

Exploring the Social World - Quantitative Block: Statistics

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Welcome

This is the website for “Exploring the Social World - Quantitative Block: Statistics” (module **ENVS225**) at the University of Liverpool. This block of the module is designed and delivered by Dr. Gabriele Filomena and Dr. Zi Ye from the Geographic Data Science Lab at the University of Liverpool. The module seeks to provide hands-on experience and training in introductory statistics for human geographers.

The website is **free to use** and is licensed under the [Attribution-NonCommercial-NoDerivatives 4.0 International](#). A compilation of this web course is hosted as a GitHub repository that you can access:

- As an [html website](#).
- As a [GitHub repository](#).

Contact

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Overview

Aim and Learning Objectives

This sub-module aims to provide training and skills on a set of basic quantitative research methods for data collection, analysis, and interpretation. You will learn how to define coherent, relevant research questions, utilise various research quantitative methods, and identify appropriate methodologies to tackle your research questions. **This block serves as the foundation for the dissertation and fieldwork modules.**

Background

Data and research are key pillars of the global economy and society today. We need rigorous approaches to collecting and analysing both the statistics that can tell us ‘how much’ and if there are observable relationships between phenomena; and the information gives us a nuanced understanding of cultural contexts and human dynamics. Quantitative skills enable us to explore and measure socio-economic activities and processes at large scales, while qualitative skills enable understanding of social, cultural, and political contexts and diverse lived experiences. Rather than being in opposition, qualitative and quantitative research can complement one another in the investigation of today’s pressing research questions.

To these ends, this block will help you develop your quantitative (statistical) skills, as critical tools. This course will help you understand what quantitative statistical researchers use and develop a set of research techniques that can be used in your field classes and dissertations.

Learning objectives:

- Understand how to explore a dataset, containing a number of observations described by a set of variables.
- Demonstrate an understanding in the application and interpretation of commonly used quantitative research methods.
- Demonstrate an understanding of how to work with quantitative data to address real-world research questions.

Module Structure

Staff: Dr Zi Ye and Dr Gabriele Filomena

Where and When

Quantitative Block (Weeks 7-12):

- **Lecture:** 10 am – 10.45 am Fridays
- **PC Practical sessions:** 11am – 1 pm, following the Lecture

Week 7: Central Teaching Hub: PC Teaching Centre BLUE+GREEN+ORANGE ZONES

Week 8 -12: Central Teaching Hub, PCTC

Lectures will introduce and explain the fundamentals of quantitative methods, with the opportunity to apply the method introduced in the labs later in the week.

The computer practical sessions, will give you the chance to use and apply quantitative methods to real-world data. These are primarily self-directed sessions, but with support on hand if you get stuck. Support and training in R will be provided through these sessions. Weekly sessions will be driven by empirical research questions.

Week	Topic	Format	Staff
7	Introduction & Review	Lecture and Computer Lab Practical	GF
8	Single & Multiple Linear Regression	Lecture and Computer Lab Practical	GF
9	Multiple Linear Regression with Categorical Variables	Lecture and Computer Lab Practical	ZY
10	Logistic Regression	Lecture and Computer Lab Practical	ZY
11	Data Visualisation	Lecture and Computer Lab Practical	GF
12	Summary and Assessment Support	Lecture and Computer Lab Practical	ZY

Software and Data

For quantitative training sessions, ensure you have installed and/or have access to **RStudio**. To run the analysis and reproduce the code in R, you need the following software installed on your machine:

- R-4.2.2
- RStudio 2022.12.0-353

To install and update:

- R, download the appropriate version from [The Comprehensive R Archive Network \(CRAN\)](#).
- RStudio, download the appropriate version from [here](#).

This software is already installed on University Machines. But you will need it to run the analysis on your personal devices.

Data

Example datasets could be accessed through Canvas or the [GitHub](#) Repository of the module. These include:

- 2021 UK Census Data.
- 2021 Annulation Population Survey.
- 2016 Family Resource Survey.

Note: The Annual Population Survey requires the completion of a form prior to its usage, as it is licensed.

Assessment

Deadline: Tuesday 7th January 2025. **Word count:** 2000 words - including tables, excluding references.

The assignment **Data Exploration and Analysis** consists of writing a research report using one of the regression techniques learned during the module. The basic idea is to put in practice the methods learned during the quantitative block of the module. You are required to apply a linear or logistic regression model to the data provided for the module. The report needs to include the following sections (in brackets, % of the whole length):

- Introduction (5%).
- Literature Review (20%).
- Methods and data (30%).
- Results and discussion (40%).
- Conclusion (5%).
- Reference List.

Required Report Structure

1. Introduction

- Context: Why is the topic relevant or worth being investigated?
- Brief discussion of existing literature.
- Knowledge gap and Aim.
- Research questions.

2. Literature review

- More detailed Literature review, i.e. what do we already know about this subject
- Rationale for including certain predictor variables in the model.
- What knowledge gap remains that this article will address? (includes “not studied before in this area”). *Note: there is no expectation on totally original research. The focus is on a clean, sensible, data analysis situated in existing ideas.*

3. Methodology:

- A brief introduction to the dataset being analysed (who collected it? When? How many responses? etc.)

- A description of the variables chosen to be analysed.
- A description of any transformation made to the original data, i.e. turning a continuous variable of income into intervals, or reducing the number of age groups from 11 to 3.
- A description and justification of the statistical techniques used in the subsequent analysis (i.e. the Multivariate regression model: Multiple or Logistic Linear Regression).

4. Results and Discussion

- Descriptive statistics and summary of the variables employed.
- Correct interpretation of correlation coefficients.
- Usage and results of an appropriate multivariate regression model.
- Interpretation of the results, including links and contrasts to existing literature.
- Selective illustrations (graphs and tables) to make your findings as clear as possible.

5. Conclusion

- Summary of main findings.
- Limitations of study (self-critique).
- Highlight any implications derived from the study.

Follow this structure and include **ALL** these points, do not make your life harder.

How to get there?

The first stage is to identify **ONE** a relevant research question to be addressed. Based on the chosen question, you will need to identify a dependent (or outcome) variable which you want to explain, and at least two relevant independent variables that you can use to explain the chosen dependent variable. The selection of variables should be informed by the literature and empirical evidence.

To detail in the Methods Section: Once the variables have been chosen, you will need to describe the data and **appropriate** type of regression to be used for the analysis. You need to explain any transformation done to the original data source, such as reclassifying variables, or changing variables from continuous to nominal scales. You also need to briefly describe the data use: source of data, year of data collection, indicate the number of records used, state if you are using individual records or geographical units, explain if you are selecting a sample, and any relevant details. You also need to identify type of regression to be used and why.

To detail in the Results and Discussion Section: Firstly, you need to provide two types of analyses. First, you need to provide a descriptive analysis of the data. Here you could use tables and/or plots reporting relevant descriptive statistics, such as the mean, median and standard deviation; variable distributions using histograms; and relationships between

variables using correlation matrices or scatter plots. Secondly, you need to present an estimated regression model or models and the interpretation of the estimated coefficients. You need a careful and critical analysis of the regression estimates. You should think that you intend to use your regression models to advice your boss who is expecting to make some decisions based on the information you will provide. As part of this process, you need to discuss the model assessment results for the overall model and regression coefficients. Remember to substantiate your arguments using relevant literature and evidence, and present results clearly in tables and graphs.

How is it graded?

Grade	Score Range	UG	Descriptor	Assignment Expectations
Fail	0-34%	Fail	Inadequate	<p>Literature Review: Lacks relevance and fails to justify variable choice. Evidence is irrelevant or missing, providing no support to the research question.</p> <p>Methods: Data is not described, and the regression model is entirely missing. No appropriate statistical method is applied.</p> <p>Results and Discussion: No descriptive statistics, graphs, or tables are provided. Model results and interpretation are absent.</p> <p>Structure and References: Report is disorganized with significant referencing and citation errors throughout.</p>

Grade	Score Range	UG	Descriptor	Assignment Expectations
Narrow Fail	35-39%	Fail	Highly Deficient	<p>Literature Review: Review is present but lacks coherence and fails to justify variable choice. Evidence is poorly aligned with the research question and mostly irrelevant.</p> <p>Methods: Minimal data description; the regression model is missing but some statistical methods are mentioned.</p> <p>Results and Discussion: Few or no descriptive statistics or visuals are present. Statistical methods are unclear or incorrectly applied. Results are vague and lack meaningful interpretation.</p> <p>Structure and References: Report structure is poor, with referencing errors in multiple sections.</p>

Grade	Score Range	UG	Descriptor	Assignment Expectations
Third / Fail	40-49%	Third (UG)	Deficient	<p>Literature Review: Relevant literature is partially addressed but lacks depth, with limited justification for variable choice. Evidence is minimally aligned with the research question.</p> <p>Methods: A very basic data description is provided, but the selected regression model is deeply inadequate or incorrect (e.g., multiple linear regression for a categorical outcome; logistic regression for a continuous outcome).</p> <p>Results and Discussion: Descriptive statistics or visuals may be present but insufficient. Model results are presented with little to no interpretation.</p> <p>Structure and References: Report structure is present but lacks clarity, with inconsistencies</p>

Grade	Score Range	UG	Descriptor	Assignment Expectations
2.2 / Pass	50-59%	2.2 (UG)	Adequate	<p>Literature Review: Addresses relevant literature but with limited justification of variable choices. Evidence generally supports the research question but lacks detail.</p> <p>Methods: Data description is present but brief; a regression model is included but applied illogically or incorrectly (e.g., multiple linear regression for a categorical outcome; logistic regression for a continuous outcome) and with little explanation.</p> <p>Results and Discussion: Basic descriptive statistics, graphs, or tables are presented; the regression model is applied with some inaccuracies and/or interpretation is minimal.</p> <p>Structure and References: Report is mostly organized</p>

Grade	Score Range	UG	Descriptor	Assignment Expectations
2.1 / Merit	60-69%	2.1 (UG)	Good	<p>Literature Review: Relevant literature is discussed, with some justification for variable choice. Evidence supports the research question well.</p> <p>Methods: Data is described with some detail, though potential data transformations are under-explored. The regression model is appropriate for the selected variable types.</p> <p>Results and Discussion: Descriptive statistics and visuals are provided. Model results are discussed, though interpretation lacks depth. Findings are compared to existing literature.</p> <p>Structure and References: Report is logically structured and clear, with mostly correct citations.</p>

Grade	Score Range	UG	Descriptor	Assignment Expectations
First / Distinction	70-79%	First (UG)	Very Good	<p>Literature Review: Strong grasp of relevant literature, with well-justified variable selection. Evidence aligns well with the research question.</p> <p>Methods: Data is comprehensively described with consideration of relevant transformations. The regression model is appropriate and well-justified.</p> <p>Results and Discussion: Descriptive statistics and clear visuals support findings. Model results are accurately interpreted with strong connections to existing literature.</p> <p>Structure and References: Report has a coherent, professional structure with only minor referencing errors.</p>

Grade	Score Range	UG	Descriptor	Assignment Expectations
High First / High Distinction	80-100%	High First (UG)	Excellent to Outstanding	<p>Literature Review: Critical and thorough literature review with strong, well-justified variable selection. Evidence fully supports the research question with insightful connections.</p> <p>Methods: Detailed data description and transformation steps are clearly articulated. Regression model is expertly applied and justified.</p> <p>Results and Discussion: Comprehensive descriptive statistics, graphs, and tables are provided. Model results are innovatively interpreted with strong links to existing research.</p> <p>Structure and References: Report is professionally structured, with flawless citations and a high standard of organization.</p>

In summary:

1. **Introduction:** Should establish the topic's relevance, present a concise literature overview, identify a knowledge gap, and outline research questions.
2. **Literature Review:** Requires an in-depth review of relevant studies, justification for chosen independent variables, and identification of a potential knowledge gap or unexplored area aligned with the chosen research question.
3. **Methods and Data:** Should describe the dataset, variable transformations, and justify the regression technique. Key transformations, such as reclassifying variables, should be explained with clarity and relevance.
4. **Results and Discussion:** Involves presenting descriptive statistics, followed by a clear regression analysis. Discussion should interpret results, compare findings with existing literature, and include meaningful tables and graphs.
5. **Conclusion:** Summarize findings, discuss limitations, and suggest future directions.
6. **Referencing:** Requires correct and consistent citations and a well-structured reference list.

Employing a novel dataset, i.e. not employed during the practical sessions, for the assignment will be awarded with a higher grade. For example, the quantitative dataset from [Secondary datasets for Human Geography and Planning Students: 202425-ENVS203](#).

Assessment: How to submit

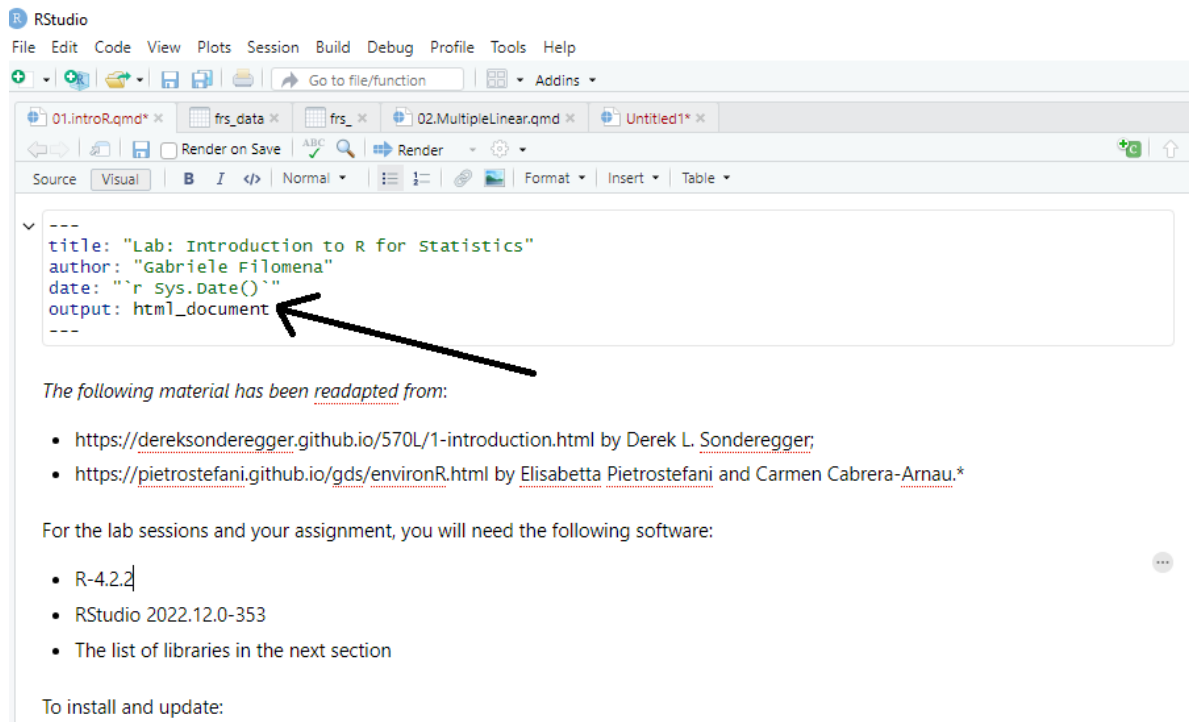
You should submit a `.pdf` file, that is a rendered version of a Quarto Markdown file (`qmd` file). This will allow you to write a research paper that also includes your working code, without the need of including the data (rendered `.qmd` files are executed before being converted to R).

How to get a PDF?

1. **Install Quarto:** Make sure you have Quarto installed. You can download it from quarto.org.
2. **LaTeX Installation:** For PDF output, you'll need a LaTeX distribution like **TinyTeX** from R, by executing this in the R console:

```
install.packages("tinytex")
tinytex::install_tinytex()
```

3. **Open the Quarto File:** Open your `.qmd` file in RStudio.
4. **Set Output Format:** In the YAML header at the top of your Quarto file, specify `pdf` under `format`:



```
title: "Your Document Title"
author: "Anonymous" # do not change
format: pdf
```

5. Click the **Render** button in the RStudio toolbar (next to the Knit button).

1 Lab: Introduction to R for Statistics

The following material has been readapted from:

- <https://dereksonderegger.github.io/570L/1-introduction.html> by Derek L. Sonderegger;
- <https://pietrostefani.github.io/gds/envIRON.html> by Elisabetta Pietrostefani and Carmen Cabrera-Arnau

The lecture's slides can be found [here](#).

For the lab sessions and your assignment, you will need the following software:

- R-4.2.2
- RStudio 2022.12.0-353
- The list of libraries in the next section

To install and update:

- R, download the appropriate version from [The Comprehensive R Archive Network \(CRAN\)](#)
- RStudio, download the appropriate version from [Posit](#)

1.1 R?

R is an open-source program that is commonly used in Statistics. It runs on almost every platform and is completely free and is available at www.r-project.org. Most of the cutting-edge statistical research is first available on R.

R is a script based language, so there is no point and click interface. While the initial learning curve will be steeper, understanding how to write scripts will be valuable because it leaves a clear description of what steps you performed in your data analysis. Typically you will want to write a script in a separate file and then run individual lines. This saves you from having to retype a bunch of commands and speeds up the debugging process.

1.2 R(Studio) Basics

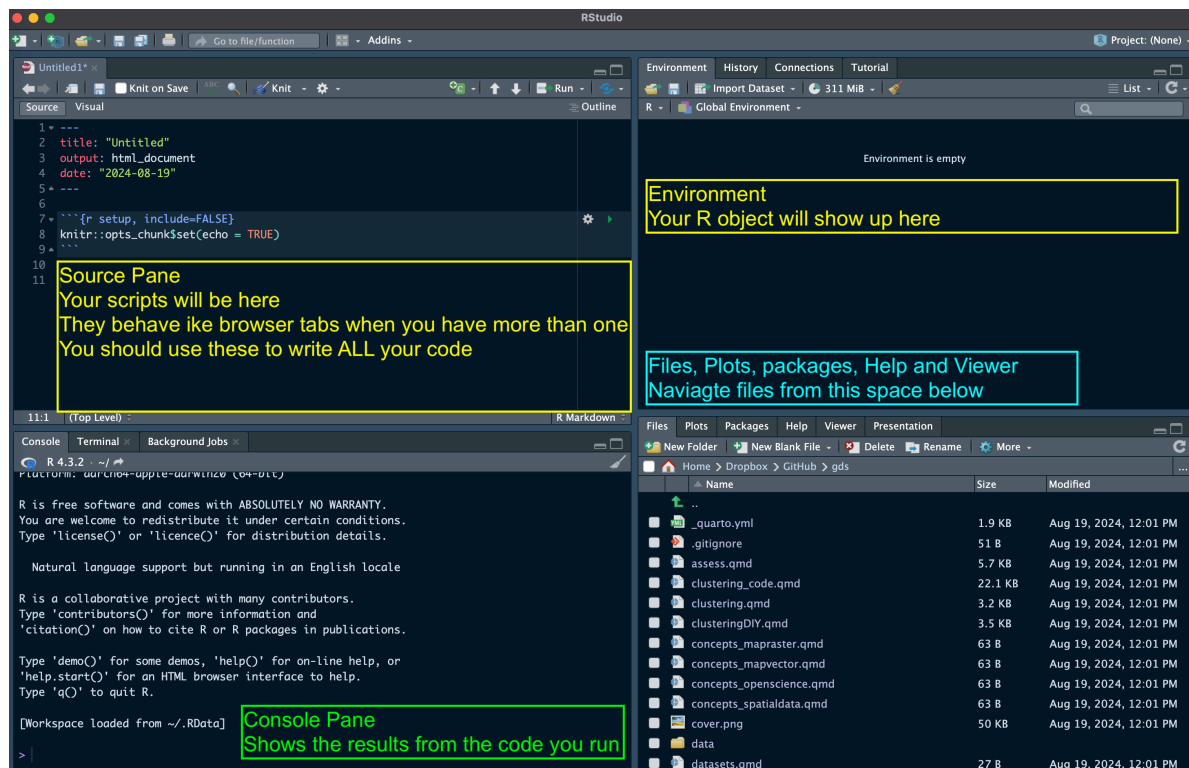
We will be running R through the program RStudio which is located at rstudio.com. When you first open up RStudio the console window gives you some information about the version of R you are running and then it gives the prompt `>`. This prompt is waiting for you to input a command. The prompt `+` tells you that the current command is spanning multiple lines. In a script file you might have typed something like this:

```
for( i in 1:5 ){  
  print(i)  
}
```

Finding help about a certain function is very easy. At the prompt, just type `help(function.name)` or `?function.name`. If you don't know the name of the function, your best bet is to go to the web page www.rseek.org which will search various R resources for your keyword(s). Another great resource is the coding question and answer site [stackoverflow](https://stackoverflow.com).

1.2.1 Starting a session in RStudio

Upon startup, RStudio will look something like this.



Note: the **Pane Layout** and **Appearance** settings can be altered:

- on Windows by clicking RStudio>Tools>Global Options>Appearance or Pane Layout
- on Mac OS by clicking RStudio>Preferences>Appearance or Pane Layout.

You will also have a standard white background; but you can choose specific [themes](#).

Source Panel (Top-Left)

This is where you write, edit, and view scripts, R Markdown/Quarto documents, or R scripts. It allows:

- Editing Scripts: Write and edit R scripts or documents (`.R`, `.Rmd`, `.qmd`).
- Executing the Code: Run lines, blocks, or the entire script directly from the editor.

Console Panel (Bottom-Left)

The Console is the main place to run R commands interactively. It allows:

- Executing the Code: Type and run R commands directly.
- Viewing outputs, warnings, and errors for immediate feedback.
- Browsing and reusing past commands (History Tab).
- Toggling between the R Console, and the Terminal (you don't really need the latter).

Environment Panel (Top-Right)

This panel helps track variables, functions, and the history of commands used. It contains:

- Environment Tab: Shows all current variables, datasets, and objects in your session, including their structure and values.
- History Tab: Provides a record of past commands. You can re-run or move commands to the console or script.

Files / Plots / Packages / Help Panel (Bottom-Right)

This multifunctional panel is for file navigation, plotting, managing packages, viewing help, and managing jobs. It contains:

- Files Tab: Navigate, open, and manage files and directories within your project.
- Plots Tab: Displays plots generated in your session. You can export or navigate through multiple plots here.
- Packages Tab: Lists installed packages and allows you to install, load, and update packages.
- Help Tab: Displays help documentation for R functions, packages, and other resources. You can search for documentation by typing a function or package name.

Important: Unless you are working with a script, you will be likely writing code on the console.

At the start of a session, it's good practice clearing your R environment (console):

```
rm(list = ls())
```

In R, we are going to be working with **relative paths**. With the command `getwd()`, you can see where your working directory is currently set.

```
getwd()
```

For ENVS225, download the [material](#) of the module and unzip it wherever you like.

The folder structure should look like:

```
stats/  
  data/  
  labs_img/  
  labs/
```

You can delete other sub-folders (e.g. docs).

This should be on your personal computer or if on a local machine, I suggest using the directory M: to store the folder, it can be accessed from every computer.

Then, in R Studio - on Windows by clicking RStudio>Tools>Global Options>General.. - on Mac OS by clicking RStudio>Preferences>Appearance or Pane Layout...

browse and set the folder you just created as your working directory.

Check if that has been applied.

```
getwd()
```

File paths in R work like this:

File Path	Description
MyFile.csv	Look in the working directory for MyFile.csv.
MyFolder/MyFile.csv	In the working directory, there is a subdirectory called MyFolder and inside that folder is MyFile.csv.

You do not need to set your working directory if you are using an R-markdown or Quarto document and you have it saved in the right location. The pathway will start from where your document is saved.

1.2.2 Using the console

Try to use the console to perform a few operations. For example type in:

```
1+1
```

```
[1] 2
```

Slightly more complicated:

```
print("hello world")
```

```
[1] "hello world"
```

If you are unsure about what a command does, use the “Help” panel in your Files pane or type `?function` in the console. For example, to see how the `dplyr::rename()` function works, type in `?dplyr::rename`. When you see the double colon syntax like in the previous command, it’s a call to a package without loading its library.

1.2.3 R as a simple calculator

You can use R as a simple calculator. At the prompt, type `2+3` and hit enter. What you should see is the following

```
# Some simple addition  
2+3
```

```
[1] 5
```

In this fashion you can use R as a very capable calculator.

```
6*8
```

```
[1] 48
```

```
4^3
```

```
[1] 64
```

```
exp(1) # exp() is the exponential function
```

```
[1] 2.718282
```

R has most constants and common mathematical functions you could ever want. For example, the absolute value of a number is given by `abs()`, and `round()` will round a value to the nearest integer.

```
pi # the constant 3.14159265...
```

```
[1] 3.141593
```

```
abs(1.77)
```

```
[1] 1.77
```

Whenever you call a function, there will be some arguments that are mandatory, and some that are optional and the arguments are separated by a comma. In the above statements the function `abs()` requires at least one argument, and that is the number you want the absolute value of.

When functions require more than one argument, arguments can be specified via the order in which they are passed or by naming the arguments. So for the `log()` function, for example, which calculates the logarithm of a number, one can specify the arguments using the named values; the order wouldn't matter:

```
# Demonstrating order does not matter if you specify  
# which argument is which  
log(x=5, base=10)
```

```
[1] 0.69897
```

```
log(base=10, x=5)
```

```
[1] 0.69897
```

When we don't specify which argument is which, R will decide that `x` is the first argument, and `base` is the second.

```
# If not specified, R will assume the second value is the base...  
log(5, 10)
```

```
[1] 0.69897
```

```
log(10, 5)
```

```
[1] 1.430677
```

When we want to specify the arguments, we can do so using the `name=value` notation.

1.2.4 Variables Assignment

We need to be able to assign a value to a variable to be able to use it later. R does this by using an arrow `<-` or an equal sign `=`. While R supports either, for readability, I suggest people pick one assignment operator and stick with it.

Variable names cannot start with a number, may not include spaces, and are case sensitive.

```
var <- 2*7.5      # create two variables  
another_var = 5   # notice they show up in 'Environment' tab in RStudio!  
var
```

```
[1] 15
```

```
var * another_var
```

```
[1] 75
```

As your analysis gets more complicated, you'll want to save the results to a variable so that you can access the results later. *If you don't assign the result to a variable, you have no way of accessing the result.*

1.2.5 Working with Scripts

R Scripts (.R files)

Traditional script files look like this:

```
# Problem 1
# Calculate the log of a couple of values and make a plot
# of the log function from 0 to 3
log(0)
log(1)
log(2)
x <- seq(.1,3, length=1000)
plot(x, log(x))

# Problem 2
# Calculate the exponential function of a couple of values
# and make a plot of the function from -2 to 2
exp(-2)
exp(0)
exp(2)
x <- seq(-2, 2, length=1000)
plot(x, exp(x))
```

In RStudio you can create a new script by going to **File -> New File -> R Script**. This opens a new window in RStudio where you can type commands and functions as a common text editor.

This looks perfectly acceptable as a way of documenting what one does, but this script file doesn't contain the actual results of commands you ran, nor does it show you the plots. Also anytime you want to comment on some output, it needs to be offset with the commenting character `#`. It would be nice to have both the commands and the results merged into one document. This is what the R Markdown file does for us.

R Markdown (.Rmd and .qmd files)

The R Markdown is an implementation of the Markdown syntax that makes it extremely easy to write webpages or scientific documents that include code. This syntax was extended to allow users to embed R code directly into more complex documents. Perhaps the easiest way to understand the syntax is to look at an at the [RMarkdown website](#).

The R code in a R Markdown document (.rmd file extension) can be nicely separated from regular text using the three backticks (3 times `'`, see below) and an instruction that it is R code that needs to be evaluated. A code chunk will look like:

```
for (i in 1:5) {print(i)}
```

```
[1] 1  
[1] 2  
[1] 3  
[1] 4  
[1] 5
```

In ENVS225: In this module we will be using `.qmd` a more flexible development of `.rmd` files.

Markdown files present several advantages compared to writing your code in the console or just using scripts. You'll save yourself a huge amount of work by embracing Markdown files from the beginning; you will keep track of your code and your steps, be able to document and present how you did your analysis (helpful when writing the methods section of a paper), and it will make it easier to re-run an analysis after a change in the data (such as additional data values, transformed data, or removal of outliers) or once you spot an error. Finally, it makes the script more readable.

1.2.6 R Packages

One of the greatest strengths about R is that so many people have developed add-on packages to do some additional function. To download and install the package from the Comprehensive R Archive Network (CRAN), you just need to ask RStudio it to install it via the menu **Tools -> Install Packages...** Once there, you just need to give the name of the package and RStudio will download and install the package on your computer.

Once a package is downloaded and installed on your computer, it is available, but it is not loaded into your current R session by default. To improve overall performance only a few packages are loaded by default and the you must explicitly load packages whenever you want to use them. You only need to load them once per session/script.

```
library(dplyr) # load the dplyr library, will be useful later
```

1.3 Practice: Dataset and Dataframes

First of all, create a new Markdown document. We use the **File -> New File -> Quarto Document...** dropdown option, and a menu will appear asking you for the document title, author, and preferred output type. You can select HTML, but you will need your assignment to be submitted in PDF; more on that later.

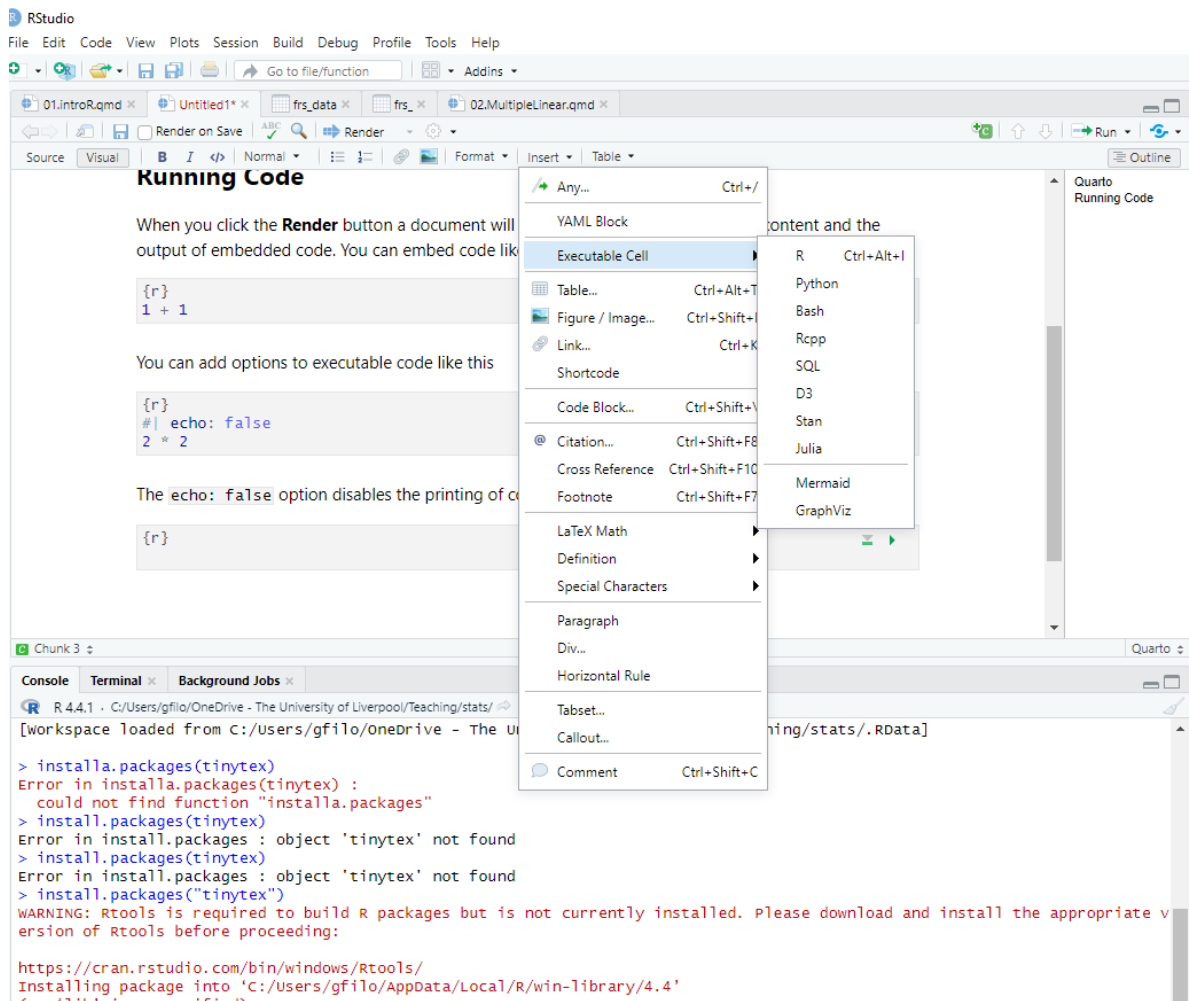
Follow the practical below. You can describe what you are doing in normal text. See [here](#) for how to format normal text in Markdown documents

Remember, when you want to write code in a markdown document you have to enclose it like this:

```
```{r}

```
```

or you can insert it manually:



Within this module we will be working with data stored in so-called datasets. A dataset is a structured collection of data points that represent various measurements or observations, often organized in a tabular format with rows and columns. A dataset might contain information

about different locations, such as neighborhoods or cities, with each row representing a place and each column detailing characteristics like population density, average income, or number of green parks. For example, a dataset could be compiled to study patterns in urban mobility, where the data includes the number of daily commuters, the distance they travel, and the mode of transport they use. Datasets provide the essential building blocks for statistical analysis; they enable exploring relationships, identifying patterns, and drawing conclusions about certain phenomena.

