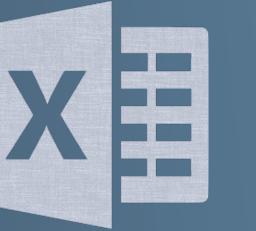


FROM  EXCEL TO 



WHO ARE WE?

1. Center for Health Data Science (HeaDS) - <https://heads.ku.dk/>

SUND Center, which includes a KU data lab

- Courses & Workshops, Seminars, etc.
- Health DS Consultations
- Commissioned Research
- Matchmaking
- Commissioned Supervision



Thilde Terkelsen ¹



Diana Andrejeva ¹



Tugce Karaderi ¹



Henrike Zschach ¹



Adrija Kalvisa ²

2. ReNEW NNF Center for Stem Cell Medicine

3. Data Science Laboratory (DSL) - <https://datalab.science.ku.dk/>



— FROM EXCEL TO R

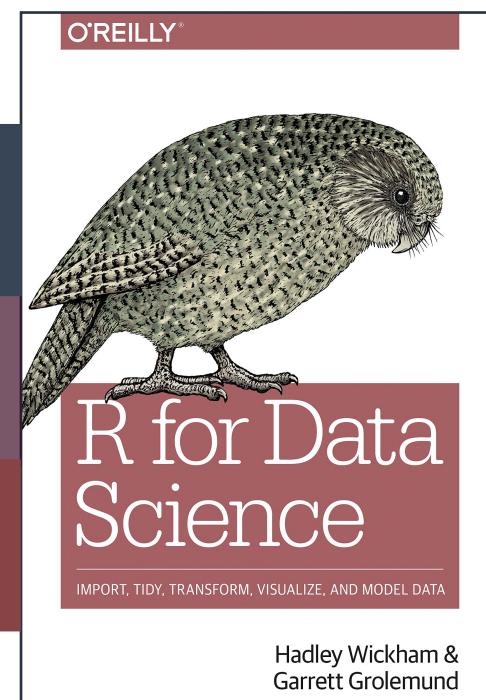
THE PRACTICALS



Two days: 9.00-16.30. There will be coffee breaks, we promise ☕

“R for Data Science” - a generally useful book on R, also for this course

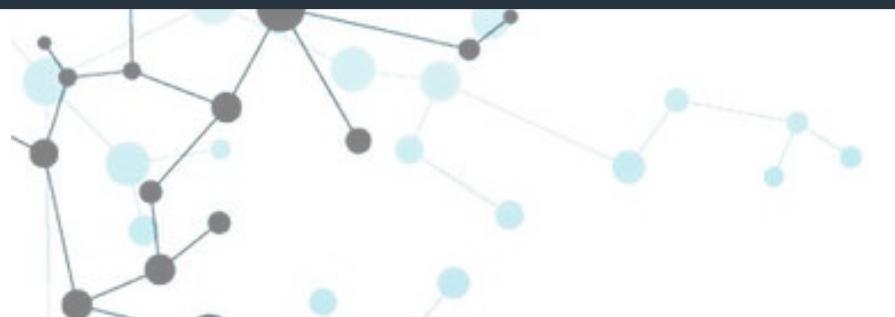
The course is build on hands-on presentations (.R, .Rmd) & exercises



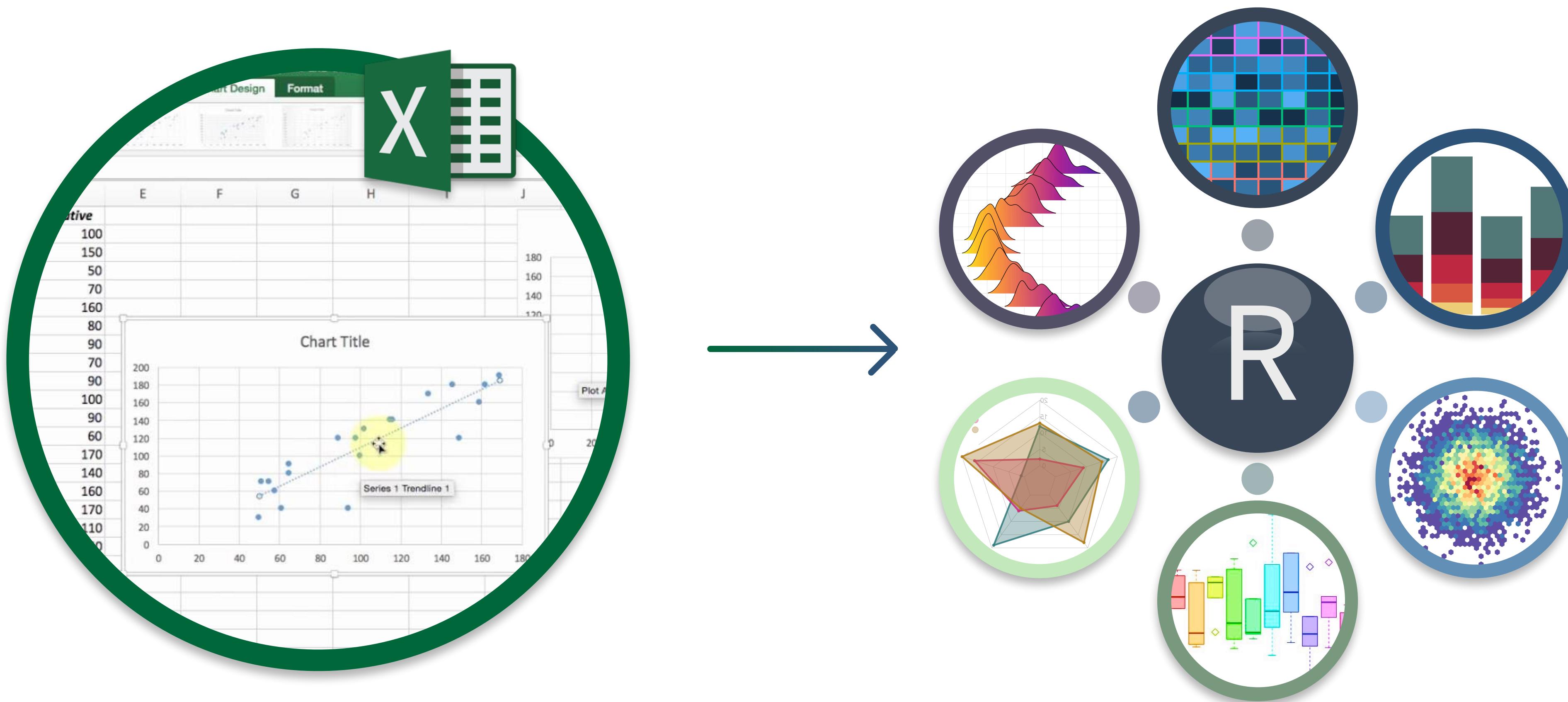
Download and install the newest version of R (<https://cran.r-project.org/>)

Download and install the newest version of R-studio (<http://www.rstudio.com/download>)

Download the course material and place it somewhere you can find it again!
<https://github.com/Center-for-Health-Data-Science/FromExceltoR>



WELCOME TO FROM EXCEL TO R

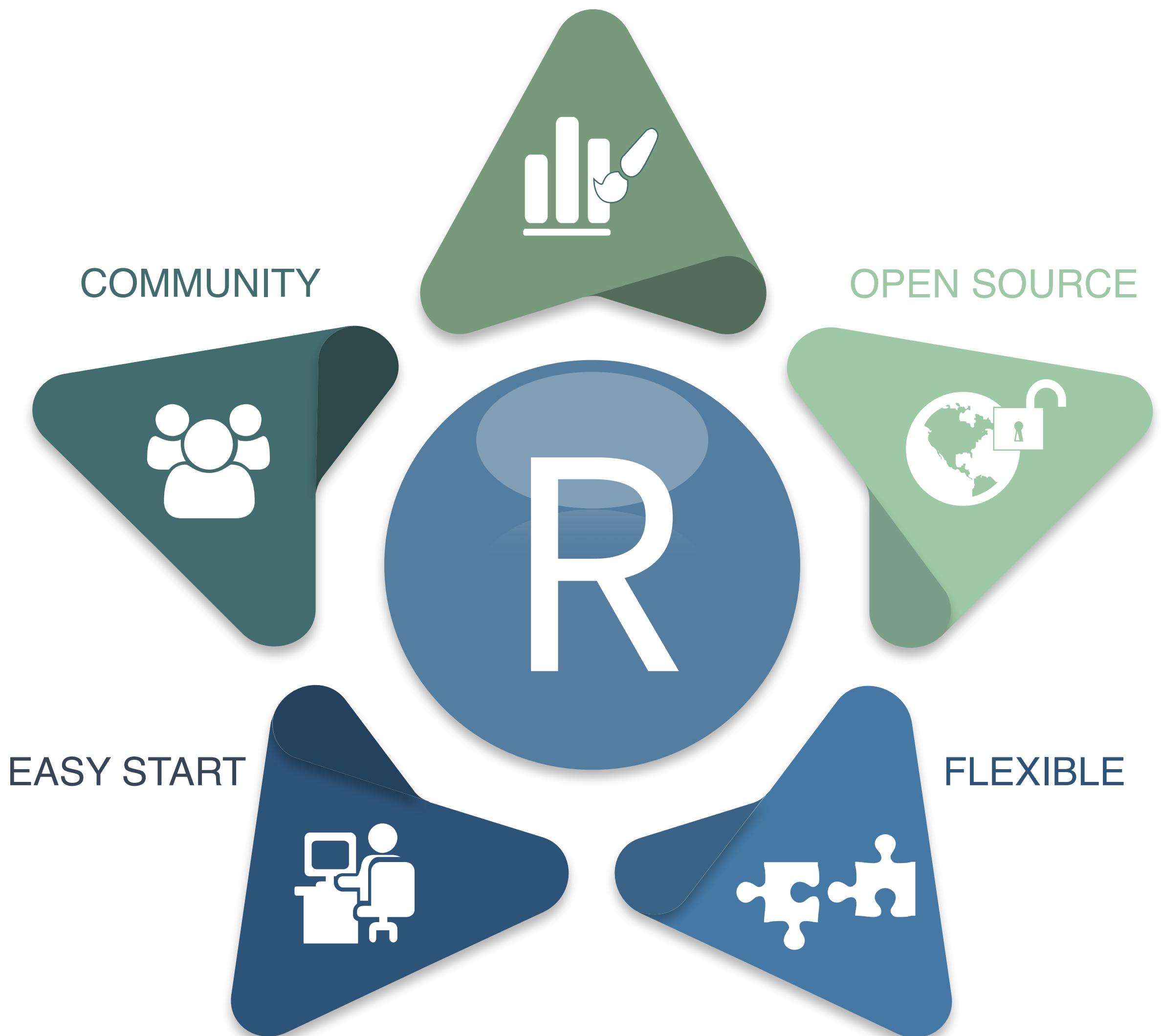


WHY R ?

- **Open Source**
- **Easy to get started with:**
Compatible with all systems, great support
- **Large Community:**
R-packages, pipelines, tutorials, help pages
- **Flexible Language:**
Plugins, git/github, R Shiny, Rmarkdown, ...
- **Customisable Graphics**

R has its **limitations**, but now fewer than ever

GRAPHICS

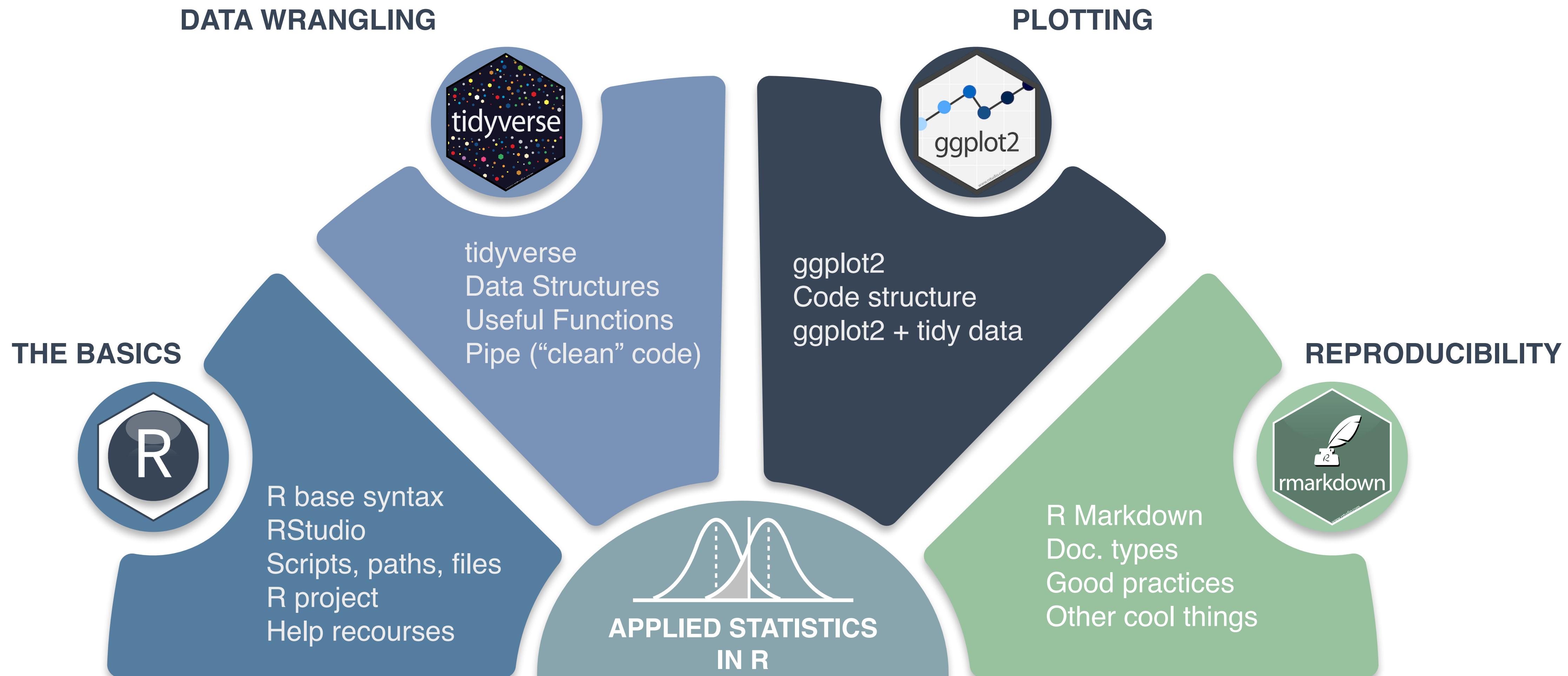


A COMPARISON

FROM EXCEL TO R



WHAT WILL YOU LEARN IN THIS COURSE?



