

Ewen Harrison and Riinu Ots

HealthyR: R for healthcare data analysis

Never trust a data scientist - they are always plotting.

Contents

List of Tables	xii
List of Figures	xiii
Preface	xv
I Data wrangling and visualisation	1
1 Your first R plots	3
1.1 Data	3
1.2 First plot	4
1.2.1 Question	5
1.2.2 Exercise	5
1.3 Comparing bars of different height	6
1.3.1 Stretch each bar to 100%	6
1.3.2 Plot each bar next to each other	6
1.4 Facets (panels)	7
1.5 Extra: using aesthetics outside of the aes()	8
1.5.1 Setting a constant fill	8
1.5.2 Exercise	9
1.5.3 Exercise	10
1.6 Two geoms for barplots: <code>geom_bar()</code> or <code>geom_col()</code>	10
1.7 Solutions	11
2 R Basics	13
2.1 Getting help	13
2.2 Objects and functions	14
2.3 Working with Objects	18
2.3.1 Exercise	19

2.4	Loading data	19
2.4.1	Exercise	20
2.4.2	Other ways to investigate objects	20
2.4.3	Exercise	21
2.4.4	Exercise	21
2.5	Operators	21
2.5.1	Exercise	23
2.5.2	Exercise	23
2.6	Types of variables	24
2.6.1	Characters	24
2.6.2	Factors	24
2.6.3	Numbers	25
2.6.4	Specifying variable types	25
2.6.5	Exercise	26
2.7	Importing data	26
2.8	Adding columns to dataframes	27
2.9	Rounding numbers	29
2.9.1	Exercise	29
2.10	The <code>combine</code> function: <code>c()</code>	29
2.10.1	Exercise	30
2.11	The <code>paste()</code> function	31
2.11.1	Exercise	32
2.12	Combining two dataframes	32
2.12.1	Exercise	33
2.13	The <code>summary()</code> function	33
2.13.1	When pipe sends data to the wrong place	35
2.13.2	Exercise	35
2.14	Extra: Creating a dataframe from scratch	36
2.14.1	Exercise	37
2.15	Solutions	37
3	Summarising data	41
3.1	Data	41
3.2	Tidyverse packages: <code>ggplot2</code> , <code>dplyr</code> , <code>tidyr</code> , etc.	43
3.3	Basic functions for summarising data	45
3.4	Subgroup analysis: <code>group_by()</code> and <code>summarise()</code>	45
3.4.1	Exercise	47

3.4.2	Exercise	47
3.5	<code>mutate()</code>	48
3.5.1	Exercise	48
3.5.2	Optional advanced exercise	49
3.6	Wide vs long: <code>spread()</code> and <code>gather()</code>	52
3.6.1	Wide format	53
3.6.2	Exercise	53
3.6.3	Long format	55
3.6.4	Exercise	56
3.7	Sorting: <code>arrange()</code>	56
3.8	Factor handling	58
3.8.1	Exercise	58
3.8.2	<code>fct_collapse()</code> - grouping levels together	62
3.8.3	<code>fct_relevel()</code> - change the order of levels	62
3.8.4	<code>fct_recode()</code> - rename levels	63
3.8.5	Converting factors to numbers	64
3.8.6	Exercise	64
3.9	Long Exercise	66
3.10	Extra: formatting a table for publication	66
3.11	Solution: Long Exercise	67
4	Different types of plots	69
4.1	Data	69
4.2	Scatter plots/bubble plots - <code>geom_point()</code>	70
4.2.1	Exercise	71
4.3	Line chart/timeplot - <code>geom_line()</code>	72
4.3.1	Exercise	73
4.3.2	Advanced example	74
4.3.3	Advanced Exercise	74
4.4	Box-plot - <code>geom_boxplot()</code>	75
4.4.1	Exercise	76
4.4.2	Dot-plot - <code>geom_dotplot()</code>	77
4.5	Barplot - <code>geom_bar()</code> and <code>geom_col()</code>	78
4.5.1	Exercise	79
4.6	All other types of plots	80
4.7	Specifying <code>aes()</code> variables	81
4.8	Extra: Optional exercises	82

4.8.1	Exercise	82
4.8.2	Exercise	84
4.9	Solutions	85
5	Fine tuning plots	87
5.1	Data and initial plot	87
5.2	Scales	88
5.2.1	Logarithmic	88
5.2.2	Expand limits	89
5.2.3	Zoom in	91
5.2.4	Exercise	92
5.2.5	Axis ticks	92
5.2.6	Swap the axes	93
5.3	Colours	94
5.3.1	Using the Brewer palettes:	94
5.3.2	Legend title	95
5.3.3	Choosing colours manually	96
5.4	Titles and labels	99
5.4.1	Annotation	99
5.4.2	Annotation with a superscript and a variable	101
5.5	Text size	102
5.5.1	Legend position	103
5.6	Saving your plot	105
II	Data analysis	107
6	Tests for continuous outcome variables	111
6.1	Continuous data	111
6.2	The Question	112
6.3	Get the data	112
6.4	Check the data	112
6.5	Plot the data	114
6.5.1	Histogram	115
6.5.2	Q-Q plot	115
6.5.3	Boxplot	117
6.6	Compare the means of two groups	119
6.6.1	T-test	119

6.6.2	Two-sample t -tests	119
6.6.3	Paired t -tests	121
6.7	Compare the mean of one group	124
6.7.1	One sample t -tests	124
6.8	Compare the means of more than two groups	126
6.8.1	ANOVA	126
6.8.2	Assumptions	128
6.8.3	Pairwise testing and multiple comparisons	129
6.9	Non-parametric data	131
6.9.1	Transforming data	131
6.9.2	Non-parametric test for comparing two groups	133
6.9.3	Non-parametric test for comparing more than two groups	135
6.10	Finalfit approach	136
6.11	Conclusions	136
6.12	Exercises	137
6.12.1	Exercise 1	137
6.12.2	Exercise 2	137
6.12.3	Exercise 3	137
6.12.4	Exercise 4	137
6.13	Exercise solutions	138
7	Linear regression	143
7.1	Data	143
7.2	Plotting	143
7.2.1	Exercise	144
7.2.2	Exercise	145
7.3	Simple linear regression	145
7.3.1	Exercise	146
7.3.2	Model information: <code>summary()</code> , <code>tidy()</code> , <code>glance()</code>	147
7.4	If you are new to linear regression	148
7.4.1	Exercise - Residuals	148
7.5	Multiple linear regression	149
7.5.1	Exercise	149
7.5.2	Exercise	150

7.5.3	Exercise	151
7.5.4	Optional (Advanced) Exercise	151
7.6	Very advanced example	153
7.7	Solutions	153
8	Tests for categorical variables	155
8.1	Data	155
8.1.1	Recap on factors	155
8.2	Chi-squared test / Fisher's exact test	156
8.2.1	Plotting	156
8.3	Analysis	158
8.3.1	Using base R	158
8.3.2	Using <code>CrossTable</code>	159
8.3.3	Exercise	161
8.3.4	Fisher's exact test	161
8.4	Summarising multiple factors (optional)	165
8.5	Summarising factors with <code>library(finalfit)</code>	165
8.5.1	Summarising factors with <code>library(tidyverse)</code>	166
8.5.2	Example	166
8.5.3	Exercise	167
9	Logistic regression	169
9.1	What is Logistic Regression?	169
9.2	Definitions	171
9.3	Odds and probabilities	171
9.3.1	Odds ratios	172
9.4	Melanoma dataset	174
9.4.1	Doing logistic regression in R	174
9.5	Setting up your data	175
9.5.1	Worked Example	175
9.6	Creating categories	176
9.6.1	Exercise	176
9.6.2	Always plot your data first!	177
9.7	Basic: One explanatory variable (predictor)	180
9.7.1	Worked example	180
9.7.2	Exercise	182

9.8	Finalfit package	183
9.9	Summarise a list of variables by another variable	183
9.10	<code>finalfit</code> function for logistic regression	184
9.11	Adjusting for multiple variables in R	185
9.11.1	Worked Example	185
9.11.2	Exercise	186
9.12	Advanced: Fitting the best model	187
9.12.1	Extra material: Diagnostics plots	188
10	Time-to-event data and survival	191
10.1	Data	191
10.2	Kaplan-Meier survival estimator	192
10.2.1	KM analysis for whole cohort	193
10.2.2	Model	193
10.2.3	Life table	193
10.2.4	KM plot	194
10.2.5	Exercise	196
10.2.6	Log-rank test	197
10.3	Cox proportional hazard regression	198
10.3.1	Model	198
10.3.2	Assumptions	200
10.3.3	Exercise	201
10.4	Dates in R	201
10.4.1	Converting dates to survival time	201
10.5	Solutions	202
III	Workflow	205
11	Notebooks and markdown	207
12	Missing data	209
13	Encryption	211
14	Exporting tables and plots	213
15	RStudio settings, good practise	215
15.1	Script vs Console	215

15.2 Starting with a blank canvas	215
Bibliography	217
Index	219

List of Tables

2.1	Example of a table (=tibble once read into R), including missing values - denoted NA (Not applicable/Not available).	14
3.1	alldata	48
3.2	summarise example	49
3.3	mutate_example	49



List of Figures



Preface

Version 0.3.1

Contributors: Riinu Ots, Ewen Harrison, Tom Drake, Peter Hall, Kenneth McLean.

This work is licensed under the Creative Commons Attribution-NonCommercial-NoDerivs 3.0 United States License. To view a copy of this license, visit <http://creativecommons.org/licenses/by-nc-nd/3.0/us/>

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 understood 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

August 2019

Structure of the book

Chapters ?? 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 3.4.4 (2018-03-15)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.5 LTS
##
## Locale:
##   LC_CTYPE=en_GB.UTF-8
##   LC_NUMERIC=C
##   LC_TIME=en_GB.UTF-8
##   LC_COLLATE=en_GB.UTF-8
##   LC_MONETARY=en_GB.UTF-8
##   LC_MESSAGES=en_GB.UTF-8
##   LC_PAPER=en_GB.UTF-8
##   LC_NAME=C
##   LC_ADDRESS=C
##   LC_TELEPHONE=C
##   LC_MEASUREMENT=en_GB.UTF-8
##   LC_IDENTIFICATION=C
##
## Package version:
##   base64enc_0.1.3  bookdown_0.7      compiler_3.4.4
##   digest_0.6.20   evaluate_0.13     glue_1.3.1
##   graphics_3.4.4  grDevices_3.4.4  highr_0.8
##   htmltools_0.3.6 jsonlite_1.6      knitr_1.22
##   magrittr_1.5     markdown_0.9      methods_3.4.4
##   mime_0.6         Rcpp_1.0.1        rmarkdown_1.12.4
##   stats_3.4.4      stringi_1.4.3     stringr_1.4.0
##   tinytex_0.11     tools_3.4.4       utils_3.4.4
```

```
##   xfun_0.6           yaml_2.2.0
```

Package names are in bold text (e.g., **rmarkdown**), and in-line 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")
```

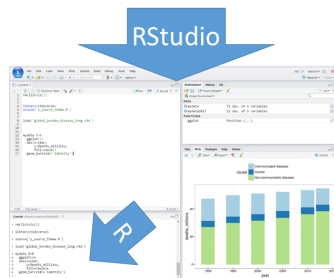
```
install.packages("devtools")

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").







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")
```

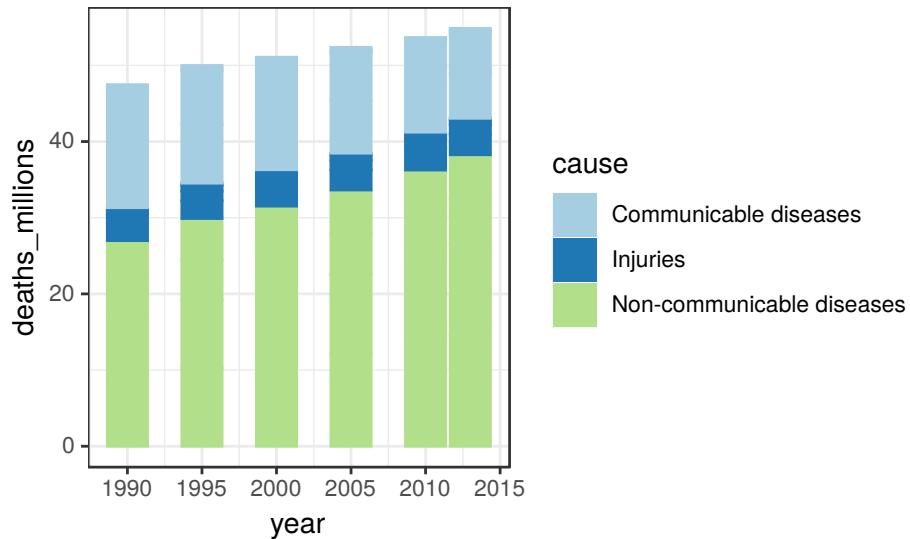
After loading the datasets, investigate your Environment tab (top-right). You will see two things listed: `mydata` and `mydata2013`, which is a subset of `mydata`.

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.

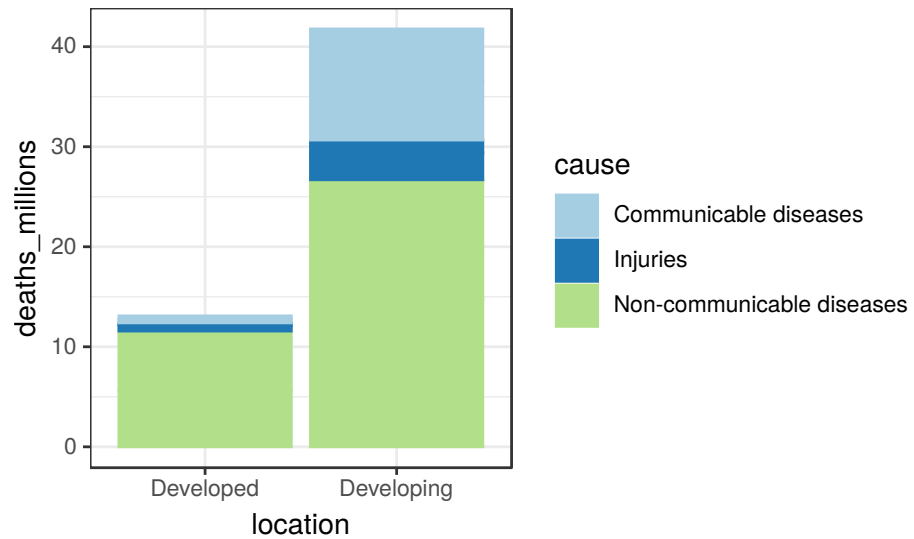
`geom_()` stands for **geometric**.

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:

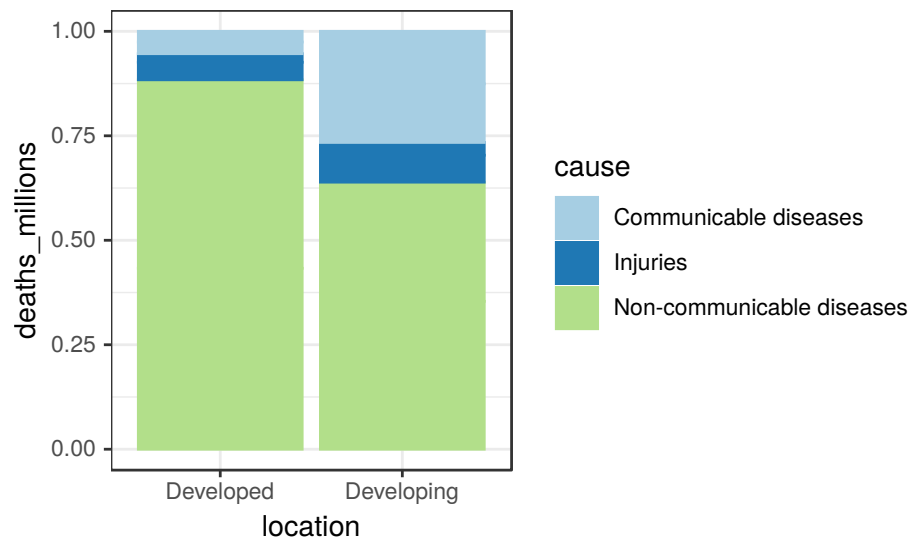


1.3 Comparing bars of different height

1.3.1 Stretch each bar to 100%

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

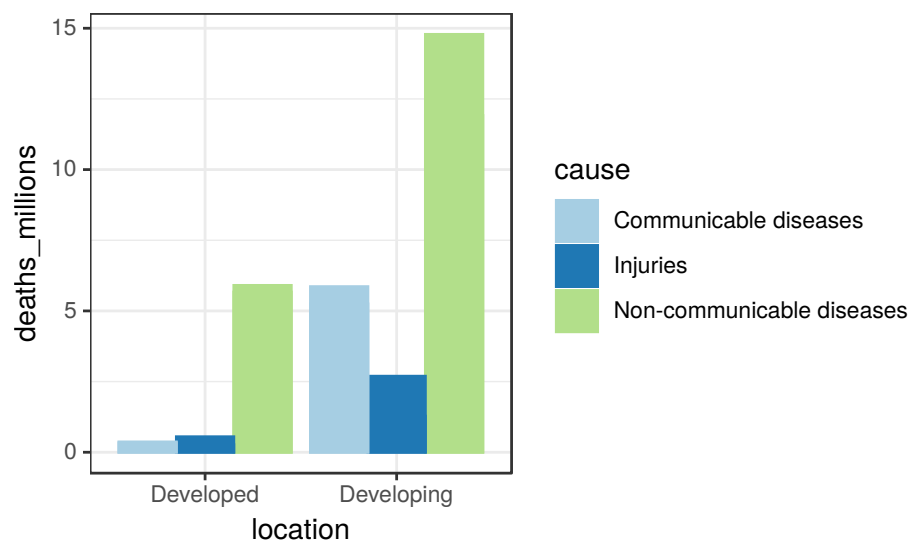
```
mydata2013 %>%
  ggplot(aes(x      = location,
             y      = deaths_millions,
             fill    = cause,
             colour  = cause)) +
  geom_col(position = "fill")
```



1.3.2 Plot each bar next to each other

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

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

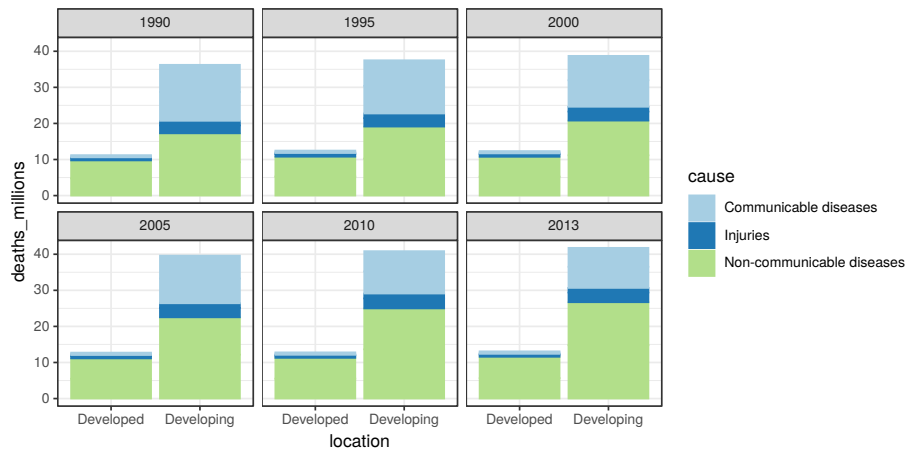


1.4 Facets (panels)

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)
```

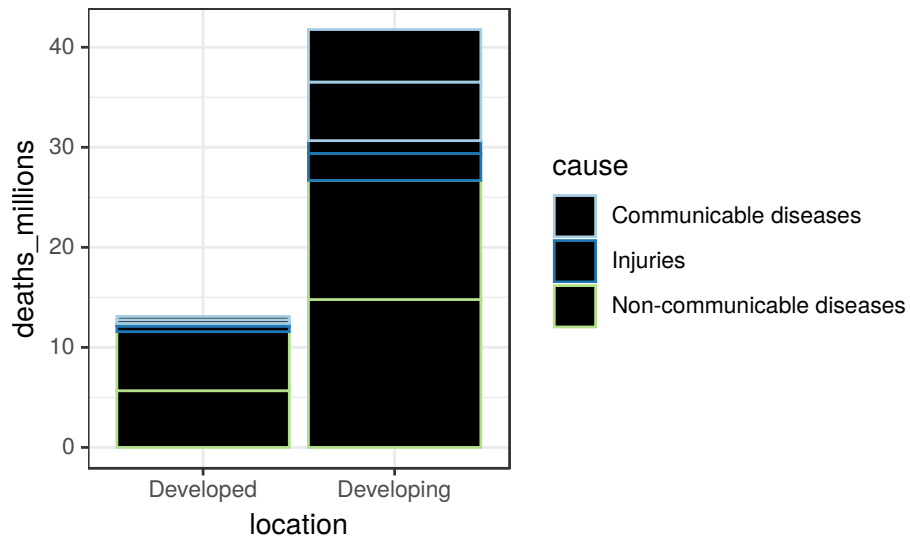


1.5 Extra: using aesthetics outside of the aes()

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")
```



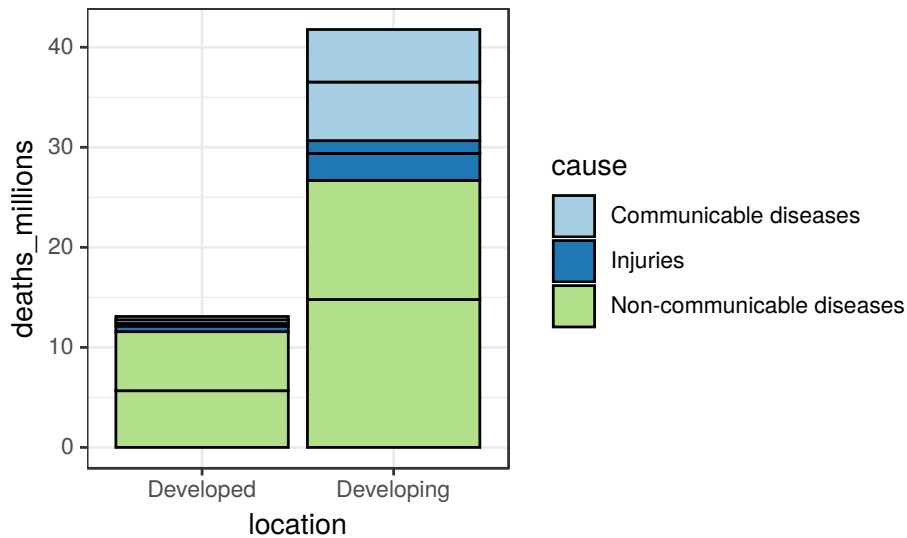
Setting aesthetics (`x`, `y`, `fill`, `colour`, etc.) outside of `aes()` sets them to a constant value. R can recognise a lot of colour names, e.g., try “cornflowerblue”, “firebrick”, or just “red”, “green”, “blue”, etc. For a full list, search Google for “Colours in R”. R also knows HEX codes, e.g.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

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

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

Now, regular does not mean it can't have missing values. Missing values are denoted **NA** that 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. We will come back to handling missing values later, but let's return to introducing objects and functions.