Examples of everyday datasets:

- **Premier League Standings:** Each row represents a team, with columns for points, games played, wins, draws, and losses.
- **Movie Dataset:** Each row represents a movie, with columns showing its title, genre, release year, director, and rating.
- **Weather Dataset:** Each row shows a day's weather in a city, with columns for temperature, humidity, wind speed, and precipitation.

Usually, data is organized in

- **Columns** of data representing some trait or variable that we might be interested in. In general, we might wish to investigate the relationship between variables.
- **Rows** represent a single object on which the column traits are measured.

For example, in a grade book for recording students scores throughout the semester, there is one row for every student and columns for each assignment. A greenhouse experiment dataset will have a row for every plant and columns for treatment type and biomass.

1.3.1 Datasets in R

In R, we want a way of storing data where it feels just as if we had an Excel Spreadsheet where each row represents an observation and each column represents some information about that observation. We will call this object a **data.frame**, an R representation of a data set. The easiest way to understand data frames is to create one.

Task: Copy the code below in your markdown. Create a **data.frame** that represents an instructor's grade book, where each row is a student, and each column represents some sort of assessment.

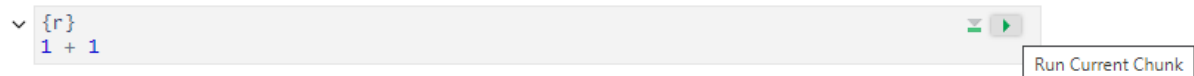
```
Grades <- data.frame(
  Name   = c('Bob', 'Jeff', 'Mary', 'Valerie'),
  Exam.1 = c(90, 75, 92, 85),
  Exam.2 = c(87, 71, 95, 81)
)
# Show the data.frame
```



```
# View(Grades) # show the data in an Excel-like tab. Doesn't work when knitting
Grades         # show the output in the console. This works when knitting
```

```
      Name Exam.1 Exam.2
1      Bob      90      87
2      Jeff      75      71
3      Mary      92      95
4 Valerie      85      81
```

To execute just one chunk of code press the green arrow top-right of the chunk:


 {r}
 1 + 1
 Run Current Chunk

R allows two different ways to access elements of the `data.frame`. First is a matrix-like notation for accessing particular values.

| Format | Result |
|--------|---|
| [a,b] | Element in row a and column b |
| [a,] | All of row a |
| [,b] | All of column b |

Because the columns have meaning and we have given them column names, it is desirable to want to access an element by the name of the column as opposed to the column number.

Task: Copy and Run:

```
Grades[, 2]      # print out all of column 2
```

```
[1] 90 75 92 85
```

```
Grades$Name      # The $-sign means to reference a column by its label
```

```
[1] "Bob"      "Jeff"      "Mary"      "Valerie"
```

1.3.2 Importing Data in R

From: https://raw.githubusercontent.com/dereksonderegger/570L/master/07_DataImport.Rmd

Usually we won't type the data in by hand, but rather load the data from some package. Reading data from external sources is a necessary skill.

Comma Separated Values Data

To consider how data might be stored, we first consider the simplest file format: the comma separated values file (`.csv`). In this file type, each of the "cells" of data are separated by a comma. For example, the data file storing scores for three students might be as follows:

```
Able, Dave, 98, 92, 94
Bowles, Jason, 85, 89, 91
Carr, Jasmine, 81, 96, 97
```

Typically when you open up such a file on a computer with MS Excel installed, Excel will open up the file assuming it is a spreadsheet and put each element in its own cell. However, you can also open the file using a more primitive program (say Notepad in Windows, TextEdit on a Mac) you'll see the raw form of the data.

Having just the raw data without any sort of column header is problematic (which of the three exams was the final?). Ideally we would have column headers that store the name of the column.

```
LastName, FirstName, Exam1, Exam2, FinalExam
Able, Dave, 98, 92, 94
Bowles, Jason, 85, 89, 91
Carr, Jasmine, 81, 96, 97
```

Reading (`.csv`) files

To make R read in the data arranged in this format, we need to tell R three things:

1. Where does the data live? Often this will be the name of a file on your computer, but the file could just as easily live on the internet (provided your computer has internet access).
2. Is the first row data or is it the column names?
3. What character separates the data? Some programs store data using tabs to distinguish between elements, some others use white space. R's mechanism for reading in data is flexible enough to allow you to specify what the separator is.

The primary function that we'll use to read data from a file and into R is the function `read.csv()`. This function has many optional arguments but the most commonly used ones are outlined in the table below.

| Argument | Default | Description |
|-------------------------------|-----------|---|
| <code>file</code> | Required | A character string denoting the file location. |
| <code>header</code> | TRUE | Specifies whether the first line contains column headers. |
| <code>sep</code> | "," | Specifies the character that separates columns. For <code>read.csv()</code> , this is usually a comma. |
| <code>skip</code> | 0 | The number of lines to skip before reading data; useful for files with descriptive text before the actual data. |
| <code>na.strings</code> | "NA" | Values that represent missing data; multiple values can be specified, e.g., <code>c("NA", "-9999")</code> . |
| <code>quote</code> | " | Specifies the character used to quote character strings, typically " or '. |
| <code>stringsAsFactors</code> | FALSE | Controls whether character strings are converted to factors; FALSE means they remain as character data. |
| <code>row.names</code> | NULL | Allows specifying a column as row names, or assigning NULL to use default indexing for rows. |
| <code>colClasses</code> | NULL | Specifies the data type for each column to speed up reading for large files, e.g., <code>c("character", "numeric")</code> . |
| <code>encoding</code> | "unknown" | Sets the text encoding of the file, which can be useful for files with special or international characters. |

Most of the time you just need to specify the file. |

Task: Let's read in a dataset of terrorist attacks that have taken place in the UK:

```
attacks <- read.csv(file = '../data/attacksUK.csv') # where the data lives
View(attacks)
```

1.4 Practice: Descriptive Statistics

1.4.1 Summarizing Data

It is very important to be able to take a data set and produce summary statistics such as the mean and standard deviation of a column. For this sort of manipulation, we use the package `dplyr`. This package allows chaining together many common actions to form a particular task.

The foundational operations to perform on a data set are:

- **Subsetting** - Returns a with only particular columns or rows
 - `select` - Selecting a subset of columns by name or column number.
 - `filter` - Selecting a subset of rows from a data frame based on logical expressions.
 - `slice` - Selecting a subset of rows by row number.
- `arrange` - Re-ordering the rows of a data frame.
- `mutate` - Add a new column that is some function of other columns.
- `summarise` - calculate some summary statistic of a column of data. This collapses a set of rows into a single row.

Each of these operations is a function in the package `dplyr`. These functions all have a similar calling syntax,; - The first argument is a data set,; - Subsequent arguments describe what to do with the input data frame and you can refer to the columns without using the `df$column` notation.

All of these functions will return a data set.

The `dplyr` package also includes a function that “pipes” commands together. The idea is that the `%>%` operator works by translating the command `a %>% f(b)` to the expression `f(a,b)`. This operator works on any function `f`. The beauty of this comes when you have a suite of functions that takes input arguments of the same type as their output. For example if we wanted to start with `x`, and first apply function `f()`, then `g()`, and then `h()`, the usual R command would be `h(g(f(x)))` which is hard to read because you have to start reading at

the innermost set of parentheses. Using the pipe command `%>%`, this sequence of operations becomes `x %>% f() %>% g() %>% h()`. For example:

```
Grades # Recall the Grades data
```

| | Name | Exam.1 | Exam.2 |
|---|---------|--------|--------|
| 1 | Bob | 90 | 87 |
| 2 | Jeff | 75 | 71 |
| 3 | Mary | 92 | 95 |
| 4 | Valerie | 85 | 81 |

```
# The following code takes the Grades data.frame and calculates  
# a column for the average exam score, and then sorts the data  
# according to the that average score
```

```
Grades %>%  
  mutate( Avg.Score = (Exam.1 + Exam.2) / 2 ) %>%  
  arrange( Avg.Score )
```

| | Name | Exam.1 | Exam.2 | Avg.Score |
|---|---------|--------|--------|-----------|
| 1 | Jeff | 75 | 71 | 73.0 |
| 2 | Valerie | 85 | 81 | 83.0 |
| 3 | Bob | 90 | 87 | 88.5 |
| 4 | Mary | 92 | 95 | 93.5 |

Keep it in mind, it is not necessary to memorise this.

Let's consider the **summarize** function to calculate the mean score for **Exam.1**. Notice that this takes a data frame of four rows, and summarizes it down to just one row that represents the summarized data for all four students.

```
library(dplyr) # load the library  
Grades %>%  
  summarize( Exam.1.mean = mean( Exam.1 ) )
```

| | Exam.1.mean |
|---|-------------|
| 1 | 85.5 |

Similarly you could calculate the **standard deviation** for the exam as well.

```

Grades %>%
  summarize( Exam.1.mean = mean( Exam.1 ),
             Exam.1.sd   = sd( Exam.1 ) )

```

```

Exam.1.mean Exam.1.sd
1          85.5  7.593857

```

Task: Write the code above in your markdown file and run it. Do not to copy it this time.

Let's go back to the terrorist attacks. There are attacks perpetrated by several different groups. Each record is a single attack and contains information about who perpetrated the attack, what year, how many were killed and how many were wounded. You can get a glimpse of the dataframe with the function head

```
head(attacks, n = 10)
```

| | nrKilled | nrWound | year | country | group |
|----|----------|---------|------|----------------|------------------------------|
| 1 | 0 | 0 | 2005 | United Kingdom | Abu Hafs al-Masri Brigades |
| 2 | 0 | 0 | 2005 | United Kingdom | Abu Hafs al-Masri Brigades |
| 3 | 0 | 0 | 2005 | United Kingdom | Abu Hafs al-Masri Brigades |
| 4 | 0 | 0 | 2005 | United Kingdom | Abu Hafs al-Masri Brigades |
| 5 | 0 | 1 | 1982 | United Kingdom | Abu Nidal Organization (ANO) |
| 6 | 0 | 0 | 2014 | United Kingdom | Anarchists |
| 7 | 0 | 0 | 2014 | United Kingdom | Anarchists |
| 8 | 0 | 0 | 2014 | United Kingdom | Anarchists |
| 9 | 0 | 0 | 2014 | United Kingdom | Anarchists |
| 10 | 0 | 0 | 2014 | United Kingdom | Anarchists |

| | attack | target |
|----|--------------------------------|-----------------------------|
| 1 | Bombing/Explosion | Transportation |
| 2 | Bombing/Explosion | Transportation |
| 3 | Bombing/Explosion | Transportation |
| 4 | Bombing/Explosion | Transportation |
| 5 | Assassination | Government (Diplomatic) |
| 6 | Facility/Infrastructure Attack | Business |
| 7 | Facility/Infrastructure Attack | Business |
| 8 | Facility/Infrastructure Attack | Business |
| 9 | Facility/Infrastructure Attack | Private Citizens & Property |
| 10 | Facility/Infrastructure Attack | Police |

| | weapon |
|---|---------------------------|
| 1 | Explosives/Bombs/Dynamite |
| 2 | Explosives/Bombs/Dynamite |

```

3 Explosives/Bombs/Dynamite
4 Explosives/Bombs/Dynamite
5           Firearms
6           Incendiary
7           Incendiary
8           Incendiary
9           Incendiary
10          Incendiary

```

We might want to compare different actors and see the mean and standard deviation of the number of people wound, by each group's attack, across time. To do this, we are still going to use the `summarize`, but we will precede that with `group_by(group)` to tell the subsequent `dplyr` functions to perform the actions separately for each breed.

```

attacks %>%
  group_by( group) %>%
  summarise( Mean = mean(attacks$nrWound),
             Std.Dev = sd(attacks$nrWound))

```

```

# A tibble: 38 x 3
  group                Mean Std.Dev
  <chr>                <dbl>   <dbl>
1 Abu Hafs al-Masri Brigades 0.963    7.22
2 Abu Nidal Organization (ANO) 0.963    7.22
3 Anarchists                0.963    7.22
4 Animal Liberation Front (ALF) 0.963    7.22
5 Animal Rights Activists    0.963    7.22
6 Armenian Secret Army for the Liberation of Armenia 0.963    7.22
7 Black September           0.963    7.22
8 Continuity Irish Republican Army (CIRA) 0.963    7.22
9 Dissident Republicans      0.963    7.22
10 Informal Anarchist Federation 0.963    7.22
# i 28 more rows

```

Task: Write the code above in your markdown file and run it. Try out another categorical variable instead of `group` (e.g. `year`) and `nrKilled` instead of `nrWound`.

Let's now move to another dataset to address a research question. For illustration purposes, we will use the **Family Resources Survey (FRS)**. The FRS is an annual survey conducted by the UK government that collects detailed information about the income, living conditions, and resources of private households across the United Kingdom. Managed by the Department

for Work and Pensions (DWP), the FRS provides data that is essential for understanding the economic and social conditions of households and informing public policy.

Consider questions such as:

- How many respondents (persons) are there in the 2016-17 FRS?
- How many variables (population attributes) are there?
- What types of variables are present in the FRS?
- What is the most detailed geography available in the FRS?

Task: To answer these questions, load and inspect the dataset.

```
# the FRS dataset should be already loaded, otherwise
frs_data <- read.csv("../data/FamilyResourceSurvey/FRS16-17_labels.csv")

# Display basic structure
glimpse(frs_data)
```

```
Rows: 44,145
Columns: 45
$ household      <int> 6087, 6101, 6103, 6122, 6134, 6136, 6138, 6140, 6143, ~
$ family         <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
$ person         <int> 5, 3, 3, 3, 2, 4, 4, 3, 3, 4, 4, 3, 4, 2, 5, 3, 4, 3, ~
$ country        <chr> "England", "England", "England", "Northern Ireland", ~
$ region         <chr> "London", "South East", "Yorks and the Humber", "Nort~
$ age_group      <chr> "05-10", "05-10", "05-10", "05-10", "05-10", "05-10", ~
$ sex            <chr> "Female", "Male", "Male", "Female", "Female", "Female~
$ marital_status <chr> "Single", "Single", "Single", "Single", "Single", "Si~
$ ethnicity      <chr> "Mixed / multiple ethnic groups", "White", "White", "~
$ hrp            <chr> "Not HRP", "Not HRP", "Not HRP", "Not HRP", "Not HRP"~
$ rel_to_hrp     <chr> "Son/daughter (incl. adopted)", "Son/daughter (incl. ~
$ lifestage      <chr> "Child (0-17)", "Child (0-17)", "Child (0-17)", "Chil~
$ dependent      <chr> "Dependent", "Dependent", "Dependent", "Dependent", "~
$ arrival_year   <chr> "UK Born", "UK Born", "UK Born", "UK Born", "UK Born"~
$ birth_country  <chr> "Dependent child", "Dependent child", "Dependent chil~
$ care_hours     <chr> "0 hours per week", "0 hours per week", "0 hours per ~
$ educ_age       <chr> "Dependent child", "Dependent child", "Dependent chil~
$ educ_type      <chr> "School (full-time)", "School (full-time)", "School (~
$ fam_youngest   <chr> "7", "4", "0", "7", "0", "9", "10", "0", "3", "10", "~
$ fam_toddlers   <int> 0, 1, 1, 0, 2, 0, 0, 2, 1, 0, 0, 1, 0, 1, 0, 0, 0, 1, ~
$ fam_size       <int> 4, 4, 4, 3, 4, 4, 3, 5, 4, 4, 3, 4, 4, 3, 5, 4, 4, 4, ~
$ happy          <chr> "Dependent child", "Dependent child", "Dependent chil~
$ health         <chr> "Not known", "Not known", "Not known", "Not known", "~
```



```

$ hh_accom_type      <chr> "Terraced house/bungalow", "Detached house/bungalow",~
$ hh_benefits        <int> 10868, 0, 1768, 8632, 8372, 1768, 1768, 1768, 0, 0, 1~
$ hh_composition     <chr> "Three or more adults, 1+ children", "One adult femal~
$ hh_ctax_band       <chr> "Band D", "Band F", "Band A", "Band B", "Band A", "Ba~
$ hh_housing_costs   <chr> "4316", "10296", "5408", "Northern Ireland", "5720", ~
$ hh_income_gross    <int> 54236, 180804, 26936, 19968, 17992, 76596, 31564, 366~
$ hh_income_net      <int> 44668, 120640, 23556, 19968, 17992, 62868, 29744, 287~
$ hh_size            <int> 5, 4, 4, 3, 4, 4, 4, 5, 4, 4, 4, 4, 4, 5, 5, 4, 4, 4,~
$ hh_tenure          <chr> "Mortgaged (including part rent / part own)", "Mortga~
$ highest_qual       <chr> "Dependent child", "Dependent child", "Dependent chil~
$ income_gross       <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
$ income_net         <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
$ jobs              <chr> "Dependent child", "Dependent child", "Dependent chil~
$ life_satisf        <chr> "Dependent child", "Dependent child", "Dependent chil~
$ nssec              <chr> "Dependent child", "Dependent child", "Dependent chil~
$ sic_chapter        <chr> "Dependent child", "Dependent child", "Dependent chil~
$ sic_division       <chr> "Dependent child", "Dependent child", "Dependent chil~
$ soc2010            <chr> "Dependent child", "Dependent child", "Dependent chil~
$ work_hours         <chr> "Dependent child", "Dependent child", "Dependent chil~
$ workstatus         <chr> "Dependent Child", "Dependent Child", "Dependent Chil~
$ years_ft_work      <chr> "Dependent child", "Dependent child", "Dependent chil~
$ survey_weight      <int> 2315, 1317, 2449, 427, 1017, 1753, 1363, 1344, 828, 1~

```

and summary:

```
summary(frs_data)
```

| household | family | person | country |
|---------------|---------------|--------------|------------------|
| Min. : 1 | Min. :1.000 | Min. :1.00 | Length:44145 |
| 1st Qu.: 4816 | 1st Qu.:1.000 | 1st Qu.:1.00 | Class :character |
| Median : 9673 | Median :1.000 | Median :2.00 | Mode :character |
| Mean : 9677 | Mean :1.106 | Mean :1.98 | |
| 3rd Qu.:14553 | 3rd Qu.:1.000 | 3rd Qu.:3.00 | |
| Max. :19380 | Max. :6.000 | Max. :9.00 | |

| region | age_group | sex | marital_status |
|------------------|------------------|------------------|------------------|
| Length:44145 | Length:44145 | Length:44145 | Length:44145 |
| Class :character | Class :character | Class :character | Class :character |
| Mode :character | Mode :character | Mode :character | Mode :character |

ethnicity

hrp

rel_to_hrp

lifestage

| | | | |
|------------------|------------------|------------------|------------------|
| Length:44145 | Length:44145 | Length:44145 | Length:44145 |
| Class :character | Class :character | Class :character | Class :character |
| Mode :character | Mode :character | Mode :character | Mode :character |

| | | | |
|------------------|------------------|------------------|------------------|
| dependent | arrival_year | birth_country | care_hours |
| Length:44145 | Length:44145 | Length:44145 | Length:44145 |
| Class :character | Class :character | Class :character | Class :character |
| Mode :character | Mode :character | Mode :character | Mode :character |

| | | | |
|------------------|------------------|------------------|----------------|
| educ_age | educ_type | fam_youngest | fam_toddlers |
| Length:44145 | Length:44145 | Length:44145 | Min. :0.0000 |
| Class :character | Class :character | Class :character | 1st Qu.:0.0000 |
| Mode :character | Mode :character | Mode :character | Median :0.0000 |
| | | | Mean :0.2557 |
| | | | 3rd Qu.:0.0000 |
| | | | Max. :4.0000 |

| | | | |
|---------------|------------------|------------------|------------------|
| fam_size | happy | health | hh_accom_type |
| Min. :1.000 | Length:44145 | Length:44145 | Length:44145 |
| 1st Qu.:2.000 | Class :character | Class :character | Class :character |
| Median :2.000 | Mode :character | Mode :character | Mode :character |
| Mean :2.599 | | | |
| 3rd Qu.:4.000 | | | |
| Max. :9.000 | | | |

| | | | |
|---------------|------------------|------------------|------------------|
| hh_benefits | hh_composition | hh_ctax_band | hh_housing_costs |
| Min. : 0 | Length:44145 | Length:44145 | Length:44145 |
| 1st Qu.: 0 | Class :character | Class :character | Class :character |
| Median : 1768 | Mode :character | Mode :character | Mode :character |
| Mean : 5670 | | | |
| 3rd Qu.:10192 | | | |
| Max. :54080 | | | |

| | | | |
|-----------------|----------------|--------------|------------------|
| hh_income_gross | hh_income_net | hh_size | hh_tenure |
| Min. : -326092 | Min. : -334776 | Min. : 1.00 | Length:44145 |
| 1st Qu.: 22256 | 1st Qu.: 20748 | 1st Qu.:2.00 | Class :character |
| Median : 35984 | Median : 31512 | Median :3.00 | Mode :character |
| Mean : 46076 | Mean : 37447 | Mean :2.96 | |
| 3rd Qu.: 57252 | 3rd Qu.: 47008 | 3rd Qu.:4.00 | |
| Max. :1165216 | Max. :1116596 | Max. :9.00 | |

| | | | |
|--------------|----------------|----------------|--------------|
| highest_qual | income_gross | income_net | jobs |
| Length:44145 | Min. : -354848 | Min. : -358592 | Length:44145 |

```

Class :character  1st Qu.:    52  1st Qu.:    0  Class :character
Mode  :character  Median : 12740  Median : 12012  Mode  :character
                        Mean  : 17305  Mean   : 14204
                        3rd Qu.: 23712  3rd Qu.: 20384
                        Max.   :1127360  Max.   :1110928
life_satisf      nssec      sic_chapter      sic_division
Length:44145     Length:44145     Length:44145     Length:44145
Class :character  Class :character  Class :character  Class :character
Mode  :character  Mode  :character  Mode  :character  Mode  :character

```

```

      soc2010      work_hours      workstatus      years_ft_work
Length:44145     Length:44145     Length:44145     Length:44145
Class :character  Class :character  Class :character  Class :character
Mode  :character  Mode  :character  Mode  :character  Mode  :character

```

```

survey_weight
Min.   : 221
1st Qu.: 1097
Median : 1380
Mean   : 1459
3rd Qu.: 1742
Max.   :39675

```

1.4.2 Understanding the Structure of the FRS Datafile

In the FRS data structure, each row represents a person, but:

- Each person is nested within a family.
- Each family is nested within a household.

Below is an example dataset structure:

| household | family | person | region | age_group | sex | marital_status | to_hrp |
|-----------|--------|--------|--------|-----------|--------|-----------------------------------|--------|
| 1 | 1 | 1 | London | 40-44 | Female | Married/Civil
partner-
ship | Spouse |

| household | family | person | region | age_group | sex | marital_status | rel_to_hrp |
|-----------|--------|--------|----------------------|-----------|--------|---------------------------|------------------------------|
| 1 | 1 | 2 | London | 40-44 | Male | Married/Civil partnership | Household Representative |
| 1 | 1 | 3 | London | 5-10 | Male | Single | Son/daughter (incl. adopted) |
| 1 | 1 | 4 | London | 5-10 | Female | Single | Son/daughter (incl. adopted) |
| 1 | 1 | 5 | London | 16-19 | Male | Single | Step-son/daughter |
| 2 | 1 | 1 | Scotland | 35-39 | Male | Single | Household Representative |
| 3 | 1 | 1 | Yorks and the Humber | 35-39 | Female | Married/Civil partnership | Household Representative |
| 3 | 1 | 2 | Yorks and the Humber | 35-39 | Male | Married/Civil partnership | Spouse |
| 3 | 1 | 3 | Yorks and the Humber | 5-10 | Male | Single | Step-son/daughter |
| 4 | 1 | 1 | Wales | 0-4 | Male | Single | Son/daughter (incl. adopted) |
| 4 | 1 | 2 | Wales | 60-64 | Male | Married/Civil partnership | Household Representative |
| 4 | 1 | 3 | Wales | 55-59 | Female | Married/Civil partnership | Spouse |
| 4 | 2 | 3 | Wales | 30-34 | Female | Single | Son/daughter (incl. adopted) |

The first five people in the FRS all belong to the same household (household 1); they also all belong to the same family. This family comprises a married middle-aged couple plus their three children, one of whom is a stepson.

The second household (household 2) comprises only one person – a single middle-aged male. The third household comprises another married couple, this time with two children.

Superficially the fourth household looks similar to households 1 and 2: a married couple plus their daughter. The difference is that this particular married couple is nearing retirement age,

and their daughter is middle-aged. Consequently, despite being a child of the married couple, the middle-aged daughter is treated as a separate ‘family’ (family 2 in the household). This is because the FRS (and Census) define a ‘family’ as a couple plus any ‘dependent’ children. A dependent child is defined as a child who is either ‘aged 0-15 or aged 16-19, unmarried and in full-time education. All children aged 16-19 who are married or no longer in full-time education are regarded as ‘independent’ adults who form their own family unit, as are all children aged 20+.

The inclusion of all persons in a household allows us more flexibility in the types of research question we can answer. For example, we could explore how the likelihood of a woman being in paid employment `WorkStatus` is influenced by the age of the youngest child still living in her family (if any) `fam_youngest`.

In the FRS (and Census), a “family” is defined as a couple and any “dependent” children. Dependent children are defined as those aged 0–15, or aged 16–19 if unmarried and in full-time education.

1.4.3 Explore the Distribution of Your Outcome Variable

Before starting your analysis, it is critical to know the type of scale used to measure your outcome variable: is it categorical or continuous? Here we will start off by exploring a continuous variable which can then turn into a categorical variable (e.g. top earners: yes or no). We explore the income distribution in the UK by first looking at the low and high end of the distribution ie. What sorts of people have high (or low) incomes?

In the FRS each person’s annual income is recorded, both gross (pre-tax) and net (post-tax). This income includes all income sources, including earnings, profits, investment returns, state benefits, occupational pensions etc. As it is possible to make a loss on some of these activities, it is also possible (although unusual) for someone’s gross or net annual income in a given year to be negative (representing an overall loss).

Task: Load the FRS dataset into your R environment, if it’s not already loaded, and inspect the data.

```
# Load the dataset (replace 'frs_data.csv' with the actual file path)
frs_data <- read.csv("../data/FamilyResourceSurvey/FRS16-17_labels.csv")
```

Open the dataset in RStudio’s **Data Viewer** to explore its structure, including the `income_gross` and `income_net` variables.

```
# Open the data in the RStudio Viewer
View(frs_data)
```

in the **Data Viewer** tab, scroll horizontally to locate the `income_gross` and `income_net` columns. If columns are listed alphabetically, they will appear near other attributes that start with “income.”

You should notice two things:

- Incomes are recorded to the nearest £, NOT in income bands.
- Dependent children almost all have a recorded income of £0.

This second observation highlights the somewhat loose wording of our question above (*What sorts of people have high (or low) incomes?*). To avoid reaching the somewhat banal conclusion that those with the lowest of all incomes are almost all children, we should re-frame the question more precisely as *What sorts of people (excluding dependent children) have low incomes?*

Task: Determine the Scale of the Outcome Variable.

```
# Summarize income variables
summary(frs_data$income_gross)
```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|---------|---------|--------|-------|---------|---------|
| -354848 | 52 | 12740 | 17305 | 23712 | 1127360 |

```
# Summarize income variables
summary(frs_data$income_net)
```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|---------|---------|--------|-------|---------|---------|
| -358592 | 0 | 12012 | 14204 | 20384 | 1110928 |

Task: Exclude Dependent Children.

You need to select all cases (persons) that are independent, that is where the variable `dependent` has values different from `!= "Dependent"` or equal `== "Independent"`.

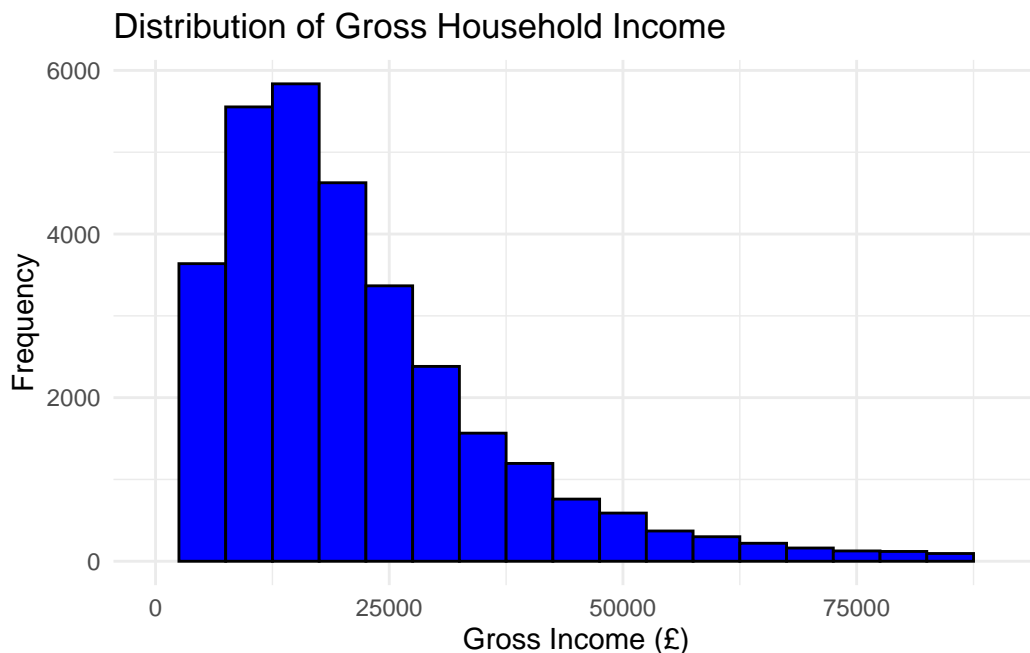
```
# Filter to include only independent persons
frs_independent <- frs_data %>% filter(dependent != "Dependent")
```

Task: Create a basic histogram (a visualisation lecture is scheduled later on).

The income variables in the FRS are all scale variables so a good starting point is to examine its distribution looking at a histogram of `income_gross`.

```
library(ggplot2)

ggplot(frs_independent, aes(x = income_gross)) +
  geom_histogram(binwidth = 5000, fill = "blue", color = "black") +
  labs(
    title = "Distribution of Gross Household Income",
    x = "Gross Income (£)",
    y = "Frequency"
  ) +
  xlim(0, 90000) +
  theme_minimal()
```



You should see the histogram below. It reveals that the income distribution is very skewed with few people earning high salaries and the majority earning just over or less 35,000 annually.

Task: Adopt a regrouping strategy.

You can also cross-tabulate gross (or net) income with any of the other variables in the FRS to your heart's content – or can you?

Again, here is important to recall that the income variables in the FRS are all 'scale' variables; in other words, they are precise measures rather than broad categories. Consequently, every single person in the FRS potentially has their own unique income value. That could make for a table c. 44,000 rows long (one row per person) if each person has their own unique value.

The solution is to create a categorical version of the original income variable by assigning each person to one of a set of income categories (income bands). Having done this, cross-tabulation then becomes possible.

But which strategy to use? Equal intervals, percentiles or ‘ad hoc’. Here I would suggest that ‘ad hoc’ is best: all you want to do is to allocate each independent adult to one of three arbitrarily defined groups: ‘low’, ‘middle’ and ‘high’ income. **Define Low and High Income Thresholds**

Define thresholds for income categories:

- Low-income threshold: £_____
- High-income threshold: £_____

Task: Create a New Variable Based on Regrouping of Original Variable.

Recode `income_gross` into categories based on the chosen thresholds.

```
# Define thresholds for income categories
LOW_THRESHOLD <- 10000 # Replace with the upper limit for low income
HIGH_THRESHOLD <- 50000 # Replace with the lower limit for high income

# Define income categories based on thresholds
frs_independent <- frs_independent %>%
  mutate(income_category = case_when(
    income_gross <= LOW_THRESHOLD ~ "Low",
    income_gross >= HIGH_THRESHOLD ~ "High",
    TRUE ~ "Middle" ))
```

The `mutate()` function in R, from the **dplyr** package, is used to add or modify columns in a data frame. It allows you to create new variables or transform existing ones by applying calculations or conditional statements directly within the function.

