4", "5", "6", "7", "8", "9",
                                    "10", "11", "12", "13", "14"),
                         after = rep("7", 15))

table(sdcCombined@manipKeyVars$AGEYRS, useNA = "ifany")
##
##    7   20   30   40   50   60   65 <NA>
## 4731 1847 1220  889  554  314  325  188

sdcCombined <- calcRisks(sdcCombined)
# Recode EDUCY (highest level of educ compl)
table(sdcCombined@manipKeyVars$EDUCY, useNA = "ifany")
##
##    0    1    2    3    4    5    6 <NA>
## 1582 4755 1062  330  139   46  104 2050

# 0 - No education, 1 - Pre-school/ Primary not completed,
# 2 -  Completed primary, but less than completed lower secondary
# 3 - Completed lower secondary (or post-primary vocational education)
#     but less than completed upper secondary
# 4 - Completed upper secondary (or extended vocational/technical education),
# 5 - Post secondary technical
# 6 - University and higher
sdcCombined <- groupVars(sdcCombined, var = "EDUCY", before = c("3", "4", "5", "6"),
                         after = c("3", "3", "3", "3")) # completed lower secondary or higher
table(sdcCombined@manipKeyVars$EDUCY, useNA = "ifany")
##
##    0    1    2    3 <NA>
## 1582 4755 1062  619 2050

# Recode INDUSTRY1 ()
table(sdcCombined@manipKeyVars$INDUSTRY1, useNA = "ifany")
##
##    1    2    3    4    5    6    7    8    9   10 <NA>
## 5300   16  153    2   93  484   95   17   70  292 3546

```

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```
# 1 - Agriculture and Fishing, 2 - Mining, 3 - Manufacturing, 4 -  Electricity and Utilities
# 5 - Construction, 6 - Commerce, 7 - Transportation, Storage and  Communication, 8 - Financial, Insurance and Real Estate
# 9 - Services: Public Administration, 10 - Other Services, 11 - Unspecified
sdcCombined <- groupVars(sdcCombined, var = "INDUSTRY1", before = c("1", "2"),
                         after = c("1", "1")) # primary
sdcCombined <- groupVars(sdcCombined, var = "INDUSTRY1", before = c("3", "4", "5"),
                         after = c("2", "2", "2")) # secondary
sdcCombined <- groupVars(sdcCombined, var = "INDUSTRY1", before = c("6", "7", "8", "9", "10"),
                         after = c("3", "3", "3", "3", "3")) # tertiary
table(sdcCombined@manipKeyVars$INDUSTRY1, useNA = "ifany")
##
##    1    2    3 <NA>
## 5316  248  958 3546
```

Local suppression

The recoding has reduced the risk already considerably. We use local suppression to achieve the required level of k-anonymity. Generally, the required level of k-anonymity for PUF files is 3 or 5. In this case study, we require 5-anonimity. Listing **??** shows the suppression pattern without specifying an importance vector. All suppressions are made in the variable “AGEYRS”. This is the variable with the highest number of different values, and hence considered first by the algorithm. We try different suppression patterns by specifying importance vectors, but we decide that the pattern without importance vector yields the best result. This is also the result with the lowest total number of suppressions. Less than 1 percent suppression in the age variable is acceptable. We could reduce this number by further recoding the variable “AGEYRS”.

Listing 12.40: Local suppression to reach 5-anonimity

```
# Local suppression without importance vector
sdcCombined <- localSuppression(sdcCombined, k = 5, importance = NULL)

# Number of suppressions per variable
print(sdcCombined, "ls")
## Local Suppression:
##      KeyVar | Suppressions (#) | Suppressions (%)
##      GENDER |                0 |            0.000
##         REL |                0 |            0.000
##     MARITAL |                0 |            0.000
##      AGEYRS |               91 |            0.904
##       EDUCY |                0 |            0.000
##   INDUSTRY1 |                0 |            0.000
```

Randomization of order of records

The records in the dataset are ordered by region and household ID. There is a certain geographical order of the households within the regions, due to the way the households IDs were assigned. Intruders could reconstruct suppressed values by using this structure. To prevent this, we randomly reorder the records within the regions. Listing **??** shows how to do this in *R*. We first count the number of records per region

Note: Some records have their region value suppressed, so we include the count of NAs.

Subsequently, we draw randomly household IDs, in such way that the regional division is respected. Finally, we sort the file by the new, randomized, individual ID (“IDP”). Households with suppressed values for “REGION” will be last in the reordered file. Before randomizing the order, we extract the data from the *sdcMicro* object "sdcCombined" as shown in Listing **??**.