A table can live anywhere: on paper, in a Spreadsheet, in an SQL database, or it can live in 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. Once you read it into R (import it), we call it a tibble. When you are in one of your very cool R sessions and read in a table, it goes into this session's Environment. 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 only use tibbles.

So, the tibble `mydata` example of an object that lives in the Environment of your R Session. A function that you may want to apply on numeric data is `mean()`. R functions always have brackets after their name. This is for two reasons. First, to easily differentiate them from objects - which don't have 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 the R function `mean()` some data to average. 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, 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, R then gives us a pretty clear Error (our first Error in this book!) saying 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 which is a data type with just two potential values TRUE/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 - `na.rm` - the NA values). This 'removal' only means excluded from the calculation, it does not affect the actual tibble (`mydata`) holding the columns and rows. R is case sensitive, so it has to be `na.rm`, not `NA.rm` etc. There is no need to try to memorise 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. Information about functions (Help) is built into R, so an internet connection is not required for this.

Make sure to always separate 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 on the output document means you as well as your colleagues can always be clear on when the results were last updated.

```
Sys.time()
```

```
## [1] "2019-07-18 16:36:43 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 functions behaviour. When we say “the function returns”, we are referring to its output. The returned object can be different to its input object. In our `mean()` examples, 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

It’s sometimes difficult to appreciate how coding works without trying it first. These exercises will show you how R works.

We’ll first create an object and call it `a`, we will give the object `a` a value of 1. In R the equals `=` sign tells R to give the object on the left of the sign the value of whatever is on the right of the sign.

```
a = 1
```

In your environment panel, you should see `a` appear under the **Values** section.

Now, lets create `b` and give it a value of 2.

```
b = 2
```

Lets now add `a` and `b` together to create the object `c`

```
c = a + b

# Print the value of c to the Console

c # should return the number 3
```

```
## [1] 3
```

All of R is just an extension of this: applying more complex functions (calculations) across more complex objects.

It's important to appreciate that objects can be more than just single numbers too. They can be entire spreadsheets, which in R are known as **tibbles** (or in base R: **data frames**).

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

2.3.1 Exercise

Create 3 new variables, **d**, **e**, **f** with values 6, 7, 8 using the different assignment operators.

```
d = 6
e <- 7
8 -> f
```

2.4 Loading data

Before we load a new dataset, we should clear our experiments from the previous section. Restart R by pressing `Ctrl+Shift+F10` or `Select Section -> Restart R` from the menu above.

Now the environment is clear, lets load in the data:

```
library(tidyverse) # Tidyverse is the package which contains some of the co  
mydata = read_csv("global_burden_disease_short.csv")
```

But how can we look at the data we just loaded? How do we know which variables it contains? Hint: the Environment tab.

2.4.1 Exercise

Answer these question about your data:

1. At present, how many variables are there?
2. How many deaths were there from communicable diseases in 1990? Hint: clicking on columns when Viewing a tibble orders it.

2.4.2 Other ways to investigate objects

In most cases, you can rely on the Environment tab to see how many variables you have. If, however, the dataset you are using is too big to easily navigate within, you might need to use `names(mydata)`, `head(mydata)`, or `str(mydata)`.

Furthermore, we can select a single column using the dollar sign: `$`.

So if we type:

```
mydata$deaths
```

```
## [1] 16149409 26993493 4325788 15449045 29897069 4639869 14775502  
## [8] 31521934 4776852 13890709 33637815 4833919 12431802 36259550  
## [15] 4970846 11809640 38267197 4786929
```


R will give us all the data for that variable.

2.4.3 Exercise



Image source: <https://cran.r-project.org/web/packages/magrittr/vignettes/magrittr.html>

Re-write `names(mydata)` and `head(mydata)` using the pipe (`%>%`).
Use the keyboard shortcut `Ctrl+Shift+M` to insert it.

2.4.4 Exercise

How many unique values does the `cause` variable have? Hint:
`mydata$cause` piped into `unique()` piped into `length()`.

2.5 Operators

Operators are symbols in R Code that tell R how to handle different pieces of data or objects.

Here are the main operators:

`=`, `<-`, `==`, `<`, `>`, `<=`, `>=`

Some of these perform a test on data. A good example of this is the ‘==’ operator.

This tells R to compare two things and ask if they are equal. If they are equal R will return ‘TRUE’, if not R will return ‘FALSE’.

On your R cheat sheet, you can see what the others do. Here is a reminder:

Symbol	What does	Example	Example result
= or <-	assigns	x = 2	the value of x is now 2
==	Equal?	x == 2	TRUE
!=	Not equal?	x != 1	TRUE
<	Less than	x < 2	FALSE
>	Greater than	x > 1	TRUE
<=	Less than or equal to	x <= 2	TRUE
>=	Greater than or equal to	x >= 1	TRUE
%>%	sends data into a function	x %>% print()	2
::	indicates package	dplyr::count()	count() fn. from the dplyr p
->	assigns	2 -> x	the value of x is now 2
&	AND	x > 1 & x < 3	TRUE
	OR	x > 3 x == 3	TRUE
%in%	is value in list	x %in% c(1,2,3)	TRUE
\$	select a column	mydata\$year	1990,1996,...
c()	combines values	c(1, 2)	1, 2
#	comment	#Rinu changed this	ignored by R

For example, if we wanted to select the years in the Global Burden of disease study after 2000 (and including 2000) we could type the following:

```
mydata %>%
  filter(year >= 2000)
```

To save this as a new object we would then write:

```
mydata_out = mydata %>%  
  filter(year >= 2000)  
  
# Or we could write  
  
mydata %>%  
  filter(year >= 2000) -> mydata_out
```

How would you change the above code to only include years greater than 2000 (so not including 2000 itself too)? Hint: look at the table of operators above (also in your HealthyR QuickStart Sheet).

2.5.1 Exercise

Modify the above example to filter for only year 2000, not all years greater than 2000. Save it into a variable called `mydata_year2000`.

2.5.2 Exercise

Let's practice this and combine multiple selections together.

This `|` means OR and `&` means AND.

From `mydata`, select the lines where year is either 1990 or 2013 and cause is "Communicable diseases":

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

2.6 Types of variables

consider structuring as per here: https://finalfit.org/articles/data_prep.html

Like many other types of statistical software, R needs to know the variable type of each column. The main types are:

2.6.1 Characters

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). We can specify these using the `as.character()` function. Characters are displayed in-between `"` (or `'`).

2.6.2 Factors

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

- The values factor levels can take is fixed. For example, if the levels of your column called `sex` are “Male” and “Female” and you try to add a new patient where sex is called just “F” you will get a warning from R. If `sex` was a character column rather than a factor R would have no problem with this and you would end up with “Male”, “Female”, and “F” in your column.
- Levels have an order. When we plotted the different causes of death in the last session, R ordered them alphabetically (because `cause` was a character rather than a factor). But if you want to use a non-alphabetical order, e.g. “Communicable diseases”-“Non-communicable diseases”-“Injuries”, we need make `cause`

into a factor. Making a character column into a factor enables us to define and change the order of the levels. Furthermore, there are useful tools such as `fct_inorder` or `fct_infreq` that can order factor levels for us.

These can be huge benefits, especially as a lot of medical data analyses include comparing different risks to a reference level. Nevertheless, the fussiness of factors can sometimes be unhelpful or even frustrating. For example, if you really did want to add a new level to your `gender` column (e.g., “Prefer not to say”) you will either have to convert the column to a character, add it, and convert it back to a factor, or use `fct_expand` to add the level and then add your new line.

2.6.2.1 Exercise

Temporarily type `fct_inorder` anywhere in your script, then press F1. Read the **Description** in the Help tab and discuss with your neighbour how `fct_inorder` and `fct_infreq` would order your factor levels.

2.6.3 Numbers

Self-explanatory! These are numbers. In R, we specify these using the `as.numeric()` function. Numbers without decimal places are sometimes called integers. Click on the blue arrow in front of `mydata` in the Environment tab and see that `year` is an `int` (integer) whereas `deaths` is a `num` (numeric).

2.6.4 Specifying variable types

```
as.character(mydata$cause)

as.numeric(mydata$year)
```

```
factor(mydata$year)

#Lets save the cause as a factor

mydata$cause = factor(mydata$cause)

#Now lets print it out

mydata$cause
```

2.6.5 Exercise

Change the order of the levels in `mydata$cause` so that “Non-communicable diseases” come before “Injuries”. Hint: use `F1` to investigate examples of how `fct_relevel()` works.

2.7 Importing data

For historical reasons, R’s default functions (e.g. `read.csv()` or `data.frame()`) convert all characters to factors automatically (for more on this see forcats.tidyverse.org¹). But it is usually more convenient to deal with characters and convert some of the columns to factors when necessary.

Base R:

```
mydata = read.csv("global_burden_disease_short.csv", stringsAsFactors = FALSE)
```

The tidyverse version, `read_csv()`, has `stringsAsFactors` set to

¹<http://forcats.tidyverse.org>

FALSE by default (and it is a lot faster than `read.csv()` when reading in large datasets).

Tidyverse:

```
mydata = read_csv("global_burden_disease_short.csv")

## Parsed with column specification:
## cols(
##   cause = col_character(),
##   year = col_double(),
##   deaths = col_double()
## )
```

You can use the “Import Dataset” button in the Environment tab to get the code for importing data from Excel, SPSS, SAS, or Stata.

2.8 Adding columns to dataframes

If we wanted to add in a new column or variable to our data, we can simply use the dollar sign ‘\$’ to create a new variable inside a pre-existing piece of data:

```
mydata$new = 1

mydata$new2 = 1:18
```

Run these lines and click on `mydata` in the Environment tab to check this worked as expected.

Conversely, if we want to delete a specific variable or column we can use the ‘NULL’ function, or alternatively ask R to `select()` the data without the new variable included.

```
mydata$new = NULL

mydata = mydata %>%
  select(-new2)
```

We can make new variables using calculations based on variables in the data too.

The mutate function is useful here. All you have to specify within the mutate function is the name of the variable (this can be new or pre-existing) and where the new data should come from.

There are two equivalent ways of defining new columns based on a calculation with a previous column:

mutate formally introduced in later chapter. Need to think how best to present this in book.

```
# First option

mydata$years_from_1990 = mydata$year - 1990
mydata$deaths_millions = mydata$deaths/1000000

# Second option (mutate() function)

mydata = mydata %>%
  mutate(years_from_1990 = year-1990,
         deaths_millions = deaths/1000000)
```

Throughout this course we will be using both of these ways to create or modify columns. The first option (using the \$) can look neater when changing a single variable, but when combining multiple ones you will end up repeating mydata\$. mutate() removes the duplication, but it does add a new line and brackets.

2.9 Rounding numbers

We can use `round()` to round the new variables to create integers.

2.9.1 Exercise

Round the new column `deaths_millions` to no decimals:

```
## [1] 16 27  4 15 30  5 15 32  5 14 34  5 12 36  5 12 38  5
```

- How would you round it to 2 decimals? Hint: use F1 to investigate `round()`.
- What do `ceiling()` and `floor()` do? Hint: sometimes you want to round a number up or down.

2.10 The combine function: `c()`

The combine function combines several values: `c()`

The combine function can be used with numbers or characters (like words or letters):

```
examplelist = c("Red", "Yellow", "Green", "Blue")  
  
# Ask R to print it by executing it on its own line  
  
examplelist  
  
## [1] "Red"      "Yellow"   "Green"    "Blue"
```

2.10.1 Exercise

There are 18 lines (observations) in `mydata`. Create a new variable using `c()` with 18 values (numbers, words, whichever you like, e.g. like we created `examplelist`). Then add it as new column to `mydata$newlist`. Advanced version: do this using a combination of `rep()` and `c()`.

2.11 The `paste()` function

The `paste()` function is used to paste several words or numbers into one character variable/sentence.

In the paste function we need to specify what we would like to combine, and what should separate the components. By default, the separation is a space, but we can change this using the `sep =` option within the paste function.

So, for example if we wanted to make a sentence:

```
#  
#paste("Edinburgh", "is", "Great")  
  
# Lets add in full stops  
  
paste("Edinburgh", "is", "Great", sep = ".")  
  
## [1] "Edinburgh.is.Great"  
  
# separator needs to go in "" as it is a character  
  
# If we really like Edinburgh  
  
#paste("Edinburgh", "is", "Great", sep = "!")  
  
# If we want to make it one word  
  
#paste("Edinburgh", "is", "Great", sep = "") # no separator (still need the
```

We can also join two different variables together using `paste()`:

```
paste("Year is", mydata$year)
```

```
## [1] "Year is 1990" "Year is 1990" "Year is 1990" "Year is 1995"
## [5] "Year is 1995" "Year is 1995" "Year is 2000" "Year is 2000"
## [9] "Year is 2000" "Year is 2005" "Year is 2005" "Year is 2005"
## [13] "Year is 2010" "Year is 2010" "Year is 2010" "Year is 2013"
## [17] "Year is 2013" "Year is 2013"
```

2.11.1 Exercise

Fix this code:

Hint: Think about characters and quotes!

```
paste(Today is, Sys.Date() )
```

2.12 Combining two dataframes

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 demonstrate the join does not 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.



2.12.1 Exercise

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

2.13 The `summary()` function

In R, the `summary()` function provides a quick way of summarising both data or the results of statistical tests.

Lets get a quick summary of all the variables inside the Global Burden of Disease dataset. It will work for whole datasets and single variables too.

```
mydata %>% summary()
```

```
##   cause          year      deaths      years_from_1990
## Length:18      Min.   :1990  Min.   : 4325788  Min.   : 0.00
## Class :character 1st Qu.:1995  1st Qu.: 4868151  1st Qu.: 5.00
## Mode  :character Median :2002  Median:14333106 Median:12.50
##              Mean  :2002  Mean  :17189854  Mean  :12.17
##              3rd Qu.:2010  3rd Qu.:29171175  3rd Qu.:20.00
##              Max.   :2013  Max.   :38267197  Max.   :23.00
## deaths_millions
## Min.   : 4.00
## 1st Qu.: 5.00
## Median :14.50
## Mean   :17.22
## 3rd Qu.:29.25
## Max.   :38.00
```

This even works on statistical tests (we will learn more about these later):

```
# lm stands for linear model
lm(deaths ~ year, data = mydata) %>% summary()
```

```
##
## Call:
## lm(formula = deaths ~ year, data = mydata)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13480641 -11791203  -2889909   12818624  19999627
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -181988644  736014812  -0.247    0.808
## year          99482     367606   0.271    0.790
##
```

```
## Residual standard error: 12590000 on 16 degrees of freedom
## Multiple R-squared:  0.004556,    Adjusted R-squared:  -0.05766
## F-statistic: 0.07324 on 1 and 16 DF,  p-value: 0.7901
```

2.13.1 When pipe sends data to the wrong place

Note that our usual way of doing things with the pipe would not work here:

```
mydata %>%
  lm(deaths ~ year) %>%
  summary()
```

This is because the pipe tries to send data into the first place of the function (first argument), but `lm()` wants the formula (`deaths ~ year`) first, then the dataframe. We can bypass this using `data = .` to tell the pipe where to put mydata:

```
mydata %>%
  lm(deaths ~ year, data = .) %>%
  summary()
```

2.13.2 Exercise

Try adding a new variable called `death_over_10m` which indicates whether there were more than 10 million deaths for a cause. The new variable should take the form ‘Yes’ or ‘No’.

Then make it into a factor.

Then use `summary()` to find out about it!

```
mydata = mydata %>%
  mutate(death_over_10m = ifelse(deaths >= 10000000, "Yes", "No")) # Using ifelse
```

```
mydata$death_over_10m = as.factor(mydata$death_over_10m)

mydata$death_over_10m %>% summary()
```

```
## No Yes
## 6 12
```

2.14 Extra: Creating a dataframe from scratch

It is rare that you will need to create a data frame by hand as most of the time you will be reading in a data from a .csv or similar. But in some cases (e.g. when creating special labels for a plot) it might be useful, so this is how to create one:

```
patient_id = paste0("ID", 1:10)
sex        = rep(c("Female", "Male"), 5)
age        = 18:27

newdata = data_frame(patient_id, sex, age)
```

```
## Warning: `data_frame()` is deprecated, use `tibble()`.
## This warning is displayed once per session.
```

```
# same as

newdata = data_frame(
  patient_id = paste0("ID", 1:10), #note the commas
  sex        = rep(c("Female", "Male"), 5),
  age        = 18:27
)
```

If we used `data.frame()` instead of `data_frame()`, all our char-

acter variables (`patient_id`, `sex`) would become factors automatically. This might make sense for `sex`, but it doesn't for `patient_id`.

2.14.1 Exercise

Create a new dataframe called `my_dataframe` that looks like this:

Hint: Use the functions `paste0()`, `seq()` and `rep()`

```
## # A tibble: 10 x 3
##   patient_id age sex
##   <chr>      <dbl> <chr>
## 1 ID11      15 Male
## 2 ID12      20 Male
## 3 ID13      25 Male
## 4 ID14      30 Male
## 5 ID15      35 Male
## 6 ID16      40 Female
## 7 ID17      45 Female
## 8 ID18      50 Female
## 9 ID19      55 Female
## 10 ID20     60 Female
```

2.15 Solutions

2.5.3

```
mydata %>% names()
mydata %>% head()
mydata %>% str()
```

2.5.4

```
mydata$cause %>% unique() %>% length()
```

```
## [1] 3
```

2.6.2

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

2.7.5

```
mydata$cause %>% fct_relevel("Injuries", after = 1)
```

2.10.1

```
mydata$deaths_millions = round(mydata$deaths_millions)  
  
# or  
mydata$deaths_millions = mydata$deaths_millions %>% round()
```

2.11.1

```
examplelist = c("Red", "Yellow", "Green", "Blue",  
                "Red", "Yellow", "Green", "Blue",  
                "Red", "Yellow", "Green", "Blue",  
                "Red", "Yellow", "Green", "Blue",  
                "Green", "Blue")
```

#Let's see what we've made by using print

```
mydata$newlist = examplelist
```

using rep()

```
examplelist2 = rep(c("Green", "Red"), 9)
```

2.12.1

```
paste("Today is", Sys.Date())
```

2.15.1

```
my_dataframe = data_frame(  
  patient_id = paste0("ID", 11:20),  
  age        = seq(15, 60, 5),  
  sex        = c( rep("Male", 5), rep("Female", 5))  
)
```



3

Summarising data

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

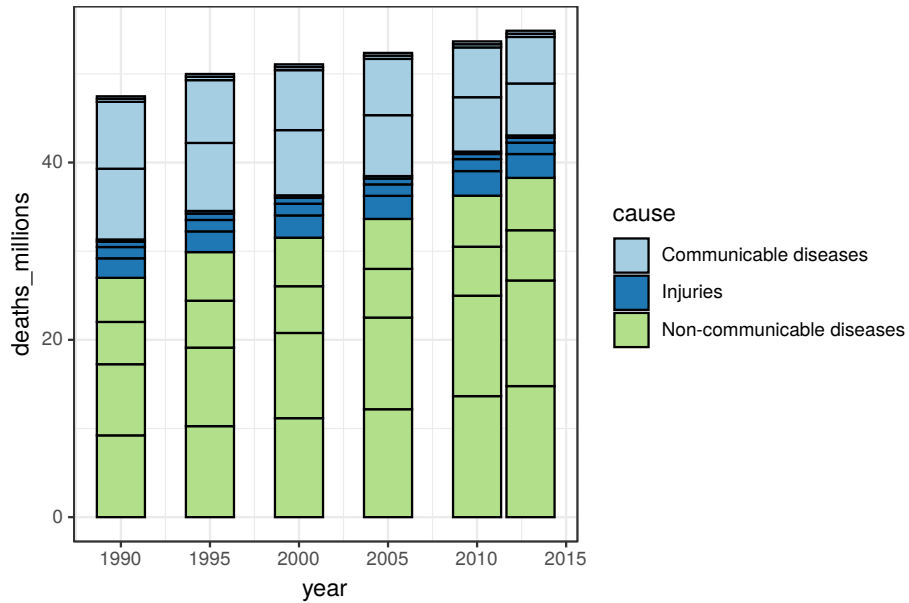
3.1 Data

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("healthy_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, tidyr, forcats, etc.

R LINGUA: LIBRARY VS PACKAGE

REAL LIFE



library

book

=

=

R

library

package

I went to the **library** to use the **English dictionary** (it was in the **library**)
 I then ordered a **specialised book** ("General Surgery") to read

I used **R** to calculate the **means and medians** of my data
 I then loaded a **specialised package** ("survival") to calculate the **means and medians**

```
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:

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

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

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

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

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

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.

