## MH2010 Practical session 29<sup>th</sup> Jan 2020

- Introduction to RStudio

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@B\_A\_Palmer





### R is for Resources

### Vignettes



### Webpages



#### eBooks







### Cheatsheets



Data Scientists Ireland

**Data Scientists IRL** 

@DataSci Ireland Follows you

in Ireland.

Promoting the Data Science professions

#### Twitter



#### Mara Averick @dataandme tidyverse @ @rstudio, # hoop head, gnashgab, blatherskite, lesser 1/2 of @batpigandme 👫 🐽

Massachusetts

@RLangTip One tip per day M-F on the R programming language #rstats. Brought to you by the R community team at

One R Tip a Day









O Cork, Ireland

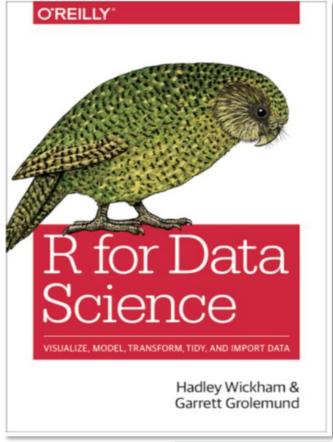
& darrendahly.github.io



Kara Woo @kara\_woo

Research scientist at @sagebio. Data curation, visualization, #rstats, reproducibility, open science, ballet

### R is for Resources





@hadleywickham



Garrett Grolemund @StatGarrett Books ♣ psyTeachR

#### Course Books



#### Level 1: Grassroots

Our first-year undergraduate course covers current state of psychological science and what Open Science is as well as its importance. It also aims to make students confident and competent at using RStudio as a tool to achieve good data management skills.

Authors: Emily Nordmann, Heather Woods

Contact: Emily Nordmann

Contributors: Jack Taylor, Shannon McNee



#### Level 2: Practical

Our second-year undergraduate course covers data skills such as R Markdown, data wrangling with tidyverse, and data visualisation with ggplot2. It also introduces statistical concepts such as permutation tests, NHST, alpha, power, effect size, and sample size. Semester 2 focusses on correlations and the general linear model.

Authors: Phil McAleer, Helena Paterson

Contact: Phil McAleer



#### Level 3: Statistical Models (Coming Soon)

This third-year undergraduate course teaches students how to specify, estimate, and interpret statistical models corresponding to various study designs, using a General Linear Models approach.

Author: Dale Barr



#### **MSc Conversion**

This book contains materials for students on the MSc Conversion in Psychological Studies/Science, a one-year postgraduate degree for students with a non-psychology undergraduate degree. This research methods course covers core data skills that allow you to manipulate and analyse quantitative data.