Explanation of the code

- `frs_independent %>%`: The pipe operator `%>%` sends `frs_independent` into `mutate()`, allowing us to apply transformations without reassigning it repeatedly.
- `mutate()`: Starts the transformation process by defining new or modified columns.
- `income_category = case_when(...)`:
 - This creates a new column named `income_category`.
 - The `case_when()` function defines conditions for assigning values to this new column.
- `case_when()`:
 - `case_when()` is used here to assign categorical labels based on conditions.

- `income_gross <= LOW_THRESHOLD ~ "Low"`: If `income_gross` is less than or equal to `LOW_THRESHOLD`, `income_category` will be labeled “Low.”
- `income_gross >= HIGH_THRESHOLD ~ "High"`: If `income_gross` is greater than or equal to `HIGH_THRESHOLD`, `income_category` will be labeled “High.”
- `TRUE ~ "Middle"`: Any values not meeting the previous conditions are labeled “Middle.”

Task: Add some Metadata.

Define metadata for the new variable by labeling income categories.

```
# Add metadata by converting to a factor and defining labels

frs_independent$income_category <- factor(frs_independent$income_category,
                                           levels = c("Low", "Middle", "High"), labels = c("<= £10,000", "£10,001 - £49,999", ">= £50,000"))
```

Task: Check your work.

Examine the frequency distribution of the variable you have just created. Both variables should have the same number of missing cases, unless:

- Missing cases in the old variable have been intentionally converted into valid cases in the new variable.
- You forgot to allocate a new value to one of the old variable categories, in which case the new variable will have more missing cases than the old variable.

```
# Frequency distribution of income categories
table(frs_independent$income_category)
```

| | | |
|------------|-------------------|------------|
| <= £10,000 | £10,001 - £49,999 | >= £50,000 |
| 8584 | 22981 | 2271 |

After preparing the data, use cross-tabulations to compare income levels across demographic groups.

```
# Cross-tabulate income category by age group, nationality, etc.
table(frs_independent$income_category, frs_independent$age_group)
```

| | 16-19 | 20-24 | 25-29 | 30-34 | 35-39 | 40-44 | 45-49 | 50-54 | 55-59 | 60-64 |
|-------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| <= £10,000 | 373 | 680 | 492 | 558 | 474 | 511 | 554 | 652 | 781 | 826 |
| £10,001 - £49,999 | 263 | 1241 | 1802 | 2056 | 2052 | 1948 | 1995 | 1967 | 1749 | 1772 |
| >= £50,000 | 1 | 8 | 59 | 186 | 314 | 331 | 334 | 356 | 237 | 177 |

| | 65-69 | 70-74 | 75+ |
|-------------------|-------|-------|------|
| <= £10,000 | 773 | 744 | 1166 |
| £10,001 - £49,999 | 2073 | 1554 | 2509 |
| >= £50,000 | 144 | 56 | 68 |

Explore income distribution across different regions.

```
# Cross-tabulate income category by region
table(frs_independent$income_category, frs_independent$region)
```

| | East Midlands | East of England | London | North East | North West |
|-------------------|---------------|-----------------|--------|------------|------------|
| <= £10,000 | 562 | 665 | 740 | 357 | 878 |
| £10,001 - £49,999 | 1550 | 1855 | 1850 | 979 | 2347 |
| >= £50,000 | 135 | 245 | 367 | 48 | 174 |

| | Northern Ireland | Scotland | South East | South West | Wales |
|-------------------|------------------|----------|------------|------------|-------|
| <= £10,000 | 874 | 1212 | 895 | 588 | 399 |
| £10,001 - £49,999 | 2305 | 3234 | 2563 | 1707 | 971 |
| >= £50,000 | 123 | 322 | 367 | 149 | 63 |

| | West Midlands | Yorks and the Humber |
|-------------------|---------------|----------------------|
| <= £10,000 | 744 | 670 |
| £10,001 - £49,999 | 1892 | 1728 |
| >= £50,000 | 164 | 114 |

Tips for Cross-Tabulation

- Place the income variable in the columns.
- Add multiple variables in the rows to create simultaneous cross-tabulations.

2 Lab: Correlation, Single, and Multiple Linear Regression

In this week's practical, we will review how to calculate and visualise correlation coefficients between variables. This practical is split into two parts. The first part focuses on measuring the correlation between and visualising the relationship between **continuous variables**. The second part goes through the implementation of a Linear Regression Model, again between continuous variables.

Before getting into it, have a look at this [resource](#), it really helps understand how regression models work.

The lecture's slides can be found [here](#).

Learning Objectives:

- Visualise the association between two continuous variables using a scatterplot.
- Measure the strength of the association between two variables by calculating their correlation coefficient.
- Build a formal regression model.
- Understand how to estimate and interpret a multiple linear regression model.

Notes: *Note for the practical: copy/edit/document the code in your own .qmd file. The code is supposed to be run as if the script was placed in the course folder or in the folder `labs`.*

Note on file paths: When calling the `read.csv` function, the path will vary depending on the location of the script it is being executed or your working directory (WD):

1. **If the script or your WD is in a sub-folder** (e.g., `labs`), use `"../data/Census2021/EW_DistrictPercentages.csv"`. The `..` tells R to go one level up to the main directory (`stats/`) and then access the `data/` folder. **Example:** `read.csv("../data/Census2021/EW_DistrictPercentages.csv")`.
2. **If the script is in the main directory** (e.g. inside `stats/`), you can access the data directly using `"data/Census2021/EW_DistrictPercentages.csv"`. Here, no `..` is necessary as the `data/` folder is directly accessible from the working directory. **Example:** `read.csv("data/Census2021/EW_DistrictPercentages.csv")`

2.1 Part I. Correlation

2.1.1 Data Overview: Descriptive Statistics:

Let's start by picking **one dataset derived from the English-Wales 2021 Census data**. You can choose one dataset that aggregates data either at a) county, b) district, or c) ward-level. Lower Tier Local Authority-, Region-, and Country-level data is also available in the data folder.

see also: <https://canvas.liverpool.ac.uk/courses/77895/pages/census-data-2021>

```
# Load necessary libraries
library(ggplot2)
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

`filter`, `lag`

The following objects are masked from 'package:base':

`intersect`, `setdiff`, `setequal`, `union`

```
options(scipen = 999, digits = 4) # Avoid scientific notation and round to 4 decimals globally

# load data
census <- read.csv("../data/Census2021/EW_DistrictPercentages.csv") # District level
```

We're using a (district/ward/etc.)-level census dataset that includes:

- % of population with poor health (variable name: `pct_Very_bad_health`).
- % of population with no qualifications (`pct_No_qualifications`).
- % of male population (`pct_Males`).
- % of population in a higher managerial/professional occupation (`pct_Higher_manager_prof`).

First, let's get some descriptive statistics that help identify general trends and distributions in the data.

```
# Summary statistics
summary_data <- census %>%
  select(pct_Very_bad_health, pct_No_qualifications, pct_Males, pct_Higher_manager_prof) %>%
  summarise_all(list(mean = mean, sd = sd))
summary_data
```

```
      pct_Very_bad_health_mean pct_No_qualifications_mean pct_Males_mean
1                1.173                17.9                48.97
      pct_Higher_manager_prof_mean pct_Very_bad_health_sd pct_No_qualifications_sd
1                13.22                0.3401                3.959
      pct_Males_sd pct_Higher_manager_prof_sd
1                0.6605                4.73
```

Q1. Complete the table below by specifying each variable type (continuous or categorical) and reporting its mean and standard deviation.

| Variable Name | Type (Continuous or Categorical) | Mean | Standard Deviation |
|-------------------------|----------------------------------|------|--------------------|
| pct_Very_bad_health | | | |
| pct_No_qualifications | | | |
| pct_Males | | | |
| pct_Higher_manager_prof | | | |

2.1.2 Simple visualisation for continuous data

You can visualise the relationship between two continuous variables using a scatter plot. Using the chosen census datasets, visualise the association between the % of population with bad health (`pct_Very_bad_health`) and each of the following:

- the % of population with no qualifications (`pct_No_qualifications`);
- the % of population aged 65 to 84 (`pct_Age_65_to_84`);
- the % of population in a married couple (`pct_Married_couple`);
- the % of population in a Higher Managerial or Professional occupation (`pct_Higher_manager_prof`).

```
# Scatterplot for each variable variables
variables <- c("pct_No_qualifications", "pct_Age_65_to_84", "pct_Married_couple", "pct_Higher_manager_prof")

# Loop to create scatterplots and calculate correlations
# x and y variables for each scatter plot,
for (var in variables) {
```

```
# Scatterplot
ggplot(census, aes_string(x = var, y = "pct_Very_bad_health")) +
  geom_point() +
  labs(title = paste("Scatterplot of pct_Very_bad_health vs", var),
       x = var, y = "pct_Very_bad_health") +
  theme_minimal()
}
```

Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
 i Please use tidy evaluation idioms with `aes()`.
 i See also `vignette("ggplot2-in-packages")` for more information.

Q2. Which of the associations do you think is strongest, which one is the weakest?

As noted, before, an observed association between two variables is no guarantee of causation. It could be that the observed association is:

- simply a chance one due to sampling uncertainty;
- caused by some third underlying variable which explains the spatial variation of both of the variables in the scatterplot;
- due to the inherent arbitrariness of the boundaries used to define the areas being analysed (the ‘Modifiable Area Unit Problem’).

Q3. Setting these caveats to one side, are the associations observed in the scatterplots suggestive of any causative mechanisms of bad health?

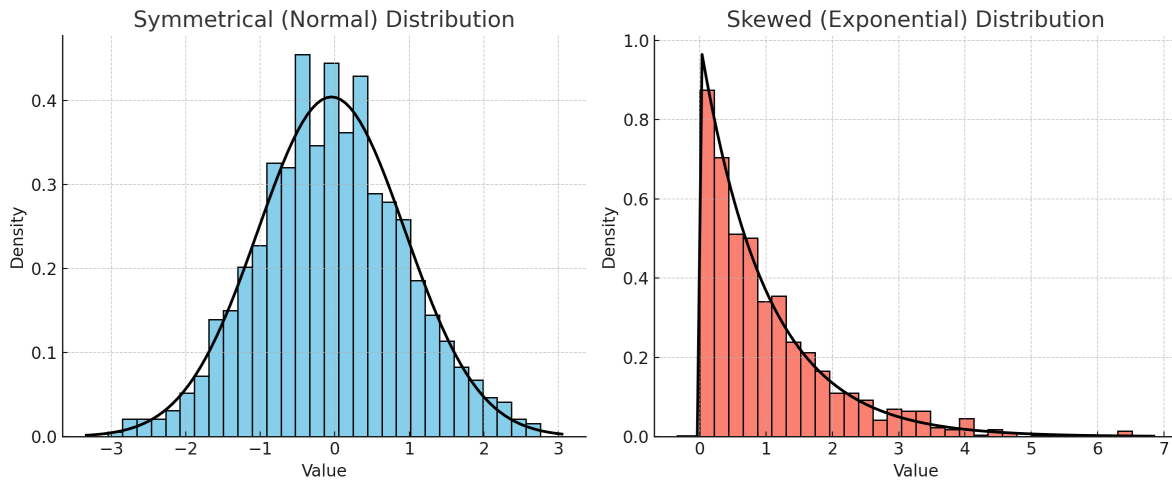
Rather than relying upon an impressionistic view of the strength of the association between two variables, we can measure that association by calculating the relevant correlation coefficient. The Table below identifies the statistically appropriate measure of correlation to use between two continuous variables.

| Variable Data Type | Measure of Correlation | Range |
|--|------------------------|----------|
| Both symmetrically distributed | Pearson’s | -1 to +1 |
| One or both with a skewed distribution | Spearman’s Rank | -1 to +1 |

Different Calculation Methods: Pearson’s correlation assumes linear relationships and is suitable for symmetrically distributed (normally distributed) variables, measuring the strength of the linear relationship. Spearman’s rank correlation, however, works on ranked data, so it’s more suitable for skewed data or variables with non-linear relationships, measuring the strength and direction of a monotonic relationship.

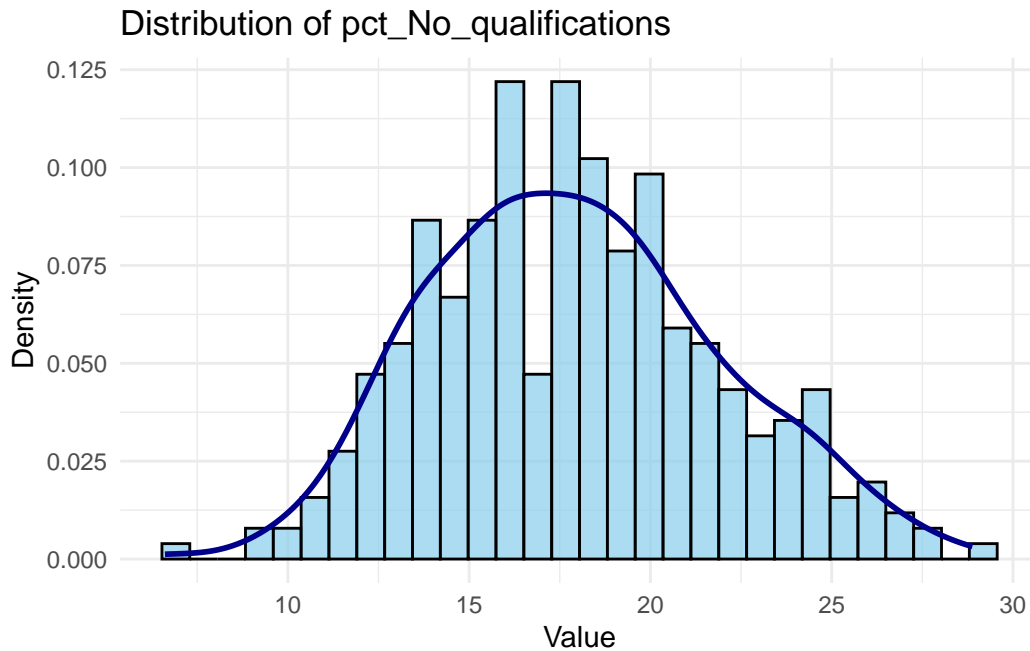
When calculating correlation for a single pair of variables, select the method that best fits their data distribution:

- Use **Pearson's** if both variables are symmetrically distributed.
- Use **Spearman's** if one or both variables are skewed.



You can check the distribution of a variable (e.g. `pct_No_qualifications`) like this:

```
# Plot histogram with density overlay for a chosen variable (e.g., 'pct_No_qualifications')
ggplot(census, aes(x = pct_No_qualifications)) +
  geom_histogram(aes(y = after_stat(density)), bins = 30, color = "black", fill = "skyblue") +
  geom_density(color = "darkblue", linewidth = 1) +
  labs(title = "Distribution of pct_No_qualifications", x = "Value", y = "Density") +
  theme_minimal()
```



When analyzing multiple pairs of variables, using different measures (Pearson for some pairs, Spearman for others) creates inconsistencies since Pearson and Spearman values aren't directly comparable in size due to their different calculation methods. To maintain consistency across comparisons, calculate **both Pearson's and Spearman's correlations** for each pair, e.g. do the trends align (both showing strong, weak, or moderate correlation in the same direction)? This consistency check can give confidence that the relationships observed are not dependent on the correlation method chosen. While in a report you'd typically include only one set of correlations (usually Pearson's if the relationships appear linear), calculating both can validate that your observations aren't an artifact of the correlation method.

Research Question 1: Which of our selected variables are most strongly correlated with % of population with bad health?

To answer this question, complete the Table below by editing/running this code:.

Pearson correlations

```
pearson_correlation <- cor(census$pct_Very_bad_health,
  census$pct_No_qualifications, use = "complete.obs", method = "pearson")

# Display the results
cat("Pearson Correlation:", pearson_correlation, "\n")
```

Pearson Correlation: 0.7619

Spearman correlations:

```
spearman_correlation <- cor(census$pct_Very_bad_health,
  census$pct_No_qualifications, use = "complete.obs", method = "spearman")

cat("Spearman Correlation:", spearman_correlation, "\n")
```

Spearman Correlation: 0.7781

| Covariates | Pearson | Spearman |
|---|---------|----------|
| pct_Very_bad_health - pct_No_qualifications | | |
| pct_Very_bad_health - pct_Age_65_to_84 | | |
| pct_Very_bad_health - pct_Married_couple | | |
| pct_Very_bad_health - pct_Higher_manager_prof | | |

What can you make of this numbers?

If you think you have found a correlation between two variables in our dataset, this doesn't mean that an association exists between these two variables in the population at large. The uncertainty arises because, by chance, the random sample included in our dataset might not be fully representative of the wider population.

For this reason, we need to verify whether the correlation is statistically significant,

```
# significance test for pearson, for example
pearson_test <- cor.test(census$pct_Very_bad_health,
  census$pct_No_qualifications, method = "pearson", use = "complete.obs")
pearson_test
```

Pearson's product-moment correlation

```
data: census$pct_Very_bad_health and census$pct_No_qualifications
t = 21, df = 329, p-value <0.0000000000000002
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.7127 0.8037
sample estimates:
cor
0.7619
```

Look at <https://www.rdocumentation.org/packages/stats/versions/3.6.2/topics/cor.test> for details about the function. But in general, when calculating the correlation between two variables, a **p-value** accompanies the correlation coefficient to indicate the statistical significance of the observed association. This p-value tests the null hypothesis that there is no association between the two variables (i.e., that the correlation is zero).

When interpreting p-values, certain thresholds denote different levels of confidence. A p-value less than 0.05 is generally considered statistically significant at the 95% confidence level, suggesting that we can be 95% confident there is an association between the variables in the broader population. When the p-value is below 0.01, the result is significant at the 99% confidence level, meaning we have even greater confidence (99%) that an association exists. Sometimes, on research papers or tables significance levels are denoted with asterisks: one asterisk (*) typically indicates significance at the 95% level ($p < 0.05$), two asterisks (**) significance at the 99% level ($p < 0.01$), three asterisks (***) significance at the 99.99% level ($p < 0.01$).

Typically, p-values are reported under labels such as “Sig (2-tailed),” where “2-tailed” refers to the fact that the test considers both directions (positive and negative correlations). Reporting the exact p-value (e.g., $p = 0.002$) is more informative than using thresholds alone, as it gives a clearer picture of how strongly the data contradicts the null hypothesis of no association.

In a nutshell, lower p-values suggest a stronger statistical basis for believing that an observed correlation is not due to random chance. A statistically significant p-value reinforces confidence that an association is likely to exist in the wider population, though it does not imply causation.

2.1.3 Part. 2: Implementing a Linear Regression Model

A key goal of data analysis is to explore the potential factors of health at the local district level. So far, we have used cross-tabulations and various bivariate correlation analysis methods to explore the relationships between variables. One key limitation of standard correlation analysis is that it remains hard to look at the associations of an outcome/dependent variable to multiple independent/explanatory variables at the same time. Regression analysis provides a very useful and flexible methodological framework for such a purpose. Therefore, we will investigate how various local factors impact residents’ health by building a multiple linear regression model in R.

We use `pct_Very_bad_health` as a proxy for residents’ health.

Research Question 2: How do local factors affect residents’ health?

Dependent (or Response) Variable:

- % of population with bad health (`pct_Very_bad_health`).

Independent (or Explanatory) Variables:

- % of population with no qualifications (pct_No_qualifications).
- % of male population (pct_Males).
- % of population in a higher managerial/professional occupation (pct_Higher_manager_prof).

Load some other Libraries

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v forcats   1.0.0      v stringr   1.5.1
v lubridate 1.9.3      v tibble    3.2.1
v purrr     1.0.2      v tidyr     1.3.1
v readr     2.1.5
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(broom)
```

and the data (if not loaded):

```
# Load dataset
census <- read.csv("../data/Census2021/EW_DistrictPercentages.csv")
```

Regression models are the standard method for constructing predictive and explanatory models. They tell us how changes in one variable (the target variable or independent variable, Y) are *associated with* changes in explanatory variables, or dependent variables, X_1, X_2, X_3 (X_n), etc. Classic linear regression is referred to *Ordinary least squares* (OLS) regression because they estimate the relationship between one or more independent variables and a dependent variable Y using a hyperplane (i.e. a multi-dimensional line) that minimises the sum of the squared difference between the observed values of Y and the values predicted by the model (denoted as \hat{Y} , Y -hat).

Having seen **Single Linear Regression** in class - where the relationship between one independent variable and a dependent variable is modeled - we can extend this concept to situations where more than one explanatory variable might influence the outcome. While single linear regression helps us understand the effect of **ONE** variable in isolation, real-world phenomena are often influenced by multiple factors simultaneously. Multiple linear regression addresses

this complexity by allowing us to model the relationship between a dependent variable and multiple independent variables, providing a more comprehensive view of how various explanatory variables contribute to changes in the outcome.

Here, regression allows us to examine the relationship between people's health rates and multiple dependent variables.

Before starting, we define two hypotheses:

- **Null hypothesis** (H_0): For each variable X_n , there is no effect of X_n on Y .
- **Alternative hypothesis** (H_1): There is an effect of X_n on Y .

We will test if we can reject the null hypothesis.

2.1.4 Model fit

```
# Linear regression model
model <- lm(pct_Very_bad_health ~ pct_No_qualifications + pct_Males + pct_Higher_manager_prof, data = census)
summary(model)
```

Call:

```
lm(formula = pct_Very_bad_health ~ pct_No_qualifications + pct_Males +
    pct_Higher_manager_prof, data = census)
```

Residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|---------|---------|--------|--------|
| -0.4911 | -0.1357 | -0.0368 | 0.0985 | 0.7669 |

Coefficients:

| | Estimate | Std. Error | t value | Pr(> t) |
|-------------------------|----------|------------|---------|--------------------------|
| (Intercept) | 4.00293 | 0.87981 | 4.55 | 0.0000076 *** |
| pct_No_qualifications | 0.05283 | 0.00591 | 8.94 | < 0.0000000000000002 *** |
| pct_Males | -0.07353 | 0.01785 | -4.12 | 0.0000479 *** |
| pct_Higher_manager_prof | -0.01318 | 0.00494 | -2.67 | 0.008 ** |

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

Residual standard error: 0.213 on 327 degrees of freedom

Multiple R-squared: 0.61, Adjusted R-squared: 0.607

F-statistic: 171 on 3 and 327 DF, p-value: <0.0000000000000002

Code explanation

`lm()` Function:

- `lm()` stands for “linear model” and is used to fit a linear regression model in R.
- The formula syntax `pct_Very_bad_health ~ pct_No_qualifications + pct_Males + pct_Higher_manager_prof` specifies a relationship between:
 - **Dependent Variable:** `pct_Very_bad_health`.
 - **Independent Variables:** `pct_No_qualifications`, `pct_Males`, and `pct_Higher_manager_prof`.
The model is trained on the `data` dataset.

Storing the Model: The `model <-` syntax stores the fitted model in an object called `model`.

`summary(model)` provides a detailed output of the model’s results, including:

- **Coefficients:** Estimates of the regression slopes (i.e., how each independent variable affects `pct_Very_bad_health`).
- **Standard Errors:** The variability of each coefficient estimate.
- **t-values** and **p-values:** Indicate the statistical significance of the effect of each independent (explanatory) variable.
- **R-squared** and **Adjusted R-squared:** Show how well the independent variables explain the variance in the dependent variable.
- **F-statistic:** Tests the overall significance of the model.

We can focus only on certain output metrics:

```
# Regression coefficients
coefficients <- tidy(model)
coefficients
```

```
# A tibble: 4 x 5
  term                estimate std.error statistic  p.value
  <chr>              <dbl>    <dbl>    <dbl>    <dbl>
1 (Intercept)        4.00      0.880      4.55 7.58e- 6
2 pct_No_qualifications 0.0528   0.00591    8.94 2.99e-17
3 pct_Males          -0.0735   0.0178   -4.12 4.79e- 5
4 pct_Higher_manager_prof -0.0132  0.00494   -2.67 7.97e- 3
```

These are:

- **Regression Coefficient Estimates.**
- **P-values.**
- **Adjusted R-squared.**

2.1.5 How to interpret the output metrics

2.1.5.1 Regression Coefficient Estimates

The **Estimate** column in the output table tells us the rate of change between each dependent variable X_n and Y .

Intercept: In the regression equation, this is β_0 and it indicates the value of Y when X_n are equal to zero.

Slopes: These are the other regression coefficients of an independent variable, e.g. β_1 , i.e. estimated average changes in Y for a one unit change in an independent variable, e.g. X_1 , when all other dependent or explanatory variables are held constant.

There are two key points worth mentioning:

- **The unit of X and Y :** you need to know what the units are of the independent and dependent variables. For instance, one unit could be one year if you have an age variable, or a one percentage point if the variable is measured in percentages (all the variables in this week's practical).
- **All the other explanatory variables are held constant.** It means that the coefficient of an explanatory variable X_1 (e.g. β_1) should be interpreted as: a one unit change in X_1 is associated with β_1 units change in Y , keeping other values of explanatory variables (e.g. X_2 , X_3) constant – for instance, $X_2 = 0.1$ or $X_3 = 0.4$.

For the independent variable X , we can derive how changes of 1 unit for the independent are associated with the changes in `pct_Very_bad_health`, for example:

- The association of `pct_No_qualifications` is positive and strong: each increase in 1% of `pct_No_qualifications` is associated with an increase of 0.05% of very bad health rate.
- The association of `pct_Males` is negative and strong: each decrease in 1% of `pct_Males` is associated with an increase of 0.07% of `pct_Very_bad_health` in the population in England and Wales.
- The association of `pct_Higher_manager_prof` is negative but weak: each decrease in 1% of `pct_Higher_manager_prof` is associated with an increase of 0.013% of `pct_Very_bad_health`.

2.1.5.2 P-values and Significance

The ***t tests*** of regression coefficients are used to judge the statistical inferences on regression coefficients, i.e. associations between independent variables and the outcome variable. For a t-statistic of a dependent variable, there is a corresponding ***p-value*** that indicates different levels of significance in the column `Pr(>|t|)` and the asterisks *****.

- ******* indicates “changes in X_n are significantly associated with changes in Y at the <0.001 level”.
- ****** suggests that “changes in X_n are significantly associated with changes in Y between the 0.001 and ($<$) 0.01 levels”.
- Now you should know what ***** means: The significance is between the 0.01 and 0.05 levels, which means that we observe a less significant (but still significant) relationship between the variables.

P-value provide a measure of how significant the relationship is; it is an indication of whether the relationship between X_n and Y found in this data could have been found by chance. Very small p-values suggest that the level of association found here might **not** have come from a random sample of data.

In this case, we can say:

- Given that the p-value is indicated by *******, changes in `pct_No_qualifications` and `pct_Males` are significantly associated with changes in `pct_Very_bad_health` at the <0.001 level; the association is highly statistically significant; we can be confident that the observed relationship between these variables and `pct_Very_bad_health` is not due to chance.
- Given that the p-value is indicated by ******, changes in `pct_Higher_manager_prof` are significantly associated with changes in `pct_Very_bad_health` at the 0.001 level. This means that the association between the independent and dependent variable is not one that would be found by chance in a series of random sample 99.999% of the time.

In both cases we can then confidently reject the **Null** hypothesis (H_0 : no association between dependent and independent variables exist).

Remember, If the *p-value* of a coefficient is smaller than 0.05, that coefficient is statistically significant. In this case, you can say that the relationship between this independent variable and the outcome variable is *statistically* significant. Contrarily, if the *p-value* of a coefficient is larger than 0.05 you can conclude that there is no evidence of an association or relationship between the independent variable and the outcome variable.

2.1.5.3 R-squared and Adjusted R-squared

These provide a measure of model fit. They are calculated as the difference between the actual value of Y and the value predicted by the model. The **R-squared** and **Adjusted R-squared** values are statistical measures that indicate how well the independent variables in your model explain the variability of the dependent variable. Both R-squared and Adjusted R-squared help us understand how closely the model’s predictions align with the actual data. An R-squared of 0.6, for example, indicates that 60% of the variability in Y is explained by the independent variables in the model. The remaining 40% is due to other factors not captured by the model.

Adjusted R-squared also measures the goodness of fit, but it adjusts for the number of independent variables in the model, accounting for the fact that adding more variables can artificially inflate R-squared without genuinely improving the model. This is especially useful when comparing models with different numbers of independent variables. If Adjusted R-squared is close to or above 0.6, as in your example, it implies that the model has a **strong explanatory power** while not being overfit with unnecessary explanatory variables.

A high R-squared and Adjusted R-squared indicate that the model captures much of the variation in the data, making it more reliable for predictions or for understanding the relationship between Y and the explanatory variables. However Low R-squared values suggest (e.g. 0.15) that the model might be missing important explanatory variables or that the relationship between Y and the selected explanatory variables is not well-captured by a linear approach.

An R-squared and Adjusted R-squared over 0.6 are generally seen as signs of a **well-fitting model** in many fields, though the ideal values can depend on the context and the complexity of the data.

2.1.6 Interpreting the Results

`coefficients`

```
# A tibble: 4 x 5
  term                estimate std.error statistic  p.value
  <chr>                <dbl>    <dbl>    <dbl>    <dbl>
1 (Intercept)         4.00      0.880      4.55 7.58e- 6
2 pct_No_qualifications 0.0528   0.00591     8.94 2.99e-17
3 pct_Males          -0.0735   0.0178    -4.12 4.79e- 5
4 pct_Higher_manager_prof -0.0132  0.00494    -2.67 7.97e- 3
```

Q4. Complete the table above by filling in the coefficients, t-values, p-values, and indicating if each variable is statistically significant.

| Variable Name | Coefficients | t-values | p-values | Significant? |
|-------------------------|--------------|----------|----------|--------------|
| pct_No_qualifications | | | | |
| pct_Males | | | | |
| pct_Higher_manager_prof | | | | |

From the lecture notes, you know that the Intercept or Constant represents the estimated average value of the outcome variable when the values of all independent variables are equal to zero.

Q5. When values of `pct_Males`, `pct_No_qualifications` and `pct_Higher_manager_prof` are all *zero*, what is the % of population with very bad health? Is the intercept term meaningful? Are there any districts (or zones, depending on the dataset you chose) with zero percentages of persons with no qualification in your data set?

Q6. Interpret the regression coefficients of `pct_Males`, `pct_No_qualifications` and `pct_Higher_manager_prof`. Do they make sense?

2.1.7 Identify factors of % bad health

Now combine the above two sections and identify factors affecting the percentage of population with very bad health. Fill in each row for the direction (positive or negative) and significance level of each variable.

| Variable Name | Positive or Negative | Statistical Significance |
|--------------------------------------|----------------------|--------------------------|
| <code>pct_No_qualifications</code> | | |
| <code>pct_Higher_manager_prof</code> | | |
| <code>pct_Males</code> | | |

Q7. Think about the potential conclusions that can be drawn from the above analyses. Try to answer the research question of this practical: How do local factors affect residents' health? Think about causation *vs* association and consider potential confounders when interpreting the results. How could these findings influence local health policies?

2.2 Part C: Practice and Extension

If you haven't understood something, if you have doubts, even if they seem silly, ask.

1. Finish working through the practical.
2. Revise the material.
3. Extension activities (optional): Think about other potential factors of very bad health and test your ideas with new linear regression models.

3 Lab: Correlation and Multiple Linear Regression with Qualitative Variables

The lecture's slides can be found [here](#).

In last week, we introduced Multiple Linear Regression (MLR) - a statistical method that models the relationship between a dependent variable and two or more independent variables, allowing researchers to examine how various predictors jointly influence an outcome. By using the following R, we create and interpret the model:

```
model <- lm(pct_Very_bad_health ~ pct_No_qualifications + pct_Males + pct_Higher_manager_pro.  
data = census)  
  
summary(model)
```

In a regression model, independent/predictor variables could be continuous or categorical (or qualitative). While continuous variables capture quantitative effects, **categorical variables provide insights into differences across groups**. When we say categorical variables, we normally mean:

- Nominal Data: categorical data without natural order. E.g. Gender, Colour, Country...
- Ordinal Data: categorical data with a meaningful order. E.g. Education level, Customer satisfaction, Grade...

By blending continuous and categorical predictors, MLR with categorical variables enhances the model's ability to reflect real-world complexities and improves interpretability, as it allows analysts to assess how each category or group within a independent variable influences the dependent variable.

For most categorical (especially the *nominal*) variables, they cannot be included in the regression model directly as a continuous independent variable. Instead, these qualitative independent variables should be included in regression models by using the **dummy variable** approach, transforming categorical information into a numerical format suitable for regression analysis.

However, R provides a powerful way, by automatively handling with such process when the categorical variable is designated as a factor and to be included in the regression model. This makes it much easier for you to use categorical variables in the regression model to assess the effects of categorical groupings on the dependent variable alongside continuous predictors.

Learning Objectives:

In this week's practical we are going to

- Analysis of categorical/qualitative variables
- Estimate and interpret a multiple linear regression model with categorical variables
- Make predictions using a regression model

3.1 Analysis categorical variables

Recall in Week 7, you get familiar to R by using the Family Resource Survey data. Today we will keep explore the data by using its categorical variables. As usual we first load the necessary libraries.

