

Do you have a github account?  
Give us a star! :)

# Welcome!

Please download all of the course material:

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[tinyurl.com/introRData](https://tinyurl.com/introRData) > [Clone or download ▾](#) > [Download ZIP](#)

and store it in a single, accessible folder on your computer. **Don't forget to unzip!**

# Introduction to R & data

---

- Part I: Basics of R
- Lunch (~12:15)
- Part II: Modern R with tidyverse
- Final remarks (~17:00)

move the samples from the data  
{r}  
select the samples to keep  
keepsamples <- row.names(pheno[  
apply sample selection to  
counts.sub <- counts.sub[,keepsamples]  
pheno.sub <- pheno[keepsamples]  
mt.assay <- mt.assay[,keepsamples]  
rld.sub <- rld[,keepsamples]

# Quick intro: this is us! And who are you?

---

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# What's with those sticky notes?

---

I need some assistance, please!

I have finished the exercise and am ready to move on!

No sticky note?



# Introduction to R & data

---

## Part 1: Basics of R



# What is R?

---

- Widely used programming language for data analysis
- Based on statistical programming language **S** (1976)
- Developed by **Ross Ihaka & Robert Gentleman** (1995)
- Very active community, with many (often subject-specific) packages



# We will work in RStudio

---

- Integrated Development Environment for R
- Founded by JJ Allaire, available since 2010
- Bloody useful! Let's take a look: please open RStudio!

# The Rstudio interface



The image shows the RStudio interface with four main panels:

- script**: The top-left panel displays an R script named "programming\_exercise.R". The code reads an "iris" database, removes the "Species" column, creates a new data frame with a single column of measurements, and calculates the average size for each measurement. The text "script" is overlaid on this panel.
- environment**: The top-right panel shows the Global Environment tab with the message "Environment is empty". The text "environment" is overlaid on this panel.
- console**: The bottom-left panel shows the R console output. It includes the R version information, a copyright notice, a warranty statement, natural language support information, and details about the R project. The text "console" is overlaid on this panel.
- files**: The bottom-right panel shows tabs for Files, Plots, Packages, Help, and Viewer. The Packages tab is selected. The text "files plots packages help" is overlaid on this panel.

# The Rstudio interface

A screenshot of the RStudio interface. The top navigation bar includes tabs for 'Console', 'Terminal', 'File', 'Edit', 'Tools', 'Help', and 'Addins'. A 'Project: (None)' indicator is on the right. The main area is divided into four panes:

- Console** (red background): Displays the standard R startup message and license information.
- Environment** (blue background): Shows the 'Global Environment' tab with the message 'Environment is empty'.
- Plots** (purple background): Shows the 'Files' tab with icons for file operations like 'New', 'Open', 'Save', 'Zoom', 'Export', and 'Viewer'.
- Packages** (pink background): Shows the 'Plots' tab with icons for file operations like 'New', 'Open', 'Save', 'Zoom', 'Export', and 'Viewer'.

Large white text overlays are placed over the bottom-right panes:

- 'environment' over the Environment pane
- 'history' over the Environment pane
- 'files' over the Packages pane
- 'plots' over the Packages pane
- 'packages' over the Plots pane
- 'help' over the Plots pane

# Have you downloaded the course material?

---

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# R syntax & the console

---

- Data types in R
- Combining data
- First functions

move the samples from the data  
\* {r}  
select the samples to keep  
keepsamples <- row.names(pheno[  
apply sample selection to  
counts.sub <- counts.sub[,ke  
pheno.sub <- pheno[keepsampl  
nt.assay <- nt.assay[,keeps  
eld.sub <- rld[,keepsample]

# A quick note on notes

---

- The console is for execution, not for storage
- Everything we do is on the slides!
- BUT: you can store, if you want, by copy-pasting to a text document
- Do you want to write notes in between?

```
# write your notes in the console like this  
# using a #hash sign.  
# pressing enter will do nothing.  
# go ahead and try!
```

# Variable assignment

---

>

# Variable assignment

---

```
> x <- 6
```

# Variable assignment

```
> x <- 6
```

```
> x <- "hi!"
```

```
> 6 -> x
```

```
> x = 6
```

```
> 6 = x
```

```
Error in 6 = x : invalid (do_set) left-hand side to assignment
```

# Base R Cheat Sheet

## Variable Assignment

```
> a <- 'apple'  
> a  
[1] 'apple'
```

# Maths Functions

---

```
> x * 3
```

```
[1] 18
```

```
> y <- x + 2
```

```
> log2(y)
```

```
[1] 3
```

## Maths Functions

`log(x)`

Natural log.

`sum(x)`

Sum.

`exp(x)`

Exponential.

`mean(x)`

Mean.

`max(x)`

Largest element.

`median(x)`

Median.

`min(x)`

Smallest element.

`quantile(x)`

Percentage quantiles.

`round(x, n)`

Round to n decimal places.

`rank(x)`

Rank of elements.

`signif(x, n)`

Round to n significant figures.

`var(x)`

The variance.

`cor(x, y)`

Correlation.

`sd(x)`

The standard deviation.

# Exercise

---

1. Make the following calculation in R:

$$\frac{(1 + 5) \times (7 - 2)}{9}$$

2. Assign the result of the calculation to a variable.
3. Bonus: Round off the result to 1 decimal. *Tip: Use the **Maths Functions** section of your cheat sheet!*

# Exercise

---

1. Make the following calculation in R:

$$\frac{(1 + 5) \times (7 - 2)}{9}$$

```
> ((1+5)*(7-2))/9
```

2. Assign the result of the calculation to a variable.

```
> MyCalc <- ((1+5)*(7-2))/9
```

3. Bonus: Round off the result to 1 decimal. *Tip: Use the Maths Functions section of your cheat sheet!*

```
> round(MyCalc, 1)
```

# Another data type: logical

---

T	TRUE
F	FALSE

```
> T  
[1] TRUE
```

```
> 1==1  
[1] TRUE
```

```
> 2!=4  
[1] TRUE
```

== is equal to  
!= is not  
>= larger than or equal to  
< smaller than

# Combining data: creating vectors

---

```
> c(1,2,3)                                a numeric vector  
[1] 1 2 3 ←
```

```
> c("a","b","c")                            a character vector  
[1] "a" "b" "c" ←
```

```
> c(T,TRUE,F)                             a logical vector  
[1] TRUE TRUE FALSE ←
```

# Vector functions

---

```
> p <- 1:5  
> p  
[1] 1 2 3 4 5  
> mean(p)  
[1] 3  
> p * 2  
[1] 2 4 6 8 10  
> q <- 5:1  
> p * q  
[1] 5 8 9 8 5
```

p * 2		
p	2	
1	2	2
2	2	4
3	2	6
4	2	8
5	2	10

p * q		
p	q	
1	5	5
2	4	8
3	3	9
4	2	8
5	1	5

```
> table(p*q)  
5 8 9  
2 2 1
```

# Exercise

---

1. Make the following vector using `seq()`:

```
[1] 8 10 12 14
```

2. Make another vector using `rep()`:

```
[1] 7 7 7 7
```

3. Combine all three functions `c()`, `rep()`, and `seq()` to generate this vector:

```
> MyVec <- ...
```

```
> MyVec
```

```
[1] 12 12 12 4 5 6
```

4. Bonus: can you sort the values in the last vector from low to high?

# Exercise

---

1. Make the following vector using `seq()`:

```
> seq(8,14, by=2)
[1] 8 10 12 14
```

2. Make another vector using `rep()`:

```
> rep(7,4)
[1] 7 7 7 7
```

3. Combine all three functions `c()`, `rep()`, and `seq()` to generate this vector:

```
> MyVec <- c(rep(12,3), seq(4,6))
> MyVec
[1] 12 12 12 4 5 6
```

4. Bonus: can you sort the values in the last vector from low to high?

```
> sort(MyVec)
```

# Vectors and factors

---

```
> chars <- c("a", "b", "a", "c")
```

```
> chars
```

```
[1] "a" "b" "a" "c"
```

```
> F_chars <- as.factor(chars)
```

```
> F_chars
```

```
[1] a b a c
```

```
Levels: a b c
```

```
> as.character(F_chars)
```

```
[1] "a" "b" "a" "c"
```

# Vectors and factors

---

```
> nums <- 10:13  
> nums  
[1] 10 11 12 13  
  
> F_nums <- as.factor(nums)  
> F_nums  
[1] 10 11 12 13  
Levels: 10 11 12 13  
  
> as.numeric(F_nums)  
[1] 1 2 3 4
```

**A factor is defined by its levels.**  
Turning a factor into numeric specifies the order of the levels, but loses their content.

# Exercise

---

1. Generate a vector that contains numeric, logical, and character elements.

```
> vt <- ...
```

2. Turn it into a factor.

```
> ft <- ...
```

3. See what happens to the content when you convert this factor into numeric, logical, and character vectors.

*(Hint: check the cheat sheet element ‘Types’ for the functions.)*

# Exercise

---

1. Generate a vector that contains numeric, logical, and character elements.

```
> vt <- c(T,T,2,4,"apple","orange")
```

2. Turn it into a factor.

```
> ft <- as.factor(vt)
```

3. See what happens to the content when you convert this factor into numeric, logical, and character vectors.

(*Hint: check the cheat sheet element ‘Types’ for the functions.*)

```
> as.numeric(ft)
```

```
[1] 5 5 1 2 3 4
```

```
> as.logical(ft)
```

```
[1] TRUE TRUE NA NA NA NA
```

```
> as.character(ft)
```

```
[1] "TRUE"    "TRUE"    "2"      "4"      "apple"   "orange"
```

# But what if there *is no data*? Introducing: NA

```
> ft <- c(T,T,2,4,"apple","orange")  
> ft <- as.logical(ft)  
> ft  
[1] TRUE TRUE     NA     NA     NA     NA  
> factor(ft)  
[1] TRUE TRUE <NA> <NA> <NA> <NA>  
Levels: TRUE
```

NA = Not Available

Name	Age	Pet
Ann	33	Cat
Bob	25	<b>None</b>
Chloe	21	Iguana
Dan	45	<b>NA</b>

In other words:

We **know** that Bob has **no pets**.

We **do not know** if Dan has pets.

## Exercise: predict the answer

---

```
> NA == NA
```

Predict the results. Does the (real) answer make sense to you?

## Exercise: predict the answer

---

```
> NA == NA
```

```
[1] NA
```

Predict the results. Does the (real) answer make sense to you?

```
> is.na(NA)
```

```
[1] TRUE
```

# NA != NULL

---

**NA** Information is **Not Available**

**NULL** Information **does not exist**

**“None” or 0** Data entry specifying **content of 0**

## Exercise: predict the answer

---

```
> is.na(NA)
```

```
[1] TRUE
```

```
> is.null(NULL)
```

```
[1] TRUE
```

Predict the results. Does the (real) answer make sense to you?

```
> is.null(NA)
```

```
> is.na(NULL)
```

## Exercise: predict the answer

---

```
> is.na(NA)
```

```
[1] TRUE
```

```
> is.null(NULL)
```

```
[1] TRUE
```

Predict the results. Does the (real) answer make sense to you?

```
> is.null(NA)
```

```
[1] FALSE
```

```
> is.na(NULL)
```

## Exercise: predict the answer

---

```
> is.na(NA)
```

```
[1] TRUE
```

```
> is.null(NULL)
```

```
[1] TRUE
```

Predict the results. Does the (real) answer make sense to you?

```
> is.null(NA)
```

```
[1] FALSE
```

```
> is.na(NULL)
```

```
[1] logical(0)
```

# Vectors, lists, and data frames

---

```
> v1 <- 4:6  
> v2 <- rep(3,3)
```

```
> c(v1,v2)  
[1] 4 5 6 3 3 3
```

```
> list(v1,v2)  
[[1]]  
[1] 4 5 6
```

```
[[2]]  
[1] 3 3 3
```

```
> data.frame(v1,v2)  
   v1 v2  
1   4  3  
2   5  3  
3   6  3
```

	how many dimensions?	function
vector	1	c()
list	any number	list()
data frame	2	data.frame()

# Let's breathe and recap!

---

What data types have you encountered so far?

`logical`

`numeric`

`character`

How can data be absent?

`NA` (not available)

`NULL` (non-existent)

And what data collections have you encountered?

`vector` (one dimension)

`factor` (one dimension, level-based)

`data frame` (two dimensions)

`list` (++ dimensions)

# Functions

---

What functions have you encountered so far?

```
> c()  
> rep()  
> as.logical()  
> data.frame()  
> is.na()  
> table()  
...
```

And do you still know what they mean? And how to use them? **No?**

```
> ?table()  
> help.search("standard deviation")
```

(or use the Help window to the right of your console)

# Help!

table {base}  function & package names

R Documentation

## Cross Tabulation and Table Creation

### Description

table uses the cross-classifying factors to build a contingency table of the counts at each combination of factor levels.

### Usage

table(...,  how would you use the function?  
exclude = if (useNA == "no") c(NA, NaN),  
useNA = c("no", "ifany", "always"),  
dnn = list.names(...), deparse.level = 1)

wait what? These are extra arguments. If you see argument = "default" then the setting is already specified, so you won't have to.

as.table(x, ...)  functions so related they share a help page  
is.table(x)

```
## S3 method for class 'table'  
as.data.frame(x, row.names = NULL, ...)
```

# Help? Scroll down!

---

## Examples

```
require(stats) # for rpois and xtabs
## Simple frequency distribution
table(rpois(100, 5))
## Check the design:
with(warpbreaks, table(wool, tension))
table(state.division, state.region)

# simple two-way contingency table
with(airquality, table(cut(Temp, quantile(Temp))), Month))

a <- letters[1:3]
table(a, sample(a))                      # dnn is c("a", "")
table(a, sample(a), deparse.level = 0) # dnn is c("", "")
table(a, sample(a), deparse.level = 2) # dnn is c("a", "sample(a)")

## xtabs() <-> as.data.frame.table() :
UCBAdmissions ## already a contingency table
DF <- as.data.frame(UCBAdmissions)
class(tab <- xtabs(Freq ~ ., DF)) # xtabs & table
## tab *is* "the same" as the original table:
all(tab == UCBAdmissions)
```

# Take a break!

---



# Selecting vector elements by position

```
> m <- 8:4  
> m  
[1] 8 7 6 5 4
```

```
> m[2]  
[1] 7
```

```
> m[1:3]  
[1] 8 7 6
```

Selecting Vector Elements	
By Position	
<b>x[4]</b>	The fourth element.
<b>x[-4]</b>	All but the fourth.
<b>x[2:4]</b>	Elements two to four.
<b>x[-(2:4)]</b>	All elements except two to four.
<b>x[c(1, 5)]</b>	Elements one and five.

# Selecting vector elements by value

```
> m <- 8:4  
[1] 8 7 6 5 4  
  
> m[m>5]  
[1] 8 7 6  
  
> m>5  
[1] TRUE TRUE TRUE FALSE FALSE  
  
> m[m %in% c(6,8,11)]  
[1] 8 6  
  
> m[NA]  
[1] NA NA NA NA NA
```

m	m>5	result
8	TRUE	8
7	TRUE	7
6	TRUE	6
5	FALSE	
4	FALSE	

## Selecting Vector Elements

### By Value

`x[x == 10]` Elements which are equal to 10.

`x[x < 0]` All elements less than zero.

`x[x %in% c(1, 2, 5)]` Elements in the set 1, 2, 5.

### Named Vectors

`x['apple']` Element with name 'apple'.

# Exercise

---

1. Generate a vector with numbers from 5 to 10.  
*(If you can, try to use vector notation `p:q` or the function `seq()` for this!)*

```
> m <- ...
```

2. Return only the 2<sup>nd</sup> and 4<sup>th</sup> number in the vector.

```
> m[ ... ]
```

3. Return only numbers larger than 8.

```
> m[ ... ]
```

# Exercise

---

1. Generate a vector with numbers from 5 to 10.  
*(If you can, try to use vector notation `p:q` or the function `seq()` for this!)*

```
> m <- 5:10
```

2. Return only the 2<sup>nd</sup> and 4<sup>th</sup> number in the vector.

```
> m[c(2,4)]
```

3. Return only numbers larger than 8.

```
> m[m>8]
```

# Indexing lists

---

```
> v1 <- 4:6
> v2 <- rep(3,3)
> myList <- list(v1,v2)
> myList[1]          select the first list element
[[1]]
[1] 4 5 6
> myList[[1]]        select the content of the first list element
[1] 4 5 6
> myList[[1]][2]
[1] 5
> myList[1][2]
[[1]]
NULL
```

# Indexing a data frame

---

## Matrix subsetting

`df[ , 2]`



`df[2, ]`



row

column

`df[2, 2]`



name	age	pet
Ann	33	Cat
Bob	25	None
Chloe	21	Iguana
Dan	45	NA

# Indexing a data frame

```
> df[,2]  
[1] 33 25 21 45  
> df[, "age"]  
[1] 33 25 21 45  
> df$age  
[1] 33 25 21 45
```

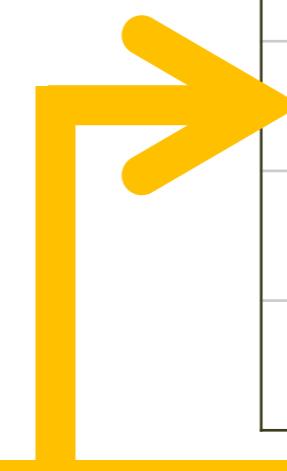
```
> df[2,]  
  name age  pet  
2  Bob  25 None  
> df[df$name=="Bob",]  
  name age  pet  
2  Bob  25 None
```

```
> df[df$name=="Bob", "age"]  
[1] 25
```

df[,2]  
df[, "age"]  
df\$age



name	age	pet
Ann	33	Cat
Bob	25	None
Chloe	21	Iguana
Dan	45	NA



df[2,]  
df[df\$name=="Bob", ]

# Exercise

---

1. Generate a simple data frame like this:

```
> df <- data.frame(name=c("Ann", "Bob", "Chloe", "Dan"),  
                    age=c(33, 25, 21, 45))
```

2. Return **only the names** of everyone in your data frame under 30.

*(Hint: what information should you use for row indexing? What information should you use for column indexing?)*

3. Bonus: can you use vector indexing on a column to achieve the same result?

# Exercise

---

1. Generate a simple data frame like this:

```
> df <- data.frame(name=c("Ann", "Bob", "Chloe", "Dan"),  
                    age=c(33, 25, 21, 45))
```

2. Return only the names of everyone in your data frame under 30.

(Hint: what information should you use for row indexing? What information should you use for column indexing?)

```
> df[df$age<30, "name"]  
> df[df$age<30, 1]
```



indexing the dataframe **df**

3. Bonus: can you use vector indexing on a column to achieve the same result?

```
> df$name[df$age<30]  
[1] Bob   Chloe
```



indexing the vector **df\$name**

Levels: Ann Bob Chloe Dan

# Which bracket does what?

---

- [ ] **Indexing** vectors, lists, dataframes...
- ( ) Passing **arguments** to functions
- { } **Defining content** of loops, functions, etc.

