RAS module R case study guide

Childhood vaccination coverage survey in Greece, 2006

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Introduction

Version history

This case study was originally written by the following authors:

- Kostas Danis
- Dimitris Papamichail
- Takis Panagiotopoulos

An R companion guide for the computer practicals accompanying the case study was developed in 2017 by:

- Patrick Keating
- Alexander Spina
- Alexandre Blake

This was updated in 2018 by:

- Ashley Sharpe

Further updates were made in 2022, to replace base R code with more modern functions from `tidyverse` packages and to add an alternative mixed-methods based approach for section 5 following the introduction of this approach in the STATA version of the case study guide by Emily White Johansson in 2022. The R guide was updated in 2022 by:

- Amy Mikhail
- Alexander Spina

Guide for use

This guide has been designed for use in two different ways; which one to follow will depend on how experienced you are in using R for analysis, and also your familiarity with the statistical concepts being covered. We recommend that facilitators choose which method to follow after discussing with their groups to determine the level of R experience and background knowledge on the statistical concepts.

Facilitator suggestions for group work

We recommend that regardless of which method you choose, the learning objectives remain focused on gaining an understanding of the statistical and epidemiological concepts to apply, particularly around sampling and survey design.

Method 1 - run as a paper discussion-based case study

Choose this method if participants have limited to no experience with R, or the group is very mixed, or there is less background familiarity with the statistical concepts. The tasks in sessions 1 to 3 can mostly be completed by hand with a calculator; for sessions 4 and 5 the results tables can be the focus of the discussion. If you are using this method, we recommend you click on the button to `hide code` at the top of the html version of this document. This will make the text easier to read. The `R coding tips` sections can be skipped, and participants can refer to these later in their own time if they wish.

Method 2 - run as a computer practical

Choose this method if at least the majority of participants in the group are already using R in their work and ideally, have also undertaken the Outbreak and MVA module computer practicals in R. We recommend that a Microsoft Teams meeting be set up for each group (even face to face groups) so that facilitators can share their screen (with the sound muted if in person). Facilitators should install all the required packages on the computer they will be using, and attempt to knit this R markdown file prior to the course.

It is also recommended that participants attempt to install all the required packages before starting the course. It is advisable to allocate some time outside of that allocated for this case study, to troubleshoot package install problems, at the beginning of the course. Prior experience has shown that installation problems can be time consuming to resolve.

We suggest that the case study begins as for the discussion-based method, with groups reading the background information and considering the questions and how they would go about completing the tasks together. Participants may then attempt to run the code on their computers, first reading and following the R coding tips and then by running each R markdown chunk and inspecting and discussing the output. For any troubleshooting, facilitators can share their screens to demonstrate solutions or explain particular aspects of how the code works, using live demonstration techniques.

If participants are encountering difficult to resolve problems with R, these are most likely to be due to their R set up and the security settings on their computers (which are becoming increasingly complex in most institutions). To avoid running out of time for conceptual epidemiological discussions, we recommend encouraging participants to pair up with other

group members that do not have these issues, for the rest of the session. Further troubleshooting with setup and package install issues can then be addressed during the breaks.

Prerequisites for participants

This guide is not intended to be an introduction to R, so if you wish to follow the case study by running the R code, it is essential to have a working knowledge of R syntax (particularly the syntax used by `dplyr` and `tidyverse` packages). Understanding the R universe, syntax and the way that packages work to undertake data cleaning, management and manipulation tasks is a massive topic, and outside the scope of this guide. If you are relatively new to R, however, you may find it helpful to work through the main data management chapters in the online Epidemiologist R handbook prior to undertaking this case study. This is a relatively new resource that was created especially for epidemiologists who want to get started using R. Wherever possible, in this guide we have used the approaches demonstrated in the Epidemiologist R handbook to undertake the generic data manipulation tasks; you may therefore also find it useful as a reference.

The R coding tips for each session focus principally on explaining the R functions necessary to undertake the analytical aspects of the task in question. Some guidance is also provided on ways to present the results. When a new function is introduced, a description of how it works is included in the text, and each line of code is also annotated.

Note that some prior knowledge about descriptive, single variable and multivariable analysis is expected from previous modules (i.e. Outbreak module, MVA).

Setup

R guide structure

This guide is for participants who wish to undertake the RAS vaccine coverage case study using R as the primary analysis software. All the information required to complete the case study has been included. The following materials have been provided in the participant pack:

1. This guide, available in three formats:
    - interactive HTML file to view in your internet browser
    - static Microsoft Word document which can be edited and printed
    - static .pdf document which can be printed
2. `data` folder containing the required data sets for this case study:
    - `Sampling_frames.xlsx`
    - `vaccine4.dta`
    - `vaccine5.dta`
3. `RAS_VCE_R_packages2install.R`: R script for installing required packages
4. `RAS_VCE_R_code_2022.Rmd`: R markdown with coding solutions for each task

You may find it easier to view and work through the html file in your internet browser, as it has the following advantages:

1. You can use the interactive contents links to jump to different sessions or tasks throughout the document
2. Each practical session is presented in a separate tab
3. You can use the `code` buttons to reveal or hide the code chunks

The R markdown file can be used to run each chunk of code and explore the results as is, or alternatively, to modify the code if participants wish to explore the R functions in more depth.

The case study is broken into 5 sessions, each of which consist of one or more tasks to complete. For each session, you are presented with the following sub-sections:

- Introductory background (text)
- Task description (text)
- R coding tips (text and code)
- Answers to the questions and tasks (tables and text)

A note on similarities with the STATA case study guide:

This R guide has been aligned as far as possible with the original STATA guide; this means that the same statistical methods are used in both guides. However, you may find minor differences in the numeric results; this is usually due to differences in rounding or minor

differences in the calculations between the two software platforms. None the less, the results from both platforms should yield the same interpretation.

R packages

It is advisable to have up-to-date versions of R and RStudio installed. The code in this guide was updated and tested using:

- R version 4.1.3 (2022-03-10)
- RStudio version 2022.02.0 Build 443

This guide uses packages from the `tidyverse` which are being used more and more for data analysis, due to their easy to read and efficient coding syntax.

The packages required for this case study can be installed by running the code below. This code has also been made available as a separate R script in the participant pack, called `RAS_VCE_R_packages2install.R`. It uses the `pload()` function from the `pacman` package as this will check the user's library for required packages, install them if they are missing, and then load them into the current R session. Once the packages are installed, you will also need to rerun this code chunk at the beginning of each session, to ensure that all the required packages are loaded.

```
# Packages to install *before* running pacman pload():
#######################################################

# Ensures the package "pacman" is installed
if (!require("pacman")) install.packages("pacman", quiet = TRUE)

# Ensure the package "remotes" is installed
if (!require("remotes")) install.packages("remotes", quiet = TRUE)

# Install the epikit package from Github:
if (!require("epikit")) remotes::install_github("R4EPI/epikit", quiet = TRUE)

# Install the sitrep package from Github:
if (!require("sitrep")) remotes::install_github("R4EPI/sitrep", quiet = TRUE)


# Install and/or load required packages:
########################################
pacman::p_load(

  # Project and file management
  ##############################
  here,      # file paths relative to R project root folder
  rio,       # import/export of many types of data
  rmarkdown, # reading and printing RAS R markdown guide
  knitr,     # reading and printing RAS R markdown guide

  # Package install and management
  ##################################
  pacman,   # package install/load
  remotes,  # install from github
```

```
  # General data management
  ##########################
  tidyverse,   # includes many packages for tidy data wrangling:
  #dplyr,      # data management
  #tidyr,      # data management
  #ggplot2,    # data visualization
  #stringr,    # work with strings and characters
  #forcats,    # work with factors
  #lubridate,  # work with dates
  #purrr       # iteration and working with lists
  janitor,     # data cleaning
  matchmaker,  # data cleaning

  # Summary tables:
  ##########################
  flextable,   # Creating printable summary tables
  officer,     # Fine tuning flextables
  gtsummary,   # making descriptive and statistical tables
  smd,         # Helper functions for gtsummary tables
  labelled,    # Labelling variables and values
  scales,      # helper functions
  Hmisc,       # Summary functions

  # Analysis:
  ##########################
  pps,         # Probability proportional to size (PPS) sampling
  sampler,     # Calculate sample size
  srvyr,       # Create survey design and calculate vaccination coverage
  survey,      # Support for srvyr functions
  fixest,      # Multivariable models with multiple fixed effects
  broom.mixed  # Extract tidy table of mixed effects model results
)

# Check for and install Github packages:
pacman::p_load_gh(

  # Packages for survey analysis and mixed effects:
  ################################################
  "R4EPI/epikit",     # Functions for survey analysis
  "R4EPI/sitrep"      # Function wrappers for survey analysis
)
```

We recommend that when you run this code for the first time, you check the output carefully for any errors that could indicate a failure to install some packages. If you do encounter any errors or other difficulties, please ask a facilitator for help during the pre-case study session that is dedicated to this.

A useful test to ensure packages have been installed correctly, is to close RStudio after running this code the first time, then reopen RStudio and run this code chunk. If you find that R is still trying to install packages, this likely means that some packages failed to install

the first time. If all packages and their dependencies installed correctly the first time, rerunning this code chunk should simply load the packages into your R environment.

Data management

File organisation:

The R practical material for this case study is available in a zip folder called `RAS_VCE_participant_pack`. You can download this folder here or from the EVA platform. Once you have downloaded it, unzip the file and save it on your computer. We recommend saving this file to a location that is not connected to OneDrive or to any other Shared Drive, if possible, as this can sometimes interfere with package installs or other functionality.

There is an R project file (`RAS_VCE_R_project.Rproj`) in this folder and we suggest you begin this practical session by double clicking on this file to open it.

In the `Files` pane of your RStudio window, you should see a folder called `rcode`. Click on this folder in the RStudio pane to view the contents. Once you are inside this folder, you should see an R markdown file called `RAS_VCE_R_code_2022.Rmd` . Click on this file to open it. It contains all the code chunks that are also present in this guide, but without explanatory text. This file is for you to run and explore the code in each chunk, modify and experiment with the code if you wish, and make your own notes.

The data sets have been stored in a sub-folder called `data`.

Note that the relative file paths used for importing data in this guide assume the above folder structure.

Importing data sets:

The data sets can be easily imported using the `import()` function from the `rio` package, combined with the `here` package to construct relative file paths.

Most of the data sets are STATA `.dta` files, while the data required for the first three excercises is saved in a Microsoft Excel workbook. Both file types can be read in to R using `rio::import()` and specifying the relevant arguments.

The data dictionary for each data set is included in the appendices at the end of this guide.

Case study

Description

This case study is built around a national survey that used stratified cluster sampling to estimate the vaccination coverage of six year-old children in Greece and to identify predicting factors of complete and timely vaccination status. Teaching methods will include presentations, interactive exercises and exercises using computers.

Objectives

The aim of this case study is to equip participants with the tools to design and conduct a cross-sectional study to estimate vaccination coverage and analyse data from a cross-sectional survey. At the end of the course, participants should have acquired the following skills:

1. Epidemiological skills:

- Select the appropriate method to estimate vaccination coverage
- Understand the principles of basic sampling methods, including stratification and cluster sampling
- Select an appropriate sampling scheme
- Calculate the required sample size
- Identify methods of data collection to estimate vaccination coverage
- Interpret the results of the various analyses
- Communicate findings

2. Computer skills:

- Calculate sample size
- Automatically select study participants from a sampling frame with different sampling methods
- Perform descriptive analysis by calculating weighted proportions
- Calculate vaccine coverage estimates using a survey design
- Conduct an analytical study using a cross-sectional survey with a stratified cluster sampling design
- Present descriptive and analytical results in publication-ready tables

Case study sessions

This case study consists of the following 5 sessions:

- *Session 1:* Sampling
- *Session 2:* Sample size calculation
- *Session 3:* From analysis plan to data collection
- *Session 4:* Descriptive statistics with weighted proportions

- *Session 5:* Analysis of associations with having a fully vaccinated child

Duration of the case study: 7-9 hours (additional 3-4 hours for the optional sessions)

Background

Vaccine-preventable diseases are still a public health burden worldwide, largely due to suboptimal vaccination coverage, and constitute an important component of the health care debate in many countries. To improve vaccination coverage and reach high immunisation levels, the reasons for inadequate vaccinations need to be identified and addressed.

Vaccination in Greece

In Greece, vaccines included in the National Vaccination Programme (NVP) (Box 1) are provided free of charge to all residents (including immigrants) in primary health care centres or health insurance clinics. Childhood vaccination coverage is not monitored routinely. Several ad-hoc studies have been conducted occasionally at local level using non-representative samples. Most of the current knowledge on immunisation uptake is based on two national population-based surveys conducted in 1997 and in 2001 using representative samples of children attending the first year of Greek Grammar school (children born in 1991) and of two-year olds (children born in 1997), respectively. Results of those surveys showed high vaccination coverage [93.5% and 98.9% for the 3rd dose of diphtheria-tetanus toxoid and pertusis (DTP) vaccine; and 89.1% and 93.7% for the 1st dose of measles-mumps-rubella (MMR) vaccine in 1997 and 2001, respectively]. However, an outbreak of measles in 2006 revealed low coverage among the Roma minority (1% of the population) and immigrants (8% of the population) who accounted for 55% and 15% of all cases, respectively.

Box 1- *Recommended childhood vaccination schedule according to the National Vaccination Programme (NVP) at the time of the study in Greece*

Recommended age	DTaP[a]	Hib[b]	IPV[a]	MMR[a]	HepB[b]	MCV[c]	PCV7[c]	Var[c]	BCG	dT
2 months	Yes	Yes	Yes		Yes	Yes	Yes			
4 months	Yes	Yes	Yes		Yes	Yes	Yes			
6 months	Yes	Yes					Yes			
6-18 months			Yes		Yes					
12-15 months		Yes		Yes			Yes			
12-18 months								Yes		
15-18 months	Yes					Yes				
4-6 years	Yes		Yes	Yes						
6 years									Yes	

Recommended age	DTaP[a]	Hib[b]	IPV[a]	MMR[a]	HepB[b]	MCV[c]	PCV7[c]	Var[c]	BCG	dT
11-18 years										Yes
13-18 years								Yes		
>18 years										Yes

[a]DTaP, IPV & MMR were introduced in the NVP before 1990

[b]Hib & HepB introduced in 1998 and 2002, respectively

[c]MCV, PCV7 and Var introduced in 2006 (although MCV was available in pharmacies since 2001)

Scenario

You work at the national public health institute and you are asked to provide data on vaccination coverage of children in Greece and identify the potential reasons for low vaccination uptake.

Glossary

Acronym or term	Meaning
BCG	Bacillus Calmette-Guérin
DTP	Diphtheria-Tetanus-Pertusis vaccine
DTaP	Diphtheria-acellular Tetanus-Pertusis vaccine
dt	reduced diphtheria toxoid-Tetanus toxoid
Hib	Haemophilus Influenzae type b
IPV	Inactivated Poliomyelitis Vaccine
MMR	Measles Mumps Rubella vaccine
OPV	Oral Poliomyelitis Vaccine
HepB	Hepatitis B
HepA	Hepatitis A
MCV	Meningococcal Conjugate Vaccine
Men C	Meningitis C
PCV7	Pneumococcal Heptavalent Vaccine
PR	Prevalence Ratio
RR	Risk ratio / Rate ratio
OR	Odds Ratio
95% CI	95% Confidence Intervals

Practical sessions

S1: Sampling frames

Session overview

This session focuses on how to select a representative sample from a specified population, using basic and more complex sampling methods.

By the end of this session, participants should be able to:

- understand the principles of basic sampling methods
- identify different sampling design options for a vaccination coverage survey
- understand the meaning of target and sample populations, primary and final sampling units, and sampling frame
- understand complex designs, especially cluster sampling and stratification
- identify the necessary number of sampling units in different strata in a survey
- draw a simple random sample
- draw a systematic sample
- generate random numbers using R
- draw a simple random sample with probability proportional to size

This session consists of 6 Tasks:

- *Task 1.1* – Sampling strategy
- *Task 1.2* – Use stratification
- *Task 1.3* – Select a simple random sample (generate random numbers)
- *Task 1.4* – Select a systematic sample
- *Task 1.5* – Select a sample with probability proportional to size
- *Task 1.6* – Cluster sampling

1.1: Sampling strategy

Background:

The aim of the study was to estimate the vaccination coverage among 6-year-old children in Greece and identify reasons for incomplete vaccination status.

The specific objectives were to:

1. estimate the vaccination coverage of 6-year-old children for all vaccines included in the National Vaccination Programme:
   - overall in Greece
   - by geographical region (6 regions, urban and rural areas)
   - by minority group (i.e. immigrants, Greek Muslims, Greek Roma)

2. examine the associations between socioeconomic status, parental beliefs and attitudes towards immunisation, and perceptions of barriers to vaccination on complete vaccination status among 6-year old children

Task instructions:

Discuss and answer the following questions:

1. What sampling frames might be available?
2. What are some necessary prerequisites for using them?
3. What options of sampling schemes would you consider?
4. What are the advantages and disadvantages of each one?
5. Explain in plain language the sampling strategy chosen by the researchers and describe the different steps of sampling.
6. In the selected sampling design:
    - what is the target population?
    - what is the study population?
    - what are the primary sampling units?
    - what are the final sampling units?
    - what sampling frame could be used?
7. "Samples of approximately equal size were selected in each region":
    - Why do you think this was done?
    - What complexity does it introduce?

Researcher selected strategies:

Q 1 - 2 (Sampling frames and prerequisites):

You may consider the following sampling frames:

- Resident registries from local authorities (complete and updated)
- Patient registries from primary care services (relatively complete)
- Child vaccination registries (if available)
- Telephone directories to identify families (exhaustive - there are usually multiple operators and networks)
- Social security registry of parents (information on children might not be available)
- School registries (in this case, a large proportion of the population should attend school)

In this survey the researchers decided to take a sample of 1st grade school children.To assess whether this study population is appropriate, it would be necessary to have information on:

- whether attendance in primary school is compulsory
- provision for children with handicap or other health problems and for children living in special social circumstances
- possible educational institutions for 6 year-old children other than "primary schools"
- existence of special education, private schools, minority schools, religious schools etc.
- school attendance of the general childhood population as well as of children belonging to special groups (e.g. immigrants, Roma etc.).

A full list of school children was impossible to obtain. Nevertheless, it was feasible to get a list of all schools in the country, with number of first grade classes in each school.

Q 3 - 4 (Sampling schemes, advantages and disadvantages):

The following options of sampling schemes should be considered:

A. Sampling of children (final sampling units):

- 1st stage: cluster sampling with schools as clusters of children
- Advantage: simplicity
- Disadvantage: large clusters if no further sampling in 2nd stage is used

B. Two-stage cluster sampling:

- 1st stage: cluster sampling with schools-classes as clusters of children
- 2nd stage: all children in school or school-class
- Advantage: smaller clusters than previous option, simple to organise

C. Multi-stage cluster sampling:

- 1st stage: cluster sampling with school-classes as clusters of children
- 2nd stage: sample of children in each school-class from the 1st stage
- Advantage: more efficient design

D. Sampling of school-classes or schools (clusters, primary sampling units):

- Simple random sample of school classes or schools
- Advantage: theoretically correct, simple to analyse
- Disadvantage 1: wide distribution across country (practical difficulties)
- Disadvantage 2: adequate sample size / region not ensured (see objectives)

E. Systematic sample of school classes or schools:

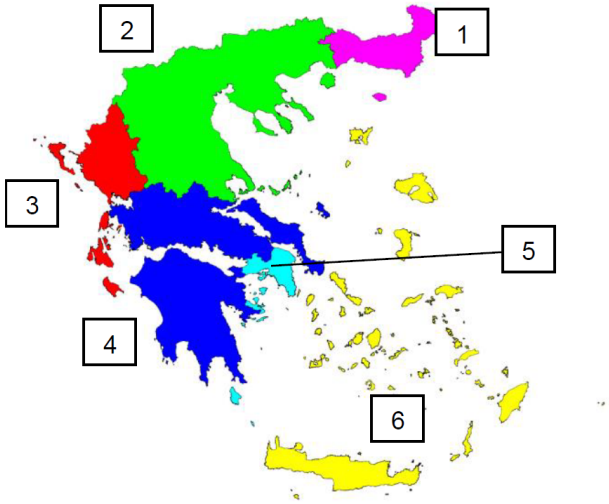
- No particular advantage compared to simple random sampling

F. Stratification by region:

- Advantage 1: more efficient design (the more the regions are heterogeneous between and homogeneous within themselves in terms of vaccination coverage, the more efficient the design, i.e. the narrower the confidence intervals)
- Advantage 2: adequate sample size in each region is ensured

G. Stratification by region and by urban/rural area:

- Advantage: more efficient design (as for regional strata above).



Note: (1) Thraki; (2) Macedonia-Thessalia; (3) Ipeiros-Ionian Islands; (4) Peloponissos-Sterea; (5) Attiki; (6) Crete-Aegean Islands.

Fig. 1.1 - Map of Greece with regions used in stratification

The researchers decided to use the following sampling strategy: stratified cluster sampling of first-grade school children, using school classes as clusters and stratification by region (see map) and urban/rural area; approximately equal sample size was used in each region,

and within each region sample size in urban/rural areas was proportional to size; all children in each school-class were selected.

Q 5 (Explain chosen sampling strategy):

A national sample of first grade school children was selected using the following sampling strategy:

- The country was divided into six geographical region (Figure 1.1)
- Each region, apart from the capital region (Attica), was further subdivided into urban and rural areas, to create 11 strata. According to the National Statistical Authority of Greece, urban areas are defined as towns/cities with 2,000 population or more, while rural areas as villages/towns with less than 2,000 population
- A sample of approximately equal size was taken in each region
- Within each region, samples were selected with probability proportional to the size of urban and rural areas
- School classes were used as clusters of children
- A simple random sample of school classes was selected in each stratum
- All children in the selected school classes (clusters) were selected in the final sample.

Q 6 (Metrics for chosen sample design):

The following metrics describe the chosen sample design:

- Target population: 6-year-old children in Greece
- Study population: children attending first grade of primary school
- Primary sampling units: school classes
- Final sampling units: individual children
- Sampling frame: list of all schools in each stratum, with number of first grade classes in each school.

Q 7 (Rationale for selecting samples of equal size per region):

The researchers had set as their objective to estimate vaccination coverage by geographical region. Therefore, the sample size would have to be adequate in each and every region in order to have estimates of acceptable precision. As a consequence, the researchers chose to get samples of equal size in each region. (In fact, they aimed at a somewhat higher precision for the region of Attiki, and therefore the sample size for this region was somewhat larger).

As the population of each region is different, opting for equal sample size in each region leads to different sampling fractions for each region. This means that weighting should be used in the analysis (for national level results) to take account of the different sampling fractions of the regions. This increases the complexity of the analysis.

1.2: Stratified proportional sampling

Background:

Stratified sampling is used when the population consists of distinct subgroups (strata), which differ with respect to the feature under study. In this study, researchers expected urban and rural areas in each region to be different in terms of vaccination coverage. Therefore, the same proportion of clusters (school classes) was taken from each stratum within a region to ensure that they were all adequately represented.

Your first task is to calculate the number of classes to sample in each region and rural / urban stratum.

Task instructions:

Using the data provided in table 1.2 below (which can be imported into R from the `table1_2` worksheet of the `Sampling_frames.xlsx` Microsoft Excel workbook in the `data` sub-folder):

1. Within each region, calculate the number of clusters (school classes) to sample from;
2. Calculate the number of classes for each urban / rural stratum relative to the population size;
3. Aim to include 50 school classes from each region;
4. Assume that all school classes have an equal number of students;
5. Append your results to table 1.2 (percentage and number of classes to sample for each urban and rural stratum in each of the 6 regions) to complete it.

Table 1.2 - Number of children aged 5 - 9 years in Greece by region and urban/rural area

Region	Urban	Rural	TOTAL
Thraki	11624	6884	18508
Macedonia-Thessalia	116322	47101	163423
Ipeiros-Ionian Islands	11446	15449	26895
Peloponissos-Sterea	55770	44132	99902
Attiki	174493	1667	176160
Crete-Aegean Islands	36374	24752	61126
TOTAL	406029	139985	546014

R coding tips:

First, import the summary data from table 1.2.

This table is currently in wide format, but to calculate the number of classes to sample from in each strata, it needs to be converted to long format (i.e. 'tidy data') so that a single column defines the strata (urban or rural) and another column contains the population for each stratum. We can do this with the `tidyr::pivot_longer()` function.