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

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

```
mutate_example %>%
  slice(1:5) %>%
```

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

```
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.

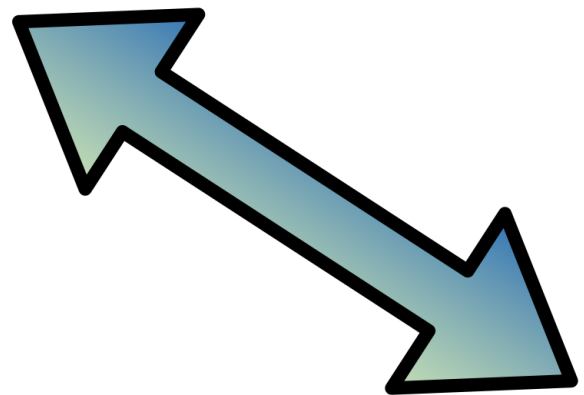
```
mydata %>%
  group_by(year, cause) %>%
```

```
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
Communicable diseases	0.6	0.7	0.7	0.7	0.7
Injuries	0.9	1	0.9	0.9	0.9
Non-communicable diseases	9.7	10.8	10.7	11.1	11.1

Developing countries:	1990	1995	2000	2005	2010
Communicable diseases	15.5	14.8	14.1	13.2	12.5
Injuries	3.5	3.6	3.8	3.9	4.0
Non-communicable diseases	17.3	19.1	20.8	22.5	24.2

[illegible]

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()
```

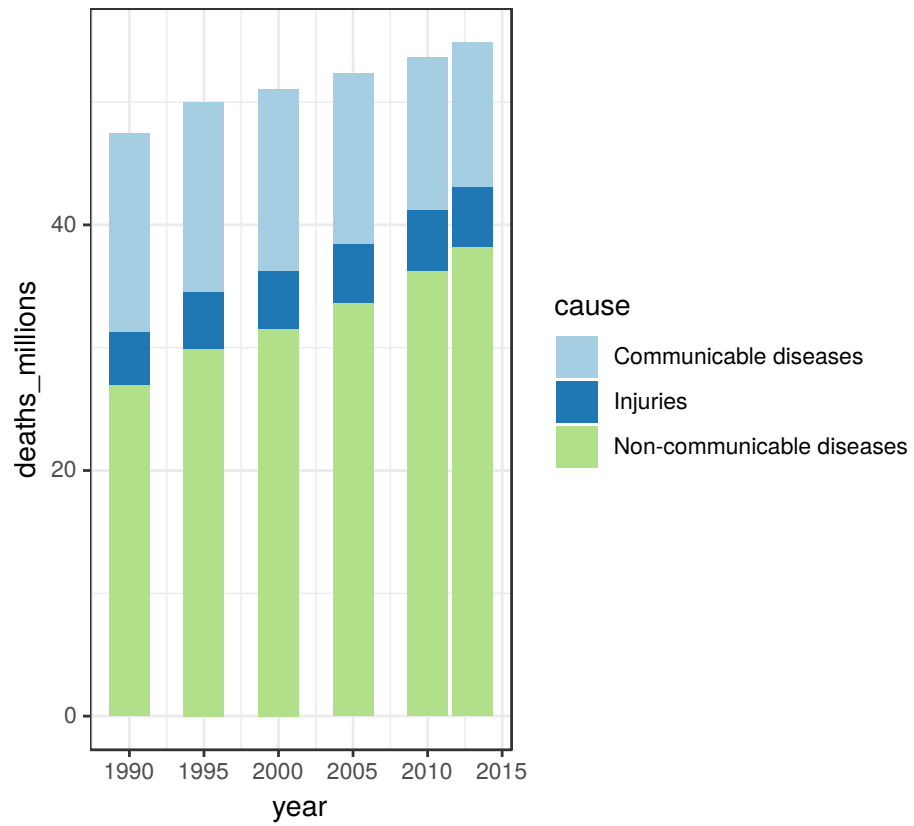
3.8 Factor handling

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.

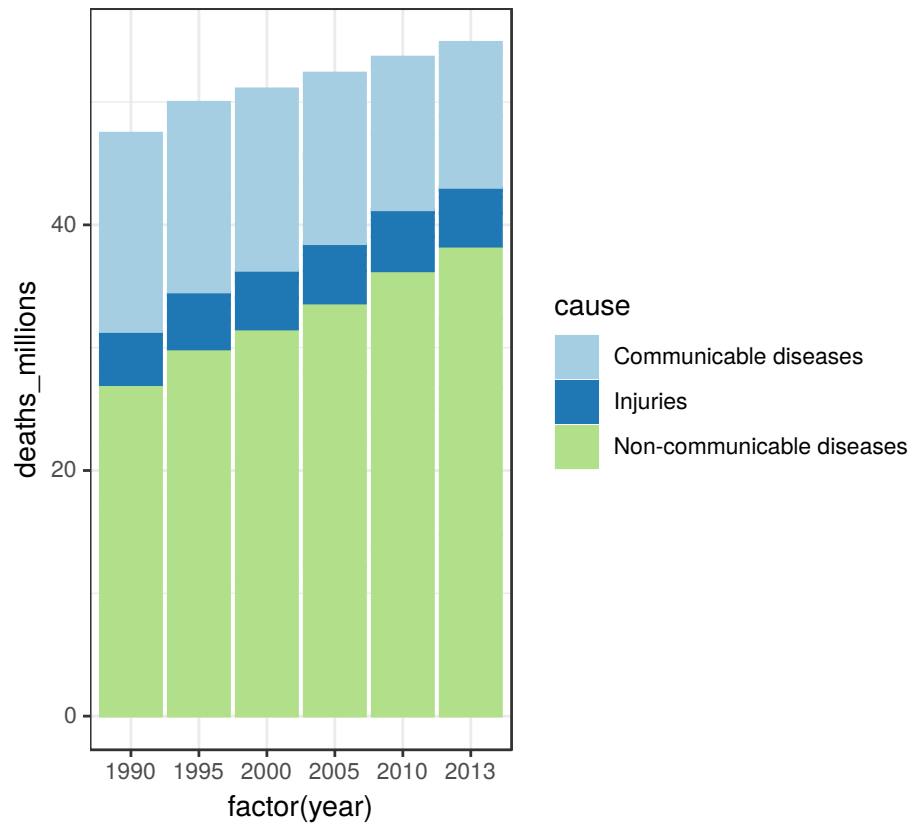
3.8.1 Exercise

Explain how and why these two plots are different.

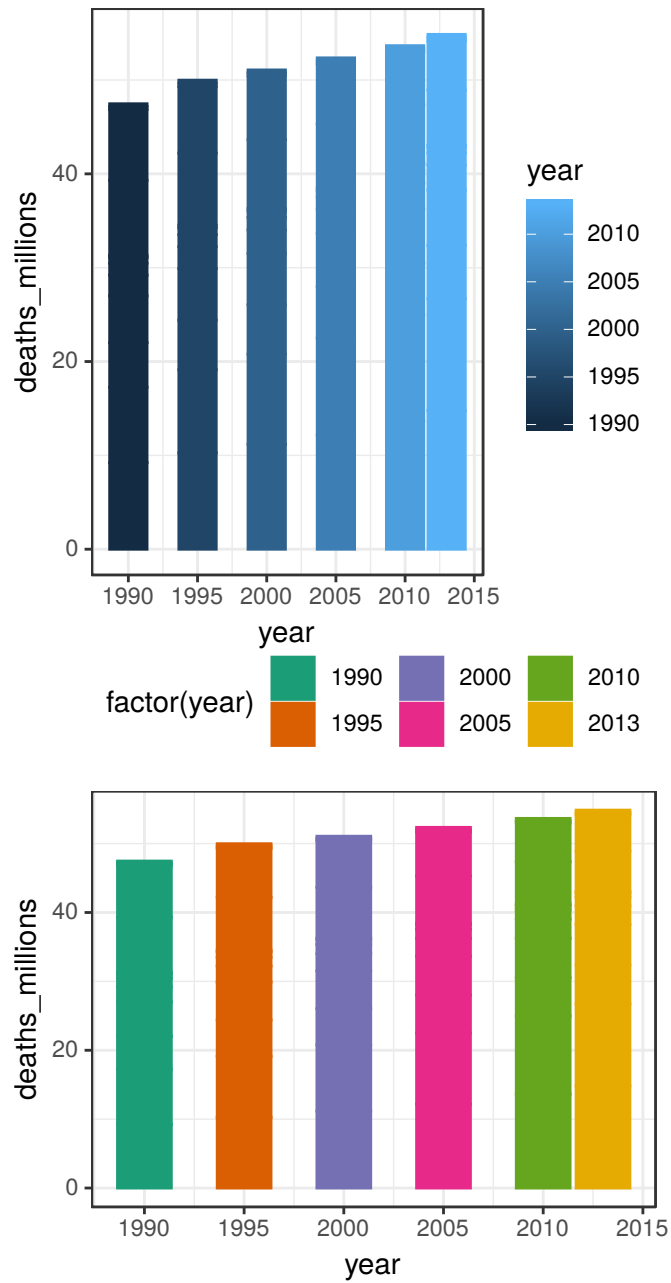
```
mydata %>%  
  ggplot(aes(x = year, y = deaths_millions, fill = cause))+  
  geom_col()
```



```
mydata %>%  
  ggplot(aes(x = factor(year), y = deaths_millions, fill = cause, colour =  
    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$cause %>%
  fct_collapse("Non-communicable and injuries" = c("Non-communicable disea
mydata$cause2
```

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

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

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

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

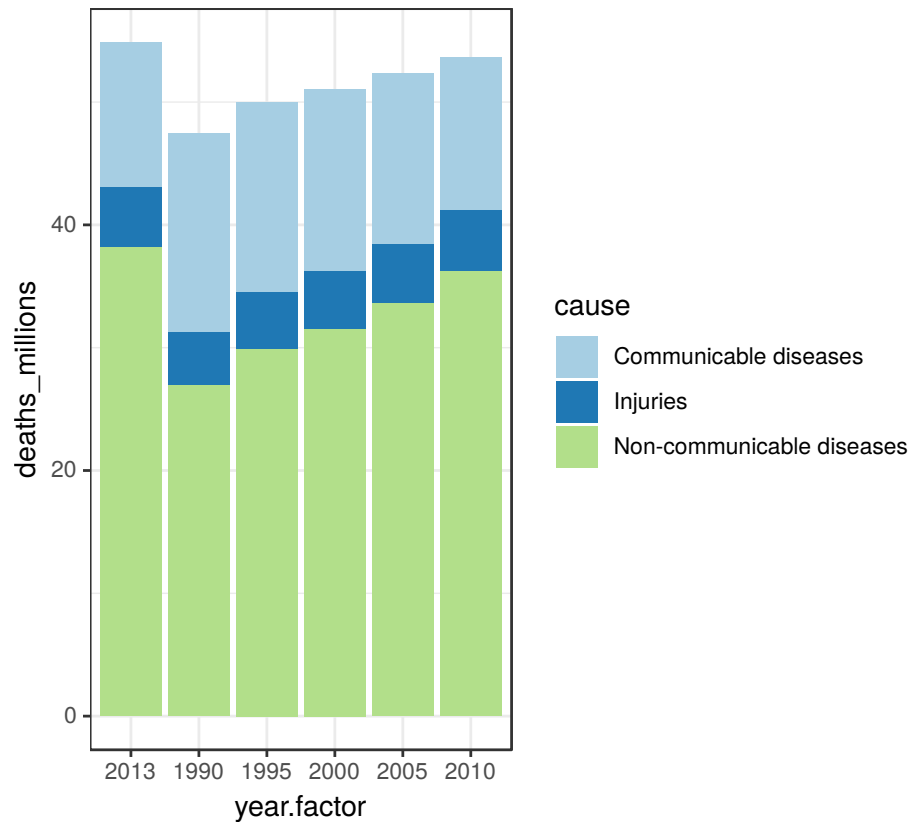
3.8.3 `fct_relevel()` - change the order of levels

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 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
      " (", round(percenta
        "%)"
      )
    ) %>%
  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
##
```

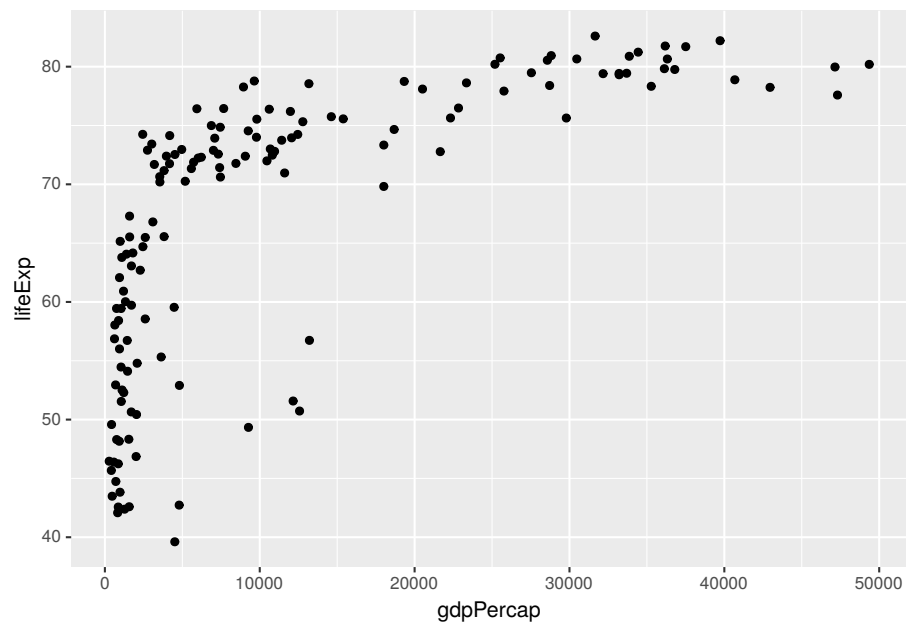
```
mydata$year %>% unique()
```

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

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

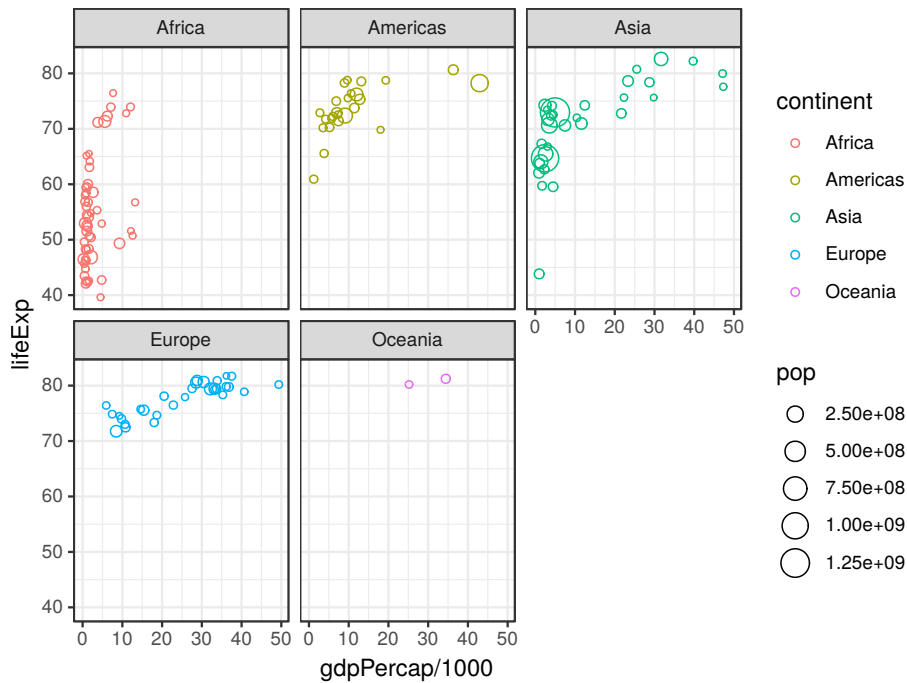
Plot life expectancy against GDP per capita (`x = gdpPercap`, `y=lifeExp`) at year 2007:

```
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:

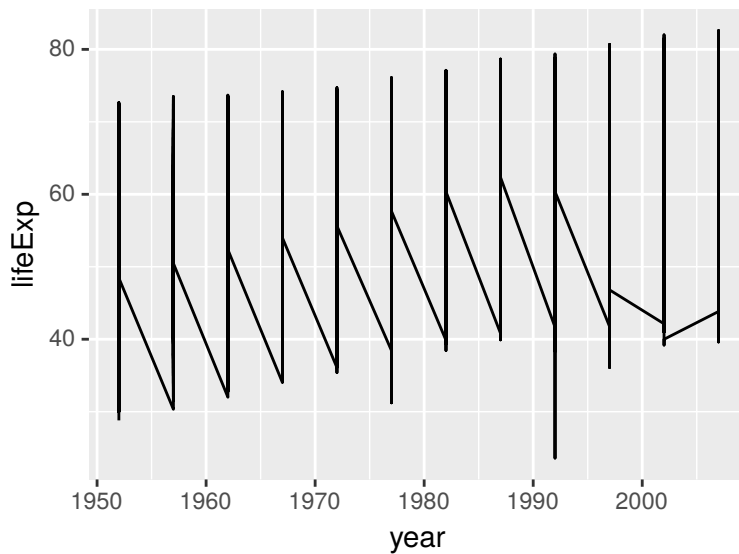


- Add points: `geom_point()`
 - Change point type: `shape = 1` (or any number from your Quickstart Sheet) inside the `geom_point()`
- Colour each country point by its continent: `colour=continent` to `aes()`
- Size each country point by its population: `size=pop` to `aes()`
- Put the country points of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

4.3 Line chart/timeplot - `geom_line()`

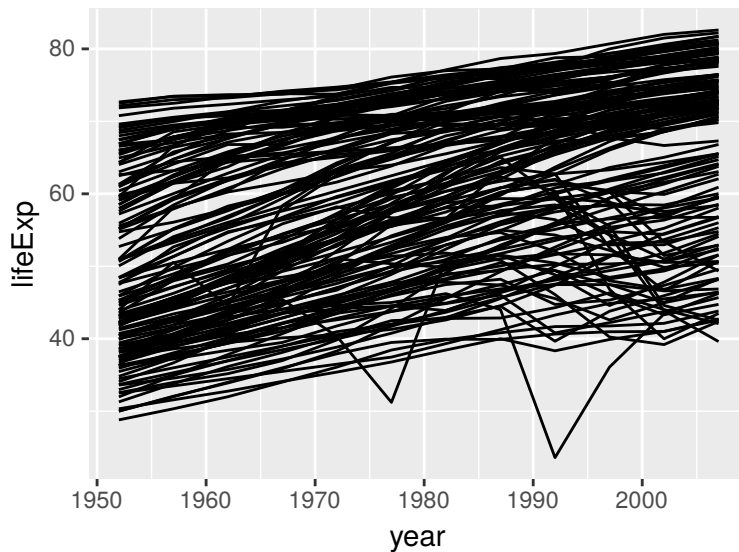
Plot life expectancy against year (`x = year`, `y=lifeExp`), add `geom_line()`:

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



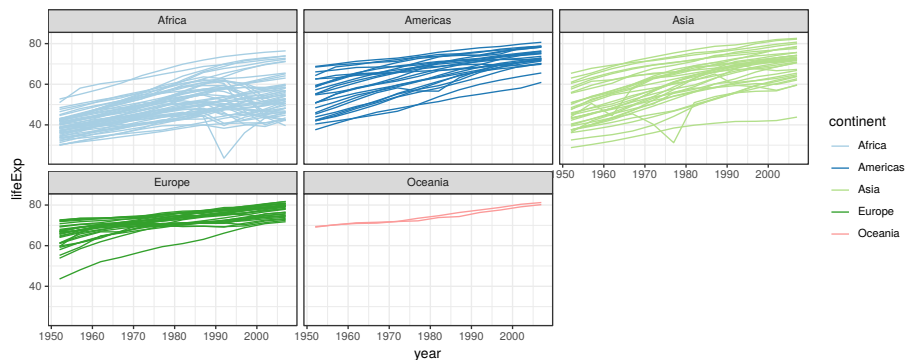
The reason you now see this weird zig-zag is that, using the above code, R does not know you want a connected line for each country. Specify how you want data points grouped to lines: `group = country` in `aes()`:

```
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:



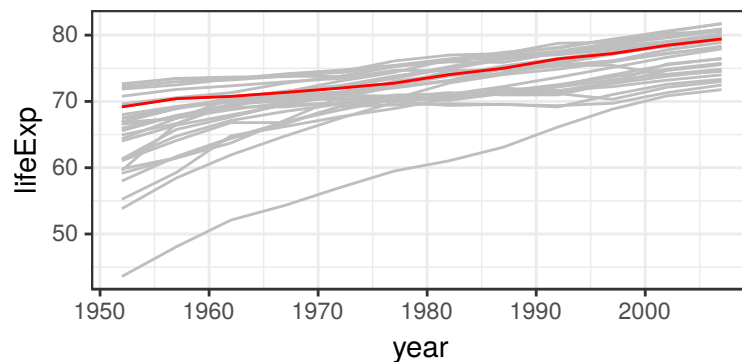
- Colour lines by continents: `colour=continent` to `aes()`
- Similarly to what we did in `geom_point()`, you can even size the line thicknesses by each country's population: `size=pop` to `aes()`
- Continents on separate panels: `+ facet_wrap(~continent)`
- Make the background white: `+ theme_bw()`

- Use a nicer colour scheme: `+ scale_colour_brewer(palette = "Paired")`

4.3.2 Advanced example

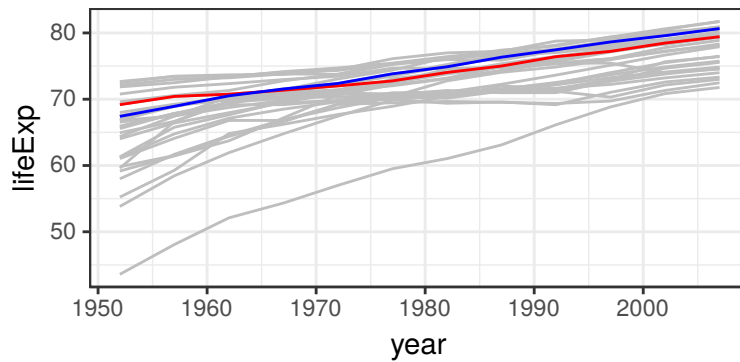
For European countries only (`filter(continent == "Europe") %>%`), plot life expectancy over time in grey colour for all countries, then add United Kingdom as a red line:

```
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:

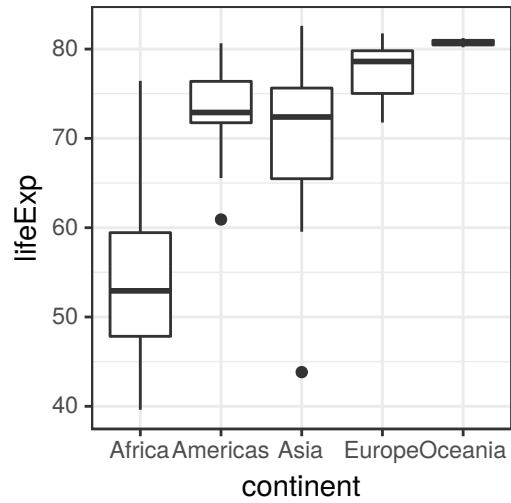


4.4 Box-plot - `geom_boxplot()`

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

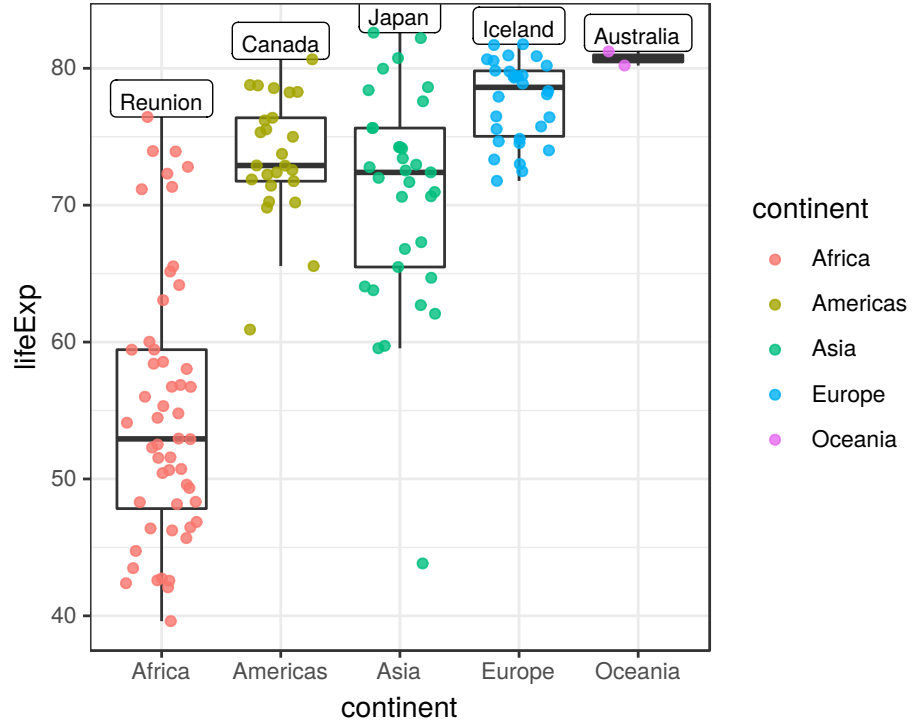
- `filter(year == 2007) %>%`
- `x = continent, y = lifeExp`
- `+ geom_boxplot()`