Some tips to avoid R returning can't find data errors:

Check your working directory by

```
getwd()
```

Check the relative path of your data folder on your PC/laptop, make sure you know the relative path of your data from your working directory, returned by `getwd()`.

Library knowledge used in today:

- **dplyr**: a basic library provides a suite of functions for data manipulation
- **ggplot2**: a widely-used data visualisation library to help you create nice plots through layered plotting.
- **tidyverse**: a collection of R packages designed for data science, offering a cohesive framework for data manipulation, visualization, and analysis. Containing dplyr, ggplot2 and other basic libraries.
- **broom**: a part of the tidyverse and is designed to convert statistical analysis results into tidy data frames.
- **forcats**: designed to work with factors, which are used to represent categorical data. It simplifies the process of creating, modifying, and ordering factors.
- **vcd**: visualise and analyse categorical data.

A useful shortcut to format your code: select all your code lines, use Ctrl+Shift+A for automatically format them in a tidy way.

3.1.1 Data overview

```
if(!require("dplyr"))  
  install.packages("dplyr",dependencies = T)
```

Loading required package: dplyr

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
# Load necessary libraries  
if(!require("ggplot2"))  
  install.packages("ggplot2",dependencies = T)
```

Loading required package: ggplot2

```
if(!require("broom"))  
  install.packages("broom",dependencies = T)
```

Loading required package: broom

```
library(dplyr)  
library(ggplot2)  
library(broom)
```

Or we can use library `tidyverse` which includes `ggplot2`, `dplyr`, `broom` and other fundamental libraries together already, remember you need first install the package if you haven't by using `install.packages("tidyverse")`.

```
if(!require("tidyverse"))
  install.packages("tidyverse",dependencies = T)
```

Loading required package: tidyverse

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v forcats   1.0.0      v stringr   1.5.1
v lubridate 1.9.3      v tibble    3.2.1
v purrr     1.0.2      v tidyr     1.3.1
v readr     2.1.5
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(tidyverse)
```

We will also use forcat library, so

```
if(!require("forcats"))
  install.packages("forcats")

library(forcats)
```

Exactly as you did in previous weeks, we first load in the dataset:

```
frs_data <- read.csv("../data/FamilyResourceSurvey/FRS16-17_labels.csv")
```

Recall in previous weeks, we used the following code to overview the dataset. Familiar yourself again by using them:

```
View(frs_data)
glimpse(frs_data)
```

and also `summary()` to produce summaries of each variable

```
summary(frs_data)
```

You may notice that for the numeric variables such as *hh_income_gross* (household gross income) and *work_hours* (worked hours per week), the `summary()` offers useful descriptive statistics. While for the qualitative information, such as *age_group* (age group), *highest_qual* (Highest educational qualification), *marital_status* (Marital status) and *nssec* (Socio-economic status), the `summary()` function is not that useful by providing mean or median values.

Performing descriptive analysis for categorical variables or qualitative variables, we focus on summarising the frequency and distribution of categories within the variable. This analysis helps understand the composition and diversity of categories in the data, which is especially useful for identifying patterns, common categories, or potential data imbalances.

```
# Frequency count
table(frs_data$age_group)
```

```

 0-4 05-10 11-15 16-19 20-24 25-29 30-34 35-39 40-44 45-49 50-54 55-59 60-64
2914 3575 2599 1858 1929 2353 2800 2840 2790 2883 2975 2767 2775
65-69 70-74 75+
2990 2354 3743
```

```
table(frs_data$highest_qual)
```

```

A-level or equivalent      Degree or above      Dependent child
              5260              9156              10298
      GCSE or equivalent      Not known              Other
              9729              6820              2882
```

```
table(frs_data$marital_status)
```

```

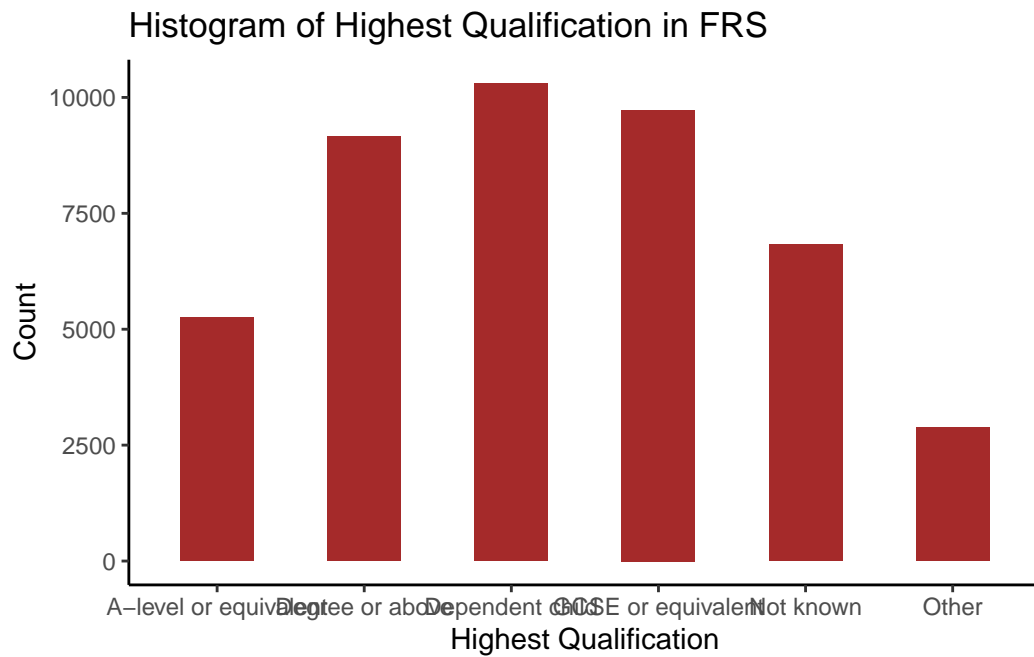
              Cohabiting Divorced/civil partnership dissolved
              4015              2199
Married/Civil partnership              Separated
              18195              747
              Single              Widowed
              16663              2326
```

```
table(frs_data$nssec)
```

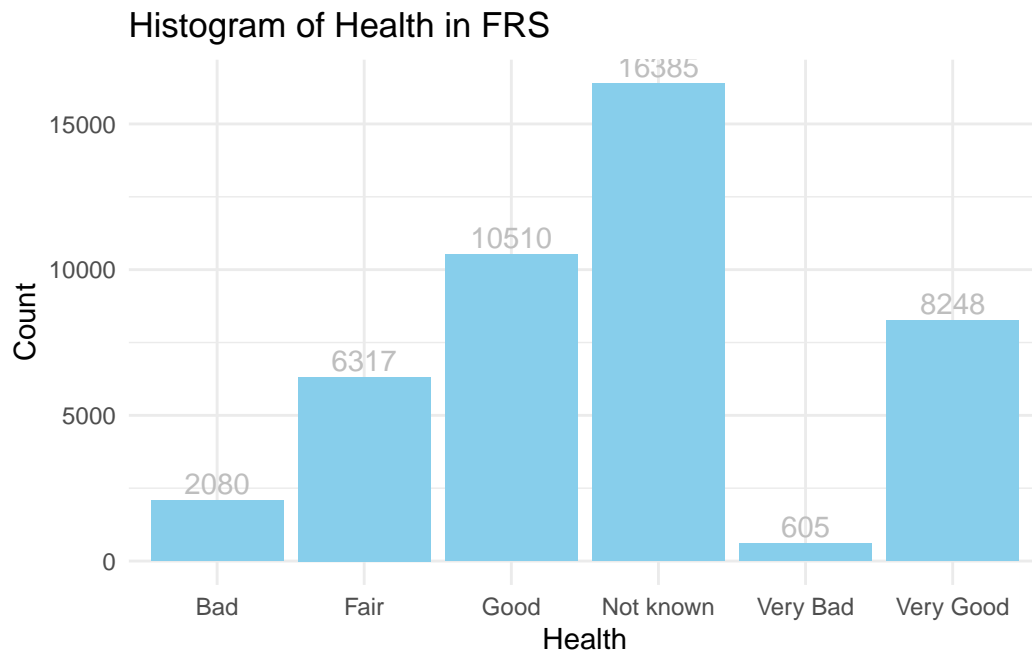
| | |
|---|-------|
| Dependent child | 10299 |
| Full-time student | 963 |
| Higher professional occupations | 3004 |
| Intermediate occupations | 4372 |
| Large employers and higher managers | 1025 |
| Lower managerial and professional occupations | 8129 |
| Lower supervisory and technical occupations | 2400 |
| Never worked or long-term unemployed | 1516 |
| Not classifiable | 107 |
| Routine occupations | 4205 |
| Semi-routine occupations | 5226 |
| Small employers and own account workers | 2899 |

By using `ggplot2`, it is easy to create some nice descriptive charts for the categorical variables, such like what you did for the continuous variables last week.

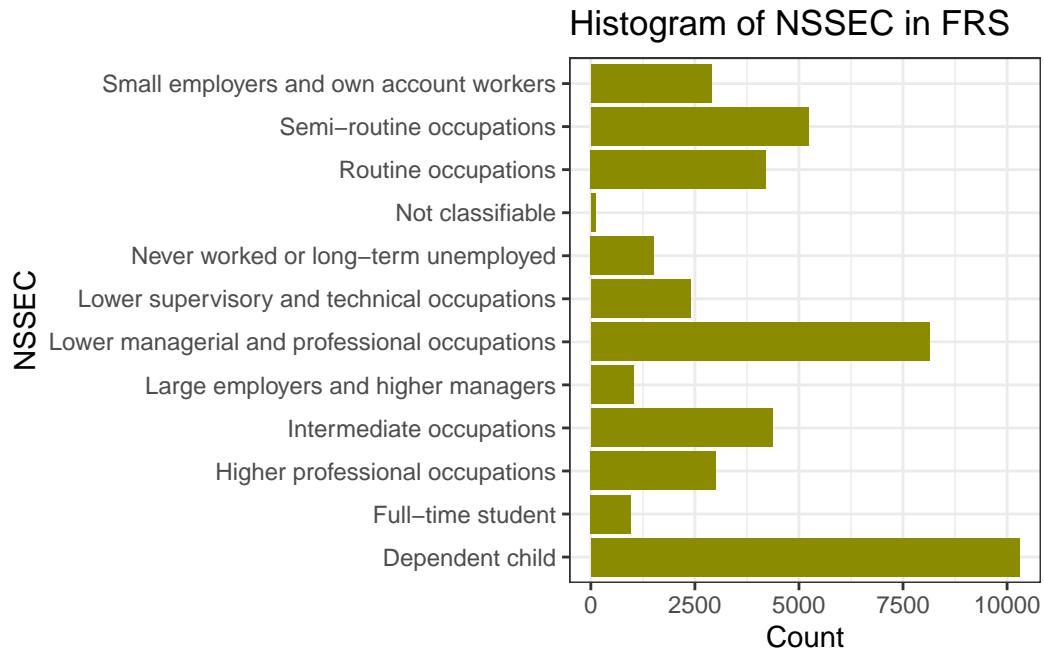
```
ggplot(frs_data, aes(x = highest_qual)) +
  geom_bar(fill="brown",width=0.5) +
  labs(title = "Histogram of Highest Qualification in FRS", x = "Highest Qualification", y =
  theme_classic())#choose theme type, try theme_bw(), theme_minimal() see differences
```



```
ggplot(frs_data, aes(x = health)) +
  geom_bar(fill="skyblue") +
  geom_text(stat = "count", aes(label = ..count..), vjust = -0.3, colour = "grey")+ #add text
  labs(title = "Histogram of Health in FRS", x = "Health", y = "Count")+ #set text info
  theme_minimal()
```

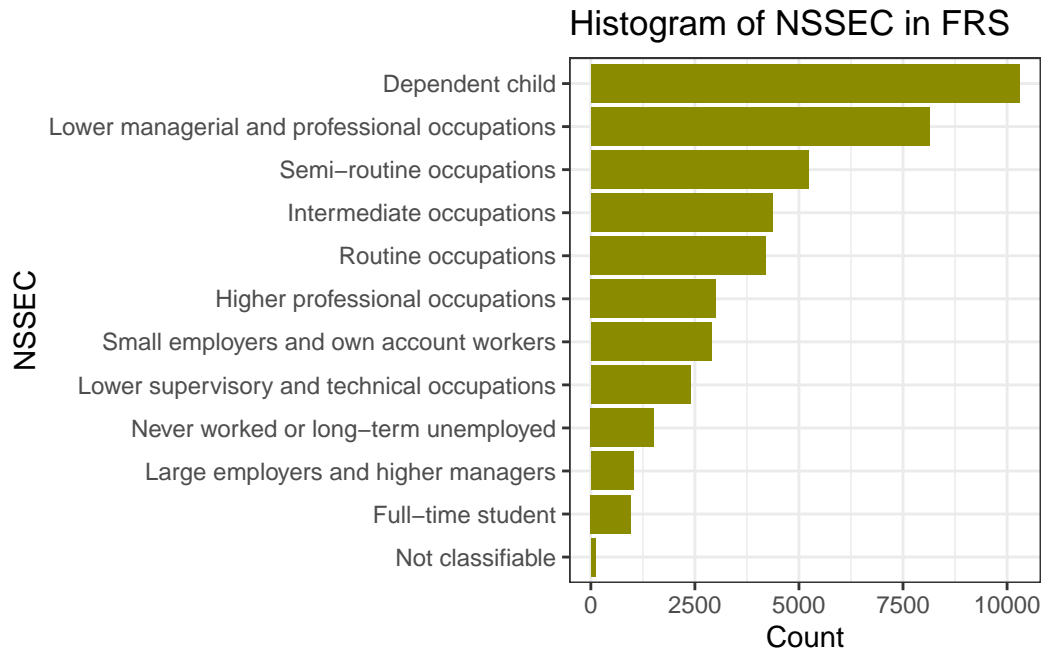



```
ggplot(frs_data, aes(x = nssec)) +
  geom_bar(fill = "yellow4") +
  labs(title = "Histogram of NSSEC in FRS", x = "NSSEC", y = "Count") +
  coord_flip()+ #Flip the Axes, add a # in front of this line, to make the code in gray and y
  theme_bw()
```



If we want to reorder the Y axis by from highest to lowest, we use the functions in `forcats` library. `fct_infreq()`: orders by the value's frequency of the variable `nssec`. `fct_rev()`: reverses the order to go from highest to lowest.

```
ggplot(frs_data, aes(x = fct_rev(fct_infreq(nssec)))) +
  geom_bar(fill = "yellow4") +
  labs(title = "Histogram of NSSEC in FRS", x = "NSSEC", y = "Count") +
  coord_flip()+ #Flip the Axes, add a # in front of this line, to make the code in gray and y
  theme_bw()
```



You can change the variables in `ggplot()` to make your own histogram chart for the variables you are interested in. You will learn more of visualisation methods in Week11's practical.

3.1.2 Correlation

Q1. Which of the associations do you think is strongest? Which is the weakest?

As before, rather than relying upon an impressionistic view of the strength of the association between two variables, we can measure that association by calculating the relevant correlation coefficient.

To calculate the correlation between categorical data, we first use Chi-squared test to assess the independence between pairs of categorical variables, then we use Cramer's V to measure the strength of association - the correlation coefficients in R.

Pearson's chi-squared test (2) is a statistical test applied to sets of categorical data to evaluate how likely it is that any observed difference between the sets arose by chance. If the p-value is low (typically < 0.05), it suggests a significant association between the two variables.

```
chisq.test(frs_data$health, frs_data$happy)
```

```
Warning in chisq.test(frs_data$health, frs_data$happy): Chi-squared
approximation may be incorrect
```

Pearson's Chi-squared test

```
data: frs_data$health and frs_data$happy  
X-squared = 45594, df = 60, p-value < 2.2e-16
```

If you see a warning message of Chi-squared approximation may be incorrect. This is because some expected frequencies in one or more cells of the cross-tabular (health * happy) are too low. The df means degrees of freedom and it related to the size of the table and the number of categories in each variable. The most important message from the output is the estimated p-value, which shows as p-value < 2.2e-16 (2.2 with 16 decimals move to the left, it is a very small number so written in scientific notation). P-value of the chi-squared test is far smaller than 0.05, so we can say the correlation is statistically significant.

Cramér's V is a measure of association for categorical (nominal or ordinal) data. It ranges from 0 (no association) to 1 (strong association). The main downside of using Cramer's V is that no information is provided on whether the correlation is positive or negative. This is not a problem if the variable pair includes a nominal variable but represents an information loss if the both variables being correlated are ordinal.

```
# Install the 'vcd' package if not installed  
if(!require("vcd"))  
install.packages("vcd", repos = "https://cran.r-project.org", dependencies = T)
```

Loading required package: vcd

Warning: package 'vcd' was built under R version 4.4.2

Loading required package: grid

```
library(vcd)  
  
# creat the crosstable  
crosstab <- table(frs_data$health, frs_data$happy)  
  
# Calculate Cramér's V  
assocstats(crosstab)
```

| | X ² | df | P(> X ²) |
|------------------|----------------|----|----------------------|
| Likelihood Ratio | 54036 | 60 | 0 |
| Pearson | 45594 | 60 | 0 |

```
Phi-Coefficient      : NA
Contingency Coeff.: 0.713
Cramer's V           : 0.454
```

```
#you can also directly calculate the assoication between variables
assocstats(table(frs_data$health, frs_data$age_group))
```

```
                X^2 df P(> X^2)
Likelihood Ratio 26557 75      0
Pearson          23854 75      0
```

```
Phi-Coefficient      : NA
Contingency Coeff.: 0.592
Cramer's V           : 0.329
```

Research Question 1. Which of our selected person-level variables is most strongly correlated with an individual's health status?

Use the codes of Chi-test and Cramer's V to answer this question by completing Table 1.

Table 1 Person-level correlations with health status

| Covariates | | Correlation
Coefficient
<i>Cramer's V</i> | Statistical
Significance
<i>p-value</i> |
|---------------|-----------------------|---|---|
| <i>health</i> | <i>age_group</i> | | |
| <i>Health</i> | <i>highest_qual</i> | | |
| <i>health</i> | <i>marital_status</i> | | |
| <i>Health</i> | <i>nssec</i> | | |

3.2 Implementing a linear regression model with a qualitative independent variable

Research Question 2: How does health vary across regions in the UK?

The practical is split into two main parts. The first focuses on implementing a linear regression model with a qualitative independent variable. **Note that** you need first to set the reference category (baseline) as the outcomes of the model reflects the **differences** between categories with the baseline. The second part focuses prediction based the estimated linear regression model.

First we load the UK district-level census dataset.

```
# load data
LAcensus <- read.csv("../data/Census2011/UK_DistrictPercentages.csv") # Local authority level
```

Using the district-level census dataset “**UK_DistrictPercentages.csv**”, the variable “Region” (labelled as Government Office Region) is used to explore regional inequality in health.

Familiar yourself with the dataset by using the same codes as last week:

```
#view the data
View(LAcensus)
glimpse(LAcensus)
```

The `names()` function returns all the column names.

```
names(df)
```

The `dim()` function can merely returns the number of rows and number of columns.

```
dim(LAcensus)
```

```
[1] 406 128
```

There are 406 rows and 130 columns in the dataset. It would be very hard to scan through the data if we use so many variables altogether. Therefore, we can select several columns to tailor for this practical. You can of course include other variables you are interested in also by their names:

```
df <- LAcensus %>% select(c("pct_Long_term_ill",
                           "pct_No_qualifications",
                           "pct_Males",
                           "pct_Higher_manager_prof",
                           "Region"))
```

Simply descriptive of this new data

```
summary(df)
```

| pct_Long_term_ill | pct_No_qualifications | pct_Males |
|-------------------|-----------------------|---------------|
| Min. :11.20 | Min. : 6.721 | Min. :47.49 |
| 1st Qu.:15.57 | 1st Qu.:19.406 | 1st Qu.:48.67 |
| Median :18.41 | Median :23.056 | Median :49.09 |
| Mean :18.27 | Mean :23.257 | Mean :49.10 |
| 3rd Qu.:20.72 | 3rd Qu.:26.993 | 3rd Qu.:49.48 |
| Max. :27.97 | Max. :40.522 | Max. :55.47 |

| pct_Higher_manager_prof | Region |
|-------------------------|----------------|
| Min. : 4.006 | Min. : 1.000 |
| 1st Qu.: 7.664 | 1st Qu.: 3.000 |
| Median : 9.969 | Median : 6.000 |
| Mean :10.747 | Mean : 6.034 |
| 3rd Qu.:12.986 | 3rd Qu.: 8.000 |
| Max. :37.022 | Max. :12.000 |

Now we can retrieve the “Region” column from the data frame by simply use `df$Region`. But what if we want to understand the data better, like the following questions?

Q2. How many categories do the variable “Region” entail? How many local authority districts does each region include?

Simply use the function `table()` would return you the answer.

```
table(df$Region)
```

```

 1  2  3  4  5  6  7  8  9 10 11 12
40 47 33 12 39 67 37 30 21 22 32 26

```

The numbers in Region column indicate different regions in the UK - 1: East Midlands; 2: East of England; 3: London; 4: North East; 5: North West; 6: South East; 7: South West; 8: West Midlands; 9: Yorkshire and the Humber; 10: Wales; 11: Scotland; and 12: Northern Ireland.

The `table()` function tells us that this data frame contains 12 regions, and the number of LAs belongs to each region.

Now, for better interpretation of our regions with their real name rather than the code, we can create a new column named “*Region_label*” by using the following code. **R can only include the categorical variables in the **factor** type, so we set the new column *Region_label* in `factor()`

```
df$Region_label <- factor(df$Region,c(1:12),labels=c("East Midlands",
                                                    "East of England",
                                                    "London",
                                                    "North East",
                                                    "North West",
                                                    "South East",
                                                    "South West",
                                                    "West Midlands",
                                                    "Yorkshire and the Humber",
                                                    "Wales",
                                                    "Scotland",
                                                    "Northern Ireland"))
```

If you re-run the `table()` function, the output is now more readable:

```
table(df$Region_label)
```

| | | |
|---------------|-----------------|--------------------------|
| East Midlands | East of England | London |
| 40 | 47 | 33 |
| North East | North West | South East |
| 12 | 39 | 67 |
| South West | West Midlands | Yorkshire and the Humber |
| 37 | 30 | 21 |
| Wales | Scotland | Northern Ireland |
| 22 | 32 | 26 |

3.2.1 Include the categorical variables into a regression model

We will continue with a very similar regression model fitted in last week that relates Percentages long-term illness (*pct_Long_term_ill*) to Percentages no-qualification (*pct_No_qualifications*), Percentage Males (*pct_Males*) and Percentages Higher Managerial or Professional occupation (*pct_Higher_manager_prof*).

Decide which region to be set as the baseline category. The principle is that if you want to compare the (average) long term illness outcome of Region A to those of other regions, Region A should be chosen as the baseline category. For example, if you want to compare the (average) long term illness outcome of London to rest of regions in the UK, London should be selected as the baseline category.

Implement the regression model with the newly created categorical variables - *Region_label* in our case. R will automatically handle the qualitative variable as dummy variables so you don't

need to concern any of that. But you need to let R know which category of your qualitative variable is your reference category or the baseline. Here we will use London as our first go. **Note:** We choose London as the baseline category so the London region will be excluded in the independent variable list.

Therefore, first, we set London as the reference:

```
df$Region_label <- fct_relevel(df$Region_label, "London")
```

Similar to last week, we build our linear regression model, but also include the *Region_label* variable into the model.

```
model <- lm(pct_Long_term_ill ~ pct_Males + pct_No_qualifications + pct_Higher_manager_prof +
summary(model)
```

Call:

```
lm(formula = pct_Long_term_ill ~ pct_Males + pct_No_qualifications +
    pct_Higher_manager_prof + Region_label, data = df)
```

Residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|---------|---------|--------|--------|
| -3.2963 | -0.9090 | -0.1266 | 0.8168 | 5.2821 |

Coefficients:

| | Estimate | Std. Error | t value | Pr(> t) | |
|--------------------------------------|----------|------------|---------|----------|-----|
| (Intercept) | 41.54134 | 5.22181 | 7.955 | 1.95e-14 | *** |
| pct_Males | -0.75756 | 0.10094 | -7.505 | 4.18e-13 | *** |
| pct_No_qualifications | 0.50573 | 0.03062 | 16.515 | < 2e-16 | *** |
| pct_Higher_manager_prof | 0.08910 | 0.03674 | 2.426 | 0.01574 | * |
| Region_labelEast Midlands | 1.14167 | 0.35015 | 3.260 | 0.00121 | ** |
| Region_labelEast of England | -0.01113 | 0.33140 | -0.034 | 0.97322 | |
| Region_labelNorth East | 2.70447 | 0.49879 | 5.422 | 1.03e-07 | *** |
| Region_labelNorth West | 2.64240 | 0.35468 | 7.450 | 6.03e-13 | *** |
| Region_labelSouth East | 0.48327 | 0.30181 | 1.601 | 0.11013 | |
| Region_labelSouth West | 2.62729 | 0.34572 | 7.600 | 2.22e-13 | *** |
| Region_labelWest Midlands | 0.91064 | 0.37958 | 2.399 | 0.01690 | * |
| Region_labelYorkshire and the Humber | 1.03930 | 0.41050 | 2.532 | 0.01174 | * |
| Region_labelWales | 4.63424 | 0.41368 | 11.202 | < 2e-16 | *** |
| Region_labelScotland | 0.46291 | 0.38916 | 1.189 | 0.23497 | |
| Region_labelNorthern Ireland | 0.55722 | 0.42215 | 1.320 | 0.18762 | |

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

Residual standard error: 1.394 on 391 degrees of freedom

Multiple R-squared: 0.8298, Adjusted R-squared: 0.8237

F-statistic: 136.2 on 14 and 391 DF, p-value: < 2.2e-16

You have already learnt how to interpret the output of regression model last week: **Significance** (p-value), **Coefficient Estimates**, and **Model fit** (R squared and Adjusted R-squared).

Q3. Relating back to this week's lecture notes, indicate what regions have statistically significant differences in the percentage of long-term illness, compared to London?

First, the **Significance** and the **Coefficient Estimates**. By examining the P-value, which is the last column in the output table, we can see that most of the independent variables are significant predictor of `pct_Long_term_ill`.

- Similarly to last week, we learn that the changes in `pct_No_qualifications` and `pct_Males` are significantly associated with changes in `pct_Long_term_ill` at the <0.001 level (with the three asterisks ***), which is actually an indicator of highly statistically significant, while we are less confident that the observed relationship between `pct_Higher_manager_prof` and `pct_Long_term_ill` are statistically significant (with the two asterisks **). Through their coefficient estimates, we learn that:
 - The association of `pct_Males` is negative and strong: each decrease in 1% of `pct_Males` is associated with an increase of 0.75% of long term illness rate in the population of UK.
 - The association of `pct_No_qualifications` is positive and strong: each increase in 1% of `pct_No_qualifications` is associated with an increase of 0.5% of long term illness rate.
 - The association of `pct_Higher_manager_prof` is positive but weak: each increase in 1% of `pct_Higher_manager_prof` is associated with an increase of 0.08% of `pct_Long_term_ill`.
- Now comes to the dummy variables (all the items starts with `Region_label`) created by R for our qualitative variable `Region_label`: `Region_labelNorth East`, `Region_labelNorth West`, `Region_labelSouth West` and `Region_labelWales` are also statistically significant at the <0.001 level. The changes in `Region_labelEast Midlands` are significantly associated with changes in `pct_Long_term_ill` at the 0.001 level, while the changes in `Region_labelWest Midlands` and `Region_labelYorkshire and the Humber` are significantly associated with changes in `pct_Long_term_ill` at

the 0.01 level. The 0.01 level suggests that it is a mild likelihood that the relationship between these independent variables and the dependent variable is not due to random change. They are just mildly statistically significant.

- The coefficient estimates of them need to be interpreted by comparing to the reference category London. The Estimate column tells us: North East region is associated with a 2.7% higher rate of long term illness than London when the other predictors remain the same. Similarly, Wales is 4.6% higher rate of long term illness than London when the other predictors remain the same. You can draw the conclusion for the other regions in this way by using their coefficient estimate values.

Reminder: You **cannot** draw conclusion between North East and Wales, nor comparison between any regions beyond London. It is because the regression model is built for the comparison between regions to your reference category London. If we want to compare between North East and Wales, we need to set either of them as the reference category by using `df$Region_label <- fct_relevel(df$Region_label, "North East")` or `df$Region_label <- fct_relevel(df$Region_label, "Wales")`.

- `Region_labelEast of England`, `Region_labelSouth East`, `Region_labelScotland` and `Region_labelNorthern Ireland` were not found to be significantly associated with `pct_Long_term_ill`.

Last but not least, the **Measure of Model Fit**. The model output suggests the R-squared and Adjusted R-squared are of greater than 0.8 indicate a reasonably well fitting model. The model explains 83.0 % of the variance in the dependent variable. After adjusting for the number of independent variable, the model explains 82.4% of the variance. They two suggest a strong fit of the model.

Now, complete the following table.

| Region names | Higher or lower than London | Whether the difference is statistically significant (Yes or No) |
|--------------------------|-----------------------------|---|
| East Midlands | | |
| East of England | | |
| North East | | |
| North West | | |
| South East | | |
| South West | | |
| West Midlands | | |
| Yorkshire and The Humber | | |
| Wales | | |
| Scotland | | |
| Northern Ireland | | |

3.2.2 Change the baseline category

If you would like to learn about differences in long-term illness between North East and other regions in the UK, you need to change the baseline category (from London) to the North East region (with variable name "Region_2").

```
df$Region_label <- fct_relevel(df$Region_label, "North East")
```

The regression model is specified again as follows:

```
model1 <- lm(
  pct_Long_term_ill ~ pct_Males + pct_No_qualifications + pct_Higher_manager_prof + Region_label,
  data = df
)

summary(model1)
```

Call:

```
lm(formula = pct_Long_term_ill ~ pct_Males + pct_No_qualifications +
    pct_Higher_manager_prof + Region_label, data = df)
```

Residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|---------|---------|--------|--------|
| -3.2963 | -0.9090 | -0.1266 | 0.8168 | 5.2821 |

Coefficients:

| | Estimate | Std. Error | t value | Pr(> t) | |
|--------------------------------------|----------|------------|---------|----------|-----|
| (Intercept) | 44.24582 | 5.20125 | 8.507 | 3.85e-16 | *** |
| pct_Males | -0.75756 | 0.10094 | -7.505 | 4.18e-13 | *** |
| pct_No_qualifications | 0.50573 | 0.03062 | 16.515 | < 2e-16 | *** |
| pct_Higher_manager_prof | 0.08910 | 0.03674 | 2.426 | 0.015738 | * |
| Region_labelLondon | -2.70447 | 0.49879 | -5.422 | 1.03e-07 | *** |
| Region_labelEast Midlands | -1.56281 | 0.46292 | -3.376 | 0.000809 | *** |
| Region_labelEast of England | -2.71561 | 0.45836 | -5.925 | 6.87e-09 | *** |
| Region_labelNorth West | -0.06208 | 0.46209 | -0.134 | 0.893206 | |
| Region_labelSouth East | -2.22120 | 0.45667 | -4.864 | 1.67e-06 | *** |
| Region_labelSouth West | -0.07718 | 0.47482 | -0.163 | 0.870957 | |
| Region_labelWest Midlands | -1.79384 | 0.48230 | -3.719 | 0.000229 | *** |
| Region_labelYorkshire and the Humber | -1.66517 | 0.50695 | -3.285 | 0.001113 | ** |
| Region_labelWales | 1.92976 | 0.50111 | 3.851 | 0.000137 | *** |
| Region_labelScotland | -2.24157 | 0.47299 | -4.739 | 3.01e-06 | *** |

```
Region_labelNorthern Ireland      -2.14725      0.49296    -4.356 1.70e-05 ***
```

```
---
```

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

```
Residual standard error: 1.394 on 391 degrees of freedom
```

```
Multiple R-squared:  0.8298,    Adjusted R-squared:  0.8237
```

```
F-statistic: 136.2 on 14 and 391 DF,  p-value: < 2.2e-16
```

Now it is very easy to use your model to estimate the results Y (dependent variable) by setting all the input independent variable X.

```
obj_London <- data.frame(  
  pct_Males = 49.7,  
  pct_No_qualifications = 24.3,  
  pct_Higher_manager_prof = 14.7,  
  Region_label = "London"  
)  
obj_NW <- data.frame(  
  pct_Males = 49.8,  
  pct_No_qualifications = 23.3,  
  pct_Higher_manager_prof = 11.2,  
  Region_label = "North West"  
)  
obj_NE <- data.frame(  
  pct_Males = 49.8,  
  pct_No_qualifications = 23.3,  
  pct_Higher_manager_prof = 11.2,  
  Region_label = "North East"  
)  
  
predict(model1, obj_London)
```

```
      1  
17.48952
```

```
predict(model1, obj_NW)
```

```
      1  
19.23858
```

```
predict(model1, obj_NE)
```

```
1  
19.30065
```

3.2.3 Recode the Region variable and explore regional inequality in health

In many real-word studies, we might not be interested in health inequality across all regions. For example, in this case study, we are interested in health inequality between *London, Other regions in England, Wales, Scotland* and *Northern Ireland*. We can achieve this by re-grouping regions in the UK based on the variable “Region”. That said, we need to have a new grouping of regions as follows:

| Original region labels | New region labels |
|--------------------------|--------------------------|
| East Midlands | Other regions in England |
| East of England | Other regions in England |
| London | London |
| North East | Other regions in England |
| North West | Other regions in England |
| South East | Other regions in England |
| South West | Other regions in England |
| West Midlands | Other regions in England |
| Yorkshire and The Humber | Other regions in England |
| Wales | Wales |
| Scotland | Scotland |
| Northern Ireland | Northern Ireland |

Here we use `mutate()` function in R to make it happen:

```
df <- df %>% mutate(New_region_label = fct_other(  
  Region_label,  
  keep = c("London", "Wales", "Scotland", "Northern Ireland"),  
  other_level = "Other regions in England"  
))
```

This code may looks a bit complex. You can simply type `?mutate` in your console. Now in your right hand Help window, the R studio offers your the explanation of the `mutate` function. This is a common way you can use R studio to help you learn what the function `caate()` creates new columns that are functions of existing variables. Therefore, the `df %>% mutate()` means add a new column into the current dataframe `df`; the `New_region_label` in the `mutate()`

function indicates the name of this new column is `New_region_label`. The right side of the `New_region_label =` indicates the value we want to assign to the `New_region_label` in each row.

