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HealthyR: R for healthcare data analysis

Never trust a data scientist - they are always plotting.

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Preface

Version 0.3.1

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Why read this book

> We are drowning in information but starved for knowledge.
> John Naisbitt

In this age of information, the manipulation, analysis and interpretation of data has become paramount. Nowhere more so than in the delivery of healthcare. From the understanding of disease and the development of new treatments, to the diagnosis and management of individual patients, the use of data and technology is now an integral part of the business of healthcare.

Those working in healthcare interact daily with data, often without realising it. The conversion of this avalanche of information to

useful knowledge is essential for high quality patient care. An important part of this information revolution is the opportunity for everybody to become involved in data analysis. This democratisation of data analysis is driven in part by the open source software movement – no longer do we require expensive specialised software to do this.

The statistical programming language, R, is firmly at the heart of this!

This book will take an individual with little or no experience in data analysis all the way through to performing sophisticated analyses. We emphasise the importance of understanding the underlying data with liberal use of plotting, rather than relying on opaque and possibly poorly understand statistical tests. There are numerous examples included that can be adapted for your own data, together with our own R packages with easy-to-use functions.

We have a lot of fun teaching this course and focus on making the material as accessible as possible. We banish equations in favour of code and use examples rather than lengthy explanations. We are grateful to the many individuals and students who have helped refine these and welcome suggestions and bug reports via `https://github.com/SurgicalInformatics`.

Ewen Harrison and Riinu Ots

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Structure of the book

Chapter 2 introduces a new topic, and …

Software information and conventions

I used the **knitr** package (Xie, 2015) and the **bookdown** package (Xie, 2018) to compile my book. My R session information is shown below:

```
xfun::session_info()
```

```
## R version 3.6.0 (2019-04-26)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.6
##
## Locale: en_GB.UTF-8 / en_GB.UTF-8 / en_GB.UTF-8 / C / en_GB.UTF-
8 / en_GB.UTF-8
##
## Package version:
##   base64enc_0.1.3 bookdown_0.11   compiler_3.6.0
##   digest_0.6.20   evaluate_0.14   glue_1.3.1
##   graphics_3.6.0  grDevices_3.6.0 highr_0.8
##   htmltools_0.3.6 jsonlite_1.6    knitr_1.23
##   magrittr_1.5    markdown_1.0    methods_3.6.0
##   mime_0.7        Rcpp_1.0.1      rmarkdown_1.13
##   stats_3.6.0     stringi_1.4.3   stringr_1.4.0
##   tinytex_0.14    tools_3.6.0     utils_3.6.0
##   xfun_0.8        yaml_2.2.0
```

Package names are in bold text (e.g., **rmarkdown**), and inline code and filenames are formatted in a typewriter font (e.g., `knitr::knit('foo.Rmd')`). Function names are followed by parentheses (e.g., `bookdown::render_book()`).

Acknowledgments

A lot of people helped me when I was writing the book.

Frida Gomam
on the Mars

Installation

- Download R

https://www.r-project.org/

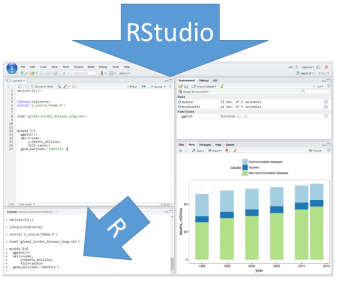
- Install RStudio

https://www.rstudio.com/products/rstudio/

- Install packages (copy these lines into the Console in RStudio):

```
install.packages("tidyverse")
install.packages("gapminder")
install.packages("gmodels")
install.packages("Hmisc")
install.packages("devtools")
devtools::install_github("ewenharrison/finalfit")
install.packages("pROC")
install.packages("survminer")
```

When working with data, don't copy or type code directly into the Console. We will only be using the Console for viewing output, warnings, and errors (and installing packages as in the previous section). All code should be in a script and executed (=Run) using Control+Enter (line or section) or Control+Shift+Enter (whole script). Make sure you are always working in a project (the right-top corner of your RStudio interface should say "HealthyR").


RStudio
R

Part I

Data wrangling and visualisation

1

Your first R plots

In this session, we will create five beautiful and colourful barplots in less than an hour. Do not worry about understanding every single word or symbol (e.g. the pipe - `%>%`) in the R code you are about to see. The purpose of this session is merely to

- gain familiarity with the RStudio interface:
  - to know what a script looks like,
  - what is the Environment tab,
  - where do your plots appear.

1.1 Data

Load the example dataset which is already saved as an R-Data file (recognisable by the file extension .rda or .RData):

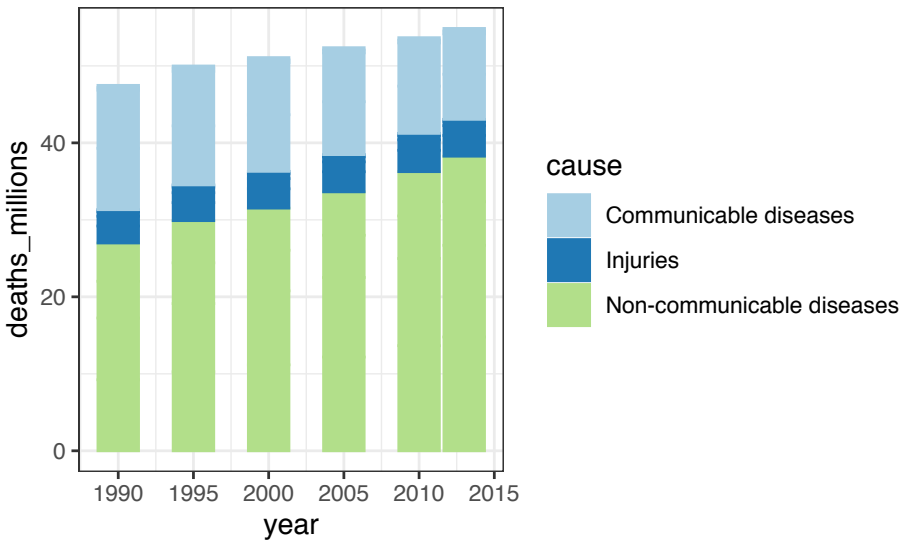
```
library(ggplot2)

source("1_source_theme.R")

load("global_burden_disease_long.rda")
```

After loading the datasets, investigate your Environment tab (top-right). You will see two things listed: `mydata` and `mydata2013`, which is a subset of mydata.

Click on the name `mydata` and it will pop up next to where your script is. Clicking on the blue button is not as useful (in this session), but it doesn't do any harm either. Try it.

1.2 First plot

```
mydata %>% #press Control-Shift-M to insert this symbol (pipe)
  ggplot(aes(x      = year,
             y      = deaths_millions,
             fill   = cause,
             colour = cause)) +
  geom_col()
```



`ggplot()` stands for **grammar of graphics plot** - a user friendly yet flexible alternative to `plot()`.

`aes()` stands for **aesthetics** - things we can see.

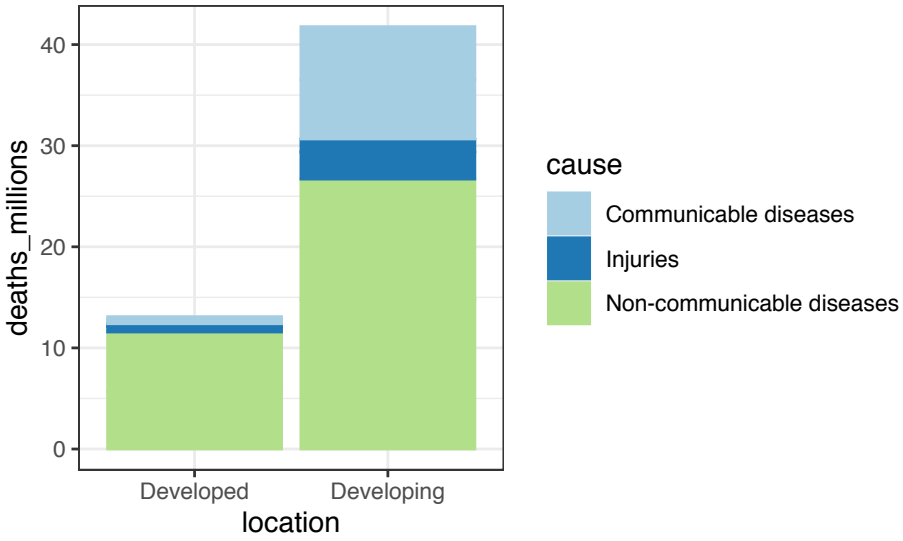
`geom_()` stands for **geometric**.

1.2.1 Question

Why are there two closing brackets - `))` - after the last aesthetic (colour)?

1.2.2 Exercise

Plot the number of deaths in Developed and Developing countries for the year 2013:

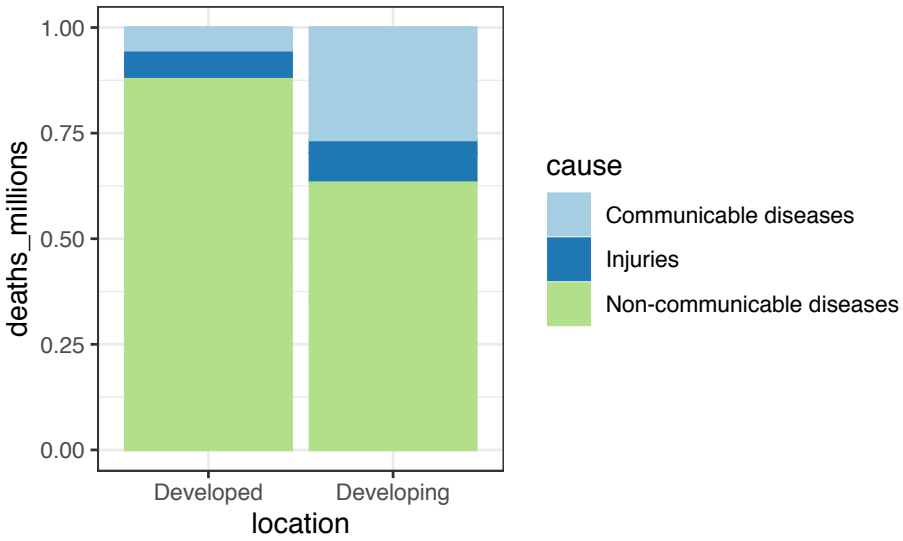


1.3 Comparing bars of different height

1.3.1 Stretch each bar to 100%

`position="fill"` stretches the bars to show relative contributions:

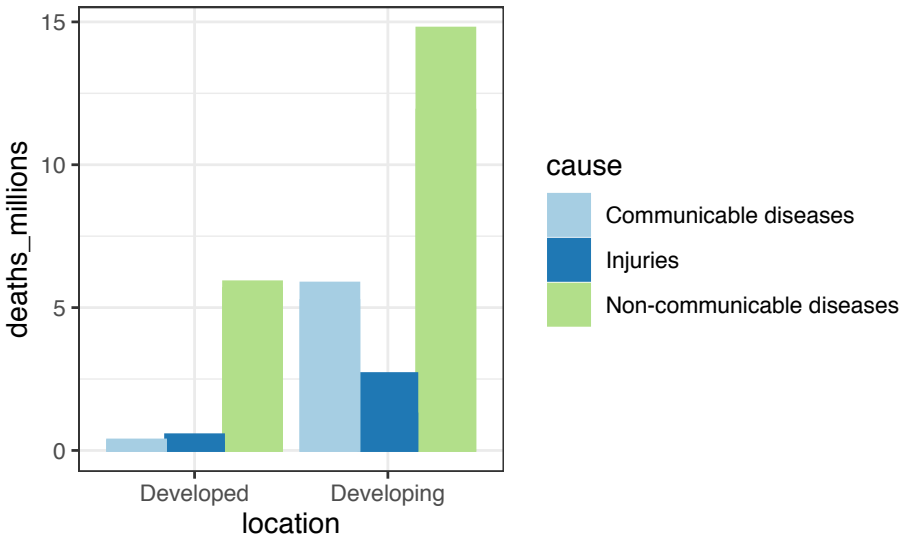
```
mydata2013 %>%
  ggplot(aes(x      = location,
             y      = deaths_millions,
             fill   = cause,
             colour = cause)) +
  geom_col(position = "fill")
```



1.3.2 Plot each bar next to each other

`position="dodge"` puts the different causes next to each rather (the default is `position="stack"`):

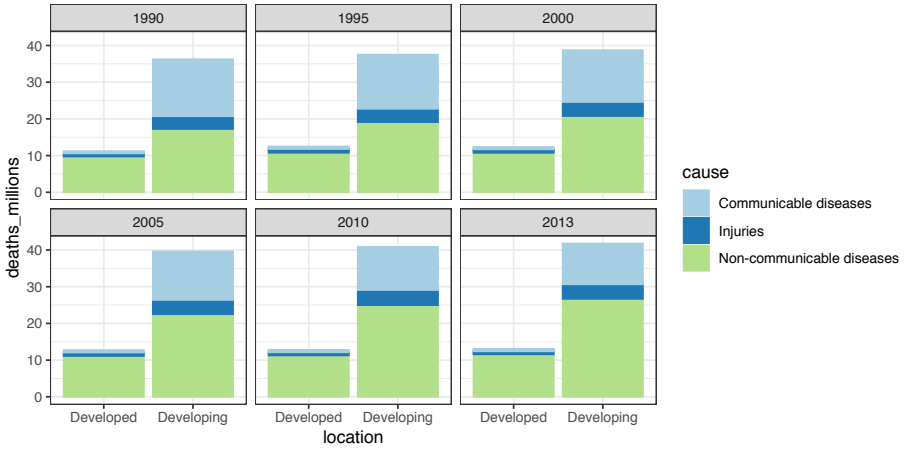
```
mydata2013 %>%
  ggplot(aes(x      = location,
             y      = deaths_millions,
             fill   = cause,
             colour = cause)) +
  geom_col(position = "dodge")
```



1.4 Facets (panels)

Going back to the dataframe with all years (1990 – 2015), add `facet_wrap(~year)` to plot all years at once:

```
mydata %>%
  ggplot(aes(x      = location,
             y      = deaths_millions,
             fill   = cause,
             colour = cause)) +
  geom_col() +
  facet_wrap(~year)
```

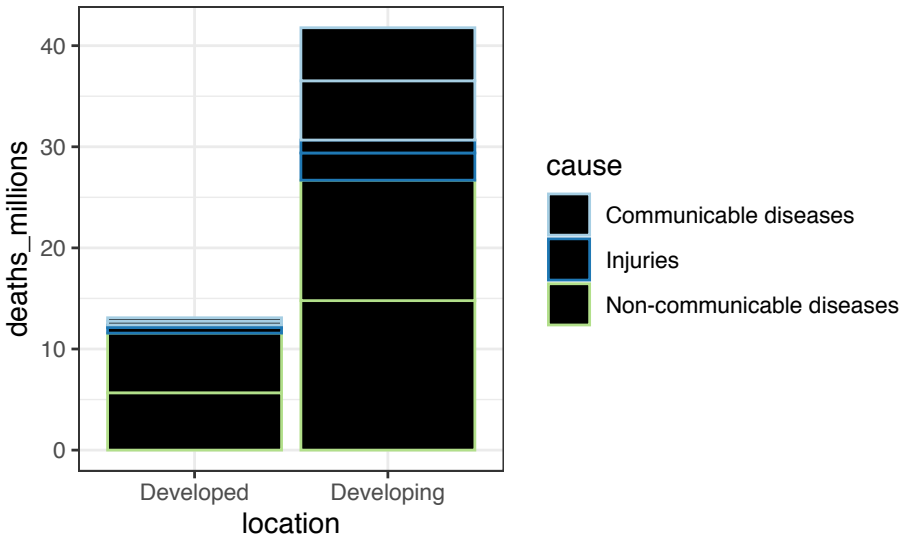


1.5 Extra: using aethetics outside of the aes()

1.5.1 Setting a constant fill

Using the `mydata2013` example again, what does the addition of `fill = "black"` in this code do? Note that putting the `ggplot(aes())` code all on one line does not affect the result.

```
mydata2013 %>%
  ggplot(aes(x = location, y = deaths_millions, fill = cause, colour = cause)) +
  geom_col(fill = "black")
```



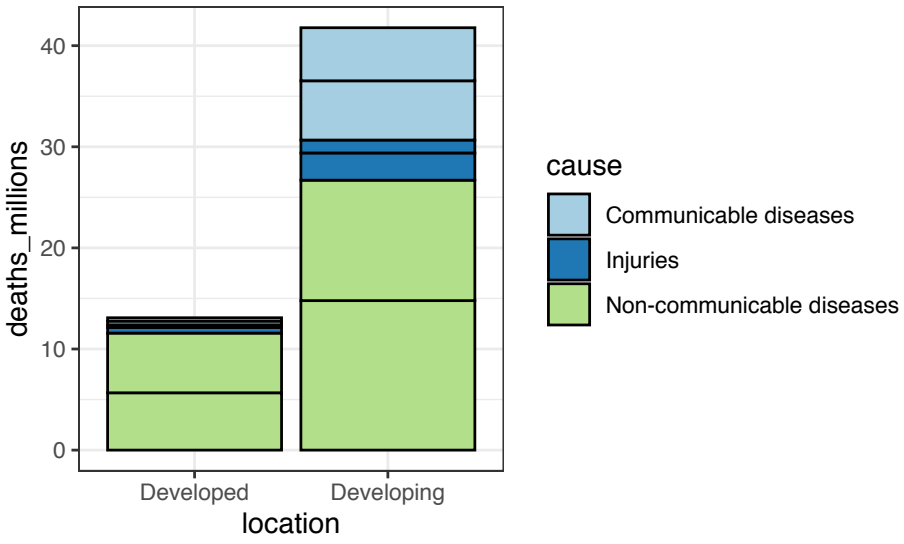
Setting aesthetics (x, y, fill, colour, etc.) outside of `aes()` sets them to a constant value. R can recognise of a lot of colour names, e.g., try "cornflowerblue", "firebrick", or just "red", "green", "blue", etc. For a full list, search Google for "Colours in R". R also knows HEX codes, e.g. `fill = "#fec3fc"` is pink.

1.5.2 Exercise

What is the difference between colour and fill in the context of a barplot?

Hint: Use `colour = "black"` instead of `fill = "black"` to investigate what `ggplot()` thinks a colour is.

```
mydata2013 %>%
  ggplot(aes(x = location, y = deaths_millions, fill = cause, colour = cause))+
  geom_col(colour = "black")
```



1.5.3 Exercise

Why are some of the words in our code quoted (e.g. `fill = "black"`) whereas others are not (e.g. `x = location`)?

1.6 Two geoms for barplots: `geom_bar()` or `geom_col()`

Both `geom_bar()` and `geom_col()` create barplots. If you:

- Want to visualise the count of different lines in a dataset - use geom_bar()
  - For example, if you are using a patient-level dataset (each line is a patient record): `mydata %>% ggplot(aes(x = sex)) + geom_bar()`
- Your dataset is already summarised - use geom_col()
  - For example, in the GBD dataset we use here, each line already includes a summarised value (`deaths_millions`)

If you have used R before you might have come across `geom_bar(stat = "identity")` which is the same as `geom_col()`.

1.7 Solutions

1.2.1: There is a double closing bracket because `aes()` is wrapped inside `ggplot()` - `ggplot(aes())`.

1.2.2:

```
mydata2013 %>%
  ggplot(aes(x      = location,
             y      = deaths_millions,
             fill   = cause,
             colour = cause)) +
  geom_col()
```

1.5.2:

On a barplot, the colour aesthetic outlines the fill. In a later session we will see, however, that for points and lines, colour is the main aesthetic to define.

1.5.3:

Words in quotes are generally something set to a constant value (e.g. make all outlines black, rather than colour them based on the cause they are representing). Unquoted words are generally variables (or functions). If the word "function" just threw you, Google "Jesse Maegan: What the h*ck is a function"

2

R Basics

The aim of this chapter is to familiarise you with how R works. We will read in data and start basic manipulations. We will be working with a shorter version of the Global Burden of Disease dataset that we met earlier.

2.1 Getting help

RStudio has a built in Help tab. To use the Help tab, click your cursor on something in your code (e.g. `read_csv()`) and press F1. This will show you the definition and some examples. However, the Help tab is only useful if you already know what you are looking for but can't remember exactly how it works. For finding help on things you have not used before, it is best to Google it. R has about 2 million users so someone somewhere has had the same question or problem.

2.2 Objects and functions

The two fundamental concepts to understand about statistical programming are objects and functions. As usual, in this book, we prefer introducing new concepts using specific examples first. And then define things in general terms after examples.

The most common data object you will be working with is a table

TABLE 2.1: Example of a table (=tibble once read into R), including missing values denoted NA (Not applicable/Not available).

id	sex	var1	var2	var3
1	Male	4	NA	2
2	Female	1	4	1
3	Female	2	5	NA
4	Male	3	NA	NA

- so something with rows and columns. It should be regular, e.g., the made-up example in Table 2.1. [1]

A table can live anywhere: on paper, in a Spreadsheet, in an SQL database, or it can live in your R Session's Environment. And yes, R sessions are as fun as they sound, almost as fun as, e.g., music sessions. We usually initiate and interface R using RStudio, but everything we talk about here (objects, functions, sessions, environment) also work when RStudio is not available, but R is. This can be the case if you are working on a supercomputer that can only serve the R Console, and not an RStudio IDE (reminder from first chapter: Integrated Development Environment). So, regularly shaped data in rows and columns is called table when it lives outside R, but once you read it into R (import it), we call it a tibble. [2] When you are in one of your very cool R sessions and read in some data, it goes into this session's Environment. Everything in your Environment needs to have a name as you can have multiple tibbles going on at the same time (`tibble` is not a name, it is the class of an object). To keep our code examples easy to follow, we call our example tibble `mydata`. In real analysis, you should give your tibbles meaningful names, e.g., `patient_data`, `lab_results`, `annual_totals`, etc.

[1] Regular does not mean it can't have missing values. Missing values are denoted `NA` which stands for either `Not available` or `Not applicable`. In same contexts, these things can have a different meaning. For example, since `var2` is `NA` for all male subjects, it may mean "Not applicable", i.e. something that can only be measured in females. Whereas in `var3`, `NA` is more likely to mean "Not available" so real missing data, e.g. lost to follow-up.

[2] There used to be an older version of tables in R - they are called data frames. In most cases, `data frames` and `tibbles` work interchangeably (and both are R objects), but `tibbles` are newer and better. Another great alternative to base R's `data frames` are `data tables`. In this book, and for most of our day-to-day work these days, we use `tibbles` though.

So, the tibble named `mydata` is example of an object that can be in the Environment of your R Session:

```
mydata
```

```
## # A tibble: 4 x 5
##      id sex     var1  var2  var3
##   <int> <chr>  <dbl> <dbl> <dbl>
## 1     1 Male       4    NA     2
## 2     2 Female     1     4     1
## 3     3 Female     2     5    NA
## 4     4 Male       3    NA    NA
```

An example of a function that can be applied on numeric data is `mean()`. R functions always have round brackets after their name. This is for two reasons. First, to easily differentiate them from objects - which don't have round brackets after their name. Second, and more important, we can put arguments in these brackets. Arguments can also be thought of as input, and in data analysis, the most common input for a function is data: we need to give `mean()` some data to average over. It does not make sense (nor will it work) to feed it the whole tibble that has multiple columns, including patient IDs and a categorical variable (`sex`). To quickly extract a single column, we use the `$` symbol like this:

```
mydata$var1
```

```
## [1] 4 1 2 3
```

You can ignore the `## [1]` at the beginning of the extracted values - this is something that becomes more useful when printing multiple lines of data as the number in the square brackets keeps count on how many values we are seeing.

We can then use `mydata$var1` as the first argument of `mean()` by putting it inside its brackets:

```
mean(mydata$var1)
```

```
## [1] 2.5
```

Which tells us that the mean of `var1` (4, 1, 2, 3) is 2.5. In this example, `mydata$var1` is the first and only argument to `mean()`. But what happens if we try to calculate the average value of `var2` (NA, 4, 5, NA)?

```
mean(mydata$var2)
```

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

We get an `NA` ("Not applicable"). We would expect to see an `NA` if we tried to, for example, calculate the average of `sex`:

```
mean(mydata$sex)
```

```
## Warning in mean.default(mydata$sex): argument is not numeric or logical:
## returning NA
```

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

In fact, in this case, R also gives us a pretty clear warning suggesting it can't compute the mean of an argument that is not numeric or logical. The sentence actually reads pretty fun, as if R was saying it was not logical to calculate the mean of something that is not numeric. But what R is actually saying that it is happy to calculate the mean of two types of variables: numerics or logicals, but what you have passed it is neither. [3]

[3]Logical is a data type with two potential values: TRUE or FALSE. We will come back to data types shortly.

So `mean(mydata$var2)` does not return an Error, but it also doesn't return the mean of the numeric values included in this column. That is because the column includes missing values (`NAs`), and R does not want to average over NAs implicitly. It is being cautious - what if you didn't know there were missing values for some patients? If you wanted to compare the means of `var1` and `var2` without any further filtering, you would be comparing samples of different size. Which might be fine if the sample sizes are sufficiently representative and the values are missing at random. Therefore, if you decide to ignore the NAs and want to calculate the mean anyway, you can do so by adding another argument to `mean()`:

```
mean(mydata$var2, na.rm = TRUE)
```

```
## [1] 4.5
```

Adding `na.rm = TRUE` tells R that you are happy for it to calculate the mean of any existing values (but to remove - `rm` - the `NA` values). This 'removal' excludes the NAs from the calculation, it does not affect the actual tibble (`mydata`) holding the dataset. R is case sensitive, so it has look exactly how the function expects it, so `na.rm`, not `NA.rm` etc. There is, however, no need to memorize how the arguments of functions are exactly spelled - this is what the Help tab (press `F1` when the cursor is on the name of the function) can remind you of. Functions' help pages are built into R, so an internet connection is not required for this.

> Make sure to separate multiple arguments with commas or R will give you an error of `Error: unexpected symbol`.

Finally, some functions do not need any arguments to work. A good example is the `Sys.time()` which returns the current time and date. This is very useful when using R to generate and update reports

automatically. Including this means you can always be clear on when the results were last updated.

```
Sys.time()
```

```
## [1] "2019-07-30 16:58:59 BST"
```

To summarise, objects and functions work hand in hand. Objects are both an input as well as the output of a function (what the function returns). The data values input into a function are usually its first argument, further arguments can be used to specify a function's behavior. When we say "the function returns", we are referring to its output (or an Error if it's one of those days). The returned object can be different to its input object. In our `mean()` examples above, the input object was a column (`mydata$var1`: 4, 1, 2, 3), whereas the output was a single value: 2.5.

2.3 Working with Objects

To create a new object into our Environment we use the equals sign:

```
a = 103
```

This reads: the variable `a` is assigned value 103. You know that the assignment worked when it shows up in the Environment tab. If we now run `a` just on its own, it gets printed back to us:

```
a
```

```
## [1] 103
```

Similarly, if we run a function without assignment to a variable, it gets printed but not saved in your Environment:

```
seq(15, 30)
```

```
##  [1] 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
```

`seq()` is a function that creates a sequence of numbers (+1 by default) between the two arguments you pass to it in its brackets. We can assign the result of `seq(15, 30)` into a variable, let's call it `example_sequence`:

```
example_sequence = seq(15, 30)
```

Doing this creates `example_sequence` in our Environment, but it does not print it.

If you save the results of an R function in a variable, it does not get printed. If you run a function without the assignment (`=`), its results get printed, but not saved in a variable.

You can call your variables (where you assigns new objects or the output of functions in) pretty much anything you want, as long as it starts with a letter. It can then include numbers as well, for example, we could have named the new variable `sequence_15_to_30`. Spaces in variable names are not easy to work with, we tend to use underscores in their place, but you could also use capitalization, e.g. `exampleSequence = seq(15, 30)`.

Finally, R doesn't mind overwriting an existing variable, for example (notice how we then include the variable on a new line to get it printed as well as overwritten):

```
example_sequence = example_sequence/2

example_sequence
```

```
##  [1]  7.5  8.0  8.5  9.0  9.5 10.0 10.5 11.0 11.5 12.0 12.5 13.0 13.5 14.0
## [15] 14.5 15.0
```

Note that many people use `<-` instead of `=`. They mean the same thing in R: both `=` and `<-` save what is on the right into the variable name on the left. There is also a left-to-right operator: `->`.

2.4 Pipe - `%>%`

The pipe - denoted `%>%` - is probably the oddest looking thing you'll see in this book. But please bear with, it is not as scary as it looks! Furthermore, it is super useful. We use the pipe to send objects into functions.

In the above examples, we calculated the mean of column `var1` from `mydata` by `mean(mydata$var1)`. With the pipe, we can rewrite this as:

```
library(tidyverse)
mydata$var1 %>% mean()
```

```
## [1] 2.5
```

Which reads: "Working with `mydata`, we select a single column called `var1` (with the `$`) **and then** calculate the `mean()`." The pipe becomes especially useful once the analysis includes multiple steps applied one after another. A good way to read and think of the pipe is **"and then"**. This piping business is not standard R functionality

and before using it in a script, you need to tell R this is what you will be doing. The pipe comes from the "magrittr" package (Figure 2.1), but loading the tidyverse will also load the pipe. So library(tidyverse) initialises everything you need (no need to include library(magrittr) explicitly).

To insert a pipe %>%, use the keyboard shortcut `Ctrl+Shift+M`.

With or without the pipe, the general rule "if the result gets printed it doesn't get saved" still applies. To save the result of the function into a new variable (so it shows up in the Environment), you need to add the name of the new variable with the assignment operator (=):

```
mean_result = mydata$var1 %>% mean()
```

FIGURE 2.1: This is not a pipe. René Magritte inspired artwork by Stefan Milton Bache (creator of %>% in R). Image source: https://cran.r-project.org/web/packages/magrittr/vignettes/magrittr.html

2.4.1 When pipe sends data to the wrong place: use `, data = .` to direct it

The pipe usually sends data to the beginning of function brackets (as most of the functions we use expect a tibble as the first argument). So `mydata %>% lm(dependent~explanatory)` is equivalent to `lm(mydata, dependent~explanatory)` (`lm()` stands for linear model introduced in detail in Chapter 7: linear regression). However, tibble first is not the order the `lm()` function expects. `lm()` wants us to specify the variables first (`dependent~explanatory`), and then wants the tibble these columns are in. So we have to use the `.` to tell the pipe to send the data to the second argument of `lm()`, not the first, e.g.

```
mydata %>%
  lm(var1~var2, data = .)
```

2.5 Reading data into R

We mentioned before that once a table (e.g. from spreadsheet or database) gets read into R we start calling it a `tibble`. The most common format data comes to us in is CSV (comma separated values). CSV is basically an uncomplicated spreadsheet with no formatting or objects other than a single table with rows and columns (no worksheets or formulas). Furthermore, you don't need special software to quickly view a CSV file - a text editor will do, and that includes RStudio.

For example, look at "example_data.csv" in the healthyr project's folder in Figure 2.2 (this is the Files pane at the bottom-right corner of your RStudio).

Clicking on a data file gives us two options: `View File` or `Import Dataset`. For very standard CSV files, we don't usually bother with the Import interface and just type in (or copy from a previous script):

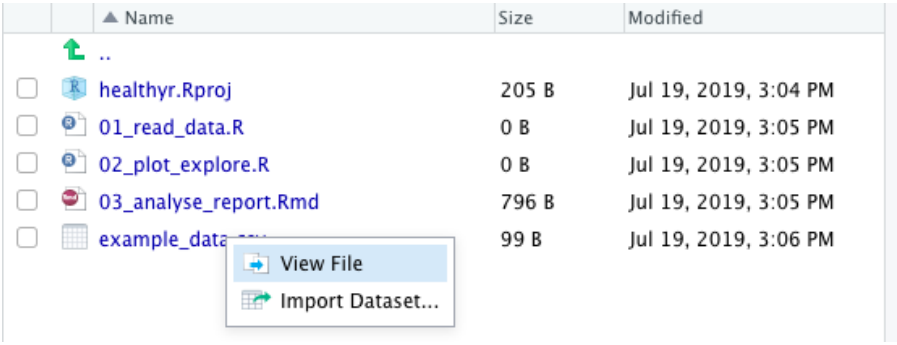


FIGURE 2.2: View or import a data file.

```
library(tidyverse)
example_data = read_csv("example_data.csv")
```

Without further arguments, `read_csv()` defaults to:

- values are delimited by commas (e.g., `id, var1, var2, ...`)
- numbers use decimal point (e.g., `4.12`), rather than decimal comma (e.g., `4,12`)
- the first line has column names (it is a "header")
- missing values are empty or denoted NA

If your file, however, is different to these, then the `Import Dataset` interface (Figure 2.2) is very useful as it will give you the relevant `read_()` syntax with all the extra arguments filled in for you.

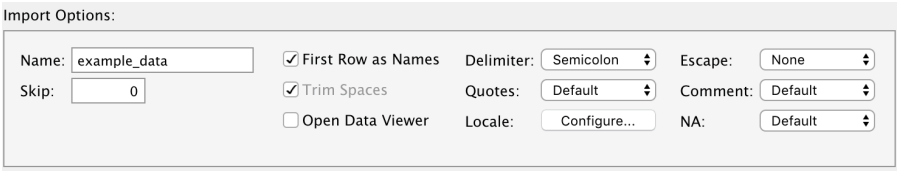


FIGURE 2.3: Import: Some of the special settings your data file might have.

After selecting the specific options for your import file (there is a friendly preview window too, so you can immediately see whether

Code Preview:

```
library(readr)
example_data <- read_delim("example_data.csv",
    ";",
    escape_double = FALSE,
    locale = locale(decimal_mark = ","),
    trim_ws = TRUE)
```

FIGURE 2.4: After using the Import Dataset window, copy-paste the resulting code into your script.

R understands the format of the your data file), DO NOT BE tempted to press the `Import` button. Yes, this will read in your dataset once, but means you have to redo the selections every time you come back to RStudio. Do copy-paste the code it gives you (e.g., Figure 2.4) into your R script - this way you can use it over and over again. Making sure all steps are recorded in scripts makes your workflow reproducible by your future self, colleagues, supervisors, extraterrestrials.

The `Import Dataset` button can also help you to read in Excel, SPSS, Stata, or SAS files (instead of `read_csv()`, it will give you `read_excel()`, `read_sav()`, `read_stata()`, or `read_sas()`).

If you've used R before or are trying to make sense of legacy scripts passed on to you by colleagues, you might see `read.csv()` rather than `read_csv()`. In short: `read_csv()` is faster and better, and in all new scripts that's what you should use. But in existing scripts that work and are tested, do not just start replacing `read.csv()` with `read_csv()`. The thing is, `read_csv()` handles categorical variables slightly differently [4]. This means that an R script written using the `read.csv()` might not work as expected any more if just replaced with `read_csv()`.

[4] It does not silently convert strings to factors, i.e., it defaults to `stringsAsFactors = FALSE`. For those not familiar with the terminology here - don't worry, we will cover this in just a few sections.

> Do not start updating and possibly breaking existing R scripts by replacing base R functions with the tidyverse ones we show here. Do use the modern functions in any new code you write.

2.5.1 Reading in the Global Burden of Disease example dataset (short version)

In the next few chapters of this book, we will be using the Global Burden of Disease datasets. The Global Burden of Disease Study (GBD) is the most comprehensive worldwide observational epidemiological study to date. It describes mortality and morbidity from major diseases, injuries and risk factors to health at global, national and regional levels. [5]

GBD data are publicly available from their website. Table 2.2 and Figure 2.5 show a very high level version of the project's data with just 3 variables: cause, year, deaths (number of people who die of each cause every year). Later, we will be using a longer dataset with different subgroups and we will show you how to summarise comprehensive datasets yourself.

```
library(tidyverse)
gbd_short = read_csv("data/global_burden_disease_SHORT.csv")
```

```
## Warning: Unknown or uninitialised column: 'year'.
```

[5] Global Burden of Disease Collaborative Network. Global Burden of Disease Study 2017 (GBD 2017) Results. Seattle, United States: Institute for Health Metrics and Evaluation (IHME), 2018. Available from http://ghdx.healthdata.org/gbd-results-tool.

TABLE 2.2: Deaths per year from three broad disease categories (short version of the Global Burden of Disease example dataset).

cause	year	deaths
Communicable diseases	1990	15,392,200
Injuries	1990	4,260,493
Non-communicable diseases	1990	26,825,621
Communicable diseases	1995	15,132,654
Injuries	1995	4,543,803
Non-communicable diseases	1995	29,407,049
Communicable diseases	2000	14,835,531
Injuries	2000	4,568,246
Non-communicable diseases	2000	31,138,228
Communicable diseases	2005	13,906,587
Injuries	2005	4,500,881
Non-communicable diseases	2005	33,015,795
Communicable diseases	2010	12,528,020
Injuries	2010	4,718,076
Non-communicable diseases	2010	35,592,216
Communicable diseases	2015	10,882,449
Injuries	2015	4,486,745
Non-communicable diseases	2015	39,452,999
Communicable diseases	2017	10,389,874
Injuries	2017	4,484,722
Non-communicable diseases	2017	41,071,133

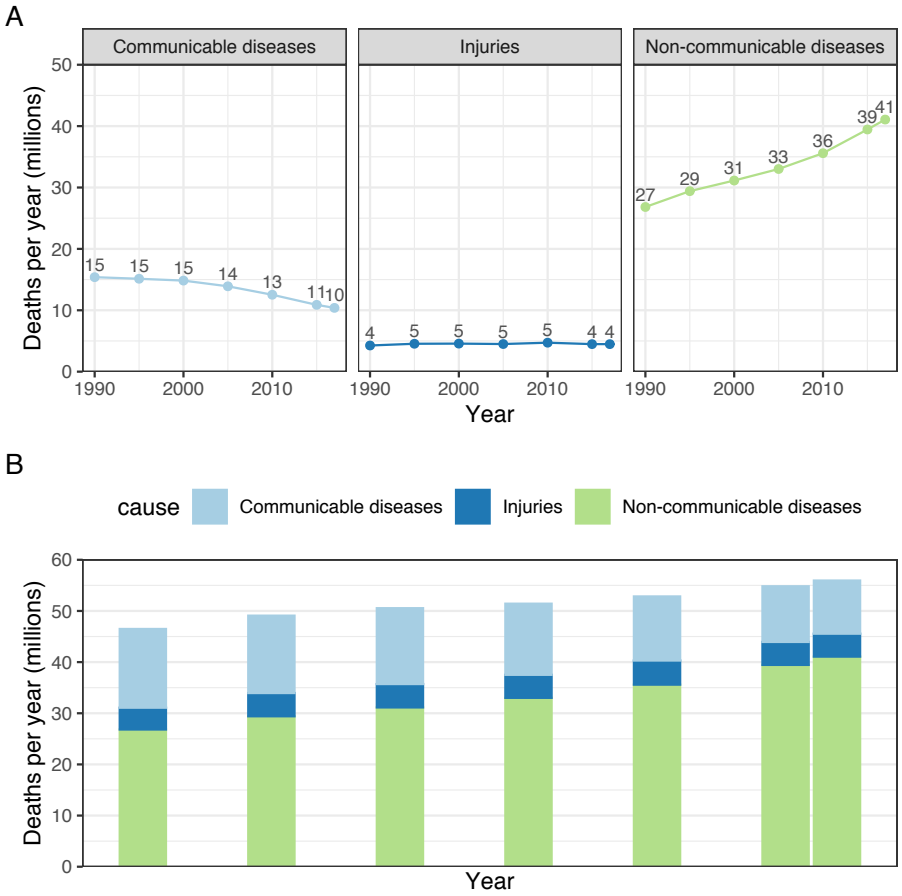


FIGURE 2.5: Causes of death from the Global Burden of Disease dataset (Table 2.2). Data on (B) is the same as (A) but stacked to show the total (sum) of all causes.

2.6 Operators for filtering data

Operators are symbols that tell R how to handle different pieces of data or objects. We have already introduced three: `$` (selects a column), `=` (assigns values or results to a variable), and the pipe - `%>%` (sends data into a function).

Other common operators are the ones we use for filtering data - these are called comparison and logical operators. This may be for creating subgroups, or for excluding outliers or incomplete cases.

The comparison operators that work with numeric data are relatively straightforward: `>`, `<`, `>=`, `<=`. The first two check whether your values are greater or less than another value, the last two check for "greater than or equal to" and "less than or equal to. These operators are most commonly spotted inside the `filter()` function:

```
gbd_short %>%
  filter(year < 1995)
```

```
## # A tibble: 3 x 3
##   cause                       year   deaths
##   <chr>                      <dbl>    <dbl>
## 1 Communicable diseases       1990 15392200
## 2 Injuries                    1990  4260493
## 3 Non-communicable diseases   1990 26825621
```

Here we send the data (`gbd_short`) to the `filter()` and ask it to retain all years that are less than 1995. The resulting tibble only includes the year 1990. Now, if we use the `<=` (less than or equal to) operator, both 1990 and 1995 pass the filter:

```
gbd_short %>%
  filter(year <= 1995)
```

```
## # A tibble: 6 x 3
##   cause                      year   deaths
##   <chr>                     <dbl>    <dbl>
## 1 Communicable diseases      1990 15392200
## 2 Injuries                   1990  4260493
## 3 Non-communicable diseases  1990 26825621
## 4 Communicable diseases      1995 15132654
## 5 Injuries                   1995  4543803
## 6 Non-communicable diseases  1995 29407049
```

Furthermore, the values either side of the operator could both be variables, e.g., `mydata %>% filter(var2 > var1)`.

To filter for values that are equal to something, we use the `==` operator. For example, the first filtering example was actually equivalent to:

```
gbd_short %>%
  filter(year == 1995)
```

```
## # A tibble: 3 x 3
##   cause                      year   deaths
##   <chr>                     <dbl>    <dbl>
## 1 Communicable diseases      1995 15132654
## 2 Injuries                   1995  4543803
## 3 Non-communicable diseases  1995 29407049
```

Accidentally using the single equals (`=` so the assignment operator) is a very common mistake and still occasionally happens to the best of us. In fact, it happens so often that the error the `filter()` function gives when using the wrong one also reminds us what the correct one was

```
gbd_short %>%
  filter(year = 1995)
```

```
## `year` (`year = 1995`) must not be named, do you need `==`?
```

> The answer to 'do you need ==?" is almost always "Yes R, I do, thank you".

But that's just because `filter()` is a clever cookie and used to this very common mistake. There are other useful functions we use these operators in, but they don't always know to tell us that we've just confused `=` for `==`. So whenever checking for equality of variables but the result is not what you expect (you'll get an Error, but not necessary with the same wording as above), remember to check your `==` operators first.

R also has two operators for combining multiple comparisons: & and |, which stand for AND and OR, respectively. For example, we can filter to only keep the earliest and latest years in the dataset:

```
gbd_short %>%
  filter(year == 1995 | year == 2017)
```

```
## # A tibble: 6 x 3
##   cause                      year   deaths
##   <chr>                     <dbl>    <dbl>
## 1 Communicable diseases      1995 15132654
## 2 Injuries                   1995  4543803
## 3 Non-communicable diseases  1995 29407049
## 4 Communicable diseases      2017 10389874
## 5 Injuries                   2017  4484722
## 6 Non-communicable diseases  2017 41071133
```

This reads: take the GBD dataset, send it to the filter to keep rows where year is equal to 1995 or year is equal to 2017. Using specific values like we've done there (1995/2017) is called "hard-coding", which is fine if we know for sure we don't want to apply the same script on an updated dataset. But a cleverer way of achieving the same thing is to use the `min()` and `max()` functions:

TABLE 2.3: Filtering operators.

Operators	Meaning
==	Equal to
!=	Not equal to
<	Less than
>	Greater than
<=	Less than or equal to
>=	Greater then or equal to
&	AND
|	OR

```
gbd_short %>%
  filter(year == max(year) | year == min(year))
```

```
## # A tibble: 6 x 3
##   cause                      year   deaths
##   <chr>                     <dbl>    <dbl>
## 1 Communicable diseases      1990 15392200
## 2 Injuries                   1990  4260493
## 3 Non-communicable diseases  1990 26825621
## 4 Communicable diseases      2017 10389874
## 5 Injuries                   2017  4484722
## 6 Non-communicable diseases  2017 41071133
```

2.6.1 Worked examples

Filter the dataset to only include the year 2000. Save this in a new variable using the assignment operator.

```
mydata_year2000 = gbd_short %>%
  filter(year == 2000)
```

Let's practice combining multiple selections together.

Reminder: '|' means OR and '&' means AND.

From `gbd_short`, select the lines where year is either 1990 or 2017 and cause is "Communicable diseases":

```
new_data_selection = gbd_short %>%
  filter((year == 1990 | year == 2013) & cause == "Communicable diseases")

# Or we can get rid of the extra brackets around the years
# by moving cause into a new filter on a new line:

new_data_selection = gbd_short %>%
  filter(year == 1990 | year == 2013) %>%
  filter(cause == "Communicable diseases")
```

The hash symbol (`#`) is used to add free text comments to R code. R will not try to run these lines, they will be ignored. Comments are an essential part of any programming code - these are notes for your future self on what and why you did.