We can then calculate the relative proportions in each stratum and from there determine the number of school classes to sample (out of 50) for each stratum within each region:

Table 1.2 **-** *Updated with proportions and number of classes to sample per stratum*

```
# Import sample frame for regions:
regions <- rio::import(here::here("data", "Sampling_frames.xlsx"),
                       which = "table1_2")

# Create new table for results:
nclasses2sample <- regions %>%

  # Convert table to tidy data:
  tidyr::pivot_longer(cols = c(Urban, Rural),        # Convert to tidy format
                      names_to = "Stratum",          # Store strata in new
col
                      values_to = "Population") %>%  # Store population in
new col

  # Calculate proportions and number of classes to sample:
  mutate(Proportion = Population/Total,              # Calculate proportions
         Nclasses = round(50*Proportion, digits = 0))# Calculate number of
classes


#################
# Print results:
################

# Convert to a flextable:
nclasses2sample_pub <- flextable::qflextable(nclasses2sample) %>%
  flextable::set_table_properties(width = 1, layout = "autofit")

# Print:
nclasses2sample_pub
```

Region	Total	Stratum	Population	Proportion	Nclasses
Thraki	18,508	Urban	11,624	0.628052734	31
Thraki	18,508	Rural	6,884	0.371947266	19
Macedonia-Thessalia	163,423	Urban	116,322	0.711784755	36
Macedonia-Thessalia	163,423	Rural	47,101	0.288215245	14
Ipeiros-Ionian Islands	26,895	Urban	11,446	0.425580963	21
Ipeiros-Ionian Islands	26,895	Rural	15,449	0.574419037	29
Peloponissos-Sterea	99,902	Urban	55,770	0.558247082	28

Region	Total	Stratum	Population	Proportion	Nclasses
Peloponissos-Sterea	99,902	Rural	44,132	0.441752918	22
Attiki	176,160	Urban	174,493	0.990537012	50
Attiki	176,160	Rural	1,667	0.009462988	0
Crete-Aegean Islands	61,126	Urban	36,374	0.595065929	30
Crete-Aegean Islands	61,126	Rural	24,752	0.404934071	20

1.3: Simple random sampling

Background:

Table 1.3 is part of the sampling frame for the stratum "rural areas of the region of Peloponissos-Sterea", where all schools have only one first grade school-class.

Questions to answer:

1. What would be the necessary steps to select a simple random sample of 22 school classes from the sampling frame (Table 1.3)?
2. What is the sampling fraction in this case?

Task instructions:

1. Generate a simple random sample of 22 school classes using random number selection in a computer programme;
2. Identify the selected school classes in the sampling frame (table 1.3);
3. Calculate the sampling fraction.

R coding tips:

The sampling frame (list of school classes in the Peleponissos-Sterea region) can be imported from the `Sampling_frames.xlsx` workbook (`table1_3` is the name of the worksheet).

The simple random sample of 22 classes can then be identified using the `dplyr` convenience function `slice_sample()` to return a random subset of 22 rows of the original sampling frame.

Table 1.3 *- Simple Random Sample of 22 school classes*

```
# Import the sampling frame of school classes in Peleponissos-Sterea:
class_frame <- rio::import(here::here("data", "Sampling_frames.xlsx"),
                           which = "table1_3")

# Perform a simple random sample to select 22 classes from the list:
msrs <- class_frame %>%

  # Subset the simple random sample of 22 classes:
  slice_sample(n = 22) %>%

  # Arrange results in ascending order by ID:
  dplyr::arrange(ID)

##################
# Print results:
################

# Convert to flextable:
```

```
msrs_pub <- flextable::qflextable(msrs) %>%
  flextable::set_table_properties(width = 1, layout = "autofit")

# Print:
msrs_pub
```

ID	School_code
1	ACH-013
17	ACH-110
21	ACH-119
22	ACH-123
23	ACH-128
24	ACH-129
28	ACH-159
31	ACH-166
32	ACH-173
38	ACH-187
43	ACH-197
44	ACH-200
49	ACH-216
50	ACH-223
74	ACH-406
77	ACH-573
80	ILIA-020
85	ILIA-030
86	ILIA-031
89	ILIA-036
91	ILIA-040
97	ILIA-048

The sampling fraction is the number of units sampled divided by the total number of units in the sampling frame, i.e.:

$$SampleFraction = \frac{n}{N}$$

where:

- n is the sample size and
- N is the total population included in the sampling frame.

```
# Calculate the sampling fraction for this example:
sample_fraction <- round(22/nrow(class_frame), digits = 2)

#################
# Print results:
################

sample_fraction
```

```
## [1] 0.22
```

1.4: Systematic sampling

Background:

Systematic sampling is similar to simple random sampling, except that the total sampling frame is divided by the desired number of sampling units to select and every *nth* row of the sampling frame is selected according to the result. This can be a useful sampling strategy when subjects are being prospectively recruited to a study, when the total size of the sampling frame is not yet clear or when it is necessary to ensure consistent sampling over multiple days with an unknown number of subjects recruited per day.

Questions to answer:

1. What is the process for a systematic sample of 22 schools among 102 schools?
2. What are the advantages and disadvantages of using systematic sampling?

Task instructions:

1. Use the same sampling frame as for the previous section (`class_frame`);
2. Divide the total number of classes in the sampling frame by the desired number of units to sample (22) to calculate the group size;
3. Randomly select one number *n* from this group size;
4. Select every *nth* row of the sampling frame to produce the systematic sample;
5. Limit the number of returned rows to the desired number of units to sample (22).

R coding tips:

After calculating the size of the groups to divide the sampling frame into, we can select a random number from this group size using the base R function `sample.int()`.

Note that you can ensure you always get the same number back by using the `set.seed()` function - this way if you send your script to someone else they would be able to reproduce the same sample.

This random number can then be fed into the `dplyr::slice()` command as shown below to select every *nth* row of the sampling frame. Note that if *n* is small / an early number in the sequence, an excess of rows may be selected. If this happens, the returned rows can be limited to the desired sample size by using the `dplyr::slice_head()` function:

Table 1.4 - *Systematic sample of school classes*

```
# Define the sampling interval - the n to systematically sample
# (i.e. every nth row to choose):
sample_n <- as.integer(nrow(class_frame)/22)

# Calculate the random starting point for systematic sampling:
sample_start <- sample.int(n = sample_n, size = 1)
```

```r
# Define rows systematically (every nth row) to filter the sampling frame:
sample_rows <- seq.int(sample_start, nrow(class_frame), sample_n)

# Now subset the sampling frame and filter for every nth row:
msystematic <- class_frame %>%

  # Select every nth row from the sampling frame:
  slice(sample_rows) %>%

  # Limit the number of returned rows to the desired sample size (22)
  slice_head(n = 22)

#################
# Print results:
################

# Convert to flextable:
msystematic_pub <- flextable::qflextable(msystematic) %>%
  flextable::set_table_properties(width = 1, layout = "autofit")

msystematic_pub
```

ID	School_code
4	ACH-027
8	ACH-055
12	ACH-093
16	ACH-107
20	ACH-118
24	ACH-129
28	ACH-159
32	ACH-173
36	ACH-184
40	ACH-191
44	ACH-200
48	ACH-215
52	ACH-230
56	ACH-276
60	ACH-294

ID	School_code
64	ACH-338
68	ACH-359
72	ACH-375
76	ACH-519
80	ILIA-020
84	ILIA-029
88	ILIA-034

Advantages:

As mentioned in the background to this task, systematic sampling can be useful when you need to undertake prospective recruitment from a theoretical sampling frame of unknown size (like the number of patients attending a clinic on a given day). However, in the context of this case study, we already have a well defined and complete sampling frame (school classes, which also list the students in each class). Because of this, a systematic sampling strategy won't provide any benefits over other methods, and we can adopt the most straight-forward approach – simple random sampling!

Disadvantages:

Bias can be introduced, if the sampling units are grouped in such a way that particular characteristics occur at regular intervals Therefore, the assumption made with systematic sampling is that there is no underlying pattern in the sampling frame.

1.5: PPS sampling

Background:

The researchers originally chose to use school classes as the sampling units, because it was assumed that all classes had similar numbers of students. An alternative sampling unit would be the schools themselves; however unlike for classes, the number of students in each school varies widely.

Probability proportional to size (PPS) sampling is a method that takes varying sample sizes in the sample units into account. This helps to avoid under-representing one subgroup in a study and yields more accurate results.

In this case study, you have been provided with a list of schools in urban areas of Attiki, which also indicates the number of grade 1 students in each school and the number of classes. This data set can be imported from the `table1_5` worksheet in the `Sampling_frames.xlsx` workbook. Schools can be selected adjusting for the size of the student population, by performing PPS sampling. The column containing the number of students in each school is used as input.

Questions to answer:

1. What does "selection without replacement" suggest?

Task instructions:

1. Use the sampling frame for Attiki schools in urban areas presented in `table1_5`
2. Select 12 schools by probability proportional to size sampling *without replacement*
3. List the schools that have been selected

R coding tips:

There are several packages available on CRAN that can perform PPS sampling. In the example code below, we will use the `sampford()` function from the `pps` package to perform the sampling without replacement, which uses the classic method developed by Sampford (1967).

We can use the indices in the results to filter the sampling frame for the 12 selected schools (using `dplyr::slice()` as above).

Note that an alternative would be to use `dplyr::slice_sample()` and supply probabilities for each school to the `weight_by` argument. To do this you would have to calculate probabilities for each school: `school_frame %>% mutate(probability = Students / sum(Students))`.

We opted for using the `pps::sampford()` function, as the documentation on methods is more transparent.

Table 1.5 *- School classes selected by Probability Proportional to Size sampling*

```r
# Import the sampling frame of urban schools with grade 1 classes in Attiki:
school_frame <- rio::import(here::here("data", "Sampling_frames.xlsx"),
                            which = "table1_5")

# Perform PPS sampling to select 12 schools:
mpps <- school_frame %>%

  # Select schools by PPS without replacement:
  slice(pps::sampford(size = Students, n = 12)) %>%

  # Arrange in ascending order by ID:
  arrange(ID)

##################
# Print results:
##################

# Convert to flextable:
mpps_pub <- flextable::qflextable(mpps) %>%
  flextable::set_table_properties(width = 1, layout = "autofit")

# Print:
mpps_pub
```

ID	Code	School	Classes	Students
5	ATT-819	ΔΗΜΟΤΙΚΟ ΝΕΑΣ ΙΩΝΙΑΣ 18ο	4	88
6	ATT-898	ΔΗΜΟΤΙΚΟ ΑΘΗΝΩΝ 123ο	4	116
13	ATT-936	ΔΗΜΟΤΙΚΟ ΜΑΡΚΟΠΟΥΛΟΥ 3ο	1	21
14	ATT-937	ΔΗΜΟΤΙΚΟ ΚΕΡΑΤΕΑΣ 3ο	4	112
16	ATT-943	ΔΗΜΟΤΙΚΟ ΑΘΗΝΩΝ 115ο	4	76
17	ATT-944	ΔΗΜΟΤΙΚΟ ΑΘΗΝΩΝ 116ο	2	40
24	ATT-972	ΔΗΜΟΤΙΚΟ ΚΑΛΛΙΘΕΑ 14ο	4	96
28	ATT-085	ΔΗΜΟΤΙΚΟ ΑΘΗΝΩΝ 125ο	2	44
33	ATT-097	ΔΗΜΟΤΙΚΟ ΖΩΓΡΑΦΟΥ 11ο	3	66
34	ATT-098	ΔΗΜΟΤΙΚΟ ΑΘΗΝΩΝ 117ο	4	88
36	ATT-104	ΔΗΜΟΤΙΚΟ ΤΑΥΡΟΥ 5ο	5	105
48	ATT-139	ΔΗΜΟΤΙΚΟ ΑΓΙΟΙ ΑΝΑΡΓΥΡΟΙ 10ο	3	54

Selection “without replacement” suggests that after selection, a school is NOT included in the draw and may not be selected again. Therefore, if a school is “selected” for a second or a third time, this is not taken into account.

1.6: Cluster sampling

Background:

Cluster sampling and stratification was used in this survey.

Questions to answer:

1. Describe the basic idea of cluster sampling and stratification.
2. What are the effects of these elements on the precision of the estimates?
3. Think of extreme situations to intuitively understand these effects.

Cluster sampling and stratification:

1. Cluster sampling:

Basic idea:

- group sampling units (or, better, use "natural" grouping of sampling units; e.g. students grouped in school-classes or schools)
- select a sample of these groups.

Effect on precision:

- decrease in precision compared to simple random sampling (for the same sample size), (confidence intervals tend to be wider)
- homogeneity between clusters and heterogeneity within clusters is an advantage: precision increased

Extreme situation:

- all clusters are 100% homogeneous between them, e.g. there is exactly the same vaccination coverage in all school-classes
- as if clusters were part of the same simple random sample

2. Stratification:

Basic idea:

- group sampling units (or, better, use "natural" grouping of sampling units; e.g. students, school-classes or schools grouped in regions)
- select a sample in each group separately

Effect on precision:

- Increase in precision compared to simple random sampling (for the same sample size), (confidence intervals tend to be narrower)
- heterogeneity between strata and homogeneity within strata is an advantage: precision increased

Extreme situation:

- all strata are 100% heterogeneous between themselves, e.g. extreme differences in vaccination coverage in different regions
- as if strata are comprised of totally different populations
- advantage in employing separate sampling procedures rather than mixing the populations

We will discuss these issues in more depth in the following session.

S2: Sample size

Session overview

One of the most important factors to consider in the design of a survey is the choice of an appropriate sample size. Studies that are too small may fail to detect important effects or obtain an imprecise estimate. Studies that are larger than necessary are a waste of time, money and other resources. In this session, you will perform all the necessary calculations to obtain the required sample size for a single proportion. The formulas are provided for each approach, so that you can initially perform your own calculations using a calculator. The R coding tips for this session then show you how to perform the same calculations using R.

A presentation on "Sample size calculation" should precede this session.

This session consists of 3 Tasks:

- *Task 2.1* – Sample size calculation for a single proportion
- *Task 2.2* – Sample size calculation for a single proportion using the design effect
- *Task 2.3* – Sample size calculation using R

Note that this case study covers only sample size calculations for a single proportion based on the precision of a study. It is not intended to cover sample size calculations based on the assessments of sample size or power for studies that compare proportions, means or incidence rates between two groups.

2.1: Single proportion sample size

Background:

The formula used to calculate confidence intervals, assuming simple random sampling can be rearranged to calculate sample size as below:

$$n = \frac{z^2 \cdot p \cdot (1-p)}{d^2}$$

However, this does not take population size into account. An adjusted version of the formula that includes a finite population correction is presented below:

$$n = \frac{z^2 \cdot p \cdot (1-p) \cdot N}{[d^2 \cdot (N-1)] + [z^2 \cdot p(1-p)]}$$

where:

- n = sample size
- N = total population
- d = precision of the estimate or Standard Error (SE)
- z = number of standard errors away from the mean of the sampling distribution ($z = 1.96$ for 95% CI)
- p = estimated proportion in the sample

Note that this expression incorporates the finite population correction (fpc) $1 - \left(\frac{n}{N}\right)$. If the population is very large relative to the sample (i.e. small sampling fraction), the fpc approximates 1 and can be reasonably omitted. If the entire population is included in the sample, the fpc becomes 0 and so does the standard error. As a rule of thumb, the fpc should not be ignored if the sampling fraction $\left(\frac{n}{N}\right)$ exceeds 5%-10% or if the total sampling population is less than 10 000 people. In that case, if the fpc is not used in the formula, the confidence intervals will be wider and the sample size larger than necessary. Otherwise, the size of the total population from which the sample is drawn has little effect in practice, and may be ignored.

Previous vaccination coverage surveys in the country have shown that vaccination coverage exceeded 85% for most vaccines. As the country was divided into 6 regions for this study, each region was considered as a separate survey and calculations were performed for each one to give the sample size with a fixed precision. The researchers decided to estimate the vaccine coverage for each of the 6 regions of the country with sufficient precision of ± 4%. This way, the precision of the overall national estimate was somewhat better than that for any single region. They also considered the response rate for a previous vaccine coverage survey of similar magnitude, which was 87.5%. The sample size was adjusted with a buffer to account for an estimated 12.5% of children in the sampling frame being non-respondents.

The following table presents the total number of pupils in the target class and age group for each region.

Table 2.1 - Total number of pupils recorded in the sampling frame, by region.

Region	Number of pupils (sampling frame)
Thraki	4201
Macedonia-Thessalia	31045
Ipeiros-Ionian Islands	5055
Peloponnisos-Sterea Ellada	17741
Attiki	30586
Kriti-Aegean Islands	12218
Greece (total)	100846

Questions to answer:

1. Based on the above formula, which parameters should you take into account for the calculation of a sample size for a single proportion, assuming simple random sampling?
2. Taking into account the population by region in table 2.1, calculate the required sample size in each region, assuming simple random sampling.
3. Adjust the sample sizes calculated in the previous step with a buffer to take into account any practical limitations you might encounter when rolling out the survey, such as non-responders.

Parameters required to calculate sample size:

The required sample size should be determined by focusing on the primary objective of the study (e.g. the estimation of vaccination coverage among 6-year-old children in Greece in this survey). To calculate the number of participants required to achieve the objectives of the survey, you should specify the following:

- *Expected frequency of the principal outcome measure (based on the main objective of the study) (e.g. expected vaccination coverage)*: The expected frequency may be obtained from previous surveys of similar subject matter. Note that the sample size will be largest when $p = 0.5$ and it decreases slowly as the difference between p and 0.5 increases. Hence, if the expected frequency is unknown, choosing 0.5 for p will always provide enough observations, irrespective of the true population proportion.

- *The desired precision of the study:* To select the appropriate sample size it is necessary to decide how precise you would like your estimate (e.g. vaccination coverage) to be. The amount of "precision" (sampling error) is represented by the width of the confidence interval around your estimate. The narrower the confidence interval (CI), the greater the precision of the estimate, but the higher the number of subjects that you need to include in the study. It is therefore necessary to decide on the width of an acceptable confidence interval. Hence, you should specify to within how many percentage points of the population value your sample estimate should be. For example, if the expected vaccination coverage is 50%, you may wish your sample estimate to be within 1%, giving a confidence interval of 49% to 51%.

- *The quantity z, that represents the number of standard errors away from the mean of the sampling distribution:* For a level of significance of 5% (95% CI), $z = 1.960$, whereas for significance levels of 10% (90% CI) or 1% (99% CI), $z = 1.645$ or $z = 2.576$, respectively.

Regional sample size calculation - task description:

1. Calculate the single proportion sample size required for each region, assuming simple random sampling;
2. Use the per region student population from table 2.1, previous vaccination coverage estimate and the desired precision presented in the background information above in your calculations;
3. Adjust your calculations to take into account the lower response rate (87.5%) achieved in previous surveys.

R coding tips:

The sampling frame sizes by region in table 2.1 can be imported into R from the `table2_1` worksheet in the `Sampling_frames.xlsx` workbook.

To calculate sample size for each region, we can use the `sampler` package. In the first instance, the `rsampcalc()` function can be used for each region. The function arguments correspond to the parameters above as follows:

- *N* = population (i.e. number of students in each region from table 2.1)
- *e* = tolerable margin of error (i.e. desired precision of +/- 4%)
- *ci* = confidence interval (i.e. 95% - the default value)
- *p* = anticipated response distribution (convert 85% vaccination coverage to proportion i.e. 0.85)
- *over* = desired over-sampling proportion (convert 87.5% response to inverse proportion i.e. 1 - 0.875)

Note that the last argument, `over` can be used to increase the sample size in order to compensate for a low response rate, by taking the inverse proportion of the response rate from previous surveys (1 - 0.875) and adding this to the calculated sample size as a buffer.

To first have a look at the sample sizes without this buffer, leave this argument on its default setting (0).

We will add the sample size calculations with and without a buffer to the table, using the `dplyr` package. We will then use the `qflextable()` function from the `flextable` package to display the results in a printable format.

Table 2.1 *- Estimated sample size by region and urban / rural residence area*

```
#########################
# Import data
#########################

# Import the sampling frame of urban schools with grade 1 classes in Attiki:
region_frame <- rio::import(here::here("data", "Sampling_frames.xlsx"),
```

```
                            which = "table2_1")

#########################
# Calculate sample size
#########################


# Calculate sample size (number of students to survey) for each region:
region_frame <- region_frame %>%

  # Create new column fpc and calculate per-region sample size
  # (with finite population correction):
  mutate(fpc = sampler::rsampcalc(N = Student_pop,
                                  e = 4,
                                  ci = 95,
                                  p = 0.85,
                                  over = 0)) %>%

  # Create new column buffer and calculate sample size again
  # this time adding a buffer for a response rate of 87.5%:
  mutate(buffer = sampler::rsampcalc(N = Student_pop,
                                  e = 4,
                                  ci = 95,
                                  p = 0.85,
                                  over = 1 - 0.875))

#########################
# Present in a table
#########################

rfpub <- region_frame %>%

  # Convert data.frame to flextable:
  flextable::qflextable()

# Print the table:
rfpub
```

Region	Student_pop	fpc	buffer
Thraki	4,201	286	322
Macedonia-Thessalia	31,045	304	342
Ipeiros-Ionian islands	5,055	289	326
Peloponnisos-Sterea Ellada	17,741	301	339
Attiki	30,586	304	342
Kriti-Aegean islands	12,218	299	337

If you calculate sample size using the first formula (without a finite population correction) this yields:

$$\frac{1.96^2 \cdot 0.85 \cdot (1 - 0.85)}{0.04^2} = 306$$

In the `fpc` results column in the table (which represents sample size with a finite population correction but without adjustment for non-responders), you can see that regions with a population size of more than 10 000 (such as Macedonia-Thessalia or Attiki) have sample sizes very close to 306, whereas the regions with populations less than 10 000 (such as Thraki and Ipeiros-Ionian Islands) have smaller sample sizes when the finite population correction is applied.

The `buffer` results column shows the sample size with a buffer to account for an estimated 12.5% of the sample frame being non-responders. This can also be calculated from the original sample size with a calculator using the following formula:

$$buffered = n \cdot (1 + pnr)$$

where:

- $buffered$ is the sample size with a buffer added for the estimated proportion of non-responders
- n is the original sample size (with or without the finite population correction)
- pnr is the estimated proportion of non-responders

2.2: Design effect

Background:

So far, you have calculated the required sample size, assuming simple random sampling. However, the more complex sampling methods used in this study result in additional variability in the sample estimate and therefore require a larger sample size. For example, in this sampling design there is variability:

- between clusters (school classes)
- between pupils within the clusters

To account for the additional variability at the different stages of complex designs, the sample size and sample estimates can be adjusted by a factor known as the design effect ($deff$). This compares the variance (i.e. the square of the Standard Error (SE)) of estimates from the more complex design used, to the variance that would come from the same sample size if simple random sampling had been used.

For cluster sampling, the variance can be calculated with the following formula:

$$SE^2 = \frac{\sum(p_i - p)^2}{m \cdot (m-1)} \cdot (1 - m/M)$$

where:

- SE^2 is the variance (square of the Standard Error)
- p_i is the proportion (e.g. vaccination coverage) in each cluster
- p is the estimated proportion for the whole population (e.g. 85% vaccination coverage)
- m is the number of clusters selected in the sample (e.g. 342 school classes in this study)
- M is the total number of clusters in the population (e.g. XX school classes in the whole country)

The design effect can then be calculated by:

$$deff = \frac{SE^2 \text{ from complex design}}{SE^2 \text{ from simple random sampling}}$$

The sample size will increase by the amount of the design effect. For example, if the design effect is estimated as 1.5, this means that in order to obtain the same precision, 50% more individuals must be studied with the complex design than with the simple random sampling strategy.

When cluster sampling is used, subjects belonging to a particular cluster (e.g. household, community, school class) tend to have characteristics which make them more similar to each other than subjects belonging to other clusters. If the outcome of interest is more likely to occur within certain clusters than others, the estimates of prevalence will be less precise than if individuals were selected at random. For this reason, the sample size required to achieve a certain level of precision must be larger for cluster sampling than simple random sampling. As mentioned earlier, to allow for the additional variability, the design effect should be estimated. Apart from the previously presented formula, the design effect can also be calculated with the intra-cluster correlation coefficient, or rho :

$$deff = 1 + (n - 1) \cdot rho$$

where:

- n is the average number of subjects per cluster and
- rho is the intra-class correlation coefficient or rate of homogeneity for the outcome of interest.

This is a measure of how different people are within a cluster (compared to people chosen randomly). This coefficient can range, in theory, from very small negative values or zero, when subjects within each cluster tend to be very diverse or representative of the sampling population (heterogeneity), to a maximum of one when subjects within each cluster are similar, but differ from cluster to cluster (homogeneity). In practice, the value of rho may be between 0.05 and 0.4 depending on the amount of variation between clusters and the variables of interest.

The value of rho (or equivalently of $deff$) can be estimated from previous surveys of similar design and subject matter. If the intra-class correlation coefficient is not available, plausible values must be estimated. Alternatively, to estimate rho, you could perform a pilot study, sampling an equal number of people (n) from some clusters and then estimating the vaccination coverage and the design effect. Subsequently, you could rearrange the above formula to calculate rho instead of $deff$.