# Programming

---

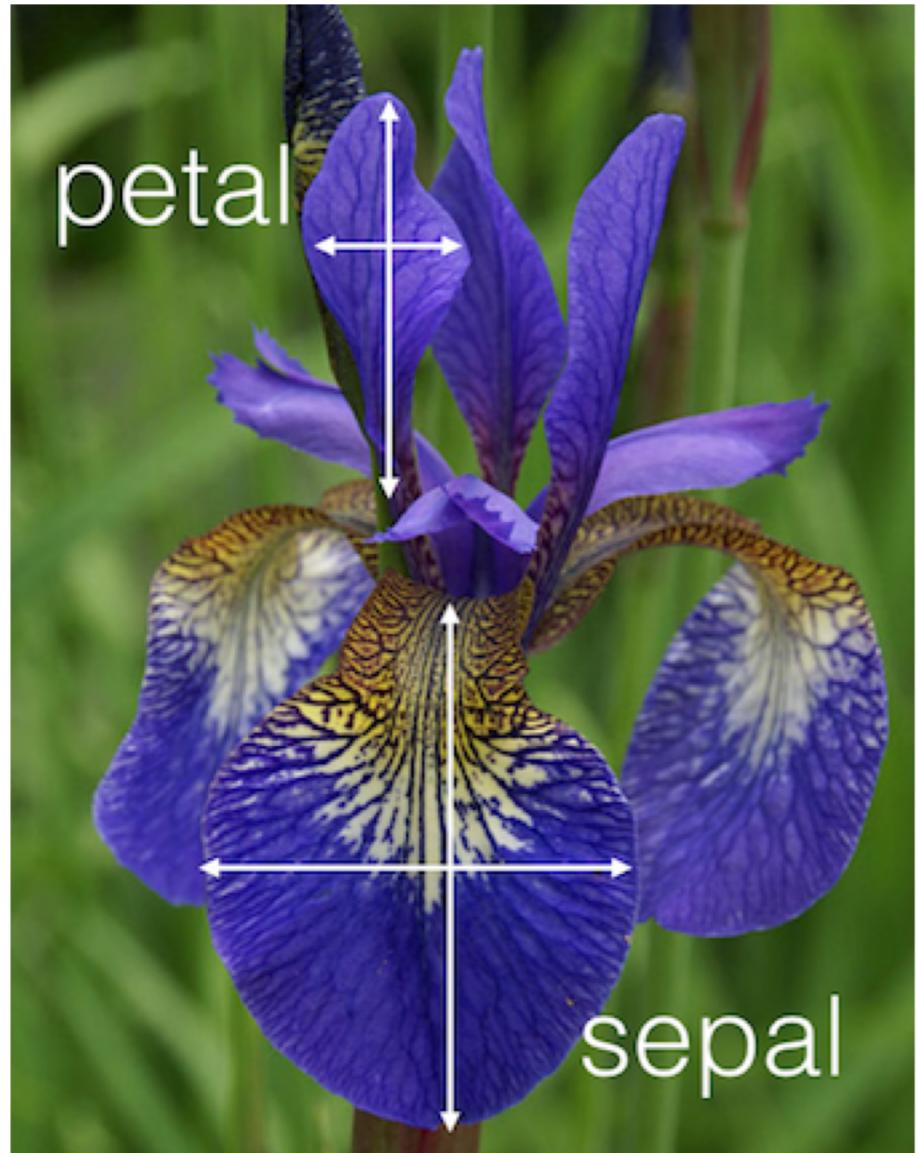
- Writing your first script
- Programming with loops and functions
- Handling and processing a dataset

```
lines(density(glnorm[,sname],na.rm=TRUE))  
move the samples from the data frame  
{r}  
select the samples to keep  
keepsamples <- row.names(pheno)  
apply sample selection to counts  
counts.sub <- counts.sub[,keepsamples]  
pheno.sub <- pheno[keepsamples]  
mt.assay <- mt.assay[,keepsamples]  
rlid.sub <- rlid[,keepsamples]
```

# Introducing a sample dataset

---

- Dataset: ‘iris’
- Standard dataset in R, measurements on 3 species of iris flowers



# Introducing a sample dataset

---

- Dataset: ‘iris’
- Standard dataset in R, measurements on 3 species of iris flowers

```
> head(iris)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

```
> summary(iris)
```

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
Min. :4.300	Min. :2.000	Min. :1.000	Min. :0.100	setosa :50
1st Qu.:5.100	1st Qu.:2.800	1st Qu.:1.600	1st Qu.:0.300	versicolor:50
Median :5.800	Median :3.000	Median :4.350	Median :1.300	virginica :50
Mean :5.843	Mean :3.057	Mean :3.758	Mean :1.199	
3rd Qu.:6.400	3rd Qu.:3.300	3rd Qu.:5.100	3rd Qu.:1.800	
Max. :7.900	Max. :4.400	Max. :6.900	Max. :2.500	

# Exercise

---

Explore the `iris` dataframe, using some of the following functions:

`head()`

`tail()`

`names()`

`summary()`

`dim()`

`str()`

Can you figure out what these functions do? What do they teach you about the kind of data in `iris`?

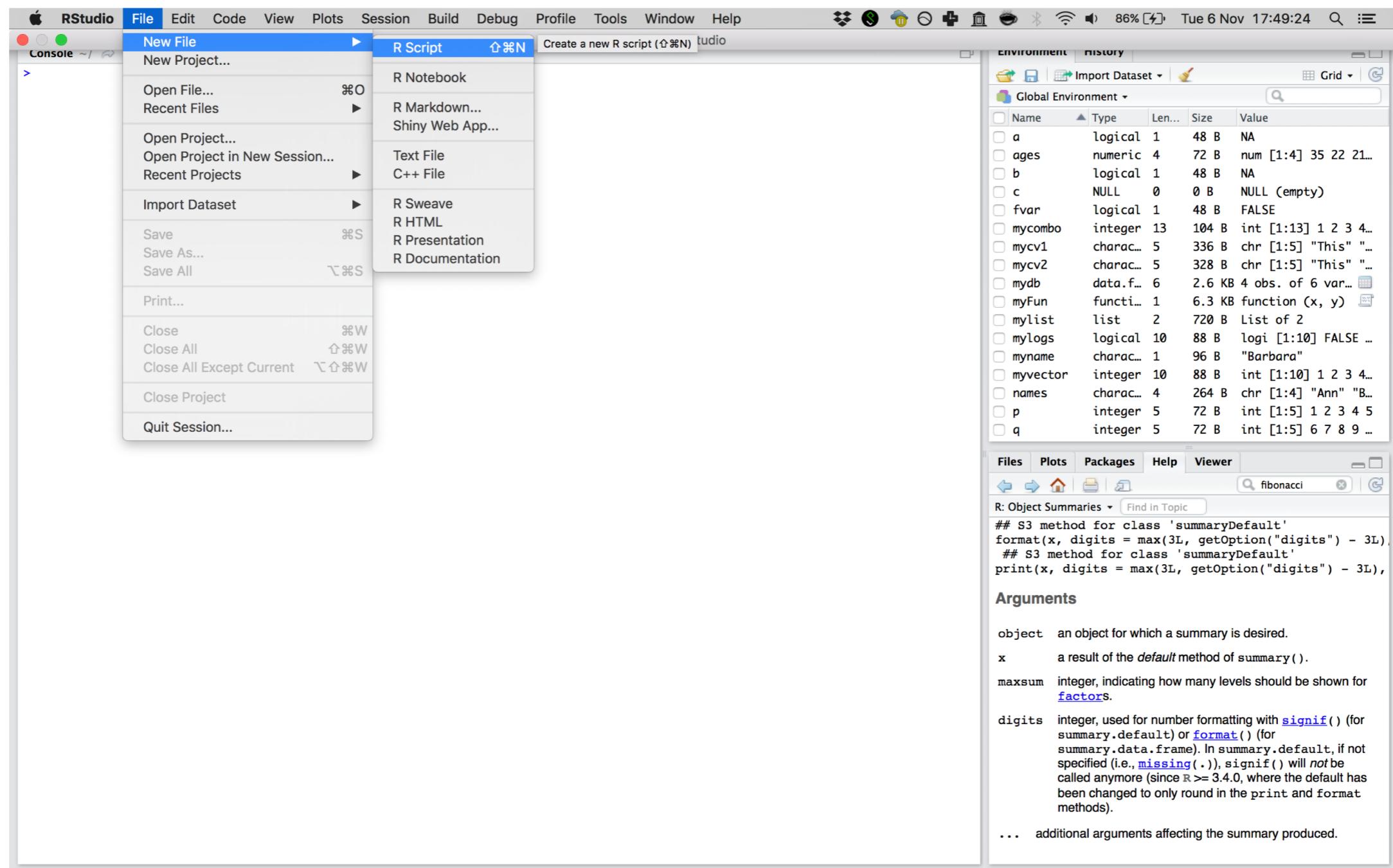
# Console and Scripts

---

Console	Code execution	-
Script	Code	Extension: .R (example_script.R)
Rmarkdown	Code + Narrative	Extension: .Rmd (example_report.Rmd)

# Ready to script?

RStudio > File > New File > R Script



# Console vs script on our slides

---

writing in the console

```
> x <- 1
```

```
> x
```

```
[1] 1
```

console output

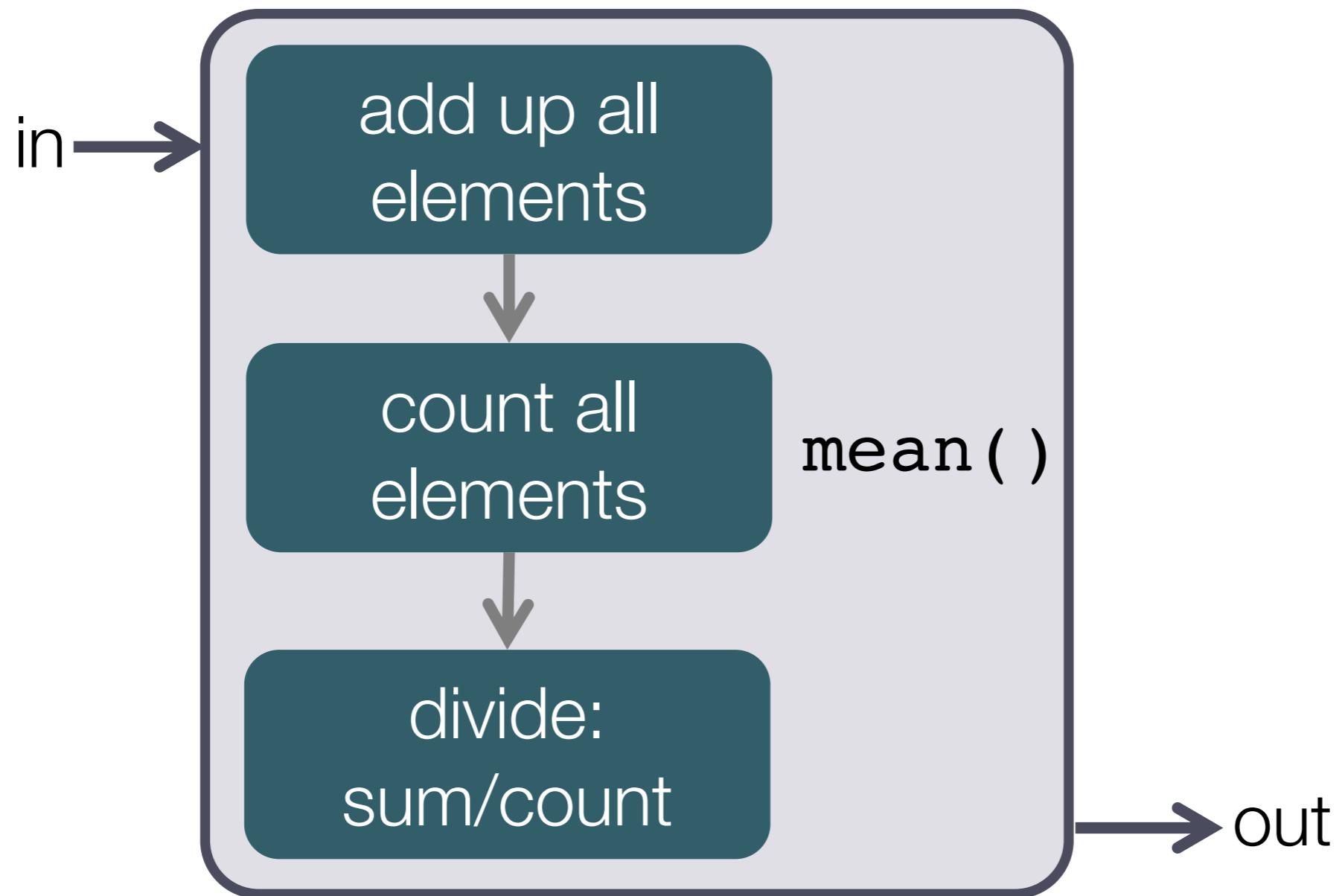
```
# Assigning the value 1 to x  
x <- 1
```

# indicates comment  
computer stops reading  
(but you should not!)

# Programming: functions

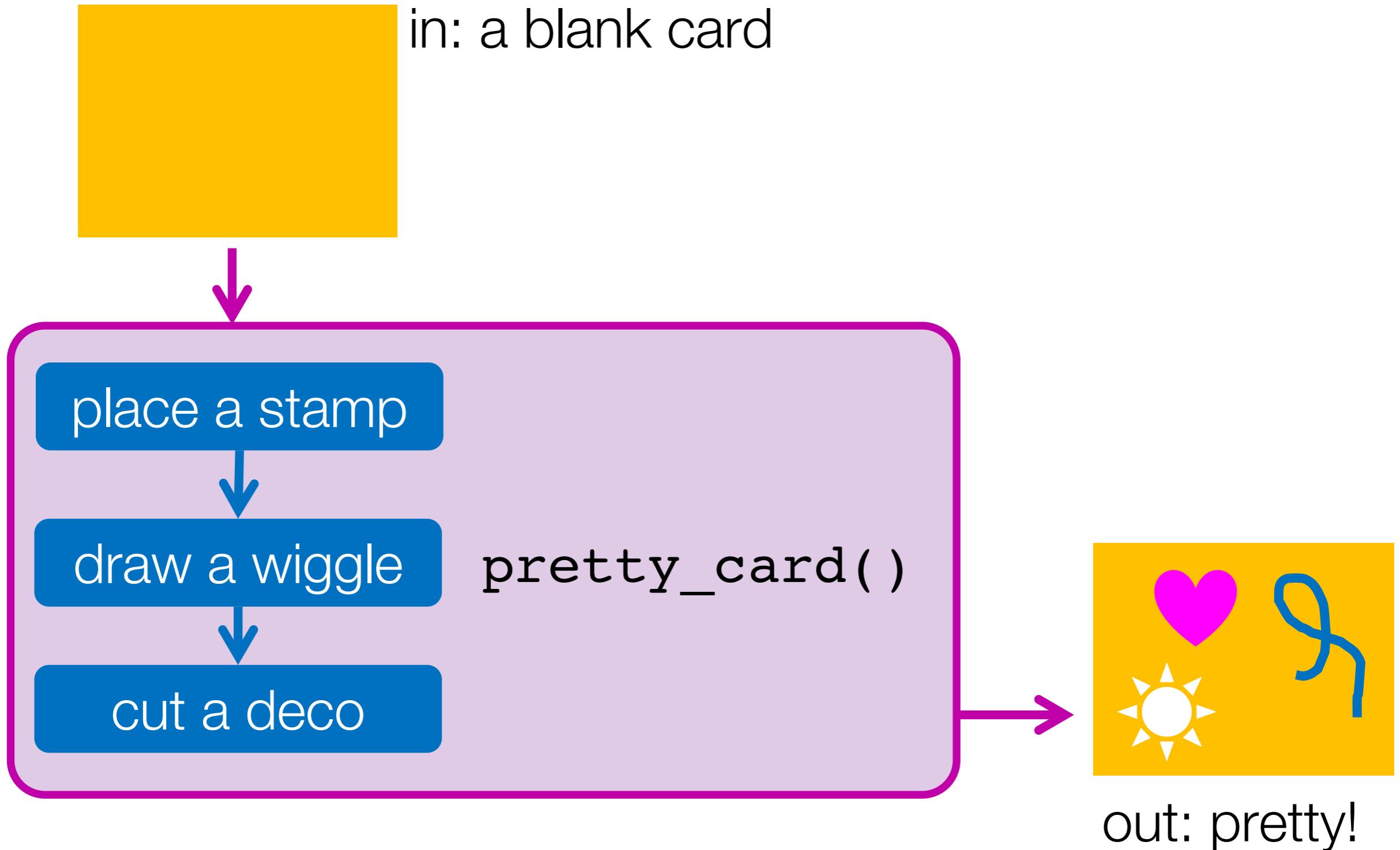
---

- Multiple instructions that form a cohesive unit
- Should be able to be repeated on different inputs



# Live exercise: the assembly line of a function

---

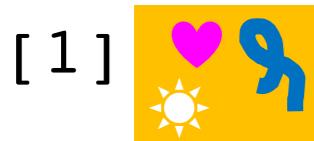


# How would this look in R?

---

```
pretty_card <- function(x){  
  x <- place_stamp(x)  
  x <- draw_wiggle(x)  
  x <- cut_deco(x)  
  return(x)  
}
```

```
> pretty_card( [ ] )
```



# Programming: functions

---

```
myFun <- function(x,y){  
  z <- x*y  
  return(z)  
}
```

```
> myFun(2,4)  
[1] 8
```

# Exercise

---

1. Write a function that takes a vector as input, and returns the mean of this vector (you can use the existing function `mean()` inside your function).

```
apply_calc <- function(...){  
  ...  
  return(...)  
}
```

2. Add further options to your function:
  - a. for example, the standard deviation (`sd()`), the minimum (`min()`), and the maximum (`max()`) of your input vector.
  - b. Put all of these calculations in a vector using the function `c()`, and return this result vector.

```
apply_calc <- function(...){  
  ...  
  
  allres <- c(...)  
  return(...)  
}
```

# Exercise

---

1. Write a function that takes a vector as input, and returns the mean of this vector (you can use the existing function `mean()` inside your function).

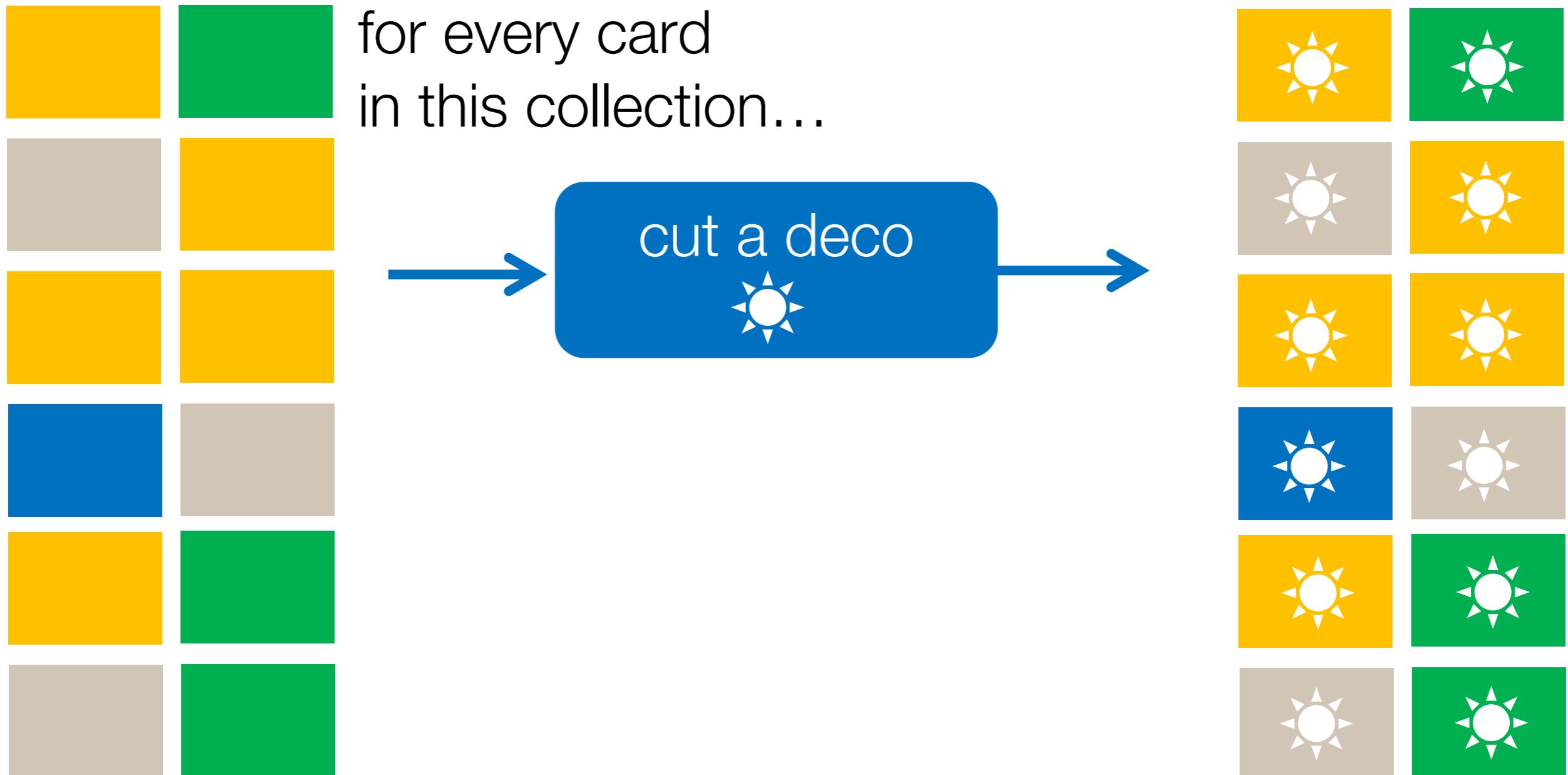
```
apply_calc <- function(x) {  
  m <- mean(x)  
  return(m)  
}
```

2. Add further options to your function:
  - a. for example, the standard deviation (`sd()`), the minimum (`min()`), and the maximum (`max()`) of your input vector.
  - b. Put all of these calculations in a vector using the function `c()`, and return this result vector.

```
apply_calc <- function(x) {  
  m <- mean(x)  
  s <- sd(x)  
  mi <- min(x)  
  ma <- max(x)  
  allres <- c(m,s,mi,ma)  
  return(allres)  
}
```

# Live exercise: the repeated action in a for-loop

---



# How would this look in R?

---

```
for(■ in [■■■■■]) {  
  cut_deco(■)  
}
```

```
[1] [■]  
[1] [■]  
[1] [■]  
[1] [■]  
[1] [■]  
[1] [■]  
[1] [■]
```

```
for(i in 1:6){  
  print(i)  
}
```

```
[1] 1  
[1] 2  
[1] 3  
[1] 4  
[1] 5  
[1] 6
```

# Exercise

---

1. Make a vector with all the column names in `iris`.

*Hint: use the function `colnames()`.*

```
iriscols <- ...
```

2. Make a for-loop that iterates over all the column names in `iris`, and prints these column names.

```
for(...){  
  ...  
}
```

3. Elaborate on this for-loop: select the corresponding column in `iris`, and print the mean. *Hint: yes, you should get a warning! Do you understand why?*

```
for(...){  
  ...  
}
```

# Exercise

---

1. Make a vector with all the column names in `iris`.

*Hint: use the function `colnames()`.*

```
iriscols <- colnames(iris)
```

2. Make a for-loop that iterates over all the column names in `iris`, and prints these column names.