2.7 The combine function: c()

The combine function is used to list several values. It is especially useful together with the `%in%` operator which can be used to filter for multiple values. Remember how the gbd_short cause column had three different causes in it:

```
gbd_short$cause %>% unique()
```

```
## [1] "Communicable diseases"     "Injuries"
## [3] "Non-communicable diseases"
```

Say we wanted to filter for communicable and non-communicable diseases. [6] We could use the OR operator - `|` like this:

[6] In this example, it would just be easier to filter(cause `!=` "Injuries") but imagine your column had more than just three different values in it.

```
gbd_short %>%
  # also filtering for a single year to keep the result concise
  filter(year == 1990) %>%
  filter(cause == "Communicable diseases" | cause == "Non-communicable diseases")
```

```
## # A tibble: 2 x 3
##   cause                      year   deaths
##   <chr>                     <dbl>    <dbl>
## 1 Communicable diseases      1990 15392200
## 2 Non-communicable diseases  1990 26825621
```

But that means we have to type in `cause` twice (and even more time if we had more different values we wanted to include). This where the `%in%` operator together with the `c()` function come in handy:

```
gbd_short %>%
  filter(year == 1990) %>%
  filter(cause %in% c("Communicable diseases", "Non-communicable diseases"))
```

```
## # A tibble: 2 x 3
##   cause                      year   deaths
##   <chr>                     <dbl>    <dbl>
## 1 Communicable diseases      1990 15392200
## 2 Non-communicable diseases  1990 26825621
```

2.8 Missing values (NAs) and filters

Filtering for missing values (NAs) needs your special attention and care. Remember the small example tibble from Table 2.1 - it has some NAs in columns `var2` and `var3`:

```
mydata
```

```
## # A tibble: 4 x 5
##      id sex     var1  var2  var3
##   <int> <chr>  <dbl> <dbl> <dbl>
## 1     1 Male       4    NA     2
## 2     2 Female     1     4     1
## 3     3 Female     2     5    NA
## 4     4 Male       3    NA    NA
```

If we now want to filter for rows where `var2` is missing, `filter(var2 == NA)` is not the way to do it, it will not work. Since R is a programming language, it can be a bit stubborn with things like these. When you ask R to do a comparison using `==` (or `<`, `>`, etc.) it expects a value on each side, but NA is not a value, it is the lack thereof. The way to filter for missing values is using the `is.na()` function:

```
mydata %>%
  filter(is.na(var2))
```

```
## # A tibble: 2 x 5
##      id sex    var1  var2  var3
##   <int> <chr> <dbl> <dbl> <dbl>
## 1     1 Male      4    NA     2
## 2     4 Male      3    NA    NA
```

We send `mydata` to the filter and keep rows where `var2` is `NA`. Note the double brackets at the end: that's because the inner one belongs to `is.na()`, and the outer one to `filter()`. Missing out a closing bracket is also a very common source of (minor, easily fixed) mistakes, and it still happens to the best of us.

If filtering for rows where `var2` is not missing, we do this[7]

```
mydata %>%
  filter(! is.na(var2))
```

[7] In this simple example, `mydata %>% filter(! is.na(var2))` could be replace by a shorthand: `mydata %>% drop_na(var2)`, but it is important to understand how the ! and `is.na()` work as there will be more complex situations where using these is necessary.

```
## # A tibble: 2 x 5
##      id sex     var1  var2  var3
##   <int> <chr>  <dbl> <dbl> <dbl>
## 1     2 Female     1     4     1
## 2     3 Female     2     5    NA
```

In R, the exclamation mark (!) means "not".

Sometimes you want to drop a specific value (e.g. an outlier) from the dataset like this. The small example tibble `mydata` has 4 rows, with the values for `var2` as follows: NA, 4, 5, NA. We can exclude the row where `var2` is equal to 5 by using the "not equals" (`!=`)[8]:

```
mydata %>%
  filter(var2 != 5)
```

```
## # A tibble: 1 x 5
##      id sex     var1  var2  var3
##   <int> <chr>  <dbl> <dbl> <dbl>
## 1     2 Female     1     4     1
```

However, you'll see that by doing this, R drops the rows where `var2` is NA as well, as it can't be sure these missing values were not equal to 5.

If you want to keep the missing values, you need to make use of the OR (`|`) operator and the `is.na()` function:

```
mydata %>%
  filter(var2 != 5 | is.na(var2))
```

```
## # A tibble: 3 x 5
##      id sex     var1  var2  var3
##   <int> <chr>  <dbl> <dbl> <dbl>
## 1     1 Male       4    NA     2
## 2     2 Female     1     4     1
## 3     4 Male       3    NA    NA
```

[8] `filter(var2 != 5)` is equivalent to `filter(! var2 == 5)`

Being caught out by missing values, either in filters or other functions is very common (remember mydata$var2 %>% mean() returns NA unless you add `na.rm = TRUE`). This is also why we insist that you always plot your data first - outliers will reveal themselves and NA values usually become obvious too.

Another thing we do to stay safe around filters and missing values is saving the results and making sure the number of rows still add up:

```
subset1 = mydata %>%
  filter(var2 == 5)

subset2 = mydata %>%
  filter(! var2 == 5)

subset1
```

```
## # A tibble: 1 x 5
##      id sex     var1  var2  var3
##   <int> <chr>  <dbl> <dbl> <dbl>
## 1     3 Female     2     5    NA
```

```
subset2
```

```
## # A tibble: 1 x 5
##      id sex     var1  var2  var3
##   <int> <chr>  <dbl> <dbl> <dbl>
## 1     2 Female     1     4     1
```

If the numbers are small, you can now quickly look at RStudio's Environment tab and figure out whether the number of observations (rows) in `subset1` and `subset2` add up to the whole dataset (`mydata`). Or use the `nrow()` function to as R to tell you what the number of rows is in each dataset:

Rows in `mydata`:

```
nrow(mydata)
```

```
## [1] 4
```

Rows in `subset1`:

```
nrow(subset1)
```

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

Rows in `subset2`:

```
nrow(subset2)
```

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

Asking R whether adding these two up equals the original size:

```
nrow(subset1) + nrow(subset2) == nrow(mydata)
```

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

As expected, this returns FALSE - because we didn't add special handling for missing values. Let's create a third subset only including rows where `var3` is NA:

Rows in `subset2`:

```
subset3 = mydata %>%
  filter(is.na(var2))

nrow(subset1) + nrow(subset2) + nrow(subset3) == nrow(mydata)
```

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

2.9 Variable types and why we care

There are three broad types of data:

- continuous (numbers), in R: numeric, double, or integer;
- categorical, in R: character, factor, or logical (TRUE/FALSE);
- date/time, in R: POSIXct date-time[9].

Values within a column all have to be the same type, but a tibble can of course hold columns of different types. Generally, R is very good at figuring out what the type your data is (in programming, this 'figuring out' is called 'parsing'). For example, when reading in data, it will tell you what it assumed for the columns:

```
library(tidyverse)
typesdata = read_csv("data/typesdata.csv")
```

```
## Parsed with column specification:
## cols(
##   id = col_character(),
##   group = col_character(),
##   measurement = col_double(),
##   date = col_datetime(format = "")
## )
```

```
typesdata
```

```
## # A tibble: 3 x 4
##   id    group     measurement date
##   <chr> <chr>           <dbl> <dttm>
## 1 ID1   Control           1.8 2017-01-02 12:00:00
## 2 ID2   Treatment         4.5 2018-02-03 13:00:00
## 3 ID3   Treatment         3.7 2019-03-04 14:00:00
```

[9]Portable Operating System Interface (POSIX) is a set of computing standards. There's nothing more to understand about this other than when R starts shouting "POSIXct this and POSIXlt that" at you, check your date and time variables

This means that a lot of the time you do not have to worry about those little `<chr>` vs `<dbl>` vs `<S3: POSIXct>` labels, R knows what its doing. But in cases of irregular or faulty input data, or when doing a lot of calculations and modifications your data, we need to be aware of these different types to be able to find and fix mistakes.

For example, consider a very similar file as above but with a couple of data entry issues:

```
typesdata_faulty = read_csv("data/typesdata_faulty.csv")
```

```
## Parsed with column specification:
## cols(
##   id = col_character(),
##   group = col_character(),
##   measurement = col_character(),
##   date = col_character()
## )
```

```
typesdata_faulty
```

```
## # A tibble: 3 x 4
##   id    group     measurement date
##   <chr> <chr>     <chr>       <chr>
## 1 ID1   Control   1.8         02-Jan-17 12:00
## 2 ID2   Treatment 4.5         03-Feb-18 13:00
## 3 ID3   Treatment 3.7 or 3.8  04-Mar-19 14:00
```

Notice R now parsed both measurement and date as characters. The first one is a data entry issue: the person taking the measurement couldn't decide which value to note down (maybe the scale was shifting between the two values) so they included both values and text "or" in the cell. A will also get parsed as a categorical variable because of a small typo, e.g., if entered as "3..7" instead of "3.7". And the reason R didn't automatically make sense of the date column is that it can't know whether which one is the month and which one year: **02-Jan-17** could stand for *02-Jan-2017* as well as *2002-Jan-17*.

Therefore, while a lot of the time you do not have to worry about variable types and can just get on with your analysis, but it is important to understand what the different types are to be ready to deal with them when issues arise.

Furthermore, since health data is generally full of categorical data, it is crucial that you do understand the difference between characters and factors (both are types of categorical variables in R with their pros and cons).

So here we go.

2.10 Numeric variables

Number are generally straightforward to handle and don't cause a lot of trouble. R usually refers to numbers as `numeric` (or `num`), but sometimes it really gets its nerd on and also calls numbers `integer` or `double`. [10] It doesn't usually matter whether R is classifying your continuous data `numeric/num/double/int`, but it is good to be aware of these different terms as you will see them in R messages.

FRIENDLY WARNING: What's about to follow is a bit dry. Furthermore, it is not essential for complete beginners - you might want to continue reading from **Characters**. Before you leave, take a mental note that sometimes numbers in R have more decimal places than it seems, and that can cause funny behavior when using the double equals operator (`==`).

Something to note about numbers is that R doesn't usually print

[10] Integers are numbers without decimal places (e.g., `1, 2, 3`), whereas `double` stands for "Double-precision floating-point" format (e.g., `1.234, 5.67890`).

more than 6 decimal places, but that doesn't mean they don't exist. For example, from the `typedata` tibble, we're taking the `measurement` column and sending it to the `mean()` function. R then calculates the mean and tells us what it is with 6 decimal places:

```
typesdata$measurement %>% mean()
```

```
## [1] 3.333333
```

Let' save that in a new object:

```
measurement_mean = typesdata$measurement %>% mean()
```

But when using the double equals operator to check if this is equivalent to a fixed value (you might do this when comparing to a threshold, or even another mean value), R returns `FALSE`:

```
measurement_mean == 3.333333
```

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

Now this doesn't seem right, does it - R clearly told us just above that the mean of this variable is 3.333333 (reminder: the actual values in the measurement column are 1.8, 4.5, 3.7). The reason the above statement is `FALSE` is because `measurement_mean` is quietly holding more than 6 decimal places.

One way to go about this is to round the mean to a reasonable number of decimal places:

```
round(measurement_mean, 3)
```

```
## [1] 3.333
```

The second argument of `round()` specifies the number of decimal places you want your number(s) rounded to. So when using `round()` in the equality statement like this, we get the expected `TRUE`:

```
round(measurement_mean, 3) == 3.333
```

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

Which is usually fine, especially if you've finished applying calculations on that number. But when you indent to use it if further calculations, then rounding should be left to the very end - to minimise rounding errors. This is where the `near()` function comes in handy:

```
library(tidyverse)
near(measurement_mean, 3.333, 0.001)
```

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

The first two arguments for `near()` are the numbers you are comparing, the third argument is the precision you are interested in. So if the numbers are equal within that precision, it returns `TRUE`. This means you get the expected result without having to round the numbers off.

2.11 Character variables

Characters (sometimes referred to as *strings* or *character strings*) in R are letters, words, or even whole sentences (an example of this

may be free text comments). Characters are displayed in-between "" (or '').

A useful way to investigate a categorical variable are the `unique()` and `n_distinct()` functions:

```
typesdata$group %>% unique()
```

```
## [1] "Control"   "Treatment"
```

```
typesdata$group %>% n_distinct()
```

```
## [1] 2
```

```
typesdata$id %>% unique()
```

```
## [1] "ID1" "ID2" "ID3"
```

```
# check whether the number of rows of typesdata is equal
# to the number of distinct values in its id column:
nrow(typesdata) == typesdata$id %>% n_distinct()
```

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

With this example `tibble` that only has three rows, it is pretty obvious that the `id` column is a unique identifier whereas the `group` column is a categorical variable. But for larger datasets, you should know how to ask these questions programmatically - can't go through 1000s of values checking if they're all the way you expect without unexpected duplicates or typos. Typos usually come out if the number of different values - result of `n_distinct()` - is greater than you expect. For example, if you expect your data to be in two groups: Control and Treatment, but `n_distinct()` says "3", it could mean that you have missing values (as NAs would also be counted as a distinct group), or that the spelling is inconsistent.

2.12 Factor variables

Factors are fussy characters. Factors are fussy because they have something called **levels.** Levels are all the unique values a factor variable could take - e.g. like when we looked at `typesdata$group %>% unique()`. Using factors rather than just characters can be useful because:

- The values factor levels can take is fixed. For example, once you tell R that `typesdata$group` is a factor with two levels: Control and Treatment, combining it with other datasets with different spellings are abbreviations for the same variable would get you a warning. This can be very helpful and useful, but it can also be a nuisance when you really do want to add in another option for a `factor` variable.
- Levels have an order. When running statistical tests on grouped data (e.g., Control vs Treatment, Adult vs Child) and the variable is just a character, not a factor, R will use the alphabetically first as the reference level. Converting a character column into a factor column enables us to define and change the order of its levels. Level order also affect plots: by default, categorical variables (i.e., think of a barplot) get ordered alphabetically, but if this is not the order we want them in, we have to make it into a factor before we plot it. The plot will then know how the order it better.

So overall, since health data is often categorical and has a reference (comparison) level, then factors are an essential way to work with these data in R. Nevertheless, the fussiness of factors can sometimes be unhelpful or even frustrating. It takes experience as an R use to know when is it easiest to keep your variables as characters and when to convert them to factors. A lot more about factor handling will be covered later in the book.

2.13 Date/time variables

R is very good for working with dates. For example, it can calculate the number of days/weeks/months between two dates, or it can be used to find a future date is (i.e., "what's the date exactly 60 days from now?"). It also knows about time zones and is happy to parse dates in pretty much any format - as long as you tell R how your date is formatted (e.g., day before month, month name abbreviated, year in 2 or 4 digits, etc.). Since R displays dates and times between quotes (""), they look similar to characters. However, it is important to know whether R has understood which of your columns contain date/time information, as which are just normal characters.

```
library(lubridate) # lubridate makes working with dates easier
current_datetime = Sys.time()
current_datetime
```

```
## [1] "2019-07-30 16:59:01 BST"
```

```
my_datetime = "2020-12-01 12:00"
my_datetime
```

```
## [1] "2020-12-01 12:00"
```

When printed, the two objects - `current_datetime` and `my_datetime` seem to have the a very similar format. But if we try to calculate the difference between these two dates, we get an error:

```
my_datetime - current_datetime
```

```
## Error in `-.POSIXt`(my_datetime, current_datetime): can only subtract from "POSIXt" objects
```

That's because when we assigned a value to `my_datetime`, R assumed the simpler type for it - so a character. We can check what the type of an object or variable is using the `class()` function:

```
current_datetime %>% class()
```

```
## [1] "POSIXct" "POSIXt"
```

```
my_datetime %>% class()
```

```
## [1] "character"
```

So we need to tell R that `my_datetime` does indeed include date/time information so we can then use it in calculations:

```
my_datetime_converted = ymd_hm(my_datetime)
my_datetime_converted
```

```
## [1] "2020-12-01 12:00:00 UTC"
```

Calculating the difference will now work:

```
my_datetime_converted - current_datetime
```

```
## Time difference of 489.834 days
```

Since R knows this is a difference between two date/time objects, it prints the in a nicely readable way. Furthermore, the result has its own type, it is a "difftime".

```
my_datesdiff = my_datetime_converted - current_datetime
my_datesdiff %>% class()
```

```
## [1] "difftime"
```

This is useful if we want to apply this time difference on another date, e.g.:

```
ymd_hm("2021-01-02 12:00") + my_datesdiff
```

```
## [1] "2022-05-07 08:00:58 UTC"
```

But if we want to use the number of days in a normal calculation, e.g., what if a measurement increased by 560 arbitrary units during this time period. We might want to calculate the increase per day like this:

```
560/my_datesdiff
```

```
## Error in `/.difftime`(560, my_datesdiff): second argument of / cannot be a "difftime" object
```

Doesn't work, does it. We need to convert `my_datesdiff` (which is a difftime value) into a numeric value by using the `as.numeric()` function:

```
560/as.numeric(my_datesdiff)
```

```
## [1] 1.143244
```

The lubridate package comes with several convenient functions for parsing dates, e.g., `ymd()`, `mdy()`, `ymd_hm()`, etc. - for a full list see lubridate.tidyverse.org.

However, if your date/time variable comes in an extra special format, then use the `parse_date_time()` function where the second argument specifies the format using these helpers:

Notation	Meaning	Example
`%d`	day as number	01-31
`%m`	month as number	01-12
`%B`	month name	January-December
`%b`	abbreviated month	Jan-Dec
`%Y`	4-digit year	2019
`%y`	2-digit year	19
`%H`	hours	12
`%M`	minutes	01
`%A`	weekday	Monday-Sunday
`%a`	abbreviated weekday	Mon-Sun

For example:

```
parse_date_time("12:34 07/Jan'20", "%H:%M %d/%b'%y")
```

```
## [1] "2020-01-07 12:34:00 UTC"
```

Furthermore, the same date/time helpers can be used to rearrange your date and time for printing:

```
Sys.time()
```

```
## [1] "2019-07-30 16:59:01 BST"
```

```
Sys.time() %>% format("%H:%M on %B-%d (%Y)")
```

```
## [1] "16:59 on July-30 (2019)"
```

You can even add plain text into the `format()` function, R will know to put the right date/time values where the `%` are:

```
Sys.time() %>% format("Happy days, the current time is %H:%M %B-%d (%Y)!")
```

```
## [1] "Happy days, the current time is 16:59 July-30 (2019)!"
```

2.14 Creating new columns - `mutate()`

The function for adding new columns (or making changes to existing ones) to a tibble is called `mutate()`. As a reminder, this is what `typesdata` looked like:

```
typesdata
```

```
## # A tibble: 3 x 4
##   id    group     measurement date
##   <chr> <chr>           <dbl> <dttm>
## 1 ID1   Control           1.8 2017-01-02 12:00:00
## 2 ID2   Treatment         4.5 2018-02-03 13:00:00
## 3 ID3   Treatment         3.7 2019-03-04 14:00:00
```

Let's say we decide to divide the column measurement by 2. A very quick way to see these values would be to pull them out using the `$` operator and then divide by 2:

```
typesdata$measurement
```

```
## [1] 1.8 4.5 3.7
```

```
typesdata$measurement/2
```

```
## [1] 0.90 2.25 1.85
```

But this becomes very cumbersome once we want to combine multiple variables from the same tibble in a calculation. So the `mutate()` is the way to go here:

```
typesdata %>%
  mutate(measurement/2)
```

```
## # A tibble: 3 x 5
##   id    group     measurement date                `measurement/2`
##   <chr> <chr>           <dbl> <dttm>                       <dbl>
## 1 ID1   Control           1.8 2017-01-02 12:00:00           0.9
## 2 ID2   Treatment         4.5 2018-02-03 13:00:00           2.25
## 3 ID3   Treatment         3.7 2019-03-04 14:00:00           1.85
```

Notice how the `mutate()` above returns the whole tibble with a new column called `measurement/2`. This is quite nice of `mutate()` already, but it would be best to give columns names that don't include characters other than underscores (_) or dots (.). So let's assign a more standard name for this new column:

```
typesdata %>%
  mutate(measurement_half = measurement/2)
```

```
## # A tibble: 3 x 5
##   id    group     measurement date                measurement_half
##   <chr> <chr>           <dbl> <dttm>                         <dbl>
## 1 ID1   Control           1.8 2017-01-02 12:00:00             0.9
## 2 ID2   Treatment         4.5 2018-02-03 13:00:00             2.25
## 3 ID3   Treatment         3.7 2019-03-04 14:00:00             1.85
```

Better. You can see that R likes the name we gave it a bit better as it's now removed the back-ticks from around it. Overall, back-ticks can be used to call out non-standard column names, so if you are forced to read in data with, e.g., spaces in column names, then the back-ticks enable calling column names that would otherwise error[11]:

[11] If this happens to you a lot, then check out `library(janitor)` and its function `clean_names()` for automatically tidying non-standard column names.

```
mydata$`Nasty column name`

# or

mydata %>%
  select(`Nasty column name`)
```

But as usual, if it gets printed, it doesn't get saved. We have two options - we can either overwrite the `typesdata` tibble (by changing the first line to `typesdata = typesdata %>%`), or we can create a new one (that appears in your Environment):

```
typesdata_modified = typesdata %>%
  mutate(measurement_half = measurement/2)

typesdata_modified
```

```
## # A tibble: 3 x 5
##   id    group     measurement date                measurement_half
##   <chr> <chr>           <dbl> <dttm>                         <dbl>
## 1 ID1   Control           1.8 2017-01-02 12:00:00             0.9
## 2 ID2   Treatment         4.5 2018-02-03 13:00:00             2.25
## 3 ID3   Treatment         3.7 2019-03-04 14:00:00             1.85
```

The `mutate()` function can also be used to create a new column with a single constant value, which in return can be used to calculate a difference for each of the existing dates:

```
library(lubridate)
typesdata %>%
  mutate(reference_date   = ymd_hm("2020-01-01 12:00"),
         dates_difference = reference_date - date) %>%
  select(date, reference_date, dates_difference)
```

```
## # A tibble: 3 x 3
##   date                reference_date      dates_difference
##   <dttm>              <dttm>              <drtn>
## 1 2017-01-02 12:00:00 2020-01-01 12:00:00 1094.0000 days
## 2 2018-02-03 13:00:00 2020-01-01 12:00:00  696.9583 days
## 3 2019-03-04 14:00:00 2020-01-01 12:00:00  302.9167 days
```

(We are then using the `select()` function to only choose the three relevant columns.)

Finally, the mutate function can be used to create a new column with a summarised value in it, e.g. the mean of another column:

```
typesdata %>%
  mutate(mean_measurement = mean(measurement))
```

```
## # A tibble: 3 x 5
##   id    group     measurement date                mean_measurement
##   <chr> <chr>           <dbl> <dttm>                         <dbl>
## 1 ID1   Control           1.8 2017-01-02 12:00:00             3.33
## 2 ID2   Treatment         4.5 2018-02-03 13:00:00             3.33
## 3 ID3   Treatment         3.7 2019-03-04 14:00:00             3.33
```

Which in return can be useful for calculating a standardized measurement (i.e. relative to the mean):

```
typesdata %>%
  mutate(mean_measurement     = mean(measurement)) %>%
  mutate(measurement_relative = measurement/mean_measurement) %>%
  select(matches("measurement"))
```

```
## # A tibble: 3 x 3
##   measurement mean_measurement measurement_relative
##         <dbl>            <dbl>                <dbl>
## 1         1.8             3.33                 0.54
## 2         4.5             3.33                 1.35
## 3         3.7             3.33                 1.11
```

2.14.1 Worked example/exercise

Round the difference to 0 decimal places using the `round()` function inside a `mutate()`. Then add a clever `matches("date")` inside the `select()` function to choose all matching columns.

Solution:

```
typesdata %>%
  mutate(reference_date   = ymd_hm("2020-01-01 12:00"),
         dates_difference = reference_date - date) %>%
  mutate(dates_difference = round(dates_difference)) %>%
  select(matches("date"))
```

```
## # A tibble: 3 x 3
##   date                reference_date      dates_difference
##   <dttm>              <dttm>              <drtn>
## 1 2017-01-02 12:00:00 2020-01-01 12:00:00 1094 days
## 2 2018-02-03 13:00:00 2020-01-01 12:00:00  697 days
## 3 2019-03-04 14:00:00 2020-01-01 12:00:00  303 days
```

You can shorten this by adding the `round()` function directly around the subtraction, so the third line becomes `dates_difference = round(reference_date - date)) %>%`. But sometimes writing calculations out longer than the absolute minimum can make them easier to understand when you return to an old script months later. Furthermore, we didn't have to save the `reference_date` as a new column, the calculation could have used the value directly: `mutate(dates_difference = ymd_hm("2020-01-01 12:00") - date) %>%`. But again, defining it makes it clearer for future self what was done. And it makes `reference_date` available for reuse in more complicated calculations within the tibble.

2.15 Conditional calculations - `if_else()`

And finally, we combine the filtering operators (`==`, `>`, `<`, etc) with the `if_else()` function to create new columns based on a condition.

```
typesdata %>%
  mutate(above_threshold = if_else(measurement > 3,
                                   "Above three",
                                   "Below three"))
```

```
## # A tibble: 3 x 5
##   id    group     measurement date                above_threshold
##   <chr> <chr>           <dbl> <dttm>              <chr>
## 1 ID1   Control           1.8 2017-01-02 12:00:00 Below three
## 2 ID2   Treatment         4.5 2018-02-03 13:00:00 Above three
## 3 ID3   Treatment         3.7 2019-03-04 14:00:00 Above three
```

We are sending `typesdata` into a `mutate()` function, we are creating a new column called `above_threshold` based on whether `measurement` is greater or less than 3. The first argument to `if_else()` is a condition (in this case that measurement is greater than 3), the second argument is the value if the condition is TRUE, and the third argument is the value if the condition is FALSE. Look at each line in the tibble above and convince yourself that the `threshold` variable worked as expected. Then look at the two closing brackets - `))` - at the end of the code and convince yourself they both need to be there.

`if_else()` and missing values tip: for rows with missing values (NAs), the condition returns neither TRUE or FALSE, it returns NA. And that might be fine, but if you want to assign a specific group/label for missing values in the new variable, you can add a fourth argument to `if_else()`, e.g., `if_else(measurement > 3, "Above three", "Below three", "Value missing")`.

2.16 Create labels - `paste()`

The `paste()` function is used to add characters together. It also works with numbers and dates which will automatically be converted to characters before being pasted together into a single label. See this example where we use all variables from `typesdata` to create a new column called `plot_label` (we `select()` for printing space):

```
typesdata %>%
  mutate(plot_label = paste(id,
                            "was last measured at", date,
                            ", and the value was",    measurement)) %>%
  select(plot_label)
```

```
## # A tibble: 3 x 1
##   plot_label
##   <chr>
## 1 ID1 was last measured at 2017-01-02 12:00:00 , and the value was 1.8
## 2 ID2 was last measured at 2018-02-03 13:00:00 , and the value was 4.5
## 3 ID3 was last measured at 2019-03-04 14:00:00 , and the value was 3.7
```

The paste is also useful when pieces of information are stored in different columns. For example, consider this made-up tibble:

```
pastedata = tibble(year  = c(2007, 2008, 2009),
                   month = c("Jan", "Feb", "March"),
                   day   = c(1, 2, 3))

pastedata
```

```
## # A tibble: 3 x 3
##    year month   day
##   <dbl> <chr> <dbl>
## 1  2007 Jan       1
## 2  2008 Feb       2
## 3  2009 March     3
```

We can use `paste()` to combine these into a single column:

```
pastedata %>%
  mutate(date = paste(day, month, year, sep = "-"))
```

```
## # A tibble: 3 x 4
##    year month   day date
##   <dbl> <chr> <dbl> <chr>
## 1  2007 Jan       1 1-Jan-2007
## 2  2008 Feb       2 2-Feb-2008
## 3  2009 March     3 3-March-2009
```

By default, `paste()` adds a space between the each value, but we can use the `sep =` argument to specify a different separator. Sometimes it is useful to use `paste0()` which does not add anything between the values (no space, no dash, etc.).

We can now tell R that the date column should be parsed as such:

```
library(lubridate)

pastedata %>%
  mutate(date = paste(day, month, year, sep = "-")) %>%
  mutate(date = dmy(date))
```

```
## # A tibble: 3 x 4
##    year month   day date
##   <dbl> <chr> <dbl> <date>
## 1  2007 Jan       1 2007-01-01
## 2  2008 Feb       2 2008-02-02
## 3  2009 March     3 2009-03-03
```

2.17 Joining multiple datasets

For combining dataframes based on shared variables we use the joins: `left_join()`, `right_join()`, `inner_join()`, or `full_join()`. Let's split some of the variables in `mydata` between two new dataframes: `first_data` and `second_data`. For demonstrating the difference between the different joins, we will only include a subset (first 6 rows) of the dataset in `second_data`:

```
# first_data  = select(mydata, year, cause, deaths_millions)
# second_data = select(mydata, year, cause, deaths_millions) %>% slice(1:6)
#
# # change the order of rows in first_data to demosntrate the join does not rely on the ordering of r
# first_data = arrange(first_data, deaths_millions)
#
# combined_left  =  left_join(first_data, second_data)
# combined_right = right_join(first_data, second_data)
# combined_inner = inner_join(first_data, second_data)
# combined_full  =  full_join(first_data, second_data)
```

Those who have used R before, or those who come across older scripts will have seen `merge()` instead of the joins. `merge()` works similarly to joins, but instead of having the four options defined clearly at the front, you would have had to use the `all = FALSE`, `all.x = all`, `all.y = all` arguments.

2.17.1 Exercise

Investigate the four new dataframes called `combined_` using the Environment tab and discuss how the different joins (left, right, inner, full) work.

3

Summarising data

In this session we will get to know our three best friends for summarising data: `group_by()`, `summarise()`, and `mutate()`.

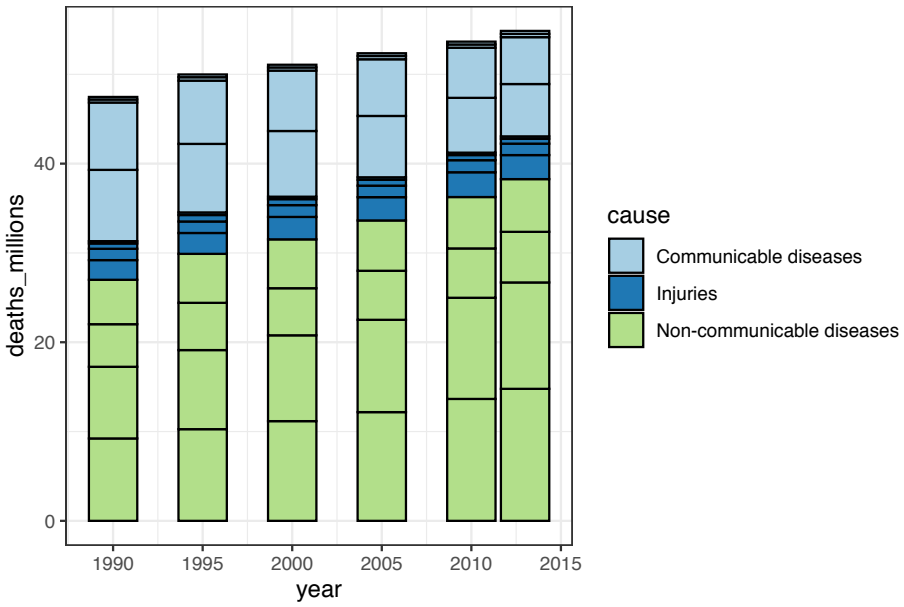
3.1 Data

In Session 2, we used a very condensed version of the Global Burden of Disease data. We are now going back to a longer one and we will learn how to summarise it ourselves.

```
source("healthyr_theme.R")
load("global_burden_disease_long.rda")
```

We were already using this longer dataset in Session 1, but with `colour=cause` to hide the fact that the total deaths in each year was made up of 12 groups of data (as the black lines on the bars indicate):

```
mydata %>%
    ggplot(aes(x = year, y = deaths_millions, fill = cause))+
    geom_col(colour = "black")
```



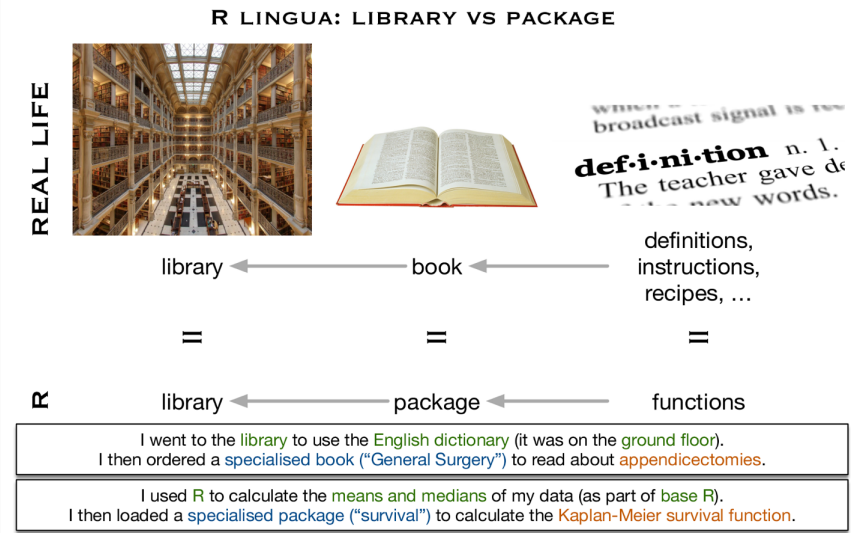

```
mydata %>%
    filter(year == 1990)
```

```
##      location                    cause    sex year deaths_millions
## 1  Developing Non-communicable diseases   Male 1990       9.2277141
## 2  Developing Non-communicable diseases Female 1990       8.0242455
## 3   Developed Non-communicable diseases   Male 1990       4.7692902
## 4   Developed Non-communicable diseases Female 1990       4.9722431
## 5  Developing                 Injuries   Male 1990       2.2039625
## 6  Developing                 Injuries Female 1990       1.2698308
## 7   Developed                 Injuries   Male 1990       0.5941184
## 8   Developed                 Injuries Female 1990       0.2578759
## 9  Developing     Communicable diseases   Male 1990       7.9819728
## 10 Developing     Communicable diseases Female 1990       7.5416376
## 11  Developed     Communicable diseases   Male 1990       0.3387820
## 12  Developed     Communicable diseases Female 1990       0.2870169
```

3.2 Tidyverse packages: ggplot2, dplyr, tidyr, etc.

Most of the functions introduced in this session come from the tidyverse family (http://tidyverse.org/), rather than Base R. Including

`library(tidyverse)` in your script loads a list of packages: ggplot2, dplyr, tidry, forcats, etc.




```
library(tidyverse)
```

3.3 Basic functions for summarising data

You can always pick a column and ask R to give you the `sum()`, `mean()`, `min()`, `max()`, etc. for it:

```
mydata$deaths_millions %>% sum()
```

```
## [1] 309.4174
```

```
mydata$deaths_millions %>% mean()
```

```
## [1] 4.297463
```

But if you want to get the total number of deaths for each `year` (or `cause`, or `sex`, whichever grouping variables you have in your dataset) you can use `group_by()` and `summarise()` that make subgroup analysis very convenient and efficient.

3.4 Subgroup analysis: `group_by()` and `summarise()`

The `group_by()` function tells R that you are about to perform subgroup analysis on your data. It retains information about your groupings and calculations are applied on each group separately. To go back to summarising the whole dataset again use `ungroup()`. Note that `summarise()` is different to the `summary()` function we used in Session 2.

With `summarise()`, we can calculate the total number of deaths per year:

```
mydata %>%
    group_by(year) %>%
    summarise(total_per_year = sum(deaths_millions)) ->
    summary_data1


mydata %>%
    group_by(year, cause) %>%
    summarise(total_per_cause = sum(deaths_millions)) ->
    summary_data2
```

- `summary_data1` includes the total number of deaths per year.
- `summary_data2` includes the number of deaths per cause per year.

year	total_per_year
1990	47
1995	50
2000	51
2005	52
2010	54
2013	55

year	cause	total_per_cause
1990	Communicable diseases	16
1990	Injuries	4
1990	Non-communicable diseases	27
1995	Communicable diseases	15
1995	Injuries	5
1995	Non-communicable diseases	30

… remaining years omitted from printing.

3.4.1 Exercise

Compare the sizes - number of rows (observations) and number of columns (variables) - of `mydata`, `summary_data1`, and `summary_data2` (in the Environment tab).

- Convince yourself that for 1990, deaths by the three causes (`summary_data2`) add up to total deaths per year (`summary_data1`).
- `summary_data2` has exactly 3 times as many rows as `summary_data1`. Why?
- `mydata` has 5 variables, whereas the summarised dataframes have 2 and 3. Which variables got dropped? Why?

3.4.2 Exercise

For each cause, calculate its percentage to total deaths in each year.

Hint: Use `full_join()` on `summary_data1` and `summary_data2`.

Solution:

TABLE 3.1: alldata

year	total_per_year	cause	total_per_cause	percentage
1990	47	Communicable diseases	16	34
1990	47	Injuries	4	9
1990	47	Non-communicable diseases	27	57
1995	50	Communicable diseases	15	31
1995	50	Injuries	5	9
1995	50	Non-communicable diseases	30	60

```
alldata = full_join(summary_data1, summary_data2)
```

```
## Joining, by = "year"
```

```
alldata$percentage = 100*alldata$total_per_cause/alldata$total_per_year %>% round()
```

`round()` defaults to 0 digits. If you want to round to a specified number of decimal places, use, e.g., round(digits = 2).

3.5 `mutate()`

Mutate works similarly to `summarise()` (as in it respects groupings set with `group_by()`), but it adds a new column into the original data. `summarise()`, on the other hand, condenses the data into a minimal table that only includes the variables specifically asked for.

3.5.1 Exercise

Investigate these examples to learn how `summarise()` and `mutate()` differ.

TABLE 3.2: summarise example

total_deaths
309

TABLE 3.3: mutate_example

location	cause	sex	year	deaths_millions	total_deaths
Developing	Non-communicable diseases	Male	1990	9	309
Developing	Non-communicable diseases	Female	1990	8	309
Developed	Non-communicable diseases	Male	1990	5	309
Developed	Non-communicable diseases	Female	1990	5	309
Developing	Non-communicable diseases	Male	1995	10	309

```
summarise_example = mydata %>%
    summarise(total_deaths = sum(deaths_millions))

mutate_example = mydata %>%
    mutate(total_deaths = sum(deaths_millions))
```

```
mutate_example %>%
  slice(1:5) %>%
  knitr::kable(digits = 0,
               booktabs = TRUE,
               caption = "mutate\\_example",
               align = "c")
```

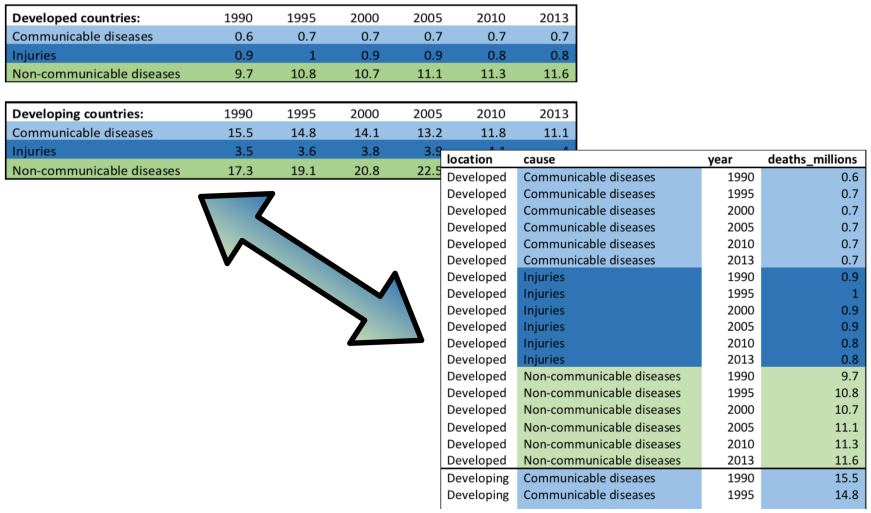
You should see that `mutate()` adds the same total number (309) to every line in the dataframe.

3.5.2 Optional advanced exercise

Based on what we just observed on how `mutate()` adds a value to each row, can you think of a way to redo **Exercise 3.4.2** without using a join? Hint: instead of creating `summary_data1` (total deaths per year) as a separate dataframe which we then merge with `summary_data2` (total deaths for all causes per year), we can use `mutate()` to add `total_per_year` to each row.

```
mydata %>%
    group_by(year, cause) %>%
    summarise(total_per_cause = sum(deaths_millions)) %>%
    group_by(year) %>%
    mutate(total_per_year = sum(total_per_cause)) %>%
    mutate(percentage = 100*total_per_cause/total_per_year) -> alldata
```

3.6 Wide vs long: `spread()` and `gather()`



Developed countries:	1990	1995	2000	2005	2010	2013
Communicable diseases	0.6	0.7	0.7	0.7	0.7	0.7
Injuries	0.9	1	0.9	0.9	0.8	0.8
Non-communicable diseases	9.7	10.8	10.7	11.1	11.3	11.6

Developing countries:	1990	1995	2000	2005	2010	2013
Communicable diseases	15.5	14.8	14.1	13.2	11.8	11.1
Injuries	3.5	3.6	3.8	3.8		
Non-communicable diseases	17.3	19.1	20.8	22.5		

location	cause	year	deaths_millions
Developed	Communicable diseases	1990	0.6
Developed	Communicable diseases	1995	0.7
Developed	Communicable diseases	2000	0.7
Developed	Communicable diseases	2005	0.7
Developed	Communicable diseases	2010	0.7
Developed	Communicable diseases	2013	0.7
Developed	Injuries	1990	0.9
Developed	Injuries	1995	1
Developed	Injuries	2000	0.9
Developed	Injuries	2005	0.9
Developed	Injuries	2010	0.8
Developed	Injuries	2013	0.8
Developed	Non-communicable diseases	1990	9.7
Developed	Non-communicable diseases	1995	10.8
Developed	Non-communicable diseases	2000	10.7
Developed	Non-communicable diseases	2005	11.1
Developed	Non-communicable diseases	2010	11.3
Developed	Non-communicable diseases	2013	11.6
Developing	Communicable diseases	1990	15.5
Developing	Communicable diseases	1995	14.8

3.6.1 Wide format

Although having data in the long format is very convenient for R, for publication tables, it makes sense to spread some of the values out into columns:

```
alldata %>%
    mutate(percentage = paste0(round(percentage, 2), "%")) %>%
    select(year, cause, percentage) %>%
    spread(cause, percentage)
```

```
## # A tibble: 6 x 4
## # Groups:   year [6]
##    year `Communicable diseases` Injuries `Non-communicable diseases`
##   <int> <chr>                   <chr>    <chr>
## 1  1990 34.02%                  9.11%    56.87%
## 2  1995 30.91%                  9.28%    59.81%
## 3  2000 28.93%                  9.35%    61.72%
## 4  2005 26.53%                  9.23%    64.24%
## 5  2010 23.17%                  9.26%    67.57%
## 6  2013 21.53%                  8.73%    69.75%
```

- `select()` pick the variables you want to keep. Try running the lines until `spread()` to see how it works.

3.6.2 Exercise

Calculate the percentage of male and female deaths for each year. Spread it to a human readable form:

Hints:

- create `summary_data3` that includes a variable called `total_per_sex`
- merge `summary_data1` and `summary_data3` into a new data frame
- calculate the percentage of `total_per_sex` to `total_per_year`
- round, add % labels
- spread

Solution:

```
mydata %>%
    group_by(year) %>%
    summarise(total_per_year = sum(deaths_millions)) ->
    summary_data1

mydata %>%
    group_by(year, sex) %>%
    summarise(total_per_sex = sum(deaths_millions)) ->
    summary_data3

alldata = full_join(summary_data1, summary_data3)
```

```
## Joining, by = "year"
```

```
result_spread = alldata %>%
  mutate(percentage = round(100*total_per_sex/total_per_year, 0)) %>%
  mutate(percentage = paste0(percentage, "%")) %>%
  select(year, sex, percentage) %>%
  spread(sex, percentage)

result_spread
```

```
## # A tibble: 6 x 3
##    year Female Male
##   <int> <chr>  <chr>
## 1  1990 47%    53%
## 2  1995 47%    53%
## 3  2000 46%    54%
## 4  2005 46%    54%
## 5  2010 46%    54%
## 6  2013 45%    55%
```

And save it into a csv file using `write_csv()`:

```
write_csv(result_spread, "gbd_genders_summarised.csv")
```

You can open a csv file with Excel and copy the table into Word or PowerPoint for presenting.

3.6.3 Long format

The opposite of `spread()` is `gather()`:

- The first argument is a name for the column that will include columns gathered from the wide columns (in this example, `Male` and `Female` are gathered into `sex`).
- The second argument is a name for the column that will include the values from the wide-format columns (the values from `Male` and `Female` are gathered into `percentage`).
- Any columns that already are condensed (e.g. year was in one column, not spread out like in the pre-course example) must be included with a negative (i.e. -year).

```
result_spread %>%
  gather(sex, percentage, -year)
```

```
## # A tibble: 12 x 3
##     year sex    percentage
##    <int> <chr>  <chr>
##  1  1990 Female 47%
##  2  1995 Female 47%
##  3  2000 Female 46%
##  4  2005 Female 46%
##  5  2010 Female 46%
##  6  2013 Female 45%
##  7  1990 Male   53%
##  8  1995 Male   53%
##  9  2000 Male   54%
## 10  2005 Male   54%
## 11  2010 Male   54%
## 12  2013 Male   55%
```

3.6.4 Exercise

Test what happens when you

- Change the order of sex and percentage:

```
result_spread %>%
  gather(percentage, sex, -year)
```

Turns out in the above example, `percentage` and `sex` were just label you assigned to the gathered columns. It could be anything, e.g.:

```
result_spread %>%
  gather(`look-I-gathered-sex`, `values-Are-Here`, -year)
```

- What happens if we omit `-year`:

```
result_spread %>%
  gather(sex, percentage)
```

`-year` was telling R we don't want the year column to be gathered together with Male and Female, we want to keep it as it is.

