

R for DNEP Day One

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By the end of today you will...

- Understand and be able to work with R and the RStudio environment.
- Be able to do basic data wrangling (aka data mangling when it goes wrong...)
- Be able to build AN(C)OVA models for different designs and be able to interpret interactions.
- Be able to build simple linear and multiple regression models in R (incl. diagnostic plots and model selection).
- Know how to produce reports using R Markdown.

Why R?

- R allows you to engage in reproducible research.
- Statistical packages in R reflect the latest advances in the fields of Statistics and Data Science.
- Linear Mixed Models (LMMs) are easy to build in R - many of the best journals now require LMMs to be used as they are more powerful and flexible than classical techniques such as ANOVA.
- Lots of amazing data visualisation packages available.
- In many institutions, the next generation of academics (PhD students, post-docs etc) are learning R skills as part of their training.
- Plays an important role in Open Science.

What role can R play in Open Science?

- R scripts are easy to share allowing for reproducibility and easy public sharing of data and code.
- R is free, open source software that is much more flexible and powerful than SPSS.
- There is an active R community continuously updating statistical tests and packages that run in R.
- As R is a programming language, it forces you to know your data.

R vs. SPSS

“SPSS is like a bus - easy to use for the standard things, but very frustrating if you want to do something that is not already pre-programmed.

R is a 4-wheel drive off-roader, with a bike on the back, a kayak on top, good walking and running shoes in the passenger seat, and mountain climbing and spelunking gear in the back.

R can take you anywhere you want to go if you take time to learn how to use the equipment, but that is going to take longer than learning where the bus stops are in SPSS.” (Greg Snow, 2010, stackoverflow.com).

In meme form...

If statistics programs/languages were cars...



O'REILLY®



R for Data Science

VISUALIZE, MODEL, TRANSFORM, TIDY, AND IMPORT DATA

Hadley Wickham &
Garrett Grolemund

Available electronically for
free at:

<http://r4ds.had.co.nz>

“Hadley Wickham, the Man Who Revolutionized R”



Chief Scientist at RStudio, author of key R packages incl. `ggplot2`, `plyr`, `dplyr` - all components of the tidyverse.

R User Groups...

R user groups exist all over the world with many in the UK (incl. Manchester)...

You can even buy the t-shirt...

UK

England

- Birmingham: [BRUM](#)
- Canterbury: [CanterburyR](#)
- Cambridge: [CambR](#)
- Coventry: [Warwick R User Group](#); [@WarwickRUG](#)
- Exeter: [Exeter R Users Group](#)
- London: [LondonR](#)
- Manchester: [ManchesterR](#)
- Newcastle: [R North East](#); [@RstatsNE](#)
- Nottingham: [Nottingham R User group](#)
- Oxford: [R user group Oxford](#); [@rusersoxford](#)
- Sheffield: [SheffieldR](#); [@Sheffield_R_](#)



RStudio

\$17



magrittr

\$17



Shiny

\$17



I like the way you R

\$17

...and conferences

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The illustration features a variety of icons related to data science and R programming. It includes a Ferris wheel, a factory building, a sun, a smartphone, a laptop displaying R code, and a small plant. The overall theme is the integration of R with real-world applications and data visualization.

useR!2017 BRUSSELS

04.07.2017 - 07.07.2017

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The logo for useR!2017 Brussels features a black network graph icon with several nodes connected by lines, symbolizing data connectivity and analysis.



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The useR!2017 Conference Brochure is online now! Take a look and find an answer to all your practical questions. A printed conference brochure will be ...

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useR! 2018

THE CONFERENCE FOR USERS OF R
JULY 10-13, 2018.
BRISBANE, AUSTRALIA.

R skills are in high demand...

February 11, 2014

R skills attract the highest salaries

Two recent salary surveys have shown that [R language](#) skills attract median salaries in excess of \$110,000 in the United States.

In the [2014 Dice Tech Salary Survey](#) of over 17,000 technology professionals, the highest-paid IT skill was R programming. While [big-data skills in general featured strongly](#) in the top tier, having R at the top of the list reflects the strong demand for skills to make sense of, and extract value from big data.

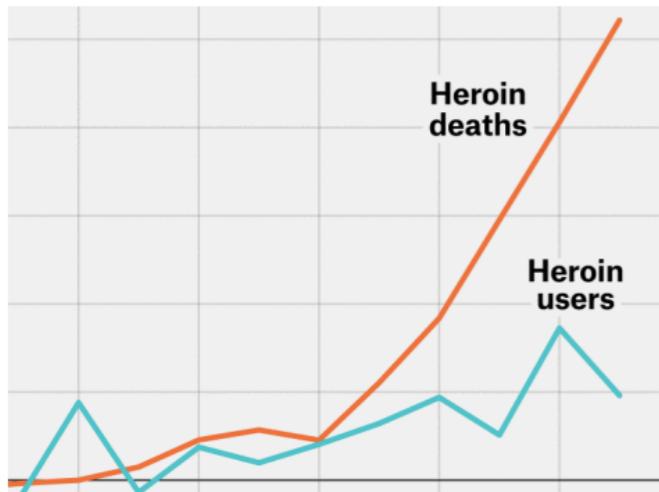
AVERAGE SALARY FOR High Paying Skills and Experience		
SKILL	2013	YR/YR CHANGE
R	\$ 115,531	n/a
NoSQL	\$ 114,796	1.6%
MapReduce	\$ 114,396	n/a
PMBok	\$ 112,382	1.3%
Cassandra	\$ 112,382	n/a
Omnigraffle	\$ 111,039	0.3%
Pig	\$ 109,561	n/a
SOA (Service Oriented Architecture)	\$ 108,997	-0.5%
Hadoop	\$ 108,669	-5.6%
Mongo DB	\$ 107,825	-0.4%

Similarly, the recent [O'Reilly Data Scientist Survey](#) also found R skills amongst those that pay in the \$110,000-\$125,000 range (albeit amongst a much smaller and specialized sample of respondents).

and R is widely used by a number of organisations...

FiveThirtyEight

Politics Sports Science & Health Economics Culture



OPIOIDS
Data On Drug Use Is Disappearing Just When We Need It Most

By Kathryn Casteel

FEATURES

THE LATEST

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JUN. 29 Data On Drug Use Is Disappearing Just When We Need It Most

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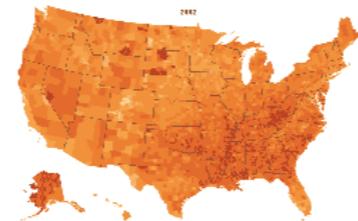
JUN. 26



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35 Years Of American Death



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How the YouGov model for the 2017 General Election works



By Douglas Rivers is a professor of political science at Stanford University and Chief Scientist at YouGov PLC.

In General Election 2017, Politics

On May 31, 2017, 6 a.m.

Share



Doug Rivers, YouGov's chief scientist, sets out how YouGov's 2017 General Election model works

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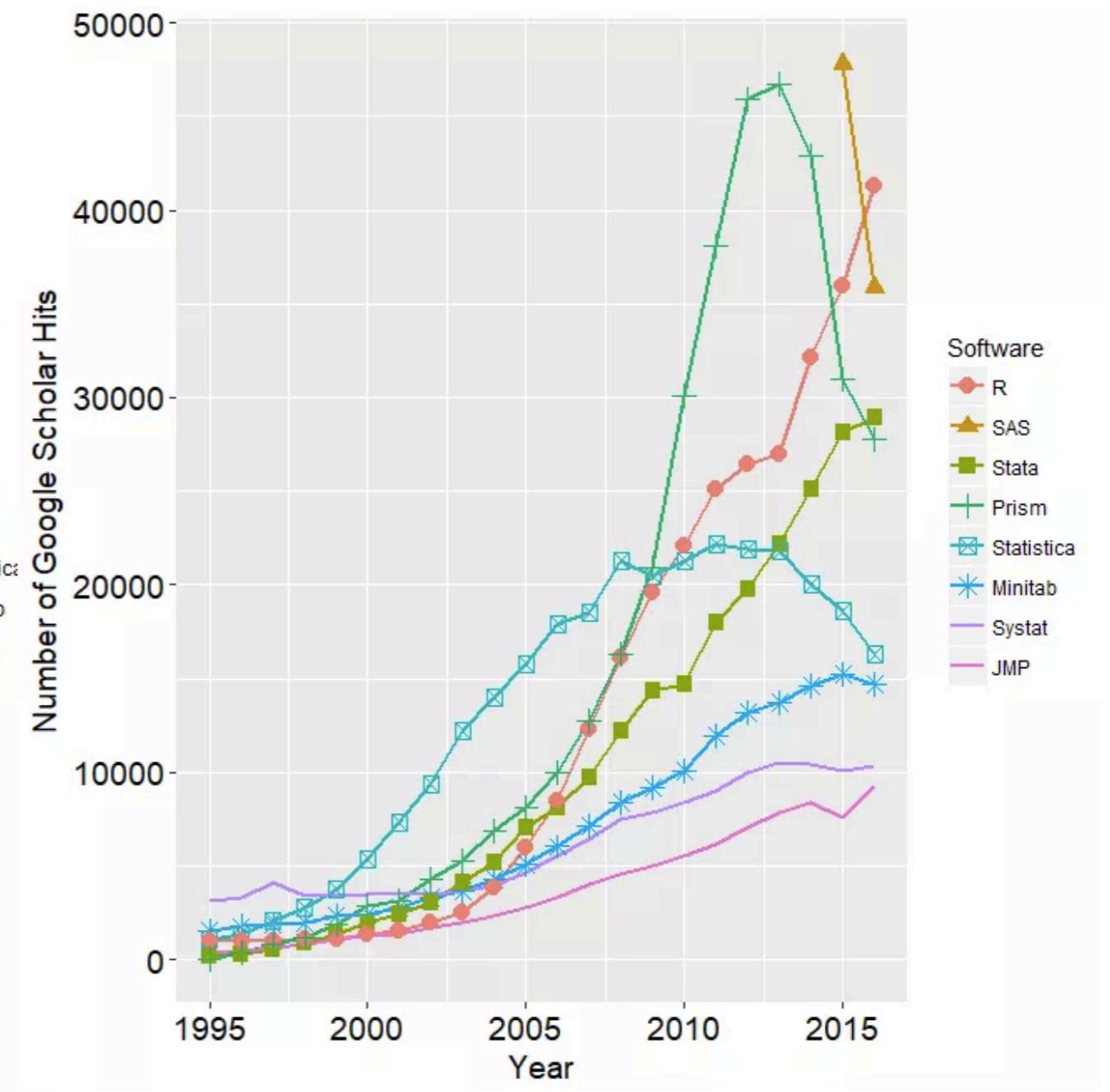
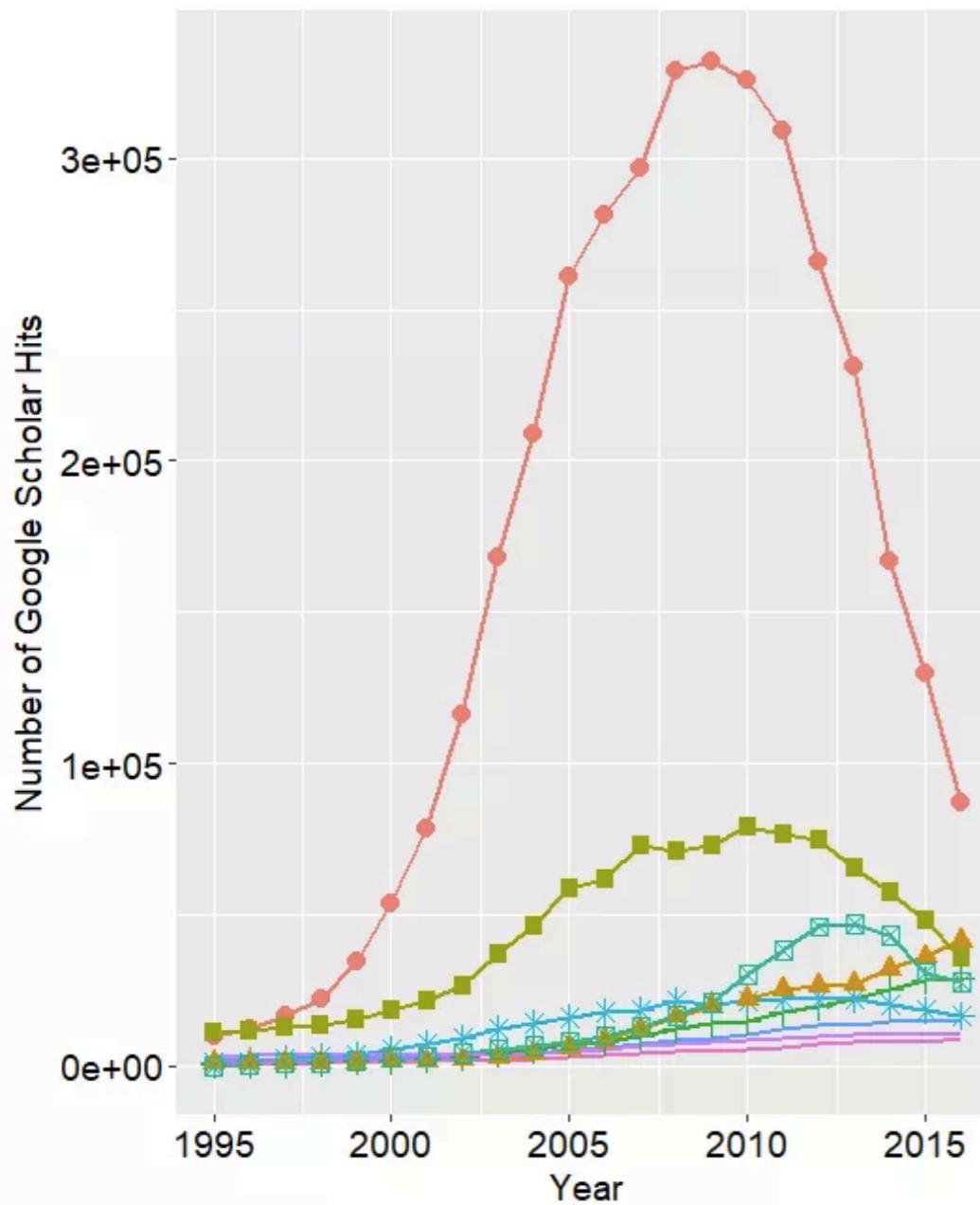
How did 2015 voters cast their ballot at the 2017 general election?

It wasn't just the kids that boosted Labour

John Humphrys - A Government Adrift?

Theresa May is now almost as unpopular as pre-campaign Corbyn

and across academia. . .



with Data Science a growing employment destination for Psychologists.



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CAREER CENTER

Hot jobs: Big-data psychologists

Wanted: Scientists who can help companies make sense of consumer and employee data.



By Rebecca Voelker

Print version: page 18

Every time you use an Internet search engine, sign up for a company "rewards" program or swipe your credit card, that information is saved and stored. The industries that amass these billions of bytes of data are increasingly hiring psychologists to help make sense of it, says Douglas Reynolds, PhD, president of APA's Div. 14 ([Society for Industrial and Organizational Psychology](#)).

"Big data, and what it means for business, is a hot topic right now," says Reynolds, who also serves as vice president of assessment technology at [Development Dimensions International Inc.](#), a human resources consulting firm. "We're in high demand."

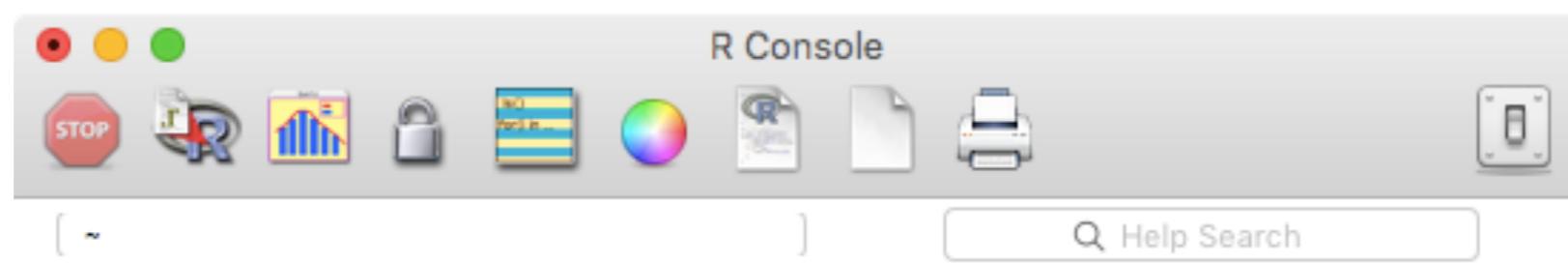
Psychologists' ability to interpret numbers and human behavior makes them key members of many industry analytics teams, adds Suzie Weaver, PhD, a psychologist and senior analytic consultant with [Epsilon](#), a global marketing and analytics company. "Analytics is at the core of everything we do, whether it's in research, the academic sphere or the business world."

Starting R

- R is open source (i.e., free to download and add to). Main R site is:
- www.r-project.org
- From here you can download R (from one of the CRAN¹ mirrors for Windows, Mac and UNIX).
- R updates regularly (you need to update manually).

¹CRAN = The Comprehensive R Archive Network

- When you first load R it looks like this:



```
R version 3.3.3 (2017-03-06) -- "Another Canoe"
Copyright (C) 2017 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin13.4.0 (64-bit)
```

```
R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.
```

```
Natural language support but running in an English locale
```

```
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.
```

```
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
```

```
[R.app GUI 1.69 (7328) x86_64-apple-darwin13.4.0]
```

```
[Workspace restored from /Users/andrewstewart/.RData]
[History restored from /Users/andrewstewart/.Rapp.history]
```

```
> |
```



- Rather than using the R interface, you should use the RStudio graphical interface.
- Download it from www.rstudio.com
- When you run RStudio, it looks like this:

RStudio File Edit Code View Plots Session Build Debug Tools Window Help

~/Desktop/Air Work/MRes 2016:17/R workshop MRes/R workshop directory/Workshop - RStudio

Addins Workshop

Workshop script2.R

```

1 library(lmerTest)
2 library(lsmeans)
3 library(pbkrtest)
4
5 #Read in First Pass Data
6 FPs <- read.csv("~/Desktop/Air Work/R analyses/Indirect Request Expt/Experiment 1 - probability of success - Libby's data/FPs")
7
8 #this sets up the contrasts so that the intercept in the mixed LMM is the grand mean (i.e., the mean of all conditions)
9 my.coding <- matrix(c(.5, -.5))
10
11 contrasts(DV$Context)<-matrix(c(.5, -.5))
12 contrasts(DV$Sentence)<-matrix(c(.5, -.5))
13
14 #construct the models with crossed random effects for subjects and items for the pre-critical, critical and post-critical regions
15 model.full <- lmer(RT ~ Context*Sentence + (1+Context*Sentence | Subject) + (1+Context*Sentence | Item), data=DV, REML=TRUE)
16 model.null <- lmer(RT ~ (1+Context*Sentence | Subject) + (1+Context*Sentence | Item), data=DV, REML=TRUE)
17
18 summary(model.full)
19 lsmeans(model.full, pairwise~Context*Sentence, adjust="none")
20
21 model.full <- lmer(RT ~ Statement*Meaning*Probability + (1:Meaning*Probability | P_c) + (1:Meaning*Probability | Item), data=FPs)
22
```

Console

```

The following object is masked from 'package:stats':
  step

> library("lsmeans", lib.loc="/Library/Frameworks/R.framework/Versions/3.3/Resources/library")
Loading required package: estimability

Attaching package: 'lsmeans'

The following object is masked from 'package:lmerTest':
  lsmeans

> model.full <- lmer(RT ~ Context*Sentence + (1+Context*Sentence | Subject) + (1+Context*Sentence | Item), data=DV, REML=TRUE)
```

Error in strsplit(keys, " *") : non-character argument

Environment

DV Global Environment

Data

DV	1680 obs. of 5 variables
my.coding	num [1:2, 1] 0.5 -0.5

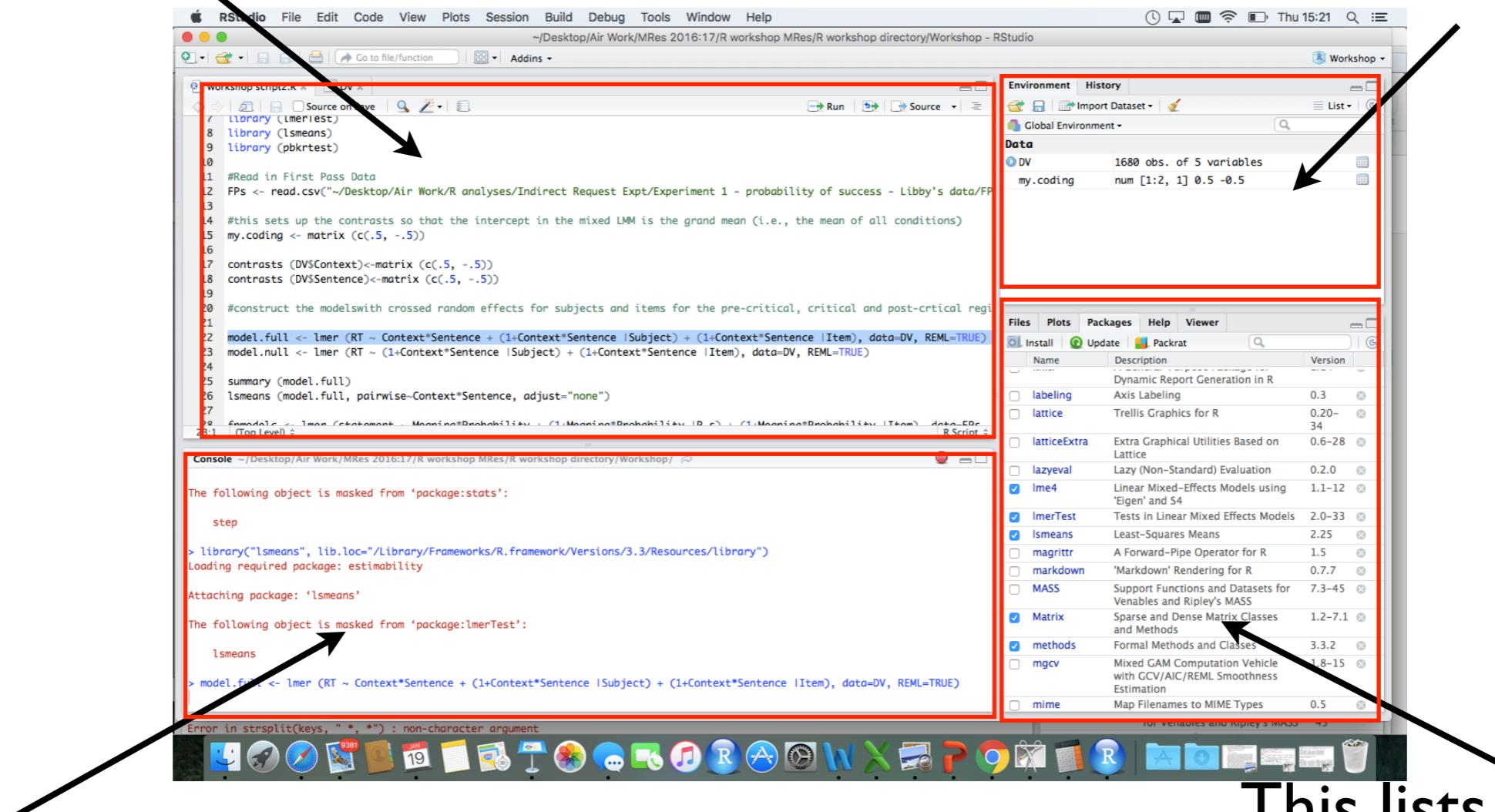
Packages

Name	Description	Version
lme4	Linear Mixed-Effects Models using 'Eigen' and S4	1.1-12
lmerTest	Tests in Linear Mixed Effects Models	2.0-33
lsmeans	Least-Squares Means	2.25
Matrix	Sparse and Dense Matrix Classes and Methods	1.2-7.1
methods	Formal Methods and Classes	3.3.2
mgcv	Mixed GAM Computation Vehicle with GCV/AIC/REML Smoothness Estimation	1.8-15
mime	Map Filenames to MIME Types	0.5

for variables and Ripley's MASS

File Applications

This is where you build your script and where data can be seen.

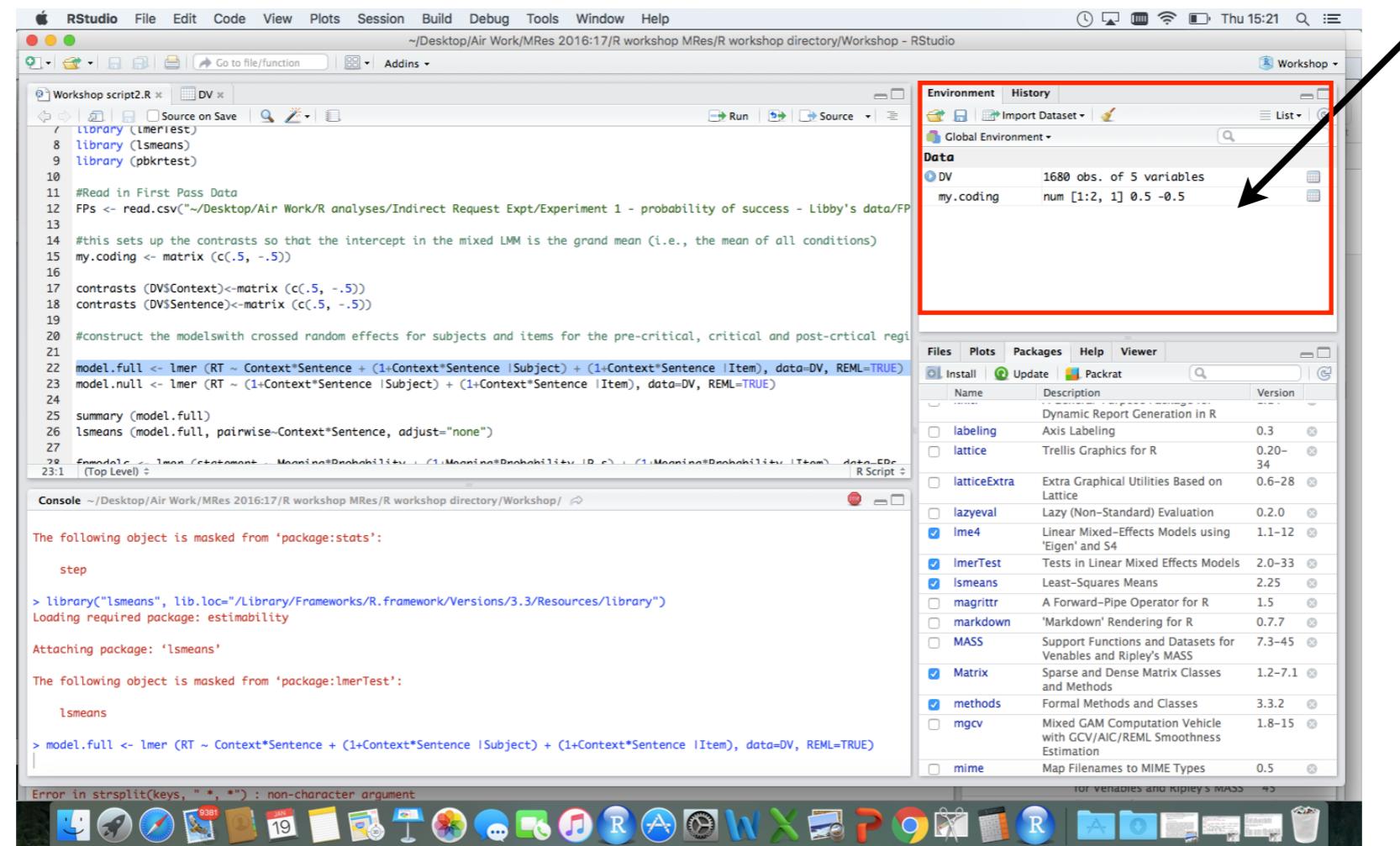


This is where you type commands.

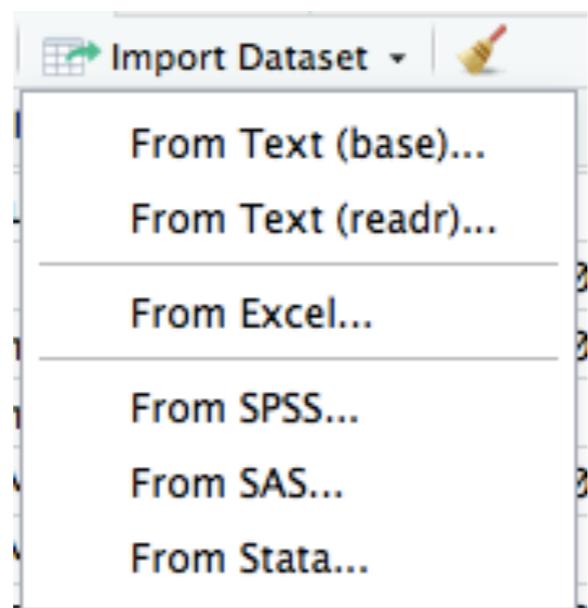
This contains information about your variables and open data sets.

This lists the packages you have loaded, and has tabs for help, graphs etc.

Here is where
you import your
data.



- Importing data (CSV (Text), Excel, SPSS, SAS and Stata format). CSV can be delimited by commas, tabs etc. Most of the time you'll use the `readr` import function...



Import Text Data

File/Url:

~/Desktop/Air Work/R analyses/R courses/R course/R Work Folder/priming data.txt

Data Preview:

Subject (integer) ▾	Priming Condition (character) ▾	RT (integer) ▾
1	LONG	500
2	LONG	551
3	LONG	479
4	LONG	567
5	LONG	522
6	SHORT	399
7	SHORT	423
8	SHORT	444
9	SHORT	410
10	SHORT	398

You can change the type of each variable by clicking on the down arrow.

You should change this to type Factor (LONG vs. SHORT).

Previewing first 50 entries.

Import Options:

Name: priming_data First Row as Names Delimiter: Tab Escape: None
Skip: 0 Trim Spaces Quotes: Default Comment: Default
 Open Data Viewer Locale: Configure... NA: Default

Code Preview:

```
library(readr)
priming_data <- read_delim("~/Desktop/Air Work/R analyses/R courses/R course/R Work Folder/priming data.txt",
                           "\t", escape_double = FALSE, trim_ws = TRUE)
View(priming_data)
```

Can change here how the columns are delimited.

This is the code that corresponds to what you're getting R Studio to do.

● R Studio now looks like this:

The screenshot shows the RStudio interface with the following components:

- Data Viewer:** On the left, a data frame named "priming_data" is displayed with columns: Subject, Priming Condition, and RT. The data consists of 10 rows of experimental results.
- Environment Browser:** In the top right, the Global Environment pane shows the "priming_data" object with a dimension of 10 obs. of 3 variables.
- Packages Browser:** In the bottom right, the Packages pane lists installed packages such as labeling, lattice, latticeExtra, lazyeval, lme4, lmerTest, lsmeans, magrittr, markdown, MASS, Matrix, methods, mgcv, mime, minqa, multcomp, and munsell.
- Console:** At the bottom left, the console displays R code and its output. The user attempts to load "priming_data" but receives an error message stating the object is not found. They then use the readr package to read a file named "priming data.txt" from a local directory, specifying column names and types. Finally, they view the resulting data frame.

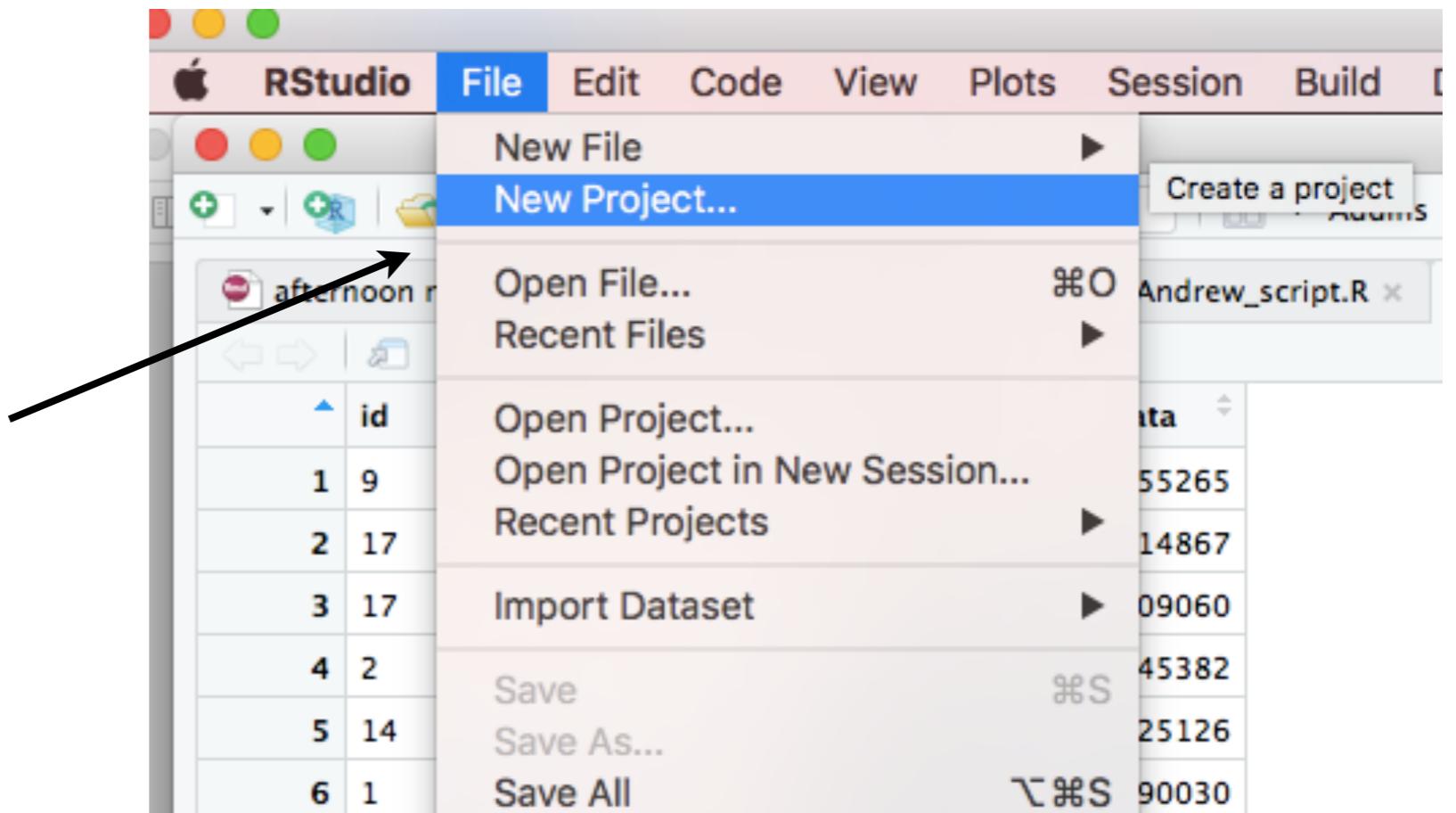
```

Console ~/Desktop/Air Work/R analyses/
>
>
>
>
>
>
> RTdata <- priming_data [c("Priming Condition", "RT")]
Error: object 'priming_data' not found
> library(readr)
> priming_data <- read_delim("~/Desktop/Air Work/R analyses/R courses/R course/R Work Folder/priming data.txt",
+   "\t", escape_double = FALSE, trim_ws = TRUE)
Parsed with column specification:
cols(
  Subject = col_integer(),
  `Priming Condition` = col_character(),
  RT = col_integer()
)
> View(priming_data)
>

```

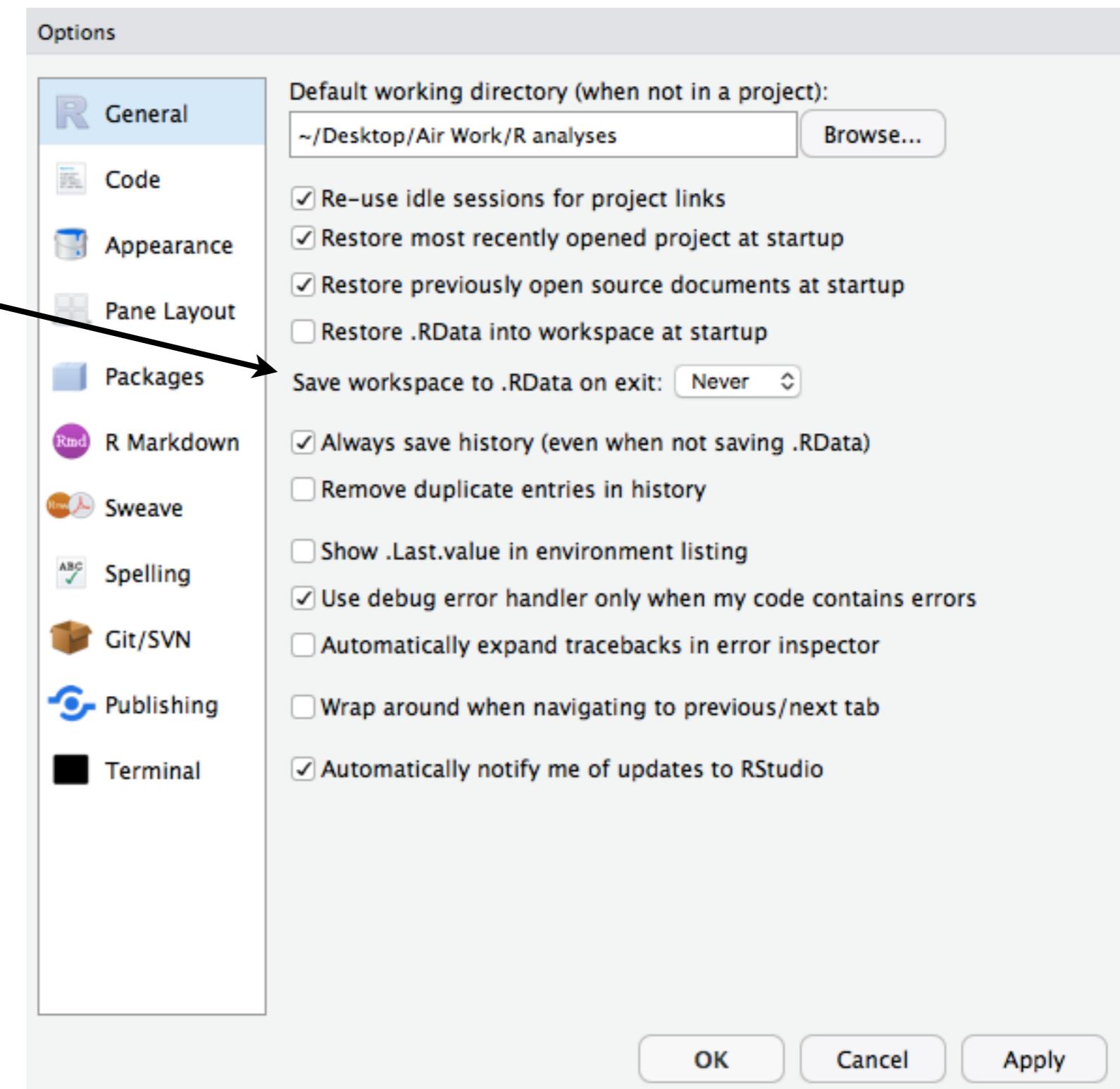
When Starting R

Always create a new project - this will keep all your files nice and organised.