PROGRAM

DATES: 24-05 & 27-05, 2024

PLACE: Faculty of Health and Medical Sciences,
Panum, Blegdamsvej 3B, 2200 København

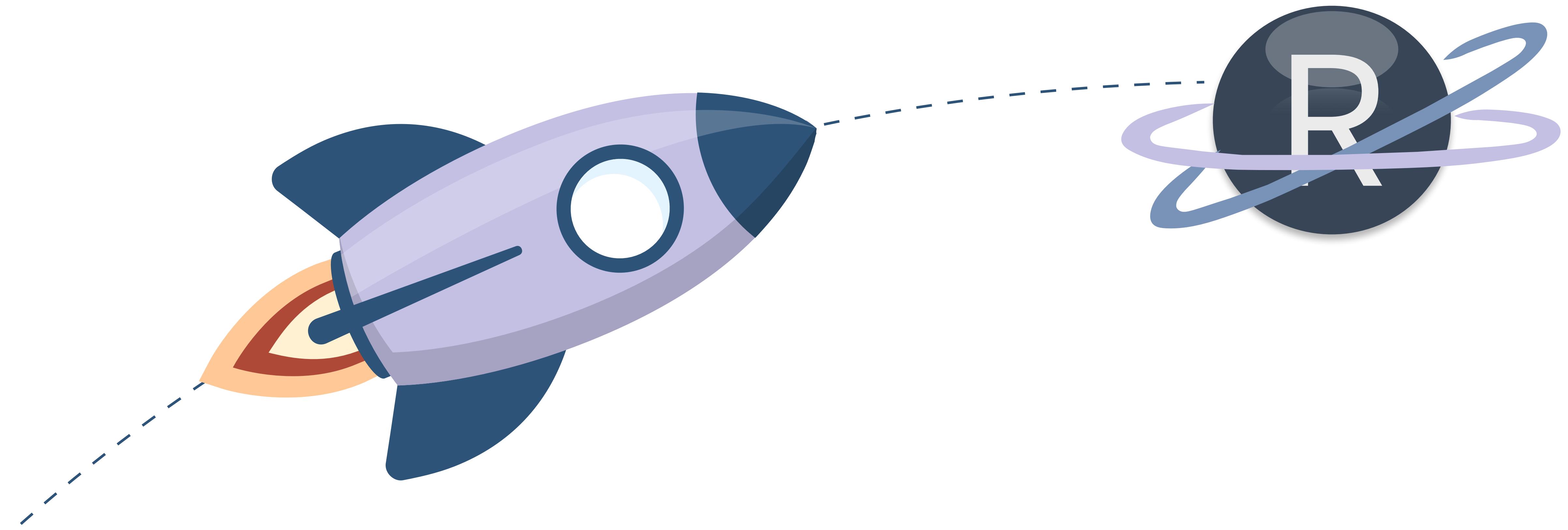
DAY 1: Holst aud.

08:30 - Installation Issues & Coffee
09:00 - Introduction to R Basics
10:00 - Rstudio Exercise
10:45 - Break
11:00 - Tidyverse
12:00 - Lunch
13:00 - Tidyverse Exercise
14:30 - Break
14:45 - Rmarkdown
15:15 - Rmarkdown Exercise
16:00 - Q&A - See you tomorrow

DAY 2: Holst aud.

08:30 - Coffee
09:00 - ggplot2
10:00 - ggplot2 Exercise
10:45 - Break
11:00 - Applied Statistics
12:00 - Lunch
13:00 - Applied Statistics
14:30 - Break
14:45 - Basic Data Analysis Exercise
15:45 - Cool things in R & Course Evaluation
16:00 - *Data Science Networking & Drinks*

— FROM EXCEL TO R
LET'S GET STARTED



R & FRIENDS



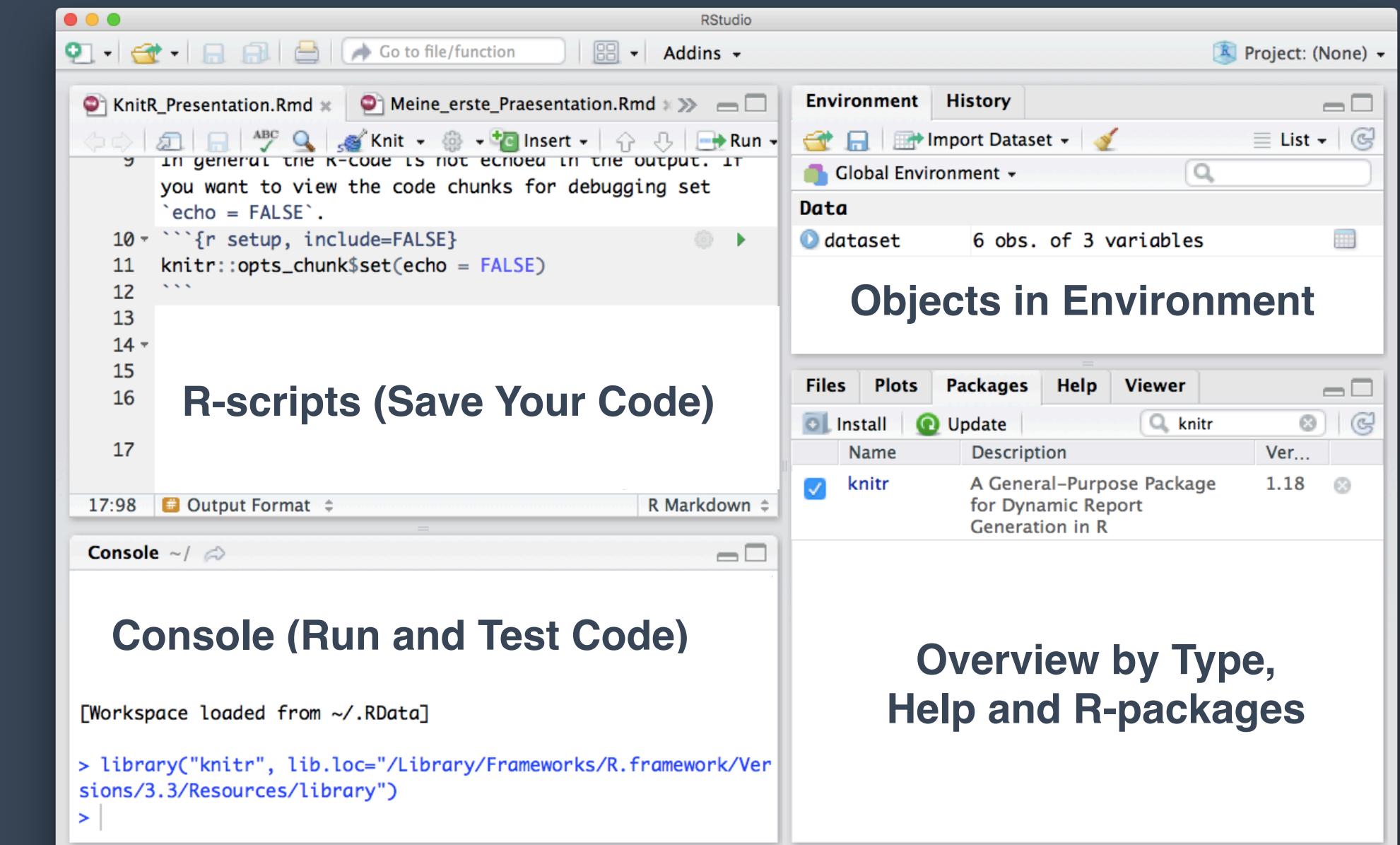
Scripting / Programming Language



Reports (html, pdf, latex)

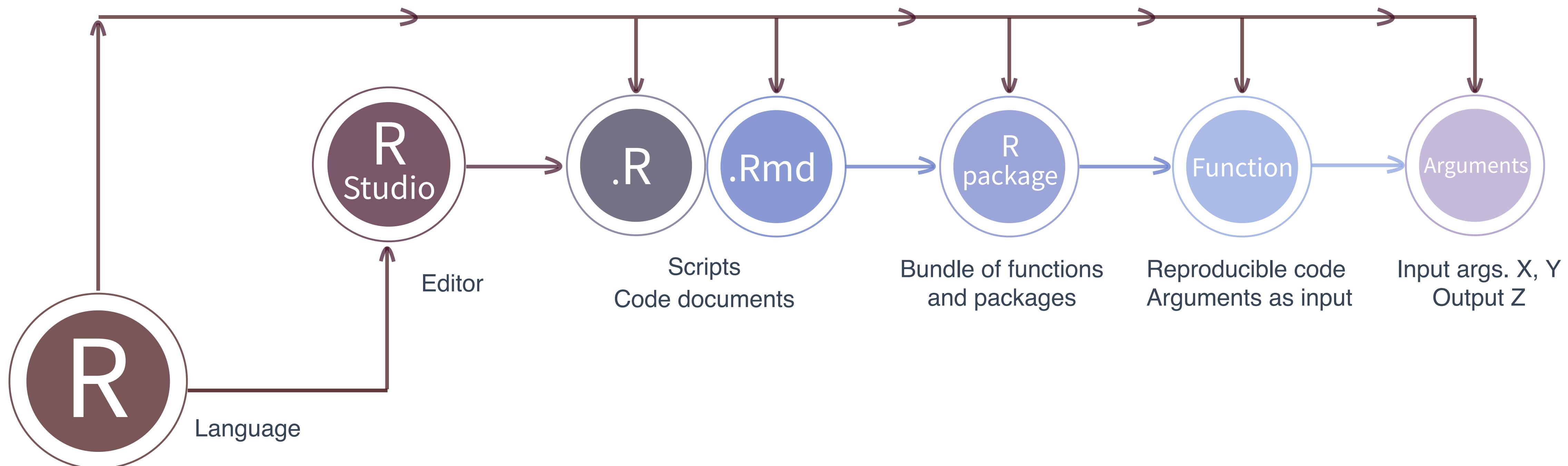


R Studio



R Code Interpreter and Editor

THE ANATOMY OF R



FIRST TIME IN R?

PACKAGES & FUNCTIONS

?*my.package*, ?*my.function*

What is it? Input?

install.packages(), *remove.packages()*

TIPS

Arrows↑↓ to find the code you ran

R studio tips: view, diagnostics

✖️⚠️ Auto-complete with tab

R-cheat sheets (<https://rstudio.com/resources/cheatsheets/>)



WORKING DIRECTORY

setwd(), *getwd()*, *list.files()*, *list.dirs()*

Where am I working from? Full/relative path.

SAVE YOUR WORK

.R, (or .Rmd)

The file with my code. Save it!

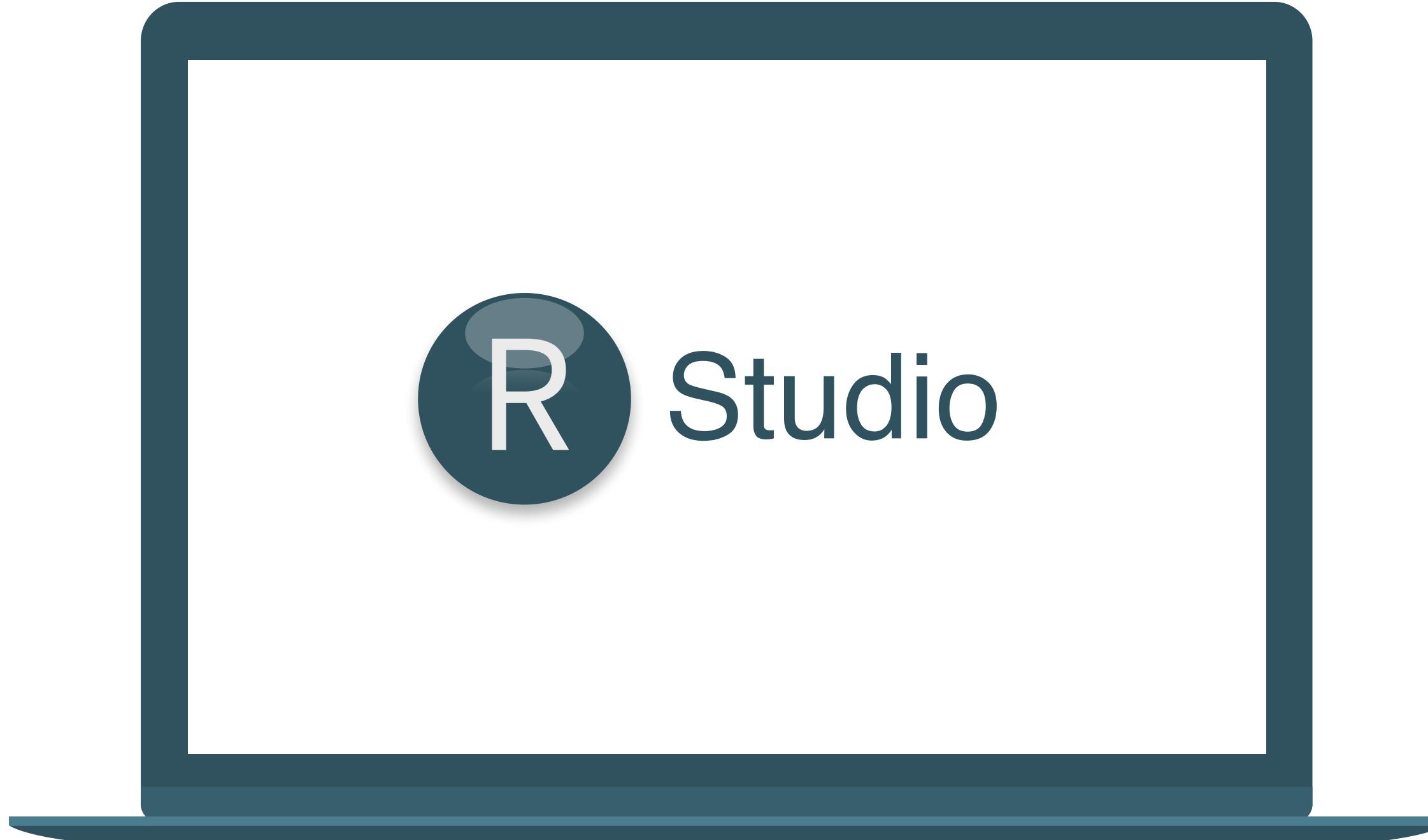
R project

Save Session, everything together

RUN CODE

Run button, highlight enter, short-cut

R STUDIO BASICS



1. R Project

File —> New Project —> New/Existing —> Create Project

2. Set Path

getwd() - Get directory
setwd() - Set directory

setwd("/Users/Tom/Rstuff") - Full path
setwd("./Rstuff") - Relative path

Session —> Set Working Directory —> Choose Directory

3. R Script

Script Icon —> R Script —> File —> Save as ...

4. Install and load a R package.

install.packages("my.package")
library (my.package) - Load package.