3.7 Sorting: `arrange()`

To reorder data ascendingly or descendingly, `use arrange()`:

```
mydata %>%
    group_by(year) %>%
    summarise(total = sum(deaths_millions))  %>%
    arrange(-year) # reorder after summarise()
```

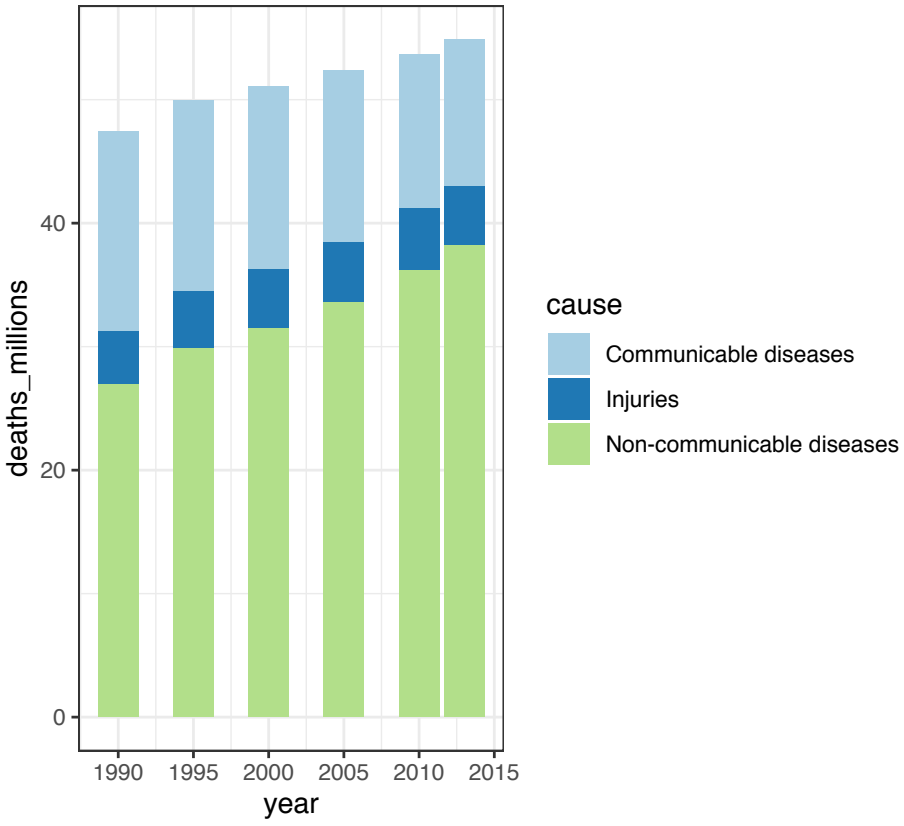
3.8 Factor handling

We talked about the pros and cons of working with factors in Session 2. Overall, they are extremely useful for the type of analyses done in medical research.

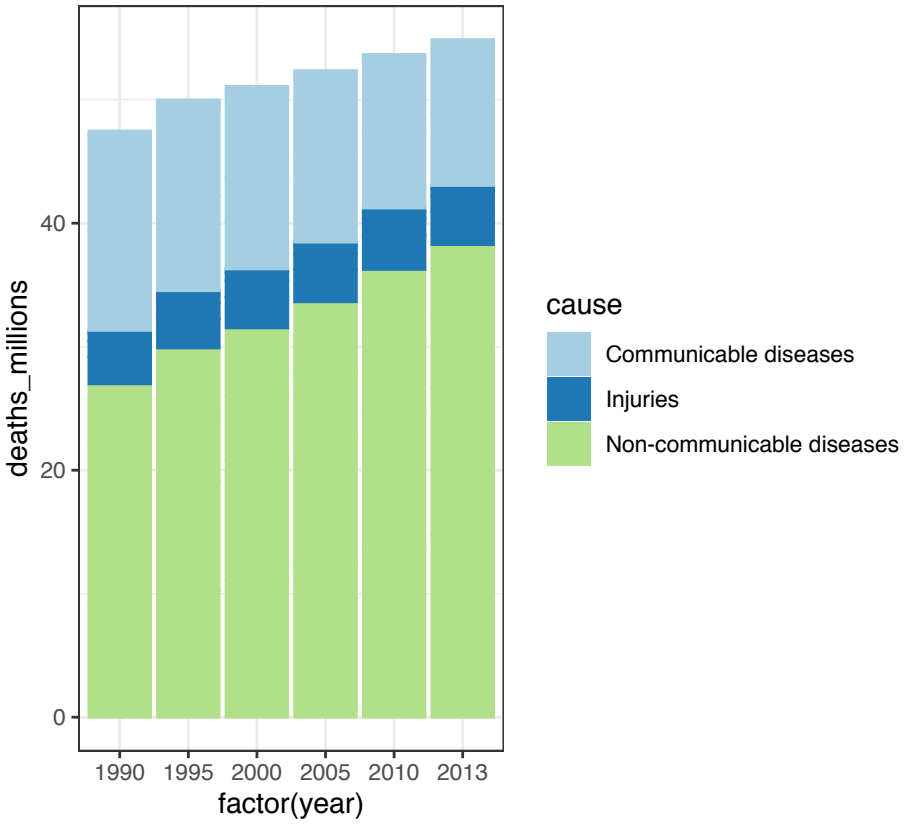
3.8.1 Exercise

Explain how and why these two plots are different.

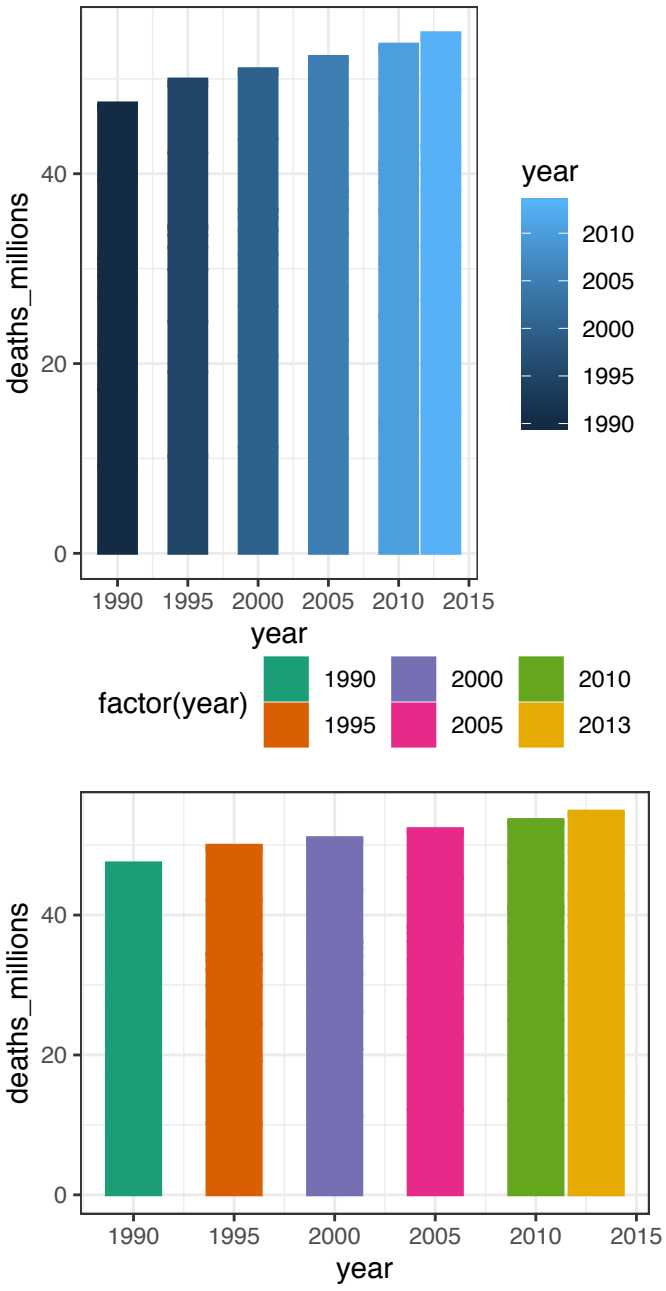
```
mydata %>%
    ggplot(aes(x = year, y = deaths_millions, fill = cause))+
    geom_col()
```



```
mydata %>%
    ggplot(aes(x = factor(year), y = deaths_millions, fill = cause, colour = cause))+
    geom_col()
```



What about these?



These illustrate why it might sometimes be useful to use numbers as factors - on the second one we have used `fill = factor(year)` as

the fill, so each year gets a distinct colour, rather than a gradual palette.

3.8.2 `fct_collapse()` - grouping levels together

```
mydata$cause  %>%
    fct_collapse("Non-communicable and injuries" = c("Non-communicable diseases", "Injuries")) ->
    mydata$cause2

mydata$cause %>% levels()
```

```
## [1] "Communicable diseases"     "Injuries"
## [3] "Non-communicable diseases"
```

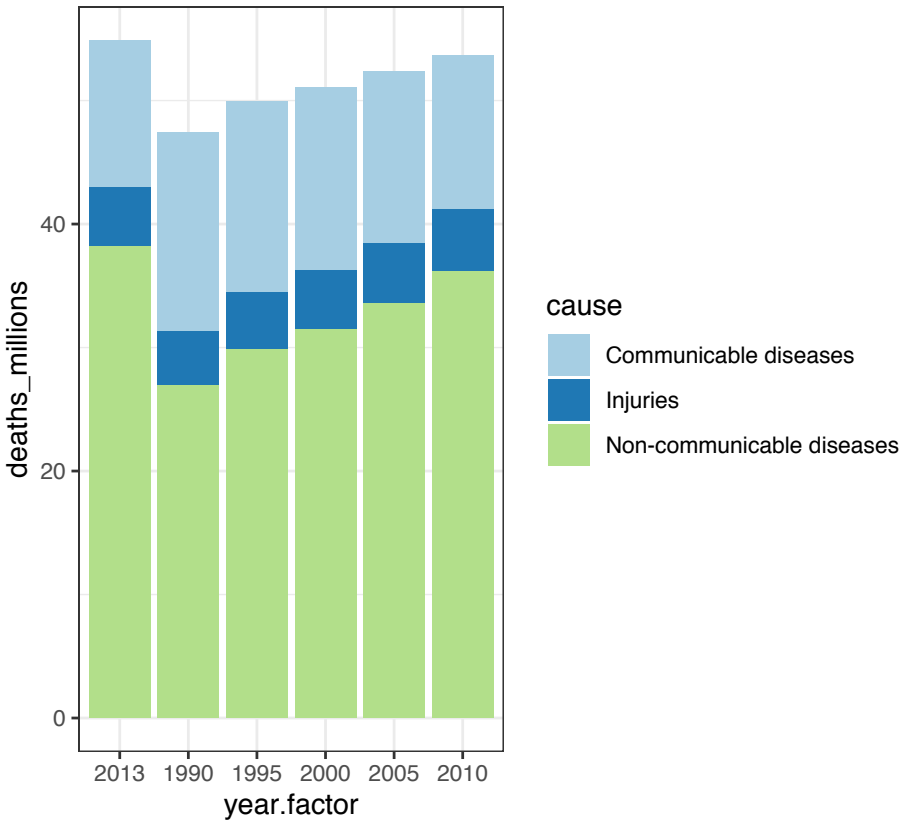
```
mydata$cause2 %>% levels()
```

```
## [1] "Communicable diseases"         "Non-communicable and injuries"
```

3.8.3 `fct_relevel()` - change the order of levels

Another reason to sometimes make a numeric variable into a factor is that we can then reorder it for the plot:

```
mydata$year %>%
  factor() %>%
    fct_relevel("2013") -> #brings 2013 to the front
    mydata$year.factor

source("1_source_theme.R")

mydata %>%
    ggplot(aes(x=year.factor, y=deaths_millions, fill=cause))+
    geom_col()
```



3.8.4 `fct_recode()` - rename levels

```
mydata$cause %>%
    levels()  # levels() lists the factor levels of a column
```

```
## [1] "Communicable diseases"     "Injuries"
## [3] "Non-communicable diseases"
```

```
mydata$cause %>%
    fct_recode("Deaths from injury" = "Injuries") %>%
    levels()
```

```
## [1] "Communicable diseases"     "Deaths from injury"
## [3] "Non-communicable diseases"
```

3.8.5 Converting factors to numbers

MUST REMEMBER: factor needs to become `as.character()` before converting to numeric or date! Factors are actually stored as labelled integers (so like number codes), only the function `as.character()` will turn a factor back into a collated format which can then be converted into a number or date.

3.8.6 Exercise

Investigate the two examples converting the `year.factor` variable back to a number.

```
mydata$year.factor
```

```
##  [1] 1990 1990 1990 1990 1995 1995 1995 1995 2000 2000 2000 2000 2005 2005
## [15] 2005 2005 2010 2010 2010 2010 2013 2013 2013 2013 1990 1990 1990 1990
## [29] 1995 1995 1995 1995 2000 2000 2000 2000 2005 2005 2005 2005 2010 2010
## [43] 2010 2010 2013 2013 2013 2013 1990 1990 1990 1990 1995 1995 1995 1995
## [57] 2000 2000 2000 2000 2005 2005 2005 2005 2010 2010 2010 2010 2013 2013
## [71] 2013 2013
## Levels: 2013 1990 1995 2000 2005 2010
```

```
mydata$year.factor %>%
    as.numeric()
```

```
##  [1] 2 2 2 2 3 3 3 3 4 4 4 4 5 5 5 5 6 6 6 6 1 1 1 1 2 2 2 2 3 3 3 3 4 4 4
## [36] 4 5 5 5 5 6 6 6 6 1 1 1 1 2 2 2 2 3 3 3 3 4 4 4 4 5 5 5 5 6 6 6 6 1 1
## [71] 1 1
```

```
mydata$year.factor %>%
    as.character() %>%
    as.numeric()
```

```
##  [1] 1990 1990 1990 1990 1995 1995 1995 1995 2000 2000 2000 2000 2005 2005
## [15] 2005 2005 2010 2010 2010 2010 2013 2013 2013 2013 1990 1990 1990 1990
## [29] 1995 1995 1995 1995 2000 2000 2000 2000 2005 2005 2005 2005 2010 2010
## [43] 2010 2010 2013 2013 2013 2013 1990 1990 1990 1990 1995 1995 1995 1995
## [57] 2000 2000 2000 2000 2005 2005 2005 2005 2010 2010 2010 2010 2013 2013
## [71] 2013 2013
```

3.9 Long Exercise

This exercise includes multiple steps, combining all of the above.

First, create a new script called "2_long_exercise.R". Then Restart your R session, add `library(tidyverse)` and load `"global_burden_disease_long.rda"`.

- Calculate the total number of deaths in Developed and Developing countries. Hint: use `group_by(location)` and `summarise(new-column-name = sum(variable-to-sum))`.
- Calculate the total number of deaths in Developed and Developing countries and for men and women. Hint: this is as easy as adding , `sex` to `group_by()`.
- Filter for 1990.
- `spread()` the `location` column.

```
## # A tibble: 2 x 3
##   sex    Developed Developing
##   <fct>      <dbl>      <dbl>
## 1 Female      5.52       16.8
## 2 Male        5.70       19.4
```

3.10 Extra: formatting a table for publication

Creating a publication table with both the total numbers and percentages (in brackets) + using `formatC()` to retain trailing zeros:

```
# Let's use alldata from Exercise 5.2:

mydata %>%
    group_by(year, cause) %>%
    summarise(total_per_cause = sum(deaths_millions)) %>%
    group_by(year) %>%
    mutate(total_per_year = sum(total_per_cause)) %>%
```

```
    mutate(percentage = 100*total_per_cause/total_per_year) -> alldata

alldata %>%
    mutate(total_percentage =
                    paste0(round(total_per_cause, 1)  %>% formatC(1, format = "f"),
                           " (", round(percentage, 1) %>% formatC(1, format = "f"),
                           "%)"
                           )
                    ) %>%
    select(year, cause, total_percentage) %>%
    spread(cause, total_percentage)
```

```
## # A tibble: 6 x 4
## # Groups:   year [6]
##    year `Communicable diseases` Injuries   `Non-communicable diseases`
##   <int> <chr>                   <chr>      <chr>
## 1  1990 16.1 (34.0%)            4.3 (9.1%) 27.0 (56.9%)
## 2  1995 15.4 (30.9%)            4.6 (9.3%) 29.9 (59.8%)
## 3  2000 14.8 (28.9%)            4.8 (9.4%) 31.5 (61.7%)
## 4  2005 13.9 (26.5%)            4.8 (9.2%) 33.6 (64.2%)
## 5  2010 12.4 (23.2%)            5.0 (9.3%) 36.3 (67.6%)
## 6  2013 11.8 (21.5%)            4.8 (8.7%) 38.3 (69.7%)
```

3.11 Solution: Long Exercise

```
mydata %>%
  filter(year == 1990) %>%
  group_by(location, sex) %>%
  summarise(total_deaths = sum(deaths_millions)) %>%
  spread(location, total_deaths)
```

4

Different types of plots

4.1 Data

We will be using the gapminder dataset:

```
library(tidyverse)
library(gapminder)

mydata = gapminder

summary(mydata)
```

```
##         country        continent        year         lifeExp
##  Afghanistan:  12   Africa  :624   Min.   :1952   Min.   :23.60
##  Albania    :  12   Americas:300   1st Qu.:1966   1st Qu.:48.20
##  Algeria    :  12   Asia    :396   Median :1980   Median :60.71
##  Angola     :  12   Europe  :360   Mean   :1980   Mean   :59.47
##  Argentina  :  12   Oceania : 24   3rd Qu.:1993   3rd Qu.:70.85
##  Australia  :  12                  Max.   :2007   Max.   :82.60
##  (Other)    :1632
##       pop              gdpPercap
##  Min.   :6.001e+04   Min.   :   241.2
##  1st Qu.:2.794e+06   1st Qu.:  1202.1
##  Median :7.024e+06   Median :  3531.8
##  Mean   :2.960e+07   Mean   :  7215.3
##  3rd Qu.:1.959e+07   3rd Qu.:  9325.5
##  Max.   :1.319e+09   Max.   :113523.1
##
```

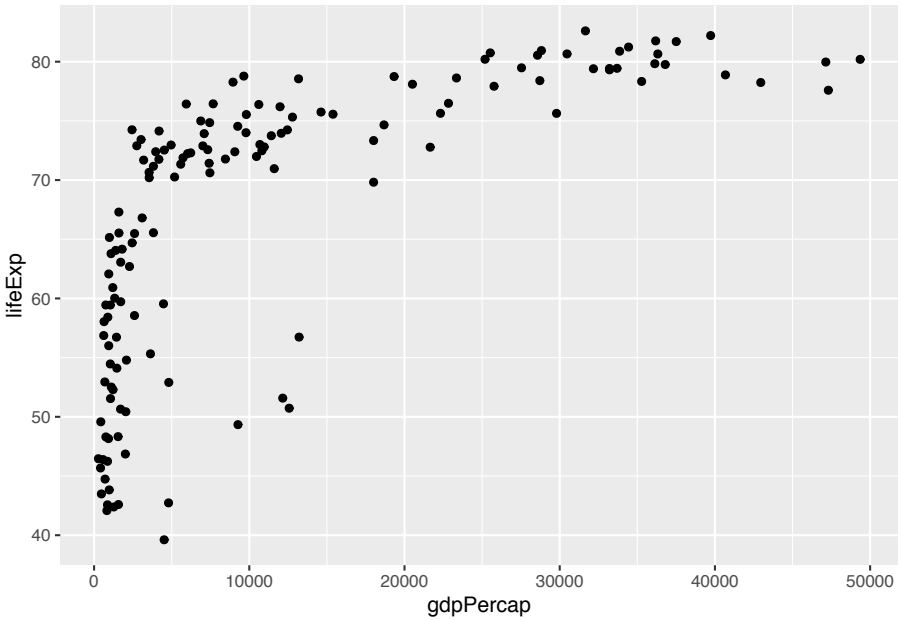
```
mydata$year %>% unique()
```

```
##  [1] 1952 1957 1962 1967 1972 1977 1982 1987 1992 1997 2002 2007
```

4.2 Scatter plots/bubble plots - `geom_point()`

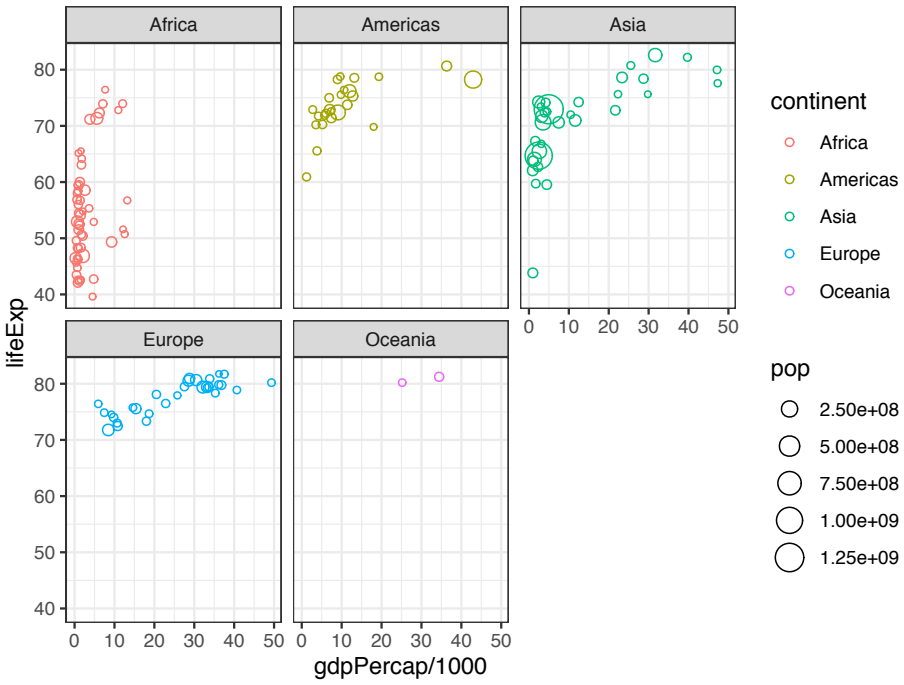
Plot life expectancy against GDP per capita (`x = gdpPercap`, `y=lifeExp`) at year 2007:

```
mydata %>%
  filter(year == 2007) %>%
  ggplot(aes(x = gdpPercap, y=lifeExp)) +
  geom_point()
```



4.2.1 Exercise

Follow the step-by-step instructions to transform the grey plot just above into this:

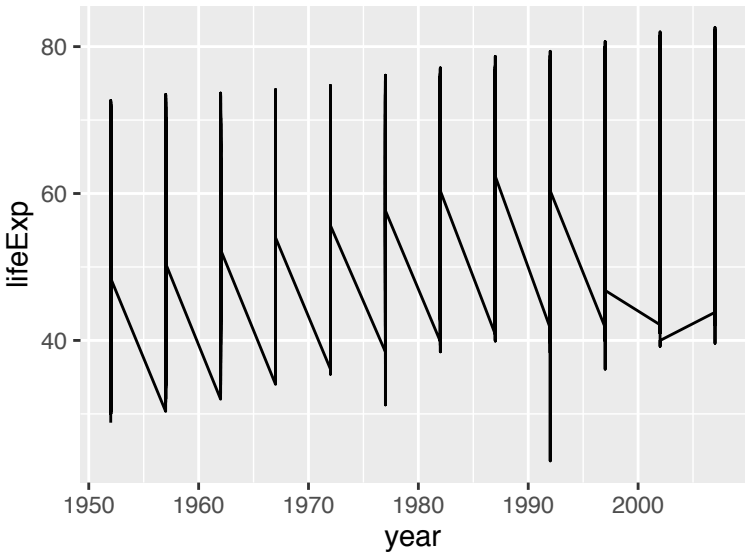


- Add points: `geom_point()`
  - Change point type: `shape = 1` (or any number from your Quickstart Sheet) inside the `geom_point()`
- Colour each country point by its continent: `colour=continent` to aes()
- Size each country point by its population: `size=pop` to aes()
- Put the country points of each continent on a separate panel: `+ facet_wrap(~continent)`
- Make the background white: `+ theme_bw()`

4.3 Line chart/timeplot - `geom_line()`

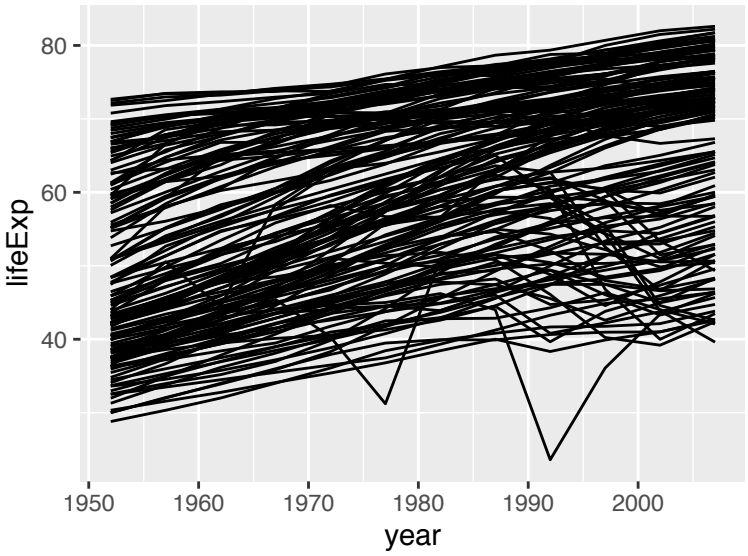
Plot life expectancy against year (`x = year, y=lifeExp`), add `geom_line()`:

```
mydata %>%
  ggplot(aes(x = year, y=lifeExp)) +
  geom_line()
```



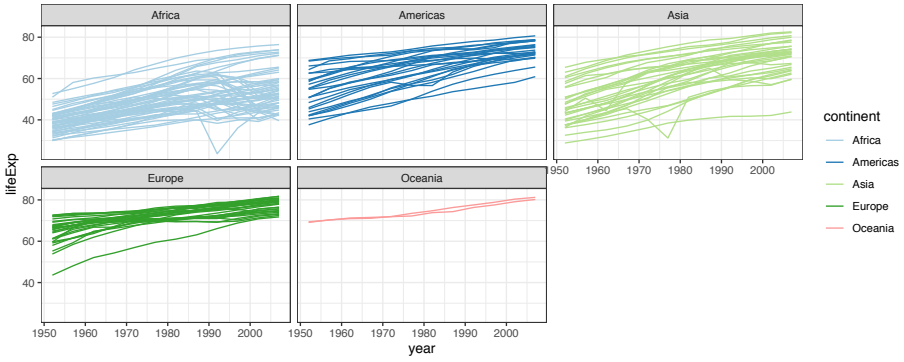
The reason you now see this weird zig-zag is that, using the above code, R does not know you want a connected line for each country. Specify how you want data points grouped to lines: `group = country` in `aes()`:

```
mydata %>%
  ggplot(aes(x = year, y=lifeExp, group = country)) +
  geom_line()
```



4.3.1 Exercise

Follow the step-by-step instructions to transform the grey plot just above into this:

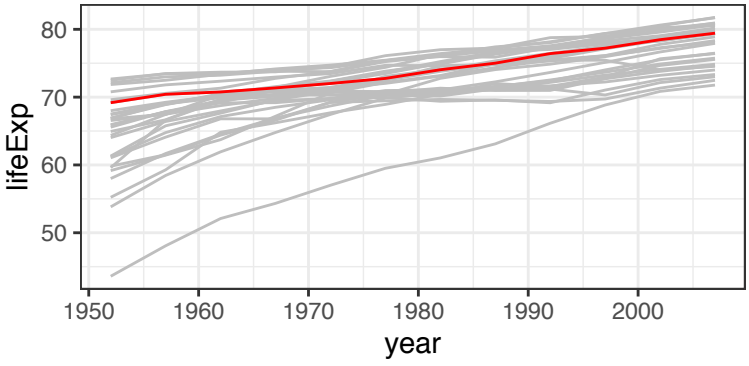


- Colour lines by continents: `colour=continent` to `aes()`
- *Similarly to what we did in `geom_point()`, you can even size the line thicknesses by each country's population:* `size=pop` *to* `aes()`
- Continents on separate panels: `+ facet_wrap(~continent)`
- Make the background white: `+ theme_bw()`
- Use a nicer colour scheme: `+ scale_colour_brewer(palette = "Paired")`

4.3.2 Advanced example

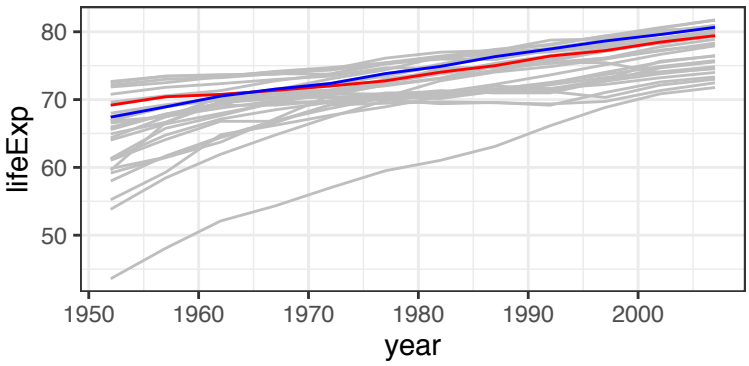
For European countries only (`filter(continent == "Europe") %>%`), plot life expectancy over time in grey colour for all countries, then add United Kingdom as a red line:

```
mydata %>%
  filter(continent == "Europe") %>% #Europe only
  ggplot(aes(x = year, y=lifeExp, group = country)) +
  geom_line(colour = "grey") +
  theme_bw() +
  geom_line(data = filter(mydata, country == "United Kingdom"), colour = "red")
```



4.3.3 Advanced Exercise

As previous, but add a line for France in blue:

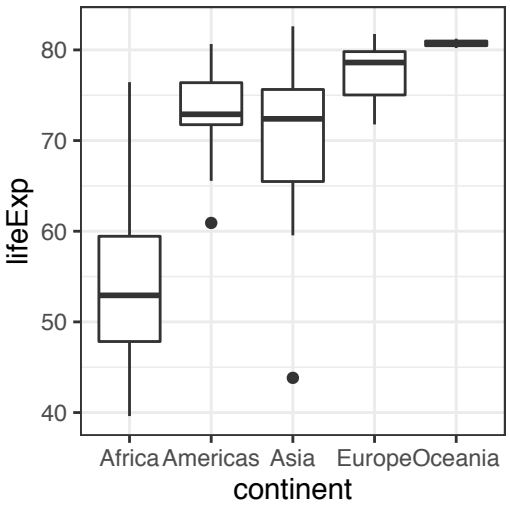


4.4 Box-plot - `geom_boxplot()`

Plot the distribution of life expectancies within each continent at year 2007:

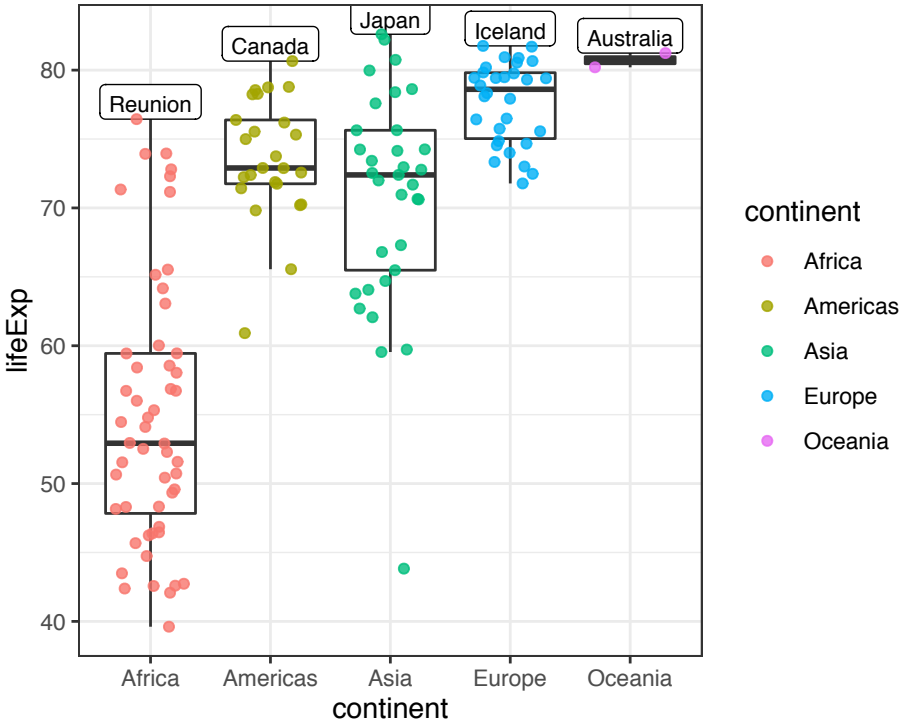
- `filter(year == 2007) %>%`
- `x = continent, y = lifeExp`
- `+ geom_boxplot()`

```
mydata %>%
  filter(year == 2007) %>%
  ggplot(aes(x = continent, y = lifeExp)) +
  geom_boxplot() +
  theme_bw()
```



4.4.1 Exercise

Add individual (country) points on top of the box plot:



Hint: Use `geom_jitter()` instead of `geom_point()` to reduce overlap by spreading the points horizontally. Include the `width=0.3` option to reduce the width of the jitter.

Optional:

Include text labels for the highest life expectancy country of each continent.

Hint 1 Create a separate dataframe called `label_data` with the maximum countries for each continent:

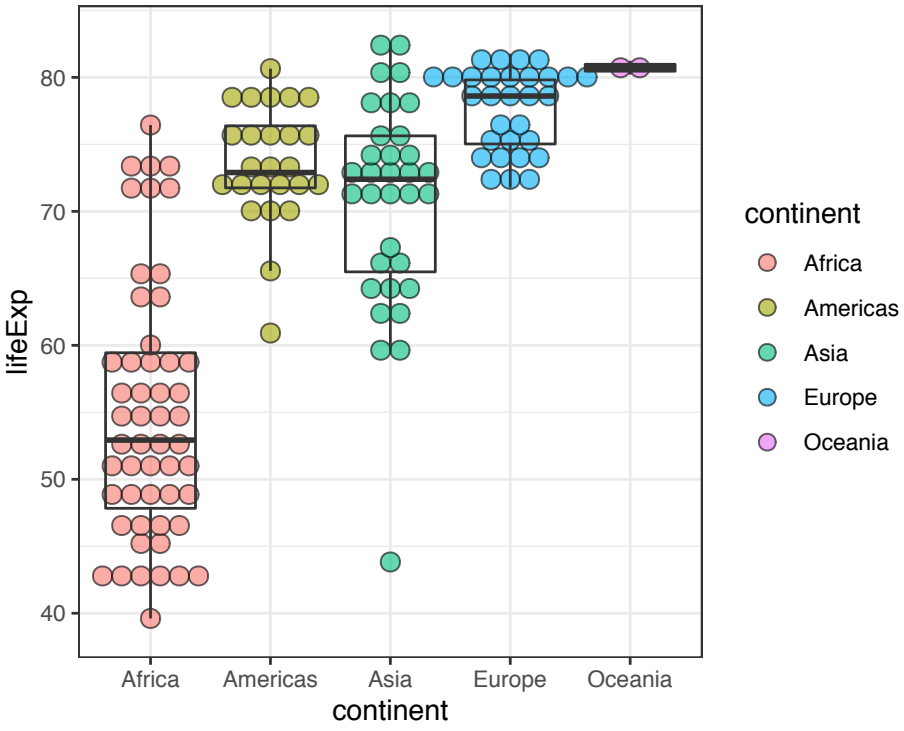
```
label_data = mydata %>%
  filter(year == max(year)) %>% # same as year == 2007
  group_by(continent) %>%
  filter(lifeExp == max(lifeExp) )
```

Hint 2 Add `geom_label()` with appropriate `aes()`:

```
+ geom_label(data = label_data, aes(label=country), vjust = 0)
```

4.4.2 Dot-plot - `geom_dotplot()`

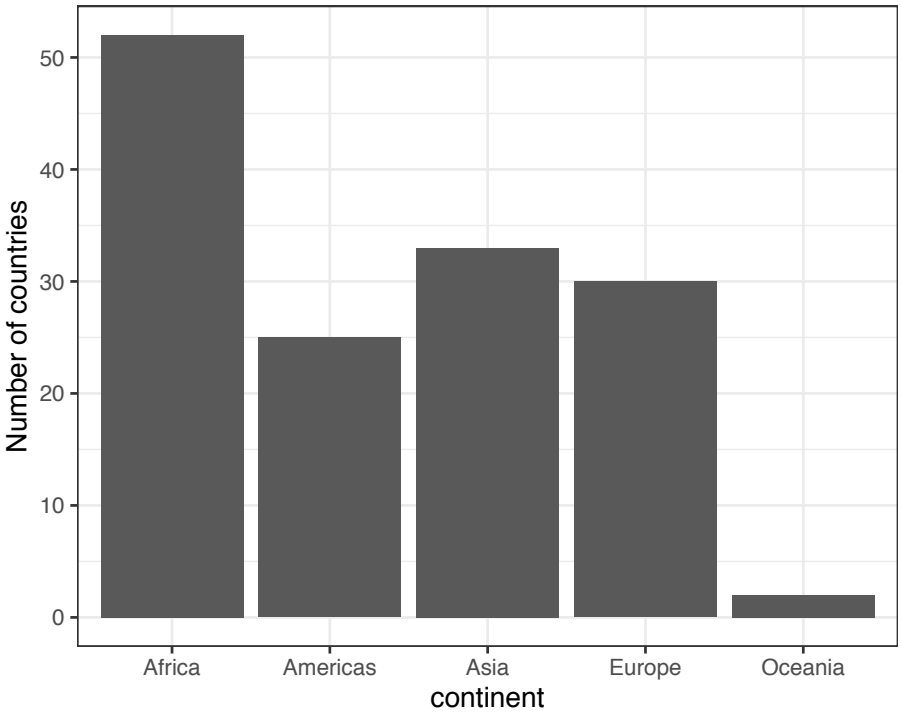
```
geom_dotplot(aes(fill=continent), binaxis = 'y', stackdir = 'center',
alpha=0.6)
```



4.5 Barplot - `geom_bar()` and `geom_col()`

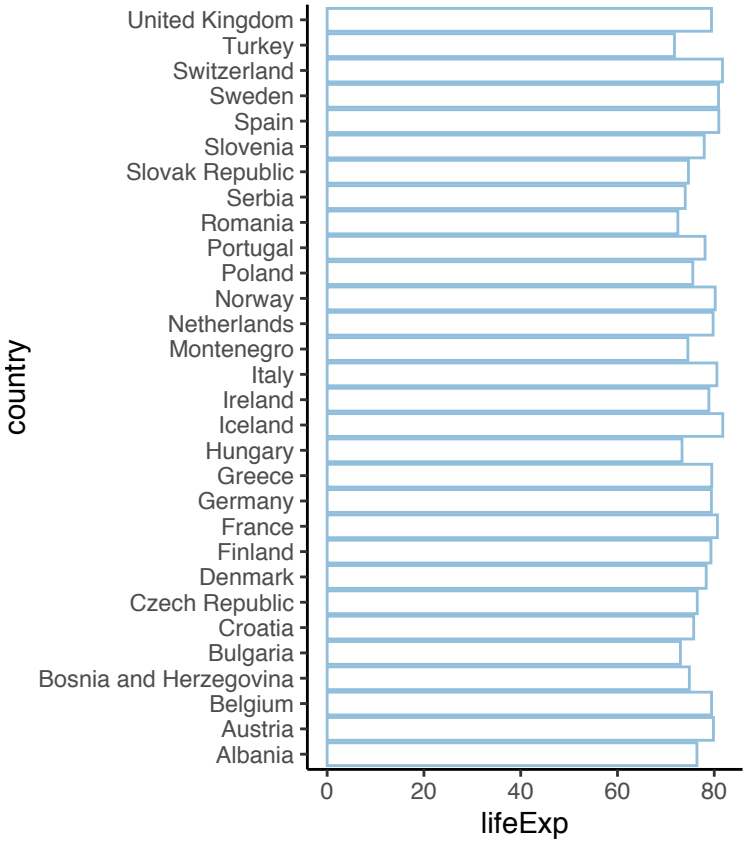
In the first module, we plotted barplots from already summarised data (using the `geom_col`), but `geom_bar()` is perfectly happy to count up data for you. For example, we can plot the number of countries in each continent without summarising the data beforehand:

```
mydata %>%
  filter(year == 2007) %>%
  ggplot(aes(x = continent)) +
  geom_bar() +
  ylab("Number of countries") +
  theme_bw()
```



4.5.1 Exercise

Create this barplot of life expectancies in European countries (year 2007). Hint: `coord_flip()` makes the bars horizontal, `fill = NA` makes them empty, have a look at your QuickStar sheet for different themes.



4.6 All other types of plots

These are just some of the main ones, see this gallery for more options: http://www.r-graph-gallery.com/portfolio/ggplot2-package/

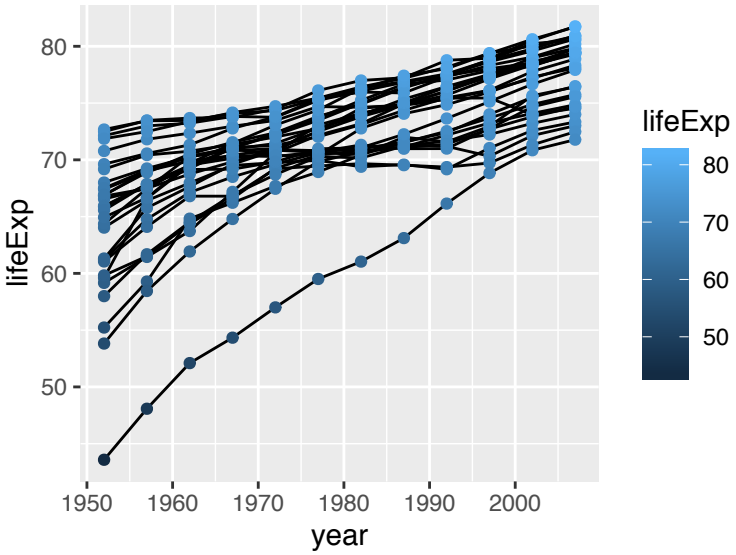
And the `ggplot()` documentation: http://docs.ggplot2.org/

Remember that you can always combine different types of plots - i.e. add lines or points on bars, etc.