```
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:

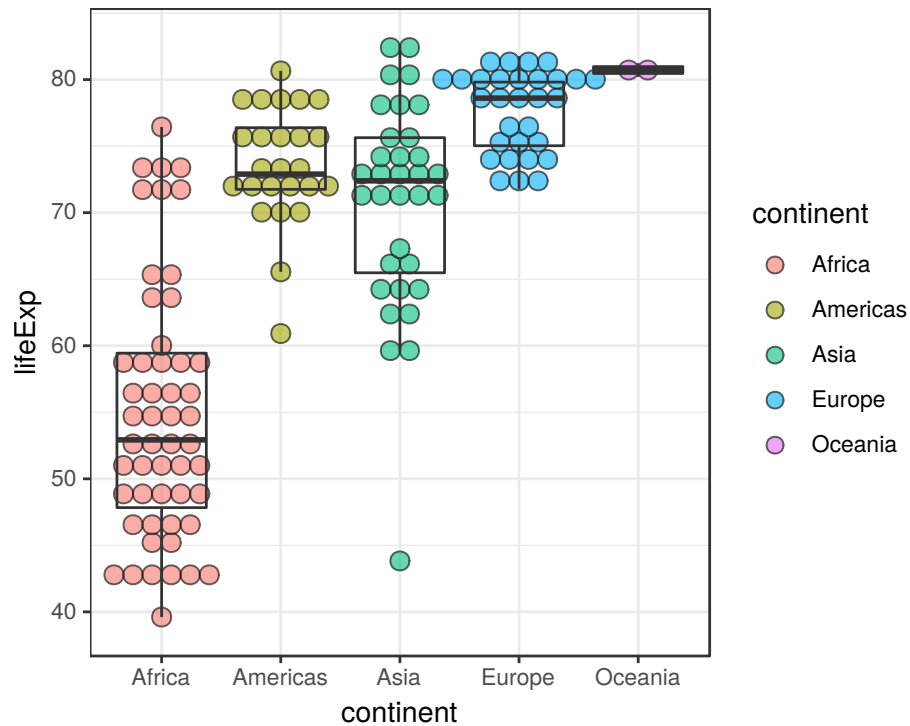
```
label_data = mydata %>%  
  filter(year == max(year)) %>% # same as year == 2007  
  group_by(continent) %>%  
  filter(lifeExp == max(lifeExp) )
```

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)
```

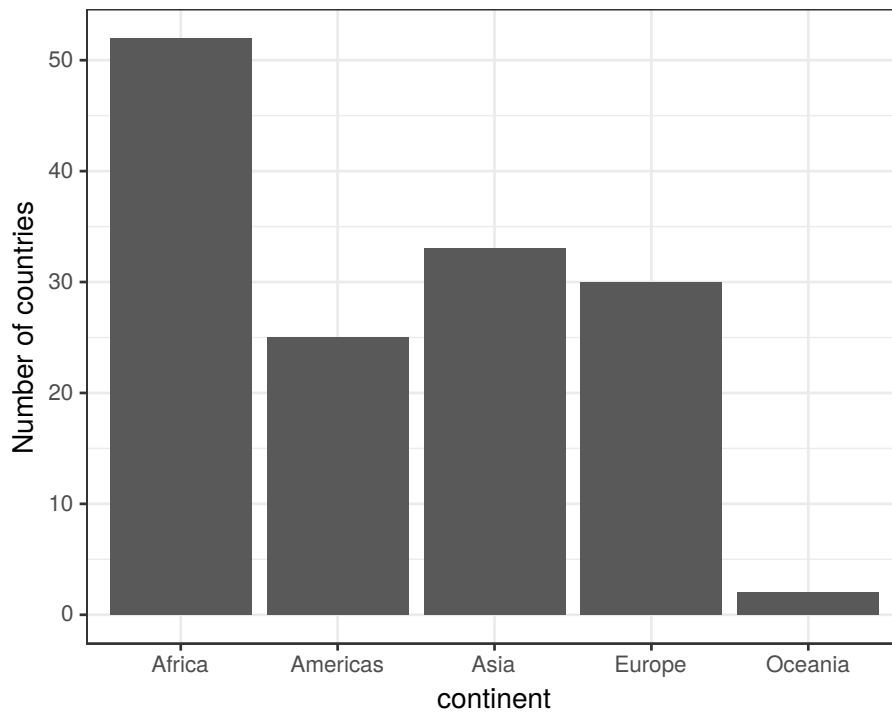


4.5 Barplot - `geom_bar()` and `geom_col()`

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:

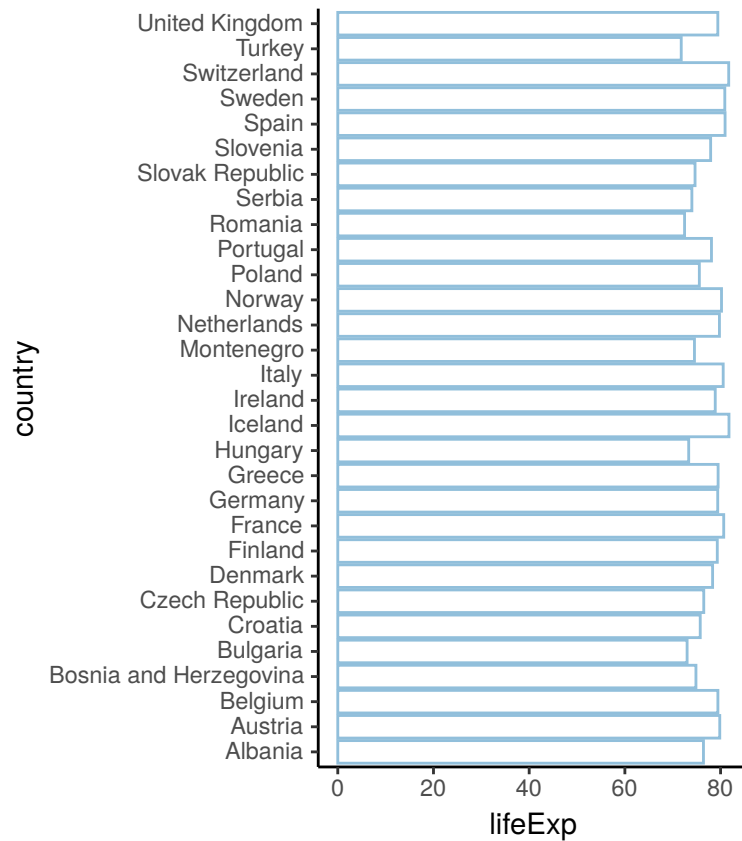
```
mydata %>%
  filter(year == 2007) %>%
  ggplot(aes(x = continent)) +
  geom_bar() +
```

```
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/>

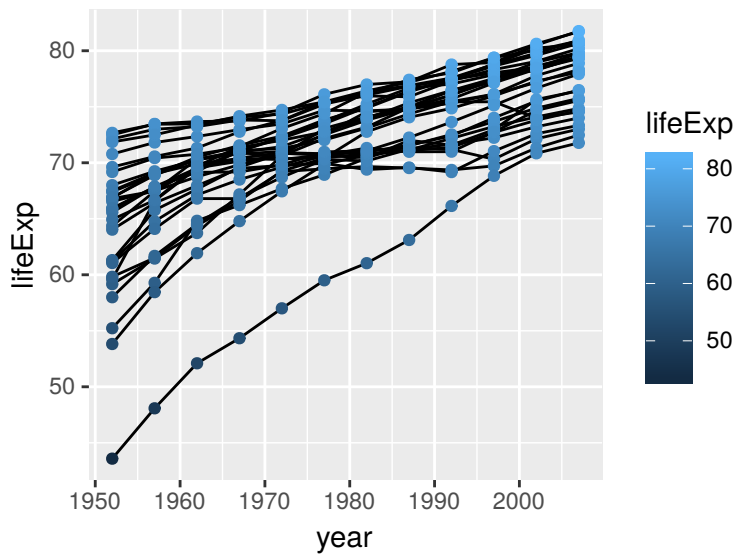
And the `ggplot()` documentation: <http://docs.ggplot2.org/>

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 f

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

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=
  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

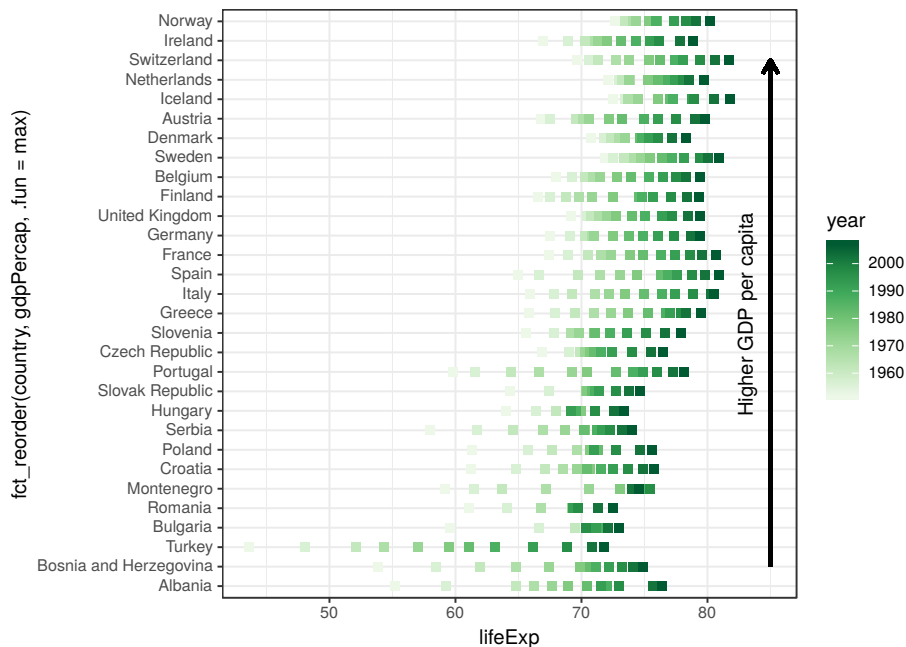
- Africa
- Americas
- Asia
- Europe
- Oceania

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",
    colour = "black", size=1,
    arrow = arrow(length = unit(0.3, "cm")))) +
  annotate("text", y = "Greece", x=83, label = "Higher GDP per capita", angl
```



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  
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 = "#91bafb", 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)

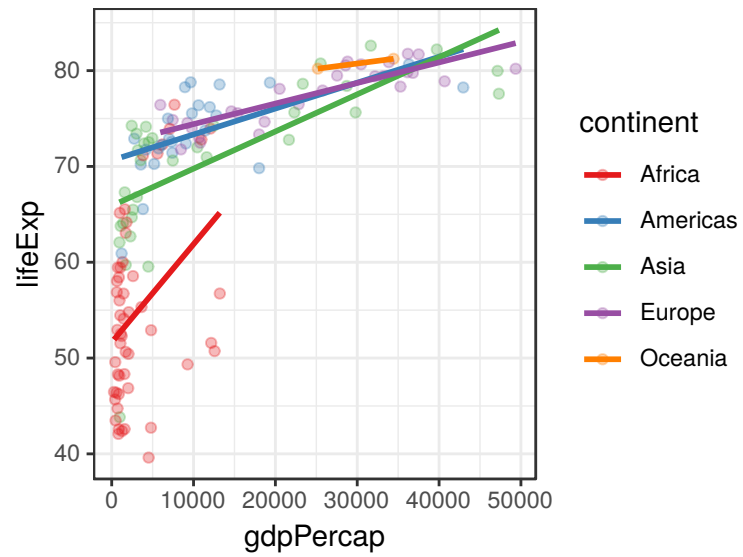
mydata = gapminder

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")

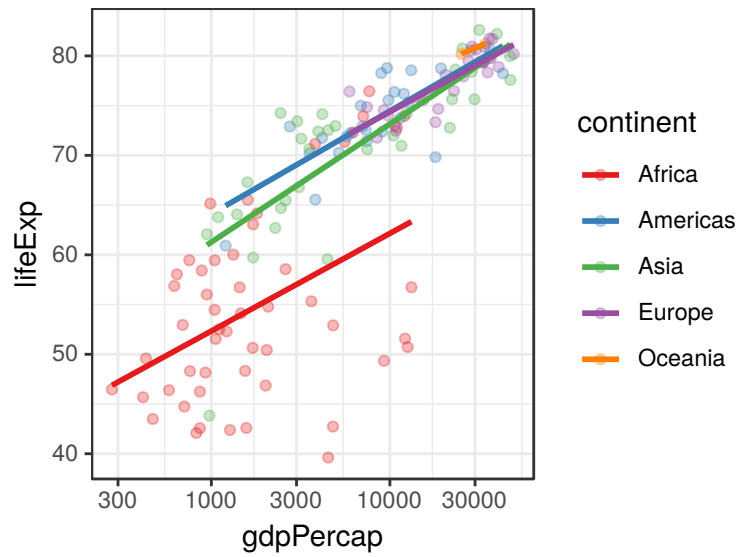
p
```



5.2 Scales

5.2.1 Logarithmic

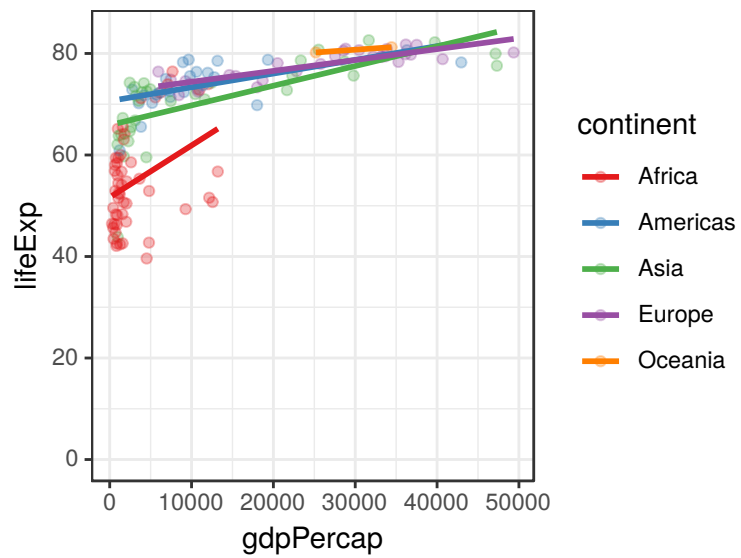
```
p +  
  scale_x_log10()
```



5.2.2 Expand limits

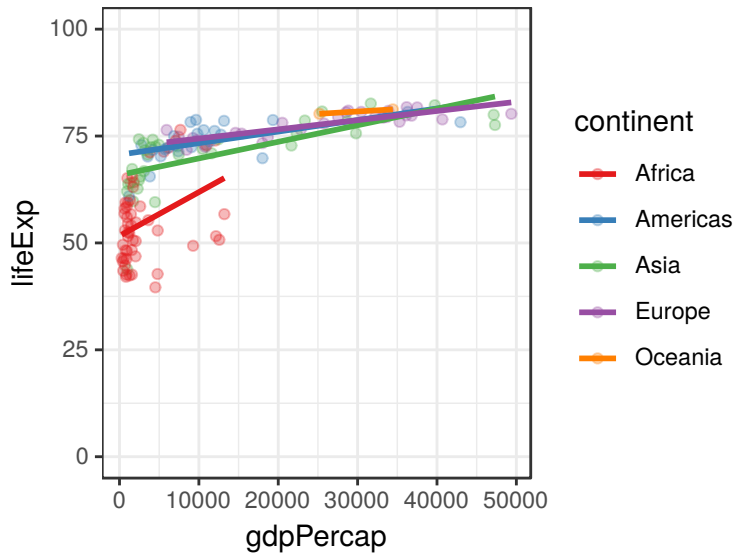
Specify the value you want to be included:

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



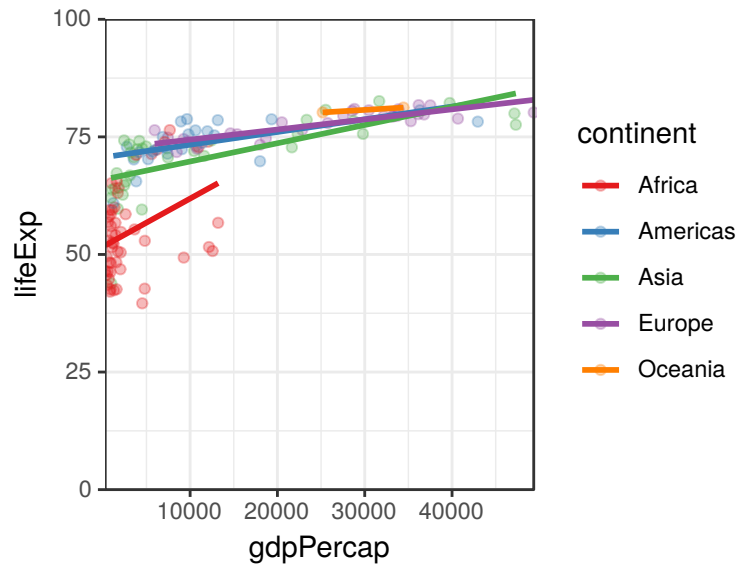
Or two:

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



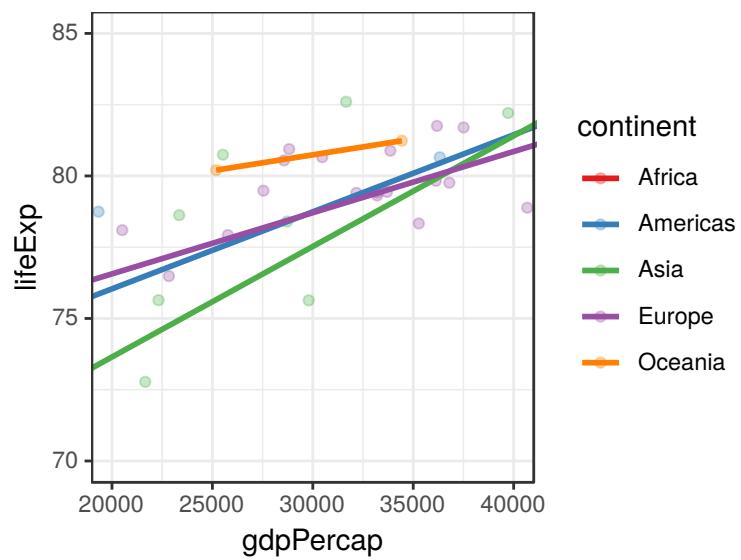
By default, `ggplot()` adds some padding around the included area (see how the scale doesn't start from 0, but slightly before). You can remove this padding with the `expand` option:

```
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))
```