```
for(i in iriscols){  
  print(i)  
}
```

3. Elaborate on this for-loop: select the corresponding column in `iris`, and print the mean. *Hint: yes, you should get a warning! Do you understand why?*

```
for(i in iriscols){  
  c <- iris[,i]  
  stat <- mean(c)  
  print(stat)  
}
```

# What's wrong? And how do we fix it?

---

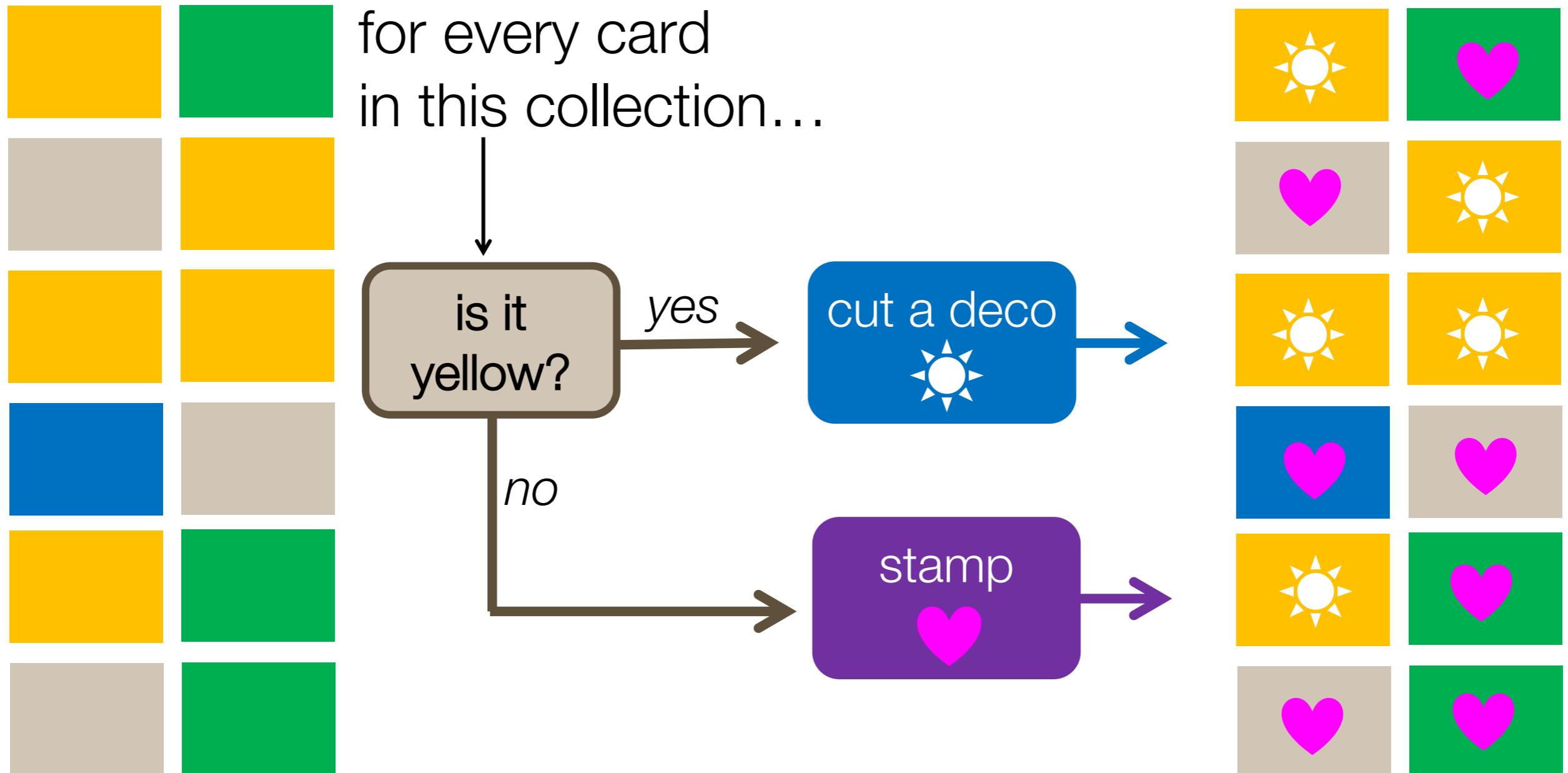
```
for(i in iriscols){  
  # select the appropriate column  
  c <- iris[,i]  
  # calculate the mean  
  stats <- mean(c)  
  # print the mean  
  print(stats)  
}
```

```
[1] 5.843333  
[1] 3.057333  
[1] 3.758  
[1] 1.199333  
[1] NA
```

Warning message:

In mean.default(c) : argument is not numeric or logical:  
returning NA

# Live exercise: the selectivity of an if-statement

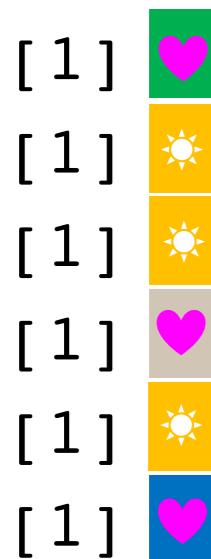


PS: note how this is still a for-loop? That's not a requirement!

# How would this look in R?

---

```
for(■ in [■■■■■]) {  
  if(■ == ■){  
    cut_deco(■)  
  } else{  
    stamp(■)  
  }  
}
```



```
for(i in 1:6){  
  if(i > 3){  
    print("Large!")  
  } else{  
    print("small...")  
  }  
}
```

```
[1] "small..."  
[1] "small..."  
[1] "small..."  
[1] "Large!"  
[1] "Large!"  
[1] "Large!"
```

# Programming: if-statement

---

```
d <- 5
```

```
if(is.na(d)){
  print("My data is missing!")
} else if(is.null(d)){
  print("My data does not even exist...")
} else{
  print("I have data!")
}
```

```
[1] "I have data!"
```

# Exercise: choose one!

---

1. Copy-paste the for-loop you made in the previous exercise. Inside this for-loop, add an if-statement, so that `mean()` is only performed on numeric vectors.

*Hint: check the function `is.numeric()`.*

```
for(i in iriscols){  
  c <- iris[,i]  
  ...  
}
```

2. Are you feeling comfortable with the material?
  - a. Open the file ‘programming\_exercise.R’
  - b. Read through the code, see if you understand it (*it is mostly the previous two exercises, but with some small tweaks!*)
  - c. Scroll down to line 32 for the exercise.
  - d. Read the bonus material — you can check your work with the code there.

# Exercise: choose one!

---

1. Copy-paste the for-loop you made in the previous exercise. Inside this for-loop, add an if-statement, so that `mean()` is only performed on numeric vectors.

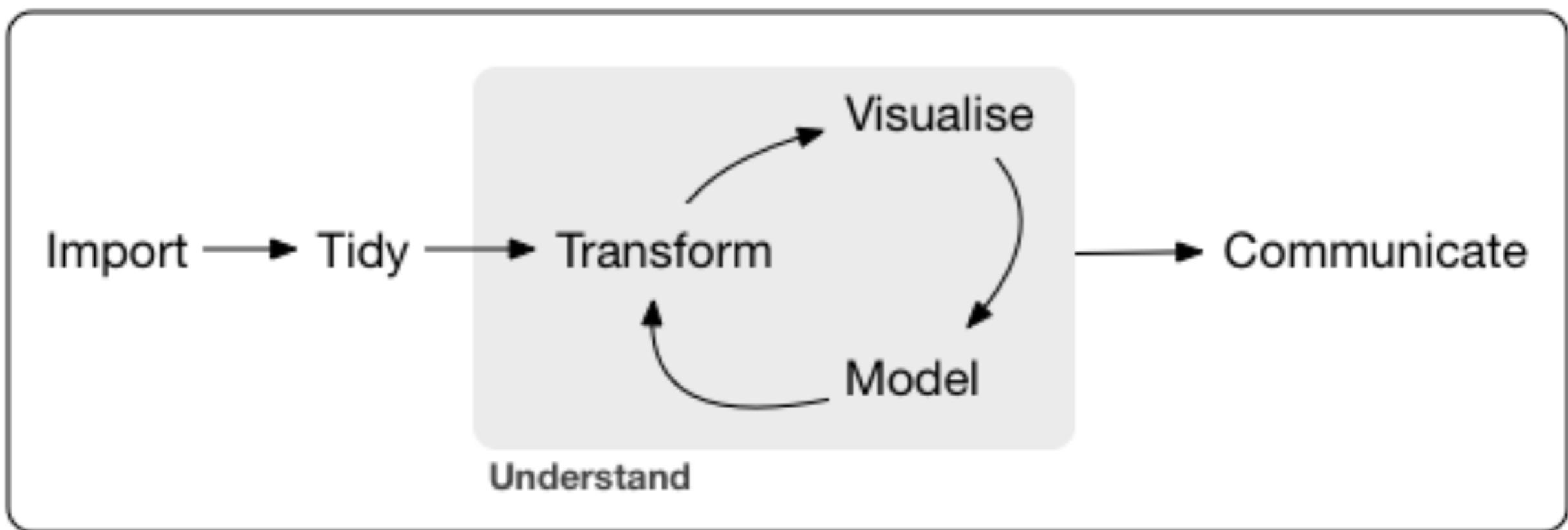
*Hint: check the function `is.numeric()`.*

```
for(i in iriscols){  
  c <- iris[,i]  
  if(is.numeric(c)){  
    stat <- mean(c)  
    print(stat)  
  }  
}
```

2. Are you feeling comfortable with the material?
  - a. Open the file ‘programming\_exercise.R’
  - b. Read through the code, see if you understand it (*it is mostly the previous two exercises, but with some small tweaks!*)
  - c. Scroll down to line 32 for the exercise.
  - d. Read the bonus material — you can check your work with the code there.

# Data science workflow: scripting is crucial

- Scripting combines commands to a comprehensive set of instructions.
- A script is code that can be **saved, reused, shared, published!**
- In short: a crucial step towards reproducible data analysis.



Program

*a single script for a single purpose!*

# Starting the script: write a header

---

```
## Date: 7 November 2018  
## Author: Barbara Vreede  
## This script was written as part of the R course  
## "Introduction to R & Data", at Utrecht University
```

# Load packages and dependencies

---

```
## Date: 7 November 2018
## Author: Barbara Vreede
## This script was written as part of the R course
## "Introduction to R & Data", at Utrecht University

# Load required packages
library(dplyr)
library(tidyr)
library(ggplot2)
```

# Custom functions

---

```
## Date: 7 November 2018
## Author: Barbara Vreede
## This script was written as part of the R course
## "Introduction to R & Data", at Utrecht University

# Load required packages
library(dplyr)
library(tidyr)
library(ggplot2)

# Functions
myFun <- function(var){
  var <- var*2*pi
  return(var)
}
```

# Starting your script: header, packages, functions

```
## Date: 7 November 2018  
## Author: Barbara Vreede  
## This script was written as part of the R course  
## "Introduction to R & Data", at Utrecht University
```

```
# Load required packages  
library(dplyr)  
library(tidyr)  
library(ggplot2)
```

```
# Functions  
myFun <- function(var){  
  var <- var*2*pi  
  return(var)  
}
```

# To check before lunch: please load tidyverse

---

```
> library(tidyverse)
— Attaching packages ━━━━━━━━━━━━━━━━ tidyverse 1.2.1 ━━━━━━━
  ggplot2 3.1.0      purrr   0.3.0
  tibble   2.0.1      dplyr    0.7.8
  tidyrr   0.8.2      stringr 1.4.0
  readr    1.3.1     forcats  0.3.0
— Conflicts ━━━━━━━━━━━━━━━━ tidyverse_conflicts() ━━━━━
  dplyr::filter() masks stats::filter()
  dplyr::lag()    masks stats::lag()
```

Enjoy your lunch!

---



# Introduction to R & data

---

## Part II: Modern R with tidyverse

## Outline part II

---

- Introduction to **tidyverse**, **rmarkdown**, and **tibble**.
- Load and save data with **readr**
- [break]
- Data visualisation with **ggplot**
- [break]
- Data transformation with **tidyr** and **dplyr**

The image shows a whiteboard with handwritten R code. The code is organized into several sections:

- A header section starting with `source("path/to/your_script.R")`.
- A section titled "move the samples from the data" containing `keepsamples <- row.names(pheno[pheno$`).
- A section titled "select the samples to keep" containing `keepsamples <- row.names(pheno[pheno$`.
- A section titled "apply sample selection to" containing `counts.sub <- counts.sub[,keepsamples]`.
- A section titled "pheno.sub" containing `pheno.sub <- pheno[keepsamples]`.
- A section titled "nt.assay" containing `nt.assay <- nt.assay[,keepsamples]`.
- A section titled "rld.sub" containing `rld.sub <- rld[,keepsamples]`.

The code uses color coding for different parts of the script, such as purple for functions like `source` and `row.names`, green for variable names like `keepsamples` and `counts.sub`, and blue for file paths and specific column names.



Tidyverse

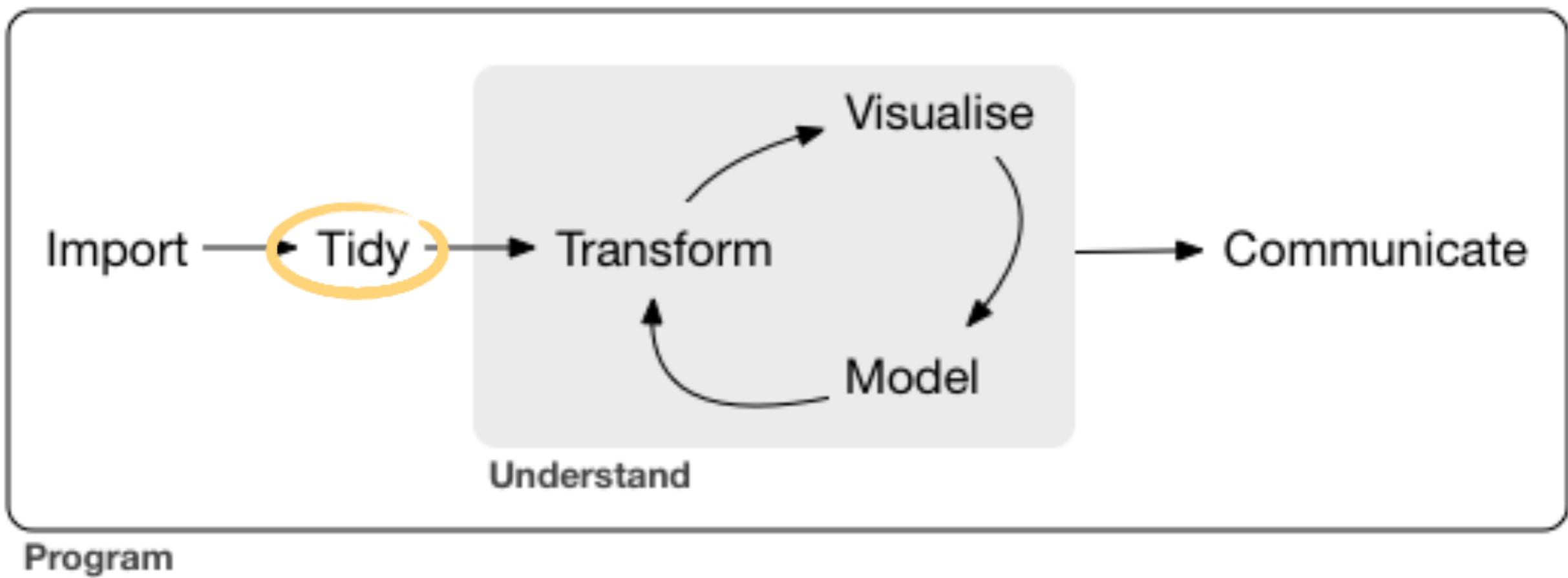
Modern R for data science

"The tidyverse is an opinionated collection of R packages designed for data science. All packages share an underlying design philosophy, grammar, and data structures."

– **tidyverse.org (2018)**

# Data science workflow

---



Tidy data ensures that further processing can be done efficiently, and reproducibly.

Tidy data is easy to manipulate, model, and visualize.

# Tidy data

multiple observations per row

- Each **variable** is a column and contains **values**
- Each **observation** is a row
- Each type of **observational unit** forms a table

values in column names

Patient	Temp	Med_A	Temp_A	Med_B	Temp_B
122030	37.0	300	37.1	NA	NA
122021	38.2	200	38.1	85	36.5
124500	38.1	300	38.0	NA	NA
126098	39.1	NA	NA	100	36.8

# Tidy data

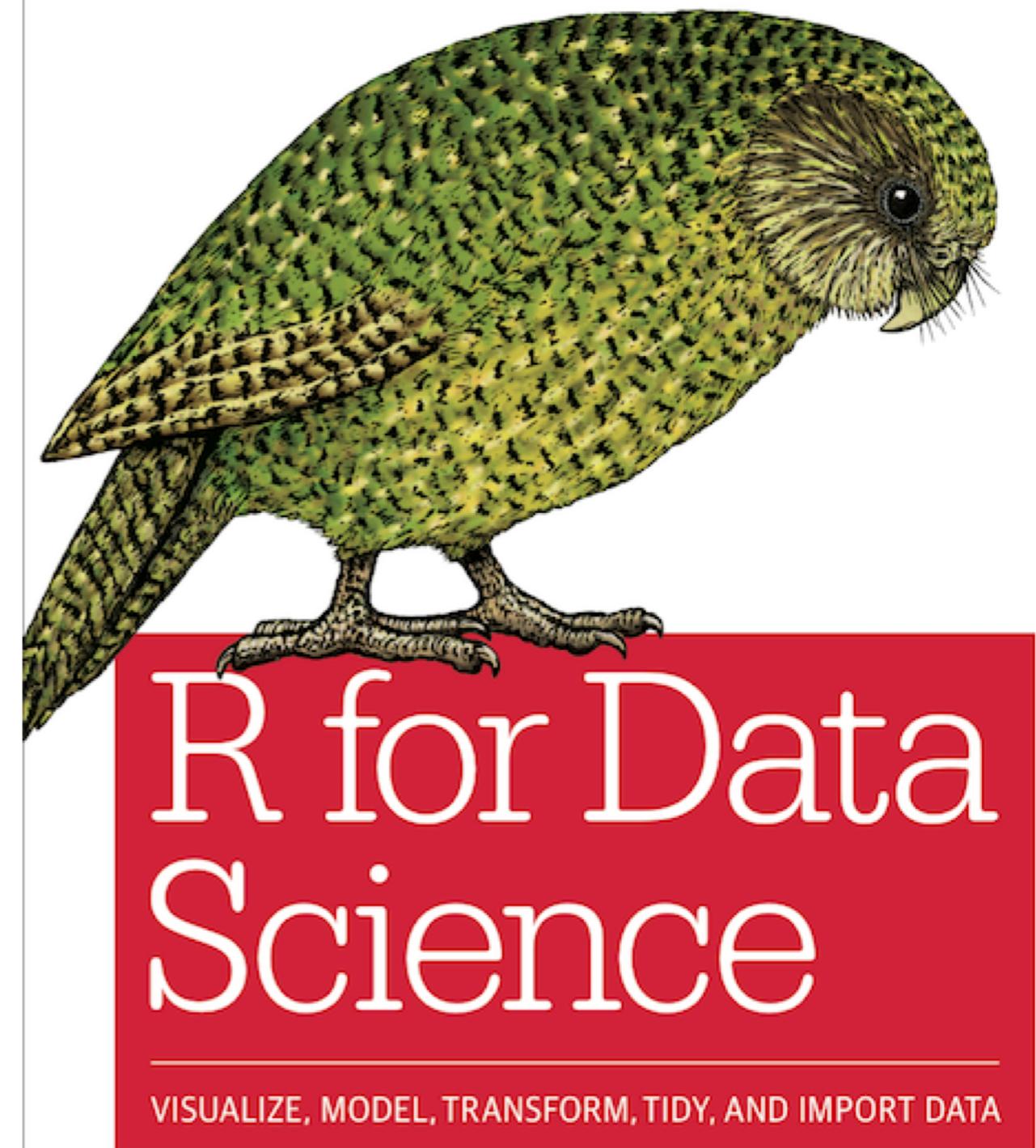
**ID no longer unique per row**  
(but can still be used to collect  
all info on single patient)

Patient	Temp	Treatment	Dose
122030	37.0	None	NA
122030	37.1	A	300
122021	38.2	None	NA
122021	38.1	A	200
122021	36.5	B	85
124500	38.1	None	NA
124500	38.0	A	300
126098	39.1	None	NA
126098	36.8	B	100

**Time series (order) lost**  
(so make sure this is  
explicit)

# Learn tidyverse

- R for Data Science (book); freely available on [r4ds.had.co.nz/](https://r4ds.had.co.nz/)



Hadley Wickham &  
Garrett Grolemund

# Learn tidyverse

- R for Data Science (book); freely available on [r4ds.had.co.nz/](https://r4ds.had.co.nz/)
- ggplot2 (book)

Hadley Wickham

**ggplot2**

Elegant Graphics for Data Analysis

# Learn tidyverse

- R for Data Science (book); freely available on [r4ds.had.co.nz/](http://r4ds.had.co.nz/)
- ggplot2 (book)
- cheatsheets  
[www.rstudio.com/resources/cheatsheets/](http://www.rstudio.com/resources/cheatsheets/)

## Data Transformation with dplyr :: CHEAT SHEET

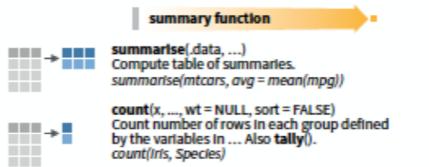


dplyr functions work with pipes and expect **tidy data**. In tidy data:



### Summarise Cases

These apply **summary functions** to columns to create a new table of summary statistics. Summary functions take vectors as input and return one value (see back).

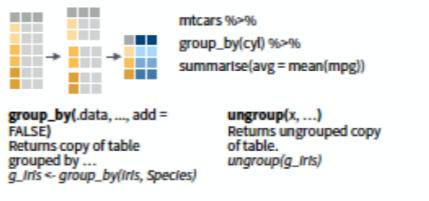


### VARIATIONS

**summarise\_all()** - Apply funs to every column.  
**summarise\_at()** - Apply funs to specific columns.  
**summarise\_if()** - Apply funs to all cols of one type.

### Group Cases

Use **group\_by()** to create a "grouped" copy of a table. dplyr functions will manipulate each "group" separately and then combine the results.

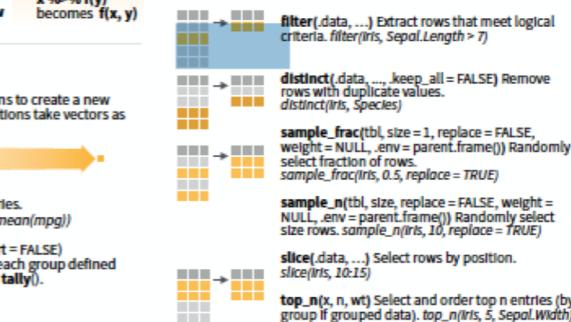


### R Studio

### Manipulate Cases

#### EXTRACT CASES

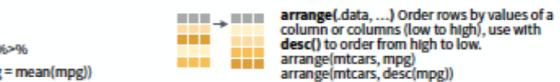
Row functions return a subset of rows as a new table.



#### Logical and boolean operators to use with filter()

< <= &lt;na() %in% ! xor()  
See ?base::logic and ?Comparison for help.

#### ARRANGE CASES



#### ADD CASES



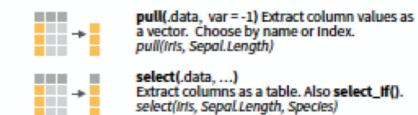
#### RENAME CASES

→ **rename(data, ...)** Rename columns.  
rename(iris, Length = Sepal.Length)

### Manipulate Variables

#### EXTRACT VARIABLES

Column functions return a set of columns as a new vector or table.



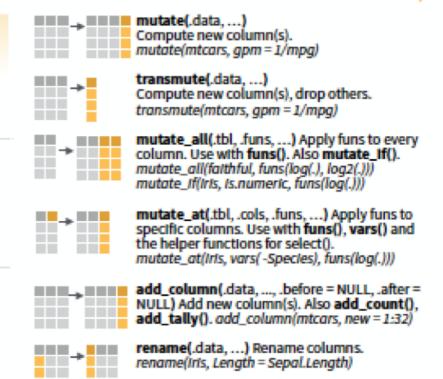
#### Use these helpers with select(), e.g. select(iris, starts\_with("Sepal"))

**contains(match)** num\_range(prefix, range) ;, e.g. mpg:cyl  
**ends\_with(match)** one\_of(...)  
**matches(match)** starts\_with(match)

#### MAKE NEW VARIABLES

These apply **vectorized functions** to columns. Vectorized funs take vectors as input and return vectors of the same length as output (see back).

#### vectorized function



### Vector Functions

#### TO USE WITH MUTATE()

**mutate()** and **transmute()** apply vectorized functions to columns to create new columns. Vectorized functions take vectors as input and return vectors of the same length as output.

#### vectorized function

**OFFSETS**  
dplyr::lag() - Offset elements by 1  
dplyr::lead() - Offset elements by -1

#### CUMULATIVE AGGREGATES

dplyr::cumall() - Cumulative all()  
dplyr::cumany() - Cumulative any()  
cummax() - Cumulative max()  
dplyr::cummean() - Cumulative mean()  
cummin() - Cumulative min()  
cumprod() - Cumulative prod()  
cumsum() - Cumulative sum()

#### RANKINGS

dplyr::cume\_dist() - Proportion of all values <=  
dplyr::dense\_rank() - rank with ties = min, no gaps  
dplyr::min\_rank() - rank with ties = min  
dplyr::ntile() - bins into n bins  
dplyr::percent\_rank() - min\_rank scaled to [0,1]  
dplyr::row\_number() - rank with ties = "first"

#### MATH

+, -, \*, /, ^, %%, %% - arithmetic ops  
log(), log2(), log10() - logs  
<, <=, >, >=, !=, == - logical comparisons  
dplyr::between() - x <= left & x <= right  
dplyr::near() - safe == for floating point numbers

#### MISC

dplyr::case\_when() - multi-case if\_else()  
dplyr::coalesce() - first non-NA values by element across a set of vectors  
dplyr::if\_else() - element-wise if() + else()  
dplyr::na\_if() - replace specific values with NA  
pmax() - element-wise max()  
pmin() - element-wise min()  
dplyr::recode() - Vectorized switch()  
dplyr::recode\_factor() - Vectorized switch() for factors

### Summary Functions

#### TO USE WITH SUMMARISE()

**summarise()** applies summary functions to columns to create a new table. Summary functions take vectors as input and return single values as output.

#### summary function

**COUNTS**  
dplyr::n() - number of values/rows  
dplyr::n\_distinct() - # of uniqueness  
sum(is.na()) - # of non-NAs

#### LOCATION

mean() - mean, also mean(!is.na())  
median() - median

#### LOGICALS

mean() - Proportion of TRUE's  
sum() - # of TRUE's

#### POSITION/ORDER

dplyr::first() - first value  
dplyr::last() - last value  
dplyr::nth() - value in nth location of vector

#### RANK

quantile() - nth quantile  
min() - minimum value  
max() - maximum value

#### SPREAD

IQR() - Inter-Quartile Range  
mad() - median absolute deviation  
sd() - standard deviation  
var() - variance

#### Row Names

Tidy data does not use rownames, which store a variable outside of the columns. To work with the rownames, first move them into a column.

rownames\_to\_column()  
Move row names into col.  
a <- rownames\_to\_column(iris, var = "C")

#### column\_to\_rownames()

Move col in row names.  
column\_to\_rownames(a, var = "C")

### Combine Tables

#### COMBINE VARIABLES

x y  
+ =  
x y

Use bind\_cols() to paste tables beside each other as they are.

bind\_cols(...) Returns tables placed side by side as a single table.  
BE SURE THAT ROWS ALIGN.

Use a "Mutating Join" to join one table to columns from another, matching values with the rows that they correspond to. Each join retains a different combination of values from the tables.

left\_join(x, y, by = NULL, copy = FALSE, suffix = c("x", "y", ...))  
Join matching values from y to x.

right\_join(x, y, by = NULL, copy = FALSE, suffix = c("x", "y", ...))  
Join matching values from x to y.

inner\_join(x, y, by = NULL, copy = FALSE, suffix = c("x", "y", ...))  
Join data. Retain only rows with matches.

full\_join(x, y, by = NULL, copy = FALSE, suffix = c("x", "y", ...))  
Join data. Retain all values, all rows.

Use by = c("col1", "col2", ...) to specify one or more common columns to match on.  
left\_join(x, y, by = "A")

Use a named vector, by = c("col1" = "col2"), to match on columns that have different names in each table.  
left\_join(x, y, by = c("C" = "D"))

Use suffix to specify the suffix to give to unmatched columns that have the same name in both tables.  
left\_join(x, y, by = c("C" = "D"), suffix = c("1", "2"))

#### COMBINE CASES

x y  
+ =  
x y

Use bind\_rows() to paste tables below each other as they are.

bind\_rows(..., id = NULL)  
Returns tables one on top of the other as a single table. Set .id to a column name to add a column of the original table names (as pictured)

intersect(x, y, ...)  
Rows that appear in both x and y.

setdiff(x, y, ...)  
Rows that appear in x but not y.

union(x, y, ...)  
Rows that appear in x or y.  
(Duplicates removed). union\_all() retains duplicates.

Use setequal() to test whether two data sets contain the exact same rows (in any order).

#### EXTRACT ROWS

x y  
+ =  
x y

Use a "Filtering Join" to filter one table against the rows of another.

semi\_join(x, y, by = NULL, ...)  
Return rows of x that have a match in y.  
USEFUL TO SEE WHAT WILL BE JOINED.

anti\_join(x, y, by = NULL, ...)  
Return rows of x that do not have a match in y.  
USEFUL TO SEE WHAT WILL NOT BE JOINED.

# Your afternoon roadmap

---

- A short explanation on screen (~15 minutes)
- Exercises in a document on your computer (~45 minutes)
  - 2-3 basic exercises
  - optional exercises, for further practice
  - reading exercises, for some extra insight into Tidyverse
- We will work with a new data set
- The exercises are presented in Rmarkdown format. We'll explain this later!



## From code to document

---

- Turn your analyses into high quality documents with Rmarkdown
- **Combine code with narrative (R with markdown)**
- Turn your analyses into high quality documents, reports, presentations and dashboards.
- ... or your note book.

# Console, Scripts and Rmarkdown

---

Console	Code execution	-
Script	Code	Extension: <b>.R</b> (example_script.R)
Rmarkdown	Code + Narrative	Extension: <b>.Rmd</b> (example_report.Rmd)

# Markdown

---