4.7 Specifying `aes()` variables

The `aes()` variables wrapped inside `ggplot()` will be taken into account by all geoms. If you put `aes(colour = lifeExp)` inside `geom_point()`, only points will be coloured:

```
mydata %>%
  filter(continent == "Europe") %>%
  ggplot(aes(x = year, y = lifeExp, group = country)) +
  geom_line() +
  geom_point(aes(colour = lifeExp))
```

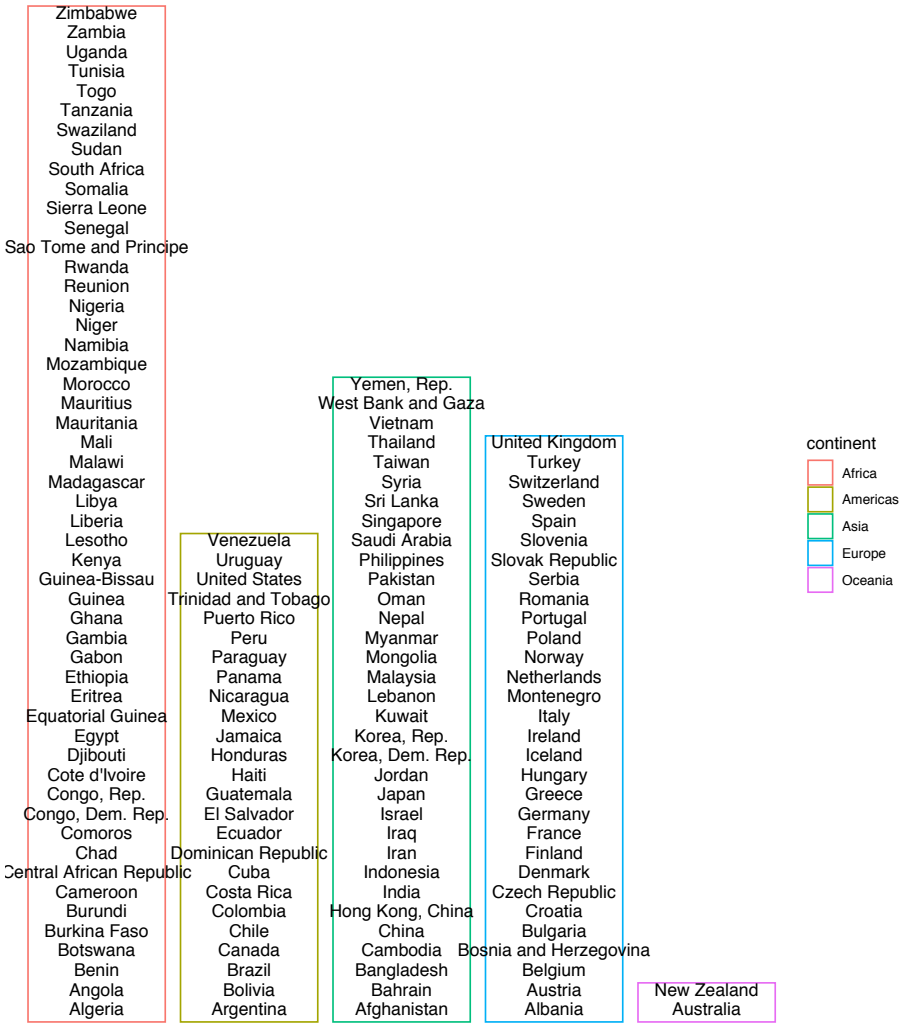


4.8 Extra: Optional exercises

4.8.1 Exercise

Make this:

```
mydata$dummy = 1  # create a column called "dummy" that includes number 1 for each country

mydata2007 = mydata %>%
  filter(year==max(year)) %>%
  group_by(continent) %>%
  mutate(country_number = cumsum(dummy))  # create a column called "country_number" that
  # is a cumulative sum of the number of countries before it - basically indexing


mydata2007 %>%
  ggplot(aes(x = continent)) +
  geom_bar(aes(colour=continent), fill = NA) +
  geom_text(aes(y = country_number, label=country), size=4, vjust=1, colour='black')+
  theme_void()
```

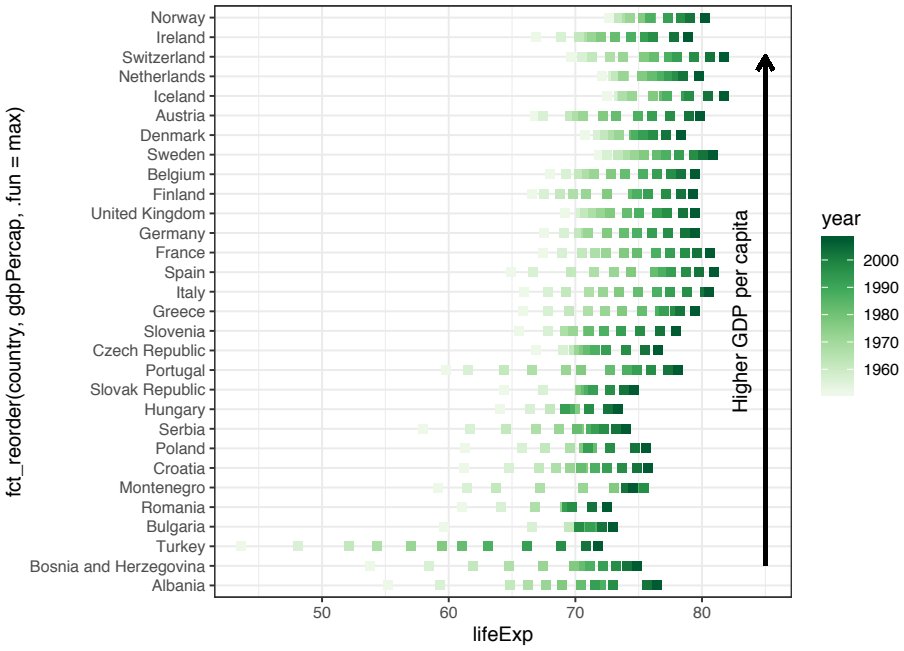

Zimbabwe
Zambia
Uganda
Tunisia
Togo
Tanzania
Swaziland
Sudan
South Africa
Somalia
Sierra Leone
Senegal
Sao Tome and Principe
Rwanda
Reunion
Nigeria
Niger
Namibia
Mozambique
Morocco
Mauritius
Mauritania
Mali
Malawi
Madagascar
Libya
Liberia
Lesotho
Kenya
Guinea-Bissau
Guinea
Ghana
Gambia
Gabon
Ethiopia
Eritrea
Equatorial Guinea
Egypt
Djibouti
Cote d'Ivoire
Congo, Rep.
Congo, Dem. Rep.
Comoros
Chad
Central African Republic
Cameroon
Burundi
Burkina Faso
Botswana
Benin
Angola
Algeria
Venezuela
Uruguay
United States
Trinidad and Tobago
Puerto Rico
Peru
Paraguay
Panama
Nicaragua
Mexico
Jamaica
Honduras
Haiti
Guatemala
El Salvador
Ecuador
Dominican Republic
Cuba
Costa Rica
Colombia
Chile
Canada
Brazil
Bolivia
Argentina
Yemen, Rep.
West Bank and Gaza
Vietnam
Thailand
Taiwan
Syria
Sri Lanka
Singapore
Saudi Arabia
Philippines
Pakistan
Oman
Nepal
Myanmar
Mongolia
Malaysia
Lebanon
Kuwait
Korea, Rep.
Korea, Dem. Rep.
Jordan
Japan
Israel
Iraq
Iran
Indonesia
India
Hong Kong, China
China
Cambodia
Bangladesh
Bahrain
Afghanistan
United Kingdom
Turkey
Switzerland
Sweden
Spain
Slovenia
Slovak Republic
Serbia
Romania
Portugal
Poland
Norway
Netherlands
Montenegro
Italy
Ireland
Iceland
Hungary
Greece
Germany
France
Finland
Denmark
Czech Republic
Croatia
Bulgaria
Bosnia and Herzegovina
Belgium
Austria
Albania
New Zealand
Australia
continent
Africa
Americas
Asia
Europe
Oceania

4.8.2 Exercise

Make this:

Hints: `coord_flip()`, `scale_color_gradient(...)`, `geom_segment(...)`, `annotate("text", ...)`

```
mydata %>%
  filter(continent == "Europe") %>%
  ggplot(aes(y = fct_reorder(country, gdpPercap, .fun=max), x=lifeExp, colour=year)) +
  geom_point(shape = 15, size = 2) +
  theme_bw() +
  scale_colour_distiller(palette = "Greens", direction = 1) +
  geom_segment(aes(yend = "Switzerland", x = 85, y = "Bosnia and Herzegovina", xend = 85),
               colour = "black", size=1,
               arrow = arrow(length = unit(0.3, "cm"))) +
  annotate("text", y = "Greece", x=83, label = "Higher GDP per capita", angle = 90)
```



4.9 Solutions

4.2.1

```
mydata %>%
  filter(year == 2007) %>%
  ggplot(  aes(x = gdpPercap/1000, #divide by 1000 to tidy the x-axis
               y=lifeExp,
               colour=continent,
               size=pop)) +
  geom_point(shape = 1) +
  facet_wrap(~continent) +
  theme_bw()
```

4.3.1

```
mydata %>%
  ggplot(  aes(x = year, y=lifeExp, group = country, colour=continent)) +
  geom_line() +
  facet_wrap(~continent) +
  theme_bw() +
  scale_colour_brewer(palette = "Paired")
```

which

Add `+  geom_line(data = filter(mydata, country == "France"), colour = "blue")`

4.4.1

```
mydata %>%
  filter(year == 2007) %>%
  ggplot(aes(x = continent, y = lifeExp)) +
  geom_boxplot(outlier.shape = NA) +
  geom_jitter(aes(colour=continent), width=0.3, alpha=0.8) + #width defaults to 0.8 of box width
  theme_bw()
```

```
mydata %>%
  filter(year == 2007) %>%
  ggplot(aes(x = continent, y = lifeExp)) +
  geom_boxplot(outlier.shape = NA) +
  geom_jitter(aes(colour=continent), width=0.3, alpha=0.8)
  theme_bw()
```

4.5.1

```
mydata %>%
  filter(year == 2007) %>%
  filter(continent == "Europe") %>%
  ggplot(aes(x = country, y = lifeExp)) +
  geom_col(colour = "#91bfdb", fill = NA) +
  coord_flip() +
  theme_classic()
```

5

Fine tuning plots

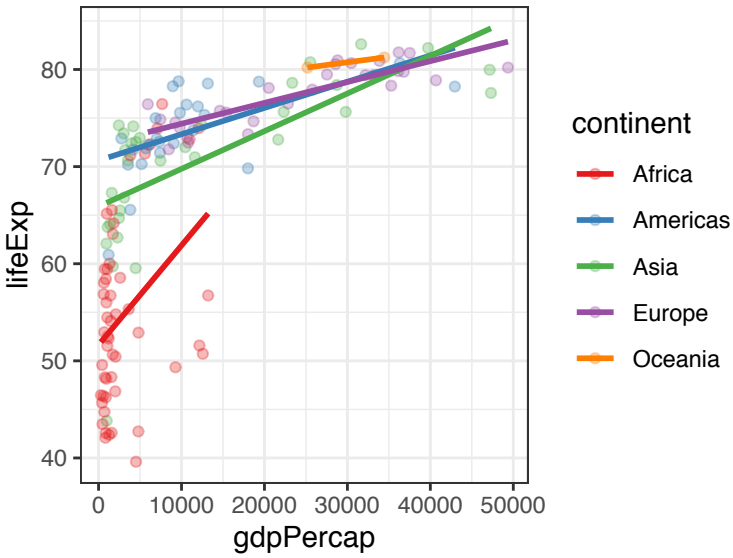
5.1 Data and initial plot

We can save a `ggplot()` object into a variable (usually called `p` but can be any name). This then appears in the Environment tab. To plot it it needs to be recalled on a separate line. Saving a plot into a variable allows us to modify it later (e.g., `p + theme_bw()`).

```
library(gapminder)
library(tidyverse)

mydata = gapminder

mydata$year %>% unique()
```

```
##  [1] 1952 1957 1962 1967 1972 1977 1982 1987 1992 1997 2002 2007
```

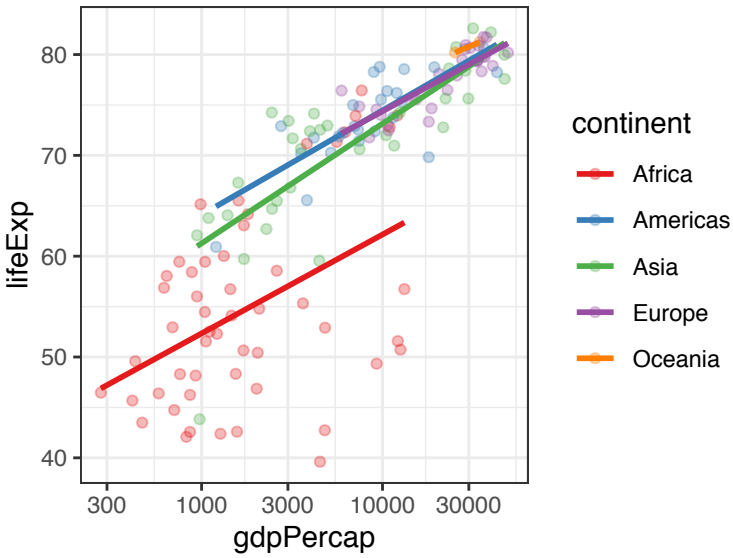
```
p = mydata %>%
  filter(year == 2007) %>%
  group_by(continent, year) %>%
  ggplot(aes(y = lifeExp, x = gdpPercap, colour = continent)) +
  geom_point(alpha = 0.3) +
  theme_bw() +
  geom_smooth(method = "lm", se = FALSE) +
  scale_colour_brewer(palette = "Set1")

p
```



5.2 Scales

5.2.1 Logarithmic

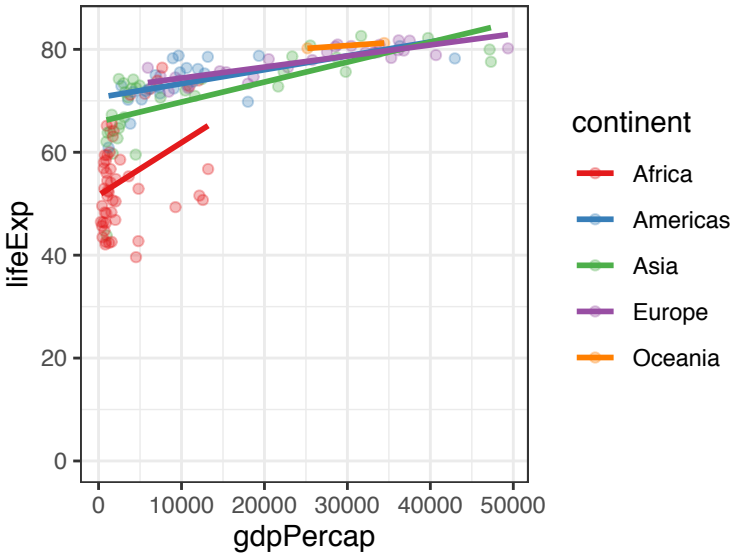
```
p +
  scale_x_log10()
```



5.2.2 Expand limits

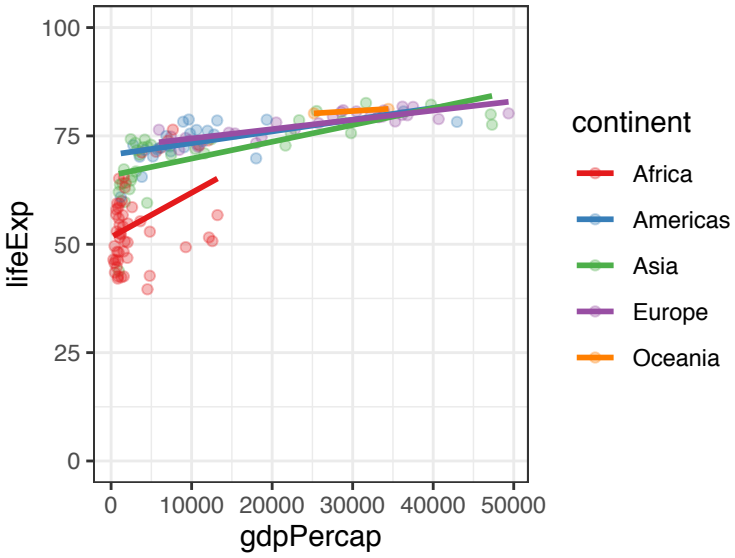
Specify the value you want to be included:

```
p +
  expand_limits(y = 0)
```



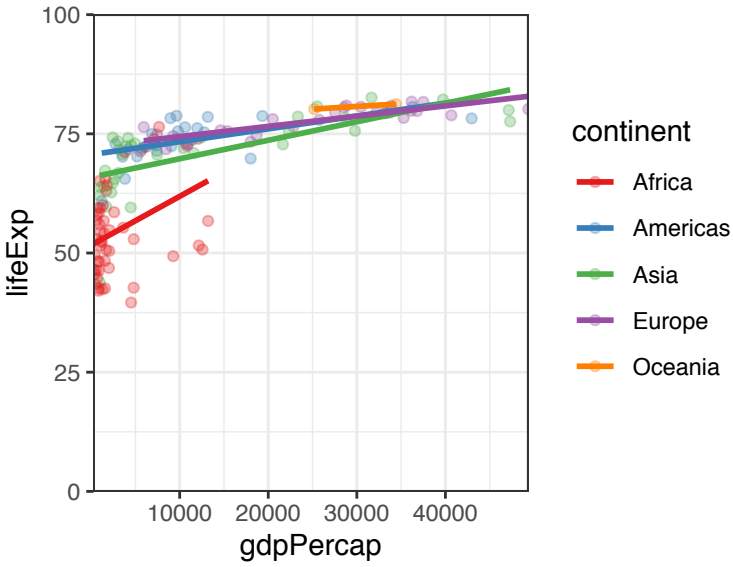
Or two:

```
p +
  expand_limits(y = c(0, 100))
```



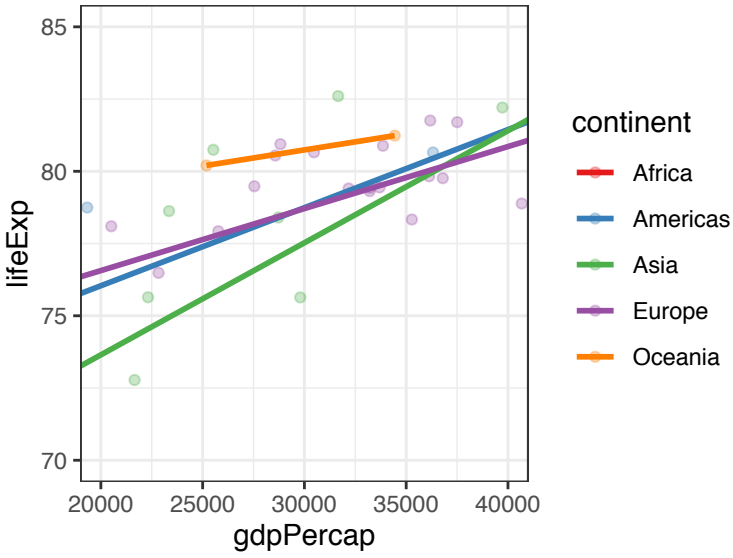
By default, `ggplot()` adds some padding around the included area (see how the scale doesn't start from 0, but slightly before). You can remove this padding with the expand option:

```
p +
  expand_limits(y = c(0, 100)) +
  coord_cartesian(expand = FALSE)
```



5.2.3 Zoom in

```
p +
  coord_cartesian(ylim = c(70, 85), xlim = c(20000, 40000))
```



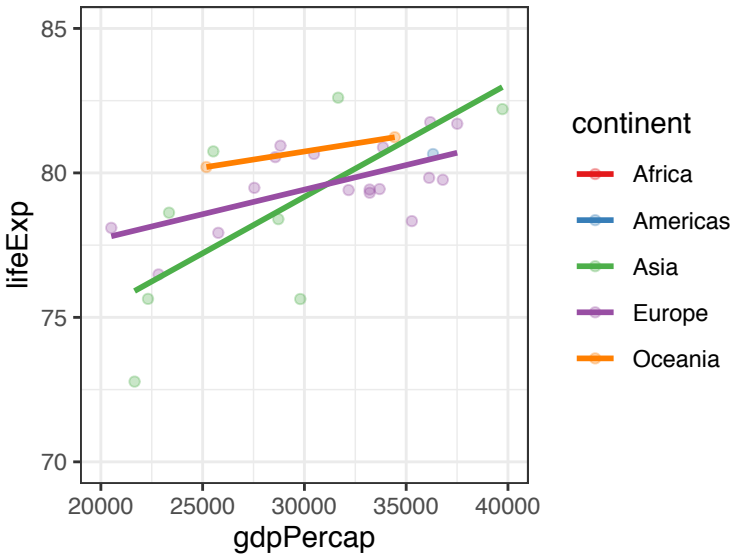
5.2.4 Exercise

How is this one different to the previous?

```
p +
  scale_y_continuous(limits = c(70, 85)) +
  scale_x_continuous(limits = c(20000, 40000))
```

```
## Warning: Removed 114 rows containing non-finite values (stat_smooth).
```

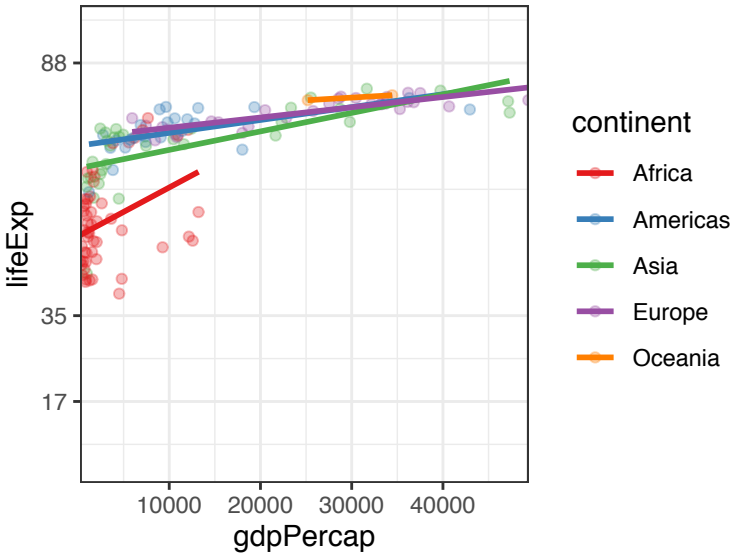
```
## Warning: Removed 114 rows containing missing values (geom_point).
```



Answer: the first one zooms in, still retaining information about the excluded points when calculating the linear regression lines. The second one removes the data (as the warnings say), calculating the linear regression lines only for the visible points.

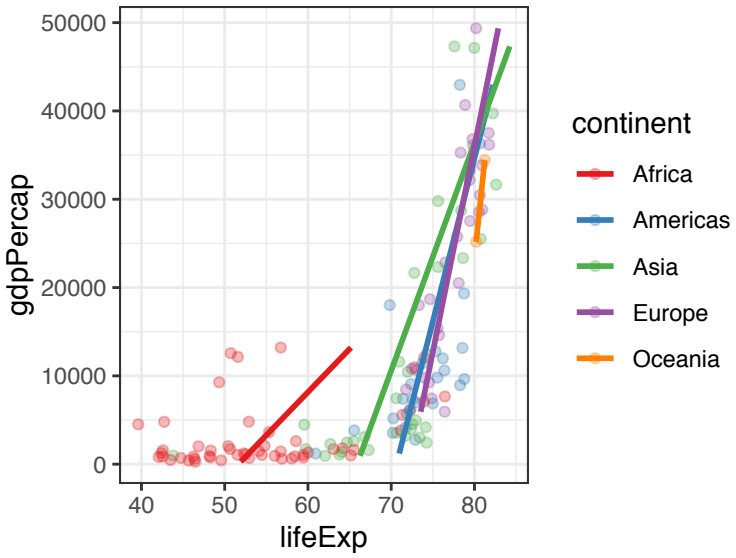
5.2.5 Axis ticks

```
p +
  coord_cartesian(ylim = c(0, 100), expand = 0) +
  scale_y_continuous(breaks = c(17, 35, 88))
```



5.2.6 Swap the axes

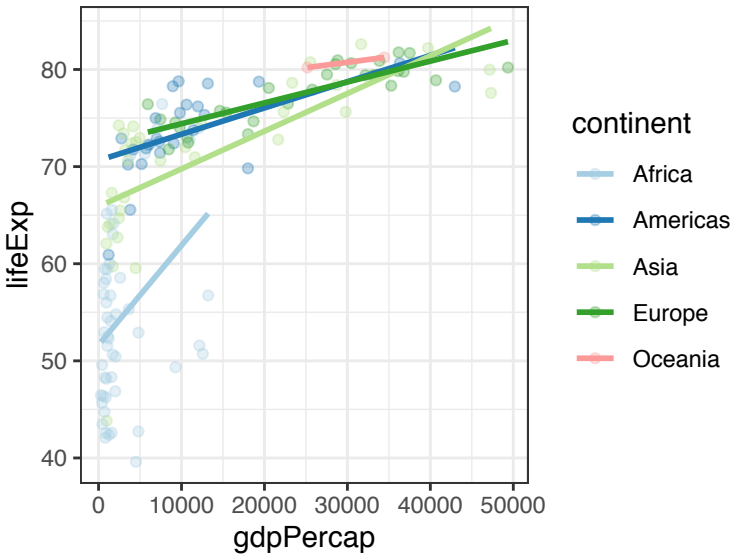
```
p +
  coord_flip()
```



5.3 Colours

5.3.1 Using the Brewer palettes:

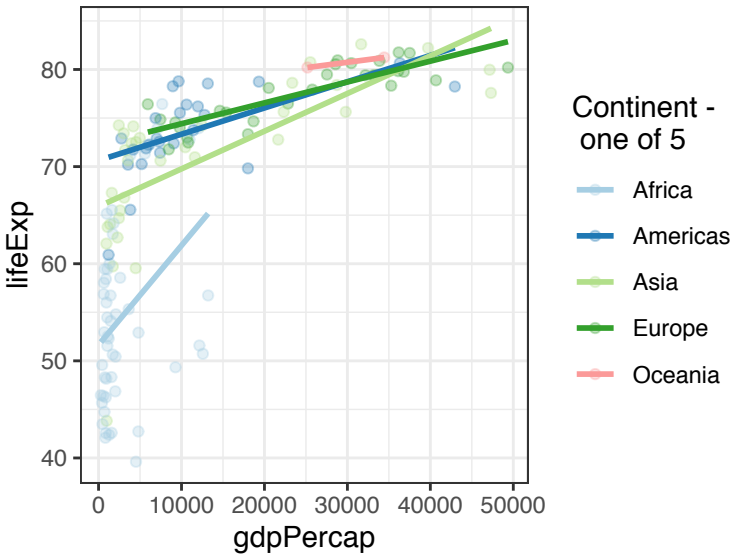
```
p +
  scale_color_brewer(palette = "Paired")
```



5.3.2 Legend title

`scale_colour_brewer()` is also a conventient place to change the legend title:

```
p +
  scale_color_brewer("Continent - \n one of 5", palette = "Paired")
```

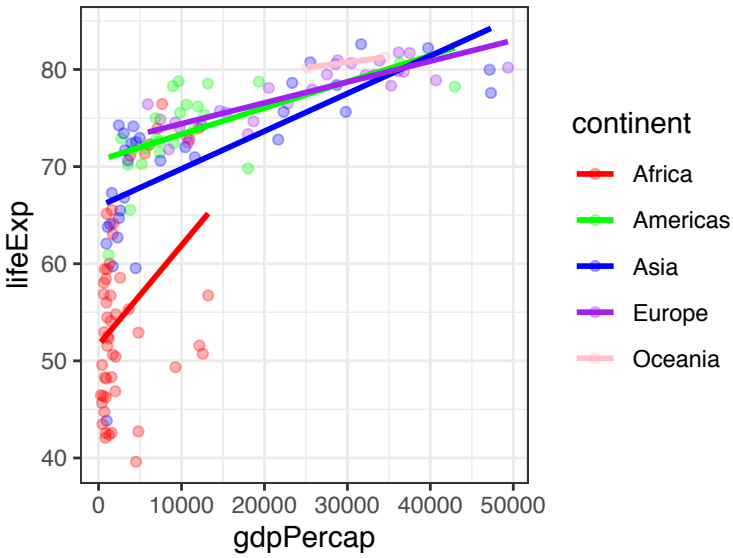


Note the `\n` inside the new legend title - new line.

5.3.3 Choosing colours manually

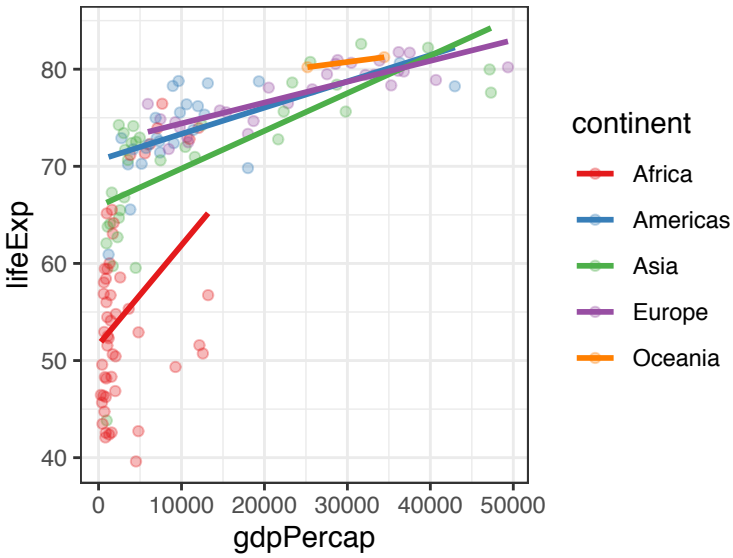
Use words:

```
p +
  scale_color_manual(values = c("red", "green", "blue", "purple", "pink"))
```



Or HEX codes (either from http://colorbrewer2.org/ or any other resource):

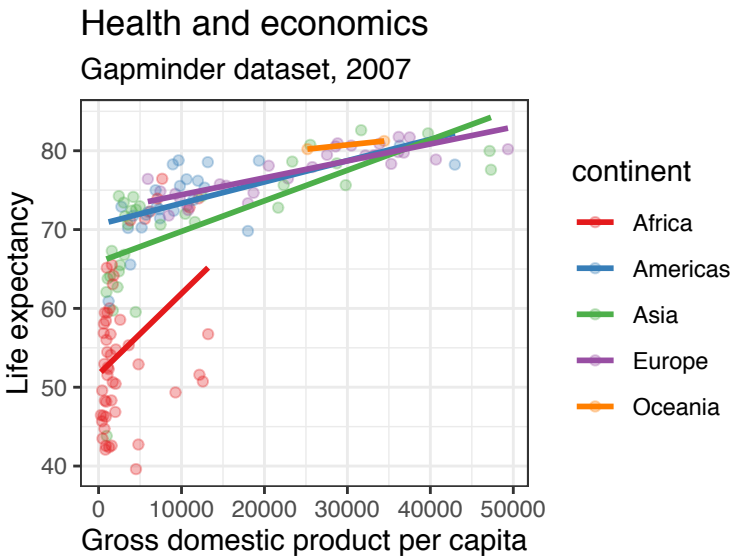
```
p +
  scale_color_manual(values = c("#e41a1c", "#377eb8", "#4daf4a", "#984ea3", "#ff7f00"))
```



Note that http://colorbrewer2.org/ also has options for *Colourblind safe* and *Print friendly*.

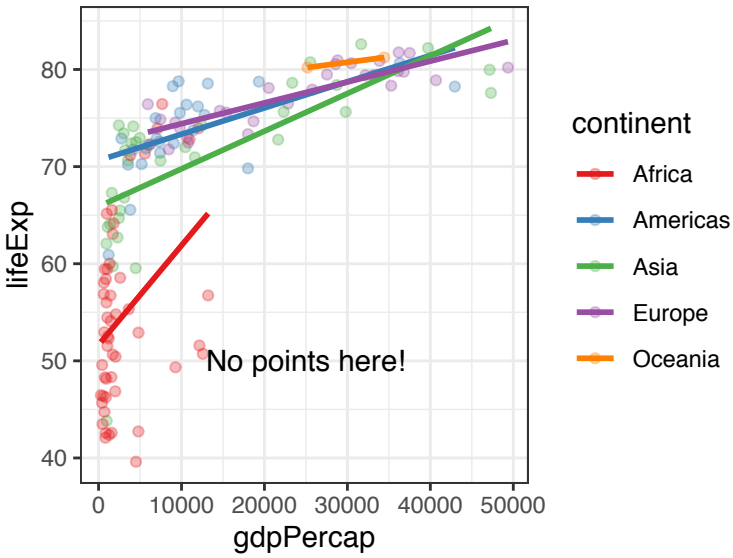
5.4 Titles and labels

```
p +
  labs(x = "Gross domestic product per capita",
       y = "Life expectancy",
       title = "Health and economics",
       subtitle = "Gapminder dataset, 2007")
```

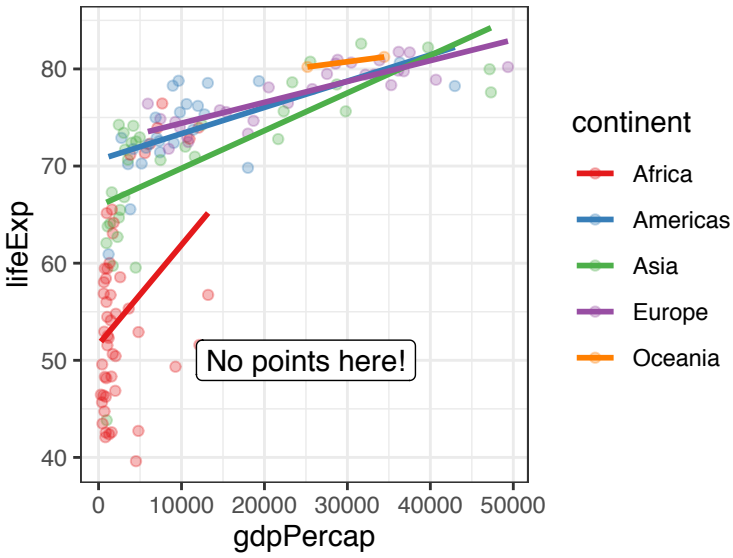


5.4.1 Annotation

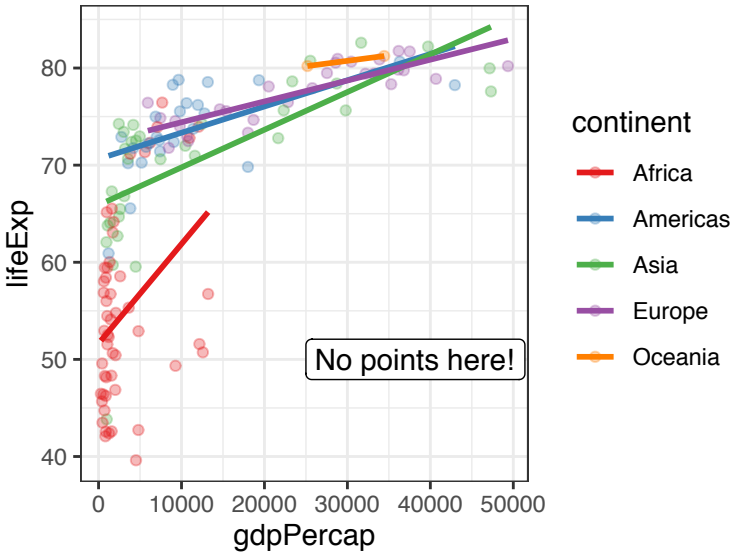
```
p +
  annotate("text",
           x = 25000,
           y = 50,
           label = "No points here!")
```




```
p +
  annotate("label",
           x = 25000,
           y = 50,
           label = "No points here!")
```



```
p +
  annotate("label",
           x = 25000,
           y = 50,
           label = "No points here!",
           hjust = 0)
```

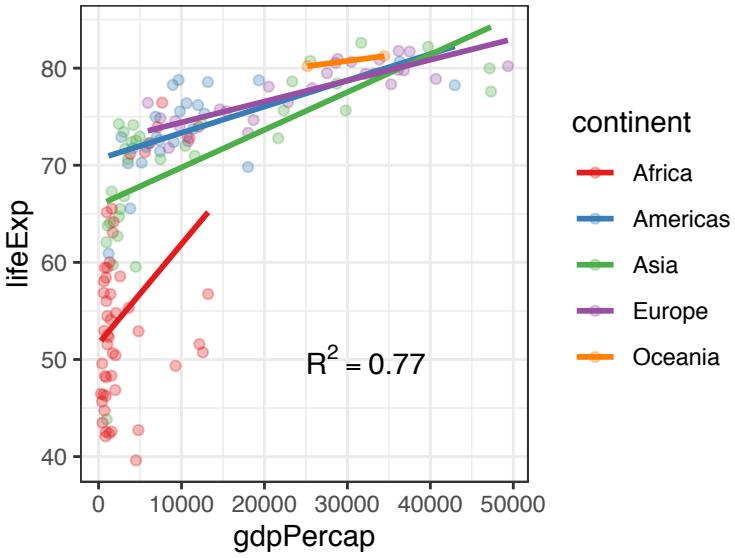


`hjust` stand for horizontal justification. It's default value is 0.5 (see how the label was centered at 25,000 - our chosen x location), 0 means the label goes to the right from 25,000, 1 would make it end at 25,000.

5.4.2 Annotation with a superscript and a variable

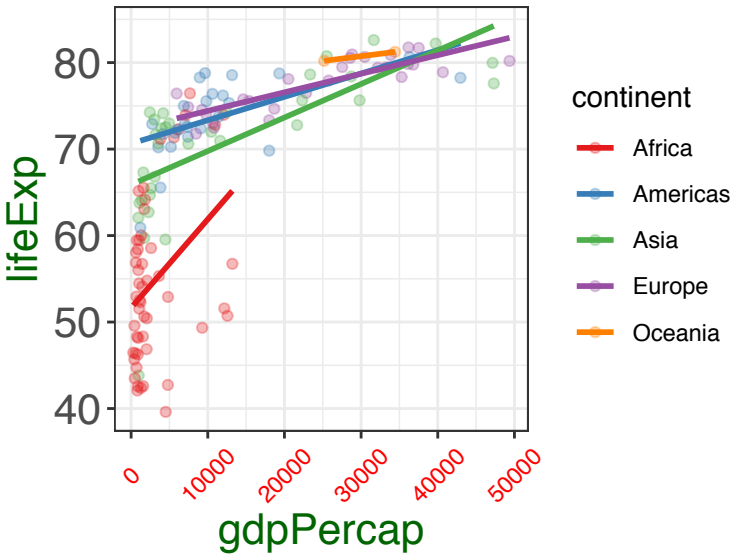
```
fit_glance = data.frame(r.squared = 0.7693465)


plot_rsquared = paste0(
  "R^2 == ",
  fit_glance$r.squared %>% round(2))


p +
```

```
  annotate("text",
           x = 25000,
           y = 50,
           label = plot_rsquared, parse = TRUE,
           hjust = 0)
```



5.5 Text size

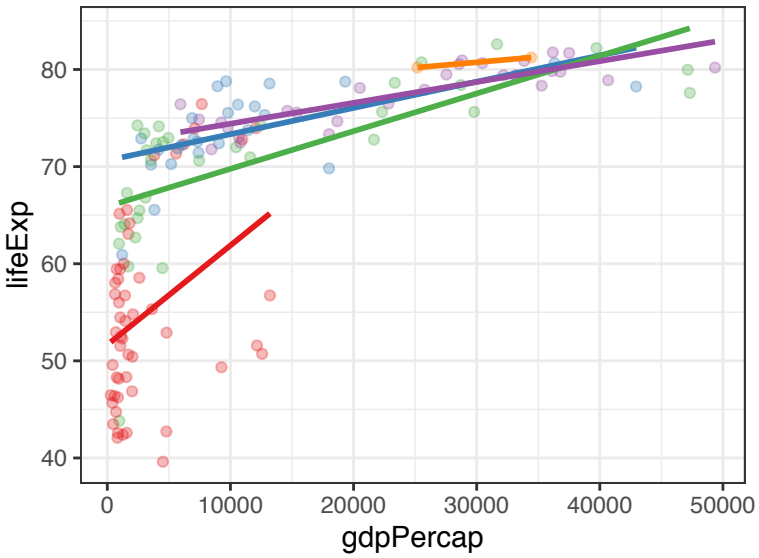
```
p +
  theme(axis.text.y = element_text(size = 16),
        axis.text.x = element_text(colour = "red", angle = 45, vjust = 0.5),
        axis.title = element_text(size = 16, colour = "darkgreen")
        )
```



5.5.1 Legend position

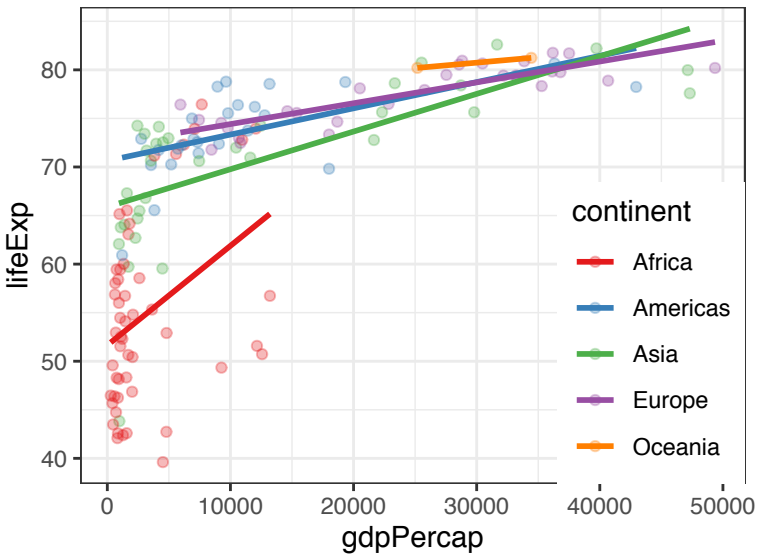
Use the following words: `"right"`, `"left"`, `"top"`, `"bottom"`, or `"none"` to remove the legend.

```
p +
  theme(legend.position = "none")
```

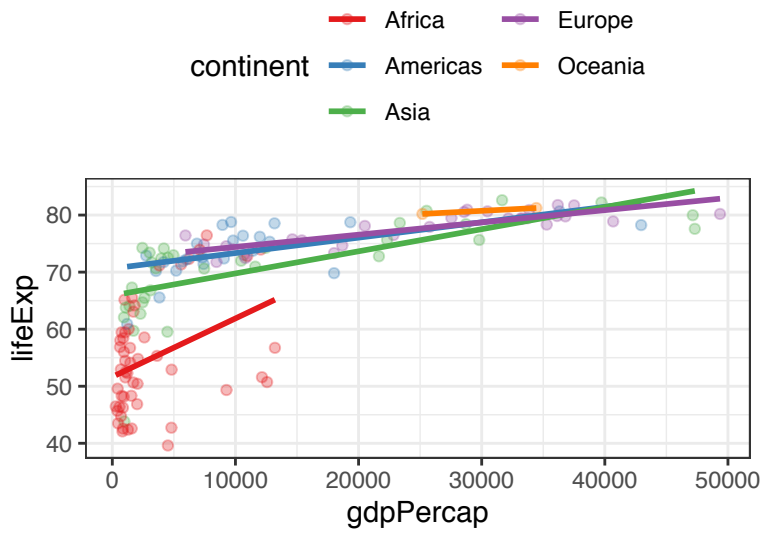


Or use relative coordinates (0–1) to give it an -y location:

```
p +
  theme(legend.position      = c(1,0),
        legend.justification = c(1,0)) #bottom-right corner
```



```
p +
  theme(legend.position = "top") +
  guides(colour = guide_legend(ncol = 2))
```



5.6 Saving your plot

```
ggsave(p, file = "my_saved_plot.png", width = 5, height = 4)
```

Part II

Data analysis

In the second part of this book, we focus specifically on the business of data analysis. That is, formulating clear questions and seeking to answer them using available datasets.

Again, we emphasise the importance of understanding the underlying data through visualisation, rather than relying on statistical tests or, heaven forbid, the p-value alone.

There are five chapters. Testing for continuous outcome variables (6) leads naturally into Linear regression (7). We would expect the majority of actual analysis done by readers to be using the methods in chapter 7 rather than 6. Similarly, Testing for categorical outcome variables (8) leads naturally to Logistic regression (9), where we would expect the majority of work to focus. Chapters 6 and 8 however do provide helpful reminders of how to prepare data for these analyses and shouldn't be skipped. Time-to-event data introduces survival analysis and includes sections on the manipulation of dates.

6

Tests for continuous outcome variables

Continuous data can be measured.
Categorical data can be counted.

6.1 Continuous data

Continuous data is everywhere in healthcare. From physiological measures in patients such as systolic blood pressure or pulmonary function tests, through to populations measures like life expectancy or disease incidence, the analysis of continuous outcome measures is common and important.

Our goal in most health data questions, is to draw a conclusion on a comparison between groups. For instance, understanding differences life expectancy between the year 2002 and 2007 or between the Africa and Europe, is usually more useful than simply describing the average life expectancy across the entire world across all of time.

The basis for comparisons between continuous measures is the distribution of the data. That word, as many which have a statistical flavour, brings on the sweats in a lot of people. It needn't. By distribution, we are simply referring to the shape of the data.

6.2 The Question

The examples in this chapter all use the data introduced previously from the amazing Gapminder project[1]. We will start by looking at the life expectancy of populations over time and in different geographical regions.

6.3 Get the data

```
# Load packages
library(tidyverse)
library(finalfit)
library(gapminder)

# Create object mydata from object gapminder
mydata = gapminder
```

6.4 Check the data

It is vital that data is carefully inspected when first read. The three functions below provide a clear summary allowing errors or miscoding to be quickly identified. It is particularity important to ensure that any missing data is identified. If you don't do this you will regret it! There are many times when an analysis has got to a relatively advanced stage before research realised the dataset was incomplete.

[1] https://www.gapminder.org/

```
glimpse(mydata) # each variable as line, variable type, first values
```

```
## Observations: 1,704
## Variables: 6
## $ country   <fct> Afghanistan, Afghanistan, Afghanistan, Afghanistan, ...
## $ continent <fct> Asia, Asia, Asia, Asia, Asia, Asia, Asia, Asia, Asia...
## $ year      <int> 1952, 1957, 1962, 1967, 1972, 1977, 1982, 1987, 1992...
## $ lifeExp   <dbl> 28.801, 30.332, 31.997, 34.020, 36.088, 38.438, 39.8...
## $ pop       <int> 8425333, 9240934, 10267083, 11537966, 13079460, 1488...
## $ gdpPercap <dbl> 779.4453, 820.8530, 853.1007, 836.1971, 739.9811, 78...
```

```
missing_glimpse(mydata) # missing data for each variable
```

```
##               label var_type    n missing_n missing_percent
## country     country    <fct> 1704         0             0.0
## continent continent    <fct> 1704         0             0.0
## year           year    <int> 1704         0             0.0
## lifeExp     lifeExp    <dbl> 1704         0             0.0
## pop             pop    <int> 1704         0             0.0
## gdpPercap gdpPercap    <dbl> 1704         0             0.0
```

```
ff_glimpse(mydata) # summary statistics for each variable
```

```
## Continuous
##               label var_type    n missing_n missing_percent       mean
## year           year    <int> 1704         0             0.0     1979.5
## lifeExp     lifeExp    <dbl> 1704         0             0.0       59.5
## pop             pop    <int> 1704         0             0.0 29601212.3
## gdpPercap gdpPercap    <dbl> 1704         0             0.0     7215.3
##                     sd     min quartile_25    median quartile_75
## year              17.3  1952.0      1965.8    1979.5      1993.2
## lifeExp           12.9    23.6        48.2      60.7        70.8
## pop       106157896.7 60011.0   2793664.0 7023595.5  19585221.8
## gdpPercap      9857.5   241.2      1202.1    3531.8      9325.5
##                    max
## year            2007.0
## lifeExp           82.6
## pop       1318683096.0
## gdpPercap     113523.1
##
```

```
## Categorical
##               label var_type    n missing_n missing_percent levels_n
## country     country    <fct> 1704         0             0.0      142
## continent continent    <fct> 1704         0             0.0        5
##                                                        levels
## country                                                     -
## continent "Africa", "Americas", "Asia", "Europe", "Oceania"
##                      levels_count               levels_percent
## country                         -                            -
## continent 624, 300, 396, 360, 24 36.6, 17.6, 23.2, 21.1,  1.4
```

As can be seen, there are 6 variables, 4 are continuous and 2 are categorical. The categorical variables are already identified as `factors`. There are no missing data.

6.5 Plot the data

We will start by comparing life expectancy between the 5 continents of the world in two different years. Always plot your data first. Never skip this step! We are particularly interested in the distribution. There's that word again. The shape of the data. Is it normal? Is it skewed? Does it differ between regions and years?

There are three useful plots which can help here:

- Histograms: examine shape of data and compare groups;
- Q-Q plots: are data normally distributed?
- Box-plots: identify outliers, compare shape and groups.

