# 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

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#### 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









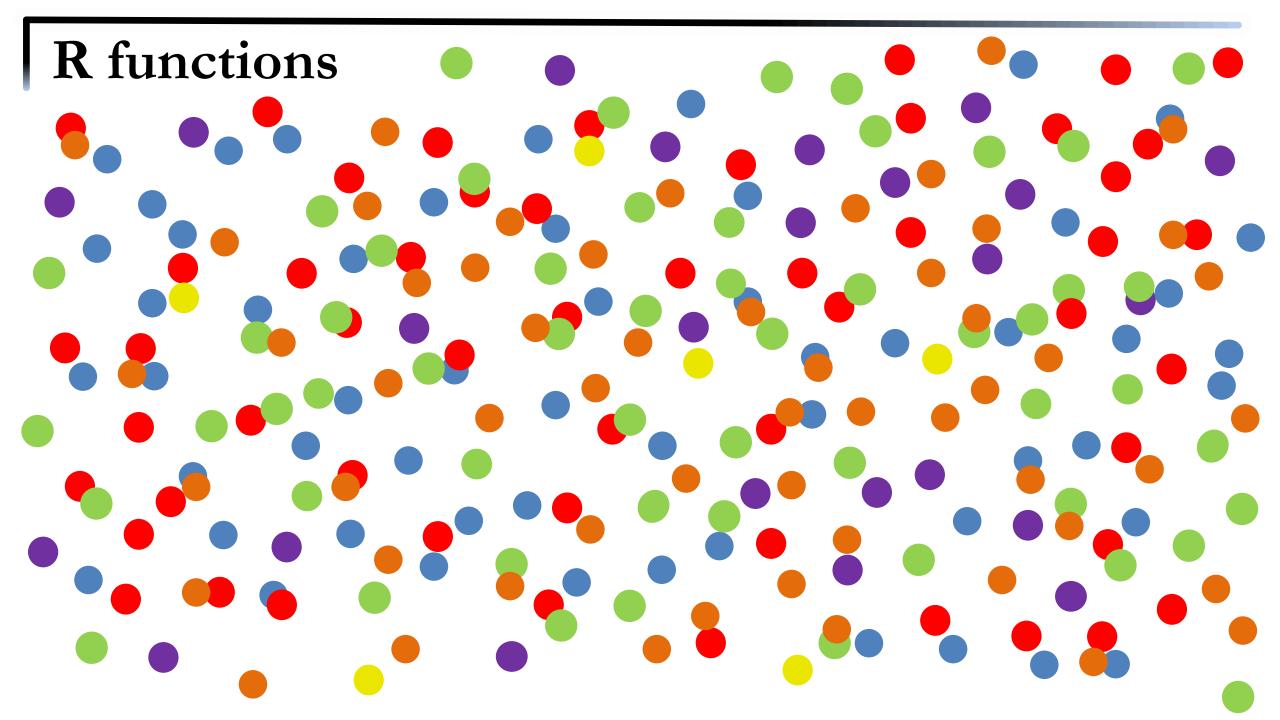
O Cork, Ireland

& darrendahly.github.io

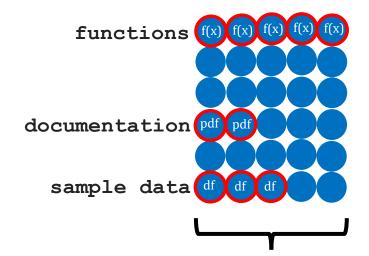


Kara Woo @kara\_woo

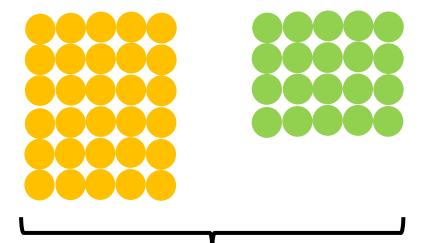
Research scientist at @sagebio. Data curation, visualization, #rstats, reproducibility, open science, ballet