```
# title
```

```
Some text about your project
```

```
## Section
```

```
More text about your project
```

```
```{r}
max(iris$Petal.Length)
min(iris$Petal.Length)
```
```

# Rmarkdown: demo

---



# Exercise: open the exercise Rmarkdown

1. RStudio > File > Open Project > introduction-to-R-and-data-github.Rproj
2. From the ‘files’ menu (bottom right), select modernR\_exercises.Rmd
3. Update the header information with your name!

# Run the first code chunk!

---

```
## Technical requirements
```

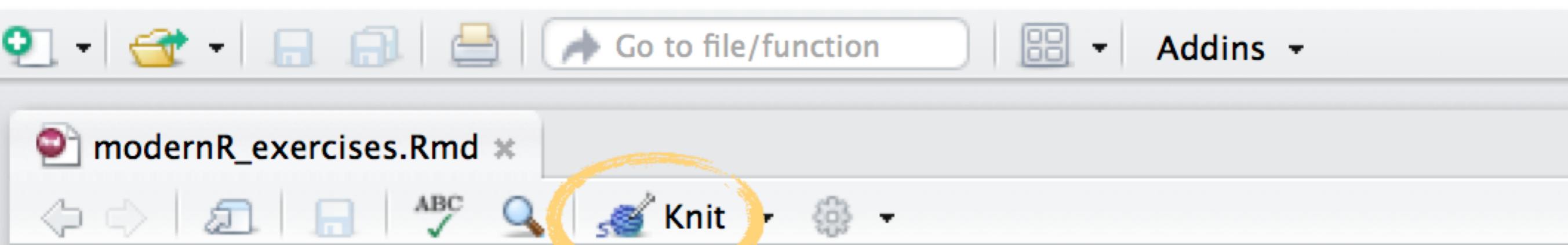
This project depends on the `tidyverse` package. Load tidyverse into your work environment.

```
```{r}
library(tidyverse)
````
```



```
> library(tidyverse)
— Attaching packages ————— tidyverse 1.2.1 —
  ggplot2 3.1.0      purrr  0.3.0
  tibble   2.0.1      dplyr   0.7.8
  tidyrr   0.8.2      stringr 1.4.0
  readr    1.3.1     forcats 0.3.0
— Conflicts ————— tidyverse_conflicts() —
  dplyr::filter() masks stats::filter()
  dplyr::lag()   masks stats::lag()
```

# All done? Time to knit!



The screenshot shows the RStudio interface with the following details:

- Toolbar:** Includes icons for file operations (New, Open, Save, Print), Go to file/function, and Addins.
- File Tab:** Shows the file name "modernR\_exercises.Rmd".
- Toolbar Buttons:** Includes back, forward, file, ABC, search, and Knit. The "Knit" button is highlighted with a yellow circle.
- Code Editor:** Displays the R Markdown code. The code includes a YAML front matter block defining the title, author, and output type (html\_document with toc: true). It also contains a note about the document being part of a workshop and a section titled "# Introduction".

```
1 ---  
2 title: "Modern R with tidyverse"  
3 author: "[Insert your name]"  
4 output:  
5   html_document:  
6     toc: true  
7 ---  
8  
9 *This document is part of the workshop **Introduction to R & Data  
10  
11 # Introduction  
12  
13 In this document, we explore Crane migration, through the GPS dat  
data was kindly provided for this course by Sasha Pekarsky at the
```

## package: Tibble

---

"Tibbles are data frames, but they tweak some older behaviours to make life a little easier."

*- Hadley Wickham*



# Tibbles

---

```
> tibble(a = 1:26, b = letters)
# A tibble: 26 x 2
      a     b
  <int> <chr>
1     1     a
2     2     b
3     3     c
4     4     d
5     5     e
6     6     f
7     7     g
8     8     h
9     9     i
10    10    j
# ... with 16 more rows
```

# Tibbles: from data.frame to tibble

---

```
> as_tibble(iris)
# A tibble: 150 x 5
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
        <dbl>       <dbl>       <dbl>       <dbl>   <fct>
1       5.10       3.50       1.40       0.200 setosa
2       4.90       3.00       1.40       0.200 setosa
3       4.70       3.20       1.30       0.200 setosa
4       4.60       3.10       1.50       0.200 setosa
5       5.00       3.60       1.40       0.200 setosa
6       5.40       3.90       1.70       0.400 setosa
7       4.60       3.40       1.40       0.300 setosa
8       5.00       3.40       1.50       0.200 setosa
9       4.40       2.90       1.40       0.200 setosa
10      4.90       3.10       1.50       0.100 setosa
# ... with 140 more rows
```

# Tibbles: from tibble to data.frame

---

```
> iris_tibble <- as_tibble(iris)
> as.data.frame(iris_tibble)
```

|    | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species |
|----|--------------|-------------|--------------|-------------|---------|
| 1  | 5.1          | 3.5         | 1.4          | 0.2         | setosa  |
| 2  | 4.9          | 3.0         | 1.4          | 0.2         | setosa  |
| 3  | 4.7          | 3.2         | 1.3          | 0.2         | setosa  |
| 4  | 4.6          | 3.1         | 1.5          | 0.2         | setosa  |
| 5  | 5.0          | 3.6         | 1.4          | 0.2         | setosa  |
| 6  | 5.4          | 3.9         | 1.7          | 0.4         | setosa  |
| 7  | 4.6          | 3.4         | 1.4          | 0.3         | setosa  |
| 8  | 5.0          | 3.4         | 1.5          | 0.2         | setosa  |
| 9  | 4.4          | 2.9         | 1.4          | 0.2         | setosa  |
| 10 | 4.9          | 3.1         | 1.5          | 0.1         | setosa  |
| 11 | 5.4          | 3.7         | 1.5          | 0.2         | setosa  |
| 12 | 4.8          | 3.4         | 1.6          | 0.2         | setosa  |
| 13 | 4.8          | 3.0         | 1.4          | 0.1         | setosa  |
| 14 | 4.3          | 3.0         | 1.1          | 0.1         | setosa  |
| 15 | 5.8          | 4.0         | 1.2          | 0.2         | setosa  |
| 16 | 5.7          | 4.4         | 1.5          | 0.4         | setosa  |

## Load and save data

---

The basics of `readr`



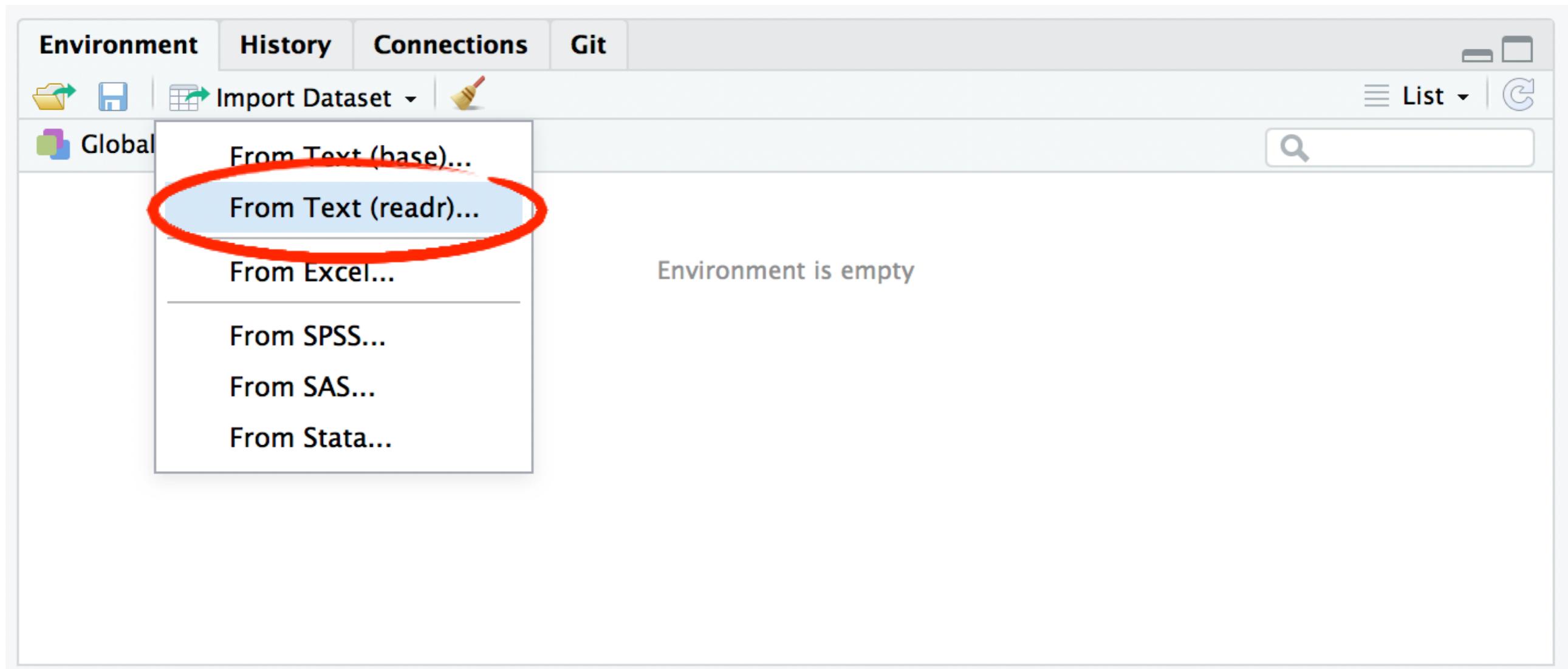
## Flat data files

---

- Most common format: Comma-separated values (CSV)
- Delimiter-separated values (also stored as CSV)
- Common delimiters:
  - comma ,
  - semicolon ;
  - tab \t

```
1 mpg;cyl;disp;hp;drat;wt;qsec;v
2 21;6;160;110;3.9;2.62;16.46;0;
3 21;6;160;110;3.9;2.875;17.02;0
4 22.8;4;108;93;3.85;2.32;18.61;
5 21.4;6;258;110;3.08;3.215;19.4
6 18.7;8;360;175;3.15;3.44;17.02
7 18.1;6;225;105;2.76;3.46;20.22
8 14.3;8;360;245;3.21;3.57;15.84
9 24.4;4;146.7;62;3.69;3.19;20;1
10 22.8;4;140.8;95;3.92;3.15;22.9
11 19.2;6;167.6;123;3.92;3.44;18.
12 17.8;6;167.6;123;3.92;3.44;18.
13 16.4;8;275.8;180;3.07;4.07;17.
14 17.3;8;275.8;180;3.07;3.73;17.
15 15.2;8;275.8;180;3.07;3.78;18;
16 10.4;8;472;205;2.93;5.25;17.98
17 10.4;8;460;215;3;5.424;17.82;0
18 14.7;8;440;230;3.23;5.345;17.4
19 32.4;4;78.7;66;4.08;2.2;19.47;
20 30.4;4;75.7;52;4.93;1.615;18.5
21 33.9;4;71.1;65;4.22;1.835;19.9
22 21.5;4;120.1;97;3.7;2.465;20.0
23 17.5;8;312;152;3.73;3.53;16.27
```

# Load data by using buttons



# Load data by using buttons

Import Text Data

File/Url:

~/surfdrive/Projects/presentations/workshops/introduction-to-R-and-data-github/data/iris.csv

Data Preview:

| Sepal.Length<br>(double) ▾ | Sepal.Width<br>(double) ▾ | Petal.Length<br>(double) ▾ | Petal.Width<br>(double) ▾ | Species<br>(character) ▾ |
|----------------------------|---------------------------|----------------------------|---------------------------|--------------------------|
| 5.1                        | 3.5                       | 1.4                        | 0.2                       | setosa                   |
| 4.9                        | 3.0                       | 1.4                        | 0.2                       | setosa                   |
| 4.7                        | 3.2                       | 1.3                        | 0.2                       | setosa                   |
| 4.6                        | 3.1                       | 1.5                        | 0.2                       | setosa                   |
| 5.0                        | 3.6                       | 1.4                        | 0.2                       | setosa                   |
| 5.4                        | 3.9                       | 1.7                        | 0.4                       | setosa                   |
| 4.6                        | 3.4                       | 1.4                        | 0.3                       | setosa                   |
| 5.0                        | 3.4                       | 1.5                        | 0.2                       | setosa                   |
| 4.4                        | 2.9                       | 1.4                        | 0.2                       | setosa                   |
| 4.9                        | 3.1                       | 1.5                        | 0.1                       | setosa                   |
| 5.4                        | 3.7                       | 1.5                        | 0.2                       | setosa                   |

Previewing first 50 entries.

Import Options:

Name:   First Row as Names  Trim Spaces  Open Data Viewer Delimiter:  Escape:  Quotes:  Comment:  Locale:  NA:

Code Preview:

```
library(readr)  
iris <- read_csv("~/surfdrive/Projects/presentations/workshops/introduction-to-R-and-data-github/data/iris.csv")  
View(iris)
```

## Read flat files

---