The previous round of this vaccination coverage survey (conducted in 1997) estimated a rho of 0.05. The mean number of pupils in first grade school classes was 20.

Questions to answer:

1. Suppose that the SE of an estimate from a complex design is 0.0265 and from a simple random sample 0.0246 and that you would need 200 subjects if you had used simple random sampling. How many subjects would you need for the complex design?
2. When calculating the design effect with rho, what is the role of the size of selected clusters on the required sample size?
3. Taking into account the cluster sampling design used, calculate the number of subjects you would need:
    a. in each region of the country and
    b. the overall required sample size

c. How many clusters would you need?

Number of subjects required for complex design:

Using the formula to calculate design effect by comparing the variance for simple and complex sampling, you should get:

$$\frac{0.0265^2}{0.0246^2} = \text{design effect of } 1.16$$

This suggests that for the complex design you would need a 16% higher number of subjects compared to those needed for simple random sampling to achieve the same precision. This means that you would need:

$$200 \times 1.16 = 232 \text{ subjects}$$

Role of selected cluster size on required sample size:

If the number of subjects in each cluster (n) is large, the product $(n-1) \cdot rho$ and the design effect will also be large, suggesting a bigger required sample size. To minimise the design effect, you should minimise the size of each cluster (n). Therefore, it follows from the formula that a large number of small clusters is better – provided that other things are equal - rather than a small number of large clusters.

Recalculating regional sample size taking into account the design effect:

Calculating the design effect with $n = 20$ and $rho = 0.05$, you should get:

$$1 + (20 - 1) \cdot 0.05 = \text{design effect of } 1.95$$

Note that rho is more likely to be constant from one survey to another, rather than the design effect that depends on the cluster sample size.

You previously estimated that you would need 350 subjects from each region, if simple random sampling were used. A design effect of 1.95 suggests that you would need almost twice the number of subjects you would have recruited if you had used simple random sampling, e.g.:

$$(350 \cdot 1.95) \cdot 6 \text{ regions} = 4095 \text{ subjects in total}$$

The number of clusters required for a study can be estimated by dividing the total number of individuals required by the average cluster size. As the mean number of pupils in first grade school classes was 20, you should get:

$$\frac{4095}{20} = 205 \text{ clusters (school classes)}$$

Note that stratification usually leads to a small reduction in the standard error of the overall estimate p (and / or equivalently in the sample size), compared to the error that would have been obtained if the survey had not been stratified. However, the improvement in precision cannot be quantified adequately to allow its use in sample-size calculations. Therefore, in this study where stratification was used, the required sample size to achieve the same precision, may have been smaller compared to the one that would have been required if stratification had not been used. You may also notice that the overall sample size

used in the study was slightly different from the one estimated here. This is because some minorities were oversampled to achieve more accurate estimates for these groups.

2.3: Sample size in R

Task description for R code:

1. Use a *rho of 0.05* and mean cluster (class) size of 20 to calculate the design effect;
2. Adjust the sample sizes calculated in task 2.1 to account for the design effect;
3. Calculate the total number of clusters required using the adjusted sample size.

R coding tips:

As for the calculation by hand / calculator, we will use the same formula to calculate the design effect in R. Note that R can be used as a calculator for simple mathematical operations; this allows these calculations to be incorporated into an R script and then applied to a column of values.

Using the table `region_frame` that we created in the previous task, we will then multiply each original sample size in the 6 regions by the calculated design effect. We will display the results in an updated `flextable`.

Next, we can add the adjusted sample sizes of all the regions together to obtain the total sample size needed for the study.

Finally, we can divide the total adjusted sample size (sum of number of students to survey in the 6 regions) by the average cluster (class) size (20).

Note that we will use the base R function `round()` to round up sample sizes to have no digits after the decimal point, since sample sizes need to be expressed in whole numbers.

Table 2.3 - *Regional sample size with adjustments for population, non-responders & design effect*

```
# Calculate the design effect given n = 20 and rho = 0.05:
deff <- 1 + (20 - 1) * 0.05

# Add new rho-adjusted sample size calculation to the table:
region_frame <- region_frame %>%

  # Calculate sample size with adjustment for the design effect:
  mutate(ndeff = round(buffer * deff, digits = 0))

# Calculate the number of clusters (school classes) required:
nclusters <- round((sum(region_frame$ndeff)) / 20, digits = 0)

##################
# Print results:
################

# Print number of clusters required:
nclusters
```

```
## [1] 196

# Convert to flextable:
rfpub <- flextable::qflextable(region_frame) %>%
  flextable::set_table_properties(width = 1, layout = "autofit")

# Print table:
rfpub
```

Region	Student_pop	fpc	buffer	ndeff
Thraki	4,201	286	322	628
Macedonia-Thessalia	31,045	304	342	667
Ipeiros-Ionian islands	5,055	289	326	636
Peloponnisos-Sterea Ellada	17,741	301	339	661
Attiki	30,586	304	342	667
Kriti-Aegean islands	12,218	299	337	657

Note that the total number of clusters required in the study is slightly smaller when the sample sizes are calculated with the finite population of each region ($n = 195$), compared to sample size calculated without taking into account regional differences in population ($n = 205$).

S3: Analysis plan

Session overview

In this session, you will consider how the analysis plan leads to a data collection instrument.

The session consists of the following task:

- *Task 3.1* – From analysis plan to data collection

To complete the work in this session you will need:

- A computer and Word programme

3.1: Data & analysis plan

Background:

Following the definitions of the objectives, you should:

- define the indicators, for each objective
- define data to be collected, for each indicator
- define data source for each piece of information to be collected
- define the data collection method, for each piece of information to be collected

Methods used to collect data are divided into quantitative and qualitative methods. To select the most appropriate data collection method for your study, you should ask yourself the following four questions:

1. Will the chosen method help to meet the objectives of the study?
2. Is the method appropriate for my study design?
3. Is the method feasible and practical?
4. Do I have the funds to use this method?

Task instructions:

Based on the objectives of the study (presented in session 1) answer the following questions:

1. Which indicators would you use for each objective?
2. Based on these indicators, what type of data would you like to collect?
3. Choose the appropriate method to collect these data.
4. Create a table for your answers with the following columns:

    a. Objective

b. Indicator

c. Data required

d. Data source(s)

e. Data collection method(s)

Data collection plan:

The study aimed to collect information on:

- *Objective 1* - vaccination status of children, nationally, by geographic area and by minority group
- *Objective 2* - demographic characteristics of children and parents/guardians
- *Objective 3* - parental perceptions on immunisation and attitudes towards vaccination
- *Objective 4* - barriers to vaccination as perceived by parents/guardians

Indicators, possible data sources and data collection methods to achieve each objective are listed in the tables below.

Objective 1: Estimate VCE for study population nationally, by region & minority

Parameter	Details
Indicator	• Number of vaccinated 6 year old children in survey • Population of surveyed 6 year old children
Data type(s)	• Vaccination status of children for each vaccine • Population of 6 year old children by region and area
Data source(s)	• Vaccination cards • Vaccination registries • Population census • School registries
Data collection	• Existing records • Self-administered questionnaires • Personal interviews

Objective 2: Association between socioeconomic characteristics and complete vaccination status

Parameter	Details
Indicator	*Descriptive:* • Proportion of children aged 6 years old with completed vaccination status by socioeconomic characteristics *Analytic:*

Parameter	Details
	• Comparison of the vaccination coverage among children with certain socioeconomic characteristics with that of children without these characteristics.
Data type(s)	• Vaccination status of each child • Demographic characteristics of the children and their parents or guardians
Data source(s)	• Vaccination cards • Vaccination registries • Population census • School registries
Data collection	• Existing records • Self-administered questionnaires • Personal interviews

Objective 3: Effect of parental beliefs and attitudes on immunisation compliance

Parameter	Details
Indicator	*Descriptive:* • Proportion of vaccinated children whose parents reported certain beliefs concerning vaccination. *Analytic:* • Comparison of the vaccination coverage among children whose parents reported certain beliefs with that of children whose parents did not report these beliefs.
Data type(s)	• Vaccination status of each child • Parental perceptions on immunisation and attitudes towards vaccination
Data source(s)	• Vaccination cards • Vaccination registries • Parents or guardians of children
Data collection	• Existing records • Self-administered questionnaires

Parameter	Details
	• Personal interviews • Focus groups

Objective 4: Effect of barriers to vaccination on complete vaccination status

Parameter	Details
Indicator	*Descriptive:* • Proportion of vaccinated children whose parents reported barriers to vaccination. *Analytic:* • Comparison of vaccination coverage among children whose parents reported barriers to vaccination with that of children whose parents did not report barriers to vaccination.
Data type(s)	• Vaccination status of each child • Parental perceived barriers to vaccination
Data source(s)	• Vaccination cards • Vaccination registries • Parents or guardians of children
Data collection	• Existing records • Self-administered questionnaires • Personal interviews • Focus groups

The researchers used three sources to collect this information:

1. School registry to obtain basic information about the school, including a list of all selected school classes and pupils and basic demographic characteristics of the selected children. An extraction form is provided in Annex 1.

2. Child vaccination booklet to gather information regarding vaccination status of children. In Greece, each child has a paper health booklet or vaccination card. The booklets/vaccination cards were photocopied and information was abstracted in a Vaccination Abstraction Form (VAF, Annex 3) that was based on the National Vaccination Programme (NVP) of Greece (Box 1).

3. Questionnaire regarding beliefs and attitudes of parents/guardians towards immunization, perceived barriers to vaccination and parental socioeconomic characteristics. Qualitative methods could have been used to gather information on perception on immunization.

The self-administered questionnaire to gather information on parental perceptions of parents/guardians towards immunization of their children (Annex 2) addressed the following issues:

- Beliefs on perceived benefits or harms of vaccination
- Perceived safety of immunizations
- Accuracy of recommendations provided by physicians
- Perceived financial, structural or health care service barriers to vaccination
- Sources of information that parents/guardians trust on immunization
- Demographic and social characteristics of parents
- Health status of child
- Identification number of respondent

The survey team consisted of 234 health professionals who received special training for the fieldwork and worked all over the country. A manual of field operations contained a detailed plan of organisational aspects and described the tasks and procedures of the study. The investigators visited the selected schools twice. During the first visit, members of the survey team handed an explanatory letter to the school headmaster providing detailed information regarding the study and asking for their cooperation. Subsequently, they handed a package for the parents/guardians containing:

1. a letter explaining the study and asking them to provide their child's vaccination booklet
2. an anonymous self-administered questionnaire asking their attitudes towards immunisation

During the second visit, the investigators received the completed questionnaires and photocopied the child's vaccination booklets.

The check-list of actions for fieldworkers is provided for information in Annex 4. The investigators then entered the data onto computers, cleaned the data and prepared for the analysis.

S4: Estimate VC

Session overview

You now have a clean data set and you are ready to analyse the data. In this session, you will:

- check if the sample is representative of the target population
- calculate the response rate and measure the potential differences between respondents and non-respondents
- estimate frequencies (or means, as appropriate) of selected covariates
- calculate sampling weights for each stratum
- estimate vaccine coverage nationally and by geographic region using the weighted proportion of sampled children vaccinated , including coveragefor different vaccines

This session consists of the following tasks:

- *Task 4.1* - Check if the sample is representative of the target population
- *Task 4.2* - Response and differences between respondents and non-respondents
- *Task 4.3* - Calculate sampling weights
- *Task 4.4* - Calculate weighted proportions
- *Task 4.5* - Estimate vaccination coverage

To complete the work in this session, you will need:

- The database `vaccine4.dta` , which is derived from two other data sets (`vaccine.dta` and `school.dta`):
  - `school.dta` contains basic information from the school registry, including a list of all selected classrooms and pupils and basic demographic characteristics of the children
  - `vaccine.dta` contain the vaccination status of children from the vaccination booklet.

A description of the variables of the two datasets is provided in Annex 5 and 6. You will find the `vaccine4.dta` data set in the `data` folder for this case study (note: although `vaccine4.dta` is a STATA data set, it can be opened in R with the `rio` package - see R coding tips below).

4.1: Sample representativeness

Background:

The first step is to check whether the sampled population is representative of the target or source population. If this is true, you can extrapolate the study results to the population from which the sample was drawn.

Questions to answer:

1. How could you show that the sampled population in your data set is representative of the source population?

Representativeness of the sampled population:

You could compare some available characteristics of the target population with those of the sampled population. For example, in this study, the age profile of participant children (mean age 6.76 years) closely resembled that of the total first year Grammar school pupils in Greece (mean age 6.68; $p = 0.16$). In addition, participant children did not differ significantly from all first year Grammar school children in terms of gender distribution ($p = 0.39$) and urban-to-rural proportion ($p = 0.86$). These suggest that the sample was representative of the source population, at least in terms of these characteristics (age, gender and urban-rural place of residence).

4.2: Respondent representativeness

Background:

The investigators compared the characteristics of respondents and non-respondents and compared them in a table. In the data set, respondents are those for whom a vaccine book was received; non-respondents are children for whom a vaccine book was not received.

Task description:

1. Determine the mean age and standard deviation of all pupils included in the survey.
2. Present counts and proportions (expressed as percentages) of surveyed pupils stratified by gender, urban/rural place of residence, minority group and country of birth.
3. Stratifying by the same variables, present counts and proportions (expressed as percentages) of respondents and non-respondents.
4. Perform a statistical test to determine if respondents differ significantly from non-respondents for each of the stratifying variables and present the results in a table.
5. What kind of bias could have been introduced due to non-response (not having a vaccine book)?
6. How would you interpret the results in the summary table in light of that limitation?

The table below lists the variables required for this task, their names and encoding:

Table 4.2 - list of required variables for respondent representativeness

No.	Variable label	Variable name	Factor level encoding
1.	Receipt of vaccine book (response)	vaccrec	No / no n - response = 0 Yes / response = 1
2.	Age of child	age	In years (with decimals)
3.	Gender	gender	Female = 0 Male = 1
4.	Urban or rural area	urban	Rural = 0 Urban = 1
5.	Minority group status	minority	General p opulation = 0 Roma = 1 Greek Muslims =

No.	Variable label	Variable name	Factor level encoding
			2 I mmigrants = 3
6.	Country of birth	country1	Other country = 0 Greece = 1

R coding tips:

The `vaccine4.dta` data only contains data for sampled students, but we can check for any differences between those that did (respondents) and didn't (non-respondents) have a vaccine book (note that subjects who did not have a vaccine book were excluded from subsequent analyses). This is encoded in the `vaccrec` variable.

We will first import the data with the `rio::import()` function. This very flexible function can be used to import many file types, including .xlsx, .csv and (in this case) .dta (the data file was exported from STATA after some initial cleaning steps).

Next, you may wish to explore the data. Using the `dplyr::describe()` command as well as the information in the data dictionary (annex 5 and 6) will give you an overview of the data set.

To ensure that the variables of interest are summarised correctly, we will convert them from the binary numeric format output from STATA to categorical labelled factors:

```
################################################
# IMPORT DATA, LABEL VARIABLES AND FACTOR LEVELS
################################################

# Import the vaccine coverage study data for session 4:
vaccine <- rio::import(here::here("data", "vaccine4.dta"))  %>%

  # Convert vaccrec to a factor and add nice display labels:
  mutate(vaccrec = factor(vaccrec,
                          levels = c(0, 1),
                          labels = c("Non-respondents", "Respondents"))) %>%

  # Convert gender to a labelled factor:
  mutate(gender = factor(gender,
                         levels = c(0, 1),
                         labels = c("Female", "Male"))) %>%

  # Convert residence area type to a labelled factor:
  mutate(urban = factor(urban,
                        levels = c(0, 1),
                        labels = c("Rural", "Urban"))) %>%
```

```
# Convert minority to a factor and add nice display labels:
mutate(minority = factor(minority,
                         levels = c(0, 1, 2, 3),
                         labels = c("General population",
                                    "Roma",
                                    "Greek Muslims",
                                    "Immigrants"))) %>%

# Convert country1 (whether from Greece or not) to a labelled factor:
mutate(country1 = factor(country1,
                         levels = c(1, 0),
                         labels = c("Greece", "Other country"))) %>%


# Label variables with pretty names for the table:
                           ##  variable name = variable label
labelled::set_variable_labels(vaccrec = "Response status",
                              age = "Age in years",
                              gender = "Gender of pupils",
                              urban = "Area type",
                              minority = "Minority group",
                              country1 = "Country of birth")
```

Now that our data is in the correct format, we can complete table 4.2 with summary statistics. To do this we will use the `tbl_summary()` function from the `gtsummary` package. This is a very useful package that facilitates creation of nicely formatted and publishable summary tables, where you can specify what methods you want to use to summarize the data. You can also choose to apply different tests or summary methods to categorical and numeric variables, with the `tidy::select()` commands `all_categorical()` and `all_continuous()`, respectively.

To create the summary table, we stratify by the `vaccrec` variable (which indicates if a vaccine book was received or not and is a proxy for survey response). We will include the following summary statistics in the table:

- *age*: mean and standard deviation
- *gender, urban residence, minority group & country of birth*: counts and proportions (%)
- *continuous variable response differences*: student's t test (`t.test()`)
- *categorical variable response differences*: chi square test (`chisq.test()`)

You can use the results of these tests to determine if the respondents are sufficiently representative of the whole population in the sampling frame, or if there is a bias in the non-responder group that needs to be taken into account.

```
################################################
# CREATE SUMMARY TABLE BY RESPONSE STATE
################################################
```

```r
# Summarise the demographics of the two groups (+/- vaccine book) in a table:
reptable <- vaccine %>%

  # Select subset of demographic variables to include in the summary table:
  dplyr::select(vaccrec, age, gender, urban, minority, country1) %>%

  # Create summary table with gtsummary:
  gtsummary::tbl_summary(

    # Stratify by group (no vaccine book = no response, has book = response):
    by = vaccrec,

    # Add summary stats (mean + SD for continuous, proportions for
categorical):
    statistic = list(all_continuous() ~ "{mean} ({sd})",
                     all_categorical() ~ "{n} ({p}%)"),

    # Exclude NA (missing values) from the table:
    missing = "no") %>%

  # Add tests of statistical significance of differences between groups:
  add_p(test = list(all_continuous() ~ "t.test",       # Continuous variables
                    all_categorical() ~ "chisq.test"), # Categorical
variables

        # Identify grouping variable:
        group = vaccrec,

        # Define any test arguments that deviate from the default:
        test.args = list(all_tests("t.test") ~ list(var.equal = FALSE),
                         all_tests("chisq.test") ~ list(simulate.p.value =
TRUE))) %>%

  # Add total numbers to column headers:
  add_overall() %>%

  # Add descriptors of the stats presented to row labels:
  add_stat_label() %>%

  # Individually label which row had which statistical test:
  separate_p_footnotes() %>%

  # Make variable names bold and italics:
  bold_labels() %>%
  italicize_labels() %>%

  # Tidy up column headers so stats are on second line:
  modify_header(update = list(all_stat_cols(FALSE) ~ "**{level}**\nN = {n}",
                              stat_0 ~ "**Overall**\nN = {N}")) %>%
```

```
  # Convert to flextable to left-align to page margin:
  as_flex_table() %>%

  # Autofit columns to fit headers and content on one line:
  flextable::set_table_properties(width = 1, layout = "autofit")


#################
# Print results
################

reptable
```

Characteristic	Overall N = 4387	Non-respondents N = 509	Respondents N = 3878	p-value
Age in years, Mean (SD)	6.57 (0.53)	6.65 (0.68)	6.56 (0.51)	0.013[1]
Gender of pupils, n (%)				0.2[2]
Female	2,180 (50%)	261 (53%)	1,919 (50%)	
Male	2,180 (50%)	231 (47%)	1,949 (50%)	
Area type, n (%)				<0.001[2]
Rural	974 (22%)	76 (15%)	898 (23%)	
Urban	3,413 (78%)	433 (85%)	2,980 (77%)	
Minority group, n (%)				<0.001[2]
General population	3,544 (82%)	323 (74%)	3,221 (83%)	
Roma	79 (1.8%)	27 (6.2%)	52 (1.3%)	
Greek Muslims	328 (7.6%)	38 (8.7%)	290 (7.5%)	
Immigrants	352 (8.2%)	49 (11%)	303 (7.8%)	
Country of birth, n (%)				0.2[2]
Greece	4,023 (94%)	379 (93%)	3,644 (94%)	
Other country	245 (5.7%)	29 (7.1%)	216 (5.6%)	

[1]Welch Two Sample t-test

[2]Pearson's Chi-squared test with simulated p-value
(based on 2000 replicates)

Summary of respondent vs. non-respondent characteristics:

In this study, respondent and non-respondent children did not differ in their sex distribution. But they differed significantly in terms of e.g. minority group ($p < 0.001$), as immigrants or Roma were less likely to participate in the study. However, due to the high response (88%) the corresponding distributions between participant and all sampled children were similar.

Sources of potential bias:

Selection bias may be introduced if non-respondents differ significantly in terms of some characteristics compared with respondents and these characteristics are associated with vaccination coverage; e.g. if the age distribution of respondents is statistically significant different from that of non-respondents. Children without a vaccination booklet (non-respondents) may be less likely to have been vaccinated (e.g. their parents may be less likely to have complied with vaccination recommendations) and therefore the vaccination coverage of respondents may have been overestimated.

Definition of main outcomes:

The investigators used the following definitions:

A. Complete vaccination status (`vacful`):

Children were considered fully vaccinated if they had received all of the following vaccinations:

1. 5 doses of poliomyelitis vaccine
2. 5 doses of DTP vaccine
3. 2 doses of MMR vaccine
4. 3 doses of hepatitis B (HBV) vaccine and
5. full vaccination for Haemophilus Influenza type b (Hib) ^[full Hib immunisation was considered as having received one of the following:]

B. Age-appropriate vaccination (`vactime`)

Children were considered age-appropriately vaccinated if they were both completely immunised and if they had received their vaccinations at an appropriate age according to the national vaccination schedule^[i.e. if they had received all of the following, according to the NVP:].

4.3: Sampling weights

As mentioned earlier, the following sampling strategy was chosen: The country was stratified into six regions, which, apart from the capital region (Attiki), were further subdivided into urban and rural areas, to create 11 strata in total (`strata`). In each region school classes (clusters = `school`) were randomly selected with probability proportional to the total number of first year grammar school pupils. The sampling frame of all school classrooms in the country for the academic year 2004-2005, was obtained from the Greek Ministry of Education. The list contained 108 538 pupils from both public and private schools.

Task description:

1. Based on the above information, did all children have the same probability of being selected regardless of where they lived?
2. Which formula would you use to calculate the probability of selecting each child?
3. Taking into account the selected sampling scheme, how would you estimate the vaccination coverage of children in the country; would you calculate simple proportions, i.e.:

$$\text{vaccination coverage} = \frac{\text{number of children vaccinated}}{\text{total number of children}}$$

4. If not, why not?
5. How would you calculate the sampling weights in this study?

Calculating and equalising the probability of selection:

As you saw in session 2, the sampling fractions used for each region were unequal (e.g. approximately 20% of children were sampled in Thraki, but only 3% in Attiki). This suggests that the probability of being selected was higher for children living in a region where a higher sampling fraction was used (e.g. Thraki) compared to regions with a lower sampling fraction (e.g. Attiki).

Note that according to the multiplicative law of probabilities, the probability of two independent events is given by the product of their individual probabilities. Two events are independent when the value taken by the first event tells us nothing about the value taken by the other, and vice versa. The probability (π) of selecting a pupil, is the product of the probability of selecting a cluster (school class) (π cluster) with the probability of selecting an individual when his class (cluster) has been selected (π pupil in cluster).

$$\pi = \pi \text{ cluster} \cdot \pi \text{ pupil in cluster}$$

Since all pupils were included within a selected cluster, π pupil in cluster $= 1$. So, the probability of an individual pupil being selected is equal to the probability of a cluster (school class) being selected:

$$\pi \text{ cluster} = \frac{n \text{ cluster}}{\sum(n \text{ cluster})}$$

where:

- n cluster is the number of clusters included in the sample and;
- $\sum(n \text{ cluster})$ is the total number of clusters in the population.

Utility of simple proportions to estimate vaccine coverage:

The simple proportions in the sample have no real use, as the distribution in the sample does not reflect the distribution in the sampled population. To allow for different probabilities of selection of children or different levels of non-response, you need to weight the observations. An estimate for each stratum may be calculated by treating each stratum as a separate survey. A stratified estimate for the whole country may then be calculated by weighting the stratum estimates by the stratum populations. In other words, you need to use sampling weights for each stratum. The idea behind sampling weights is that they are inversely proportional to the sampling fractions. So, if you have under-sampled a particular stratum, you can give it a weight that is higher than average; and conversely if you have over-sampled a particular stratum, you give it a weight that is lower than average.

Sample weighting strategies:

There are several sampling weights that could be used in this study, such as:

- the proportion of the 6 year-old population in each stratum divided by the total population of 6-year olds in the country (derived from the latest census).