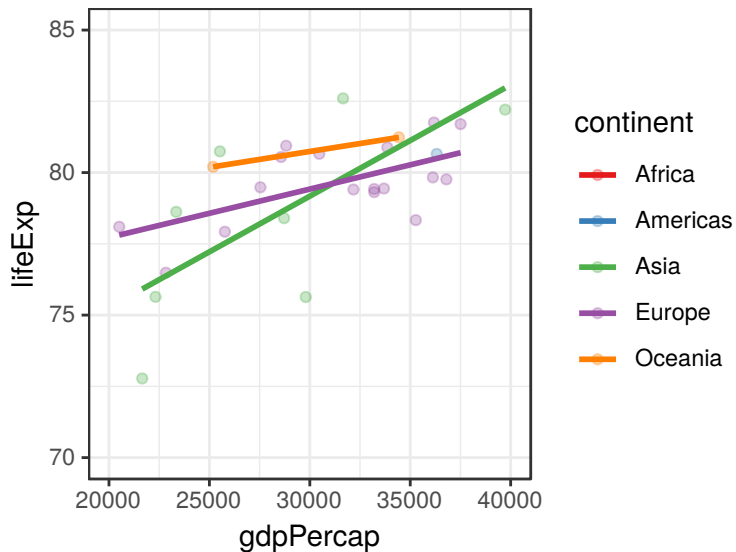
5.2.4 Exercise

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).
```

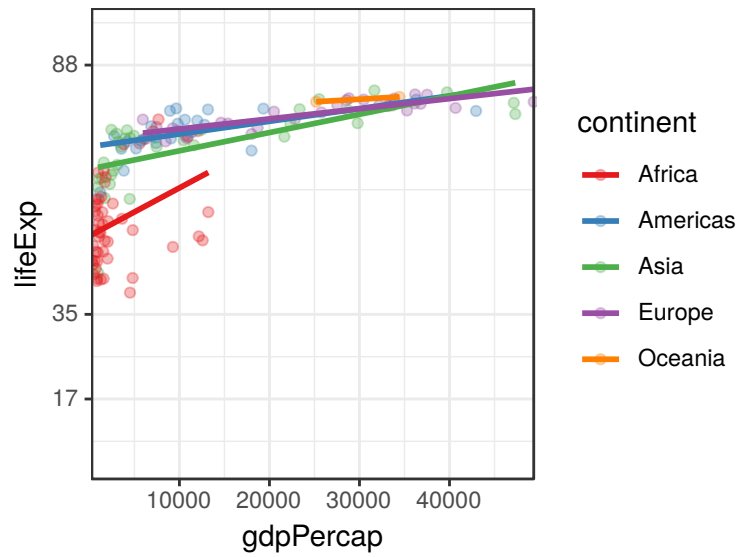
```
## Warning: Removed 114 rows containing missing values (geom_point).
```



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.

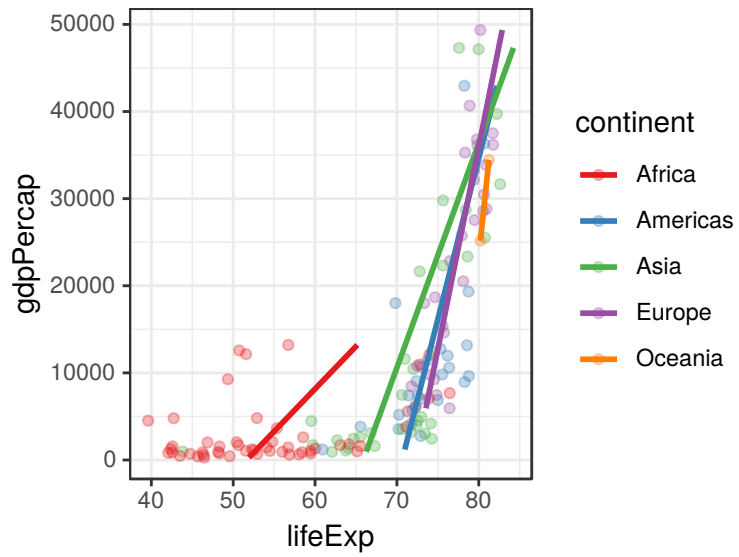
5.2.5 Axis ticks


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



5.2.6 Swap the axes

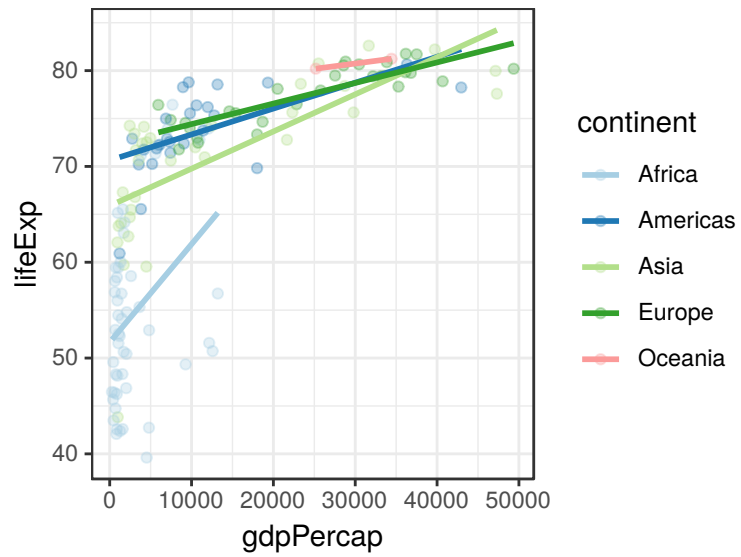
```
p +  
  coord_flip()
```



5.3 Colours

5.3.1 Using the Brewer palettes:

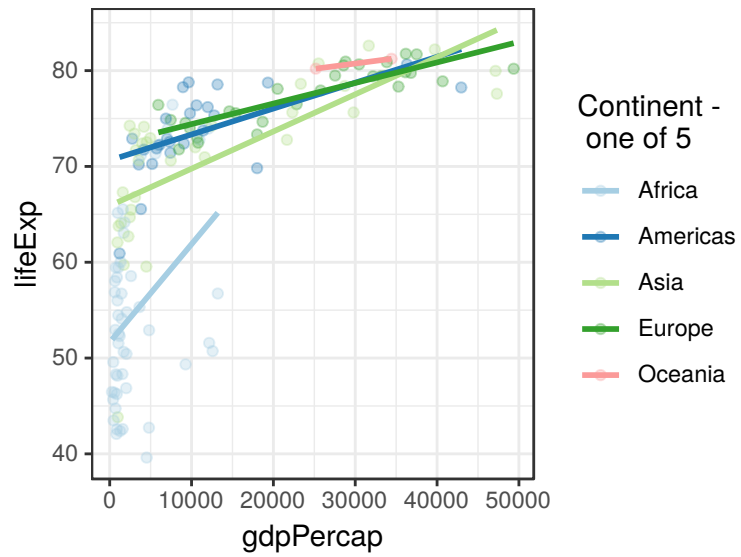
```
p +  
  scale_color_brewer(palette = "Paired")
```



5.3.2 Legend title

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

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

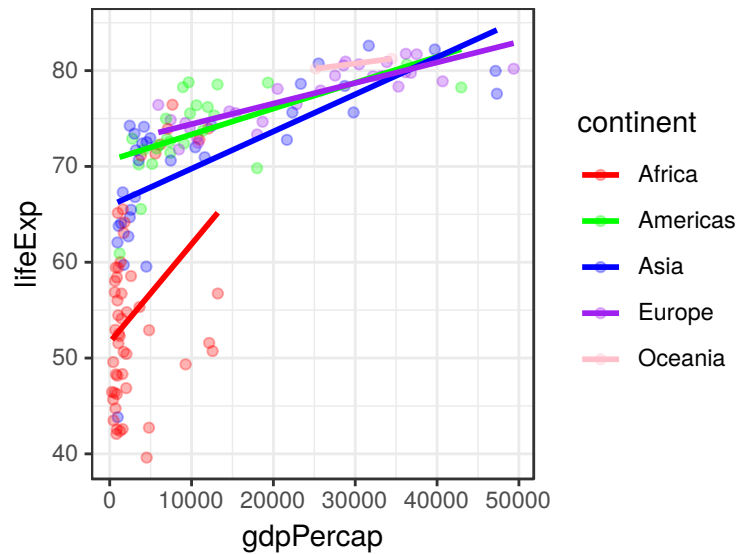


Note the `\n` inside the new legend title - new line.

5.3.3 Choosing colours manually

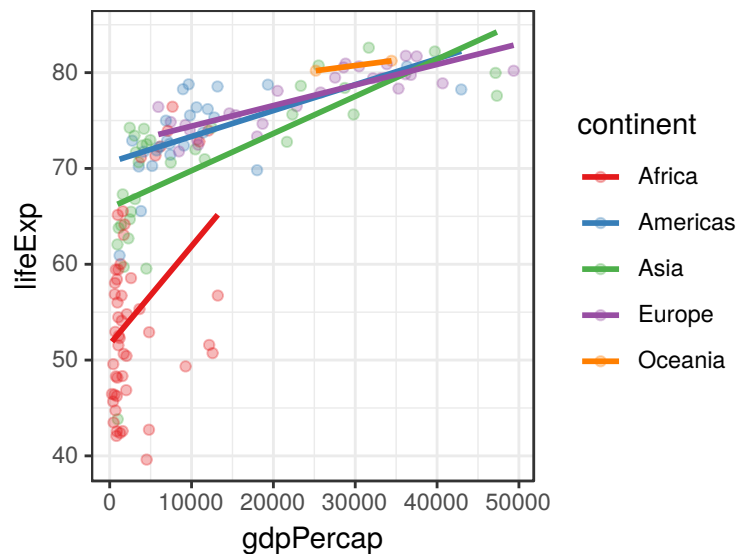
Use words:

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



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

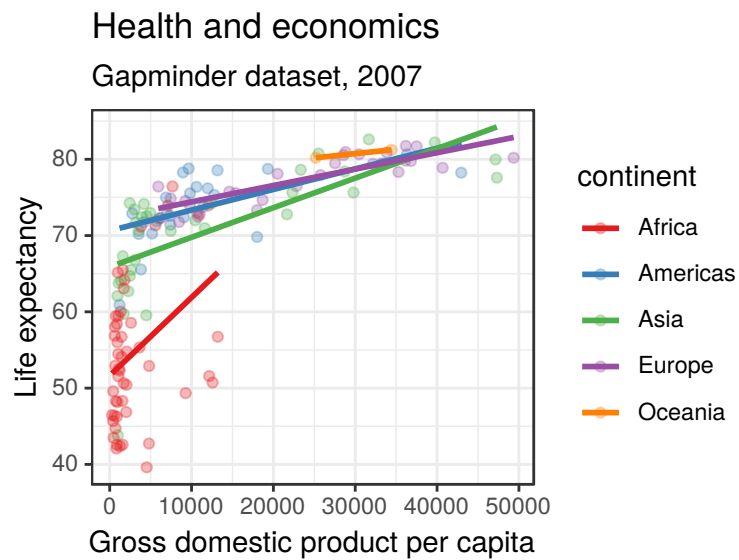
```
p +
  scale_color_manual(values = c("#e41a1c", "#377eb8", "#4daf4a", "#984ea3",
                                "#f781bf"))
```



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")
```

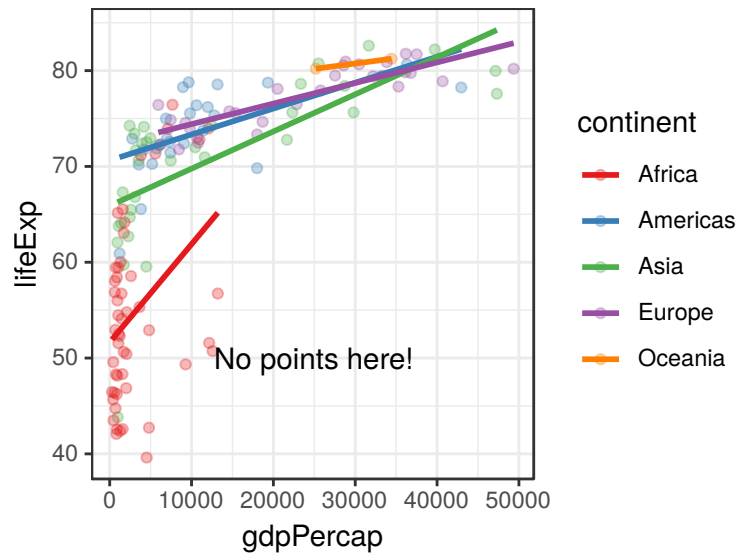


5.4.1 Annotation

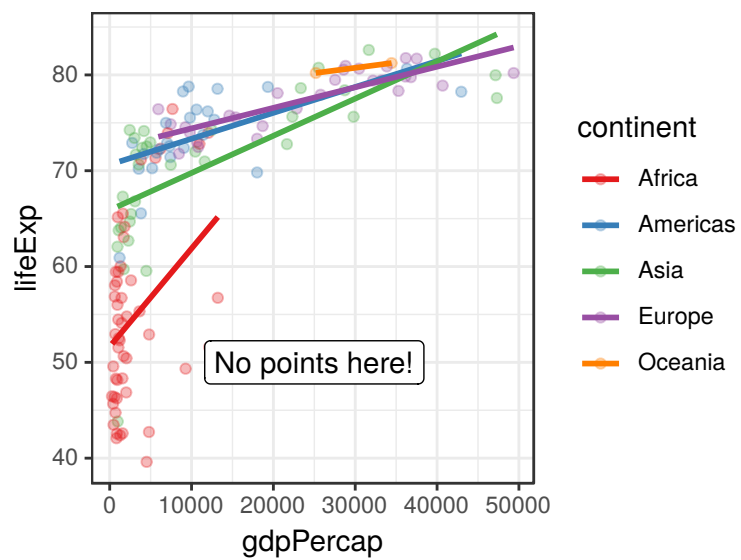
```
p +  
  annotate("text",  
          x = 25000,  
          y = 50,  
          label = "No points here!")
```

100

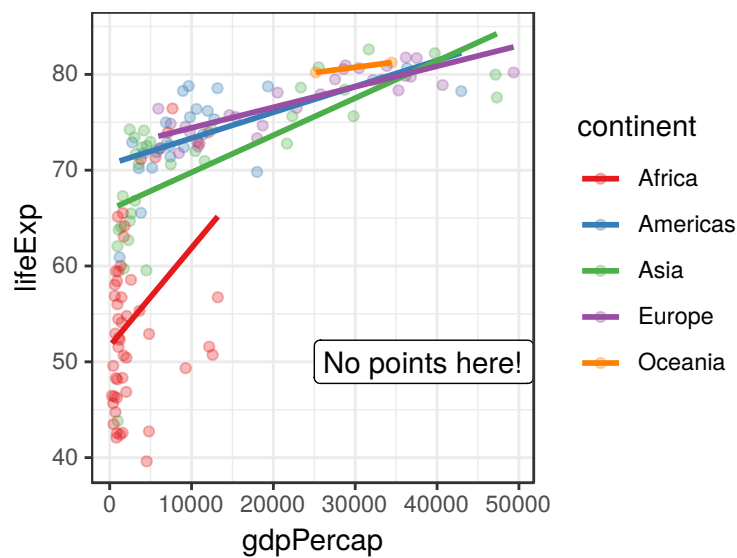
5 Fine tuning plots



```
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.

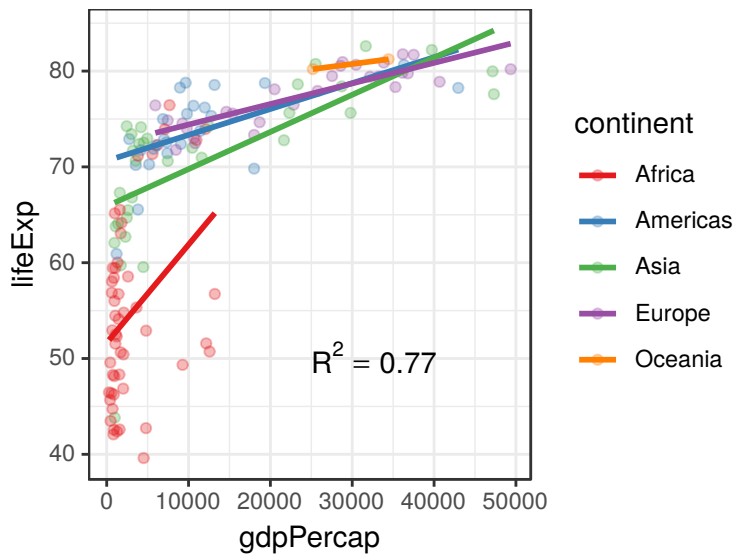
5.4.2 Annotation with a superscript and a variable

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

plot_rsquared = paste0(
  "R^2 == ",
```

```
fit_glance$r.squared %>% round(2))

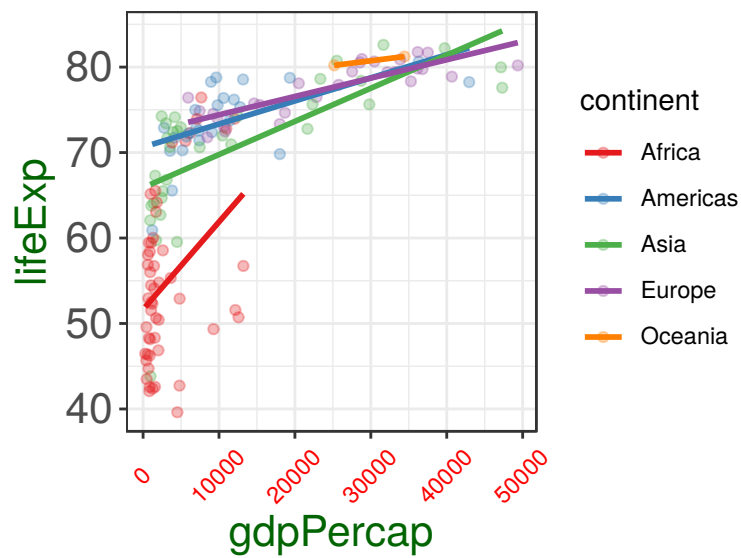
p +
  annotate("text",
    x = 25000,
    y = 50,
    label = plot_rsquared, parse = TRUE,
    hjust = 0)
```



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),
```

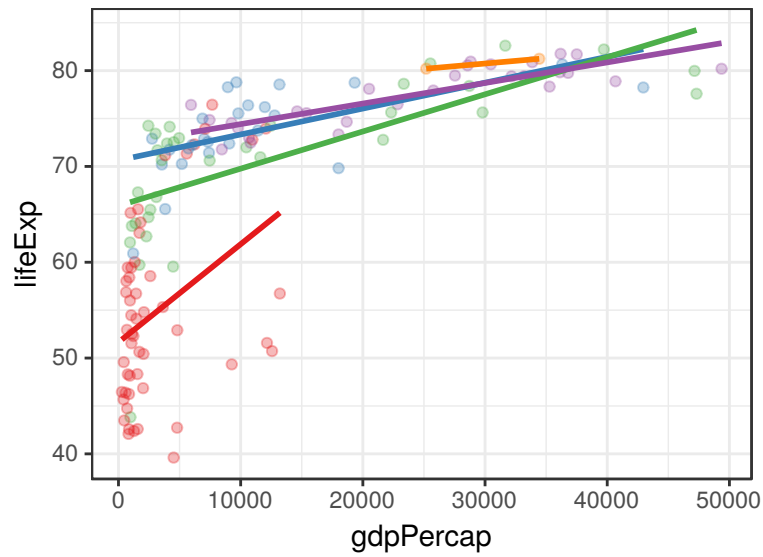
```
axis.title = element_text(size = 16, colour = "darkgreen")
)
```



5.5.1 Legend position

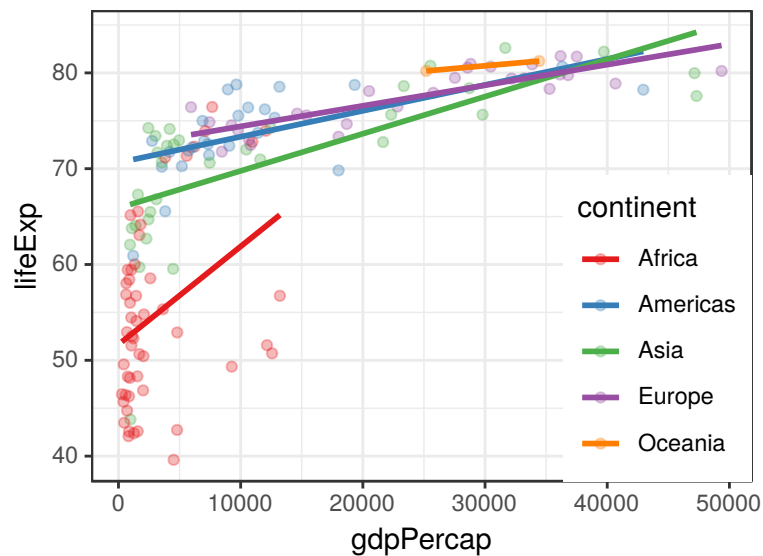
Use the following words: "right", "left", "top", "bottom", or "none" to remove the legend.

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

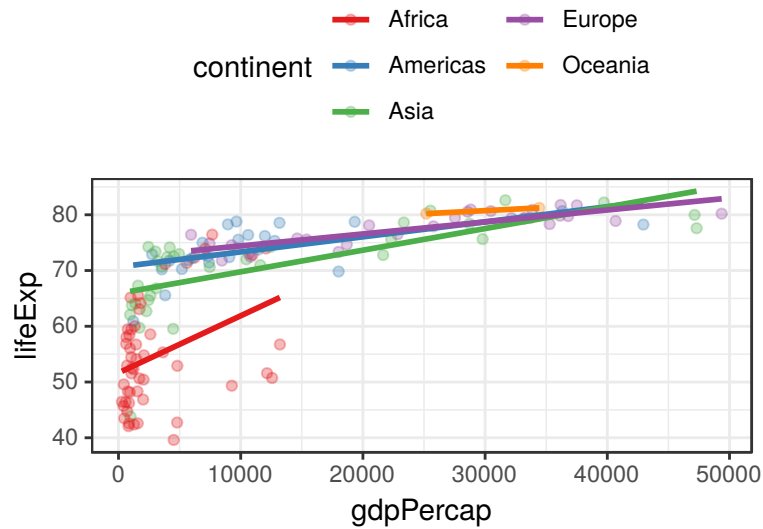


Or use relative coordinates (0–1) to give it an -y location:

```
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 project¹. 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 particularly 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

¹<https://www.gapminder.org/>

relatively advanced stage before research realised the dataset was incomplete.

```
glimpse(mydata)           # each variable on a single line, variable type, fi
```

```
## Observations: 1,704
## Variables: 6
## $ country  <fct> Afghanistan, Afghanistan, Afghanistan, Afghanistan, ...
## $ continent <fct> Asia, 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

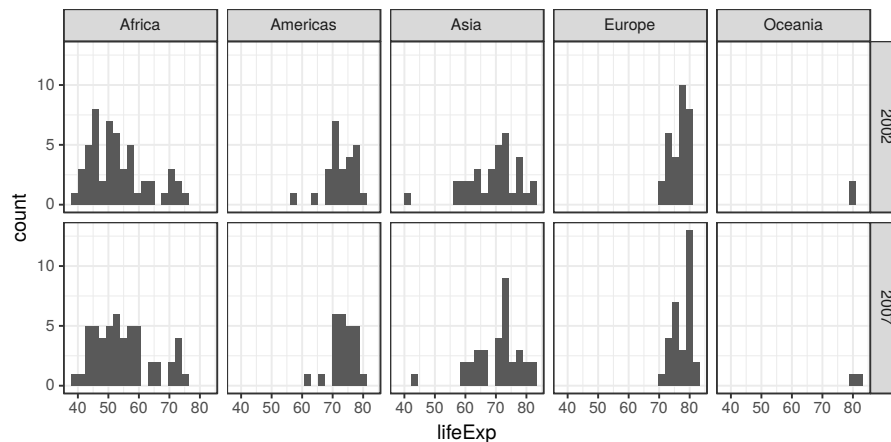
We will start by comparing life expectancy between the 5 continents of the world in two different years. Always plot your data first. Never skip this step! We are particularly interested in the distribution. There's that word again. The shape of the data. Is it normal? Is it skewed? Does it differ between 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)) %>% # only 2002 and 2007
  ggplot(aes(x = lifeExp)) +           # x-axis is life expectancy
  geom_histogram(bins = 20) +         # histogram with data chopped into
  facet_grid(year ~ continent)        # create grid of year by continent
```



```
# add scale = "free" to facet_grid to
```