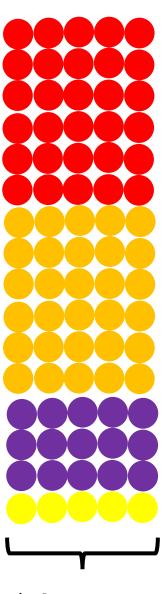
# R packages



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

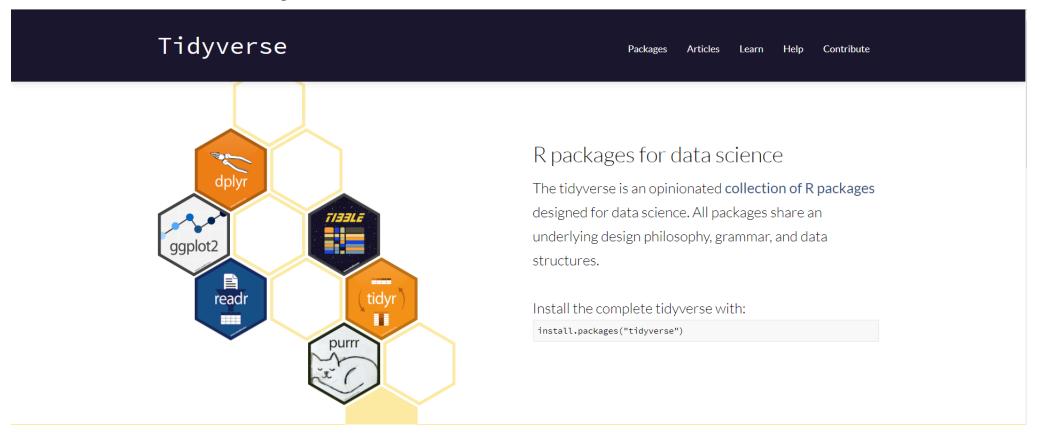


Other packages:
Install once
Update regularly
Load each session



tidyverse

### What is the tidyverse?



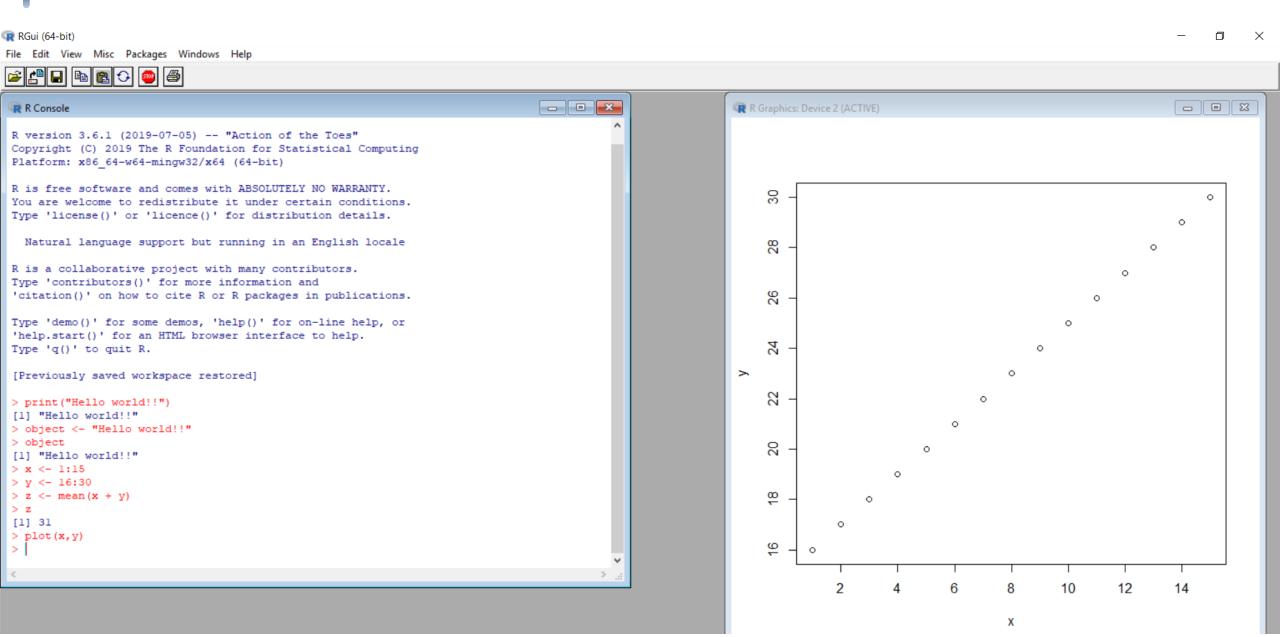
- Joined up collection of packages for data analysis
  - Consistent functions
  - Uses (tidy) data
  - Supports end-to-end workflows