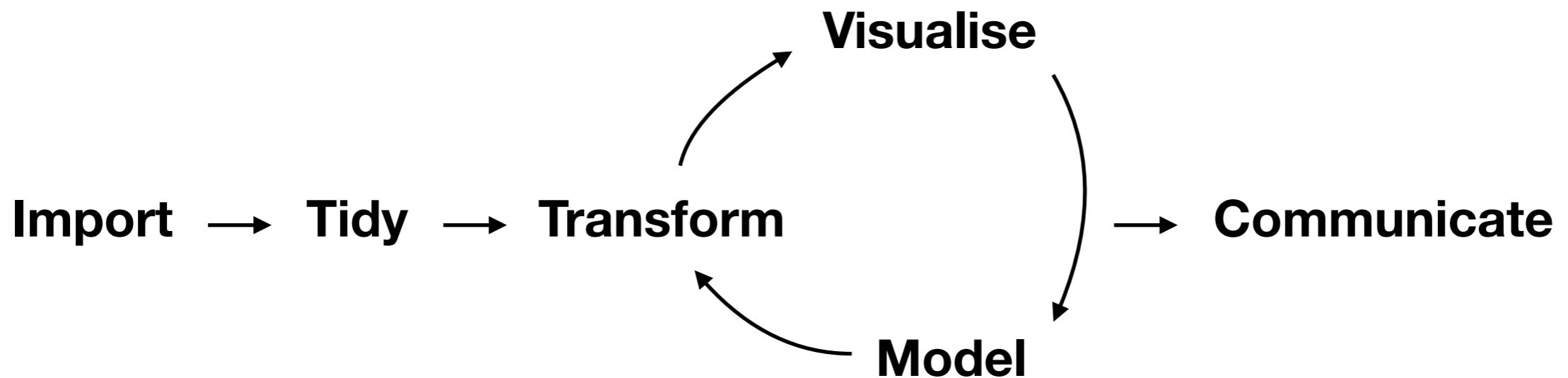
When Starting R

Under preferences,
make sure you
uncheck the saving
workspace option...

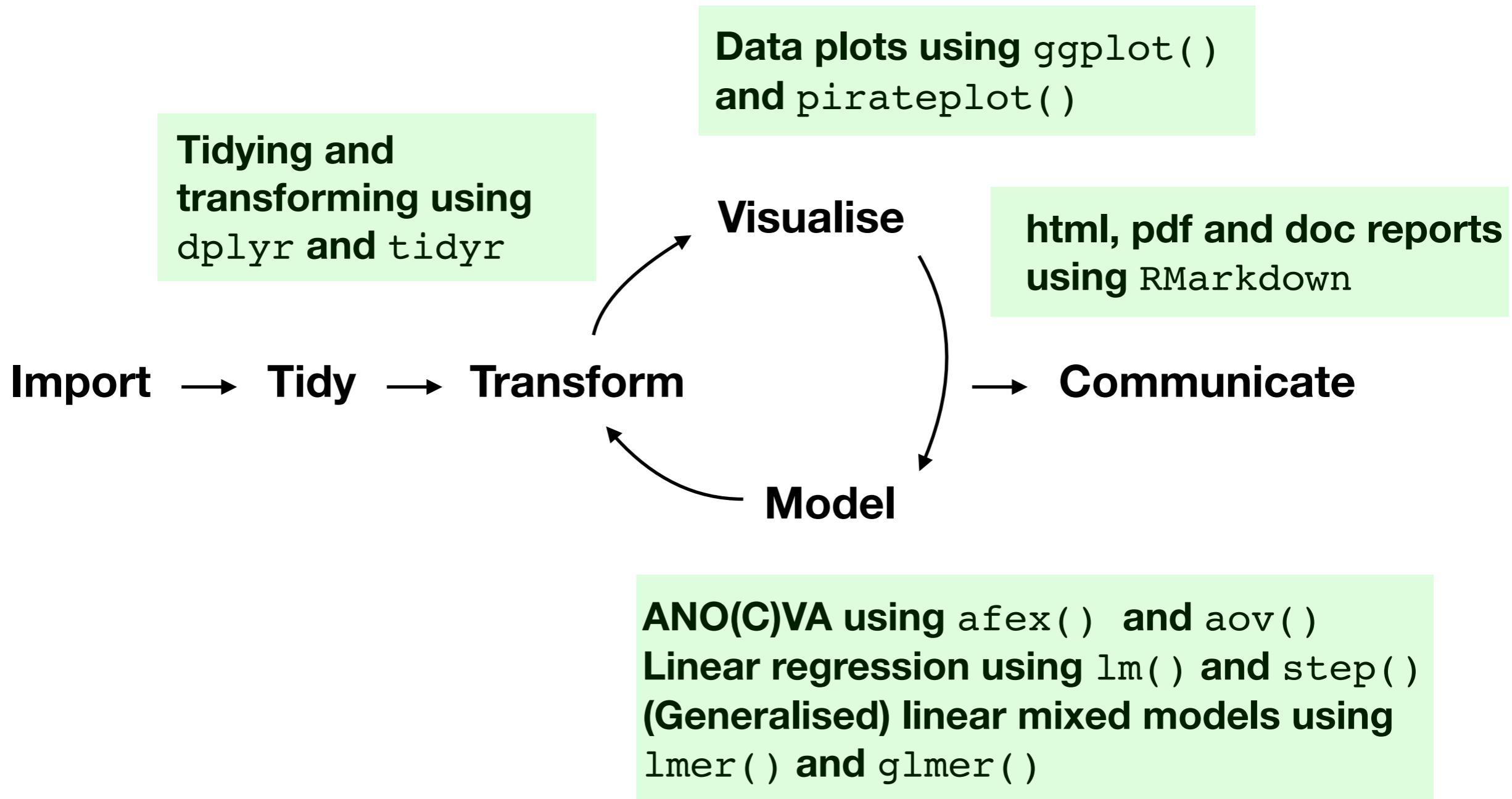


Analysis Workflow in the Tidyverse

(Garrett Grolemund and Hadley Wickham) - from Data to Write-up



Workflow



Packages in R

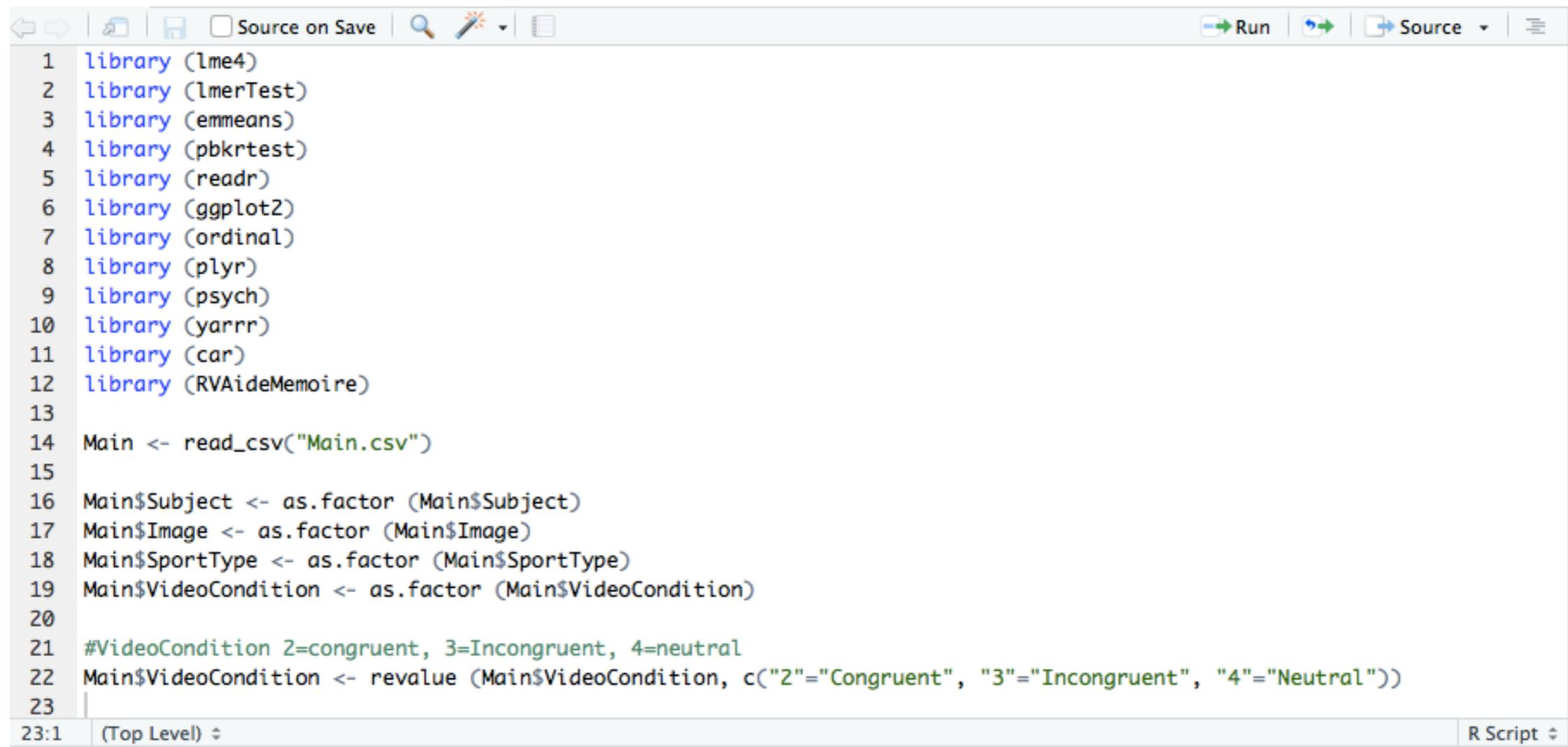
R has a number of functions already built in - but for much of what we do we need to load particular packages to let us use additional functions. We do this by:

```
> install.packages ("packagename")
```

```
> library (packagename)
```

Every time you start R afresh, you need to load the packages you will use by using the `library` function or the `require` function.

Writing Scripts in R



The screenshot shows the RStudio interface with an R script editor. The code in the editor is as follows:

```
1 library(lme4)
2 library(lmerTest)
3 library(emmeans)
4 library(pbkrtest)
5 library(readr)
6 library(ggplot2)
7 library(ordinal)
8 library(plyr)
9 library(psych)
10 library(yarrr)
11 library(car)
12 library(RVAideMemoire)
13
14 Main <- read_csv("Main.csv")
15
16 Main$Subject <- as.factor(Main$Subject)
17 Main$Image <- as.factor(Main$Image)
18 Main$SportType <- as.factor(Main$SportType)
19 Main$VideoCondition <- as.factor(Main$VideoCondition)
20
21 #VideoCondition 2=congruent, 3=Incongruent, 4=neutral
22 Main$VideoCondition <- revalue(Main$VideoCondition, c("2"="Congruent", "3"="Incongruent", "4"="Neutral"))
23
```

The status bar at the bottom indicates "23:1 (Top Level) R Script".

Ultimately you will be writing scripts that will allow yourself and others to recreate your analysis just by running the script - the code at the start of the script will load the packages your analysis needs, then load your data, tidy, transform and visualise your data, and then code for your model...

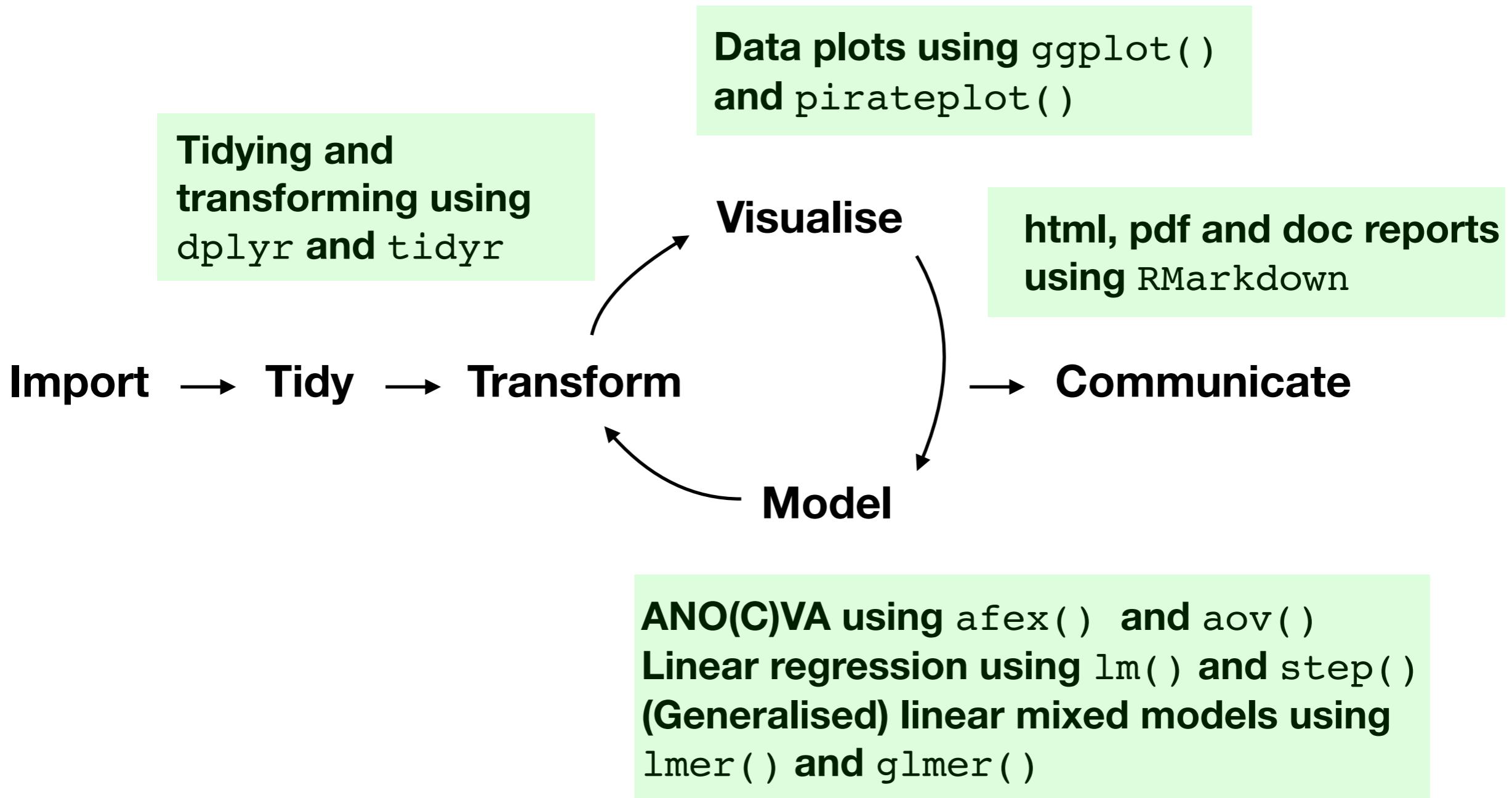
Writing Scripts in R

Scripts should have lots of comments, indicated by a # symbol - this helps others read your code, and also yourself when you look back at it later.

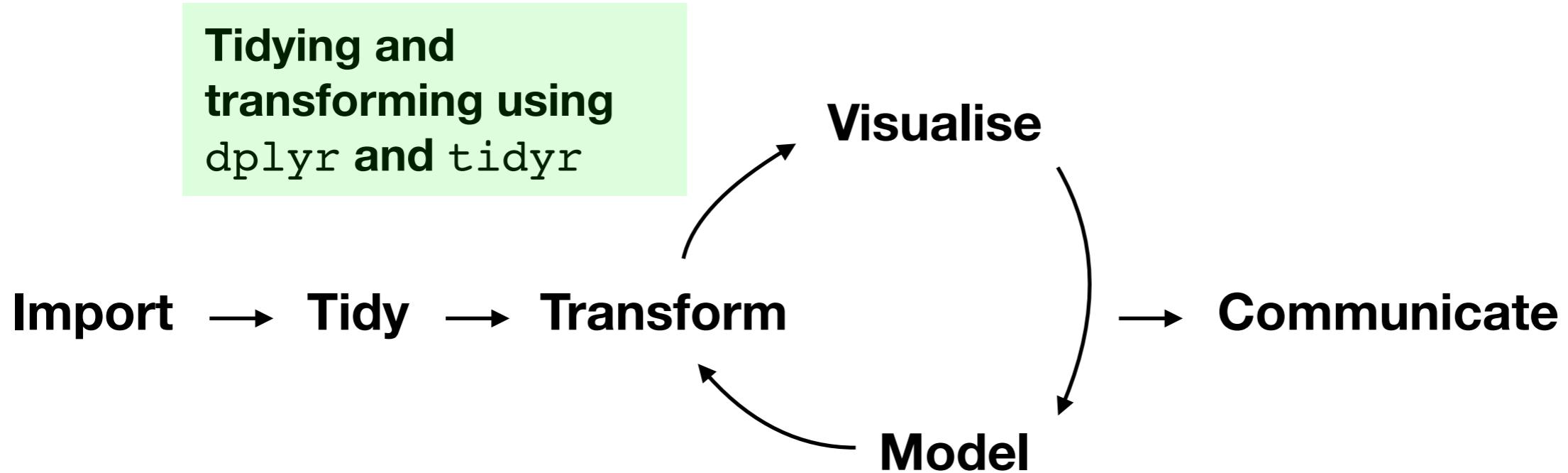
Scripts can be saved and uploaded to (e.g.) OSF, GitHub, or submitted as an electronic supplement alongside your journal submission. Even when journals don't require you to adhere to Open Science practices, it's a good idea to make your code and data available during the reviewing process - and publicly available once your paper is published.

If you aren't sharing your data and code, you aren't engaged in generating reproducible or open research...

Workflow



Tidying and Transforming Data



Tidying and Transforming Data

Imagine we have two datasets - one (called `data`) contains a large number of records of individual participants with measures of Working Memory, IQ, and reading comprehension.

If we type into the Console:

```
> View (data)
```

the data frame is displayed like this...



ID	WM	IQ	Comp
1	43	72	16
2	51	109	18
3	55	107	18
4	38	102	20
5	52	121	17
6	52	92	16
7	47	68	21
8	47	97	23
9	47	93	22
10	45	101	17
11	47	86	17
12	45	113	21
13	46	114	19
14	50	99	20

Showing 1 to 14 of 10,000 entries

To get more information about the structure of our data frame we can type:

```
> str (data)
'data.frame': 10000 obs. of 4 variables:
 $ ID   : int 1 2 3 4 5 6 7 8 9 10 ...
 $ WM   : int 43 51 55 38 52 52 47 47 47 45 ...
 $ IQ   : int 72 109 107 102 121 92 68 97 93 101 ...
 $ Comp: int 16 18 18 20 17 16 21 23 22 17 ...
```

So we have 10,000 observations with 4 variables associated with each observation - all of them of type integer.

Imagine that 48 of these 10,000 people also took part in a reading time experiment and we have their reading data (called `dataRT`) for Simple Sentence and Complex Sentence reading conditions:

```
> str (dataRT)
'data.frame': 48 obs. of 3 variables:
 $ ID           : int  9937 1506 5212 374 6757 1778 9421 5576 7326 4166 ...
 $ Simple Sentence : int  1996 2235 2177 1824 2113 2056 2037 2073 1830 1824 ...
 $ Complex Sentence: int  2551 2310 2244 2483 2567 2791 2226 2270 2640 2386 ...
```

We are interested in analysing the data of these 48 people in the data frame called `dataRT` but covarying out the effect of IQ captured in our data frame called `data`.

Problem - how can we combine these two data frames so that we end up with one data frame of 48 people, their reading times plus their individual difference measures?

Manually, in Excel we could open the two data frames as spreadsheets and cut and paste cases where the id number matches...

Probably ok for 48 participants, but what if you had 200 or 2,000?

In R, we can use the `inner_join` function from the `dplyr` package where we join the two data frames matched by ID.

```
> inner_join (data, dataRT, by=c("ID"))
```

	ID	WM	IQ	Comp	Simple Sentence	Complex Sentence
1	374	49	80	19	1824	2483
2	516	45	108	23	1800	2348
3	570	45	114	17	1942	2409
4	648	50	102	22	2167	2308
5	691	49	112	20	1816	2313
6	882	45	113	24	1848	2237
7	1033	44	100	19	1882	2219
8	1191	50	89	17	1731	2417
9	1338	50	82	21	1868	2462
10	1506	48	96	20	2235	2310

We can use the assignment symbol `<-` to assign the output of this `inner_join` function to a new variable I'm calling `dataRT_all`. We can ask for the structure of this new data frame using the `str()` function:

```
> dataRT_all <- inner_join (data, dataRT, by=(c("ID")))
> str (dataRT_all)
'data.frame': 48 obs. of 6 variables:
 $ ID           : int  374 516 570 648 691 882 1033 1191 1338 1506 ...
 $ WM          : int  49 45 45 50 49 45 44 50 50 48 ...
 $ IQ           : int  80 108 114 102 112 113 100 89 82 96 ...
 $ Comp         : int  19 23 17 22 20 24 19 17 21 20 ...
 $ Simple Sentence: int  1824 1800 1942 2167 1816 1848 1882 1731 1868 2235 ...
 $ Complex Sentence: int  2483 2348 2409 2308 2313 2237 2219 2417 2462 2310 ...
```

So we have created a new data frame of 48 participants comprised of their reading times and their individual difference measures from two separate (and different sized) data frames...with one line of code...

	ID	WM	IQ	Comp	Simple Sentence	Complex Sentence
1	374	49	80	19	1824	2483
2	516	45	108	23	1800	2348
3	570	45	114	17	1942	2409
4	648	50	102	22	2167	2308

Now imagine we find the distributions of reading times for our two conditions are positively skewed (and we discover the residuals are non-normal). We could log transform these two columns and have two new columns in our data frame - let's call them `log_Simple` and `log_Complex`. We can use the `mutate` function in the `dplyr` package to create two new columns.

```
> data_transformed <- mutate (dataRT_all, log_Simple=log (dataRT_all$`Simple Sentence`), log_Complex=log (dataRT$`Complex Sentence`))  
> data_transformed
```

	ID	WM	IQ	Comp	Simple Sentence	Complex Sentence	log_Simple	log_Complex
1	374	49	80	19	1824	2483	7.508787	7.844241
2	516	45	108	23	1800	2348	7.495542	7.745003
3	570	45	114	17	1942	2409	7.571474	7.716015
4	648	50	102	22	2167	2308	7.681099	7.817223
5	691	49	112	20	1816	2313	7.504392	7.850493
6	882	45	113	24	1848	2237	7.521859	7.934155
7	1033	44	100	19	1882	2219	7.540090	7.707962
8	1191	50	89	17	1731	2417	7.456455	7.727535
9	1338	50	82	21	1868	2462	7.532624	7.878534
10	1506	48	96	20	2235	2310	7.711997	7.777374

Perhaps we have a reason to exclude a particular participant - number 1191 for example. We can set up a logical vector which gives us a value of TRUE for all participants other than 1191:

```
> index <- data_transformed$ID!=1191  
> View (index)
```

Values are all set to TRUE
except the participant who
has the ID value of 1191

ID	Value
1	TRUE
2	TRUE
3	TRUE
4	TRUE
5	TRUE
6	TRUE
7	TRUE
8	FALSE
9	TRUE
10	TRUE
11	TRUE
12	TRUE
13	TRUE
14	TRUE
15	TRUE

Showing 1 to 15 of 48 entries

`!=` stands for “not equal to”- here is the full list of logical operators in R:

`<` less than

`<=` less than or equal to

`>` greater than

`>=` greater than or equal to

`==` exactly equal to

`!=` not equal to

`!x` Not x

`x | y` x OR y

`x & y` x AND y

`isTRUE(x)` test if X is TRUE

We can now apply our logical vector to our dataRT_all data frame and create a new filtered data frame (which I am calling filtered_data):

```
> index <- data_transformed$ID!=1191
> filtered_data <- data_transformed[index, ]
> filtered_data
```

	ID	WM	IQ	Comp	Simple Sentence	Complex Sentence	log_Simple	log_Complex
1	374	49	80	19	1824	2483	7.508787	7.844241
2	516	45	108	23	1800	2348	7.495542	7.745003
3	570	45	114	17	1942	2409	7.571474	7.716015
4	648	50	102	22	2167	2308	7.681099	7.817223
5	691	49	112	20	1816	2313	7.504392	7.850493
6	882	45	113	24	1848	2237	7.521859	7.934155
7	1033	44	100	19	1882	2219	7.540090	7.707962
9	1338	50	82	21	1868	2462	7.532624	7.878534
10	1506	48	96	20	2235	2310	7.711997	7.777374

We could then run an ANCOVA over the log transformed RTs while covarying out the individual participant effects...

Problem - imagine our data are in the wrong ‘shape’ - they are in **Wide format** (each row is one *participant*) but we need them in **Long format** (each row is one *observation*).

In SPSS, most data will be in **Wide format** with each experimental condition its own column:

	ID	Simple Sentence	Complex Sentence
1	9937	1996	2551
2	1506	2235	2310
3	5212	2177	2244
4	374	1824	2483
5	6757	2113	2567
6	1778	2056	2791
7	9421	2037	2226
8	5576	2073	2270
9	7326	1830	2640
10	4166	1824	2386

For many analyses in R, data need to be in **Long format** with each row being one observation. So, we want to transform our `dataRT` data frame so it looks like this:

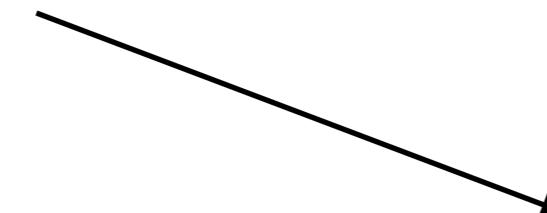
ID	Condition	RT
...

To do this we can use the `gather()` function in the `tidyverse` package.

```
> data_long <- gather (dataRT, "Condition", "RT", c("Simple Sentence", "Complex Sentence"))
```

The first parameter is the name of the data frame we want to reshape, the second is the name of the new ‘Key’ column, the third is the name of the new value column and the fourth the names of the columns we want to collapse.

We can use this to create a new data frame called `data_long` which looks like this:



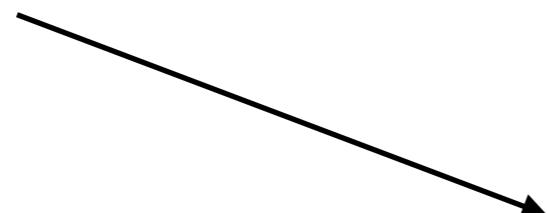
	ID	Condition	RT
1	9937	Simple Sentence	1996
2	1506	Simple Sentence	2235
3	5212	Simple Sentence	2177
4	374	Simple Sentence	1824
5	6757	Simple Sentence	2113
6	1778	Simple Sentence	2056
7	9421	Simple Sentence	2037
8	5576	Simple Sentence	2073
9	7326	Simple Sentence	1830
10	4166	Simple Sentence	1824
11	8817	Simple Sentence	1917
12	7645	Simple Sentence	2008
13	3893	Simple Sentence	2078
14	5199	Simple Sentence	2027

Showing 1 to 14 of 96 entries

And in reverse we can use the `spread()` function to go from Long to Wide data format:

```
> data_wide <- spread (data_long, "Condition", "RT", c("Simple Sentence", "Complex Sentence"))
> View (data_wide)
```

We're now back to where we started with data in Wide format:



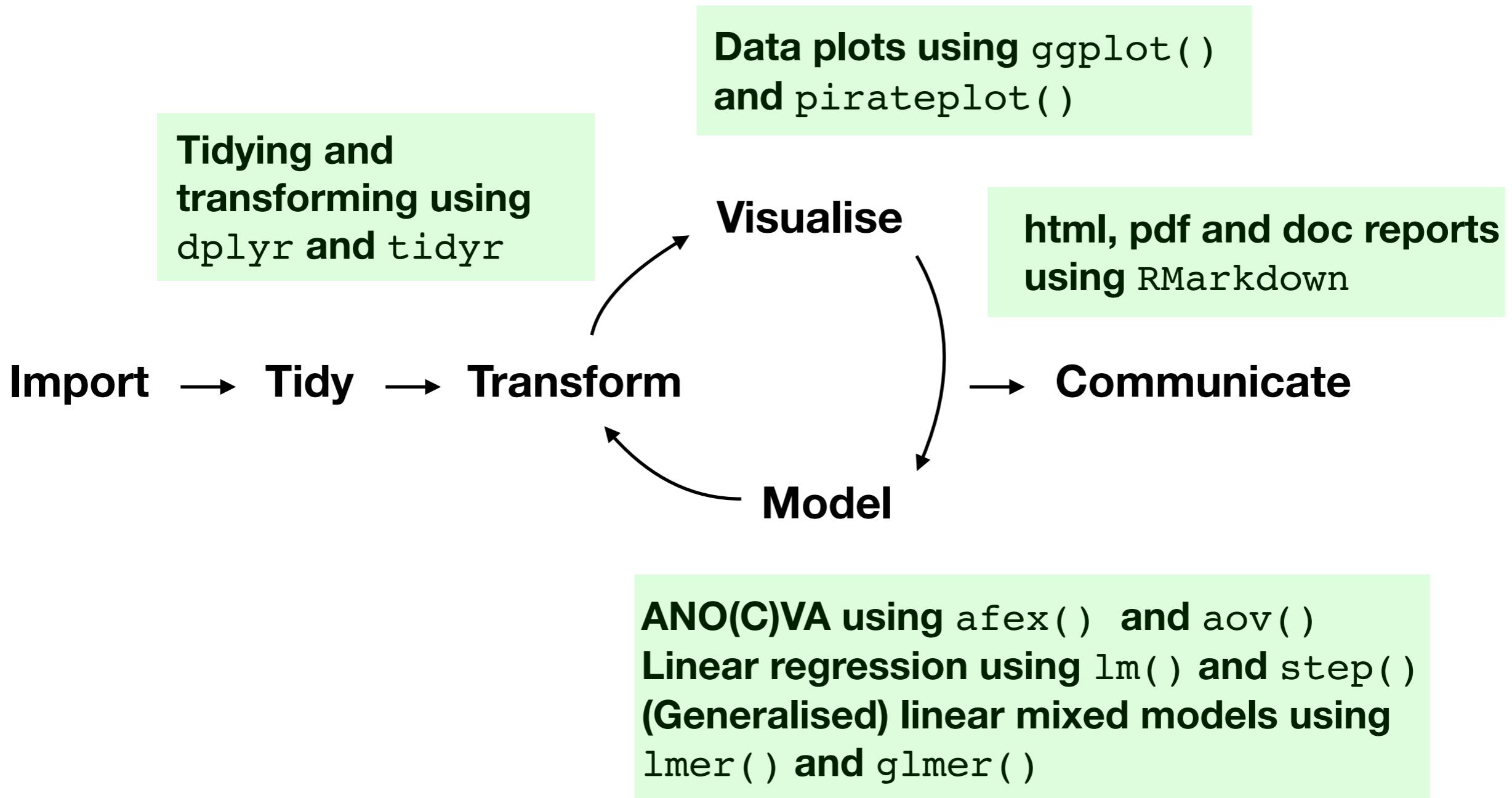
	ID	Complex Sentence	Simple Sentence
1	374	2483	1824
2	516	2348	1800
3	570	2409	1942
4	648	2308	2167
5	691	2313	1816
6	882	2237	1848
7	1033	2219	1882
8	1191	2417	1731
9	1338	2462	1868
10	1506	2310	2235
11	1521	2452	1858
12	1776	2081	1925
13	1778	2791	2056

Showing 1 to 14 of 48 entries

This is just a small example of functions in the `dplyr` and `tidyR` packages that allow you to tidy, transform, and reshape your data. All of your code for doing this should appear at the start of your analysis script so that others (and you in 5 years or 5 days time) can see exactly what you did.

