December 2023

Quality Indicators for Administrative Data[1]

User Manual For R Package on GitHub

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Version 2.1

1 Funded by the Grant: 'Methodological Advancements on the Use of Administrative Data in Official Statistics' ESRC (ES/V005456/1)

Contents

1. Project aims and objectives

The Office for National Statistics (ONS) have strategic priorities on embedding and advancing the use of administrative data into their official statistics processes. Their immediate priority is to use administrative data in the quality assurance of the 2021 census and to develop the production of administrative-based population estimates (ABPEs). A more long-term priority is the Population Statistics Transformation Programme which will feed into a recommendation to Government due in 2023 on the future of census and population statistics. In particular, the objective is to create population characteristic estimates from administrative and integrated data sources.

Motivated by these initiatives, the University of Manchester was successfully awarded an ESRC grant from April 2021 to January 2023 titled: 'Methodological Advancements on the Use of Administrative Data in Official Statistics' (ES/V005456/1). The funded research enabled collaborations with the ONS on researching and developing methods to enhance the use of administrative data in official statistics.

This user manual concerns the sub-project related to developing a quality framework and quantitative measures to assess representativeness and coverage for a single administrative data source. We use univariate and bivariate distributions obtained from high- quality large random probability surveys (such as the UK Annual Population Survey) and compare them to distributions in the administrative data on a common set of variables based on distance metrics between these distributions. In addition, we developed a Representativity (R-) Indicator that is designed for quantifying the representativeness of population groups in the administrative data. Section 2 describes the methods underpinning the R-code hosted in GitHub and Section 3 describes the R-code with a running example of its outputs. We conclude in Section 4 with troubleshooting questions and answers.

2. Quality indicators

In the R-code on GitHub we focus on quality indicators to identify errors arising from coverage and representativeness of a single administrative data source. It is vital that statistical agencies have good quality indicators to ensure the fit of administrative data to the population and to identify those sub-groups that are missing or over-covered, especially when the administrative data contributes to an integrated dataset for multisource processing or to quality assure other data sources, such as surveys and censuses.

2.1 Distance Metrics

In this section we compare distributions obtained from the administrative data with external population auxiliary information, either obtained directly from a census or estimated from a large probability-based random survey.

Denote variable v having categories $h, h = 1, 2 \dots H$ in the administrative dataset having M individuals. Let $\Delta_{h,i}^{v}$ be the 0-1 indicator for individual i being a member of category h in variable v. We can then calculate the counts for category h : $m_h^v = \sum_{i=1}^{M} \Delta_{h,i}^{v}$ and note that $\sum_{h=1}^{H} m_h^v = M$. We can also obtain the probability distribution of variable v having category $h, h = 1, 2 \dots H$ and calculate: $p_h^v = \frac{m_h^v}{M}$. We note that the variable v can also represent a cross-tabulation of two or more variables, for example age group × sex.

Now assume we have equivalent estimates of these distributions from a census, or alternatively from a large probability-based random sample of size n where every individual i in the sample has an associated survey weight w_i . The survey weights typically are calibrated to known population benchmarks and hence sum to the known population size N. In this case, $n_h^v = \sum_{i=1}^{n} w_i \Delta_{h,i}^{v}$ and $\sum_{h=1}^{H} n_h^v = N$. Moreover, the equivalent distribution is $q_h^v = \frac{n_h^v}{N}$.

The entropy measures the uniformity of the probability distributions and hence can be compared when calculated on the administrative data distribution versus the population distribution. The formula for the entropy on the probability distribution $\{p_h^v, h = 1, \dots, H\}$ is: $-\sum_h p_h^v \, log(p_h^v)$ and similarly on the probability distribution $\{q_h^v, h = 1, \dots, H\}$.

We can now use a variety of distance metrics to assess deviations between the distributions $\{p_h^v, h = 1, \dots, H\}$ and $\{q_h^v, h = 1, \dots, H\}$. In this research, we assess three distance metrics: the Indicator of Dissimilarity (Duncan and Duncan, 1955), Hellinger's Distance (HL) and the Kullback-Leibler divergence (KL). The formula for the three distance metrics is given in Table 1.

Table 1: Distance metrics between the distribution calculated from the administrative data $\{p_h^v, h = 1, \dots, H\}$ and the distribution from the population $\{q_h^v, h = 1, \dots, H\}$ on variable v

Distance Metrics	Formula	Standarize
Indicator of Dissimilarity (ID)	$\frac{1}{2}\sum_h \lvert p_h - q_h \rvert$	1-ID
Hellinger's Distance (HL)	$\frac{1}{\sqrt{2}}\sqrt{\sum_h \left(\sqrt{p_h} - \sqrt{q_h}\right)^2}$	1-HL

Kullback-Leibler Divergence (KL)	$\sum_h p_k \, log\left(\frac{p_h}{q_h}\right)$	1-KL

There are subtle differences between these distance metrics. For example, Hellinger's Distance places more weight on the smaller proportions compared to the larger proportions whereas the Indicator of Dissimilarity treats all proportions equally. More work is needed on standardizing the distance metrics into meaningful quality measures. We have yet to determine which distance metric should be used and therefore propose to include all of them in the R-code. This will facilitate more empirical work for future recommendations.

2.2 R-indicators

The R-indicator and its related partial R-indicators were originally designed to assess the representativeness of responses from a survey and are particularly useful as an objective function in the optimization of adaptive survey designs (Schouten, et al. 2009, Schouten and Shlomo, 2017). The R-indicators measure the contrast between those who are missing and not missing in the data and identify those groups that are not represented in the data. Here, we develop the R-indicator and partial R-indicators to assess the representativeness and coverage of an administrative dataset compared to a target population. Recent research by Bianchi, et al. (2019) adapts the R-indicator to the case where only population-based auxiliary information are available instead of sample-based frame information. We draw upon this research and utilize population-based auxiliary information where the population auxiliary information is obtained by weighted survey counts from a large probability-based random sample.

To calculate the population-based R-indicator, denote the response indicator r_i equal to 1 for all units in the administrative dataset. We have information available on the values $\boldsymbol{x_i} = (x_{1,i}, x_{2,i}, \ldots, x_{K,i})^T$ of a vector of K auxiliary variables $\boldsymbol{X}$, for example, sex, age group, geographical region, ethnic minority group and employment status. Therefore, each $x_{k,i}$ is a binary indicator variable. We also assume that values of $\boldsymbol{x_i}$ are observed for all individuals in the administrative dataset so that $\{x_i; i \in r\}$ is observed.

Assume we know $\boldsymbol{x_i}$ at the aggregate level: the population total $\sum_U \boldsymbol{x_i}$ and population cross-products $\sum_U \boldsymbol{x_i}\,\boldsymbol{x_i^T}$. This information is known as the population–based auxiliary information. If this information is not available at the population level we can estimate the aggregates and cross-products using a large probability-based random sample, denoted s, where each individual i in the sample has a survey weight w_i. The estimated population-based auxiliary information is then: $\sum_s w_i \boldsymbol{x_i}$ and $\sum_s w_i \boldsymbol{x_i x_i^T}$. We also know the overall total in the population, denoted by N.

Response propensities are defined as the conditional expectation of the response indicator variable r_i given the values of specified variables: $\rho_i \equiv \rho_X(\boldsymbol{x_i})$. In the population-based setting

we model the response propensities under an identity link function where the true response propensities satisfy: $\rho_i = \boldsymbol{x_i^T \beta}$, $i \in U$. For the linear probability model, the estimate of ρ_i in the sample-based scenario is given by: $\hat{\rho}_i^{OLS} = \boldsymbol{x_i^T}(\sum_{s'} d_i \boldsymbol{x_i x_i^T})^{-1} \sum_{s'} d_i \boldsymbol{x_i} r_i$, $i \in s'$, where d_i is the design weight and s' denotes the sample under analysis.

In the case of population-based auxiliary information where we know both population totals and cross-products, we note that $\sum_{s'} d_i \boldsymbol{x_i}$ and $\sum_{s'} d_i \boldsymbol{x_i x_i^T}$ are unbiased estimates for $\sum_U \boldsymbol{x_i}$ and $\sum_U \boldsymbol{x_i x_i^T}$, respectively and that in large samples we may expect that $\sum_{s'} d_i \boldsymbol{x_i} \approx \sum_U \boldsymbol{x_i}$ and $\sum_{s'} d_i \boldsymbol{x_i x_i^T} \approx \sum_U \boldsymbol{x_i x_i^T}$. It follows that, in the population-based setting, we may approximate $\hat{\rho}_i^{OLS}$ by $\hat{\rho}_i^P = \boldsymbol{x_i^T}(\sum_U \boldsymbol{x_i x_i^T})^{-1} \sum_r d_i \boldsymbol{x_i}$, $i \in r$ and we refer to the propensities as 'participation' propensities. Note that $\hat{\rho}_i^P$ is computed only on the set of individuals in the administrative data. In addition, in our setting of assessing the representativeness in administrative data, the design weight d_i is the inverse of the coverage weight: $d_i = [M/N]^{-1}$ where M is the number of individuals in the administrative dataset.

In the population-based setting, an estimator for the R-indicator is given by $\hat{R}_{\hat{\rho}^P} = 1 - 2\hat{S}_{\hat{\rho}^P}$ where $\hat{S}^2_{\hat{\rho}^P} = \frac{N}{N-1}\{\frac{1}{N}\sum_r d_i \hat{\rho}_i^P - [\frac{1}{N}\sum_r d_i]^2\}$ and $\hat{\rho}_i^P$ is estimated as above. This estimator of the R-indicator makes the estimator $\hat{S}^2_\rho$ linear in $\hat{\rho}_i^P$ which provides an advantage for size bias adjustment computations (although given the large administrative datasets, a size bias adjustment is not needed). Furthermore, we use propensity weighting by $\hat{\rho}_i^{P^{-1}}$ to adjust for coverage bias. The R-indicator measures the variation of the sub-group participation propensities. If the participation propensities are all equal and there is no variation in sub-group participation, the R-indicator would obtain a value of 1.

The unconditional partial R-indicator measures the amount of variation of the participation propensities between the categories of a variable. The larger the between-category variation is, the stronger the relationship is and the stronger the impact of the variable on a lack of representativeness. As earlier, let $\boldsymbol{x_k}$ be one of the components of the vector $\boldsymbol{X}$. The variable $\boldsymbol{x_k}$ is categorical and assume it has H categories. Let m_h denote the weighted respondent size in category h in the administrative data, for $h = 1, 2, \ldots, H$. That means $m_h = \sum_{i \epsilon r} d_i \Delta_{h,i}$ where $\Delta_{h,i}$ is the 0-1 indicator for participating unit i being a member of category h and $\sum_{h=1}^H m_h = N$ given the definition of d_i as the inverse coverage weight. Define $\hat{\bar{\rho}}_h$ the average of the participation propensities in category h of $\boldsymbol{x_k}$ for the units in the administrative dataset and $\hat{\bar{\rho}}$ the overall average participation probability based on the estimated population-based participation propensities $\hat{\rho}_i^P$. The estimate for the unconditional partial R-indicator for variable $\boldsymbol{x_k}$ is: $R_U(\boldsymbol{x_k}) = \sqrt{\frac{1}{N}\sum_{h=1}^H m_h(\hat{\bar{\rho}}_h - \hat{\bar{\rho}})^2}$. The upper bound of the unconditional partial R-indicator is 0.5. The larger the value of the partial R-indicator, the stronger the association of the variable with a lack of representativeness in the administrative dataset. By computing and comparing the unconditional partial indicators for a set of variables it can be established for which variables the relationships are strongest. The unconditional partial R-indicator at the

category level h for variable $\boldsymbol{x_k}$ is $R_U(\boldsymbol{x_k^h}) = \sqrt{\frac{m_h}{N}}\,(\hat{\bar{\rho}}_h - \hat{\bar{\rho}})$ and can assume positive and negative values. Note that at the category-level, a negative sign represents under-representation and a plus sign represents over-representation.