6.5.1 Histogram

```
mydata %>%
    filter(year %in% c(2002, 2007)) %>%
    ggplot(aes(x = lifeExp)) +       # remember aes()
    geom_histogram(bins = 20) +      # histogram with 20 bars
    facet_grid(year ~ continent)     # add scale="free" for axes to vary
```

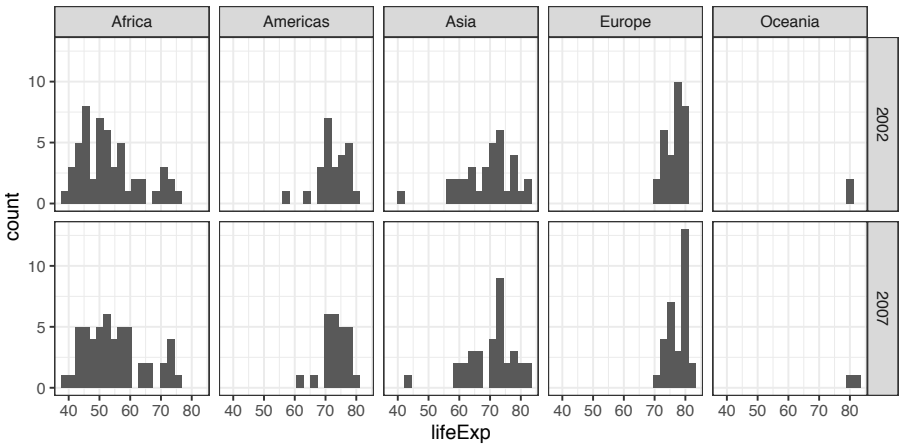


FIGURE 6.1: Histogram: country life expectancy by continent and year

What can we see? That life expectancy in Africa is lower than in other regions. That we have little data for Oceania given there are only two countries included, Australia and New Zealand. That Africa and Asia have great variability in life expectancy by country than in the Americas or Europe. That the data follow a reasonably normal shape, with Africa 2002 a little right skewed.

6.5.2 Q-Q plot

A quantile-quantile sounds complicated but is not. It is simply a graphical method for comparing the distribution (think shape) of our own data to a theoretical distribution, such as the normal distribution. In this context, quantiles are just cut points which divide our data into bins each containing the same number of observations. For example, if we have the life expectancy for 100 countries, then quartiles (note the quar-) for life expectancy are the three ages which split the observations into 4 groups each containing 25 countries. A Q-Q plot simply plots the quantiles for our data against the theoretical quantiles for a particular distributions (default below is normal). If our data follow that distribution (e.g. normal), then we get a 45 degree line on the plot.

```
mydata %>%
  filter(year %in% c(2002, 2007)) %>%
  ggplot(aes(sample = lifeExp)) +       # Q-Q plot requires `sample
  geom_qq() +                           # defaults to normal distribution
  geom_qq_line() +                      # add 45 degree line
  facet_grid(year ~ continent)
```

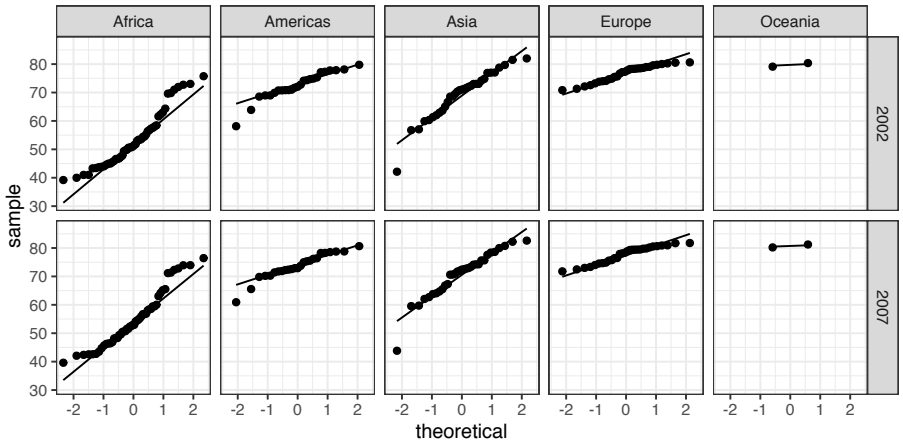


FIGURE 6.2: Q-Q plot: country life expectancy by continent and year

What can we see. We are looking to see if the data follow the 45 degree line which is included in the plot. These do reasonably, except for Africa which is curved upwards at each end, suggesting a skew.

We are frequently asked about performing a hypothesis test to check the assumption of normality, such as the Shapiro-Wilk normality test. We do not recommend this, simply because it is often non-significant when the number of observations is small but the data look skewed, and often significant when the number of observations is high but the data look reasonably normal on inspection of plots. It is therefore not useful in practice - common sense should prevail.

6.5.3 Boxplot

Boxplots are our preferred method for comparing a continuous variable such as life expectancy with a categorical explanatory variable. It is much better than a bar plot, or a bar plot with error bars, sometimes called a dynamite plot.

The box represents the median and interquartile range (where 50% of the data sits). The lines (whiskers) by default are 1.5 times the interquartile range. Outliers are represented as points.

Thus it contains information, not only on central tenancy (median), but on the variation in the data and the distribution of the data, for instance a skew should be obvious.

```
mydata %>%
  filter(year %in% c(2002, 2007)) %>%
  ggplot(aes(x = continent, y = lifeExp)) +
  geom_boxplot() +
  facet_grid(. ~ year)                    # spread by year, note `.`
```

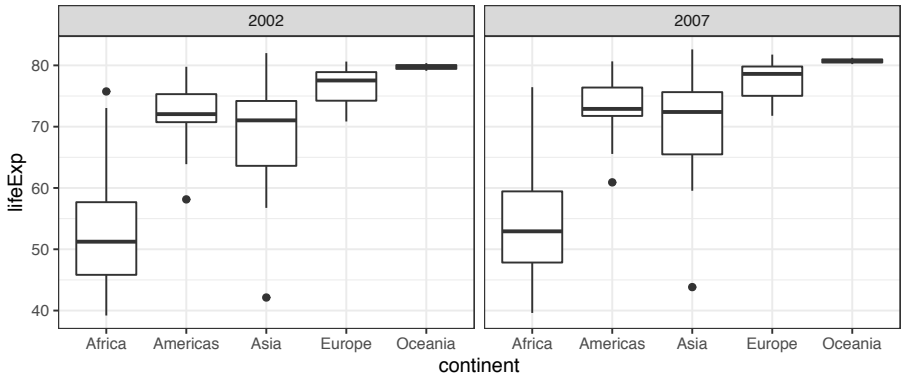


FIGURE 6.3: Boxplot: country life expectancy by continent and year

What can we see? The median life expectancy is lower in Africa than in any other continent. The variation in life expectancy is greatest in Africa and smallest in Oceania. The data in Africa looks skewed, particularly in 2002 - the lines/whiskers are unequal lengths.

We can add further arguments

```
mydata %>%
  filter(year %in% c(2002, 2007)) %>%
  ggplot(aes(x = factor(year), y = lifeExp)) +
  geom_boxplot(aes(fill = continent)) +     # add colour to boxplots
  geom_jitter(alpha = 0.4) +                # alpha = transparency
  facet_grid(. ~ continent) +               # spread by year, note `.`
  theme(legend.position = "none") +         # remove legend
  xlab("Year") +                            # label x-axis
  ylab("Life expectancy (years)") +         # label y-axis
  ggtitle(
    "Life expectancy by continent in 2002 v 2007") # add title
```

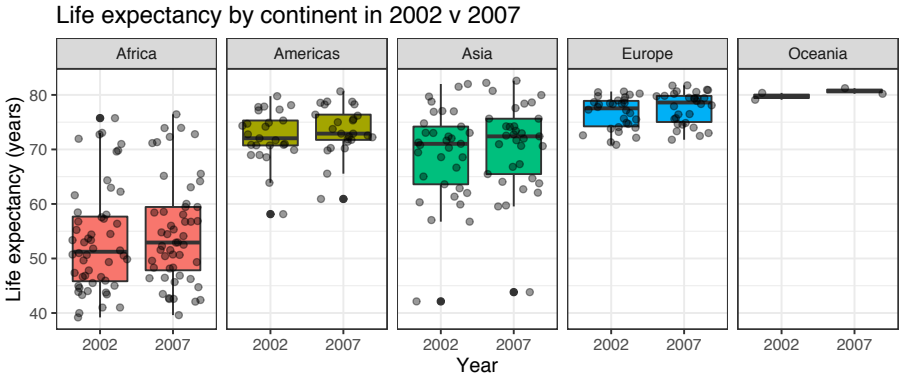


FIGURE 6.4: Boxplot with jitter points: country life expectancy by continent and year

6.6 Compare the means of two groups

6.6.1 T-test

A *t*-test is used to compare the means of two groups of continuous variables. Volumes have been written about this else where, and we won't rehearse it here.

There are various variations on the *t*-test. We will use two here.

The most useful in our context is a two-sample test if independent groups (first figure). Repeated-measures data such as comparing the same countries between years can be analysed using a paired *t*-test (second figure)

6.6.2 Two-sample *t*-tests

Referring to the first figure, let's compare life expectancy between Asia and Europe for 2007. What is imperative, is that you decide what sort of difference exists by looking at the boxplot, rather than relying on the *t*-test output. The median for Europe is clearly higher than in Asia. The distributions overlap, but it looks likely that Europe has a higher life expectancy than Asia.

```
ttest_data = mydata %>%                       # save as object testdata
  filter(year == 2007) %>%                    # 2007 only
  filter(continent %in% c("Asia", "Europe")) # Asia/Europe only

ttest_result =
  t.test(lifeExp ~ continent, data = ttest_data) # Base R t.test
ttest_result
```

```
##
##  Welch Two Sample t-test
##
## data:  lifeExp by continent
## t = -4.6468, df = 41.529, p-value = 3.389e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -9.926525 -3.913705
## sample estimates:
##   mean in group Asia mean in group Europe
##             70.72848             77.64860
```

The Welch two-sample t-test is the most flexible and copes with differences in variance (variability) between groups, as in this example. The difference in means is provided at the bottom of the output. The *t*-value, degrees of freedom (df) and p-value are all provided. The p-value is 0.00003.

The base R output is not that easy to utilise. For reference, the

results can be explored and exported. However, more straightforward methods are provided below.

```
names(ttest_result)  # Names of elements of result object
```

```
##  [1] "statistic"   "parameter"   "p.value"     "conf.int"    "estimate"
##  [6] "null.value"  "stderr"      "alternative" "method"      "data.name"
```

```
str(ttest_result)    # Details of result object
```

```
## List of 10
##  $ statistic  : Named num -4.65
##   ..- attr(*, "names")= chr "t"
##  $ parameter  : Named num 41.5
##   ..- attr(*, "names")= chr "df"
##  $ p.value    : num 3.39e-05
##  $ conf.int   : num [1:2] -9.93 -3.91
##   ..- attr(*, "conf.level")= num 0.95
##  $ estimate   : Named num [1:2] 70.7 77.6
##  ..- attr(*, "names")= chr [1:2] "mean in group Asia" "mean in group Europe"
##  $ null.value : Named num 0
##   ..- attr(*, "names")= chr "difference in means"
##  $ stderr     : num 1.49
##  $ alternative: chr "two.sided"
##  $ method     : chr "Welch Two Sample t-test"
##  $ data.name  : chr "lifeExp by continent"
##  - attr(*, "class")= chr "htest"
```

```
ttest_result$p.value # Extracted element of result object
```

```
## [1] 3.38922e-05
```

The `broom` package provides useful methods for 'tidying' common model outputs into a `tibble`.
The whole analysis can be constructed as a single piped function.

```
library(broom)
mydata %>%
  filter(year == 2007) %>%                          # 2007 only
  filter(continent %in% c("Asia", "Europe")) %>%  # Asia/Europe only
  t.test(lifeExp ~ continent, data = .) %>%
  tidy()
```

```
## # A tibble: 1 x 10
##   estimate estimate1 estimate2 statistic p.value parameter conf.low
##      <dbl>     <dbl>     <dbl>     <dbl>   <dbl>     <dbl>    <dbl>
## 1    -6.92      70.7      77.6     -4.65 3.39e-5      41.5    -9.93
## # ... with 3 more variables: conf.high <dbl>, method <chr>,
## #   alternative <chr>
```

6.6.3 When pipe sends data to the wrong place: use `, data = .` to direct it

In the code above, the `, data = .` bit is necessary because the pipe usually sends data to the beginning of function brackets. So `mydata %>% t.test(lifeExp ~ continent)` would be equivalent to `t.test(mydata, lifeExp ~ continent`. However, this is not an order that `t.test()` will accept. `t.test()` wants us to specify the formula first, and then wants the data these variables are present in. So we have to use the . to tell the pipe to send the data to the second argument of `t.test()`, not the first.

6.6.4 Paired *t*-tests

Consider that we want to compare the difference in life expectancy in Asian countries between 2002 and 2007. The overall difference is not impressive in the boxplot.

We can plot differences at the country level directly.

```
paired_data = mydata %>%                  # save as object paired_data
  filter(year %in% c(2002, 2007)) %>%  # 2002 and 2007 only
  filter(continent == "Asia")          # Asia only
```

```
paired_data %>%
  ggplot(aes(x = year, y = lifeExp,
             group = country)) +       # for individual country lines
  geom_line()
```

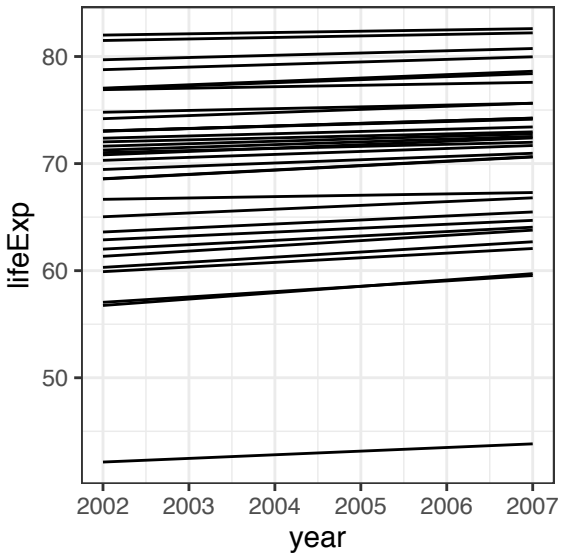


FIGURE 6.5: Line plot: Change in life expectancy in Asian countries from 2002 to 2007

What is the difference in life expectancy for each individual country. We don't usually have to produce this directly, but here is one method.

```
paired_table = paired_data %>%        # save object paired_data
  select(country, year, lifeExp) %>%  # select vars interest
  spread (year, lifeExp) %>%          # make wide table
  mutate(
    dlifeExp = `2007` - `2002`        # difference in means
  )

paired_table
```

```
## # A tibble: 33 x 4
##    country          `2002` `2007` dlifeExp
```

```
##    <fct>              <dbl>  <dbl>    <dbl>
##  1 Afghanistan         42.1   43.8    1.70
##  2 Bahrain             74.8   75.6    0.84
##  3 Bangladesh          62.0   64.1    2.05
##  4 Cambodia            56.8   59.7    2.97
##  5 China               72.0   73.0    0.933
##  6 Hong Kong, China    81.5   82.2    0.713
##  7 India               62.9   64.7    1.82
##  8 Indonesia           68.6   70.6    2.06
##  9 Iran                69.5   71.0    1.51
## 10 Iraq                57.0   59.5    2.50
## # ... with 23 more rows
```

```
# Mean of difference in years
paired_table %>% summarise( mean(dlifeExp) )
```

```
## # A tibble: 1 x 1
##   `mean(dlifeExp)`
##              <dbl>
## 1             1.49
```

On average, therefore, there is an increase in life expectancy of 1.5 years in Asian countries between 2002 and 2007. Let's test whether this number differs from zero with a paired t-test.

```
paired_data %>%
  t.test(lifeExp ~ year, data = .) # Include paired = TRUE
```

```
##
##  Welch Two Sample t-test
##
## data:  lifeExp by year
## t = -0.74294, df = 63.839, p-value = 0.4602
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -5.513722  2.524510
## sample estimates:
## mean in group 2002 mean in group 2007
##           69.23388           70.72848
```

The results show a highly significant difference. As an exercise you can repeat this analysis simply comparing the means in an unpaired manner. The resulting p-value is `R paired_data %>% t.test(lifeExp ~ year, data = .)$p.value`. Why is there such a difference between the two approaches? This emphasises just how important it is to plot the data first. The average difference of 1.5 years is highly consistent between countries, as show on the line plot, and this differs from zero. It is up to you the investigator to interpret the effect size of 1.5 y in reporting the finding.

6.7 Compare the mean of one group

6.7.1 One sample *t*-tests

We can use a *t*-test to determine whether the mean of a distribution is different to a specific value.

The paired *t*-test above is is equivalent to a one-sample *t*-test on the calculated difference in life expectancy being different to zero.

```
t.test(paired_table$dlifeExp)
```

```
##
##  One Sample t-test
##
## data:  paired_table$dlifeExp
## t = 14.338, df = 32, p-value = 1.758e-15
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  1.282271 1.706941
## sample estimates:
## mean of x
##  1.494606
```

We can compare to values other than zero. For instance, we can test whether the mean life expectancy in each continent was significantly different to 77 years in 2007. We have included some extra

code here to demonstrate how to run multiple base R tests in one pipe function.

```
mydata %>%
  filter(year == 2007) %>%          # 2007 only
  group_by(continent) %>%           # split by continent
  do(                               # dplyr function
    t.test(.$lifeExp, mu = 77) %>%  # compare mean to 77 years
      tidy()                        # tidy into tibble
    )
```

```
## # A tibble: 5 x 9
## # Groups:   continent [5]
##  continent estimate statistic  p.value parameter conf.low conf.high method
##   <fct>       <dbl>     <dbl>    <dbl>     <dbl>    <dbl>     <dbl> <chr>
## 1 Africa       54.8    -16.6  3.15e-22        51     52.1      57.5 One S~
## 2 Americas     73.6     -3.82 8.32e- 4        24     71.8      75.4 One S~
## 3 Asia         70.7     -4.52 7.88e- 5        32     67.9      73.6 One S~
## 4 Europe       77.6      1.19 2.43e- 1        29     76.5      78.8 One S~
## 5 Oceania      80.7      7.22 8.77e- 2         1     74.2      87.3 One S~
## # ... with 1 more variable: alternative <chr>
```

```
mydata %>%
  filter(year == 2007) %>%           # 2007 only
  group_by(continent) %>%            # split by continent
  group_modify(                      # dplyr function
    ~ t.test(.$lifeExp, mu = 77) %>% # compare mean to 77 years
      tidy()                         # tidy into tibble
    )
```

```
## # A tibble: 5 x 9
## # Groups:   continent [5]
##  continent estimate statistic  p.value parameter conf.low conf.high method
##   <fct>       <dbl>     <dbl>    <dbl>     <dbl>    <dbl>     <dbl> <chr>
## 1 Africa       54.8    -16.6  3.15e-22        51     52.1      57.5 One S~
## 2 Americas     73.6     -3.82 8.32e- 4        24     71.8      75.4 One S~
## 3 Asia         70.7     -4.52 7.88e- 5        32     67.9      73.6 One S~
## 4 Europe       77.6      1.19 2.43e- 1        29     76.5      78.8 One S~
## 5 Oceania      80.7      7.22 8.77e- 2         1     74.2      87.3 One S~
## # ... with 1 more variable: alternative <chr>
```

The mean life expectancy for Europe and Oceania do not differ from 77, while the others to to varying degrees. In particular, look at the confidence intervals of the tables and whether they include or exclude 77.

6.8 Compare the means of more than two groups

It may be that our question is set around a hypothesis involving more than two groups. For example, we may be interested in comparing life expectancy across 3 continents such as the Americas, Europe and Asia.

6.8.1 Plot the data

```
mydata %>%
    filter(year == 2007) %>%
    filter(continent %in%
             c("Americas", "Europe", "Asia")) %>%
    ggplot(aes(x = continent, y=lifeExp)) +
    geom_boxplot()
```

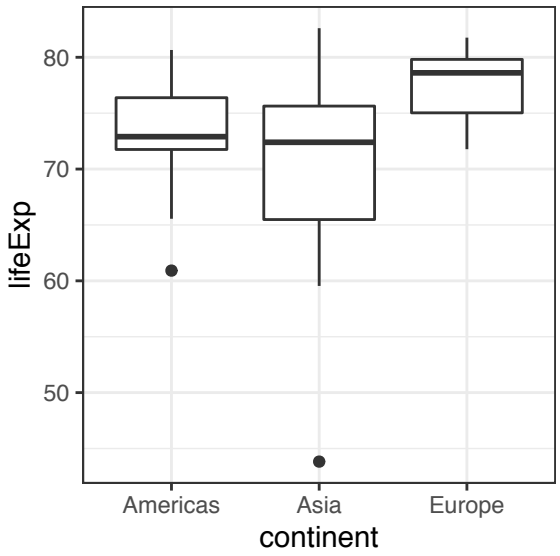


FIGURE 6.6: Boxplot: Life expectancy in selected continents for 2007

6.8.2 ANOVA

Analysis of variance is a collection of statistical tests which can be used to test the difference in means between two or more groups.

In base R form, it produces an ANOVA table which includes an F-test. This so-called omnibus test tells you whether there are any differences in the comparison of means of the included groups. Again, it is important to plot carefully and be clear what question you are asking.

```
aov_data = mydata %>%
  filter(year == 2007) %>%
  filter(continent %in% c("Americas", "Europe", "Asia"))

fit = aov(lifeExp ~ continent, data = aov_data)
summary(fit)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## continent    2  755.6   377.8   11.63 3.42e-05 ***
## Residuals   85 2760.3    32.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can conclude from this, that there is a difference in the means between at least two pairs of the included continents. As above, the output can be neatened up using the `tidy` function.

```
library(broom)
mydata %>%
  filter(year == 2007) %>%
  filter(continent %in% c("Americas", "Europe", "Asia")) %>%
  aov(lifeExp~continent, data = .) %>%
    tidy()
```

```
## # A tibble: 2 x 6
##   term         df sumsq meansq statistic    p.value
##   <chr>     <dbl> <dbl>  <dbl>     <dbl>      <dbl>
## 1 continent     2  756.  378.       11.6  0.0000342
## 2 Residuals    85 2760.   32.5      NA   NA
```

6.8.3 Assumptions

As with the normality assumption of the t-test, there are assumptions of the ANOVA model). These are covered in detail in the linear regression chapter and will not be repeated here. Suffice to say that diagnostic plots can be produced to check that the assumptions are fulfilled.

```
par(mfrow=c(2,2))
plot(fit)
```

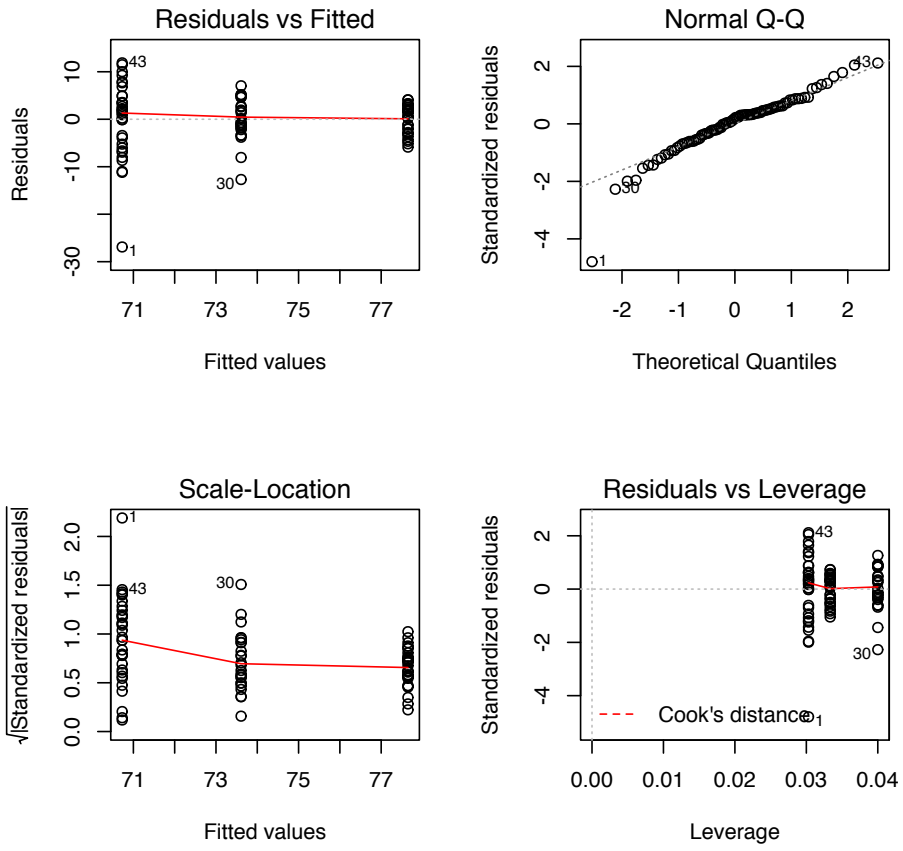


FIGURE 6.7: Diagnostic plots: ANOVA model of life expectancy by continent for 2007

```
par(mfrow=c(1,1))
```

6.8.4 Pairwise testing and multiple comparisons

When the F-test is significant, we will often want to proceed to try and determine where the differences lie. This should of course be obvious from the boxplot you have made. However, some are fixated on the p-value!

```
pairwise.t.test(aov_data$lifeExp, aov_data$continent,
                p.adjust.method = "bonferroni")
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  aov_data$lifeExp and aov_data$continent
##
##        Americas Asia
## Asia   0.180    -
## Europe 0.031    1.9e-05
##
## P value adjustment method: bonferroni
```

A matrix of pairwise p-values is produced. Here we can that there is good evidence of a difference in means between Europe and Asia.

The p-values are corrected for multiple comparisons. When performing a hypothesis test at the 5% level (alpha = 0.05), there is a 5% chance of a type 1 error. That is, a 1 in 20 chance of concluding a difference exists when it in fact does not (formally, this is rejection of a true null hypothesis). As more simultaneous statistical tests are performed, the chance of a type 1 error increases.

There are three approaches to this. The first, is to no perform any correction at all. Some advocate that the best approach is simply to present the results of all the tests that were performed, and let the sceptical reader make adjustments themselves. This is attractive, but presupposes a sophisticated readership who will take the time to consider the results in their entirety.

The second and classical approach, is to control for the so-called family-wise error rate. The "Bonferroni" correction is probably the most famous and most conservative, where the threshold for significance is lowered in proportion to the number of comparisons made. For example, if three comparisons are made, the threshold for significance is lowered to 0.017. Equivalently, any particular p-value can be multiples by 3 and the value compared to a threshold of 0.05, as is done above. The Bonferroni method is particular conservative, meaning that type 2 errors may occur (failure to identify true differences, or false negatives) in favour or minimising type 1 errors (false positives).

The third newer approach controls false-discovery rate. The development of these methods has been driven in part by the needs of areas of science where many different statistical tests are performed at the same time, for instance, examining the influence of 1000 genes simultaneously. In these hypothesis-generating settings, a higher tolerance to type 1 errors may be preferable to missing potential findings through type 2 errors. You can see in our example, that the p-values are lower with the `fdr` correction when compared to the `Bonferroni` correction.

```
pairwise.t.test(aov_data$lifeExp, aov_data$continent,
                p.adjust.method = "fdr")
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  aov_data$lifeExp and aov_data$continent
##
##        Americas Asia
## Asia   0.060    -
## Europe 0.016    1.9e-05
##
## P value adjustment method: fdr
```

Try not to get too hung up on this. Be sensible. Plot the data and look for differences. Focus on effect size, for instance, the actual difference in life expectancy in years, rather than the p-value of

a comparison test. Choose a method which fits with your overall aims. If you are generating hypotheses which you will proceed to test with other methods, the `fdr` approach may be preferable. If you are trying to capture robust effect and want to minimise type 2 errors, use a family-wise approach.

6.9 Non-parametric data

What if your data is different shape to normal or the ANOVA assumptions are not fulfilled (see linear regression chapter). As always, be sensible! Would your data be expected to be normally distributed given the data-generating process? For instance, if you examining length of hospital stay it is likely that your data are highly right skewed - most patients are discharged from hospital in a few days while a smaller number stay for a long time. Is a comparison of means ever going to be the correct approach here? Perhaps you should consider a time-to-event analysis for instance (see chapter x).

If a comparison of means approach is reasonable, but the normality assumption are not fulfilled there are two approaches,

1. Transform the data;
2. Perform non-parametric tests.

6.9.1 Transforming data

Remember, the Welch *t*-test is reasonably robust to divergence from the normality assumption, so small deviations can be safely ignored.

Otherwise, the data can be transformed to another scale to deal with a skew. A natural `log` scale is most common.

```
africa_data = mydata %>%                  # save as africa_data
  filter(year == 2002) %>%                # only 2002
  filter(continent == "Africa") %>%       # only Africa
  select(country, lifeExp) %>%            # only these variables
  mutate(
    lifeExp_log = log(lifeExp)            # log life expectancy
  )
head(africa_data)                         # inspect
```

```
## # A tibble: 6 x 3
##   country      lifeExp lifeExp_log
##   <fct>          <dbl>       <dbl>
## 1 Algeria         71.0        4.26
## 2 Angola          41.0        3.71
## 3 Benin           54.4        4.00
## 4 Botswana        46.6        3.84
## 5 Burkina Faso    50.6        3.92
## 6 Burundi         47.4        3.86
```

```
africa_data %>%
  gather(key, lifeExp, -country) %>%      # gather vals to same column
  ggplot(aes(x = lifeExp)) +
  geom_histogram(bins = 15) +             # make histogram
  facet_grid(. ~ key, scales = "free")    # facet & axes free to vary
```

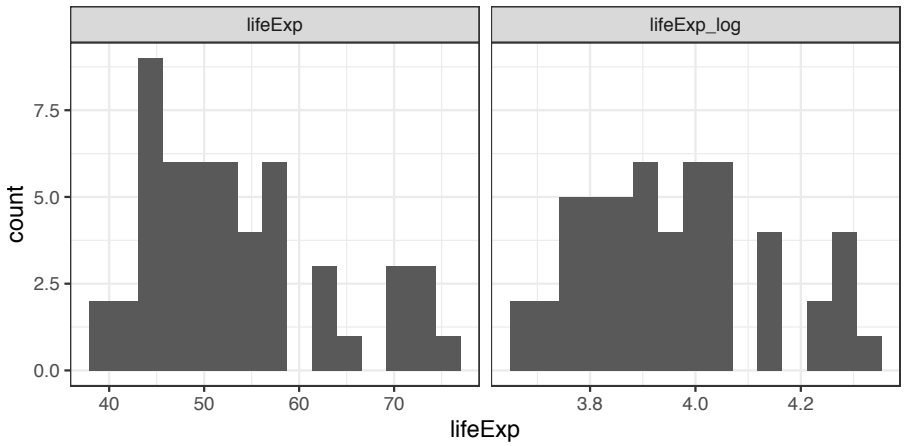


FIGURE 6.8: Histogram: Log transformation of life expectancy for countries in Africa 2002

This has worked well here. The right skew on the Africa data has been dealt with by the transformation. A parametric test such as a *t*-test can now be performed.

6.9.2 Non-parametric test for comparing two groups

The Mann-Whitney U test is also called the Wilcoxon rank-sum test and uses a rank-based method to compare two groups (note the Wilcoxon signed-rank test is for paired data). We can use if to test for a difference in life expectancies for African countries between 1982 and 2007. Let's do a histogram, Q-Q plot and boxplot first.

```
africa_plot = mydata %>%
  filter(year %in% c(1982, 2007)) %>%      # only 1982 and 2007
  filter(continent %in% c("Africa"))       # only Africa

p1 = africa_plot %>%                       # save plot as p1
  ggplot(aes(x = lifeExp)) +
  geom_histogram(bins = 15) +
  facet_grid(. ~ year)

p2 = africa_plot %>%                       # save plot as p2
  ggplot(aes(sample = lifeExp)) +          # `sample` for Q-Q plot
  geom_qq() +
  geom_qq_line() +
  facet_grid(. ~ year)

p3 = africa_plot %>%                       # save plot as p3
  ggplot(aes(x = factor(year),
             y = lifeExp)) +               # change year to factor
  geom_boxplot(aes(fill = factor(year))) + # colour boxplot
  geom_jitter(alpha = 0.4) +               # add data points
  theme(legend.position = "none")          # remove legend

library(patchwork)                         # great for combining plots
p1 / p2 | p3
```

The data is a little skewed based on the histograms and Q-Q plots. The difference between 1982 and 2007 is not particularly striking on the boxplot.

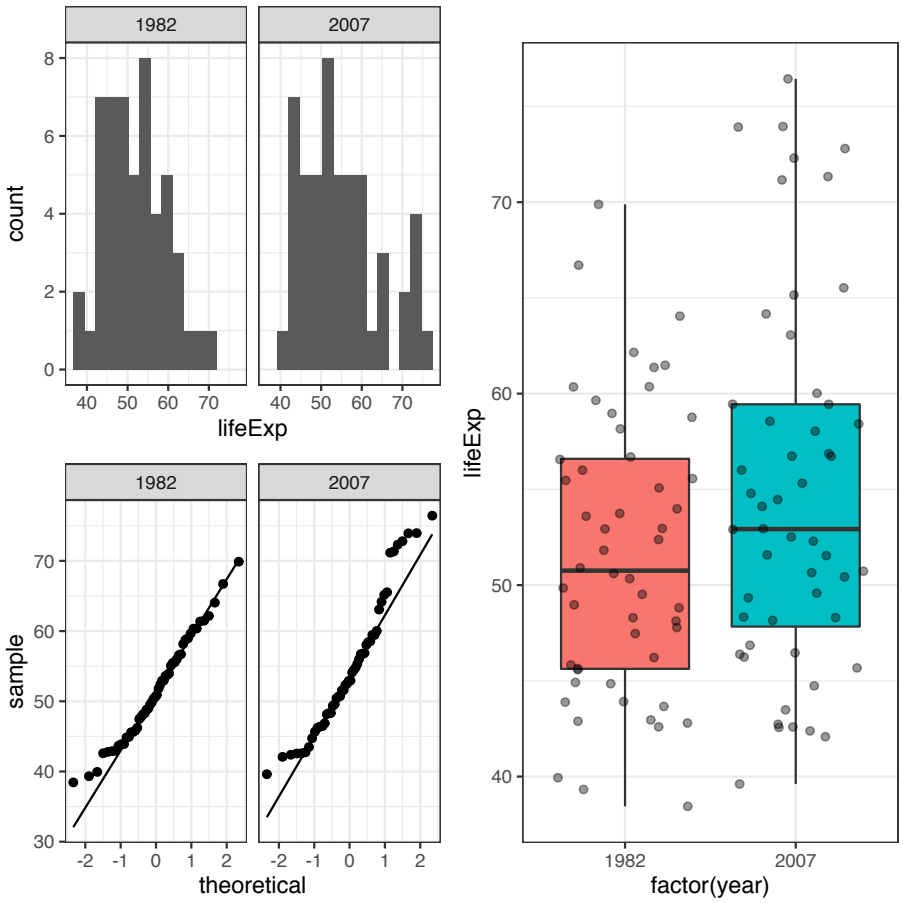


FIGURE 6.9: Panels plots: histogram, Q-Q, boxplot for life expectancy in Africa 1992 v 2007

```
africa_plot %>%
  wilcox.test(lifeExp ~ year, data = .)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  lifeExp by year
## W = 1130, p-value = 0.1499
## alternative hypothesis: true location shift is not equal to 0
```

6.9.3 Non-parametric test for comparing more than two groups

The non-parametric equivalent to ANOVA, is the Kruskal-Wallis test. It can be used in base R, or via the finalfit package below.

```
library(broom)
mydata %>%
  filter(year == 2007) %>%
  filter(continent %in% c("Americas", "Europe", "Asia")) %>%
  kruskal.test(lifeExp~continent, data = .) %>%
    tidy()
```

```
## # A tibble: 1 x 4
##   statistic   p.value parameter method
##       <dbl>     <dbl>     <int> <chr>
## 1      21.6 0.0000202         2 Kruskal-Wallis rank sum test
```

6.10 Finalfit approach

The finalfit package provides an easy to use interface for performing non-parametric hypothesis tests. Any number of explanatory variables can be tested against a so-called dependent variable. In this case, this is equivalent to a typical Table 1 in healthcare study.

```
dependent = "year"
explanatory = c("lifeExp", "pop", "gdpPercap")
mydata %>%
  filter(year %in% c(1982, 2007)) %>%       # only 1982 and 2007
  filter(continent == "Africa") %>%         # only Africa
  mutate(
    year = factor(year)                     # change year to factor
  ) %>%
  summary_factorlist(dependent, explanatory,
                     cont = "median", p = TRUE) %>%
  knitr::kable(row.names = FALSE, booktabs = TRUE,
               align = c("l", "l", "r", "r", "r", "r"),
               caption = "Life expectancy, population and GDPperCap in Africa 1982 v 2007")
```

TABLE 6.1: Life expectancy, population and GDPperCap in Africa 1982 v 2007

label	levels	1982	2007	p
lifeExp	Median (IQR)	50.8 (11.0)	52.9 (11.6)	0.150
pop	Median (IQR)	5668228.5 (8218654.0)	10093310.5 (16454428.0)	0.032
gdpPercap	Median (IQR)	1323.7 (1958.9)	1452.3 (3130.6)	0.506

6.11 Conclusions

Continuous data is frequently encountered in a healthcare setting. Liberal use of plotting is required to really understand the underlying data. Comparisons can easily made between two or more groups of data, but always remember what you are actually trying to analyse and don't become fixated on the p-value. In the next chapter, we will explore the comparison of two continuous variables together with multivariable models of datasets.

6.12 Exercises

6.12.1 Exercise 1

Make a histogram, Q-Q plot, and a box-plot for the life expectancy for a continent of your choice, but for all years. Do the data appear normally distributed?

6.12.2 Exercise 2

1. Select any 2 years in any continent and perform a *t*-test to determine whether mean life expectancy is significantly different. Remember to plot your data first.
2. Extract only the p-value from your `t.test()` output.

6.12.3 Exercise 3

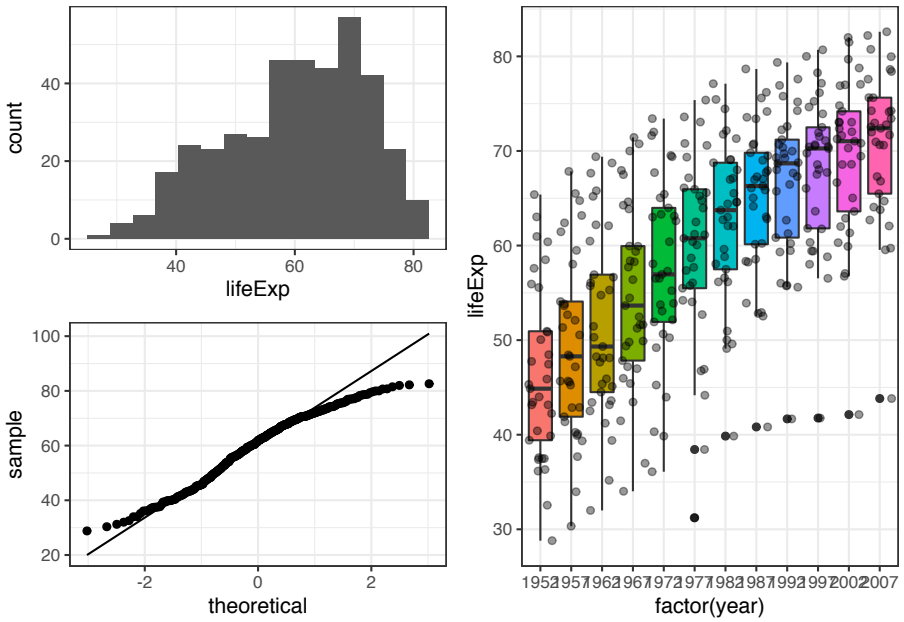
In 2007, in which continents did mean life expectancy differ from 70.

6.12.4 Exercise 4

1. Use ANOVA to determine if the population changed significantly through the 1990s/2000s in individual continents.

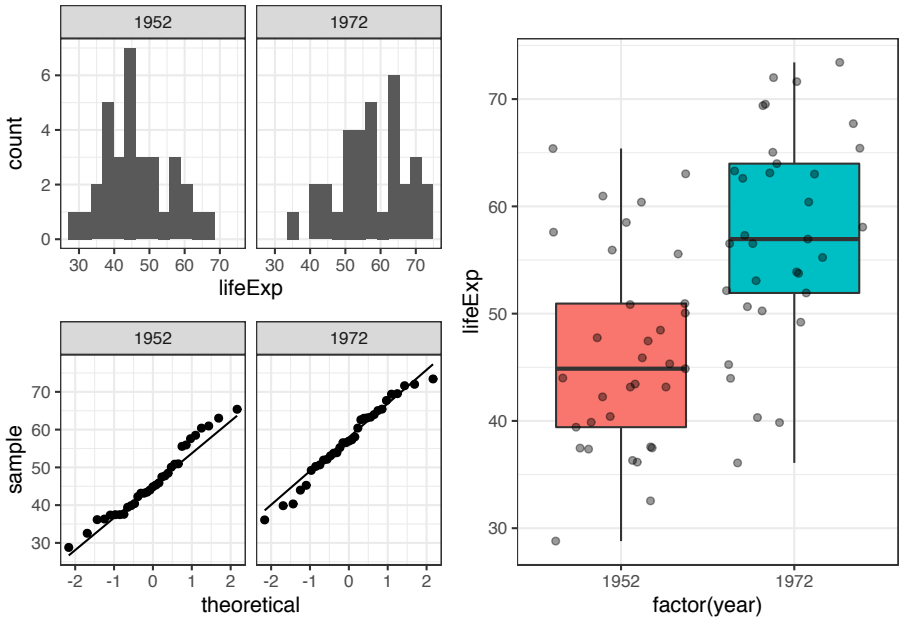
6.13 Exercise solutions

```
# Exerise 1
## Make a histogram, Q-Q plot, and a box-plot for the life expectancy
## for a continent of your choice, but for all years.
## Do the data appear normally distributed?

asia_plot = mydata %>%
  filter(continent %in% c("Asia"))

p1 = asia_plot %>%
  ggplot(aes(x = lifeExp)) +
  geom_histogram(bins = 15) #+
  #facet_grid(. ~ year)                          # no facet

p2 = asia_plot %>%
  ggplot(aes(sample = lifeExp)) +               # `sample` for Q-Q plot
  geom_qq() +
  geom_qq_line() #+
  #facet_grid(. ~ year)                          # no facet

p3 = asia_plot %>%
  ggplot(aes(x = factor(year), y = lifeExp)) +  # year as factor
  geom_boxplot(aes(fill = factor(year))) +
  geom_jitter(alpha = 0.4) +
  theme(legend.position = "none")

library(patchwork)
p1 / p2 | p3
```




```
# Exercise 2
## Select any 2 years in any continent and perform a *t*-test to
## determine whether mean life expectancy is significantly different.
## Remember to plot your data first.

asia_years = mydata %>%
  filter(continent %in% c("Asia")) %>%
  filter(year %in% c(1952, 1972))

p1 = asia_years %>%
  ggplot(aes(x = lifeExp)) +
  geom_histogram(bins = 15) +
  facet_grid(. ~ year)

p2 = asia_years %>%
  ggplot(aes(sample = lifeExp)) +
  geom_qq() +
  geom_qq_line() +
  facet_grid(. ~ year)

p3 = asia_years %>%
  ggplot(aes(x = factor(year), y = lifeExp)) +
  geom_boxplot(aes(fill = factor(year))) +
  geom_jitter(alpha = 0.4) +
  theme(legend.position = "none")
```

```
library(patchwork)
p1 / p2 | p3
```



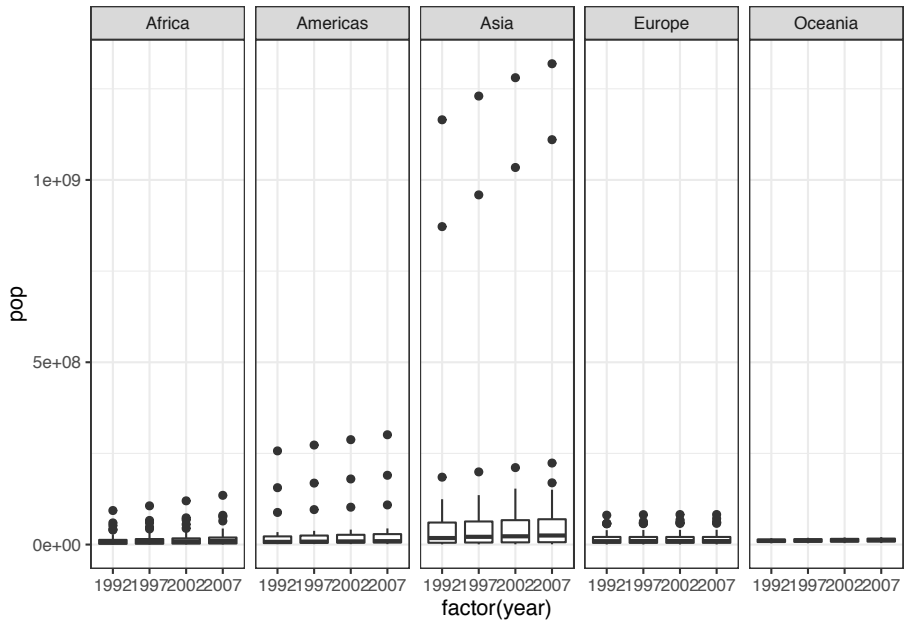

```
asia_years %>%
  t.test(lifeExp ~ year, data = .)
```

```
##
##  Welch Two Sample t-test
##
## data:  lifeExp by year
## t = -4.7007, df = 63.869, p-value = 1.428e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -15.681981  -6.327769
## sample estimates:
## mean in group 1952 mean in group 1972
##           46.31439           57.31927
```

```r
# Exercise 3
## In 2007, in which continents did mean life expectancy differ from 70
mydata %>%
  filter(year == 2007) %>%
  group_by(continent) %>%
  group_modify(
    ~ t.test(.$lifeExp, mu = 70) %>% tidy() # Somtimes awkward in the tidyverse
  )
```

```
## # A tibble: 5 x 9
## # Groups:   continent [5]
##   continent estimate statistic  p.value parameter conf.low conf.high method
##   <fct>        <dbl>     <dbl>    <dbl>     <dbl>    <dbl>     <dbl> <chr>
## 1 Africa        54.8   -11.4   1.33e-15        51     52.1      57.5 One S~
## 2 Americas      73.6     4.06  4.50e- 4        24     71.8      75.4 One S~
## 3 Asia          70.7     0.525 6.03e- 1        32     67.9      73.6 One S~
## 4 Europe        77.6    14.1   1.76e-14        29     76.5      78.8 One S~
## 5 Oceania       80.7    20.8   3.06e- 2         1     74.2      87.3 One S~
## # ... with 1 more variable: alternative <chr>
```