Tools —> Install packages —> my.package

ONLINE RESOURCES FOR R

<https://www.r-project.org/>



GET STARTED

<https://rseek.org/>

<https://rstudio.com/resources/cheatsheets/>

<http://www.cookbook-r.com/>

<https://www.statmethods.net/r-tutorial/index.html>



GRAPHICS

<https://www.r-graph-gallery.com/>

<http://r-statistics.co/Top50-Ggplot2-Visualizations-MasterList-R-Code.html>



BOOKS & COURSES

<https://www.r-bloggers.com/best-books-to-learn-r-programming/>

<https://www.datacamp.com/>

<https://www.codecademy.com/>

<https://www.coursera.org/>



OTHER RESOURCES

<https://github.com/trending/r>

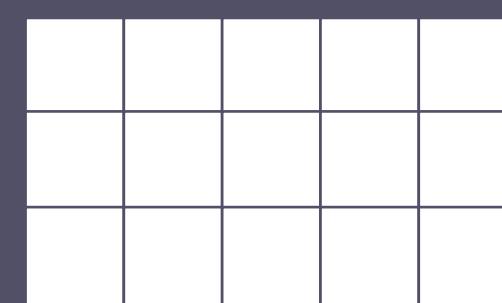
<https://blog.revolutionanalytics.com/>

<https://stackoverflow.com/questions/tagged/r>



R DATA TYPES & STRUCTURES

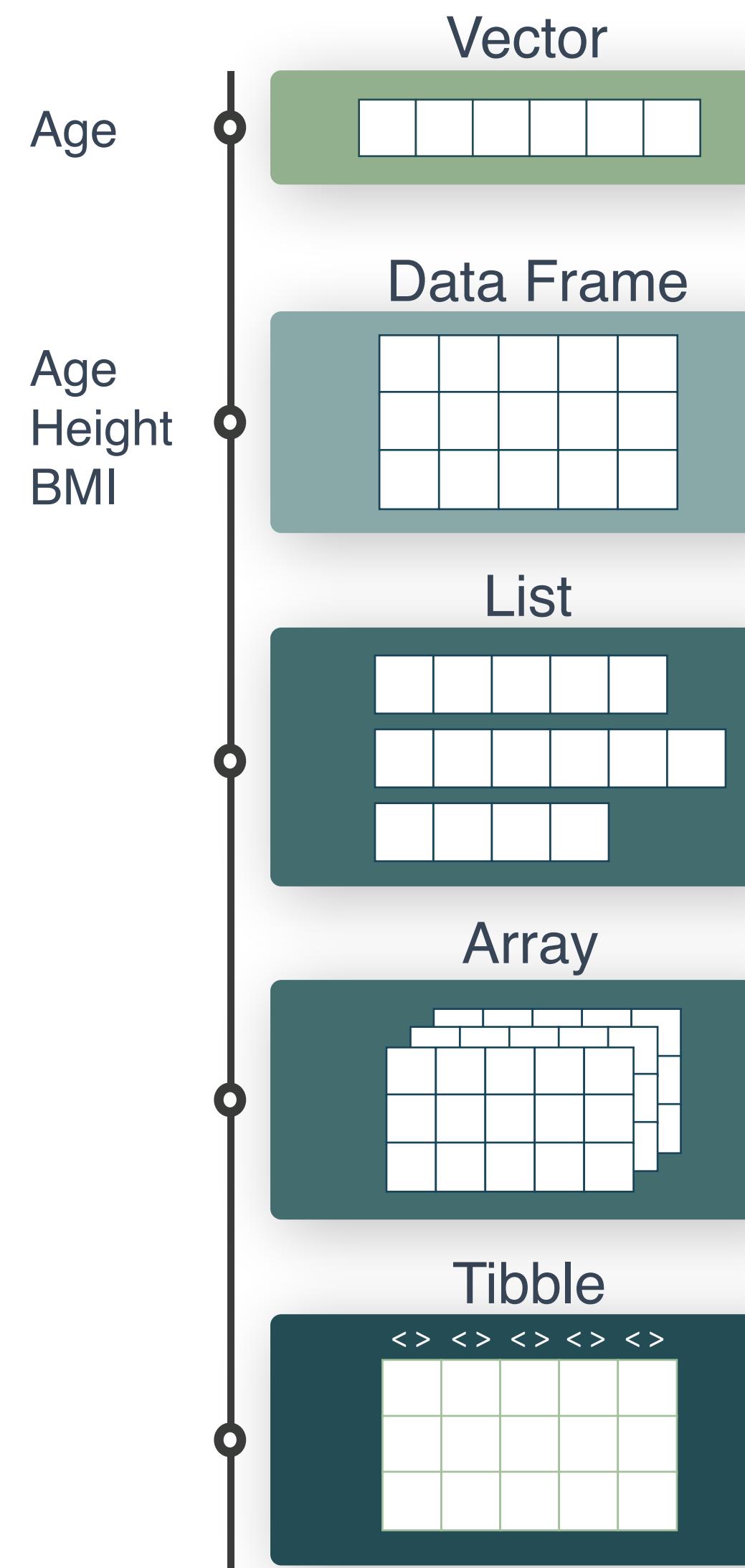
VARIABLES



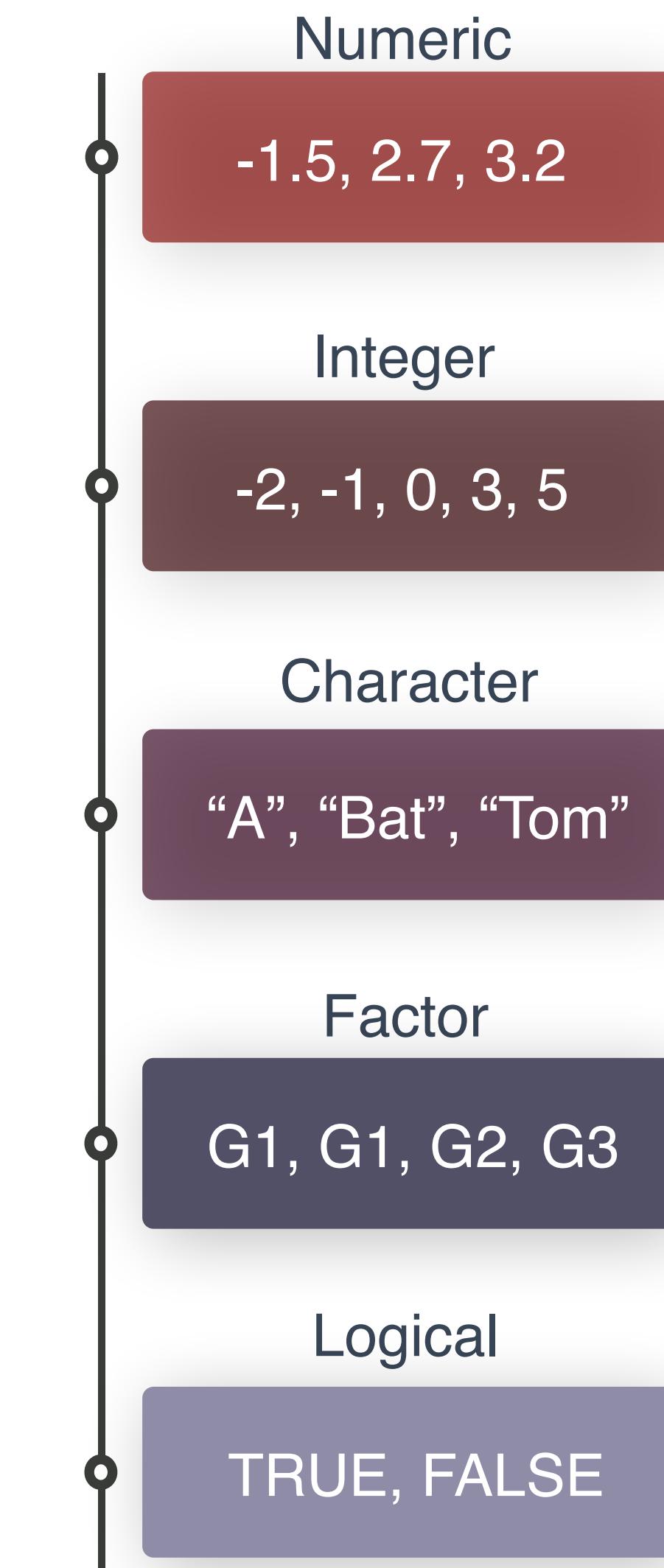
OBSERVATIONS

— FROM EXCEL TO R

DATA STRUCTURES



DATA TYPES



R BASE SYNTAX - RUN THROUGH

VARIABLE ASSIGNMENT

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

```
> x <- c(1.5, 2.6, 1.7, 3.2, 3.0, 2.9, ...)  
> x  
[1] 1.5 2.6 1.7 3.2 3.0 2.9 ...
```

READING AND WRITING DATA

Input	Output	Description
<code>df <- read.table('file.txt')</code>	<code>write.table(df, 'file.txt')</code>	Read and write a delimited text file.
<code>df <- read.csv('file.csv')</code>	<code>write.csv(df, 'file.csv')</code>	Read and write a comma separated value file. This is a special case of read.table/write.table.
<code>load('file.RData')</code>	<code>save(df, file = 'file.Rdata')</code>	Read and write an R data file, a file type special for R.

DON'T USE

Spaces in names

Special characters
% ? / | \ & \$ @

Unspecific names

Short/long names

R BASE SYNTAX - RUN THROUGH

SELECTING ELEMENTS

x[4] The fourth element.

x[-4] All but the fourth.

x[2:4] Elements two to four.

x[!(2:4)] All elements except two to four.

x[c(1, 5)] Elements one and five.

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.

R-BASE FUNCTIONS

log(x) Natural log.

exp(x) Exponential.

max(x) Largest element.

min(x) Smallest element.

round(x, n) Round to n decimal places.

sig.fig(x, n) Round to n significant figures.

cor(x, y) Correlation.

sum(x) Sum.

mean(x) Mean.

median(x) Median.

quantile(x) Percentage quantiles.

rank(x) Rank of elements.

var(x) The variance.

sd(x) The standard deviation.

CONDITIONS

a == b	Are equal	a > b	Greater than	a >= b	Greater than or equal to	is.na(a)	Is missing
a != b	Not equal	a < b	Less than	a <= b	Less than or equal to	is.null(a)	Is null

BASE R CHEAT SHEET

Basics: `getwd()`, `setwd() # location`
`install.packages('pname')`, `library(pname)`
`ls()`, `rm() # list, remove objects`
`load()`, `data()`, `save() # load, save as .Rdata`

Overview: `head(df, n=10)`, `df[1:10,]` `tail(df, n=10)`
first or last 10 rows
`class()` # data structure
`unique()`, `table() # unique vals, count vals`

Is/As type:
`is.numeric(x)` (character, factor, integer, etc.)
`as.numeric(x)` (factor, matrix, data.frame, etc.)

Other: `seq(1, 10, by = 1.0) # sequence from-to`
`rep(x, times) # replicate n times`
`sort(), reverse() # sort or reverse vector`

Read in data:
`read.xlsx('name.xlsx')`,
`read.delim('name.txt', sep = '\t')`
`read.csv('name.csv', sep=';')`

Make Data: `c() # vector`
`data.frame(x=x,y=y)`
`matrix(x, nrow = 3, ncol = 3)`
`list(x=x, y=y)`

Strings:
`paste(x, y, sep = '')`
`grep('pattern', x) # find str pattern`
`gsub('pattern', 'replace', x) # replace with`

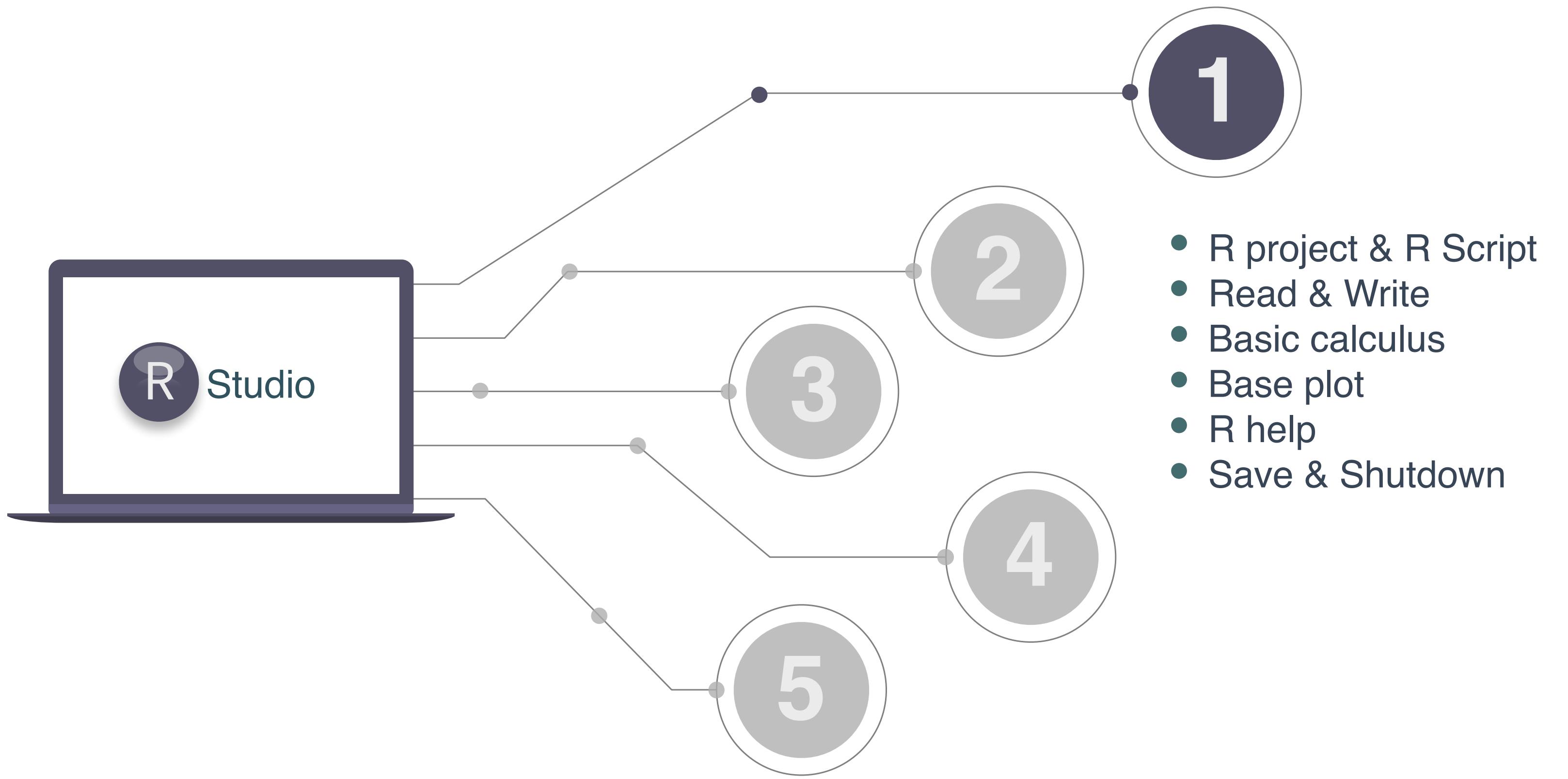
Plots: `plot(x)`
`plot(x,y) # scatter`
`hist(x) # histogram`