Listing 12.41: Randomizing the order of records within regions

```r
# Randomize order of households dataAnon and recode IDH to random
number (sort file by region)
set.seed(97254)
# Sort by region
dataAnon <- dataAnon[order(dataAnon$REGION),]

# Number of households per region
hhperregion <- table(dataAnon[match(unique(dataAnon$IDH), dataAnon$IDH), "REGION"],
                     useNA = "ifany")

# Randomized IDH (household ID)
randomHHid <- c(sample(1:hhperregion[1], hhperregion[1]),
                unlist(lapply(1:(length(hhperregion)-1),
                              function(i){sample((sum(hhperregion[1:i]) + 1):sum(hhperregion[1:(i+1)]), hhperregion[(i+1)])})))

dataAnon$IDH <- rep(randomHHid, table(dataAnon$IDH)[match(unique(dataAnon$IDH),
                                                          as.numeric(names(table(dataAnon$IDH))))])

# Sort by IDH (and region)
dataAnon <- dataAnon[order(dataAnon$IDH),]
```

Alternative options for dealing with household structure

In Step 6b we compared the disclosure risk for two cases: one with only individual level key variables and another with individual level and household level key variables combined. We decided to use only the individual level key variables to reduce the computation time and justified this choice by arguing that intruders cannot use household and individual level variables simultaneously. This might not always be the case. Therefore we explore other options to reduce the risk when taking both individual level and household level variables into account. We present two options: removing the household structure; and using options in the local suppression algorithm.

Removing household structure

We consider the risk emanating from the household structure in the dataset to be very high. We can remove the hierarchical household structure completely and treat all variables at the individual level. This entails, besides removing the household id ("IDH"), also treating variables that could be used for reconstructing households. These are, for instance, "REL" (relation to household head), "HHSIZE" (household size), and any of the household level variables, such as income and expenditure. However, not all household level variables need to be treated. For example, "REGION" is a household level variable, but the probability that this variable leads to the reconstruction of a household is low. Also, we need to reorder the records in the file, as they are sorted by households. Note that by removing the household structure, we interpret all variables as individual level variables for measuring disclosure risk. This leads to a lower need for recoding and suppression, since the hierarchical risk disappears. The reason why we did not opt for this approach is the loss of utility for the user. The household structure is an important feature of the data, and should be kept in the PUF file.

Using different options for local suppression

The long running time is mainly due to the local suppression algorithm. In the Section Local suppression we discuss options to reduce the running time of the local suppression in case of many key variables. The all-m approach reduces the running time by first considering subsets of the complete set of key variables. This reduces the complexity of the problem and leads to lower computation times. However, the total number of suppressions made is likely to be higher. Also, if not explicitly specified, it is not guaranteed that the required level for k-anonymity is automatically achieved on the complete set of key variables. It is therefore important to check the results.

12.2.14 Step 9b: Re-measure risk

We re-evaluate the risk measures selected in Step 6. Table **??** shows that local suppression, not surprisingly, has reduced the number of individuals violating 5-anonymity to 0. The global hierarchical risk was reduced to 0.02%, which corresponds to approximately 2 correct re-identifications. The highest individual hierarchical re-identification risk is 0.2%. These risk levels are acceptable for a PUF release. Furthermore, the recoding has removed any unusual combinations in the data.

Note: The risk may be underestimated by excluding the household level variables.

Table 12.25: k-anonymity violations

k-anonymity	Number of records violating	Percentage
2	0	0.0 %
3	0	0.0 %
5	0	0.0 %

12.2.15 Step 10b: Re-measure utility

We compare (cross-)tabulations before and after anonymization, which are illustrated in the *R* code to this case study. We note that due to the recoding in Step 8b, the detail in the variables is reduced. This reduces the number of necessary suppressions and is acceptable for a public use file.

12.2.16 Step 11: Audit and reporting

In the audit step, we check whether the data allow for reproduction of published figures from the original dataset and relationships between variables and other data characteristics are preserved in the anonymization process. In short, we check whether the dataset is valid for analytical purposes. There are no figures available that were published from the dataset and need to be reproducible from the anonymized data.

In Step 2, we explored the data characteristics and relationships between variables. These data characteristics and relationships have been mainly preserved, since we took them into account when choosing the appropriate anonymization methods. Since values of the variable “AGEYRS” were not perturbed, but only recoded and suppressed, we did not introduce unlikely combinations, such as a 60-year-old individual enrolled in primary education. Also, by separating the anonymization process into two parts, one for household-level variables and one for individual-level variables, the values of variables measured at the household level agree for all members of each household.

Furthermore, we drafted two reports, internal and external, on the anonymization of the case study dataset. The internal report includes the methods used, the risk before and after anonymization as well as the reasons for the selected methods and their parameters. The external report focuses on the changes in the data and the loss in utility. Focus here should be on the number of suppressions as well as the perturbative methods (PRAM). This is described in the previous steps.

Note: When creating a PUF, it is inevitable that there will be a loss of information and it is very important for the users to be aware of these changes and release them in a report that accompanies the data.

Appendix C provides examples of an internal and external report of the anonymization process of this dataset. Depending on the users and readers of the reports, the content may differ.

Note: The report() function in sdcMicro is at this point not useful, since this will only report on the SDC measures in the second case study.

However, the report should contain the entire process, including the measures applied in case study 1.

12.2.17 Step 12: Data release

The final step is the release of the anonymized dataset together with the external report. Listing **??** shows how to export the anonymized dataset as *STATA* file. The Section Read functions in R presents functions for exporting files in other data formats.

Listing 12.42: Exporting the anonymized PUF file

```
# Create STATA file
write.dta(dataframe = dataAnon, file= 'Case2DataAnon.dta', convert.dates=TRUE)
```