A 01 E 0 N 1



Emily Nordmann @emilynordmann



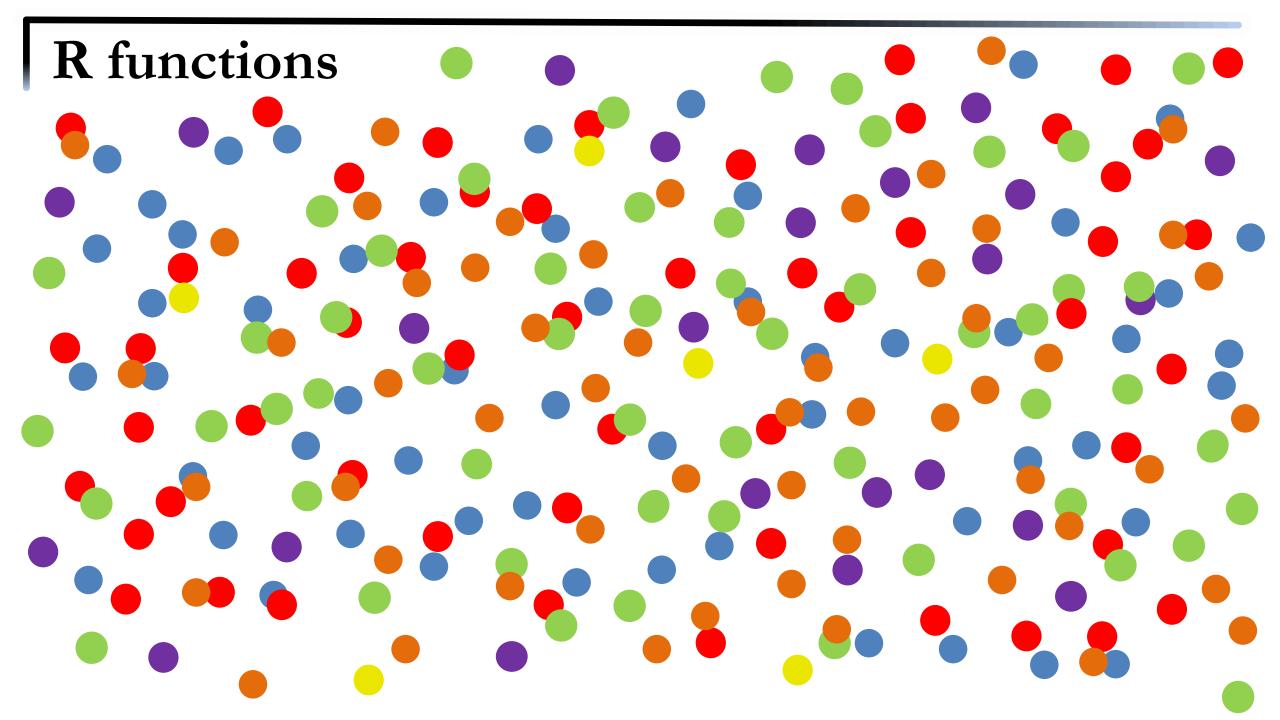
Lisa DeBruine 

@LisaDeBruine

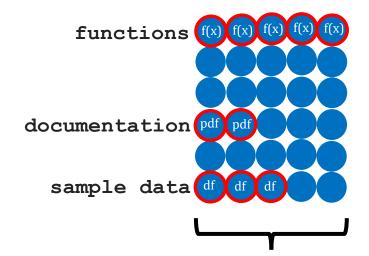


Phil McAleer

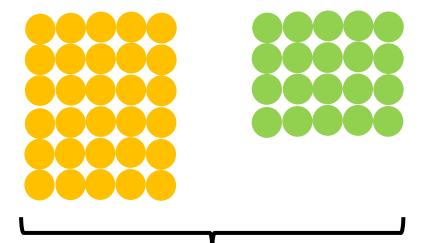
@McAleerP



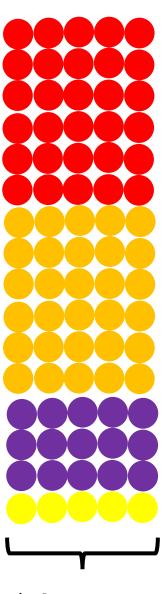
## R packages



R comes preloaded with ~30 other packages (e.g. base, stats, graphics etc.)

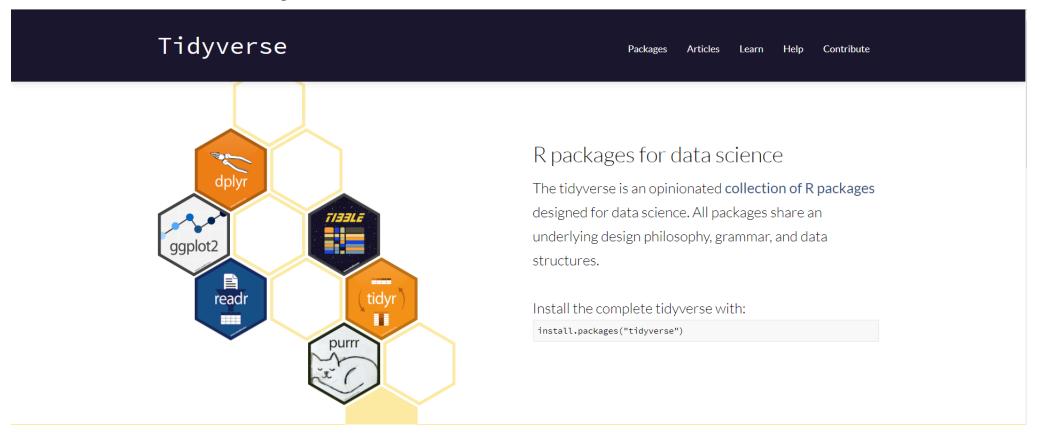


Other packages:
Install once
Update regularly
Load each session



tidyverse

### What is the tidyverse?



- Joined up collection of packages for data analysis
  - Consistent functions
  - Uses (tidy) data
  - Supports end-to-end workflows

### What is the tidyverse?

```
> install.packages(c("broom", "cli2", "crayon",
"dbplyr", "dplyr", "forcats", "ggplot2", "haven",
"hms", "httr", "jsonlite", "lubridate",
"magrittr", "modelr", "pillar", "purrr", "readr",
"readxl", "reprex", "rlang", "rstudioapi",
"rvest", "stringr", "tibble", "tidyr", "xml2")
```