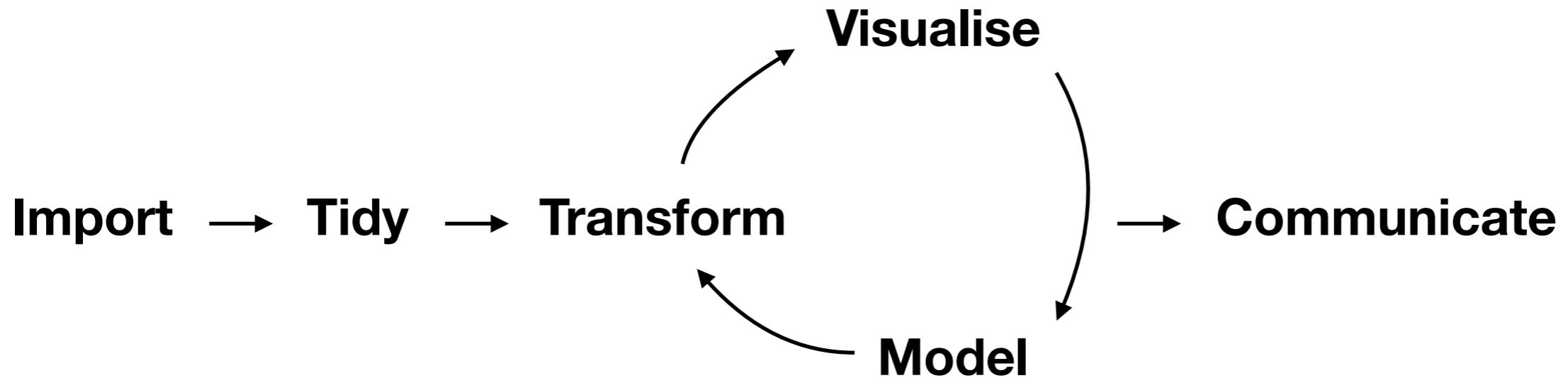
This allows for fully reproducible data preparation in the first part of your analysis workflow (important for Open Science and transparency).

Workflow



Visualise

Data plots using `ggplot()` and `pirateplot()`



Visualising Your Data

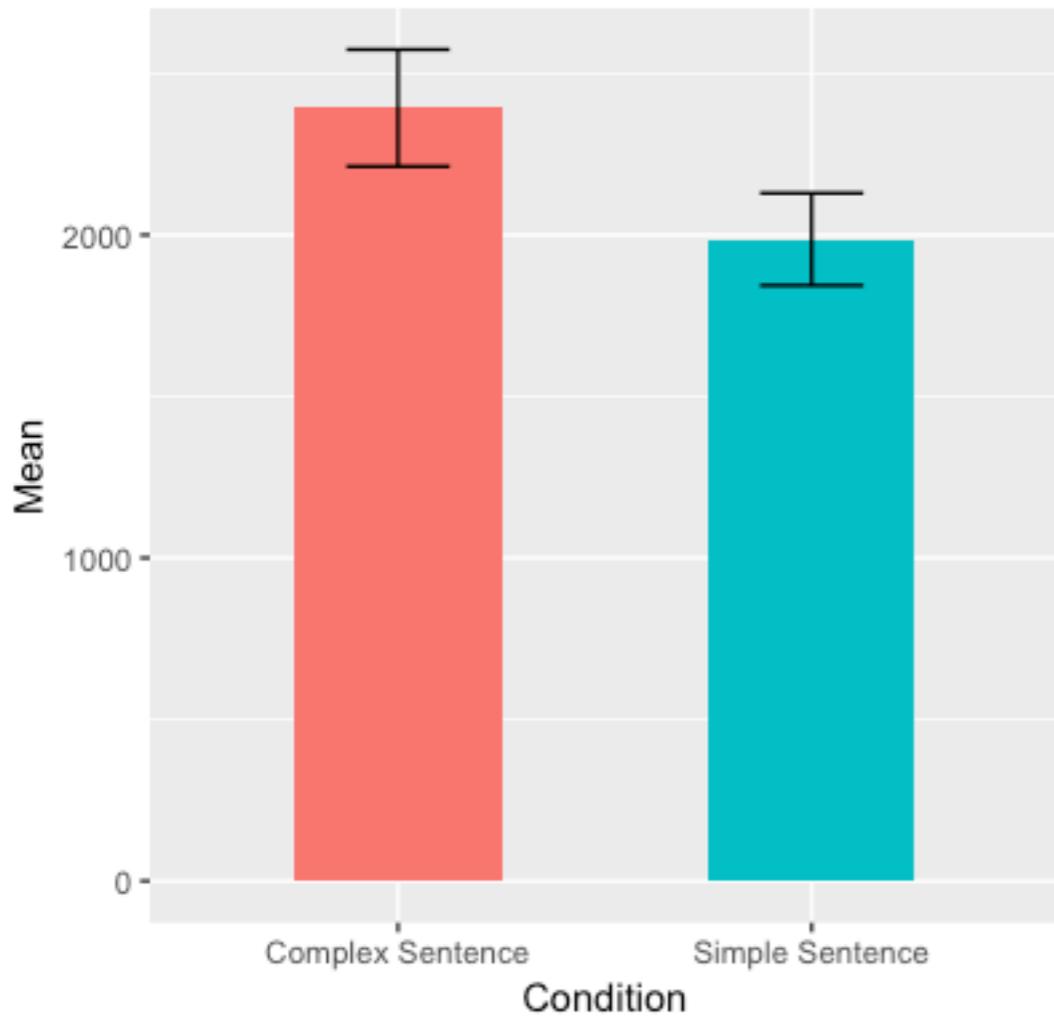
- R has a number of in built graphics functions, but you're more likely to use functions from within the `ggplot2` and `yarr` packages.

```
> library (ggplot2)
```

```
> library (yarr)
```

Bar Graphs

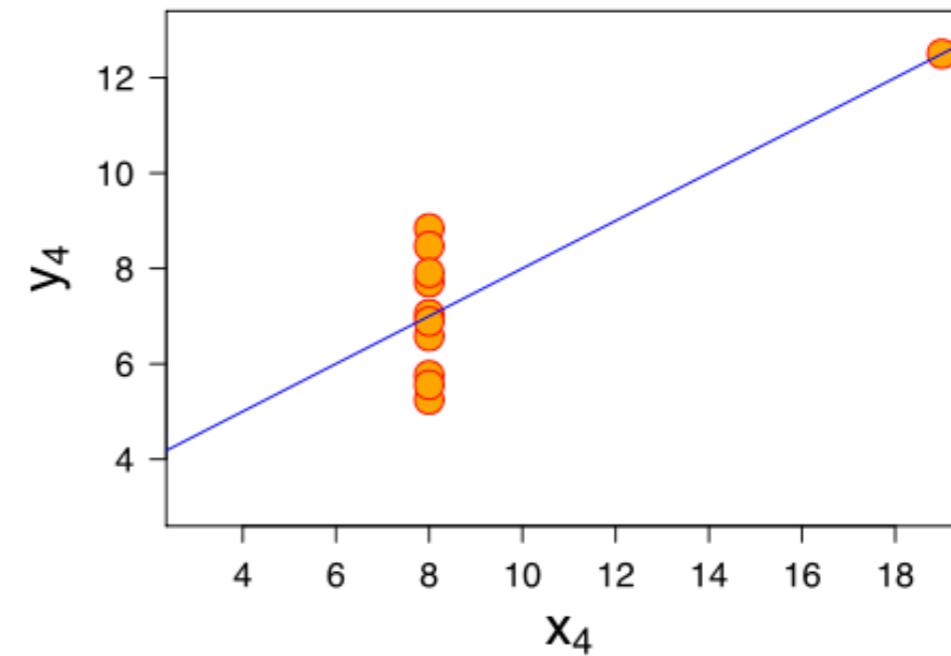
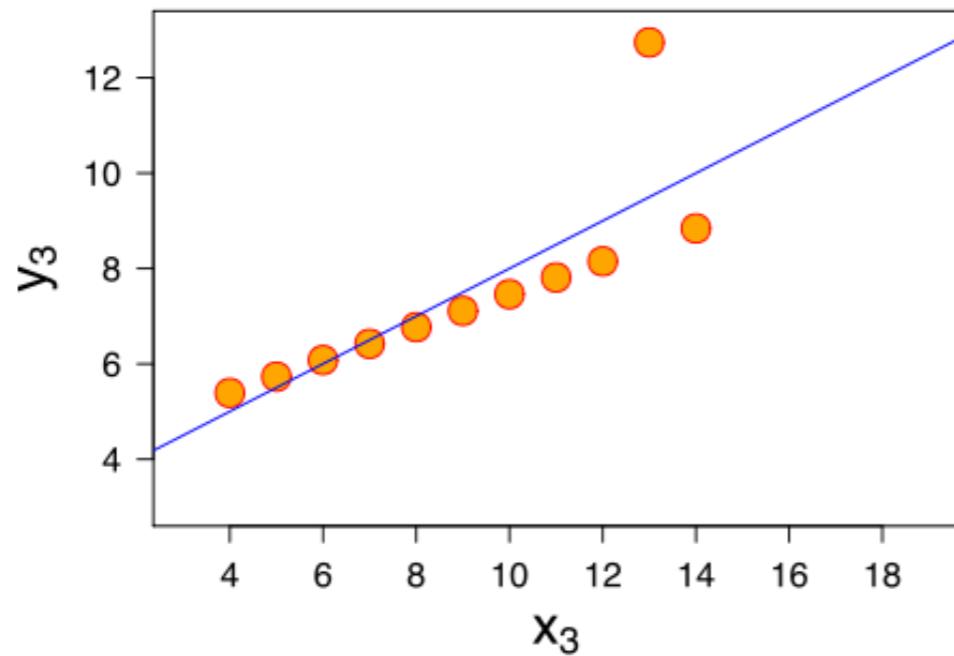
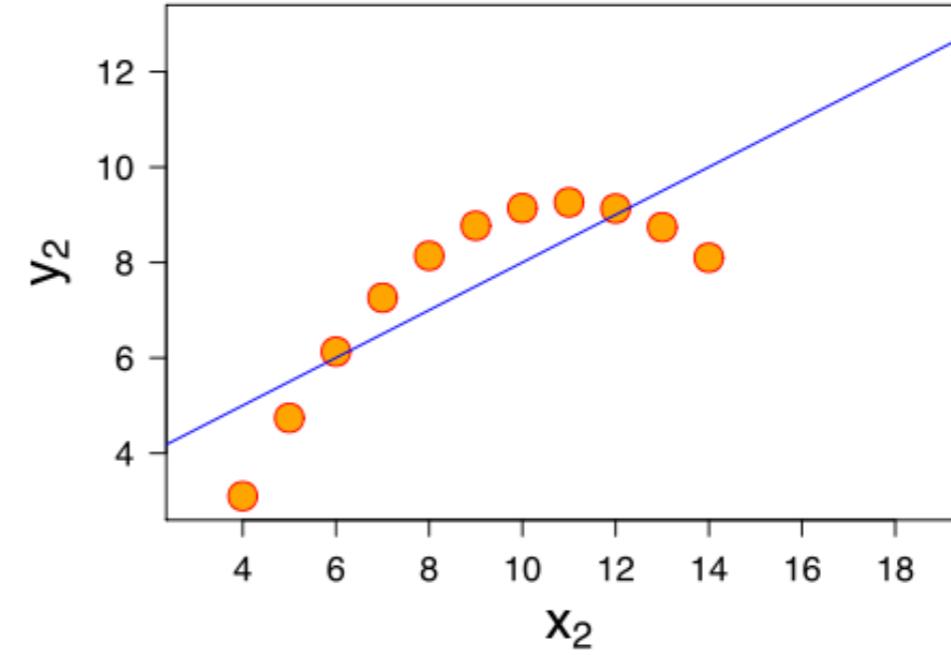
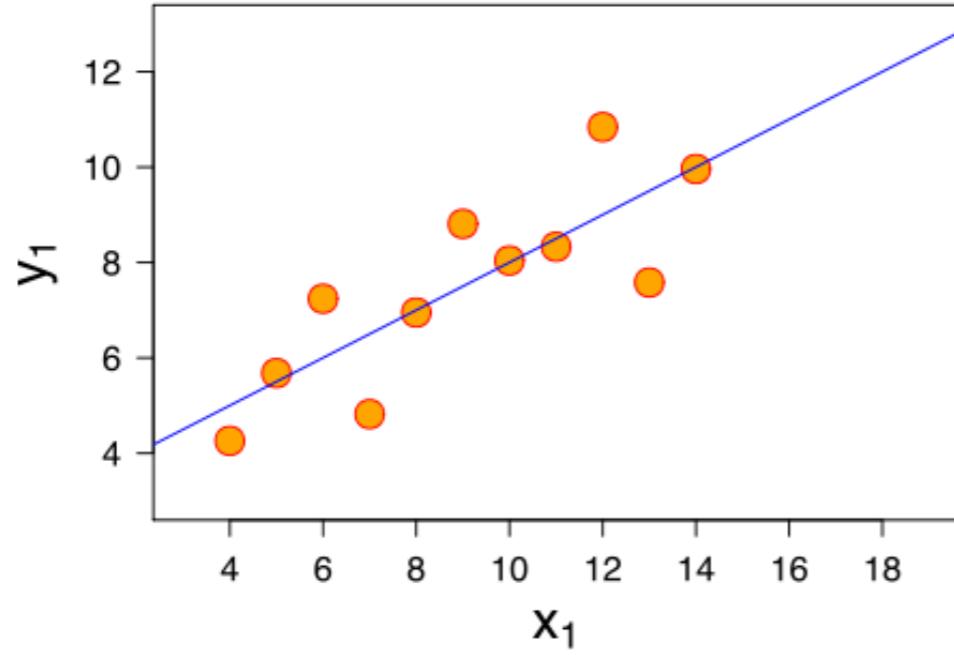
Bar chart with Error Bars



Bar graphs tend to be quite limited in terms of what they communicate. Here they communicate the means for levels of a factor and information about variance. But they don't tell us anything about the *distribution* of the data.

```
> data_summ <- data_long %>% group_by(Condition) %>% summarise(Mean = mean(RT), sd = sd(RT))
> ggplot (data_summ, aes (x=Condition, y=Mean, group=Condition, fill=Condition, ymin=Mean-sd,
+ ymax=Mean+sd)) + geom_bar(stat = "identity", width=.5) + geom_errorbar(width=.25) +
+ ggtile("Bar chart with Error Bars") + guides(fill=FALSE)
```

Anscombe's Quartet



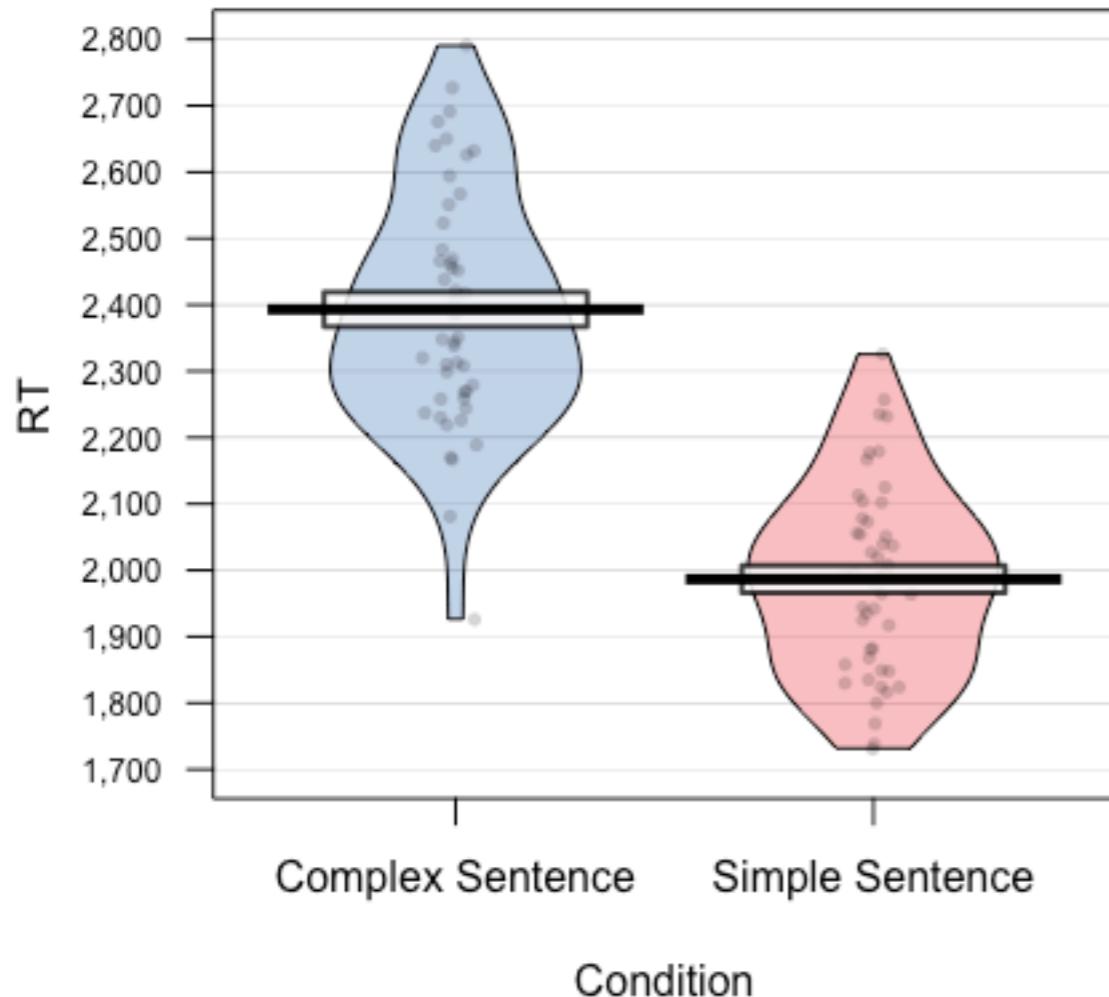
Violin Plots



Violin plots tell us about the distribution of the data. The width at any point corresponds to the *density* of the data at that value.

```
> ggplot (data_long, aes (x=Condition, y=RT, group=Condition, colour=Condition)) +  
  geom_violin() + geom_jitter(alpha=.5, position=position_jitter(0.05)) +  
  guides(colour=FALSE)
```

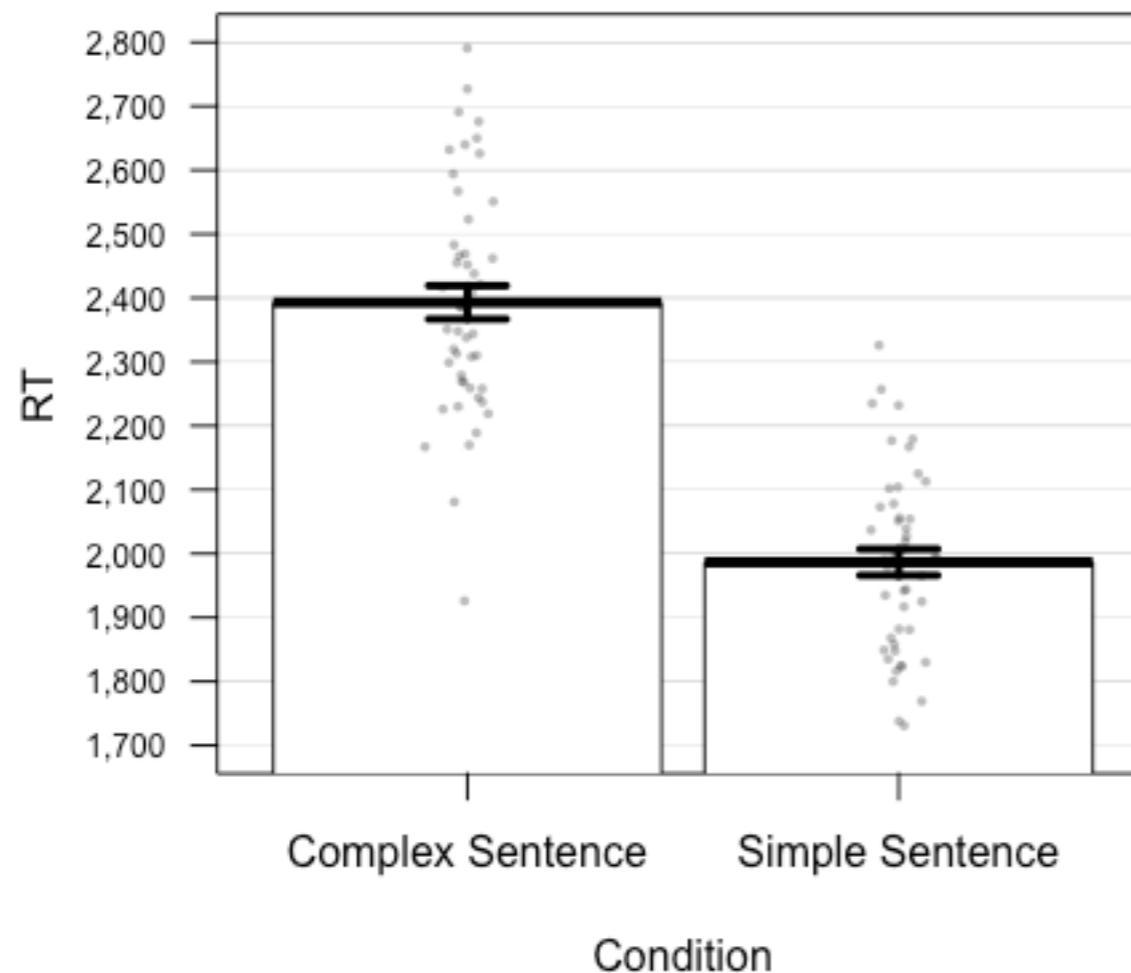
Pirate Plots



Pirate Plots are an example of RDI (Raw data, Descriptive and Inferential statistic) plots. Available in the package `yarr`. Plots include shape of distribution, mean, and SE (all changeable as parameters).

```
> pirateplot (formula=RT~Condition, data=data_long,  
inf.method="se", cex.axis=.75, theme=1)
```

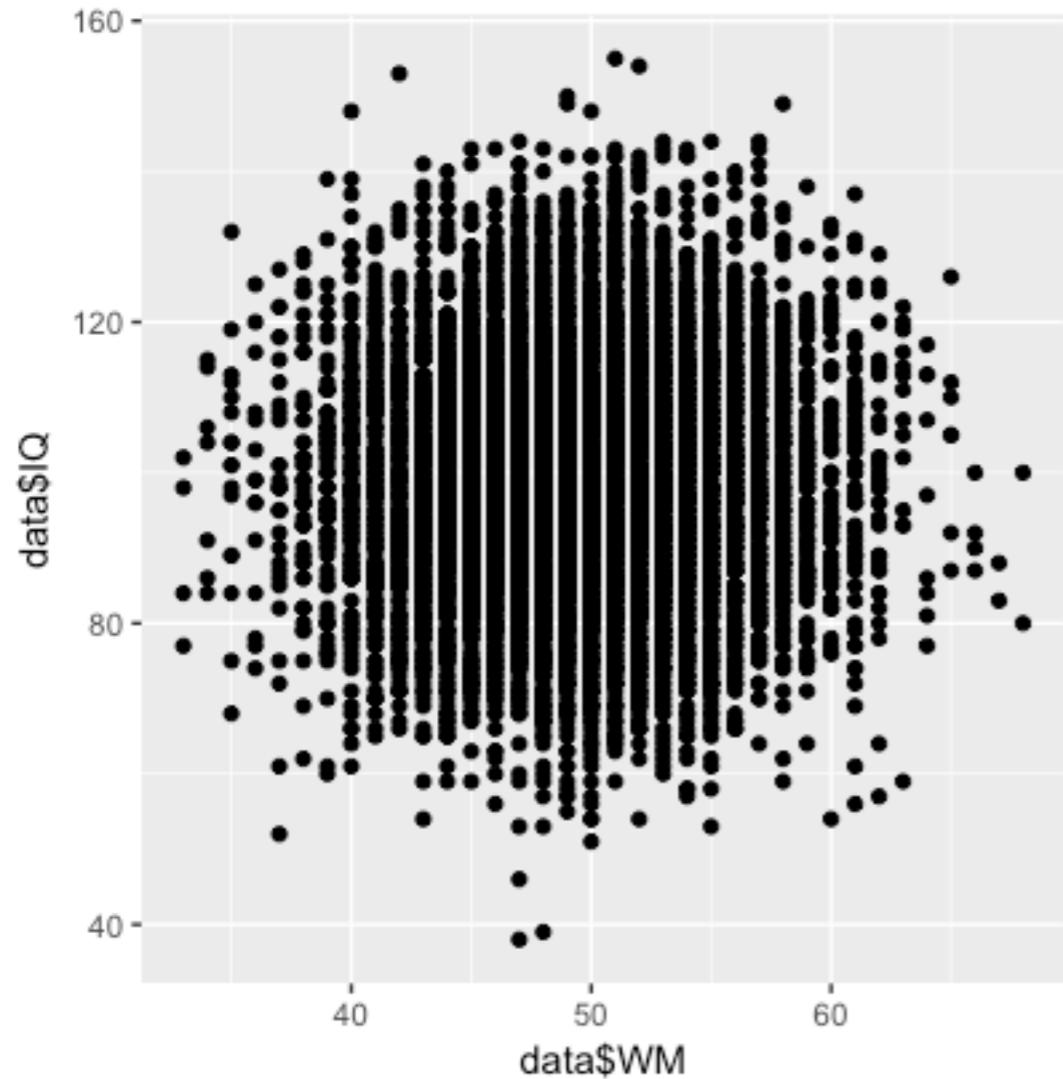
Combining Bar Graphs with Raw Data Plots



Bar graph plus the raw data.

```
> pirateplot(formula=RT~Condition, data=data_long, inf.method="se",  
cex.axis=.75, theme=4)
```

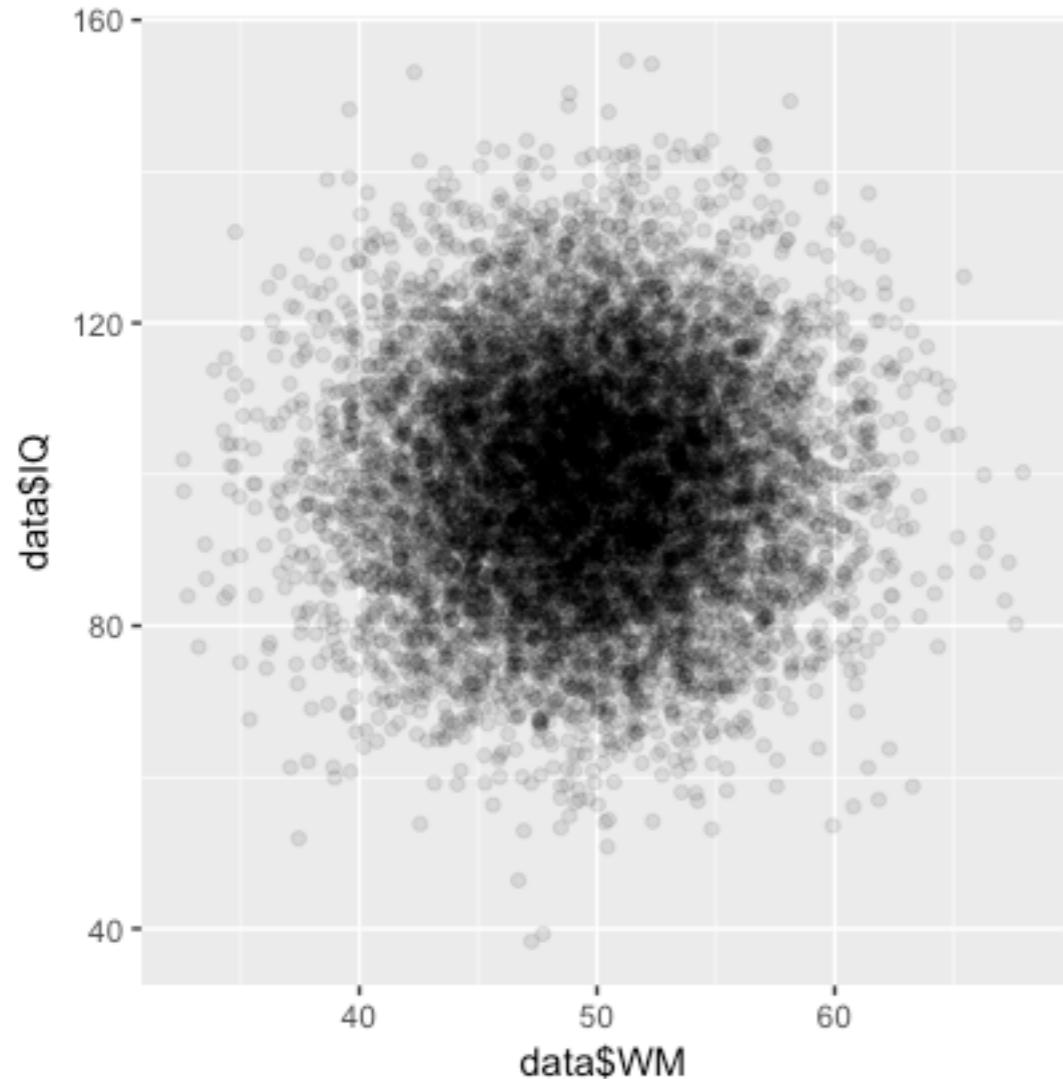
Plotting IQ against WM for our 10,000 participants



The problem of overplotting - as we have many data points, a number are plotted on top of each other so it is tricky to get a feel for the data.

```
ggplot (data, aes (x=data$WM, y=data$IQ)) + geom_point ()
```

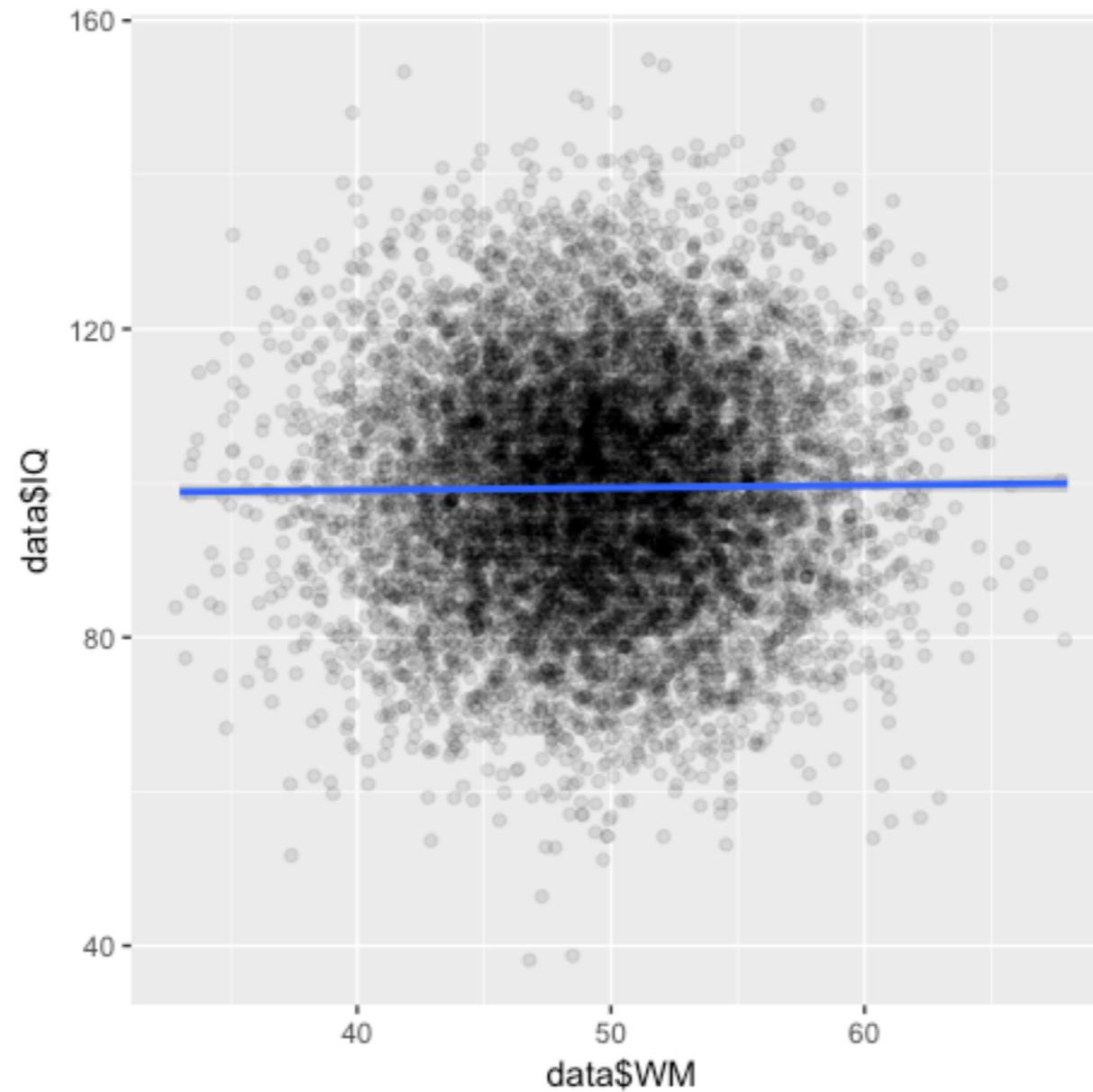
Plotting IQ against WM for our 10,000 participants



To avoid over-plotting, you can jitter the points and set them to be translucent via the alpha parameter.