Finally, we note that when producing estimates from the administrative dataset, one should weight each individual i by its inverse participation propensity: $\hat{\rho}_i^{P^{-1}}$ to adjust for coverage bias in the estimates.

The theory described here is when the administrative data is in the form of individual-level microdata. If the administrative data is very large, we can first aggregate it to a table spanned by the variables of interest (covariates) in the model prior to calculating the R-indicator and partial indicators. The description of the R-code for microdata-level administrative data is described in Section 3.5 and the description of the R-code for tabular-level administrative data in described in Section 3.6.

3. User Guide on the R-package

This package assumes that there is a Census file to obtain auxiliary population estimates and the administrative datasets under analysis. However, in real settings we would not have a Census microdata to work with, rather we would have a large probability-based survey sample for estimating population distributions. Therefore, we draw a random sample from the Census microdata to support this scenario and obtain auxiliary population totals from weighted sample counts.

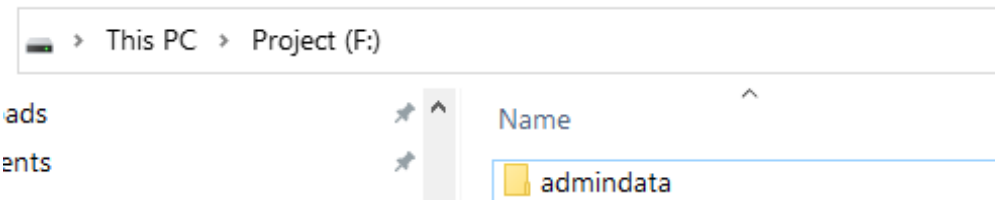
3.1 Download and inspect the contents

3.1.1 Download

Please visit the github site here: qualadmin link. Click on `Code` at the top-right corner. Then, click on `Download ZIP` to download to your local machine.

Now, the downloaded folder needs to be placed in the designated location. We recommend users decide the appropriate Drive (C, D, E, F, etc) to house the downloaded contents. Then, **create a new folder** called `admindata` in File Explorer of your PC. Users can customise the new folder name as appropriate. This is your **starting path**.

The screenshot showing **starting path**:



Under this Starting path, `F:/admindata`, place the downloaded folder from GitHub. Extract the zip folder as necessary.

As such, `F:/admindata/qualadmin` becomes the MASTER project folder. We'll set it as working directory[1] in RStudio later.

3.1.2 Downloaded contents explained

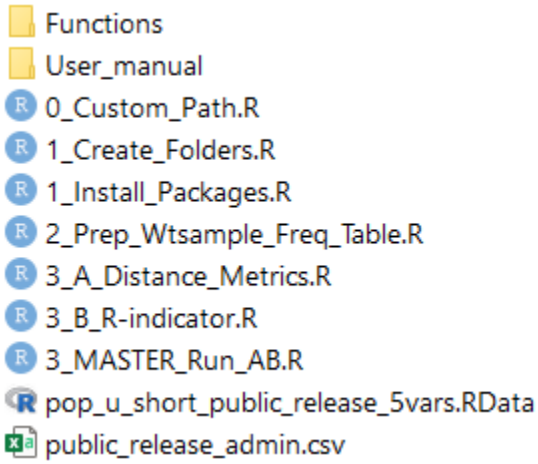
Example datasets

We provide two example data sources.

Data type	File name
Administrative	public_release_admin.csv
Census	pop_u_short_public_release_5vars.Rdata

Folders and R scripts

Under `F:\admindata\qualadmin` folder, you'll be presented with the following contents.



The **"User_manual"** folder contains instructions on using the provided R code files.

The users do not need to do anything with the folder titled **"Functions"**. These pre-defined functions are used to either enclose complex procedures or perform repetitive tasks including cleaning and computing quality indicators. There is no need to run this function file independently.

The functions will be automatically called in when the three main R script files are run:
`2_Prep_Wtsample_Freq_Table.R` `3_A_Distance_Metrics.R` `3_B_R-indicator.R`

[1] Notice that the terms, folder, directory, and path are used interchangeably in the user manual.

The `2_Prep_Wtsample_Freq_Table.R` file creates necessary data needed to compute distance metrics and R-indicators. The master file, `3_MASTER_Run_AB.R` runs the above *two* main R script files, (`3_A_Distance_Metrics.R` `3_B_R-indicator.R`) automatically in sequence.

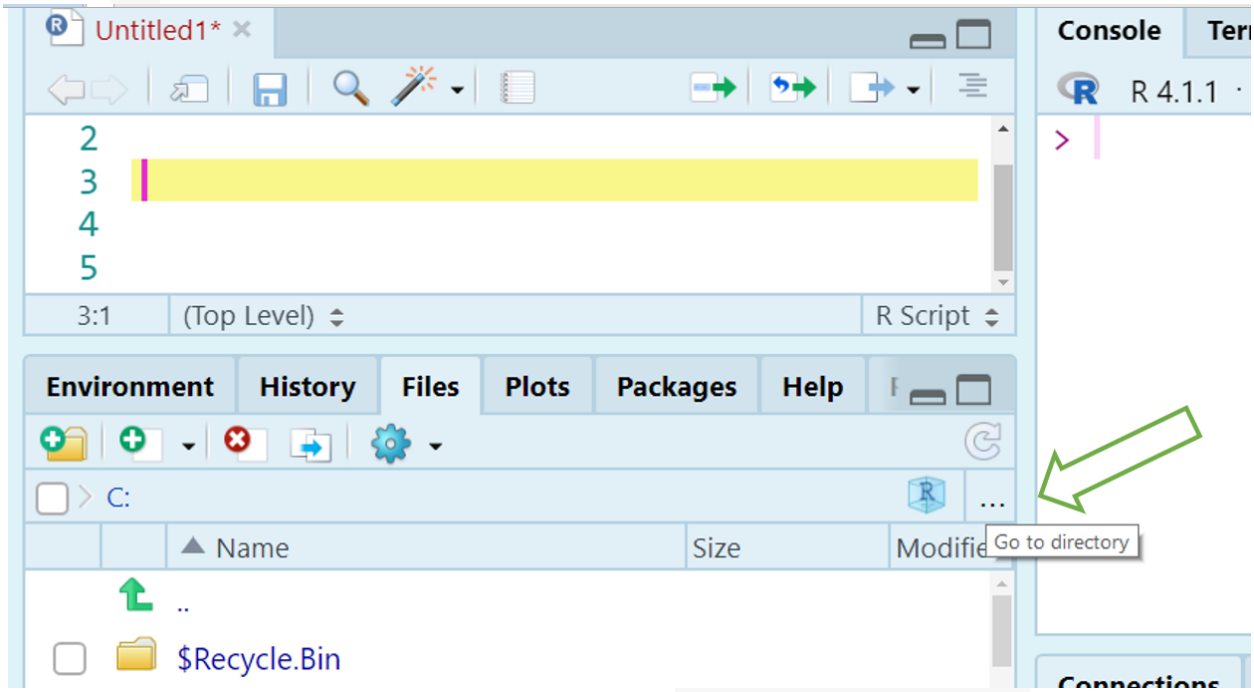
The first three files, `0_Custom_Path.R`, `1_Create_Folders.R` and `1_Install_Packages.R` can be run to get ready to run the above main analysis files, as discussed in the following section.

3.2 Launch RStudio and get ready

3.2.1 Open the entire master folder in RStudio

First, launch RStudio. Then, we need to **open the entire folder** `F:/admindata/qualadmin` where downloaded materials are located.

Unfortunately, RStudio has no feature in the menu, but you could do so by accessing **Files** tab. Click on `...` as shown below.



Then, locate the master folder. In our example, it is `F:/admindata/qualadmin`.

3.2.2 Set custom path

Click open the R script file, `0_Custom_Path.R`. Customise the starting path as needed, and set the path to indicate the master folder. The example code is:

```
# Starting path (CUSTOMISE PLEASE)
setwd("F:/admindata")

# Master project folder (USE AS IT IS)
setwd("./qualadmin")
```

```
    # Check your current directory
    getwd()
```

Please ensure to use a single forward slash `/` as above. R will print an error when backward slash `\` is used in path. For instance,

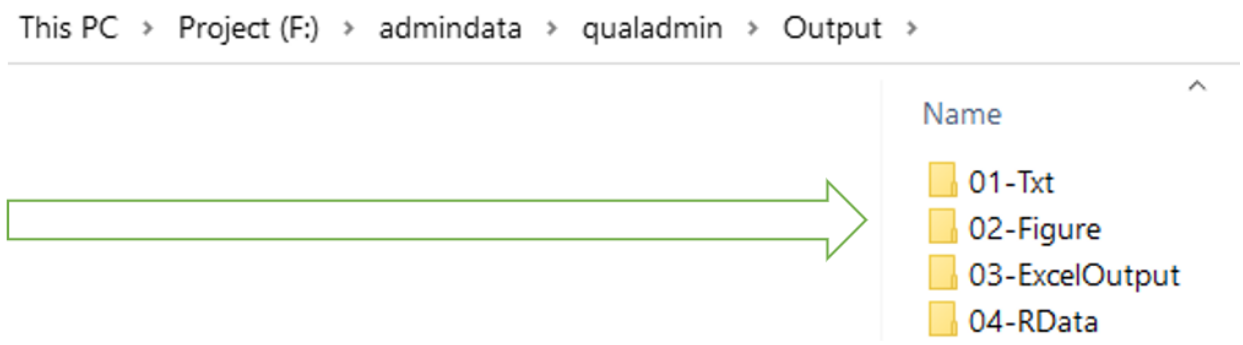
```
    setwd("F:\admindata)`
    Error: '\a' is an unrecognized escape in character string starting ""F:\a
"
```

> Please ensure your working directory is set at the master project path throughout the analytical steps.

3.2.3 Automatically create output folders

The three main R script files `2_Prep_Wtsample_Freq_Table.R`, `3_A_Distance_Metrics.R`, `3_B_R-indicator.R` produce outputs. The outputs may be text, figure or in spreadsheet form. For the existing programmes to work, users need to create dedicated output folders.

To do so, please click on the `1_Create_Folders.R` file to open. Then run the code line by line. The resulting folder structure is provided here:



3.2.4 Install packages

The final preparation step is installing packages. Open `1_Install_Packages.R` file, and run line by line.

```
        #---------------------------------
        # Install packages (Run once)
        #---------------------------------
        install.packages("tidyverse")
        install.packages("ggplot2")
        install.packages("fastDummies")
        install.packages("janitor")
```

Now, you're all set to proceed with quality measures indicators!

3.3 RUNNING 2_Prep_Wtsample_Freq_Table.R

This code file calculates the distributions of the weighted sample data. If the Census data or a weighted sample data are available, users consult 3.3.1 *Use the existing weighted sample data*. For a scenario where these data are unavailable, users can generate the data as shown in 3.3.2 *Generate a weighted sample data*.

Open the `2_Prep_Wtsample_Freq_Table.R` file.