```r
# Exercise 4
## Use Kruskal-Wallis to determine if the mean population changed
## significantly through the 1990s/2000s in individual continents.

mydata %>%
  filter(year >=1990) %>%
  ggplot(aes(x = factor(year), y = pop)) +
  geom_boxplot() +
  facet_grid(. ~ continent)
```




```
mydata %>%
  filter(year >=1990) %>%
  group_by(continent) %>%
  group_modify(
    ~ kruskal.test(pop ~ factor(year), data = .) %>% tidy()
  )
```

```
## # A tibble: 5 x 5
## # Groups:   continent [5]
##   continent statistic p.value parameter method
##   <fct>         <dbl>   <dbl>     <int> <chr>
## 1 Africa        2.10    0.553         3 Kruskal-Wallis rank sum test
## 2 Americas      0.847   0.838         3 Kruskal-Wallis rank sum test
## 3 Asia          1.57    0.665         3 Kruskal-Wallis rank sum test
## 4 Europe        0.207   0.977         3 Kruskal-Wallis rank sum test
## 5 Oceania       1.67    0.644         3 Kruskal-Wallis rank sum test
```

7

Linear regression

7.1 Regression

Regression is a method with which we can determine the existence and strength of the relationship between two or more variables. This can be thought of as drawing lines, ideally straight lines, through data points.

Linear regression is our method of choice for examining continuous outcome variables. Broadly, there are often two separate goals in regression:

- Prediction: fitting a predictive model to an observed dataset. Using that model to make predictions about an outcome from a new set of explanatory variables;
- Explanation: fit a model to explain the inter-relationships between a set of variables.

Figure 7.1 unifies the terms we will use throughout. A clear scientific question should define our `explanatory variable of interest` (x), which sometimes gets called a exposure, predictor, or independent variable. Our outcome of interest will be referred to as the `dependent` variable (y), sometimes referred to as the response. In simple linear regression, there is a single explanatory variable and a dependent variable, and we will sometimes refer to this as *univariable linear regression*. When there is more than one explanatory variable, we will call this *multivariable regression*. Avoid the term *multivariate regression*, which suggests more than one dependent variable. We don't use this method and we suggest you don't either!

Note that the dependent variable is always continuous, it cannot be a categorical variable. The explanatory variables can be either continuous or categorical.

7.2 The Question (1)

We will illustrate our examples of linear regression using a classical question which is important to many of us! This is the relationship between coffee consumption and blood pressure (and therefore cardiovascular events, such as myocardial infarction and stroke). There has been a lot of backwards and forwards over decades about whether coffee is harmful, has no effect, or is in fact beneficial. Figure 7.1 shows a linear regression example. Each point is a person and average number of cups of coffee per day is the explanatory variable of interest (x) and systolic blood pressure as the dependent variable (y). This next bit is important! These data are made up, fake, randomly generated, fabricated, not real. So please do not alter your coffee habit on the basis of these plots!

7.3 Fitting a regression line

Simple linear regression uses the *ordinary least squares* method for fitting. The details of this are beyond the scope here, but if you want to get out the linear algebra/matrix maths you did in high school, an enjoyable afternoon can be spent proving to yourself how it actually works.

Figure 7.2 aims to make this easy to understand. The maths defines a line which best fits the data provided. For the line to fit best, the distances between it and the observed data should be as small as possible. The distance from each observed point to the line is called a *residual* - one of those statistical terms that bring on the

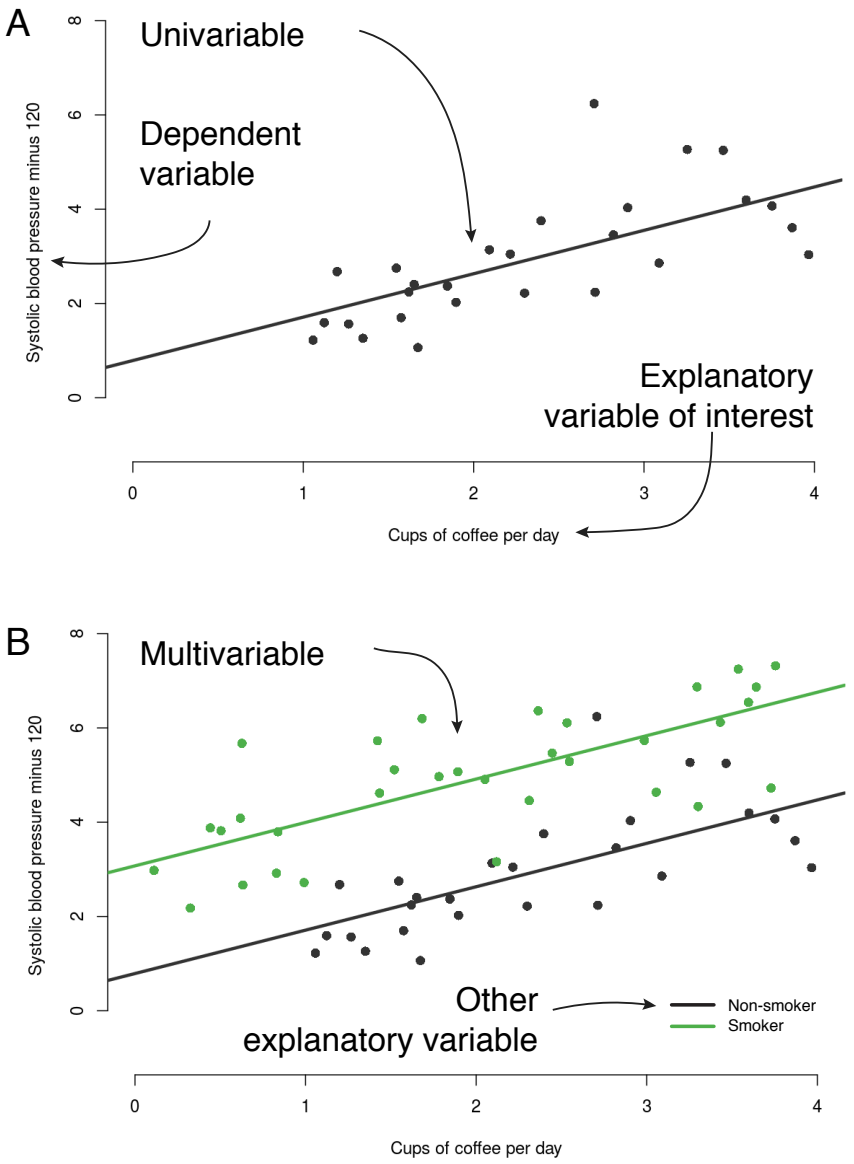


FIGURE 7.1: The anatomy of a regression plot.

sweats. It just refers to the "residual error" left over after the line is fitted.

You can use the simple regression shiny app[1] to explore the concept. We want the residuals to be as small as possible. We can square each residual (to get rid of minuses and penalise further away points) and add them up. If this number is as small as possible, the line is fitting as best it can. Or in more formal language, we want to minimise the sum of squared residuals.

7.4 When the line fits well

Linear regression modelling has four main assumptions:

1. Linear relationship between between predictors and outcome;
2. Independence of residuals;
3. Normal distribution of residuals;
4. Equal variance of residuals.

You can use the simple regression diagnostics shiny app[2] to get a handle on these.

Figure 7.3 shows diagnostic plots from the app, which we will run ourselves below.

7.4.1 Linear relationship

A simple scatter plot should show a linear relationship between the explanatory and the dependent variable, as in figure 7.3A. If the data describe a non-linear pattern (figure 7.3B), then a straight line is not going to fit it well. In this situation, an alternative model should be considered, such as including a quadratic (x^2) or polynomial term.

[1] https://argoshare.is.ed.ac.uk/simple_regression
[2] https://argoshare.is.ed.ac.uk/simple_regression_diagnostics

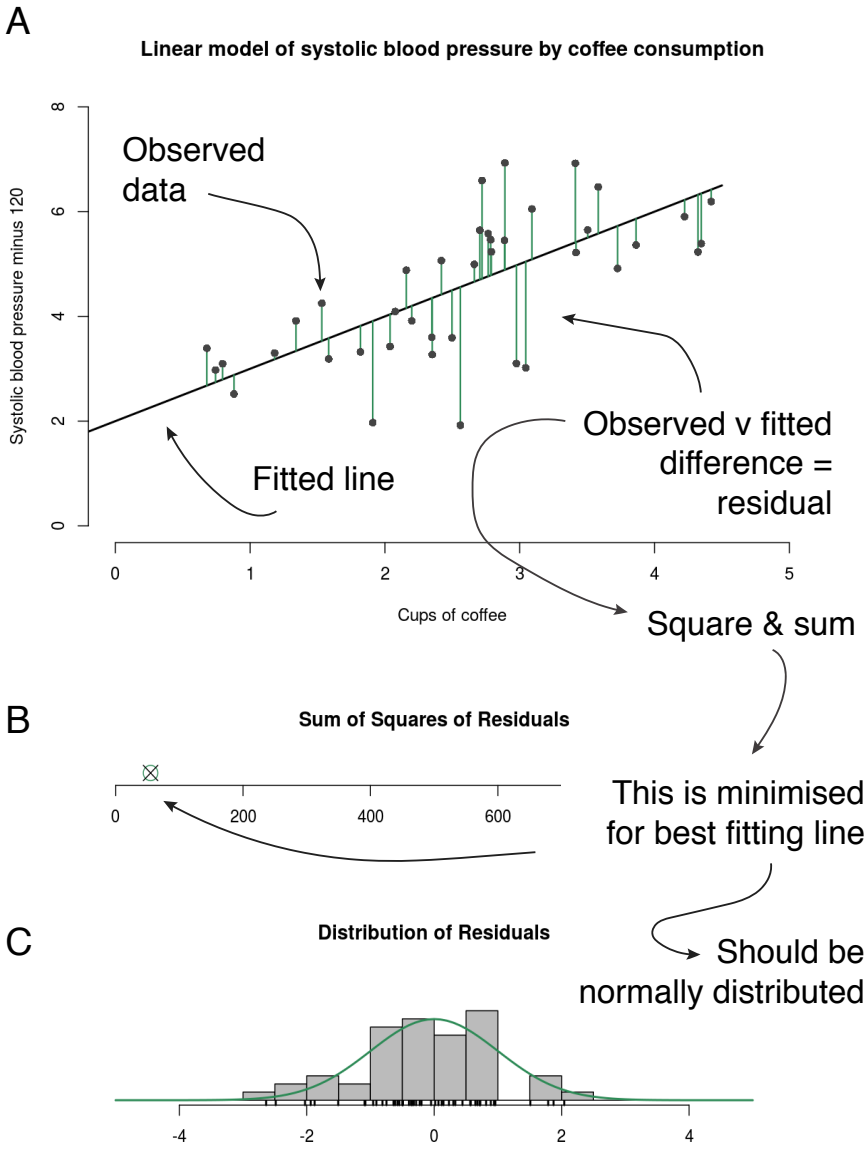


FIGURE 7.2: How a regression line is fitted.

7.4.2 Independence of residuals

The observations and therefore the residuals should be independent. This is more commonly a problem in time series data, where observations may be correlated across time with each other (autocorrelation).

7.4.3 Normal distribution of residuals

The observations should be normally distributed around the fitted line. This means that the residuals should show a normal distribution with a mean of zero (figure 7.3A). If the observations are not equally distributed around the line, the histogram of residuals will be skewed and a normal Q-Q plot will show residuals diverging from the 45 degree line (figure 7.3B). See *Q-Q plot ref.*

7.4.4 Equal variance of residuals

The distribution of the observations around the fitted line should be the same on the left side of the scatter plot as they are on the right side. Look at the fan-shaped data on the simple regression diagnostics shiny app[3]. This should be obvious on the residuals vs. fitted values plot, as well as the histogram and normal Q-Q plot.

This is really all about making sure that the line you draw through your data points is valid. It is about ensuring that the regression line is valid across the range of the explanatory variable and dependent variable. It is really about understanding the underlying data, rather than relying on a fancy statistical test that gives you a p-value.

[3] https://argoshare.is.ed.ac.uk/simple_regression_diagnostics

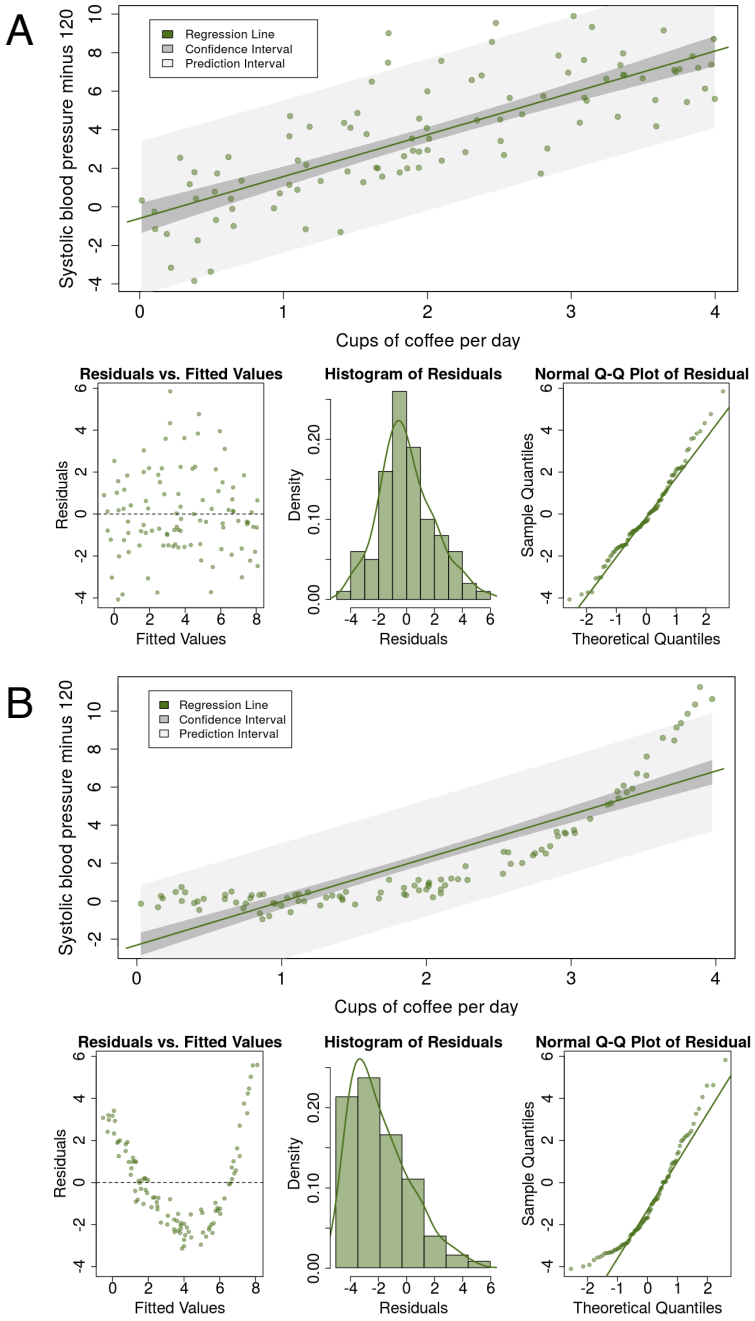


FIGURE 7.3: Regression diagnostics. Does this also appear in the contents. What about this?

7.5 The fitted line and the linear equation

We promised to keep the equations to a minimum, but this one is so important it needs to be included. But it is easy to understand, so fear not.

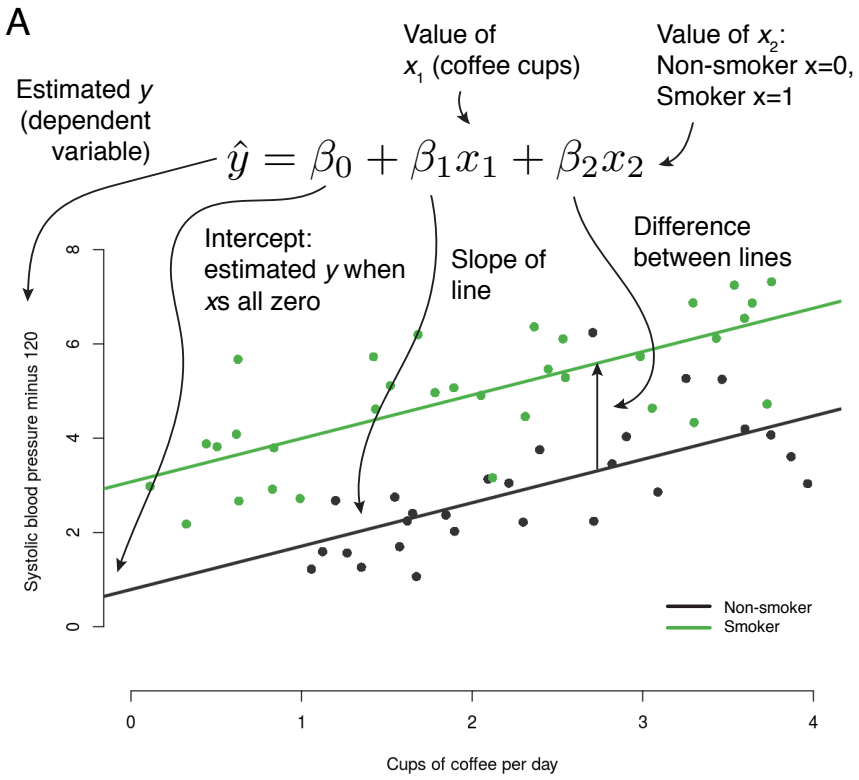
Figure 7.4 links the fitted line, the linear equation, and the output from R. Some of this will likely be already familiar to you.

Figure 7.4A shows a scatter plot with fitted lines from a multivariable linear regression model. The plot is taken from the multivariable regression shiny app[4]. Remember, these data are simulated and are not real. This app will really help you understand different regression models, more on this below. The app allows us to specify "the truth" with the sliders on the left hand side. For instance, we can set the intercept=1, meaning that when all $x = 0$, the value of the dependent variable, $\hat{y} = 1$.

Our model has a continuous explanatory variable of interest (average coffee consumption) and a further categorical variable (smoking). In the example the truth is set as $intercept = 1$, $\beta_1 = 1$ (true effect of coffee on blood pressure, gradient/slope of line), and $\beta_2 = 2$ (true effect of smoking on blood pressure). The points on the plot are simulated following the addition of random noise.

Figure 7.4B shows the default output in R for this linear regression model. Look carefully and make sure you are clear how the fitted lines, the linear equation, and the R output fit together. In this example, the random sample from our true population specified above shows $intercept = 0.67$, $\beta_1 = 1.00$ (coffee), and $\beta_2 = 2.48$ (smoking). A p-value is provided ($Pr(> |t|)$), which is the result of a null hypothesis significance test for the gradient of the line being equal to zero. Said another way, this is the probability that the gradient of the particular line is equal to zero.

[4] https://argoshare.is.ed.ac.uk/multi_regression/



B Linear regression (`lm`) output

```
Call:
lm(formula = y ~ coffee + smoking, data = df)

Residuals:
    Min      1Q  Median      3Q     Max
-1.4589 -0.6176  0.0043  0.6715  1.8748

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.68661    0.24292   2.827  0.00648 **
coffee      1.00496    0.09781  10.275 1.38e-14 ***
smoking     2.47581    0.22694  10.910 1.40e-15 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.8724 on 57 degrees of freedom
Multiple R-squared:  0.8144,    Adjusted R-squared:  0.8079
F-statistic: 125.1 on 2 and 57 DF,  p-value: < 2.2e-16
```

Function call

Distribution of residuals

Results

Adjusted R^2

$$s\hat{B}P = \beta_0 + \beta_{coffee} x_{coffee} + \beta_{smoking} x_{smoking}$$

FIGURE 7.4: Linking the fitted line, regression equation and R output.

7.6 Effect modification

Effect modification occurs when the size of the effect of the explanatory variable of interest (exposure) on the outcome (dependent variable) differs depending on the level of a third variable. Said another way, this is a situation in which an explanatory variable differentially (positively or negatively) modifies the observed effect of another explanatory variable on the outcome.

Again, this is best thought about using the concrete example provided in the multivariable regression shiny app[5].

Figure 7.5 shows three potential causal pathways.

In the first, smoking is not associated with the outcome (blood pressure) or our explanatory variable of interest (coffee consumption).

In the second, smoking is associated with elevated blood pressure, but not with coffee consumption. This is an example of effect modification.

In the third, smoking is associated with elevated blood pressure and with coffee consumption. This is an example of confounding.

7.6.1 Additive vs. multiplicative effect modification (interaction)

Depending on the field you work, will depend on which set of terms you use. Effect modification can be additive or multiplicative. We refer to multiplicative effect modification as simply including a statistical interaction.

Figure 7.6 should make it clear exactly how these work. The data have been set-up to include an interaction term. What does this mean?

[5] https://argoshare.is.ed.ac.uk/multi_regression/

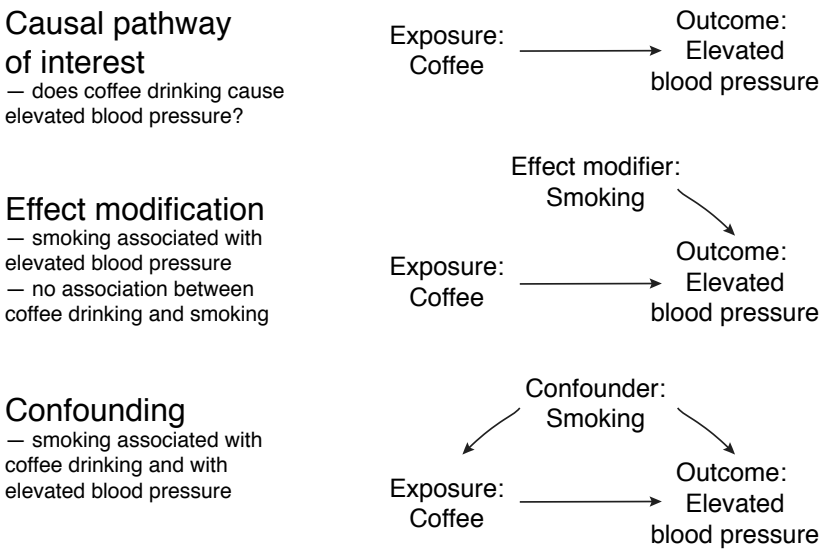


FIGURE 7.5: Causal pathways, effect modification and confounding.

- *intercept* = 1: the blood pressure ($\widehat{y}$) for non-smokers who drink no coffee (all $x = 0$);
- $\beta_1 = 1$ (`coffee`): the additional blood pressure for each cup of coffee drunk by non-smokers (slope of the line when $x_2 = 0$;
- $\beta_2 = 1$ (`smoking`): the difference in blood pressure between non-smokers and smokers who drink no coffee ($x_1 = 0$);
- $\beta_3 = 1$ (`coffee:smoking` interaction): the blood pressure ($\widehat{y}$) in addition to β_1 and β_2, for each cup of coffee drunk by smokers ($x_2 = 1$).

You may have to read that a couple of times in combination with looking at Figure 7.6.

With the additive model, the fitted lines for non-smoking vs smoking are constrained to be parallel. Look at the equation in Figure 7.6B and convince yourself that the lines can never be anything other than parallel.

A statistical interaction (or multiplicative effect modification) is a situation where the effect of an explanatory variable on the out-

come is modified in non-additive manner. In other words using our example, the fitted lines are no longer constrained to be parallel.

If we had not checked for an interaction effect, we would have inadequately described the true relationship between these three variables.

What does this mean back in reality? Well it may be biologically plausible for the effect of smoking on blood pressure to increase multiplicatively due to a a chemical interaction between cigarette smoke and caffeine, for example.

Note, we are just trying to find a model which best describes the underlying data. All models are approximations of reality.

7.7 R-squared and model fit

Figure 7.6 includes a further metric from the R output: `Adjusted R-squared`.

R-squared is another measure of how close the data are to the fitted line. It is also known as the coefficient of determination and represents proportion of the dependent variable which is explained by the explanatory variable(s). So 0.0 indicates that none of the variability in the dependent is explained by the explanatory (no relationship between data points and fitted line) and 1.0 indicates that the model explains all of the variability in the dependent (fitted line follows data points exactly).

R provides the `R-squared` and the `Adjusted R-squared`. The adjusted R-squared includes a penalty the more explanatory variables are included in the model. So if the model includes variables which do not contribute to the description of the dependent variable, the adjusted R-squared will be lower.

Looking again at Figure 7.6, in A, a simple model of coffee alone does not describe the data well (adjusted R-squared 0.38). Add smoking to the model improves the fit as can be seen by the fitted

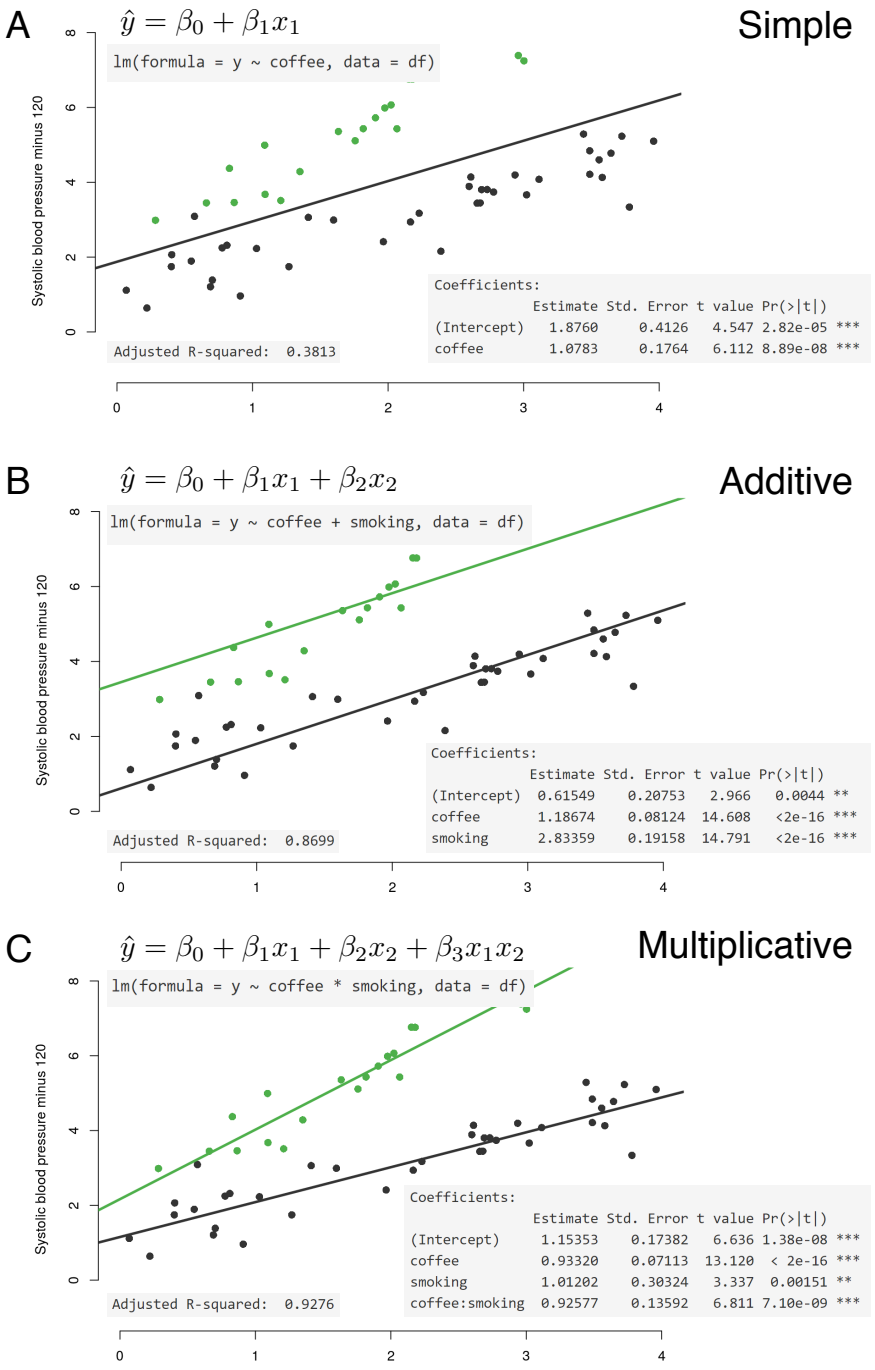


FIGURE 7.6: Multivariable linear regression with additive and multiplicative effect modification.

lines (0.87). But a true interaction exists in the actual data. By including this interaction in the model, the fit is very good indeed (0.93).

7.8 Confounding

The last important concept to mention here is confounding. Confounding is a situation in which the association between an explanatory variable (exposure) and outcome (dependent variable) is distorted by the presence of another explanatory variable.

In our example, confounding exists if there is an association between smoking and blood pressure AND smoking and coffee consumption (Figure 7.5C). This exists simply if smokers drink more coffee than non-smokers.

Figure 7.7 shows this really clearly. The underlying data have been altered so that those who drink more than two cups of coffee per day also smoke and those who drink fewer than two cups per day do not smoke. A true effect of smoking on blood pressure is entered, but NO effect of coffee on blood pressure.

If we simply fit blood pressure by coffee consumption (Figure 7.7A), then we may mistakenly conclude a relationship between coffee consumption and blood pressure. But this does not exist, because the ground truth we have set is that no relationship exists between coffee and blood pressure. We are simply seeing the effect of smoking on blood pressure, which is confounding the effect of coffee on blood pressure.

If we include the confounder in the model by adding smoking, the true relationship becomes apparent. Two parallel flat lines indicating no effect of coffee on blood pressure, but a relationship between smoking and blood pressure. This procedure is often referred to as controlling for or adjusting for confounders.

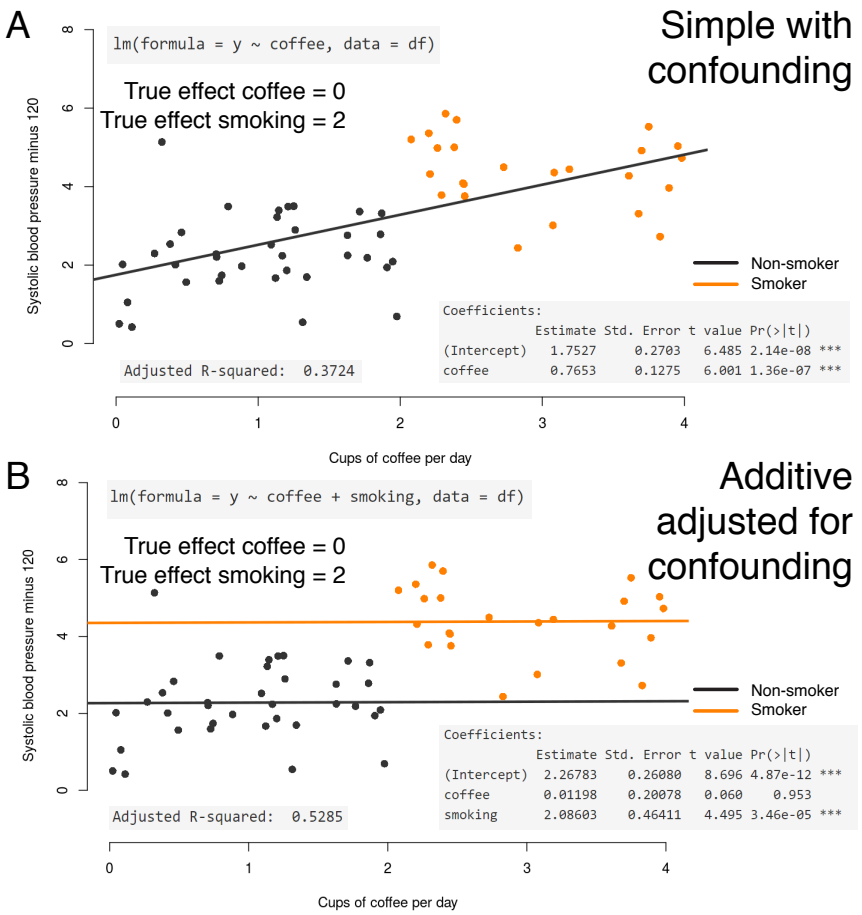


FIGURE 7.7: Multivariable linear regression with confounding of coffee drinking by smoking.

7.9 Summary

We have intentionally spent some time going through the principles and applications of linear regression because it is so important. A firm grasp of these concepts lead to an easy understanding of other regression procedures, such as logistic regression and Cox Proportional Hazards regression.

We will now perform all this ourselves in R using a gapminder dataset which you are familiar with from preceding chapters.

7.10 Fitting simple models

7.10.1 The Question (2)

We are interested in modelling the change in life expectancy for different countries over the past 60 years.

7.10.2 Get the data

```
library(tidyverse)
library(gapminder) # dataset
library(lubridate) # handles dates
library(finalfit)
library(broom)

theme_set(theme_bw())
mydata = gapminder
```

7.10.3 Check the data

Always check a new dataset, as described in 06-1

```
glimpse(mydata) # each variable as line, variable type, first values
missing_glimpse(mydata) # missing data for each variable
ff_glimpse(mydata) # summary statistics for each variable
```

7.10.4 Plot the data

Let's plot the life expectancies in European countries over the past 60 years, focussing on the UK and Turkey. We can add in simple best fit lines using `ggplot` directly.

```
p1 = mydata %>%                          # save as object p1
  filter(continent == "Europe") %>%      # Europe only
  ggplot(aes(x = year, y = lifeExp)) +   # lifeExp~year
  geom_point() +                         # plot points
  facet_wrap(~ country) +                # facet by country
  scale_x_continuous(
    breaks = c(1960, 2000))      # adjust x-axis

p2 = p1 + geom_smooth(method = "lm")    # add regression line

library(patchwork)
p1 + p2
```

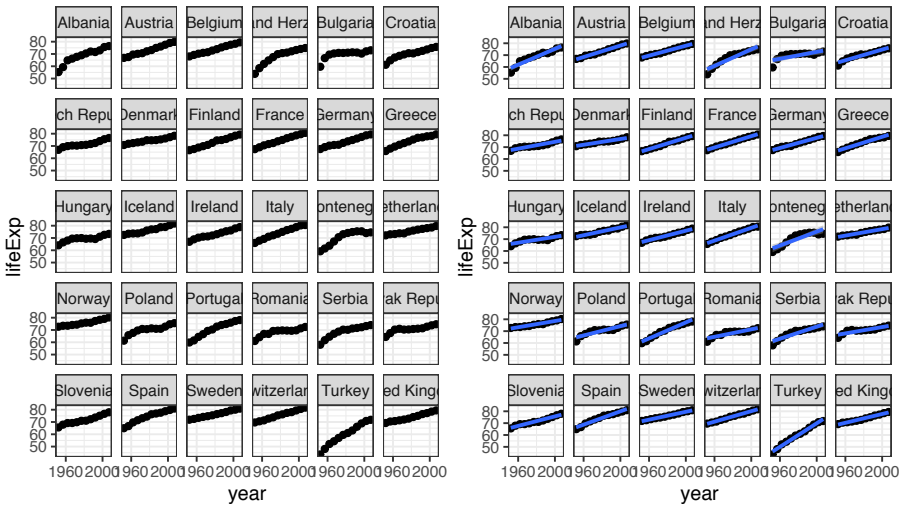


FIGURE 7.8: Scatterplot with fitted line plot: Life expectancy by year in European countries

7.10.5 Simple linear regression

As you can see, `ggplot()` is very happy to run and plot linear regression models for us. While this is sometimes convenient, we usually want to build, run, and explore these models ourselves. We can then investigate the intercepts and the slope coefficients (linear increase per year):

First let's plot two countries to compare, Turkey and United Kingdom

```
mydata %>%
  filter(country %in% c("Turkey", "United Kingdom")) %>%
  ggplot(aes(x = year, y = lifeExp, colour = country)) +
  geom_point()
```

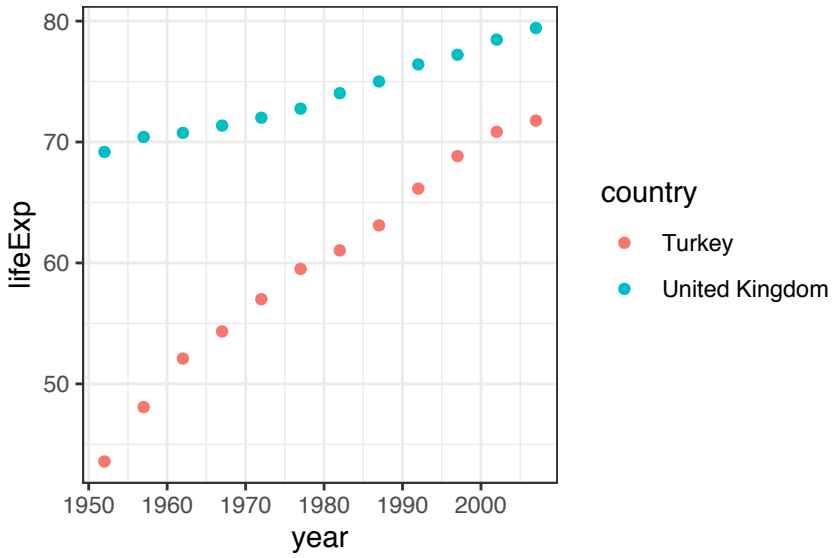


FIGURE 7.9: Scatterplot: Life expectancy by year Turkey and Europe.

The two non-parallel lines may make you think of what has been discussed above.

First, let's model the two countries separately.

United Kingdom:

```
fit_uk = mydata %>%
  filter(country == "United Kingdom") %>%
  lm(lifeExp~year, data = .)

fit_uk %>%
  summary()
```

```
##
```

```
## Call:
## lm(formula = lifeExp ~ year, data = .)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.69767 -0.31962  0.06642  0.36601  0.68165
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2.942e+02  1.464e+01  -20.10 2.05e-09 ***
## year         1.860e-01  7.394e-03   25.15 2.26e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4421 on 10 degrees of freedom
## Multiple R-squared:  0.9844, Adjusted R-squared:  0.9829
## F-statistic: 632.5 on 1 and 10 DF,  p-value: 2.262e-10
```

Turkey:

```
fit_turkey = mydata %>%
  filter(country == "Turkey") %>%
  lm(lifeExp~year, data = .)

fit_turkey %>%
  summary()
```

```
##
## Call:
## lm(formula = lifeExp ~ year, data = .)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.4373 -0.3457  0.1653  0.9008  1.1033
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -924.58989   37.97715  -24.35 3.12e-10 ***
## year           0.49724    0.01918   25.92 1.68e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.147 on 10 degrees of freedom
## Multiple R-squared:  0.9853, Adjusted R-squared:  0.9839
## F-statistic: 671.8 on 1 and 10 DF,  p-value: 1.681e-10
```

7.10.5.1 Accessing the coefficients of linear regression

A simple linear regression model will return two coefficients - the intercept and the slope (the second returned value). Compare this to the `summary()` output above.

```
fit_uk$coefficients
```

```
##  (Intercept)         year
## -294.1965876    0.1859657
```

```
fit_turkey$coefficients
```

```
##  (Intercept)         year
## -924.5898865    0.4972399
```

In this example, the intercept is telling us that life expectancy at year 0 in the United Kingdom (some 2000 years ago) was -294 years. While this is mathematically correct (based on the data we have), it obviously makes no sense in practice. It is important at all stages of data analysis, to keep "sense checking" your results.

To make the intercepts meaningful, we will add in a new column called `year_from1952` and re-run `fit_uk` and `fit_turkey` using `year_from1952` instead of `year`.

```
mydata = mydata %>%
  mutate(year_from1952 = year - 1952)

fit_uk = mydata %>%
  filter(country == "United Kingdom") %>%
  lm(lifeExp ~ year_from1952, data = .)

fit_turkey = mydata %>%
  filter(country == "Turkey") %>%
  lm(lifeExp ~ year_from1952, data = .)
```

```
fit_uk$coefficients
```

```
##   (Intercept) year_from1952
##    68.8085256     0.1859657
```

```
fit_turkey$coefficients
```

```
##   (Intercept) year_from1952
##    46.0223205     0.4972399
```

Now, the updated results tell us that in year 1952, the life expectancy in the United Kingdom was 68 years. Note that the slope (0.18) does not change. There was nothing wrong with the original model and the results were correct, the intercept was just not very useful.

7.10.5.2 Accessing all model information `tidy()` and `glance()`

In the fit_uk and fit_turkey examples above, we were using `fit_uk %>% summary()` to get R to print out a summary of the model. This summary is not, however, in a rectangular shape so we can't easily access the values or put them in a table/use as information on plot labels.

We use the `tidy()` function from `library(broom)` to get the explanatory variable specific values in a nice tibble:

```
fit_uk %>% tidy()
```

```
## # A tibble: 2 x 5
##   term          estimate std.error statistic  p.value
##   <chr>            <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)     68.8     0.240       287.  6.58e-21
## 2 year_from1952    0.186   0.00739      25.1 2.26e-10
```

In the `tidy()` output, the column `estimate` includes both the intercepts and slopes.

And we use the `glance()` function to get overall model statistics (mostly the r.squared).

```
fit_uk %>% glance()
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic  p.value   df logLik  AIC  BIC
##       <dbl>         <dbl> <dbl>     <dbl>    <dbl> <int>  <dbl> <dbl> <dbl>
## 1     0.984         0.983 0.442     633. 2.26e-10     2  -6.14  18.3  19.7
## # ... with 2 more variables: deviance <dbl>, df.residual <int>
```

7.10.6 Multivariable linear regression

Multivariable linear regression includes more than one explanatory variable. There are a few ways to include more variables, depending on whether they should share the intercept and how they interact:

Simple linear regression (exactly one predictor variable):

```
myfit = lm(lifeExp ~ year, data = mydata)
```

Multivariable linear regression (additive):

```
myfit = lm(lifeExp ~ year + country, data = mydata)
```

Multivariable linear regression (interaction):

```
myfit = lm(lifeExp ~ year * country, data = mydata)
```

This equivalent to: `myfit = lm(lifeExp ~ year + country + year:country, data = mydata)`

These examples of multivariable regression include two variables: `year` and `country`, but we could include more by adding them with `+`.

In this particular setting, it will become obvious which model is appropriate. So we have complete control over the model being fitted, we will use the `predict()` function directly to obtain our fitted line, rather than leaving it up to `ggplot`.

7.10.6.1 Model 1: year only

```
mydata_UK_T = mydata %>%
  filter(country %in% c("Turkey", "United Kingdom"))

fit_both1 = mydata_UK_T %>%
  lm(lifeExp ~ year_from1952, data = .)
fit_both1
```

```
##
## Call:
## lm(formula = lifeExp ~ year_from1952, data = .)
##
## Coefficients:
##   (Intercept)  year_from1952
##       57.4154         0.3416
```

```
pred_both1 = predict(fit_both1)

mydata_UK_T %>%
  bind_cols(pred_both = pred_both1) %>%
  ggplot() +
  geom_point(aes(x = year, y = lifeExp, colour = country)) +
  geom_line(aes(x = year, y = pred_both))
```

By fitting year only, the model ignores country. This gives us a fitted line which is the average of life expectancy in the UK and Turkey. This may be desirable, depending on the question. But here we want to best describe the data.

7.10.6.2 Model 2: year + country

```
fit_both2 = mydata_UK_T %>%
  lm(lifeExp ~ year_from1952 + country, data = .)
fit_both2
```

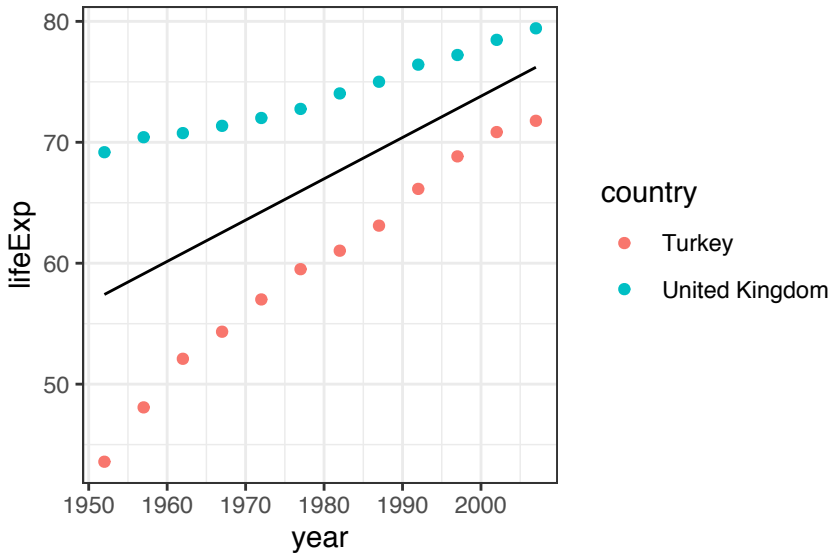


FIGURE 7.10: Scatter and line plot. Life expectancy in Turkey and the UK - univariable fit.