```
> library(readr)  
> data_iris <- read_delim("data/iris.csv", delim=',')
```

## Read flat files

---

```
> library(readr)
> data_iris <- read_delim("data/iris.csv", delim=',')
Parsed with column specification:
cols(
  Sepal.Length = col_double(),
  Sepal.Width = col_double(),
  Petal.Length = col_double(),
  Petal.Width = col_double(),
  Species = col_character()
)
```

## Read flat files

---

```
> library(readr)
> data_iris <- read_csv("data/iris.csv")
Parsed with column specification:
cols(
  Sepal.Length = col_double(),
  Sepal.Width = col_double(),
  Petal.Length = col_double(),
  Petal.Width = col_double(),
  Species = col_character()
)
```

# Exercise dataset

---

- GPS data from 39 tagged individual cranes during fall migration of 2017
- Courtesy of Sasha Pekarsky at the Hebrew University of Jerusalem, Israel
- In the ‘data’ folder of your course materials.



# Exercises

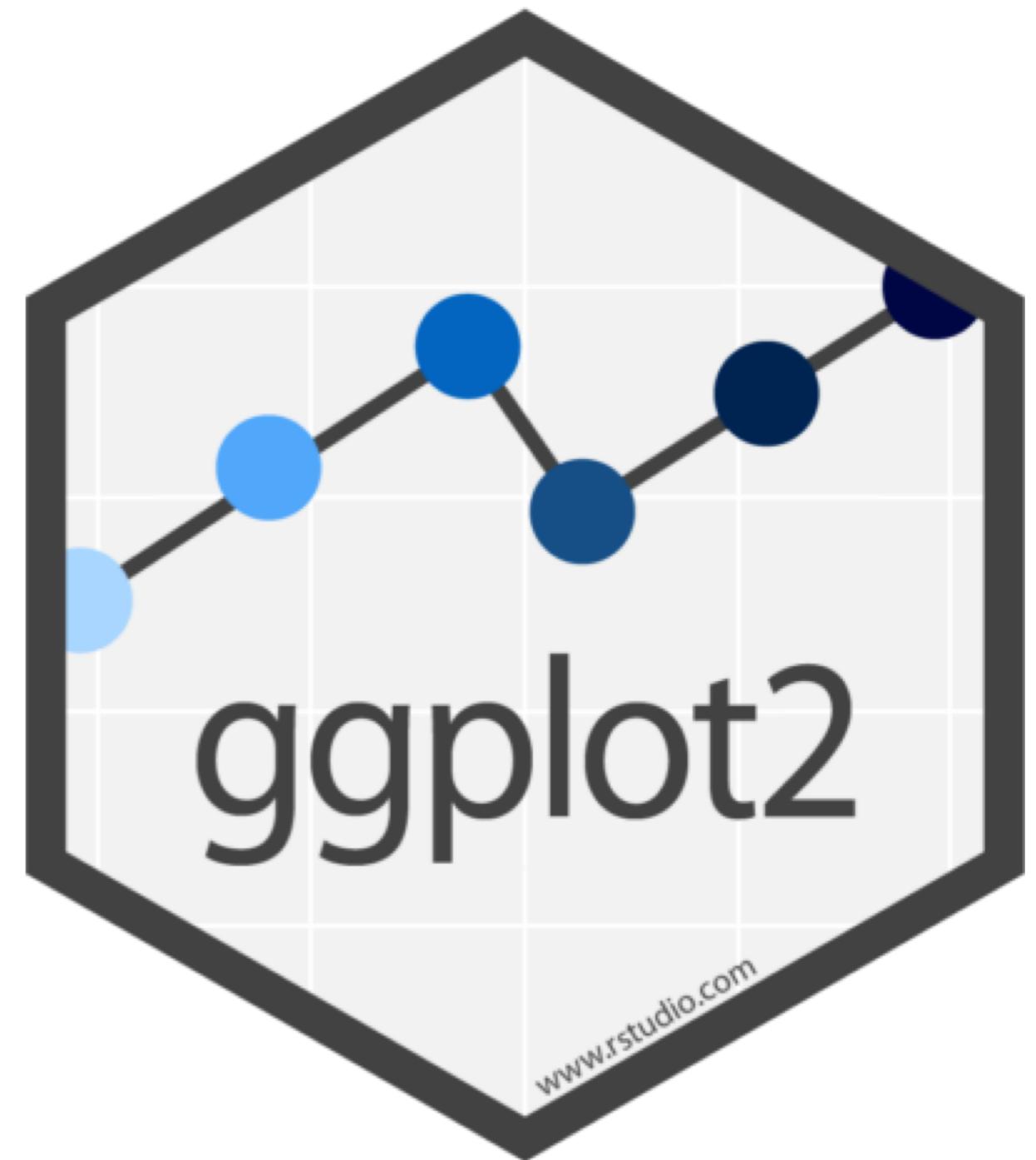
Please do basic exercises 1-I and 1-II.

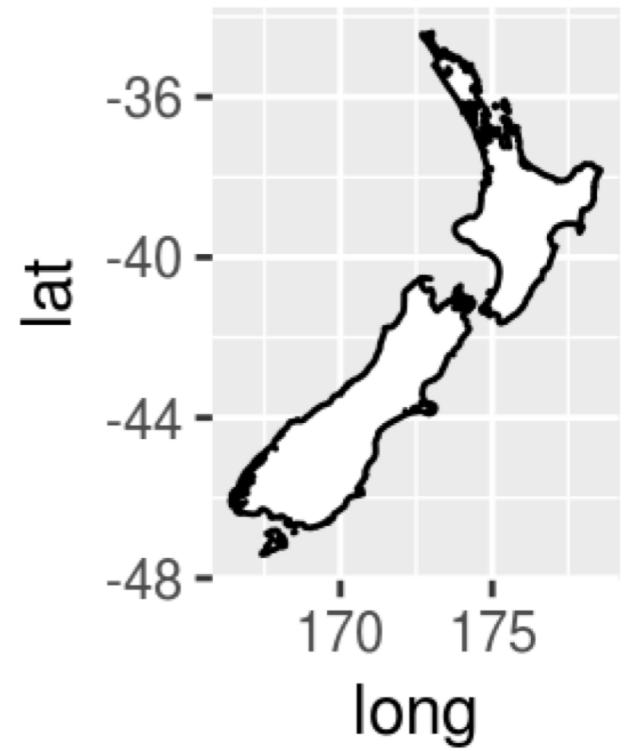
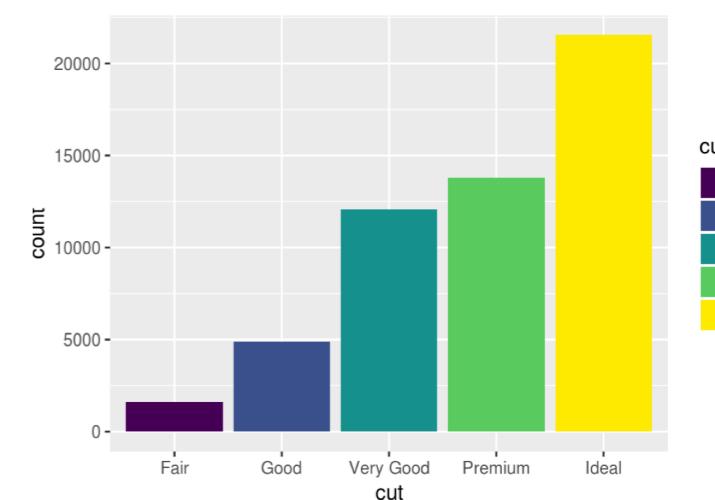
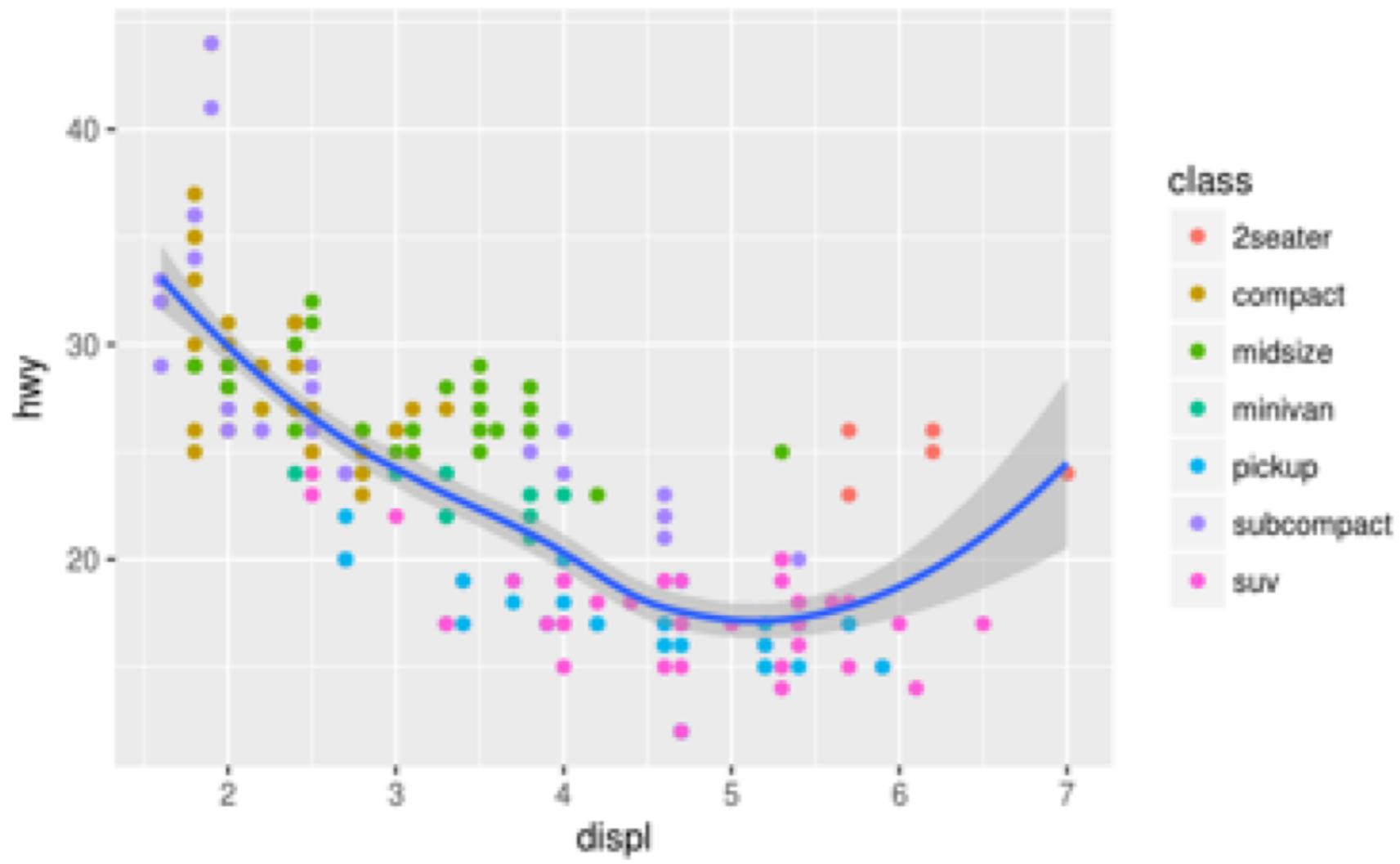
Time left? Opt for a reading exercise or optional exercise!

# Data visualisation

---

Create eye candy with ggplot2





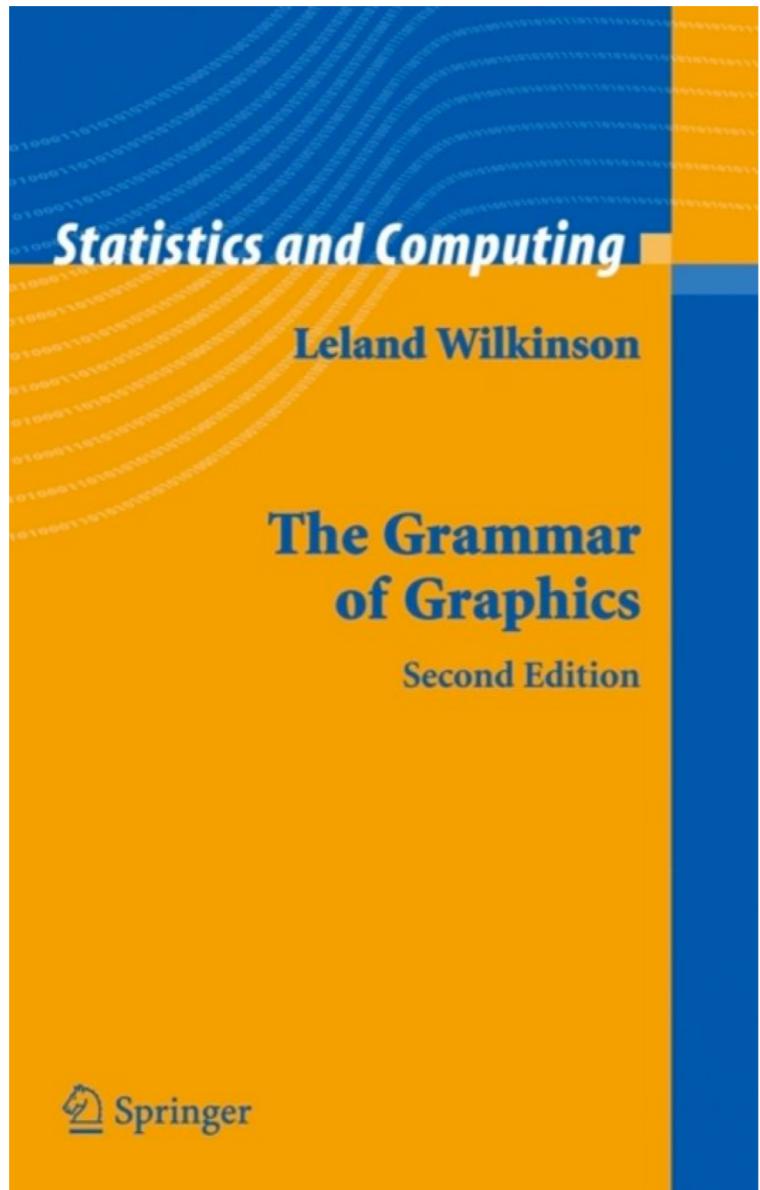
Examples of plots with R (and ggplot2)

# Data visualisation with ggplot2

---

- **ggplot2** is an extremely popular data visualisation package for R
- Simple syntax, easy to learn, nice plots
- Developed and maintained by Hadley Wickham
- Based on the book: The Grammar of Graphics (Wilkinson, 2005)

# The grammar of graphics



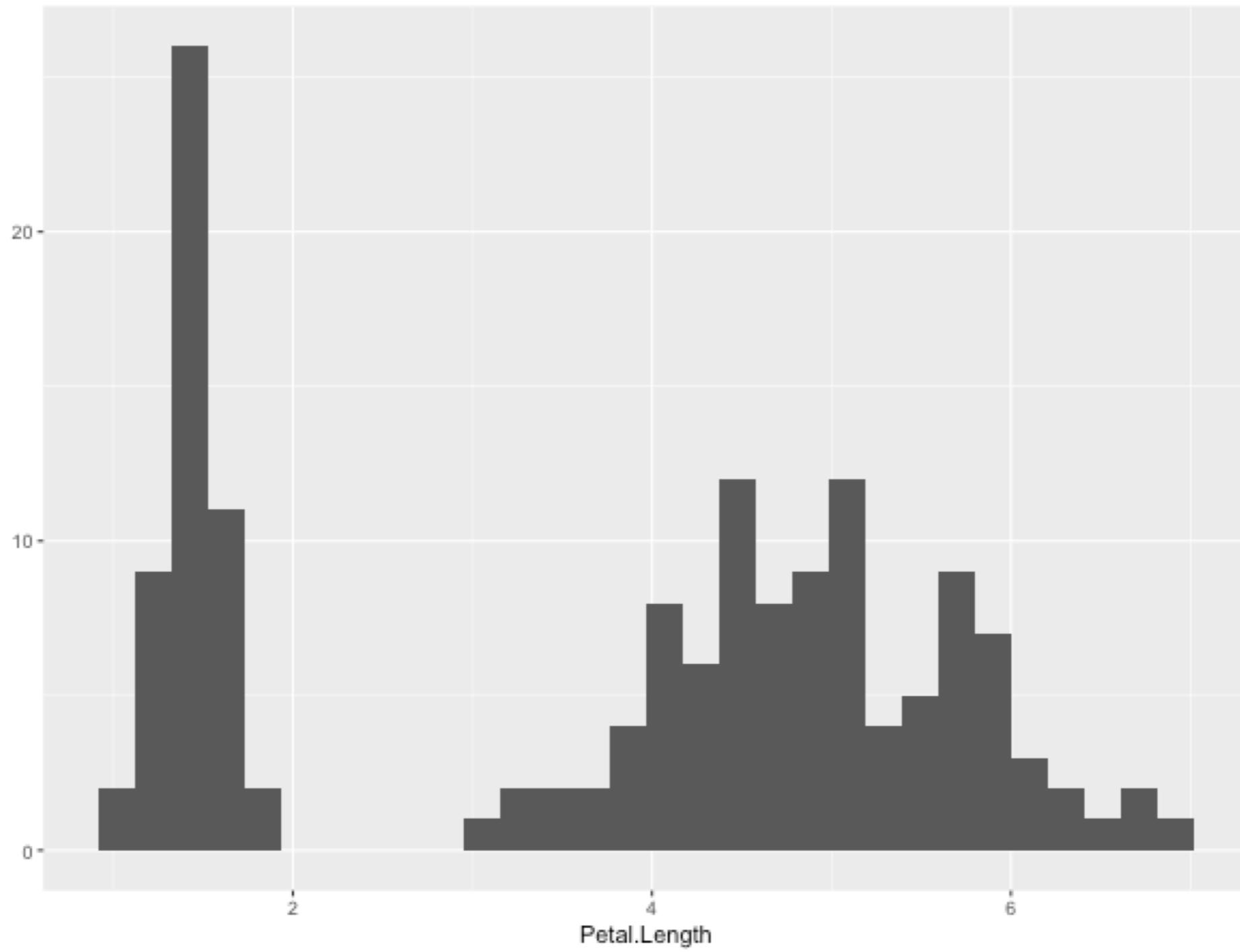
|            |   |
|------------|---|
| Data       | The variables in a tibble or data.frame   |
| Aesthetics | x- and y-axis, colour, size, alpha, shape |
| Geometries | point, line, bar, histogram               |

# Quick plotting

# Quick plots

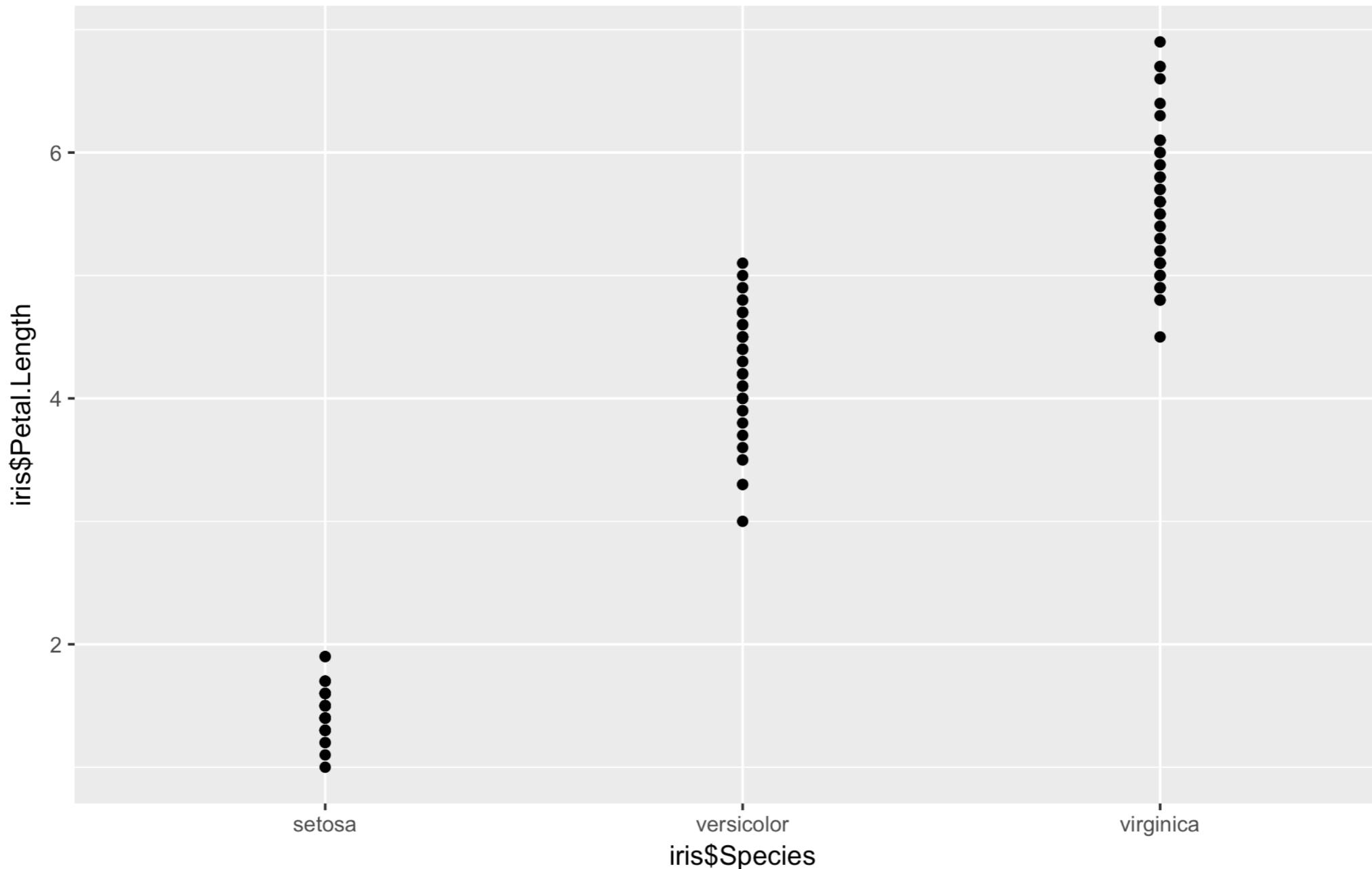
---