The top of the code file concerns checking the current directory, reading in the pre-defined functions in the R environment and loading relevant R libraries.

```
getwd()

# Run the code file with functions.
source("Functions/1_Functions.R")

# Define output file folders, path
fn_output_folder_path()

# Disable scientific notation.
options(scipen = 999)

library("dplyr")     # data manipulation
library("ggplot2")   # visualisation
library("readr")     # read large csv file
library("readxl")    # read Excel file
library("writexl")   # export to Excel
library("janitor")   # cross-tabulation
```

3.3.1 Use the existing weighted sample data

- Step 1: Read in the data.

```
df  <- read_csv("custom_wtsample.csv")

dim(df)       # obs = 1163659 (example)
glimpse(df)   # Quick glance at the data
```

Users decide which variables are to be used for tabulation. For example, users may identify the following five variables.

```
names(df)     # variable names

[1] "geog1"     "sex"       "agecode1"  "eth_code5"
[5] "econg"
```

- Step 2: Declare variables to be tabulated. Here, we declare all five variables using `var` object[2]. Users can customize the variable names here. By running the code below, R automatically saves the total number of variables, 5 in a macro called `maxvar`.

```
var <- c("geog1", "sex", "agecode1",
         "eth_code5", "econg")
maxvar <- length(var)                # No need to customise
maxvar
[1] 5
```

- Step 3: Obtain frequency table of categorical variables (count of categories).

This procedure is to assess and calculate *the distribution* of categories in the weighted sample. Users can run the pre-defined function, `fn_maxvar5_freq_table()` to perform the task. The function automatically obtains counts and structure the output in long form, organised by each variable, and by its discrete category. In case of using four variables, users can use `fn_maxvar4_freq_table()` instead[3].

```
fn_maxvar5_freq_table()
```

- Step 4: Carry out checks to see if the calculated frequency tables are accurate.

```
freq_table[1:8, 1:9]

##   seq twdigits      n          p oneway v   by1  by2
## 1   1      101  113250 0.09732308      1 1 geog1  01
## 2   2      102  148400 0.12752976      1 1 geog1  02
## 3   3      103  137450 0.11811971      1 1 geog1  03
## 4   4      104  175100 0.15047480      1 1 geog1  04
## 5   5      105   92300 0.07931938      1 1 geog1  05
## 6   6      106  497150 0.42723327      1 1 geog1  06
## 7   7      201  565350 0.48584196      1 2   sex  01
## 8   8      202  598300 0.51415804      1 2   sex  02
```

When we printed the first 8 lines and 10 variables, we can see the count, `n`, and the corresponding proportion, `p` by each variable. The following code obtains the total observation size and confirms that the total proportion adds up to 1, for `geog1` variable. Here, the total observation size can be viewed as the population size.

```
# Check whether the total adds up to 1
sum(freq_table[1:6, "n"])
```

---

[2] As the `var` object is treated as a global macro, the programme runs automatically using the information stored in global macro, and produces the results. Users can save `var` in a separate RData file and load it in each session, instead of repeating the procedure.

[3] We do not provide functions for the maximum variable size beyond five. In such cases, users can create their own functions by consulting the provided functions.

```
## [1] 1163650
```

```
        sum(freq_table[1:6, "p"])
```

```
## [1] 1
```

- Step 5: Rename and save.
- Step 6: Export the output frequency table in Excel with the file name, **Weightedsample_freq_table.xlsx**.
- Step 7: Save the R objects as RData. Done.

3.3.2 Generate a weighted sample data

- Step 1: Load a Census microdata. It is called `pop_u_short_public_release_5vars` in the provided example code.

```
        #H---------------------------------------
        ##> 1. Load Census data
        #H---------------------------------------

        load("pop_u_short_public_release_5vars.RData")
        df  <- pop_u_short_public_release_5vars
        dim(df)   # obs = 1163659
        names(df)
```

In our example Census data, we have 1,163,659 observations with five categorical variables including `geography`, `sex`, `age groups`, `ethnic groups`, and `economic activity status`. One can declare which variable to tabulate. Here, we declare all five variables using `var` object[4].

```
  var <- c("geog1", "sex", "agecode1",
           "eth_code5", "econg")
```

The description of categories, and distribution is shown below.

Variable	Category	Description	N	(%)
Total			1163659	
geog1	1	LA codes	116128	(10.0)
	2	LA codes	150139	(12.9)
	3	LA codes	137520	(11.8)
	4	LA codes	170624	(14.7)
	5	LA codes	90873	(7.8)
	6	LA codes	498375	(42.8)

[4] As the `var` object is treated as global macro, the programme runs automatically using the information stored in global macro, and produces the results.

Variable	Category	Description	N	(%)
sex	1	male	564905	(48.5)
	2	female	598754	(51.5)
agecode1	1	16-20	82426	(7.1)
	2	21-25	94643	(8.1)
	3	26-30	110296	(9.5)
	4	31-35	120398	(10.3)
	5	36-40	119393	(10.3)
	6	14-45	101711	(8.7)
	7	46-50	94209	(8.1)
	8	51-55	100159	(8.6)
	9	56-60	77799	(6.7)
	10	61-65	65833	(5.7)
	11	66-70	57305	(4.9)
	12	71-75	51263	(4.4)
	13	76-80	43678	(3.8)
	14	81+	44546	(3.8)
eth_code5	1	White	1081812	(93.0)
	2	Mixed/Multiple ethnic groups	10487	(0.9)
	3	Asian/Asian British	46446	(4.0)
	3	Black/African/Caribbean/Black British	16268	(1.4)
	4	Other ethnic group	8646	(0.7)
econg	1	In employment(FT, PT)	689140	(59.2)
	2	Unemployed	27744	(2.4)
	3	Out of workforce	446775	(38.4)

Using this prior information on the population distribution (based on the Census), we can mimic the distribution in a random sample. See the next step.

- Step 2: Then, we draw a random sample 1:50.
- Step 3: From the randomly selected sample (`1163659/50 = 23273`), we then obtain frequency table of categorical variables (count of categories). Users can run the pre-defined function, `fn_maxvar5_freq_table()` to perform the task. The function[5] automatically obtains counts and structure the output in long form, organised by each variable, and by its discrete category.

[5] We also provide `fn_maxvar4_freq_table()` for users who declare four categorical variables. We do not provide functions for the maximum variable size beyond five. In such cases, users can create their own functions by consulting the provided functions.

```
        fn_maxvar5_freq_table()
```

This procedure is to assess and calculate *the distribution* of categories in a random sample (N = 23273). Based on the counts of the randomly selected sample, we multiply the counts by 50. One may wonder why we multiply. As we *reduced* the census sample by drawing a random sample by the 1:50 ratio, we need to *convert* the shrank sample back to the original size (with the priori distribution). This explains why we multiply by 50 (Weighted Sample N = 23273 * 50 = 1163650). This completes the process of generating weighted sample survey data.

- Step 4: Carry out checks to see if the calculated frequency tables are accurate.

```
        freq_table[1:8, 1:9]
```

```
##   seq twdigits raw_n      n          p oneway v   by1 by2
## 1   1      101  2265 113250 0.09732308      1 1 geog1  01
## 2   2      102  2968 148400 0.12752976      1 1 geog1  02
## 3   3      103  2749 137450 0.11811971      1 1 geog1  03
## 4   4      104  3502 175100 0.15047480      1 1 geog1  04
## 5   5      105  1846  92300 0.07931938      1 1 geog1  05
## 6   6      106  9943 497150 0.42723327      1 1 geog1  06
## 7   7      201 11307 565350 0.48584196      1 2   sex  01
## 8   8      202 11966 598300 0.51415804      1 2   sex  02
```

When we printed the first 8 lines and 9 variables, we can see the count, `n`, and the corresponding proportion, `p` by each variable. The following code obtains the total observation size and confirms that the total proportion adds up to 1, for `geog1` variable. Here, the total observation size can be viewed as the population size.

```
        # Check whether the total adds up to 1
        sum(freq_table[1:6, "n"])
```

```
## [1] 1163650
```

```
        sum(freq_table[1:6, "p"])
```

```
## [1] 1
```

- Step 5: Rename and save.
- Step 6: Export the output frequency table in Excel with the file name, **Weightedsample_freq_table.xlsx**.
- Step 7: Save the R objects as RData. Done.

3.4 RUNNING 3A_Distance_Metrics.R

To calculate distance metrics, we first obtain one-way, and two-way frequency tables of categorical variables, and calculates proportions of each sub-category by each data source.

Previously, we dealt with frequency tables for the weighted sample data. Here, we calculate distributions of administrative data. Next, we combine master (benchmark) and admin freq tables. Then, we create domains for quality indicators, and finally compute distance metrics as part of quality indicators. We offer three different types of distance metrics. To allow comparison across the metrics, we standardise the calculations.

Users can also produce a summary table of three types of distance metrics, and visualise the results.

The preliminary step is to ensure we have benchmark data. Simply *source* the previous file as below to update it.

```
        source("2_Prep_Wtsample_Freq_Table.R")
```

Step 1: Read admin data

```
        df  <- read_csv("public_release_admin.csv")
```

```
## Rows: 1033664 Columns: 6
## -- Column specification --------------------------------------------------
------
## Delimiter: ","
## dbl (6): person_id, geog1, sex, agecode1, eth_code5, econg
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this m
essage.
```

```
        tail(df)
```

```
## # A tibble: 6 x 6
##   person_id geog1   sex agecode1 eth_code5 econg
##       <dbl>  <dbl> <dbl>    <dbl>     <dbl> <dbl>
## 1   1033659      1     1        6         1     1
## 2   1033660      6     1        6         1     1
## 3   1033661      6     2        5         1     1
## 4   1033662      5     1       12         1     3
## 5   1033663      1     2        9         1     1
## 6   1033664      6     2        9         1     1
```

The last six observations of the example admin data are shown above. As the person id goes up to 1033664, we can see there are `1033664` observations in admin data. As such, we declare all five variables for tabulations. If variables are already defined using `var`, users can skip this part.

```
  var <- c("geog1", "sex", "agecode1",
           "eth_code5", "econg")
```

Step 2: Obtain admin freq tables.

As mentioned in the previous section, we obtain frequency table of categorical variables (count of categories). Users can run the pre-defined function, `fn_maxvar5_freq_table()` to perform

the task. The function[6] automatically obtains counts and structure the output in long form, organised by each variable, and by its discrete category.

Once the frequency tables are obtained, we rename the object as `Admin_f_table_one`. Let's inspect `Admin_f_table_one`.

```
        head(Admin_f_table_one)
```

```
##   seq twdigits admin_n admin_perc oneway v   by1 by2    by3 by4 by5
## 1   1      101  137993  0.1334989      1 1 geog1  01 oneway   0   0
## 2   2      102  124051  0.1200110      1 1 geog1  02 oneway   0   0
## 3   3      103  131176  0.1269039      1 1 geog1  03 oneway   0   0
## 4   4      104  139867  0.1353119      1 1 geog1  04 oneway   0   0
## 5   5      105  142304  0.1376695      1 1 geog1  05 oneway   0   0
## 6   6      106  358273  0.3466049      1 1 geog1  06 oneway   0   0
```

```
       tail(Admin_f_table_one)
```

```
##     seq twdigits admin_n   admin_perc oneway v       by1 by2   by3 by4 by5
## 340 340   404501    8557 0.0082783187      2 4 eth_code5  04 econg   5  01
## 341 341   404502     791 0.0007652390      2 4 eth_code5  04 econg   5  02
## 342 342   404503    5007 0.0048439338      2 4 eth_code5  04 econg   5  03
## 343 343   405501    3867 0.0037410609      2 4 eth_code5  05 econg   5  01
## 344 344   405502     255 0.0002466953      2 4 eth_code5  05 econg   5  02
## 345 345   405503    3420 0.0033086187      2 4 eth_code5  05 econg   5  03
```

Step 3: Merge admin + Weighted sample freq tables

The next step is to merge two data sources and save as `freq_table2`.

```
freq_table2 <- full_join(Weightedsample_freq_table,
                  Admin_f_table_one)
```

Step 4: Compute distance metrics

Run the functions to compute three types of distance metrics.

```
        fn_distance_metrics ()
```

Step 5: Reshape for plotting

From wide form, the outputs have been reshaped to long form. Then, we keep standardised solutions. The results are as follows:

```
      fn_distance_metrics_long ()
```

[6] We also provide `fn_maxvar4_freq_table()` for users who wish to declare four categorical variables.

```
## # A tibble: 9 x 5
##   domain_id domain   indicator  index           ref
##       <int> <chr>    <chr>      <dbl>          <fct>
## 1         1 geog1    Std_Duncan 0.897           1
## 2         1 geog1    Std_HD     0.911           2
## 3         1 geog1    Std_KL     0.957           3
## 4         2 sex      Std_Duncan 0.987           1
## 5         2 sex      Std_HD     0.991           2
## 6         2 sex      Std_KL     1.00            3
## 7         3 agecode1 Std_Duncan 0.946           1
## 8         3 agecode1 Std_HD     0.953           2
## 9         3 agecode1 Std_KL     0.987           3
```

Step 8: Visualise the distance metrics

```
plot(p)
```

3.5 RUNNING 3B_R-indicator.R

This procedure computes the overall R-indicator and partial indicators when the underlying administrative data is individual-level microdata. For very large datasets, it is possible to calculate the R-indicator and partial indicators from a table aggregated to the level of the covariates (variables of interest) in the model. This procedure is described in Section 3.6.