### 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")

#### R user interface versus RStudio



#### RStudio Cloud



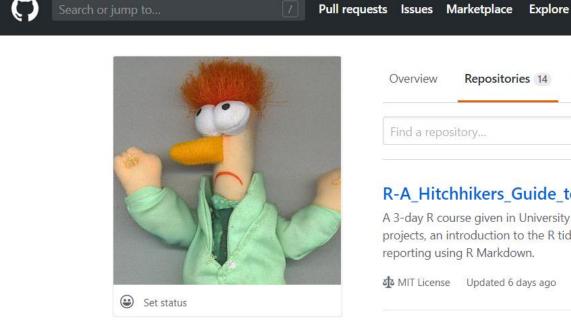
Log In Sign Up

#### Welcome to RStudio Cloud alpha

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

Get Started

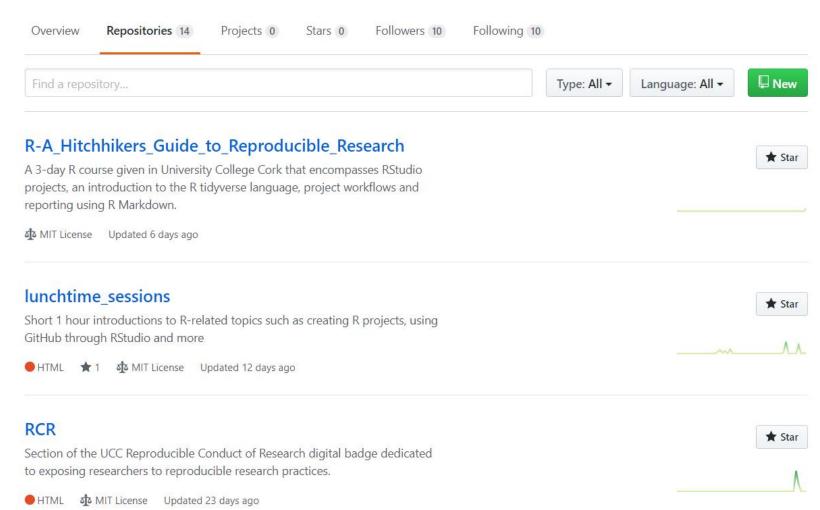
#### GitHub



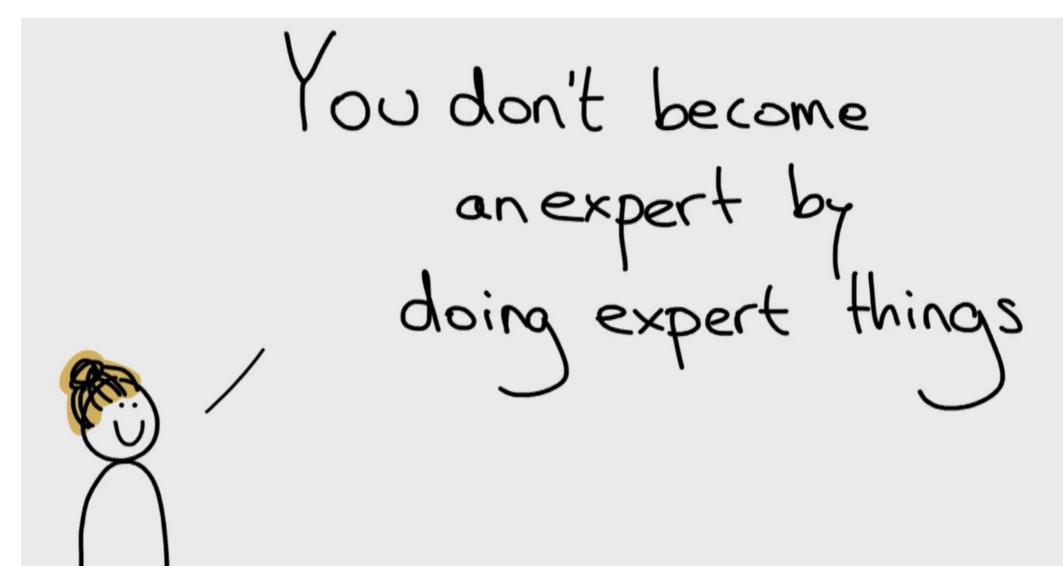
#### Brendan Palmer bapalmer







#### Central theme of this session



```
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
```

#### 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.

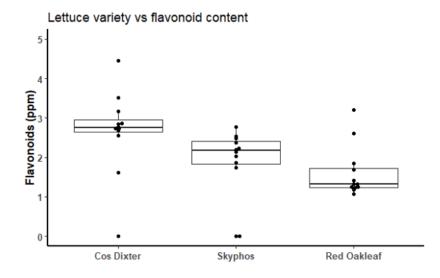
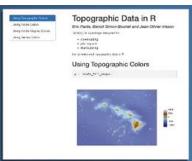
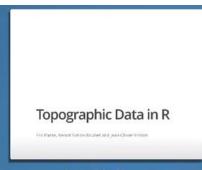


Fig. 1. Flavonoid content of three lettuce varieties under three experimental conditions.

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

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





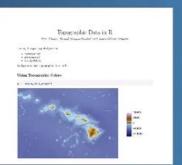












ioslides



reveal.js



rtf



tufte handout



book

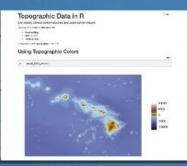


pdf



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\* × 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