GETTING
STARTED

DATA STRUCTURES
& OVERVIEW

DATA TYPES &
STRINGS

VECTORS &
BASE PLOTS



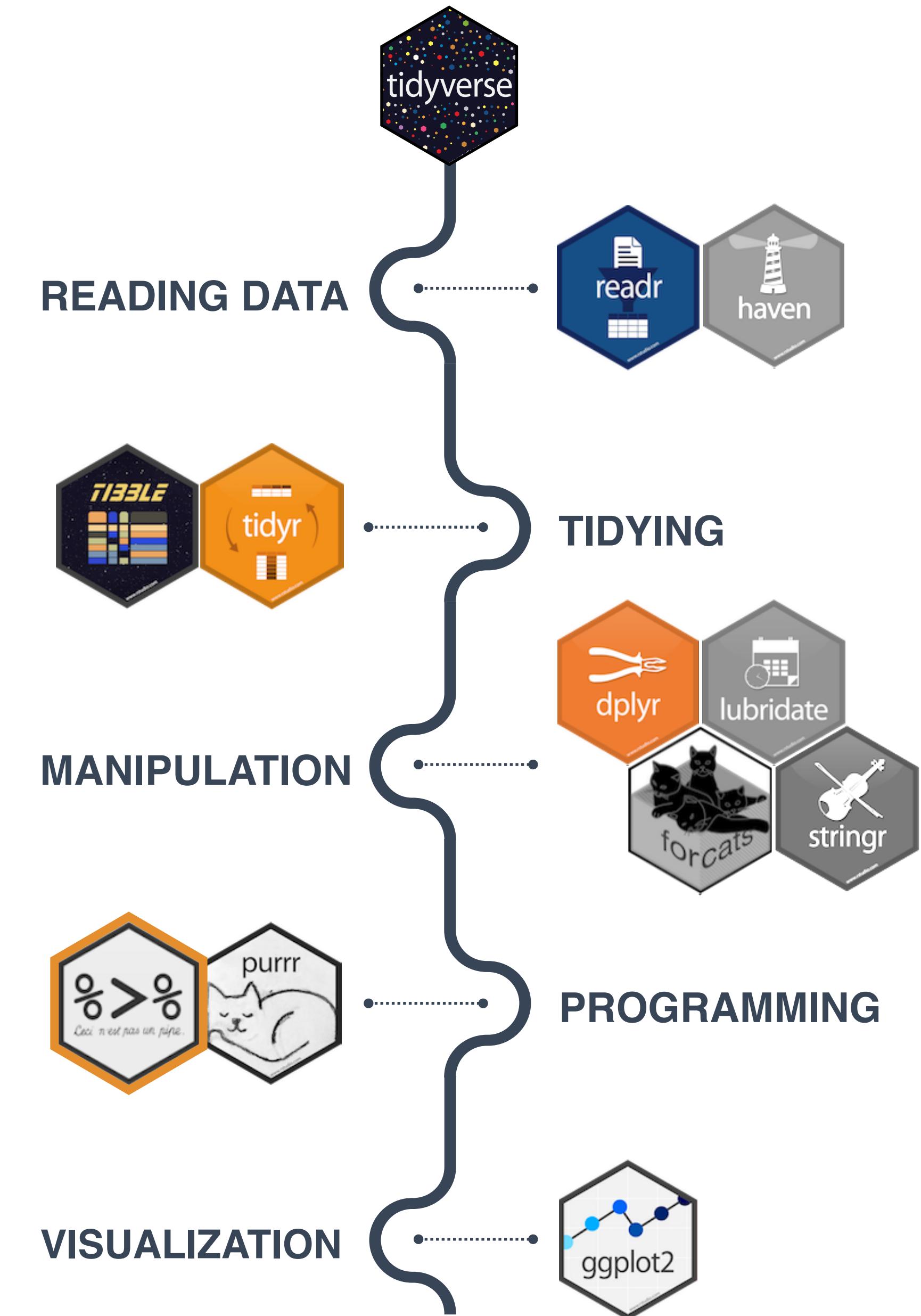
TIDYVERSE

<https://www.tidyverse.org/>

tidyverse is a collection of R packages for data science

“The packages share an underlying design philosophy, grammar, and data structures.” *Wickham and Grolemund*

tidyverse is used to “tidy up” your datasets, so they are easy to work with



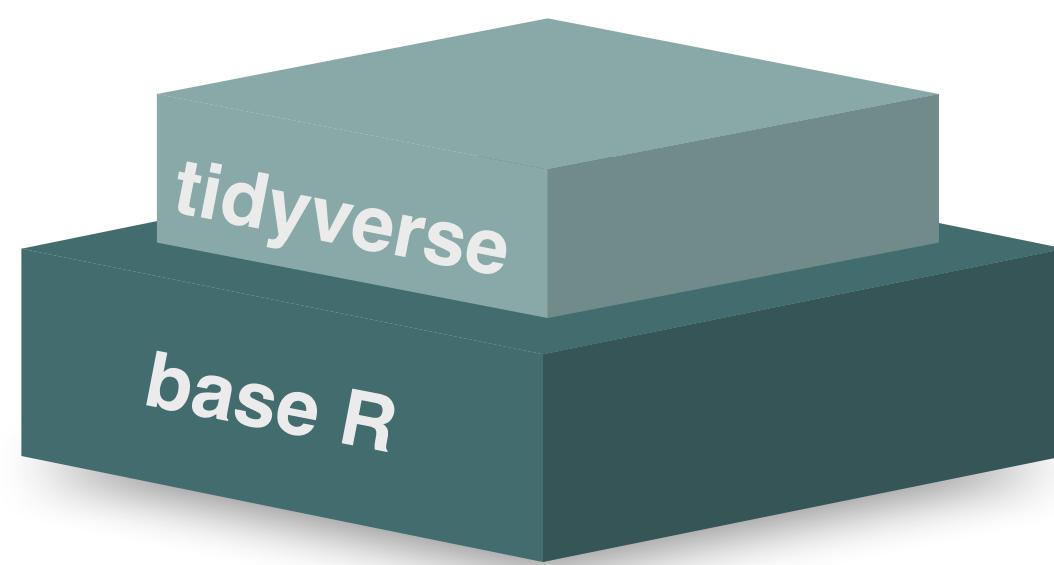
CECI N'EST PAS UNE PIPE

%>%

- You do NOT have to “choose” between tidyverse and base R

BENEFITS

- Short & well-organised code
- Tidy datasets, easy to work with
- Great documentation
- Functions with logical names & inputs



CONSIDERATIONS

- Can be less stable
- “Different syntax”
- Remember what tidyverse is made for!

base R

```
# think from the inside out  
g(f(x,y),z)
```

tidyverse

```
# no brain acrobatics  
x %>% f(y) %>% g(z)
```



pipe symbol

TIDYVERSE CHEAT SHEET

readr, tidyverse, dplyr, ...

Read Data (*readr*)

Reading tabular data

There are solutions for multiple data types
`read_excel()` # using *readxl* package
`read_table()`
`read_csv()`

Useful arguments

Skip lines: `read_csv(file, skip=1)`
Read subset: `read_csv(file, n_max=1)`

Data types

readr guesses the types of each column and tells you about it
("Parsed with column specifications: ...")

HELP

R Documentation (e.g. enter `?dplyr::filter` and see examples)

Much more info and detailed cheat sheets:

<https://brianward1428.medium.com/introduction-to-tidyverse-7b3dbf2337d5>

It also helps to google "tidyverse + whatever you want to do"

Data Tidying (*tidyr*)

Handle missing values

`drop_na()`
`fill()`
`replace_na()`

Subsetting

`tibble[:,1:5]` # returns a tibble
`tibble$colname` # returns a vector
(same as `tibble[[colname]]`)

Reorganize layout

Change between long and wide format
`gather()` # wide to long
`spread()` # long to wide

Data Manipulation (*dplyr*)

Summary

`summarise()`/`summarize()`
`count()`

Group

`group_by()`

Functions will manipulate each group separately and combine results.

Extract and sort observations # i.e. rows

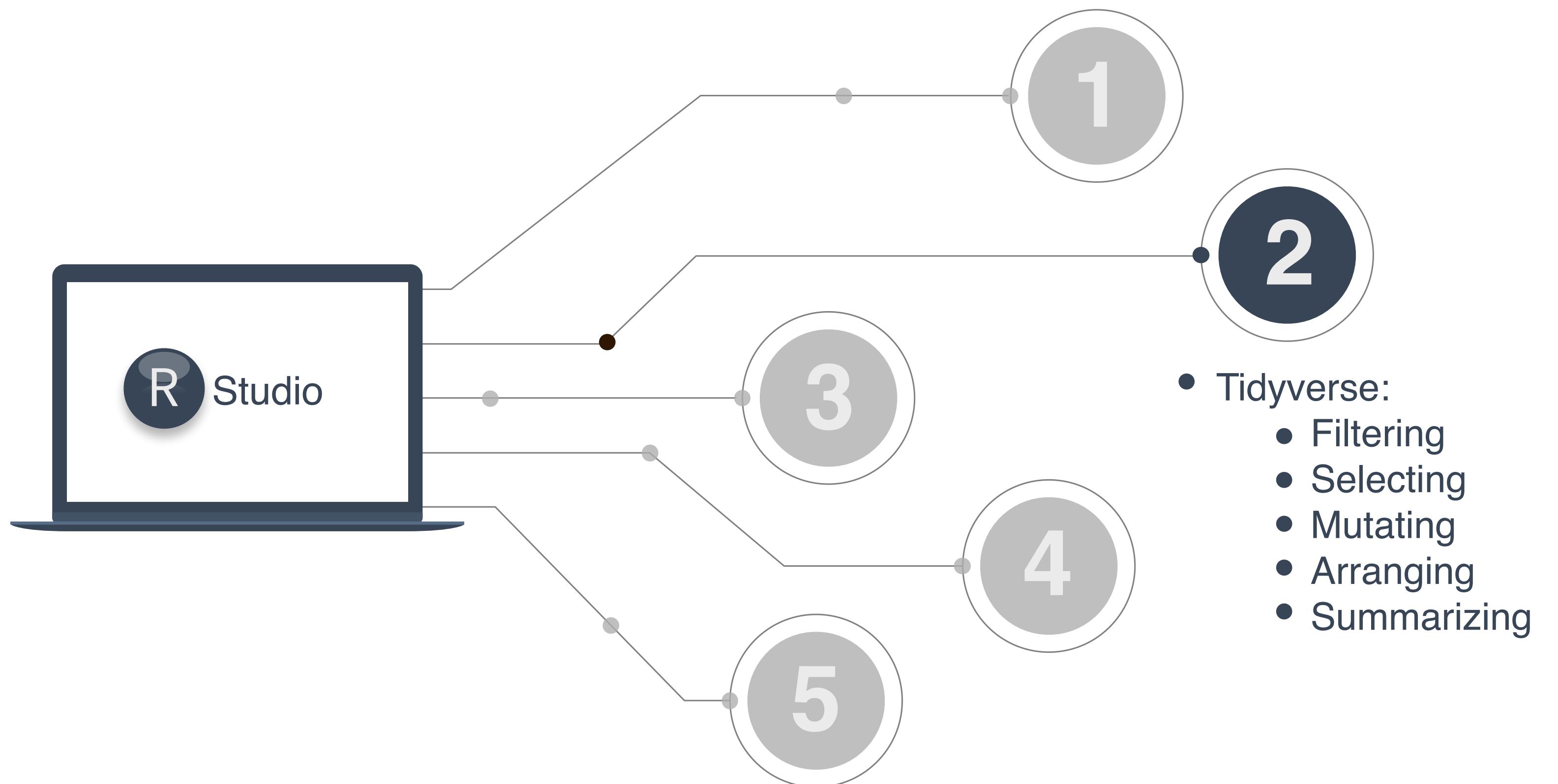
`filter()` # subset by condition
`distinct()` # subset to unique values
`top_n()` # subset by position
`arrange()` # sort low->high, other way with `desc()`

Manipulate variables # i.e. columns

`select()`
`mutate(new_name = f(column))`

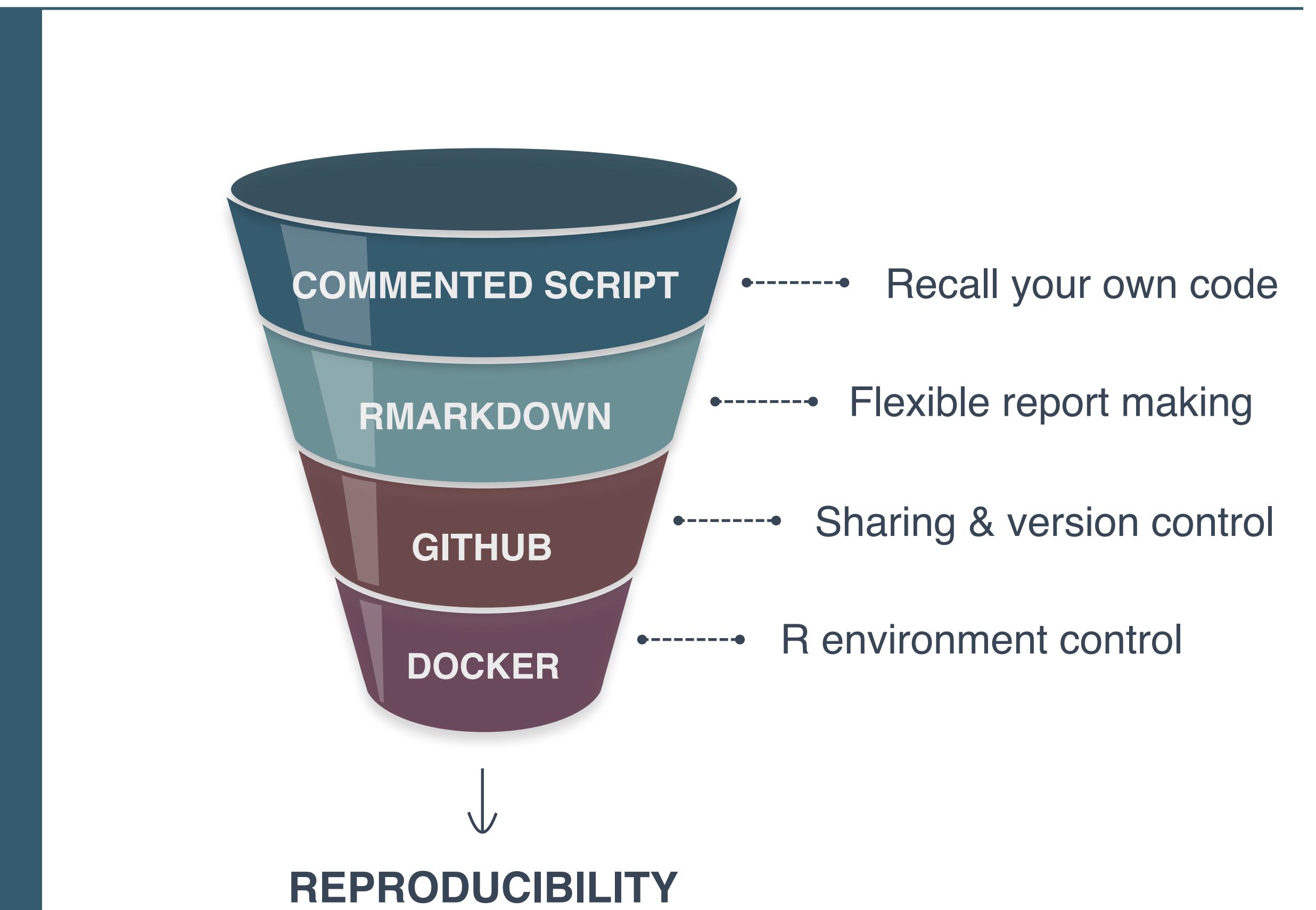
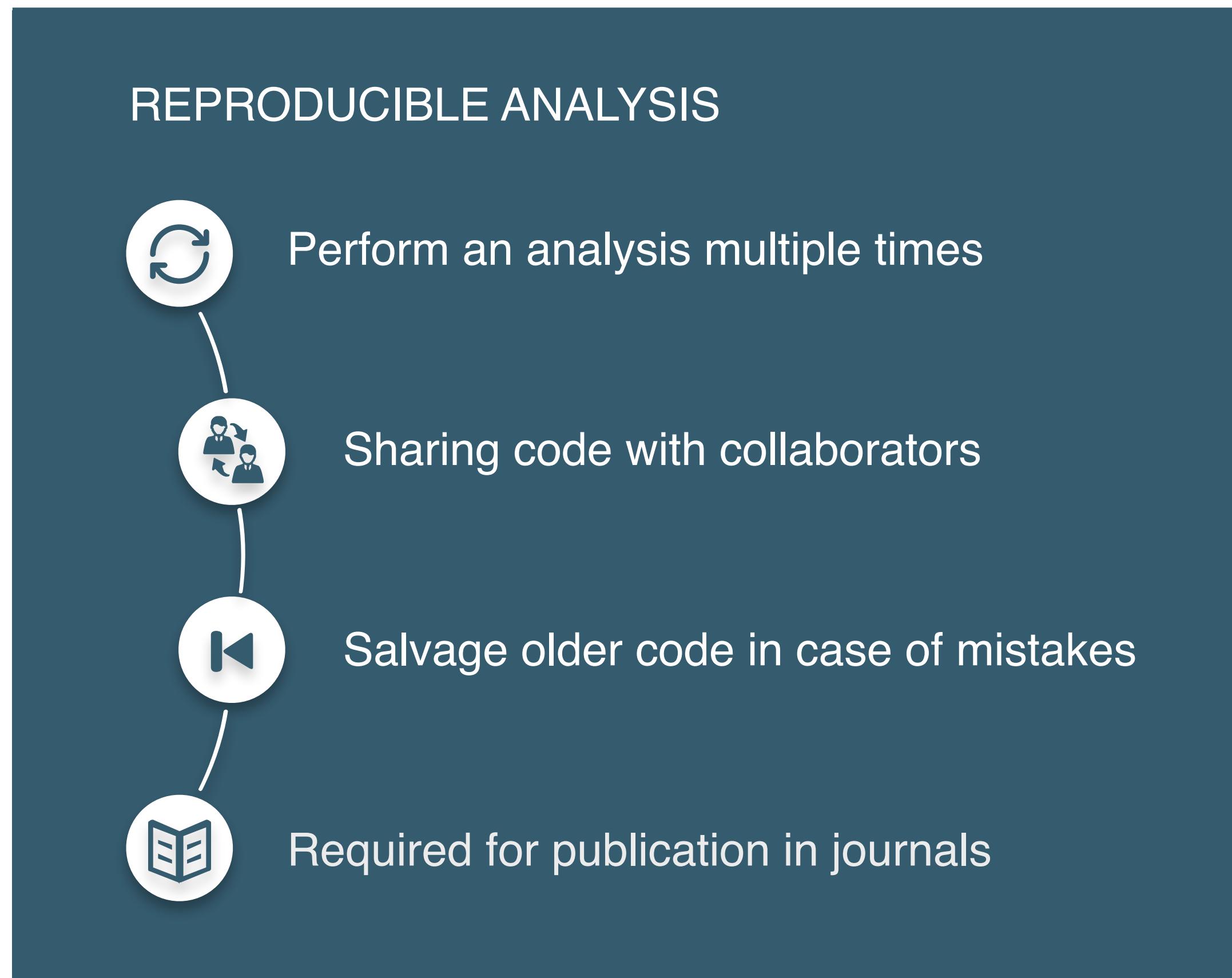
Vectorised functions