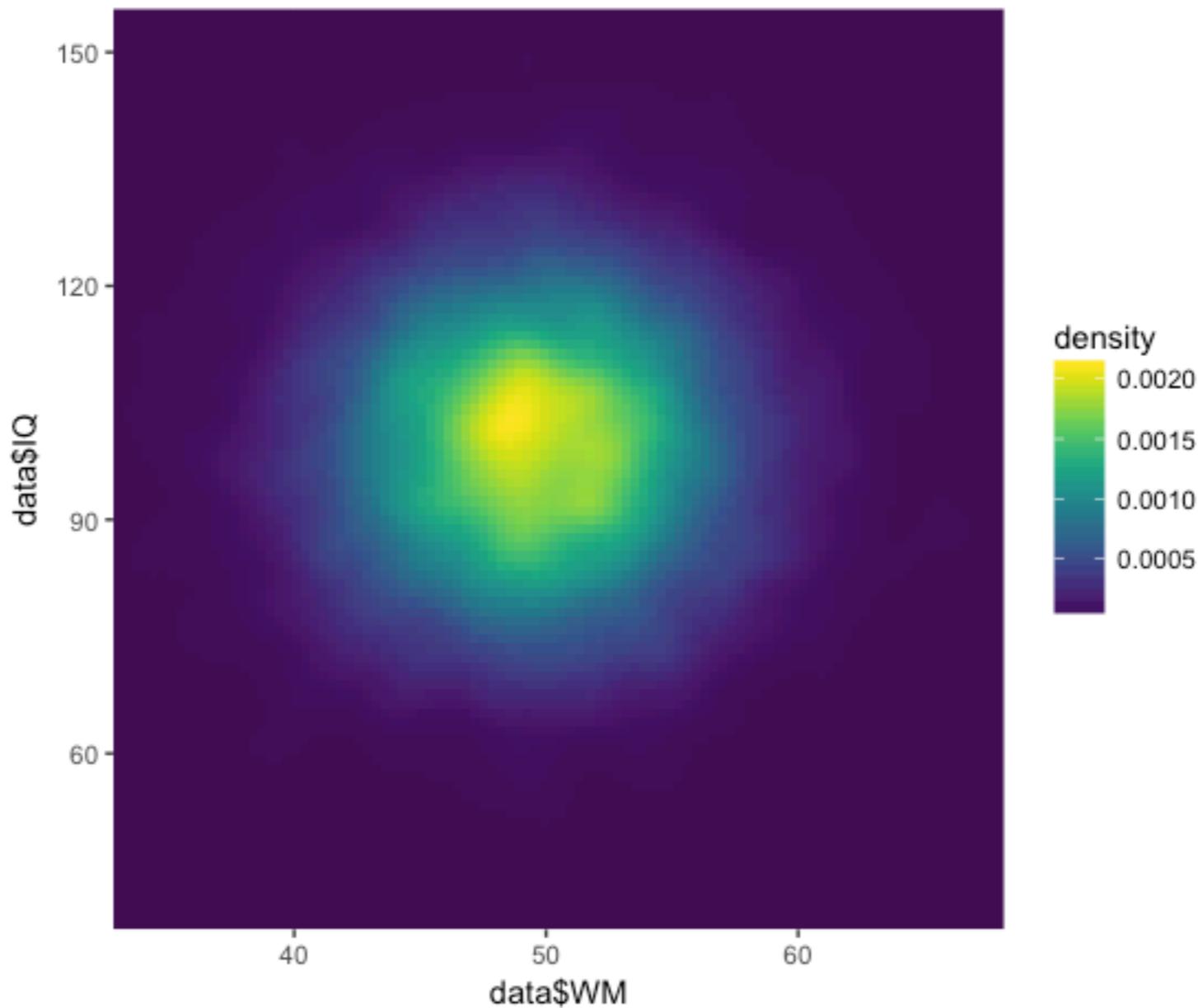
```
> ggplot (data, aes (x=data$WM, y=data$IQ)) + geom_jitter(alpha=.1,  
position=position_jitter(0.5))
```

With a regression line



```
> ggplot (data, aes (x=data$WM, y=data$IQ)) + geom_jitter(alpha=.1,  
position=position_jitter(0.5)) + geom_smooth(method="lm")
```

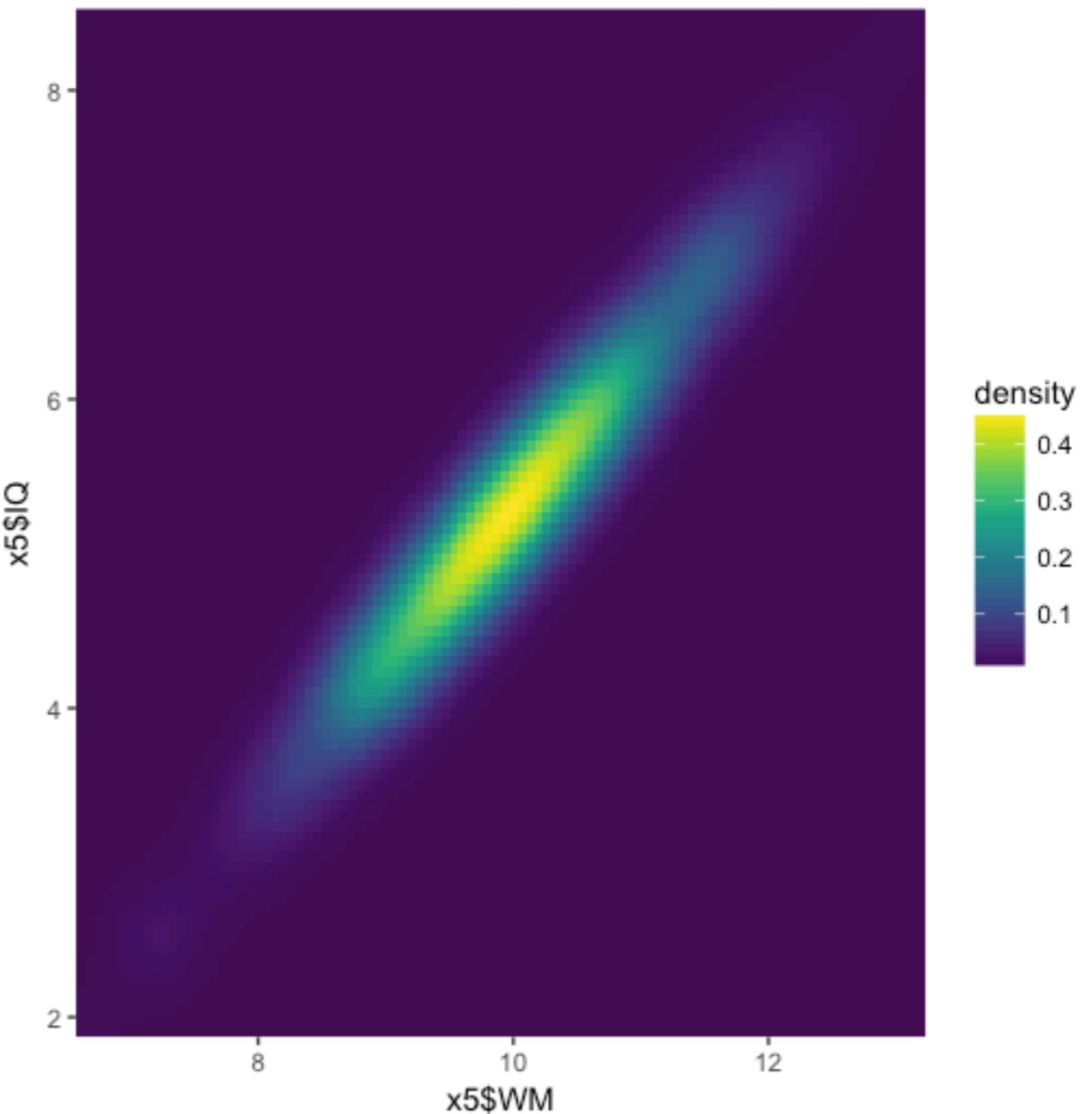
And as a Density Heat Map



```
> ggplot (data, aes (x=data$WM, y=data$IQ)) + stat_density_2d(aes(fill = ..density..), geom = 'raster', contour = FALSE) + scale_fill_viridis() + coord_cartesian(expand = FALSE)
```

If IQ and WM were perfectly (positively) correlated, we'd have something like this...

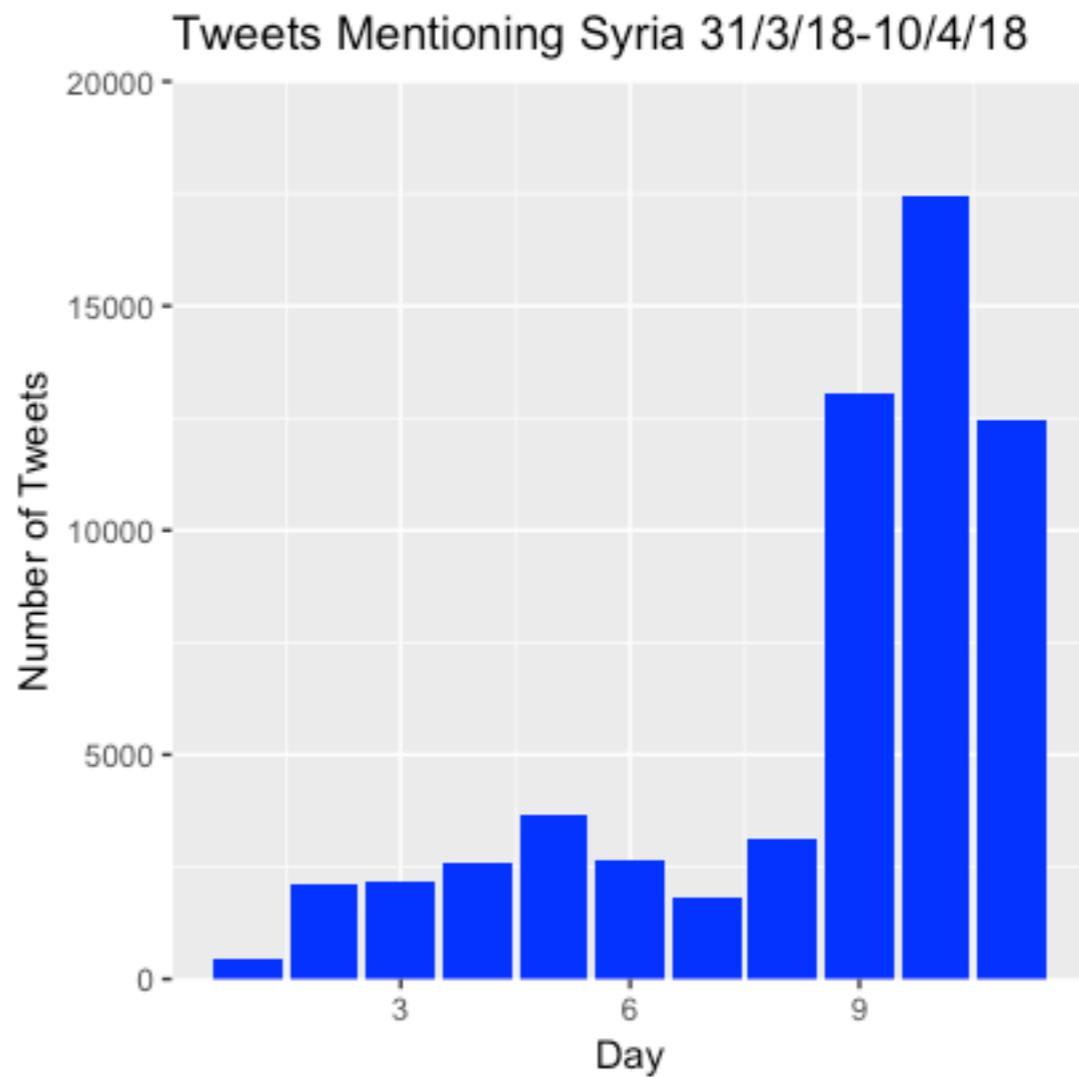
```
> #creating two perfectly correlated variables  
> set.seed(1234)  
> mysigma <- matrix (c(1,1,1,1),  
2,2)  
> x1 <- mvrnorm(n=1000,  
c(5.3,10), mysigma)  
> x5 <- as.data.frame (x1)  
> colnames(x5) <- c("IQ", "WM")  
  
> ggplot (x5, aes (x=x5$WM,  
y=x5$IQ)) +  
stat_density_2d(aes(fill  
= ..density..), geom = 'raster',  
contour = FALSE) +  
scale_fill_viridis()  
+coord_cartesian(expand = FALSE)
```



Visualising ‘Big Data’

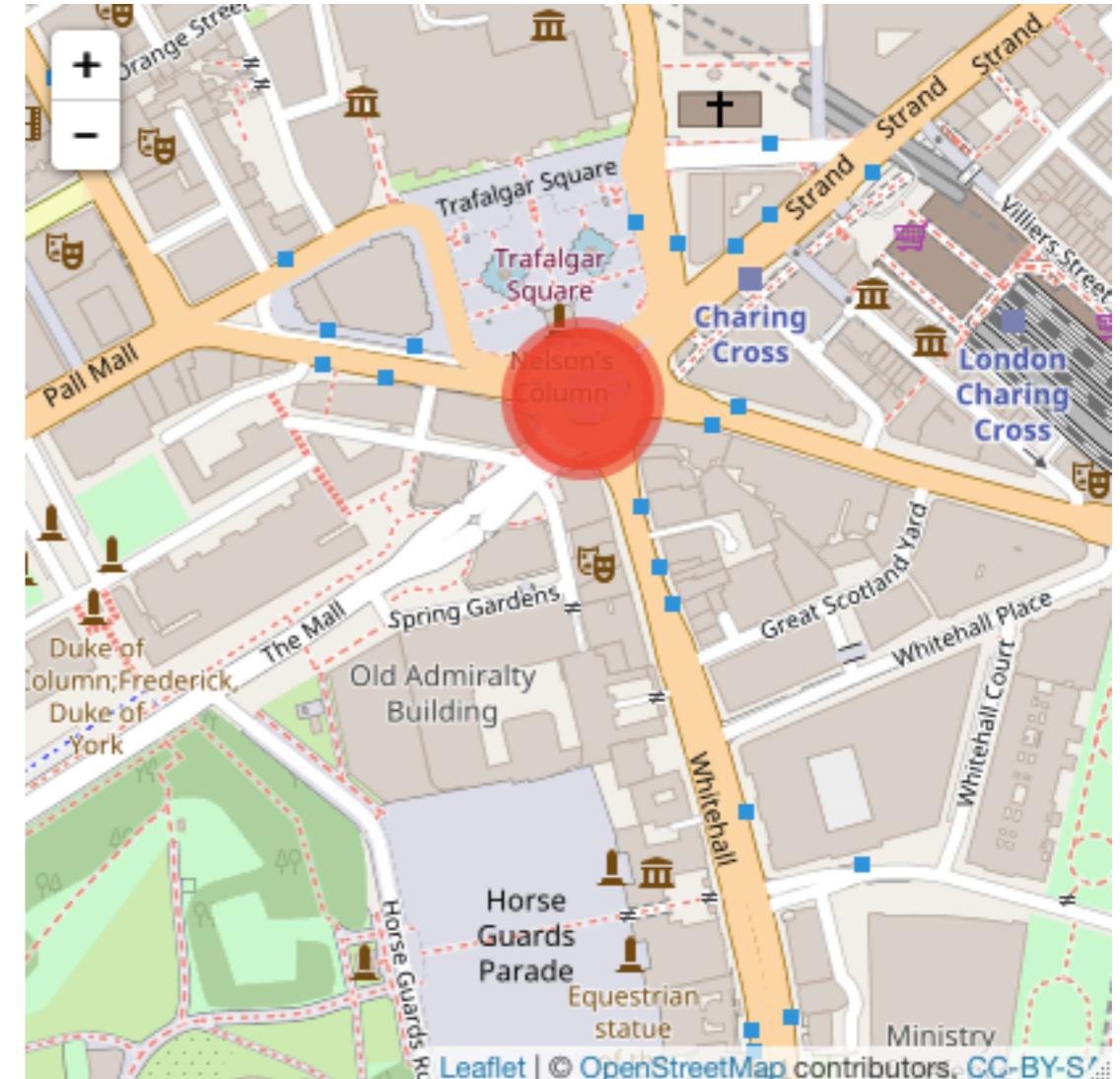
The R package, *rtweet*, can be used to scrape Twitter for mentions of particular topics. Connects via the Twitter Developer API.

In this case I scraped for up to 1,000,000 Tweets mentioning “Syria” around the time of the April chemical attack.

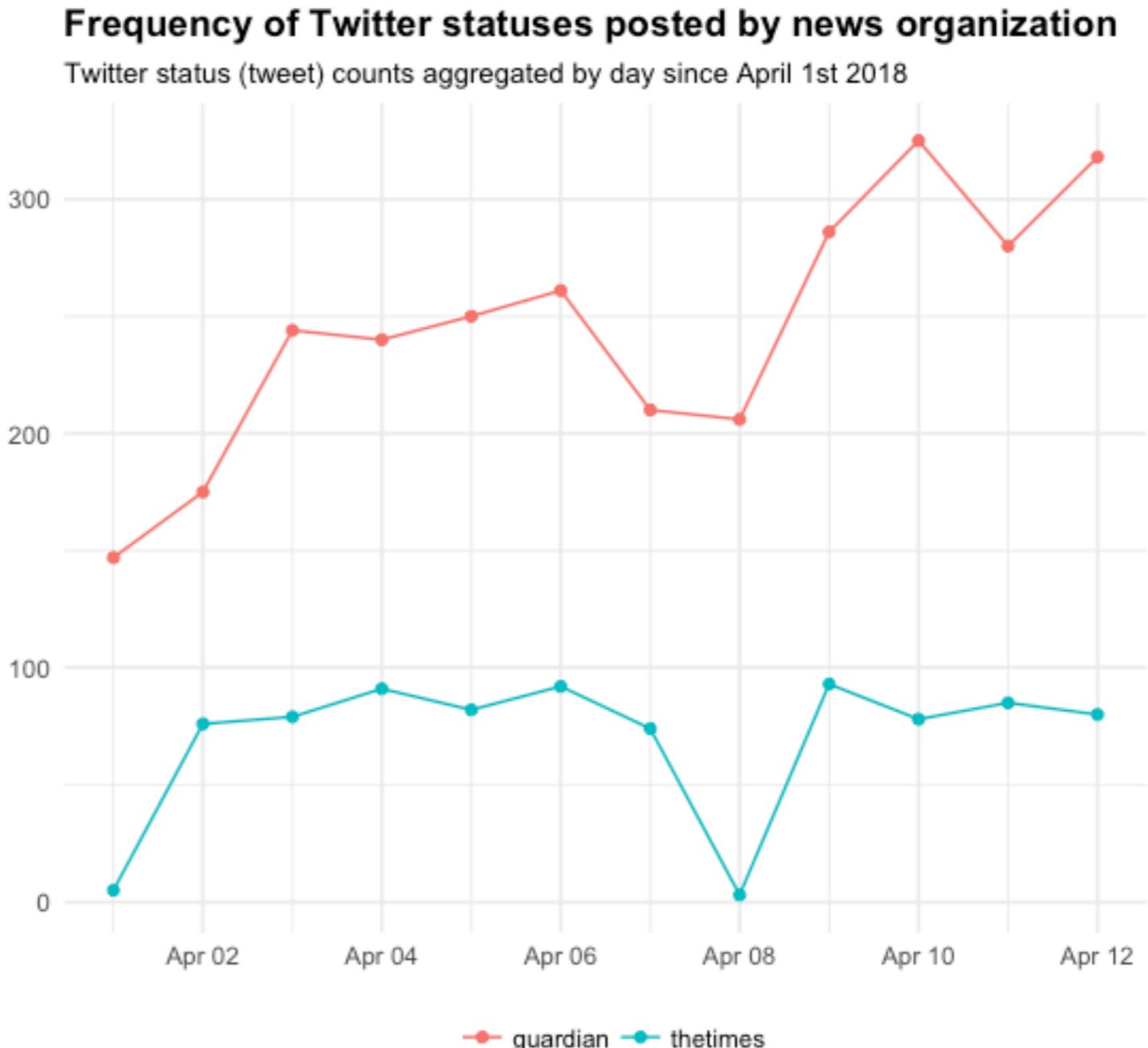


Geospatial mapping

If geospatial tagging has been activated by the user, Tweets will have geospatial co-ordinates attached to them. We can then use the *maps* and *leaflet* packages to plot the location of these Tweets.

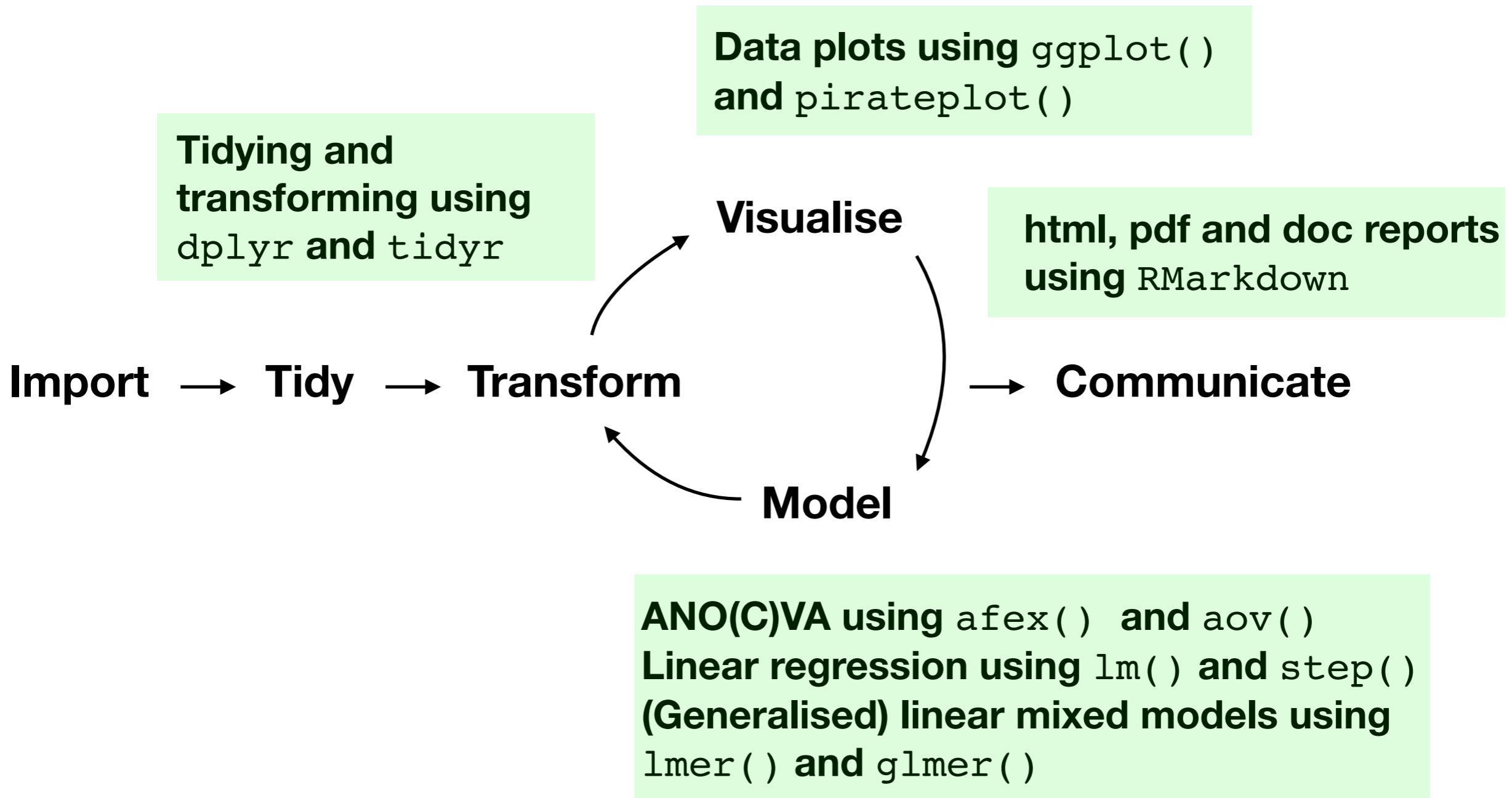


Can also focus on specific Twitter accounts and calculate (e.g.) Tweet frequency.

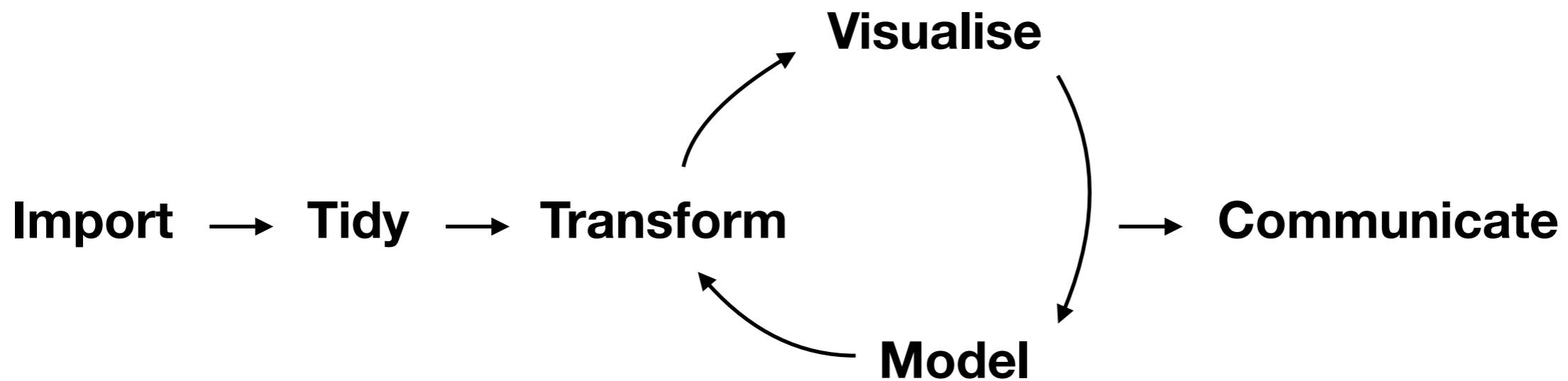


Source: Data collected from Twitter's REST API via rtweet

Workflow



Workflow



ANO(C)VA using `afex()` and `aov()`
Linear regression using `lm()` and `step()`
(Generalised) linear mixed models using `lmer()` and `glmer()`

Model

- Today we will focus on generating descriptive stats using the psych package, AN(C)OVA for different designs, and on simple linear and multiple regression (incl. model selection using AIC).
- Tomorrow we will focus on (Generalised) Linear Mixed Models. Over the last ~ 8 years they have transformed how we analyse experimental data.

You don't need to re-invent the wheel...

- For any problem you want to solve, chances are others have had the same problem, solved it and have created an R package to do exactly what you want...
- One of the many great things about R is that you can add freely available packages to your library.
- ~11,000 R packages currently available
- The sites r-bloggers.com and rweekly.org are good places to find out about new packages.

The “psych” Package

```
> install.packages ("psych")  
  
> library (psych)
```

You can read documentation about any package by typing :

```
> help (package name)
```

“psych” contains many helpful functions including *describeBy*.

To get help on any function, just type:

```
> help (function name)
```

This parameter specifies what data frame and variable we want descriptives for.

This parameter specifies how we want our descriptives grouped.

```
> describeBy (data_long$RT, group=data_long$Condition)
```

```
Descriptive statistics by group
group: Complex Sentence
  vars n   mean     sd median trimmed    mad   min   max range skew kurtosis      se
x1     1 48 2393.04 180.89 2368.5 2390.93 163.09 1926 2791   865 0.11 -0.3 26.11
-----
group: Simple Sentence
  vars n   mean     sd median trimmed    mad   min   max range skew kurtosis      se
x1     1 48 1986.6 143.07 1992 1981.72 163.83 1731 2326   595 0.27 -0.64 20.65
```

If we had a 2×2 design with Factor_1, Factor_2 and one DV in a data frame called data, to calculate the descriptives for each of our 4 conditions we would group like this:

```
> describeBy (data$DV, group=list(data$Factor_1, data$Factor_2))
```

You can type the name of the function itself (with no parameters), to see the code underlying it - great for transparency...

```
> describeBy
function (x, group = NULL, mat = FALSE, type = 3, digits = 15,
  ...)
{
  cl <- match.call()
  if (is.null(group)) {
    answer <- describe(x, type = type)
    warning("no grouping variable requested")
  }
  else {
    if (!is.data.frame(group) && !is.list(group) && (length(group) <
       NROW(x)))
      group <- x[, group]
    answer <- by(x, group, describe, type = type, ...)
    class(answer) <- c("psych", "describeBy")
  }
  if (mat) {
    ncol <- length(answer[[1]])
    n.var <- nrow(answer[[1]])
    n.col <- ncol(answer[[1]])
    n.grouping <- length(dim(answer))
    n.groups <- prod(dim(answer))
    names <- names(answer[[1]])
    row.names <- attr(answer[[1]], "row.names")
    dim.names <- attr(answer, "dimnames")
    mat.ans <- matrix(NaN, ncol = ncol, nrow = n.var * n.groups)
    labels.ans <- matrix(NaN, ncol = n.grouping + 1, nrow = n.var *
      n.groups)
    colnames(labels.ans) <- c("item", paste("group", 1:n.grouping,
      sep = ""))
    colnames(mat.ans) <- colnames(answer[[1]])
    rn <- 1:(n.var * n.groups)
    k <- 1
    labels.ans[, 1] <- seq(1, (n.var * n.groups))
    group.scale <- cumprod(c(1, dim(answer)))
    for (var in 1:(n.var * n.groups)) {
      for (group in 1:n.grouping) {
        groupi <- ((trunc((var - 1)/group.scale[group]))%%dim(answer)[group]) +
          1
        labels.ans[rn[var], group + 1] <- dim.names[[group]][[groupi]]}
```

ANOVA

- Imagine we're interested in the impact of caffeine consumption on an individual's motor performance.
- It's a between-subjects design with 3 conditions:
 - low amount of caffeine (single espresso)
 - large amount of caffeine (double espresso)
 - placebo group (water)

	Participant	Condition	Ability
1	1	Water	4.817174
2	2	Water	5.410972
3	3	Water	5.733776
4	4	Water	4.361721
5	5	Water	5.471650
6	6	Water	5.502422
7	7	Water	5.070104
8	8	Water	5.081347
9	9	Water	5.074219
10	10	Water	4.943985
11	11	Water	5.109123
12	12	Water	4.900645
13	13	Water	4.989498
14	14	Water	5.325784
15	15	Water	5.683798
16	16	Single Espresso	7.050372
17	17	Single Espresso	6.870046
18	18	Single Espresso	6.689962
19	19	Single Espresso	6.723273

Showing 1 to 20 of 45 entries

Our data look like this:

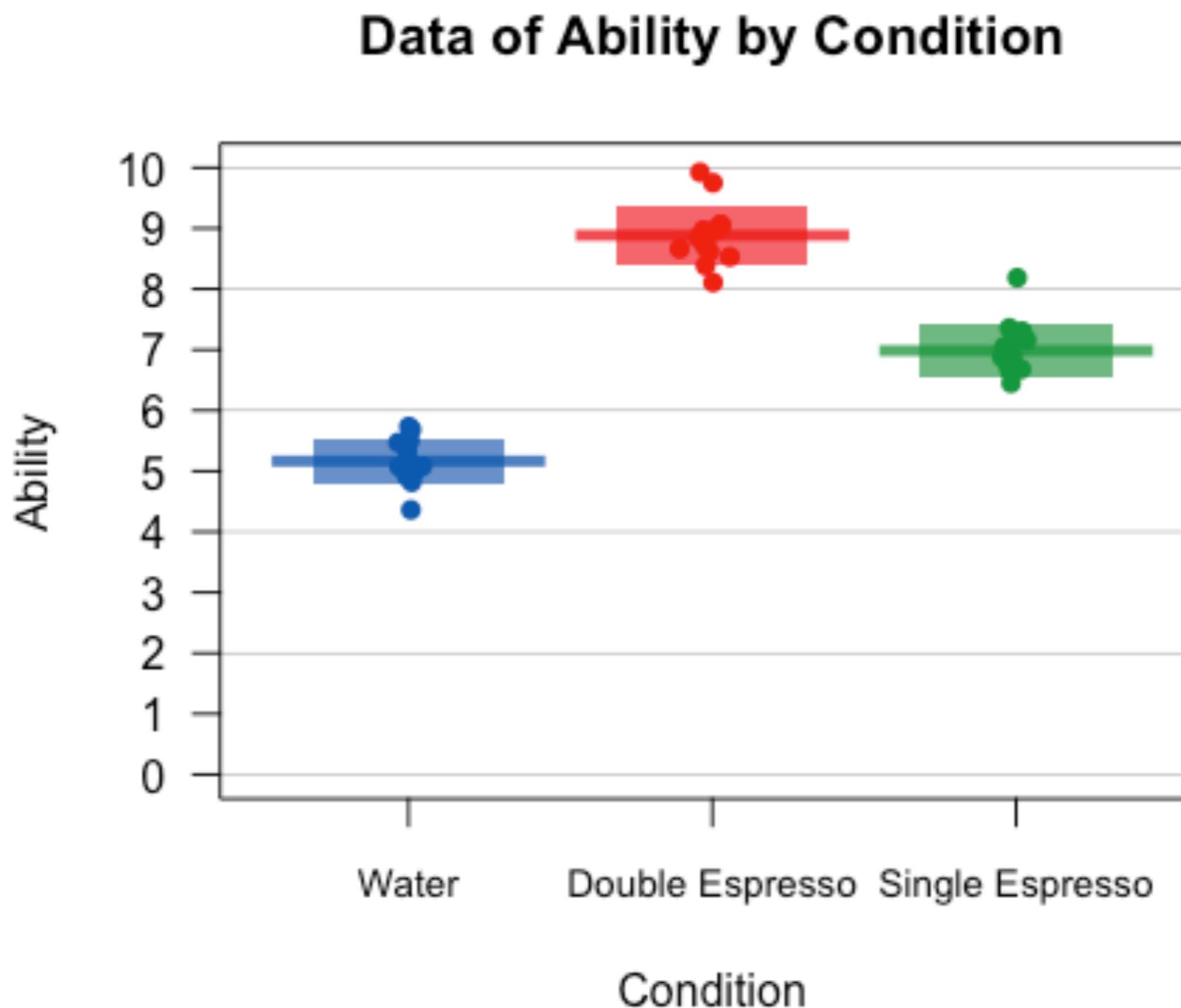
We have 45 participants, a between participants condition with 3 levels (Water vs. Single Espresso vs. Double Espresso), and Ability as our DV measured on a scale of 1-10.

First we need to load the packages we're going to use:

```
require (psych) # Gives us descriptive statistics  
require (yarr) # For building pirate plots  
require (ggplot2) # For building ggplots  
require (afex) # For Factorial ANOVA  
require (DescTools) # For generating effect sizes  
require (emmeans) # Allows us to run pairwise comparisons
```

If you haven't installed them previously, remember to type
> install.packages ("packagename")
first. Note, require basically does the same job as library.

Let's visualise the data first



Now some descriptives...

We're going to do this by using the *describeBy* function in the *Psych* package.

```
> describeBy (cond$Ability, group=cond$Condition)
```

```
> describeBy (cond$Ability, group=cond$Condition)
```

Descriptive statistics by group

group: Water

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
X1	1	15	5.17	0.36	5.08	5.18	0.36	4.36	5.73	1.37	-0.27	-0.49	0.09

group: Double Espresso

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
X1	1	15	8.89	0.47	8.85	8.87	0.31	8.11	9.92	1.81	0.72	0.05	0.12

group: Single Espresso

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
X1	1	15	6.99	0.42	6.88	6.93	0.3	6.45	8.19	1.74	1.4	1.83	0.11

Now let's run the 1-way ANOVA using the *aov* function (part of base R). We are going to assign it to a variable we are calling *model*.

```
> model <- aov(Ability ~ Condition, data=cond)
> anova(model)
Analysis of Variance Table

Response: Ability
          Df  Sum Sq Mean Sq F value    Pr(>F)
Condition   2 103.872  51.936  297.05 < 2.2e-16 ***
Residuals 42   7.343   0.175
---
Signif. codes:  0 '****' 0.001 '***' 0.01 '**' 0.05 '*' 0.1 '.' 1
```

Here's the output we get – the F value is the ratio of systematic variance to unsystematic variation. It is the Mean SS of Condition divided by Mean Residual SS.

To get the Mean Square values we divide the Sum of Squares by the associated degrees of freedom (e.g., $7.343 / 42 = 0.175$).

The ANOVA tells us we have an effect somewhere of Condition, but we don't yet know which level of this factor differs from which other level(s).