> install.packages("tidyverse")

### RStudio Cloud



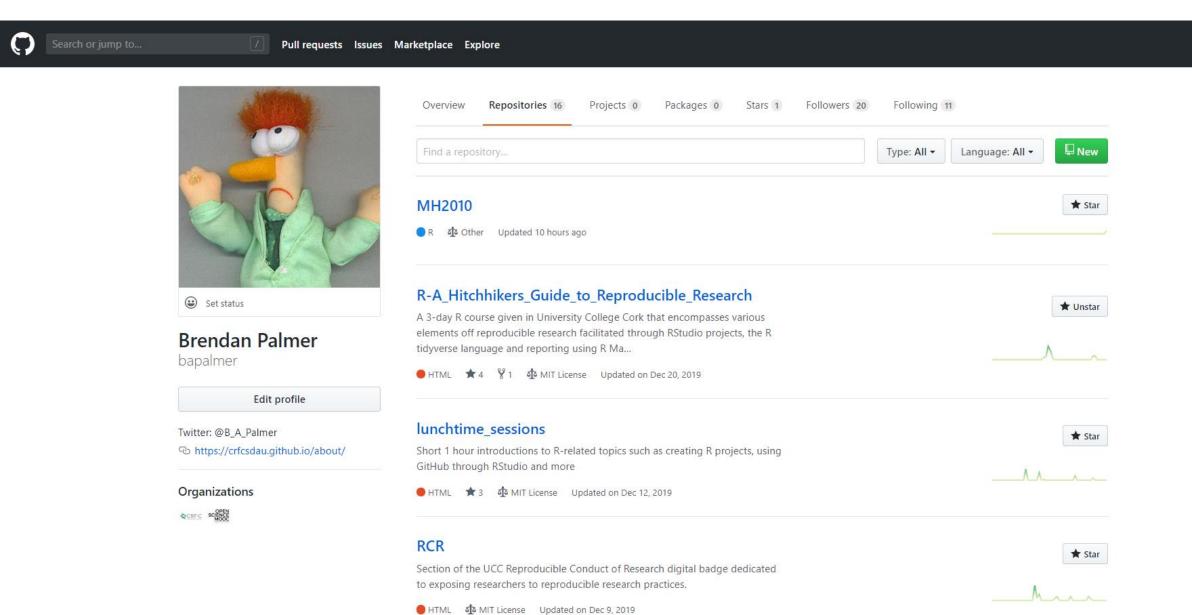
Log In Sign Up

### Welcome to RStudio Cloud alpha

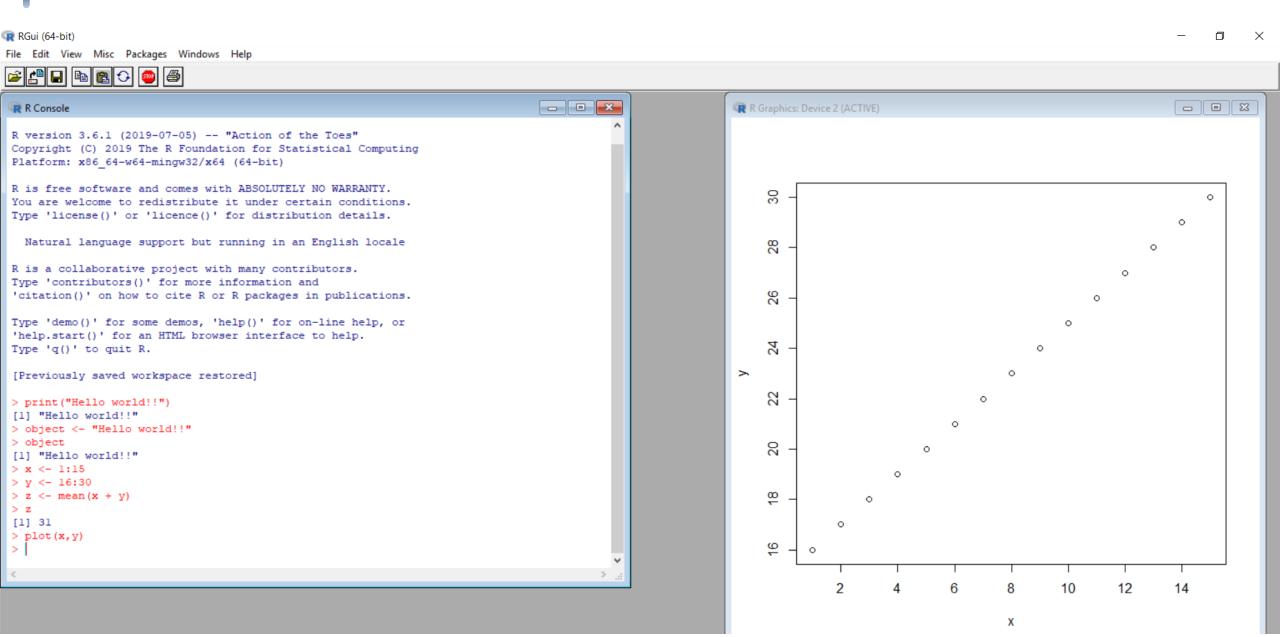
Do, share, teach and learn data science with R.