```
##
## Call:
## lm(formula = lifeExp ~ year_from1952 + country, data = .)
##
## Coefficients:
##           (Intercept)          year_from1952  countryUnited Kingdom
##               50.3023                 0.3416                14.2262
```

```
pred_both2 = predict(fit_both2)

mydata_UK_T %>%
  bind_cols(pred_both = pred_both2) %>%
  ggplot() +
  geom_point(aes(x = year, y = lifeExp, colour = country)) +
  geom_line(aes(x = year, y = pred_both, colour = country))
```

This is better, by including country in the model, we now have fitted lines better represent the data. However, the lines are constrained to be parallel. This is discussed in detail above. We need to include an interaction term to allow the effect of year on life expectancy to vary by country in a non-additive manner.

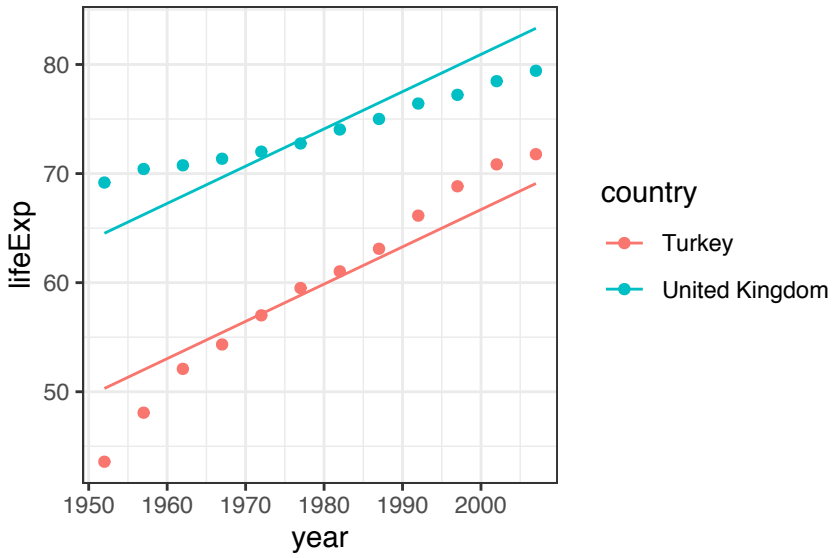


FIGURE 7.11: Scatter and line plot. Life expectancy in Turkey and the UK - multivariable additive fit.

7.10.6.3 Model 3: year * country

```
fit_both3 = mydata_UK_T %>%
  lm(lifeExp ~ year_from1952 * country, data = .)
fit_both3
```

```
##
## Call:
## lm(formula = lifeExp ~ year_from1952 * country, data = .)
##
## Coefficients:
##                           (Intercept)                         year_from1952
##                               46.0223                                0.4972
##             countryUnited Kingdom  year_from1952:countryUnited Kingdom
##                               22.7862                               -0.3113
```

```
pred_both3 = predict(fit_both3)

mydata_UK_T %>%
```

```
  bind_cols(pred_both = pred_both3) %>%
  ggplot() +
  geom_point(aes(x = year, y = lifeExp, colour = country)) +
  geom_line(aes(x = year, y = pred_both, colour = country))
```

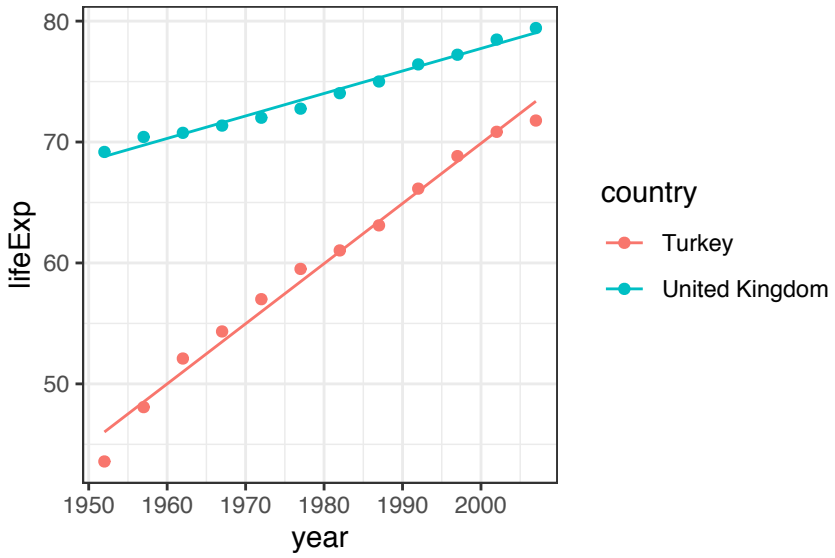


FIGURE 7.12: Scatter and line plot. Life expectancy in Turkey and the UK - multivariable multiplicative fit.

This fits the data much better than the previous two models. You can check the R-squared using 'summary(fit_both1)

Pro tip

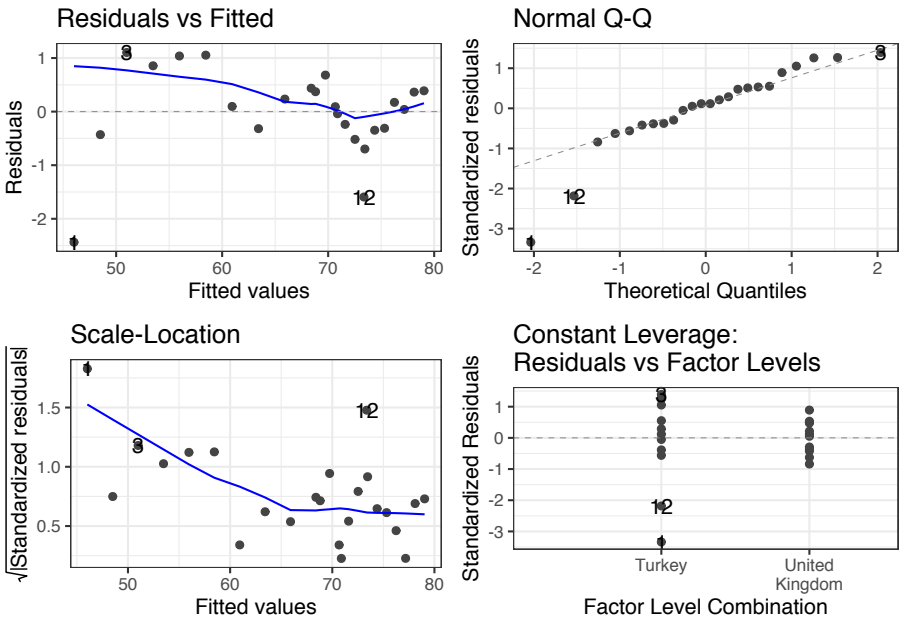
```
library(purrr)
list(fit_both1, fit_both2, fit_both3) %>%
  map_df(glance, .id = "fit")
```

```
## # A tibble: 3 x 12
##   fit   r.squared adj.r.squared sigma statistic  p.value    df logLik   AIC
##   <chr>     <dbl>         <dbl> <dbl>     <dbl>    <dbl> <int>  <dbl> <dbl>
## 1 1         0.373         0.344 7.98       13.1 1.53e- 3     2  -82.9 172.
## 2 2         0.916         0.908 2.99      114.  5.18e-12     3  -58.8 126.
## 3 3         0.993         0.992 0.869     980.  7.30e-22     4  -28.5  67.0
## # ... with 3 more variables: BIC <dbl>, deviance <dbl>, df.residual <int>
```

7.10.7 Check assumptions

The assumptions of linear regression can be checked with diagnostic plots, either by passing the fitted object (`lm()` output) to base R `plot()`, or by using the more convenient function below.

```
library(ggfortify)
autoplot(fit_both3)
```



There is no clear problem with the residuals, as we would expect from the scatterplot with fitted lines.

7.11 Fitting more complex models

7.11.1 The Question (3)

Finally in this chapter, we are going to fit a more complex linear regression model. Here, we will discuss variable selection and introduce the Akaike Information Criterion (AIC).

We will introduce a new dataset: The Western Collaborative Group Study. This classic includes data from 3154 healthy young men aged 39-59 from the San Francisco area who were assessed for their personality type. It aimed to capture the occurrence of coronary heart disease over the following 8.5 years.

We will use it however to explore the relationship between systolic blood pressure (`sbp`), weight (`weight`) and personality type (`personality_2L`).

Personality type is A: aggressive and B: passive.

7.11.2 Model fitting principles

We suggest building statistical models on the basis of the following six pragmatic principles:

1. As few explanatory variables should be used as possible (parsimony);

2. Explanatory variables associated with the outcome variable in previous studies should be accounted for;
3. Demographic variables should be included in model exploration;
4. Population stratification should be incorporated if available;
5. Interactions should be checked and included if influential;
6. Final model selection should be performed using a "criterion-based approach"

- minimise the Akaike information criterion (AIC)
- maximise the adjusted R-squared value.

This is not the law, but it probably should be. These principles are sensible as we will discuss through the rest of this book. We strongly suggest you do not use automated methods of variable selection. These are often "forward selection" or "backward elimination" methods for including or excluding particular variables

on the basis of a statistical property. In certain settings, these approaches may be found to work. However, they create an artificial distance between you and the problem you are working on. They give you a false sense of certainty that the model you have created is in some sense valid. And quite frequently, they will get it wrong.

Alternatively, you can follow the five principles above.

A variable may have previously been shown to strongly predict an outcome (think smoking and risk of cancer). This should give you good reason to consider it in your model. But perhaps you think that previous studies were incorrect, or that the variable is confounded by another. All this is fair, but it will be expected that this new knowledge is clearly demonstrated by you, so do not omit these variables before you start.

There are particular variables that are so commonly associated with particular outcomes in healthcare that they should almost always be included at the start. Age, sex, social class, and comorbidity for instance are commonly associated with survival, before you start looking at your explanatory variable of interest or checking that your randomised controlled trial is indeed balanced.

Patients are often clustered by a particular grouping variable, such as treating hospital. There will be commonalities between these patients that are likely not fully explained by your observed variables. To estimate the coefficients of your variables of interest most accurately, clustering should be accounted for in the analysis.

As demonstrated enough, the purpose of the model is to provide a best fit approximation of the underlying data. Effect modification and interactions commonly exist in heath datasets, and should be incorporated if present.

Finally, we want to assess how well our models fit the data with `model checking`. The effect of adding or removing one variable to the coefficients of the other variables in the model is very important, and will be discussed later. Measures of goodness-of-fit such as the `AIC`, can also be of great use when deciding which model choice is most valid.

7.11.3 AIC

The Akaike Information Criterion (AIC) is an alternative goodness-of-fit measure. In that sense, it is similar to the R-squared, but has a different statistical basis. It is useful because it can be used to help guide the best fit in generalised linear models such as logistic regression (ref: chapter 9). It is based on the likelihood but is also penalised for the number of variables present in the model. We aim to have as small an AIC as possible. The value of the number itself has no inherent meaning. It's use is as a comparison between different models.

7.11.4 Get the data

```
mydata = finalfit::wcgs #F1 here for details
```

7.11.5 Check the data

As always, when you receive a new dataset, carefully check that it does not contain errors.

```
##
## Attaching package: 'kableExtra'

## The following object is masked from 'package:dplyr':
##
##     group_rows
```

7.11.6 Plot the data

```
mydata %>%
  ggplot(aes(y = sbp, x = weight,
             colour = personality_2L)) +   # Personality type
  geom_point(alpha = 0.2) +                # Add transparency
  geom_smooth(method = "lm", se = FALSE)
```

TABLE 7.1: WCGS data, ff_glimpse: continous

label	var_type	n	missing_n	mean	sd	median
Subject ID	<int>	3154	0	10477.9	5877.4	11405.5
Age (years)	<int>	3154	0	46.3	5.5	45.0
Height (inches)	<int>	3154	0	69.8	2.5	70.0
Weight (pounds)	<int>	3154	0	170.0	21.1	170.0
Systolic BP (mmHg)	<int>	3154	0	128.6	15.1	126.0
Diastolic BP (mmHg)	<int>	3154	0	82.0	9.7	80.0
Cholesterol (mg/100 ml)	<int>	3142	12	226.4	43.4	223.0
Cigarettes/day	<int>	3154	0	11.6	14.5	0.0
Time to CHD event	<int>	3154	0	2683.9	666.5	2942.0

TABLE 7.2: WCGS data, ff_glimpse: categorical

label	var_type	n	missing_n	levels_n	levels	levels_count
Personality type	<fct>	3154	0	4	"A1", "A2", "B3", "B4"	264, 1325, 1216, 349
Personality type	<fct>	3154	0	2	"B", "A"	1565, 1589
Smoking	<fct>	3154	0	2	"Non-smoker", "Smoker"	1652, 1502
Corneal arcus	<fct>	3152	2	2	"No", "Yes", "(Missing)"	2211, 941, 2
CHD event	<fct>	3154	0	2	"No", "Yes"	2897, 257
Type CHD	<fct>	3154	0	4	"No", "MI_SD", "Silent_MI", "Angina"	2897, 135, 71, 51

From this plot we can see that there is a weak relationship between weight and blood pressure. In addition, there is really no meaningful effect of personality type on blood pressure. This is really important, because as you will see below, we are about to find some highly statistically significant effects in a model.

7.11.7 Linear regression with Finalfit

Finalfit is our own package and provides a convenient set of functions for fitting regression models with results presented in final tables.

There are a host of features with example code at the Finalfit website[6].

Here we will use the all-in-one `finalfit` function, which takes a

[6] https://finalfit.org

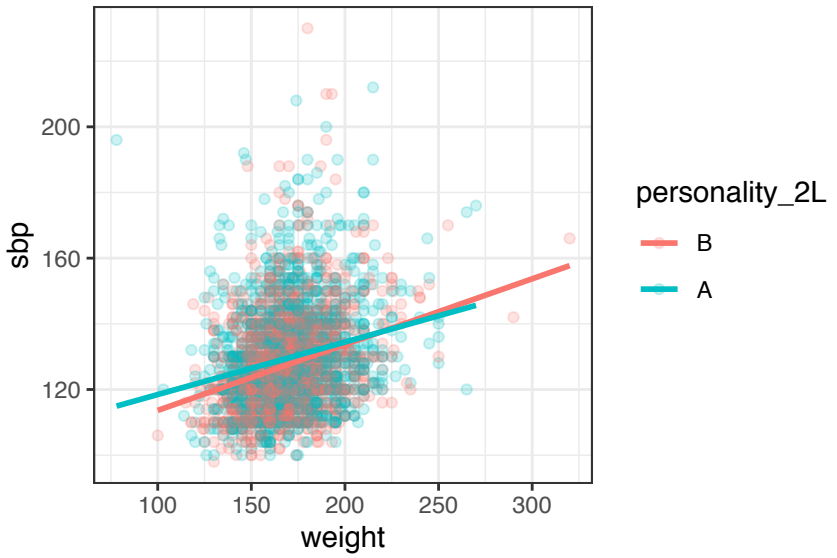


FIGURE 7.13: Scatter and line plot. Systolic blood pressure by weight and personality type.

dependent variable and one or more explanatory variables. The appropriate regression for the dependent variable is performed, from a choice of linear, logistic, and Cox Proportional Hazards regression. Summary statistics, together with a univariable and a multivariable regression analysis are produced in a final results table.

```
dependent = "sbp"
explanatory = "weight"
fit_sbp1 = mydata %>%
  finalfit(dependent, explanatory, metrics = TRUE)
```

TABLE 7.3: Linear regression: Systolic blood pressure by weight

Dependent: Systolic BP (mmHg)		Mean (sd)	Coefficient (univariable)	Coefficient (multivariable)
Weight (pounds)	[78,320]	128.6 (15.1)	0.18 (0.16 to 0.21, p<0.001)	0.18 (0.16 to 0.21, p<0.001)

The output shows us the range for weight (78 to 320 pounds) and the mean (standard deviation) systolic blood pressure for the

whole cohort. As there is only one variable, the univariable and multivariable analyses are the same (the multivariable column can be removed if desired by including `select(-5) #5th column` in the piped function). The coefficient and 95% confidence interval are provided by default. This is interpretted as: for each pound increase in weight, there is on average a corresponding increase of 0.18 mmHg in systolic blood pressure.

TABLE 7.4: Model metrics: Systolic blood pressure by weight

Number in dataframe = 3154, Number in model = 3154, Missing = 0, Log-likelihood = -12936.15, AIC = 25878.3, R-squared = 0.064, Adjusted r-squared = 0.064

The optional `metrics = TRUE` output gives us the number included in the model. This is so important as frequently people forget that in standard regression models, missing data from any variable results in the that entire row (think patient) being excluded from the analysis. See missing data section. Note the `AIC` and `Adjusted R-squared` results. The adjusted R-squared is very low - the fitted line only explains 6.4% of the variation of systolic blood pressure. This is to be expected, given our scatterplot above.

We will now add in personality type, our other variable of interest. `personality_2L` - the '2L' just mean two levels, rather than the other option for this variable of four levels.

```
dependent = "sbp"
explanatory = c("weight", "personality_2L")
fit_sbp2 = mydata %>%
  finalfit(dependent, explanatory, metrics = TRUE)
```

TABLE 7.5: Multivariable linear regression: Systolic blood pressure by weight and personality type.

Dependent: Systolic BP (mmHg)		Mean (sd)	Coefficient (univariable)	Coefficient (multivariable)
Weight (pounds)	[78,320]	128.6 (15.1)	0.18 (0.16 to 0.21, p<0.001)	0.18 (0.16 to 0.20, p<0.001)
Personality type	B	127.5 (14.4)	-	-
	A	129.8 (15.7)	2.32 (1.26 to 3.37, p<0.001)	1.99 (0.97 to 3.01, p<0.001)

TABLE 7.6: Multivariable linear regression metrics: Systolic blood pressure by weight and personality type.

Number in dataframe = 3154, Number in model = 3154, Missing = 0, Log-likelihood = -12928.82, AIC = 25865.6, R-squared = 0.068, Adjusted r-squared = 0.068

Looking first at personality type, the mean blood pressure for type A is higher than for type B. This is quantified by the univariable analysis for personality type. Althought the difference is numerically quite small (2.3 mmHg), it is staistically signficiant partly because there are a large number of patients in this study. There is little change in the size of the coefficients for each variable in the multivarible analysis, meaning that they are reasonably independent. As an exercise, check the the distribution of weight by personality type using a boxplot.

The AIC is slightly lower and the adjusted R-squared is slightly higher, meaning the model better fits the data with personality type included.

Let's now add in other variable that we think may influence systolic blood pressure.

```
dependent = "sbp"
explanatory = c("weight", "personality_2L", "age",
                "height", "chol", "smoking")
fit_sbp3 = mydata %>%
  finalfit(dependent, explanatory, metrics = TRUE)
```

TABLE 7.7: Multivariable linear regression: Systolic blood pressure by available explanatory variables.

Dependent: Systolic BP (mmHg)		Mean (sd)	Coefficient (univariable)	Coefficient (multivariable)
Weight (pounds)	[78,320]	128.6 (15.1)	0.18 (0.16 to 0.21, p<0.001)	0.24 (0.21 to 0.27, p<0.001)
Personality type	B	127.5 (14.4)	-	-
	A	129.8 (15.7)	2.32 (1.26 to 3.37, p<0.001)	1.44 (0.44 to 2.43, p=0.005)
Age (years)	[39,59]	128.6 (15.1)	0.45 (0.36 to 0.55, p<0.001)	0.43 (0.33 to 0.52, p<0.001)
Height (inches)	[60,78]	128.6 (15.1)	0.11 (-0.10 to 0.32, p=0.302)	-0.84 (-1.08 to -0.61, p<0.001)
Cholesterol (mg/100 ml)	[103,645]	128.6 (15.1)	0.04 (0.03 to 0.05, p<0.001)	0.03 (0.02 to 0.04, p<0.001)
Smoking	Non-smoker	128.6 (15.6)	-	-
	Smoker	128.7 (14.6)	0.08 (-0.98 to 1.14, p=0.883)	0.95 (-0.05 to 1.96, p=0.063)

TABLE 7.8: Model metrics: Systolic blood pressure by available explanatory variables.

Number in dataframe = 3154, Number in model = 3142, Missing = 12, Log-likelihood = -12772.04, AIC = 25560.1, R-squared = 0.12, Adjusted r-squared = 0.12

to here

```
dependent = "sbp"
explanatory = c("weight", "personality_2L", "age",
                "height", "chol", "smoking")
explanatory_multi = c("weight", "personality_2L", "age",
                      "height", "chol")
fit_sbp4 = mydata %>%
  finalfit(dependent, explanatory,
           explanatory_multi,
           keep_models = TRUE, metrics = TRUE)
```

TABLE 7.9: Multivariable linear regression: Systolic blood pressure by available explanatory variables and reduced model.

Dependent: Systolic BP (mmHg)		Mean (sd)	Coefficient (univariable)	Coefficient (multivariable)	Coefficient (multivariable reduced)
Weight (pounds)	[78,320]	128.6 (15.1)	0.18 (0.16 to 0.21, p<0.001)	0.24 (0.21 to 0.27, p<0.001)	0.23 (0.21 to 0.26, p<0.001)
Personality type	B	127.5 (14.4)	-	-	-
	A	129.8 (15.7)	2.32 (1.26 to 3.37, p<0.001)	1.44 (0.44 to 2.43, p=0.005)	1.49 (0.50 to 2.49, p=0.003)
Age (years)	[39,59]	128.6 (15.1)	0.45 (0.36 to 0.55, p<0.001)	0.43 (0.33 to 0.52, p<0.001)	0.42 (0.33 to 0.51, p<0.001)
Height (inches)	[60,78]	128.6 (15.1)	0.11 (-0.10 to 0.32, p=0.302)	-0.84 (-1.08 to -0.61, p<0.001)	-0.83 (-1.06 to -0.59, p<0.001)
Cholesterol (mg/100 ml)	[103,645]	128.6 (15.1)	0.04 (0.03 to 0.05, p<0.001)	0.03 (0.02 to 0.04, p<0.001)	0.03 (0.02 to 0.04, p<0.001)
Smoking	Non-smoker	128.6 (15.6)	-	-	-
	Smoker	128.7 (14.6)	0.08 (-0.98 to 1.14, p=0.883)	0.95 (-0.05 to 1.96, p=0.063)	-

TABLE 7.10: Model metrics: Systolic blood pressure by available explanatory variables (top) with reduced model (bottom).

Number in dataframe = 3154, Number in model = 3142, Missing = 12, Log-likelihood = -12772.04, AIC = 25560.1, R-squared = 0.12, Adjusted r-squared = 0.12
Number in dataframe = 3154, Number in model = 3142, Missing = 12, Log-likelihood = -12773.77, AIC = 25561.5, R-squared = 0.12, Adjusted r-squared = 0.12

More to add for each step above.

An important message here relates to the highly significant p-values in the table above. Should we conclude that in a "multivariable regression model controlling for weight, height, age, serum cholesterol levels and smoking status, blood pressure was significantly elevated in those with a Type A personality (1.44 (95% CI 0.44 to 2.43, p=0.005) compared with Type B. The p-value looks impressive, but the actual difference in blood pressure is only 1.4 mmHg. Even at a population level, that seems unlikely to be clinically significant. Which fits with our first thoughts when we saw the scatter plot.

8

Tests for categorical variables

8.1 Data

We are now changing to a new dataset, `melanoma`. Click on `mydata` in your environment and have a look at the values - you'll see that categorical variables are coded as numbers, rather than text. You will need to recode these numbers into proper factors.

```
library(tidyverse)
library(finalfit)
library(broom)
library(knitr)
library(kableExtra)
mydata = boot::melanoma
head(mydata) %>%
 kable(booktabs = TRUE, caption = "CAPTION") %>%
 kable_styling(font_size = 7)
```

8.1.1 Recap on factors

Press `F1` on `boot::melanoma` to see its description. Use the information from help to change the numbers into proper factors (e.g. 0 - female, 1 - male).

```
mydata$status %>%
  factor() %>%
  fct_recode("Died"  = "1",
             "Alive" = "2",
             "Died - other causes" = "3") %>%
```

TABLE 8.1: CAPTION

time	status	sex	age	year	thickness	ulcer
10	3	1	76	1972	6.76	1
30	3	1	56	1968	0.65	0
35	2	1	41	1977	1.34	0
99	3	0	71	1968	2.90	0
185	1	1	52	1965	12.08	1
204	1	1	28	1971	4.84	1

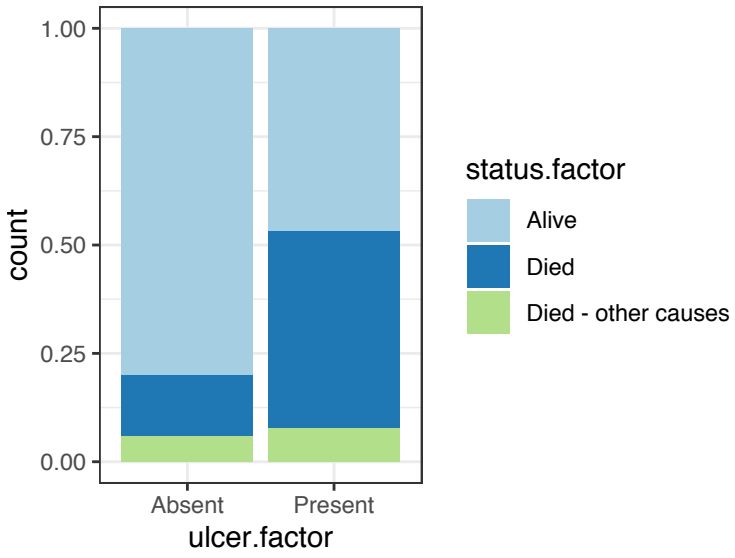
```
  fct_relevel("Alive") -> # move Alive to front (first factor level)
  mydata$status.factor    # so odds ratio will be relative to that

mydata$sex %>%
  factor() %>%
  fct_recode("Female" = "0",
             "Male" = "1") ->
  mydata$sex.factor

mydata$ulcer %>%
  factor() %>%
  fct_recode("Present" = "1",
             "Absent"  = "0") ->
  mydata$ulcer.factor

#the cut() function makes a continuous variable into a categorical variable
mydata$age %>%
  cut(breaks = c(4,20,40,60,95), include.lowest=TRUE) ->
  mydata$age.factor
```

8.2 Chi-squared test / Fisher's exact test

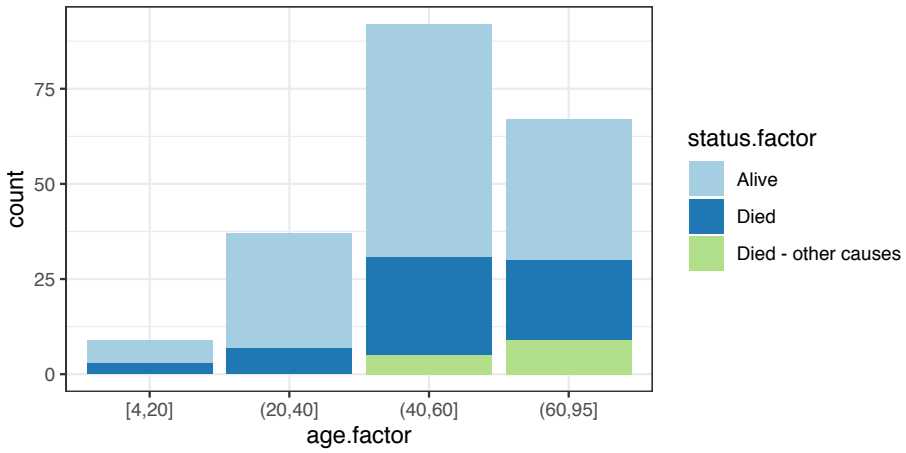
8.2.1 Plotting

Always plot new data first!

```
mydata %>%
    ggplot(aes(x = ulcer.factor, fill=status.factor)) +
      geom_bar(position = "fill") +
      theme_bw() +
      scale_fill_brewer(palette = "Paired")
```

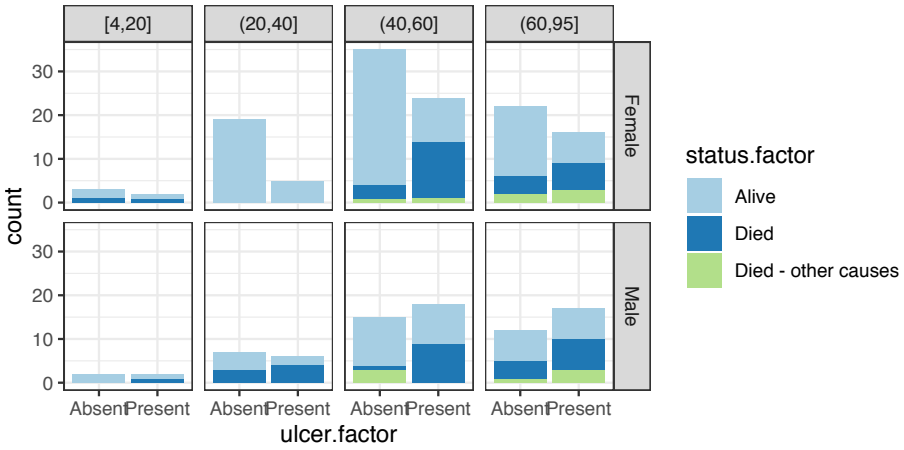



```
mydata %>%
  ggplot(aes(x = age.factor, fill = status.factor)) +
    geom_bar() +
    theme_bw() +
    scale_fill_brewer(palette = "Paired")
```




```
mydata %>%
  ggplot(aes(x = ulcer.factor, fill=status.factor)) +
```

```
    geom_bar() +
    theme_bw() +
    scale_fill_brewer(palette = "Paired") +
    facet_grid(sex.factor~age.factor)
```



8.3 Analysis

8.3.1 Using base R

First lets group together those that 'died of another cause' with those 'alive', to give a disease-specific mortality variable (`fct_collapse()` will help us).

```
mydata$status.factor %>%
    fct_collapse("Alive" = c("Alive", "Died - other causes")) ->
  mydata$status.factor
```

Let's test mortality against sex.

```
table(mydata$status.factor, mydata$sex.factor)
```

```
##
##         Female Male
##   Alive     98   50
##   Died      28   29
```

```
chisq.test(mydata$status.factor, mydata$sex.factor)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  mydata$status.factor and mydata$sex.factor
## X-squared = 4.3803, df = 1, p-value = 0.03636
```

Note that `chisq.test()` defaults to the Yates' continuity correction.

It is fine to use this, but if you have a particular need not to, turn if off with `chisq.test(mydata$status.factor, mydata$sex.factor, correct=FALSE)`.

8.3.2 Using `CrossTable`

This gives lots of useful information. It is readable in R and has lots of options, including Fisher's exact test. It is not that easy to extract results.

```r
library(gmodels)
# F1 CrossTable to see options
CrossTable(mydata$status.factor, mydata$sex.factor, chisq=TRUE)
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  205
##
##
##                      | mydata$sex.factor
## mydata$status.factor |    Female |      Male | Row Total |
## ---------------------|-----------|-----------|-----------|
##                Alive |        98 |        50 |       148 |
##                      |     0.544 |     0.868 |           |
##                      |     0.662 |     0.338 |     0.722 |
##                      |     0.778 |     0.633 |           |
##                      |     0.478 |     0.244 |           |
## ---------------------|-----------|-----------|-----------|
##                 Died |        28 |        29 |        57 |
##                      |     1.412 |     2.253 |           |
##                      |     0.491 |     0.509 |     0.278 |
##                      |     0.222 |     0.367 |           |
##                      |     0.137 |     0.141 |           |
## ---------------------|-----------|-----------|-----------|
##         Column Total |       126 |        79 |       205 |
##                      |     0.615 |     0.385 |           |
## ---------------------|-----------|-----------|-----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  5.076334     d.f. =  1     p =  0.0242546
##
## Pearson's Chi-squared test with Yates' continuity correction
## ------------------------------------------------------------
## Chi^2 =  4.380312     d.f. =  1     p =  0.03635633
##
##
```

8.3.3 Exercise

Use the 3 methods (`table`, `chisq.test`, `CrossTable`) to test `status.factor` against `ulcer.factor`.

```
table(mydata$status.factor, mydata$ulcer.factor)
chisq.test(mydata$status.factor, mydata$ulcer.factor)
```

Using `CrossTable`

```
CrossTable(mydata$status.factor, mydata$ulcer.factor, chisq=TRUE)
```

8.3.4 Fisher's exact test

An assumption of the chi-squared test is that the 'expected cell count' is greater than 5. If it is less than 5 the test becomes unreliable and the Fisher's exact test is recommended.

Run the following code.

```
library(gmodels)
CrossTable(mydata$status.factor, mydata$age.factor, expected=TRUE, chisq=TRUE)
```

```
## Warning in chisq.test(t, correct = FALSE, ...): Chi-
squared approximation
## may be incorrect
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
```

```
##
##
## Total Observations in Table:  205
##
##
##                      | mydata$age.factor
## mydata$status.factor |   [4,20] |  (20,40] |  (40,60] |  (60,95] | Row Total |
## ---------------------|----------|----------|----------|----------|----------
|----------|
##              Alive |       6 |      30 |      66 |      46 |     148 |
##                    |   6.498 |  26.712 |  66.420 |  48.371 |         |
##                    |   0.038 |   0.405 |   0.003 |   0.116 |         |
##                    |   0.041 |   0.203 |   0.446 |   0.311 |   0.722 |
##                    |   0.667 |   0.811 |   0.717 |   0.687 |         |
##                    |   0.029 |   0.146 |   0.322 |   0.224 |         |
## ---------------------|----------|----------|----------|----------|----------
|----------|
##               Died |       3 |       7 |      26 |      21 |      57 |
##                    |   2.502 |  10.288 |  25.580 |  18.629 |         |
##                    |   0.099 |   1.051 |   0.007 |   0.302 |         |
##                    |   0.053 |   0.123 |   0.456 |   0.368 |   0.278 |
##                    |   0.333 |   0.189 |   0.283 |   0.313 |         |
##                    |   0.015 |   0.034 |   0.127 |   0.102 |         |
## ---------------------|----------|----------|----------|----------|----------
|----------|
##       Column Total |       9 |      37 |      92 |      67 |     205 |
##                    |   0.044 |   0.180 |   0.449 |   0.327 |         |
## ---------------------|----------|----------|----------|----------|----------
|----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  2.019848     d.f. =  3     p =  0.5682975
##
##
##
```

Why does it give a warning? Run it a second time including `fisher=TRUE`.

```
library(gmodels)
CrossTable(mydata$status.factor, mydata$age.factor, expected=TRUE, chisq=TRUE)
```

```
##   Warning in chisq.test(t, correct = FALSE, ...): Chi-
squared approximation
```

```
## may be incorrect

##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |              Expected N |
## | Chi-square contribution |
## |           N / Row Total |
## |           N / Col Total |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  205
##
##
##                      | mydata$age.factor
## mydata$status.factor |   [4,20] |  (20,40] |  (40,60] |  (60,95] | Row Total |
## ---------------------|----------|----------|----------|----------|----------
|----------|
##              Alive |        6 |       30 |       66 |       46 |      148 |
##                    |    6.498 |   26.712 |   66.420 |   48.371 |          |
##                    |    0.038 |    0.405 |    0.003 |    0.116 |          |
##                    |    0.041 |    0.203 |    0.446 |    0.311 |    0.722 |
##                    |    0.667 |    0.811 |    0.717 |    0.687 |          |
##                    |    0.029 |    0.146 |    0.322 |    0.224 |          |
## ---------------------|----------|----------|----------|----------|----------
|----------|
##               Died |        3 |        7 |       26 |       21 |       57 |
##                    |    2.502 |   10.288 |   25.580 |   18.629 |          |
##                    |    0.099 |    1.051 |    0.007 |    0.302 |          |
##                    |    0.053 |    0.123 |    0.456 |    0.368 |    0.278 |
##                    |    0.333 |    0.189 |    0.283 |    0.313 |          |
##                    |    0.015 |    0.034 |    0.127 |    0.102 |          |
## ---------------------|----------|----------|----------|----------|----------
|----------|
##       Column Total |        9 |       37 |       92 |       67 |      205 |
##                    |    0.044 |    0.180 |    0.449 |    0.327 |          |
## ---------------------|----------|----------|----------|----------|----------
|----------|
##
##
## Statistics for All Table Factors
##
##
## Pearson's Chi-squared test
## ------------------------------------------------------------
## Chi^2 =  2.019848     d.f. =  3     p =  0.5682975
##
##
##
```

8.4 Summarising multiple factors (optional)

`CrossTable` is useful for summarising single variables. We often want to summarise more than one factor or continuous variable against our `dependent` variable of interest. Think of Table 1 in a journal article.

8.5 Summarising factors with `library(finalfit)`

This is our own package which we have written and maintain. It contains functions to summarise data for publication tables and figures, and to easily run regression analyses. We specify a `dependent` or outcome variable, and a set of `explanatory` or predictor varaibles.

```
library(finalfit)
mydata %>%
  summary_factorlist(dependent = "status.factor",
                     explanatory = c("sex.factor", "ulcer.factor", "age.factor"),
                     p = TRUE,
                     column = TRUE)
```

```
## Warning in chisq.test(tab, correct = FALSE): Chi-
squared approximation may
## be incorrect
```

```
##          label  levels     Alive      Died      p
## 5   sex.factor  Female 98 (66.2) 28 (49.1)  0.024
## 6                 Male 50 (33.8) 29 (50.9)
## 7 ulcer.factor  Absent 99 (66.9) 16 (28.1) <0.001
## 8              Present 49 (33.1) 41 (71.9)
## 1   age.factor  [4,20]   6 (4.1)   3 (5.3)  0.568
## 2              (20,40] 30 (20.3)  7 (12.3)
## 3              (40,60] 66 (44.6) 26 (45.6)
## 4              (60,95] 46 (31.1) 21 (36.8)
```

8.5.1 Summarising factors with library(tidyverse)

8.5.2 Example

Tidyverse gives the flexibility and power to examine millions of rows of your data any way you wish. The following are intended as an extension to what you have already done. These demonstrate some more advanced approaches to combining tidy functions.

```
# Calculate number of patients in each group
counted_data = mydata %>%
  count(ulcer.factor, status.factor)

# Add the total number of people in each status group
counted_data2  = counted_data %>%
  group_by(status.factor) %>%
  mutate(total = sum(n))
```

```
# Calculate the percentage of n to total
counted_data3 = counted_data2 %>%
  mutate(percentage = round(100*n/total, 1))
```

Create a combined columns of both n and percentage using paste() to add brackets around the percentage.

```
counted_data4  = counted_data3 %>%
  mutate(count_perc = paste0(n, " (", percentage, ")"))
```

Or combine everything together without the intermediate counted_data breaks.

```
mydata %>%
  count(ulcer.factor, status.factor) %>%
  group_by(status.factor) %>%
  mutate(total = sum(n)) %>%
  mutate(percentage = round(100*n/total, 1)) %>%
  mutate(count_perc = paste0(n, " (", percentage, ")")) %>%
  select(-total, -n, -percentage) %>%
  spread(status.factor, count_perc)
```

```
## # A tibble: 2 x 3
##   ulcer.factor Alive     Died
##   <fct>        <chr>     <chr>
## 1 Absent       99 (66.9) 16 (28.1)
## 2 Present      49 (33.1) 41 (71.9)
```

8.5.3 Exercise

By changing one and only one word at a time in the above block (the "Combine everything together" section)

Reproduce this:

```
##   age.factor     Alive      Died
## 1     [4,20]   6 (4.1)   3 (5.3)
## 2    (20,40] 30 (20.3)  7 (12.3)
## 3    (40,60] 66 (44.6) 26 (45.6)
## 4    (60,95] 46 (31.1) 21 (36.8)
```

And then this:

```
##   sex.factor     Alive      Died
## 1     Female 98 (66.2) 28 (49.1)
## 2       Male 50 (33.8) 29 (50.9)
```

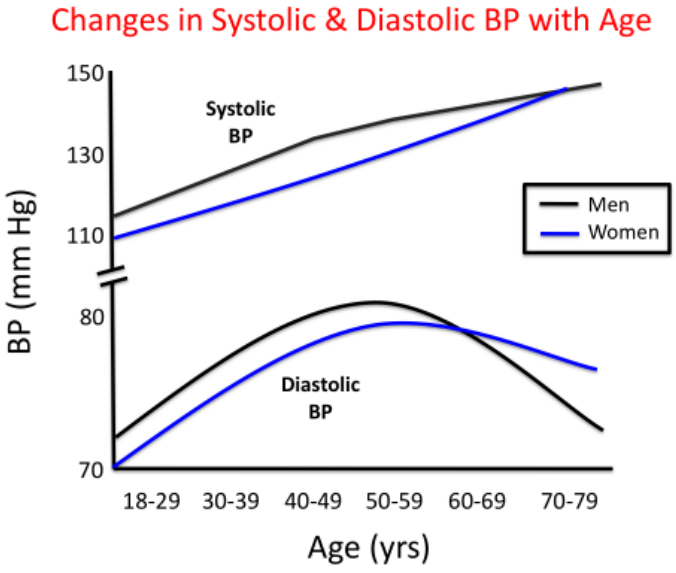
Solution: The only thing you need to change is the first variable in `count()`, e.g., `count(age.factor, ....`

9

Logistic regression

9.1 What is Logistic Regression?

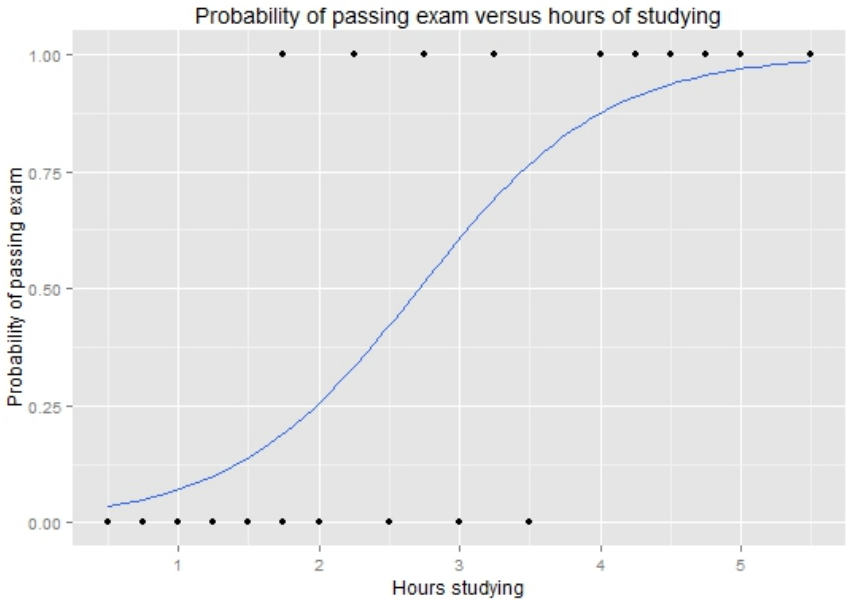
As we have seen in previously, regression analysis is a statistical process for estimating the relationships between variables. For instance, we may try to predict the blood pressure of a group of patients based on their age. As age and blood pressure are on a continuous scale, this is an example of linear regression.



Adapted from: JNC7 & Burt et al (1995) Hypertension 23:305-313

Logistic regression is an extension of this, where the variable being predicted is *categorical*. We will deal with binary logistic regression, where the variable being predicted has two levels, e.g. yes or

no, 0 or 1. In healthcare, this is usually done for an event (like death) occurring or not occurring. Logistic regression can tell us the probability of the outcome occuring.



Logistic regression lets you adjust for the effects of confounding factors on an outcome. When you read a paper that says it has adjusted for confounding factors, this is the usual method which is used.

Adjusting for confounding factors allows us to isolate the true effect of a variable upon an outcome. For example, if we wanted to know the effects of smoking on deaths from heart attacks, we would need to also control for things like sex and diabetes, as we know they contribute towards heart attacks too.

Although in binary logistic regression the outcome must have two levels, the predictor variables (also known as the explanatory variables) can be either continuous or categorical.

Logistic regression can be performed to examine the influence of one predictor variable, which is known as a univariable analysis. Or multiple predictor variables, known as a multivariable analysis.

9.2 Definitions

Dependent variable (in clinical research usually synonymous to **outcome**) - is what we are trying to explain, i.e. we are trying to identify the factors associated with a particular outcome. In binomial logistic regression, the dependent variable has exactly two levels (e.g. "Died" or "Alive", "Yes - Complications" or "No Complications", "Cured" or "Not Cured", etc.).

Explanatory variables (also known as **predictors**, **confounding** variables, or **"adjusted for"**) - patient-level information, usually including demographics (age, gender) as well as clinical information (disease stage, tumour type). Explanatory variables can be categorical as well as continuous, and categorical variables can have more than two levels.

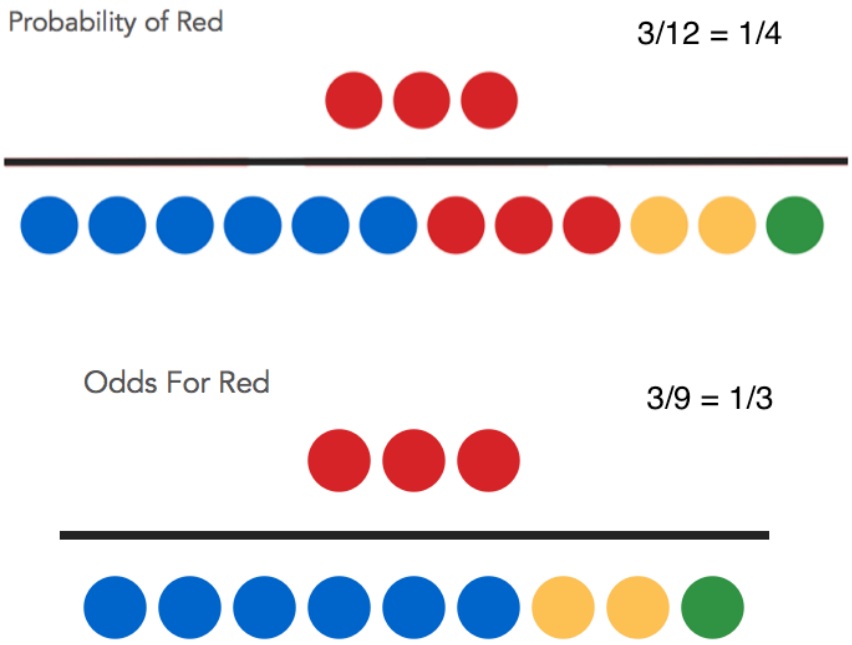
Univariable - analysis with only one Explanatory variable.

Multivariable - analysis with more than one Explanatory variable. Synonymous to "adjusted".

(**Multivariate** - technically means more than one **Dependent variable** (we will not discuss this type of analysis), but very often used interchangeably with **Multivariable**.)

9.3 Odds and probabilities

Odds and probabilities can get confusing so let's get them straight:



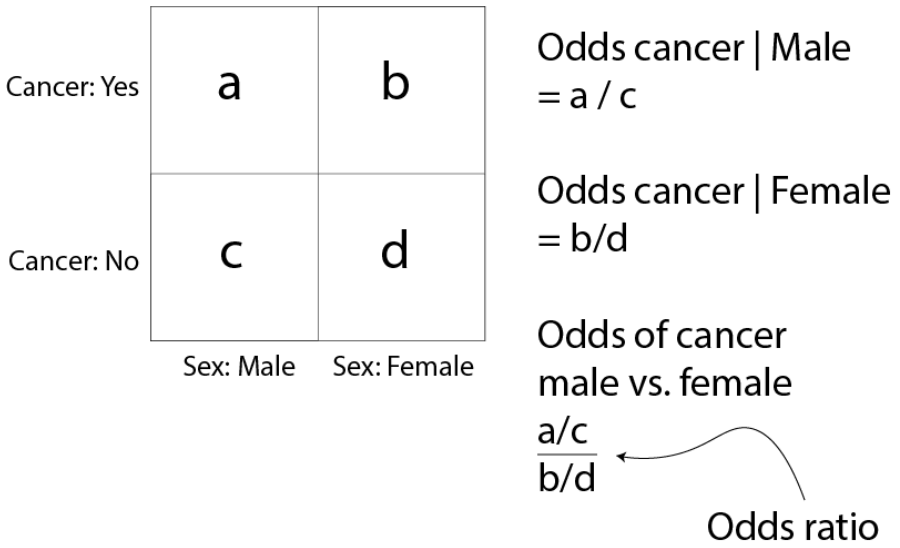
Odds and probabilities can be interconverted. For example, if the odds of a patient dying from a disease are `9 to 1` then the probability of death (also known as risk) is 10%. Odds of `1 to 1` equal 50%.

$Odds = \frac{p}{1-p}$, where p is the probability of the outcome occuring (or the circle being red).

Look at the numbers and convince yourself that this works.

9.3.1 Odds ratios

For a given categorical explanatory variable (e.g. gender), the likelihood of an outcome/dependent occuring (e.g cancer) can be expressed in a ratio of odds or odds ratio, e.g. the odds of men developing cancer is 2-times that of females, odds ratio = 2.0.



An alternative is a ratio of probabilites, called a risk ratio or relative risk. Odds ratios have useful mathematical characteristics and are the main expression of results in logistic regression analysis.

9.4 Melanoma dataset

Malignant melanoma is a cancer of the skin. It is agressive and highly invasive, making it difficult to treat.

It's classically divided into 4 stages of severity, based upon the depth of the tumour:

- Stage I: <0.5 mm depth
- Stage II: 0.5 to 1.0 mm depth
- Stage III: 1.0 to 4.0 mm depth
- Stage IV: > 4.0 mm depth

This will be important in our analysis as we will creating a new variable based upon this.

Using logistic regression, we will investigate factors associated with death from malignant melanoma.

9.4.1 Doing logistic regression in R

There are a few different ways of doing logistic regression in R. The `glm()` function is probably the most common and most flexible one to use. (`glm` stands for `generalised linear model`.)

Within the `glm()` function there are several `options` in the function we must define to make R run a logistic regression.

`data` - you must define the dataframe to be used in the regression.

`family` - this tells R to treat the analysis as a logisitic regression. For our purposes, `family` will always be `"binomial"` (as binary data follow this distribution).

`x ~ a + b + c` - this is the formula for the logistic regression, with `x` being the outcome and `a`, `b` and `c` being predictor variables.

Note the outcome is separated from the rest of the formula and

sits on the left hand side of a `~`. The confounding variables are on the right side, separated by a `+` sign.

The final `glm()` function takes the following form:

```
glm(x ~ a + b + c + d, data = data, family = "binomial")
```

9.5 Setting up your data

The most important step to ensure a good basis to start from is to ensure your variables are well structured and your outcome variable has exactly two outcomes.

We will need to make sure our outcome variables and predictor variables (the ones we want to adjust for) are suitably prepared.

In this example, the outcome variable called `status.factor` describes whether patients died or not and will be our (dependent) variable of interest.

9.5.1 Worked Example

```
library(tidyverse)

load("melanoma_factored.rda")
#Load in data from the previous session
```

Here `status.factor` has three levels: `Died`, `Died - other causes` and `Alive`. This is not useful for us, as logistic regression requires outcomes to be binary (exactly two levels).

We want to find out which variables predict death from melanoma. So we should create a new factor variable, `died_melanoma.factor`. This will have two outcomes, `Yes` (did die from melanoma) or `No` (did not die from melanoma).