We need to conduct post hoc tests to figure this out. We can conduct both Bonferroni and Tukey pairwise comparisons using the `emmeans` function - Bonferroni is slightly more conservative than Tukey.

```
> emmeans (model, pairwise~Condition, adjust="Bonferroni")
$emmeans
  Condition      emmean       SE df lower.CL upper.CL
  Water          5.165081 0.1079627 42  4.947204 5.382959
  Double Espresso 8.886287 0.1079627 42  8.668409 9.104164
  Single Espresso 6.985001 0.1079627 42  6.767124 7.202879

Confidence level used: 0.95

$contrasts
  contrast           estimate       SE df t.ratio p.value
  Water - Double Espresso -3.721205 0.1526824 42 -24.372 <.0001
  Water - Single Espresso   -1.819920 0.1526824 42 -11.920 <.0001
  Double Espresso - Single Espresso 1.901285 0.1526824 42  12.453 <.0001

P value adjustment: bonferroni method for 3 tests
```

```

> emmeans (model, pairwise~Condition, adjust="Tukey")
$emmeans
  Condition      emmean       SE df lower.CL upper.CL
  Water          5.165081 0.1079627 42  4.947204 5.382959
  Double Espresso 8.886287 0.1079627 42  8.668409 9.104164
  Single Espresso 6.985001 0.1079627 42  6.767124 7.202879

Confidence level used: 0.95

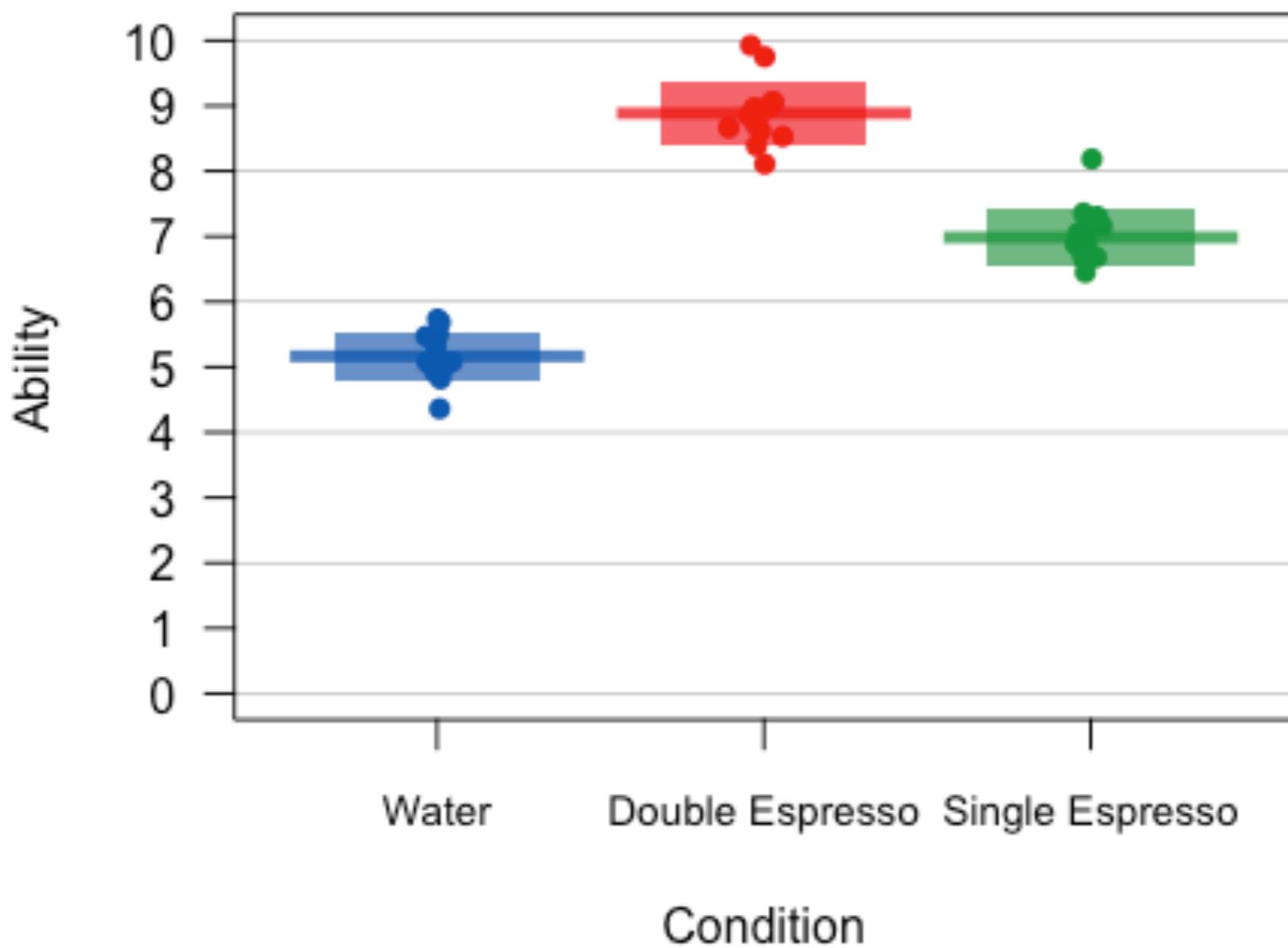
$contrasts
  contrast           estimate       SE df t.ratio p.value
  Water - Double Espresso -3.721205 0.1526824 42 -24.372 <.0001
  Water - Single Espresso   -1.819920 0.1526824 42 -11.920 <.0001
  Double Espresso - Single Espresso 1.901285 0.1526824 42  12.453 <.0001

P value adjustment: tukey method for comparing a family of 3 estimates

```

We could set `adjust="none"` if we wanted uncorrected p -values. But in this case, both Bonferroni and Tukey comparisons tell us the same thing - each condition differs from each other condition (which fits with what we saw in the graph)...

Data of Ability by Condition



Measure of Effect Size

- Effect size measures tell us how much variance can be explained by our experimental factors.
- partial η^2 is a correlation between the dependent variable and different levels of a factor.
- For designs with more than one factor it can be a useful indicator of how much variance in the dependent variable can be explained by each factor (plus any interactions between factors).

```
> EtaSq(model, type=3, anova=TRUE)
      eta.sq eta.sq.part      SS  df       MS          F   p
Condition 0.93397251  0.9339725 103.871817  2 51.9359084 297.0494  0
Residuals 0.06602749        NA    7.343252 42  0.1748393        NA NA
```

ANOVA for factorial designs

- A particularly good package for factorial ANOVA is by Henrik Singmann and called `afer`.
- Built to work like ANOVA in SPSS - uses Type III Sums of Squares with *effect coding* of contrasts. This overrides the default contrast coding in *R* which is for *dummy coding*.

Repeated measures example - I

Factor, 4 levels

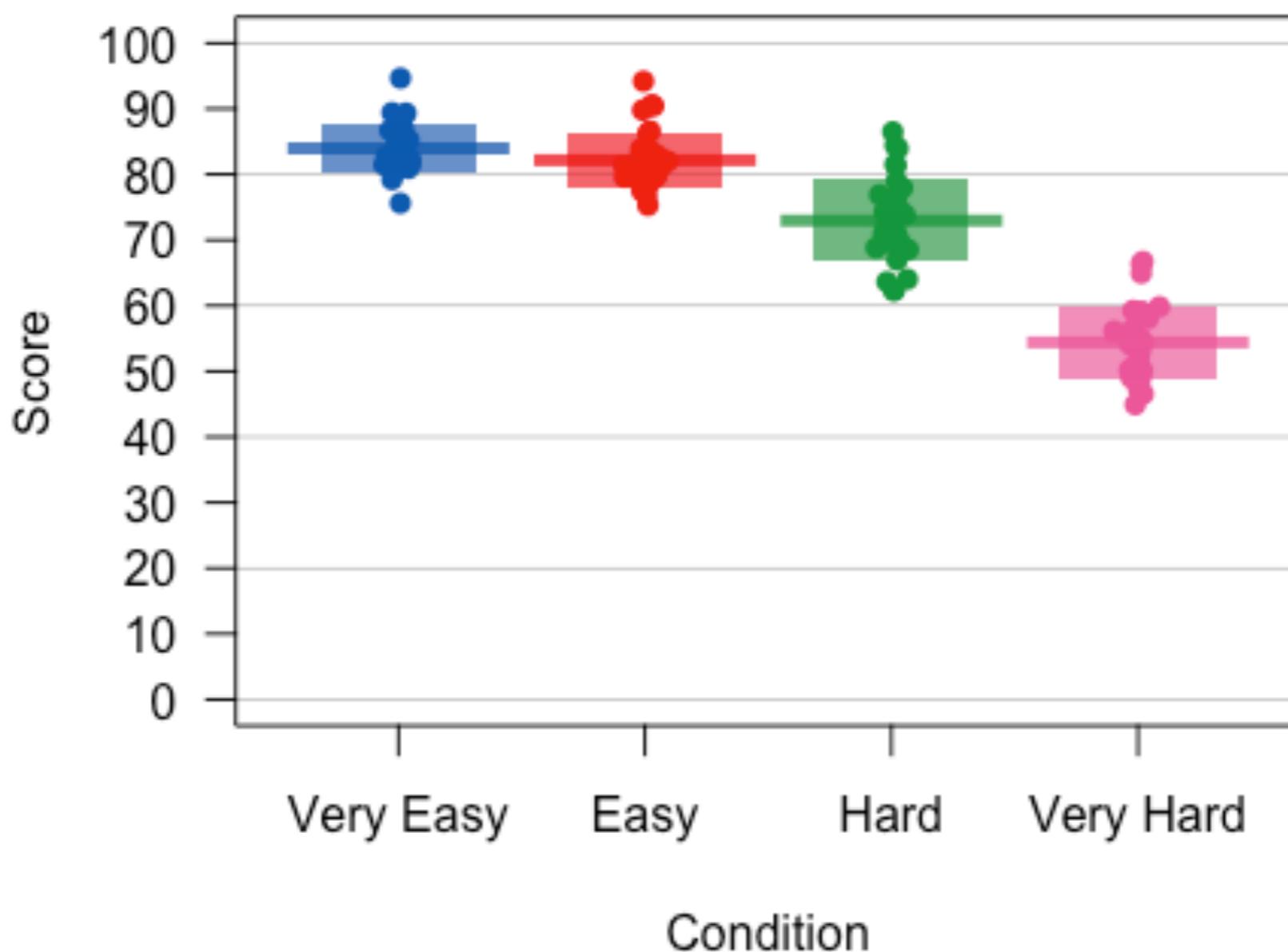
- Let's imagine we have an experiment where we asked 32 participants to memorise words of differing levels of spelling complexity - Very Easy, Easy, Hard, and Very Hard.
- They were presented with these words in an initial exposure phase. After a 30 minute break we tested them by asking them to write down all the words. We scored them as number correct for each condition.
- We want to know whether there is a difference in the number of words they remembered for each level of spelling complexity.

	Participant	Condition	Score
1	1	Very Easy	80
2	2	Very Easy	86
3	3	Very Easy	89
4	4	Very Easy	75
5	5	Very Easy	86
6	6	Very Easy	87
7	7	Very Easy	82
8	8	Very Easy	82
9	9	Very Easy	82
10	10	Very Easy	81
11	11	Very Easy	83
12	12	Very Easy	81

Showing 1 to 13 of 128 entries

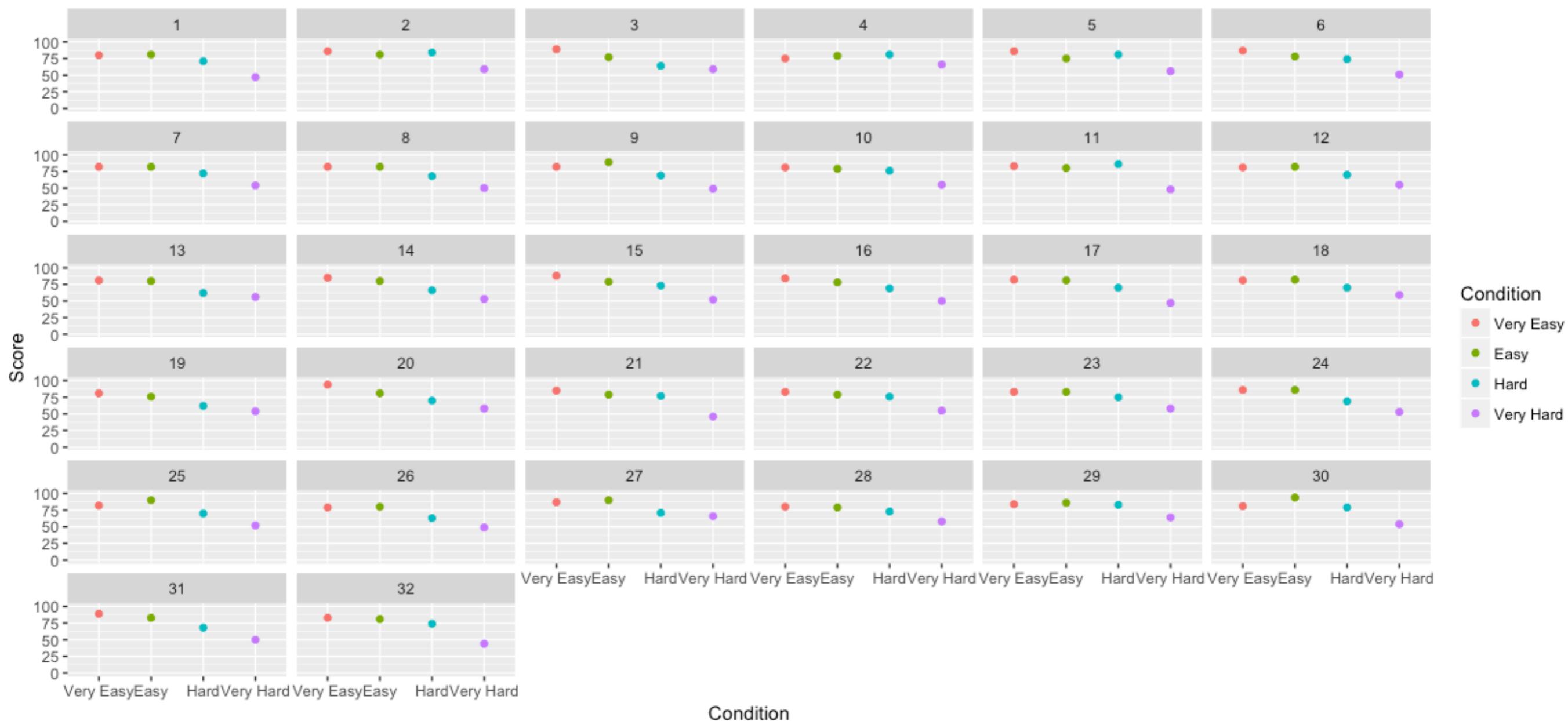
Our data are in long format with three columns - Participant, Condition, and Score.

Let's visualise the data first



We can use the `facet_wrap` function with `ggplot` to plot separate graphs for each participant on the same page:

```
> ggplot (data, aes (Condition, Score,  
colour=Condition)) + ylim(0,100) + geom_point () +  
facet_wrap (~data$Participant)
```



Now some descriptives...

We're going to do this by using the *describeBy* function in the *Psych* package.

```
> describeBy (data$Score, group=data$Condition)

  Descriptive statistics by group
group: Very Easy
    vars   n   mean     sd median trimmed   mad min max range skew kurtosis     se
X1      1 32 83.5 3.62       83    83.31 2.97   75   94     19  0.54      0.83 0.64
-----
group: Easy
    vars   n   mean     sd median trimmed   mad min max range skew kurtosis     se
X1      1 32 81.62 4.28       81    81.15 2.97   75   94     19  1.14      0.83 0.76
-----
group: Hard
    vars   n   mean     sd median trimmed   mad min max range skew kurtosis     se
X1      1 32 72.38 6.24       71    72.15 4.45   62   86     24  0.37     -0.56 1.1
-----
group: Very Hard
    vars   n   mean     sd median trimmed   mad min max range skew kurtosis     se
X1      1 32 53.97 5.5        54    53.62 5.93   44   66     22  0.42     -0.37 0.97
```

This is the our ANOVA model - we have a significant effect of Condition.

```
> model <- aov_4 (Score~Condition + (1+Condition|Participant), data=data)
> summary (model)
```

Univariate Type III Repeated-Measures ANOVA Assuming Sphericity

	SS	num Df	Error	SS	den Df	F	Pr (>F)
(Intercept)	679632	1	936.49	31	22497.36	< 2.2e-16	***
Condition	17509	3	2179.48	93	249.04	< 2.2e-16	***

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

Mauchly Tests for Sphericity

	Test statistic	p-value
Condition	0.90603	0.71042

Greenhouse-Geisser and Huynh-Feldt Corrections
for Departure from Sphericity

	GG	eps	Pr (>F[GG])
Condition	0.9401	< 2.2e-16	***

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

	HF	eps	Pr (>F[HF])
Condition	1.043895	2.615157e-44	

```
> anova (model)
Anova Table (Type 3 tests)

Response: Score
      num Df den Df     MSE      F     ges   Pr(>F)
Condition 2.8203  87.43 24.928 249.04 0.84892 < 2.2e-16 ***
---
Signif. codes:  0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The effect size is measured by ges which stands for generalised effect size (η_G^2) - this is the recommended effect size measure for repeated measures designs (Bakeman, 2005). We get this by using the *anova* function on our model. Note the dfs in this output are always corrected as if there is a violation of sphericity - to be conservative (and to avoid Type I errors) we might be better off to always choose these corrected dfs.

```
> anova (model)
Anova Table (Type 3 tests)

Response: Score
      num Df den Df      MSE          F      ges     Pr(>F)
Condition 2.8203  87.43 24.928 249.04 0.84892 < 2.2e-16 ***
---
Signif. codes:  0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So we know we have an effect of Condition, but we don't know where the difference lies...

Let's do some post hoc tests with Bonferroni corrected p -values...

```

> emmeans (model, pairwise~Condition, adjust="Bonferroni")
$emmeans
  Condition    emmean       SE   df lower.CL upper.CL
Very.Easy  83.50000 0.8861571 122.33 81.74581 85.25419
Easy        81.62500 0.8861571 122.33 79.87081 83.37919
Hard        72.37500 0.8861571 122.33 70.62081 74.12919
Very.Hard   53.96875 0.8861571 122.33 52.21456 55.72294

Confidence level used: 0.95

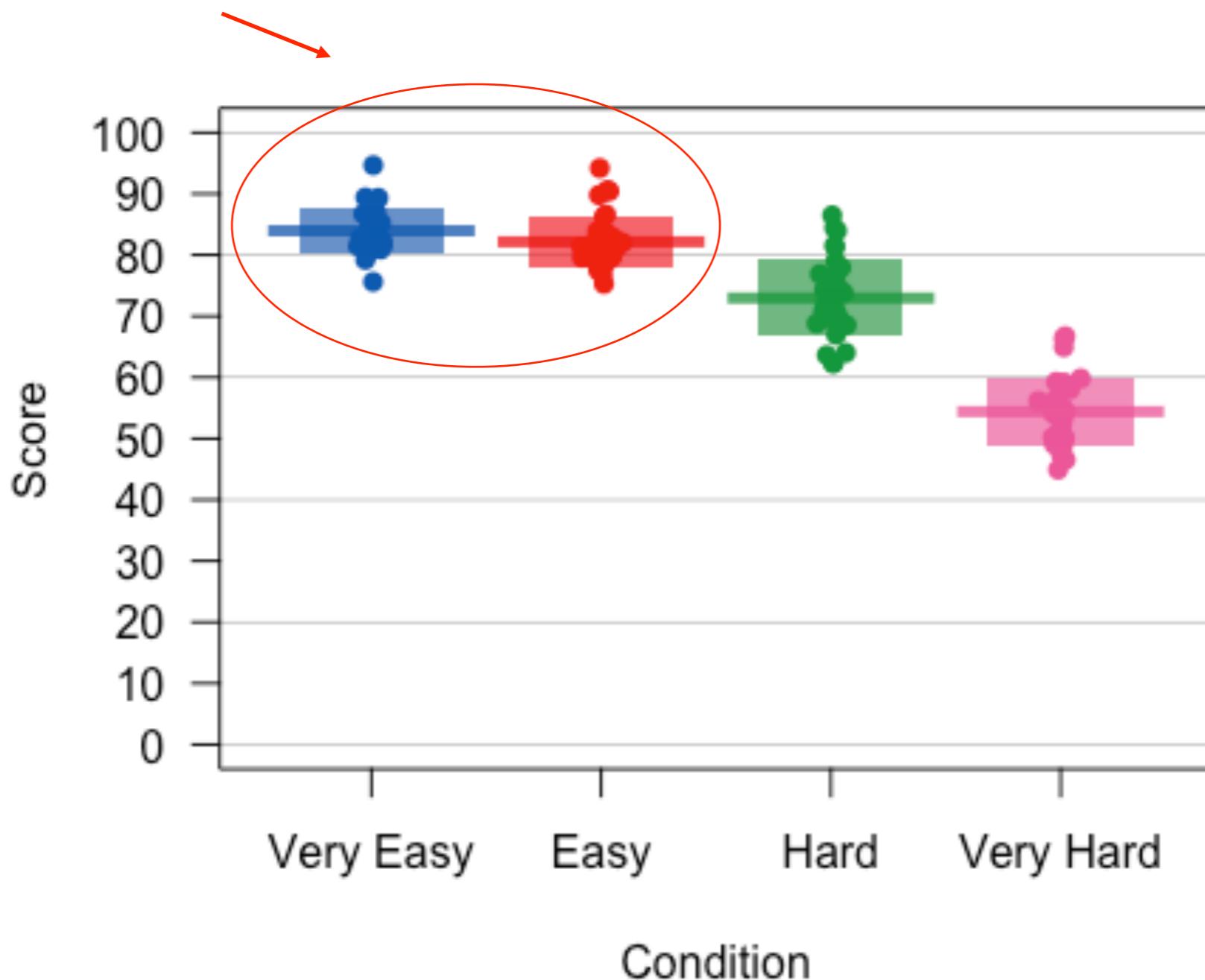
$contrasts
  contrast      estimate       SE   df t.ratio p.value
Very.Easy - Easy     1.87500 1.210249 93   1.549  0.7483
Very.Easy - Hard    11.12500 1.210249 93   9.192 <.0001
Very.Easy - Very.Hard 29.53125 1.210249 93  24.401 <.0001
Easy - Hard        9.25000 1.210249 93   7.643 <.0001
Easy - Very.Hard   27.65625 1.210249 93  22.852 <.0001
Hard - Very.Hard   18.40625 1.210249 93  15.209 <.0001

P value adjustment: bonferroni method for 6 tests

```

- We see each level differs from each other, apart from Very Easy vs. Easy (where $p = .75$).

These two are equivalent, while other pairwise differences are significant.



2 x 2 Example

- A 2 x 2 repeated measures design with the factors Sentence Type (Positive vs. Negative) and Context (Positive vs. Negative). DV is reaction time (RT).
- When the data file is in *long* format (i.e., each row is one observation):

	Subject	Item	RT	Sentence	Context
1	1	3	1270	Positive	Negative
2	1	7	739	Positive	Negative
3	1	11	982	Positive	Negative
4	1	15	1291	Positive	Negative
5	1	19	1734	Positive	Negative
6	1	23	1757	Positive	Negative
7	1	27	1052	Positive	Negative
8	2	4	1706	Positive	Negative
9	2	8	533	Positive	Negative
10	2	12	1009	Positive	Negative
11	2	16	939	Positive	Negative
12	2	20	1848	Positive	Negative
13	2	24	1435	Positive	Negative

Showing 1 to 14 of 1,680 entries

```
1 install.packages("afex")
2 library (afex)
3
4 aov_4(RT ~ Sentence*Context + (1+Sentence*Context|Subject), data=DV, na.rm=TRUE)
```

- Syntax corresponds to RT being predicted by the two factors (Sentence*Context corresponds to two main effects plus the interaction) plus the random effect by Subjects using the datafile called DV. By setting na.rm to be TRUE, we are telling the analysis to ignore individual trials where there might be missing data - effectively this calculates the condition means over the data that is present (and just ignores trial where it is missing).
- aov_4 aggregates over the grouping term in the random effect. Simply change to (1+Sentence*Context| Item) for by-item (i.e., F2) analysis. This requires the data to contain the individual observations (not aggregated as means).

By Subjects

```
> model <- aov_4 (RT ~ Sentence*Context + (1+Sentence*Context | Subject),  
  data=DV, na.rm=TRUE)  
  
> anova (model)  
Anova Table (Type 3 tests)  
  
Response: RT  


|                  | num Df | den Df | MSE    | F      | ges       | Pr(>F)    |
|------------------|--------|--------|--------|--------|-----------|-----------|
| Sentence         | 1      | 59     | 124547 | 0.6283 | 0.0016524 | 0.43114   |
| Context          | 1      | 59     | 90195  | 3.1767 | 0.0060231 | 0.07984 . |
| Sentence:Context | 1      | 59     | 93889  | 4.5967 | 0.0090449 | 0.03616 * |

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

- The output contains the main effect of Sentence, the main effect of Context, and the interaction between the two. Associated with each are the dfs, the Mean Squared Error, the F ratio, the generalized eta-squared, and p-value. Note, you can ask for partial eta-squared as effect size measure too.

By Items

```
> model1 <- aov_4 (RT ~ Sentence*Context + (1+Sentence*Context | Item),  
data=DV, na.rm=TRUE)  
  
> anova (model1)  
Anova Table (Type 3 tests)  
  
Response: RT  


|                  | num | Df | den | Df     | MSE    | F         | ges     | Pr(>F) |
|------------------|-----|----|-----|--------|--------|-----------|---------|--------|
| Sentence         |     | 1  | 27  | 203164 | 0.1221 | 0.0012553 | 0.72951 | .      |
| Context          |     | 1  | 27  | 39844  | 4.0013 | 0.0080150 | 0.05561 | .      |
| Sentence:Context |     | 1  | 27  | 40168  | 5.7687 | 0.0116070 | 0.02346 | *      |
| ---              |     |    |     |        |        |           |         |        |

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

- With the same datafile and just by changing one word in the analysis code.

Interpreting Interactions

We can build the model as before and pass the model to the function `emmeans` (remember to load the `emmeans` package) and ask for pairwise comparisons with no correction - we need to work out the Bonferroni corrected value ourselves...

```
> emmeans (model, pairwise ~ Sentence*Context, adjust="none")  
$emmeans  
  Sentence Context    emmean      SE      df lower.CL upper.CL  
Positive Positive 1579.181 57.78624 137.64 1464.917 1693.445  
Negative Positive 1627.877 57.78624 137.64 1513.614 1742.141  
Positive Negative 1594.889 57.78624 137.64 1480.625 1709.152  
Negative Negative 1473.962 57.78624 137.64 1359.698 1588.225
```

Confidence level used: 0.95

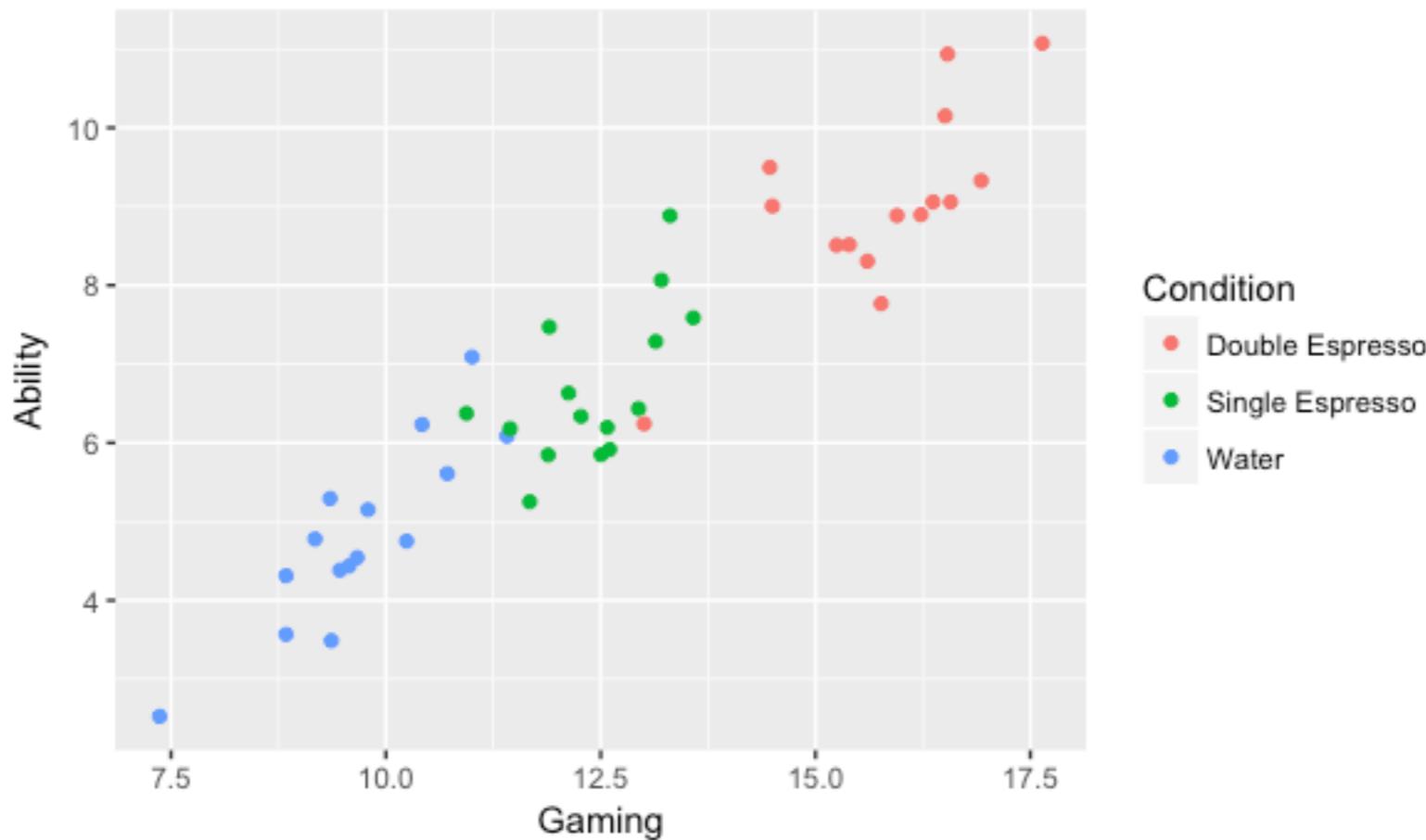
```
$contrasts  
  contrast                      estimate      SE      df t.ratio p.value  
Positive,Positive - Negative,Positive -48.69643 60.33730 115.72 -0.807 0.4213  
Positive,Positive - Positive,Negative -15.70794 55.39009 117.95 -0.284 0.7772  
Positive,Positive - Negative,Negative 105.21905 59.82499 115.06 1.759 0.0813  
Negative,Positive - Positive,Negative  32.98849 59.82499 115.06 0.551 0.5824  
Negative,Positive - Negative,Negative 153.91548 55.39009 117.95 2.779 0.0064  
Positive,Negative - Negative,Negative 120.92698 60.33730 115.72 2.004 0.0474
```

ANCOVA

- Earlier we looked at how double espresso vs. single espresso vs. water drinking (our IV) might influence people's computer game ability (our DV).
- Imagine we sampled from a new group of participants - and we think other factors that we are not manipulating might also influence the DV – e.g., practice with computer games.
- What we want is to be able to see the effect on our DV of our IV after we have removed the effects of other things (computer gaming frequency in this case).

- Now, imagine we have a measure of computer games frequency - perhaps hours per week people play computer games...
- So, in addition to manipulating the type of beverage we're giving people (i.e., double espresso vs. single espresso vs. water) we also measure how often they play computer games...
- Let's do a plot first with our DV (Ability) on the y-axis, and our covariate (Gaming Frequency) on the x-axis...

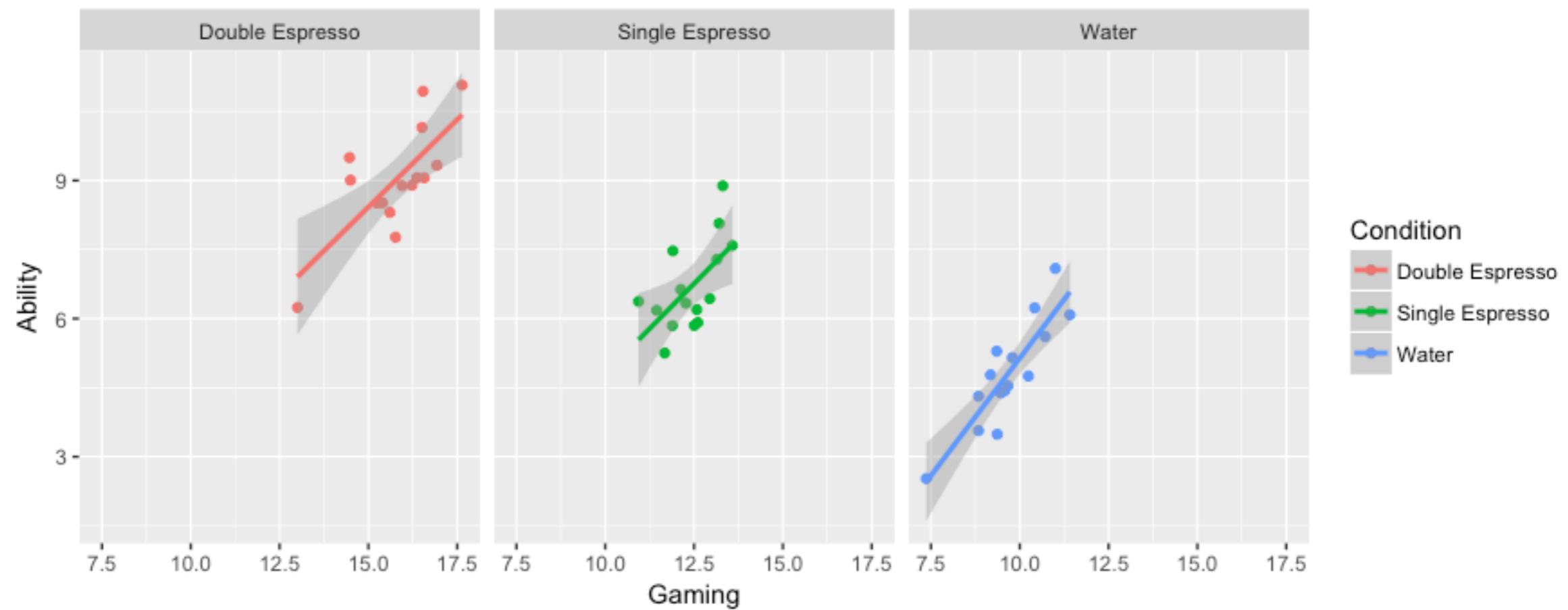
```
> ggplot (cond, aes (x=Gaming, y=Ability, colour=Condition)) + geom_point ()
```



- So we can see there's a relationship between our DV (Ability) and our covariate (Gaming Frequency)...
- We can also see our Gaming Ability groups appear to be clustering in our data by Condition...

We can look at the data separately by condition using the `facet_wrap()` function:

```
> ggplot (cond, aes (x=Gaming, y=Ability, colour=Condition)) +  
  geom_point () + facet_wrap ('Condition') +  
  geom_smooth(method='lm')
```



Running a 1-way between participants ANOVA (and ignoring the covariate)...

```
> model <- aov(Ability ~ Condition, data=cond)
> anova(model)
Analysis of Variance Table

Response: Ability
          Df  Sum Sq Mean Sq F value    Pr(>F)
Condition   2 132.746  66.373  53.432 2.882e-12 ***
Residuals 42  52.172   1.242
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The factor Condition is significant with an $F = 53.432$. We would erroneously conclude that our manipulation has had an effect...

But now let's control for the effect of our co-variate by adding it before our experimental manipulation...

```
> model_ancova <- aov(Ability ~ Gaming + Condition, data=cond)
> anova(model_ancova)
Analysis of Variance Table

Response: Ability
            Df  Sum Sq Mean Sq F value Pr(>F)
Gaming       1 161.329 161.329 292.4162 <2e-16 ***
Condition     2    0.968   0.484   0.8771 0.4236
Residuals   41  22.620   0.552
---
Signif. codes:  0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The factor Condition is now not significant with an $F < 1$. However, our covariate *Gaming Frequency* is significant. Adding it means a lot of the variance we previously attributed to our experimental factor is actually explained by our covariate (and our residual error goes down too)...