Get Started

### GitHub



### R user interface versus RStudio



```
File Edit Code View Plots Session Build Debug Profile Tools Help
      Go to file/function
                                                                                                                                                                 Pre-workshop *
                                                                                                               Environment History Connections Git
        ☐ Source on Save
                                                                                          Run 🖘 🕈 Source 🕶
                                                                                                               🚰 📊 🔛 Import Dataset 🕶 🎻
                                                                                                                                                                 ⊞ Grid ▼
                                                                                                               Global Environment •
  32
       gather(sample, expression, G0.05:U0.3) %>%
                                                                                                                cleaned_g... tbl_df 7
                                                                                                                                            11.3 ... 198430 obs. of 7...
  33
                                                                                                                nutrient_... charac... 6
                                                                                                                                            984 B Named chr [1:6] "G...
       separate(sample, c("nutrient", "rate"), sep = 1, convert = TRUE) %>%
                                                                                                                            charac... 1
                                                                                                                                            168 B "http://varianceex...
  35
                                                                                                                url
 36
       mutate(nutrient = plyr::revalue(nutrient, nutrient_names)) %>%
  37
  38
       filter(!is.na(expression), systematic_name != "")
                                                                                                                             Environment
     # Plot the clean data
 41
                                                             Code editor
     cleaned_genes_tbl %>%
 43
                                                                                                               File Plots Packages Help Viewer
       filter(BP == "leucine biosynthesis") %>%
                                                                                                                  \rangle 🔑 Zoom 😕 Export 🕶 🔞 🧳
                                                                                                                                                                Publish
                                                                                                                                                 LEU2
                                                                                                                           LEU1
       ggplot(mapping = aes(x = rate, y = expression, color = nutrient)) +
 46
       geom_point() +
       geom_smooth(method = "lm", se = FALSE) +
       facet_wrap(~ name)
     # Does this work on your system? $
  /R_Users_Workshop/PG_module/course_notes/R-A_Hitchhikers_Guide_to_Reproducible_Research/Pre-workshop/ 🔊
  GID = col_character(),
                                                                                                                                                                   Ammonia
  YORF = col_character().
                                                                                                                                                                   Glucose
  NAME = col_character()

    Leucine

                                                                                                                     Files/Plots/Help
                                                              R console

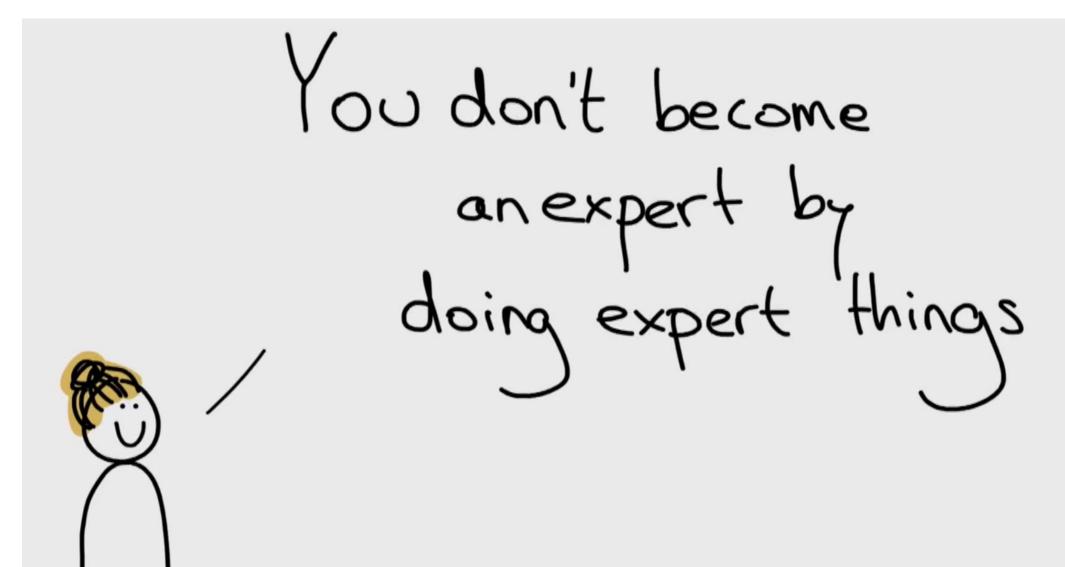
    Phosphate

See spec(...) for full column specifications.

    Sulfate

  cleaned_genes_tbl %>%
                                                                                                                                                                Uracil
    filter(BP == "leucine biosynthesis") %>%
    ggplot(mapping = aes(x = rate, y = expression, color = nutrient)) +
    geom_point() +
    geom_smooth(method = "lm", se = FALSE) +
    facet_wrap(~ name)
                                                                                                                              0.2
                                                                                                                                                    0.2
```