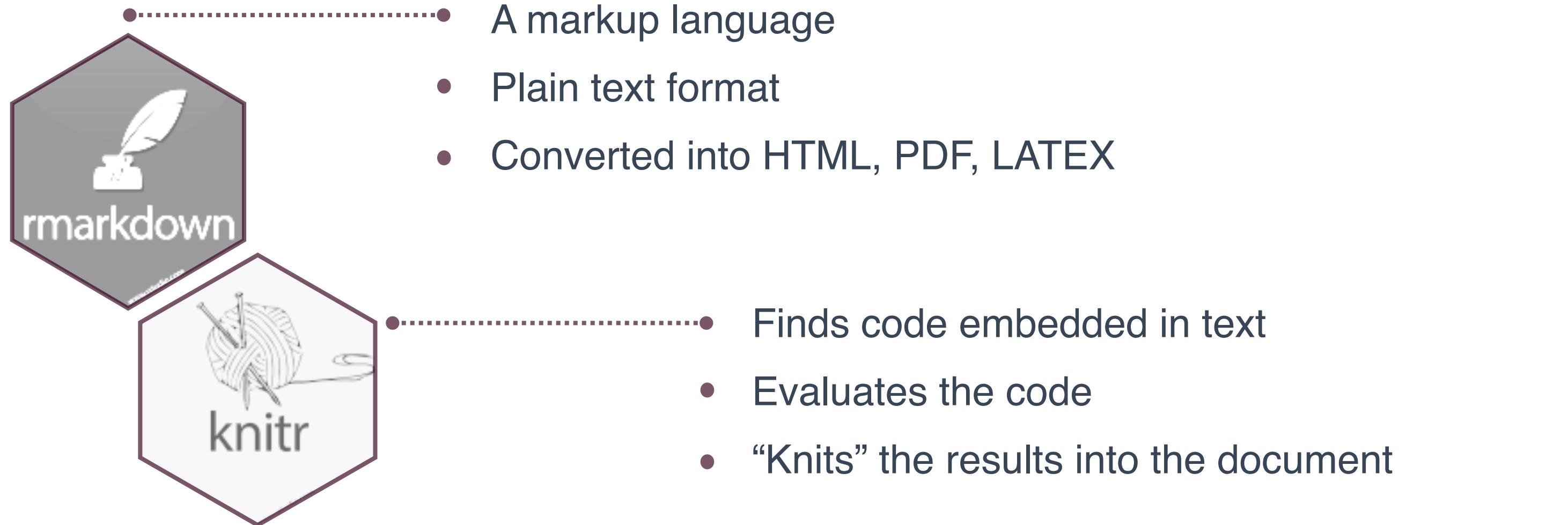
Ranking: `percent_rank()`
Math: Any arithmetic or logical operations, `between()`,
`near()`
`if_else()`



TIDYVERSE EXERCISE 2

REPRODUCIBILITY IN R





— <https://www.markdowntutorial.com/>

R SCRIPT & RMARKDOWN

HOW TO

Write code as normal •

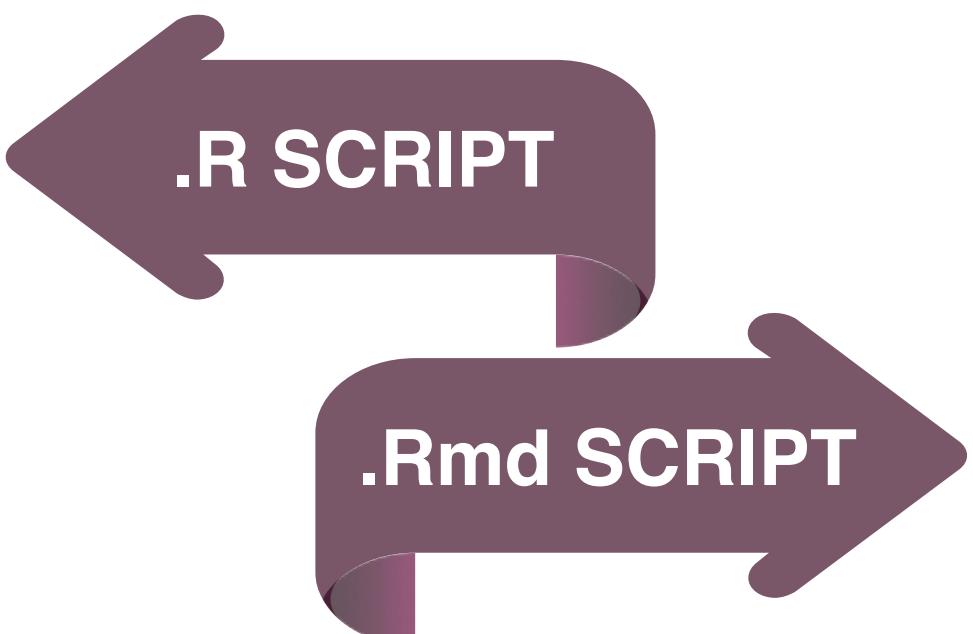
Comment text with # •

USE FOR

Testing new code •

Big data analysis •

Software development •



HOW TO

Write text as normal •

Embed code ``{r} my.code`` •

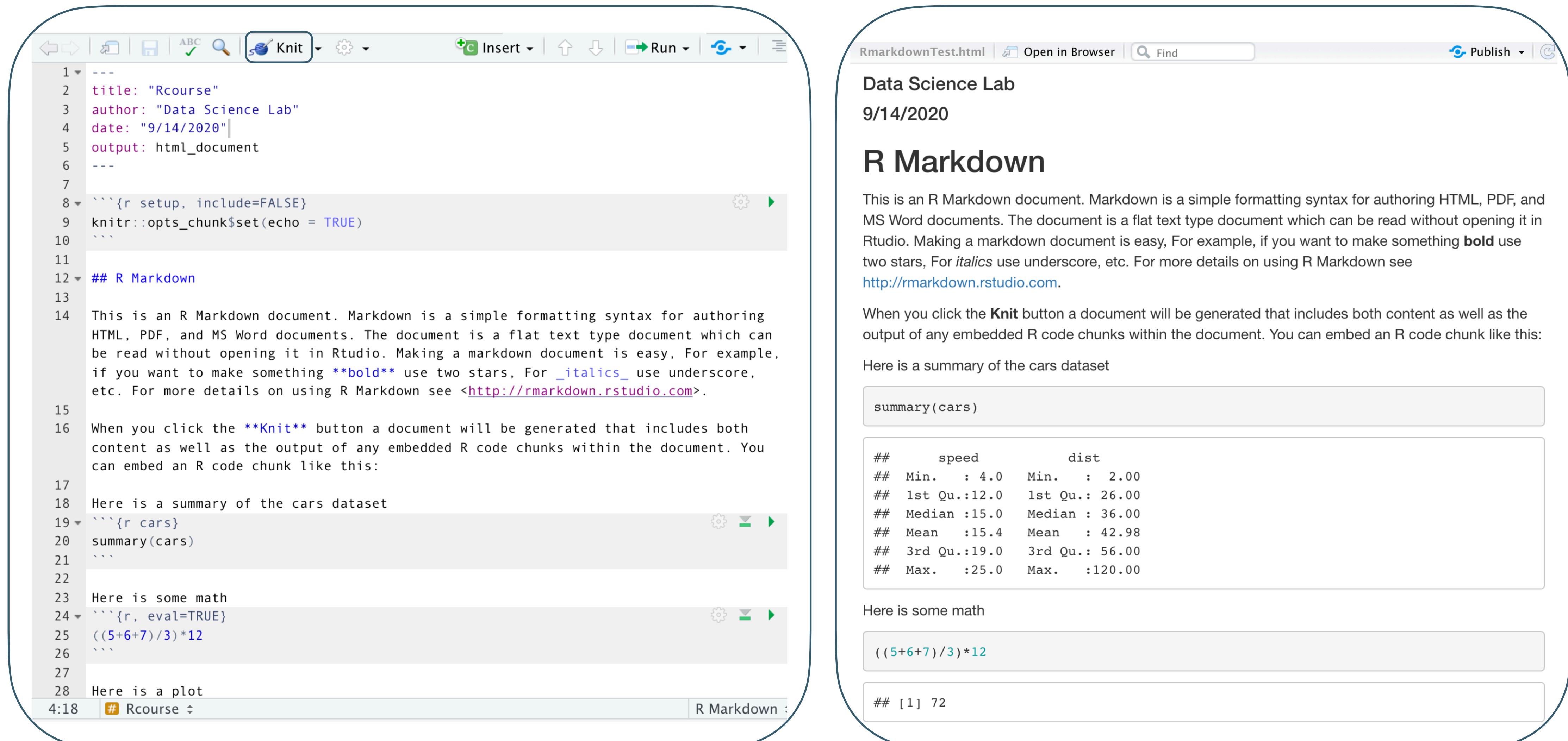
USE FOR

Reports for yourself •

Reports for collaborators •

Tutorials •

RMarkdown



The diagram illustrates the RStudio interface for R Markdown. It features two main panes: the left pane for editing the R Markdown file and the right pane for viewing the generated HTML output.

Left Pane (R Markdown Editor):

- Toolbar:** Includes icons for back, forward, file operations, ABC, search, and a prominent **Knit** button.
- Code Area:** Displays the R Markdown code. The code includes a YAML header, R code chunks, and text sections. A specific R code chunk is highlighted.
- Status Bar:** Shows the file name "R Markdown" and the line number "4:18".

Right Pane (HTML Preview):

- Toolbar:** Includes icons for Open in Browser, Find, and a Publish button.
- Content:** Displays the generated HTML document. The title is "Data Science Lab" and the date is "9/14/2020". The main section is titled "R Markdown".

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. The document is a flat text type document which can be read without opening it in RStudio. Making a markdown document is easy, For example, if you want to make something **bold** use two stars, For italics use underscore, etc. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed      dist
##  Min.   : 4.0   Min.   :  2.00
##  1st Qu.:12.0   1st Qu.: 26.00
##  Median :15.0   Median : 36.00
##  Mean   :15.4   Mean   : 42.98
##  3rd Qu.:19.0   3rd Qu.: 56.00
##  Max.   :25.0   Max.   :120.00
```

Here is some math

```
((5+6+7)/3)*12
```

```
## [1] 72
```

RMARKDOWN CHEAT

Begin .Rmd:

```
---
```

```
title: My Project Name
```

```
output:
```

```
    html_document (pdf_document, ...)
```

```
---
```

Code Chunk:

```
```{r}
```

```
some R code
```

```
```
```

Global Option:

```
```{r setup, include=FALSE}
```

```
knitr::opts_chunk$set(echo = TRUE)
```

```
```
```

GETTING
STARTED

Code Options:

```
echo (= TRUE or FALSE - print my code)
```

```
eval (= TRUE or FALSE - run my code)
```

```
warning (= TRUE or FALSE display warning messages)
```

Figure Options:

```
fig.align (= 'left', 'right', 'center')
```

```
fig.cap (= 'my figure caption')
```

```
fig.height (= n), fig.width (= n)
```

CHUNK
OPTIONS

Header:

Header size ranging from largest (one #)
to smallest (six #):
my.text, ## my.text, ### my.text, etc.

Text:

italics

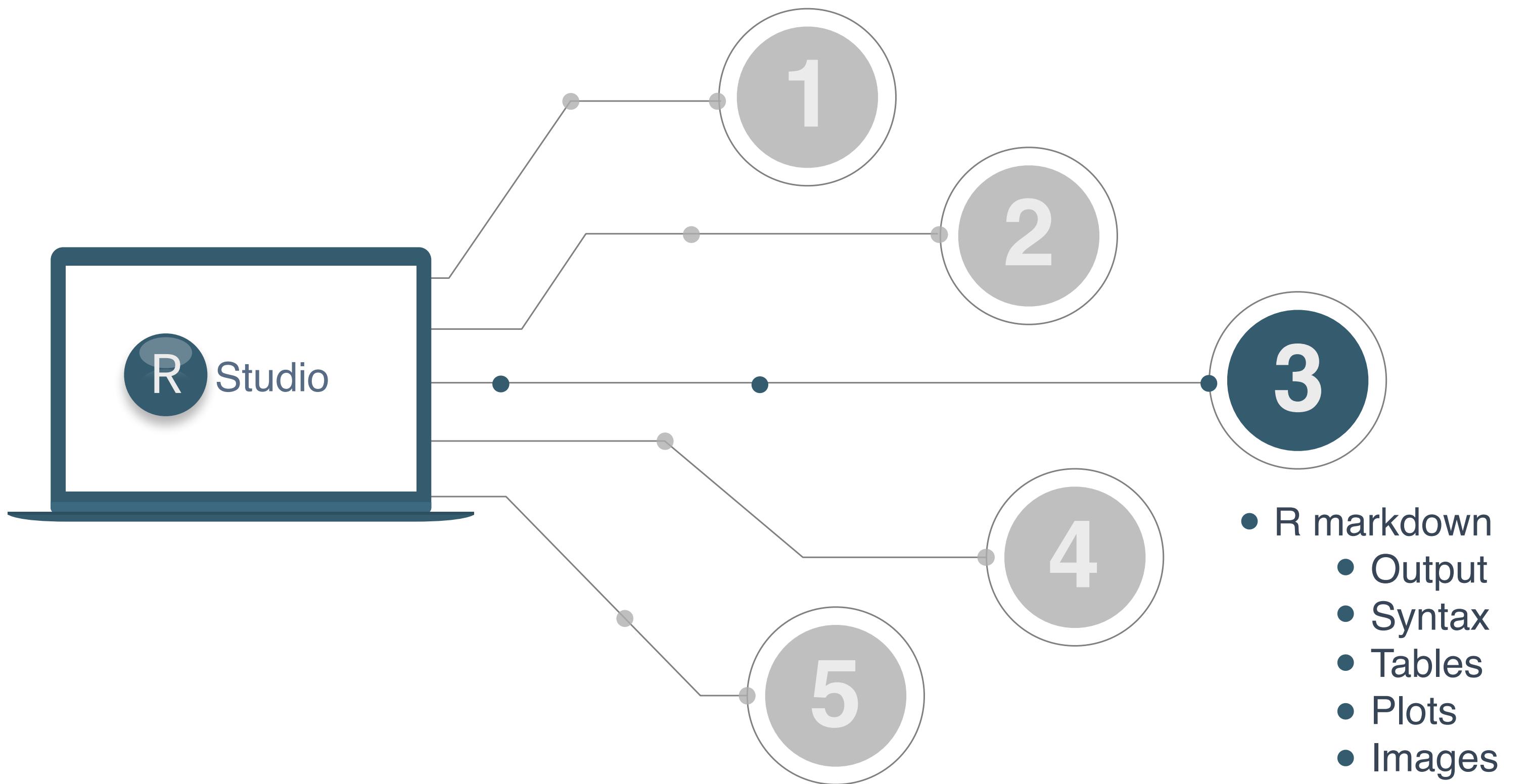
bold

`highlighted`

Lists:

- * List item1 (filled dot)
 - + sub-item1 (open dot)
- 1. List item1 (numbered)
 - i) sub-item1 (roman)

TEXT

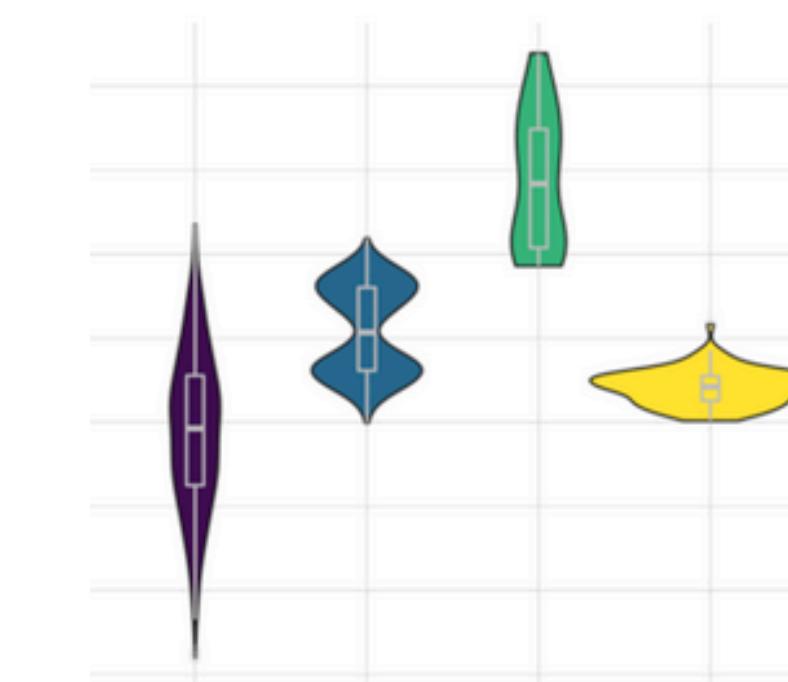


R MARKDOWN EXERCISE 3

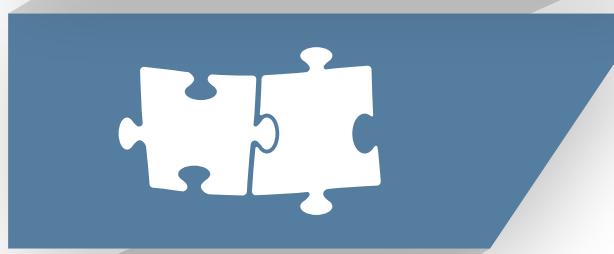
GGPLOT2 - EASY GRAPHICS



Aesthetically pleasing graphics.



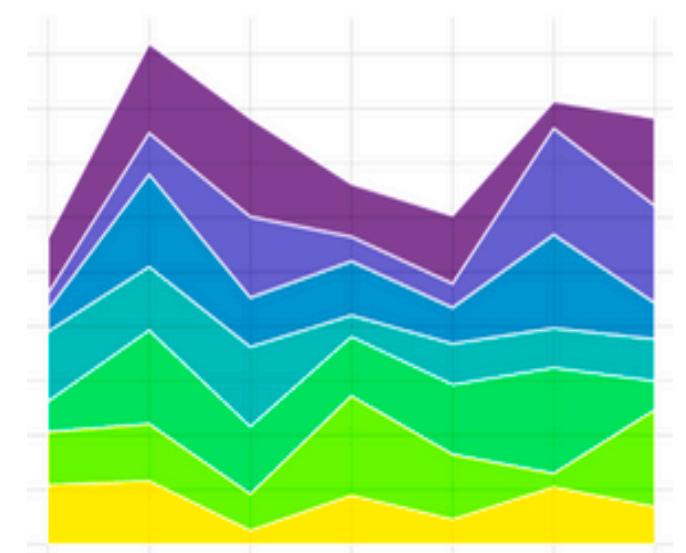
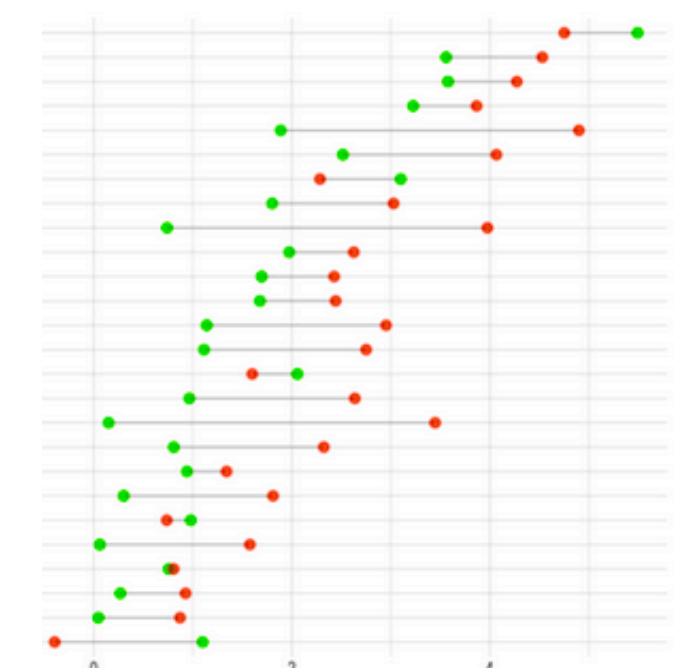
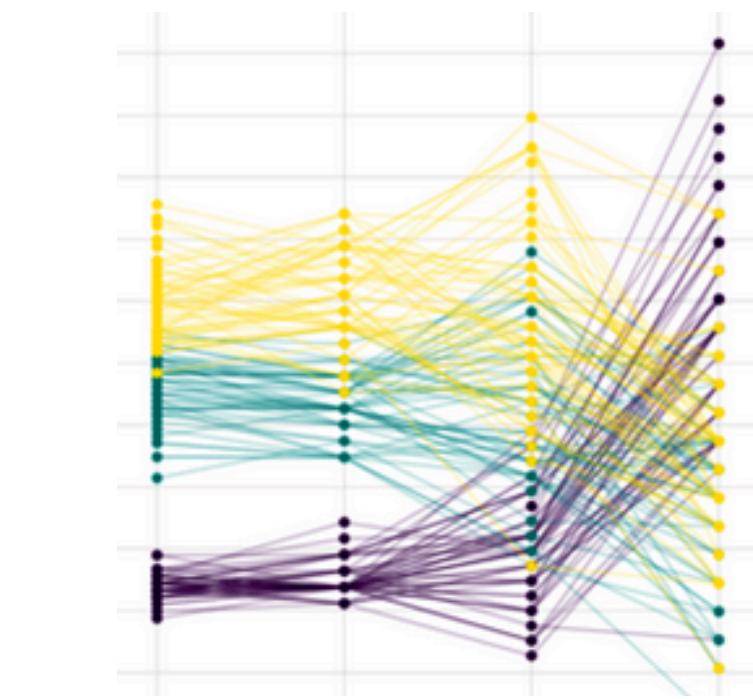
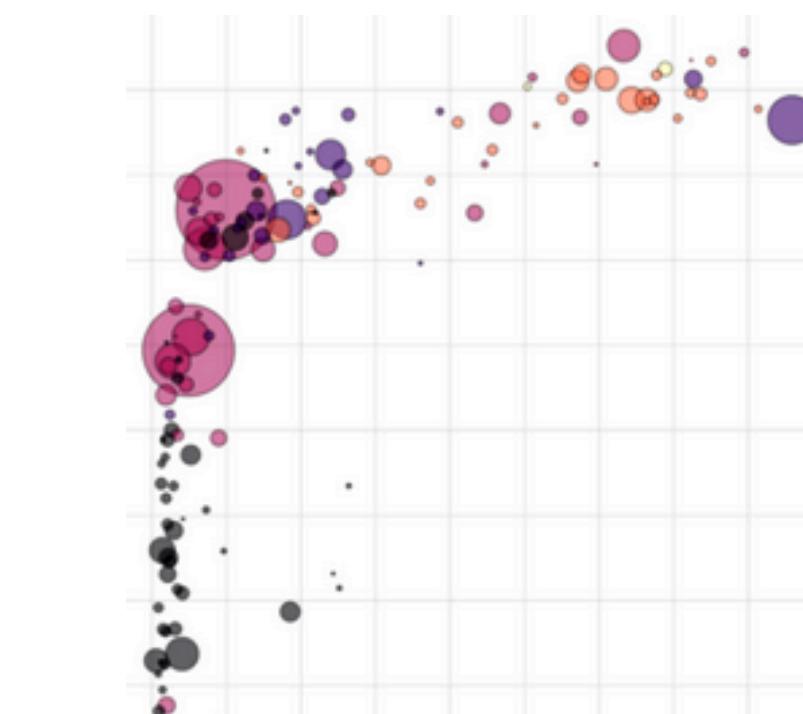
Well-defined “additive” (+) structure.



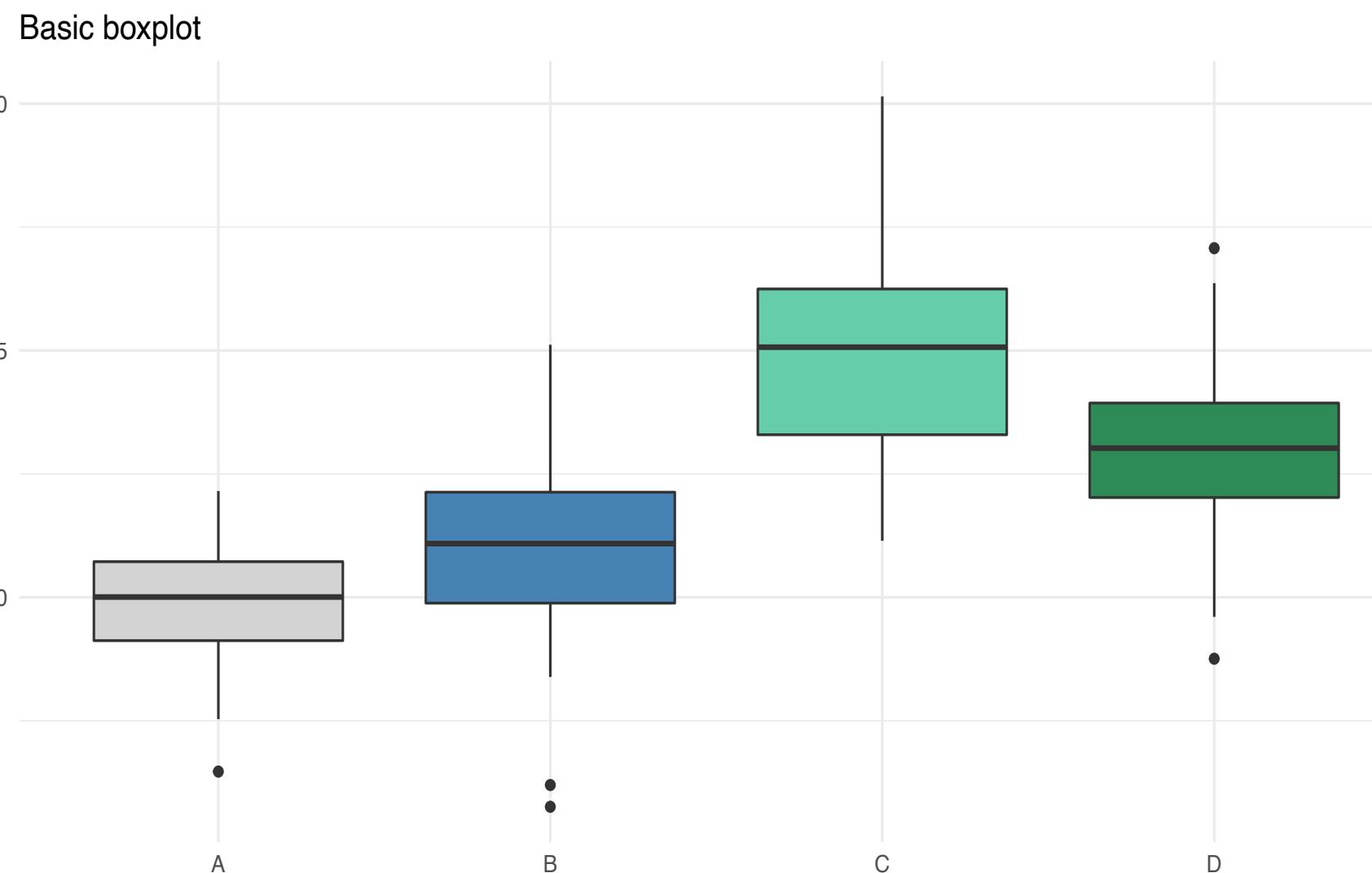
Integrates perfectly with tidy data.



Great documentation & community



GGPLOT2 ADDITIVE STRUCTURE



DATASET, SAMPLES &
OBSERVATIONS

```
ggplot(my.DS, aes(x=Sample,  
y=Measure))
```

DEFINE PLOT TYPE

```
ggplot(my.DS, aes(x=Sample,  
y=Measure))  
+ geom_boxplot()
```

COLOR BY GROUP

```
ggplot(my.DS, aes(x=Sample,  
y=Measure, fill=Sample))  
+ geom_boxplot()
```

TITLE AND LEGEND

```
... + ggtitle("Basic boxplot") +  
theme(legend.position="none",  
plot.title = element_text(size=11))
```

CUSTOM COLORS