```
> qplot(Petal.Length, data = iris)
```



# Quick plots

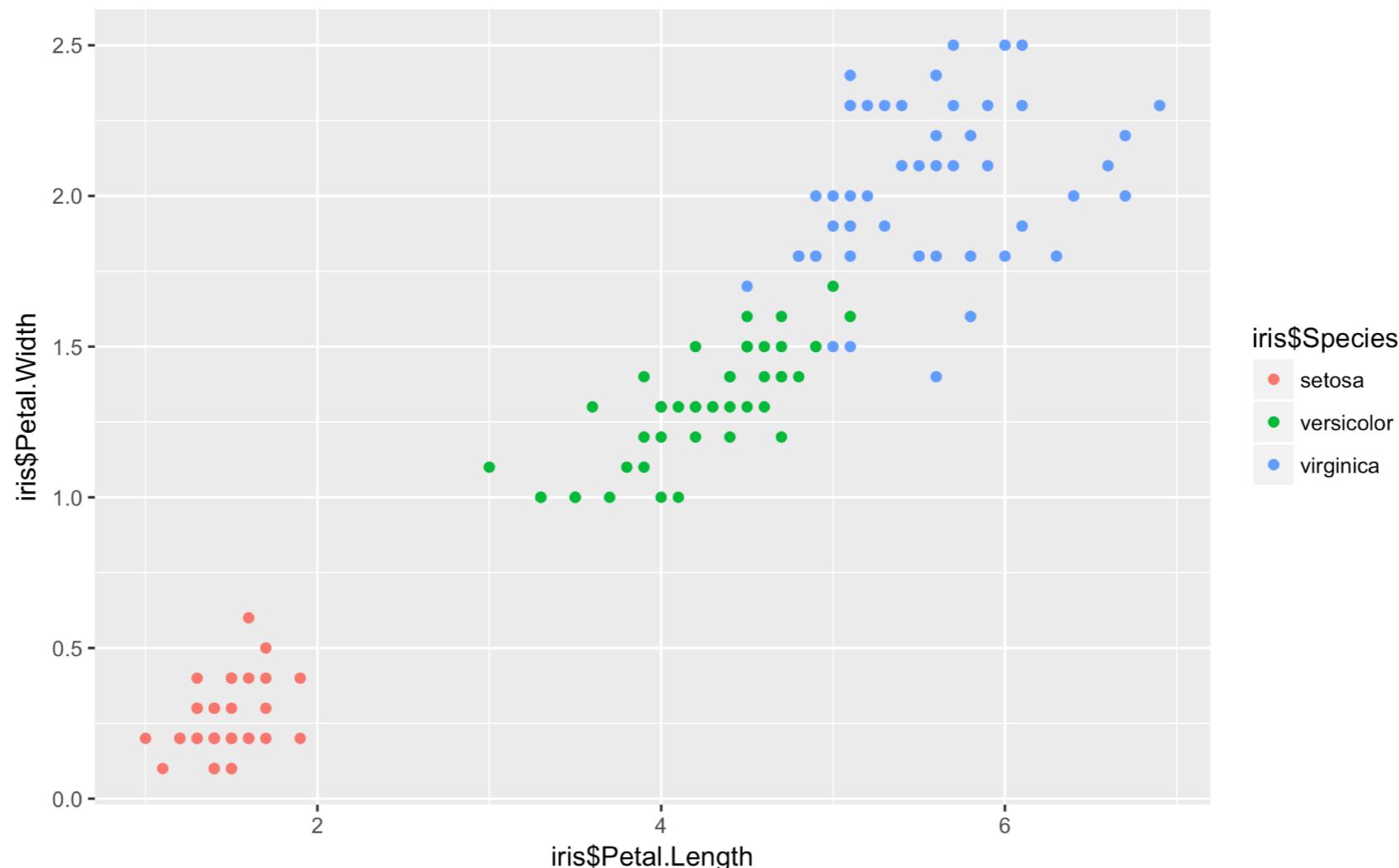
```
> qplot(Petal.Length, data = iris)
> qplot(Species, Petal.Length, data = iris)
```



# Quick plots

---

```
> qplot(Petal.Length, data = iris)
> qplot(Species, Petal.Length, data = iris)
> qplot(Petal.Length, Petal.Width, data = iris, colour=Species)
```

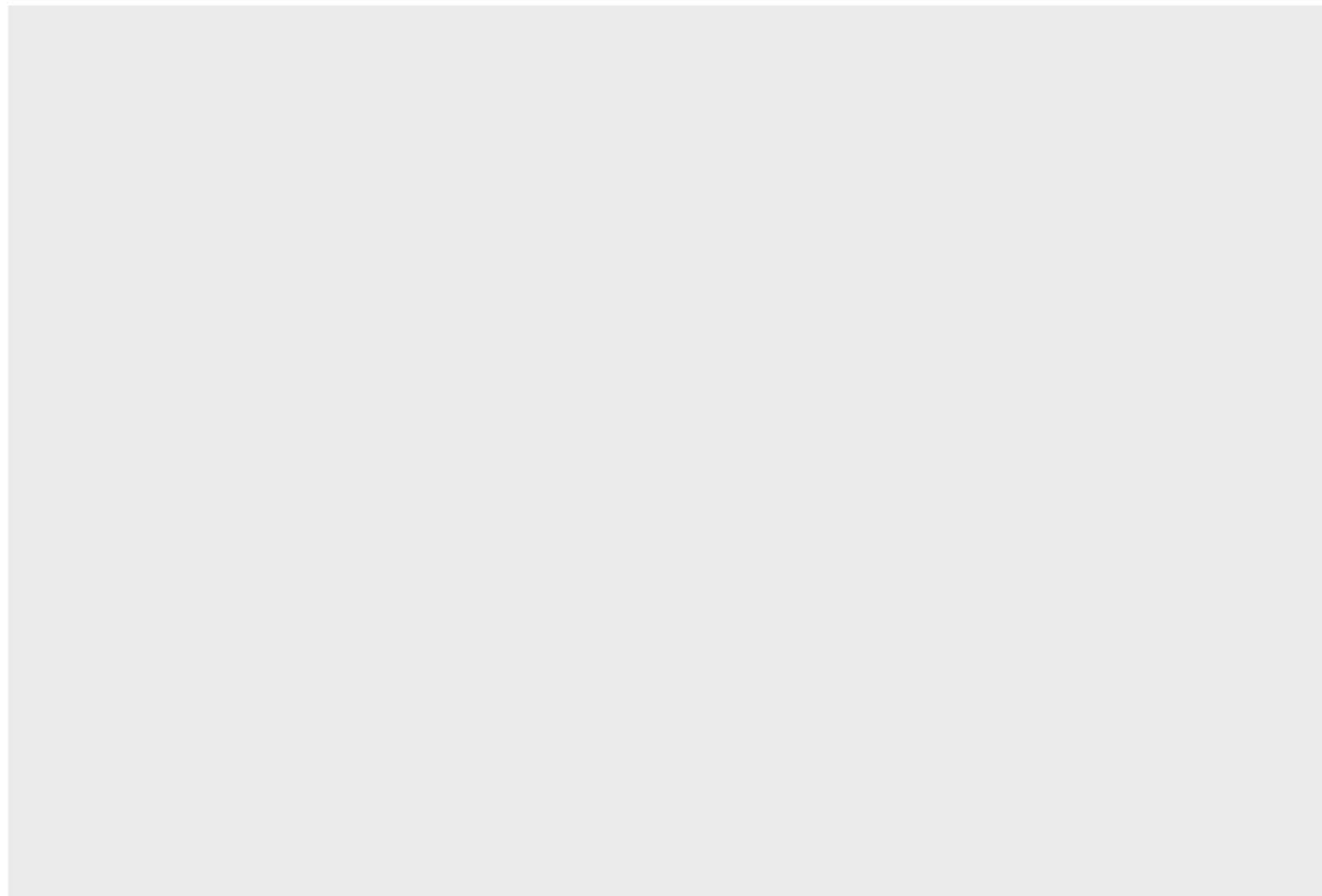


ggplot (grammar of graphics)

# ggplot: Data, aesthetics, geometrics

---

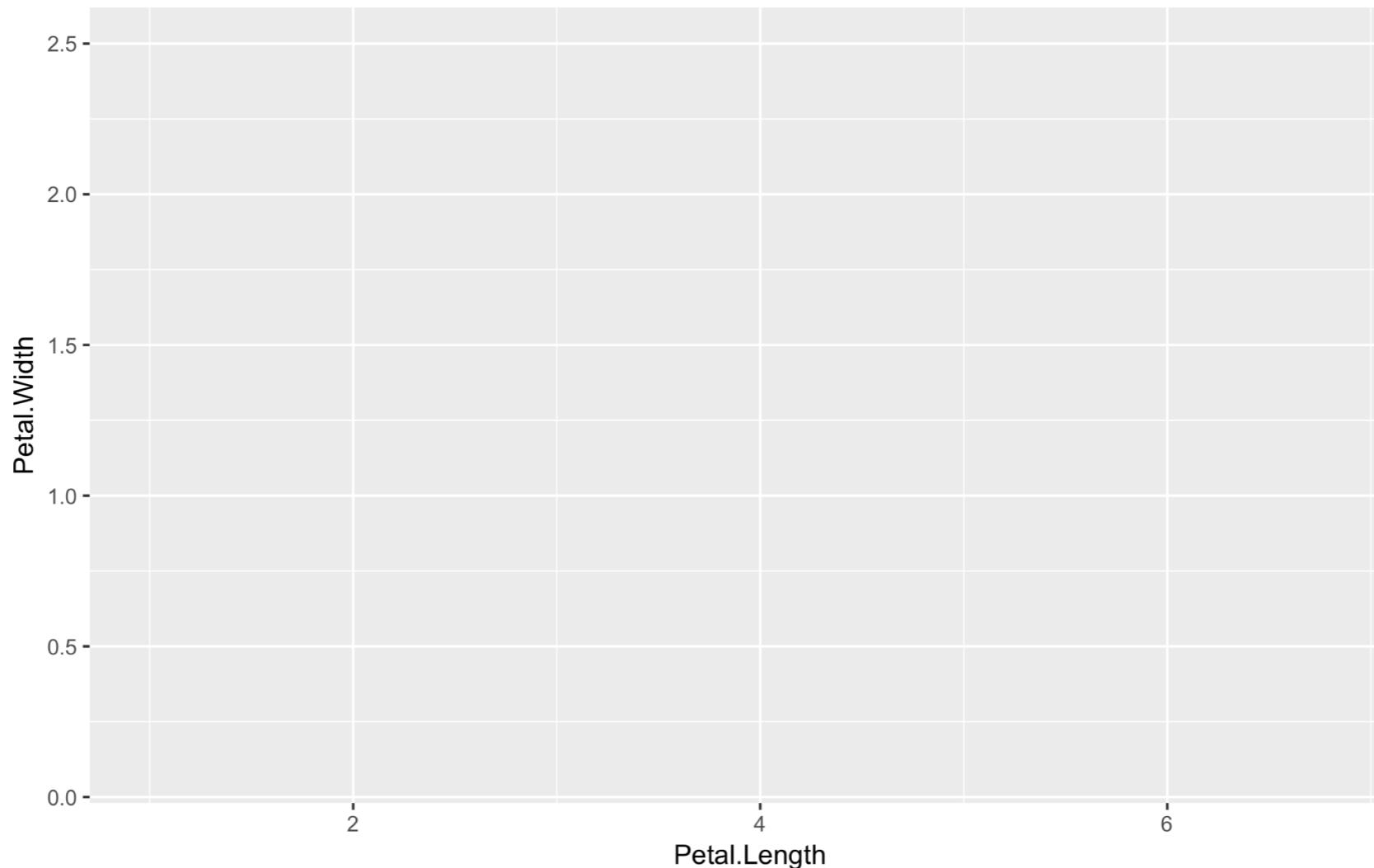
```
> ggplot(iris)
```



# ggplot: Data, aesthetics, geometrics

---

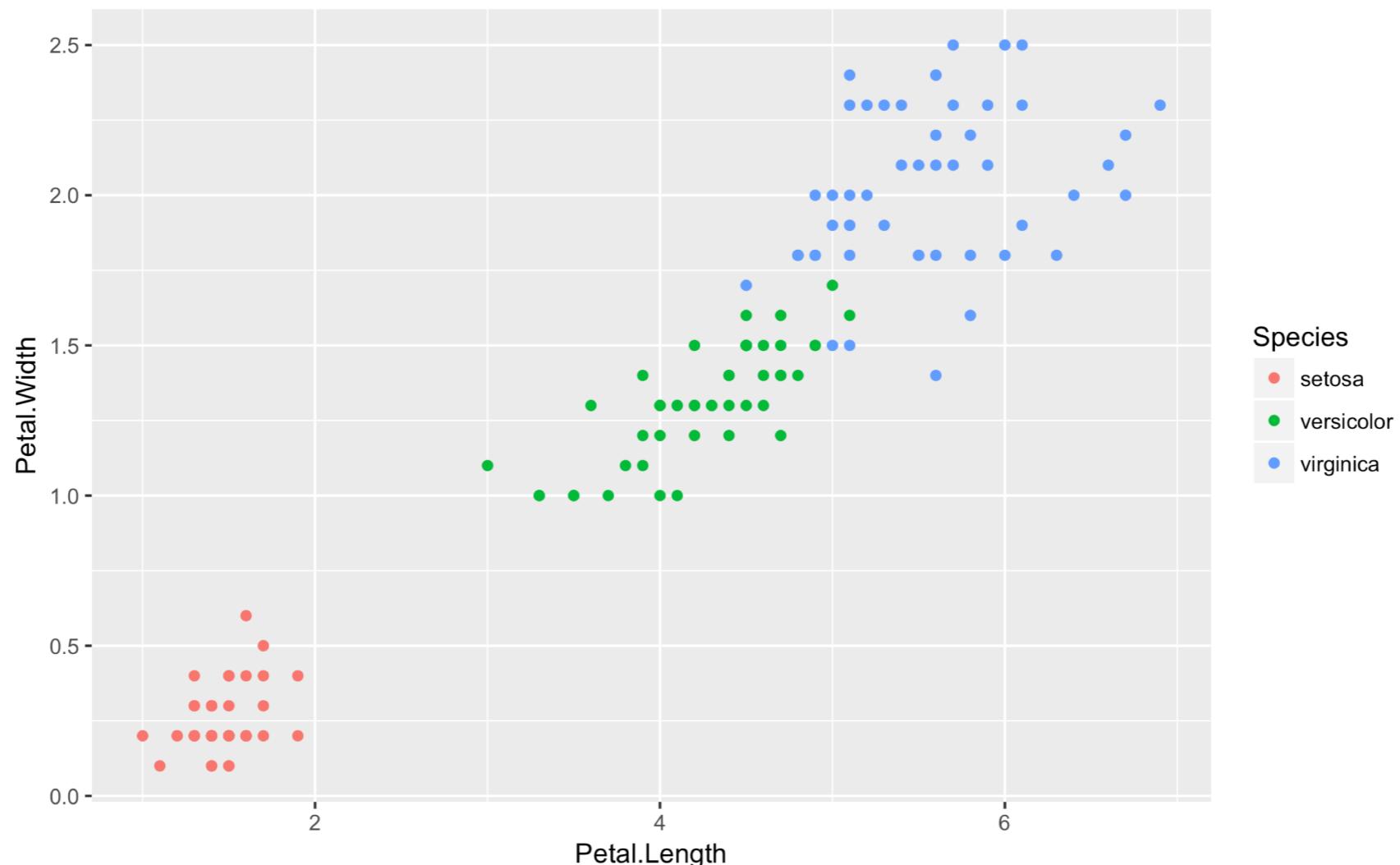
```
> ggplot(iris)  
> ggplot(iris, aes(x = Petal.Length, y = Petal.Width, colour=Species))
```



# ggplot: Data, aesthetics, geometrics

---

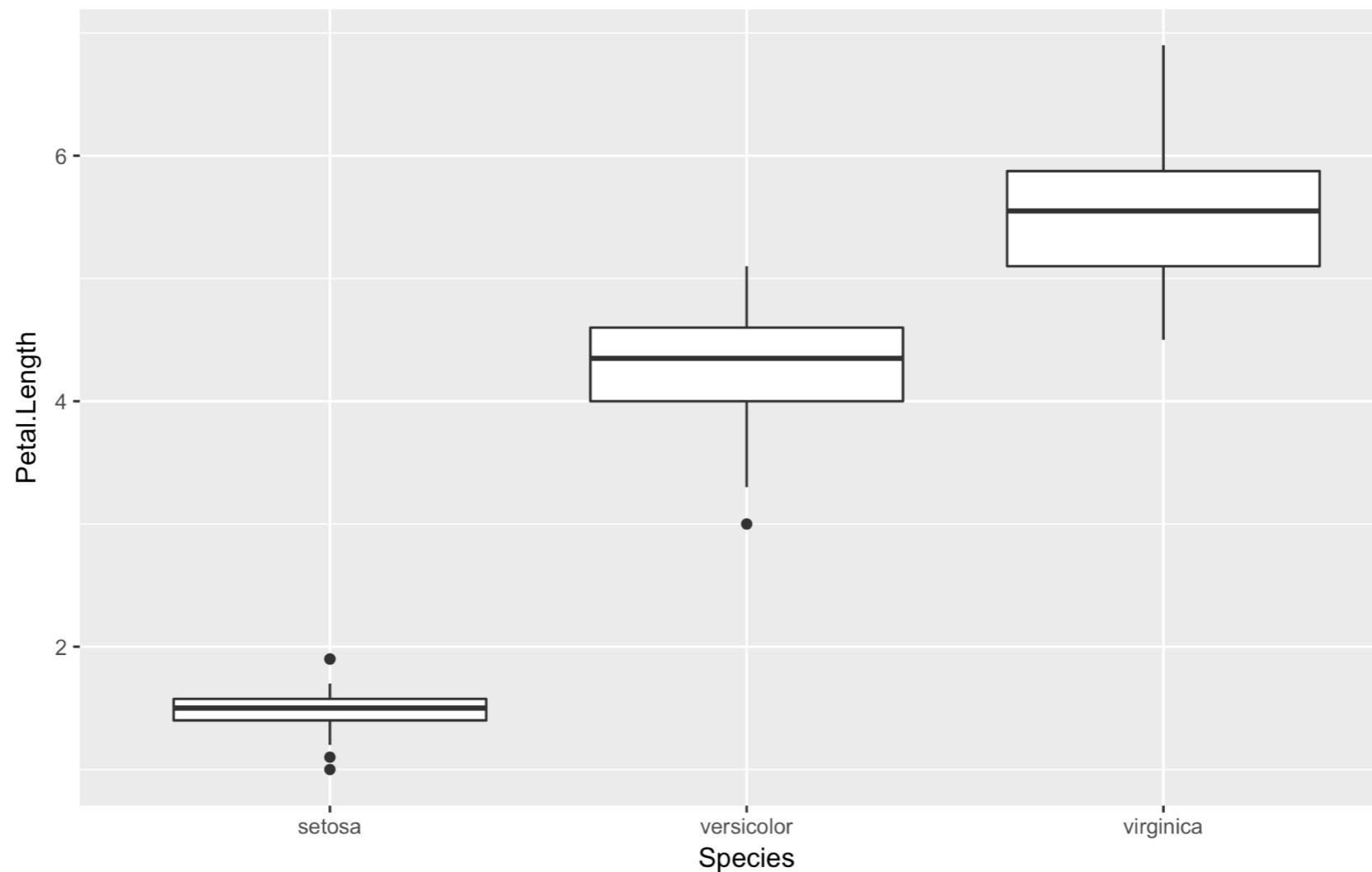
```
> ggplot(iris)  
> ggplot(iris, aes(x = Petal.Length, y = Petal.Width, colour=Species))  
> ggplot(iris, aes(x = Petal.Length, y = Petal.Width, colour=Species)) +  
  geom_point()
```



# ggplot: Multiple geometric layers

---

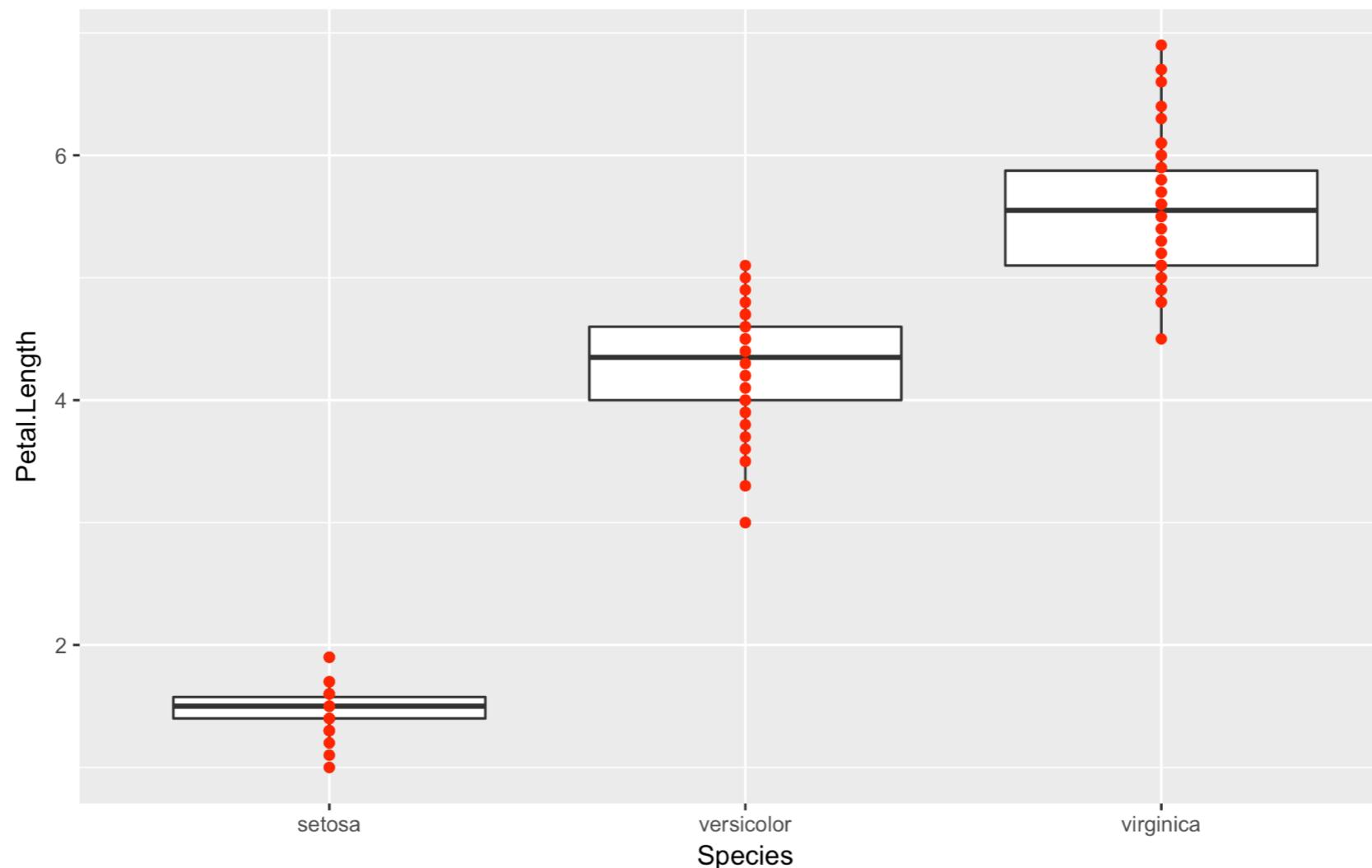
```
> ggplot(iris, aes(x = Species, y = Petal.Length)) +  
  geom_boxplot()
```



# ggplot: Multiple geometric layers

---

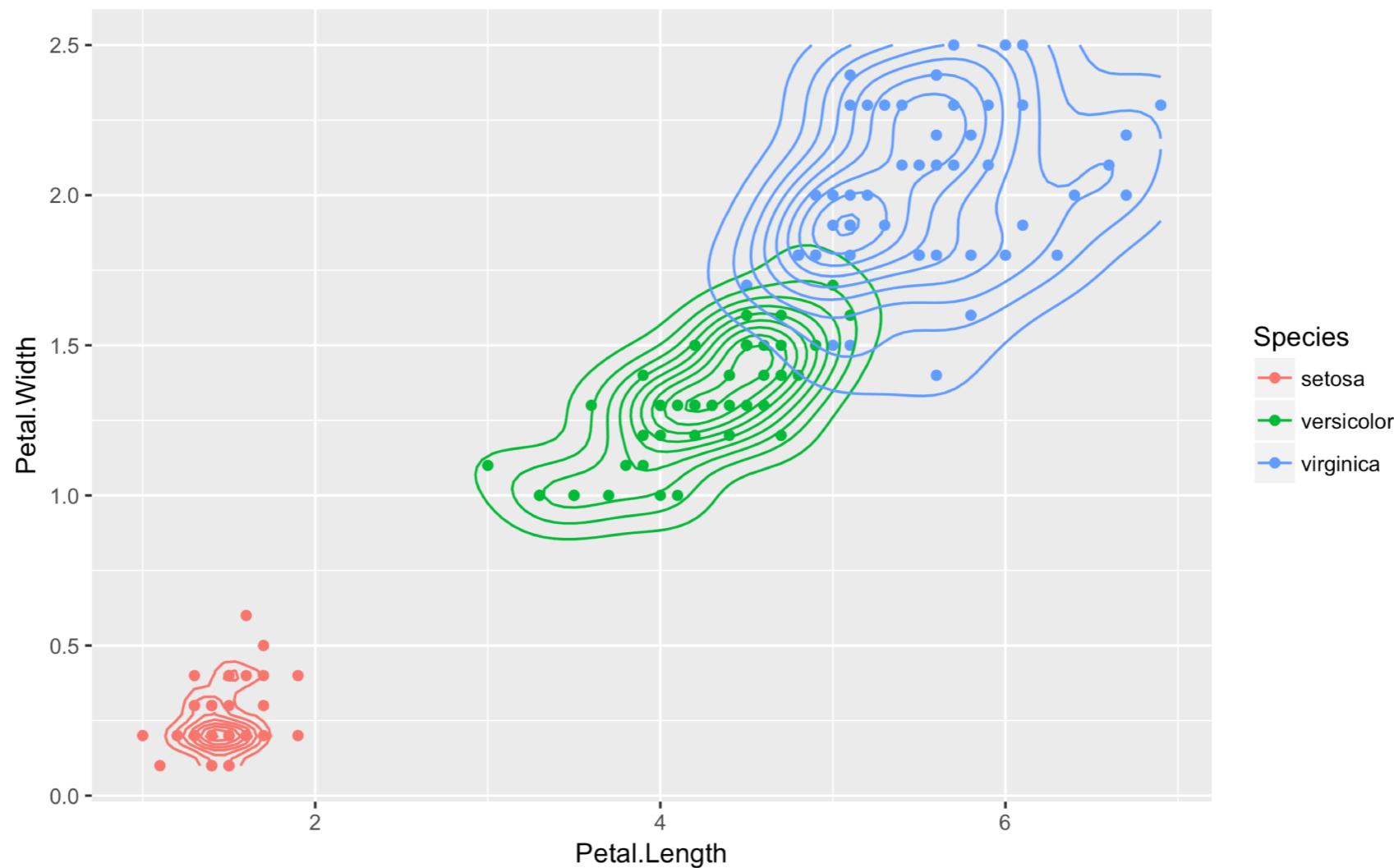
```
> ggplot(iris, aes(x = Species, y = Petal.Length)) +  
  geom_boxplot() +  
  geom_point(colour='red')
```



# ggplot: Statistical layers

---