### Central theme of this session



### R Markdown

```
Randon Paragon Para
File Edit Code View Plots Session Build Debug Profile Tools Help
                                    Nnit → 🌣 →
                                                                                                                                                                                                        © Insert - 1 ♣ ■ Run - 5 -
                  title: "This is a reproducible document"
                   author: "Dr. Brendan Palmer"
                   date: "18th June 2019"
                               fia width: 6
        10-# This is the beginning of the project
        12 Our initial reports might be restricted to lab meetings etc. We can use R
                   Markdown to show the code we are using, so that the meetings are not just a
                   demonstration of the results, but also an examination of the `code` used to obtain
                   them.
        13
        14 - ## Data overview
                            {r packages and setup, include = FALSE}
                                                                                                                                                                                                                                                         ☆ 🏝 🕨
        16
        17 knitr::opts_chunk$set(echo = FALSE, message = FALSE, warning = FALSE)
        18
                   library(tidyverse)
                     library(knitr)
        22
        23
        24 The plot below is call from the ggplot object entitled `report_plot` created in
                   the script `03_final_analysis.R`.
        25
                            {r Plots from script, echo = FALSE}
                                                                                                                                                                                                                                                         ☆ ▼ →
        27
                  source("scripts/03_final_analysis.R")
        29
        30 # The location of the Rmd file dictates whether the path to other files is intact
```

#### This is a reproducible document

Dr. Brendan Palmer

18th June 2019

#### This is the beginning of the project

Our initial reports might be restricted to lab meetings etc. We can use R Markdown to show the code we are using, so that the meetings are not just a demonstration of the results, but also an examination of the code used to obtain them.

#### Data overview

The plot below is call from the ggplot object entitled report\_plot created in the script 03\_final\_analysis.R.

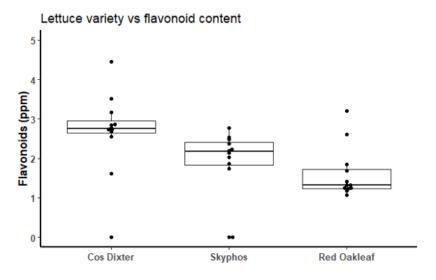
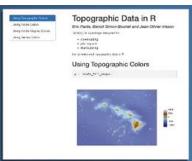
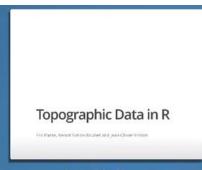


Fig. 1. Flavonoid content of three lettuce varieties under three experimental conditions.

Or we can also recreate the code within the R Markdown document as seen below.

### What has R Markdown ever done for us?





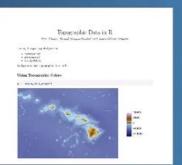












ioslides



reveal.js



rtf



tufte handout



book

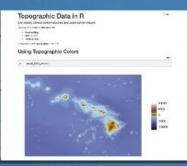


pdf



Word

dashboard



notebook

slidy



beamer

markdown



latex

### package vignette



custom template

website



shiny app

### R Markdown

YAML header

Chunks of code

Plain text with data outputs from R code

Chunks of code

title: "Diamond sizes" date: 2016-08-25

output: html\_document

{r setup, include = FALSE}
library(ggplot2)
library(dplyr)
smaller <- diamonds %>%
filter(carat <= 2.5)</pre>