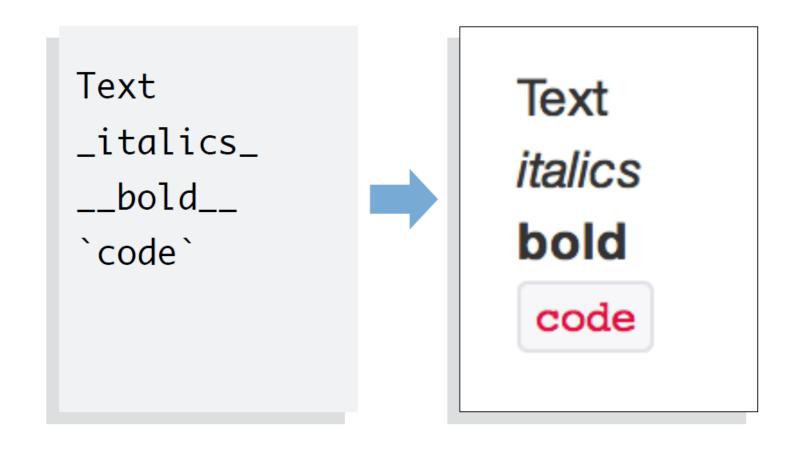
**Header 3** 

**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: {}



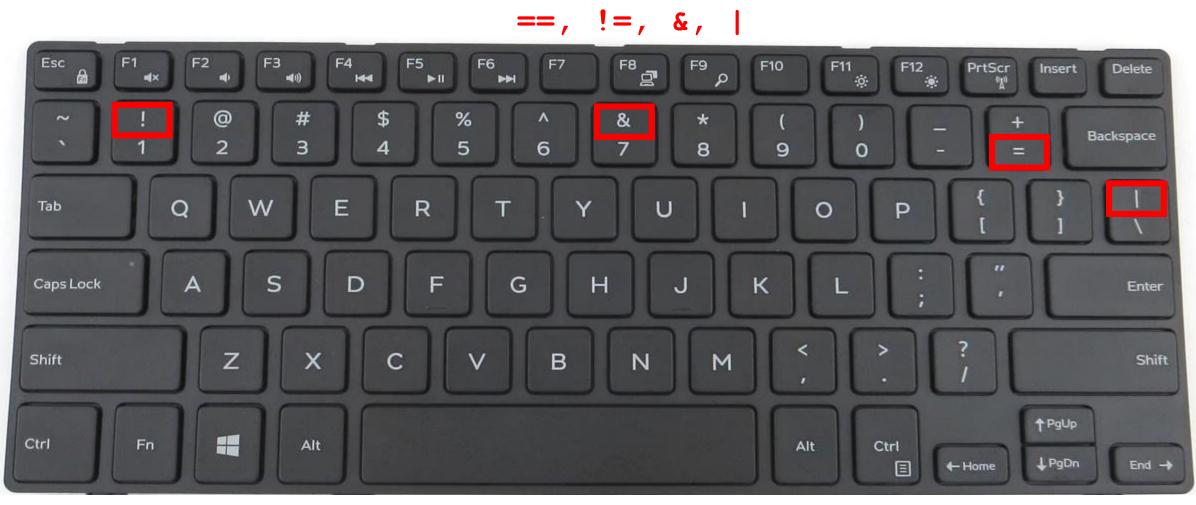
You can comment out your code using the hash key: #



Dollar sign allows you extract elements by name: \$



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



