Getting started with

Dr Saskia Freytag

Webinar for Australian Biocommons

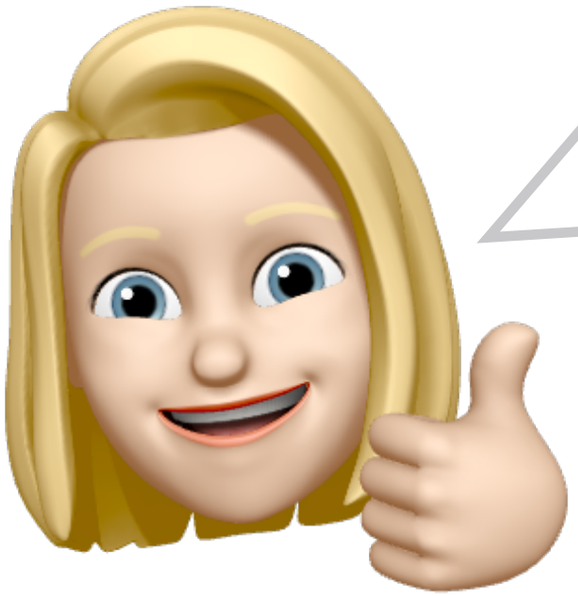
To me R is a:

- Programming language

Console | Terminal | Jobs

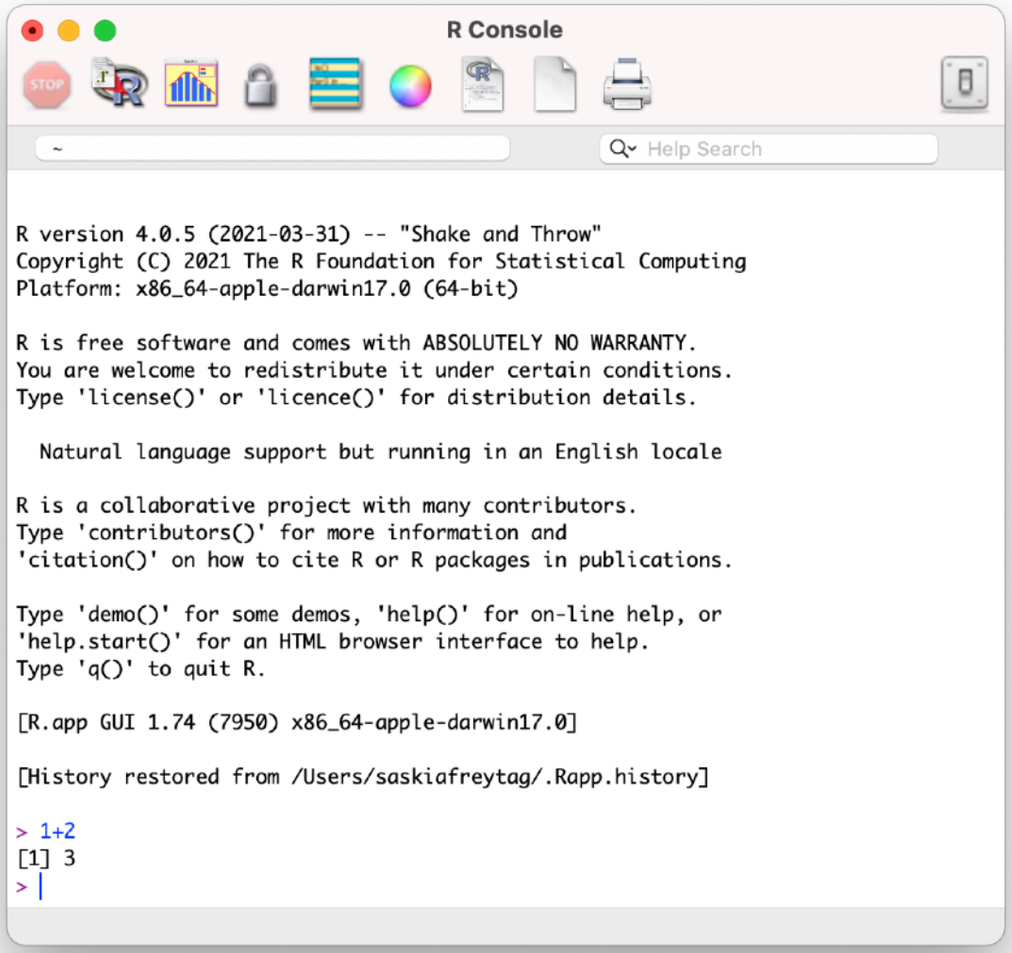
/cloud/project/

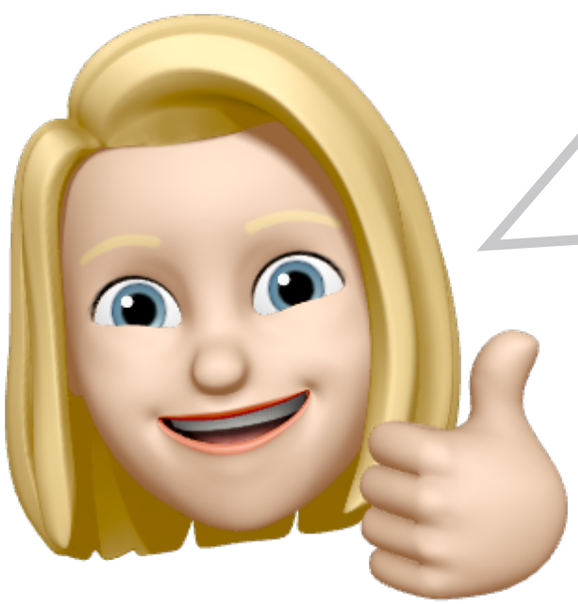
```
> # if statement
> x <- -3
> if (x < 0) {
+   print("x is a negative number")
+ } else if (x == 0) {
+   print("x is zero")
+ } else {
+   print("x is a positive number")
+ }
[1] "x is a negative number"
>
> # else if statement
> x <- 0
> if (x < 0) {
+   print("x is a negative number")
+ } else if (x == 0) {
+   print("x is zero")
+ } else {
+   print("x is a positive number")
+ }
[1] "x is zero"
>
> # else statement
> x <- 5
> if (x < 0) {
+   print("x is a negative number")
+ } else if (x == 0) {
+   print("x is zero")
+ } else {
+   print("x is a positive number")
+ }
[1] "x is a positive number"
>
```



To me R is a:

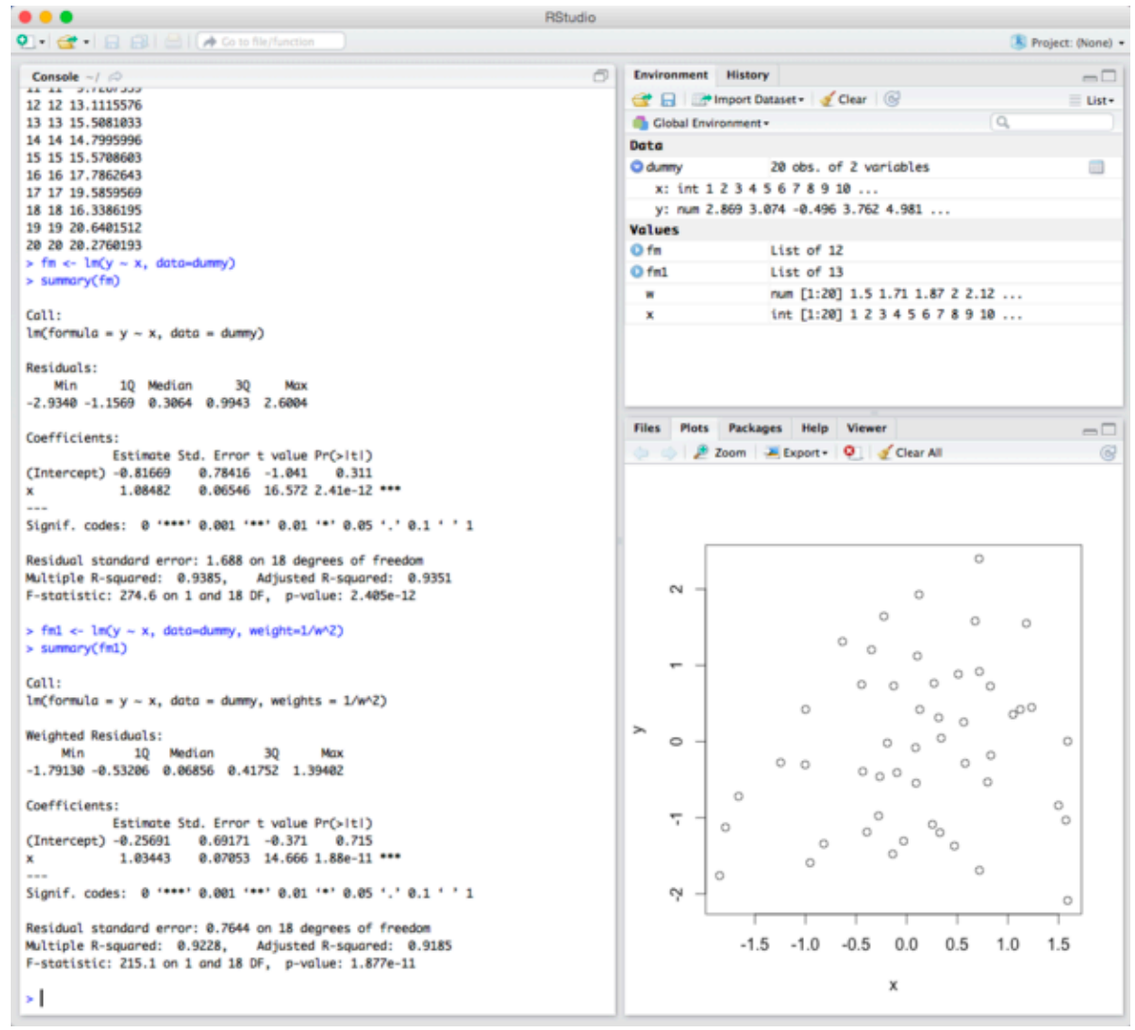
- Calculator

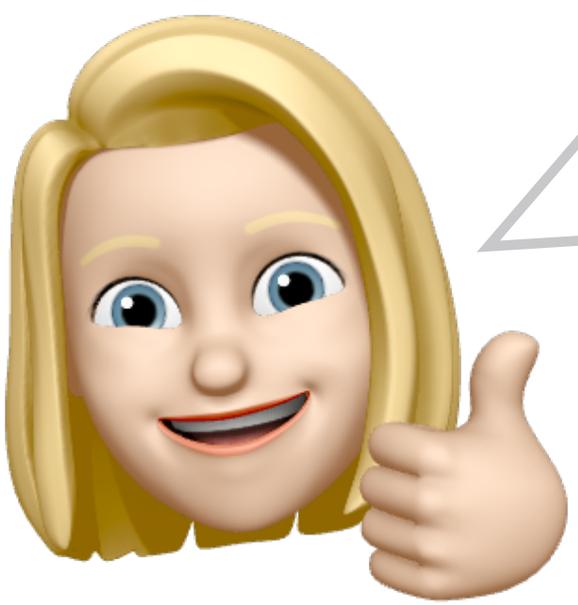




To me R is a:

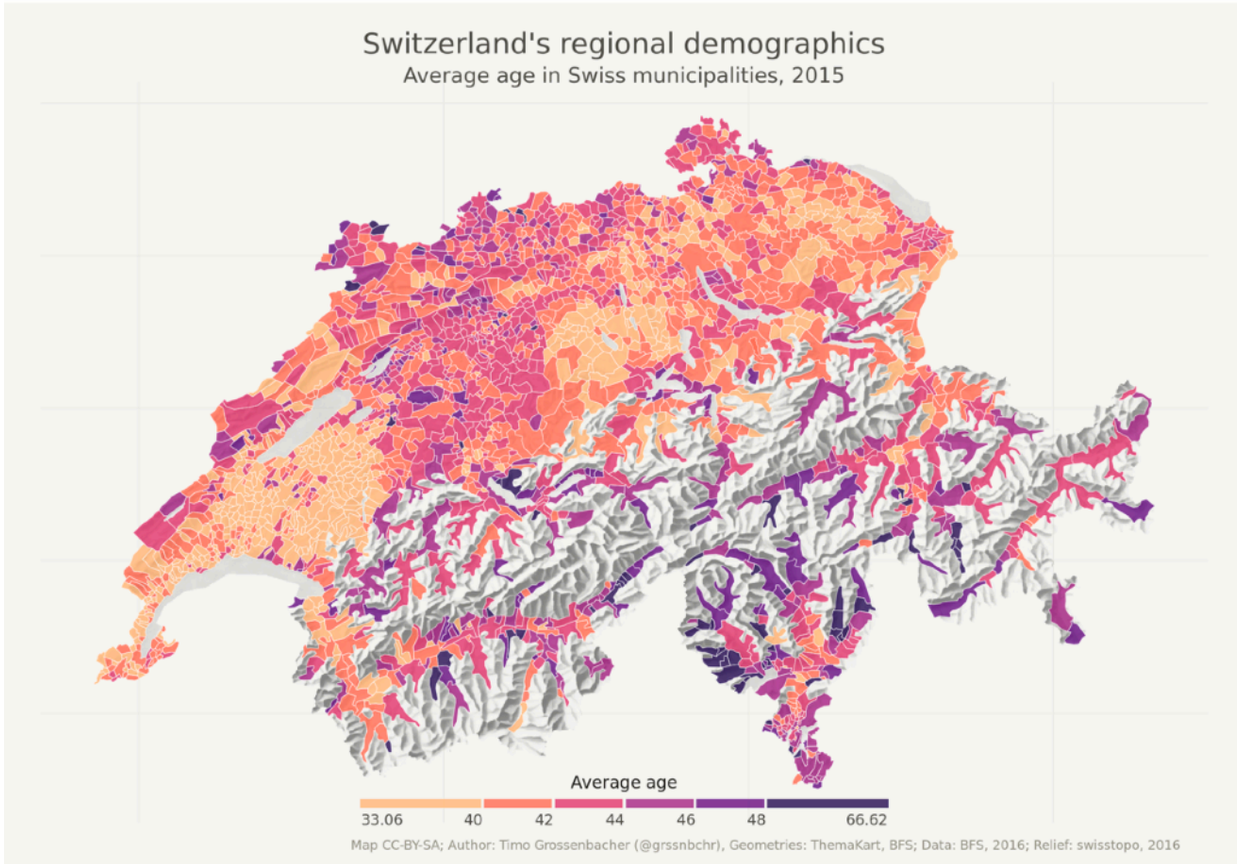
- Statistical analysis tool

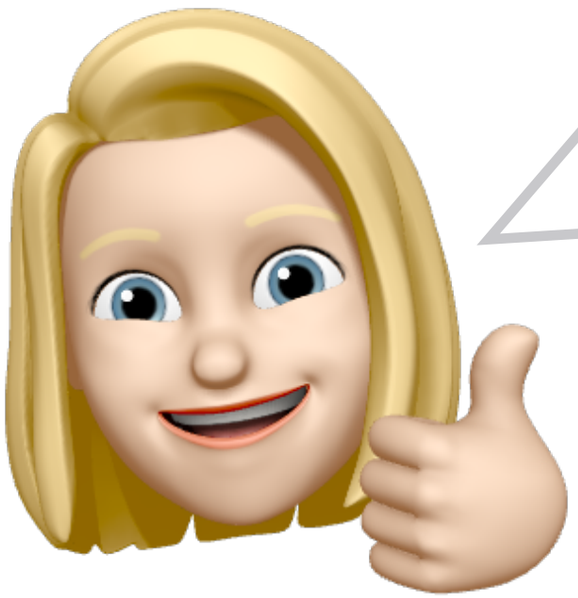




To me R is a:

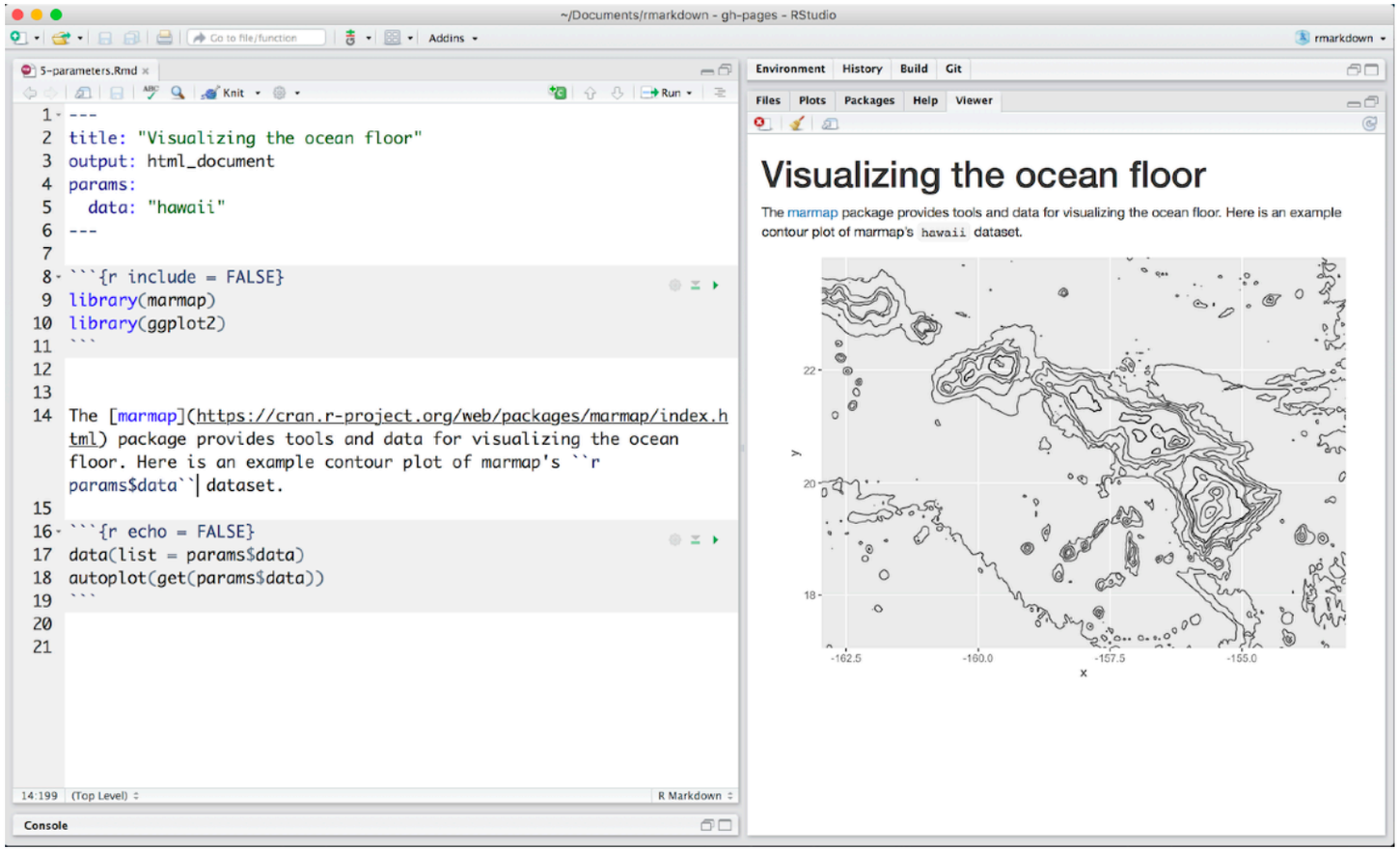
- Visualisation platform

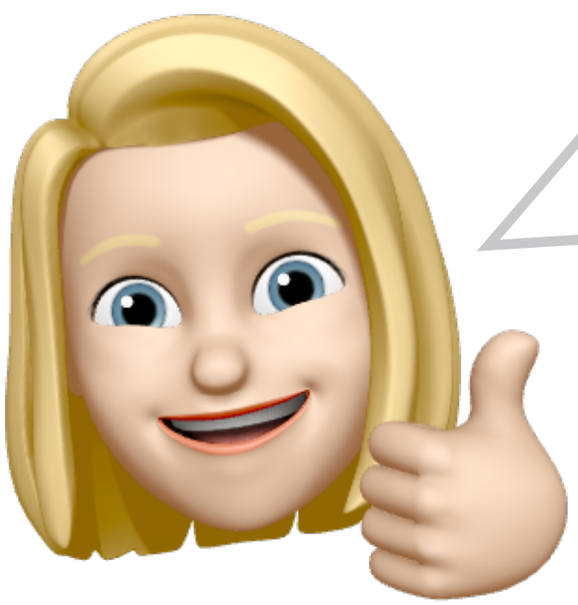




To me R is a:

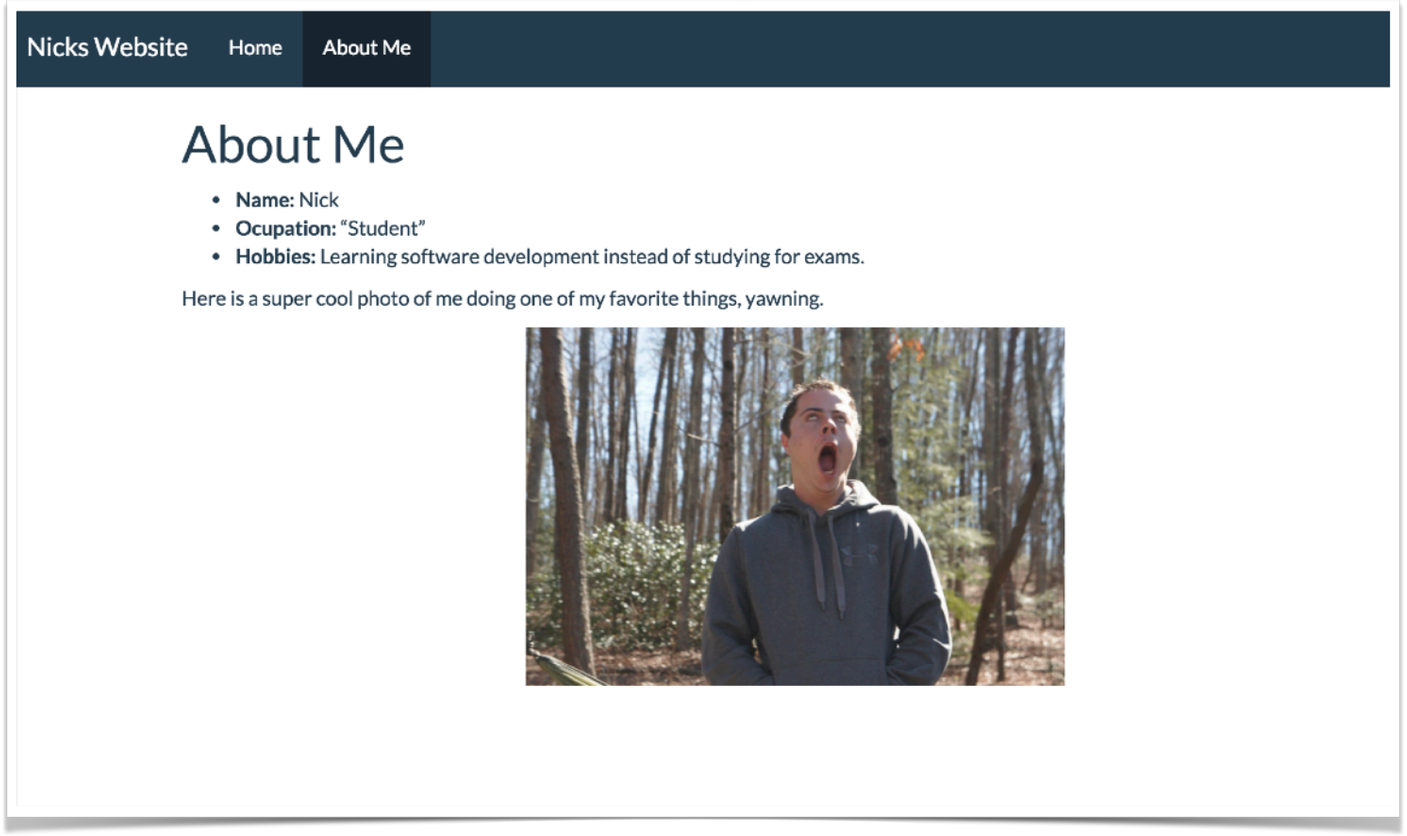
- Document editor

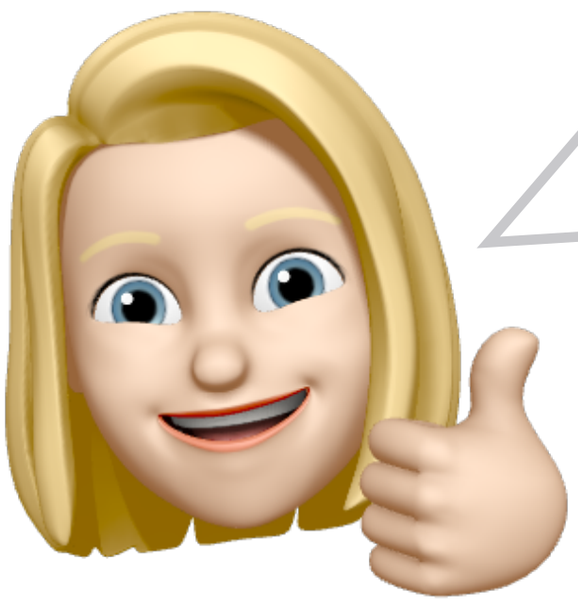




To me R is a:

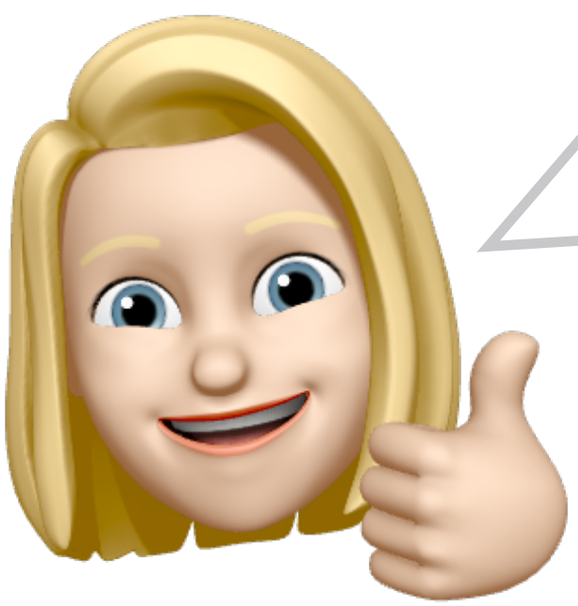
- Website editor





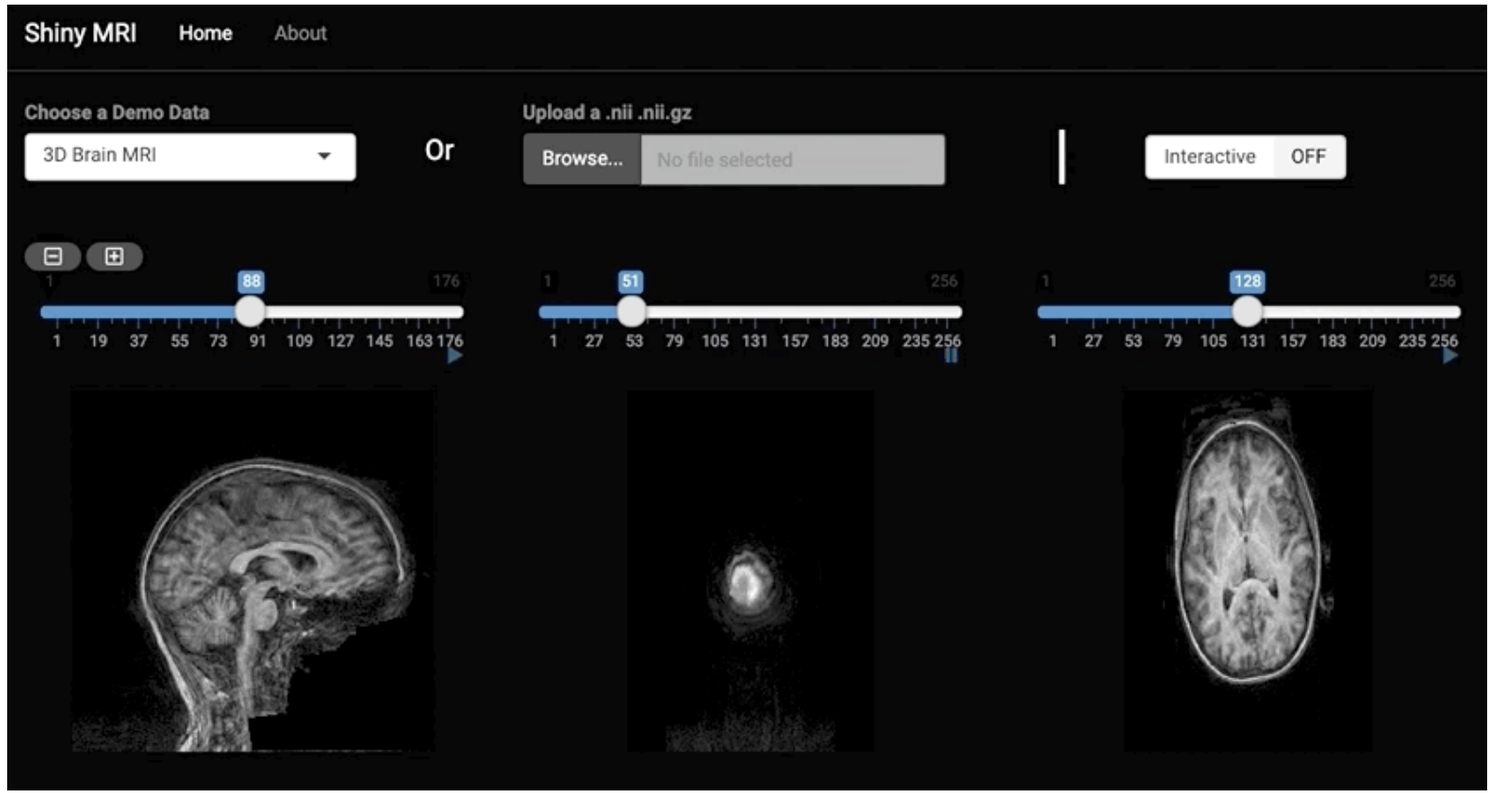
To me R is a:

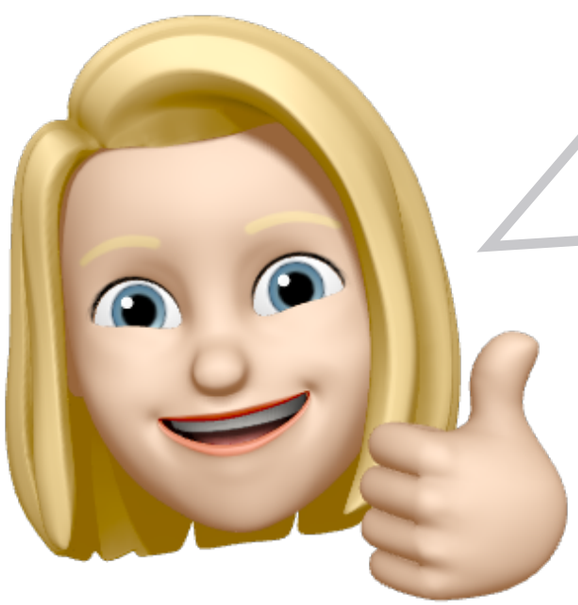
- Presentation editor



To me R is a:

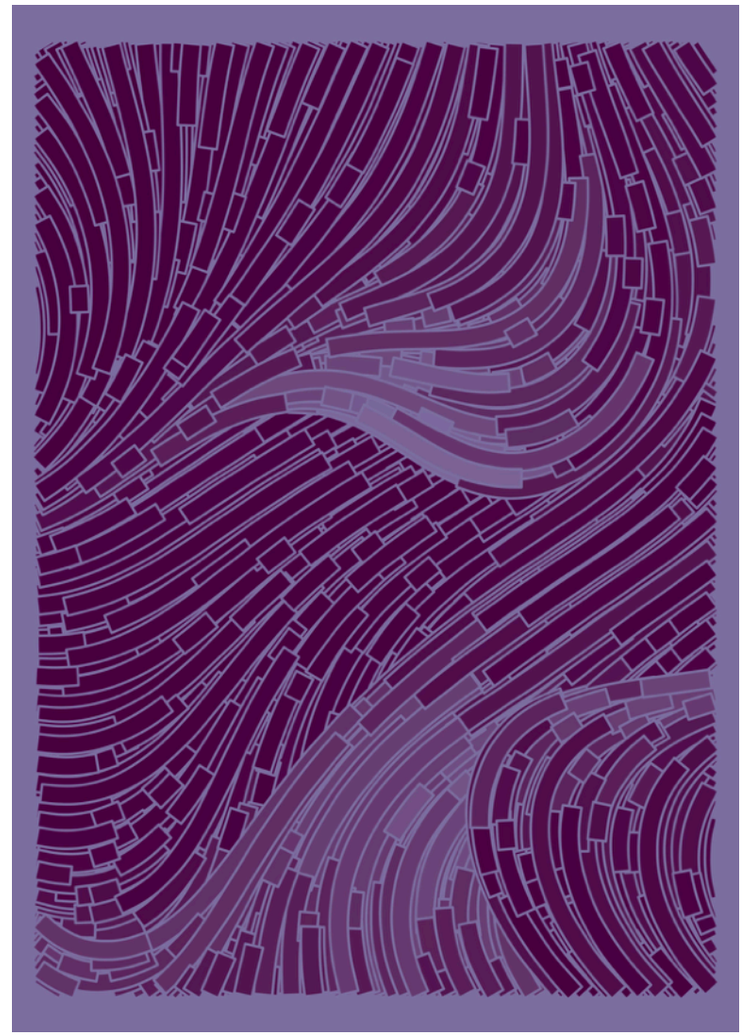
- Application maker

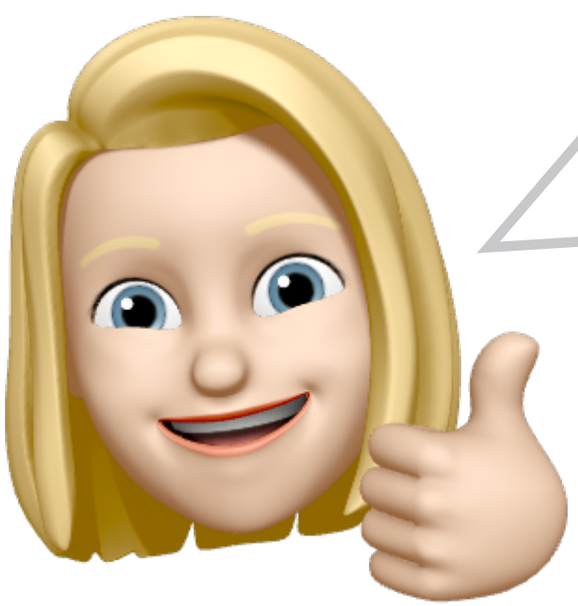




To me R is a:

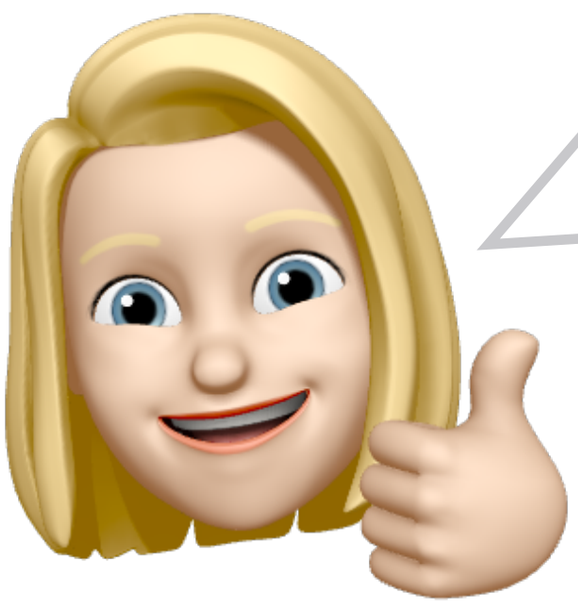
- Art generator





To me R is a:

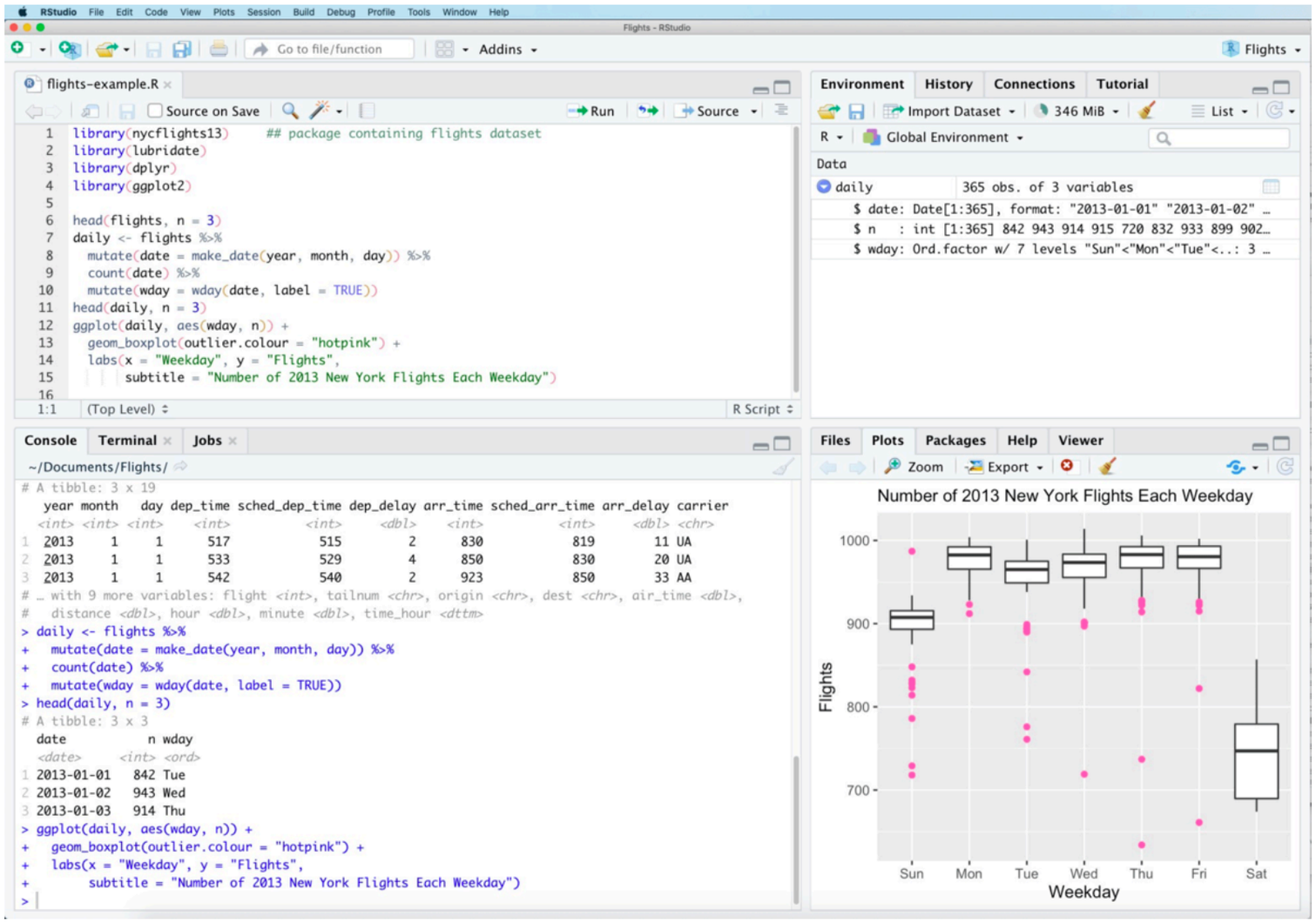
- Community



RStudio - a natural home for R and more

Source:
Recipes

Environment/etc.:
Ingredients



Console/etc.:
Cooking stove

Plotting pane/etc.:
Platting

Cool extra features

and so many extra helpful features, such as tab complete, search, code snippets, …