```
> ggplot(iris, aes(x = Petal.Length, y = Petal.Width, colour=Species)) +  
  geom_point() +  
  stat_density_2d()
```



# Exercises

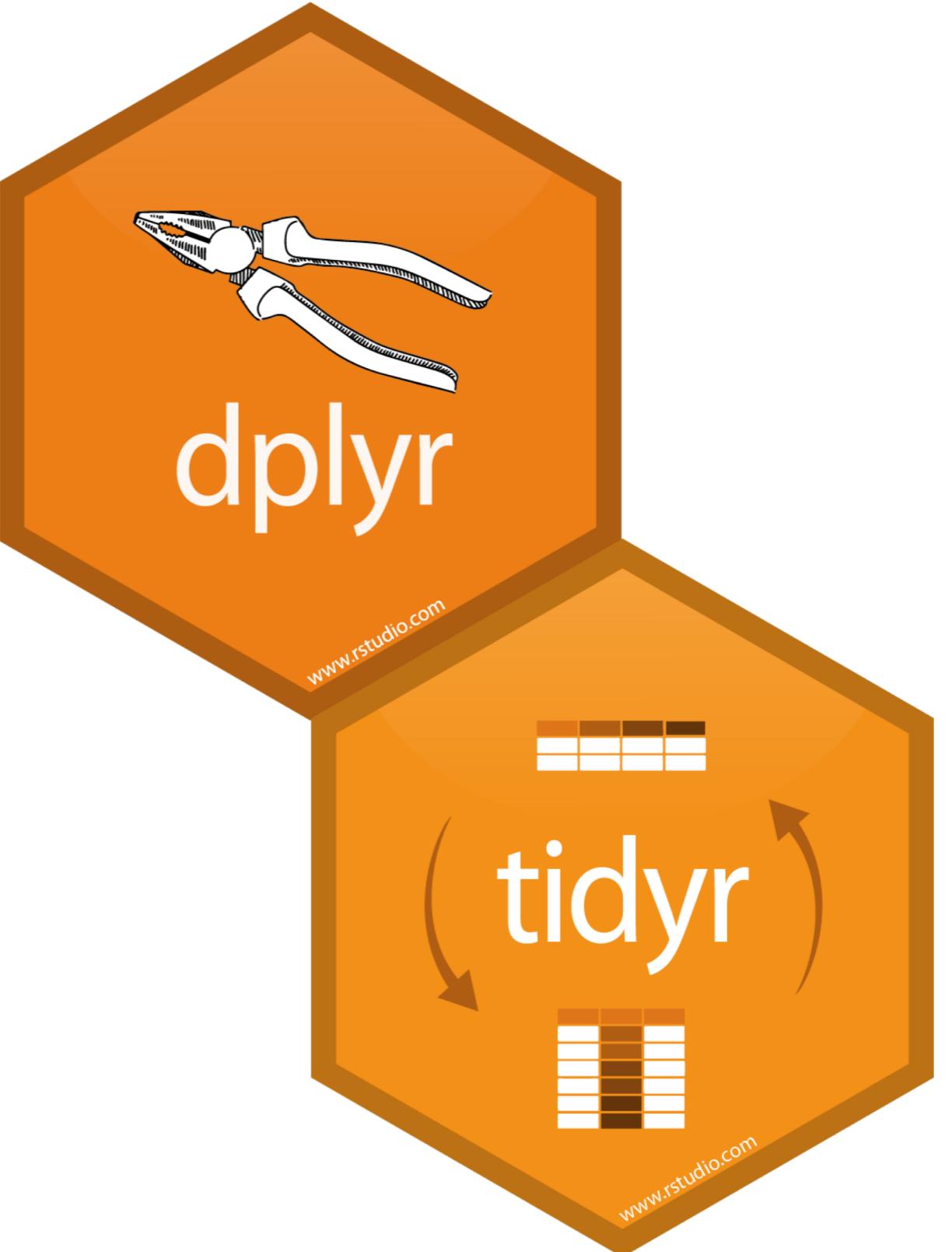
Please do basic exercises 2-I and 2-II.

Time left? Opt for a reading exercise or optional exercise!

# Data transformation

---

Explore the power of **dplyr** and **tidyr**



# Data Transformation with dplyr :: CHEAT SHEET



dplyr functions work with pipes and expect **tidy data**. In tidy data:



Each **variable** is in its own **column**



Each **observation**, or **case**, is in its own **row**

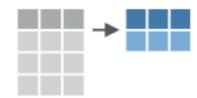


`x %>% f(y)` becomes `f(x, y)`

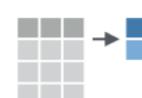
## Summarise Cases

These apply **summary functions** to columns to create a new table of summary statistics. Summary functions take vectors as input and return one value (see back).

### summary function



`summarise(.data, ...)`  
Compute table of summaries.  
`summarise(mtcars, avg = mean(mpg))`



`count(x, ..., wt = NULL, sort = FALSE)`  
Count number of rows in each group defined by the variables in ... Also **tally()**.  
`count(iris, Species)`

### VARIATIONS

`summarise_all()` - Apply funs to every column.

`summarise_at()` - Apply funs to specific columns.

`summarise_if()` - Apply funs to all cols of one type.

## Group Cases

Use **group\_by()** to create a "grouped" copy of a table.

dplyr functions will manipulate each "group" separately and then combine the results.



`mtcars %>%`  
`group_by(cyl) %>%`  
`summarise(avg = mean(mpg))`

`group_by(.data, ..., add = FALSE)`

Returns copy of table

grouped by ...

`g_iris <- group_by(iris, Species)`

`ungroup(x, ...)`

Returns ungrouped copy of table.

`ungroup(g_iris)`

## Manipulate Cases

### EXTRACT CASES

Row functions return a subset of rows as a new table.



`filter(.data, ...)` Extract rows that meet logical criteria. `filter(iris, Sepal.Length > 7)`



`distinct(.data, ..., .keep_all = FALSE)` Remove rows with duplicate values.  
`distinct(iris, Species)`



`sample_frac(tbl, size = 1, replace = FALSE, weight = NULL, .env = parent.frame())` Randomly select fraction of rows.  
`sample_frac(iris, 0.5, replace = TRUE)`



`sample_n(tbl, size, replace = FALSE, weight = NULL, .env = parent.frame())` Randomly select size rows.  
`sample_n(iris, 10, replace = TRUE)`



`slice(.data, ...)` Select rows by position.  
`slice(iris, 10:15)`

`top_n(x, n, wt)` Select and order top n entries (by group if grouped data).  
`top_n(iris, 5, Sepal.Width)`

### Logical and boolean operators to use with filter()

<      <=      is.na()      %in%      |      xor()  
>      >=      !is.na()      !      &

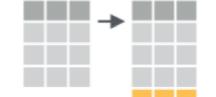
See `?base::logic` and `?Comparison` for help.

### ARRANGE CASES



`arrange(.data, ...)` Order rows by values of a column or columns (low to high), use with `desc()` to order from high to low.  
`arrange(mtcars, mpg)`  
`arrange(mtcars, desc(mpg))`

### ADD CASES



`add_row(.data, ..., .before = NULL, .after = NULL)`  
Add one or more rows to a table.  
`add_row(faithful, eruptions = 1, waiting = 1)`

## Manipulate Variables

### EXTRACT VARIABLES

Column functions return a set of columns as a new vector or table.



`pull(.data, var = -1)` Extract column values as a vector. Choose by name or index.  
`pull(iris, Sepal.Length)`



`select(.data, ...)`  
Extract columns as a table. Also `select_if()`.  
`select(iris, Sepal.Length, Species)`

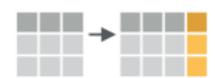
Use these helpers with `select()`,  
e.g. `select(iris, starts_with("Sepal"))`

`contains(match)`    `num_range(prefix, range)` ;, e.g. `mpg:cyl`  
`ends_with(match)`    `one_of(...)`  
`matches(match)`    `starts_with(match)` -, e.g. `-Species`

### MAKE NEW VARIABLES

These apply **vectorized functions** to columns. Vectorized funs take vectors as input and return vectors of the same length as output (see back).

### vectorized function



`mutate(.data, ...)`  
Compute new column(s).  
`mutate(mtcars, gpm = 1/mpg)`



`transmute(.data, ...)`  
Compute new column(s), drop others.  
`transmute(mtcars, gpm = 1/mpg)`



`mutate_all(.tbl, .funs, ...)` Apply funs to every column. Use with `funs()`. Also `mutate_if()`.  
`mutate_all(faithful, funs(log(.), log2(.)))`  
`mutate_if(iris, is.numeric, funs(log(.)))`



`mutate_at(.tbl, .cols, .funs, ...)` Apply funs to specific columns. Use with `funs()`, `vars()` and the helper functions for `select()`.  
`mutate_at(iris, vars(-Species), funs(log(.)))`



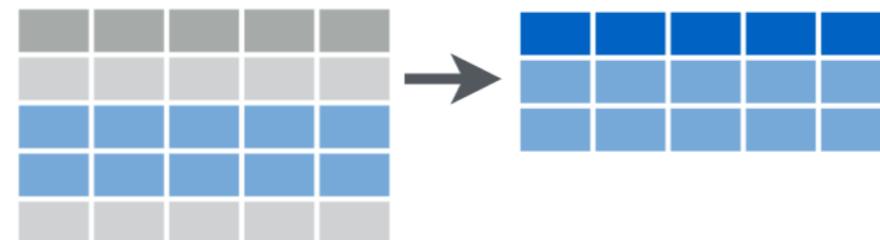
`add_column(.data, ..., .before = NULL, .after = NULL)` Add new column(s). Also `add_count()`, `add_tally()`.  
`add_column(mtcars, new = 1:32)`



`rename(.data, ...)` Rename columns.  
`rename(iris, Length = Sepal.Length)`

`filter()`

## Subset Observations (Rows)



## Function: filter()

---

```
> filter(iris, Species=="virginica")
```

## Function: filter()

---

```
> filter(iris, Species=="virginica")
# A tibble: 50 x 5
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
        <dbl>       <dbl>       <dbl>       <dbl>   <fct>
1       6.30       3.30       6.00       2.50 virginica
2       5.80       2.70       5.10       1.90 virginica
3       7.10       3.00       5.90       2.10 virginica
4       6.30       2.90       5.60       1.80 virginica
5       6.50       3.00       5.80       2.20 virginica
6       7.60       3.00       6.60       2.10 virginica
7       4.90       2.50       4.50       1.70 virginica
8       7.30       2.90       6.30       1.80 virginica
9       6.70       2.50       5.80       1.80 virginica
10      7.20       3.60       6.10       2.50 virginica
# ... with 40 more rows
```

## Function: filter()

---

```
> filter(iris, Species=="virginica", Sepal.Length>= 7.5)
```

## Function: filter()

---

```
> filter(iris, Species=="virginica", Sepal.Length>= 7.5)
# A tibble: 6 x 5
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
        <dbl>       <dbl>       <dbl>       <dbl>   <fct>
1       7.60       3.00       6.60       2.10 virginica
2       7.70       3.80       6.70       2.20 virginica
3       7.70       2.60       6.90       2.30 virginica
4       7.70       2.80       6.70       2.00 virginica
5       7.90       3.80       6.40       2.00 virginica
6       7.70       3.00       6.10       2.30 virginica
```

## Function: filter()

---

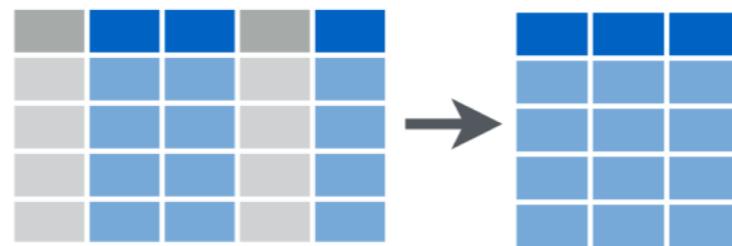
```
> filter(iris, Species=="virginica", Sepal.Length>= 7.5)
# A tibble: 6 x 5
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
        <dbl>       <dbl>      <dbl>      <dbl>   <fct>
1       7.60       3.00      6.60      2.10 virginica
2       7.70       3.80      6.70      2.20 virginica
3       7.70       2.60      6.90      2.30 virginica
4       7.70       2.80      6.70      2.00 virginica
5       7.90       3.80      6.40      2.00 virginica
6       7.70       3.00      6.10      2.30 virginica
```

Same as:

```
> filter(iris, Species=="virginica" & Sepal.Length>= 7.5)
```

`select()`

## Subset Variables (Columns)



## Function: select()

---

```
> select(iris, Sepal.Length, Sepal.Width, Species)
```

## Function: select()

---

```
> select(iris, Sepal.Length, Sepal.Width, Species)
# A tibble: 150 × 3
  Sepal.Length Sepal.Width Species
        <dbl>       <dbl> <fct>
1         5.10       3.50 setosa
2         4.90       3.00 setosa
3         4.70       3.20 setosa
4         4.60       3.10 setosa
5         5.00       3.60 setosa
6         5.40       3.90 setosa
7         4.60       3.40 setosa
8         5.00       3.40 setosa
9         4.40       2.90 setosa
10        4.90       3.10 setosa
# ... with 140 more rows
```

## Function: select()

---

```
> select(iris, Sepal.Length, Sepal.Width, Species)  
> select(iris, starts_with("Sepal"), Species)
```

## Function: select()

---

```
> select(iris, Sepal.Length, Sepal.Width, Species)
> select(iris, starts_with("Sepal"), Species)
# A tibble: 150 × 3
  Sepal.Length Sepal.Width Species
        <dbl>      <dbl> <fct>
1         5.10      3.50 setosa
2         4.90      3.00 setosa
3         4.70      3.20 setosa
4         4.60      3.10 setosa
5         5.00      3.60 setosa
6         5.40      3.90 setosa
7         4.60      3.40 setosa
8         5.00      3.40 setosa
9         4.40      2.90 setosa
10        4.90      3.10 setosa
# ... with 140 more rows
```

## Function: select()

---

```
> select(iris, Sepal.Length, Sepal.Width, Species)
> select(iris, starts_with("Sepal"), Species)
> select(iris, -starts_with("Petal"))
```

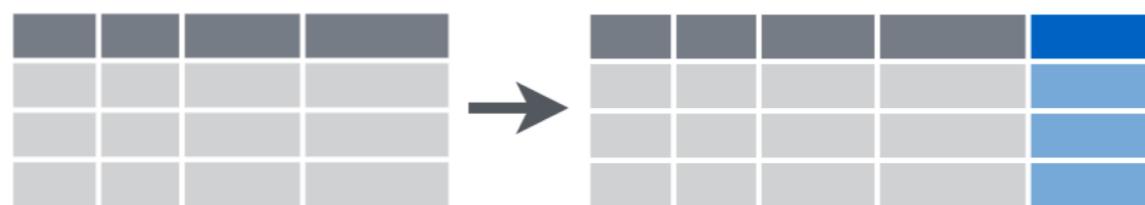
## Function: select()

---