Tilde operator for use in formulas: ~

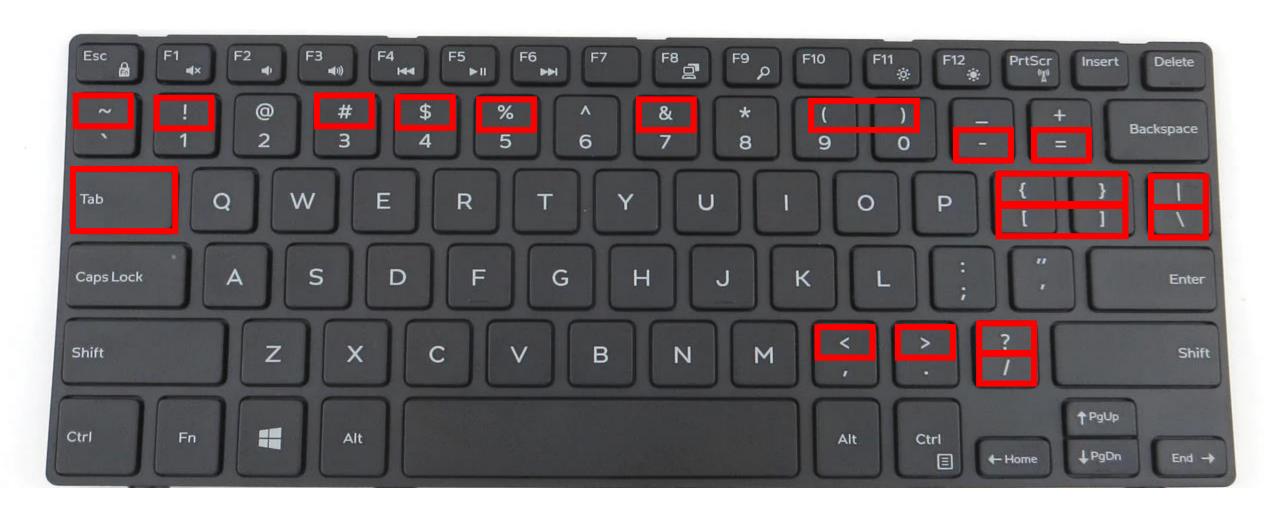


Tab key for autocomplete



Backslash and forward slash





# 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

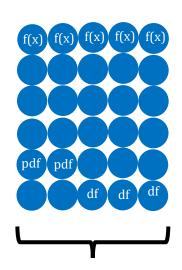
#### Three main types of data structure

```
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)
```