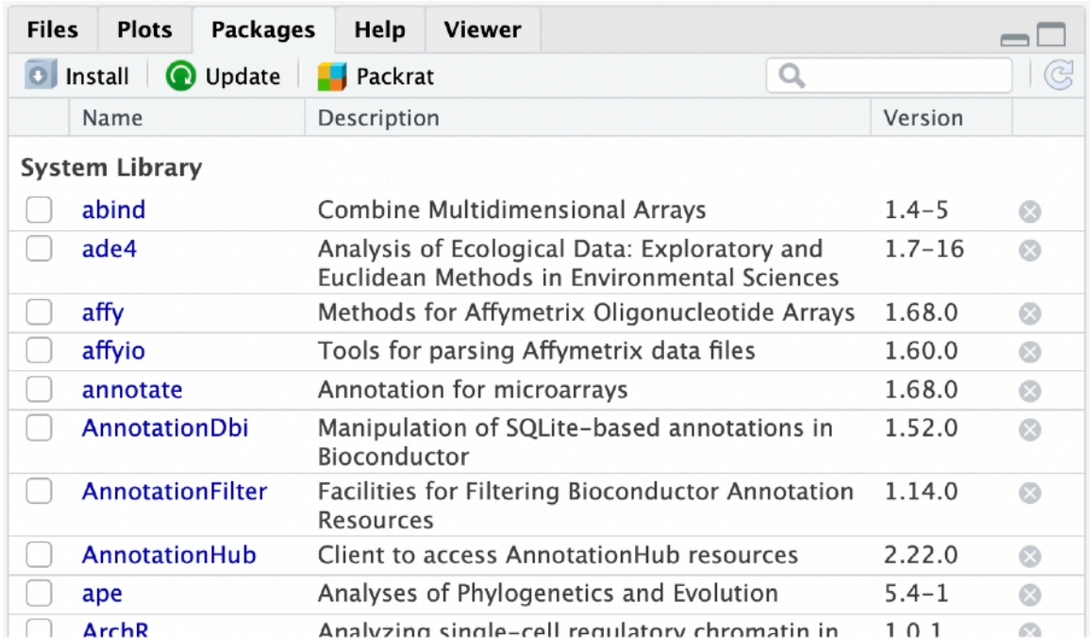
Extending the R universe with packages

Repositories such as CRAN and Bioconductor allow you to install packages that add further functionality

```
> install.packages("ggplot2")
trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.0/ggplot2_3.3.
5.tgz'
Content type 'application/x-gzip' length 4125428 bytes (3.9 MB)
==================================================
downloaded 3.9 MB


The downloaded binary packages are in
        /var/folders/h9/0dch4nrd7w50dkjtx5w2jfwh0000gn/T//RtmpzBNYsJ/dow
nloaded_packages
> library(ggplot2)
> |
```

For example the reticulate package allows you to interface with python



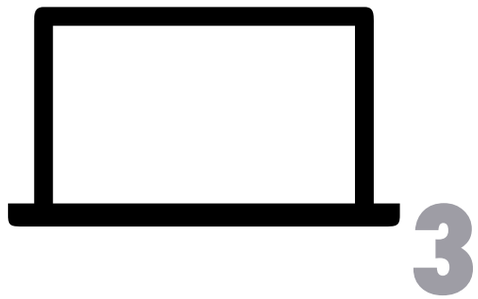
For Bioconductor use BiocManager::install

Tackling your project with R

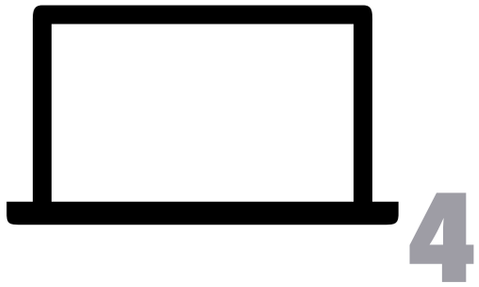
Common steps in your R data analysis project:

Organise project

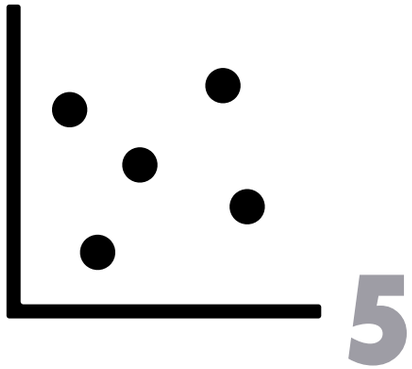
Read in data



Data wrangling



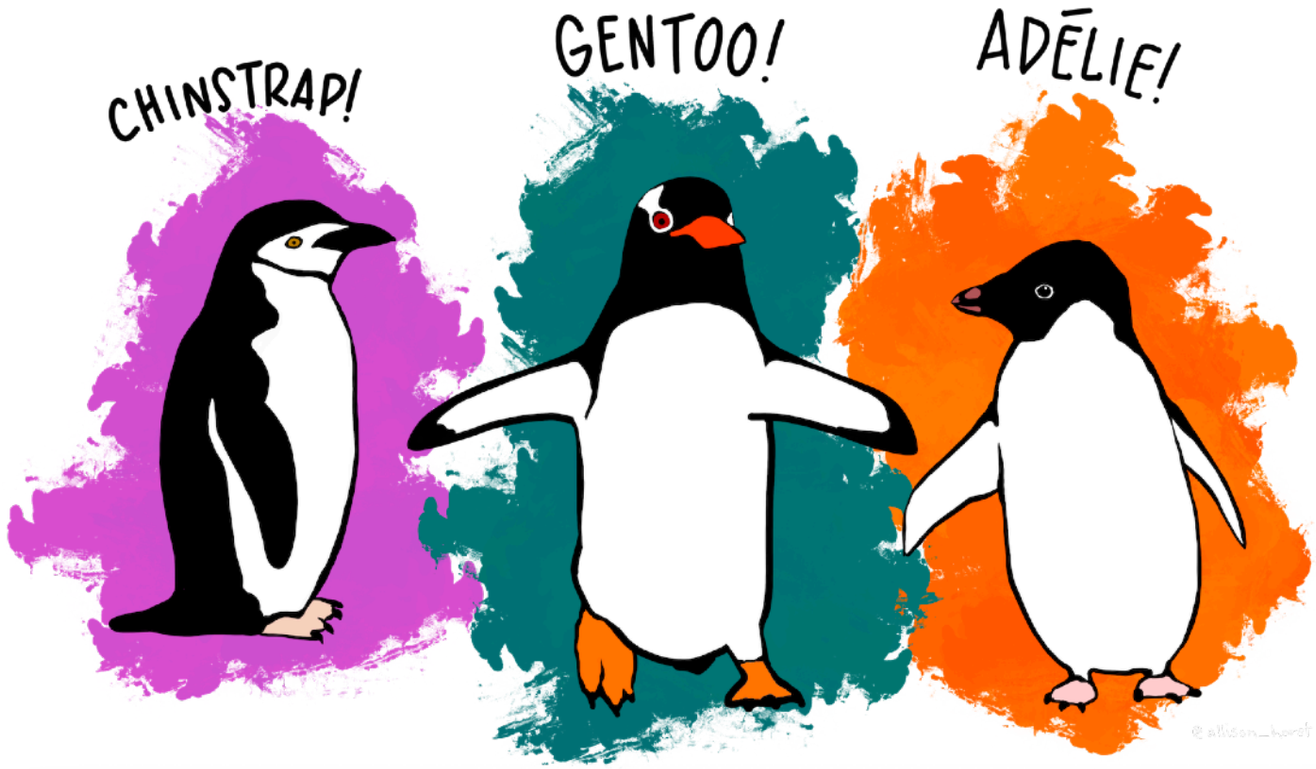
Analysis

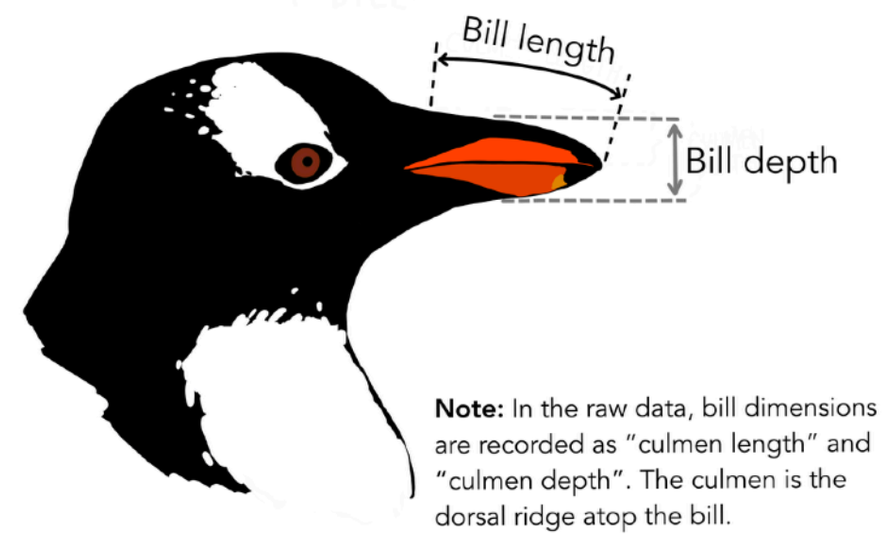


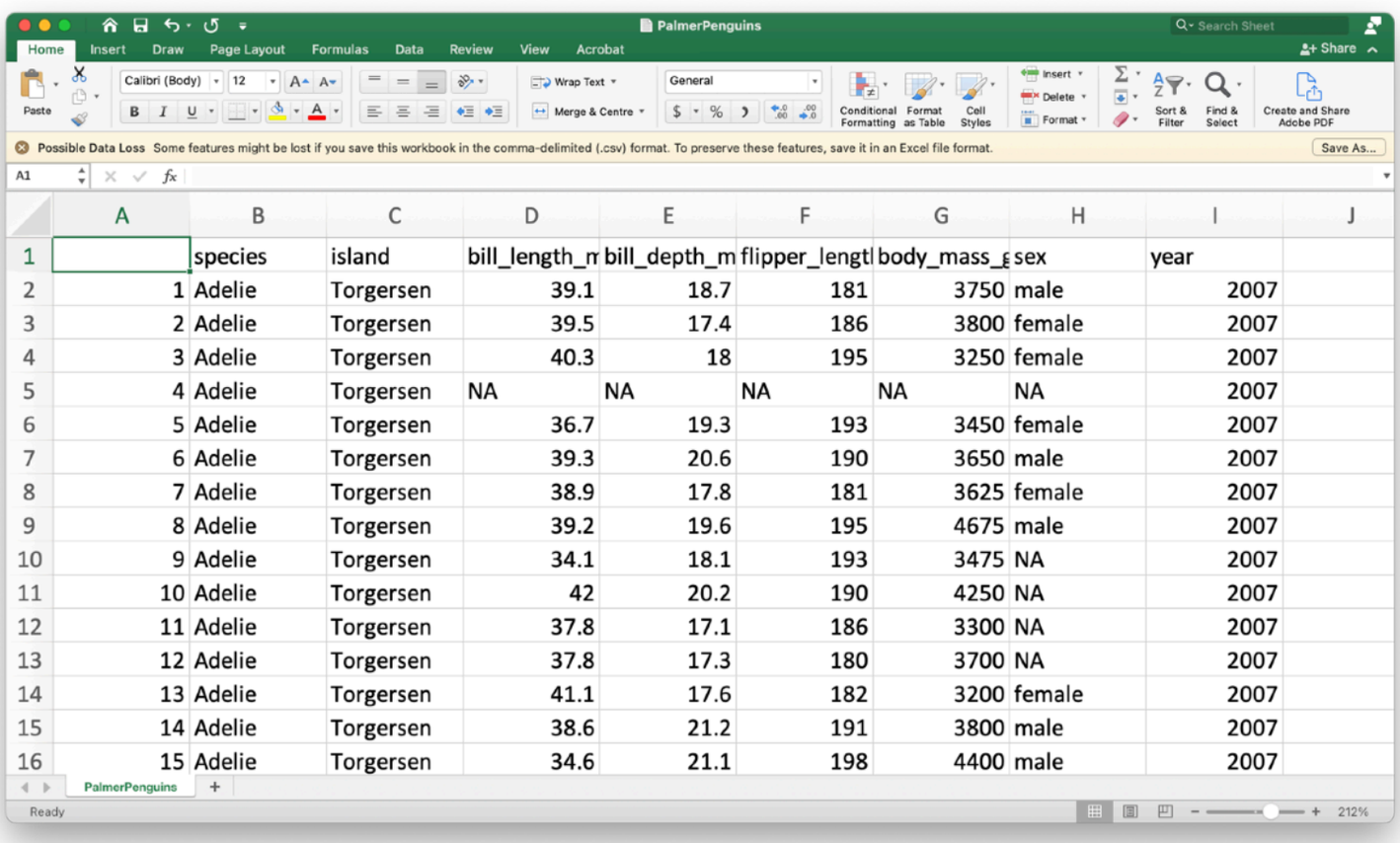
Visualisation

Report

Taking you through a project example

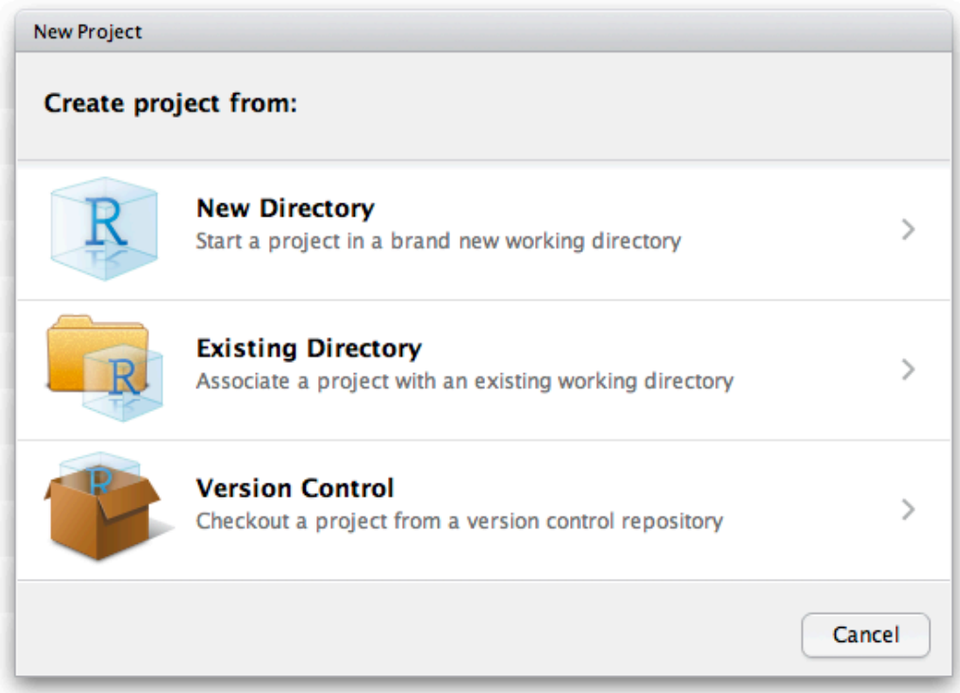


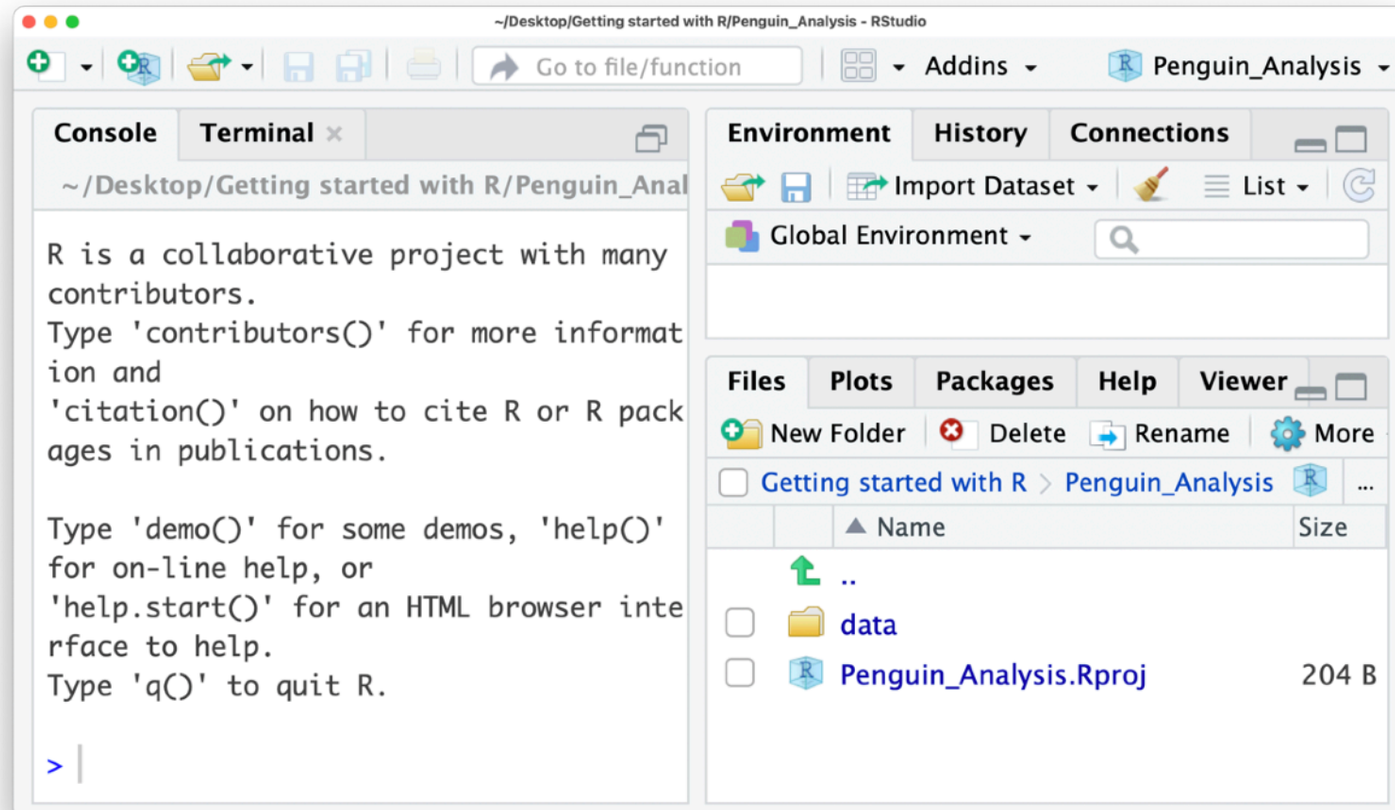


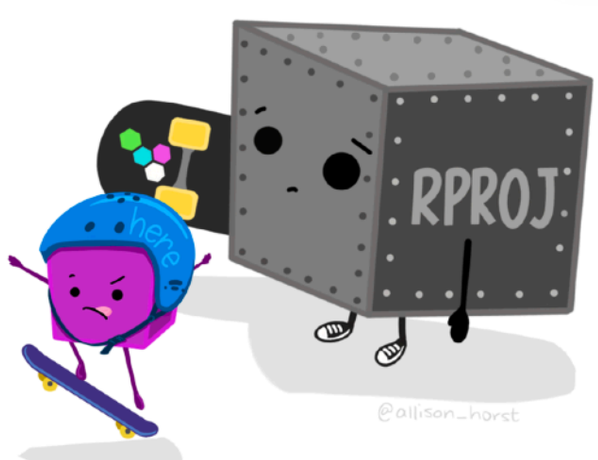


	A	B	C	D	E	F	G	H	I
1		species	island	bill_length_m	bill_depth_m	flipper_lengt	body_mass_g	sex	year
2	1	Adelie	Torgersen	39.1	18.7	181	3750	male	2007
3	2	Adelie	Torgersen	39.5	17.4	186	3800	female	2007
4	3	Adelie	Torgersen	40.3	18	195	3250	female	2007
5	4	Adelie	Torgersen	NA	NA	NA	NA	NA	2007
6	5	Adelie	Torgersen	36.7	19.3	193	3450	female	2007
7	6	Adelie	Torgersen	39.3	20.6	190	3650	male	2007
8	7	Adelie	Torgersen	38.9	17.8	181	3625	female	2007
9	8	Adelie	Torgersen	39.2	19.6	195	4675	male	2007
10	9	Adelie	Torgersen	34.1	18.1	193	3475	NA	2007
11	10	Adelie	Torgersen	42	20.2	190	4250	NA	2007
12	11	Adelie	Torgersen	37.8	17.1	186	3300	NA	2007
13	12	Adelie	Torgersen	37.8	17.3	180	3700	NA	2007
14	13	Adelie	Torgersen	41.1	17.6	182	3200	female	2007
15	14	Adelie	Torgersen	38.6	21.2	191	3800	male	2007
16	15	Adelie	Torgersen	34.6	21.1	198	4400	male	2007