- the proportion of the total number of school classes in each stratum divided by the total number of school-classes in the country.
- the proportion of first year Grammar school classes (6-year old pupils) in each stratum divided by the total first year Grammar school classes in the country

The researchers calculated sample weights for each stratum, according to the number of 6-year old pupils in each stratum, which was derived from the sampling frame. They preferred the weights based on number of children, because this allowed for different class sizes in different strata.

Calculating sampling weights:

1. Based on the information provided in `Table 4.3`, calculate the sampling fraction and sampling weights for each of the 11 strata and add them to the table.
2. Add a new variable to your data set containing the calculated per-stratum sampling weights.

R coding tips:

Table 4.2 can be imported into R from the `table4_2` worksheet in the `Sampling_frames.xlsx` workbook. This table contains the names, IDs and urban / rural status of the 11 strata, along with the total student population from the sampling frame and the number of students selected in each stratum.

The sampling fraction and weights can easily be calculated and added in two new columns to the imported table with `dplyr` using the formulas below.

The sampling fraction is given by:

$$Samplefraction = \frac{n}{N}$$

The sampling weights are the inverse of the sample fraction:

$$Weight = \frac{1}{\left(\frac{n}{N}\right)}$$

```
##########################################
# CALCULATE SAMPLE FRACTIONS AND WEIGHTS
##########################################

# Import the summary information on the 11 strata (table 4.2):
strata_frame <- rio::import(here::here("data", "Sampling_frames.xlsx"),
                            which = "table4_2") %>%

  # Add a new column and calculate the sample fractions for each stratum:
  mutate(Sample_fraction = Selected_pupils / Total_pupils) %>%

  # Add a new column and calculate the sample weights for each stratum:
  mutate(Sample_weights = 1 / Sample_fraction)
```

Now we can print the calculated sample fractions and weights in a `flextable` :

Table 4.2 - *Per-stratum sampling fractions and sample weights*

```
# Show summary in a flextable:
tab42pub <- strata_frame %>%

  # Convert to flextable:
  flextable::qflextable() %>%

  # Autofit column widths to text:
  flextable::set_table_properties(width = 1, layout = "autofit")

# Print the table:
tab42pub
```

Stratum_id	Stratum_name	Area_type	Total_pupils	Selected_pupils	Sample_fraction	Sample_weights
11	Ipiros	urban	3,282	435	0.13254113	7.544828
12	Ipiros	rural	1,773	247	0.13931190	7.178138
21	Aegean	urban	8,609	477	0.05540713	18.048218
22	Aegean	rural	3,609	188	0.05209199	19.196809
31	Macedonia	urban	24,311	572	0.02352844	42.501748
32	Macedonia	rural	6,734	109	0.01618652	61.779817
41	Attica	urban	30,345	1,029	0.03391003	29.489796
51	Sterea	urban	12,928	512	0.03960396	25.250000
52	Sterea	rural	4,813	158	0.03282776	30.462025
61	Thrace	urban	3,069	388	0.12642555	7.909794
62	Thrace	rural	1,132	272	0.24028269	4.161765

Finally, we can add the calculated sample weights to the `vaccine` data set with a `dplyr::left_join()`:

```
# Add calculated fraction and weights to vaccine data set:
vaccine <- vaccine %>%

  # Join the fraction and weights from strata_frame to the vaccine data set:
  left_join(y = dplyr::select(.data = strata_frame, # Identify second data
set

                              # Identify columns to add:
                              Stratum_id,       # Column to match on in 2nd
```

```
data
                                Sample_fraction,  # Sample fractions to add to
data
                                Sample_weights),  # Sample weights to add to
data

            # Indicate ID columns to join by:
            by = c("strata" = "Stratum_id"))
```

4.4: Weighted proportions

Background:

You will now calculate weighted vaccination coverage as proportions.

You can think of a weighted proportion as:

- a weighted average of each observation of 0 and 1, where the weights for each stratum are equal to $\frac{N_i}{n_i}$ (i.e. inversely proportional to the sampling fraction of the ith stratum), where N_i is the total population of the stratum i and n_i is the sample size of stratum i; or
- as a weighted average of the stratum specific proportions, where the weights are equal to N_i (i.e. proportional to the stratum population sizes).

The formula for any weighted average of y, using weight w, is:

$$\text{weighted average} = \frac{\sum(w_i \cdot y_i)}{\sum(w_i)}$$

where:

- w_i is the weight to apply and
- y_i is the estimate to weight

So, there are two formulas that can be used:

1. *Formula 4.1*: $\frac{\sum\left(\frac{N_i}{n_i} \cdot x_i\right)}{\sum\left(\frac{N_i}{n_i}\right)}$ where the $\sum$ is over all observations and $x_i = 0$ or $x_i = 1$, or;
2. *Formula 4.2:* $\frac{\sum(N_i \cdot p_i)}{\sum(N_i)}$ where p_i is the stratum-specific proportion

The researchers aimed to obtain separate estimates for the urban and rural sectors of the population in each region (strata) as well as of the whole country.

Task description:

1. First, restrict the `vaccine` data set to respondents only (children for whom a vaccination booklet was available, i.e. `vaccrec == "Respondents"`).
2. Next, calculate the vaccination coverage of MMR-2 (variable name `mmr2yn`) for each stratum and add the results in a new column to `Table 4.2` (from the previous task).
3. Suppose there are only three strata (strata 11, 12 and 21) in the country. Based on the information provided in `Table 4.2`, calculate the weighted proportion of children vaccinated with MMR-2 in the country (three strata only). Use a handheld calculator or code in R.

4. Finally, calculate the weighted proportion of children vaccinated with MMR-2 in the whole country, using all 11 strata.

R coding tips:

A. Preparing the data set:

First we need to convert the `vaccrec` and `strata` variables to character class, as this is what the `survey` package expects.

We will also filter on the `vaccrec` variable using `dplyr::filter()` and selecting only those records where `vaccrec == "Respondents"`.

```
##########################################
# PREPARE AND FILTER THE DATA SET
##########################################

# Create new table of weighted MMR-2 vaccine coverage by strata:
s44data <- vaccine %>%

  # Convert vaccrec and strata to character:
  mutate(vaccrec = as.character(vaccrec),
         strata = as.character(strata)) %>%

  # Filter for respondents only:
  dplyr::filter(vaccrec == "Respondents")
```

B. Create the survey design:

You will need to set up a stratified survey design, which can be achieved with the `srvyr` package `as_survey_design()` function. This takes the following arguments:

- *ids* - this is for the variable containing cluster IDs - in this case we will not use it and set to 1[1]
- *weights* - enter the name of the `Sample_weights` variable here
- *strata* - enter the name of the variable containing the `strata` here

```
# Create the survey design:
s44design <- s44data %>%

  # Create survey design:
  srvyr::as_survey_design(ids = 1,
```

[1] Although the researchers did have clusters in their survey design (school classes), for simplicity you have just been given the sampling frames (population and number of pupils selected) for the 11 strata (urban and rural areas in each of the 6 regions). Therefore, you can undertake this task as if there were only strata and no clusters in the design.

```
                        weights = Sample_weights,
                        strata = strata)
```

C. Calculate weighted proportions (vaccine coverage estimates):

You can then apply this survey design object to the `tab_survey()` function from the `sitrep` package, which will calculate the weighted proportions, as shown below. Note that the `sitrep` package is not yet available on CRAN, but it can be installed from Github (see package install section). For other ways to calculate weighted proportions, have a look at the Survey chapter in the Epidemiologist R handbook.

The `sitrep::tab_survey()` function takes the following arguments:

- The data set with the survey design applied (can be piped in)
- The variable to calculate proportions on
- *strata* - the variable containing the strata
- *keep* - which of the values or factor levels of the variable of interest to calculate proportions for (for vaccination coverage, only vaccinated individuals need to be kept, e.g. `mmr2yn == 1`)
- *method* - which method to use to calculate the weighted proportions. Note that the default method is `logit`, but we have selected the `xlogit` method as this is closer to the approach taken in STATA.
- *wide* - whether to present the results in a wide or long format table (long format is better for multiple variables; to set to long format use `wide = FALSE`).
- *deff* - whether to include the design effect in the results table (`TRUE`) or not (`FALSE`).
- *pretty* - whether to convert results to percentages (`TRUE`) or not (`FALSE`). We have selected `FALSE` because this is not the final results table and we want to do some further formatting on the numbers.

A note on statistical methods:

The `sitrep::tab_survey()` function uses methods to calculate the proportions, confidence intervals and design effect from the `survey::svyciprop()` function. If you type `?survey::svyciprop` in the console to look at the help page for this function, you will find further details on the different methods available. The method we have chosen, `xlogit` computes confidence intervals for the calculated proportions in the following way:

1. Estimate the mean and standard error
2. Apply a logit transform to the mean
3. Use the delta method to transform the standard error estimate
4. Compute a confidence interval for the logit mean

5. Back-transform to the probability scale

Further discussion on this method and its origins is available in this StackExchange post.

```
# Calculate weighted vaccine coverage for MMR-2:
mmr2cov <- s44design %>%

  # Create weighted proportions:
  sitrep::tab_survey(mmr2yn,           # The variable to calculate
proportions on
                     strata = strata,  # The variable containing the strata
                     keep = c(1),      # The value of interest (mmr2
vaccinated)
                     method = "xlogit",# Log transformation of the mean
                     wide = FALSE,     # Long format better for a lot of
strata
                     deff = TRUE,      # Include the design effect in the
output
                     pretty = FALSE) %>% # Do not convert to percent (yet)

  # Convert strata back to numeric for merging:
  mutate(strata = strtoi(strata))
```

D. Calculate the weighted population fraction:

Next, we will merge the results (weighted proportions) to the `strata_frame` table we were working with earlier, using a `dplyr::left_join()` as before.

Then we can calculate the weighted population fraction as follows:

$$\text{Weighted population fraction} = N_i \cdot p_i$$

where:

- N_i is the total number of pupils in the study population per stratum and
- p_i is the calculated weighted proportion of MMR-2 vaccinated children from the study.

We will store the weighted population fraction in a new variable called `pop_frac`.

```
##########################################
# CALCULATE TOTAL WEIGHTED VACCINE COVERAGE
##########################################

# Add the results to the strata_frame table:
strata_frame <- strata_frame %>%

  # Add MMR-2 weighted vaccine coverage to strata_frame:
  dplyr::left_join(y = dplyr::select(.data = mmr2cov,
                                     strata,
                                     proportion,
                                     proportion_low,
```

```
                                        proportion_upp),
                    by = c("Stratum_id" = "strata")) %>%

  # Calculate weighted fraction of population:
  mutate(pop_frac = Total_pupils * proportion)
```

E. Calculate total weighted proportions for the country:

You have been asked to first calculate the total weighted vaccination coverage estimate for the first three strata only, and then for all 11 strata. In both cases, this can be achieved by:

$$\text{Total weighted VCE} = \frac{\sum(wp_i \cdot N_i)}{\sum(N_i)}$$

where:

- wp_i are the weighted proportions for each stratum and
- N_i is the population for each stratum

We can use the `dplyr::slice()` function to extract the first three rows of data to summarise (corresponding to the first three strata).

Then we can use `dplyr::summarise()` to calculate total weighted VCE using the above formula.

Finally we can use `dplyr::pull()` to print the result.

Task 4.4 - total weighted vaccination coverage for three strata

```
################################################
# CALCULATE TOTAL WEIGHTED VACCINATION COVERAGE
################################################

# Calculate total VCE for the first 3 strata:
vc_total_03 <- strata_frame %>%

  # Keep the first three rows:
  slice(1:3) %>%

  # Calculate the percentage:
  summarise(round((sum(pop_frac) / sum(Total_pupils)) * 100, digits = 2)) %>%

  # Get the number out of the data.frame:
  pull()

# Print the results:
vc_total_03
```

```
## [1] 73.21
```

Task 4.4 - total weighted vaccination coverage for eleven strata

```r
# Calculate total VCE for all 11 strata:
vc_total_11 <- strata_frame %>%

  # Calculate the percentage:
  summarise(round(sum(pop_frac) / sum(Total_pupils) * 100, digits = 2)) %>%

  # Get the number out of the dataframe
  pull()

# Print the results:
vc_total_11
```

```
## [1] 75.98
```

F. Present per-stratum weighted proportions in a table:

Finally, we will tidy up the format of the results (round up to two decimal places etc. for easier reading) and publish the results to a `flextable`. We will not go into details about `flextable` formatting syntax here, but you can read more about this in the Epidemiologist R handbook.

Table 4.4 - *Weighted vaccination coverage estimates by region and area classification, Greece*

```r
##########################################
# DISPLAY STRATIFIED RESULTS IN A TABLE
##########################################

# Create a pretty flextable of the results:
mmr2pubtable <- strata_frame %>%

  # Convert vaccine coverage estimates and 95% CIs to percent:
  mutate(across(
    .cols = tidyr::starts_with("proportion"),
    .fns = ~ scales::percent(.x, accuracy = 0.01, suffix = NULL))) %>%

  # Combine 95% CIs in one column:
  tidyr::unite(col = "mmr2_95ci",
               tidyr::starts_with("proportion_"),
               sep = " - ",
               remove = TRUE) %>%

  # Select columns for the final table:
  dplyr::select(1:7, proportion, mmr2_95ci) %>%

  # Reduce Sample fraction to two decimal places for display:
  mutate(across(
    .cols = tidyr::starts_with("Sample_"),
    .fns = ~ round(.x, digits = 2))) %>%

  # Convert to a flextable:
  flextable::flextable() %>%
```

```
  # Add nice theme:
  flextable::theme_booktabs(bold_header = TRUE) %>%

  # Add labels:
  flextable::set_header_labels(values = list(Stratum_id = "Stratum",
                                             Stratum_name = "Area",
                                             Area_type = "Type",
                                             Total_pupils = "Population",
                                             Selected_pupils = "Surveyed",
                                             Sample_fraction = "Fraction",
Sample_weights = "Weights",
                                             proportion = "MMR-2 VCE",
                                             mmr2_95ci = "95% CI")) %>%

  # Left-align first column (stratum ID):
  flextable::align(j = 1, align = "left", part = "all") %>%

  # Right-align last 2 columns (weighted VCE and 95% CI):
  flextable::align(j = 8:9, align = "right", part = "all") %>%

  # Adjust column widths to fit text:
  flextable::set_table_properties(width = 1, layout = "autofit")


##################
# Print results
################

mmr2pubtable
```

Stratum	Area	Type	Population	Surveyed	Fraction	Weights	MMR-2 VCE	95% CI
11	Ipiros	urban	3,282	435	0.13	7.54	67.97	63.11 - 72.47
12	Ipiros	rural	1,773	247	0.14	7.18	63.88	57.37 - 69.91
21	Aegean	urban	8,609	477	0.06	18.05	77.14	72.93 - 80.86
22	Aegean	rural	3,609	188	0.05	19.20	72.09	64.85 - 78.34
31	Macedonia	urban	24,311	572	0.02	42.50	78.24	74.52

Stratum	Area	Type	Population	Surveyed	Fraction	Weights	MMR-2 VCE	95% CI
								- 81.55
32	Macedonia	rural	6,734	109	0.02	61.78	83.96	75.55 - 89.87
41	Attica	urban	30,345	1,029	0.03	29.49	76.67	73.68 - 79.41
51	Sterea	urban	12,928	512	0.04	25.25	72.14	67.86 - 76.05
52	Sterea	rural	4,813	158	0.03	30.46	66.21	58.04 - 73.51
61	Thrace	urban	3,069	388	0.13	7.91	82.57	78.04 - 86.33
62	Thrace	rural	1,132	272	0.24	4.16	75.00	69.19 - 80.03

4.5: Vaccination coverage

Background:

You will now estimate the vaccination coverage of children for different vaccines and in different settings, using `srvyr::as_survey_design()` to define the survey design, and `sitrep::tab_survey()` to estimate vaccination coverage in R.

You will create and present your results in two tables, with the following objectives:

- *Table 4.5.1* - explore the impact of different survey designs on vaccine coverage estimates;
- *Table 4.5.2* - estimate vaccine coverage for different sub-populations in the study

Task description:

A - Table 4.5.1:

Calculate the proportion of children that were fully vaccinated (using the variable `vacful`) and corresponding 95% confidence intervals with the following survey designs:

- as if simple random sampling were used;
- allowing for weights by `strata`;
- allowing for weights by `strata` and clustering by `school` class;
- allowing for weights, clustering and stratification (separate result for each stratum).

You will also need to calculate:

- the design effect (for each estimate of vaccination coverage)
- the intra-class correlation coefficient or rho (for the whole study).

B - Table 4.5.2:

Estimate vaccination coverage for all the vaccines in the data set separately (including the total sub-population N, 95% CI and the design effect) for the following sub-groups:

- overall population
- different minority groups (`minority`)
- urban and rural areas (`urban`)

Then perform the same calculations for these sub-groups, this time looking at:

- complete vaccination (`vacful`)
- timeliness of vaccination (`vactime`)

Combine your results in a table and discuss any differences you observe between sub-population groups, coverage for different vaccines, or other points of interest.

R coding tips:

We recommend you begin with the `vaccine` data set that you already imported and modified during the preceding tasks in session 4.

You will be using the following key R coding strategies to create the tables, most of which you have already encountered during previous tasks:

1. `dplyr` package for all data manipulation tasks and for piping `%>%` lines of code together;
2. `srvyr::as_survey_design()` to define the survey design;
3. `sitrep::tab_survey()` to estimate vaccination coverage;
4. `flextable::qflextable()` and other `flextable` functions to create and format results tables;
5. `purrr::map()` to iterate through each vaccine and estimate vaccination coverage for each one.

The `map()` functions from the `purrr` package (which is part of the `tidyverse`) simplify the process of looping through multiple variables and performing the same operations on each of them (like a for loop).

Remember that the formula for calculating the design effect $deff$ was presented in task 2.2. You can use the same formula to solve for rho (the intra-cluster correlation coefficient) by extracting the design effect from the output of the `sitrep::tab_survey()` command that you will be using to estimate vaccine coverage.

Code for table 4.5.1:

A - simple random sampling:

In the first code chunk, we will set the survey design for simple random sampling. Note that there is no design effect, because there are no strata, clusters or weights in this design. We can represent this with 1.

```
#####################################
# 01. SIMPLE RANDOM SAMPLING
#####################################

# Use this first result as the base row of table 4.5.1
# Results for the other survey designs can be appended to the same table

# Create new table of full vaccine coverage by (a) simple random sampling:
table451a <- vaccine %>%

  # Convert vaccrec to character:
  mutate(vaccrec = as.character(vaccrec)) %>%

  # Filter for respondents only:
  dplyr::filter(vaccrec == "Respondents") %>%

  # Create survey design for SRS:
  srvyr::as_survey_design(ids = 1,            # No cluster variable
                          weights = NULL,     # No weights
                          strata = NULL) %>%  # No strata

  # Create proportions for fully vaccinated:
  sitrep::tab_survey(vacful,           # The variable to calculate
proportions on
                     strata = NULL,    # Simple random sampling has no strata
                     keep = c(1),      # The value of interest (fully
vaccinated)
                     method = "xlogit",# Use CDC SUDAAN method
                     wide = FALSE,     # Long format better for tabulating
results
                     deff = TRUE,      # Include the design effect in the
output
                     pretty = FALSE) %>% # Do not merge VCE and 95% CI yet

  # Add a design column to describe each survey design:
  mutate(design = "Simple random sampling") %>%

  # Update the design effect where NA to 1 (representing no effect):
  mutate(deff = replace_na(deff, 1))
```

B - Sampling with weights:

We can compute vaccine coverage with weights by repeating the steps in the previous chunk, but this time including the `Sample_weights` variable in the survey design. The results can then be appended to the previous table.

```
#####################################
# 02. SAMPLING WITH WEIGHTS
#####################################

# Create new table of full vaccine coverage by (b) sampling with weights:
table451b <- vaccine %>%

  # Convert vaccrec to character:
  mutate(vaccrec = as.character(vaccrec)) %>%

  # Filter for respondents only:
  dplyr::filter(vaccrec == "Respondents") %>%

  # Create survey design for sampling with weights:
  srvyr::as_survey_design(ids = 1,                  # No clustering
                          weights = Sample_weights, # This time include
weights
                          strata = NULL) %>%        # No strata

  # Create proportions for fully vaccinated:
  sitrep::tab_survey(vacful,           # The variable to calculate
proportions on
                     strata = NULL,    # Weighted sampling has no strata
                     keep = c(1),      # The value of interest (fully
vaccinated)
                     na.rm = TRUE,     # Remove missing values
                     wide = FALSE,     # Long format better for a lot of
strata
                     deff = TRUE,      # Include the design effect in the
output
                     method = "xlogit",# Use CDC SUDAAN method
                     pretty = FALSE) %>% # Do not merge VCE and 95% CI yet

  # Add a design column:
  mutate(design = c("Sample weights"))
```

C - Sampling with weights and clustering:

As before, we can repeat the same code, this time adding `school` classes as clusters to the `ids` argument in the call to survey design:

```
########################################
# 03. CLUSTER SAMPLING WITH WEIGHTS
########################################

# Create new table of full vaccine coverage by (C) cluster sampling with
weights:
table451c <- vaccine %>%

  # Convert vaccrec to character:
  mutate(vaccrec = as.character(vaccrec)) %>%

  # Filter for respondents only:
  dplyr::filter(vaccrec == "Respondents") %>%

  # Create survey design for sampling with weights:
  srvyr::as_survey_design(ids = school,              # Clustering by school
class
                          weights = Sample_weights,  # Use sampling weights
                          strata = NULL) %>%         # No strata

  # Create proportions for fully vaccinated:
  sitrep::tab_survey(vacful,           # The variable to calculate
proportions on
                     strata = NULL,    # Weighted sampling has no strata
                     keep = c(1),      # The value of interest (fully
vaccinated)
                     wide = FALSE,     # Long format better for a lot of
strata
                     deff = TRUE,      # Include the design effect in the
output
                     method = "xlogit",# Use CDC SUDAAN method
                     pretty = FALSE) %>% # Do not merge VCE and 95% CI yet

  # Add a design column:
  mutate(design = c("Sample weights + clusters"))
```

D - Cluster sampling with weights and strata:

We can again repeat the same code, this time adding the `strata` to the survey design. We will not add strata to the `tab_survey()` command, however, as to complete table 4.5.1, we need the total population estimate rather than the estimates for each stratum. The stratification is however taken into account in the survey design.

We will also round up the results to make them easier to read, and print them to a `flextable()`.

```
########################################
# 04. CLUSTER SAMPLING, WEIGHTS & STRATA
########################################

# Create table of full vaccine coverage by (d) cluster sampling, weights &
strata:
table451d <- vaccine %>%

  # Convert vaccrec to character:
  mutate(vaccrec = as.character(vaccrec)) %>%

  # Convert strata to character:
  mutate(strata = as.character(strata)) %>%

  # Filter for respondents only:
  dplyr::filter(vaccrec == "Respondents") %>%

  # Create survey design for sampling with weights, clusters & strata:
  srvyr::as_survey_design(ids = school,             # Cluster by school class
                          weights = Sample_weights, # Include sample weights
                          strata = strata) %>%      # Include strata

  # Create proportions for fully vaccinated:
  sitrep::tab_survey(vacful,           # The variable to calculate
proportions on
                     strata = NULL,    # To get the total we will leave this
NULL
                     keep = c(1),      # The value of interest (fully
vaccinated)
                     wide = FALSE,     # Long format better for a lot of
strata
                     deff = TRUE,      # Include the design effect in the
output
                     method = "xlogit",# Use CDC SUDAAN method
                     pretty = FALSE) %>% # Do not merge VCE and 95% CI yet

  # Add a design column:
  mutate(design = c("Sample weights + clusters + strata"))
```

Now that the table is complete, we can tidy up the decimal points and convert the estimates and confidence intervals to percentages to make them easier to read.