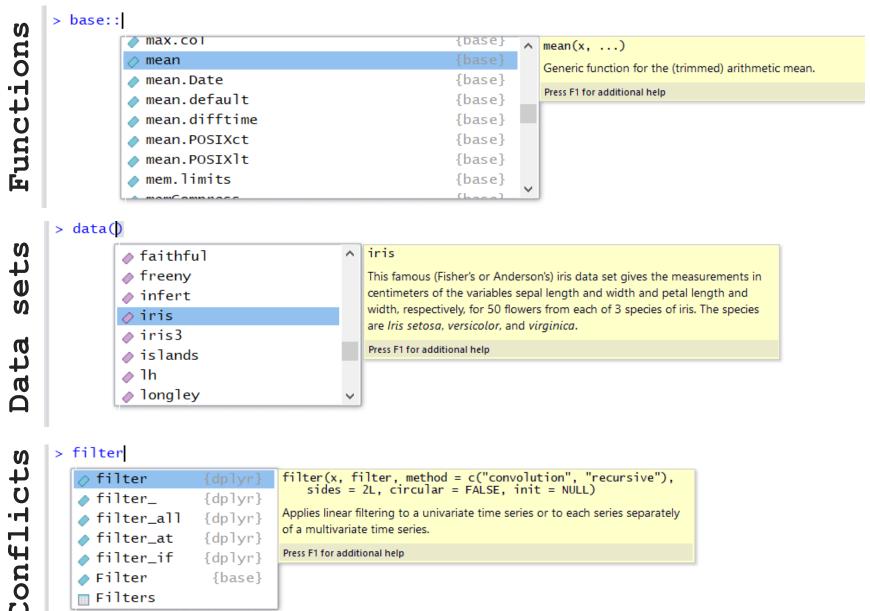
# Walkthrough example script

- 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

### 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)
```

#### **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)
- 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

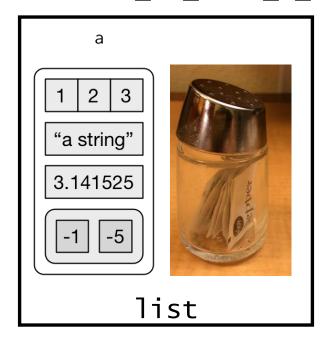
### Types of data structures

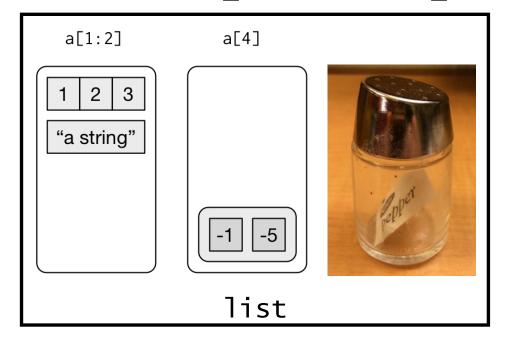
### Indexing

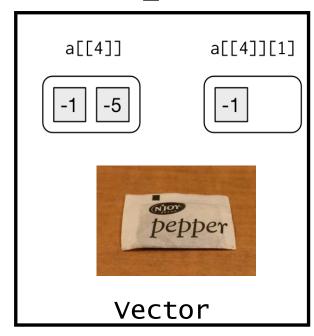
```
- Indexing can occur in one or two dimensions
- One dimension:
    new_object <- c(1, 2, 3)
    new_object[1]
    [1] 1
- Two dimensions
    a_data_frame[1, 1] # i.e [Row number 1, Column number 1]
    a data frame$number[1] # i.e. Column called number, row 1</pre>
```

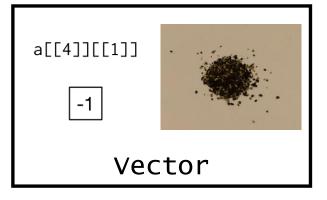
### Indexing

- # 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