We have data about 'r nrow(diamonds)'
diamonds. Only
'r nrow(diamonds) - nrow(smaller)' are
larger than
2.5 carats. The distribution of the
remainder is shown below:

{r, echo = FALSE}
smaller %>%
ggplot(aes(carat)) +
geom\_freqpoly(binwidth = 0.01)

### R Markdown

### Knit the document

#### Insert new chunk

example report.Rmd\* × -0 Rnit → 💮 → Insert ▼ | ↑ ↓ | → Run ▼ | • ▼ 2 title: "This is a reproducible document" author: "Dr. Brendan Palmer" A YAML date: "2nd August 2019" output: header word\_document: fig\_height: 4 fig\_width: 6 10 11- # This is the beginning of the project 12 13 Our initial reports might be restricted to lab meetings etc. We can use `R Markdow Click to run all show the code we are using, so that the meetings are not just a demonstration of 1 Text formatted results, but also an examination of the `code` used to obtain them. code chunks 14 with Markdown 15 - ## Data overview 16 17 The plot below is call from the ggplot object entitled `report\_plot` created in the script `03\_final\_analysis.R`. 18 19 -```{r Plots from script, echo = FALSE} ∰ ¥ 20 library(tidyverse) library(knitr) 23 Code 24 source("scripts/03\_final\_analysis.R") chunk 25

# The location of the Rmd file dictates whether the path to other files is intact

above

Run code in the chunk

27

29

report\_plot

### R Markdown - Headers

```
# Header 1

## Header 2

### Header 3

#### Header 4

##### Header 5

###### Header 6
```



# Header 1 Header 2

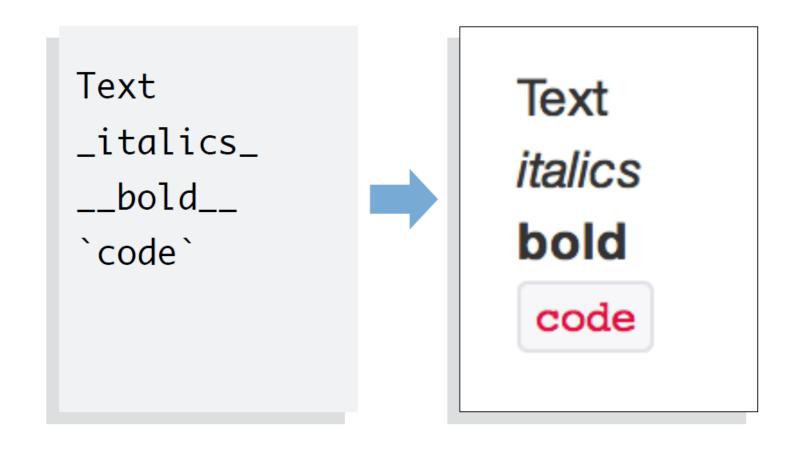
**Header 3** 

**Header 4** 

**Header 5** 

Header 6

## R Markdown - Formatting



### R Markdown - Lists

### Bullets

- \* bullet 1
- \* bullet 2

Numbered list

- 1. item 1
- 2. item 2

### **Bullets**

- bullet 1
- bullet 2

### Numbered list

- 1. item 1
- 2. item 2



## R Markdown - Hyperlinks



### Basics of R code

Symbol	What it does	Example 1	Example 2
<-	Assign operator Creates new objects	<pre>&gt; x &lt;- 5 &gt; x [1] 5</pre>	<pre>&gt; y &lt;- "This" &gt; y [1] "This"</pre>
c()	Helps create objects with more than one element	> A	<pre>&gt; w &lt;- c("This", "is", "easy! ") &gt; w [1] "This" "is" "easy!"</pre>
#	Computer ignores what is written. Used for adding notes to code	<del>-</del>	<pre>&gt; print("hello") [1] "hello"</pre>
%>%	<u> </u>	> data %>% do_something_to(data)	<pre>&gt; data %&gt;%   do_something_to(data) %&gt;%   do_something_else_to(data)</pre>
%in%	returns a logical vector indicating if there is a match	> "x" %in% c("x", "y", "z") [1] TRUE	> c("x", "y", "z") %in% "x" [1] TRUE FALSE FALSE
?	Access help	> ?mean()	<pre>&gt; ?geom_point()</pre>

FYI: R is case sensitive!! Name.of.data ≠ name.of.data

Assignment operator: <-



Functions take arguments inside round brackets: function()



Indexing occurs inside square brackets: []