Rather than calculating over the raw means which are:

Water Group = 4.82

Double Espresso Group = 9.02

Single Espresso Group = 6.69

```
> describeBy (cond$Ability, group=cond$Condition)
```

Descriptive statistics by group

group: Double Espresso

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
x1	1	15	9.02	1.19	9.01	9.07	0.73	6.24	11.07	4.83	-0.26	0.16	0.31

group: Single Espresso

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
x1	1	15	6.69	0.98	6.37	6.63	0.78	5.25	8.88	3.63	0.69	-0.53	0.25

group: Water

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
x1	1	15	4.82	1.16	4.75	4.82	0.8	2.53	7.09	4.56	0.03	-0.57	0.3

The calculation is performed over the *adjusted* means (which take into consideration the influence of the covariate):

Water Group = 7.33

Double Espresso Group = 6.32

Single Espresso Group = 6.87

```
> emmeans (model_ancova, pairwise~Condition, adjust="none")
$emmeans
  Condition        emmean       SE df lower.CL upper.CL
  Double Espresso 6.319464 0.4152816 41 5.480786 7.158142
  Single Espresso  6.871614 0.1934303 41 6.480974 7.262255
  Water            7.327960 0.3931110 41 6.534056 8.121864
```

Confidence level used: 0.95

If our experimental factor in the ANCOVA had been significant, we could have looked at the pairwise comparisons reported by `emmeans` to determine what condition was different from what other condition...

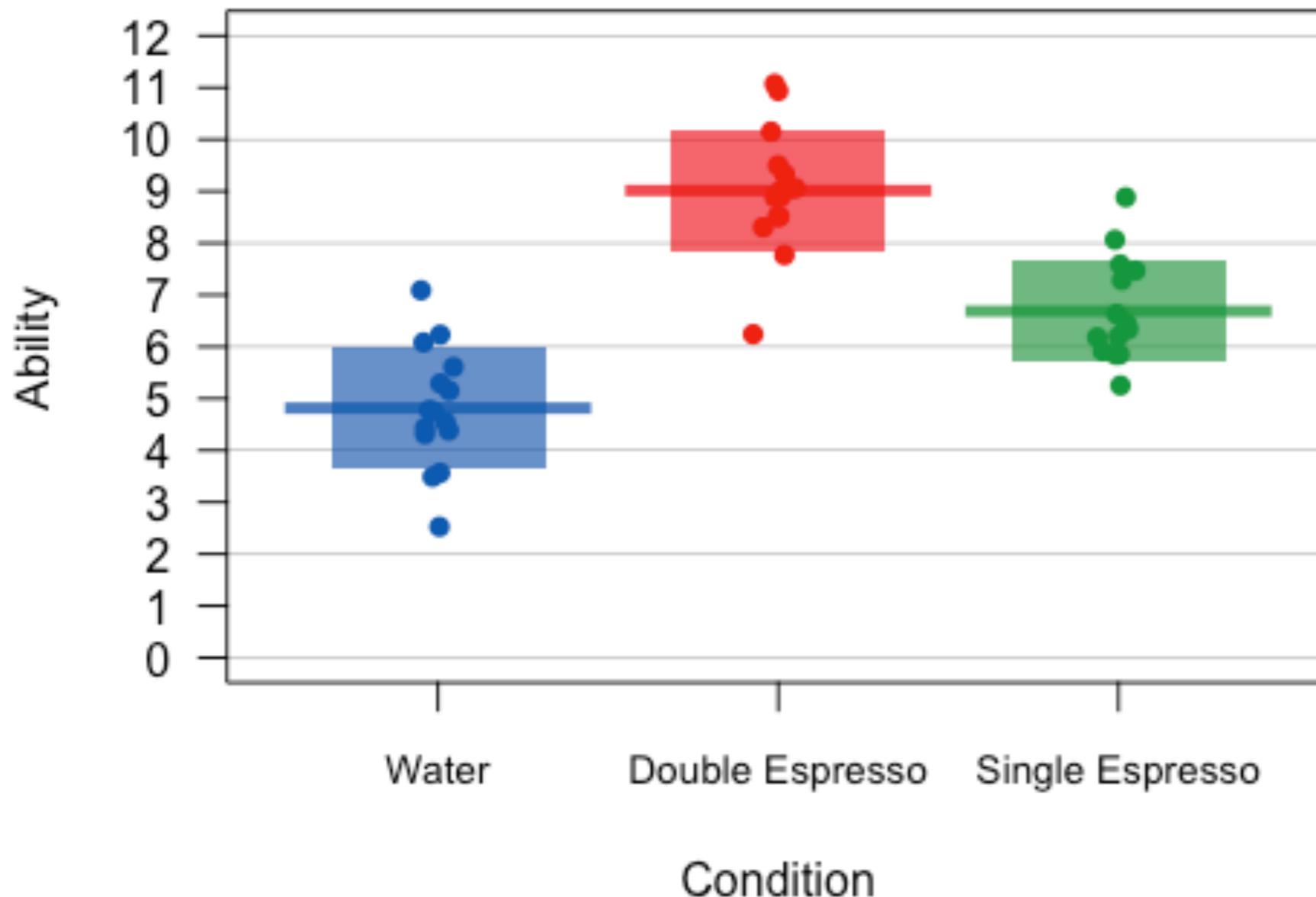
\$contrasts	contrast	estimate	SE	df	t.ratio	p.value
	Double Espresso - Single Espresso	-0.5521505	0.4779448	41	-1.155	0.2547
	Double Espresso - Water	-1.0084959	0.7614421	41	-1.324	0.1927
	Single Espresso - Water	-0.4563454	0.4179276	41	-1.092	0.2812

But once we take account of the influence of our covariate we found no effect of Condition...

AN(C)OVA as a special case of regression...

- Let's return to the example we looked at for ANCOVA - and let's forget the covariate for a moment...
- We looked at how double espresso vs. single espresso vs. water drinking (our IV) might influence people's motor task performance (our DV).

Data of Ability by Condition



Water mean = 4.82
Double Espresso mean = 9.02
Single Espresso mean = 6.69

- First we need to use dummy coding of the levels of our experimental factor - which is the default coding in *R* for factors...

```
> contrasts (cond$Condition)
          Double Espresso Single Espresso
Water                  0                 0
Double Espresso        1                 0
Single Espresso         0                 1
```

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Double Espresso}) + \beta_2(\text{Single Espresso}) + \varepsilon$$

The Intercept is our reference category (Water) with coding (0, 0), while the dummy coding for Double Espresso is (1, 0) and for Single Espresso (0, 1)

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Double Espresso}) + \beta_2(\text{Single Espresso}) + \varepsilon$$

We want to calculate β_1 and β_2

```
> lm1 <- lm(Ability ~ Condition, data=cond)
> lm1

Call:
lm(formula = Ability ~ Condition, data = cond)

Coefficients:
(Intercept) ConditionDouble Espresso ConditionSingle Espresso
              4.817                  4.199                  1.871
```

The intercept is 4.817 (which is the mean of our Water group), β_1 is 4.2, and β_2 is 1.87

To work out the mean Ability of our Double Espresso Group:

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Double Espresso}) + \beta_2(\text{Single Espresso}) + \varepsilon$$

$$\text{Ability} = 4.82 + 4.2(1) + 1.87(0) + \varepsilon$$

$$\text{Ability} = 4.82 + 4.2 + \varepsilon$$

$$\text{Ability} = 9.02 + \varepsilon$$

To work out the mean Ability of our Single Espresso Group:

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Double Espresso}) + \beta_2(\text{Single Espresso}) + \varepsilon$$

$$\text{Ability} = 4.82 + 4.2(0) + 1.87(1) + \varepsilon$$

$$\text{Ability} = 4.82 + 1.87 + \varepsilon$$

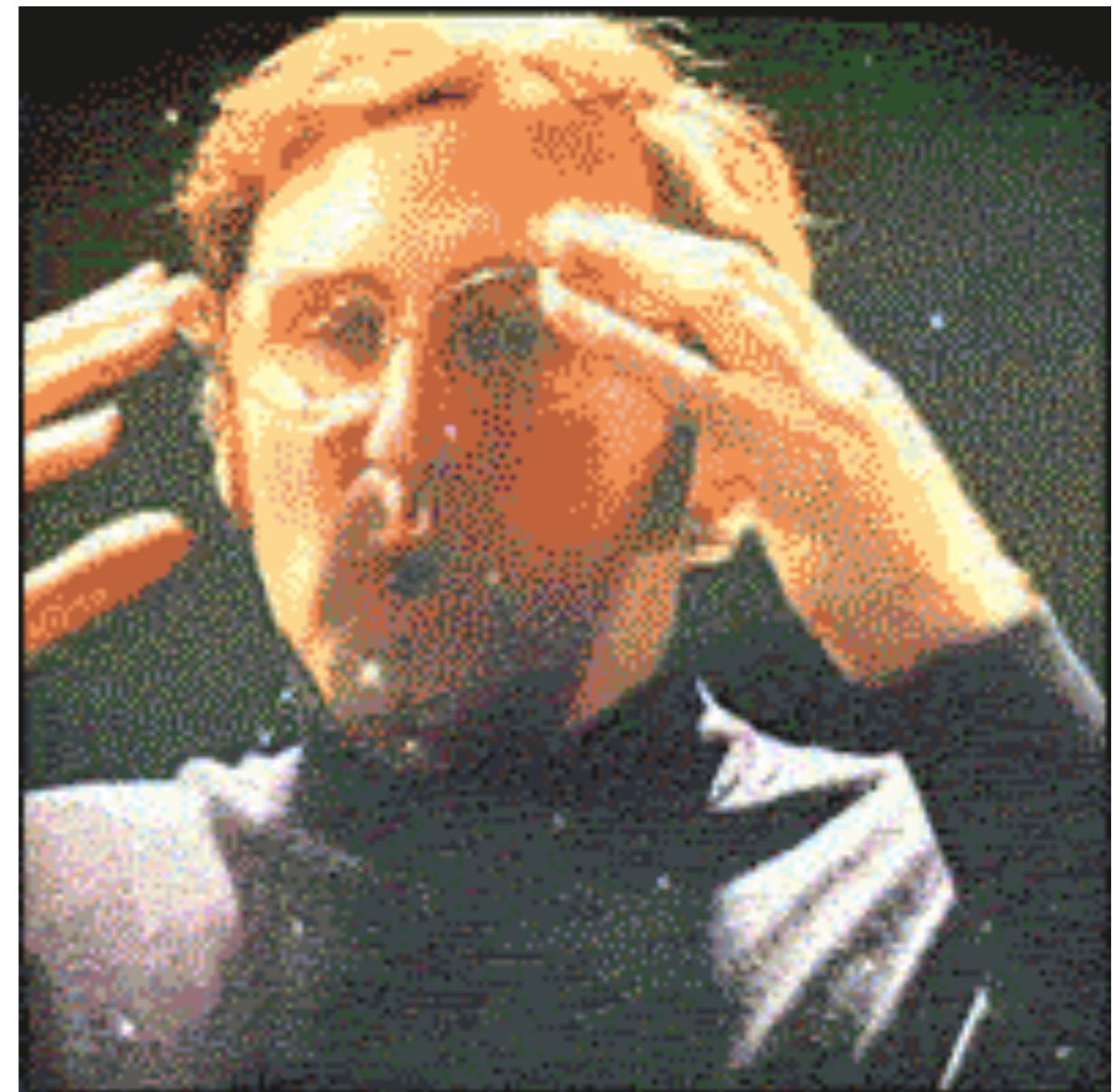
$$\text{Ability} = 6.69 + \varepsilon$$

Which are the exact same means generated by the ANOVA...

Water mean = 4.82

Double Espresso mean = 9.02

Single Espresso mean = 6.69



We can do ANCOVA like this too - let's consider our co-variate of Gaming frequency...

The *adjusted* means from the ANCOVA (which take into consideration the influence of the covariate) were:

Water Group = 7.33

Double Espresso Group = 6.32

Single Espresso Group = 6.87

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Gaming}) + \beta_2(\text{Double Espresso}) + \beta_3(\text{Single Espresso}) + \varepsilon$$

Add the covariate to our model *before* the experimental factor:

```
> lm2 <- lm(Ability ~ Gaming + Condition, data=cond)
> lm2
```

Call:
lm(formula = Ability ~ Gaming + Condition, data = cond)

Coefficients:

(Intercept)	Gaming	ConditionDouble Espresso	ConditionSingle Espresso
-3.4498	0.8538	-1.0085	-0.4563

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Gaming}) + \beta_2(\text{Double Espresso}) + \beta_3(\text{Single Espresso}) + \varepsilon$$

The β_2 and β_3 coefficients tell us the difference between each group mean (i.e., the adjusted mean) compared to the reference Group (Water) when taking into account the covariate of Gaming frequency:

β_2 is the difference between the Double Espresso and Water group adjusted means ($= -1.01$) while β_3 is the difference between the Double Espresso and Water group adjusted means ($= -0.46$)...

Let's check - the following are the adjusted means output by the ANCOVA model:

Water Group = 7.33

Double Espresso Group = 6.32

Single Espresso Group = 6.87

Difference between the Water and Double Espresso Group is 1.01 and the difference between the Water and Single Espresso Group is 0.46...

We can work out the mean of our reference group (Water) by plugging in the values to our equation - note that Gaming is not a factor and we need to enter the mean of this variable (which is 12.62296). So,...

$$\text{Ability} = \text{Intercept} + \beta_1(\text{Gaming}) + \beta_2(\text{Double Espresso}) + \beta_3(\text{Single Espresso}) + \varepsilon$$

$$\text{Ability} = -3.4498 + 0.8538(12.62296) + (-1.0085)(0) + (-0.4563)(0) + \varepsilon$$

$$\text{Ability} = -3.4498 + 10.777 + \varepsilon$$

$$\text{Ability} = 7.33 + \varepsilon$$

7.33 is the adjusted mean for the Water group...which is what we had from calling the *emmeans* function following the ANCOVA...

Multiple Regression in R

In Formula One, we suspect that the amount of money a team invests in their cars positively influences how many points the team scores in the championship. We also suspect that other factors influence how many points are scored - we have measures of car performance, driver age (in years) and media coverage. We want to determine the regression equation to account for the influence of these 4 predictors on the points scored by a team...

First we will build a linear model with all 4 predictors, then a second model with just the intercept (i.e., the mean) - we then compare them - is the model with the 4 predictors a better fit to our data than the model with just the mean?

```
> model.full <- lm (Points ~ Investment + Car_performance + Age + Media_coverage,  
data=regression)  
> model.null <- lm (Points ~ 1, data=regression)  
> anova (model.full, model.null)  
Analysis of Variance Table  
  
Model 1: Points ~ Investment + Car_performance + Age + Media_coverage  
Model 2: Points ~ 1  
  Res.Df   RSS Df Sum of Sq    F    Pr(>F)  
1     95  884.4  
2     99 1043.1 -4   -158.73 4.2625 0.003236 **  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The F-ratio comparing our two models is 4.2625 indicating our model with all the predictors is a better fit than our model with just the intercept (the mean). We then need to get our parameter estimates using the function `summary ()`

```
> summary (model.full)
```

Call:

```
lm(formula = Points ~ Investment + Car_performance + Age +  
Media_coverage,  
data = regression)
```

Residuals:

Min	1Q	Median	3Q	Max
-11.8120	-1.7164	-0.1836	1.9258	7.8733

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-268.72776	106.03555	-2.534	0.01290 *
Investment	0.38025	0.10566	3.599	0.00051 ***
Car_performance	-0.86504	0.56151	-1.541	0.12675
Age	-0.27148	0.26726	-1.016	0.31231
Media_coverage	0.02055	0.04777	0.430	0.66809

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

Residual standard error: 3.051 on 95 degrees of freedom

Multiple R-squared: 0.1522, Adjusted R-squared: 0.1165

F-statistic: 4.263 on 4 and 95 DF, p-value: 0.003236

Here we have our parameter estimates and the t-tests associated with our predictors.

Here are the R-squared and Adjusted R-squared values (which reflects number of predictors in our model).

```
> #as Investment is the only significant predictor, let's drop the others  
> model2 <- lm (Points ~ Investment, data=regression)  
> anova (model.full, model2)
```

```
> anova (model.full, model2)  
Analysis of Variance Table
```

```
Model 1: Points ~ Investment + Car_performance + Age + Media_coverage  
Model 2: Points ~ Investment  
  Res.Df   RSS Df Sum of Sq    F Pr(>F)  
1     95 884.40  
2     98 921.52 -3   -37.119 1.3291 0.2695
```

OK, so the models do not differ significantly by this test - we can also use another measure of goodness-of-fit - AIC (Akaike Information Criterion). AIC tells us how much information in our data is not captured by each model - lower values are better - can only be interpreted in a relative sense (i.e., comparing one model to another)...

```
> #choose model on basis of lower AIC value  
> AIC (model.full)  
[1] 513.7622  
> AIC (model2)  
[1] 511.8735
```

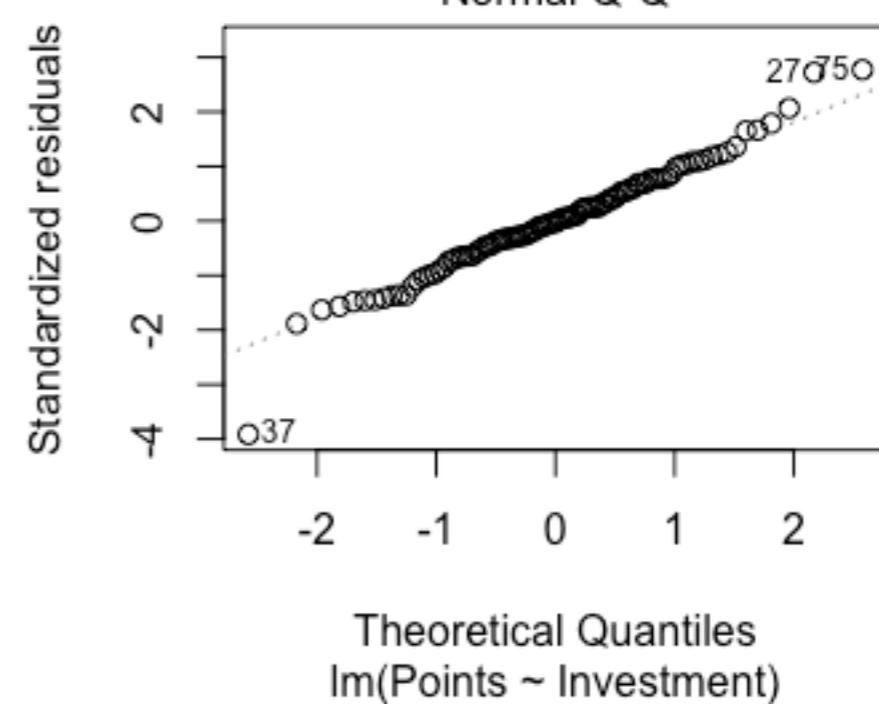
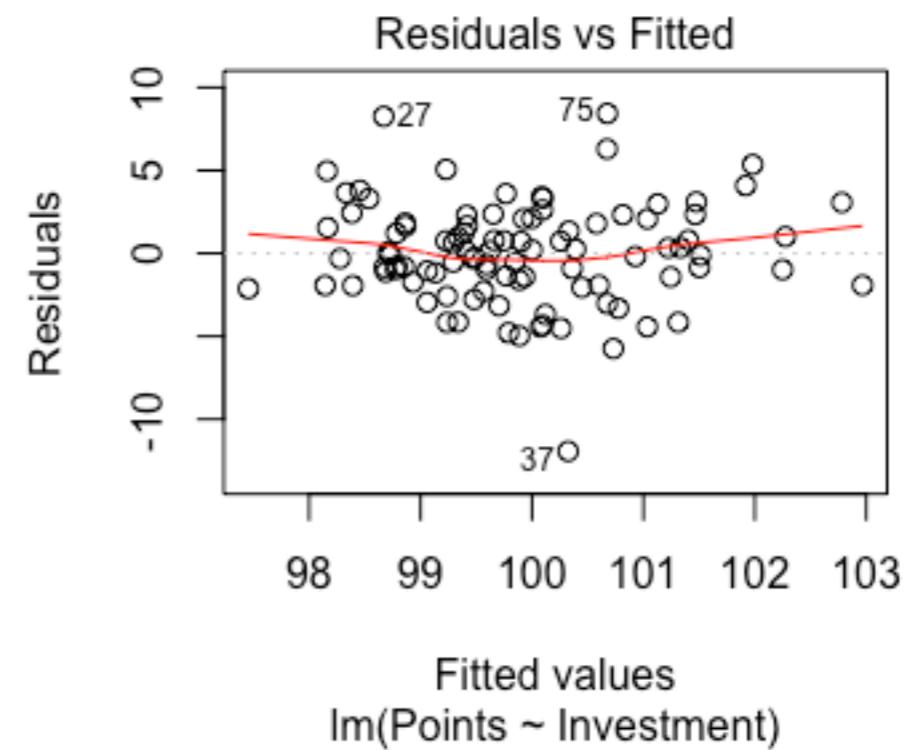
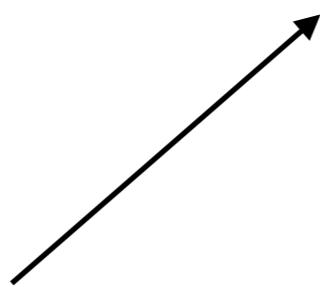
As `model2` has the lower AIC value (so more information in our data is explained by `model2` than by `model.full`), we would be justified in selecting that as our ‘best’ model. AIC penalises models with increasing number of parameters (but not as much as BIC) so gives us a good trade-off of fitting our data and model complexity.

Now let’s look at some diagnostic plots...

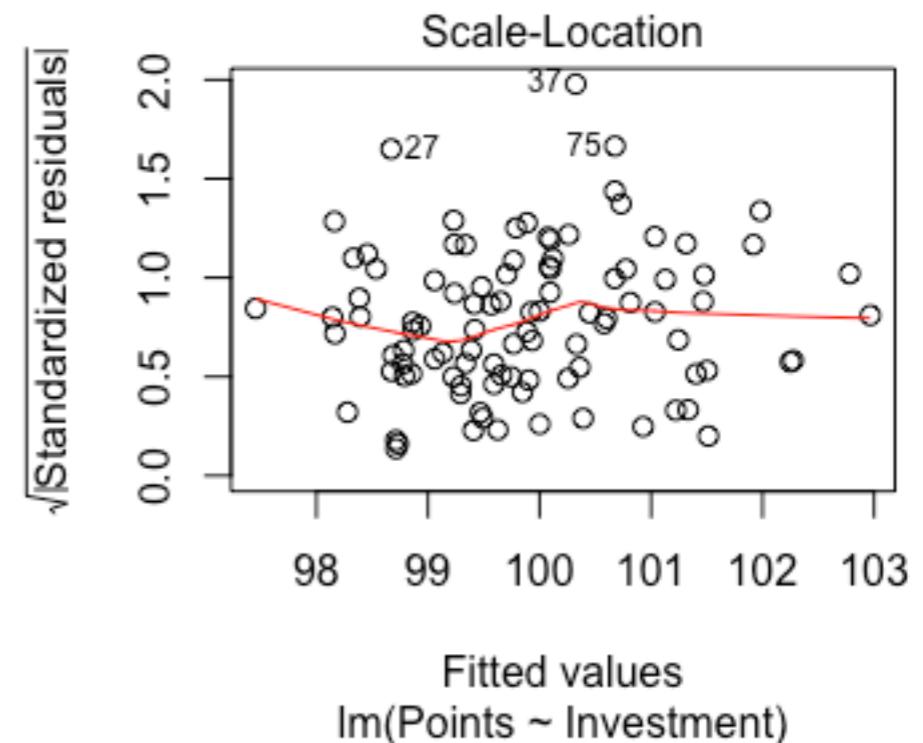
We can use the following command to get some visual representations of model fit:

```
> plot (model2)
```

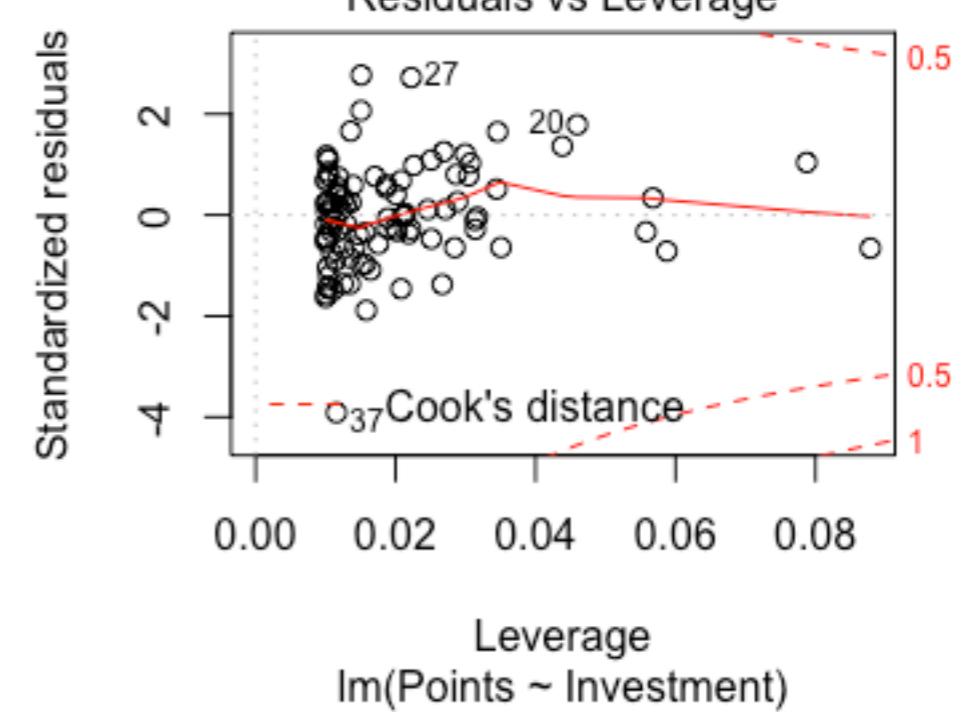
We should have a similar distribution of points (via LOESS Curve Fitting) either side of zero - if we don't it would suggest non-random errors (see Durbin Watson test later). Point 37 looks a bit off both in the Residuals vs. Fitted plot, and also in the Q-Q plot.



The Scale-Location plot shows if residuals are spread equally along the ranges of predictors. We used this to check the assumption of equal variance (homoscedasticity). We really want to see a horizontal line with equally, randomly spread points.



The Residuals vs. Leverage plot tells us about influential outliers (i.e., outliers that are affecting our model) - when cases are outside of Cook's distance (beyond the dashed line) it means they are having an influential affect on the regression model - we'd might want to exclude these points and rebuild our model.



Durbin Watson Test

- This tests for the non-independence of errors - our errors need to be independent (one of the assumptions of regression). This test needs the `car` package to be loaded.

```
> durbinWatsonTest(model2)
   lag Autocorrelation D-W Statistic p-value
   1      0.07517027     1.830761    0.354
Alternative hypothesis: rho != 0
```

A D-W value of 2 means that there is no autocorrelation in the sample - our calculated value is pretty close to that - $p = .354$ so we conclude our errors are independent of each other.

Stepwise Regression Based on AIC Improvement

Rather than building our regression model step by step manually, we can use the `step` function in R - it takes a starting model, and then uses forwards or backwards procedures (or a combination of both) to produce the best model.

We need to install the `MASS` library.

Let's apply the procedure to `model.null` and `model.full` as our limits - we can specify the stepwise procedure with the parameter "direction":

```
> library (MASS)  
  
> steplimitsboth <- step(model.null, scope=list (upper=model.full),  
  direction = "both")
```

- Let's focus on the combined method that adds predictors which improve model fit, and removes ones that don't - based on minimising AIC:

```
> summary (steplimitsboth)

Call:
lm(formula = Points ~ Investment + Car_performance, data = regression)

Residuals:
    Min      1Q  Median      3Q     Max 
-11.9048 -1.6602 -0.1308  1.9264  7.7338 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -251.3167   102.1767  -2.460 0.015678 *  
Investment     0.3562     0.1020   3.493 0.000722 *** 
Car_performance -0.8959     0.5489  -1.632 0.105868    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.041 on 97 degrees of freedom
Multiple R-squared:  0.1402, Adjusted R-squared:  0.1225 
F-statistic: 7.908 on 2 and 97 DF,  p-value: 0.0006582
```

We can see the procedure has settled on the model with Investment and Car_performance. AIC value of this model is 511.1639

Stepwise Regression Based on Adjusted R Squared Improvement

- Use the `ols_step_forward` function to work out the model with predictors entered on the basis of improvement via p -value and adjusted R^2 . For this we need the package `olsrr`.

```
#using ols_step_forward  
  
> install.packages ("olsrr")  
> library (olsrr)  
> pmodel <- ols_step_forward(model.full)  
> pmodel
```

```
> pmodel  
Forward Selection Method
```

Candidate Terms:

- 1 . Investment
- 2 . Car_performance
- 3 . Age
- 4 . Media_coverage

Selection Summary						
Step	Variable Entered	Adj.		C (p)	AIC	RMSE
		R-Square	R-Square			
1	Investment	0.1166	0.1076	2.9872	511.8735	3.0665
2	Car_performance	0.1402	0.1225	2.3410	511.1639	3.0408
3	Age	0.1505	0.1240	3.1850	511.9567	3.0382

In Step 1 ‘Investment’ is added first, in Step 2 ‘Car_performance’ is then added etc. We end up with the same final model as we had based on AIC improvement.

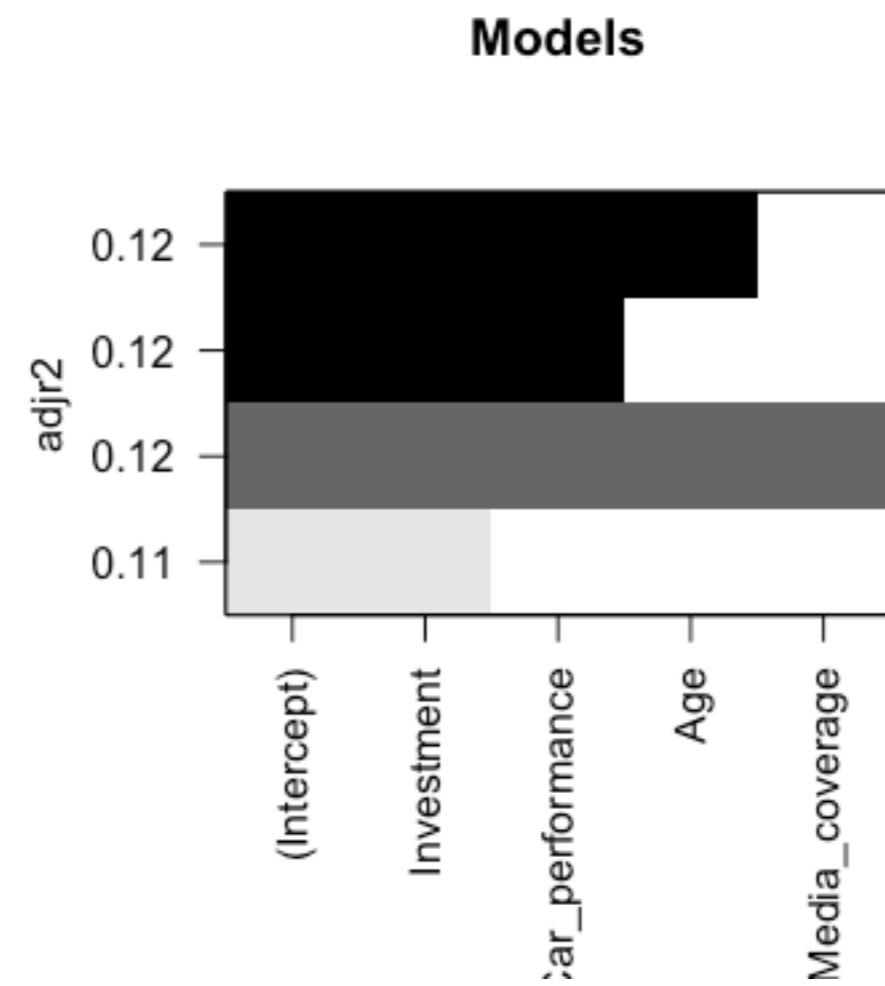
Mallow’s Cp is another measure of model fit (low is good).

Adjusted R-squared (which penalises as more predictors are added) is highest for model with the 3 predictors - but AIC tells a slightly different story...

Residual Mean Square Error.

- Visualise the possible models (incl. the one with the largest adjusted R² value) using the *leaps* package.

```
> library (leaps)
> leapsmodels <- regsubsets (Points ~
Investment + Car_performance + Age +
Media_coverage, data=regression)
> plot (leapsmodels, scale="adjr2",
main="Models")
```



Collinearity?

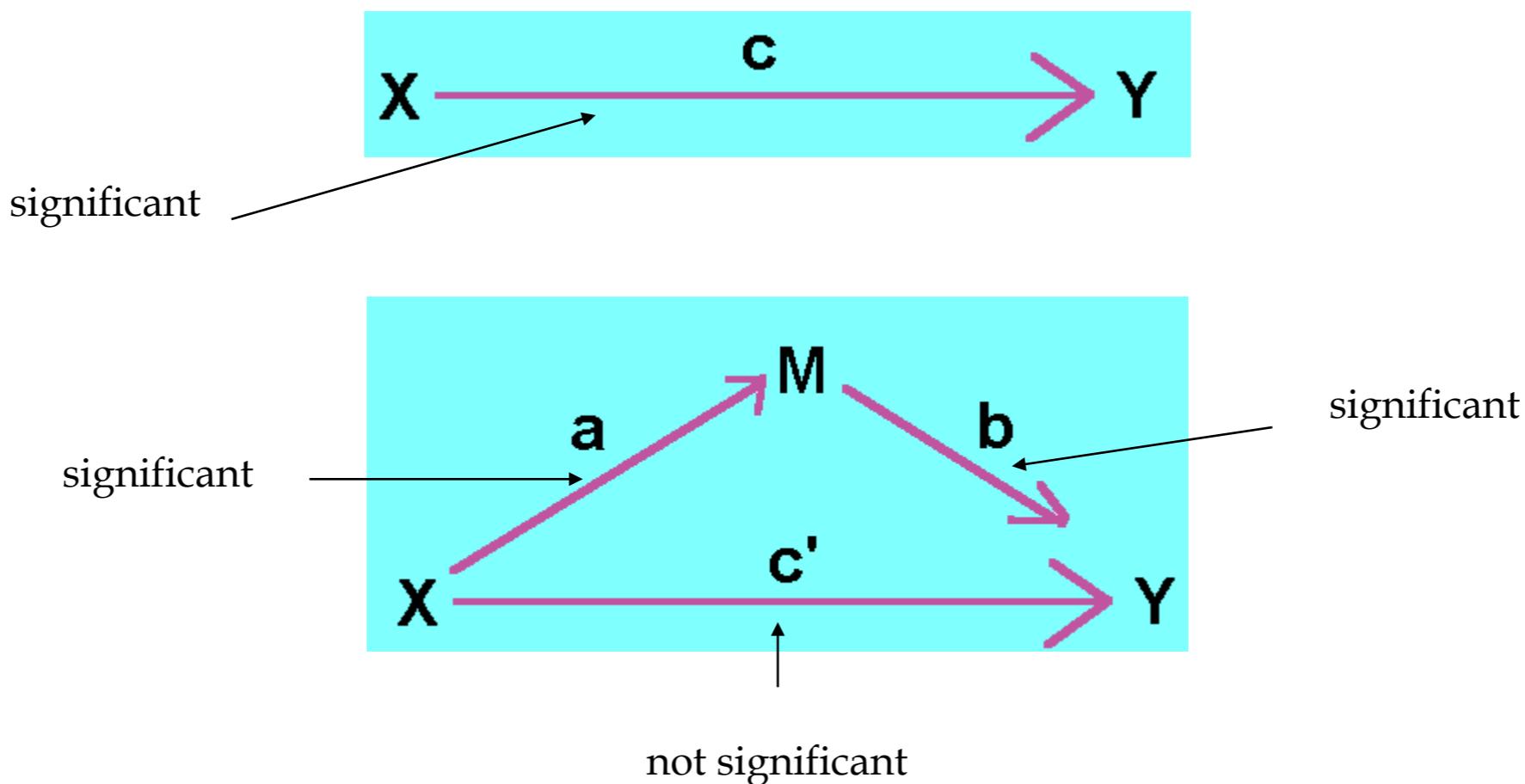
- We can apply the `vif()` function to our model - it will work out the VIF values for each of our variables - `vif()` is in the `car` package so don't forget to load that...