Table 4.5.1 - *Vaccination coverage estimates with different survey designs*

```
# Bind results together in one table:
table451 <- dplyr::bind_rows(table451a, # VCE with Simple random sampling
                             table451b, # VCE with weights
                             table451c, # VCE with weights + clustering
                             table451d) # VCE with weights + clustering +
strata


# Create publishable table of results:
table451pub <- table451 %>%

  # Now we can convert the estimates and 95% CI to percentages:
  mutate(
    across(
      # for each column which has proportion in the name
      contains("proportion"),
      # convert to a percentage
      ~ scales::percent(.x, accuracy = 0.01))) %>%

  # And finally we can trim the decimal places for other columns:
  mutate(deff = round(deff, digits = 2)) %>%

  # Create merged column for 95% CIs:
  tidyr::unite(
    # name the new column CI95
    col = "CI95",
    # state which two columns to combine
    proportion_low, proportion_upp,
    # separate the values with a dash
    sep = " - ",
    # drop the old columns
    remove = TRUE
    ) %>%

  # Select the columns to print:
  dplyr::select(design,
                deff,
                n,
                proportion,
                CI95) %>%

  # Lastly we can convert it to a flextable for printing:
  flextable::qflextable() %>%

  # Add labels:
  flextable::set_header_labels(values = list(design = "Survey design",
                                             deff = "Design effect",
                                             n = "VCE (n)",
                                             proportion = "VCE (%)",
```

```
                                          CI95 = "95% CI")) %>%

  # Right-align last 2 columns (weighted VCE and 95% CI):
  flextable::align(j = 4:5, align = "right", part = "all") %>%

  # Adjust column widths to fit text:
  flextable::set_table_properties(width = 1, layout = "autofit")


##################
# Print results
#################

table451pub
```

Survey design	Design effect	VCE (n)	VCE (%)	95% CI
Simple random sampling	1.00	2,350.00	60.99%	59.44% - 62.52%
Sample weights	1.41	55,831.77	62.96%	61.17% - 64.71%
Sample weights + clusters	2.37	55,831.77	62.96%	60.62% - 65.23%
Sample weights + clusters + strata	2.36	55,831.77	62.96%	60.63% - 65.23%

Interpreting the design effects:

Estimations are modified when the sampling design is taken into account:

- allowing for the sample weight modifies the estimate of vaccination coverage
- allowing for the clustering (or multistage design) decreases the precision of the estimate (higher variance and design effect)
- allowing for the stratification improves the precision of the estimate (lower variance and design effect)

Note that the point estimate depends on the weights only, while the 95% CIs depend on everything (weights, stratification and clustering).

A design effect of 1.346 suggests that the variability (variance or the square of the standard error) of the estimate under the chosen design is 34.6% larger than that of the same-sized simple random sampling. Similarly, a design effect of 2.255 suggests that the variability of the estimate allowing for clustering, stratification and sampling weights is 125.5% larger than that would come from the same sample size if simple random sampling were used.

E - Estimating the intra-class correlation coefficient:

We can solve for rho (intra-class correlation coefficient) using the equation that was presented in task 2.2, with the following values as input:

- Mean school class (cluster) size: **20**

- Design effect from the weighted, stratified cluster sampling: **2.36**

This can be calculated as follows:

$$rho = \frac{(deff - 1)}{(n - 1)}$$

where:

- rho is the intra-class correlation coefficient
- $deff$ is the design effect
- n is the mean size of clusters

```
# Calculate ICC:
study_rho <- (2.36 - 1) / (20 - 1)

# Print result:
study_rho
```

```
## [1] 0.07157895
```

As mentioned earlier, rho is the proportion of the total variation in the outcome that is between clusters; this measures the degree of similarity or correlation between subjects within the same cluster. The larger rho is (the tendency for subjects within a cluster to be similar), the greater the size of the design effect and the larger the number of additional subjects required to achieve the same precision.

Note that in the sample size calculations in session 2, the design effect and rho were expected to be higher (2 and 0.05, respectively). Hence, the sample size actually achieved was slightly smaller and the estimates were a bit less precise than originally expected.

Code for table 4.5.2

In this section, we will include weights, clusters and strata in all the survey designs and estimate vaccine coverage (*n* and %), 95% confidence intervals and the design effect for:

1. Each vaccine, separately : dtp3yn, dtp4yn, dtp5yn, mmr1yn, mmr2yn, hibprmyn, hibfulyn, hbv3yn, mnc1yn, pne1yn and var1yn) ;
2. For DTP-3 (dtp3yn) also stratify by minority and urban/rural residence;
3. For complete vaccination (`vacful`) also stratify by minority and urban/rural residence;
4. For timeliness of vaccination (`vactime`) also stratify by minority and urban / rural residence.

We will then combine the results in a single table as for the previous section.

Because most of this code is repetitive we will use the `map()` function from the `purrr` package to iterate (repeat) code for each of this variables. This may seem scary at first, but try to remember that we are just using the functions from previous sessions and running them multiple times, once for each variable. `purrr` will store the output in a list object, but using `bind_rows()` we can easily and simply combine these in to a single data frame.

We will first create the survey design (which is the same for the whole table):

```
vce_design <- vaccine %>%

  # Convert vaccrec to character:
  mutate(vaccrec = as.character(vaccrec)) %>%

  # Convert strata to character:
  mutate(strata = as.character(strata)) %>%

  # Filter for respondents only:
  dplyr::filter(vaccrec == "Respondents") %>%

    # Create survey design for sampling with weights, clusters & strata:
  srvyr::as_survey_design(ids = school,
                          weights = Sample_weights,
                          strata = strata)
```

Next, we will create the first results for DTP3 (3-dose anti- diphtheria, tetanus and pertussis vaccine) stratified by minority group and then by urban / rural area of residence using the `tab_survey()` function from the `sitrep` package, and `purr::map()` to loop over the two stratifiers.

Note that `strata` in the survey design refers to how the sampling protocol was stratified - this is distinct from the `strata` argument in `tab_survey()` , which will calculate separate vaccine coverage estimates for each level of the stratifying variable.

```
##############################################
# Estimate VC for DTP3 by minority and urban:
##############################################


restab452a <- purrr::map(
  # for each of the variables listed
  .x = c("minority", "urban"),
  # run the following function (replacing x with each variable one-by-one)
  .f = function(x) {

    # using the study design object
    vce_design %>%
      # Create proportions for DTP3 stratified by the current variable being
run:
      sitrep::tab_survey(dtp3yn,
                         # purrr replaces x with "minority" and then with
"urban"
                         # x is in curly brackets so it is interpreted as a
                         # variable name instead of a character
                         strata = {x},
                         keep = c(1),
                         na.rm = TRUE,
                         method = "xlogit",
                         wide = FALSE,
                         deff = TRUE,
                         pretty = FALSE) %>%

      # Rename minority column to stratum:
      # Note that here we dont need curly brackets
      # (because we want it to be a character)
      rename(stratum = x) %>%

      # Remove row with missing values:
      filter(!is.na(stratum))
  }
) %>%
  ## pull the results out of lists and in to a single dataframe
  bind_rows()
```

For the next set of variables to tabulate, we do not require stratification. Instead of iterating over the stratifying variable, we can iterate over each of the vaccines to get an overall estimate for each.

```
# Create a list of variables (vaccines) to estimate vaccine coverage with:
varlist <- c("dtp4yn",
             "dtp5yn",
             "mmr1yn",
             "mmr2yn",
             "hibprmyn",
             "hibfulyn",
```

```
              "hbv3yn",
              "mnc1yn",
              "pne1yn",
              "var1yn")


restab452b <- purrr::map(
  # for each of the variables listed
  .x = varlist,
  # run the following function (replacing x with each variable one-by-one)
  .f = function(x) {

    vce_design %>%
      # purrr replaces x with each of the vaccines listed
        # x is in curly brackets so it is interpreted as a
        # variable name instead of a character
      sitrep::tab_survey({x},
                         strata = NULL,
                         keep = c(1),
                         na.rm = TRUE,
                         method = "xlogit",
                         wide = FALSE,
                         deff = TRUE,
                         pretty = FALSE) %>%

      # Create stratum column:
    mutate(stratum = "Overall")
  }
) %>%
  bind_rows()
```

Next, we can look at vaccine completeness, stratified by minority group and urban/rural residence. We repeat the above process to run each of the variables through the strata argument of the `tab_survey()` function from `sitrep`.

```
restab452c <- purrr::map(
  .x = c("minority", "urban"),
  .f = function(x) {

    vce_design %>%
      sitrep::tab_survey(vacful,
                         # purrr replaces x with "minority" and then with
"urban"
                         # x is in curly brackets so it is interpreted as a
                         # variable name instead of a character
                         strata = {x},
                         keep = c(1),
                         na.rm = TRUE,
                         method = "xlogit",
                         wide = FALSE,
                         deff = TRUE,
```

```
                          pretty = FALSE) %>%

      # Rename minority column to stratum:
      rename(stratum = x)  %>%

      # Remove row with missing values:
      filter(!is.na(stratum))
  }
) %>%
  bind_rows()
```

Finally we can repeat the same process for vaccination timeliness. Note that we could have saved some repeating code by nesting `map()` arguments, to iterate over both vaccines and strata groups. For simplicity, we have not done this, but if you have extra time - try this out.

```
restab452d <- purrr::map(
  .x = c("minority", "urban"),
  .f = function(x) {

    vce_design %>%
      sitrep::tab_survey(vactime,
                         # purrr replaces x with "minority" and then with
"urban"
                         # x is in curly brackets so it is interpreted as a
                         # variable name instead of a character
                         strata = {x},
                         keep = c(1),
                         na.rm = TRUE,
                         method = "xlogit",
                         wide = FALSE,
                         deff = TRUE,
                         pretty = FALSE) %>%

      # Rename minority column to stratum:
      rename(stratum = x) %>%

      # Remove row with missing values:
      filter(!is.na(stratum))
  }
) %>%
  bind_rows()
```

Lastly, we can combine all the tables together and tidy up the decimals and add percentages to make the results easier to read, as before.

Table 4.5.2 - *Vaccination coverage estimates stratified by population sub-groups*

```
# combine each of the result tables in to one
restabpub <- bind_rows(restab452a,
                       restab452b,
                       restab452c,
                       restab452d
                       ) %>%
  # to be able to ignore the value column (which only contains 1s)
  ungroup()


# Create publishable table of results:
restabpub <- restabpub %>%

  # Now we can convert the estimates and 95% CI to percentages:
  mutate(
    across(
      # for each column which has proportion in the name
      contains("proportion"),
      # convert to a percentage
      ~ scales::percent(.x, accuracy = 0.01))) %>%

  # And finally we can trim the decimal places for other columns:
  mutate(across(c(n, deff),
                ~ round(.x, digits = 2))) %>%

  # Create merged column for 95% CIs:
  tidyr::unite(
    # name the new column CI95
    col = "CI95",
    # state which two columns to combine
    proportion_low, proportion_upp,
    # separate the values with a dash
    sep = " - ",
    # drop the old columns
    remove = TRUE
    ) %>%

  # Select the columns to print:
  dplyr::select(variable,
                stratum,
                deff,
                n,
                proportion,
                CI95) %>%

  # Recode variable names to nice labels for printing (see data dictionary):
  mutate(variable = dplyr::recode(variable,
                                  dtp3yn = "DTP: 3 doses",
                                  dtp4yn = "DTP: 4 doses",
```

```
                                  dtp5yn = "DTP: 5 doses",
                                  mmr1yn = "MMR: 1 dose",
                                  mmr2yn = "MMR: 2 doses",
                                  hibprmyn = "HiB: partial",
                                  hibfulyn = "HiB: full",
                                  hbv3yn = "HBV: 3 doses",
                                  mnc1yn = "Men C: 1 dose",
                                  pne1yn = "Pneumo: 1 dose",
                                  var1yn = "Varicella: 1 dose",
                                  vacful = "Fully vaccinated",
                                  vactime = "Timely vaccination")) %>%

  # Lastly we can convert it to a flextable for printing:
  flextable::qflextable() %>%

  # Merge cells in the vaccine colum as the values are repeated:
  flextable::merge_v(j = c("variable"), target = c("variable")) %>%

  # Add labels:
  flextable::set_header_labels(values = list(variable = "Vaccine",
                                             stratum = "Stratum",
                                             deff = "Design effect",
                                             n = "VCE (n)",
                                             proportion = "VCE (%)",
                                             CI95 = "95% CI")) %>%

  # Right-align last 2 columns (weighted VCE and 95% CI):
  flextable::align(j = 5:6, align = "right", part = "all") %>%

  # Add borders under the merged cells:
  flextable::hline(i = rle(cumsum(.$body$spans$columns[,1] ))$values,
                   border = fp_border(style = "solid", width = 1)) %>%

  # Fix thickness of bottom border:
  fix_border_issues() %>%

  # Add bottom border back:
  flextable::hline_bottom(border = fp_border(style = "solid", width = 2),
                          part = "body") %>%

  # Adjust column widths to fit text:
  flextable::set_table_properties(width = 1, layout = "autofit")

##################
# Print results
#################

restabpub
```

Vaccine	Stratum	Design effect	VCE (n)	VCE (%)	95% CI
DTP: 3 doses	General population	2.97	78,513.23	99.52%	99.12% - 99.74%
	Roma	4.04	806.59	79.65%	55.95% - 92.35%
	Greek Muslims	2.34	1,597.77	96.31%	91.77% - 98.39%
	Immigrants	2.80	7,368.36	98.99%	96.40% - 99.72%
	Rural	6.97	16,653.61	98.37%	96.76% - 99.19%
	Urban	6.97	71,969.94	99.39%	98.93% - 99.65%
DTP: 4 doses	Overall	1.91	87,865.44	98.35%	97.70% - 98.81%
DTP: 5 doses	Overall	1.71	80,472.99	90.07%	88.80% - 91.22%
MMR: 1 dose	Overall	1.75	87,813.85	98.29%	97.67% - 98.75%
MMR: 2 doses	Overall	3.10	67,899.19	76.00%	73.60% - 78.24%
HiB: partial	Overall	1.45	80,408.32	90.00%	88.83% - 91.06%
HiB: full	Overall	1.51	76,325.71	85.43%	84.04% - 86.72%
HBV: 3 doses	Overall	1.75	85,147.72	95.30%	94.36% - 96.10%
Men C: 1 dose	Overall	2.76	64,162.29	71.82%	69.45% - 74.07%
Pneumo: 1 dose	Overall	1.74	4,095.83	4.58%	3.80% - 5.52%
Varicella: 1 dose	Overall	2.65	11,595.27	12.98%	11.38% - 14.76%
Fully vaccinated	General population	2.14	52,238.06	66.61%	64.20% - 68.94%
	Roma	3.40	245.60	24.25%	9.13% - 50.52%

Vaccine	Stratum	Design effect	VCE (n)	VCE (%)	95% CI
	Greek Muslims	1.85	849.63	51.22%	40.56% - 61.76%
	Immigrants	1.71	2,197.89	30.31%	25.03% - 36.18%
	Rural	6.38	9,610.30	57.06%	50.56% - 63.33%
	Urban	6.38	46,221.47	64.34%	61.85% - 66.75%
Timely vaccination	General population	1.64	42,600.03	55.39%	52.85% - 57.91%
	Roma	0.80	18.05	2.15%	0.22% - 17.75%
	Greek Muslims	1.44	491.35	30.52%	23.30% - 38.85%
	Immigrants	1.69	1,232.06	16.96%	12.39% - 22.77%
	Rural	4.94	7,773.62	47.46%	40.45% - 54.57%
	Urban	4.94	36,766.93	52.12%	49.48% - 54.74%

Summarizing the results:

- Vaccination coverage was high for vaccines included in the NVP before 1990 (i.e. DTP, Po, MMR). However, the uptake of 2 doses of MMR was much lower than the WHO target of 95%.
- Vaccination coverage was satisfactory for Hib and HepB that were introduced in the NVP in 1998 and 2002, respectively.
- Uptake for vaccines introduced in the NVP in 2006 ranged from high (MNC that was available in the pharmacies earlier) to very low (PCV7 and Var)
- Vaccination uptake was lower among Greek Roma and to a lesser degree among immigrants
- There were no substantial differences in the vaccination coverage in urban and rural areas.

Types of practices administering vaccines:

The investigators also estimated the weighted proportions of practices administering MMR-1 and other vaccines. Almost 70% of MMR-1 vaccines were administered in private practices. Approximately 90% of the first doses of MMR among Greek Roma were administered in state practices, with the corresponding proportions among immigrants, Greek Muslims and the general population being 53%, 45% and 26%, respectively. Similar patterns were observed for most, but not all, vaccines.

S5: Modelling PR

Background to the analytical study:

During the study, parents/ guardians of participating children were asked to complete a self-administered questionnaire, indicating their agreement with statements on perceived benefits or harms of and barriers to immunization on a four-point scale, with possible responses ranging from "completely agree" to "completely disagree". These answers were transformed to ordinal numeric scores between 1 and 4, with the maximum score corresponding to "completely agree" for the positively worded statements or "completely disagree" for the negatively worded statements.

Definition of positive opinion towards vaccination:

A balanced positive opinion towards immunization was defined as agreement with the following two positively worded statements:

- "Vaccinations are necessary for my child" and
- "I keep my child's vaccination up to date, according to scientific advice"

and disagreement with the following two negatively worded statements:

- "I fear that vaccines may harm my child" and
- "Natural childhood disease is certainly preferable to vaccination"

The scores from each of these statements were summed up, with higher scores denoting more positive beliefs regarding vaccination. Based on these scores, balanced positive opinion was classified as strong (score > 7.5), moderate (score between 6.0 and 7.5) and weak (score <6.0).

Uncritical positive opinion towards immunization was defined as agreement with the following two statements:

- "Children should be immunized immediately with every newly licensed vaccine" and
- "Vaccines are completely safe and never harm child's health"

Other statements addressed issues regarding newly licensed vaccines, perceived safety of vaccination, accuracy of recommendations, financial profit and perceived financial, structural or health care service barriers to vaccination.

Session overview

In this session, you will describe beliefs and attitudes of parents/guardians towards immunization, their perceived barriers to vaccination and their socioeconomic characteristics. You will subsequently identify which of those factors are associated with low vaccination coverage.

This session consists of the following tasks:

- *Task 5.1* - Describe parental characteristics, beliefs towards vaccination and perceived barriers to immunization
- *Task 5.2* - Identify unadjusted (crude) associations with having a fully vaccinated child
- *Task 5.3* - Identify adjusted associations of parental characteristics, parental beliefs towards vaccination and perceived barriers to immunization with having a fully vaccinated child

To complete the work in this session, you will need:

The database `vaccine5.dta` that is derived from the three data sets (`vaccine.dta`, `school.dta` and `quest.dta`); `quest.dta` contains information from the self-administered questionnaire completed by parents/guardians regarding beliefs and attitudes towards immunization, perceived barriers to vaccination and parental socioeconomic characteristics. A description of the variables of the three datasets is provided in the appendix. All these datasets have been simplified for the purpose of this case study.

The researchers are interested in finding out if there is any correlation between parental beliefs and the vaccination status of their child. The following table lists the variables you will be working with in this session and any recoding or transformation required:

Table 5.0.1 - list of variables required for session 5 tasks

Characteristic or belief	Variable name	Class	Transform
Sample weights (numeric value)	weight	Numeric	-
Urban / rural region (numeric stratum ID)	strata	Factor	Convert to factor
School class (numeric cluster ID)	school	Factor	Convert to factor
Fully vaccinated status (outcome measure)	vacful	Binary (0, 1)	-
Minority group status	minority	Factor	New ref: Roma
Mother's age at child's birth	mage	Factor	<25, 25-29, >=30
Number of other siblings	osib1	Factor	>=3, 1-2, 0
Father's education (no. years)	educf	Factor	Convert to factor
Balanced positive opinion on vaccination (L)	a1posg	Factor	Convert to factor
Balanced positive opinion on vaccination (B)	a1posyn	Factor	Convert to factor

Characteristic or belief	Variable name	Class	Transform
Uncritical positive opinion on vaccination	u ncritical	Factor	Convert to factor
Vaccination is necessary for my child	a1x1g	Factor	Convert to factor
Vaccines may harm my child	a1x2g	Factor	Convert to factor
Natural infection preferable to vaccination	a1x5g	Factor	Convert to factor
Barrier: long distance to immunization site	a3x1g	Factor	Convert to factor
Barrier: inconvenient opening hours	a3x2g	Factor	Convert to factor
Barrier: high cost of vaccines	a3x5g	Factor	Convert to factor

You will use te first three variables (`weight`, `strata` and `school`) to create the survey design, as before. In task 5.3 where the survey design is not needed, `school` will still be used to define the clusters.

Throughout this session, you will use the binary variable `vacful` as the outcome measure. Note that this variable is already in the correct format for inclusion in the analytic tasks (1 = fully vaccinated).

The next four variables (minority group, mother's age at child's birth, number of other siblings and father's education in years) represent key characteristics about the parents or family of the child who has been enrolled in the study. Each of these variables will require some transformation before analysis, as they will be easier to interpret as categorical factors (ordered for the last three).

Variables that are currently classified as numeric and continuous (e.g. mother's age at child's birth) will need to be converted to factors with each level / group defined as detailed in table 5.0 above.

For each factor, you may wish to consider how to order the factor levels and also which level to assign as the reference, to best facilitate interpretation. Specific instructions on this are provided in the relevant tasks.

The remaining 9 variables represent statements on beliefs about vaccination and barriers to vaccination. Parents were asked to indicate whether they agreed or disagreed with each statement, on a Likhert scale. Eight of these variables have been converted to binary answers (0 = no / disagree, 1 = yes / agree) for convenience. Note that the question on balanced positive opinion on vaccination is represented in two different ways; Likhert (no opinion, moderate, strong) and binary (no / yes). There is likely to be some autocorrelation or co-linearity between these two variables, which you will explore in task 5.3, when choosing what to include in the model.

As before, please refer to the following appendices for full details on how these variables are coded:

- Annex 5: `school` data set (contains basic demographic variables on recruited children)
- Annex 6: `vaccine` data set (contains the vaccine records of recruited children)
- Annex 7: `quest` data set (encoded, scaled answers to the parental questionnaire on vaccine beliefs)

5.1: Descriptive analysis

Background:

In this task, you will perform descriptive analysis and calculate the survey design-adjusted proportions of study children by certain parental characteristics;

- membership of a minority group
- mother's age at childbirth
- number of other siblings in the family

You will present your results in a new table (`table 5.1`). Consider the implications of these proportions on study power before estimating vaccine coverage in the next task.

Task description:

Using the data set `vaccine5.dta` you will:

1. Create an age group variable for mother's age (`mage`) as follows: (<25, 25-29, >=30 years)
2. Create categories for number of other siblings in the family (`osib1`) : (>=3, 1-2, 0)
3. Create appropriate labels for the recoded variables
4. Estimate the proportions for each of the parental characteristics listed below, using a survey design that takes into account the weights, clustering and strata that were used during the sampling.

The parental characteristics to estimate proportions for in table 5.1 are as follows:

Table 5.0.2 - parental characteristics to include

Variable description	Variable name	Comments
Minority group	`minority`	Convert to factor and add factor level labels
Mother's age at childbirth	`mage`	Create age groups: <25, 25-29, >=30
Number of other siblings	`osib1`	Divide into categories: >=3, 1-2, 0

R coding tips:

A - Data import and preparation

First, we will import the data `vaccine5.dta` which you can find in the `data` folder, as before.

Because we will use the same data set for the rest of this session, we will also prepare (recode or reclassify, as necessary) the other variables required for tasks 5.2 and 5.3 in this data preparation step. The purpose of the recoding is to make the results easier to interpret in the models.

01. Reclassifying categorical variables as factors

Note that several categorical variables (such as `minority`) are currently interpreted by R as being numeric. We can update these variables to labelled factors using the base R function `factor()`. Refer to appendices 5, 6 and 7 to obtain the labels for the different factor levels in each variable.

02. Converting numeric variables to ordered categories

We can create ordered categorical versions of the variables `mage` (mother's age group), `osib1` (number of siblings) and `educf` (number of years of father's education) using the dplyr function `case_when()`. We will supply labels for each level of the new variables as character strings.

03. Reordering factor levels

Next, we will convert the two new categorical variables to an ordered factor, by using the `forcats::fct_relevel()` function. You can check that the factor levels are in the correct order with `levels()`.

Note:

In the code below, the recoding of all the variables has been piped together using `%>%` so that the data set only has to be imported and named once, at the top of the piping chain. This is for convenience and is useful practice to reduce duplication in your code, thus making it more readable.