The right side of `New_region_label` is

```
fct_other(Region_label, keep=c("London","Wales","Scotland","Northern Ireland"),
other_level="Other regions in England")
```

By using the code, the `fct_other()` function checks whether each value in the `Region_label` column is one of the **keep** regions: “London”, “Wales”, “Scotland”, or “Northern Ireland”. If the region is not in this list, the value is replaced with the label “Other regions in England”. If the region is one of these four, the original value in `Region_label` is kept. This process categorizes regions that are outside of the four specified ones into a new group labeled “Other regions in England”, while preserving the original labels for the specified regions.

Now we use the same way to examine our new column `New_region_label`:

```
table(df$New_region_label)
```

| | | |
|------------------|--------------------------|----------|
| London | Wales | Scotland |
| 33 | 22 | 32 |
| Northern Ireland | Other regions in England | |
| 26 | 293 | |

Comparing with the `Region_label`, we now can see the mutate worked:

```
df[,c("Region_label","New_region_label")]
```

Now you will have a new qualitative variable named `New_region_label` in which the UK is divided into five regions: London, Other regions in England, Wales, Scotland and Northern Ireland.

Based on the newly generated qualitative variable `New_region_label`, we can now build our new linear regression model. Don't forget:

(1) R need to deal with the categorical variables in regression model in the factor type;

```
class(df$New_region_label)
```

```
[1] "factor"
```

The `class()` returns the type of the variable. The `New_region_label` is already a factor variable. If not, we need to convert it by the `as.factor()`, as we used above.

```
df$New_region_label = as.factor(df$New_region_label)
```

2) Let R know which region you want to use as the baseline category. Here I will use London again, but of course you can choose other regions.

```
df$New_region_label <- fct_relevel(df$New_region_label, "London")
```

The linear regression window is set up below. This time we include `New_region_label` rather than `Region_label` as the region variable:

```
model2 <- lm(
  pct_Long_term_ill ~ pct_Males + pct_No_qualifications + pct_Higher_manager_prof + New_region_label,
  data = df
)

summary(model2)
```

Call:

```
lm(formula = pct_Long_term_ill ~ pct_Males + pct_No_qualifications +
    pct_Higher_manager_prof + New_region_label, data = df)
```

Residuals:

```
      Min       1Q   Median       3Q      Max
-4.6719 -1.1252 -0.0556  0.9564  7.3768
```

Coefficients:

| | Estimate | Std. Error | t value | Pr(> t) |
|--|-----------|------------|---------|----------|
| (Intercept) | 47.217525 | 5.795439 | 8.147 | 4.86e-15 |
| pct_Males | -0.834471 | 0.113398 | -7.359 | 1.07e-12 |
| pct_No_qualifications | 0.472354 | 0.032764 | 14.417 | < 2e-16 |
| pct_Higher_manager_prof | 0.000497 | 0.040851 | 0.012 | 0.990300 |
| New_region_labelWales | 4.345262 | 0.471088 | 9.224 | < 2e-16 |
| New_region_labelScotland | 0.143672 | 0.442989 | 0.324 | 0.745863 |
| New_region_labelNorthern Ireland | 0.264425 | 0.474074 | 0.558 | 0.577314 |
| New_region_labelOther regions in England | 1.071719 | 0.312746 | 3.427 | 0.000674 |

```
(Intercept) ***
```



```

pct_Males ***
pct_No_qualifications ***
pct_Higher_manager_prof
New_region_labelWales ***
New_region_labelScotland
New_region_labelNorthern Ireland
New_region_labelOther regions in England ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.609 on 398 degrees of freedom
Multiple R-squared:  0.7693,    Adjusted R-squared:  0.7653
F-statistic: 189.6 on 7 and 398 DF,  p-value: < 2.2e-16

```

Q4. Are there statistically significant differences in the percentage of people with long-term illness between London and Scotland, and between London and Wales, controlling for other variables? What conclusions could be drawn in terms of regional differences in health outcome?

3.3 Predictions using fitted regression model

3.3.1 Write down the % illness regression model with the new region label categorical variables

Relating to this week's lecture, the % *pct_Long_term_ill* is equal to:

[write down the model]

Q5. Now imagine that the values of variables *pct_Males*, *pct_No_qualifications*, and *pct_Higher_manager_prof* are 49, 23 and 11, respectively, what would the percentage of persons with long-term illness in Wales and London be?

Check the answer at the end of this practical page.

3.4 Income inequality with respect to gender and health status

In this section, we will work with individual-level data ("FRS 2016-17_label.csv") again to explore income inequality with respect to gender and health status.

To explore income inequality, we need to work with a data set excluding dependent children. In addition, we look at individuals who are the representative persons of households. Therefore, we will select cases (or samples) that meet both conditions.

We want R to select persons only if they are the representative persons of households and they are not dependent children. The involved variables are `hrp` and `Dependent` for the categories “Household Reference Person” and “independent”, you can select the appropriate cases. We also want to exclude the health variable reported as “Not known”.

```
frs_df <- frs_data %>% filter(hrp == "HRP" &
                             dependent == "Independent" & health != "Not known")
```

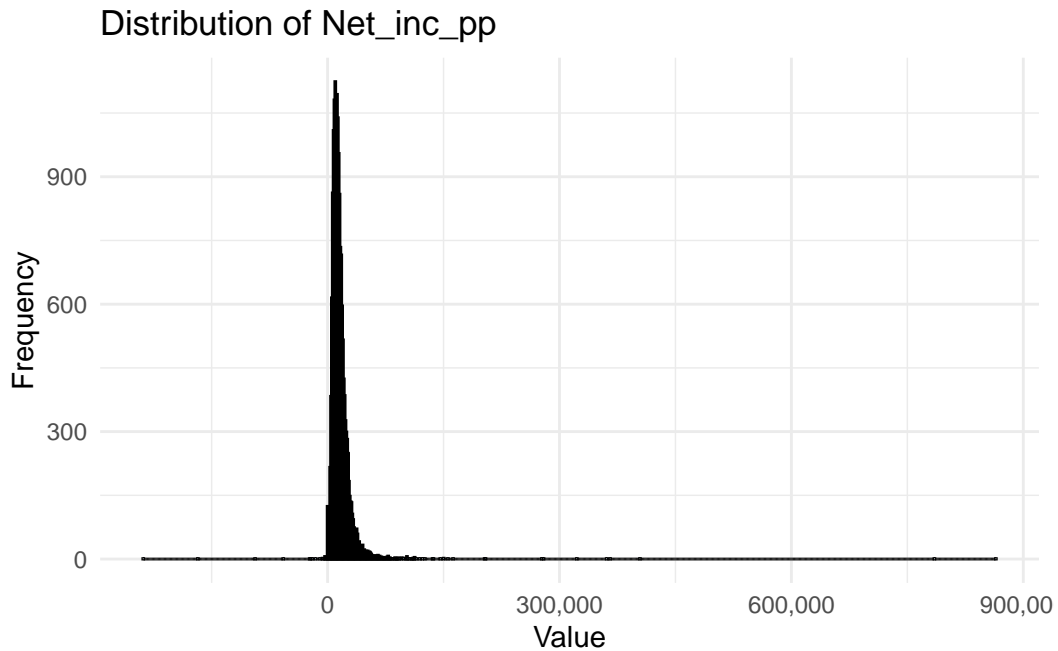
Then, we create a new numeric variable `Net_inc_perc` indicate net income per capita as our dependent variable:

```
frs_df$Net_inc_pp = frs_df$hh_income_net / frs_df$hh_size
summary(frs_df$Net_inc_pp)
```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|---------|---------|--------|-------|---------|--------|
| -238160 | 9074 | 13347 | 15834 | 19136 | 864812 |

The distribution of the net household income per capita can be visualised by using `ggplot()`

```
ggplot(frs_df, aes(x = Net_inc_pp)) +
  geom_histogram(
    bins = 1000,
    color = "black",
    fill = "skyblue",
    alpha = 0.7
  ) +
  labs(title = "Distribution of Net_inc_pp", x = "Value", y = "Frequency") +
  scale_x_continuous(labels = scales::label_comma()) + # Prevent scientific notation on the
  theme_minimal()
```



Our two qualitative independent variables “sex” and “health”. Let’s first know what they look like:

```
table(frs_df$sex)
```

```
Female  Male
 7647   9180
```

```
table(frs_df$health)
```

```
Bad      Fair      Good  Very Bad  Very Good
1472     4253     6277      426     4399
```

Remember what we did in the Region long-term illness practical previously before we put the qualitative variable into the regression model? Yes. First, make sure they are in factor type and Second, decide the reference category. Here, I will use Female and Very Bad health status as my base categories. You can decide what you wish to use. This time, I use the following codes to combine these two steps in one line.

```
frs_df$sex <- fct_relevel(as.factor(frs_df$sex), "Female")
frs_df$health <- fct_relevel(as.factor(frs_df$health), "Very Bad")
```

Implement the regression model with the two qualitative independent variables.

```
model_frs <- lm(Net_inc_pp ~ sex + health, data = frs_df)
summary(model_frs)
```

Call:

```
lm(formula = Net_inc_pp ~ sex + health, data = frs_df)
```

Residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|-------|--------|------|--------|
| -255133 | -6547 | -2213 | 3515 | 845673 |

Coefficients:

| | Estimate | Std. Error | t value | Pr(> t) |
|-----------------|----------|------------|---------|--------------|
| (Intercept) | 12115.5 | 762.9 | 15.881 | < 2e-16 *** |
| sexMale | 2091.2 | 240.6 | 8.691 | < 2e-16 *** |
| healthBad | -102.8 | 854.3 | -0.120 | 0.904205 |
| healthFair | 1051.3 | 789.0 | 1.332 | 0.182751 |
| healthGood | 2766.0 | 777.4 | 3.558 | 0.000375 *** |
| healthVery Good | 4931.8 | 787.8 | 6.260 | 3.95e-10 *** |

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

Residual standard error: 15530 on 16821 degrees of freedom

Multiple R-squared: 0.01646, Adjusted R-squared: 0.01616

F-statistic: 56.29 on 5 and 16821 DF, p-value: < 2.2e-16

The result can be formatted by:

```
library(broom)
tidy(model_frs)
```

A tibble: 6 x 5

| term | estimate | std.error | statistic | p.value |
|---------------|----------|-----------|-----------|----------|
| <chr> | <dbl> | <dbl> | <dbl> | <dbl> |
| 1 (Intercept) | 12116. | 763. | 15.9 | 2.21e-56 |

| | | | | | |
|---|-----------------|-------|------|--------|----------|
| 2 | sexMale | 2091. | 241. | 8.69 | 3.90e-18 |
| 3 | healthBad | -103. | 854. | -0.120 | 9.04e- 1 |
| 4 | healthFair | 1051. | 789. | 1.33 | 1.83e- 1 |
| 5 | healthGood | 2766. | 777. | 3.56 | 3.75e- 4 |
| 6 | healthVery Good | 4932. | 788. | 6.26 | 3.95e-10 |

Q6. What conclusions could be drawn in terms of income inequalities with respect to gender and health status? Also think about the statistical significance of these differences.

3.5 Extension activities

The extension activities are designed to get yourself prepared for the Assignment 2 in progress. For this week, try whether you can:

- Present descriptive statistics for independent variable and the dependent variable: counts, percentages, a centrality measure, a spread measure, histograms or any relevant statistic
- Report the observed association between the dependent and independent variables: correlation plus a graphic or tabular visualisation
- Briefly describe and critically discuss the results
- Think about other potential factors of long-term illness and income, and then test your ideas with linear regression models
- Summaries your model outputs and interpret the results.

Answer of the written down model and Q5

The model of the new region label is: $pct_Long_term_ill (\%) = 47.218 + (-0.834) * pct_Males (\%) + 0.472 * pct_No_qualifications (\%) + 1.072 * Other\ Regions\ in\ England + 4.345 * Wales$

So if the values of variables *pct_Males*, *pct_No_qualifications*, and *pct_Higher_manager_prof* are 49, 23 and 11,

the model of Wales will be: $pct_Long_term_ill (\%) = 47.218 + (-0.834) * 49 + 0.472 * 23 + 1.072 * 0 + 4.345 * 1 = 21.553$ (you can direct paste the number sentence into your R studio Console and the result will be returned)

the model of London will be: $pct_Long_term_ill (\%) = 47.218 + (-0.834) * 49 + 0.472 * 23 + 1.072 * 0 + 4.345 * 0 = 17.208$

You can also make a new object like

```
obj_London <- data.frame(
  pct_Males = 49,
  pct_No_qualifications = 23,
  pct_Higher_manager_prof = 11,
  New_region_label = "London"
)
obj_Wales <- data.frame(
  pct_Males = 49,
  pct_No_qualifications = 23,
  pct_Higher_manager_prof = 11,
  New_region_label = "Wales"
)
predict(model2, obj_London)
```

```
      1
17.19808
```

```
predict(model2, obj_Wales)
```

```
      1
21.54334
```

Therefore, the percentage of persons with long-term illness in Wales and London be 21.5% and 17.2% separately. If you got the right answers, then congratulations you can now use regression model to make prediction.

4 Lab: LogisticRegression

Last week, we learnt how to use qualitative variables in multiple linear regression model to understand the relationship between independent variables $X_1 \dots X_n$ and the dependent variable Y . Today we will learn to use logistic regression for binary dependent variable. A **logistic regression model** is a type of regression analysis used when the dependent variable is binary (e.g., “success/failure” or “0/1”). It estimates the probability of one outcome relative to the other using a logistic function. This model is commonly used in situations like predicting disease presence (yes/no) or customer churn (stay/leave). The independent variables can be continuous, categorical, or a mix of both. The model’s output is in the form of odds ratios, showing how predictors affect the likelihood of the outcome.

The lecture’s slides can be found [here](#).

Learning objectives

An understanding of, and ability to:

- Estimate and interpret a logistic regression model
- Assess the model fit

The application context of a binomial logistic regression model is when the dependent variable under investigation is a binary variable. Usually, a value of 1 for this dependent variable means the occurrence of an event; and, 0 otherwise. For example, the dependent variable for this practical is whether a person is a long-distance commuter i.e. 1, and 0 otherwise.

In this week’s practical, we are going to apply logistic regression analysis in an attempt to answer the following research question:

RESEARCH QUESTION: Who is willing to commute long distances?

The practical is split into two main parts. The first focuses on implementing a binary logistic regression model with R. The second part focuses the interpretation of the resulting estimates.

4.1 Preparing the input variables

Prepare the data for implementing a logistic regression model. The data set used in this practical is the “sar_sample_label.csv” and “sar_sample_code.csv”. The SAR is a snapshot of census microdata, which are individual level data. The data sample has been drawn and anonymised from census and known as the Samples of Anonymised Records (SARs).

You may need to download the two datasets from our [github website](#) if you haven't. The two csv are actually the same dataframe, only one uses the label as the value but the other uses the code. We will first read in both for the data overview the labels are more friendly, and then we focus on using “sar_sample_code.csv” in the regression model as it is easier for coding.

```
if(!require("tidyverse"))
  install.packages("tidyverse",dependencies = T, repos = "https://cloud.r-project.org/")
if(!require("broom"))
  install.packages("broom",dependencies = T, repos = "https://cloud.r-project.org/")

library(tidyverse)
library(broom)
```

```
sar_label <- read_csv("../data/SAR/sar_sample_label.csv")
```

```
Rows: 50000 Columns: 39
```

```
-- Column specification -----
Delimiter: ","
```

```
chr (39): country, region, county, la_group, age_group, sex, marital_status,...
```

```
i Use `spec()` to retrieve the full column specification for this data.
```

```
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
sar_code <- read_csv("../data/SAR/sar_sample_code.csv")
```

```
Rows: 50000 Columns: 39
```

```
-- Column specification -----
Delimiter: ","
```

```
dbl (39): country, region, county, la_group, age_group, sex, marital_status,...
```

```
i Use `spec()` to retrieve the full column specification for this data.
```

```
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```



```
View(sar_label)
View(sar_code)

glimpse(sar_label)
glimpse(sar_code)
```

```
summary(sar_code)
summary(sar_label)
```

The outcome variable is a person's commuting distance captured by the variable "work_distance".

```
table(sar_label$work_distance)
```

```

10 to <20 km
      3650
 2 to <5 km
      4414
20 to <40 km
      2014
40 to <60km
      572
 5 to <10 km
      4190
60km or more
      703
Age<16 or not working
      25975
      At home
      2427
Less than 2 km
      4028
No fixed place
      1943
Work outside England and Wales but within UK
      29
      Work outside UK
      21
Works at offshore installation (within UK)
      34
```

```
table(sar_code$work_distance)
```

```

      -9      1      2      3      4      5      6      7      8      9     10     11     12
25975  4028  4414  4190  3650  2014   572   703  2427  1943   29   21   34

```

There are a variety of categories in the variable, however, we are only interested in commuting distance and therefore in people reporting their commuting distance. Thus, we will explore the numeric codes of the variable ranging from 1 to 8.

| Code for Work_distance | Categories |
|------------------------|--|
| 1 | Less than 2 km |
| 2 | 2 to <5 km |
| 3 | 5 to <10 km |
| 4 | 10 to <20 km |
| 5 | 20 to <40 km |
| 6 | 40 to <60 km |
| 7 | 60km or more |
| 8 | At home |
| 9 | No fixed place |
| 10 | Work outside England and Wales but within UK |
| 11 | Work outside UK |
| 12 | Works at offshore installation (within UK) |

As we are also interested in exploring whether people with different socio-economic statuses (or occupations) tend to be associated with varying probabilities of commuting over long distances, we further filter or select cases.

```
table(sar_label$nssec)
```

```

      Child aged 0-15
      9698
Full-time student
      3041
Higher professional occupations
      3162
Intermediate occupations
      5288

```

```

Large employers and higher managers
909
Lower managerial and professional occupations
8345
Lower supervisory and technical occupations
2924
Never worked or long-term unemployed
2261
Routine occupations
4660
Semi-routine occupations
5893
Small employers and own account workers
3819

```

```
table(sar_code$nssec)
```

```

 1    2    3    4    5    6    7    8    9   10   12
909 3162 8345 5288 3819 2924 5893 4660 2261 3041 9698

```

Using `nssec`, we select people who reported an occupation, and delete cases with numeric codes from 9 to 12, who are *unemployed, full-time students, children* and *not classifiable*.

| Code for nssec | Category labels |
|----------------|---|
| 1 | Large employers and higher managers |
| 2 | Higher professional occupations |
| 3 | Lower managerial and professional occupations |
| 4 | Intermediate occupations |
| 5 | Small employers and own account workers |
| 6 | Lower supervisory and technical occupations |
| 7 | Semi-routine occupations |
| 8 | Routine occupations |
| 9 | Never worked or long-term employed |
| 10 | Full-time student |
| 11 | Not classifiable |
| 12 | Child aged 0-15 |

Now, similar to next week, we use the `filter()` to prepare our dataframe today. You may already realise that using `sar_code` is easier to do the filtering.

```
sar_df <- sar_code %>% filter(work_distance<=8 & nssec <=8 )
```

Q1. Summarise the frequencies of the two variables “work_distance” and “nssec” with the new data.

Recode the “work_distance” variable into a binary dependent variable

A simple way to create a binary dependent variable representing long-distance commuting is to use the `mutate()` function as discussed in last week’s practical session. Before creating the binary variables from the “work_distance” variable, we need to define *what counts as a long-distance commuting move*. Such definition can vary. Here we define a long-distance commuting move as any commuting move over a distance above 60km (the category of “60km or more”).

```
sar_df <- sar_df %>% mutate(  
  New_work_distance = if_else(work_distance >6, 1,0))
```

Q2. Check the new `sar_df` dataframe with new column named `New_work_distance` by using the codes you have learnt.

Prepare your “nssec” variable before the regression model

The `nssec` is a categorical variable. Therefore, as we’ve learnt last week, before adding the categorical variables into the regression model, we need first make it a factor and then identify the reference category.

We are interested in whether people with occupations being “Higher professional occupations” are associated with a lower probability of commuting over long distances when comparing to people in other occu

```
sar_df$nssec <- relevel(as.factor(sar_df$nssec), ref = "2")
```

4.2 Implementing a logistic regression model

The binary dependent variable is long-distance commuting, variable name `New_work_distance`.

The independent variables are gender and socio-economic status.

For gender, we use male as the baseline.

```
sar_df$sex <- relevel(as.factor(sar_df$sex),ref="1")
```

For socio-economic status, we use code 5 (Small employers and Own account workers) as the baseline category to explore whether people work as independent employers show lower probability of commuting longer than 60km compared with other occupations.

```
#create the model
m.glm = glm(New_work_distance~sex + nssec,
             data = sar_df,
             family= "binomial")
# inspect the results
summary(m.glm)
```

Call:

```
glm(formula = New_work_distance ~ sex + nssec, family = "binomial",
     data = sar_df)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|-------------|----------|------------|---------|--------------|
| (Intercept) | -1.67337 | 0.05329 | -31.401 | < 2e-16 *** |
| sex2 | -0.36678 | 0.04196 | -8.742 | < 2e-16 *** |
| nssec1 | -0.12881 | 0.11306 | -1.139 | 0.255 |
| nssec3 | -0.38761 | 0.06467 | -5.994 | 2.05e-09 *** |
| nssec4 | -1.03079 | 0.08439 | -12.214 | < 2e-16 *** |
| nssec5 | 1.22639 | 0.06489 | 18.898 | < 2e-16 *** |
| nssec6 | -1.38992 | 0.10919 | -12.730 | < 2e-16 *** |
| nssec7 | -1.43909 | 0.09002 | -15.986 | < 2e-16 *** |
| nssec8 | -1.48534 | 0.09646 | -15.398 | < 2e-16 *** |

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 20441 on 33025 degrees of freedom
 Residual deviance: 17968 on 33017 degrees of freedom
 AIC: 17986

Number of Fisher Scoring iterations: 6

```
# odds ratios
exp(coef(m.glm))
```

| (Intercept) | sex2 | nssec1 | nssec3 | nssec4 | nssec5 |
|-------------|------|--------|--------|--------|--------|
|-------------|------|--------|--------|--------|--------|

| | | | | | |
|-----------|-----------|-----------|-----------|-----------|-----------|
| 0.1876138 | 0.6929649 | 0.8791416 | 0.6786766 | 0.3567267 | 3.4088847 |
| nssec6 | nssec7 | nssec8 | | | |
| 0.2490946 | 0.2371432 | 0.2264258 | | | |

```
# confidence intervals
exp(confint(m.glm, level = 0.95))
```

Waiting for profiling to be done...

| | 2.5 % | 97.5 % |
|-------------|-----------|-----------|
| (Intercept) | 0.1688060 | 0.2080319 |
| sex2 | 0.6381810 | 0.7522773 |
| nssec1 | 0.7017990 | 1.0935602 |
| nssec3 | 0.5981911 | 0.7708192 |
| nssec4 | 0.3020431 | 0.4205270 |
| nssec5 | 3.0037298 | 3.8739884 |
| nssec6 | 0.2002766 | 0.3073830 |
| nssec7 | 0.1984396 | 0.2824629 |
| nssec8 | 0.1869397 | 0.2729172 |

Q3. If we want to explore whether people with occupation being “Large employers and higher managers”, “Higher professional occupations” and “Routine occupations” are associated with higher probability of commuting over long distance when comparing to people in other occupation, how will we prepare the input independent variables and what will be the specified regression model?

Hint: use `mutate()` to create a new column, set the value of “Large employers and higher managers”, “Higher professional occupations” and “Routine occupations” as original, while the rest as “Other occupations” (recall in Lab 3 what we did for assigning the regions not within “London”, “Wales”, “Scotland” and “Northern Ireland” as “Other Regions in England”). Here by using the SAR in code format, we can make this more easier by using:

```
sar_df <- sar_df %>% mutate(New_nssec = fct_other(
  nssec,
  keep = c("1", "2", "8"),
  other_level = "0"
))
```

Or by using `if_else` and `%in%` in R, we can achieve the same result. `%in%` is an operator used to test if elements of one vector are present in another. It returns `TRUE` for elements found and `FALSE` otherwise.

```
sar_df <- sar_df %>% mutate(New_nssec = if_else(!nssec %in% c(1,2,8), "0", nssec))
```

Use “Other occupations” (code: 0) as the reference category by `relevel(as.factor())` and then create the regression model: `glm(New_work_distance~sex + New_nssec, data = sar_df, family= "binomial")`. Can you now run the model by yourself? Find the answer at the end of the practical.

4.2.1 Model fit

We include the R library `pscl` for calculate the measures of fit.

```
if(!require("pscl"))
  install.packages("pscl", repos = "https://cloud.r-project.org/")
```

Loading required package: `pscl`

Warning: package 'pscl' was built under R version 4.4.2

Classes and Methods for R originally developed in the
Political Science Computational Laboratory
Department of Political Science
Stanford University (2002-2015),
by and under the direction of Simon Jackman.
hurdle and zeroinfl functions by Achim Zeileis.

```
library(pscl)
```

Relating back to this week’s lecture notes, what is the Pseudo R^2 of the fitted logistic model (from the Model Summary table below)?

```
# Pseudo R-squared
pR2(m.glm)
```

fitting null model for pseudo-r2

| | llh | llhNull | G2 | McFadden | r2ML |
|------|---------------|---------------|--------------|--------------|--------------|
| | -8.983928e+03 | -1.022037e+04 | 2.472890e+03 | 1.209785e-01 | 7.214246e-02 |
| r2CU | | | | | |
| | 1.563288e-01 | | | | |

```
# or in better format
pR2(m.glm) %>% round(4) %>% tidy()
```

fitting null model for pseudo-r2

```
# A tibble: 6 x 2
  names      x
  <chr>    <dbl>
1 llh      -8984.
2 llhNull  -10220.
3 G2        2473.
4 McFadden  0.121
5 r2ML      0.0721
6 r2CU      0.156
```

- **llh**: The log-likelihood of the fitted model.
- **llhNull**: The log-likelihood of the null model (without predictors).
- **G2**: The likelihood ratio statistic, showing the model's improvement over the null model.
- **McFadden**: McFadden's pseudo R-squared (a common measure of model fit).
- **r2ML**: Maximum likelihood pseudo R-squared.
- **r2CU**: Cox & Snell pseudo R-squared.

Different from the multiple linear regression, whose R-squared indicates % of the variance in the dependent variables that is explained by the independent variable. In logistic regression model, R-squared is not directly applicable. Instead, we use pseudo R-squared measures, such as McFadden's pseudo R-squared, or Cox & Snell pseudo R-squared to provide an indication of model fit. For the individual level dataset like SAR, value around 0.3 is considered good for well-fitting.

4.2.2 Statistical significance of regression coefficients or covariate effects

Similar to the statistical inference in a linear regression model context, p-values of regression coefficients are used to assess significances of coefficients; for instance, by comparing p-values to the conventional level of significance of 0.05:

- If the p-value of a coefficient is smaller than 0.05, the coefficient is statistically significant. In this case, you can say that the relationship between an independent variable and the outcome variable is *statistically* significant.

· If the p-value of a coefficient is larger than 0.05, the coefficient is statistically insignificant. In this case, you can say or conclude that there is no statistically significant association or relationship between an independent variable and the outcome variable.

4.2.3 Interpreting estimated regression coefficients

- The interpretation of coefficients (B) and odds ratios (Exp(B)) for the independent variables differs from that in a linear regression setting.
- Interpreting the regression coefficients.
 - o For the variable **sex**, a negative sign and the odds ratio estimate indicate that the probability of commuting over long distances for female is 0.693 times less likely than male (the reference group), with the confidence intervals (CI) or likely range between 0.6 to 0.7, holding all other variables constant (the socio-economic classification variable). Put it differently, being females reduces the probability of long-distance commuting by 30.7% (1-0.693).
 - o For variable **nssec**, a positive significant and the odds ratio estimate indicate that the probability of long-distance commuting for those whose socio-economic classification as:
 - small employers and own account workers (nssec=5) are 3.409 times more likely than the higher prof occupations, holding all other variables constant (the Sex variable), with a likely range (CI) of between 3.0 to 3.8.
 - the p-value of Large employers and higher managers (nssec=1) is > 0.05 , so there is no statistically significant relationship between large employers and higher managers and long-distance commuting.
 - Routine occupations (nssec=8) are 0.226 times (or 22.6%) less likely than the higher professional occupations, with the CI between 0.18 to 0.27. when other variable constant. Or, we can see being routine occupations decreases the probability of long-distance commuting by 77.4% (1-0.226).

Q4. Interpret the regression coefficients (i.e. Exp(B)) of variables “nssec=Lower managerial and professional occupations” and “nssec=Semi-routine occupation”.

Q5. Could you identify significant factors of commuting over long distances?

4.2.4 Prediction using fitted regression model

Relating to this week’s lecture, the log odds of the person who is will to long-distance commuting is equal to:

Log odds of long-distance commuting = $0.188 + 0.693 * \text{sexFemale} + 0.679 * \text{nssec3} + 0.357 * \text{nssec4} + 3.409 * \text{nssec5} + 0.249 * \text{nssec6} + 0.237 * \text{nssec7} + 0.226 * \text{nssec8}$

By using R, you can create the object you would like to predict. Here we created three person, see whether you can interpret their gender and socio-economic classification?

```
objs <- data.frame(sex=c("1","2","1"),nssec=c("7","3","5"))
```

Then we can predict by using our model `m.glm`:

```
predict(m.glm, objs,type = "response")
```

```
          1          2          3  
0.04259618 0.08108050 0.39007797
```

So let us look at these three people. The first one, for a male who classified as Semi-routine occupation in NSSEC, the probability of he travel over 60km to work is only 4.26%. For the second one, a female who is in Lower managerial and professional occupation, the probability of long-distance commuting is 8.11%. Now you know the prediction outcomes for our last person.

4.3 Extension activities

The extension activities are designed to get yourself prepared for the Assignment 2 in progress. For this week, try whether you can:

- Select a regression strategy and explain why a linear or logistic model is appropriate
- Perform one or a series of regression models, including different combinations of your chosen independent variables to explain and/or predict your dependent variable

Answer for the model in Q3

In Q3, we want to explore whether people with occupation being “Large employers and higher managers”, “Higher professional occupations” and “Routine occupations” are associated with higher probability of commuting over long distance when comparing to people in other occupation. So we create the variable `New_nssec` with 0 “Other occupations”, but still keep “1”, “2” and “8” still as original categories.

So we can first have a check of our new variable `New_nssec`:

```
table(sar_df$New_nssec)
```

| | | | |
|-------|-----|------|------|
| 0 | 1 | 2 | 8 |
| 24615 | 887 | 3055 | 4469 |

Then we set the reference categories: `sex` as 1 (male) and `New_nssec` as 0, which is “Other occupations”:

```
sar_df$sex <- relevel(as.factor(sar_df$sex),ref="1")
sar_df$New_nssec <- relevel(as.factor(sar_df$New_nssec),ref="0")
```

Now, we build the logistic regression model and check out the outcomes:

```
model_new = glm(New_work_distance~sex + New_nssec, data = sar_df, family= "binomial")
summary(model_new)
```

Call:

```
glm(formula = New_work_distance ~ sex + New_nssec, family = "binomial",
    data = sar_df)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|-------------|----------|------------|---------|--------------|
| (Intercept) | -1.92955 | 0.02786 | -69.253 | < 2e-16 *** |
| sex2 | -0.61757 | 0.03936 | -15.688 | < 2e-16 *** |
| New_nssec1 | 0.19183 | 0.10336 | 1.856 | 0.0634 . |
| New_nssec2 | 0.32582 | 0.05678 | 5.738 | 9.58e-09 *** |
| New_nssec8 | -1.14082 | 0.08434 | -13.526 | < 2e-16 *** |

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 20441 on 33025 degrees of freedom
Residual deviance: 19868 on 33021 degrees of freedom
AIC: 19878

Number of Fisher Scoring iterations: 6

For the model interpretation, we need:

```
# odds ratios
exp(coef(model_new))
```

```
(Intercept)      sex2  New_nssec1  New_nssec2  New_nssec8
    0.1452137    0.5392528    1.2114691    1.3851650    0.3195562
```

```
# confidence intervals
exp(confint(model_new, level = 0.95))
```

Waiting for profiling to be done...