```
> vif (steplimitsboth)
Investment  Car_performance
      1.005772          1.005772
```

- As a rule of thumb VIF greater than 10 suggests a multicollinearity issue (although greater than 5 has been suggested too - more conservative).
- For our case, we don't have a collinearity problem as the VIF values are relatively low.

Mediation Effects

- At times, a variable's predicting power of an outcome is lost (complete mediation) or significantly reduced (partial mediation) when another predictor is introduced.
- This added variable mediates the initial effect by its absence and cancels the effect by its presence.



Step 1: The initial variable is correlated with the outcome.

- X is the predictor and Y the outcome variable (path c).

Step 2: Show that the initial variable is correlated with the mediator.

- X is the predictor and M is the outcome variable in the regression equation (path a).

Step 3: Show that the mediator affects the outcome variable.

- X and M are both predictors and Y is the outcome variable (path b).
- X (and not just M) is included so that the initial variable could be controlled in establishing the effect of the mediator on the outcome.

Step 4: After introducing M the effect of X on Y controlling for M (path c') should be zero.

Mediation in R

- Imagine we are interested in whether the number of hours since dawn (X) affects the subjective ratings of wakefulness (Y) of 100 graduate students through the consumption of coffee (M).
- Our datafile is called Meddata - we are also using the stargazer package to produce our table - so need to:

```
> install.packages("stargazer")
> library (stargazer)
```

The 4 Steps (Baron and Kenny Method)

1. Estimate the relationship between X on Y (hours since dawn on degree of wakefulness) - Path “c” must be significantly different from 0; must have a total effect between the IV & DV
2. Estimate the relationship between X on M (hours since dawn on coffee consumption) - Path “a” must be significantly different from 0; IV and mediator must be related.
3. Estimate the relationship between M on Y controlling for X (coffee consumption on wakefulness, controlling for hours since dawn) - Path “b” must be significantly different from 0; mediator and DV must be related. - The effect of X on Y decreases with the inclusion of M in the model
4. Estimate the relationship between Y on X controlling for M (wakefulness on hours since dawn, controlling for coffee consumption) - Should be non-significant and nearly 0.

Step 1

```
> #1. Total effect
> fit <- lm(Y ~ X, data=Meddata)
> summary(fit)

Call:
lm(formula = Y ~ X, data = Meddata)

Residuals:
    Min      1Q  Median      3Q     Max 
-10.917 -3.738 -0.259  2.910 12.540 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 19.88368   14.26371   1.394   0.1665    
X             0.16899    0.08116   2.082   0.0399 *  
---
Signif. codes:  0 '****' 0.001 '***' 0.01 '**' 0.05 '*' 0.1 ' .' 1

Residual standard error: 5.16 on 98 degrees of freedom
Multiple R-squared:  0.04237, Adjusted R-squared:  0.0326 
F-statistic: 4.336 on 1 and 98 DF,  p-value: 0.03993
```

Step 2

```
> #2. Path A (X on M)
> fita <- lm(M ~ X, data=Meddata)
> summary(fita)

Call:
lm(formula = M ~ X, data = Meddata)

Residuals:
    Min      1Q  Median      3Q     Max 
-9.5367 -3.4175 -0.4375  2.9032 16.4520 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 6.04494   13.41692   0.451   0.653    
X            0.66252    0.07634   8.678 8.87e-14 ***  
---
Signif. codes:  0 '****' 0.001 '***' 0.01 '**' 0.05 '*' 0.1 '.' 1 

Residual standard error: 4.854 on 98 degrees of freedom
Multiple R-squared:  0.4346, Adjusted R-squared:  0.4288 
F-statistic: 75.31 on 1 and 98 DF,  p-value: 8.872e-14
```

Step 3

```
> #3. Path B (M on Y, controlling for X)
> fitb <- lm(Y ~ M + X, data=Meddata)
> summary(fitb)
```

Call:
lm(formula = Y ~ M + X, data = Meddata)

Residuals:

Min	1Q	Median	3Q	Max
-9.3651	-3.3037	-0.6222	3.1068	10.3991

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	17.32177	13.16216	1.316	0.191
M	0.42381	0.09899	4.281	4.37e-05 ***
X	-0.11179	0.09949	-1.124	0.264

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

Residual standard error: 4.756 on 97 degrees of freedom
Multiple R-squared: 0.1946, Adjusted R-squared: 0.1779
F-statistic: 11.72 on 2 and 97 DF, p-value: 2.771e-05

Step 4

```
> #4. Reversed Path C (Y on X, controlling for M)
> fitc <- lm(X ~ Y + M, data=Meddata)
> summary(fitc)
```

Call:
lm(formula = X ~ Y + M, data = Meddata)

Residuals:

Min	1Q	Median	3Q	Max
-14.438	-2.573	-0.030	3.010	11.779

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	96.11234	9.27663	10.361	< 2e-16 ***
Y	-0.11493	0.10229	-1.124	0.264
M	0.69619	0.08356	8.332	5.27e-13 ***

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

Residual standard error: 4.823 on 97 degrees of freedom
Multiple R-squared: 0.4418, Adjusted R-squared: 0.4303
F-statistic: 38.39 on 2 and 97 DF, p-value: 5.233e-13

```
> stargazer(fit, fita, fitb, fitc, type = "text", title = "Baron and Kenny Method")
```

Baron and Kenny Method

Dependent variable:				
	Y (1)	M (2)	Y (3)	X (4)
Y				-0.115 (0.102)
M			0.424*** (0.099)	0.696*** (0.084)
X	0.169** (0.081)	0.663*** (0.076)	-0.112 (0.099)	
Constant	19.884 (14.264)	6.045 (13.417)	17.322 (13.162)	96.112*** (9.277)
Observations	100	100	100	100
R2	0.042	0.435	0.195	0.442
Adjusted R2	0.033	0.429	0.178	0.430
Residual Std. Error	5.160 (df = 98)	4.854 (df = 98)	4.756 (df = 97)	4.823 (df = 97)
F Statistic	4.336** (df = 1; 98)	75.313*** (df = 1; 98)	11.715*** (df = 2; 97)	38.389*** (df = 2; 97)

Note:

*p<0.1; **p<0.05; ***p<0.01

Step 1 shows a significant positive relationship between hours since dawn (X) and wakefulness (Y).

Our Path A model (Step 2) shows that hours since down (X) is also positively related to coffee consumption (M).

Our Path B model (Step 3) shows that coffee consumption (M) positively predicts wakefulness (Y) when controlling for hours since dawn (X).

Finally, (Step 4) wakefulness (Y) does not predict hours since dawn (X) when controlling for coffee consumption (M).

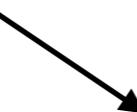
Since the relationship between hours since dawn and wakefulness is no longer significant when controlling for coffee consumption, this suggests that coffee consumption does in fact mediate this relationship.

Determining the significance of our mediator

- With the Baron and Kenny approach, we can use the Sobel test to determine the p-value associated with the influence of our mediator.
- We need to first install the package called `multilevel` so remember then to load it: `library (multilevel)`
- This is what we are interested in - it's the z-value of the effect of our mediator - you can calculate the 2-tailed p-value from the normal distribution like this:

```
> 2 * (1-pnorm(3.83939))  
[1] 0.0001233404
```

```
> sobel(Meddata$X, Meddata$M, Meddata$Y)  
$`Mod1: Y~X`  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 19.8836805 14.2637142 1.394004 0.16646905  
pred 0.1689931 0.0811601 2.082220 0.03992761  
  
$`Mod2: Y~X+M`  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 17.3217682 13.16215851 1.316028 1.912663e-01  
pred -0.1117904 0.09949262 -1.123605 2.639537e-01  
med 0.4238113 0.09899469 4.281152 4.371472e-05  
  
$`Mod3: M~X`  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 6.0449365 13.41692114 0.4505457 6.533122e-01  
pred 0.6625203 0.07634187 8.6783345 8.871741e-14  
  
$Indirect.Effect  
[1] 0.2807836  
  
$SE  
[1] 0.07313234  
  
$z.value  
[1] 3.83939  
  
$N  
[1] 100
```



Mediation via Bootstrapping

- Sobel test can be quite conservative - *bootstrapping* and the *mediation* package a more powerful method to investigate mediation effect. Bootstrapping better for small samples.
- Imagine you have a sample of n measurements, you can sample this in many ways as long as you allow some values to appear more than once and others to be left out (sampling with replacement). Calculate the mean lots of times (one for each sampling - often as many as 10,000) and work out the CIs and other population parameter estimates. This is *bootstrapping*.

The Mediation Package

- Based on Preacher & Hayes (2004) - more power than Sobel test
 - well suited for small sample sizes.
- Need to build two models - one for direct effect of our predictors and one for the effect of our predictor and mediator.

```
> require (mediation)
> fitM <- lm(M ~ X, data=Meddata) #IV on M; Hours since dawn predicting coffee
consumption
> fitY <- lm(Y ~ X + M, data=Meddata) #IV and M on DV; Hours since dawn and
coffee predicting wakefulness
```

- Then use the **mediate** function in the mediation package to compare the two models - allows us to estimate effect of the mediator...

```
> fitMed <- mediate(fitM, fitY, treat="X", mediator="M")
> summary(fitMed)
```

```
> summary(fitMed)
```

Causal Mediation Analysis

Quasi-Bayesian Confidence Intervals

	Estimate	95% CI Lower	95% CI Upper	p-value
ACME	0.276803	0.144987	0.43	<2e-16 ***
ADE	-0.115043	-0.316462	0.07	0.268
Total Effect	0.161760	0.000729	0.31	0.048 *
Prop. Mediated	1.653327	0.507091	9.66	0.048 *

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

Sample Size Used: 100

Simulations: 1000

- By running this we get the Average Causal Mediation Effects (ACME), our Average Direct Effects (ADE), combined indirect and direct effects (Total Effect), and the ratio of these estimates (Prop. Mediated).
- The ACME is the indirect effect of M (Total Effects - ADE) and the associated p-value value tells us if our mediation effect is significant.
- We can bootstrap our data and fit a model based on our estimated population parameters (which is recommended over the default CI estimation method above)...

```
> fitMedBoot <- mediate(fitM, fitY, boot=TRUE, sims=10000,  
treat="X", mediator="M")  
> summary(fitMedBoot)
```

```
> summary(fitMedBoot)
```

Causal Mediation Analysis

Nonparametric Bootstrap Confidence Intervals with the Percentile Method

	Estimate	95% CI Lower	95% CI Upper	p-value
ACME	0.28078	0.14112	0.43	<2e-16 ***
ADE	-0.11179	-0.29548	0.09	0.273
Total Effect	0.16899	-0.00862	0.35	0.066 .
Prop. Mediated	1.66151	-3.92801	10.91	0.066 .

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

Sample Size Used: 100

Simulations: 10000

- We now see that the ACME is the only one that is significant - this tells us we have a significant moderator - with no direct effect of our predictor or combined effect of predictor and moderator when the moderator is taken into consideration. In this case, it's the same story as we found with the Baron and Kenny method.

Moderation Effects

- Moderation tests whether a variable (Z) affects the direction and/or strength of the relation between an IV (X) and a DV (Y).
- In other words, moderation tests for interactions that affect when relationships between variables occur.
- Imagine we are interested in whether the relationship between the number of hours of sleep (X) a student receives and the attention that they pay to this lecture (Y) is influenced by their consumption of coffee (Z).

Our predictor variables are X and Z - good idea to centre them (i.e., mean of zero) using the `scale` function. It is important to centre both the moderator and predictor to reduce multicollinearity and make interpretation easier.

```
#Centering Data
Xc      <- c(scale(X, center=TRUE, scale=FALSE)) #Centering IV;
hours of sleep
Zc      <- c(scale(Z, center=TRUE, scale=FALSE)) #Centering
moderator; coffee consumption
```

```
> fitMod <- lm(Y ~ Xc + Zc + Xc:Zc) #Model interacts IV & moderator  
> summary(fitMod)
```

Call:

```
lm(formula = Y ~ Xc + Zc + Xc : Zc)
```

Residuals:

Min	1Q	Median	3Q	Max
-21.466	-8.972	-0.233	6.180	38.051

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	48.54443	1.17286	41.390	< 2e-16 ***
Xc	5.20812	0.34870	14.936	< 2e-16 ***
Zc	1.10443	0.15537	7.108	2.08e-10 ***
Xc:Zc	0.23384	0.04134	5.656	1.59e-07 ***

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

Residual standard error: 11.65 on 96 degrees of freedom

Multiple R-squared: 0.7661, Adjusted R-squared: 0.7587

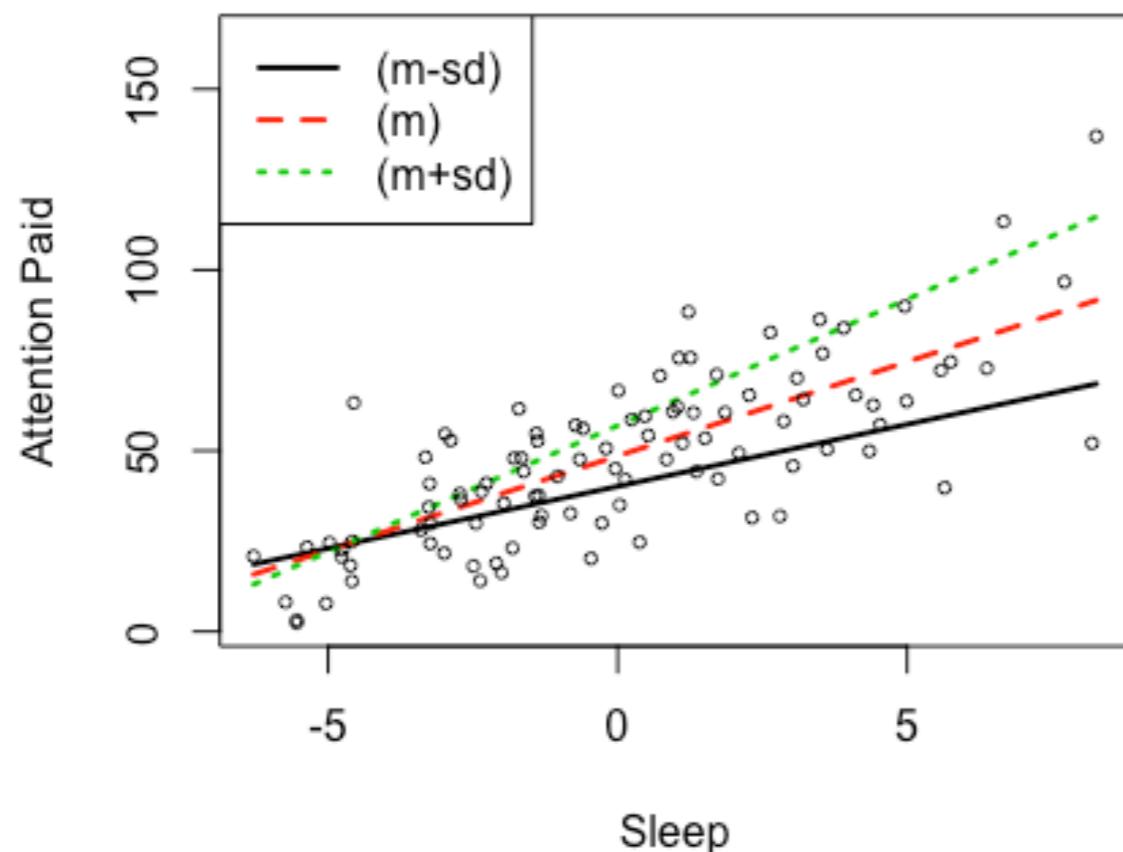
F-statistic: 104.8 on 3 and 96 DF, p-value: < 2.2e-16

We can use the `plotSlopes` function in the `rockchalk` package to plot the slopes (1 SD above and 1 SD below the mean) of the moderating effect.

The plot below shows that those who drank less coffee (the black line) paid more attention with the more sleep they got last night, but paid less attention overall than average (the red line).

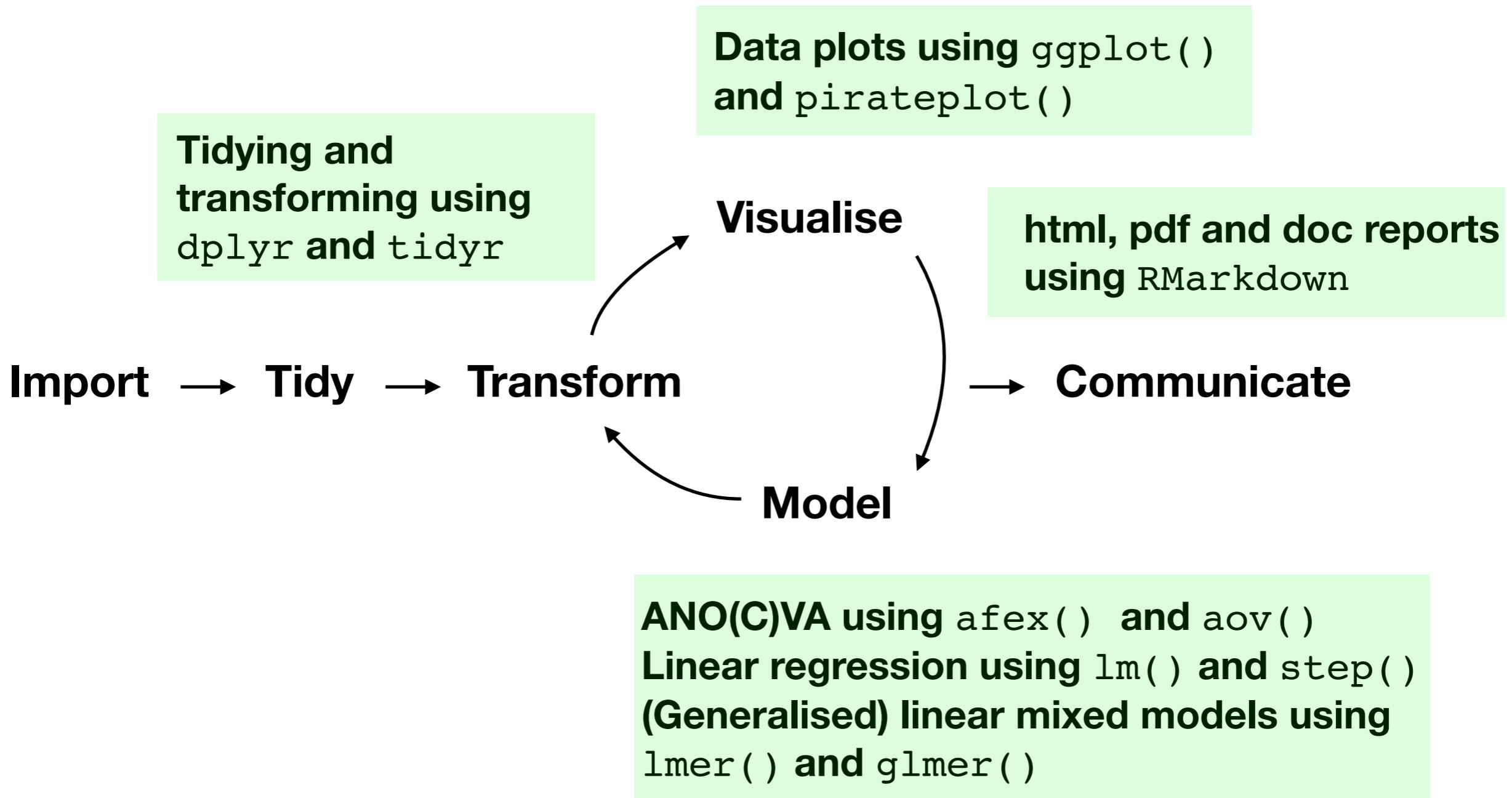
Those who drank more coffee (the green line) paid more attention when they slept more as well and paid more attention than average.

The difference in the slopes for those who drank more or less coffee shows that coffee consumption moderates the relationship between hours of sleep and attention paid.

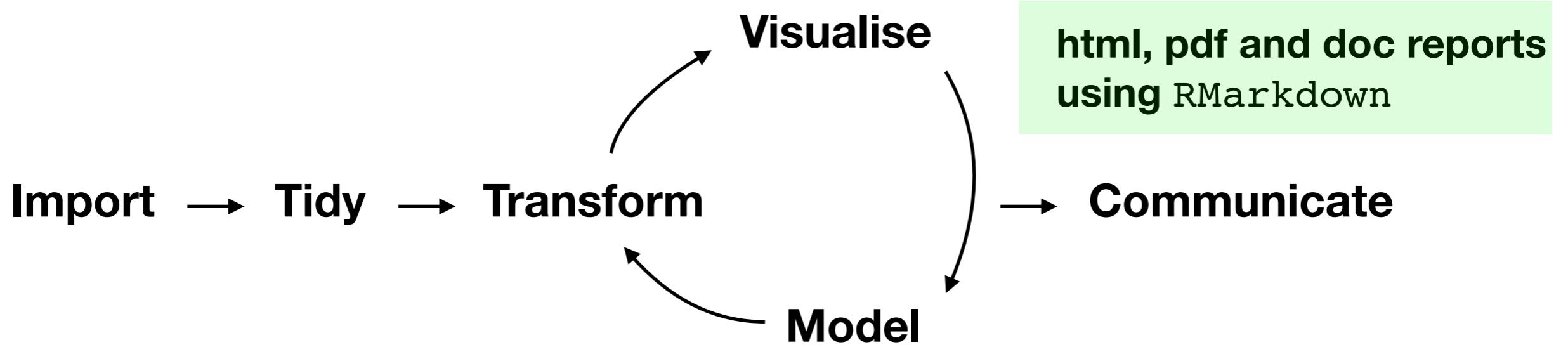


```
ps <- plotSlopes(fitMod,
plotx="Xc", modx="Zc", xlab =
"Sleep", ylab = "Attention
Paid", modxVals = "std.dev")
```

Workflow



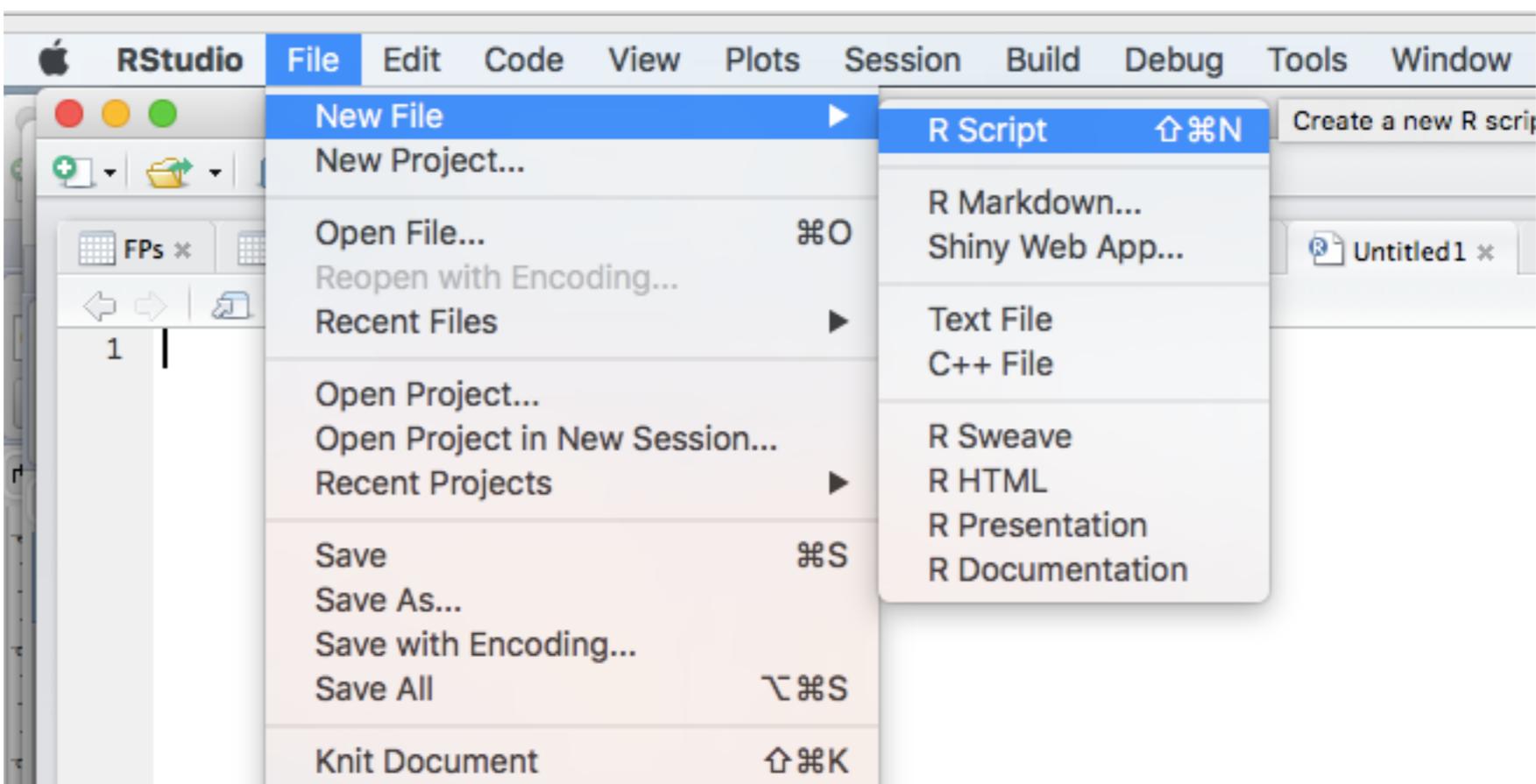
Communicate

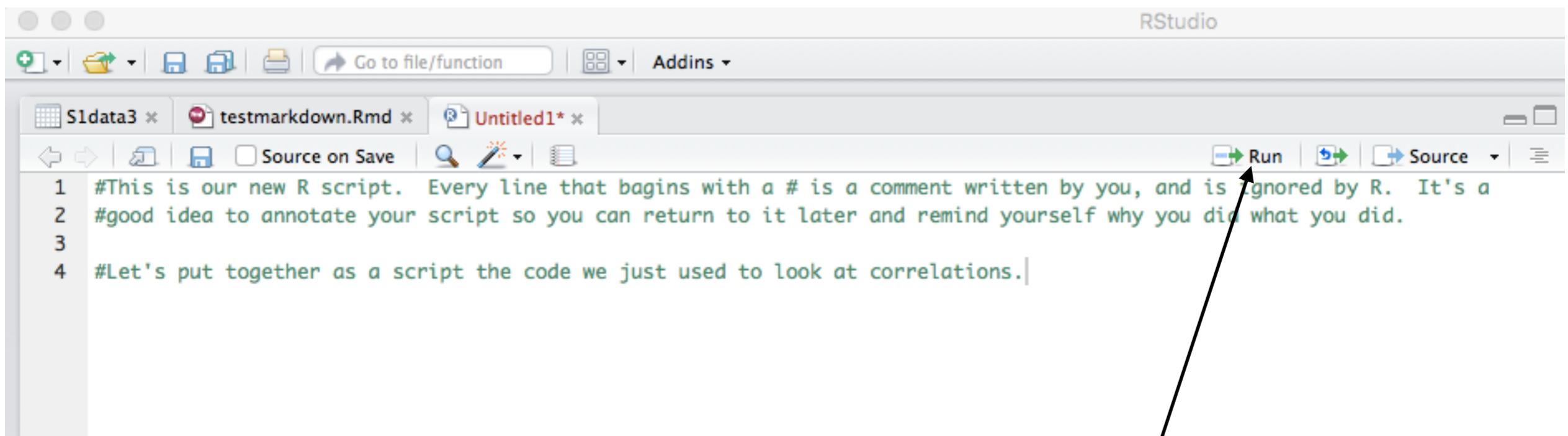


Writing Scripts in R

- Rather than simply writing commands line by line in the console, we can create a *script* containing multiple lines of code.
- This script can then be re-run whenever you want, and also could be submitted alongside your paper to a journal for review (along with your data).
- Providing the raw data from your work, plus your analysis script allows other researchers to see exactly how you analysed your data. Transparency in the age of the open science is key.

Create a new R script like this:





The screenshot shows the RStudio interface. In the top bar, there are icons for file operations like Open, Save, and Print, followed by a "Go to file/function" search bar and a "Addins" dropdown. Below the top bar, the main window has tabs for "S1data3", "testmarkdown.Rmd", and "Untitled1*". The "Untitled1*" tab contains the following R code:

```
1 #This is our new R script. Every line that begins with a # is a comment written by you, and is ignored by R. It's a
2 #good idea to annotate your script so you can return to it later and remind yourself why you did what you did.
3
4 #Let's put together as a script the code we just used to look at correlations.
```

The "Run" button, which has a green arrow pointing to it, is located in the toolbar below the code editor. The "Source" button is also visible in the same row.

Once it's written, you can either run your entire script by highlighting it all (CMD-A in OSX) and clicking on 'Run', or you can highlight sections of your script and run only those (by clicking 'Run' once you have highlighted the code you are interested in). CMD-Return will also Run the highlighted code.

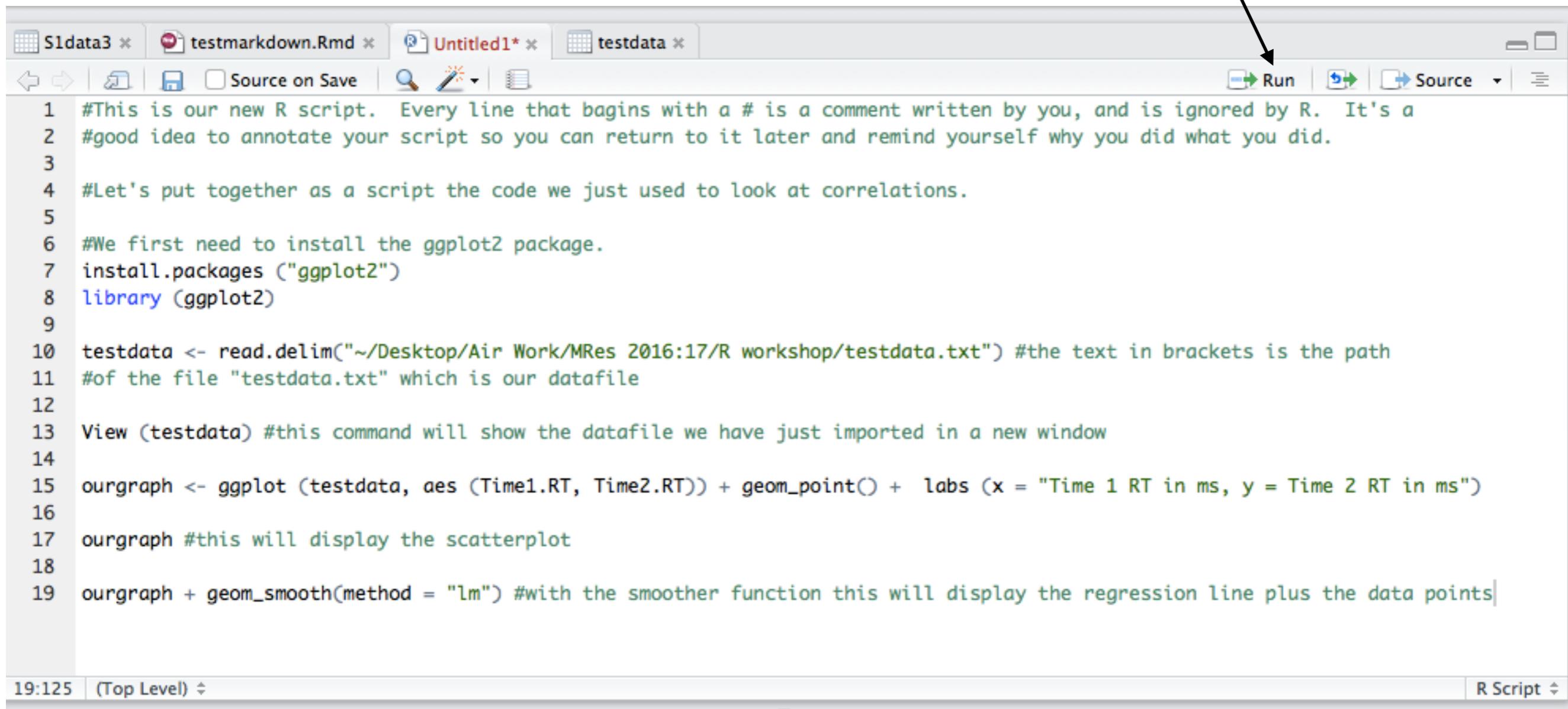
The screenshot shows the RStudio interface with several tabs at the top: S1data3, testmarkdown.Rmd, Untitled1*, and testdata*. Below the tabs is a toolbar with icons for back, forward, save, and search. The main area contains the following R code:

```
1 #This is our new R script. Every line that begins with a # is a comment written by you, and is ignored by R. It's a
2 #good idea to annotate your script so you can return to it later and remind yourself why you did what you did.
3
4 #Let's put together as a script the code we just used to look at correlations.
5
6 #We first need to install the ggplot2 package.
7 install.packages ("ggplot2")
8 library (ggplot2)
9
10 testdata <- read.delim("~/Desktop/Air Work/MRes 2016:17/R workshop/testdata.txt") #the text in brackets is the path
11 #of the file "testdata.txt" which is our datafile
12
13 View (testdata) #this command will show the datafile we have just imported in a new window
14
15 ourgraph <- ggplot (testdata, aes (Time1.RT, Time2.RT)) + geom_point() + labs (x = "Time 1 RT in ms, y = Time 2 RT in ms")
16
17 ourgraph #this will display the scatterplot
18
19 ourgraph + geom_smooth(method = "lm") #with the smoother function this will display the regression line plus the data points|
```

At the bottom left, the status bar shows "19:125 (Top Level)". At the bottom right, it says "R Script".

We've started writing our script - it includes comments (prefixed by #), the code to load the ggplot2 package, the code to load our data, and the code to plot our data, first as a scatterplot, then with the regression line.

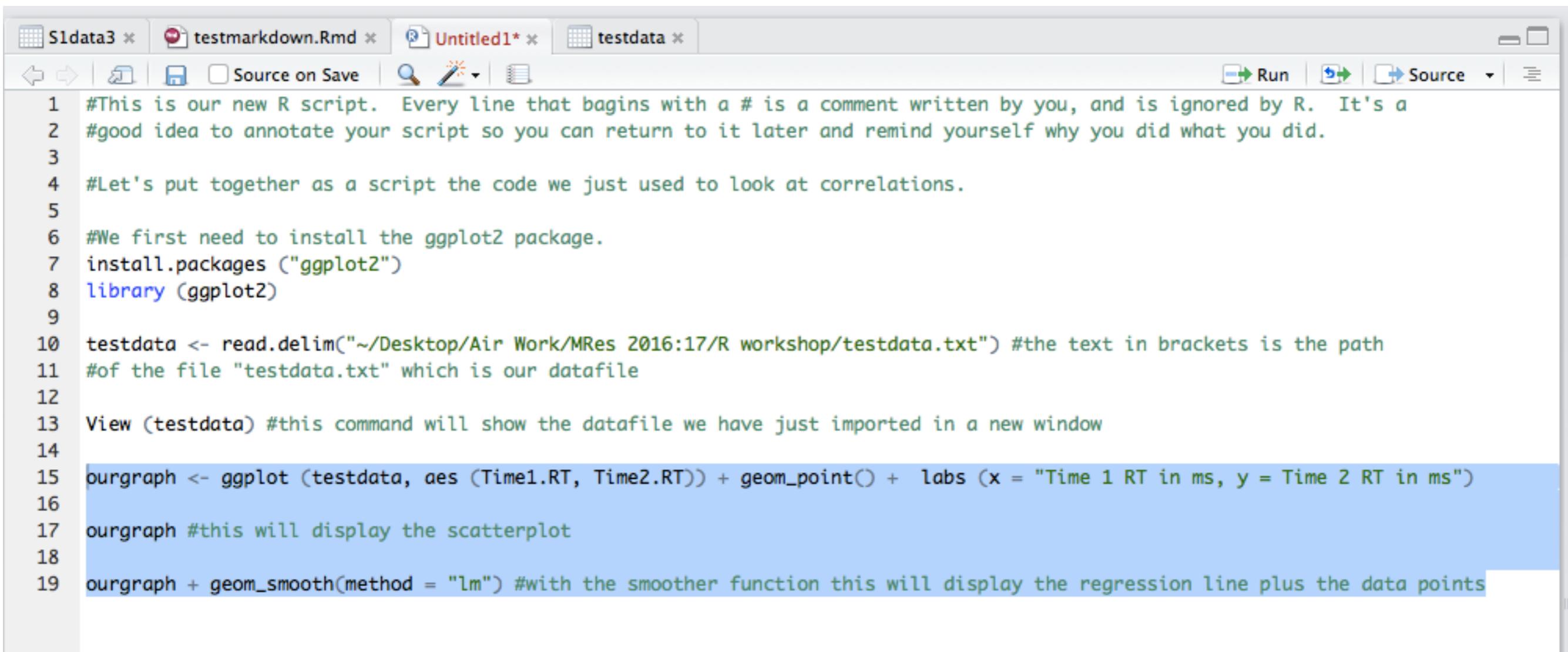
We first need to highlight, and then click on ‘Run’ to run the whole script.



The screenshot shows the RStudio interface with an R script open. The script contains code for reading a data file, installing the ggplot2 package, and creating a scatterplot with a regression line. A black arrow points from the text above to the 'Run' button in the toolbar, indicating where to click to execute the script.