Functions are defined inside curly brackets: {}



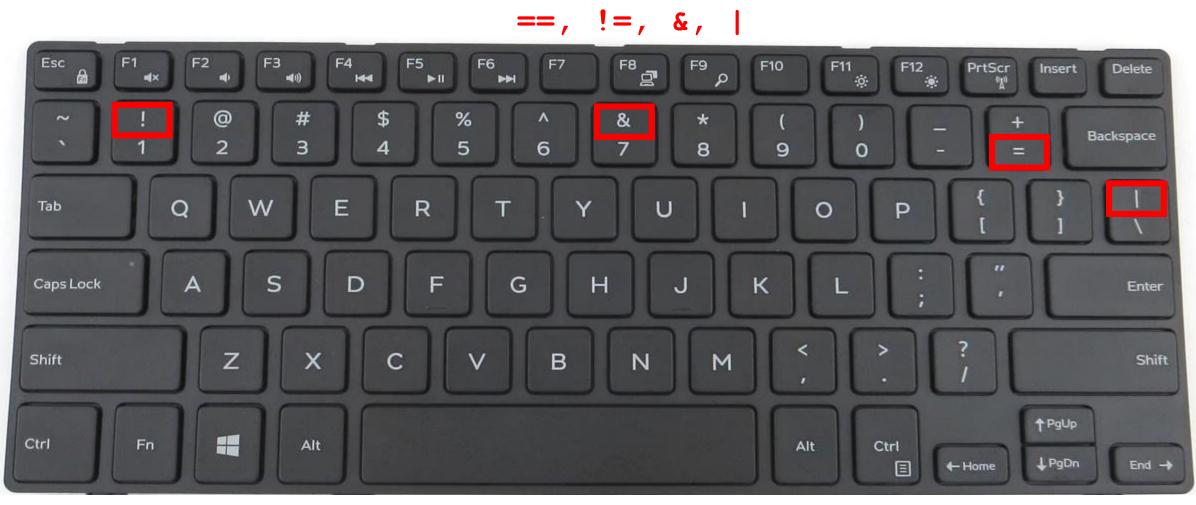
You can comment out your code using the hash key: #



Dollar sign allows you extract elements by name: \$



Logical TRUE/FALSE operators equals, not equals, and, or:



Tilde operator for use in formulas: ~



Tab key for autocomplete



## To understand R, remember the following

- Everything that exists is an object
- Everything that happens is a function

## Creating objects

```
For most of us, R is simply the creation of and manipulation
of objects:
new object \leftarrow c(1, 2, 3)
- the objects are then fed into functions to create amazing
 new objects
amazing new object <- function (new object)
Broadly speaking the following is true in R:
information
> data frame <- function(information)</pre>
      <- function(data frame)
> plot
> model <- function(data frame)</pre>
```

### Naming objects

There are a few simple rules to follow initially:

- Object names must start with a letter and can only contain letters, numbers, '' and '.'
- Certain characters should not be used, e.g:
  - c is the concatenate function 'c()'
  - T is used as shorthand for TRUE
  - F is used as shorthand for FALSE

### Three main types of data structure

```
The main data types are;
# double (for double precision floating point numbers)
typeof(1.23)
# character
typeof("string")
# logical
typeof (FALSE)
# missing values are represented by NA
example \leftarrow c(1, 2, NA, 4)
```

### Nested functions

It is possible to 'nest' functions within functions ...

```
round(mean(sample(pop, n, replace = FALSE)), 2)
```

- sample(pop, n, replace = FALSE) will give us a numeric vector
- mean(numeric vector) will calculate the mean of this vector
- round(mean, 2) will round up the answer to two decimal places

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## Types of data structure

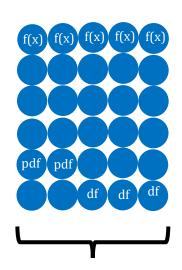
- Vectors come in two forms

```
A: Atomic vectors contain exactly one type of data
           <-c(1, 2, 0.5, -0.5, 3.4)
all numbers
all characters <- c("One", "too", "3")
all logical
           <- c(TRUE, FALSE) # NOTE: Type it out</pre>
B: Lists allow combinations of different types of data
this is a list <- list(1, TRUE, "Three", "4")
typeof(this is a list)
[1] "list"
this is also a list <- list(all numbers, all characters)
```