```
              2.5 %    97.5 %
(Intercept) 0.1374508 0.1533142
sex2        0.4991249 0.5824112
New_nssec1  0.9846735 1.4770819
New_nssec2  1.2380128 1.5467297
New_nssec8  0.2698515 0.3756702
```

```
# model fit
pR2(model_new) %>% round(4) %>% tidy()
```

fitting null model for pseudo-r2

Warning in tidy.numeric(.): 'tidy.numeric' is deprecated.
See help("Deprecated")

```
# A tibble: 6 x 2
  names      x
  <chr>    <dbl>
1 llh      -9934.
2 llhNull -10220.
3 G2        573.
4 McFadden  0.028
5 r2ML      0.0172
6 r2CU      0.0373
```

5 Lab: Data Visualisation with ggplot

The lecture's slides can be found [here](#).

5.1 Part 1: Towards the Assignment (30 min, or till when you feel you are good to go)

1. Identify a possible topic:
 - Load your dataset(s) in Rstudio.
 - Define your Research Question.
 - Identify the related variables to analyse.
2. Discuss ideas:
 - Get feedback on feasibility and the clarity of research questions.

5.2 Part 2 - Visualisation: ggplot2 Functions and Arguments

For this session you need the following libraries:

```
install.packages(c("ggplot2", "dplyr", "tidyr", "kableExtra", "ggridges",  
"RColorBrewer", "broom", "scales", "corrplot", "vtable"))
```

If necessary install them by moving the line into a code chunk.

The **ggplot2** package in R is one of the most powerful tools for creating publication-quality visualisations. It uses a layered approach to building plots, starting with data, then adding mappings, geometries, and other components.

A ggplot2 plot is built step by step:

```
ggplot(data, aes(x = <X-axis variable>, y = <Y-axis variable>, <other aesthetics>)) +  
  <geom_function()> +  
  <scales/themes/other layers>
```

5.2.1 ggplot()

- Initializes the plotting system.
- Main arguments:
- `data`: A data frame containing the variables to be plotted.
- `aes()`: Aesthetic mappings to connect data variables to visual properties like `x`, `y`, `color`, `fill`, `size`, etc.

```
library(ggplot2)
```

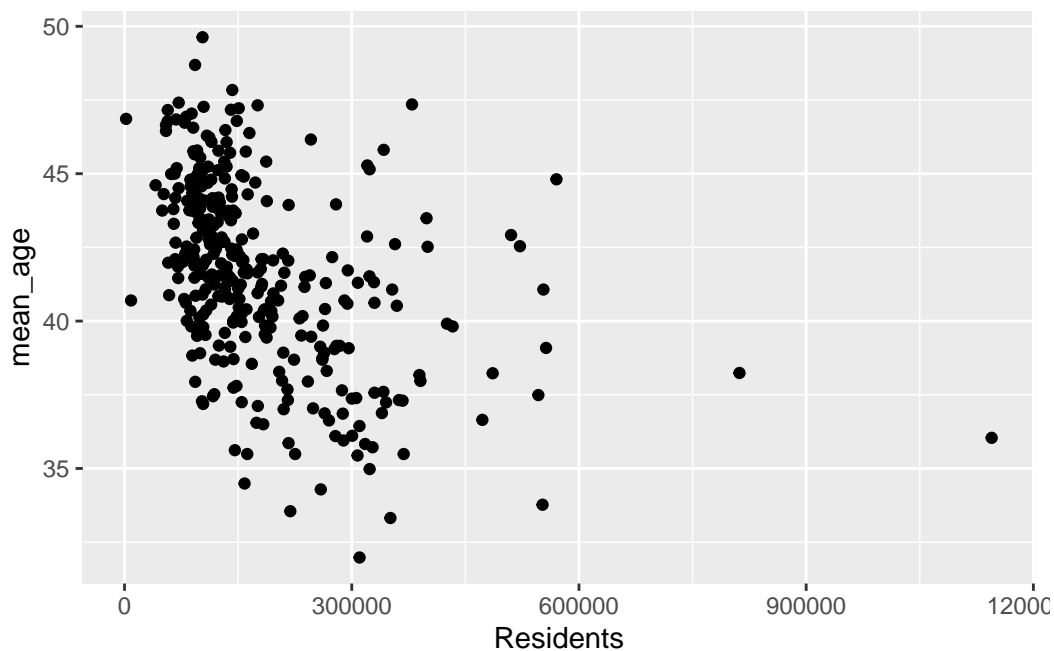
Example:

Let's load the data first:

```
census_data <- read.csv("../data/Census2021/EW_DistrictPercentages.csv")
```

Plotting Number of residents vs age (mean).

```
ggplot(data = census_data, aes(x = Residents, y = mean_age)) +  
  geom_point()
```



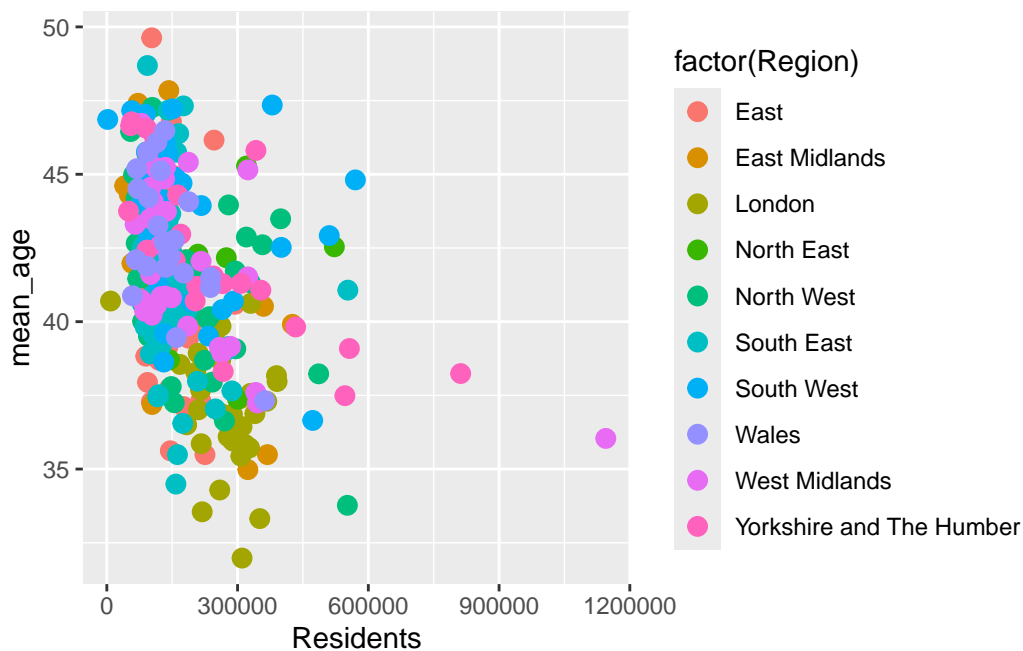
5.2.2 Geometries in ggplot2

You can plot the following geometries in ggplot:

| Geometry | Function | Use Case |
|-----------|-------------------------------|-----------------------------------|
| Point | <code>geom_point()</code> | Scatterplots |
| Line | <code>geom_line()</code> | Line plots |
| Bar | <code>geom_bar()</code> | Bar charts |
| Histogram | <code>geom_histogram()</code> | Histograms |
| Boxplot | <code>geom_boxplot()</code> | Boxplots |
| Density | <code>geom_density()</code> | Density plots |
| Smooth | <code>geom_smooth()</code> | Add regression or smoothing lines |

Example: Scatterplot with `geom_point()`

```
ggplot(census_data, aes(x = Residents, y = mean_age, color = factor(Region))) +  
  geom_point(size = 3)
```



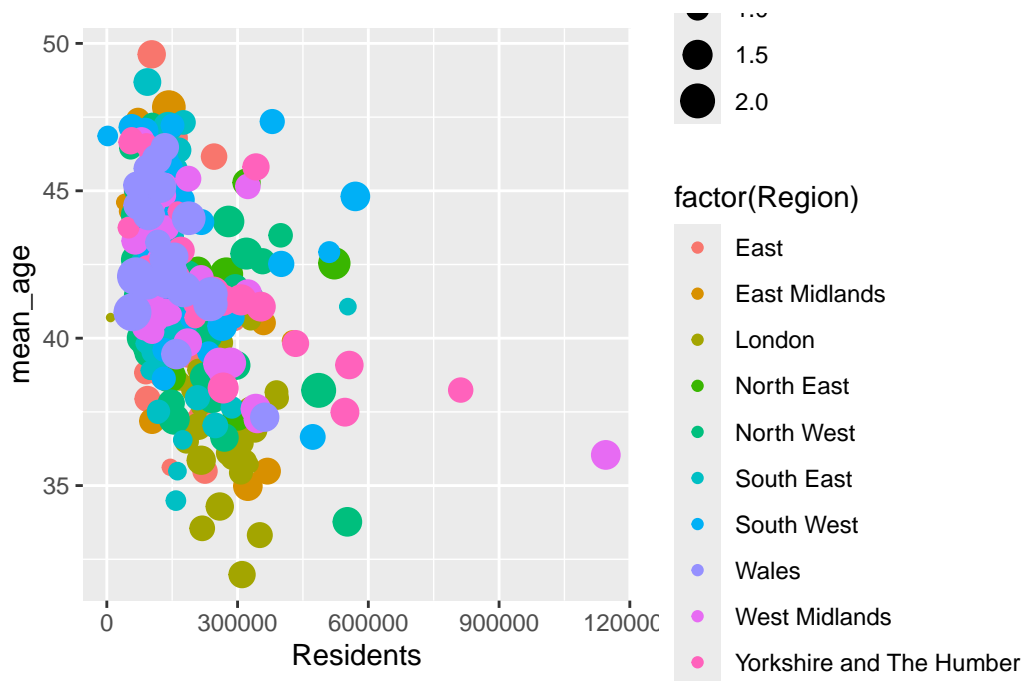
5.2.3 Aesthetics: `aes()`

- Maps data variables to visual properties.

- Common aesthetics:
- **x**: X-axis variable.
- **y**: Y-axis variable.
- **color**: Changes point/line colors based on a variable.
- **fill**: Fills bars/areas based on a variable.
- **size**: Controls the size of points/lines.

Example: Adding color and size aesthetics

```
ggplot(census_data, aes(x = Residents, y = mean_age, color = factor(Region), size = pct_Very.  
geom_point()
```



What's missing in the plot above?How can this be improved?

5.2.4 Faceting: facet_*

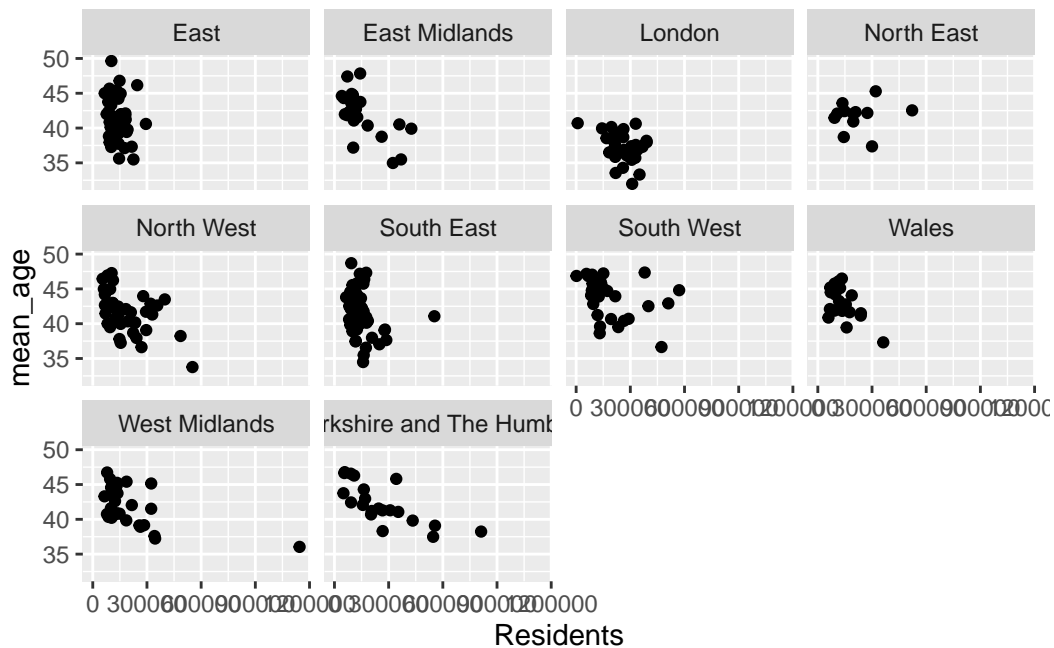
Faceting splits data into subsets and creates multiple small plots.

| Function | Description |
|------------------------------------|----------------------------------|
| <code>facet_wrap(~var)</code> | Wraps plots across rows/columns. |
| <code>facet_grid(row ~ col)</code> | Creates a grid layout for plots. |

Faceting is a technique to create multiple plots based on subsets of your data. It is particularly useful for comparing relationships or distributions across categories. By breaking down a dataset into smaller pieces according to a categorical variable, faceting helps visualise data trends or differences within subgroups. For instance, `facet_wrap(~ Region)` creates individual plots for each category in the Region variable, aligning them into rows and columns. Alternatively, `facet_grid(row ~ col)` creates a more structured layout, where two categorical variables determine the rows and columns of the grid.

Faceting is essential when dealing with data that needs to be compared across multiple dimensions. For example, a scatterplot faceted by sex can show how a relationship differs for males and females. Similarly, faceted histograms can reveal differences in the distribution of a variable across categories.

```
ggplot(census_data, aes(x = Residents, y = mean_age)) +
  geom_point() +
  facet_wrap(~Region)
```



What are the issues here?

5.2.5 Themes (`theme_*`)

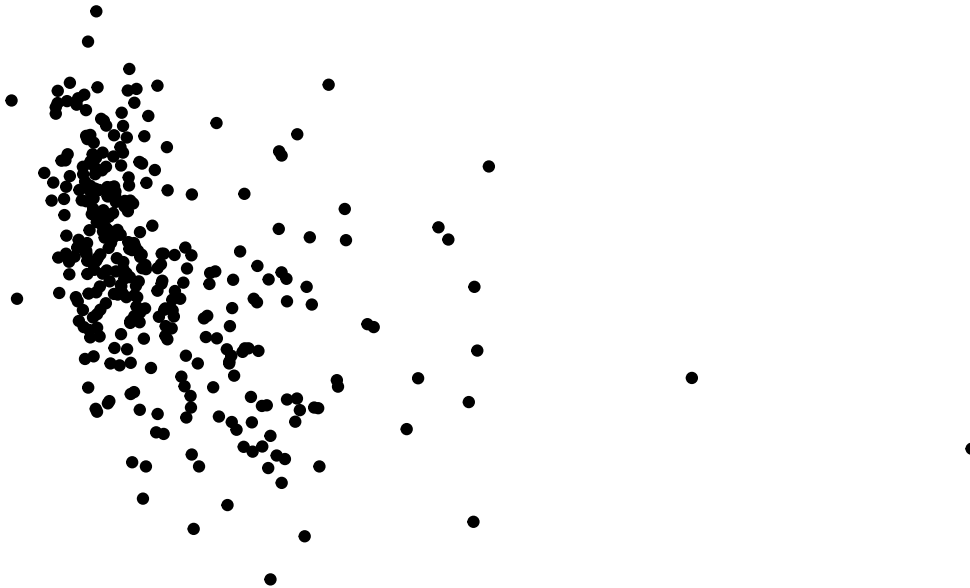
Themes control the overall appearance of the plot.

| Function | Effect |
|------------------------------|--------------------------------|
| <code>theme_minimal()</code> | Simple and clean theme. |
| <code>theme_classic()</code> | Classic-style plots. |
| <code>theme_dark()</code> | Dark background. |
| <code>theme_void()</code> | Minimal with no axes or grids. |

Applying a theme

```
ggplot(data = census_data, aes(x = Residents, y = mean_age)) +
  geom_point() +
  theme_void() +
  labs(title = "Visualisation with Void Theme")
```

Visualisation with Void Theme



What do you think? Is this any good?

5.2.6 Scales

Scales adjust color, size, and axis properties.

| Scale | Description |
|-----------------------------------|--------------------------------------|
| <code>scale_color_manual()</code> | Customizes colors for lines/points. |
| <code>scale_fill_brewer()</code> | Predefined color palettes for fills. |
| <code>scale_x_continuous()</code> | Modifies X-axis properties. |
| <code>scale_y_continuous()</code> | Modifies Y-axis properties. |

`scale_color` functions modify the outline color of elements like points, lines, or the border of shapes, while `scale_fill` functions modify the interior fill color of shapes like bars, tiles, or boxes. Both are used to control aesthetics based on a variable mapped in `aes()` but apply to different visual aspects of the plot.

Example: Customizing axis and colors

The `RColorBrewer` library provides pre-defined color palettes specifically designed for data visualisation, ensuring clarity and accessibility. It includes sequential, diverging, and qualitative palettes suitable for various data types and visualisation needs.

Have a look at: <https://r-graph-gallery.com/38-rcolorbrewers-palettes.html>

```
# Automatically determine the number of colors needed

num_levels <- length(unique(census_data$Region))
```

The `num_levels` variable is a dynamic way to determine the number of unique levels in a categorical variable, such as `Region`. This approach is particularly helpful when you don't know in advance how many categories exist in the dataset.

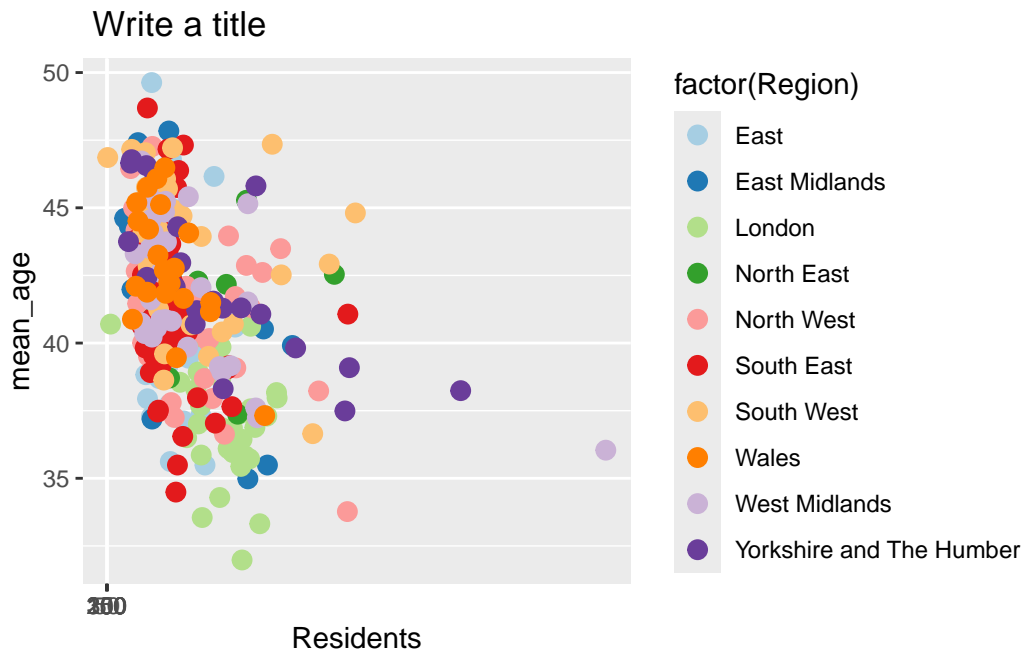
The code above calculates the number of unique categories in the `Region` variable, ensuring that your plot's color palette matches the data's requirements. Based on the value of `num_levels`, you can choose an appropriate color palette from libraries like `RColorBrewer`. For example:

```
library(RColorBrewer)
# Use an appropriate Brewer palette based on the number of levels
palette <- if (num_levels <= 8) "Set2" else "Paired" # Choose a palette with enough colors
```

This dynamically selects a palette suitable for the number of categories. If there are 8 or fewer levels, the `Set2` palette is used; for more levels, `Paired` ensures enough distinct colors (there's several palettes, check the link above for more).

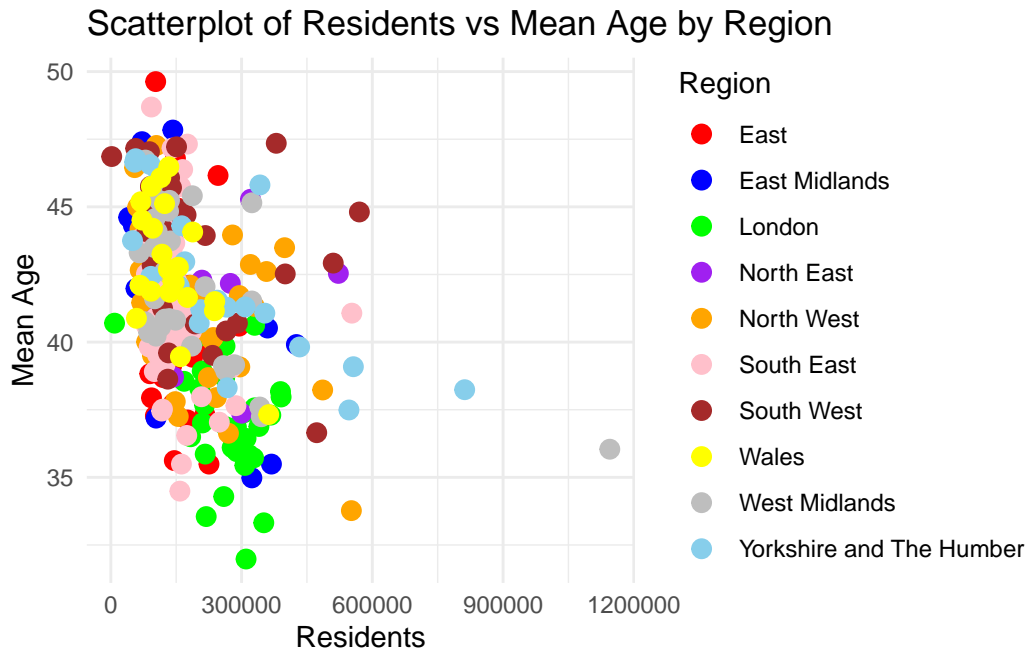
When applying the palette in `ggplot2`, the function `scale_color_brewer(palette = palette)` ensures that the plot assigns colors based on the selected scheme. This process avoids hardcoding colors or palettes and ensures the plot adapts to changes in the data, such as when categories are added or removed.

```
ggplot(census_data, aes(x = Residents, y = mean_age, color = factor(Region))) +
  geom_point(size = 3) +
  scale_color_brewer(palette = palette) + # Dynamically chosen palette
  scale_x_continuous(breaks = seq(50, 350, 50)) +
  labs(title = " Write a title")
```



You can also create your own palette of colours.

```
ggplot(census_data, aes(x = Residents, y = mean_age, color = factor(Region))) +
  geom_point(size = 3) +
  scale_color_manual(values = c("red", "blue", "green", "purple", "orange", "pink", "brown", "grey")) +
  labs(
    title = "Scatterplot of Residents vs Mean Age by Region",
    x = "Residents",
    y = "Mean Age",
    color = "Region"
  ) +
  theme_minimal()
```



Consider in general, that there's several functions associated to scales

| Category | Function | Description | Example Usage |
|-----------------------|--------------------------------------|---|--|
| Discrete Color Scales | <code>scale_color_brewer()</code> | Use pre-defined discrete palettes from RColorBrewer. | <code>scale_color_brewer(palette = "Set1")</code> |
| | <code>scale_fill_brewer()</code> | Fill colors for discrete variables from RColorBrewer. | <code>scale_fill_brewer(palette = "Pastel2")</code> |
| | <code>scale_color_manual()</code> | Manually assign colors for discrete variables. | <code>scale_color_manual(values = c("red", "blue", "green"))</code> |
| | <code>scale_fill_manual()</code> | Manually assign fill colors for discrete variables. | <code>scale_fill_manual(values = c("purple", "orange", "yellow"))</code> |
| | <code>scale_color_viridis_d()</code> | Use discrete palettes from the viridis package (colorblind-friendly). | <code>scale_color_viridis_d(option = "plasma")</code> |
| | <code>scale_fill_viridis_d()</code> | Fill discrete variables with viridis palettes. | <code>scale_fill_viridis_d(option = "cividis")</code> |

| Category | Function | Description | Example Usage |
|-------------------------|--------------------------------------|---|---|
| Continuous Color Scales | <code>scale_color_gradient()</code> | Two-color gradient for continuous variables. | <code>scale_color_gradient(low = "blue", high = "red")</code> |
| | <code>scale_fill_gradient()</code> | Two-color gradient for continuous fill variables. | <code>scale_fill_gradient(low = "green", high = "yellow")</code> |
| | <code>scale_color_gradient2()</code> | Diverging gradient with a midpoint for continuous variables. | <code>scale_color_gradient2(low = "blue", mid = "white", high = "red", midpoint = 0)</code> |
| | <code>scale_fill_gradient2()</code> | Diverging gradient with a midpoint for continuous fill variables. | <code>scale_fill_gradient2(low = "purple", mid = "gray", high = "orange", midpoint = 50)</code> |
| | <code>scale_color_gradientn()</code> | Multi-color gradient for continuous variables. | <code>scale_color_gradientn(colors = c("blue", "green", "yellow", "red"))</code> |
| | <code>scale_fill_gradientn()</code> | Multi-color gradient for continuous fill variables. | <code>scale_fill_gradientn(colors = c("lightblue", "white", "pink"))</code> |
| | <code>scale_color_viridis_c()</code> | Continuous color scales from viridis. | <code>scale_color_viridis_c(option = "magma")</code> |
| | <code>scale_fill_viridis_c()</code> | Continuous fill scales from viridis. | <code>scale_fill_viridis_c(option = "inferno")</code> |
| Axis Scales | <code>scale_x_continuous()</code> | Customize numeric X-axis with limits and breaks. | <code>scale_x_continuous(limits = c(0, 100), breaks = seq(0, 100, 10))</code> |
| | <code>scale_y_continuous()</code> | Customize numeric Y-axis with limits and labels. | <code>scale_y_continuous(labels = scales::percent_format())</code> |
| | <code>scale_x_log10()</code> | Logarithmic transformation for X-axis. | <code>scale_x_log10()</code> |
| | <code>scale_y_log10()</code> | Logarithmic transformation for Y-axis. | <code>scale_y_log10()</code> |
| | <code>scale_x_reverse()</code> | Reverse the X-axis direction. | <code>scale_x_reverse()</code> |

| Category | Function | Description | Example Usage |
|-----------------------|--------------------------------------|--|---|
| Shape and Size Scales | <code>scale_y_reverse()</code> | Reverse the Y-axis direction. | <code>scale_y_reverse()</code> |
| | <code>scale_shape_manual()</code> | Manually assign shapes to categories for points. | <code>scale_shape_manual(values = c(19, 17, 15))</code> |
| | <code>scale_size_continuous()</code> | Scale the size of points based on a continuous variable. | <code>scale_size_continuous(range = c(1, 10))</code> |
| | <code>scale_size_manual()</code> | Manually specify point sizes for categorical variables. | <code>scale_size_manual(values = c(2, 4, 6))</code> |

5.2.7 Additional Functions for Customization

- `labs()`: Adds labels for axes, title, and legend.
- `coord_flip()`: Flips X and Y axes for horizontal plots.

Labeling:

```
# labels
labs(
  title = "Plot Title",
  x = "X-Axis Label",
  y = "Y-Axis Label",
  color = "Legend Title"
)
```

```
$x
[1] "X-Axis Label"
```

```
$y
[1] "Y-Axis Label"
```

```
$colour
[1] "Legend Title"
```

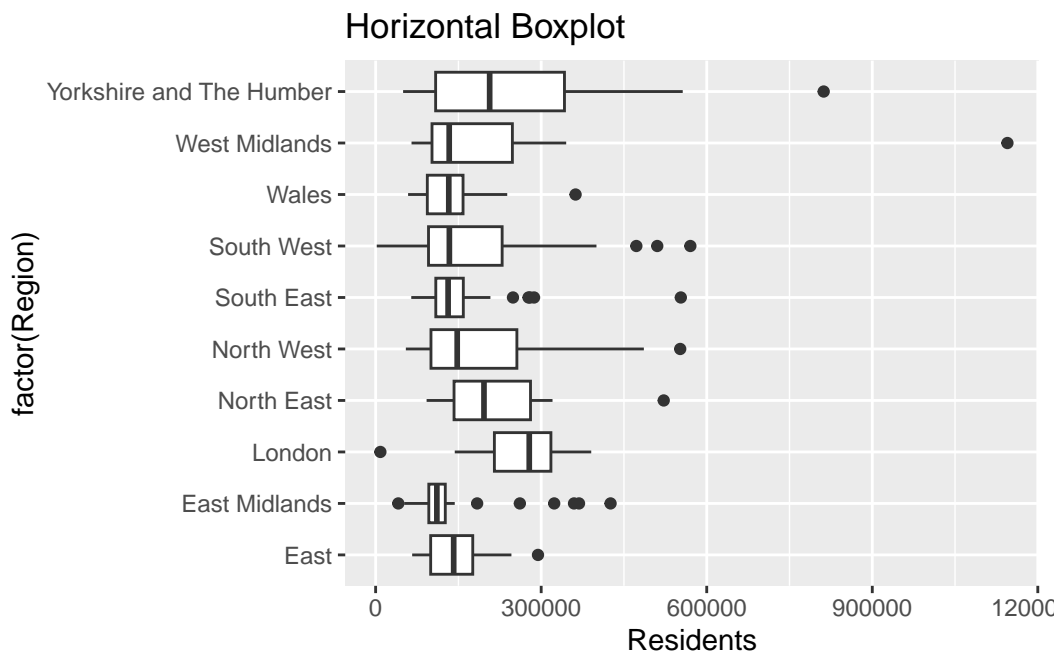
```
$title
[1] "Plot Title"
```

```
attr("class")
```

```
[1] "labels"
```

Flipping:

```
# flipping
ggplot(census_data, aes(x = factor(Region), y = Residents)) +
  geom_boxplot() +
  coord_flip() +
  labs(title = "Horizontal Boxplot")
```



Key Tips for ggplot2:

- Start with simple plots and incrementally add layers (+).
- Use themes (`theme_minimal()`, `theme_classic()`) to clean up your plots.
- Explore palettes with `RColorBrewer` or `viridis` for colorblind-friendly options.

5.3 Part 3 - Visualisation: Making decent graphs (1h)

This section demonstrates how to create **publication-quality visualisations** in R using `ggplot2`.

Learning goals Developing an understanding of, and ability to create academic standard data visualisations.

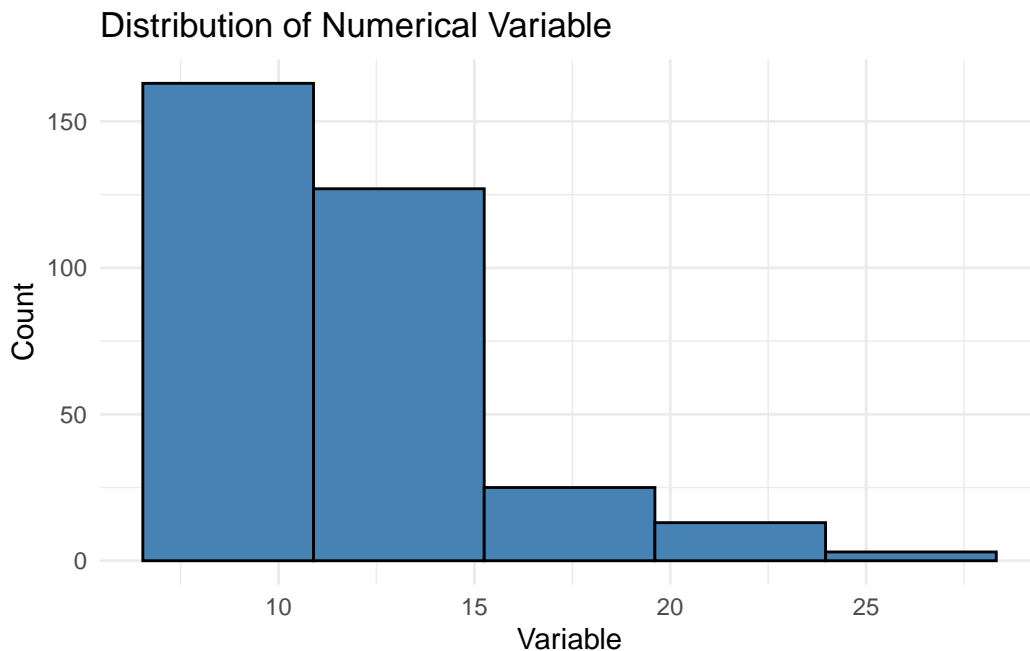
Let's load the datasets first Check the paths, you may need to remove the “.”