Users can also proceed with computing *partial* R-indicators by category level, and variable level. The procedure can be computationally extensive. This is noted in the relevant section, so that users can allow some time to execute the code.

On this example, we will prepare the sample and population distributions and calculate an R-indicator for 5 variables: geog1 (6), sex (2), agecode1 (14) and eth_cod5 (5) and econg (3).

As part of administrative data preparation, each of the variables should have their categories numbered 1,2,3…. We will use these numbers instead of the original names of the categories because it will enable us to do loops through the data. This is to facilitate building design matrix using dummy variables.

Along with administrative data, we also need benchmark data from Census. Assuming users have no access to Census data, we replace Census with weighted sample counts. The auxiliary data file contains these weighted sample counts.

As such, we will read in both administrative and auxiliary data files separately and compute R-indicators using matrix syntax in R. Due to the complexity of the procedure, we provide defined functions that users can execute with ease in practice. Users can consult `Functions/1_Functions.R` file for more details on the algorithm and operationalisation.

Step 1: Prepare an Auxiliary data file

From the frequency table generated by using the weighted sample, we will prepare an ***auxiliary data file*** to be used for R-indicator computation procedures. This auxiliary file is used as the benchmark. In essence, the auxiliary data file is a summary of the distributions, containing the population proportions of each category from the defined variables in row vectors. Please note that the population proportions concerning the last categories are to be removed.

Obtain the population size and population proportions

From the previous steps, we identified the population size of 1,116,350 (`popsize` = 1163650) from the weighted sample. For R-indicator calculations, along with the total population size, we also need to compute the *population proportions*, `meanpop`, by variables which are `geography`, `sex`, `age groups`, `ethnic groups`, and `economic activity status`. Users can simply run the function, `fn_meanpop_auxiliary()` to achieve this goal.

```
load(file = "Output/04-RData/Weightedsample_freq_table.RData")

fn_meanpop_auxiliary()
```

Exerpts of the function is provided below to aid readers' understanding.

```
# Compute meanpop
auxiliary  <- freq_table %>%
          filter(oneway == 1) %>%
          group_by(by1) %>%
          mutate(meanpop = n / popsize) %>%
          ungroup()  %>%
```

```
                    dplyr::select(seq, count = n, by1,
                     v, by2, meanpop, raw_n)
```

We first remove two-way and keep the one-way frequency table only. Then, by variable-level (indicated by the variable, `by1)`, we compute `meanpop`. As seen before, the count of each category is stored in `n`. The `meanpop` is obtained by dividing `n` by `popsize`. For example, the value of **meanpop** for first category of `geog1` is calculated as `113250/1163650 = 0.0973`, and the second category of `geog1` is `148400/1163650 = 0.1275` and so on.

Let's look at the intermediate properties of auxiliary data. We can see the count and proportion of each variable (`by1`) and the sub-category (`by2`) for five variables. The population size is indicated as `1163560` (shown in the first row, under `count` column).

```
        print(auxiliary)
```

```
##    seq   count       by1 v by2     meanpop raw_n     type
## 1    1 1163650     total 0  00 1.000000000     0 wtsample
## 2    2  113250     geog1 1  01 0.097323078  2265 wtsample
## 3    3  148400     geog1 1  02 0.127529756  2968 wtsample
## 4    4  137450     geog1 1  03 0.118119710  2749 wtsample
## 5    5  175100     geog1 1  04 0.150474799  3502 wtsample
## 6    6   92300     geog1 1  05 0.079319383  1846 wtsample
## 7    7  497150     geog1 1  06 0.427233275  9943 wtsample
## 8    8  565350       sex 2  01 0.485841963 11307 wtsample
## 9    9  598300       sex 2  02 0.514158037 11966 wtsample
## 10  10   84600  agecode1 3  01 0.072702273  1692 wtsample
## 11  11   93300  agecode1 3  02 0.080178748  1866 wtsample
## 12  12  111200  agecode1 3  03 0.095561380  2224 wtsample
## 13  13  124250  agecode1 3  04 0.106776092  2485 wtsample
## 14  14  118200  agecode1 3  05 0.101576935  2364 wtsample
## 15  15   99950  agecode1 3  06 0.085893525  1999 wtsample
## 16  16   95800  agecode1 3  07 0.082327160  1916 wtsample
## 17  17   95600  agecode1 3  08 0.082155287  1912 wtsample
## 18  18   78450  agecode1 3  09 0.067417179  1569 wtsample
## 19  19   67600  agecode1 3  10 0.058093069  1352 wtsample
## 20  20   57950  agecode1 3  11 0.049800198  1159 wtsample
## 21  21   50650  agecode1 3  12 0.043526834  1013 wtsample
## 22  22   42250  agecode1 3  13 0.036308168   845 wtsample
## 23  23   43850  agecode1 3  14 0.037683152   877 wtsample
## 24  24 1083250 eth_code5 4  01 0.930907060 21665 wtsample
## 25  25   10450 eth_code5 4  02 0.008980364   209 wtsample
## 26  26   45600 eth_code5 4  03 0.039187041   912 wtsample
## 27  27   16300 eth_code5 4  04 0.014007648   326 wtsample
## 28  28    8050 eth_code5 4  05 0.006917888   161 wtsample
## 29  29  691300     econg 5  01 0.594078976 13826 wtsample
## 30  30   28250     econg 5  02 0.024277059   565 wtsample
## 31  31  444100     econg 5  03 0.381643965  8882 wtsample
```

Now, we prepare the data to build design matrix using dummy variables. To do so, from the total number of categories for each variable, we need to remove the **last** category of each

categorical variable (`group_by(by1)`). The last category is defined by `max(by2)` and removed accordingly. The first row (`seq == 1`) is not subject to this procedure and kept in the data. As shown in the code below, we keep rows if `lastcat == 0`, while filtering out cases which are the last category. We then drop the indicator for the last category (`dplyr::select(-c(lastcat_, lastcat))`). Here, we explicitly instruct R to use `dplyr` package to access `select` function[7].

```
        col_auxiliary <- auxiliary %>%
             group_by(by1) %>%
             mutate(
              lastcat_ = ifelse(by2 == max(by2), 1, 0),
              lastcat = ifelse(seq == 1, 0, lastcat_)
             ) %>%
             filter(lastcat == 0) %>%
             dplyr::select(-c(lastcat_, lastcat)) %>%
             ungroup()
```

Notice that from 5 variables, geog1 (6), sex (2), agecode1 (14) and eth_cod5 (5) and econg (3), we now have 1+(nvar-1) for each variable so here it is 1+5+1+13+4+3=26 rows. We create a macro, `numcat` to store this information on the total row.

```
nrow(col_auxiliary)

## [1] 26

numcat <- nrow(col_auxiliary)
numcat

## [1] 26
```

To inspect the setup on dummy variables (to be created later), let's produce a cross-tabulation by `by1` and `by2`.

```
  dummychk <- col_auxiliary
  dummychk %>% tabyl(by1, by2)

            00 01 02 03 04 05 06 07 08 09 10 11 12 13
  agecode1   0  1  1  1  1  1  1  1  1  1  1  1  1  1
  econg      0  1  1  0  0  0  0  0  0  0  0  0  0  0
  eth_code5  0  1  1  1  1  0  0  0  0  0  0  0  0  0
  geog1      0  1  1  1  1  1  0  0  0  0  0  0  0  0
  sex        0  1  0  0  0  0  0  0  0  0  0  0  0  0
  total      1  0  0  0  0  0  0  0  0  0  0  0  0  0
```

[7] This is to avoid warning messages from R when R searches for a particular function from two competing packages.

All look good. At this stage, we keep `meanpop` only, dropping other columns, and print `meanpop` in a single column (column vector). This column will be transposed before we save it as row vectors. Before reshaping the data, we carefully inspect the values of `meanpop`.

```
        # Print the column vector, meanpop
        print(col_auxiliary)
```

```
## # A tibble: 26 x 1
##    meanpop
##      <dbl>
##  1 1
##  2 0.0973
##  3 0.128
##  4 0.118
##  5 0.150
##  6 0.0793
##  7 0.486
##  8 0.0727
##  9 0.0802
## 10 0.0956
## 11 0.107
## 12 0.102
## 13 0.0859
## 14 0.0823
## 15 0.0822
## 16 0.0674
## 17 0.0581
## 18 0.0498
## 19 0.0435
## 20 0.0363
## 21 0.931
## 22 0.00898
## 23 0.0392
## 24 0.0140
## 25 0.594
## 26 0.0243
```

Reshape and save benchmark data as row vectors

We use `t(col_auxiliary)` to transpose and tidy the reshaped data. We then generate `ttt` as an indicator of benchmark data. We use this indicator for merging with the administrative data later. Finally, save the data as `popmean_row_vector`.

```
# Transpose to arrange in row vector format.
  temp <- t(col_auxiliary)
  temp <- as.data.frame(temp)
  row.names(temp) <- 1:nrow(temp)

# generate merge id, ttt.
  temp$ttt  <- 0
```

```
# Rename variables "popmean1- popmean26"
  names(temp) <- c(paste0("popmean", 1:numcat), "ttt")

# SAVE
  popmean_row_vector <- temp
```

Let's see the row vector names, "popmean1- popmean26" and `ttt`.

```
  names(popmean_row_vector)
```

```
##  [1] "popmean1"  "popmean2"  "popmean3"  "popmean4"  "popmean5"  "popmean6"
##  [7] "popmean7"  "popmean8"  "popmean9"  "popmean10" "popmean11" "popmean12"
## [13] "popmean13" "popmean14" "popmean15" "popmean16" "popmean17" "popmean18"
## [19] "popmean19" "popmean20" "popmean21" "popmean22" "popmean23" "popmean24"
## [25] "popmean25" "popmean26" "ttt"
```

```
    popmean_row_vector[, 1:5]
```

```
##   popmean1   popmean2  popmean3  popmean4  popmean5
## 1        1 0.09732308 0.1275298 0.1181197 0.1504748
```

Now, our benchmark data preparation is complete.