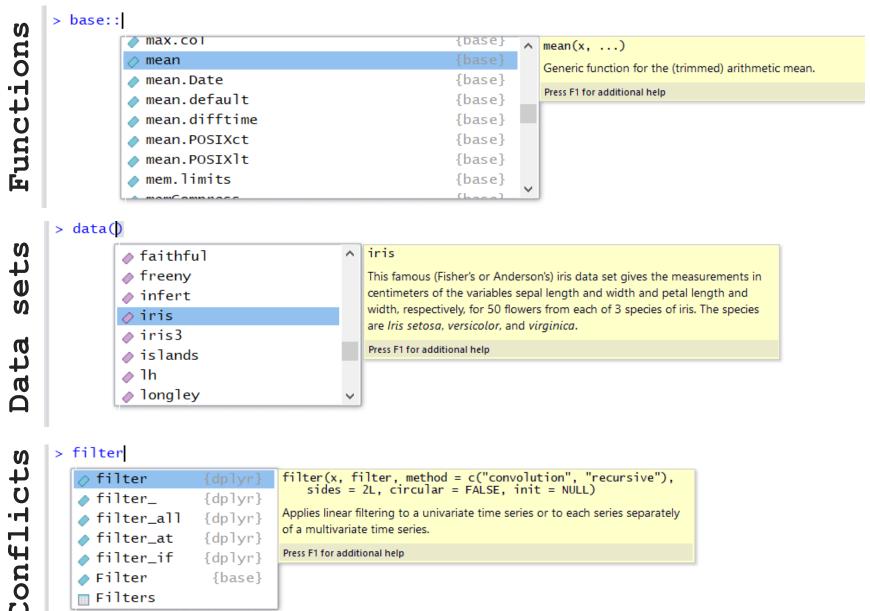
## Walkthrough example script

- scripts/01\_baseR\_introduction.R

## Package contents



Base R: Comes preloaded



## Walkthrough example script

- scripts/02\_navigating\_R\_packages.R

## Practical notes

- docs/frequentist\_inference.Rmd

### **OPTIONAL EXTRAS**

## Types of data structure

- # Matrices/Arrays:
- You can have a matrix of two or more dimensions a matrix <- matrix(1:9, 3, 3)</p>
- Vectors and matrices can only contain **one** type of data
- VERY VERY NB: If you try to create a vector with more than one data type, then it will undergo coercion to the least common denominator
- The coercion rule goes:

  logical -> integer -> numeric -> complex -> character
- You can perform coercions yourself on vectors

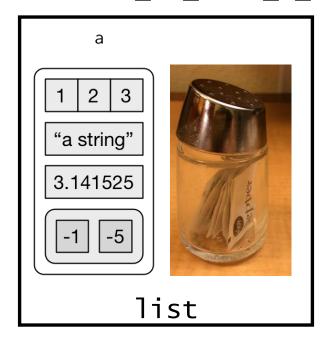
## Types of data structures

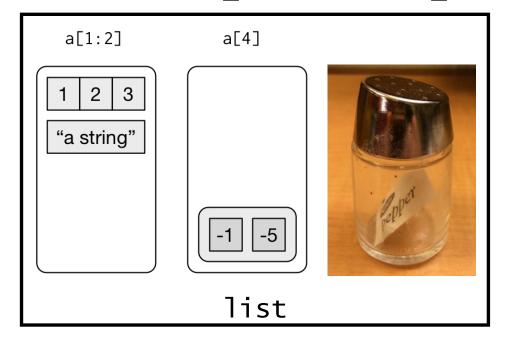
## Indexing

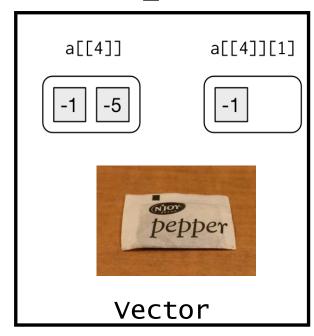
```
- Indexing can occur in one or two dimensions
- One dimension:
    new_object <- c(1, 2, 3)
    new_object[1]
    [1] 1
- Two dimensions
    a_data_frame[1, 1] # i.e [Row number 1, Column number 1]
    a data frame$number[1] # i.e. Column called number, row 1</pre>
```

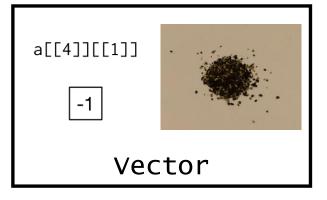
## Indexing

- # Recall
- this is also a list <- list(all numbers, all characters, all logical)









- # Important
- [ extracts a sublist, results will be a list
- [[ extracts a single component

# Try it out for yourself

- scripts/03\_practice\_worksheet.R