```
> select(iris, Sepal.Length, Sepal.Width, Species)
> select(iris, starts_with("Sepal"), Species)
> select(iris, -starts_with("Petal"))
# A tibble: 150 × 3
  Sepal.Length Sepal.Width Species
        <dbl>      <dbl> <fct>
1         5.10      3.50 setosa
2         4.90      3.00 setosa
3         4.70      3.20 setosa
4         4.60      3.10 setosa
5         5.00      3.60 setosa
6         5.40      3.90 setosa
7         4.60      3.40 setosa
8         5.00      3.40 setosa
9         4.40      2.90 setosa
10        4.90      3.10 setosa
# ... with 140 more rows
```

`mutate()`

## Make New Variables



## Function: mutate()

---

```
> mutate(iris,  
       petal_area = pi * Petal.Length/2 * Petal.Width/2)
```

# Function: mutate()

---

```
> mutate(iris,
        petal_area = pi * Petal.Length/2 * Petal.Width/2)
# A tibble: 150 x 6
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species  petal_area
          <dbl>       <dbl>        <dbl>       <dbl> <fct>      <dbl>
1         5.1        3.5         1.4        0.2 setosa     0.220
2         4.9        3.0         1.4        0.2 setosa     0.220
3         4.7        3.2         1.3        0.2 setosa     0.204
4         4.6        3.1         1.5        0.2 setosa     0.236
5         5.0        3.6         1.4        0.2 setosa     0.220
6         5.4        3.9         1.7        0.4 setosa     0.534
7         4.6        3.4         1.4        0.3 setosa     0.330
8         5.0        3.4         1.5        0.2 setosa     0.236
9         4.4        2.9         1.4        0.2 setosa     0.220
10        4.9        3.1         1.5        0.1 setosa     0.118
# ... with 140 more rows
```

## Function: mutate()

---

```
> mutate(iris,  
        # compute the area of a single petal  
        petal_area = pi * Petal.Length/2 * Petal.Width/2,  
        # abbreviate the name of the species  
        Species_abbr = substring(Species, 1, 3)  
)
```

# Function: mutate()

---

```
> mutate(iris,
  # compute the area of a single petal
  petal_area = pi * Petal.Length/2 * Petal.Width/2,
  # abbreviate the name of the species
  Species_abbr = substring(Species, 1, 3)
)
# A tibble: 150 x 7
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species petal_area Species_abbr
  <dbl>       <dbl>        <dbl>        <dbl> <fct>      <dbl> <chr>
1     5.1        3.5         1.4         0.2 setosa      0.220 set 
2     4.9        3           1.4         0.2 setosa      0.220 set 
3     4.7        3.2         1.3         0.2 setosa      0.204 set 
4     4.6        3.1         1.5         0.2 setosa      0.236 set 
5     5           3.6         1.4         0.2 setosa      0.220 set 
6     5.4        3.9         1.7         0.4 setosa      0.534 set 
7     4.6        3.4         1.4         0.3 setosa      0.330 set 
8     5           3.4         1.5         0.2 setosa      0.236 set 
9     4.4        2.9         1.4         0.2 setosa      0.220 set 
10    4.9        3.1         1.5         0.1 setosa      0.118 set 
# ... with 140 more rows
```

# gather() and spread()



**tidy::gather(cases, "year", "n", 2:4)**  
Gather columns into rows.



**tidy::spread(pollution, size, amount)**  
Spread rows into columns.

# Tidy data is long data

---

- Each **variable** is a column and contains **values**
- Each **observation** is a row
- Each type of **observational unit** forms a table

| Patient | Temp | Med_A | Temp_A | Med_B | Temp_B |
|---------|------|-------|--------|-------|--------|
| 122030  | 37.0 | 300   | 37.1   | NA    | NA     |
| 122021  | 38.2 | 200   | 38.1   | 85    | 36.5   |
| 124500  | 38.1 | 300   | 38.0   | NA    | NA     |
| 126098  | 39.1 | NA    | NA     | 100   | 36.8   |

# Wide and long data

---

```
# A tibble: 150 x 6
  Species observation Petal.Length Petal.Width Sepal.Length Sepal.Width
  <chr>     <int>        <dbl>      <dbl>       <dbl>      <dbl>
1 setosa      1         1.40      0.200      5.10      3.50
2 setosa      2         1.40      0.200      4.90      3.00
3 setosa      3         1.30      0.200      4.70      3.20
4 setosa      4         1.50      0.200      4.60      3.10
5 setosa      5         1.40      0.200      5.00      3.60
6 setosa      6         1.70      0.400      5.40      3.90
7 setosa      7         1.40      0.300      4.60      3.40
8 setosa      8         1.50      0.200      5.00      3.40
9 setosa      9         1.40      0.200      4.40      2.90
10 setosa     10        1.50      0.100     4.90      3.10
# ... with 140 more rows
```

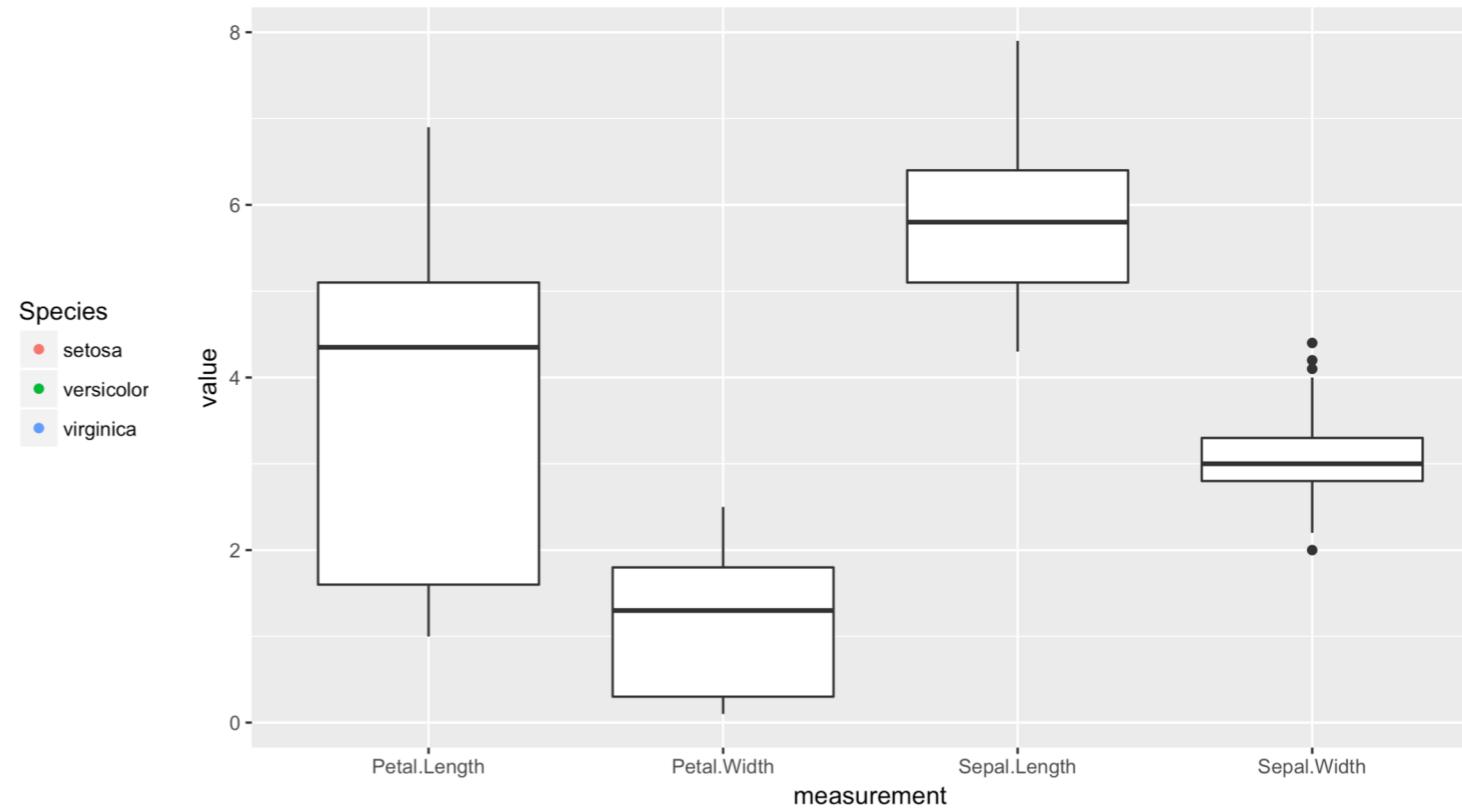
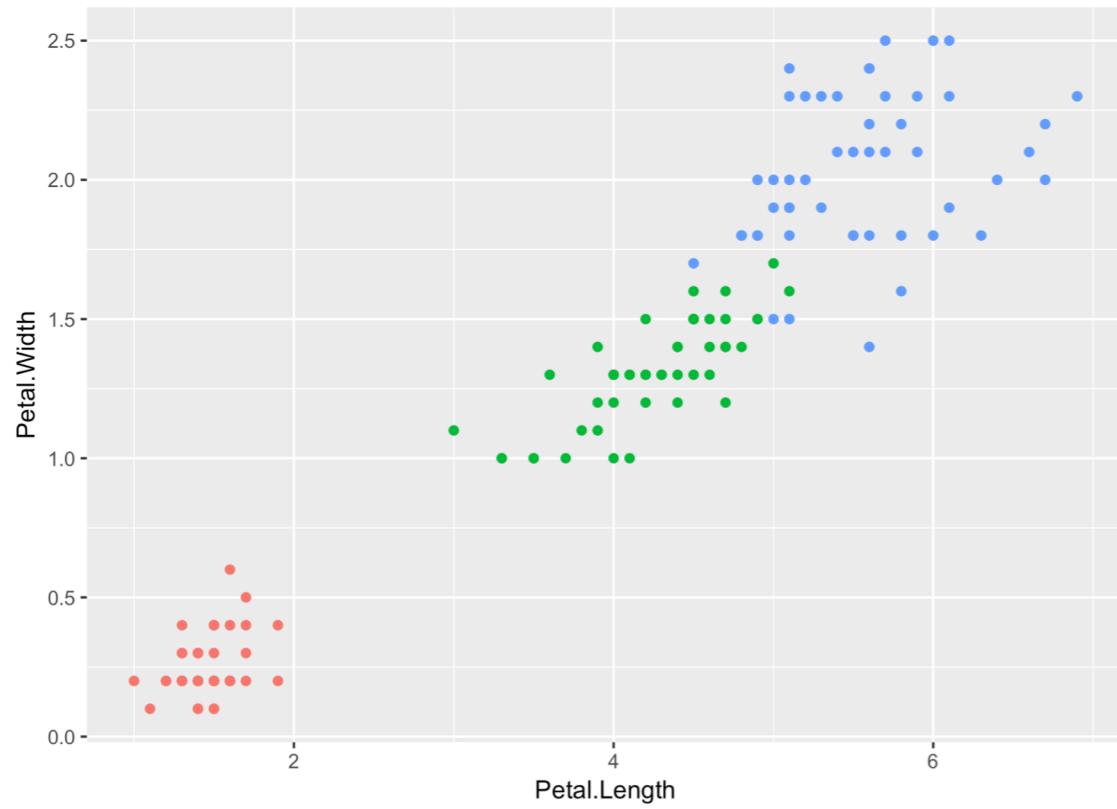
```
# A tibble: 600 x 4
  Species observation measurement value
  <chr>     <int>      <chr>      <dbl>
1 setosa      1 Sepal.Length 5.10
2 setosa      1 Sepal.Width  3.50
3 setosa      1 Petal.Length 1.40
4 setosa      1 Petal.Width  0.200
5 setosa      2 Sepal.Length 4.90
6 setosa      2 Sepal.Width  3.00
7 setosa      2 Petal.Length 1.40
8 setosa      2 Petal.Width  0.200
9 setosa      3 Sepal.Length 4.70
10 setosa     3 Sepal.Width  3.20
# ... with 590 more rows
```

- More information per row
  - Combines all measurements on a single individual
  - Necessary to plot matching measurements
- More information per column
  - No values as column headers (tidy)
  - Single observation in single row (tidy)
  - Necessary to plot large amounts of data in a single plot

# Wide

# vs.

# Long



- More information per row
- Combines all measurements on a single individual
- **Necessary to plot matching measurements**

- More information per column
- No values as column headers (tidy)
- Single observation in single row (tidy)
- **Necessary to plot large amounts of data in a single plot**

# Function: gather()

```
> iris_obs <- mutate(iris, observation = 1:n())
> iris_obs
# A tibble: 150 x 6
#>   Sepal.Length Sepal.Width Petal.Length Petal.Width Species observation
#>   <dbl>       <dbl>      <dbl>       <dbl>    <chr>        <int>
#> 1     5.10      3.50       1.40      0.200  setosa         1
#> 2     4.90      3.00       1.40      0.200  setosa         2
#> 3     4.70      3.20       1.30      0.200  setosa         3
#> 4     4.60      3.10       1.50      0.200  setosa         4
#> 5     5.00      3.60       1.40      0.200  setosa         5
#> 6     5.40      3.90       1.70      0.400  setosa         6
#> 7     4.60      3.40       1.40      0.300  setosa         7
#> 8     5.00      3.40       1.50      0.200  setosa         8
#> 9     4.40      2.90       1.40      0.200  setosa         9
#> 10    4.90      3.10       1.50      0.100  setosa        10
# ... with 140 more rows
```

headers

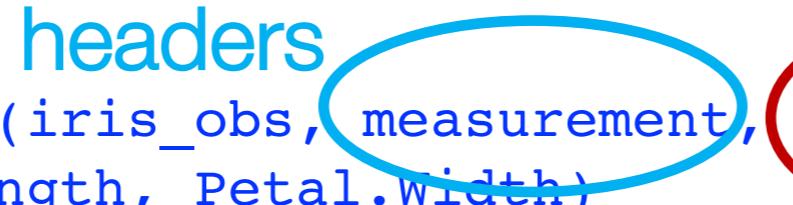
|    | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species | observation |
|----|--------------|-------------|--------------|-------------|---------|-------------|
|    | <dbl>        | <dbl>       | <dbl>        | <dbl>       | <chr>   | <int>       |
| 1  | 5.10         | 3.50        | 1.40         | 0.200       | setosa  | 1           |
| 2  | 4.90         | 3.00        | 1.40         | 0.200       | setosa  | 2           |
| 3  | 4.70         | 3.20        | 1.30         | 0.200       | setosa  | 3           |
| 4  | 4.60         | 3.10        | 1.50         | 0.200       | setosa  | 4           |
| 5  | 5.00         | 3.60        | 1.40         | 0.200       | setosa  | 5           |
| 6  | 5.40         | 3.90        | 1.70         | 0.400       | setosa  | 6           |
| 7  | 4.60         | 3.40        | 1.40         | 0.300       | setosa  | 7           |
| 8  | 5.00         | 3.40        | 1.50         | 0.200       | setosa  | 8           |
| 9  | 4.40         | 2.90        | 1.40         | 0.200       | setosa  | 9           |
| 10 | 4.90         | 3.10        | 1.50         | 0.100       | setosa  | 10          |

content

# Function: gather()

```
> iris_obs <- mutate(iris, observation = 1:n())
> iris_obs
> iris_long <- gather(iris_obs, measurement, value, Sepal.Length,
Sepal.Width, Petal.Length, Petal.Width)
> iris_long
# A tibble: 600 x 4
  Species observation measurement value
  <chr>       <int> <chr>      <dbl>
1 setosa         1 Sepal.Length 5.10 
2 setosa         1 Sepal.Width  3.50 
3 setosa         1 Petal.Length 1.40 
4 setosa         1 Petal.Width  0.200
5 setosa         2 Sepal.Length 4.90 
6 setosa         2 Sepal.Width  3.00 
7 setosa         2 Petal.Length 1.40 
8 setosa         2 Petal.Width  0.200
9 setosa         3 Sepal.Length 4.70 
10 setosa        3 Sepal.Width  3.20
# ... with 590 more rows
```

headers content



| Species   | observation | measurement  | value |
|-----------|-------------|--------------|-------|
| <chr>     | <int>       | <chr>        | <dbl> |
| 1 setosa  | 1           | Sepal.Length | 5.10  |
| 2 setosa  | 1           | Sepal.Width  | 3.50  |
| 3 setosa  | 1           | Petal.Length | 1.40  |
| 4 setosa  | 1           | Petal.Width  | 0.200 |
| 5 setosa  | 2           | Sepal.Length | 4.90  |
| 6 setosa  | 2           | Sepal.Width  | 3.00  |
| 7 setosa  | 2           | Petal.Length | 1.40  |
| 8 setosa  | 2           | Petal.Width  | 0.200 |
| 9 setosa  | 3           | Sepal.Length | 4.70  |
| 10 setosa | 3           | Sepal.Width  | 3.20  |

## Function: spread()

column to  
headers

column to be split

```
> iris_wide <- spread(iris_long, measurement, value)
```

```
> iris_wide
```

```
# A tibble: 150 x 6
```

| Species                  | observation | Petal.Length | Petal.Width | Sepal.Length | Sepal.Width |
|--------------------------|-------------|--------------|-------------|--------------|-------------|
| <chr>                    | <int>       | <dbl>        | <dbl>       | <dbl>        | <dbl>       |
| 1 setosa                 | 1           | 1.40         | 0.200       | 5.10         | 3.50        |
| 2 setosa                 | 2           | 1.40         | 0.200       | 4.90         | 3.00        |
| 3 setosa                 | 3           | 1.30         | 0.200       | 4.70         | 3.20        |
| 4 setosa                 | 4           | 1.50         | 0.200       | 4.60         | 3.10        |
| 5 setosa                 | 5           | 1.40         | 0.200       | 5.00         | 3.60        |
| 6 setosa                 | 6           | 1.70         | 0.400       | 5.40         | 3.90        |
| 7 setosa                 | 7           | 1.40         | 0.300       | 4.60         | 3.40        |
| 8 setosa                 | 8           | 1.50         | 0.200       | 5.00         | 3.40        |
| 9 setosa                 | 9           | 1.40         | 0.200       | 4.40         | 2.90        |
| 10 setosa                | 10          | 1.50         | 0.100       | 4.90         | 3.10        |
| # ... with 140 more rows |             |              |             |              |             |

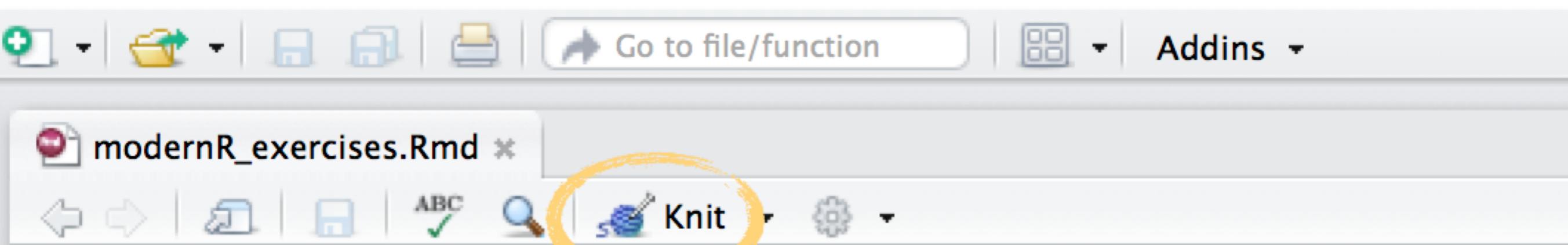
necessary for grouping!

# Exercises

Please do basic exercises 3-I and 3-II.

Time left? Opt for a reading exercise or optional exercise!

# All done? Time to knit!



The screenshot shows the RStudio interface with the 'modernR\_exercises.Rmd' file open in the editor. The 'Knit' button in the toolbar is highlighted with a yellow circle. The code in the file is as follows:

```
1 ---  
2 title: "Modern R with tidyverse"  
3 author: "[Insert your name]"  
4 output:  
5   html_document:  
6     toc: true  
7 ---  
8  
9 *This document is part of the workshop **Introduction to R & Data  
10  
11 # Introduction  
12  
13 In this document, we explore Crane migration, through the GPS dat  
data was kindly provided for this course by Sasha Pekarsky at the
```

# Introduction to R & data

---

Before you leave...

# Other RDM workshops

---

- <https://www.uu.nl/en/research/research-data-management/tools-services/training-and-workshops>
- Learn to write your Data Management Plan (online course)
- Quickstart to Research Data Management

# R Cafe

---

Monthly event for R programmers at UU/UMCU. Be part of the R community! Work on your own project, and ask (or answer!) questions.

More info on:  
[github.com/UtrechtUniversity/R-data-cafe](https://github.com/UtrechtUniversity/R-data-cafe)

(Or subscribe to the newsletter, check the RDM support website...)

Mondays, 15-17, Bucheliuszaal (6.18) UB

Next edition: Monday 15/4, 15:00-17:00



We love feedback! It's how we learn....

Please send your feedback, remarks, questions to Barbara: [b.m.i.vreede@uu.nl](mailto:b.m.i.vreede@uu.nl)

**Or generate an issue on github!**

[tinyurl.com/introRData](http://tinyurl.com/introRData)

```
useR <- function(){
  print("Good luck and see you!")
}
useR()
```