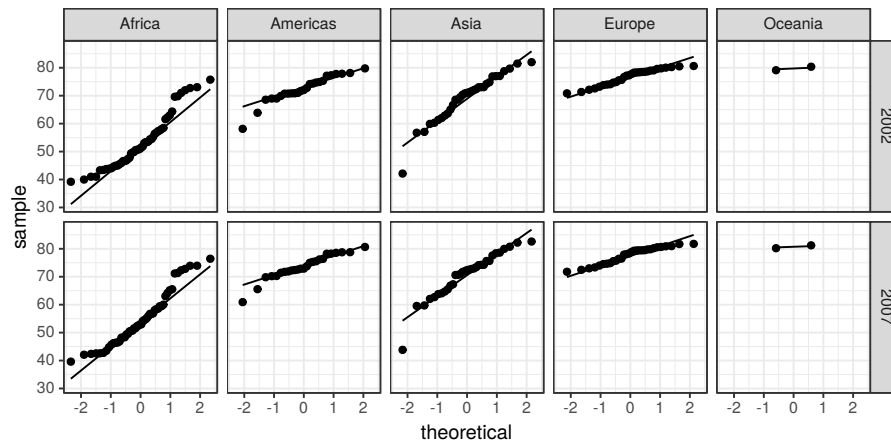
What can we see? That life expectancy in Africa is lower than in other regions. That we have little data for Oceania given there are only two countries included, Australia and New Zealand. That Africa and Asia have great variability in life expectancy by country than in the Americas or Europe. That the 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)) %>% # only 2002 and 2007
  ggplot(aes(sample = lifeExp)) +      # Q-Q plot requires `sample`, rather
  geom_qq() +                          # geom for qq plot, defaults to normal
  geom_qq_line() +                     # add 45 degree line
  facet_grid(year ~ continent)
```



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.

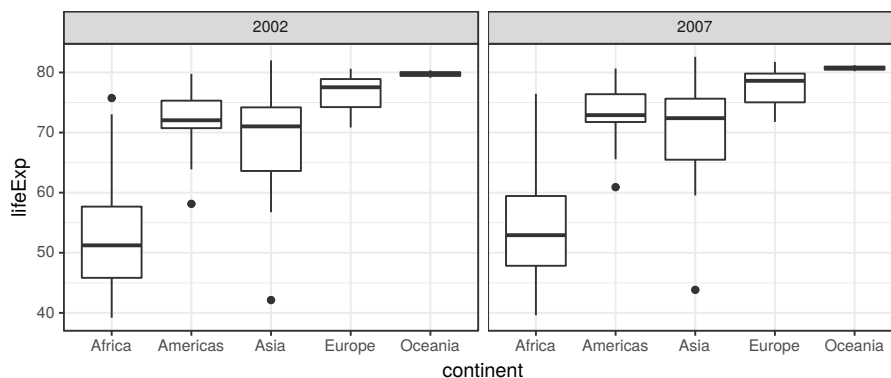
6.5.3 Boxplot

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 tendency (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)) %>%           # only 2002 and 2007
  ggplot(aes(x = continent, y = lifeExp)) +      # specify x and y axes, requires
  geom_boxplot() +                               # specify boxplot
  facet_grid(. ~ year)                          # spread by year, note `.`
```

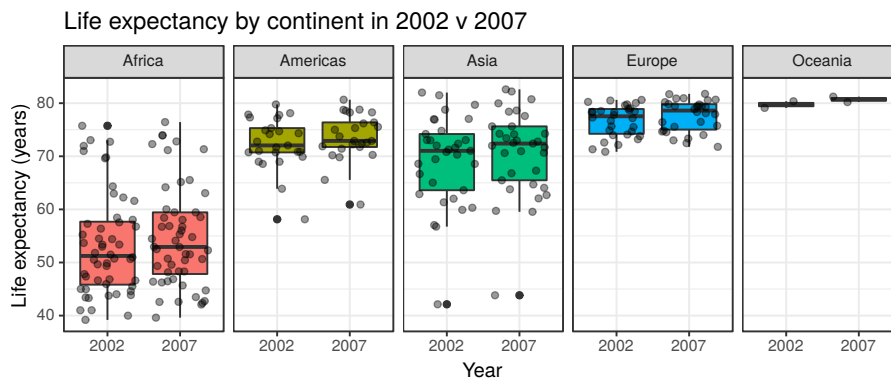


What can we see? The median life expectancy is lower in Africa than in any other continent. The variation in life expectancy is greatest in Africa and smallest in Oceania. The data in Africa looks skewed, particularly in 2002 - the lines/whiskers are unequal lengths.

We can add further arguments

```
mydata %>%
  filter(year %in% c(2002, 2007)) %>%
  ggplot(aes(x = factor(year), y = lifeExp)) +
  geom_boxplot(aes(fill = continent)) +
  geom_jitter(alpha = 0.4) +
  facet_grid(. ~ continent) +
  theme(legend.position = "none") +
  xlab("Year") +
  ylab("Life expectancy (years)") +
  ggtitle("Life expectancy by continent in 2002 v 2007")
```

only 2002 and 2007
specify x and y variables
add colour to boxplots
add data points, semi-transparent
spread by year, not continent
remove legend
adjust x-axis
adjust y-axis
add title



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 elsewhere, 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 %>%  
  filter(year == 2007) %>%  
  filter(continent %in% c("Asia", "Europe"))  
  
ttest_result =  
  t.test(lifeExp ~ continent, data = ttest_data)  
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" "alternative" "method" "data.name"
```

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

```
## List of 9
##  $ 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     : atomic [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"
```

```
## $ 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) %>% # Filter for 2007 only
  filter(continent %in% c("Asia", "Europe")) %>% # Filter for Asia and Europe
  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 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.

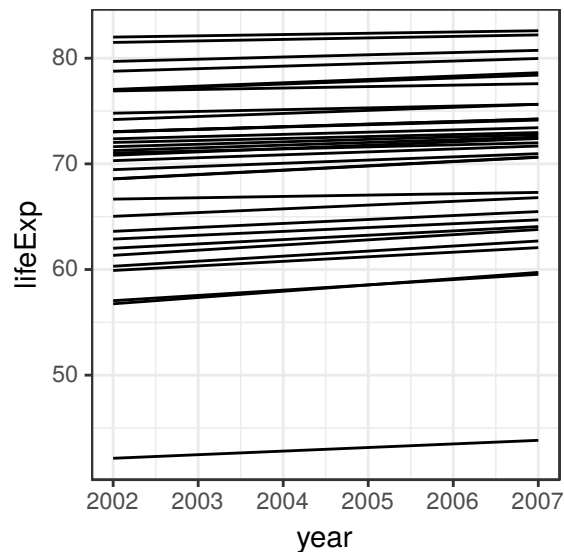
We can plot differences at the country level directly.

```

paired_data = mydata %>% # Save object with name paired_data
  filter(year %in% c(2002, 2007)) %>% # Filter for 2002 and 2007 only
  filter(continent == "Asia") # Filter for Asia

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

```



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 with name paired_data
  select(country, year, lifeExp) %>% # Select variables of interest
  spread(year, lifeExp) %>% # Make wide table
  mutate(
    dlifeExp = `2007` - `2002` # Calculate 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 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) %>%           # filter for 2007 only
  group_by(continent) %>%           # split data into chunks by continent
  do(                                # dplyr function useful in this setting
    t.test(.$lifeExp, mu = 77) %>%   # compare mean lifeExp for each continent
    tidy()                          # tidy into tibble
  )
```

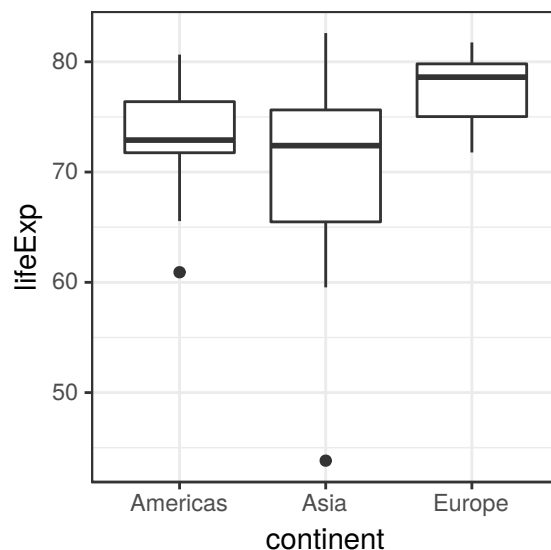
```
## # A tibble: 5 x 9
## # Groups:   continent [5]
##   continent estimate statistic p.value parameter conf.low conf.high method
##   <fct>      <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl> <chr>
## 1 Africa      54.8    -16.6  3.15e-22     51    52.1    57.5 One S~
## 2 Americas    73.6     -3.82 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. ### Plot the data

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



6.8.1 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.

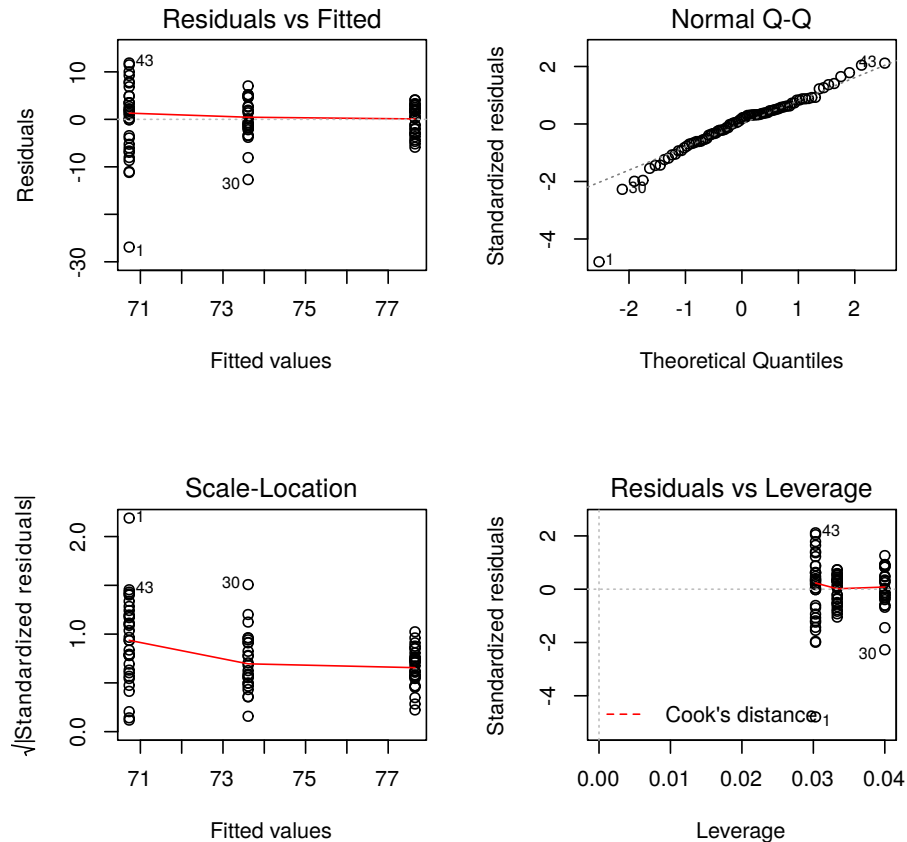
```
library(broom)
mydata %>%
  filter(year == 2007) %>%
  filter(continent %in% c("Americas", "Europe", "Asia")) %>%
  aov(lifeExp~continent, data = .) %>%
  tidy()
```

```
## # 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
```

6.8.2 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)
```



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

6.8.3 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 see 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 not 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 multiplied by 3 and the value compared to a threshold of 0.05, as is done above. The Bonferroni method is particularly conservative, meaning that type 2 errors may occur (failure to identify true differences, or false negatives) in favour of 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 %>%           # new object 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

```

```

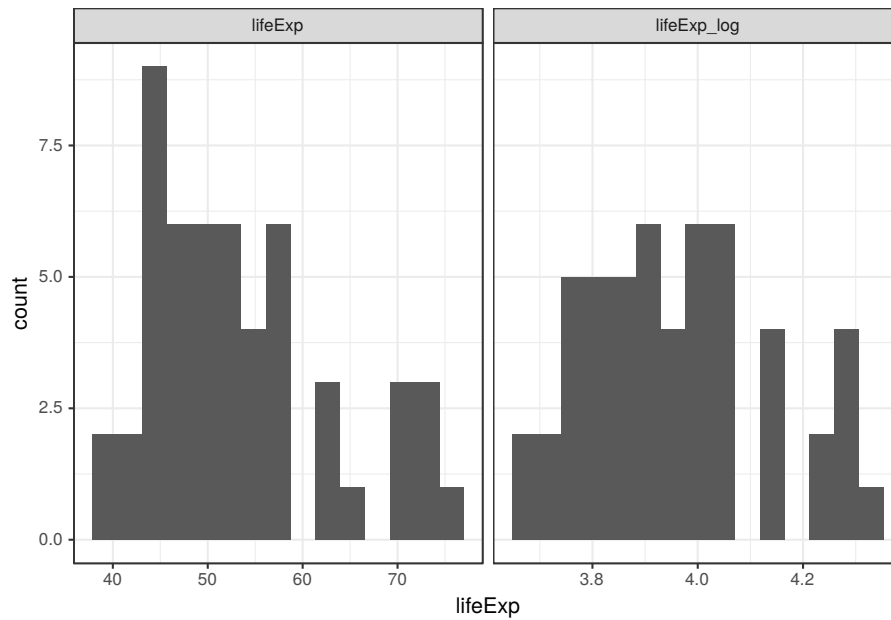
## # A tibble: 6 x 3
##   country      lifeExp lifeExp_log
##   <fct>        <dbl>     <dbl>
## 1 Algeria      71.0        4.26
## 2 Angola       41.0        3.71
## 3 Benin        54.4        4.00
## 4 Botswana     46.6        3.84
## 5 Burkina Faso 50.6        3.92
## 6 Burundi     47.4        3.86

```

```

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

```

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 it 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)) %>%           # Filter for 1982 and 2007
  filter(continent %in% c("Africa"))             # Filter for Africa only

p1 = africa_plot %>%                             # Plot saved as object p1
  ggplot(aes(x = lifeExp)) +
```

```

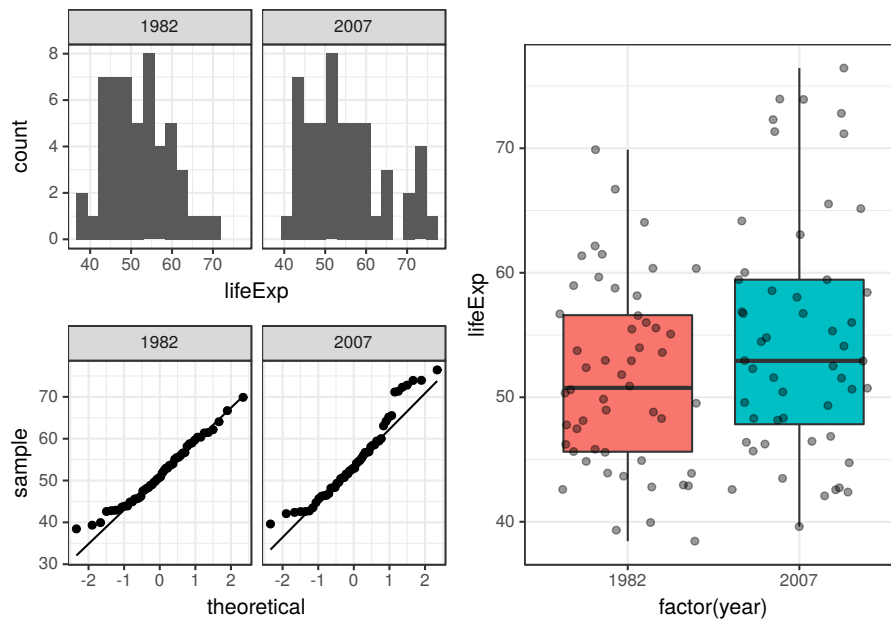
geom_histogram(bins = 15) +                               # bins can be adjusted based
facet_grid(. ~ year)

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

p3 = africa_plot %>%                                     # Plot saved as object p3
  ggplot(aes(x = factor(year), y = lifeExp)) +             # Year is numeric, specify
  geom_boxplot(aes(fill = factor(year))) +                 # Colour in boxplot
  geom_jitter(alpha = 0.4) +                               # Include individual data points
  theme(legend.position = "none")                          # Remove legend

library(patchwork)                                         # Great package for combining
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.

```
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)) %>%           # Filter for 1982 and 2007
  filter(continent == "Africa") %>%           # Filter for Africa only
  mutate(
    year = factor(year)                         # Change year to a factor
  ) %>%
  summary_factorlist(dependent, explanatory,
                      cont = "median", p = TRUE) %>%
  knitr::kable(row.names = FALSE,
               align = c("l", "l", "r", "r", "r", "r"))
```

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 be 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

```

# Exercise 1
## Make a histogram, Q-Q plot, and a box-plot for the life expectancy for a

asia_plot = mydata %>%
  filter(continent %in% c("Asia")) # Filter for Asia only

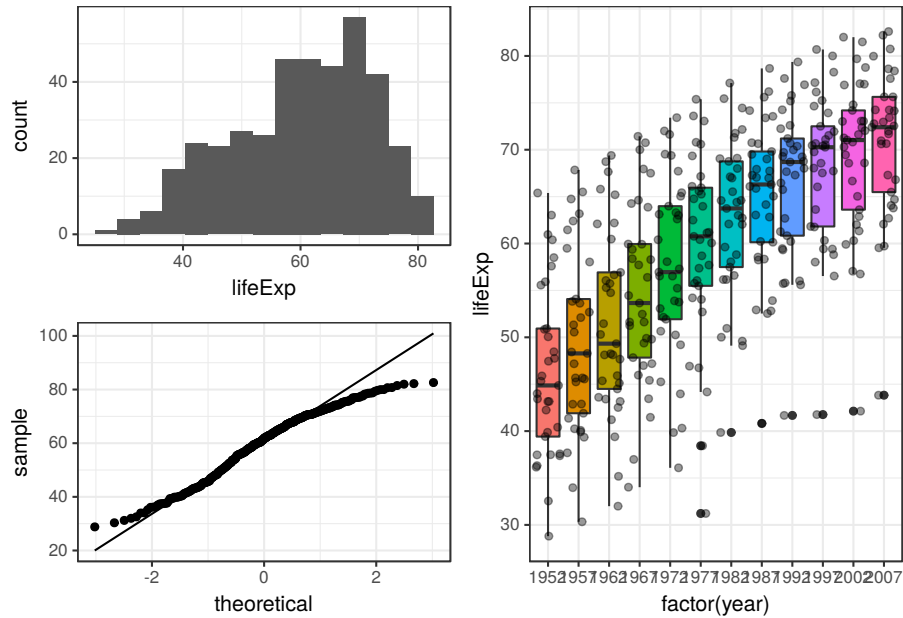
p1 = asia_plot %>% # Plot saved as object p1
  ggplot(aes(x = lifeExp)) +
  geom_histogram(bins = 15) #+ # bins can be adjusted base
  #facet_grid(. ~ year) # years, not included, so a

p2 = asia_plot %>% # Plot saved as object p2
  ggplot(aes(sample = lifeExp)) + # remember `sample` for Q-Q
  geom_qq() +
  geom_qq_line() #+
  #facet_grid(. ~ year) # years not included, so a

p3 = asia_plot %>% # Plot saved as object p3
  ggplot(aes(x = factor(year), y = lifeExp)) + # Year is numeric, specify
  geom_boxplot(aes(fill = factor(year))) + # Colour in boxplot
  geom_jitter(alpha = 0.4) + # Include individual data points
  theme(legend.position = "none") # Remove legend

library(patchwork) # Great package for combining plots
p1 / p2 | p3

```

*# Exercise 2*

*## Select any 2 years in any continent and perform a *t*-test to determine
Remember to plot your data first.*

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

*# filter for Asia only
filter for 1952 and 1972*

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

*# Plot saved as object p1
bins can be adjusted base*

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

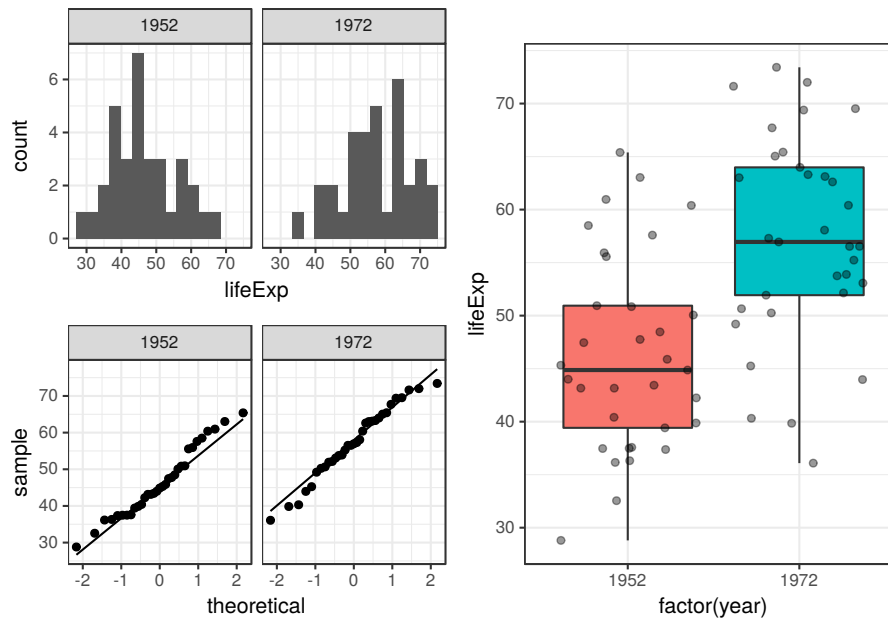
*# Plot saved as object p2
remember `sample` for Q-Q
years not included, so all*

```

p3 = asia_years %>%
  ggplot(aes(x = factor(year), y = lifeExp)) + # Plot saved as object p3
  geom_boxplot(aes(fill = factor(year))) + # Year is numeric, specify .
  geom_jitter(alpha = 0.4) + # Colour in boxplot
  theme(legend.position = "none") # Include individual data points
                                   # Remove legend

library(patchwork) # Great package for combining plots
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
```

Exercise 3

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

```
mydata %>%
```

```
  filter(year == 2007) %>%
```

```
  group_by(continent) %>%
```

```
  do(
```

```
    t.test(.$lifeExp, mu = 70) %>% tidy()
```

It's sometimes a little awkward

```
)
```

```
## # 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>
```

Exercise 4

Use Kruskal-Wallis to determine if the mean population changed significantly

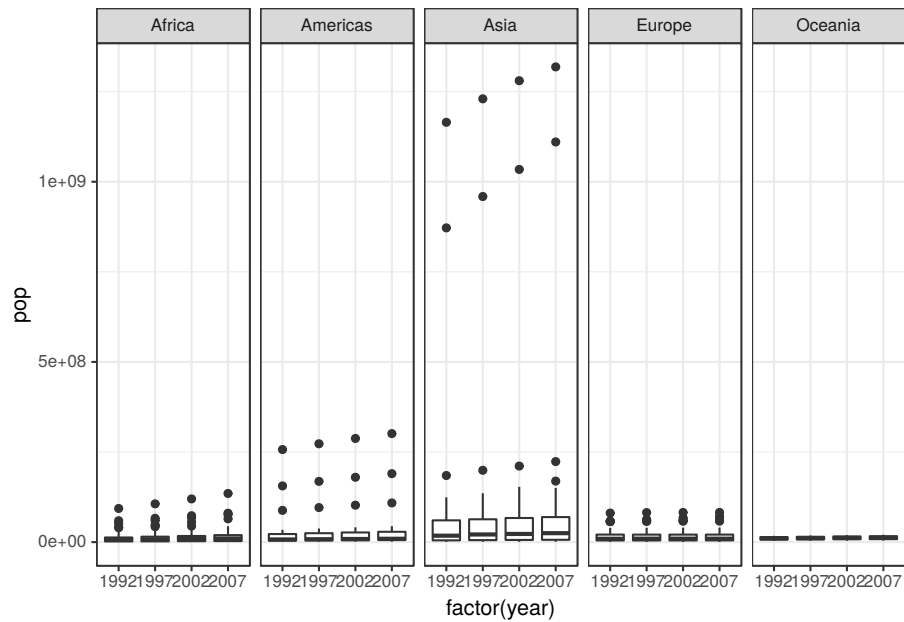
```
mydata %>%
```

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

```
  ggplot(aes(x = factor(year), y = pop)) +
```

```
  geom_boxplot() +
```

```
  facet_grid(. ~ continent)
```



```
mydata %>%
  filter(year >=1990) %>%
  group_by(continent) %>%
  do(
    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 Data

We will be using the same gapminder dataset as in the last two sessions.