Step 2: Prepare the administrative data

Open the administrative data and keep only variables of interest. Notice the sample size is 1,033,664. Rename variables to be consistent with the weighted sample data and sort as necessary. *Please note that sorting is not required.* The programme will detect the number of variables, and categories automatically.

```
aa  <- read_csv("public_release_admin.csv")

nrow(aa) # 1033664
## [1] 1033664

# rename, keep variables of interest and sort
aa <- aa %>%
 dplyr::select(-person_id) %>%
 arrange(geog1, sex, agecode1, eth_code5, econg)

head(aa)
##   geog1  sex agecode1 eth_code5 econg
## 1 <dbl> <dbl> <dbl>    <dbl>   <dbl>
## 2    1   1        1         1     1
## 3    1   1        1         1     1
## 4    1   1        1         1     1
## 5    1   1        1         1     1
## 6    1   1        1         1     1
```

Step 3: Compute R-indicator

Once steps 1 and 2 are completed, we are set to carry out computing the R-indicator. These procedures are automated via pre-defined functions using complex matrix and data management syntax.

By running the single function below, users can produce estimates of overall and partial R indicators. Please note that some procedures can be computationally intensive.

```
fn_RUN_R_indicator()
```

Once the function is executed, users can proceed with the next steps 4 and 5 to export the output.

The function, `fn_RUN_R_indicator()`, consists of multiple sub-functions. Note that we have eight sub-functions that permit us to compute overall R-indicators, along with additional functions for obtaining partial R-indicators.

```
fn_design_matrix()
fn_freq()
fn_respmean()
fn_des_pop_respmean()
fn_gh()
fn_R_indicator()
fn_rindicatorall()
fn_partial()
```

Each function will perform a particular task and generate intermediate properties stored in objects including `design_matrix`, `respmean`, `des_pop_respmean`, `gh`, `R_indicator` and , `rindicatorall` as indicated in the function name. The final output, partial R-indicators, can be found in the data object, `partial`.

Let's go over one function at a time.

fn_design_matrix()

The utility of `fn_design_matrix()` is to build design matrix. Starting with ensuring that the admin data only contains the declared variables and factorise them, the function defines macro variables, `resppop` and `rrate` using the data object, `aa`. To prepare for design matrix, the code creates dummy variables, using **fastDummies** R library package. Once all dummy variables generated, we need to remove the last category. As such, the function detects the categories of each variable and drops the last category.

Let's see the `design_matrix` object, which contains the original variables, and the design matrix with weights. The last few columns are printed below. As des1 denotes intercept, all values of des1 is set at 1. As the first six observations show geog1 = 1, the dummy column *geog1_1* is initially created internally (not shown) before being renamed as `des2`. Then, the next gego1 dummy column, *geog1_2* (where, geog1 = 2) is generated, which will subsequently be named as `des3`. Since the first six rows are geog1 = 1, the values of columns from `des3` to

`des6` (geog1 = 2, geog1 = 3, geog1 = 4, geog1 = 5, respectively) become 0. We also notice that the dummy for the last geog1 category, *geog1_6* (geog1 = 6), is omitted. As such, the next column, `des7` concerns *sex_1* (where sex = 1) while `des8` denotes *agecode1_1* (agecode1=1).

```
   head(design_matrix)
```

```
##   geog1 sex agecode1 eth_code5 econg des1 des2 des3 des4 des5 des6 des7 des8
## 1     1   1        1         1     1    1    1    0    0    0    0    1    1
## 2     1   1        1         1     1    1    1    0    0    0    0    1    1
## 3     1   1        1         1     1    1    1    0    0    0    0    1    1
## 4     1   1        1         1     1    1    1    0    0    0    0    1    1
## 5     1   1        1         1     1    1    1    0    0    0    0    1    1
## 6     1   1        1         1     1    1    1    0    0    0    0    1    1
##   des9 des10 des11 des12 des13 des14 des15 des16 des17 des18 des19 des20 des21
## 1    0     0     0     0     0     0     0     0     0     0     0     0     1
## 2    0     0     0     0     0     0     0     0     0     0     0     0     1
## 3    0     0     0     0     0     0     0     0     0     0     0     0     1
## 4    0     0     0     0     0     0     0     0     0     0     0     0     1
## 5    0     0     0     0     0     0     0     0     0     0     0     0     1
## 6    0     0     0     0     0     0     0     0     0     0     0     0     1
##   des22 des23 des24 des25 des26 finalwgt piinv ttt
## 1     0     0     0     1     0 1.125753     1   0
## 2     0     0     0     1     0 1.125753     1   0
## 3     0     0     0     1     0 1.125753     1   0
## 4     0     0     0     1     0 1.125753     1   0
## 5     0     0     0     1     0 1.125753     1   0
## 6     0     0     0     1     0 1.125753     1   0
```

The weights are calculated by the inverse of *rrate* (`finalwgt = 1/rrate`). The column, `ttt`, is to be used as a merging id.

fn_freq()

We then prepare a data object, `freq`, to hold the summary of the admin data. It will be merged with the R-indicator summary.

```
   print(freq, n =  nrow(freq))
```

```
## # A tibble: 31 × 5
##     count domain_     n_cat domain_n cum_count
##     <dbl> <chr>       <chr>    <dbl>     <dbl>
##  1      0 des1        1            0         0
##  2 137993 geog1_1     1            1   1033664
##  3 124051 geog1_2     2            1   1033664
##  4 131176 geog1_3     3            1   1033664
##  5 139867 geog1_4     4            1   1033664
##  6 142304 geog1_5     5            1   1033664
##  7 358273 geog1_6     6            1   1033664
##  8 489228 sex_1       1            2   1033664
```

```
##  9 544436 sex_2       2            2   1033664
## 10  55659 agecode1_1  1            3   1033664
## 11  64496 agecode1_2  2            3   1033664
## 12  81222 agecode1_3  3            3   1033664
## 13 113740 agecode1_4  4            3   1033664
## 14 112863 agecode1_5  5            3   1033664
## 15  96444 agecode1_6  6            3   1033664
## 16  89764 agecode1_7  7            3   1033664
## 17  95381 agecode1_8  8            3   1033664
## 18  73902 agecode1_9  9            3   1033664
## 19  62717 agecode1_10 10           3   1033664
## 20  54730 agecode1_11 11           3   1033664
## 21  48803 agecode1_12 12           3   1033664
## 22  41664 agecode1_13 13           3   1033664
## 23  42279 agecode1_14 14           3   1033664
## 24 962692 eth_code5_1 1            4   1033664
## 25   8928 eth_code5_2 2            4   1033664
## 26  40147 eth_code5_3 3            4   1033664
## 27  14355 eth_code5_4 4            4   1033664
## 28   7542 eth_code5_5 5            4   1033664
## 29 609471 econg_1     1            5   1033664
## 30  23289 econg_2     2            5   1033664
## 31 400904 econg_3     3            5   1033664
```

fn_respmean() : admin data distributions as row vectors

The `fn_respmean()` prepares the distributions of the administrative data. Using the data object, `design_matrix`, we obtain the proportions based on weighted sample counts. and produces a row vector called *respmean*. For example, the proportion of geog1_1 is stored at des2. The des3 column is for geog1_2 and so on. The intermediate output is shown below.

```
   print(respmean_column)
```

```
##       respmn_list
## des2  0.133498045
## des3  0.120010312
## des4  0.126903278
## des5  0.135311305
## des6  0.137669402
## des7  0.473294375
## des8  0.053846088
## des9  0.062395050
## des10 0.078576032
## des11 0.110035664
## des12 0.109186611
## des13 0.093302969
## des14 0.086840545
## des15 0.092274309
```

```
## des16 0.071494865
## des17 0.060673742
## des18 0.052947192
## des19 0.047213509
## des20 0.040306793
## des21 0.931339320
## des22 0.008636618
## des23 0.038838998
## des24 0.013887337
## des25 0.589621450
## des26 0.022529970
```

Once we obtain the respmean in a column, we transpose and save respmean as row vectors.

fn_des_pop_respmean()

This function allows us to combine design matrix, popmean and respmean vectors in a single dataset.

First, merging the corresponding `popmean_row_vector` from the benchmark data we prepared at the step 1 earlier, we combine both mean vectors from the two data sources. The combined mean vectors are stored at the `pop_respmean` data object. We then combine the *design matrix* with the `pop_respmean` and store the data at `des_pop_respmean`.

```
   head(des_pop_respmean, n = 3)
```

```
##   geog1 sex agecode1 eth_code5 econg des1 des2 des3 des4 des5 des6 des7 des8
## 1     1   1        1         1     1    1    1    0    0    0    0    1    1
## 2     1   1        1         1     1    1    1    0    0    0    0    1    1
## 3     1   1        1         1     1    1    1    0    0    0    0    1    1
##   des9 des10 des11 des12 des13 des14 des15 des16 des17 des18 des19 des20 des21
## 1    0     0     0     0     0     0     0     0     0     0     0     0     1
## 2    0     0     0     0     0     0     0     0     0     0     0     0     1
## 3    0     0     0     0     0     0     0     0     0     0     0     0     1
##   des22 des23 des24 des25 des26 finalwgt piinv popmean1   popmean2  popmean3
## 1     0     0     0     1     0 1.125753     1        1 0.09732308 0.1275298
## 2     0     0     0     1     0 1.125753     1        1 0.09732308 0.1275298
## 3     0     0     0     1     0 1.125753     1        1 0.09732308 0.1275298
##    popmean4  popmean5   popmean6 popmean7   popmean8   popmean9  popmean10
## 1 0.1181197 0.1504748 0.07931938 0.485842 0.07270227 0.08017875 0.09556138
## 2 0.1181197 0.1504748 0.07931938 0.485842 0.07270227 0.08017875 0.09556138
## 3 0.1181197 0.1504748 0.07931938 0.485842 0.07270227 0.08017875 0.09556138
##   popmean11 popmean12  popmean13  popmean14  popmean15  popmean16  popmean17
## 1 0.1067761 0.1015769 0.08589352 0.08232716 0.08215529 0.06741718 0.05809307
## 2 0.1067761 0.1015769 0.08589352 0.08232716 0.08215529 0.06741718 0.05809307
## 3 0.1067761 0.1015769 0.08589352 0.08232716 0.08215529 0.06741718 0.05809307
##   popmean18  popmean19  popmean20 popmean21   popmean22  popmean23  popmean24
## 1 0.0498002 0.04352683 0.03630817 0.9309071 0.008980364 0.03918704 0.01400765
## 2 0.0498002 0.04352683 0.03630817 0.9309071 0.008980364 0.03918704 0.01400765
```

```
## 3 0.0498002 0.04352683 0.03630817 0.9309071 0.008980364 0.03918704 0.01400765
##   popmean25  popmean26 respmean1 respmean2 respmean3 respmean4 respmean5
## 1  0.594079 0.02427706         1  0.133498 0.1200103 0.1269033 0.1353113
## 2  0.594079 0.02427706         1  0.133498 0.1200103 0.1269033 0.1353113
## 3  0.594079 0.02427706         1  0.133498 0.1200103 0.1269033 0.1353113
##   respmean6 respmean7  respmean8  respmean9 respmean10 respmean11 respmean12
## 1 0.1376694 0.4732944 0.05384609 0.06239505 0.07857603  0.1100357  0.1091866
## 2 0.1376694 0.4732944 0.05384609 0.06239505 0.07857603  0.1100357  0.1091866
## 3 0.1376694 0.4732944 0.05384609 0.06239505 0.07857603  0.1100357  0.1091866
##   respmean13 respmean14 respmean15 respmean16 respmean17 respmean18 respmean19
## 1 0.09330297 0.08684054 0.09227431 0.07149487 0.06067374 0.05294719 0.04721351
## 2 0.09330297 0.08684054 0.09227431 0.07149487 0.06067374 0.05294719 0.04721351
## 3 0.09330297 0.08684054 0.09227431 0.07149487 0.06067374 0.05294719 0.04721351
##   respmean20 respmean21  respmean22 respmean23 respmean24 respmean25 respmean26
## 1 0.04030679  0.9313393 0.008636618   0.038839 0.01388734  0.5896214 0.02252997
## 2 0.04030679  0.9313393 0.008636618   0.038839 0.01388734  0.5896214 0.02252997
## 3 0.04030679  0.9313393 0.008636618   0.038839 0.01388734  0.5896214 0.02252997
##   seq responsesamp1
## 1   1             1
## 2   2             1
## 3   3             1
```

fn_gh()

Once the combined dataset, `des_pop_respmean`, is ready, we compute the difference from the mean vectors.