```
mydata$status.factor %>%
  fct_collapse("Yes" = c("Died"),
               "No"  = c("Alive", "Died - other causes")) ->
  mydata$died_melanoma.factor

mydata$died_melanoma.factor %>% levels()
```

```
## [1] "No"  "Yes"
```

9.6 Creating categories

Now that we have set up our outcome variable, we should ensure our predictor variables are prepared too.

Remember the stages of melanoma? This is an important predictor of melanoma Mortality based upon the scientific literature.

We should take this into account in our model.

9.6.1 Exercise

Create a new variable called `stage.factor` to encompass the stages of melanoma based upon the thickness. In this data, the `thickness` variable is measured in millimetres too.

```
#the cut() function makes a continuous variable into a categorical variable
mydata$thickness %>%
    cut(breaks = c(0,0.5,1,4, max(mydata$thickness, na.rm=T)),
            include.lowest = T) ->
mydata$stage.factor

mydata$stage.factor %>% levels()
```

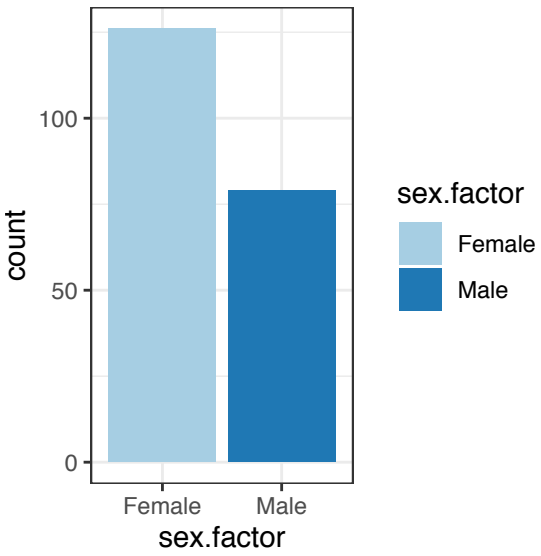
```
## [1] "[0,0.5]"  "(0.5,1]"  "(1,4]"    "(4,17.4]"
```

```
mydata$stage.factor %>%
  fct_recode("Stage I"   = "[0,0.5]",
             "Stage II"  = "(0.5,1]",
             "Stage III" = "(1,4]",
             "Stage IV"  = "(4,17.4]"
    ) -> mydata$stage.factor

mydata$stage.factor %>% levels()
```

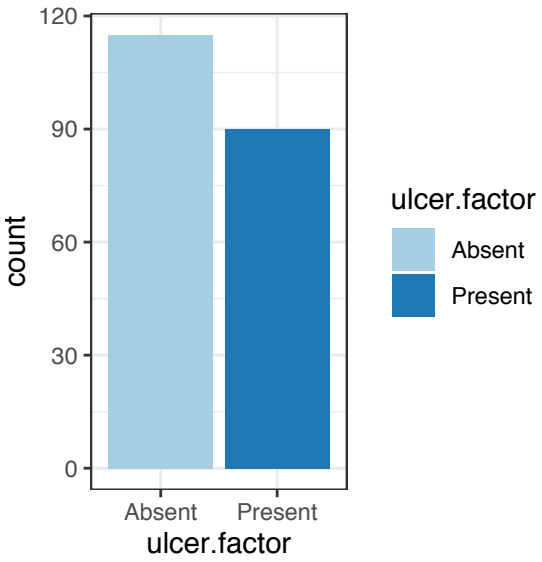
```
## [1] "Stage I"   "Stage II"  "Stage III" "Stage IV"
```

9.6.2 Always plot your data first!

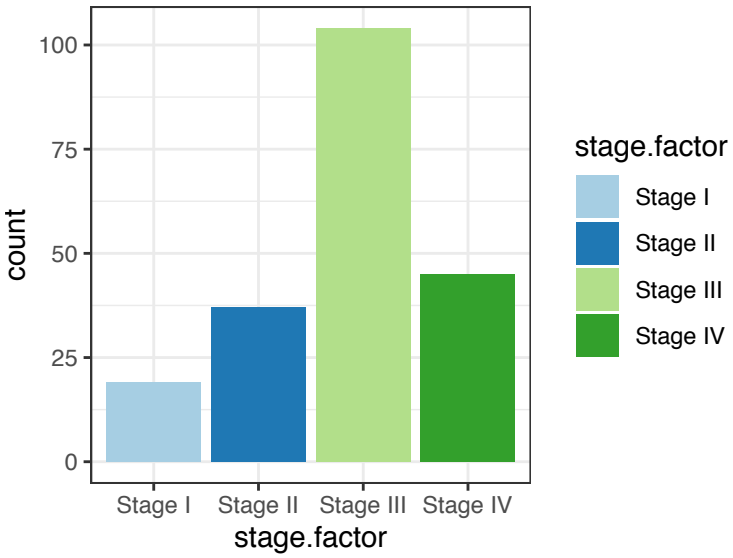
```
source("1_source_theme.R")

mydata %>%
  ggplot(aes(x = sex.factor)) +
  geom_bar(aes(fill = sex.factor))
```



```
mydata %>%
  ggplot(aes(x = ulcer.factor)) +
  geom_bar(aes(fill = ulcer.factor))
```

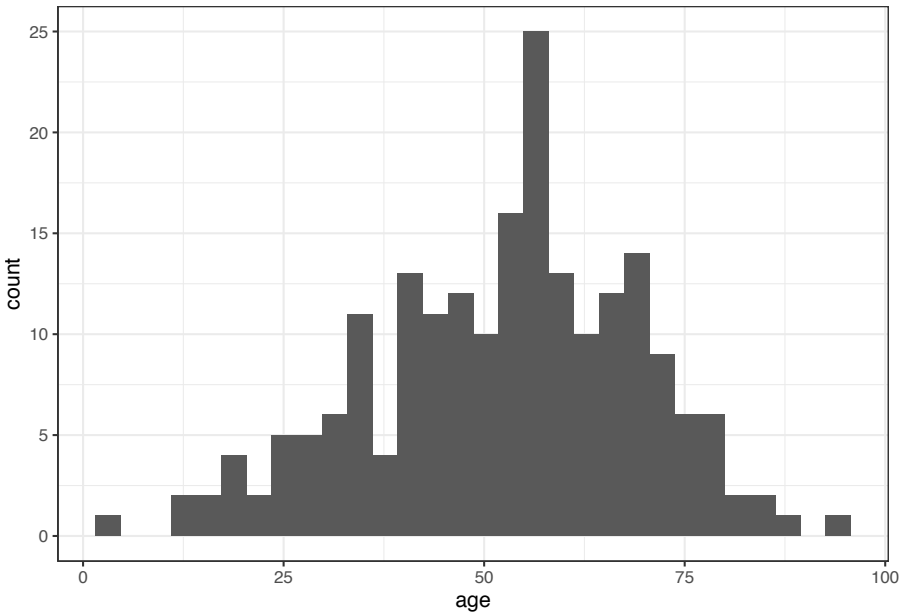



```
mydata %>%
  ggplot(aes(x = stage.factor)) +
  geom_bar(aes(fill = stage.factor))
```




```
mydata %>%
  ggplot(aes(x = age)) +
  geom_histogram(aes(fill = age))
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Now we are ready for some modelling!

9.7 Basic: One explanatory variable (predictor)

Lets find out what the influence of each predictor/confounding variable is on mortality from melanoma, which may help inform a more complicated regression, with multiple predictors/confounders.

We'll start with whether the patient was male or female:

9.7.1 Worked example

First we need to create a regression model using `glm()`. We will then summarise it using `summary()`

Note, we need to use the `family` option. Specifying `'binomial'` in `family` tells `glm()` to switch to logistic regression.

```
#Create a model

glm(died_melanoma.factor ~ sex.factor, data = mydata, family = "binomial")
```

```
##
## Call:  glm(formula = died_melanoma.factor ~ sex.factor, family = "binomial",
##     data = mydata)
##
## Coefficients:
##    (Intercept)  sex.factorMale
##         -1.253           0.708
##
## Degrees of Freedom: 204 Total (i.e. Null);  203 Residual
## Null Deviance:       242.4
## Residual Deviance: 237.4     AIC: 241.4
```

```
model1 = glm(died_melanoma.factor ~ sex.factor, data = mydata, family = "binomial")

summary(model1)
```

```
##
## Call:
## glm(formula = died_melanoma.factor ~ sex.factor, family = "binomial",
##     data = mydata)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9565  -0.7090  -0.7090   1.4157   1.7344
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -1.2528     0.2143  -5.846 5.03e-09 ***
## sex.factorMale   0.7080     0.3169   2.235   0.0254 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 242.35  on 204  degrees of freedom
## Residual deviance: 237.35  on 203  degrees of freedom
## AIC: 241.35
##
## Number of Fisher Scoring iterations: 4
```

Now we have created the model - fantastic!

But this doesn't mean a lot to humans reading a paper - or us in fact.

The estimate output of `summary(model_1)` represents the logarithm of the odds ratio. The odds ratio would be a lot easier to understand.

Therefore, to sort that out we should exponentiate the output of the model! The `exp()` function will do this.

```
exp(model1$coefficients)
```

```
##    (Intercept) sex.factorMale
##      0.2857143      2.0300000
```

This gives us an odds ratio of 2.03 for males. That is to say, males are twice as likely to die from melanoma than females.

Now a confidence interval might be handy. As this will be the logarithm of the confidence interval, we should exponentiate it to make it understandable.

```
exp(confint(model1))
```

```
## Waiting for profiling to be done...
```

```
##                    2.5 %    97.5 %
## (Intercept)    0.1843592 0.4284939
## sex.factorMale 1.0914854 3.7938450
```

The 2.5% is the lower bound and the 97.5% is the upper bound of the 95% confidence interval.

So we can therefore say that being male doubles your chances of dying from melanoma with an Odds Ratio of 2.03 (95% confidence interval of 1.09 to 3.79)

9.7.2 Exercise

Repeat this for all the variables contained within the data, particulary:

`stage.factor`, `age`, `ulcer.factor`, `thickness` and `age.factor`.

Write their odds ratios and 95% confidence intervals down for the next section!

Congratulations on building your first regression model in R!

9.8 Finalfit package

We have developed our `finalfit` package to help with advanced regression modelling. We will introduce it here, but not go into detail.

See www.finalfit.org for more information and updates.

9.9 Summarise a list of variables by another variable

We can use the `finalfit` package to summarise a list of variables by another variable. This is very useful for "Table 1" in many studies.

```
library(finalfit)
dependent   = "died_melanoma.factor"
explanatory = c("age", "sex.factor")

table_result = mydata %>%
  summary_factorlist(dependent, explanatory, p = TRUE)
```

label	levels	No	Yes	p
age	Mean (SD)	51.5 (16.1)	55.1 (17.9)	0.189
sex.factor	Female	98 (77.8)	28 (22.2)	0.024
	Male	50 (63.3)	29 (36.7)	

9.10 `finalfit` function for logistic regression

We can then use the `finalfit` function to run a logistic regression analysis with similar syntax.

```
dependent   = "died_melanoma.factor"
explanatory = c("sex.factor")

model2 = mydata %>%
  finalfit(dependent, explanatory)
```

Dependent: died_melanoma.factor		No	Yes	OR (univariabl
sex.factor	Female	98 (66.2)	28 (49.1)	
	Male	50 (33.8)	29 (50.9)	2.03 (1.09-3.79, p=0.02

9.11 Adjusting for multiple variables in R

Your first models only included one variable. It's time to scale them up.

Multivariable models take multiple variables and estimates how each variable predicts an event. It adjusts for the effects of each one, so you end up with a model that calculates the adjusted effect estimate (i.e. the odds ratio), upon an outcome.

When you see the term 'adjusted' in scientific papers, this is what it means.

9.11.1 Worked Example

Lets adjust for `age` (as a continuous variable), `sex.factor` and `stage.factor`. Then output them as odds ratios.

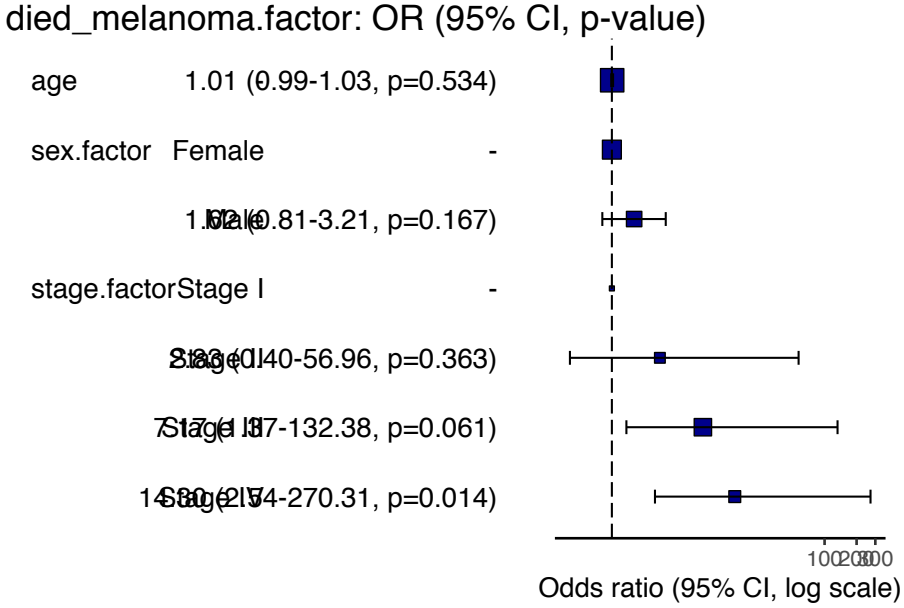
```
dependent   = "died_melanoma.factor"
explanatory = c("age", "sex.factor", "stage.factor")

model3 = mydata %>%
  finalfit(dependent, explanatory)
```

Dependent: died_melanoma.factor		No	Yes	OR
age	Mean (SD)	51.5 (16.1)	55.1 (17.9)	1.01 (0.99-1.
sex.factor	Female	98 (66.2)	28 (49.1)	
	Male	50 (33.8)	29 (50.9)	2.03 (1.09-3.
stage.factor	Stage I	18 (12.2)	1 (1.8)	
	Stage II	32 (21.6)	5 (8.8)	2.81 (0.41-56.
	Stage III	75 (50.7)	29 (50.9)	6.96 (1.34-128.
	Stage IV	23 (15.5)	22 (38.6)	17.22 (3.13-322.

```
or_plot(mydata, dependent, explanatory)
```

```
## Waiting for profiling to be done...
## Waiting for profiling to be done...
## Waiting for profiling to be done...
```

```
## Warning: Removed 2 rows containing missing values (geom_errorbarh).
```



When we enter age into regression models, the effect estimate is provided in terms of per unit increase. So in this case it's expressed in terms of an odds ratio per year increase (i.e. for every year in age gained odds of death increases by 1.02).

9.11.2 Exercise

Create a regression that includes `ulcer.factor`.

9.12 Advanced: Fitting the best model

Now we have our preliminary model. We could leave it there.

However, when you publish research, you are often asked to supply a measure of how well the model fitted the data.

There are different approaches to model fitting. Come to our course HealthyR-Advanced: Practical Logistic Regression. At this we describe use of the Akaike Information Criterion (AIC) and the C-statistic.

The C-statistic describes discrimination and anything over 0.60 is considered good. The closer to 1.00 the C-statistic is, the better the fit.

The AIC measure model fit with lower values indicating better fit.

These metrics are available here:

```
mydata %>%
  finalfit(dependent, explanatory, metrics=TRUE)
```

```
## Waiting for profiling to be done...
## Waiting for profiling to be done...
## Waiting for profiling to be done...
## Waiting for profiling to be done...
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

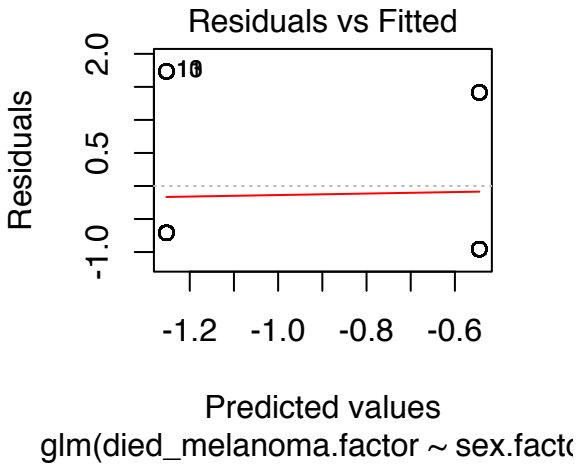
```
## [[1]]
##   Dependent: died_melanoma.factor                    No         Yes
## 1                             age Mean (SD) 51.5 (16.1) 55.1 (17.9)
## 2                      sex.factor    Female   98 (66.2)   28 (49.1)
## 3                                      Male   50 (33.8)   29 (50.9)
## 4                    stage.factor   Stage I   18 (12.2)     1 (1.8)
## 5                                  Stage II   32 (21.6)     5 (8.8)
## 6                                 Stage III   75 (50.7)   29 (50.9)
## 7                                  Stage IV   23 (15.5)   22 (38.6)
```

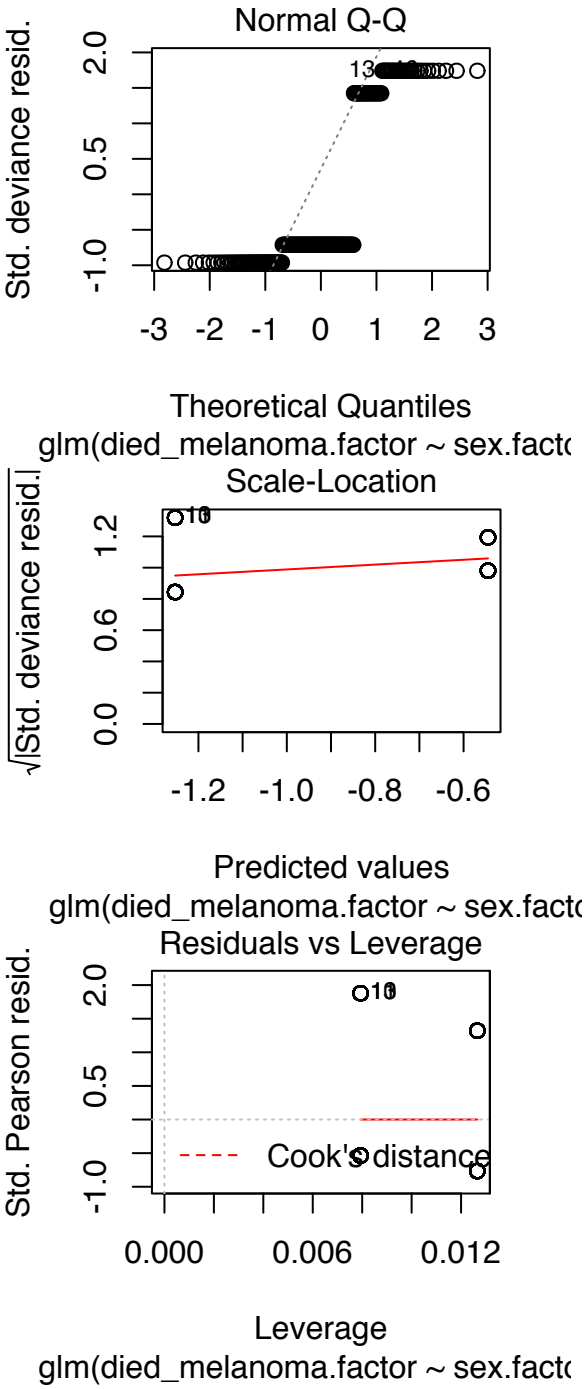
```
##               OR (univariable)           OR (multivariable)
## 1    1.01 (0.99-1.03, p=0.163)    1.01 (0.99-1.03, p=0.534)
## 2                            -                            -
## 3    2.03 (1.09-3.79, p=0.025)    1.62 (0.81-3.21, p=0.167)
## 4                            -                            -
## 5   2.81 (0.41-56.12, p=0.362)   2.83 (0.40-56.96, p=0.363)
## 6  6.96 (1.34-128.04, p=0.065)  7.17 (1.37-132.38, p=0.061)
## 7 17.22 (3.13-322.85, p=0.008) 14.30 (2.54-270.31, p=0.014)
##
## [[2]]
## [1] "Number in dataframe = 205, Number in model = 205, Missing = 0, AIC = 232.3, C-
statistic = 0.708, H&L = Chi-sq(8) 3.63 (p=0.889)"
```

9.12.1 Extra material: Diagnostics plots

While outwith the objectives of this course, diagnostic plots for `glm` models can be produced by:

```
plot(model1)
```




Normal Q-Q
Std. deviance resid.
Theoretical Quantiles
glm(died_melanoma.factor ~ sex.facto
Scale-Location
√|Std. deviance resid.|
Predicted values
glm(died_melanoma.factor ~ sex.facto
Residuals vs Leverage
Std. Pearson resid.
Cook's distance
Leverage
glm(died_melanoma.factor ~ sex.facto

10

Time-to-event data and survival

10.1 Data

The `boot::melanoma` dataset was introduced in chapter 7.

In the previous session, we used logistic regression to investigate death by calculating odds ratios for different factors at a single point in time.

```
library(tidyverse)
library(broom)
library(survival)
library(survminer)
mydata = boot::melanoma

mydata$status %>%
    factor() %>%
    fct_recode("Died" = "1",
                          "Alive" = "2",
                          "Died - other causes" = "3") %>%
    fct_relevel("Alive") -> # move Alive to front (first factor level)
    mydata$status.factor    # so OR will be relative to that

mydata$sex %>%
    factor() %>%
    fct_recode("Female" = "0",
                          "Male"   = "1") ->
    mydata$sex.factor

mydata$ulcer %>%
    factor() %>%
    fct_recode("Present" = "1",
                          "Absent" = "0") ->
    mydata$ulcer.factor

mydata$age %>%
```

```
    cut(breaks = c(4,20,40,60,95), include.lowest=TRUE) ->
    mydata$age.factor
```

10.2 Kaplan-Meier survival estimator

The Kaplan-Meier (KM) survival estimator is a non-parametric statistic used to estimate the survival function from time-to-event data.

'Time' is time from event to last known status. This status could be the event, for instance death. Or could be when the patient was last seen, for instance at a clinic. In this circumstance the patient is considered 'censored'.

```
survival_object = Surv(mydata$time, mydata$status.factor == "Died")

# It is often useful to convert days into years
survival_object = Surv(mydata$time/365, mydata$status.factor == "Died")

# Investigate this:
head(survival_object) # + marks censoring in this case "Died of other causes"
# Or that the follow-up ended and the patient is censored.
```

```
## [1] 0.02739726+ 0.08219178+ 0.09589041+ 0.27123288+ 0.50684932  0.55890411
```

10.2.1 KM analysis for whole cohort

10.2.2 Model

The survival object is the first step to performing univariable and multivariable survival analyses. A univariable model can then be fitted.

If you want to plot survival stratified by a single grouping variable, you can substitute "survival_object ~ 1" by "survival_object ~ factor"

```
# For all patients
my_survfit = survfit(survival_object ~ 1, data = mydata)
my_survfit # 205 patients, 57 events
```

```
## Call: survfit(formula = survival_object ~ 1, data = mydata)
##
##       n  events  median 0.95LCL 0.95UCL
##     205      57      NA      NA      NA
```

10.2.3 Life table

A life table is the tabular form of a KM plot, which you may be familiar with. It shows survival as a proportion, together with confidence limits. The whole table is shown with, `summary(my_survfit)`.

```
summary(my_survfit, times = c(0, 1, 2, 3, 4, 5))
```

```
## Call: survfit(formula = survival_object ~ 1, data = mydata)
##
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##     0    205       0    1.000  0.0000        1.000        1.000
##     1    193       6    0.970  0.0120        0.947        0.994
##     2    183       9    0.925  0.0187        0.889        0.962
##     3    167      15    0.849  0.0255        0.800        0.900
##     4    160       6    0.818  0.0274        0.766        0.874
##     5    122       9    0.769  0.0303        0.712        0.831
```

```
# 5 year survival is 77%

# Help is at hand
help(summary.survfit)
```

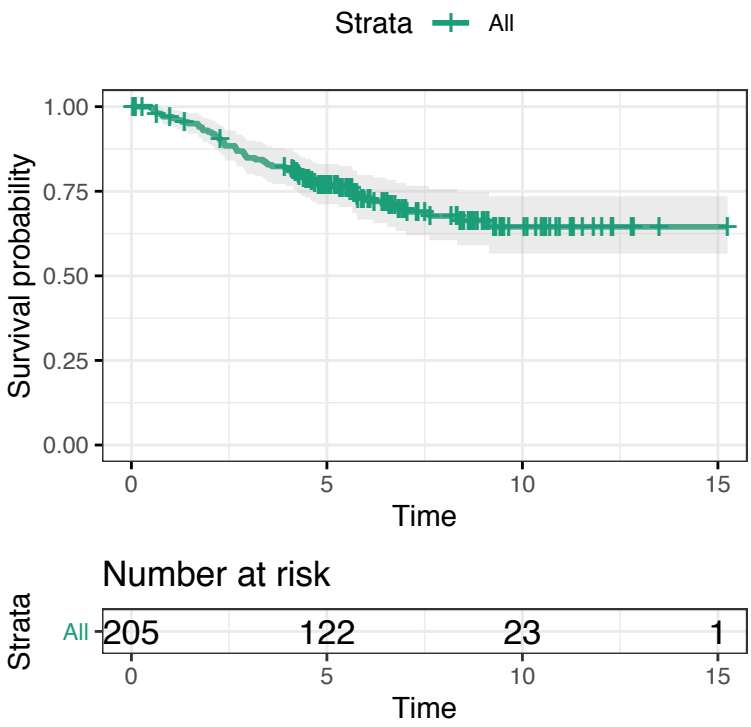
10.2.4 KM plot

A KM plot can easily be generated using the `survminer` package.

For more information on how the survminer package draws this

plot, or how to modify it: http://www.sthda.com/english/wiki/survminer-r-package-survival-data-analysis-and-visualization and https://github.com/kassambara/survminer

```
library(survminer)
my_survplot = ggsurvplot(my_survfit, data = mydata,
           risk.table = TRUE,
           ggtheme = theme_bw(),
           palette = 'Dark2',
           conf.int = TRUE,
           pval=FALSE)
my_survplot
```



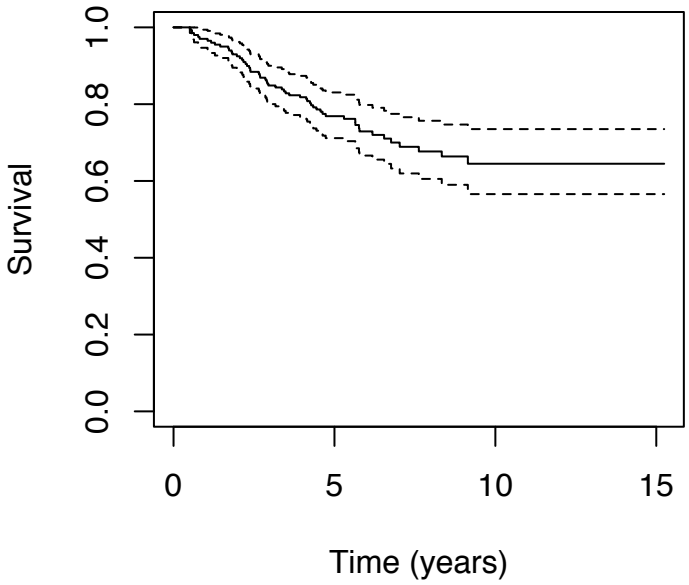

```
# Note can also take `ggplot()` options.
my_survplot$plot +
    annotate('text', x = 5, y = 0.25, label='Whole cohort')
```

Here is an alternative plot in base R to compare. Not only does

this produce a more basic survival plot, but tailoring the plot can be more difficult to achieve.

Furthermore, appending a life table ('risk.table') alongside the plot can also be difficult, yet this is essential for interpretation.

```
plot(my_survfit, mark.time=FALSE, conf.int=TRUE,
         xlab="Time (years)", ylab="Survival")
```



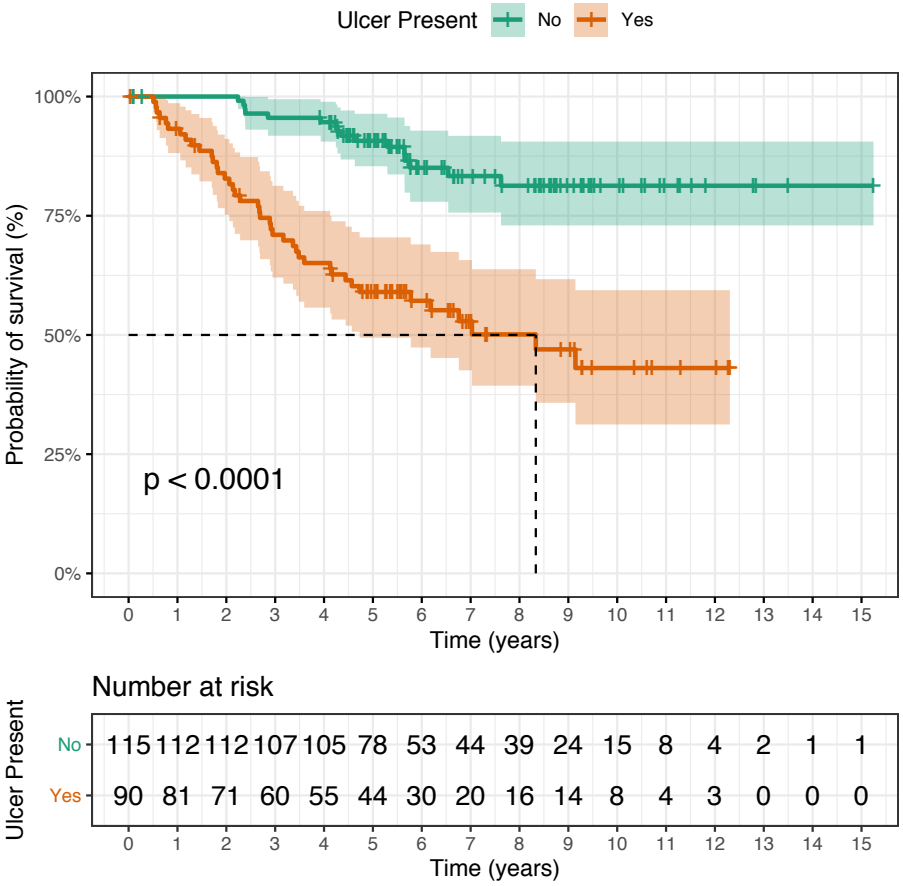
10.2.5 Exercise

Using the above scripts, perform a univariable Kaplan Meier analysis to determine if `ulcer.factor` influences overall survival. Hint: `survival_object ~ ulcer.factor`.

Try modifying the plot produced (see Help for ggsurvplot). For example:

- Add in a medial survival lines: `surv.median.line="hv"`
- Alter the plot legend: `legend.title = "Ulcer Present", legend.labs = c("No", "Yes")`

- Change the y-axis to a percentage: `ylab = "Probability of survival (%)", surv.scale = "percent"`
- Display follow-up up to 10 years, and change the scale to 1 year: `xlim = c(0,10), break.time.by = 1)`



10.2.6 Log-rank test

Two KM survival curves can be compared using the log-rank test. Note survival curves can also be compared using a Wilcoxon test that may be appropriate in some circumstances.

This can easily be performed in `library(survival)` using the function `survdiff()`.

```
survdiff(survival_object ~ ulcer.factor, data = mydata)
```

```
## Call:
## survdiff(formula = survival_object ~ ulcer.factor, data = mydata)
##
##                         N Observed Expected (O-E)^2/E (O-E)^2/V
## ulcer.factor=Absent   115       16     35.8      10.9      29.6
## ulcer.factor=Present   90       41     21.2      18.5      29.6
##
##  Chisq= 29.6  on 1 degrees of freedom, p= 5e-08
```

Is there a signficiant difference between survival curves?

10.3 Cox proportional hazard regression

10.3.1 Model

Multivariable survival analysis can be complex with parametric and semi-parametric methods available. The latter is performed using a Cox proportional hazard regression analysis.

```
# Note several variables are now introduced into the model.
# Variables should be selected carefully based on published methods.

my_hazard = coxph(survival_object~sex.factor+ulcer.factor+age.factor, data=mydata)
summary(my_hazard)
```

```
## Call:
## coxph(formula = survival_object ~ sex.factor + ulcer.factor +
##     age.factor, data = mydata)
##
##   n= 205, number of events= 57
##
##                         coef exp(coef) se(coef)      z Pr(>|z|)
## sex.factorMale       0.48249   1.62011  0.26835  1.798   0.0722 .
## ulcer.factorPresent  1.38972   4.01372  0.29772  4.668 3.04e-06 ***
## age.factor(20,40]   -0.40628   0.66613  0.69339 -0.586   0.5579
## age.factor(40,60]   -0.04513   0.95588  0.61334 -0.074   0.9414
```

```
## age.factor(60,95]    0.17889   1.19588  0.62160  0.288   0.7735
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                     exp(coef) exp(-coef) lower .95 upper .95
## sex.factorMale         1.6201     0.6172    0.9575     2.741
## ulcer.factorPresent    4.0137     0.2491    2.2394     7.194
## age.factor(20,40]      0.6661     1.5012    0.1711     2.593
## age.factor(40,60]      0.9559     1.0462    0.2873     3.180
## age.factor(60,95]      1.1959     0.8362    0.3537     4.044
##
## Concordance= 0.735  (se = 0.031 )
## Likelihood ratio test= 34.08  on 5 df,   p=2e-06
## Wald test            = 30.19  on 5 df,   p=1e-05
## Score (logrank) test = 35.21  on 5 df,   p=1e-06
```

```
library(broom)
tidy(my_hazard)
```

```
## # A tibble: 5 x 7
##   term         estimate std.error statistic   p.value conf.low conf.high
##   <chr>           <dbl>     <dbl>     <dbl>     <dbl>    <dbl>     <dbl>
## 1 sex.factorMale   0.482     0.268    1.80     7.22e-2  -0.0435     1.01
## 2 ulcer.factorPr~  1.39      0.298    4.67     3.04e-6   0.806      1.97
## 3 age.factor(20,~ -0.406     0.693   -0.586    5.58e-1  -1.77       0.953
## 4 age.factor(40,~ -0.0451    0.613   -0.0736   9.41e-1  -1.25       1.16
## 5 age.factor(60,~  0.179     0.622    0.288    7.74e-1  -1.04       1.40
```

The interpretation of the results of model fitting are beyond the aims of this course. The exponentiated coefficient (`exp(coef)`) represents the hazard ratio. Therefore, patients with ulcers are 4-times more likely to die at any given time than those without ulcers.

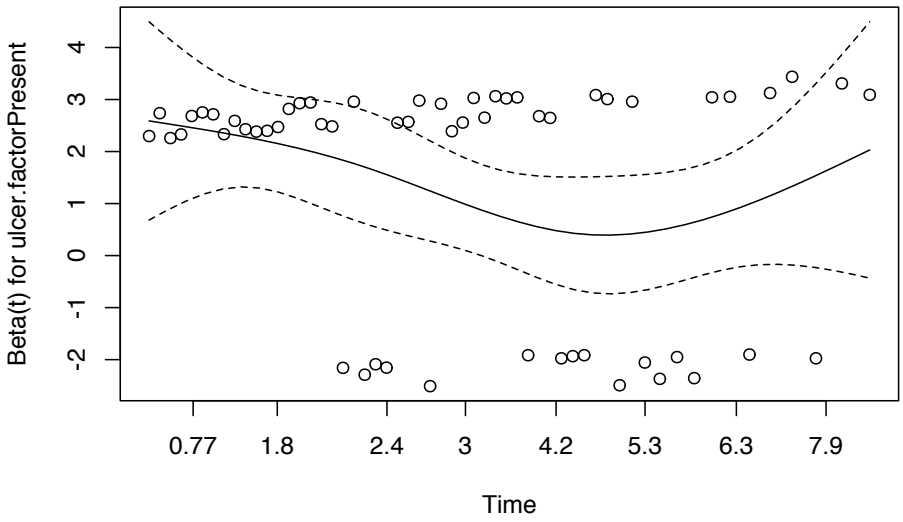
10.3.2 Assumptions

The CPH model presumes 'constant hazards'. That means that the risk associated with any given variable (like ulcer status) shouldn't get worse or better over time. This can be checked.

```
ph = cox.zph(my_hazard)
ph
```

```
##                         rho chisq      p
## sex.factorMale      -0.104 0.647 0.4212
## ulcer.factorPresent -0.238 3.135 0.0766
## age.factor(20,40]    0.110 0.716 0.3976
## age.factor(40,60]    0.194 2.222 0.1361
## age.factor(60,95]    0.146 1.257 0.2622
## GLOBAL                  NA 6.949 0.2244
```

```
# GLOBAL shows no overall violation of assumptions.
# Ulcer.status is borderline significant

# Plot Schoenfield residuals to evaluate PH
plot(ph, var=2) # ulcer.status is variable 2
```




```
# help(plot.cox.zph)
```

Hazard decreases a little between 2 and 5 years, but is acceptable.

10.3.3 Exercise

Create a new CPH model, but now include the variable `thickness` as a variable. How would you interpret the output? Is it an independent predictor of overall survival in this model? Are CPH assumptions maintained?

10.4 Dates in R

10.4.1 Converting dates to survival time

In the melanoma example dataset, we already had the time in a convenient format for survial analysis - survival time in days since the operation. This section shows how to convert dates into "days from event". First we will generate a dummy operation date and censoring date based on the melanoma data.

```
library(lubridate)
first_date = ymd("1966-01-01")           # let's create made-up dates for the operations
last_date = first_date + days(nrow(mydata)-1) # assume tone every day from 1-Jan 1966
operation_date = seq(from = first_date, to = last_date, by = "1 day") # create dates

mydata$operation_date = operation_date # add the created sequence to melanoma dataset
```

Now we will to create a 'censoring' date by adding `time` from the melanoma dataset to our made up operation date.

Remember the censoring date is either when an event occurred (e.g. death) or the last known alive status of the patient.

```
mydata = mydata %>%
  mutate(censoring_date = operation_date + days(time))

# (Same as doing:):
mydata$censoring_date = mydata$operation_date + days(mydata$time)
```

Now consider if we only had the `operation date` and `censoring date`. We want to create the `time` variable.

```
mydata = mydata %>%
  mutate(time_days = censoring_date - operation_date)
```

The `Surv()` function expects a number (`numeric` variable), rather than a `date` object, so we'll convert it:

```
# Surv(mydata$time_days, mydata$status==1) # this doesn't work

mydata %>%
  mutate(time_days_numeric = as.numeric(time_days))  ->
  mydata

survival_object = Surv(mydata$time_days_numeric, mydata$status.factor == "Died") # this works as expe
```

10.5 Solutions

9.2.2

```
# Fit survival model
my_survfit.solution = survfit(survival_object ~ ulcer.factor, data = mydata)

# Show results
my_survfit.solution
summary(my_survfit.solution, times=c(0,1,2,3,4,5))

# Plot results
my_survplot.solution = ggsurvplot(my_survfit.solution,
                          data = mydata,
                          palette = 'Dark2',
                          risk.table = TRUE,
                          ggtheme = theme_bw(),
                          conf.int = TRUE,
                          pval=TRUE,
```

```
                        # Add in a medial survival line.
                        surv.median.line="hv",

                        # Alter the plot legend (change the names)
                        legend.title = "Ulcer Present",
                        legend.labs = c("No", "Yes"),

                        # Change the y-axis to a percentage
                        ylab = "Probability of survival (%)",
                        surv.scale = "percent",

                        # Display follow-up up to 10 years, and change the scale to 1 year
                        xlab = "Time (years)",
                        # present narrower X axis, but not affect survival estimates.
                        xlim = c(0,10),
                        # break X axis in time intervals by 1 year
                        break.time.by = 1)

my_survplot.solution
```

9.3.3

```
# Fit model
my_hazard = coxph(survival_object~sex.factor+ulcer.factor+age.factor+thickness, data=mydata)
summary(my_hazard)

# Melanoma thickness has a HR 1.12 (1.04 to 1.21).
# This is interpretted as a 12% increase in the
# risk of death at any time for each 1 mm increase in thickness.

# Check assumptions
ph = cox.zph(my_hazard)
ph
# GLOBAL shows no overall violation of assumptions.
# Plot Schoenfield residuals to evaluate PH
plot(ph, var=6)
```

Part III

Workflow

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Notebooks and markdown

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Missing data

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Encryption

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Exporting tables and plots

15

RStudio settings, good practise

15.1 Script vs Console

Throughout this course, don't copy or type code directly into the Console. We will only be using the Console for viewing output, warnings, and errors. All code should be in a script and executed (=run) using Ctrl+Enter (line or section) or Ctrl+Shift+Enter (whole script). Make sure you are always working in a project (the right-top corner of your RStudio interface should say "HealthyR").

15.2 Starting with a blank canvas

In the first session we loaded some data that we then plotted. When we import data, R stores it and displays it in the Environment tab.

It's good practice to restart R before commencing new work. This is to avoid accidentally using the wrong data or functions stored in the environment.
Restarting R only takes a second!

- Restart R (Ctrl+Shift+F10 or select it from Session -> Restart R).

RStudio has a default setting that is no longer considered best practice. You should do this once:

- Go to Tools -> Global Options -> General and set “Save .RData on exit” to Never. This does not mean you can’t or shouldn’t save your work in .RData files. But it is best to do it consciously and load exactly what you need to load, rather than letting R always save and load everything for you, as this could also include broken data or objects.

Bibliography

Xie, Y. (2015). *Dynamic Documents with R and knitr*. Chapman and Hall/CRC, Boca Raton, Florida, 2nd edition. ISBN 978-1498716963.

Xie, Y. (2018). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.7.15.

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