```
frs_data <- read.csv("../data/FamilyResourceSurvey/FRS16-17_labels.csv")
census_data <- read.csv("../data/Census2021/EW_DistrictPercentages.csv")
```

5.3.1 Distribution of 1 Numerical variable:

Histogram

```
ggplot(census_data, aes(x = pct_Age_20_to_29)) +
  geom_histogram(bins = 5, fill = "steelblue", color = "black") +
  labs(title = "Distribution of Numerical Variable", x = "Variable", y = "Count") +
  theme_minimal()
```

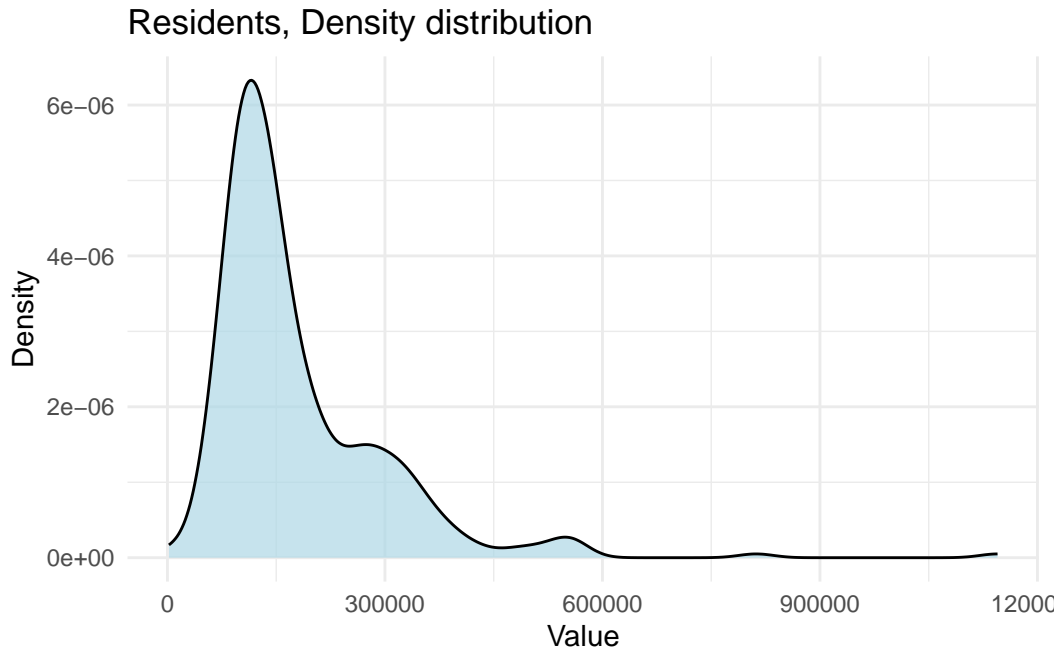


The **bins** parameter in a histogram determines the number of intervals (bins) into which the data range is divided. Each bin represents a range of values along the x-axis, and the height of each bar shows the count of observations within that range. For example, if **bins = 5**, the data is divided into five equal-width intervals. Using fewer bins results in a coarser view of the data, while more bins provide a finer, more detailed representation. However, too many bins

can make the histogram appear cluttered and difficult to interpret. The width of each bin is automatically calculated by dividing the range of the data by the number of bins.

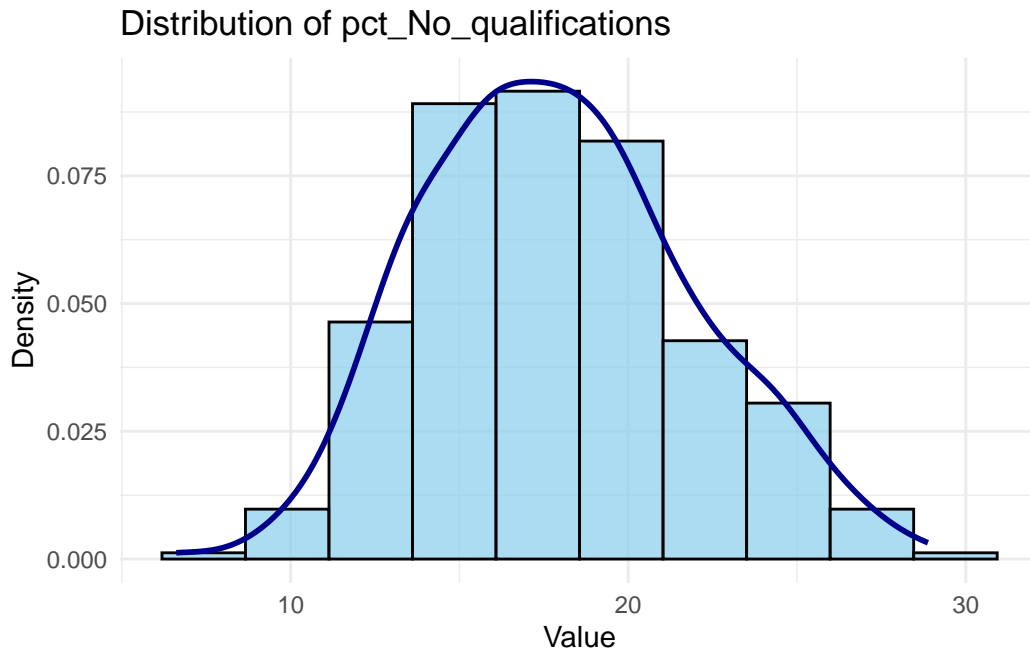
Density Plot

```
ggplot(census_data, aes(x = Residents)) +  
  geom_density(fill = "lightblue", alpha = 0.7) +  
  labs(title = "Residents, Density distribution", x = "Value", y = "Density") +  
  theme_minimal()
```



Histogram + Density Distribution

```
# Plot histogram with density overlay for a chosen variable (e.g., 'pct_No_qualifications')  
ggplot(census_data, aes(x = pct_No_qualifications)) +  
  geom_histogram(aes(y = after_stat(density)), bins = 10, color = "black", fill = "skyblue") +  
  geom_density(color = "darkblue", linewidth = 1) +  
  labs(title = "Distribution of pct_No_qualifications", x = "Value", y = "Density") +  
  theme_minimal()
```



Box Plot

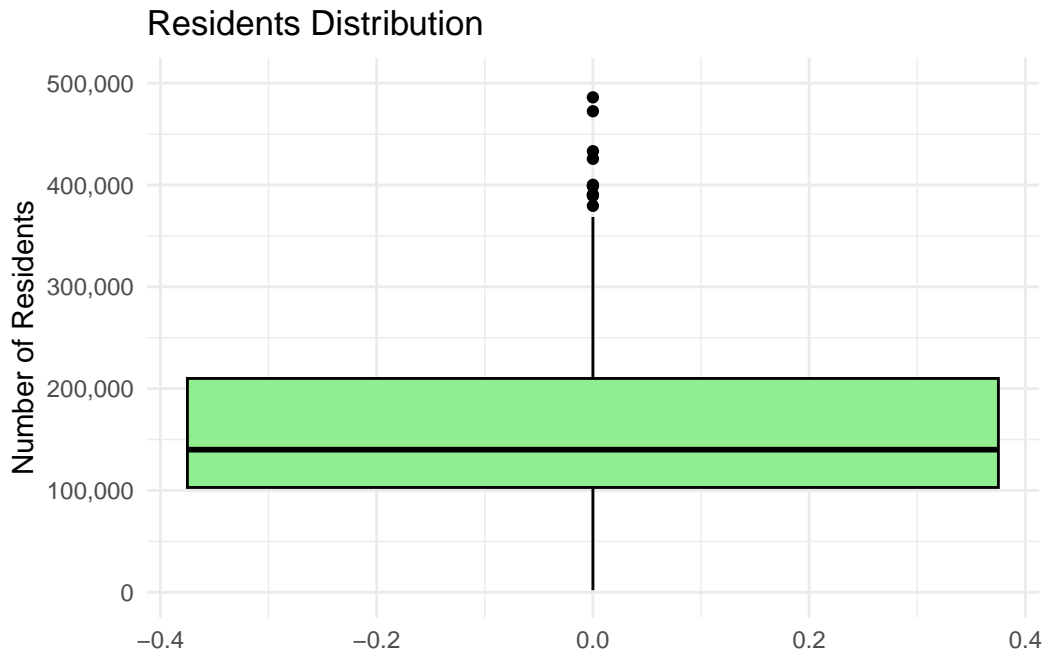
A box plot, also known as a box-and-whisker plot, is a graphical representation of the distribution of a dataset. It displays the minimum, first quartile (Q1), median (Q2), third quartile (Q3), and maximum values, with the central box representing the interquartile range (IQR) from Q1 to Q3. The whiskers extend from the box to show the range of the data, excluding outliers. Outliers are typically represented as individual points outside the whiskers.

The box plot provides a concise summary of the data distribution, highlighting the spread, center, and potential skewness.

```
library(scales) # For label_comma()

ggplot(census_data, aes(y = Residents)) +
  geom_boxplot(fill = "lightgreen", color = "black") +
  labs(title = "Residents Distribution", y = "Number of Residents") +
  theme_minimal() +
  scale_y_continuous(
    limits = c(0, 500000),
    labels = label_comma() # Properly placed within scale_y_continuous()
  )
```

Warning: Removed 9 rows containing non-finite outside the scale range (`stat_boxplot()`).



```
# Setting axis limits for better readability and applying comma-separated format to large numbers
```

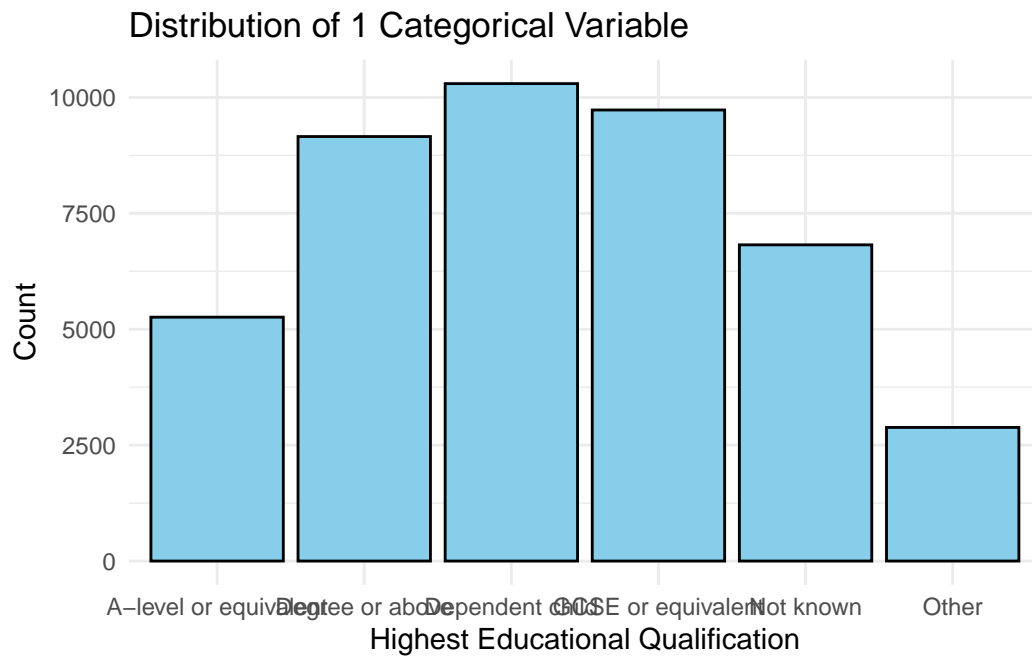
This looks kind of sad with just one variable, but it's the best way, usually, to plot distributions for numerical variables.

Notice the **outliers**. Outliers are data points that deviate significantly from the overall pattern of a dataset. They can arise due to measurement errors, variability in the data, or the presence of extreme values. Outliers can heavily influence statistical analyses, such as means or regression models, potentially leading to misleading conclusions. Identifying and addressing outliers is crucial to ensure robust and accurate results. Boxplots allow spotting them, along with interquartile range (IQR) analysis.

5.3.2 Distribution of 1 Categorical variable:

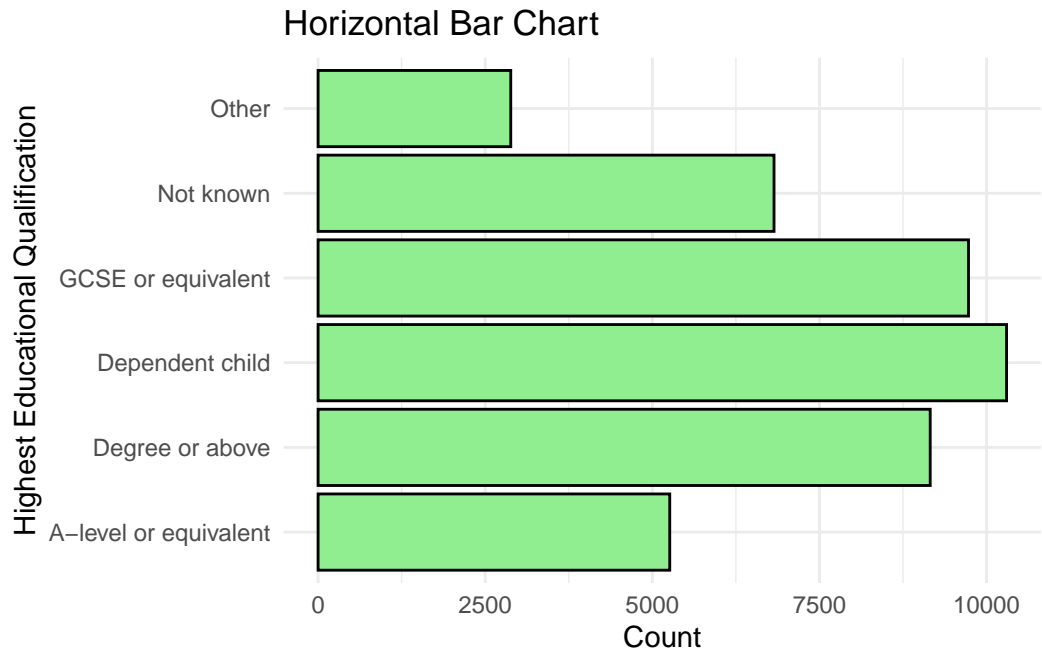
Bar Chart

```
ggplot(frs_data, aes(x = highest_qual)) +
  geom_bar(fill = "skyblue", color = "black") +
  labs(title = "Distribution of 1 Categorical Variable", x = "Highest Educational Qualification") +
  theme_minimal()
```



Horizontal Bar Chart

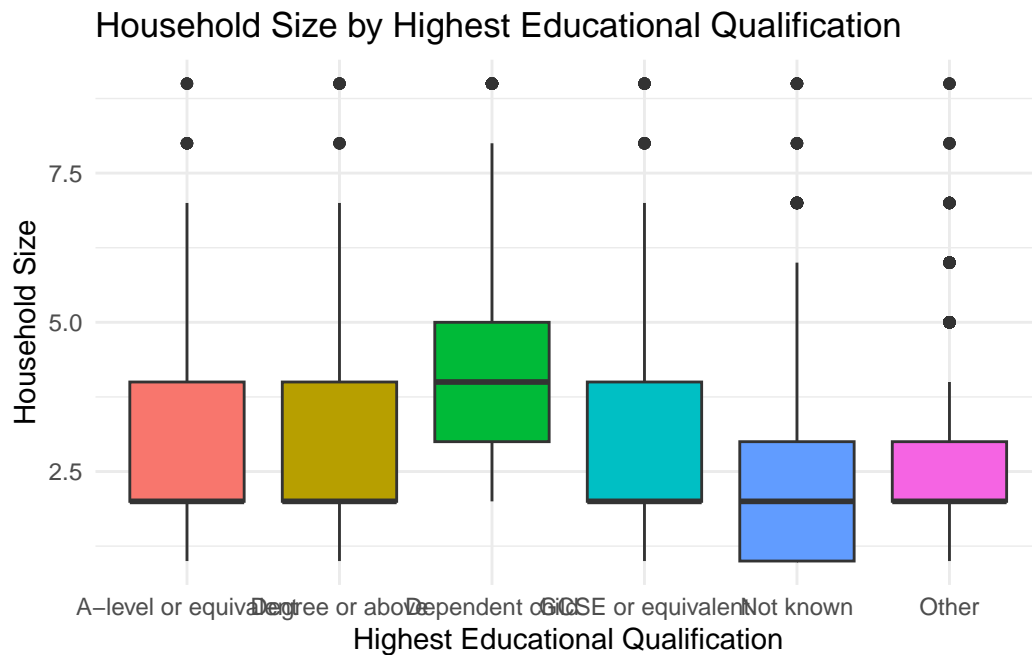
```
ggplot(frs_data, aes(x = highest_qual)) +  
  geom_bar(fill = "lightgreen", color = "black") +  
  labs(title = "Horizontal Bar Chart", x = "Highest Educational Qualification", y = "Count", )  
  coord_flip() + #just flipping  
  theme_minimal()
```



5.3.3 Comparing variables

1 numerical, 1 categorical: Boxplot

```
ggplot(frs_data, aes(x = highest_qual, y = hh_size, fill = highest_qual)) +  
  geom_boxplot() +  
  labs(  
    title = "Household Size by Highest Educational Qualification",  
    x = "Highest Educational Qualification",  
    y = "Household Size"  
  ) +  
  theme_minimal() +  
  theme(legend.position = "none") # don't need this
```



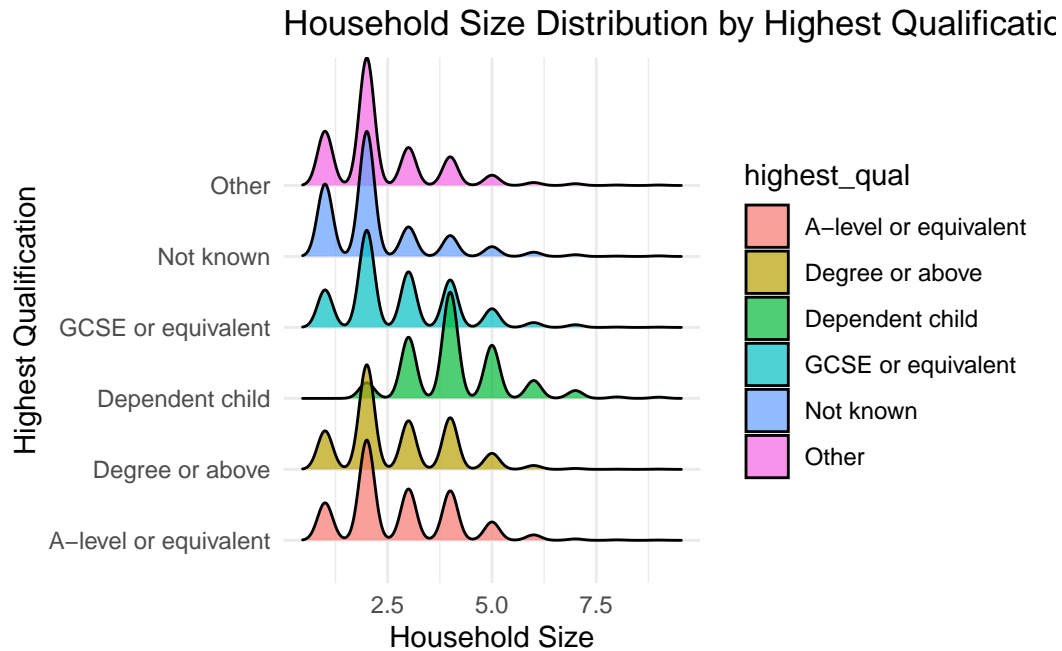
1 numerical, 1 categorical: Density Ridges

```
library(ggrridges) # need a library for this
```

Warning: package 'ggrridges' was built under R version 4.4.2

```
ggplot(frs_data, aes(x = hh_size, y = highest_qual, fill = highest_qual)) +
  geom_density_ridges(alpha = 0.7) +
  labs(
    title = "Household Size Distribution by Highest Qualification",
    x = "Household Size",
    y = "Highest Qualification"
  ) +
  theme_minimal()
```

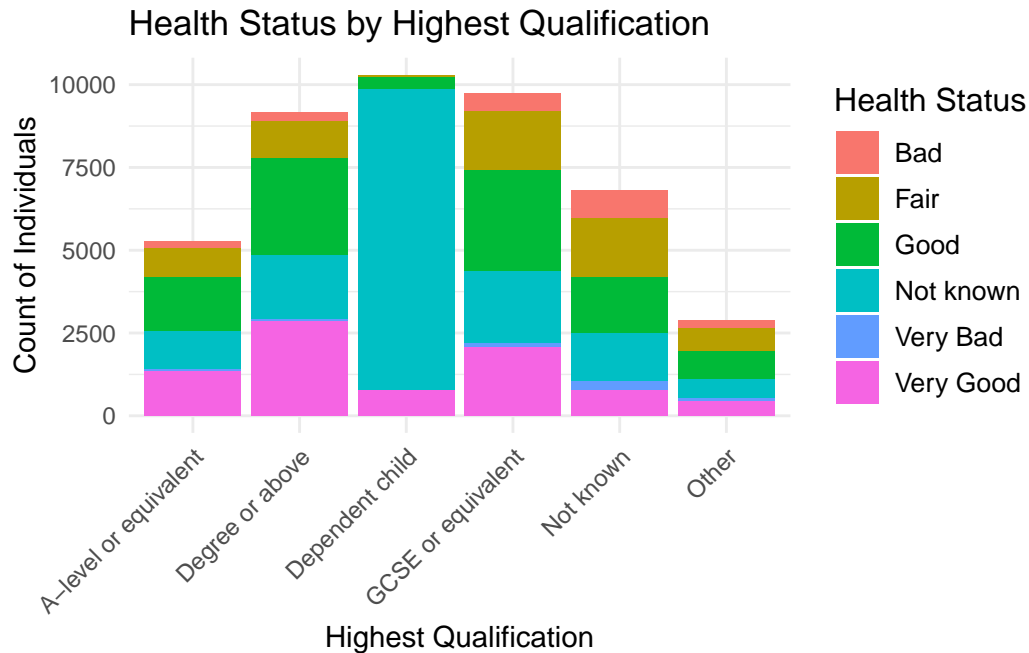
Picking joint bandwidth of 0.18



2 Categorical Variables: Stacked Bar Chart

Note the adjustments made for making the labels look better

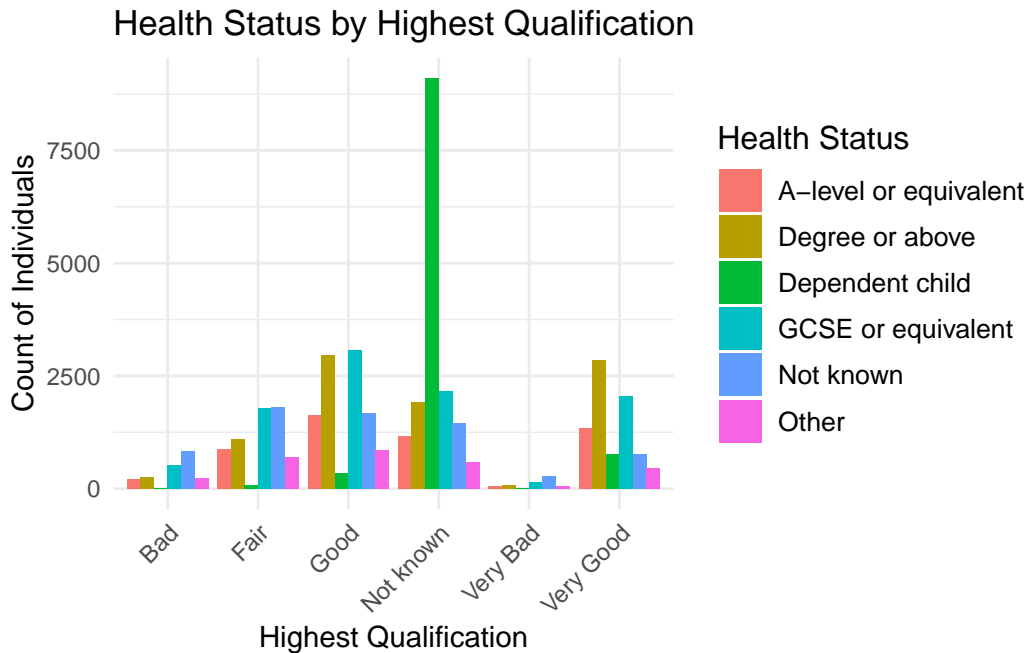
```
ggplot(frs_data, aes(x = highest_qual, fill = health)) +
  geom_bar(position = "stack") +
  labs(
    title = "Health Status by Highest Qualification",
    x = "Highest Qualification",
    y = "Count of Individuals",
    fill = "Health Status"
  ) +
  theme_minimal() +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1), # Rotate X-axis labels for readability
    legend.title = element_text(size = 12),           # Adjust legend title size
    legend.text = element_text(size = 10)             # Adjust legend text size
  )
```

Side-by-Side Bar Chart (Two-Way Frequency Distribution)

This type of chart can get messy.

```
ggplot(frs_data, aes(x = health, fill = highest_qual)) +
  geom_bar(position = "dodge") +
  labs(
    title = "Health Status by Highest Qualification",
    x = "Highest Qualification",
    y = "Count of Individuals",
    fill = "Health Status"
  ) +
  theme_minimal() +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1),
    legend.title = element_text(size = 12),
    legend.text = element_text(size = 10)
  )
```



2 Categorical Variable counts to percentages: Stacked Percentage Graph

One can also convert the counts of two categorical variables to percentages. In this case, we aim to visualise the proportional distribution of one categorical variable (**health**) across levels of another categorical variable (**highest_qual**) using a stacked percentage bar chart. First, we create a cross-tabulation to count the occurrences of each combination of Health and Qualification categories. These counts are then converted into a percentage format relative to the total counts for each Qualification category. This transformation allows us to represent the relative proportions rather than absolute counts, facilitating comparison across categories.

A *cross tabulation* (or contingency table) is a statistical tool used to analyze the relationship between two or more categorical variables. It organizes data into a table format where:

- Rows represent the categories of one variable.
- Columns represent the categories of another variable.
- Cells display the counts or frequencies of data points that fall into each combination of the row and column categories.

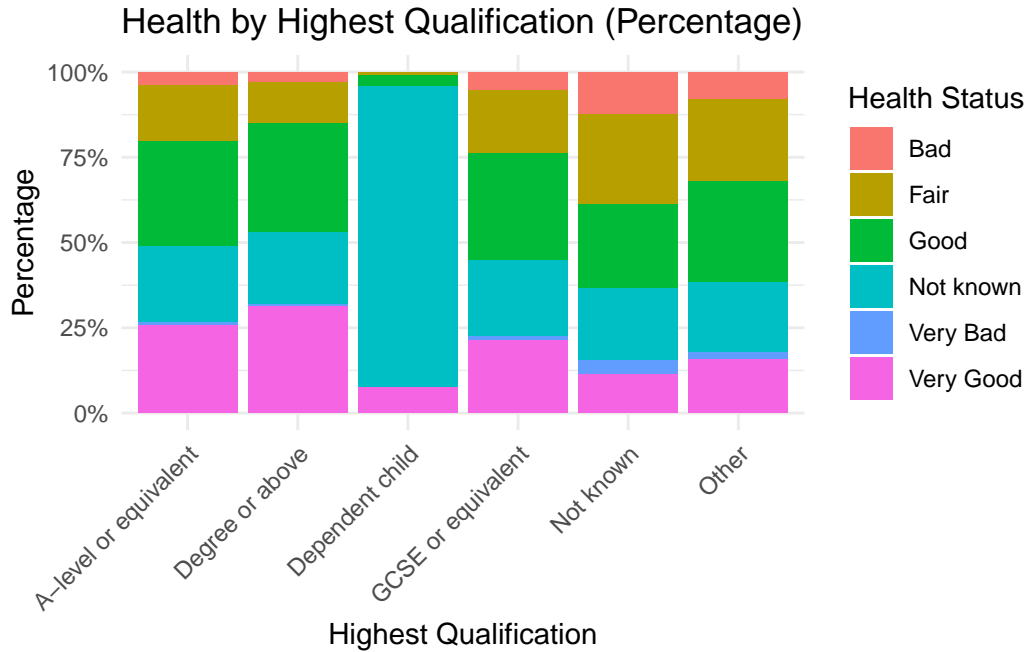
```
# Create a cross-tabulation of observed counts
cross_tab <- table(frs_data$health, frs_data$highest_qual)

# Convert the cross-tabulation to a data frame
cross_tab_df <- as.data.frame(cross_tab)
colnames(cross_tab_df) <- c("Health", "Qualification", "Percentage")
```

The data is reshaped into a data frame for compatibility with **ggplot2**, where a stacked bar

chart with percentage scaling (`position = "fill"`) is generated. The result is a plot that shows how Health statuses are distributed proportionally within each Qualification level.

```
# Create a stacked percentage bar chart
ggplot(cross_tab_df, aes(x = Qualification, y = Percentage, fill = Health)) +
  geom_bar(stat = "identity", position = "fill") +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(
    title = "Health by Highest Qualification (Percentage)",
    x = "Highest Qualification",
    y = "Percentage",
    fill = "Health Status"
  ) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



3+ Numerical Variables: Boxplot

To compare three numerical variables using boxplots in `ggplot2`, one needs to reshape the data to a long format so that each numerical variable is treated as a category in a single column.

Here's how you can do it, using `tidyverse`

```
library(tidyverse) # we need tidyverse for this
```

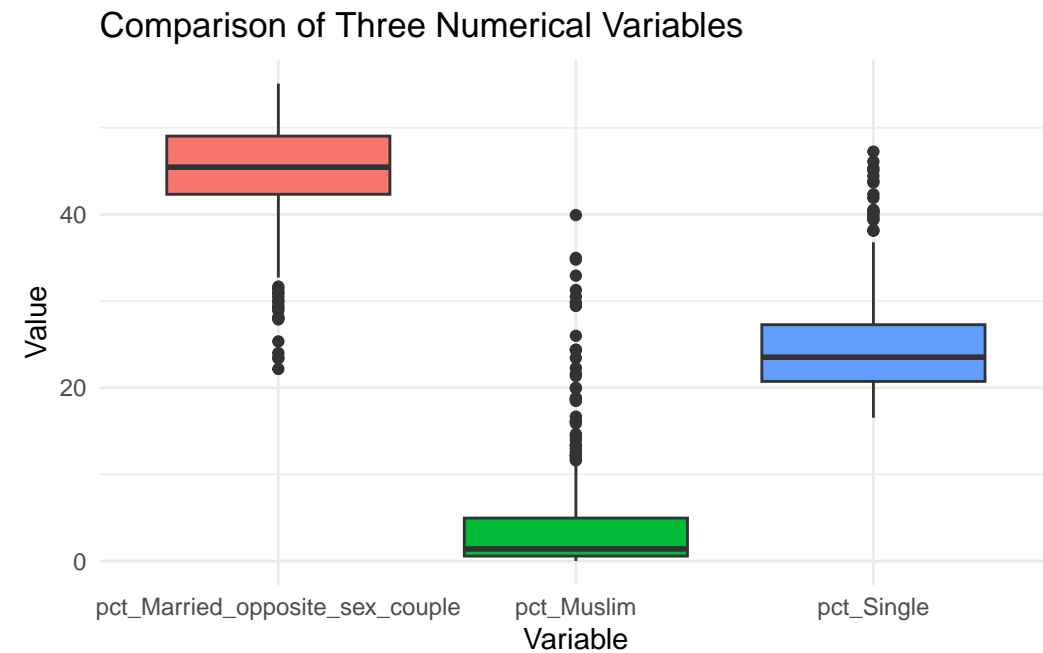
```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr      1.1.4      v readr      2.1.5
v forcats    1.0.0      v stringr    1.5.1
v lubridate  1.9.3      v tibble     3.2.1
v purrr      1.0.2      v tidyr      1.3.1
-- Conflicts ----- tidyverse_conflicts() --
```

```
x readr::col_factor() masks scales::col_factor()
x purrr::discard()     masks scales::discard()
x dplyr::filter()      masks stats::filter()
x dplyr::lag()          masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
# Reshape the data into long format
long_data <- census_data %>%
  pivot_longer(
    cols = c(pct_Single, pct_Muslim, pct_Married_opposite_sex_couple),
    names_to = "Variable",
    values_to = "Value"
  )
```

The code above reshapes the data from a wide format to a long format using the `pivot_longer()` function from the `tidyverse` package. In the original dataset, each column represents a separate variable (e.g., `pct_Single`, `pct_Muslim`, ..), and their values are stored in individual columns. The transformation collapses these columns into two new columns: one for the variable names (`Variable`) and another for their corresponding values (`Value`). This format is useful for plotting or analysis where variables are treated uniformly, such as when creating boxplots or facet grids in `ggplot2`.