In the `fn_r_indicator_4_gh()`, we compute the difference from the mean vectors and the weight variables. Excerpts of the code from the function below show that the differences are stored in `rsam` and `psam`. By merging *rsam* and *psam* with the intermediate data object, `des_pop_respmean`, we obtain the `gh` data. This concludes the pre-matrix preparation part.

```
  # use df for programming.
  df <-  data.frame(des_pop_respmean)

  # Prep for loop.
  des_col      <-  c(paste0("des"     , 1:numcat))
  respmean_col <-  c(paste0("respmean", 1:numcat))
  popmean_col  <-  c(paste0("popmean" , 1:numcat))

  des          <-  df[, des_col]
  respmean     <-  df[, respmean_col]
  popmean      <-  df[, popmean_col]

  rsam         <-  des - respmean
  psam         <-  des - popmean
  rpsam        <-  data.frame(rsam, psam)

  # Rename variables
  colnames(rpsam) <- c(paste0("rsam", 1:numcat),
                       paste0("psam", 1:numcat))
```

```
  # Combine
  gh <-  cbind(des_pop_respmean, rpsam)
```

fn_R_indicator()

The `fn_R_indicator()` uses matrix syntax to calculate propensity scores, prior to computing R-indicators. We calculate two kinds of propensity scores – one that used only population information (roipop, or prop_pop) and the other which used a mixture of the response data and the population information (roimix, or prop_mix). In this manual, we demonstrate using *prop_mix*.

```
   print(R_indicator)
```

```
## [1] 0.4960263
```

fn_rindicatorall()

In this step, we take the sum of the weights, finalwgt, and the average of the propensity scores for each of the categories of variables, which are stored in fbar and mrphat columns.

```
   print(rindicatorall)
```

```
##       fbar1    fbar2     fbar3       fbar4     fbar5   mrphat1   mrphat2
## 1  155346.0 550749.7  62658.27 1083753.082 686113.60 1.2004888 0.9362283
## 2  139650.7 612900.3  72606.54   10050.720  26217.65 0.9041243 0.9809375
## 3  147671.7       NA  91435.88   45195.592 451318.75 1.0212640        NA
## 4  157455.6       NA 128043.11   16160.179        NA 0.8602353        NA
## 5  160199.1       NA 127055.82    8490.427        NA 1.3362734        NA
## 6  403326.8       NA 108572.09          NA        NA 0.7531388        NA
## 7        NA       NA 101052.06          NA        NA        NA        NA
## 8        NA       NA 107375.41          NA        NA        NA        NA
## 9        NA       NA  83195.37          NA        NA        NA        NA
## 10       NA       NA  70603.83          NA        NA        NA        NA
## 11       NA       NA  61612.44          NA        NA        NA        NA
## 12       NA       NA  54940.11          NA        NA        NA        NA
## 13       NA       NA  46903.36          NA        NA        NA        NA
## 14       NA       NA  47595.70          NA        NA        NA        NA
##      mrphat3   mrphat4   mrphat5 seq
## 1  0.6487130 0.9601892 0.9530622   1
## 2  0.7066057 0.9244880 0.8909178   2
## 3  0.7677695 0.9518284 0.9739849   3
## 4  0.9860914 0.9520912        NA   4
## 5  1.0216912 1.0058556        NA   5
## 6  1.0303194        NA        NA   6
## 7  1.0059449        NA        NA   7
## 8  1.0571924        NA        NA   8
## 9  1.0104442        NA        NA   9
## 10 0.9975692        NA        NA  10
## 11 1.0125800        NA        NA  11
## 12 1.0291411        NA        NA  12
```

```
## 13 1.0479060        NA        NA  13
## 14 1.0296841        NA        NA  14
```

The function also computes the overall mean of propensity scores.

```
mrphatall <- mean(gh_prop_mix$roi)
mrphatall
## [1] 0.9597769
```

fn_partial()

The category and variable-level partical R-indicators can be otained by running `fn_partial()`. The output below shows variable-level and category-level R-indicator estimates.

```
    partial[1:17, c(1:4, 6:8)]

##    seq level    domain R_indicator_summary  count n_cat domain_n
## 1    1     0   Overall         0.496026315     NA  <NA>       NA
## 2    2     0 mrphatall         0.959776861     NA  <NA>       NA
## 3    3    99   resppop  1033664.0000000000     NA  <NA>       NA
## 4    4     1     geog1         0.210337414     NA  <NA>       NA
## 5    5     1       sex         0.022322665     NA  <NA>       NA
## 6    6     1  agecode1         0.123628959     NA  <NA>       NA
## 7    7     1 eth_code5         0.005447982     NA  <NA>       NA
## 8    8     1     econg         0.014550224     NA  <NA>       NA
## 9    9    99      des1                  NA      0     1        0
## 10  10     3   geog1_1         0.087950135 137993     1        1
## 11  11     3   geog1_2        -0.019279482 124051     2        1
## 12  12     3   geog1_3         0.021903908 131176     3        1
## 13  13     3   geog1_4        -0.036616129 139867     4        1
## 14  14     3   geog1_5         0.139694673 142304     5        1
## 15  15     3   geog1_6        -0.121654343 358273     6        1
## 16  16     3     sex_1        -0.016200550 489228     1        2
## 17  17     3     sex_2         0.015357199 544436     2        2
```

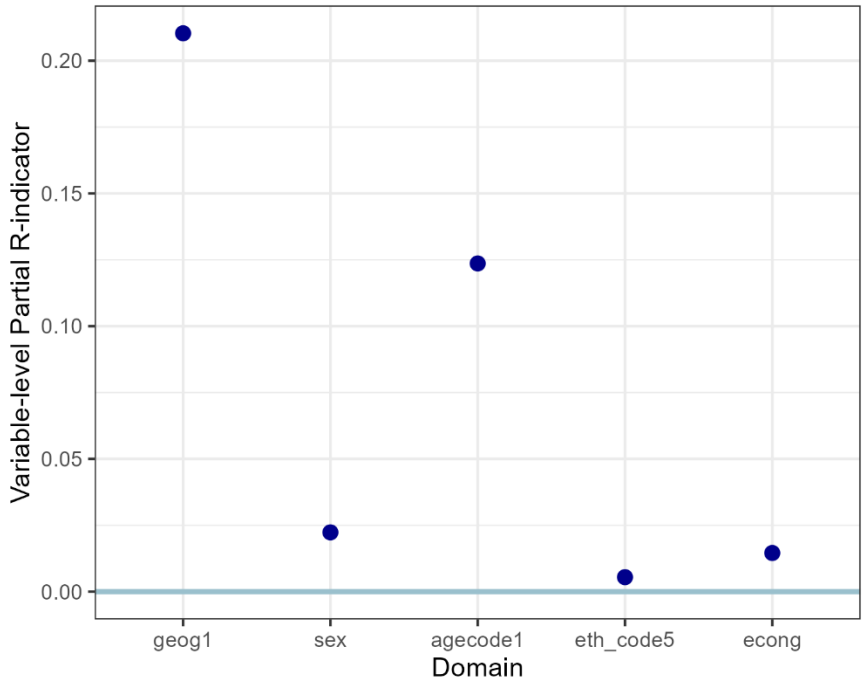
Step 4: Save in Excel and inspect

At this stage, users can inspect the output accordingly. Let's have a look. Here, we can see the overall R-indicator is estimated as 0.496 based the administrative data (N=1033664). Looking at the variable-level R-indicator (see rows 4-8), geog1 was seen to have the greatest R-indicator (0.04) compared to econg (0.0002).

Step 5: Visualise using scatterplots

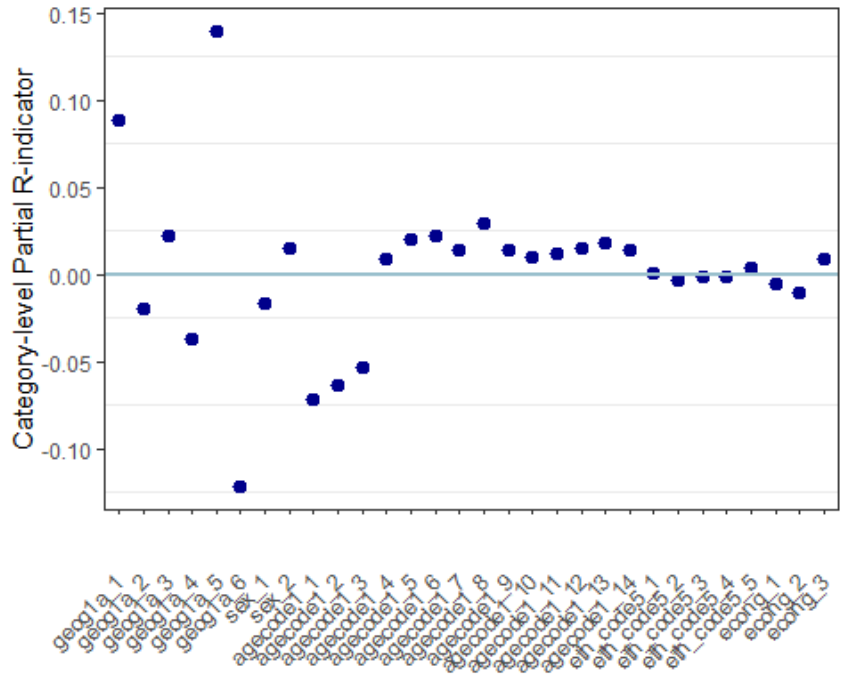
The visualisation of R-indicator by the variable level is shown as an example:

```
plot(p1)
```



And for R-indicator by the category-level:

```
plot(p2)
```



3.6 RUNNING 3B_Table-based R-indicator

For very large administrative datasets, it is possible to aggregate the microdata to a frequency table spanned by the variables of interest (covariates) in the model prior to calculating R-indicators and partial indicators. The computation of the indicators will then be based on the *frequencies* in the table rather than the microdata. The procedures are less computationally intensive than those of microdata level R-indicators described in Section 3.5.

Follw the instructions given for Section 3.5 Step 1 and 2 and proceed with the following steps.

Step 3: Compute R-indicator

In the table-based R-indicator approach, administrative data will be reduced in the form of a table defined by the covariates of interest. The principle is largely the same as the earlier approach in 3.5, but the dataset have records of aggregates defined by the cells of the table (spanned by the variables of interest), and we need to use the aggregated sums as weights at the cell level: the variable 'piinv' is now the cell count in the table and the variable 'finalwgt' is the aggregated inverse response rate (defined as the population size divided by the administrative size) in the cell of the table.

The overall and partial R indicators can be computed by running the single function below.

```
fn_RUN_table_based_R_indicator()
```

After the function is executed, users can proceed with the next steps by producing a summary table in an Excel file and visualizing the variable-level and category-level R-indicators.