```
library(tidyverse)
library(gapminder) # dataset
library(lubridate) # handles dates
library(broom)     # transforms statistical output to data frame

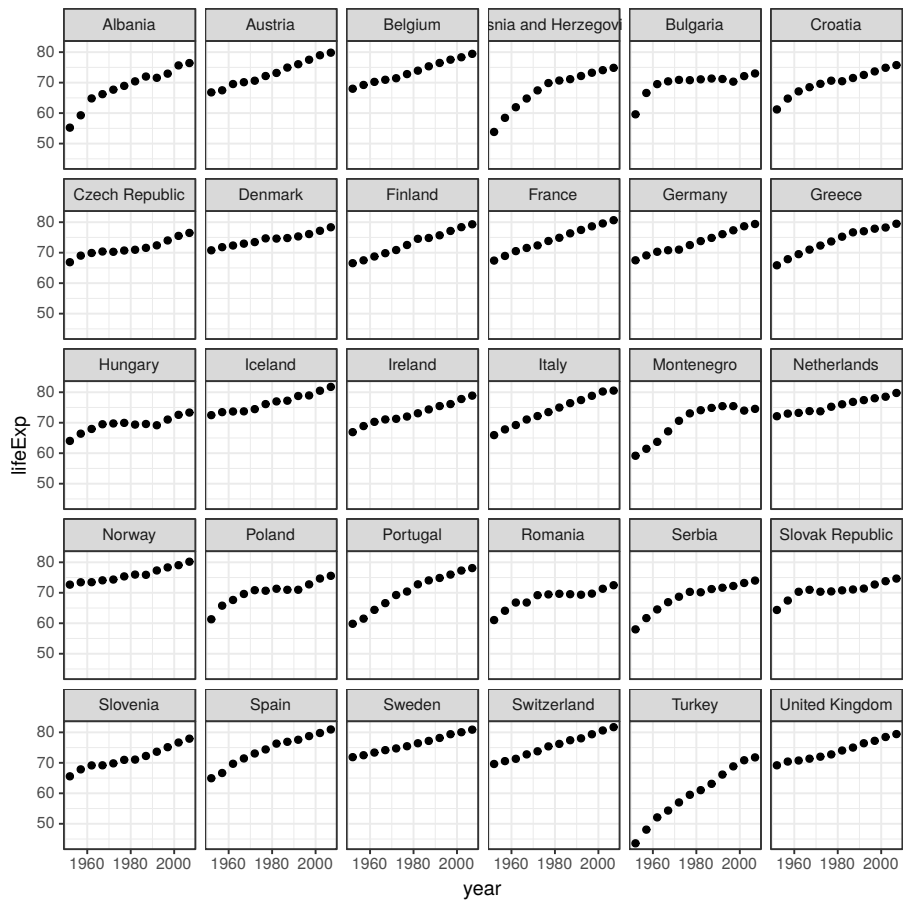
mydata = gapminder
```

7.2 Plotting

Let's plot the life expectancies in European countries over the past 60 years:

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

```
theme_bw() +
scale_x_continuous(breaks = c(1960, 1980, 2000))
```



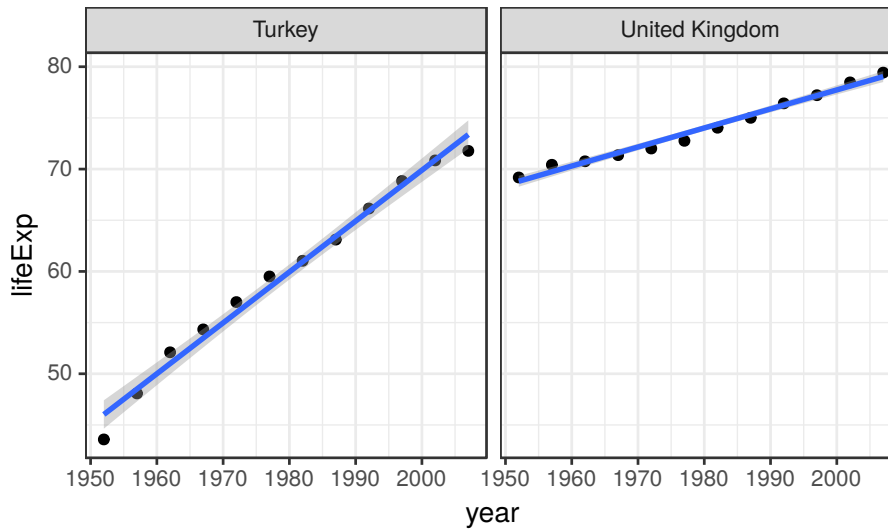
7.2.1 Exercise

Save the above filter into a new variable called `eurodata`:

```
eurodata = mydata %>%
  filter(continent == "Europe")
```

7.2.2 Exercise

Create the same plot as above (life expectancy over time), but for just Turkey and the United Kingdom, and add linear regression lines. Hint: use + `geom_smooth(method = "lm")` for the lines. `lm()` stands for linear model.



7.3 Simple linear regression

As you can see, `ggplot()` is very happy to run and plot linear regression for us. To access the results, however, we should save the full results of the linear regression models into variables in our Environment. We can then investigate the intercepts and the slope coefficients (linear increase per year):

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

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

```
fit_uk$coefficients
```

```
fit_turkey$coefficients
```

```
## (Intercept)      year  
## -294.1965876    0.1859657  
## (Intercept)      year  
## -924.5898865    0.4972399
```

7.3.1 Exercise

To make the intercepts more meaningful, add a new column called `year_from1952` and redo `fit_turkey` and `fit_uk` using `year_from1952` instead of `year`.

```
mydata$year_from1952 = mydata$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
```

```
fit_turkey$coefficients
```

```
## (Intercept) year_from1952
## 68.8085256 0.1859657
## (Intercept) year_from1952
## 46.0223205 0.4972399
```

7.3.2 Model information: `summary()`, `tidy()`, `glance()`

Accessing all other information about our regression model:

```
fit_uk %>% summary()
```

```
##
## Call:
## lm(formula = lifeExp ~ year_from1952, 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)  68.808526  0.240079  286.61 < 2e-16 ***
## year_from1952  0.185966  0.007394   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
```

```
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
```

```
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>
```

7.4 If you are new to linear regression

See these interactive Shiny apps provided by RStudio:

https://gallery.shinyapps.io/simple_regression/

https://gallery.shinyapps.io/multi_regression/

(`library(shiny)` is an R package for making your output interactive)

7.4.1 Exercise - Residuals

Open the first Shiny app (“Simple regression”). Move the sliders until the red lines (residuals*) turn green - this means you’ve made the line fit the points as well as possible. Look at the intercept and slope - discuss with your neighbour or a tutor what these numbers mean and how they affect the straight line on the plot.

*Residual is how far away each point (observation) is from the

linear regression line. (In this example it's the linear regression line, but residuals are relevant in many other contexts as well.)

7.5 Multiple linear regression

Multiple linear regression includes more than one predictor 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=eurodata)
```

Multiple linear regression (additive):

```
myfit = lm(lifeExp~year+country, data=eurodata)
```

Multiple linear regression (all interactions):

```
myfit = lm(lifeExp~year*country, data=eurodata)
```

These examples of multiple regression include two variables: `year` and `country`, but we could include more by just adding them with `+`.

7.5.1 Exercise

Open the second Shiny app (“Multiple regression”) and see how:

- In simple regression, there is only one intercept and slope for the whole dataset.
- Using the additive model (`lm(formula = y ~ x + group)`) the two lines (one for each group) have different intercepts but the same slope. However, the `lm()` summary seems to only include one line called “(Intercept)”, how to find the intercept for the second group of points?

- Using the interactive model (`lm(formula = y ~ x*group)`) the two lines have different intercepts and different slopes.

7.5.2 Exercise

Convince yourself that using an fully interactive multivariable model is similar to running several separate simple linear regression models. Remember that we calculate the life expectancy in 1952 (intercept) and improvement per year (slope) for Turkey and the United Kingdom:

```
fit_uk %>%
  tidy() %>%
  mutate(estimate = round(estimate, 2)) %>%
  select(term, estimate)
```

```
## # A tibble: 2 x 2
##   term          estimate
##   <chr>          <dbl>
## 1 (Intercept)    68.8
## 2 year_from1952  0.19
```

```
fit_turkey %>%
  tidy() %>%
  mutate(estimate = round(estimate, 2)) %>%
  select(term, estimate)
```

```
## # A tibble: 2 x 2
##   term          estimate
##   <chr>          <dbl>
## 1 (Intercept)    46.0
## 2 year_from1952  0.5
```

(The lines `tidy()`, `mutate()`, and `select()` are only included for neater presentation here, you can use `summary()` instead.)

We can do this together using `year_from1952*country` in the `lm()`:

```
mydata %>%
  filter(country %in% c("Turkey", "United Kingdom")) %>%
  lm(lifeExp ~ year_from1952*country, data = .) %>%
  tidy() %>%
  mutate(estimate = round(estimate, 2)) %>%
  select(term, estimate)
```

```
## # A tibble: 4 x 2
##   term                estimate
##   <chr>              <dbl>
## 1 (Intercept)        46.0
## 2 year_from1952       0.5
## 3 countryUnited Kingdom 22.8
## 4 year_from1952:countryUnited Kingdom -0.31
```

Now. It may seem like R has omitted Turkey but the values for Turkey are actually in the Intercept = 46.02 and in `year_from1952` = 0.50. Can you make out the intercept and slope for the UK? Are they the same as in the simple linear regression model?

7.5.3 Exercise

Add a third country (e.g. “Portugal”) to `filter(country %in% c("Turkey", "United Kingdom"))` in the above example. Do the results change?

7.5.4 Optional (Advanced) Exercise

Run separate linear regression models for every country in the dataset at the same time and putting it all in two neat dataframes (one for the coefficients, one for the summary statistics):

```

linfit_coefficients = mydata %>%
  group_by(country) %>%
  do(
    tidy(
      lm(lifeExp~year, data=.)
    )
  )

linfit_overall = mydata %>%
  group_by(country) %>%
  do(
    glance(
      lm(lifeExp~year, data=.)
    )
  )

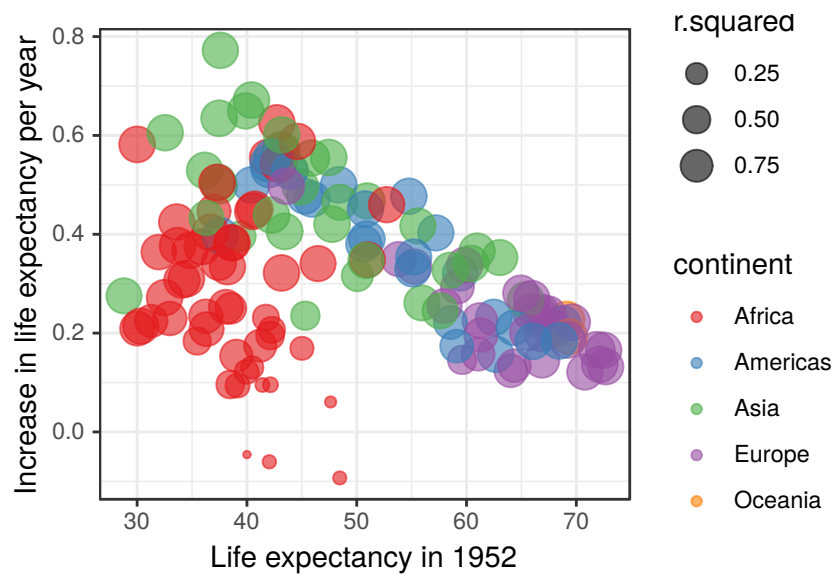
```

Plot the linear regression estimate (improvement per year between 1952 – 2007), size the points by their r-squared values, and colour the points by continent (hint: you will have to join `mydata`, `linfit_coefficients` %>% `filter(term == "year")`, and `linfit_overall`):

```

mydata %>%
  filter(year == 1952) %>%
  full_join(linfit_coefficients %>% filter(term == "year"), by = "country")
  full_join(linfit_overall, by = "country") %>%
  ggplot(aes(x = lifeExp, y = estimate, colour = continent, size = r.squared)) +
  geom_point(alpha = 0.6) +
  theme_bw() +
  scale_colour_brewer(palette = "Set1") +
  ylab("Increase in life expectancy per year") +
  xlab("Life expectancy in 1952")

```



7.6 Very advanced example

Or you can do the above in a nested tibble/data frame:

```
nested_linreg = mydata %>%
  group_by(country) %>%
  nest() %>%
  mutate(model = purrr::map(data, ~ lm(lifeExp ~ year, data = .)))
```

7.7 Solutions

6.2.2

```
mydata %>%  
  filter(country %in% c("United Kingdom", "Turkey")) %>%  
  ggplot(aes(x = year.formatted, y = lifeExp)) +  
  geom_point() +  
  facet_wrap(~country) +  
  theme_bw() +  
  geom_smooth(method = "lm")
```

6.5.3

```
mydata %>%  
  filter(country %in% c("Turkey", "United Kingdom", "Portugal")) %>%  
  lm(lifeExp ~ year_from1952*country, data = .) %>%  
  tidy() %>%  
  mutate(estimate = round(estimate, 2)) %>%  
  select(term, estimate)
```

Overall, the estimates for Turkey and the UK do not change, but Portugal becomes the reference (alphabetically first) to which you can subtract or add the relevant lines for Turkey and the UK.

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)
mydata = boot::melanoma
```

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$status %>%
  factor() %>%
  fct_recode("Died" = "1",
            "Alive" = "2",
            "Died - other causes" = "3") %>%
  fct_relevel("Alive") -> # move Alive to front (first factor level)
mydata$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

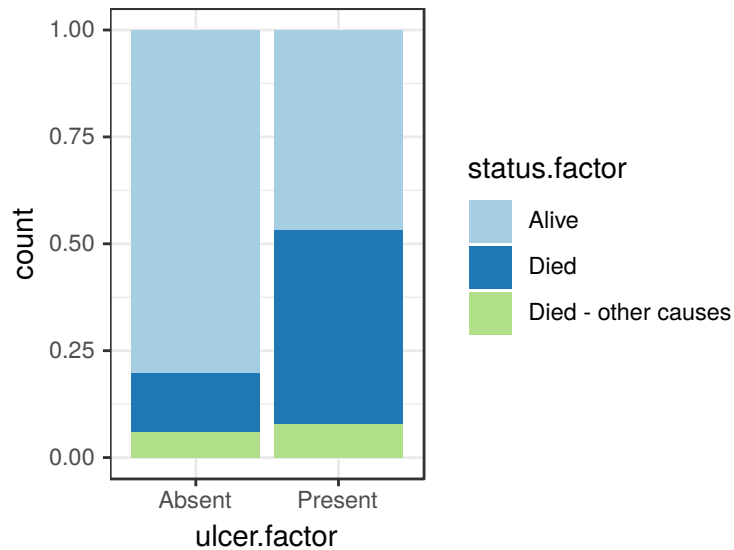
#the cut() function makes a continuous variable into a categorical variable
mydata$age %>%
  cut(breaks = c(4,20,40,60,95), include.lowest=TRUE) ->
mydata$age.factor
```

8.2 Chi-squared test / Fisher's exact test

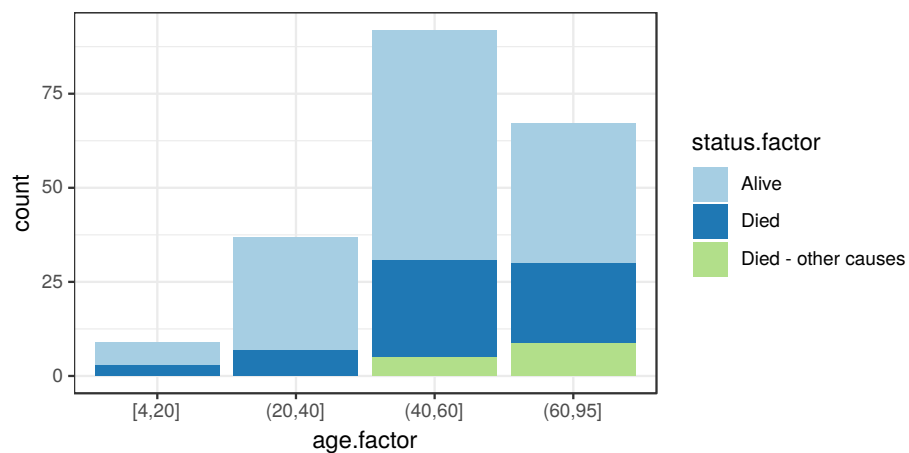
8.2.1 Plotting

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")
```

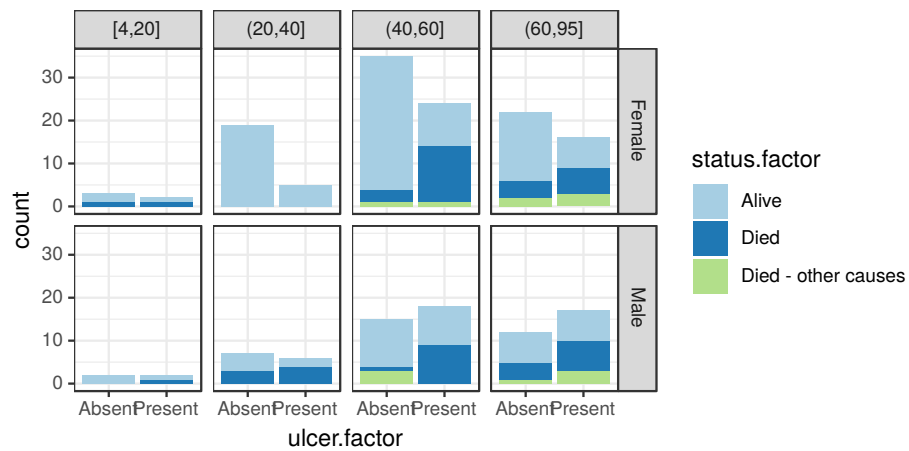



```
mydata %>%
  ggplot(aes(x = age.factor, fill = status.factor)) +
  geom_bar() +
  theme_bw() +
  scale_fill_brewer(palette = "Paired")
```



```
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 let's 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 it 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.

```
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 variables.

```
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,`

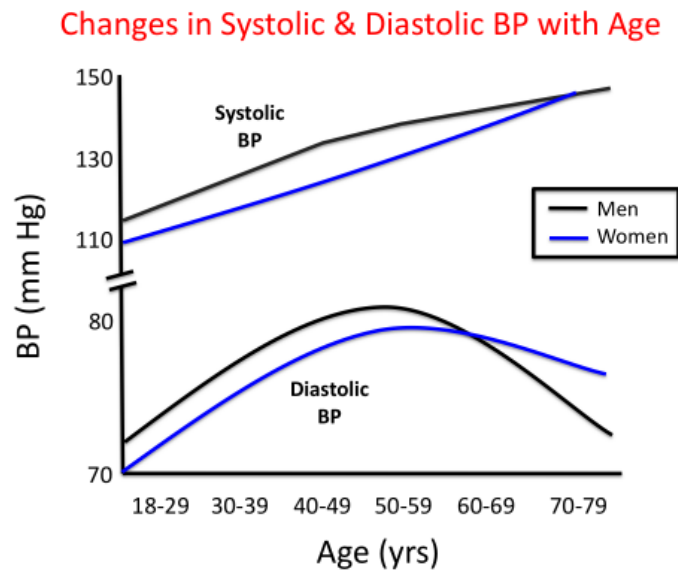


9

Logistic regression

9.1 What is Logistic Regression?

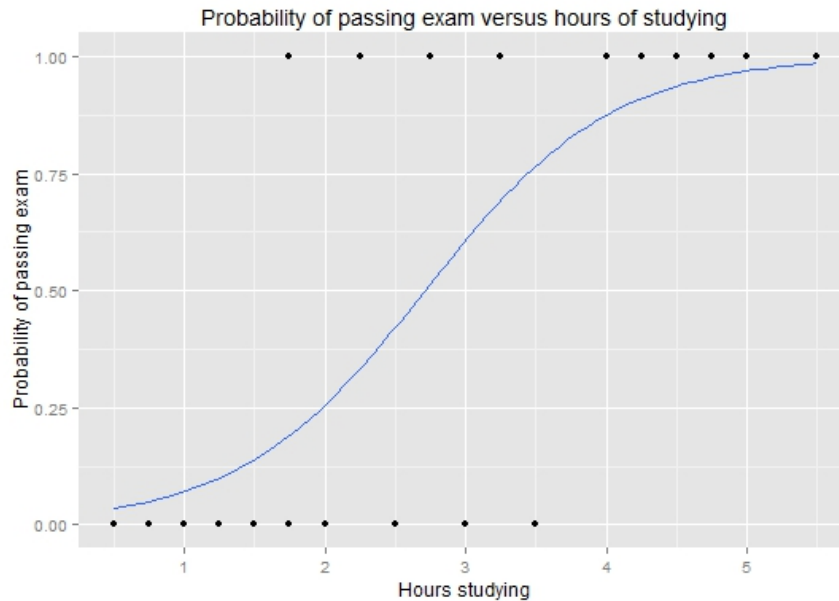
As we have seen in previously, regression analysis is a statistical process for estimating the relationships between variables. For instance, we may try to predict the blood pressure of a group of patients based on their age. As age and blood pressure are on a continuous scale, this is an example of 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 regres-

sion, 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 occurring.



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”.