Organise your project





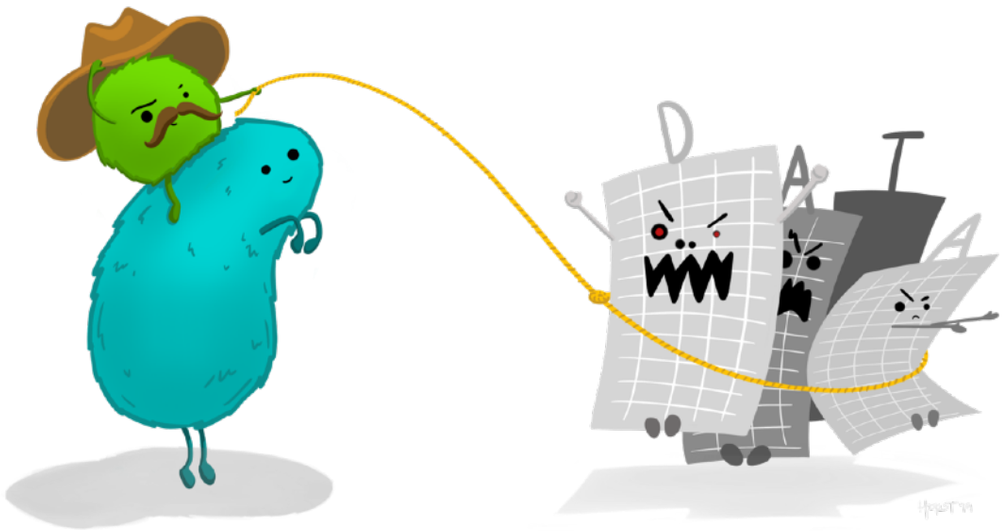


Read in your data

```
> data <- read.csv("data/PalmerPenguins.csv")
> head(data)
  X species    island bill_length_mm bill_depth_mm
1 1  Adelie Torgersen           39.1          18.7
2 2  Adelie Torgersen           39.5          17.4
3 3  Adelie Torgersen           40.3          18.0
4 4  Adelie Torgersen             NA            NA
5 5  Adelie Torgersen           36.7          19.3
6 6  Adelie Torgersen           39.3          20.6
  flipper_length_mm body_mass_g    sex year
1               181        3750   male 2007
2               186        3800 female 2007
3               195        3250 female 2007
4                NA          NA   <NA> 2007
5               193        3450 female 2007
6               190        3650   male 2007
```

`NA` - not available, i.e. missing data

... and many more specialised packages



Wrangle your data into shape

```
> data <- data %>% filter(!is.na(bill_length_mm))
> head(data)
  X species    island bill_length_mm bill_depth_mm flipper_length_mm
1 1  Adelie Torgersen           39.1          18.7               181
2 2  Adelie Torgersen           39.5          17.4               186
3 3  Adelie Torgersen           40.3          18.0               195
4 5  Adelie Torgersen           36.7          19.3               193
5 6  Adelie Torgersen           39.3          20.6               190
6 7  Adelie Torgersen           38.9          17.8               181
  body_mass_g    sex year
1        3750   male 2007
2        3800 female 2007
3        3250 female 2007
4        3450 female 2007
5        3650   male 2007
6        3625 female 2007
```

... and many more specialised packages

Analysis time

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data.

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

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Home » BiocViews

All Packages

Bioconductor version 3.13 (Release)

Autocomplete biocViews search:

- Software (2041)
  - AssayDomain (819)
  - BiologicalQuestion (866)
  - Infrastructure (480)
  - ResearchField (953)
  - StatisticalMethod (762)
  - Technology (1301)
  - WorkflowStep (1121)
- AnnotationData (976)
- ExperimentData (406)
- Workflow (29)

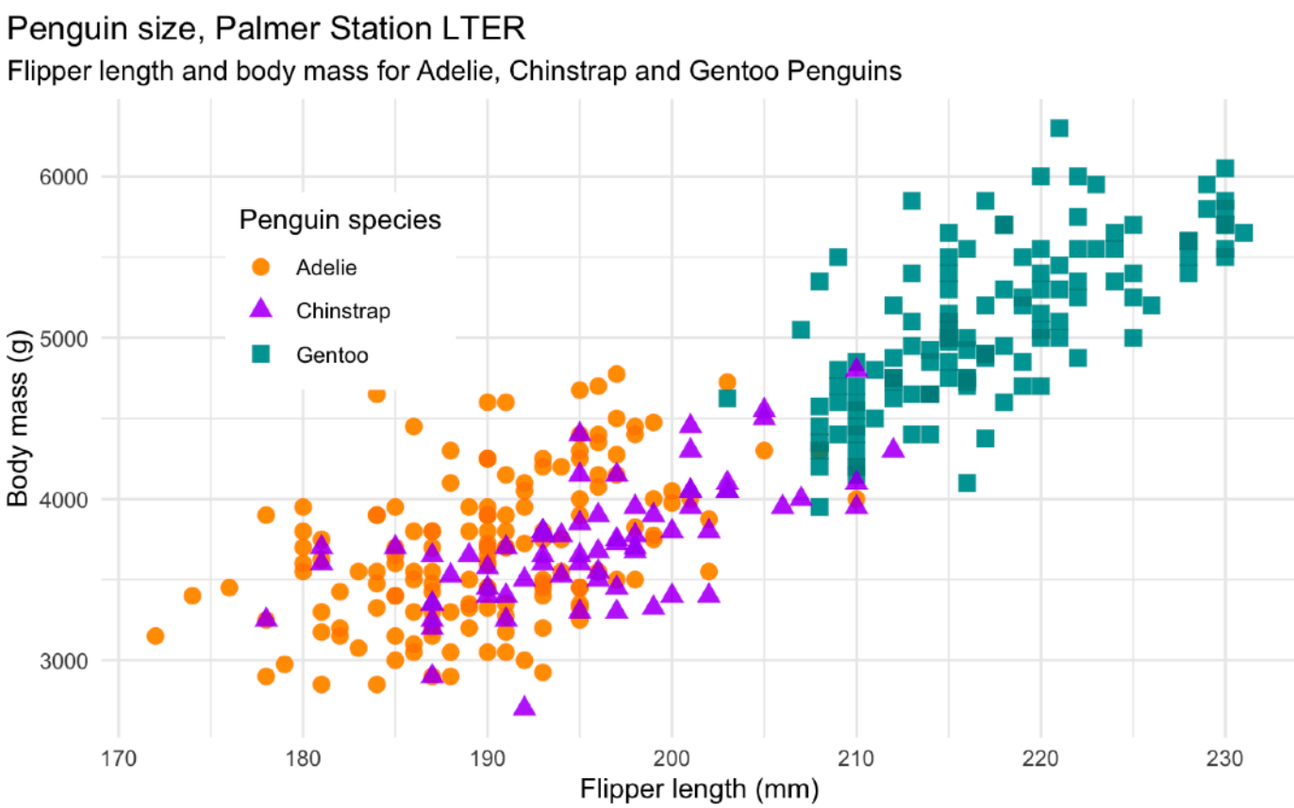
Packages found under Software:

Rank based on number of downloads: lower numbers are more frequently downloaded.

Show All entries Search table:

Package	Maintainer	Title	Rank
BiocGenerics	Bioconductor Package Maintainer	S4 generic functions used in Bioconductor	1
BiocVersion	Bioconductor Package Maintainer	Set the appropriate version of Bioconductor packages	2
S4Vectors	Bioconductor Package Maintainer	Foundation of vector-like and list-like containers in Bioconductor	3
IRanges	Bioconductor Package Maintainer	Foundation of integer range manipulation in Bioconductor	4
Biobase	Bioconductor Package Maintainer	Biobase: Base functions for Bioconductor	5
zlibbioc	Bioconductor Package Maintainer	An R packaged zlib-1.2.5	6
GenomeInfoDb	Bioconductor Package Maintainer	Utilities for manipulating chromosome names, including modifying them to follow a particular naming style	7

Visualise your results




```
ggplot(data, aes(x, y, color)) +
geom_something() + theme()
```

Summarise it in a report

Penguins

Saskia Freytag
01/08/2021

Read in data

```
data <-  read.csv("data/PalmerPenguins.csv")
```

Exploring factors

The penguins data has three factor variables:

```
data %>%
  dplyr::select(where(is.factor)) %>%
  glimpse()
```