However, if you prefer to see the impact of each step on the data set separately, you could break the chain into separate steps (piping from the `vaccine` data set for each step). You can also highlight the existing piped code to just before the relevant pipe operator and press `Ctrl + Enter` to run e.g. just the first step, the first and second step or the first second and third step etc.

```
############################################################
# 02. IMPORT DATA, CONVERT TO FACTORS, LABEL & ORDER LEVELS
############################################################

# Import vaccine5.dta:
vaccine <- rio::import(here::here("data", "vaccine5.dta"))  %>%

  # Convert minority to a labelled factor:
```

```r
  mutate(minority = factor(minority,
                           levels = c(0, 1, 2, 3),
                           labels = c("General population",
                                      "Roma",
                                      "Greek Muslims",
                                      "Immigrants"))) %>%

  # Create new categorical variable (agegroup) from mother's age:
  mutate(magegroup = case_when(

    # Logical criteria      Label
    mage < 25               ~ "Under 25",
    between(mage, 25, 29)   ~ "25 - 29",
    mage >= 30              ~ "30 or over")) %>%

  # Convert to a factor and put the age groups in ascending order:
  mutate(magegroup = forcats::fct_relevel(magegroup,
                                          "Under 25",
                                          "25 - 29",
                                          "30 or over")) %>%

  # Create new categorical variable for number of siblings:
  mutate(nsibcat = case_when(

    # Logical criteria      Label
    osib1 >= 3              ~ "3 or more",
    between(osib1, 1, 2)    ~ "1 - 2",
    osib1 == 0              ~ "No siblings")) %>%

  # Convert to a factor and put the categories in descending order:
  mutate(nsibcat = forcats::fct_relevel(nsibcat,
                                        "3 or more",
                                        "1 - 2",
                                        "No siblings")) %>%

  # Convert school (numeric IDs) to a factor:
  mutate(school = factor(school)) %>%

  # Create a labeled factor from educf for father's education:
  mutate(educf = factor(educf,
                           levels = c(2, 3, 4, 6),
                           labels = c("Grammar school (< 9 years)",
                                      "High school (9 - 11 years)",
                                      "College (12 years)",
                                      "University (> 12 years)"))) %>%

  # Create labelled factor for a1posg (balanced positive opinion, 3
categories):
  mutate(a1posg = factor(a1posg,
                         levels = c(0, 1, 2),
```

```
                          labels = c("No positive opinion",
                                     "Moderate positive opinion",
                                     "Strong positive opinion")))
```

04. Bulk processing: reclassifying a list of variables as factors

Lastly, there are a number of additional variables to include in tasks 5.2 and 5.3, where parental responses to questions about vaccination have been recorded as binary (no = 0, yes = 1). In preparation for the analysis, we will recode these as factors. Because they all have the same number of factor levels (n = 2) and because the two factor levels have the same labels ('no' or 'yes'), we can do this conversion in one go, using the dplyr convenience function `across()` with the list of variables to convert.

To facilitate this process, we will first create a list containing the names of all of the binary variables, as character strings. We will also create another list that contains both the binary variables and the other explanatory variables listed in table 5.0 that we want to iterate through in each analysis step.

We can then put the original variable names and a column of apply human readable labels in a data frame. Later, we can use the `matchmaker::match_vec()` function to recode, and automatically annotate results tables (so that the variable / question label appears in tables instead of the variable name).

```
############################
# 01. CREATE VARIABLE LISTS
############################

# First we create a list of binary variables to label:
binary_vars <- c("a1posyn",
                 "uncritical",
                 "a1x1g",
                 "a1x2g",
                 "a1x5g",
                 "a3x1g",
                 "a3x2g",
                 "a3x5g")

# Now iterate through the list of binary variables to convert them to
factors:
vaccine <- vaccine %>%
  # Mutate across list of binary variables to convert all to labelled
factors:
  mutate(across(
    .cols = c(all_of(binary_vars)),    # Columns to loop through: all
binary_vars
    .fns = ~factor(.x,                 # Function to apply: convert to factor
      levels = c(0, 1),                # Stipulate levels from existing
values
      labels = c("no", "yes"))))       # Label levels as no and yes
```

```
# Next, create a list of all variables to analyse:
allvars <- c("minority",
             "magegroup",
             "educf",
             "nsibcat",
             "a1posg",
             binary_vars)

# Create a list of nice labels for allvars:
allvarlabs <- c("Minority group",
                "Mother's age at childbirth",
                "Father's education",
                "Number of siblings",
                "Balanced positive opinion on vaccination: likhert",
                "Balanced positive opinion on vaccination: binary",
                "Uncritical positive opinion on vaccination",
                "Vaccination is necessary for my child",
                "Vaccines may harm my child",
                "Natural disease preferable to vaccines",
                "Long distance to immunization site",
                "Inconvenient opening hours",
                "Cost of vaccines")

# Create a dataframe of original variable names and labels to use in
recoding:
recoders <- cbind(allvars, allvarlabs)
```

B - Survey design

We will then create the survey design, including weights, clustering and strata, using `srvyr::as_survey_design()` as before. You will need the following variables to do this:

- `weight` : contains sampling weights as calculated earlier;
- `strata` : contains the 11 strata (urban/rural areas within the 6 regions);
- `school` : contains the ID number for each school class (cluster).

```
vce_design <- vaccine %>%

  # Create survey design:
  srvyr::as_survey_design(ids = school,      # This is the cluster variable
                          weights = weight,  # These are the sample weights
                          strata = strata)   # These are the 11 strata
```

C - Estimate stratified proportions:

Here we will calculate estimated proportions of each factor level in minority group, mother's age group and number of siblings (in categories), taking into account the survey design. We will use the `sitrep::tab_survey()` function to estimate the proportions, and `purrr::map()` to loop through the three variables of interest, `minority` , `magegroup` and `nsibcat`.

Notes:

1. Estimated proportions may be bigger or smaller than the actual proportions in the sample, because the survey design is used to estimate what the proportions in the population at large are likely to be.

2. In the `sitrep::tab_survey()` function we will set the argument `keep` to `TRUE` , since this time we want to calculate relative proportions for all the different factor levels in each variable. This is in contrast to when we were calculating vaccine coverage in the previous section; where we set `keep = c(1)` to indicate that we only wanted to calculate the proportion of vaccinated individuals (in all the vaccine variables, `vaccinated = 1`, while `not vaccinated = 0`).

```
# Create a list of variables:
varlist <- c("minority",
             "magegroup",
             "nsibcat")

# Loop over the variables:
restab452a <- purrr::map(

  # For each of the variables listed:
  .x = varlist,

  # Run the following function
  # (replacing x with each variable one-by-one)
  .f = function(x) {

    # Apply the study design:
    vce_design %>%

      # purrr replaces x with each of the variables listed
      # x is in curly brackets so it is interpreted as a
      # variable name instead of a character
      sitrep::tab_survey({x},
                         strata = NULL,
                         keep = TRUE,
                         na.rm = TRUE,
                         method = "xlogit",
                         wide = FALSE,
                         deff = TRUE,
                         pretty = FALSE)
  }

) %>%
  bind_rows()
```

D - create summary table of results

In this code chunk, we will use `flextable` as before, to create a publishable summary of the results.

Table 5.1 - *Counts and proportions of parental characteristics adjusted by survey design*

```r
# Create publishable table of results:
restabpub <- restab452a %>%

  # Now we can convert the estimates and 95% CI to percentages:
  mutate(across(contains("proportion"), ~ scales::percent(.x, accuracy =
0.01))) %>%

  # And finally we can trim the decimal places for other columns:
  mutate(across(c(n, deff), ~ round(.x, digits = 2))) %>%

  # Create merged column for 95% CIs:
  tidyr::unite(col = "CI95",
               proportion_low, proportion_upp,
               sep = " - ",
               remove = TRUE) %>%

  # Add nice names for stratifier variables to the table:
  mutate(variable = case_when(
    variable == "minority"   ~ "Minority group",
    variable == "magegroup"  ~ "Mother's age at childbirth",
    variable == "nsibcat"    ~ "Number of other siblings")) %>%

  # Select the columns to print:
  dplyr::select(variable,
                value,
                deff,
                n,
                proportion,
                CI95) %>%

  # Lastly we can convert it to a flextable for printing:
  flextable::qflextable() %>%

  # Merge cells in the stratifier colum as the values are repeated:
  flextable::merge_v(j = "variable", target = "variable") %>%

  # Add labels:
  flextable::set_header_labels(values = list(variable = "Stratifier",
                                             value = "Stratum",
                                             deff = "Design effect",
                                             n = "VCE (n)",
                                             proportion = "VCE (%)",
                                             CI95 = "95% CI")) %>%

  # Right-align last 2 columns (weighted VCE and 95% CI):
  flextable::align(j = 5:6, align = "right", part = "all") %>%

  # Add borders under the merged cells:
  flextable::hline(i = rle(cumsum(.$body$spans$columns[,1] ))$values,
                   border = fp_border(style = "solid", width = 1)) %>%
```

```
  # Add bottom border back:
  flextable::hline_bottom(border = fp_border(style = "solid",
                                             width = 2),
                          part = "body") %>%

  # Fix thickness of bottom border:
  fix_border_issues() %>%

  # Adjust column widths to fit text:
  flextable::set_table_properties(width = 1, layout = "autofit")



################
# Print results
###############

restabpub
```

Stratifier	Stratum	Design effect	VCE (n)	VCE (%)	95% CI
Minority group	General population	2.71	71,758.97	89.75%	87.98% - 91.28%
	Roma	4.48	613.05	0.77%	0.35% - 1.69%
	Greek Muslims	2.08	1,404.21	1.76%	1.23% - 2.50%
	Immigrants	2.57	6,179.91	7.73%	6.43% - 9.26%
Mother's age at childbirth	Under 25	1.38	617.59	0.78%	0.51% - 1.21%
	25 - 29	1.98	10,399.34	13.21%	11.71% - 14.87%
	30 or over	2.03	67,699.67	86.00%	84.28% - 87.57%
Number of other siblings	3 or more	2.07	5,640.21	7.17%	6.03% - 8.51%
	1 - 2	1.51	60,638.37	77.10%	75.34% - 78.77%
	No siblings	1.76	12,372.89	15.73%	14.19% - 17.41%

Summarising the results:

Parents/guardians indicated a high degree of perceived necessity of immunization with the vast majority agreeing that vaccination is beneficial for their children. In addition, 76% considered that vaccines are completely safe and never harm child health and 45% felt that children should be immediately immunized with every newly introduced vaccine (data not shown here), reflecting an uncritical positive opinion on vaccination. Only 3% feared that vaccines may expose their child to a substantial risk, suggesting minimal concerns over the side effects of vaccines. Nevertheless, one fifth reported that natural childhood disease may be preferable to vaccination, reflecting perceptions of less susceptibility to and severity of vaccine preventable diseases. More skepticism was observed regarding new vaccines and accuracy of recommendations with approximately one third feeling confused due to conflicting physicians' opinions, almost half stating the need to cross-check doctors' recommendations and about 60% believing that new vaccines are developed for financial profit (data not shown here). Despite these statements, however, parents/guardians indicated a high degree of compliance with the current official recommendations on vaccination, with almost all stating that they would keep their child's immunization up-to-date, following the current scientific advice (data not shown).

Among all respondents, cost (including the cost of the visit to an immunization provider, the fee for vaccine administration and the cost of the vaccine itself) was the barrier most commonly identified. About one fifth of respondents cited long distance to vaccination location and/or inconvenient opening hours of the immunization sites as important barriers to immunization. Other obstacles less commonly reported (not shown here) included lack of accurate information regarding immunization, unfriendly behavior of immunization staff or poor organization of services, lack of confidence in social insurance doctors, lack of paediatricians and long waiting times for appointments.

5.2: Crude associations

Background:

In this task, you will continue with analysis of parental characteristics and attitudes towards vaccination and look at the associations between these factors and vaccination coverage. You will do this by calculating bivariate statistics (vaccine coverage stratified by different parental characteristics and attitudes) as well as crude (unadjusted) prevalence ratios (univariable analysis). If you have extra time, you can also perform univariable analysis to calculate crude odds ratios.

Below is a brief description of the rationale for the analytical approach used in this session. Further reading on these issues is provided at the end of this guide in the references section.

Bivariate statistics:

As a first step in the analytical study, it is important to tabulate bivariate statistics, or create a 2x2 table, which describe the proportion and number of fully vaccinated children (outcome) by each of the potential exposure variables, e.g., parental characteristics, parental beliefs/attitudes about immunization, and perceived barriers to vaccination. Similar to the previous sections, the tabulation of summary statistics for the target population use weighted proportions to account for different probabilities of selection of children into the study sample.

Study of associations:

For the analyses of associations between potential exposures and the outcome, there is (arguably) less concern about the representativeness of identified associations for the target population. In addition, it may be difficult to assume that the estimates of associations, and their corresponding uncertainty intervals, would in fact be applicable to the whole population. For these reasons, weights are not used in regression models in this case study. Nevertheless, the analysis of cluster sample surveys must take into account the clustering of observations within primary sampling units (i.e. school classes) due to the complex survey design. Multilevel models, also known as mixed-effects models, are used in these situations in order to adjust for non-independence of study observations, and depending on the research interest, quantify the extent of clustering at the contextual level (e.g., schools, hospitals, neighbourhoods). To account for the cluster sampling design in our analysis, the primary sampling unit (school class) is specified as the random effect, or cluster variable, and all potential exposure variables are specified in the multilevel model as fixed effects nested within the primary sampling unit (school class).

Measures of associations:

Logistic regression models are often used to study associations in cross-sectional studies with binary outcomes (e.g., having a fully vaccinated child or not). However, these models estimate an odds ratio as the measure of association. Odds ratios overestimate the risk ratio when an outcome is common, or roughly above 10% prevalence. The odds ratio may therefore not be interpreted as a risk of the disease outcome, which is generally easier to understand and is the preferred measure of association. In these situations, it is preferable

to estimate a prevalence ratio as a better approximation of the risk ratio. This can be done using a Poisson regression model with robust error variance. For these reasons, this case study uses the prevalence ratio as the measure of association to estimate the risk of having a fully vaccinated child. As an optional activity at the end of this session, we provide commands to calculate the odds ratio using a mixed-effects logistic regression model, which still provides a valid measure of association but the coefficient (odds ratio) will be more difficult to interpret than a risk ratio.

Task description:

1. Tabulate bivariate statistics (create a 2x2 table) to describe parental characteristics, parental beliefs/attitudes about immunization and perceived barriers to vaccination in relation to the binary outcome of having a fully vaccinated child (`vacful`) or not. Use the explanatory variables listed in table 5.0.1 and the same survey design as for previous sections, taking into account weights (`weight`), clustering (`school`) and strata (`strata`).

2. Calculate crude measures of association, with corresponding 95% confidence intervals, between the above factors and having a fully vaccinated child (using `vacful` as the study outcome). Use a Poisson regression mixed effects model with robust error variance to calculate prevalence ratios, taking clustering into account by including `school` as the random effect, or cluster variable.

3. If you have time, complete the optional exercise and calculate crude odds ratios, using `vacful` as the outcome measure and the factors listed in table 5.0.1 as explanatory variables. As with prevalence ratios, include `school` as the random effect or cluster variable.

R coding tips:

A - Counts of fully vaccinated children:

In this section we will create a table of counts for fully vaccinated children (`vacful`), cross-tabulated by each of the variables listed in `allvars`. We can use the `sitrep` function `tab_linelist()` to generate the counts for each factor level in each variable from `allvars`.

We will also add human readable question labels to the variable names, which will make the final results table easier to understand. We will use this as the base table and add other results to it in the following sections.

```
restab52a <- vaccine %>%

  # Filter for those that are fully vaccinated only:
  dplyr::filter(vacful == 1) %>%

  # Create summary table:
  sitrep::tab_linelist(all_of(allvars)) %>%

  # Drop un-weighted proportions variable
  # (we will add weighted proportions later)
  dplyr::select(-proportion) %>%

  # We can use our dataframe of labels to recode the variable column
  # Note the quotations to define which variables in recoders to use
  # you could also simply remove these as the default recodes from col 1 to 2
  mutate(variable = matchmaker::match_vec(variable,
                                          dictionary = recoders,
                                          from = "allvars", to =
"allvarlabs"))
```

B - Vaccination coverage stratified by parental characteristics and beliefs:

Here we will repeat the same procedure using `sitrep::tab_survey()` as demonstrated in previous sections to estimate full vaccination coverage (`vacful`), taking into account weights, strata and clustering in `vce_design` and stratifying the results by each of the variables in `allvars`.

We will loop through each of the variables using `purrr::map()` as before.

We will then append the results to the table of counts we created in the previous section, using `bind_cols()` .

```
##################################
# 01. Calculate VCE proportions:
##################################

restab_vce <- purrr::map(

  # allvars is the list of variables to loop through that we already created:
  .x = allvars,
  .f = function(x) {

    vce_design %>%

      # VCE will be calculated for vacful
      sitrep::tab_survey(vacful,
                         # Each variable in allvars is a stratum
                         strata = all_of({x}),
                         # We are only interested in vacful == 1
                         keep = c(1),
                         na.rm = TRUE,
                         method = "xlogit",
                         wide = FALSE,
                         deff = TRUE,
                         pretty = FALSE) %>%

      # Rename factor level column to value:
      dplyr::rename(response = x) %>%

      # Remove rows with missing values:
      filter(!is.na(response)) %>%

      # Add the variable name to make merging more accurate:
      mutate(variable = x)

    }

  ) %>%

  # Bind the results from each variable into a data.frame:
  bind_rows() %>%
```

```
  # Remove value = 1 grouping (from vacful == 1)
  ungroup %>%

  # Trim the decimal places for other columns:
  mutate(across(c(n, deff),
                ~ round(.x, digits = 2))) %>%

  # Convert the estimates and 95% CI to percentages:
  mutate(across(contains("proportion"),
                ~ scales::percent(.x,                    # Cols to convert to %
                          accuracy = 0.1,      # No. decimal places
                          suffix = ""))) %>%   # Do not add % sign

  # Create merged column for 95% CIs:
  tidyr::unite(col = "CI95",                       # Name of new column in
quotes
               proportion_low, proportion_upp,     # Two columns to combine
               sep = " - ",                        # Separator between values
               remove = TRUE) %>%                  # Remove old columns

  # Rename proportion column to avoid confusion when merging tables:
  dplyr::rename(vce_prop = proportion) %>%

  # Add human readable labels to variable column:
  mutate(variable = matchmaker::match_vec(variable, recoders))  %>%

  # Select the columns to keep:
  dplyr::select(variable,          # Variable name from allvars (to group)
                value = response, # Rename to match restab52a (to group)
                deff,             # Design effect for reference
                n,                # Estimated count for reference
                vce_prop,         # VCE (%) to add to table
                CI95)             # VCE 95% CIs for reference
```

This survey estimated that in total, 63.8% of children in Greece were fully vaccinated at the time of the survey. Among Roma, Greek Muslims and immigrant groups, the percentage of fully vaccinated children were 40.1% (95% CI: 22.7 - 60.4), 52.8% (95% CI: 40.8 - 64.5) and 29.9% (95% CI: 24.7 - 35.8), respectively. In comparison, 67.1% (95% CI: 64.5 - 69.6) of children in non-minority groups in Greece were fully vaccinated at the time of the survey.

Now we can bind the first two tables together:

```
# Join vaccine coverage to counts table:
restab52b <- restab52a %>%

  # Merge the two tables with a left join on variable and response:
  left_join(y = dplyr::select(.data = restab_vce,
                              variable,
                              value,
                              vce_prop),
```

```
            # Join by both variable and value
            # This is safer than value alone
            # as yes/no answers are not unique
            by = c("variable", "value")) %>%

  # Add brackets around vaccine coverage estimate proportion:
  # note variables are between curly brackets {} within double quotation
marks
  mutate(vce_prop = stringr::str_glue("({vce_prop})")) %>%

  # Create combined count and estimated vaccine coverage column:
  tidyr::unite(col = "n_vce",
               n, vce_prop,
               sep = " ",
               remove = TRUE)
```

D - Crude vaccination prevalence ratios by parental characteristics and beliefs:

In this section, you will create a Poisson mixed effects model with robust error variance to calculate crude prevalence ratios, using the `feglm()` function from the `fixest` package. This package was specifically designed to make it easier to replicate model designs from STATA code in R. You can read more about the methods in the package vignette. There are also some helpful cheat sheets that show how to convert model code from STATA to R using the `fixest` package (see here and here).

Importantly for this case study, the `fixest` package also has an implementation of the Huber sandwich estimator; alternately this method is referred to as the heteroskedasticity-consistent error correction for robust error variance. In the `fixest` package, this method can be selected by setting the `vcov` argument to `hetero` (the R equivalent of STATA's `vce(robust)`). Use of this correction should result in more accurate estimates of standard errors (and therefore confidence intervals).

The `fixest::feglm()` function is specifically designed for generalised linear models with one or multiple fixed effects (the explanatory variables - in this case parental characteristics). It will also take a clustering variable (e.g. school) and use this in combination with the selected error variance method (e.g. hetero) to calculate the standard errors.

The function takes the following key arguments:

- *fml* (model formula): in the format `outcome ~ dependent` (e.g. `vacful ~ minority`)
- *family*: select the type of model and link method, e.g. `poisson(link = "log")`
- *vcov*: select error variance method and variable to cluster by, e.g. `hetero ~ school`
- *data*: name the data set, e.g. `vaccine`

Note:

1. The data set can also be piped directly into the model, if desired
2. The outcome variable for Poisson models should be binary encoded as (0, 1)

3. The explanatory variables can be factors (with any number of levels) or numeric

First, we will regress full vaccination status (`vacful`) against minority group membership (`minority`) and inspect the results to get a sense of how the model works. We will use `fixest::etable()` to look at the overall summary figures for the model.

We will then use the `broom.mixed` package (which is part of the tidyverse) to extract the estimates, 95% confidence intervals and *p* values into a table.

Note that in R, for models where the `link` is set to "log" or "logit", estimates will be calculated as log to the base 10, by default. In order to obtain prevalence, risk or odds ratios, these estimates and their 95% confidence intervals need to be exponentiated. The `tidy()` function in the `broom` and `broom.mixed` packages will already do this for commonly used models, when the argument `exponentiate` is set to `TRUE`. However, this has not yet been implemented for the `fixest` package as it is still relatively new. Fortunately, we can easily exponentiate the extracted estimates by using the base R function `exp()`.

Table 5.2.1 - *Vaccination prevalence ratio by minority group*

```
# Create the model:
model1 <- fixest::feglm(fml = vacful ~ minority,          # Model formula
                        family = poisson(link = "log"),  # Model type
                        vcov = hetero ~ school,          # SE method &
cluster
                        data = vaccine)                  # Data set

# View a summary of the results:
fixest::etable(model1)

##                                    model1
## Dependent Var.:                    vacful
##
## Constant              -0.4145*** (0.0134)
## minorityRoma           -0.8848** (0.2847)
## minorityGreekMuslims  -0.2504*** (0.0635)
## minorityImmigrants    -0.7388*** (0.0953)
## ____________________ ____________________
## S.E. type             Heteroskedast.-rob.
## Observations                        3,404
## Squared Cor.                      0.04257
## Pseudo R2                         0.01039
## BIC                               6,211.6
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Use the broom.mixed package to extract prevalence ratios and 95% CI:
model1tab <- broom.mixed::tidy(x = model1,
                               conf.int = TRUE,
                               conf.method = "Wald") %>%

  # Exponentiate estimate and 95% CIs:
```

```
  mutate(across(
    .cols = c(estimate, starts_with("conf.")),
    .fns = exp)) %>%

  # Round up numeric columns to 2 decimal places:
  mutate(across(
    .cols = where(is.numeric),
    .fns = round, digits = 2)) %>%

  # Convert to flextable for printing:
  flextable::qflextable()

# View the results:
model1tab
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	0.66	0.01	-31.03	0	0.64	0.68
minorityRoma	0.41	0.28	-3.11	0	0.24	0.72
minorityGreek Muslims	0.78	0.06	-3.94	0	0.69	0.88
minorityImmigrants	0.48	0.10	-7.76	0	0.40	0.58

This model shows that compared to the reference level (general population), the included minority groups (Roma, Greek Muslims and Immigrants) all had significantly lower vaccination prevalence ratios (the prevalence ratios are all less than 1 and the 95% confidence intervals do not cross 1).

We can now take advantage of the convenience function `purrr::map()`, to iterate through all the variables in our list (`allvars`) and calculate vaccination prevalence ratios for each of them. As before, this is most easily accomplished if we first create a function to specify the arguments in the model that will stay the same for all the variables:

```
# Function to create Poisson fixed effects model with robust errors:
poisson_tabulator <- function(predictor) {

  # Construct model formula:
  pm_formula = as.formula(stringr::str_glue("vacful ~ {predictor}"))

  # Construct the poisson model clustering by school with robust errors:
  modtab = fixest::feglm(fml = pm_formula,
                         family = poisson(link = "log"),
                         vcov = hetero ~ school,
                         data = vaccine) %>%

    # Extract the results in a table:
    broom.mixed::tidy(conf.int = TRUE,
                      conf.method = "Wald") %>%
```

```
    # Exponentiate estimate and 95% CIs:
    mutate(across(
      .cols = c(estimate, starts_with("conf.")),
      .fns = exp)) %>%

    # Round up numeric columns to 2 decimal places:
    mutate(across(
      .cols = where(is.numeric),
      .fns = round, digits = 2)) %>%

    # Merge lower and upper 95% CI in a new column:
    tidyr::unite(col = "95% CI",
                 starts_with("conf."),
                 sep = " - ",
                 remove = TRUE) %>%

    # Remove intercept:
    dplyr::filter(term != "(Intercept)")

  # Return the results table:
  return(modtab)

}
```

Next, we will apply the function to each of the variables in `allvars` by looping through them with `purrr::map()`.

Note that the results are identified by the variable name and factor level concatenated together in one word, which is not easy for external readers to interpret. To fix this, we will split the variable names and factor levels into two separate columns, `variable` and `value` using the `stringr` package functions `str_extract()` and `str_remove()`. The `|` symbol in R means `OR` and can be used to search for any of the variables in `allvars` when pasted between the variable names (e.g. `minority|magegroup|educf` means `minority` OR `magegroup` OR `educf`).