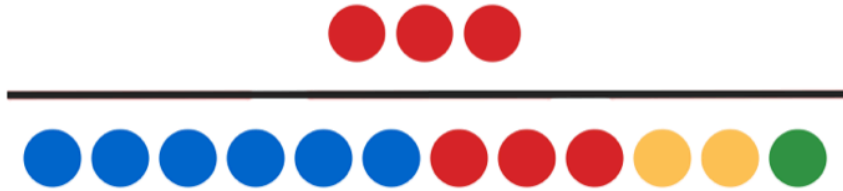
(**Multivariate** - technically means more than one **Dependent variable** (we will not discuss this type of analysis), but very often used interchangeably with **Multivariable**.)

9.3 Odds and probabilities

Odds and probabilities can get confusing so let’s get them straight:

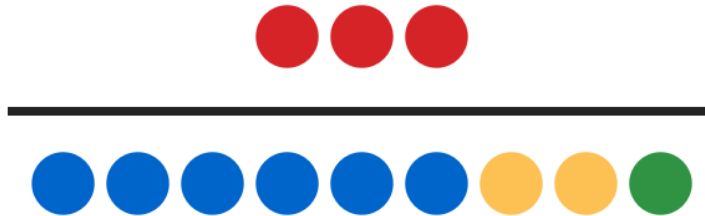
Probability of Red

$$3/12 = 1/4$$



Odds For Red

$$3/9 = 1/3$$



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 occurring (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 occurring (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.

Cancer: Yes	a	b	Odds cancer Male = a / c
Cancer: No	c	d	Odds cancer Female = b / d
	Sex: Male	Sex: Female	Odds of cancer male vs. female $\frac{a/c}{b/d}$ Odds ratio

An alternative is a ratio of probabilities, 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 aggressive 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 logisitc 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()
```

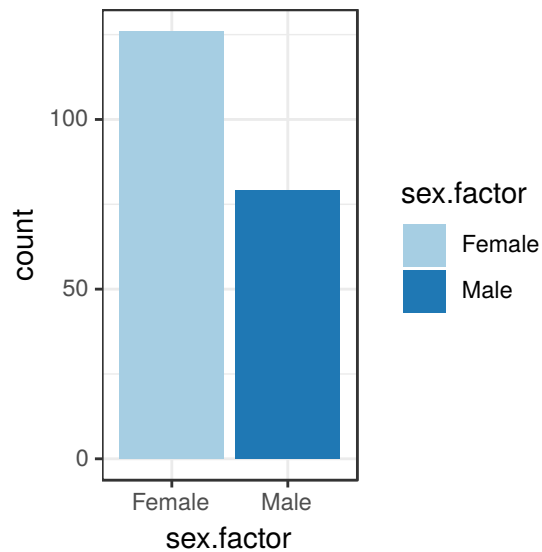
```
## [1] "[0,0.5]" "(0.5,1]" "(1,4]" "(4,17.4]"
```

```
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()
```

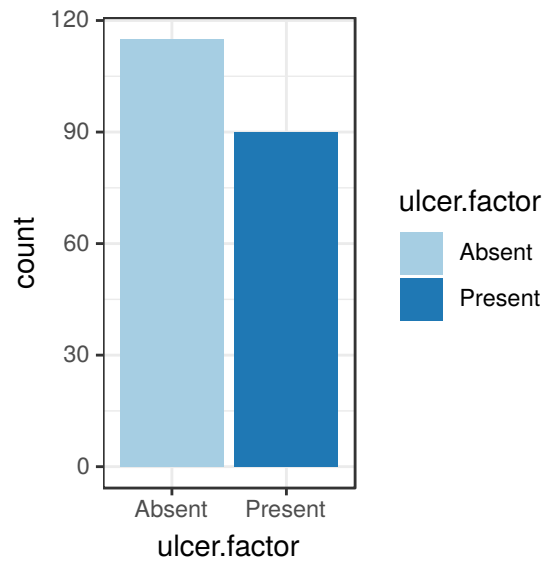
```
## [1] "Stage I" "Stage II" "Stage III" "Stage IV"
```

9.6.2 Always plot your data first!

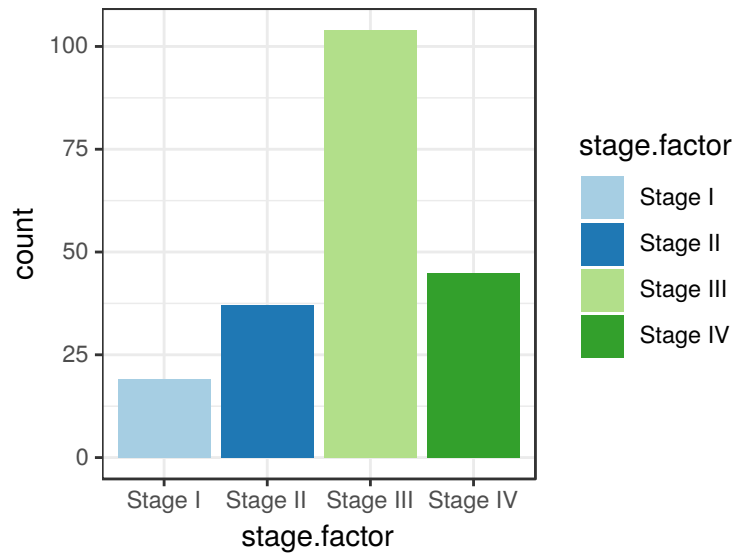
```
source("1_source_theme.R")  
  
mydata %>%  
  ggplot(aes(x = sex.factor)) +  
  geom_bar(aes(fill = sex.factor))
```



```
mydata %>%  
  ggplot(aes(x = ulcer.factor)) +  
  geom_bar(aes(fill = ulcer.factor))
```

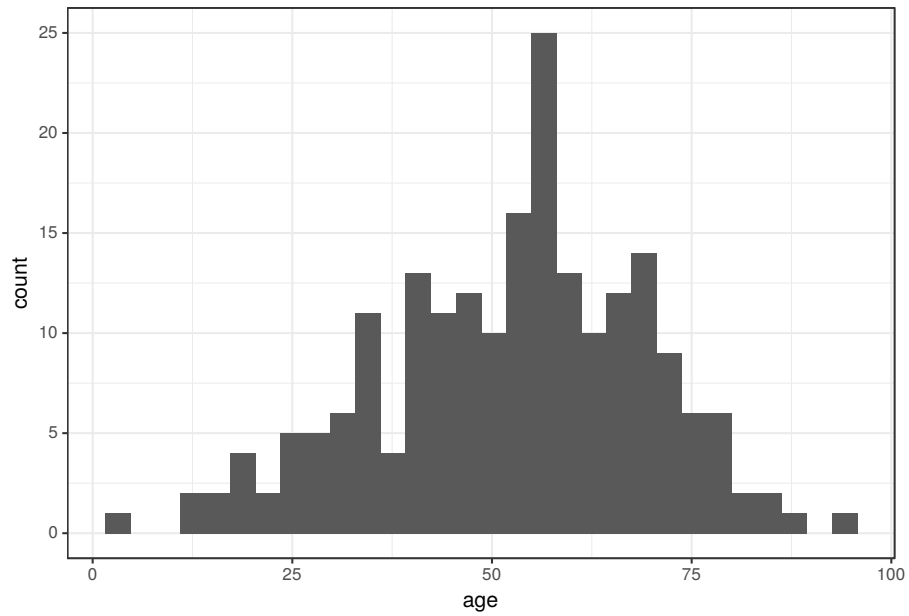


```
mydata %>%  
  ggplot(aes(x = stage.factor)) +  
  geom_bar(aes(fill = stage.factor))
```



```
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, particularly:

`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 (univariable)
sex.factor	Female	98 (66.2)	28 (49.1)	
	Male	50 (33.8)	29 (50.9)	2.03 (1.09-3.79, p=0.023)

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)
```

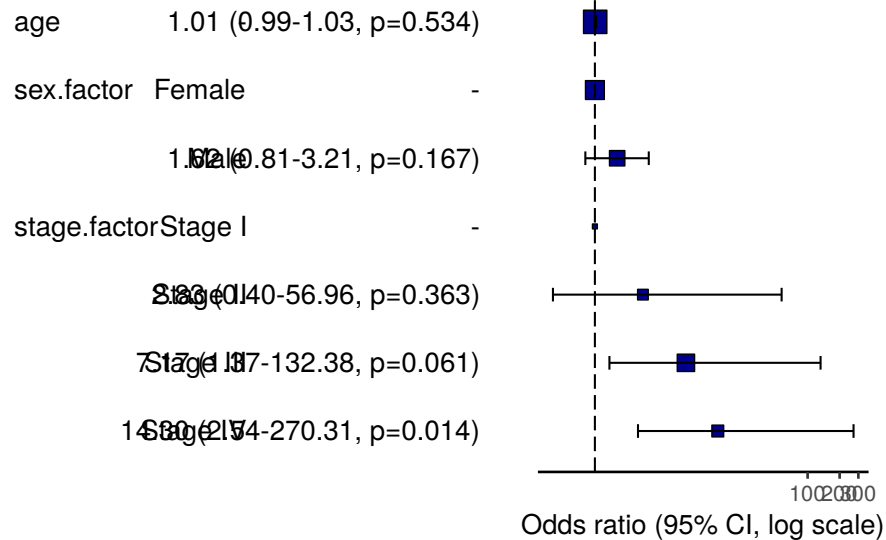
Dependent: died_melanoma.factor		No	Yes	OR
age	Mean (SD)	51.5 (16.1)	55.1 (17.9)	1.01 (0.99-1.02)
sex.factor	Female	98 (66.2)	28 (49.1)	
	Male	50 (33.8)	29 (50.9)	2.03 (1.09-3.81)
stage.factor	Stage I	18 (12.2)	1 (1.8)	
	Stage II	32 (21.6)	5 (8.8)	2.81 (0.41-56.1)
	Stage III	75 (50.7)	29 (50.9)	6.96 (1.34-128.1)
	Stage IV	23 (15.5)	22 (38.6)	17.22 (3.13-322.1)

```
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).
```

died_melanoma.factor: OR (95% CI, p-value)



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`.

Now we have our preliminary model. We could leave it there.

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 AIC measure model fit with lower values indicating better fit.

```
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

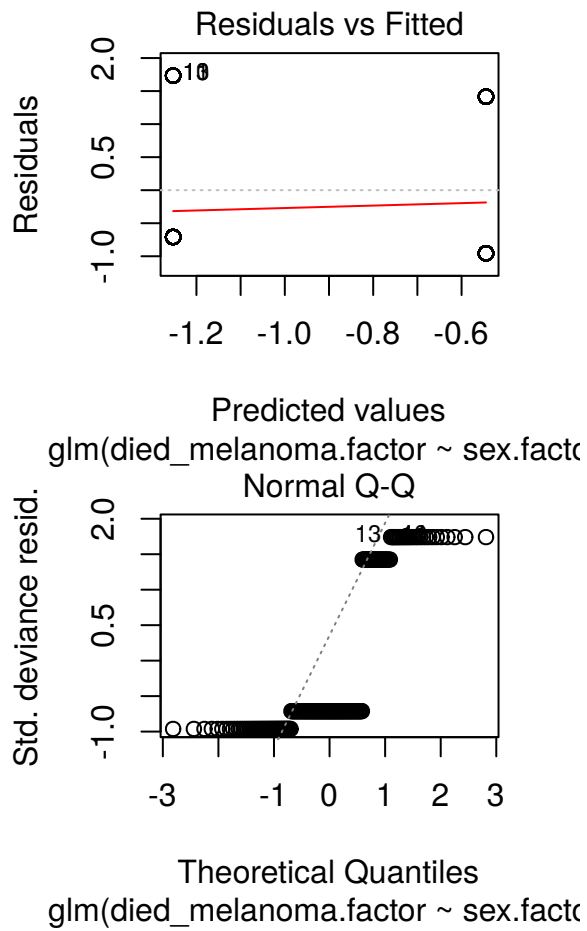
## [[1]]
##   Dependent: died_melanoma.factor      No      Yes
## 1              age Mean (SD) 51.5 (16.1) 55.1 (17.9)
## 2              sex.factor   Female  98 (66.2)  28 (49.1)
## 3                      Male   50 (33.8)  29 (50.9)
## 4              stage.factor Stage I  18 (12.2)   1 (1.8)
## 5                      Stage II  32 (21.6)   5 (8.8)
```

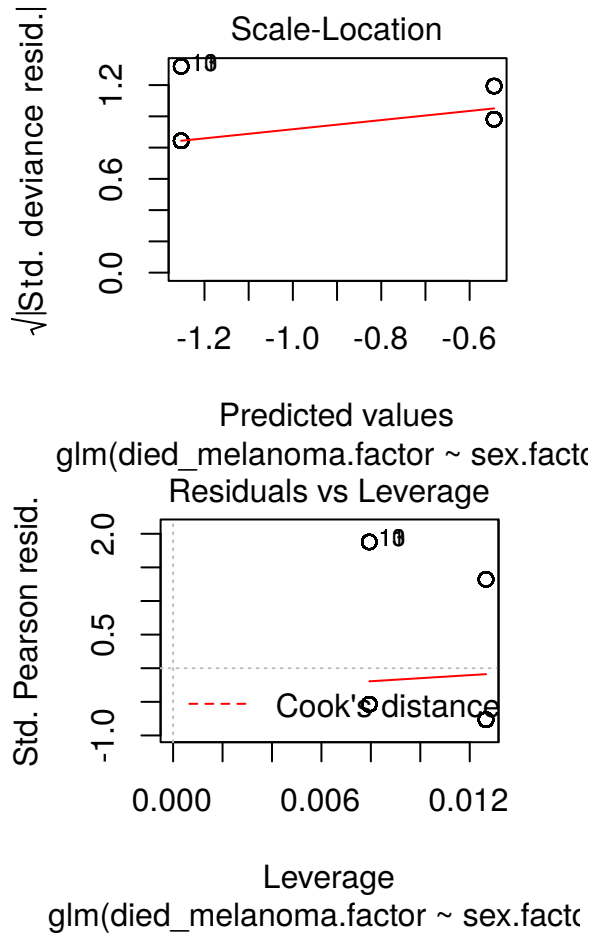
```
## 6          Stage III  75 (50.7)  29 (50.9)
## 7          Stage IV  23 (15.5)  22 (38.6)
##          OR (univariable)      OR (multivariable)
## 1    1.01 (0.99-1.03, p=0.163)  1.01 (0.99-1.03, p=0.534)
## 2          -                      -
## 3    2.03 (1.09-3.79, p=0.025)  1.62 (0.81-3.21, p=0.167)
## 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"
```

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)
```



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 cause"
# 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
```

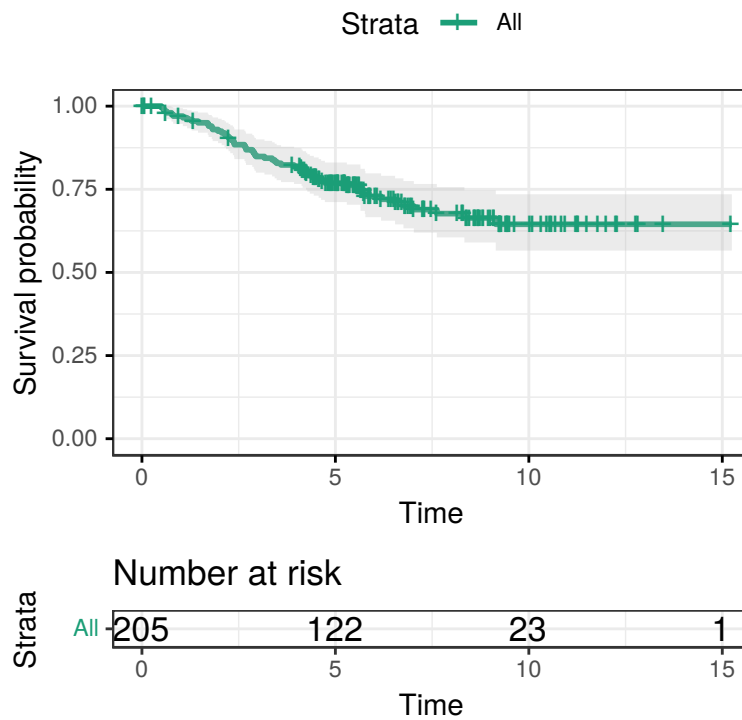
```
help(summary.survfit)
```

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
```

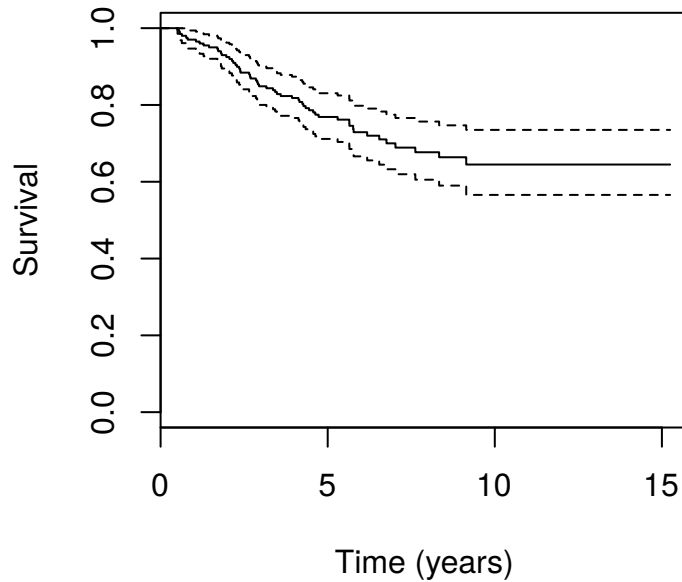


```
# Note can also take `ggplot()` options.
my_survplot$plot +
  annotate('text', x = 5, y = 0.25, label='Whole cohort')
```

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")
```

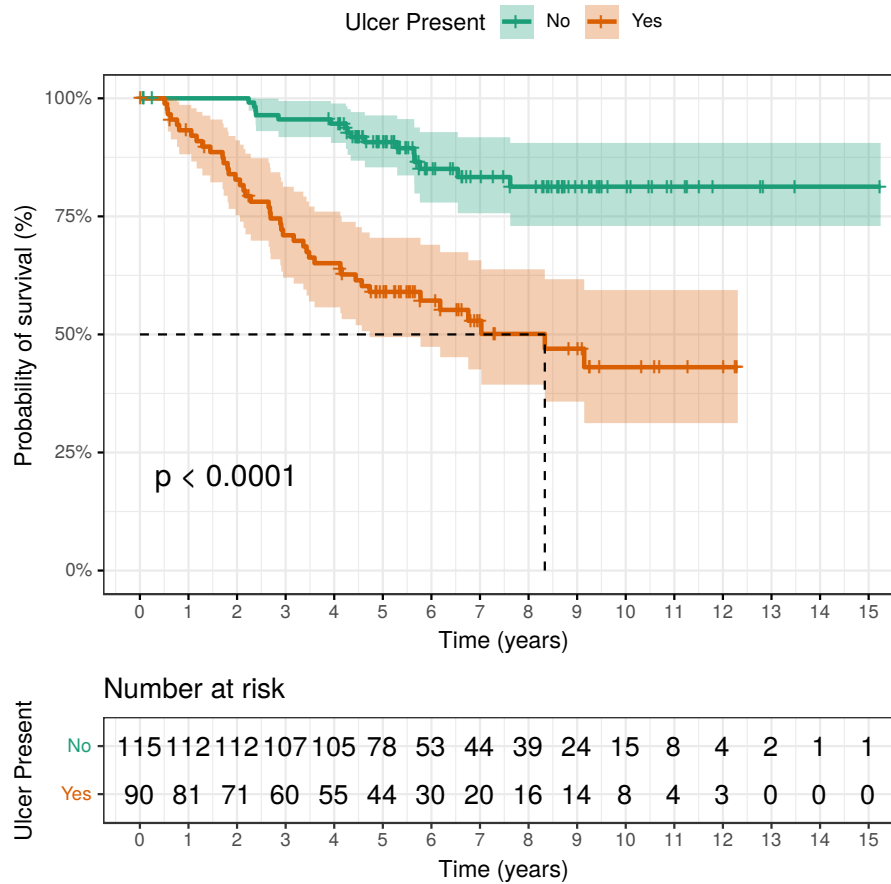


10.2.5 Exercise

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 `survdif()`.

```
survdif(survival_object ~ ulcer.factor, data = mydata)
```

```
## Call:
```

```
## survdif(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 significant 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=m
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 = 0.04 )
## Rsquare= 0.153  (max possible= 0.937 )
## 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

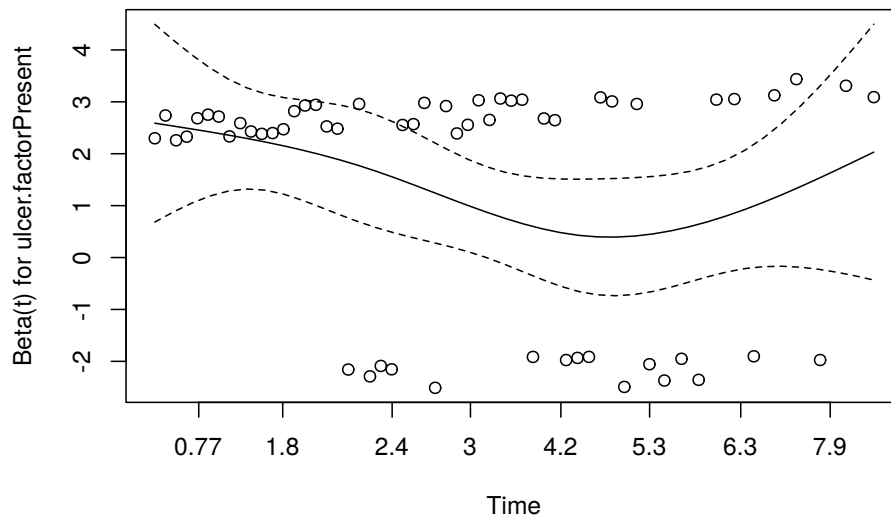
The CPH model presumes ‘constant hazards’. That means that the risk associated with any given variable (like ulcer status) shouldn’t get worse or better over time. This can be checked.

```
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 Schoenfeld 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 survival 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
last_date = first_date + days(nrow(mydata)-1) # assume one every day from 1
operation_date = seq(from = first_date, to = last_date, by = "1 day") # create
mydata$operation_date = operation_date # add the created sequence to melanoma
```

Now we will 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 == "Di
```

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
  xlab = "Time (years)",
  # present narrower X axis, but not affect survival
  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+thickne
summary(my_hazard)

# Melanoma thickness has a HR 1.12 (1.04 to 1.21).
# This is interpreted 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 Schoenfeld residuals to evaluate PH
plot(ph, var=6)
```




Part III

Workflow



11

Notebooks and markdown



12

Missing data



13

Encryption



14

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.



Index

bookdown, [xi](#)

knitr, [xi](#)