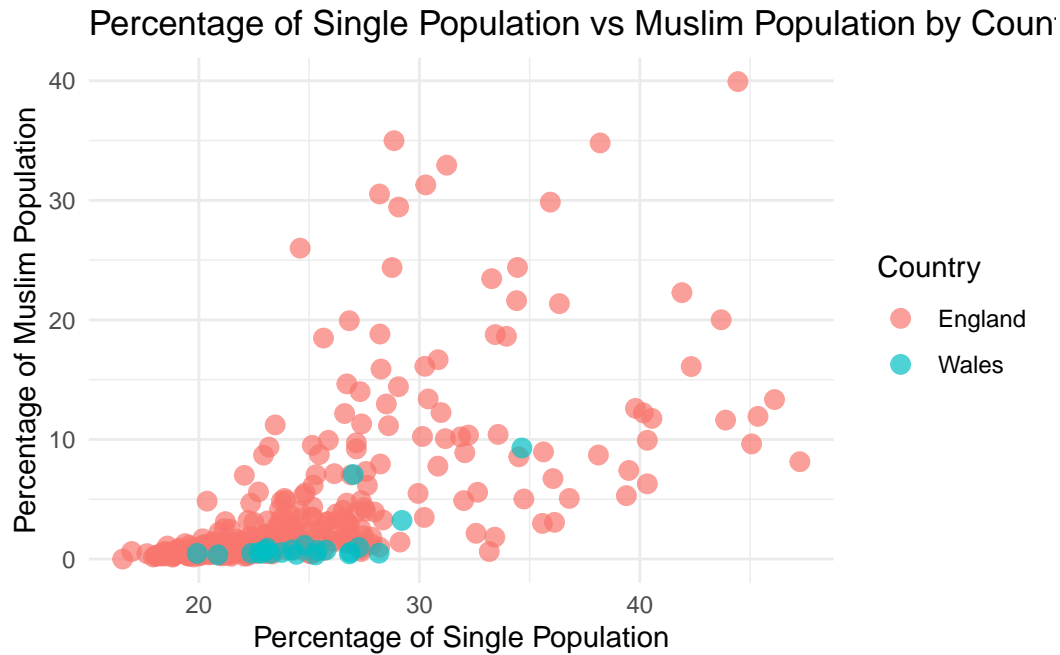
```
# Create the boxplot
ggplot(long_data, aes(x = Variable, y = Value, fill = Variable)) +
  geom_boxplot() +
  labs(
    title = "Comparison of Three Numerical Variables",
    x = "Variable",
    y = "Value"
  ) +
  theme_minimal() +
  theme(legend.position = "none")
```



5.3.4 Visualising Relationships:

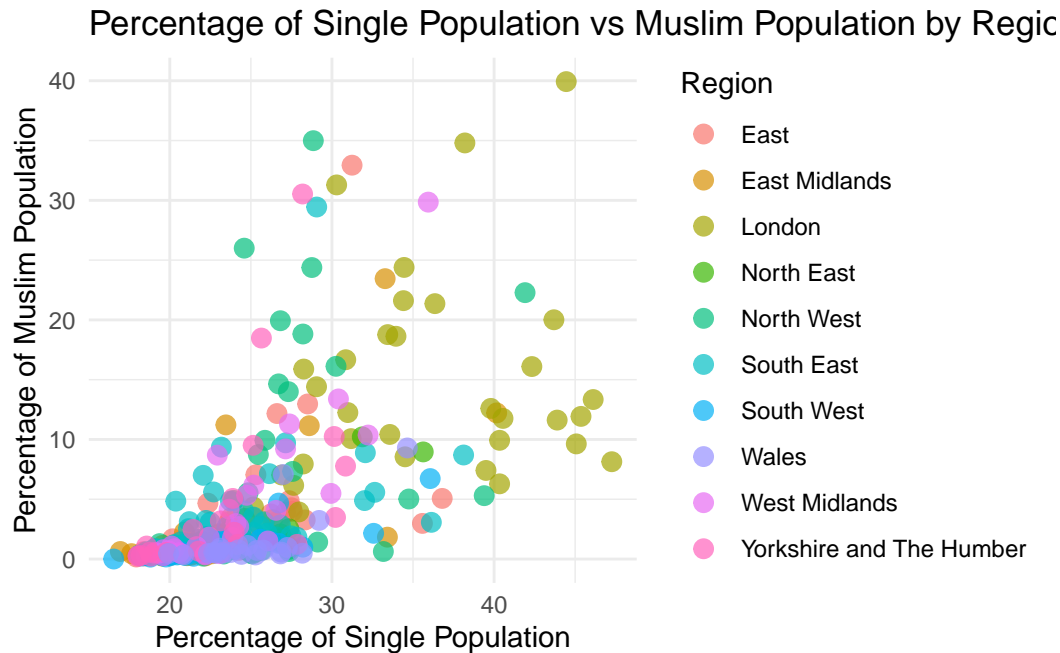
2 Numerical Variables: Scatterplot

```
ggplot(census_data, aes(x = pct_Single, y = pct_Muslim, color = factor(Country))) +
  geom_point(size = 3, alpha = 0.7) +
  labs(
    title = "Percentage of Single Population vs Muslim Population by Country",
    x = "Percentage of Single Population",
    y = "Percentage of Muslim Population",
    color = "Country"
  ) +
  theme_minimal()
```



2 Numerical Variables + 1 Catecorical: Scatterplot

```
ggplot(census_data, aes(x = pct_Single, y = pct_Muslim, color = factor(Region))) +
  geom_point(size = 3, alpha = 0.7) +
  labs(
    title = "Percentage of Single Population vs Muslim Population by Region",
    x = "Percentage of Single Population",
    y = "Percentage of Muslim Population",
    color = "Region"
  ) +
  theme_minimal()
```



3+ Numerical Variables: Correlogram

A correlogram is a visual representation of a correlation matrix, where the strength and direction of relationships between numerical variables are displayed. The matrix is typically a grid, with variables listed along both the rows and columns. Each cell in the matrix shows the correlation coefficient between two variables.

The library `corrplot` would do it for us. Check: <https://cran.r-project.org/web/packages/corrplot/vignettes/corrplot-intro.html> for deeper customisation.

In the `corrplot` package, a correlogram can use colors, shapes, or numbers to represent the correlation. For example, colors ranging from blue to red often signify negative to positive correlations, while white may indicate no correlation. Similarly, circles or other shapes can vary in size to depict the strength of the relationship. The `corrplot` function simplifies creating correlograms with customizable options. For example, using `method = "number"` places correlation coefficients in each cell, while `method = "circle"` represents correlations graphically.

Correlograms are valuable for quickly identifying patterns or strong relationships between variables, such as spotting which features might influence one another in a dataset

```
library(corrplot)
```

```
Warning: package 'corrplot' was built under R version 4.4.2
```

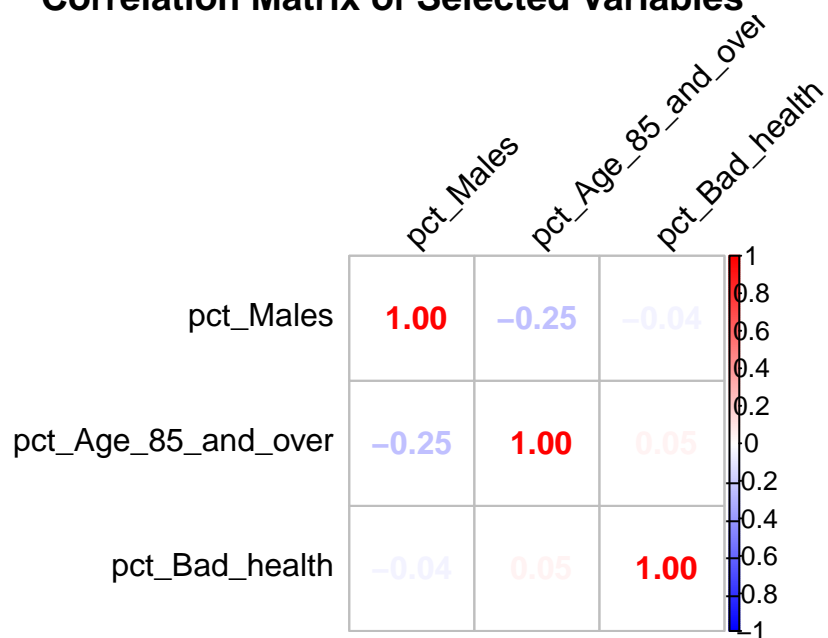
```
corrplot 0.95 loaded
```

```
# Select the necessary variables from the dataset
selected_vars <- census_data[, c("pct_Males", "pct_Age_85_and_over", "pct_Bad_health")]

# Calculate the correlation matrix
cor_matrix <- cor(selected_vars, use = "complete.obs")

# Generate the correlation plot
corrplot(cor_matrix,
  method = "number", # Display numbers
  col = colorRampPalette(c("blue", "white", "red"))(200), # Color gradient
  tl.col = "black", # Text color for labels
  tl.srt = 45, # Rotate text labels
  title = "Correlation Matrix of Selected Variables",
  mar = c(0, 0, 1, 0)) # Adjust margins
```

Correlation Matrix of Selected Variables



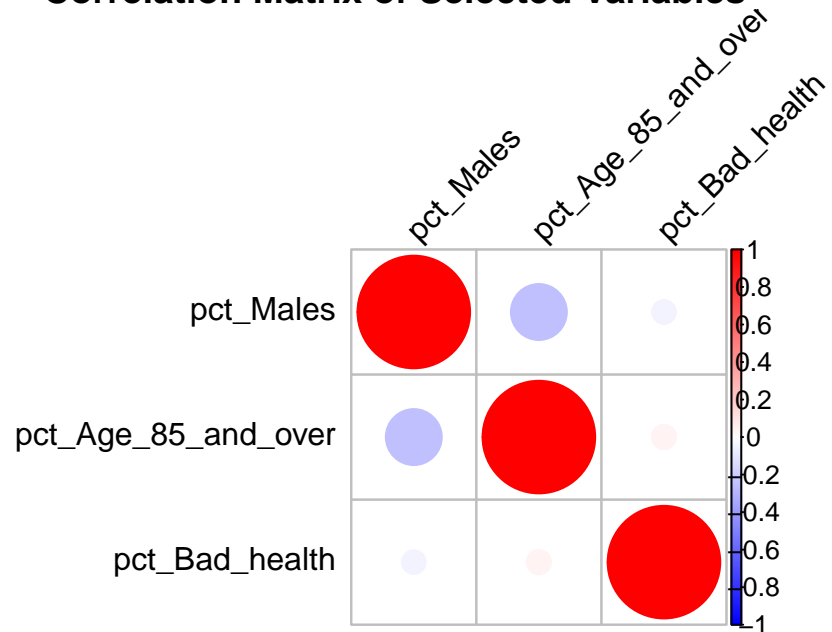
We can also include circles to graphically represent correlations.

```
# Generate the correlation plot with circles
corrplot(cor_matrix,
  method = "circle", # Display circles
  col = colorRampPalette(c("blue", "white", "red"))(200), # Color gradient
  tl.col = "black", # Text color for labels
  tl.srt = 45, # Rotate text labels
```



```
title = "Correlation Matrix of Selected Variables",
mar = c(0, 0, 1, 0)) # Adjust margins
```

Correlation Matrix of Selected Variables



3+ Numerical Variables: Scatterplot matrix

Preparation:

```
library(tidyverse)

# Select the variables
selected_vars <- census_data[, c("pct_Males", "pct_Single", "pct_Bad_health")]

# Create pairwise combinations of variable names
scatter_data <- expand_grid(
  Variable1 = names(selected_vars),
  Variable2 = names(selected_vars)
)

# Add the data values for the pairs
scatter_data <- scatter_data %>%
  rowwise() %>%
  mutate(
    Value1 = list(selected_vars[[Variable1]]), # Extract values for Variable1
```

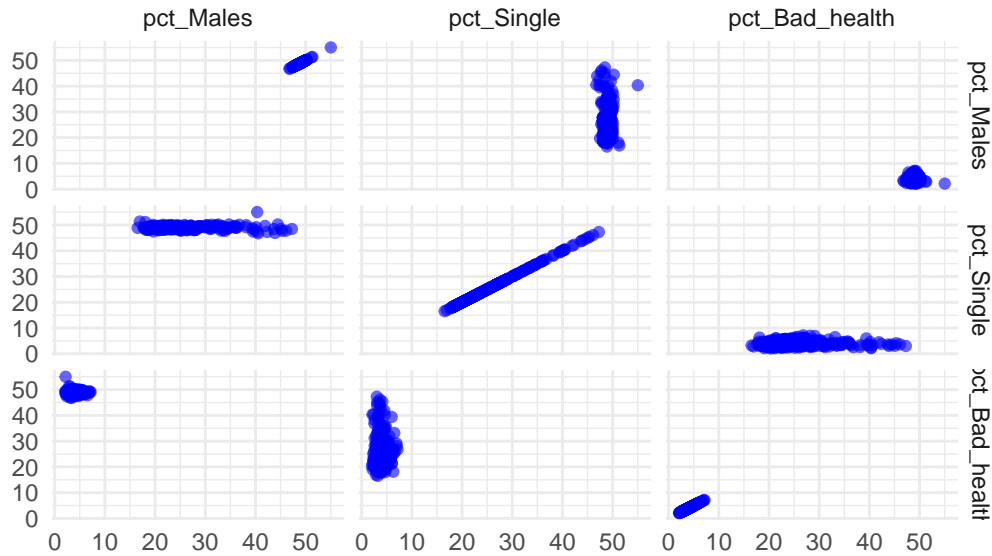
```
Value2 = list(selected_vars[[Variable2]]) # Extract values for Variable2
) %>%
unnest(c(Value1, Value2)) # Unnest the lists into rows
```

This code is used to create a dataset that facilitates generating pairwise scatterplots between selected variables from a dataset. First, it selects the variables of interest (`pct_Males`, `pct_Single`, and `pct_Bad_health`) from the `census_data` dataset and stores them in a new data frame called `selected_vars`. Then, the `expand.grid()` function is used to generate all possible combinations of these variables, resulting in a data frame with two columns, `Variable1` and `Variable2`, where each row represents a pair of variables (e.g., `pct_Males` vs `pct_Single`). Finally, the `mutate()` function is applied to map the actual values of the paired variables (`Variable1` and `Variable2`) to two new columns, `Value1` and `Value2`. These columns contain the corresponding data points for the variable pair, enabling the creation of scatterplots where `Value1` is plotted against `Value2` for each combination.

Visualisation:

```
ggplot(scatter_data, aes(x = Value1, y = Value2)) +
  geom_point(alpha = 0.6, color = "blue") +
  facet_grid(Variable1 ~ Variable2, scales = "free") +
  labs(
    title = "Correlation Matrix",
    x = "",
    y = ""
  ) +
  theme_minimal()
```

Correlation Matrix



You can also include a categorical variable through colouring. Let's try with Country.

```
# Ensure the original data includes the 'Country' variable
selected_vars <- census_data[, c("pct_Males", "pct_Single", "pct_Bad_health", "Country")]

# Create pairwise combinations of variable names (excluding 'Country')
scatter_data <- expand_grid(
  Variable1 = names(selected_vars)[-4], # Exclude 'Country'
  Variable2 = names(selected_vars)[-4]
)

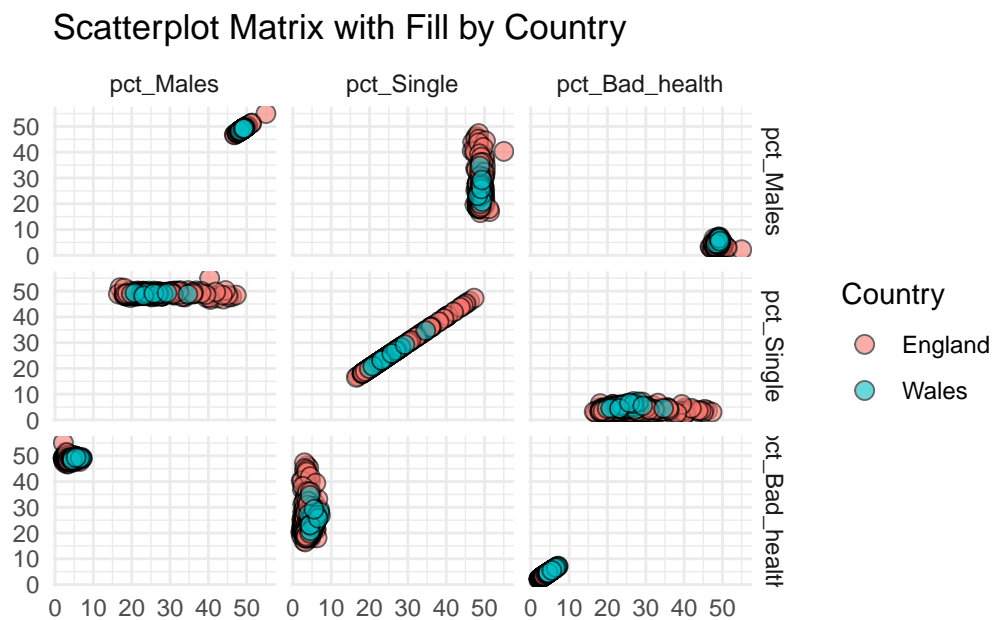
# %>% filter(Variable1 != Variable2) # Remove self-comparisons

# Add the data values for the pairs
scatter_data <- scatter_data %>%
  rowwise() %>%
  mutate(
    Value1 = list(selected_vars[[Variable1]]), # Extract values for Variable1
    Value2 = list(selected_vars[[Variable2]]), # Extract values for Variable2
    Country = list(selected_vars$Country)      # Include 'Country' in the data
  ) %>%
  unnest(c(Value1, Value2, Country)) # Unnest the lists into rows
```

Now, the scatter_data includes the Country column, which can be used to map fill in

ggplot:

```
ggplot(scatter_data, aes(x = Value1, y = Value2, fill = Country)) +
  geom_point(alpha = 0.6, shape = 21, size = 3) + # Use shape with fill (e.g., 21)
  facet_grid(Variable1 ~ Variable2, scales = "free") +
  labs(
    title = "Scatterplot Matrix with Fill by Country",
    x = "",
    y = "",
    fill = "Country"
  ) +
  theme_minimal()
```



1 Numerical Variables, 2+ Categorical Variables: Boxplot faceting

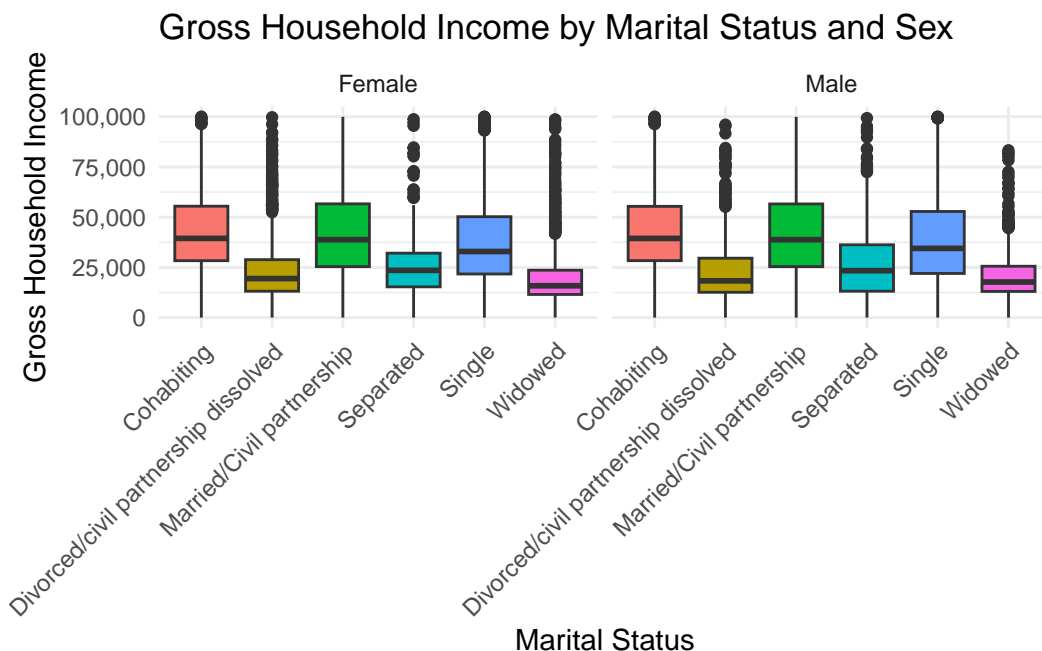
```
ggplot(frs_data, aes(x = marital_status, y = hh_income_gross, fill = marital_status)) +
  geom_boxplot() +
  facet_wrap(~ sex) +
  scale_y_continuous(
    limits = c(0, 100000), # limit the y-axis
    labels = label_comma() # Properly placed within scale_y_continuous()
  ) +
  labs(
```

```

title = "Gross Household Income by Marital Status and Sex",
x = "Marital Status",
y = "Gross Household Income"
) + # Removed 'fill' label to avoid legend creation
theme_minimal() +
theme(
  axis.text.x = element_text(angle = 45, hjust = 1), # Rotate x-axis labels for readability
  legend.position = "none" # Corrected to lowercase 'none'
)

```

Warning: Removed 2769 rows containing non-finite outside the scale range (``stat_boxplot()``).



1 Numerical Variables, 2+ Cateorical Variables: Violin Plot faceting

A violin plot combines aspects of a box plot and a density plot. It displays the distribution of a continuous variable, showing its probability density across different levels of a categorical variable. The plot consists of a vertical axis representing the variable of interest and horizontal axes that group data by categorical variables. The shape of the “violin” represents the distribution’s density, often mirrored on both sides, making it easier to see the spread and skewness of the data.

```
ggplot(frs_data, aes(x = marital_status, y = hh_income_gross, fill = marital_status)) +
  geom_violin() +
  facet_wrap(~ sex) +
  scale_y_continuous(
    limits = c(0, 100000),
    labels = label_comma() # Properly placed within scale_y_continuous()
  ) +
  labs(
    title = "Gross Household Income by Marital Status and Sex",
    x = "Marital Status",
    y = "Gross Household Income"
  ) + # Removed 'fill' label to avoid legend creation
  theme_minimal() +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1), # Rotate x-axis labels for readability
    legend.position = "none" # Corrected to lowercase 'none'
  )
)
```

Warning: Removed 2769 rows containing non-finite outside the scale range (``stat_ydensity()``).

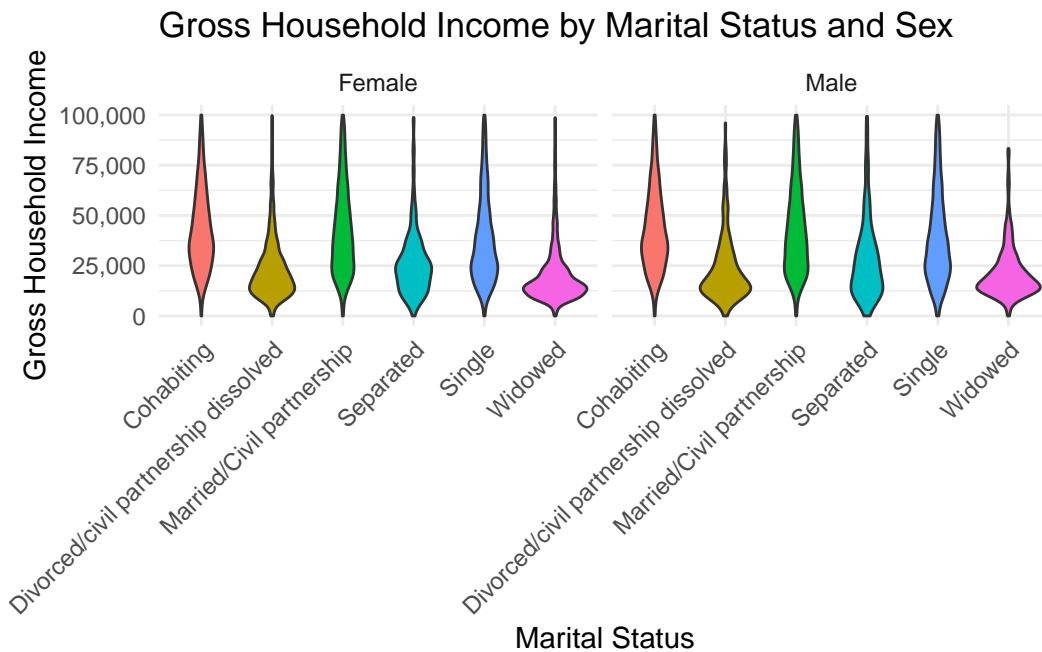


Table 5.6: Summary Statistics

| Variable | N | Mean | Std. Dev. | Min | Pctl. 25 | Pctl. 75 | Max |
|-------------------------|-----|------|-----------|------|----------|----------|-----|
| pct_Very_bad_health | 331 | 1.2 | 0.34 | 0.55 | 0.92 | 1.4 | 2.4 |
| pct_No_qualifications | 331 | 18 | 4 | 6.6 | 15 | 20 | 29 |
| pct_Males | 331 | 49 | 0.66 | 47 | 49 | 49 | 55 |
| pct_Higher_manager_prof | 331 | 13 | 4.7 | 5.5 | 9.8 | 16 | 40 |

5.4 Part 4: Publication-Ready Tables

We will be using `kableExtra` to create nicely formatted tables for a series of outputs in Rstudio:

```
library(kableExtra)
```

Warning: package 'kableExtra' was built under R version 4.4.2

Attaching package: 'kableExtra'

The following object is masked from 'package:dplyr':

```
group_rows
```

5.4.1 Summarising datasets

Only for summarising statistics we use `vtable` that makes use of `kableExtra` behind the scenes. You can use the function `st()` or `sumtable()`, they do the same thing. See <https://cran.r-project.org/web/packages/vtable/vignettes/sumtable.html>

```
library(vtable)
```

Warning: package 'vtable' was built under R version 4.4.2

```
# Generate the summary table
st(census_data, vars = c("pct_Very_bad_health", "pct_No_qualifications", "pct_Males", "pct_Higher_manager_prof"))
```

5.4.2 Creating a Well-Formatted Table from a Cross Tabulation

We can also convert a basic cross tabulation to a nice table

```
# cross tabulation
cross_tab <- table(frs_data$health, frs_data$highest_qual)

# Convert the cross-tabulation to a data frame
cross_tab_df <- as.data.frame(cross_tab)
```

This will output lots of rows, but it's just an example.

```
colnames(cross_tab_df) <- c("Health", "Qualification", "Percentage")

cross_tab_df %>%
  kbl(caption = "Health and Educational Qualification") %>%
  kable_styling(full_width = FALSE, position = "left") %>%
  add_header_above(c(" " = 1, "Highest Educational Qualification" = 2))
```

- **Rename Columns:** `colnames(cross_tab_df) <- c("Health", "Qualification", "Percentage")`. This assigns new column names to the data frame `cross_tab_df`.
- **Generate a Table with kable:** `cross_tab_df %>% kbl(caption = "Health and Educational Qualification")`. This uses the `kbl` function from the `kableExtra` package to create a basic, well-formatted table. The `caption` argument adds a title to the table: “Health and Educational Qualification.”
- **Style the Table:** `%>% kable_styling(full_width = FALSE, position = "left")`. This enhances the appearance of the table with the `kable_styling` function. `full_width = FALSE` ensures the table is not stretched to the full width of the document or webpage; `position = "left"`: Aligns the table to the left side of the page.
- **Add a Header Row:** `%>% add_header_above(c(" " = 1, "Highest Educational Qualification" = 2))` Adds an additional header row above the table; `" " = 1` the first column (“Health”) has a blank header in this new row; `"Highest Educational Qualification" = 2`: The next two columns (“Qualification” and “Percentage”) are grouped under the label “Highest Educational Qualification.”

5.4.3 Creating a Well-Formatted Table from a Cross Tabulation

Finally, we can derive a table to show the Multiple Linear Regression results.

Table 5.7: Health and Educational Qualification

| Health | Highest Educational Qualification | |
|-----------|-----------------------------------|------------|
| | Qualification | Percentage |
| Bad | A-level or equivalent | 200 |
| Fair | A-level or equivalent | 868 |
| Good | A-level or equivalent | 1626 |
| Not known | A-level or equivalent | 1163 |
| Very Bad | A-level or equivalent | 55 |
| Very Good | A-level or equivalent | 1348 |
| Bad | Degree or above | 262 |
| Fair | Degree or above | 1097 |
| Good | Degree or above | 2953 |
| Not known | Degree or above | 1923 |
| Very Bad | Degree or above | 67 |
| Very Good | Degree or above | 2854 |
| Bad | Dependent child | 22 |
| Fair | Dependent child | 67 |
| Good | Dependent child | 342 |
| Not known | Dependent child | 9100 |
| Very Bad | Dependent child | 7 |
| Very Good | Dependent child | 760 |
| Bad | GCSE or equivalent | 524 |
| Fair | GCSE or equivalent | 1785 |
| Good | GCSE or equivalent | 3061 |
| Not known | GCSE or equivalent | 2165 |
| Very Bad | GCSE or equivalent | 133 |
| Very Good | GCSE or equivalent | 2061 |
| Bad | Not known | 841 |
| Fair | Not known | 1804 |
| Good | Not known | 1674 |
| Not known | Not known | 1447 |
| Very Bad | Not known | 279 |
| Very Good | Not known | 775 |
| Bad | Other | 231 |
| Fair | Other | 696 |
| Good | Other | 854 |
| Not known | Other | 587 |
| Very Bad | Other | 64 |
| Very Good | Other | 450 |

Table 5.8: Regression Results: Predicting Very Bad Health Percentage

| Term | Coefficients | | | |
|-------------------------|--------------|------------|---------|---------|
| | Estimate | Std. Error | t Value | P Value |
| (Intercept) | 4.003 | 0.880 | 4.550 | 0.000 |
| pct_No_qualifications | 0.053 | 0.006 | 8.937 | 0.000 |
| pct_Males | -0.074 | 0.018 | -4.121 | 0.000 |
| pct_Higher_manager_prof | -0.013 | 0.005 | -2.670 | 0.008 |

```
# Load required libraries
library(broom)

# Fit the regression model
model <- lm(pct_Very_bad_health ~ pct_No_qualifications + pct_Males + pct_Higher_manager_prof,
            data = census_data)
```

Let's tidy up the regression output.

```
regression_table <- tidy(model) %>%
  select(term, estimate, std.error, statistic, p.value) %>%
  rename(
    Term = term,
    Estimate = estimate,
    `Std. Error` = std.error,
    `t value` = statistic,
    `P value` = p.value
  )
```

Create and style the regression table

```
regression_table %>%
  kbl(
    caption = "Regression Results: Predicting Very Bad Health Percentage",
    digits = 3,
    col.names = c("Term", "Estimate", "Std. Error", "t Value", "P Value")
  ) %>%
  kable_styling(full_width = FALSE, bootstrap_options = c("striped", "hover", "condensed")) %>%
  column_spec(2:5, width = "3cm") %>% # Adjust column widths
  add_header_above(c(" " = 1, "Coefficients" = 4)) # Add grouped header
```

- `kable_styling()` This function customizes the appearance of a **kable** table. The arguments used are:
 - `full_width = FALSE`: Ensures the table is not stretched to fill the entire width of the page.
 - `bootstrap_options = c("striped", "hover", "condensed")`:
 - * **striped**: Adds alternating row colors for better readability.
 - * **hover**: Highlights rows when hovered over with the mouse (for HTML tables).
 - * **condensed**: Reduces the table’s vertical spacing, making it more compact.
- `column_spec(2:5, width = "3cm")`. This function customizes specific columns of the table.
 - `2:5`: Targets columns 2 through 5 for styling.
 - `width = "3cm"`: Sets the width of these columns to 3 cm, ensuring uniform and readable column sizes.
- `add_header_above(c(" " = 1, "Coefficients" = 4))`. This function adds an additional header row above the table. This is used to customize the header of a table.
 - `" " = 1`: Leaves the first column (e.g., the Term column) without a header, spanning 1 column.
 - `"Coefficients" = 4`: This part means that columns 2, 3, 4, and 5 will be grouped together under one header, which is labeled as “Coefficients” (4 here indicates the other 4 tables). Essentially, these columns will have the same header, which makes the table more readable and organized.

Have a look here for some details on **kableExtra** <https://bookdown.org/yihui/rmarkdown-cookbook/kableextra.html>.

5.5 Part 5: Play with the code

- Experiment with different variables and aesthetics to deepen your understanding of `ggplot2`.
- Test modifying labels, themes, and colour schemes to create tailored visualisations.