The function, `fn_RUN_table_based_R_indicator()`, is composed of eight sub-functions:

```
fn_t_design_matrix()
fn_freq()
fn_t_respmean()
fn_t_des_pop_respmean()
fn_gh()
fn_t_R_indicator()
fn_t_rindicatorall()
fn_t_R_indicators_partial()
```

Some functions can be used for both microdataset-based and table-based R-indicator computation. The function names containing `t` indicates that the computation concerns table-based R indicators. Users can run each sub-function to understand the procedure as necessary.

fn_t_design_matrix()

By running `fn_t_design_matrix()`, users can build a table spanned by the variables that will define the pop-based R-indicator, merge with the administrative data, identify missing cells, and perform a data reduction to organise the data characterised by the unique pattern, raw count, and aggregate weights for each pattern.

Build a Table and identify missing cells

In the provided dataset, we have 5 variables: geog1 (6), sex (2), agecode1 (14) and eth_cod5 (5) and econg (3). As such, the total theoretically-possible combinations of each variable will be 2520(6×2×1×4×5×3). We can verify that the size of 2520 as the last row number indicates 2520.

```
nrow(pp)

## [1] 2520
```

Let's request R to print the first 30 rows of the untreated table, `pp`, that illustrate the structure of the table.

```
head(pp, n = 30)

##    pp_seq geog1 sex agecode1 eth_code5 econg
## 1       1     1   1        1         1     1
## 2       2     1   1        1         1     2
## 3       3     1   1        1         1     3
## 4       4     1   1        1         2     1
## 5       5     1   1        1         2     2
## 6       6     1   1        1         2     3
## 7       7     1   1        1         3     1
## 8       8     1   1        1         3     2
## 9       9     1   1        1         3     3
## 10     10     1   1        1         4     1
## 11     11     1   1        1         4     2
## 12     12     1   1        1         4     3
## 13     13     1   1        1         5     1
## 14     14     1   1        1         5     2
## 15     15     1   1        1         5     3
## 16     16     1   1        2         1     1
## 17     17     1   1        2         1     2
## 18     18     1   1        2         1     3
## 19     19     1   1        2         2     1
## 20     20     1   1        2         2     2
## 21     21     1   1        2         2     3
## 22     22     1   1        2         3     1
## 23     23     1   1        2         3     2
## 24     24     1   1        2         3     3
## 25     25     1   1        2         4     1
## 26     26     1   1        2         4     2
## 27     27     1   1        2         4     3
## 28     28     1   1        2         5     1
## 29     29     1   1        2         5     2
## 30     30     1   1        2         5     3
```

The unique combination of each variable category is indicated by the pattern identifier, `pp_seq`. As seen, pp_seq spans up to 2520. Our goal is to examine the frequency of each pattern using

the administrative data, before computing weights. This is carried out in several stages as depicted in Figure 1 below.

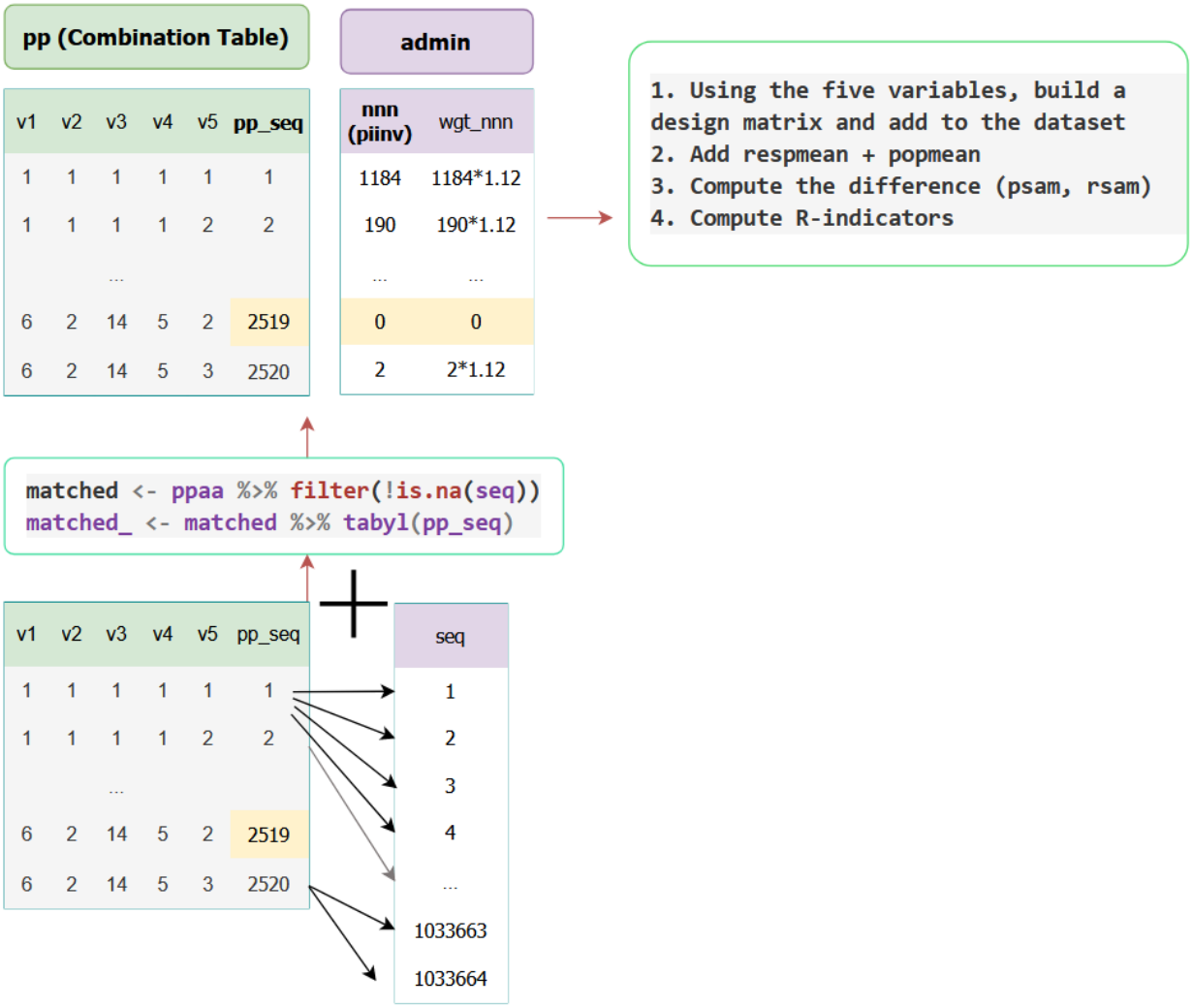


Figure 1 Illustration of obtaining pp combination table and the frequency of each combination

By merging this table with the administrative data, we can identify the *pp_seq* by each row/observation in the administrative data. As this is theoretical, not all this unique combination will be found in the administrative data, and unfound combination patterns or missing cells are to be expected. We will examine those missing cells shortly.

```
## >> Merge ----
# Recall  nrow(aa) = 1033664
ppaa  <- aa %>% dplyr::full_join(pp)
ppaa  <- ppaa %>% arrange(seq)
  nrow(ppaa)              # 1034120
```

Once we merge the `pp` table, consisting of 2520 rows, with the admin data, `aa`, the identifier of the pp, `pp_seq`, is distributed across the admin data. If the unique combination pattern between two data sources is matched, the observation in the admin data, `seq` will display a corresponding pp_seq. If the matching pattern is not found in admin data, `seq` will indicate missing. We can verify the extent of missing cells (n = 456).

The following output displays the last 11 rows. As seen, the pattern identifier 116, which corresponds to the theoretically possible combination pattern of 1-1-8-4-2 among geog1, sex, agecode1, eth_code5, and econg variables' categories, is missing in the admin data.

```
missing  <- nrow(mi); missing
```

```
## [1] 456
```

```
ppaafrom <- nrow(ppaa) - missing - 4
ppaato   <- ppaafrom + 10
print(ppaa[ppaafrom: ppaato, ])
```

```
## # A tibble: 11 × 8
##    geog1 sex   agecode1 eth_code5 econg     seq finalwgt pp_seq
##    <fct> <fct> <fct>    <fct>     <fct>   <int>    <dbl>  <int>
##  1 6     2     14       4         3     1033660     1.13   2517
##  2 6     2     14       4         3     1033661     1.13   2517
##  3 6     2     14       4         3     1033662     1.13   2517
##  4 6     2     14       5         3     1033663     1.13   2520
##  5 6     2     14       5         3     1033664     1.13   2520
##  6 1     1     8        4         2          NA    NA       116
##  7 1     1     11       2         2          NA    NA       155
##  8 1     1     11       4         2          NA    NA       161
##  9 1     1     11       5         2          NA    NA       164
## 10 1     1     12       2         2          NA    NA       170
## 11 1     1     12       3         2          NA    NA       173
```

Organise the data by the Table and add weights

Please note that the weights, `finalwgt` column was computed in the administrative data. To obtain finalwgt, We first calculate the *response rate*, which is the admin size divided by the population size, `nrow(aa)/popsize`. The weights are computed by the inverse of *response rate* (finalwgt = 1/rrate). This can be treated as the *global weight*, as all observations have the consistent value, 1.125753.

At this stage, we reduce the data and organise by `pp_seq` (n = 2520), the combination pattern, and the raw count, `nnn`. We then apply appropriate weights, depending on the missingness represented by seq. For the non-missing seq, we tabulate pp_seq to obtain the raw count of each entry before applying the global weight, 1.125753 to the raw count. See the `wgt_nnn` column (wgt_nnn = nnn × finalwgt_global). The dataset is saved in `pall`.

```
1184 * finalwgt_global
```

```
## [1] 1332.891
```

```r
sum(pall$wgt_nnn) ; popsize  # match with the popsize = 1163650
```

```
## [1] 1163650
```

```
## [1] 1163650
```

For the missing seq, 0 weight is applied. Here's the summary.

```r
head(pall, n = 3); tail(pall, n = 3)
```

```
##   geog1 sex agecode1 eth_code5 econg  nnn finalwgt_global      wgt_nnn piinv
## 1     1   1        1         1     1 1184        1.125753     1332.891  1184
## 2     1   1        1         1     2  190        1.125753      213.893   190
## 3     1   1        1         1     3 2103        1.125753     2367.458  2103
##   pp_seq
## 1      1
## 2      2
## 3      3
```

```
##      geog1 sex agecode1 eth_code5 econg nnn finalwgt_global     wgt_nnn  piinv
## 2518     6   2       14         5     1   0              NA     0.000000     0
## 2519     6   2       14         5     2   0              NA     0.000000     0
## 2520     6   2       14         5     3   2        1.125753     2.251505     2
##      pp_seq
## 2518   2518
## 2519   2519
## 2520   2520
```

Design matrix added

Now, using the five variables, we build a design matrix. To achieve this, we will create dummy variables for each variable and drop the last category, while keeping nnn (= piinv, raw count) and wgt_nnn. The intermediate results before renaming columns as des2-des26 are shown below. As demonstrated, the last category of the econg variable, econg_3 is dropped.

```r
tail(design_matrix_temp, n = 3)
```

```
##      geog1 sex agecode1 eth_code5 econg des1 geog1_1 geog1_2 geog1_3 geog1_4
## 2518     6   2       14         5     1    1       0       0       0       0
## 2519     6   2       14         5     2    1       0       0       0       0
## 2520     6   2       14         5     3    1       0       0       0       0
##      geog1_5 sex_1 agecode1_1 agecode1_2 agecode1_3 agecode1_4 agecode1_5
## 2518       0     0          0          0          0          0          0
## 2519       0     0          0          0          0          0          0
## 2520       0     0          0          0          0          0          0
##      agecode1_6 agecode1_7 agecode1_8 agecode1_9 agecode1_10 agecode1_11
## 2518          0          0          0          0           0           0
## 2519          0          0          0          0           0           0
## 2520          0          0          0          0           0           0
##      agecode1_12 agecode1_13 eth_code5_1 eth_code5_2 eth_code5_3 eth_code5_4
## 2518           0           0           0           0           0           0
## 2519           0           0           0           0           0           0
## 2520           0           0           0           0           0           0
```

```
##      econg_1 econg_2      wgt_nnn  piinv
## 2518       1       0     0.000000     0
## 2519       0       1     0.000000     0
## 2520       0       0     2.251505     2
```