```
# Apply the model to the list of variables called 'allvars':
poiscrudetab <- allvars %>%

  # Loop them through the 'poison_tabulator' function we just created:
  purrr::map(poisson_tabulator) %>%

  # Bind the results into a single table:
  bind_rows() %>%

  # Split term into two columns (variable name and level / value):
  dplyr::mutate(

    # Create variable col (strings in 'term' that match any of allvars):
    variable = stringr::str_extract(term,
                                    str_c(allvars, collapse = "|")),
```

```
    # Create value col (whats left after strings matching allvars are
removed):
    value = stringr::str_remove(term,
                                str_c(allvars, collapse = "|"))) %>%

    # Add human readable labels to values in the variable column:
    mutate(variable = matchmaker::match_vec(variable, recoders)) %>%

    # Remove unnecessary columns:
    dplyr::select(-term, -std.error, -statistic) %>%

    # Reorder new columns:
    relocate(c(variable, value), .before = estimate) %>%

    # Put estimate with 95% CI:
    relocate(p.value, .before = estimate)
```

Finally, generic `dplyr` functions can be used to further arrange the results as desired and they can be printed with the `flextable` package, as before.

Table 5.2.2 - *Vaccination prevalence ratios by parental characteristics and beliefs*

```
poiscrudetabpub <- poiscrudetab %>%

  # Convert to a flextable:
  flextable::qflextable() %>%

  # Merge cells in the vaccine colum as the values are repeated:
  flextable::merge_v(j = c("variable"), target = c("variable")) %>%

  # Label column headers:
  flextable::set_header_labels(values = list(
    variable = "Parameter",
    value = "Characteristic",
    p.value = "P value",
    estimate = "Prevalence ratio",
    `95% CI` = "95% CI")) %>%

  # Right align numeric results columns:
  flextable::align(j = 3:5,
                   align = "right",
                   part = "all") %>%

  # Add highlighting of significant values:
  flextable::bg(i = ~ p.value < 0.05,
                j = 3:5,
                bg = "yellow") %>%

  # Add border lines under the merged cells:
  flextable::hline(i = rle(cumsum(.$body$spans$columns[,1] ))$values,
                   border = fp_border(style = "solid", width = 1)) %>%
```

```
  # Fix thickness of bottom border:
  fix_border_issues() %>%

  # Add bottom border back:
  flextable::hline_bottom(border = fp_border(style = "solid", width = 2),
                          part = "body") %>%

  # Adjust column widths to fit text:
  flextable::set_table_properties(width = 1, layout = "autofit")


###################
# Print the table:
poiscrudetabpub
```

Parameter	Characteristic	P value	Prevalence ratio	95% CI
Minority group	Roma	0.00	0.41	0.24 - 0.72
	Greek Muslims	0.00	0.78	0.69 - 0.88
	Immigrants	0.00	0.48	0.4 - 0.58
Mother's age at childbirth	25 - 29	0.14	1.40	0.9 - 2.18
	30 or over	0.01	1.79	1.16 - 2.77
Father's education	High school (9 - 11 years)	0.44	1.04	0.94 - 1.16
	College (12 years)	0.00	1.15	1.06 - 1.26
	University (> 12 years)	0.00	1.30	1.19 - 1.41
Number of siblings	1 - 2	0.00	1.30	1.14 - 1.47
	No siblings	0.00	1.29	1.12 - 1.48
Balanced positive opinion on vaccination: likhert	Moderate positive opinion	0.06	1.35	0.99 - 1.84

Parameter	Characteristic	P value	Prevalence ratio	95% CI
	Strong positive opinion	0.01	1.49	1.1 - 2.03
Balanced positive opinion on vaccination: binary	yes	0.01	1.47	1.08 - 1.99
Uncritical positive opinion on vaccination	yes	0.24	0.97	0.92 - 1.02
Vaccination is necessary for my child	yes	0.42	1.56	0.53 - 4.56
Vaccines may harm my child	yes	0.00	0.77	0.65 - 0.92
Natural disease preferable to vaccines	yes	0.01	0.90	0.84 - 0.97
Long distance to immunization site	yes	0.00	0.83	0.77 - 0.89
Inconvenient opening hours	yes	0.00	0.89	0.83 - 0.96
Cost of vaccines	yes	0.42	1.02	0.97 - 1.08

We can now merge these results with the table containing counts and vaccine coverage, using the`variable` and `value` columns to ensure the matches are unique. Note that in the Poisson crude prevalence ratios table, we removed the intercepts (reference values). When the two tables are merged, the prevalence ratio for reference values will present as missing (`NA`) which we can then recode to `ref` with the `tidyr::replace_na()` function.

```
########################################
# Subsetting Poisson results for merge:
########################################

# Subset the necessary columns to merge:
poiscrudetabmini <- poiscrudetab %>%

  # Combine prevalence ratios and 95% CIs in one column:
  mutate(pr_95 = str_glue("{estimate} ({`95% CI`})")) %>%

  # Remove unnecessary columns:
  dplyr::select(-estimate, -`95% CI`, -p.value)


################################################
# Merge vaccine coverage and prevalence ratios:
################################################

# Merge the two tables with a left join on variable and value columns:
restab52c <- restab52b %>%

  # Join the counts / vaccine coverage table to the poisson table on
response:
  left_join(y = dplyr::select(.data = poiscrudetabmini,

                              # Columns to include:
                              variable,
                              value,
                              pr_95),

            # Join by variable and value to ensure unique matches:
            by = c("variable", "value")) %>%

  # Encode the missing values for intercepts as 'ref'
  # Otherwise leave the rest of the values as they are:
  mutate(pr_95 = tidyr::replace_na(pr_95, "ref"))
```

E - Crude odds ratios for vaccination by parental characteristics and beliefs (optional exercise)

If you have extra time, it may be interesting to calculate crude odds ratios and compare them to the prevalence ratios that we calculated in the previous section.

This can easily be done by repeating the same steps used to calculate prevalence ratios, but this time selecting `family = binomial(link = "logit")` instead of Poisson in the `fixest::feglm()` function.

Below is the code to do this, wrapping the model commands in a function as before and applying it to `allvars` . For convenience, we will then add the results to the table we already created, so that we can see them all together.

```
##############################################
# 01. Function to tabulate crude odds ratios
##############################################

# Function to create Poisson fixed effects model with robust errors:
or_tabulator <- function(predictor) {

  # Construct model formula:
  pm_formula = as.formula(str_glue("vacful ~ {predictor}"))

  # Construct the poisson model clustering by school with robust errors:
  modtab = fixest::feglm(fml = pm_formula,
                         family = binomial(link = "logit"),
                         vcov = hetero ~ school,
                         data = vaccine) %>%

    # Extract the results in a table:
    broom.mixed::tidy(conf.int = TRUE,
                      conf.method = "Wald") %>%

    # Exponentiate estimate and 95% CIs:
    mutate(across(
      .cols = c(estimate, starts_with("conf.")),
      .fns = exp)) %>%

    # Round up numeric columns to 2 decimal places:
    mutate(across(
      .cols = where(is.numeric),
      .fns = round, digits = 2)) %>%

    # Merge lower and upper 95% CI in a new column:
    tidyr::unite(col = "95% CI",
                 starts_with("conf."),
                 sep = " - ",
                 remove = TRUE) %>%

    # Remove intercept:
    dplyr::filter(term != "(Intercept)")

  # Return the results table:
  return(modtab)

}
```

Now we can apply the `or_tabulator` function to `allvars` :

```
# Apply the model to the list of variables called 'allvars':
orcrudetab <- allvars %>%

  # Loop them through the 'poison_tabulator' function we just created:
```

```
  purrr::map(or_tabulator) %>%

  # Bind the results into a single table:
  bind_rows() %>%

  # Split term into two columns (variable name and level / value):
  dplyr::mutate(

    # Create variable col (strings in 'term' that match any of allvars):
    variable = stringr::str_extract(term,
                                    str_c(allvars, collapse = "|")),
    # Create value col (whats left after strings matching allvars are
removed):
    value = stringr::str_remove(term,
                                str_c(allvars, collapse = "|"))) %>%

    # Add human readable labels to values in the variable column:
    mutate(variable = matchmaker::match_vec(variable, recoders)) %>%

    # Remove unnecessary columns:
    dplyr::select(-term, -std.error, -statistic) %>%

    # Reorder new columns:
    relocate(c(variable, value), .before = estimate) %>%

    # Put estimate with 95% CI:
    relocate(p.value, .before = estimate)
```

We can merge the crude odds ratios with the table that now contains vaccination coverage and prevalence ratios:

```
########################################
# Subsetting Poisson results for merge:
########################################

# Subset the necessary columns to merge:
orcrudetabmini <- orcrudetab %>%

  # Combine prevalence ratios and 95% CIs in one column:
  mutate(or_95 = str_glue("{estimate} ({`95% CI`})")) %>%

  # Remove unnecessary columns:
  dplyr::select(-estimate, -`95% CI`, -p.value)


################################################
# Merge vaccine coverage and prevalence ratios:
################################################

# Merge the two tables with a left join on variable and value columns:
```

```
restab52d <- restab52c %>%

  # Join the counts / vaccine coverage table to the poisson table on
response:
  left_join(y = dplyr::select(.data = orcrudetabmini,

                              # Columns to include:
                              variable,
                              value,
                              or_95),

            # Join by variable and value to ensure unique matches:
            by = c("variable", "value")) %>%

  # Encode the missing values for intercepts as 'ref'
  # Otherwise leave the rest of the values as they are:
  mutate(or_95 = tidyr::replace_na(or_95, "ref"))
```

Finally, we can print the combined results table using `flextable` as before:

Table 5.2.3 - *Crude measures of association between vaccination and parental characteristics*

```
crudefinaltabpub <- restab52d %>%

  # Convert to a flextable:
  flextable::qflextable() %>%

  # Merge cells in the vaccine colum as the values are repeated:
  flextable::merge_v(j = c("variable"), target = c("variable")) %>%

  # Label column headers:
  flextable::set_header_labels(values = list(
    variable = "Parameter",
    value = "Characteristic",
    n_vce = "N (VCE)",
    pr_95 = "Prevalence ratio (95% CI)",
    or_95 = "Odds ratio (95% CI)")) %>%

  # Right align numeric results columns:
  flextable::align(j = 3:5,
                   align = "right",
                   part = "all") %>%

  # Add borders under the merged cells:
  flextable::hline(i = rle(cumsum(.$body$spans$columns[,1] ))$values,
                   border = fp_border(style = "solid", width = 1)) %>%

  # Fix thickness of bottom border:
  fix_border_issues() %>%

  # Add bottom border back:
```

```
  flextable::hline_bottom(border = fp_border(style = "solid", width = 2),
                          part = "body") %>%

  # Adjust column widths to fit text:
  flextable::set_table_properties(width = 1, layout = "autofit")


##################
# Print the table:
crudefinaltabpub
```

Parameter	Characteristic	N (VCE)	Prevalence ratio (95% CI)	Odds ratio (95% CI)
Minority group	General population	1904 (67.1)	ref	ref
	Roma	9 (40.1)	0.41 (0.24 - 0.72)	0.19 (0.09 - 0.42)
	Greek Muslims	126 (52.8)	0.78 (0.69 - 0.88)	0.54 (0.42 - 0.71)
	Immigrants	77 (29.9)	0.48 (0.4 - 0.58)	0.24 (0.18 - 0.31)
Mother's age at childbirth	Under 25	13 (38.6)	ref	ref
	25 - 29	247 (52.8)	1.4 (0.9 - 2.18)	1.81 (0.9 - 3.66)
	30 or over	1823 (65.8)	1.79 (1.16 - 2.77)	3.24 (1.63 - 6.42)
Father's education	Grammar school (< 9 years)	300 (55.9)	ref	ref
	High school (9 - 11 years)	302 (58.5)	1.04 (0.94 - 1.16)	1.1 (0.86 - 1.4)
	College (12 years)	706 (64.6)	1.15 (1.06 - 1.26)	1.41 (1.15 - 1.74)
	University (> 12 years)	666 (70.5)	1.3 (1.19 - 1.41)	2.01 (1.62 - 2.5)
Number of siblings	3 or more	124 (48.6)	ref	ref
	1 - 2	1630 (65.3)	1.3 (1.14 - 1.47)	1.82 (1.4 - 2.35)

Parameter	Characteristic	N (VCE)	Prevalence ratio (95% CI)	Odds ratio (95% CI)
	No siblings	336 (65.4)	1.29 (1.12 - 1.48)	1.78 (1.31 - 2.41)
Balanced positive opinion on vaccination: likhert	No positive opinion	24 (52.3)	ref	ref
	Moderate positive opinion	330 (59.6)	1.35 (0.99 - 1.84)	1.83 (1.05 - 3.18)
	Strong positive opinion	1663 (65.5)	1.49 (1.1 - 2.03)	2.38 (1.39 - 4.06)
Balanced positive opinion on vaccination: binary	no	24 (52.3)	ref	ref
	yes	1993 (64.5)	1.47 (1.08 - 1.99)	2.26 (1.33 - 3.86)
Uncritical positive opinion on vaccination	no	1068 (65.2)	ref	ref
	yes	988 (63.1)	0.97 (0.92 - 1.02)	0.92 (0.8 - 1.06)
Vaccination is necessary for my child	no	2 (51.1)	ref	ref
	yes	2093 (64.0)	1.56 (0.53 - 4.56)	2.49 (0.41 - 14.9)
Vaccines may harm my child	no	1882 (64.4)	ref	ref
	yes	64 (54.8)	0.77 (0.65 - 0.92)	0.55 (0.39 - 0.79)
Natural disease preferable to vaccines	no	1637 (65.6)	ref	ref
	yes	359 (58.5)	0.9 (0.84 - 0.97)	0.77 (0.64 - 0.92)
Long distance to immunization site	no	1700 (66.0)	ref	ref
	yes	356 (56.0)	0.83 (0.77 - 0.89)	0.63 (0.53 - 0.75)
Inconvenient opening hours	no	1646 (65.3)	ref	ref

Parameter	Characteristic	N (VCE)	Prevalence ratio (95% CI)	Odds ratio (95% CI)
	yes	383 (59.6)	0.89 (0.83 - 0.96)	0.75 (0.63 - 0.89)
Cost of vaccines	no	1244 (64.4)	ref	ref
	yes	795 (63.8)	1.02 (0.97 - 1.08)	1.06 (0.92 - 1.23)

Interpreting the results (Table 5.2.3):

Socioeconomic factors:

Based on crude prevalence ratios (unadjusted for other factors), children were less likely to be fully vaccinated if they belonged to a minority group, were born to a younger mother, had 3+ siblings, or if their father was less educated.

Beliefs and attitudes towards immunization:

Based on crude prevalence ratios (unadjusted for other factors), children were less likely to be fully vaccinated if the parents held negative opinions about vaccination, believed that vaccines may harm their child, or believed that natural childhood disease is preferable to vaccination compared to parents who did not hold these beliefs.

Barriers to immunization:

Based on crude prevalence ratios (unadjusted for other factors), children were less likely to be fully vaccinated if their parents believed that it was a long distance to the immunization site or if they believed the immunization site had inconvenient opening hours, compared to parents who did not hold these beliefs.

5.3: Adjusted associations

Background:

This task will build on the previous task, calculating prevalence ratios as before but in a multivariable, multilevel model, using all the same variables as for task 5.2.

Key considerations:

1. Because this is a clustered sampling survey, the model must take into account the non-independence of observations within the primary sampling unit (in this case school classes).

2. This can be achieved with mixed effect models, specifying the primary sampling unit (school class) as the random effect, or cluster variable and regressing the outcome (`vacful`) against all the explanatory variables (parent characteristics and attitudes towards vaccination) as fixed effects nested within school classes.

3. As for unadjusted measures of association, calculating prevalence ratios from poisson regression with robust error variance is likely to give better estimates than odds ratios calculated from logistic regression, as these tend over-estimate the risk ratio when an outcome is common (~ > 10%).

4. Robust error variance refers to the Huber correction for calculating standard errors (the square root of the elements on the diagonal of the covariance matrix), also known as heteroskedasticity-consistent standard errors. This is sometimes referred to as the Huber sandwich estimator.

5. This approach (poisson mixed effects model with robust error variance) follows the strategy first proposed by Zou et al. (2004) - however for an alternative perspective favouring the log-binomial method for moderate prevalence and/or sample size, see Petersen and Deddens (2008). Note that in this data set we have already seen that the vaccination coverage estimate is quite high (mean 58.5, median 63.1 from table 5.2.3), so the Poisson approach is more appropriate.

Task description:

In this task you will need to undertake the following steps:

1. Build a model to calculate adjusted measures of association (prevalence ratios) taking clustering into account as before, this time including all the variables from table 5.0 in the model as fixed effects;
2. Check for any multi-colinearity;
3. Use the Wald test to identify which variables to keep in the final model and/or which are significantly associated with vaccination;
4. Present the results of the final model (adjusted prevalence ratios and 95% CI) in a table.

R coding tips:

Before proceeding, we can consider if we are happy with the reference values that were used for each categorical variable in task 5.2. Note that for the first variable, `minority`, using `General population` as the reference value yielded a prevalence ratio of less than 1 for all the other groups. It might be more intuitive to use `Roma` as the reference group, since this group has the lowest vaccination coverage. We can change the reference value by changing the order of the factor levels, using `forcats::fct_relelevel()` as shown below:

```
# Using the vaccine data:
vaccine <- vaccine %>%

  # Change the order of the factor levels so Gen Pop comes last
  # This will make Roma the first level:
  dplyr::mutate(minority = forcats::fct_relevel(.f = minority,
                                                "General population",
                                                after = Inf))
```

As before, we will use the `fixest::feglm()` function to create the Poisson model with robust error variance and calculate prevalence ratios. This time, however, instead of calculating prevalence ratios for each explanatory variable separately, we will create a model formula that includes all the variables, so that the adjusted estimates will reflect the relative contribution of each variable to the model.

In R, we can create a multivariable model and include all the variables in `allvars` as fixed effects, by separating them with a + sign in the model formula, e.g. `fml = vacful ~ minority + magegroup`.

As we have a lot of variables to include in the model (n = 13), it would be more convenient to pass them to the model in the list we already made (`allvars`). Fortunately, the `fixest` package has a convenient way for us to code this: we can simply put the name of our variable list in the model formula, enclosed in square brackets and preceded by a dot: `fml = vacful ~ .[allvars]`. The model will be built by placing a plus sign between each of the explanatory variables in `allvars` on the right hand side of the tilde (~).

```
# Create the Poisson model with robust error variance:
modelres <- vaccine %>%

  # Create fixed effects poisson model clustering by school:
  fixest::feglm(fml = vacful ~ .[allvars],
                family = poisson(link = "log"),
                vcov = hetero ~ school)
```

The `fixest::feglm()` function has a number of other convenient features. You may have noticed that after running the model:

- Missing values were automatically removed (and the message tells you how many);
- Where co-linearity is detected between variables, one of the variables is automatically removed.

In this case, the variable `a1posyn` has been removed because it is co-linear with `a1posg`. This is expected, given that both these variables are alternative ways of coding responses to the same question (does the respondent have a balanced positive opinion on vaccination); `a1posyn` is the binary version (with yes or no as answers), while `a1posg` is the categorical multi-level version (with no, moderate or strong positive opinion as possible answers).

If you wish to inspect the co-linearity scores, you can do this by viewing the `$collin.var` element of the model results:

```
# View which elements of the model have been determined to be colinear:
modelres$collin.var

## [1] "a1posynyes"

# View the colinearity coefficients for each element of the model:
modelres$collin.coef

##                      (Intercept)           minorityGreek Muslims
##                     -1.485094873                      0.480180743
##              minorityImmigrants      minorityGeneral population
##                     -0.173606814                      0.568974530
##                 magegroup25 - 29             magegroup30 or over
##                      0.555846725                      0.683856754
## educfHigh school (9 - 11 years)         educfCollege (12 years)
##                      0.009367583                      0.061936454
##    educfUniversity (> 12 years)                     nsibcat1 - 2
##                      0.123080067                      0.273198848
##              nsibcatNo siblings a1posgModerate positive opinion
##                      0.295597102                      0.040244864
##   a1posgStrong positive opinion                       a1posynyes
##                      0.079427042                              NA
##                    uncriticalyes                         a1x1gyes
##                      0.056169176                     -0.565787411
##                         a1x2gyes                         a1x5gyes
##                     -0.106672115                     -0.051909100
##                         a3x1gyes                         a3x2gyes
##                     -0.068276759                     -0.043829466
##                         a3x5gyes
##                      0.045982099

# View a summary of the model results:
fixest::etable(modelres)

##                                      modelres
## Dependent Var.:                        vacful
##
## Constant                         -1.485** (0.4540)
## minorityGreekMuslims               0.4802 (0.3701)
## minorityImmigrants                -0.1736 (0.3848)
## minorityGeneralpopulation          0.5690 (0.3659)
## magegroup25-29                    0.5558. (0.3171)
## magegroup30orover                 0.6839* (0.3142)
```

```
## educfHighschool(9-11years)       0.0094 (0.0604)
## educfCollege(12years)            0.0619 (0.0524)
## educfUniversity(>12years)       0.1231* (0.0520)
## nsibcat1-2                    0.2732*** (0.0773)
## nsibcatNosiblings             0.2956*** (0.0842)
## a1posgModeratepositiveopinion    0.0402 (0.2219)
## a1posgStrongpositiveopinion      0.0794 (0.2375)
## uncriticalyes                   0.0562. (0.0296)
## a1x1gyes                       -0.5658* (0.2261)
## a1x2gyes                        -0.1067 (0.1176)
## a1x5gyes                        -0.0519 (0.0638)
## a3x1gyes                        -0.0683 (0.0496)
## a3x2gyes                        -0.0438 (0.0452)
## a3x5gyes                         0.0460 (0.0308)
## ______________________________ ___________________
## S.E. type                     Heteroskedas.-rob.
## Observations                              2,517
## Squared Cor.                            0.06336
## Pseudo R2                               0.01445
## BIC                                     4,747.2
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can now extract the model results and put them in a table, using `broom.mixed::tidy()` as before:

```
# Extract the model results into a table:
modeltab <- modelres %>%

  # Extract the results in a table:
  broom.mixed::tidy(conf.int = TRUE,
                    conf.method = "Wald") %>%

  # Exponentiate the estimates and 95% CI to convert to prevalence ratios:
  dplyr::mutate(across(c(estimate, starts_with("conf.")), exp)) %>%

  # Remove intercept (estimate for reference values):
  dplyr::filter(term != "(Intercept)") %>%

  # Split term into two columns (variable name and level / value):
  dplyr::mutate(
    # Create variable col (strings in 'term' that match any of allvars):
    variable = stringr::str_extract(term,
                                    str_c(allvars, collapse = "|")),
    # Create value col (whats left after strings matching allvars are
removed):
    value = stringr::str_remove(term,
                                str_c(allvars, collapse = "|"))) %>%

  # Round to 2 decimal places in numeric columns:
  mutate(across(
```

```
    .cols = where(is.numeric),
    .fns = round, digits = 2)) %>%

  # Merge lower and upper 95% CI in a new column:
  tidyr::unite(col = "95% CI",
               starts_with("conf."),
               sep = " - ",
               remove = TRUE) %>%

  # Remove unnecessary columns:
  dplyr::select(-term, -std.error, -statistic) %>%

  # Reorder new columns:
  relocate(c(variable, value), .before = estimate) %>%

  # Put estimate with 95% CI:
  relocate(p.value, .before = estimate)
```

Note that the reference levels are not included in the table; it would be useful to add these to facilitate interpretation of the results. In R, the reference value is always the first level in a factor. We can identify which is the first level by using the `dplyr` function `first()` and combining it with the base R function to extract the levels,
e.g. `first(levels(vaccine$minority)` .

We can do this for all the variables in `allvars` by using `summarise(across(allvars, …))` . Then we can `pivot_longer()` to orientate the resultant table so that it can be merged with the table containing the model results.

```
# Extract reference levels for all the variables in allvars:
reflevels <- vaccine %>%

  # Get first level of each factor in allvars:
  summarise(across(.cols = allvars,                  # Use columns in allvars
                   .fns = ~ first(levels(.x)))) %>% # Get first factor level

  # Transpose the results:
  pivot_longer(cols = everything(),   # Transpose all columns from previous
step
               names_to = "variable", # Put the variable names in col
'variable'
               values_to = "reference") # Put the ref values in col
'reference'


################################

# Merge reference values with model results table:
modeltab <- modeltab %>%

  # Join the reference values to modeltab:
```

```
  left_join(y = reflevels,
            by = "variable") %>%

  # Move the new reference column:
  relocate(reference, .before = value) %>%

  # Add more human readable labels to the variable column:
  mutate(variable = matchmaker::match_vec(variable, recoders))
```

Finally, we can present the results in a publishable table, using `flextable` .