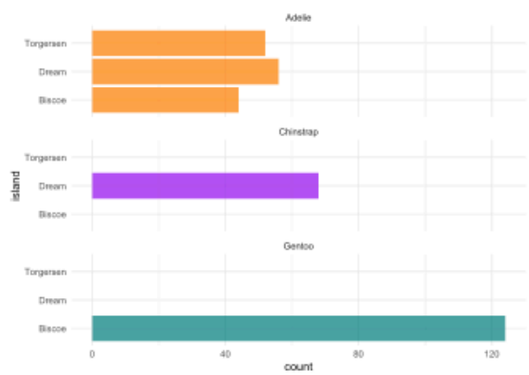
```
## Rows: 344
## Columns: 0
```

```
# Count penguins for each species / island
data %>%
  count(species, island, .drop = FALSE)
```

```
##     species    island   n
## 1    Adelie    Biscoe  44
## 2    Adelie     Dream  56
## 3    Adelie Torgersen  52
## 4 Chinstrap     Dream  68
## 5    Gentoo    Biscoe 124
```

```
ggplot(data, aes(x = island, fill = species)) +
  geom_bar(alpha = 0.8) +
  scale_fill_manual(values = c("darkorange","purple","cyan4"),
                    guide = FALSE) +
  theme_minimal() +
  facet_wrap(~species, ncol = 1) +
  coord_flip()
```

```
## Warning: It is deprecated to specify `guide = FALSE` to remove a guide. Please
## use `guide = "none"` instead.
```

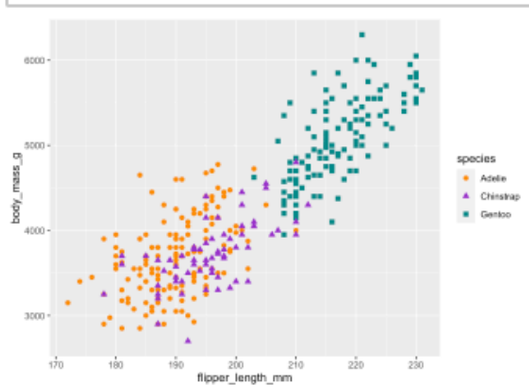


Exploring scatterplots

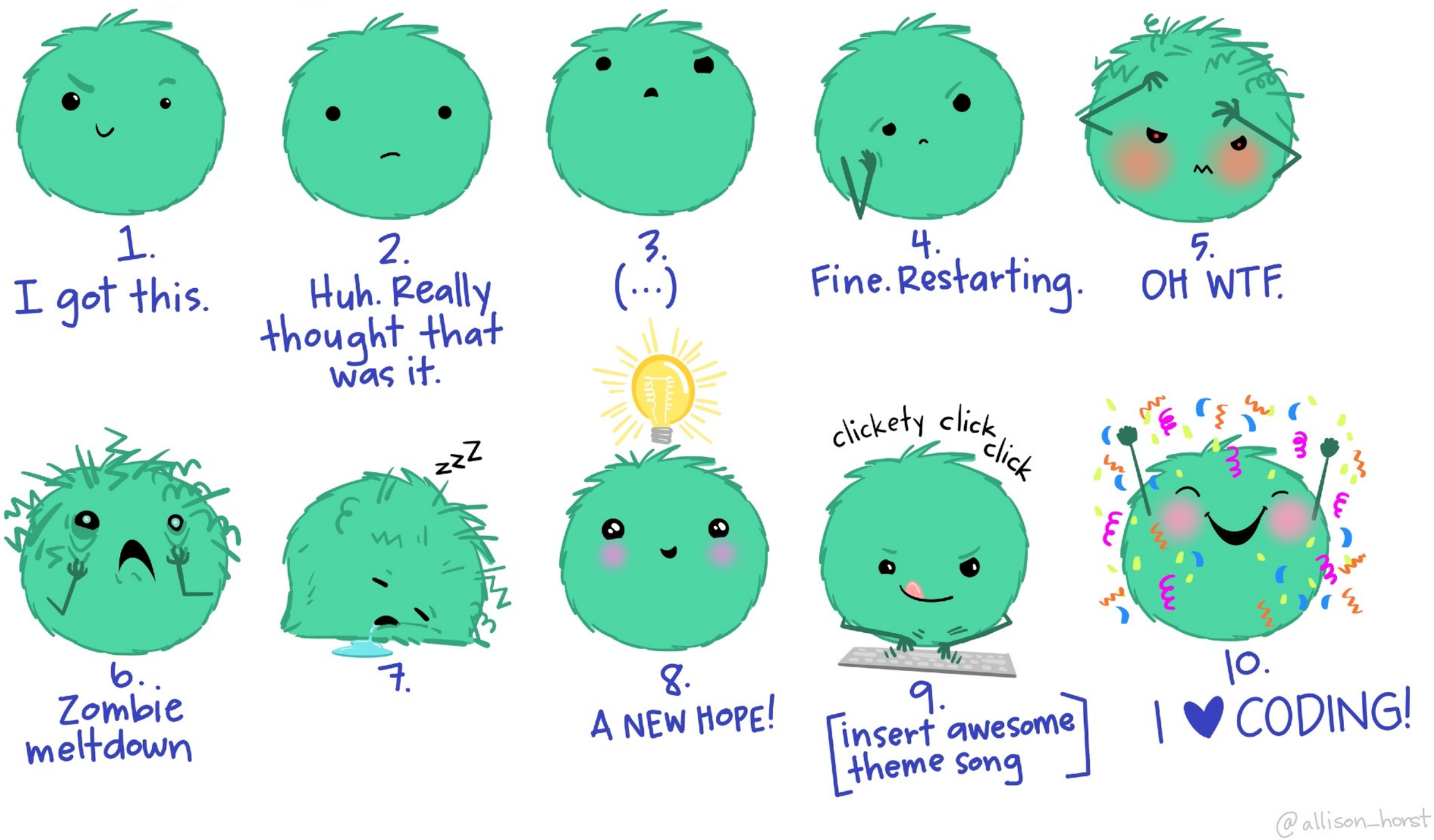
The penguins data also has four continuous variables, making six unique scatterplots possible!

```
ggplot(data = data, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species,
                 shape = species),
             size = 2) +
  scale_color_manual(values = c("darkorange","darkorchid","cyan4"))
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```



Debugging in R



Debugging in R

Error messages can be helpful, google them.

Use R 's interactive capabilities to your advantage.

Make it repeatable.

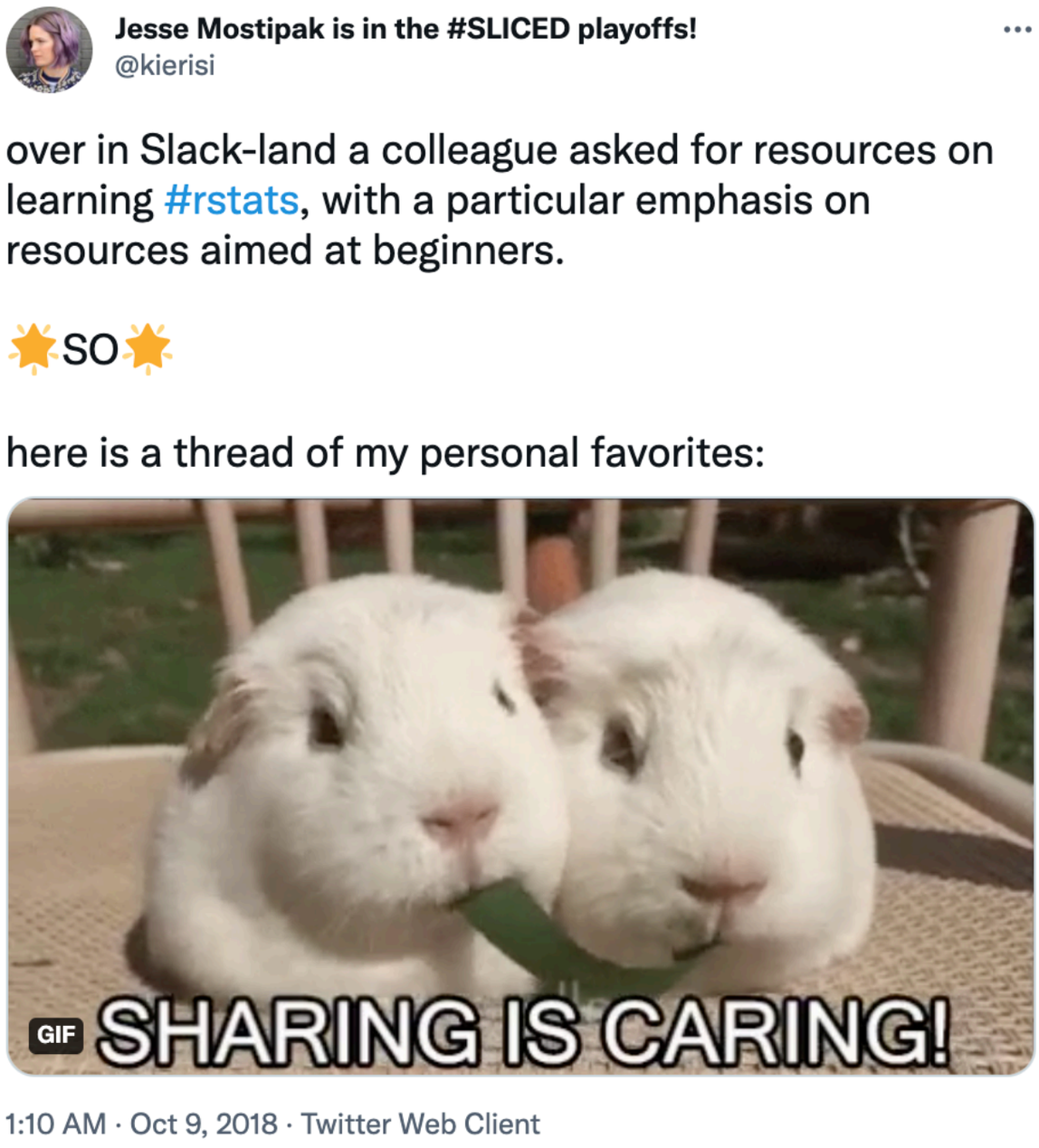
Remember R really, really wants to complete any call.

```
> 1+c(1,3,4)
[1] 2 4 5
```

Finding help for R

- stackoverflow
- #rstats twitter
- rOpenScience forum
- RStudio community
- Bioconductor support forum
- RLadies slack

Best R resources for beginners



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- R for Data Science
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- swirl

Question and Answer Time