```
1 #This is our new R script. Every line that begins with a # is a comment written by you, and is ignored by R. It's a
2 #good idea to annotate your script so you can return to it later and remind yourself why you did what you did.
3
4 #Let's put together as a script the code we just used to look at correlations.
5
6 #We first need to install the ggplot2 package.
7 install.packages ("ggplot2")
8 library (ggplot2)
9
10 testdata <- read.delim("~/Desktop/Air Work/MRes 2016:17/R workshop/testdata.txt") #the text in brackets is the path
11 #of the file "testdata.txt" which is our datafile
12
13 View (testdata) #this command will show the datafile we have just imported in a new window
14
15 ourgraph <- ggplot (testdata, aes (Time1.RT, Time2.RT)) + geom_point() + labs (x = "Time 1 RT in ms, y = Time 2 RT in ms")
16
17 ourgraph #this will display the scatterplot
18
19 ourgraph + geom_smooth(method = "lm") #with the smoother function this will display the regression line plus the data points|
```

- But maybe we already have the `ggplot2` package and our data loaded. What if we just want to run the portion of the script associated with generating the graph? We simply highlight it, then click on ‘Run’.

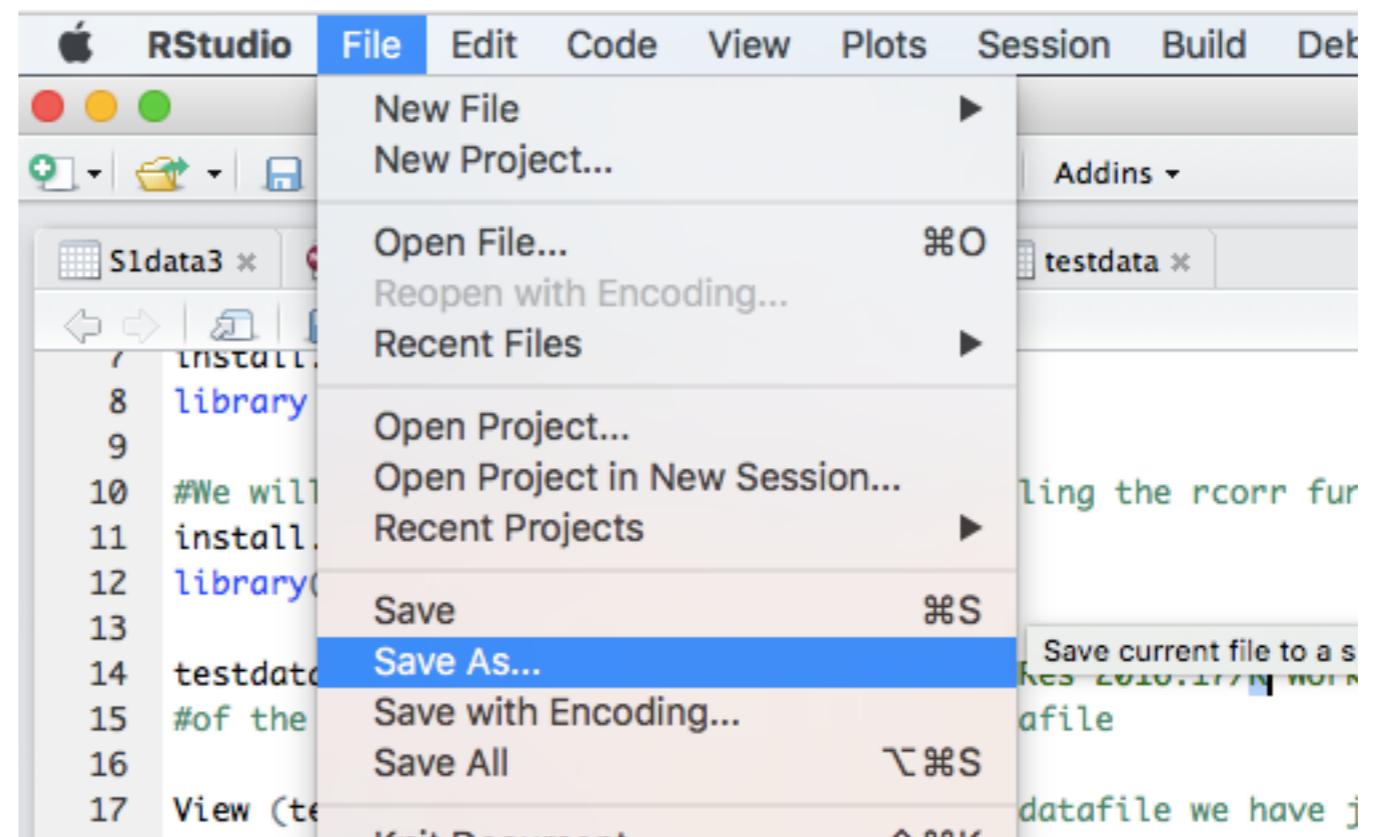


The screenshot shows the RStudio interface with several tabs at the top: S1data3, testmarkdown.Rmd, Untitled1*, and testdata. The testdata tab is active. The main area contains an R script:

```
1 #This is our new R script. Every line that begins with a # is a comment written by you, and is ignored by R. It's a
2 #good idea to annotate your script so you can return to it later and remind yourself why you did what you did.
3
4 #Let's put together as a script the code we just used to look at correlations.
5
6 #We first need to install the ggplot2 package.
7 install.packages ("ggplot2")
8 library (ggplot2)
9
10 testdata <- read.delim("~/Desktop/Air Work/MRes 2016:17/R workshop/testdata.txt") #the text in brackets is the path
11 #of the file "testdata.txt" which is our datafile
12
13 View (testdata) #this command will show the datafile we have just imported in a new window
14
15 ourgraph <- ggplot (testdata, aes (Time1.RT, Time2.RT)) + geom_point() + labs (x = "Time 1 RT in ms, y = Time 2 RT in ms")
16
17 ourgraph #this will display the scatterplot
18
19 ourgraph + geom_smooth(method = "lm") #with the smoother function this will display the regression line plus the data points
```

The lines from 15 to 19 are highlighted in blue, indicating they are selected for execution.

Once your
script is finished,
don't forget to
save it...



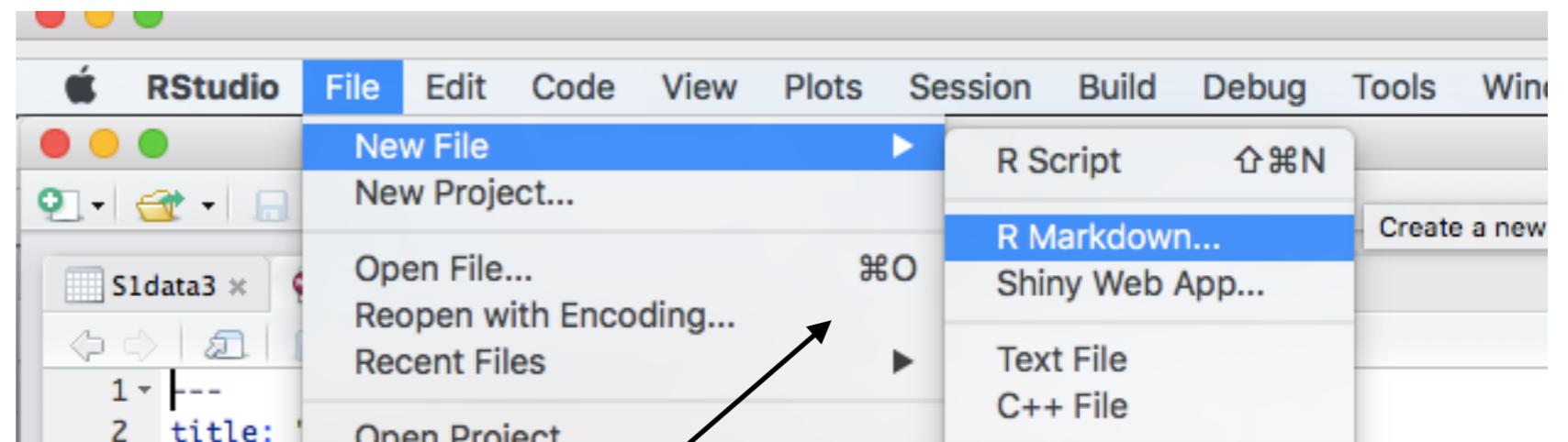
R Markdown

- You can create publishable reports using R Markdown. Such reports contain your code (which you can copy from your R script), the output associated with executing that code, plus comments that you write explaining what you're doing.
- To install it, simply install the R Markdown package:

```
> install.packages ("rmarkdown")
```

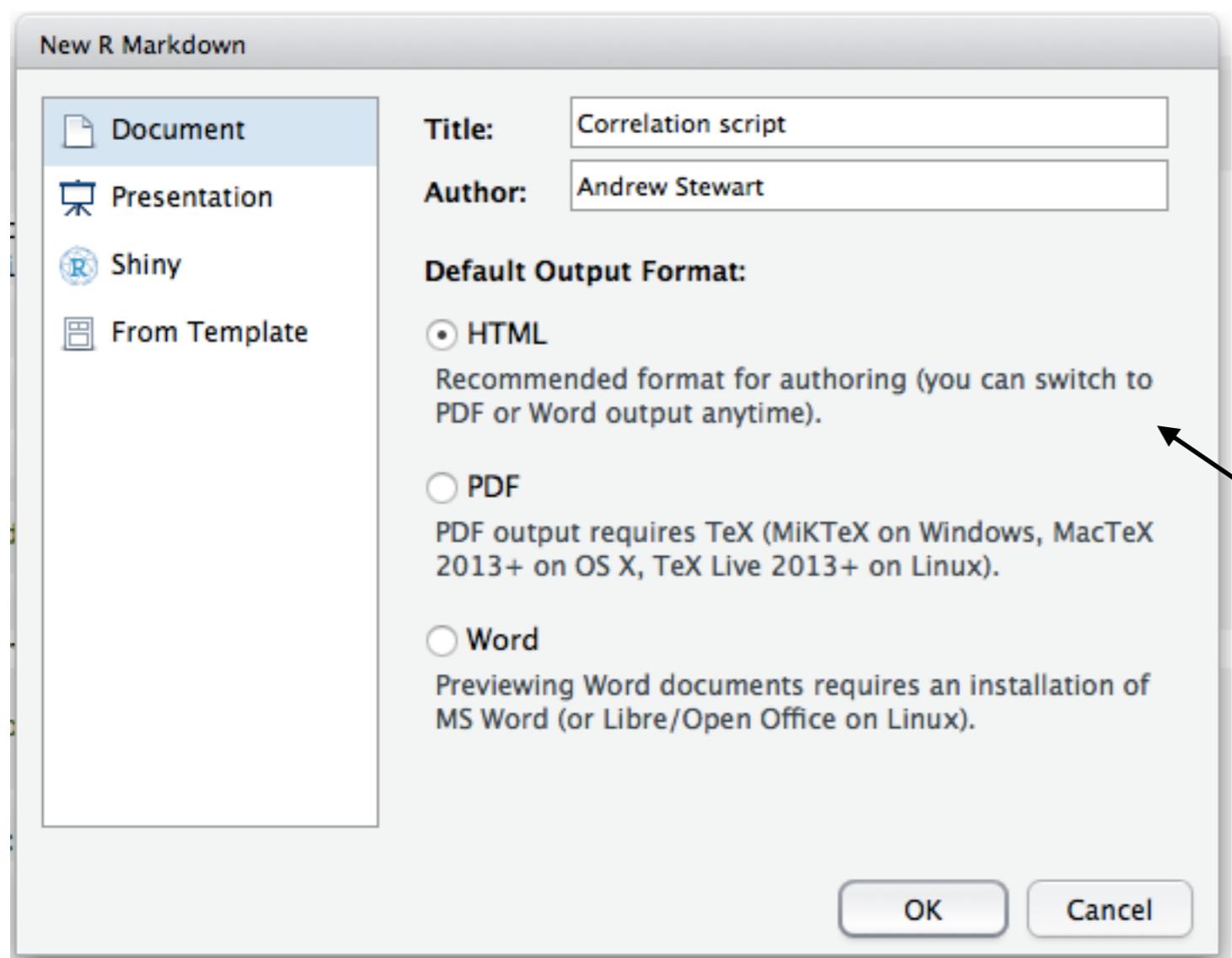
```
> library (rmarkdown)
```

Whenever you want to produce an R Markdown document, make sure you have the *rmarkdown* package loaded.



Start a new R Markdown script. We are going to write a Markdown script incorporating the correlation script we just saw.

Call your document something sensible and specify what type of file it should be. I'm choosing a **HTML** for this one. You *might* need to install a **latex** file to build a **PDF** (if so, R will tell you), otherwise you can build a **Word** file.



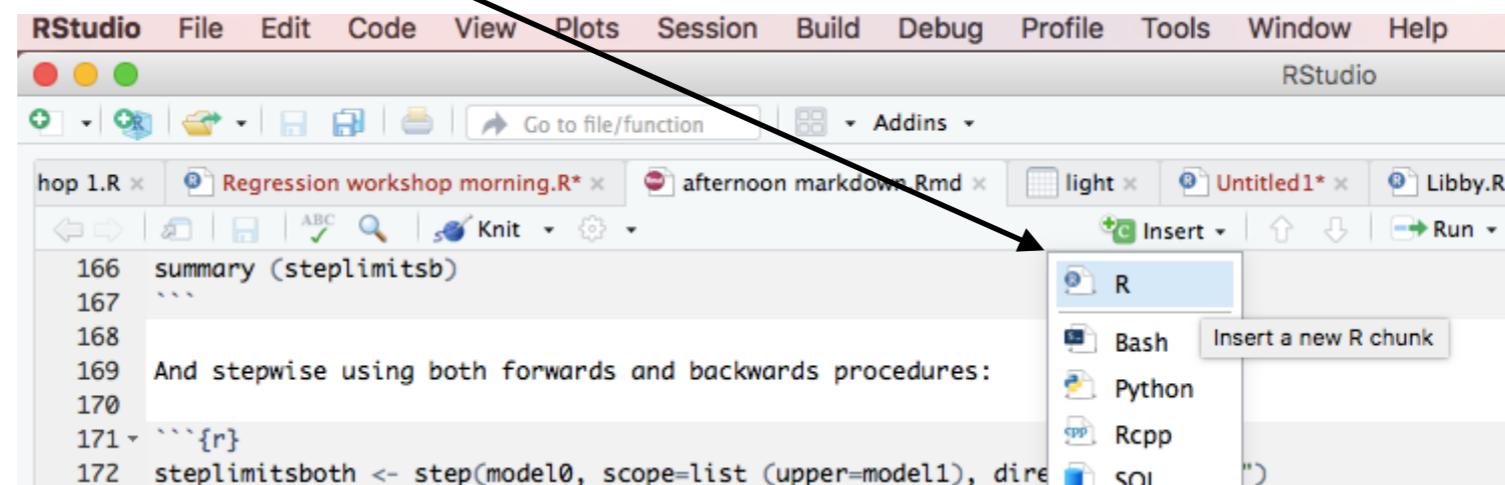
Our Markdown script is comprised of R code (grey background) and comments that will appear in the Markdown document (white background).

```
1 - ---
2   title: "Correlation script"
3   author: "Andrew Stewart"
4   date: "1/12/2017"
5   output: html_document
6 -
7
8 - ````{r setup, include=FALSE}
9   knitr::opts_chunk$set(echo = TRUE)
10 -
11
12 - ## R Markdown
13
14 This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more
15 details on using R Markdown see <http://rmarkdown.rstudio.com>.
16
17 When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded
18 R code chunks within the document. You can embed an R code chunk like this:
19
20 - ````{r cars}
21   summary(cars)
22 -
23
24 - ## Including Plots
25
26 - ````{r pressure, echo=FALSE}
27   plot(pressure)
28 -
29
30 Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.
31
```

```
1 ---  
2 title: "Correlation script"  
3 author: "Andrew Stewart"  
4 date: "1/12/2017"  
5 output: html_document  
6 ---  
7  
8 ```{r setup, include=FALSE}  
9 knitr::opts_chunk$set(echo = TRUE)  
10 ```  
11  
12 This is our new R script that is in an R Markdown document. All of this text will appear in the Notebook. Every line that begins with a # is a comment written by you, and is ignored by R. However, it will appear in the Notebook.  
13  
14 Let's put together as a script the code we just used to look at correlations.  
15  
16 We first need to install the ggplot2 package.  
17  
18 ```{r, warning=FALSE, message=FALSE}  
19 install.packages ("ggplot2", repos="http://cran.rstudio.com/")  
20 library (ggplot2)  
21 ```  
22 We will also need the Hmisc package for calling the rcorr function  
23 ```{r, warning=FALSE, message=FALSE}  
24 install.packages ("Hmisc", repos="http://cran.rstudio.com/")  
25 library(Hmisc)  
--
```

Also note, I am using `warning=FALSE` and `message=FALSE` parameters to stop such text from appearing in the document we're creating. Obviously, if any **have** appeared, you need to be sure they're not serious/relevant. In these case, the warnings relate to a different version number.

- To insert R code in your Markdown document, click on the Insert button, and select ‘R’.



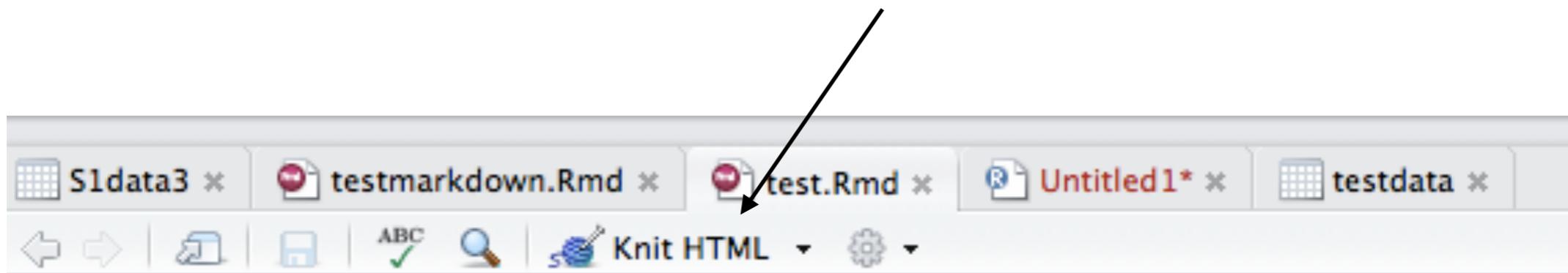
A screenshot of the RStudio code editor. It displays the following R code:

```
28 ````{r}
29 testdata <- read.delim("~/Desktop/Air Work/MRes 2016:17/R workshop/testdata.txt") #the text in brackets is the path
30 #of the file "testdata.txt" which is our datafile
31 time1 <- testdata$Time1.RT
32 time2 <- testdata$Time2.RT
33 ````
```

An arrow points from the text below to the green arrow icon at the end of the code chunk.

You can click on this arrow , just to run the chunk of R code delimited by ````

- Once you have your R Markdown script written (with appropriate in-text annotations to describe what you're doing, and why) you then need to 'Knit' the code together to produce your report in the format you have chosen:



A screenshot of the RStudio interface. The top menu bar shows several open files: 'S1data3', 'testmarkdown.Rmd', 'test.Rmd' (which is currently active), 'Untitled1*', and 'testdata'. Below the menu bar is a toolbar with various icons. A red arrow points to the 'Knit HTML' icon, which is the fourth icon from the left. The main workspace below contains the following R Markdown code:

```
1 ---  
2 title: "Correlation script"  
3 author: "Andrew Stewart"  
4 date: "1/12/2017"  
5 output: html_document
```

Correlation script

Andrew Stewart

1/12/2017

This is our new R script that is in an R Markdown document. All of this text will appear in the Notebook. Every line that begins with a # is a comment written by you, and is ignored by R. However, it will appear in the Notebook.

Let's put together as a script the code we just used to look at correlations.

We first need to install the ggplot2 package.

```
install.packages ("ggplot2", repos="http://cran.rstudio.com/")

## 
## The downloaded binary packages are in
## /var/folders/95/f9g_lcxj1777n_w285nmptmm0000gn/T//RtmpjNs3Ku/downloaded_packages

library (ggplot2)
```

We will also need the Hmisc package for calling the rcorr function

```
install.packages ("Hmisc", repos="http://cran.rstudio.com/")

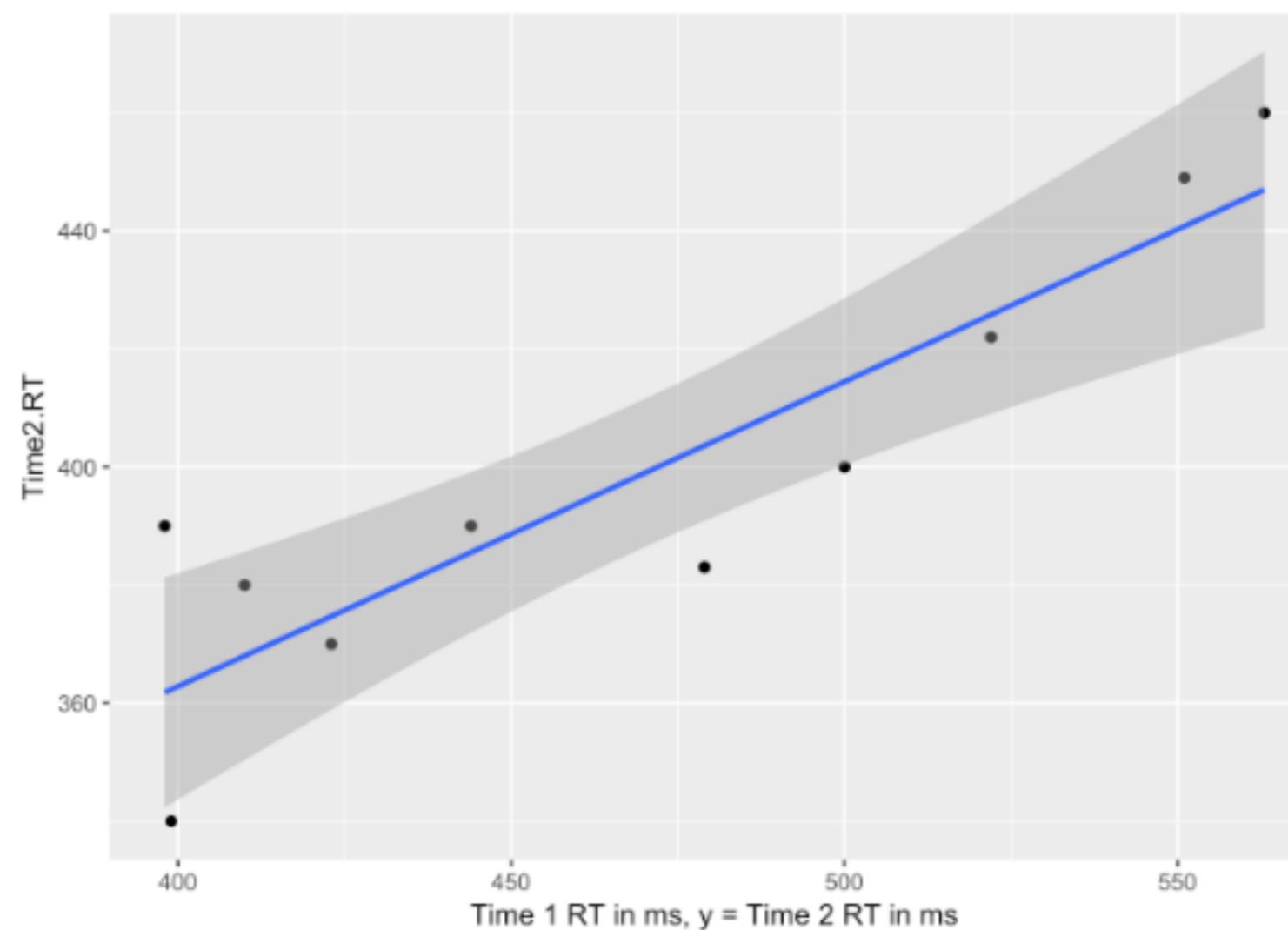
## 
## The downloaded binary packages are in
## /var/folders/95/f9g_lcxj1777n_w285nmptmm0000gn/T//RtmpjNs3Ku/downloaded_packages

library(Hmisc)

testdata <- read.delim("~/Desktop/Air Work/MRes 2016:17/R workshop/testdata.txt") #the text in brackets is the path
#of the file "testdata.txt" which is our datafile
time1 <- testdata$Time1.RT
time2 <- testdata$Time2.RT
```

You can use double hashes to make a title bigger. Below, you will see our plot plus the regression line.

```
ourgraph <- ggplot (testdata, aes (Time1.RT, Time2.RT)) + geom_point() + labs (x = "Time 1 RT in ms, y = Time 2 RT in ms")
ourgraph + geom_smooth(method = "lm") #with the smoother function this will display the regression line plus the data points
```



```
time1 <- testdata$Time1.RT  
time2 <- testdata$Time2.RT  
  
rcorr (time1, time2)
```

```
##      x     y  
## x 1.00 0.89  
## y 0.89 1.00  
##  
## n= 10  
##  
##  
## P  
##      x     y  
## x      5e-04  
## y 5e-04
```

We should probably include some text here which interprets the correlation we have found between our two variables.

Your R Markdown report should contain descriptions of what you're doing which each chunk of code, and any decisions you make as it which analysis to focus on (e.g., interpreting interaction effects). Good commenting helps those read the code, including yourself at some future point.

Sharing your analysis

Journals are increasingly requesting analysis code and data to be published alongside the published paper (and sometimes at the review stage).

You can share your analysis and data even at the submission stage using something like GitHub or OSF.

Git is a powerful tool that allows for the version control in collaborative projects, and the sharing of code and projects.

You can set up a GitHub account, and install GitHub Desktop on your own computer.

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ajstewartlang

Senior Lecturer in the Division of Neuroscience and Experimental Psychology, University of Manchester.

University of Manchester [http://personalpages.manchester.ac.uk/~ajstewartlang/](#) Joined 21 days ago

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ajstewartlang Capitalisation corrected

Latest commit `7e14ea2` 3 hours ago

Both Expts comparison

Tidied up code with consistent labelling

3 hours ago

Expt 1 Script and data

Tidied up code with consistent labelling

3 hours ago

Expt 2 Script and data

Tidied up code with consistent labelling

3 hours ago

README.txt

Capitalisation corrected

3 hours ago

README.txt

The repository "Both Expts comparison" contains the R analysis script and RT data for both experiments in 1 file. The conditions are relabeled to congruent vs. incongruent to allow a comparison of the magnitude of the congruency effect across the two experiments.

The repository "Expt 1 Script and Data" contains the R analysis script for the Anger/Fear experiment, the RT data, the accuracy data and the two data files (containing the word "graph") used by ggplot2 to graph the means and SEs.

The repository "Expt 2 Script and Data" contains the R analysis script for the Happy/Sad experiment, the RT data, the accuracy data and the two data files (containing the word "graph") used by ggplot2 to graph the means and SEs.

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ajstewartlang Tidied up code with consistent labelling	Latest commit de7b584 3 hours ago
..	
AngerFearAcc.csv	Tidied up code with consistent labelling
AngerFearRT.csv	Tidied up code with consistent labelling
AngerFeargraphacc.csv	R code and data
AngerFeargraphdata.csv	R code and data
Expt1_AngerFear_script.R	Tidied up code with consistent labelling

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Affective-Theory-of-Mind-Inferences / Expt 1 Script and data / Expt1_AngerFear_script.R

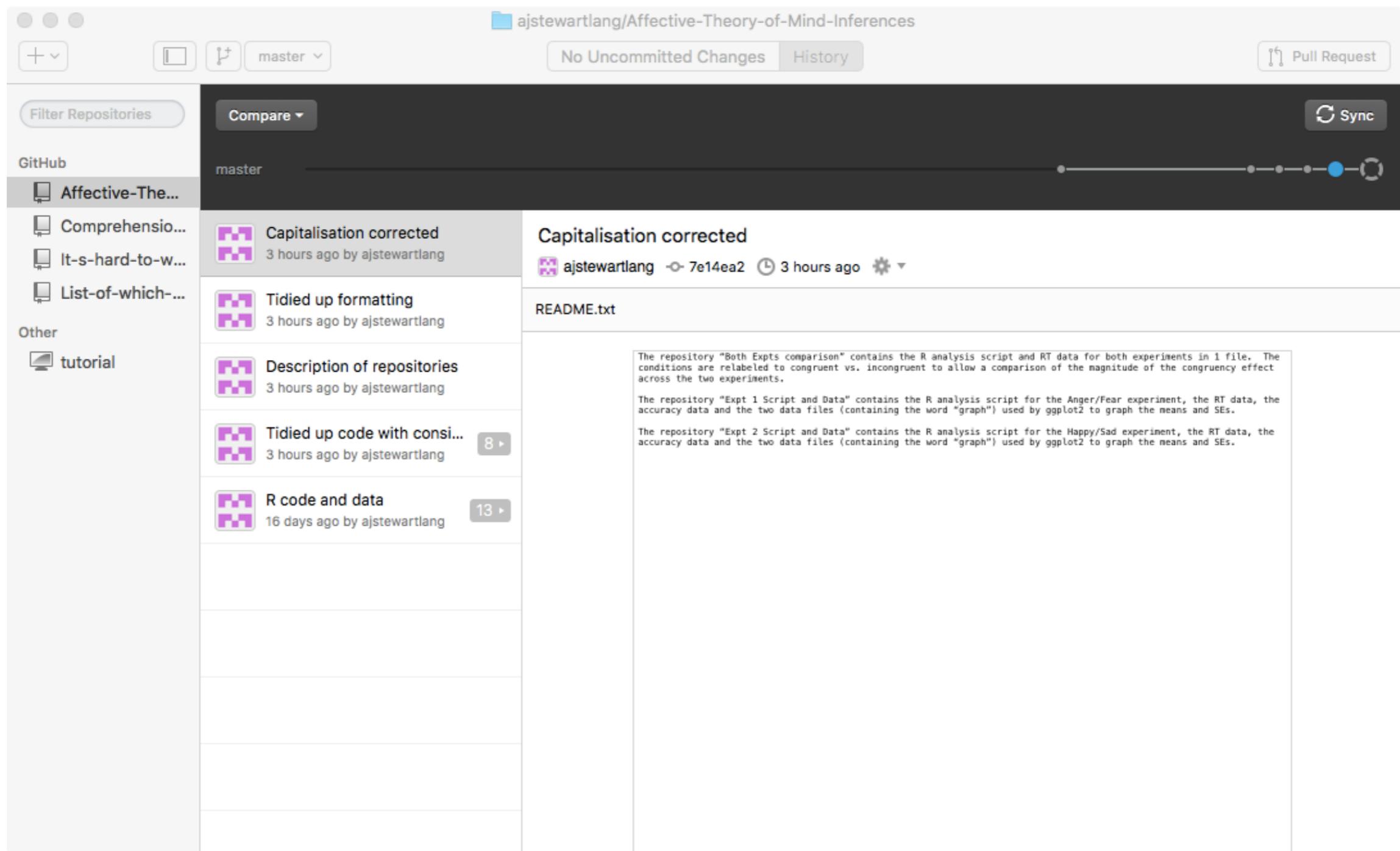
ajstewartlang Tidied up code with consistent labelling de7b584 3 hours ago

0 contributors

59 lines (46 sloc) | 3.17 KB Raw Blame History

```
1 library(lme4)
2 library(lmerTest)
3 library(lsmeans)
4 library(pbkrtest)
5 library(readr)
6 library(ggplot2)
7
8 #script for AngerFear RT and accuracy data analysis with arousal
9
10 #this is the analysis of the RT data
11 AngerFearRT <- read_csv("~/AngerFearRT.csv")
12
13 AngerFearRT$StoryEmotion <- as.factor(AngerFearRT$StoryEmotion)
14 AngerFearRT$FaceExpression <- as.factor(AngerFearRT$FaceExpression)
15
16 contrasts(AngerFearRT$StoryEmotion) <- matrix(c(.5, -.5))
17 contrasts(AngerFearRT$FaceExpression) <- matrix(c(.5, -.5))
18
19 #with Subject, Vignette, and Face as crossed random effects with arousal
20 #full model does not converge so need to drop interaction term from the random effects - in addition, Face random effect has only random in
21 modelRTAr1 <- lmer(RT ~ StoryEmotion*FaceExpression*Arousal + (1+StoryEmotion+FaceExpression|Subject) + (1+StoryEmotion+FaceExpression|Vig
22 summary(modelRTAr1)
23 modelRT <- lmer(RT ~ StoryEmotion*FaceExpression + (1+StoryEmotion+FaceExpression|Subject) + (1+StoryEmotion+FaceExpression|Vignette) + (1
24 anova(modelRTAr1, modelRT)
25
26 #difference between models not signif - arousal does not interact with effect so drop arousal from subsequent analysis
27
28 modelRTnull <- lmer(RT ~ (1+StoryEmotion+FaceExpression|Subject) + (1+StoryEmotion+FaceExpression|Vignette) + (1+FaceExpression|Face),
29 anova(modelRT, modelRTnull)
30 summary(modelRT)
```

This is GitHub Desktop



This Afternoon

- In the PC cluster, you'll get to work on data visualisation and modelling via ANOVA and Regression using R.
- Remember to write your code in a script - rather than writing it one command at a time.

Tomorrow

- We will focus entirely on (generalised) linear mixed models (GLMMs).
- GLMMs can be used pretty much any time you could use AN(C)OVA or regression. Except they are much more powerful and flexible (allowing for unbalanced designs, missing data, ordinal DVs, and non-normal data).

Recommended Online Resource

The following website is a fantastic interactive book that covers many of analyses (and is what the mediation content is based on) - if you want to expand your R skills, it is well worth a visit:

<http://ademos.people.uic.edu/index.html>