For convenience, we have highlighted the elements of the model that are significant according to the Wald test (which is the method we selected to calculate *p* values when extracting the model results with `broom.mixed::tidy()`). If desired, you could limit the final model to include only variables that contain levels which are statistically significant according to the Wald test.

Table 5.3 - *Adjusted measures of association between vaccination status & parental characteristics*

```
modeltabpub <- modeltab %>%

  # Convert to a flextable:
  flextable::qflextable() %>%

  # Merge cells in the vaccine colum as the values are repeated:
  flextable::merge_v(j = c("variable"), target = c("variable", "reference"))
%>%

  # Label column headers:
    flextable::set_header_labels(values = list(
      variable = "Parameter",
      reference = "Reference level",
      value = "Characteristic",
      p.value = "P value (Wald)",
      estimate = "Prevalence ratio",
      `95% CI` = "95% CI")) %>%

  # Right align numeric results columns:
  flextable::align(j = 4:6, align = "right", part = "all") %>%

  # Add highlighting of significant values:
  flextable::bg(i = ~ p.value < 0.05,
                j = 4:6,
                bg = "yellow") %>%

  # Add borders under the merged cells:
  flextable::hline(i = rle(cumsum(.$body$spans$columns[,1] ))$values,
                   border = fp_border(style = "solid", width = 1)) %>%

  # Fix thickness of bottom border:
```

```
  fix_border_issues() %>%

  # Add bottom border back:
  flextable::hline_bottom(border = fp_border(style = "solid", width = 2),
                          part = "body") %>%

  # Adjust column widths to fit text:
  flextable::set_table_properties(width = 1, layout = "autofit")



###############
# Print table:
###############

modeltabpub
```

Parameter	Reference level	Characteristic	P value (Wald)	Prevalence ratio	95% CI
Minority group	Roma	Greek Muslims	0.19	1.62	0.78 - 3.34
		Immigrants	0.65	0.84	0.4 - 1.79
		General population	0.12	1.77	0.86 - 3.62
Mother's age at childbirth	Under 25	25 - 29	0.08	1.74	0.94 - 3.25
		30 or over	0.03	1.98	1.07 - 3.67
Father's education	Grammar school (< 9 years)	High school (9 - 11 years)	0.88	1.01	0.9 - 1.14
		College (12 years)	0.24	1.06	0.96 - 1.18
		University (> 12 years)	0.02	1.13	1.02 - 1.25
Number of siblings	3 or more	1 - 2	0.00	1.31	1.13 - 1.53
		No siblings	0.00	1.34	1.14 - 1.59
Balanced positive opinion on vaccination:	No positive opinion	Moderate positive opinion	0.86	1.04	0.67 - 1.61

Parameter	Reference level	Characteristic	P value (Wald)	Prevalence ratio	95% CI
likhert		Strong positive opinion	0.74	1.08	0.68 - 1.72
Uncritical positive opinion on vaccination	no	yes	0.06	1.06	1 - 1.12
Vaccination is necessary for my child	no	yes	0.01	0.57	0.36 - 0.88
Vaccines may harm my child	no	yes	0.36	0.90	0.71 - 1.13
Natural disease preferable to vaccines	no	yes	0.42	0.95	0.84 - 1.08
Long distance to immunization site	no	yes	0.17	0.93	0.85 - 1.03
Inconvenient opening hours	no	yes	0.33	0.96	0.88 - 1.05
Cost of vaccines	no	yes	0.14	1.05	0.99 - 1.11

Conclusions

Summary

This study identified several independent determinants of complete vaccination status among 6-year old Greek school children included in the survey. Complete vaccination coverage was significantly lower among children who belonged to a minority group, who had siblings in the household, whose mothers were <30 years, whose father had low educational levels, and whose parents/guardians did not believe that vaccination was necessary for a child. These findings indicate that socioeconomic factors may be more important determinants of immunization coverage than parental immunization beliefs and perceived barriers to vaccination.

Recommendations

Based on the findings of this study, the following identified groups merit increased attention in future interventions designed to improve immunization delivery in Greece:

1. minority groups, especially Roma and immigrants
2. families with many children
3. young mothers, and
4. households headed by fathers with low educational level

   (possibly reflecting low socioeconomic status of the families)

Interventions aimed at those high-risk families, although difficult to deliver, may have the greatest effects on community immunization rates.

In addition, parents/guardians must be educated about the necessity of vaccinations for children's health.

There is a need for policies to overcome structural and health care system barriers to immunization, and identify effective and comprehensive approaches for improving the immunization levels of children in high-risk groups.

References

Case study:

1. Danis K, Georgakopoulou T, Stavrou T, Laggas D and Panagiotopoulos T (2010). Socioeconomic factors play a more important role in childhood vaccination coverage than parental perceptions: a cross-sectional study in Greece. *Vaccine* **28**(7):1861-1869.
2. Danis K, Georgakopoulou T, Stavrou T, Laggas D, and Panagiotopoulos T (2010). Predictors Of Childhood Vaccination Uptake: A Cross-sectional Study In Greece. *Proceedings in Vaccinology* **2**(1), 86-91.

Prevalence ratio versus odds ratio:

1. Barros AJD and Hirakata VN (2003). Alternatives for logistic regression in cross-sectional studies: an empirical comparison of models that directly estimate the prevalence ratio. *BMC Medical Research Methodology* **3**(21).
2. Zou G. A (2004). Modified poisson regression approach to prospective studies with binary data. *American Journal of Epidemiology* **159**(702).

Model- versus design-based approaches to complex survey analysis:

1. Skinner C and Wakefield J (2017). Introduction to the design and analysis of complex survey data. *Statistical Science* **32**(165).
2. Lovasi GS, Fink DS, Mooney SJ and Link BG (2017). Model-based and design-based inference goals frame how to account for neighborhood clustering in studies of health in overlapping context types. Population Health **3**(600).

Appendix

Forms used in the study are presented below (annex 1 - 4). In addition, the data dictionaries for the data sets that you will use in this case study can be found in annexes 5 - 7.

A1

Form 1. List of students in school-class

District: ..... **School/Class:** ..... **Total number of students in school class:** .....

	SCHID(1)	Student's Surname and Name	Gender		Date of birth			Country of birth	Minority group (2)					Question-naire received	Vaccination record received	Date of receiving vaccination record
			Male	Female	DAY	MONTH	YEAR									
(3)	4	Papadopoulou Maria	1	(2)	23	6	99	GR	(0)	1	2	3	9	✓	✓	8/12
1			1	2					0	1	2	3	9			
2			1	2					0	1	2	3	9			
3			1	2					0	1	2	3	9			
4			1	2					0	1	2	3	9			
5			1	2					0	1	2	3	9			
6			1	2					0	1	2	3	9			
7			1	2					0	1	2	3	9			
8			1	2					0	1	2	3	9			
9			1	2					0	1	2	3	9			
10			1	2					0	1	2	3	9			
11			1	2					0	1	2	3	9			
12			1	2					0	1	2	3	9			
13			1	2					0	1	2	3	9			
14			1	2					0	1	2	3	9			
15			1	2					0	1	2	3	9			
16			1	2					0	1	2	3	9			

(1)SCHID: Student's ID in school class (2) 0: no minority group 1: Greek Roma 2: Greek Muslim 3:Immigrant 9:Unknown (3) Example of completion

School registry extraction form

A2

Vaccination Beliefs Questionnaire

For office use only

county	school/class	Student ID

A. Beliefs, attitudes and barriers towards childhood immunization

A1. Beliefs and attitudes towards immunization

You will find below certain beliefs and attitudes of some parents towards immunization. Please tick the appropriate box (✓) if you agree or disagree with the following statements. An example is provided below. There are not "right" or "wrong" answers to those. We would simply like to see what you think of them.

Example

	Please tick the appropriate box (✓) if you agree or disagree with the following statements.	Agree	Rather agree	Rather disagree	Disagree	I do not know
1	Most vaccines are administered by a pediatrician		✓			

	Please tick the appropriate box (✓) if you agree or disagree with the following statements.	Agree	Rather agree	Rather disagree	Disagree	I do not know
1	Do you believe that vaccination is necessary for your child?					
2	I'm concerned that vaccines may harm my child					
3	Children should be immunized with no delay with every new licensed vaccine					
4	I usually need to crosscheck my physician's advice regarding the immunization for my child					
5	Natural disease is preferable to vaccination					
6	I'm confused with childhood vaccines, because of physicians' conflicting opinions					
7	Even now as an adult I'm scared of vaccines and injections, due to bad experiences as a child					
8	The more vaccines a child gets, the better it is for his health					
9	The state provides very limited information on new vaccines to reduce funding for new immunizations					
10	I try to keep my child's immunization up to date, according to the latest scientific advice					
11	Vaccines are completely safe and cannot harm child's health					
12	Campaigns for new vaccines are done for financial profit					

A2. How much do you trust the following sources for accurate information on vaccines?

	How much do you trust . . . :	Very much	Enough	Average	Little	I do not know
1	... your child's physician?	1	2	4	5	9
2	... the immunization nurse (if available)?	1	2	4	5	9
3	... your friends or relatives?	1	2	4	5	9
4	... the ministry of health?	1	2	4	5	9
5	... parents books?	1	2	4	5	9
6	... magazines for parents?	1	2	4	5	9
7	... news in newspapers or tv?	1	2	4	5	9
8	... reports in newspapers?	1	2	4	5	9
9	... tv programmes on immunization??	1	2	4	5	9

A3. Problems/ barriers to vaccination

You will find below some problems/barriers that sometimes parents face for their child's immunization. Please let us know if you have also faced such problems. If YES, please state (tick the appropriate box (✓) if you consider them as Small, Average or Big problems.

	Did you experience problems with any of the following during your child's immunization?	Problem			
		NO	YES		
			Small	Average	Big
1	... long distance to the immunization site?	1	2	4	5
2	...inconvenient opening hours of the immunization site?	1	2	4	5
3	... lack of accurate information on vaccines?	1	2	4	5
4	... high cost of the vaccines?	1	2	4	5
5	... high cost of the immunization visit?	1	2	4	5
6	... inappropriate/unfrendly behavior of the immunization staff?	1	2	4	5
7	... anything else?	1	2	4	5
	If OTHER problem, please specify.....				

B. Medical history and family characteristics of your child

We would now like to ask you a couple of things regarding the health and family characteristics of your child.

B1. Did your child stay in the Maternity hospital or the Neonatal Intensive Care Unit for more than a week at birth?

Please tick the box (✓)

☐ 1 Yes ☐ 2 No

If YES: ► **For how long?** .....

► **For which health conditions;**

Please specify.....

.....

B2. Has you child ever been admitted (i.e. spent the night) to a hospital?

Please tick the box (✓) as appropriate

☐ 1 Yes ☐ 2 No

If YES: ► **How many times?** .....

► **For which health conditions;**

Please specify.....

.....

B3. Does your child have insurance coverage?

Please tick the box (✓) as appropriate

- State insurance: ☐ 1 NAI ☐ 2 OXI
- Private insurance: ☐ 1 NAI ☐ 2 OXI

B4. What is .....?

- mother's age : ☐ years ☐ 9 I do not know
- father's age : ☐ years ☐ 9 I do not know

B5. What is the educational level of child's parents?

Please tick the box (✓) as appropriate

	Mother	Father
• Primary school not completed . . .	☐ 1	☐ 1
• Primary school completed	☐ 2	☐ 2
• Grammar school completed	☐ 3	☐ 3
• High school completed.	☐ 4	☐ 4
• College	☐ 5	☐ 5
• Higher Education	☐ 6	☐ 6
• University	☐	☐
• Other	☐ 7	☐ 7
If OTHER, please specify	. . . . .	. . . . .
• I do not know	☐ 9	☐ 9

B6. How many persons live in your household (including yourself and your child)

- Number of persons living in your household (including yourself and your child) ☐

B7. Does your child have other siblings?

Please tick the box (✓) as appropriate

☐ 1 Yes ☐ 2 No

If YES: ▶ **How many?** . . . . . .

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▶ **Questionnaire completed by:**

☐ 1 Mother ☐ 2 Father ☐ 3 Grandmother

☐ 4 Other Please specify . . . . . .

▶ **Date of completion of questionnaire:** . . . . . / . . . . . / . . . . .

Thank you for your cooperation

Please return the completed questionnaire at your child's school

A3

Vaccination Abstraction Form

		Code	
► Region:			[REGION]
► School/Class:			[SCHOOL]
► Surname / Name:			[SCHID]
► Gender:	1. MALE 2. FEMALE 9. UNKNOWN		[GENDER]
► Date of birth:	___ / ___ / ___		[DOB]
► Field worker:			[FIELDW]
► Date of vaccination record collection:	___ / ___ / ___		[DATECOL]
► Record type:	1. HEALTH BOOKLET 2. VACCINATION CARD 3. OTHER		[RECT]

Vaccines/doses carried out by child

For each vaccine/dose, write down: 1. whether vaccination was done (check Y/N) (circle appropriate option),
2. date of vaccination (DD/MM/YY),
3. vaccine type, where necessary (circle appropriate option).

1) Vaccines of National Vaccination Programme starting at 1st year of life

	Dose 1	*Dose 2*	*Dose 3*	*Dose 4*	*Dose 5*	*Dose 6*	
DTP	Y N	Y N	Y N	Y N	Y N	Y N	[DTP-]
DATE							
POLIO	Y N	Y N	Y N	Y N	Y N	Y N	[POL-]
DATE							
Vaccine type	OPV - IPV - UNK	OPV - IPV - UNK	OPV - IPV - UNK	OPV - IPV - UNK	OPV - IPV - UNK	OPV - IPV - UNK	[POLTYP-]

	Dose 1	*Dose 2*	*Dose 3*	*Dose 4*	
HIB	Y N	Y N	Y N	Y N	[HIB-]
DATE					
HEP B	Y N	Y N	Y N	Y N	[HBV-]
DATE					
MEN C	Y N	Y N	N	Y N	[MEN-]
DATE					
PNEUMO	Y N	Y N	N	Y N	[PNU-]
DATE					

2) Vaccines of National Vaccination Programme starting at 2nd year of life

	Dose 1		Dose 2		Dose 3		Dose 4		
MMR	Y	N	Y	N	Y	N	Y	N	[MMR-]
DATE									
MEASLES	Y	N	Y	N		N	Y	N	[MSL-]
DATE									
RUBELLA	Y	N	Y	N		N	Y	N	[RUB-]
DATE									
MUMPS	Y	N	Y	N		N	Y	N	[MUM-]
DATE									

3) BCG, INFLUENZA

	First dose		Last dose		Total number of doses	
BCG	Y	N	Y	N		[BCG-]
DATE					[BCGN]	
INFLU-ENZA	Y	N	Y	N		[FLU-]
DATE					[FLUN]	

4) Other vaccines / special indications

	Dose 1		Dose 2		Dose 3		Dose 4		
VARI-CELLA	Y	N	Y	N	Y	N	Y	N	[VAR-]
DATE									
HEP A	Y	N	Y	N	Y	N	Y	N	[HAV-]
DATE									

OTHER	Y	N	[OTHER]

	Dose 1		Dose 2		Dose 3		Dose 4		
OTHER-A	Y	N	Y	N	Y	N	Y	N	OTHERA-]
DATE									
	Y	N	Y	N	Y	N	Y	N	

OTHER-B DATE					OTHERB-]

Place of vaccination: public/private sector

(Circle appropriate option)

	NO VACCINATION	PUBLIC SECTOR	PRIVATE SECTOR	VACCINATION ABROAD	UNKNOWN SECTOR	
DTP - dose 1	0	1	2	3	9	[DTP1PLC]
DTP - dose 4	0	1	2	3	9	[DTP4PLC]
DTP - dose 5	0	1	2	3	9	[DTP5PLC]
HIB - dose 1	0	1	2	3	9	[HIB1PLC]
HEP B - dose 1	0	1	2	3	9	[HBV1PLC]
MEN C - dose 1	0	1	2	3	9	[MEN1PLC]
PNEUMO - dose 1	0	1	2	3	9	[PNU1PLC]
MMR (OR MCV*) - dose 1	0	1	2	3	9	[MCV1PLC]
MMR (OR MCV*) - dose 2	0	1	2	3	9	[MCV2PLC]
BCG - dose 1	0	1	2	3	9	[BCG1PLC]
Influenza - dose 1	0	1	2	3	9	[FLU1PLC]
Varicella - dose 1	0	1	2	3	9	[VAR1PLC]
HEP A - dose 1	0	1	2	3	9	[HAV1PLC]

* measles containing vaccine

A4

Form 2. Fieldworker's check-list of actions

District: . . . . . School/Class: . . . . . .

SCHID (1)	Student's Surname and Name	Letter & Questionnaire given	Date that Questionnaire was given	Completed Questionnaire received	Vaccination record received	Date that Vaccination record was received	Photocopy of vaccination record	Check of photocopies and fill in gaps	Prepare feedback note on vaccination status for parents	Return vaccination record + feedback note to parents
4	Papadopoulou Mary	✓	6/12	✓	✓	8/12	✓	✓	✓	✓

(1)SCHID: Student's ID in school class

Field worker's checklist

A5

Table A5 - Data dictionary for "School" database

Variable	Type	Encoding	Definition
school	Numeric		School/Class
schid	Numeric		Student's ID in school class
vaccrec	Numeric	0:No, 1:Yes	Vaccination Booklet received
qsrec	Numeric	0:No, 1:Yes	Questionnaire received
id	Numeric		(school x 100)+schid
region	Numeric		
urban	Numeric	0: Rural, 1:Urban	Rural/Urban
gender	Numeric	0:Female, 1:Male, 9:Unknown	Gender (from school record)
dob1	Date		Date of birth (from school record)
country	String		Country of birth
minority	Numeric		Minority group
minoryn	Numeric	0:No, 1:Yes, 9:Unknown	Belongs to minority group
datecol	Date		Date of booklet collection

A6

Table A6 - Data dictionary for "Vaccine" database

Variable	Type	Encoding	Definition
id	Numeric		Unique identifier of students
weight	Numeric		
datecol	Numeric		Date of booklet collection
agey	Numeric		Age in years
dob	Date		Date of birth (from vaccination booklet)
dtp1	Date		1st dose of DTP vaccine
dtp2	Date		2nd dose of DTP vaccine

Variable	Type	Encoding	Definition
dtp3	Date		3rd dose of DTP vaccine
dtp4	Date		4th dose of DTP vaccine
dtp5	Date		5th dose of DTP vaccine
po1	Date		1st dose of Polio vaccine
po2	Date		2nd dose of Polio vaccine
po3	Date		3rd dose of Polio vaccine
po4	Date		4th dose of Polio vaccine
po5	Date		5th dose of Polio vaccine
potyp1	Numeric	1:OPV, 2:IPV, 9:Unknown	Polio 1st dose vaccine type
potyp2	Numeric	1:OPV, 2:IPV, 9:Unknown	Polio 2nd dose vaccine type
potyp3	Numeric	1:OPV, 2:IPV, 9:Unknown	Polio 3rd dose vaccine type
potyp4	Numeric	1:OPV, 2:IPV, 9:Unknown	Polio 4th dose vaccine type
potyp5	Numeric	1:OPV, 2:IPV, 9:Unknown	Polio 5th dose vaccine type
bcg1	Date		1st dose of BCG vaccine
bcgl	Date		Last dose of BCG vaccine
bcgn	Numeric		Total number of BCG vaccine doses
msl1	Date		1st dose of Measles vaccine
msl2	Date		2nd dose of Measles vaccine
msl3	Date		3rd dose of Measles vaccine
rub1	Date		1st dose of Rubella vaccine
rub2	Date		2nd dose of Rubella vaccine
rub3	Date		3rd dose of Rubella vaccine
mu1	Date		1st dose of Mumps vaccine
mu2	Date		2nd dose of Mumps vaccine
mu3	Date		3rd dose of Mumps vaccine
mmr1	Date		1st dose of MMR vaccine

Variable	Type	Encoding	Definition
mmr2	Date		2nd dose of MMR vaccine
mmr3	Date		3rd dose of MMR vaccine
hbv1	Date		1st dose of HBV vaccine
hbv2	Date		2nd dose of HBV vaccine
hbv3	Date		3rd dose of HBV vaccine
hbv4	Date		4th dose of HBV vaccine
hav1	Date		1st dose of HAV vaccine
hav2	Date		2nd dose of HAV vaccine
hav3	Date		3rd dose of HAV vaccine
hav4	Date		4th dose of HAV vaccine
hib1	Date		1st dose of HIB vaccine
hib2	Date		2nd dose of HIB vaccine
hib3	Date		3rd dose of HIB vaccine
hib4	Date		4th dose of HIB vaccine
mnc1	Date		1st dose of MEN C vaccine
mnc2	Date		2nd dose of MEN C vaccine
mnc3	Date		3rd dose of MEN C vaccine
mnc4	Date		4th dose of MEN C vaccine
flu1	Date		1st dose of Influenza vaccine
flul	Date		Last dose of Infuenza vaccine
flun	Date		Total number of Influenza vaccine doses
var1	Date		1st dose of Varicella vaccine
var2	Date		2nd dose of Varicella vaccine
pne1	Date		1st dose of Pneumo vaccine
pne2	Date		2nd dose of Pneumo vaccine
pne3	Date		3rd dose of Pneumo vaccine

Variable	Type	Encoding	Definition
pne4	Date		4th dose of Pneumo vaccine
other	Numeric	0:No, 1:Yes	Other vaccine YES/NO
dtp1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of DTP-1 administration
dtp4plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of DTP-4 administration
dtp5plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of DTP-5 administration
bcg1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of BCG-1 administration
mmr1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of (MMR or MCV)-1 administration
mmr2plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of (MMR or MCV)-2 administration
hbv1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of HBV-1 administration
hav1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of HAV-1 administration
hib1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of HIB-1 administration
mnc1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of MEN C-1 administration
pne1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of PNU-1 administration
var1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of VAR-1 administration
flu1plc	Numeric	0:No vaccination, 1: State, 2:Private, 3:Abroad	Place of FLU-1 administration

A7

Table A7 - Data dictionary for "Quest" database

Variable	Type	Encoding	Definition
A1. Beliefs and attitudes towards immunization			

Variable	Type	Encoding	Definition
a1x1	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	Do you believe that vaccination is necessary for your child?
a1x2	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	I'm concerned that vaccines may harm my child
a1x3	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	Children should be immunized with no delay with every new licensed vaccine
a1x4	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	I usually need to crosscheck my physician's advice regarding the immunization for my child
a1x5	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	Natural disease is preferable to vaccination
a1x6	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	I'm confused with childhood vaccines, because of physicians' conflicting opinions
a1x7	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	Even now as an adult I'm scared of vaccines and injections, due to bad experiences as a child
a1x8	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	The more vaccines a child gets, the better it is for his health
a1x9	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	The state provides very limited information on new vaccines to reduce funding for new immunizations
a1x10	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	I try to keep my child's immunization up to date, according to the latest scientific advice
a1x11	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	Vaccines are completely safe and cannot harm child's health
a1x12	Numeric	1:Agree, 2:Rather agree, 3:Rather disagree, 4:Disagree, 9:Don't know	Campaigns for new vaccines are done for financial profit
A3. Which of the following present a problem for the immunization of your child?			
a3x1	Numeric	1:No, 2:small problem, 3:average problem, 4:big	Long distance to the immunization site

Variable	Type	Encoding	Definition
		problem	
a3x2	Numeric	1:No, 2:small problem, 3:average problem, 4:big problem	The OPENING HOURS OF the immunization site
a3x3	Numeric	1:No, 2:small problem, 3:average problem, 4:big problem	Lack of accurate information on vaccines
a3x4	Numeric	1:No, 2:small problem, 3:average problem, 4:big problem	High cost of the vaccines
a3x5	Numeric	1:No, 2:small problem, 3:average problem, 4:big problem	High cost of the immunization visit
a3x6	Numeric	1:No, 2:small problem, 3:average problem, 4:big problem	Inappropriate/unfriendly behaviour of the immunization staff
a3x7	Numeric	1:No, 2:small problem, 3:average problem, 4:big problem	Anything else
a3a1	String	text	Please specify
B1. Medical history and family characteristics of your child			
b3st	Numeric	0:No, 1:Yes	Did your child have state insurance coverage?
b3pr	Numeric	0:No, 1:Yes	Did your child have private insurance coverage?
mage	Numeric		Age of the mother
agef	Numeric		Age of the father
b5m	Numeric	1:Kindergarten, 2:Grammar school, 3:High school, 4:College, 5:Higher education, 6:University, 7:other	Mother's educational level (last academic year completed)
b5f	Numeric	1:Kindergarten, 2:Grammar school, 3:High school, 4:College, 5:Higher education, 6:University, 7:other	Father's educational level (last academic year completed)
b6	Numeric		How many persons live in your household (including yourself and your

Variable	Type	Encoding	Definition
			child)
b7	Numeric	0:No, 1:Yes	Are there other siblings in the household?
b7ad	Numeric		If YES, how many brother/sisters?