To complete the function, these dummy variable columns (from gegog1_1 to econg_2) are renamed as des1-des26.

fn_freq()

This function creates a summary of the admin data to be merged in the R-indicator summary.

fn_t_respmean() : admin data distributions as row vectors

Similar to `popmean_row_vector` in 3.5, Step 1, we build a dataset containing the proportions of each variable's category (dummy column) as they appear in the administrative data. Note that this time when working with tabular data we need to *weight* the sum with the global weight, 1.125753. For example, for the first dummy column, *geog1_1*, we first obtain the total count of geog1_1 = 137993. Then, respmean is computed by `(137993 * finalwgt_global)/popsize`.

```
finalwgt_global; popsize
```

```
## [1] 1.125753
```

```
## [1] 1163650
```

```
(137993 *1.125753)/1163650
```

```
## [1] 0.1334989
```

```
(137993 * finalwgt_global)/popsize
```

```
## [1] 0.1334989
```

The function repeats this process across columns. The computed proportions are printed below.

```
Respmean_column
```

```
##             respmn_list
## geog1_1     0.133498045
## geog1_2     0.120010312
## geog1_3     0.126903278
## geog1_4     0.135311305
## geog1_5     0.137669402
## sex_1       0.473294375
## agecode1_1  0.053846088
## agecode1_2  0.062395050
## agecode1_3  0.078576032
## agecode1_4  0.110035664
## agecode1_5  0.109186611
## agecode1_6  0.093302969
```

```
## agecode1_7  0.086840545
## agecode1_8  0.092274309
## agecode1_9  0.071494865
## agecode1_10 0.060673742
## agecode1_11 0.052947192
## agecode1_12 0.047213509
## agecode1_13 0.040306793
## eth_code5_1 0.931339320
## eth_code5_2 0.008636618
## eth_code5_3 0.038838998
## eth_code5_4 0.013887337
## econg_1     0.589621450
## econg_2     0.022529970
```

The function then reshapes the data into a single row, in order to save these proportions in row vectors. As seen earlier, we rename each column as respmean1- respmean 26.

fn_des_pop_respmean()

The procedure is the same as seen earlier in 3.5. We now merge design matrix, popmean and respmean vectors.

fn_gh()

We compute the difference from the mean vectors.

fn_t_R_indicator()

The `fn_t_R_indicator()` allows us to compute propensity scores using matrix syntax. The computation of R-indicator relies on the propensity scores. As a preliminary step in the table-based R-indicator computation, the rsam and psam columns are being multiplied with the square root of `piinv`, which is the cell total for each unique combination in the table.

```
head(gh[, c("seq", "gg", "piinv", " wgt_nnn")])
```

```
##   seq        gg piinv     wgt_nnn
## 1   1 34.409301  1184  1332.891152
## 2   2 13.784049   190   213.893006
## 3   3 45.858478  2103  2367.457849
## 4   4  3.316625    11    12.383279
## 5   5  2.449490     6     6.754516
## 6   6  9.433981    89   100.191987
```

The corresponding syntax is provided below.

```
  px          <- as.matrix(gh[, psam_col])
  rx          <- as.matrix(gh[, rsam_col])
  gh   <- gh %>% mutate(gg = sqrt(piinv))
  gg   <- gh[, "gg"]
  pxm  <-  px * gg          # weighted_psam
```

```
  xxpm <-  t(pxm) %*% pxm
  rxm  <-  rx * gg          # weighted_rsam
  xxrm <-  t(rxm) %*% rxm
```

Subsequently, the function calculates propensity score, and the overall R-indicator.

We also compute weighted propensity scores by multiplying propensity scores, `roi`, by aggregate weights, `wgt_nnn`. Recall *wgt_nnn = n × finalwgt_global*.

```
gh_prop_mix <- gh_prop_mix %>%
         mutate(roi_wgt = roi * wgt_nnn)
head(gh_prop_mix_[, c("seq", var[1], "roi_wgt", "roi", "wgt_nnn") ])
```

```
##   seq geog1     roi_wgt       roi     wgt_nnn
## 1   1     1 1124.107366 0.8433602  1332.891152
## 2   2     1  178.256671 0.8333918   213.893006
## 3   3     1 2059.171606 0.8697817  2367.457849
## 4   4     1   10.459251 0.8446269    12.383279
## 5   5     1    5.637714 0.8346585     6.754516
## 6   6     1   87.272074 0.8710484   100.191987
```

fn_t_rindicatorall()

The function computes the mean of weighted propensity scores across variables in loop. This is the sum of weighted propensity scores divided by the sum of final weights for each category of a variable. The equivalent expression using *one* variable without using loop is shown for illustration purposes. Please note the programme uses for loop function in R.

```
gh_prop_mix_ %>% group_by(geog1) %>%
  summarise(
   wgt_nnn_sum = sum(wgt_nnn),
   roi_wgt_sum = sum(roi_wgt) ) %>%
  mutate(
   roiwgtsum_dv_wgtnnnsum = roi_wgt_sum/wgt_nnn_sum )
```

```
## # A tibble: 6 × 4
## geog1   wgt_nnn_sum   roi_wgt_sum       roiwgtsum_dv_wgtnnnsum
##   <fct>       <dbl>       <dbl>                        <dbl>
## 1 1         155346.     186491.                        1.20
## 2 2         139651.     126262.                        0.904
## 3 3         147672.     150812.                        1.02
## 4 4         157456.     135449.                        0.860
## 5 5         160199.     214070.                        1.34
## 6 6         403327.     303761.                        0.753
```

```
186491.1 / 155346.0
```

```
## [1] 1.200489
```

The function also computes the overall mean of propensity scores.

```
mrphatall <- sum(df$roi_wgt) / sum(df$wgt_nnn)
mrphatall
## [1] 0.9597769
```

fn_partial()

The category and variable-level partical R-indicators can be otained by running `fn_partial()`.

The function concludes with exporting the results to a spreadsheet. For next steps, see section 3.5.

4. Troubleshooting Questions and Answers

4.1 Questions and Answers

How do I know where to customise the code to suit my needs?

Unless indicated as "Customise as needed", users can run the code as it is. Please consult each code file.

How to use Starting path in multiple machines?

If users plan to use different machines, simply by changing the "starting path", users can carry out the analysis with minimal disruption. To achieve this, please ensure to use the consistent master project folder name.

What are the commonly used commands?

Most commonly used commands in the tidyverse package are:

```
  arrange : sort variables.
  bind_rows: append multiple dataframes.
  mutate  : manipulate variables, and
            create new variables based on old variables.
  select  : order, and keep(drop) variables of interest.
  shell.exec: launch a software and opens the target file (Windows PC only)
```

How to free up memory space and speed up RStudio?

You can remove objects that you no longer need.

```
  # To remove objects except for certain objects
  ls()

  keepobjectslist <- c("a", "b", "c")
```

```
  rm(list = ls()[!ls() %in% keepobjectslist])
  ls()
```

I get error messages when a pre-defined function is used.

Users can inspect the codes used in the function, and identify the issues. It is recommended NOT edit the function file directly, as the functions are used repeatedly, and the interlinked sections may not run as expected. Where preferable, users may copy the codes in the function, and use locally with minor tweaks.

How do I modify pre-defined functions?

Users can modify `1_Functions.R` under the *Functions* folder.

```
# 1_Functions.R
fn_output_folder_path <- function() {

  currentdate <<- Sys.Date()
  txtpath   <<- "Output/01-Txt/"
  figpath   <<- "Output/02-Figure/"
  xlsxpath  <<- "./Output/03-ExcelOutput/"
  Rdatapath <<- "Output/04-RData/"
}
```

We can check how the output folder names are set as path to save the results during the analytical process.

```
fn_output_folder_path()
```

Let's run the function. We can see that xlsxpath is set as `"./Output/03-ExcelOutput/"`.

```
xlsxpath

## [1] "./Output/03-ExcelOutput/"
```

Let's customise the xlsxpath, by renaming the folder name. If we customise `1_Functions.R` file, we can edit the information enclosed in the brackets. Notice that we use `<<-` with functions so that the object created by a function will exist in the global R environment. This is very important.

Alternatively, we could ignore the pre-defined function and just write relevant lines of code and keep it in the main R script file. For instance, we could put output_folder_path at the top of the `2_Prep_Wtsample_Freq_Table.R`. Here, we edited the `xlsxpath`. Notice that `fn_output_folder_path <- function() {  }` is removed.

```
    xlsxpath_2 <- "./Output/03-Excel/"

    xlsxpath_2

## [1] "./Output/03-Excel/"
```

```
    #H-------------------------------------
    ## > Step 1. Load Census data
    #H-------------------------------------
    # load("pop_u_short_before_sim_5vars.RData")
```

Notice that we use `<-`. Using `<<-` is not necessary here. Users can remember the usage of `<-` and can modify the functions as appropriate, should the function incur errors.

What approaches are taken in programming?

When loop is used, base R functions were used (table, tapply, etc). For data manipulation, tidyverse package was used extensively. This strategy is partly to improve readability of the code.

To enhance users' workflow, output files are programmed to launch using the pre-defined functions.

Can I ignore Warning messages?

Some packages alert users with compatibility issues arising from old version. These can be ignored. For example,

```
  library("fastDummies")
  Warning message:
  package 'fastDummies' was built under
  R version 4.1.2

  library(rlist)
  Warning message:
  package 'rlist' was built under R version 4.1.2
```

What version of R is used?

Tested with Windows PC. R version used: 4.1.1 RStudio version: RStudio 2022.12.0 Build 353.

4.2 Troubleshooting

Unused argument error

For example, `sim %>% select(geog1)` the select command can cause an error:

```
Error in select(., geog1) :
  unused arguments (geog1)
```

This maybe due to the conflict in packages.

The error can be fixed by adding the name of the package used, dplyr, explicitly. `sim %>% dplyr::select(geog1)`

I get errors when computing…

Please inspect zero cells, and ensure 0 (numeric value) is entered for n and perc, as well as admin_n and admin_perc. Errors may occur with NA coding and data attributes(character, factor, numeric).

I am experiencing slowness in computation.

R can be not responsive if memory is full. Please identify bottlenecks and remove them. It may be due to certain commands. For example, `View(object)` command could take a while if the object is huge in size. Unless one should inspect the data, suppress the View command to expedite the computation where possible.

It can also be the case that for loop functions can be slow as well. In some instances, removing objects may help as this procedure can free up memory space. See above commonly used commands for more information.

Error: cannot allocate vector of size xxxx.x Gb

If matrix symbols have entered mistakenly, R shows an error message like this. Please double check whether there are any mistakes. For instance, one may have typed `a*b` instead of `a%*%b`. Users can type `memory.limit()` to check the current memory limit and increase as necessary.

This concludes the manual. Thank you for taking the time reading the material. Please get in touch with any query or errata at demystify.stats@gmail.com.

References

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Citation

Please cite this work as:

Kim, Sook & Shlomo, Natalie (2023). “Quality Indicators for Administrative Data User Manual For R Package on GitHub, version 2.1”, available at https://github.com/sook-tusk/qualadmin