```
... + scale_fill_manual(values =  
c("lightgray", "steelblue",  
"aquamarine3", "seagreen4"))
```

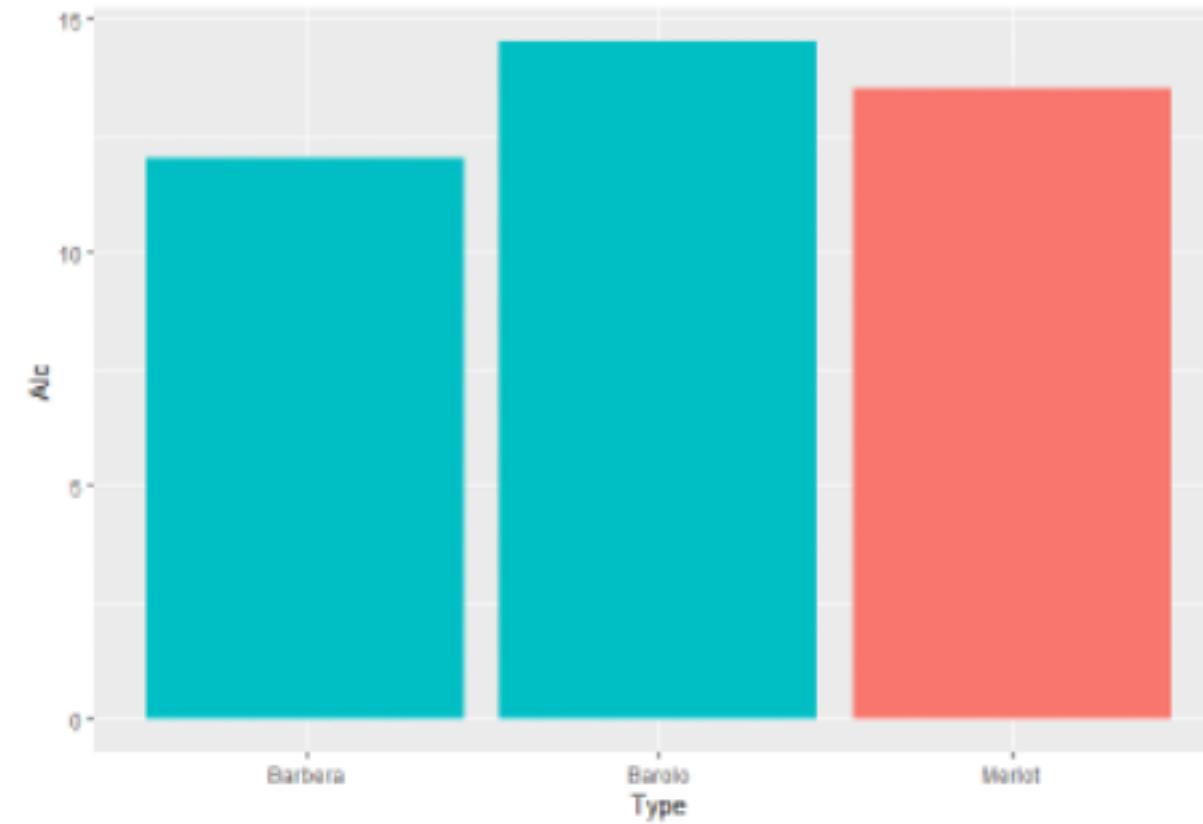
BACKGROUND

```
+ theme_minimal()
```

GGPLOT BASIC STRUCTURE

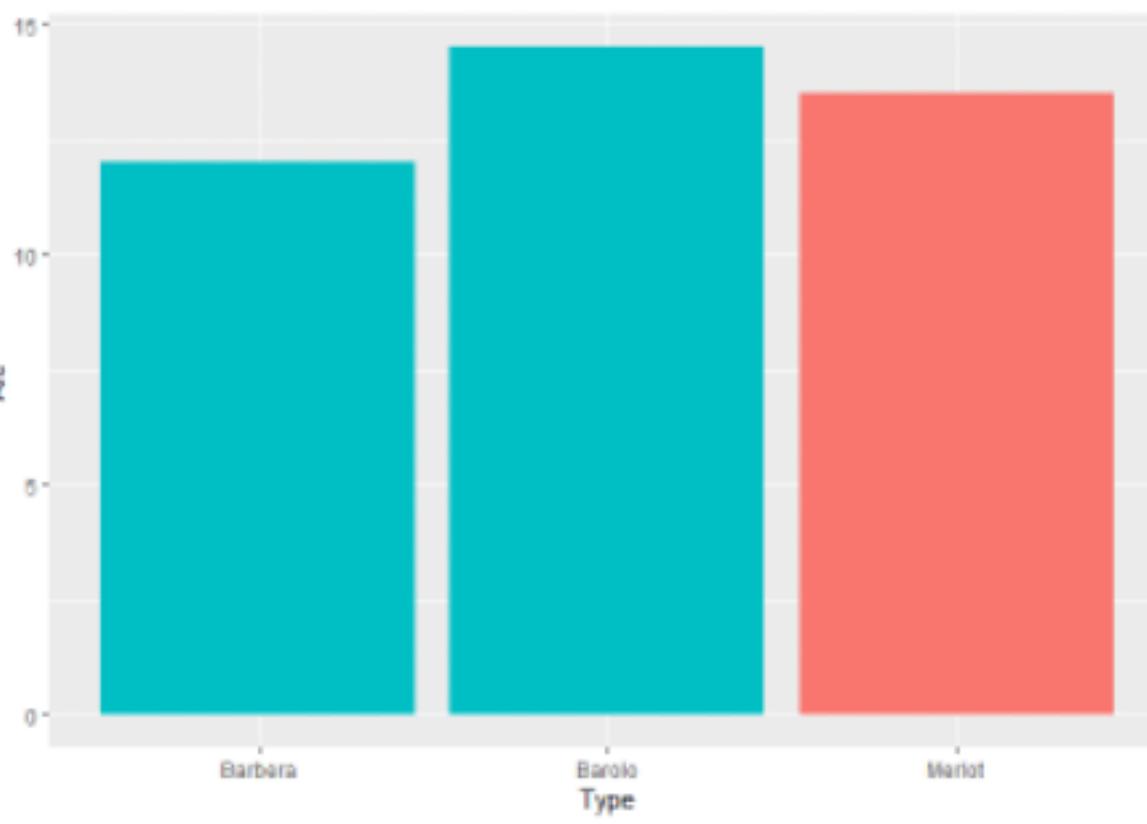
Geoms inherit the parameters from the ggplot they are added to:

```
ggplot(my_wine,
aes(x=Type, y=Alc, fill=Country))
+ geom_col()
```



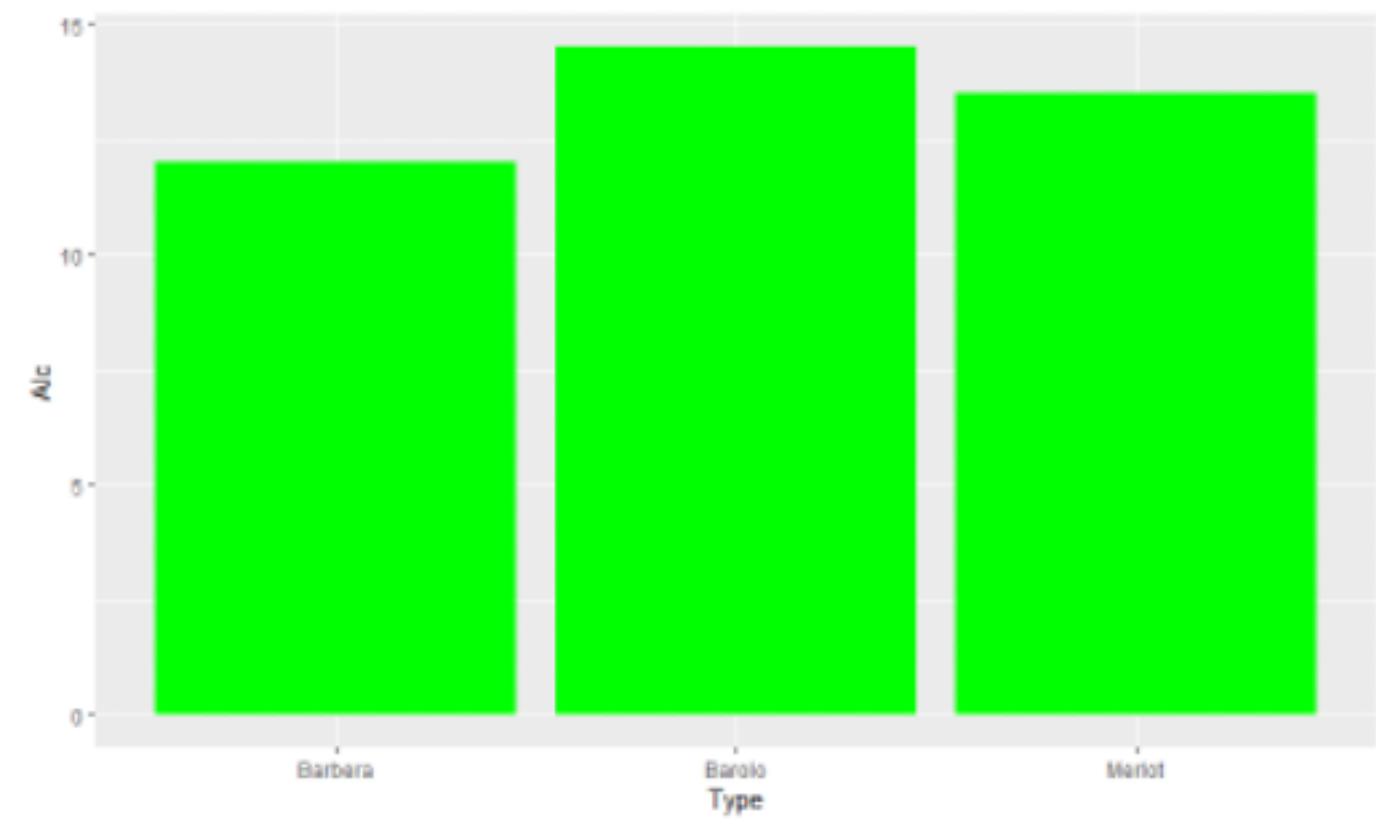
Alternatively, you can specify additional parameters directly in the geom:

```
ggplot(my_wine,
aes(x=Type, y=Alc))
+ geom_col(aes(fill=Country))
```



Things outside the aes are applied to everything!

```
ggplot(my_wine,
aes(x=Type, y=Alc))
+ geom_col(fill='green')
```



GGPLOT CHEAT SHEET

Define Plot:

```
ggplot(data = my.data,  
aes(x = x.var, y = y.var))
```

Add Plot Type:

- + geom_point()
- + geom_line()
- + geom_boxplot()
- + geom_col()
- + geom_density()
- + geom_histogram()

One Color:

```
ggplot(..., aes(...,  
color = "green"))
```

Color Fill by Group:

```
ggplot(..., aes(...,  
fill = group.var))
```

Custom Colors:

- + scale_*_manual(values = c())
- ex: scale_color_manual(values = c("blue", "pink"))

More Colors:

- + scale_fill_grey(start = 0.2, end = 0.8)
- + scale_fill_gradient(low="white", high="red")

Grid Theme:

- + theme_bw()
- + theme_minimal()
- + theme_dark()
- + theme_*

Labels:

- + ggtitle(...)
- + xlab(...)
- + ylab(...)

Text:

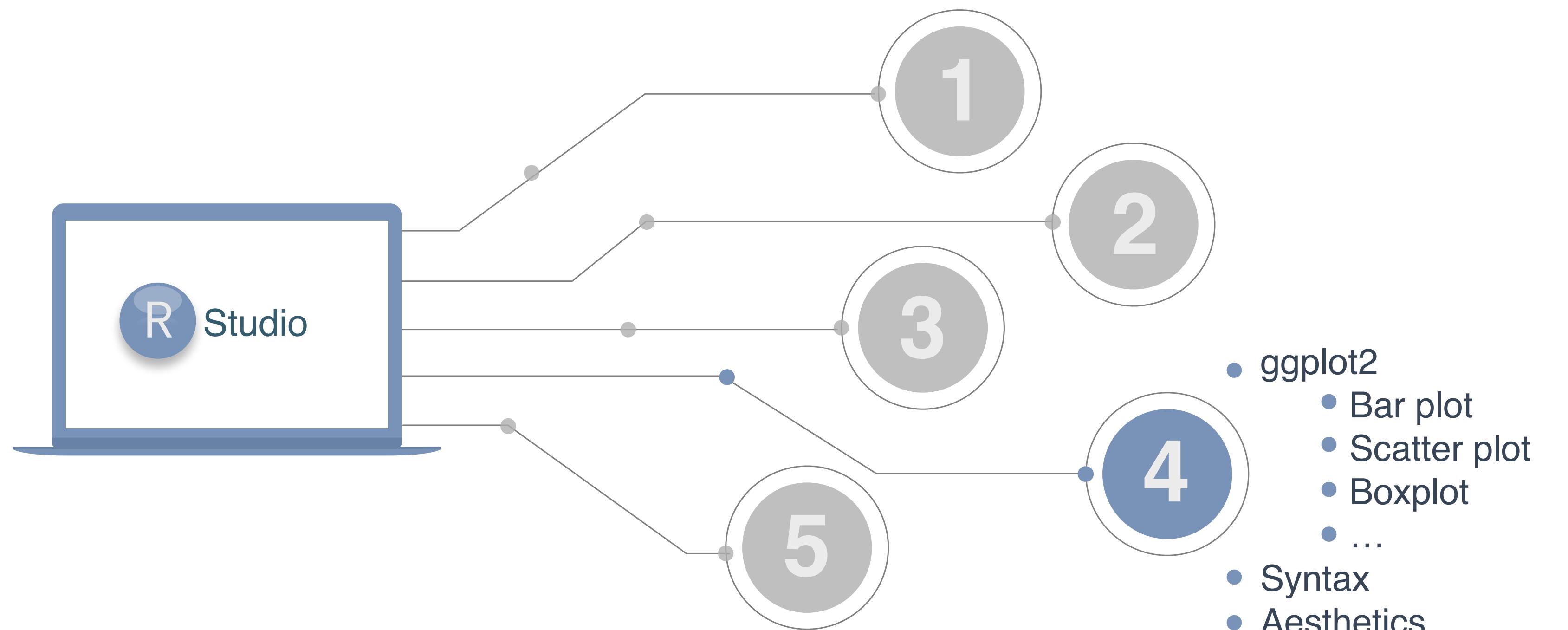
- + theme(* = element_text())
- + theme(axis.title = element_text(angle = 90, colour= "red"),
legend.text = element_text(size = 8, face = "bold"))

GET
STARTED

COLORS

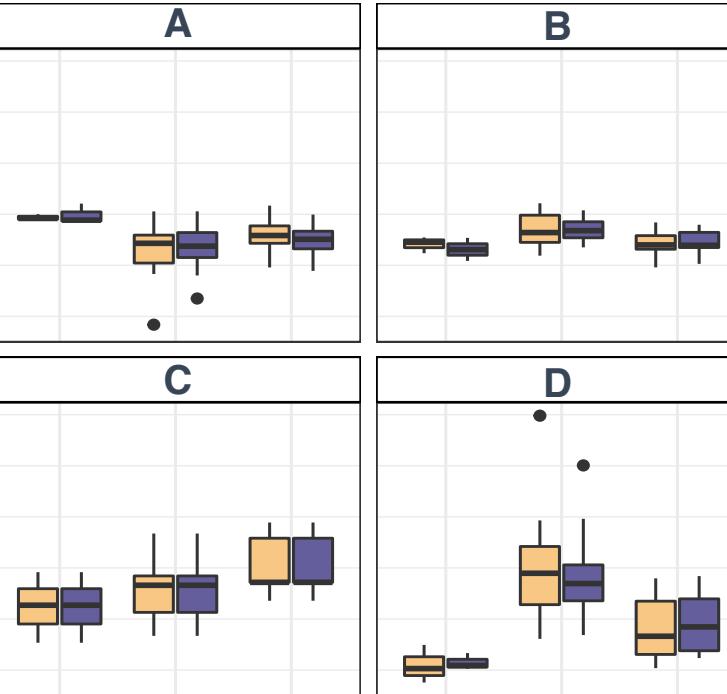
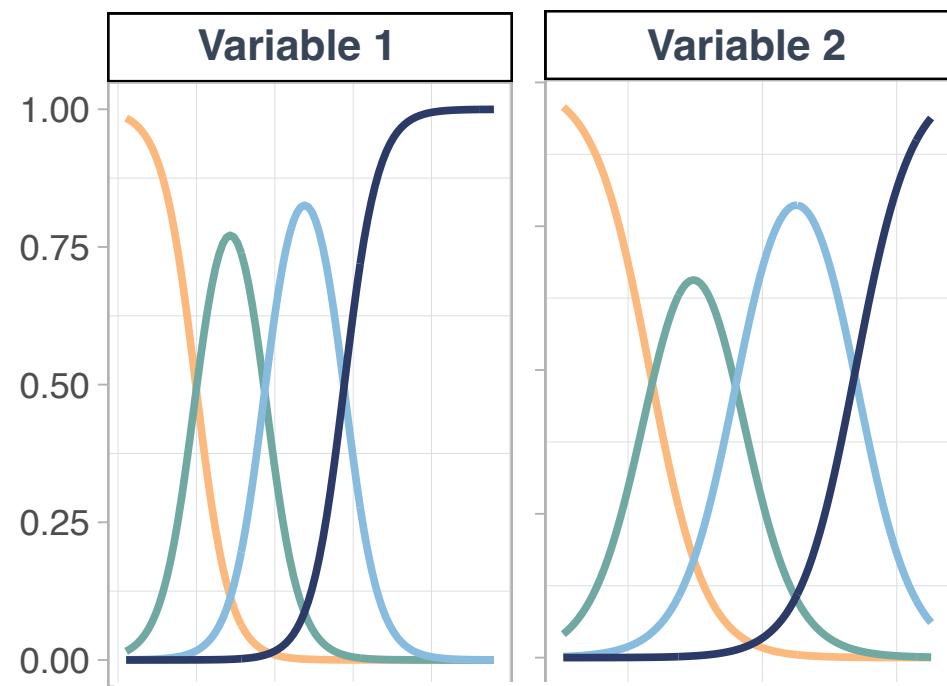
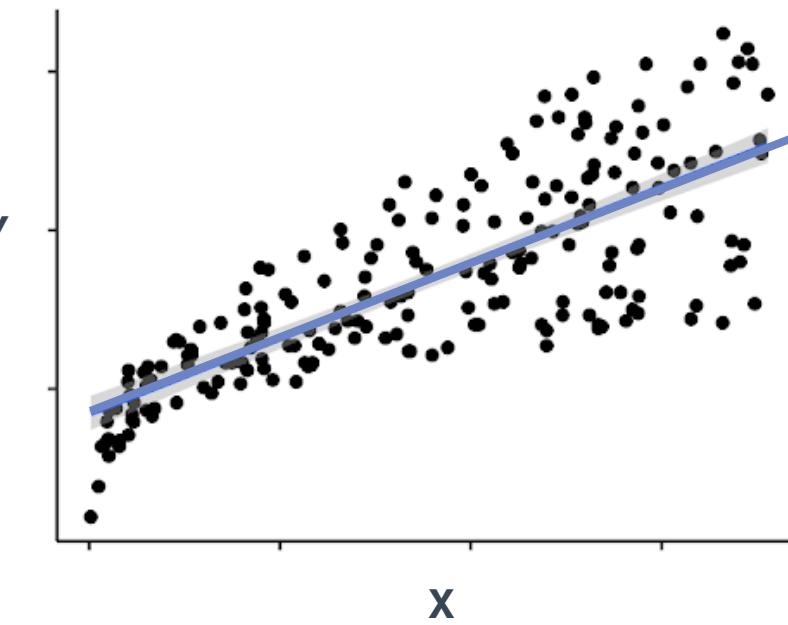
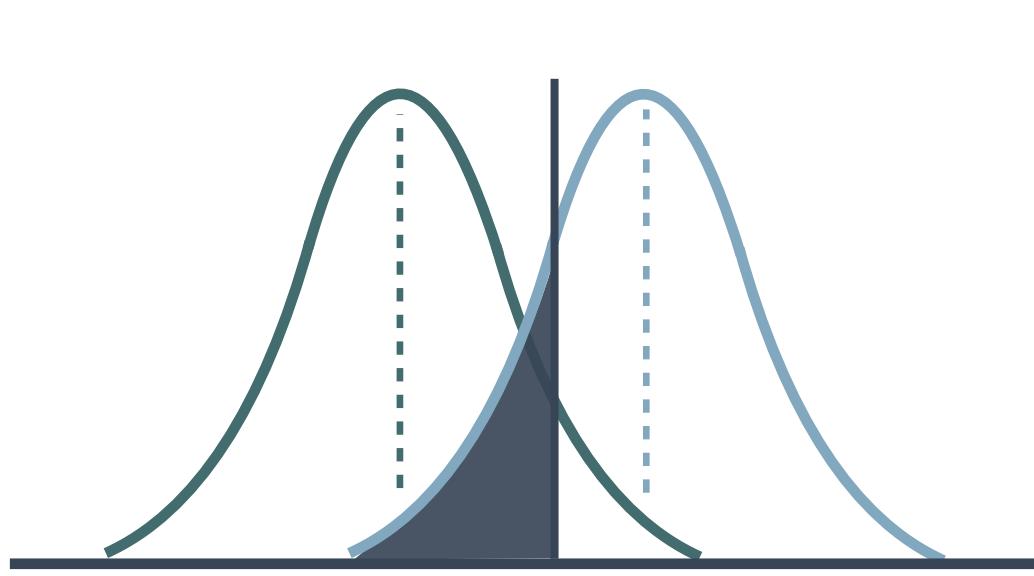
COLOR SCALES
& THEMES

TEXT



— GGPlot2 EXERCISE 4

R - A STATISTICAL SCRIPTING LANGUAGE



MODEL FUNCTIONS

`lm()`, `glm()`
`lmer()`, `glmer()`,
`nls()`, ...

EMMEANS PACKAGE

`emmeans()`,
`pairs()`, `cld()`

APPLY TO MODEL

`summary()`, `anova()`,
`confint()`, `predict()`,
`drop1()`, `update()`,
`step()`, ...

MORE FUNCTIONS

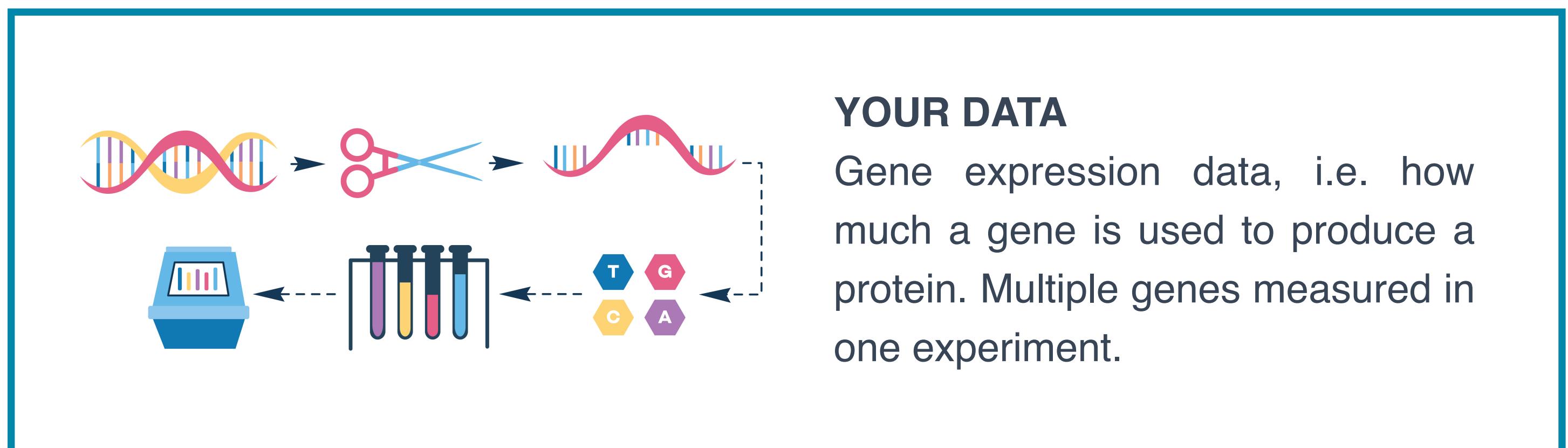
`t.test()`, `cor()`,
`cor.test()`, `aov()`,
`quantile()`,
`p.adjust()`,
`rank()`, ...

Let's use R in a statistical analysis



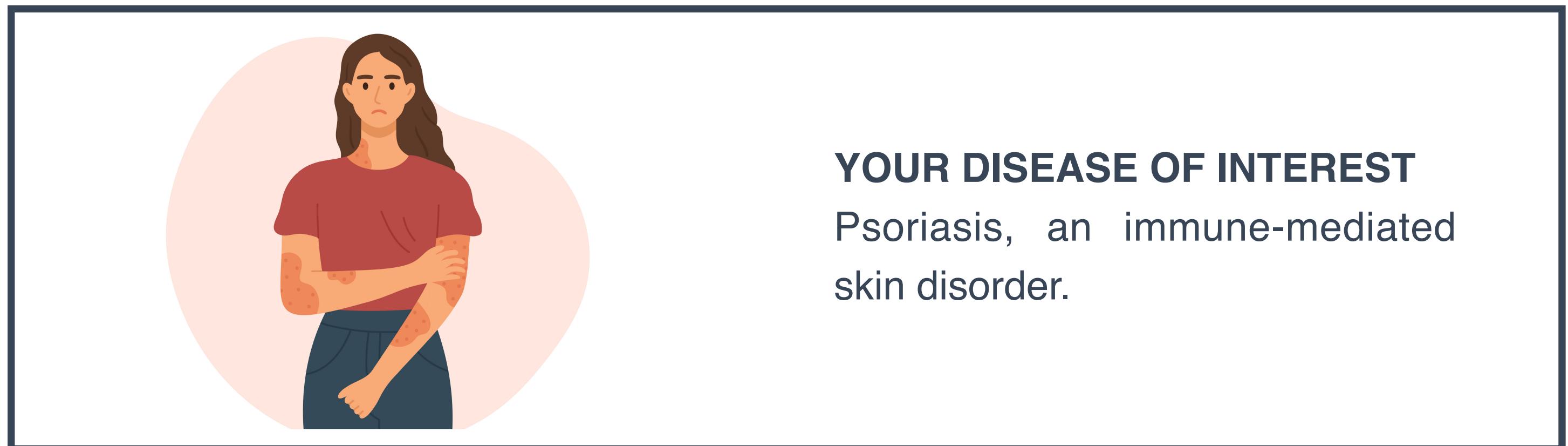
YOU

The researcher with R skills!



YOUR DATA

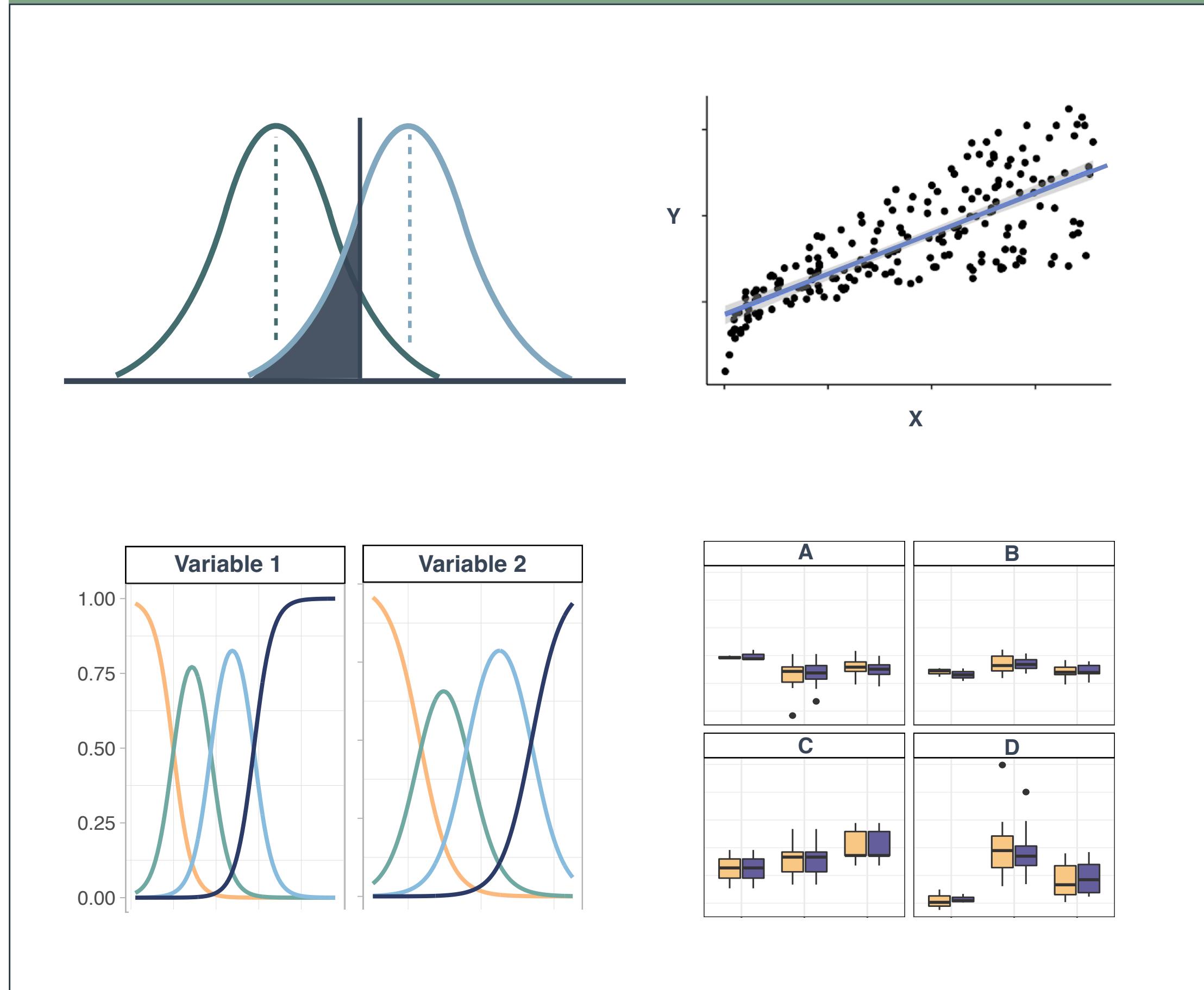
Gene expression data, i.e. how much a gene is used to produce a protein. Multiple genes measured in one experiment.



YOUR DISEASE OF INTEREST

Psoriasis, an immune-mediated skin disorder.

R - A STATISTICAL SCRIPTING LANGUAGE



During this session:

- *Cooperatively* discuss and share ideas about the data
- Apply steps of basic statistical analysis for hypothesis testing consistent with the given data
- Suggest conclusions based on your analysis, regarding the association between psoriasis and gene expression levels

STATS CHEAT SHEET

Import Data:

```
read_excel("my.data.xlsx")
```

Overview of Data:

```
summary(my.data)  
nrow(my.data)
```

```
length(my.data)  
names(my.data)
```

Linear:

```
lm(y~x, data=my.data)  
confint(model)
```

Logistic:

```
glm(y~x,  
data=my.data)
```

Linear Mixed:

```
lmer(y~x + (1|z),  
data=my.data)
```

Check Model:

```
summary(model)  
par(mfrow=c(2,2))  
plot(model)
```

ANOVA:

```
anova(model2, model1)
```

F-Test:

```
drop1(model, test="F")
```

Emmeans:

```
emmeans(model, ~x)  
pairs(emmeans(model, ~x))
```

Check Type:

```
table(my.data$x)  
is.numeric(my.data$x)  
is.factor(my.data$x)
```

Change Type:

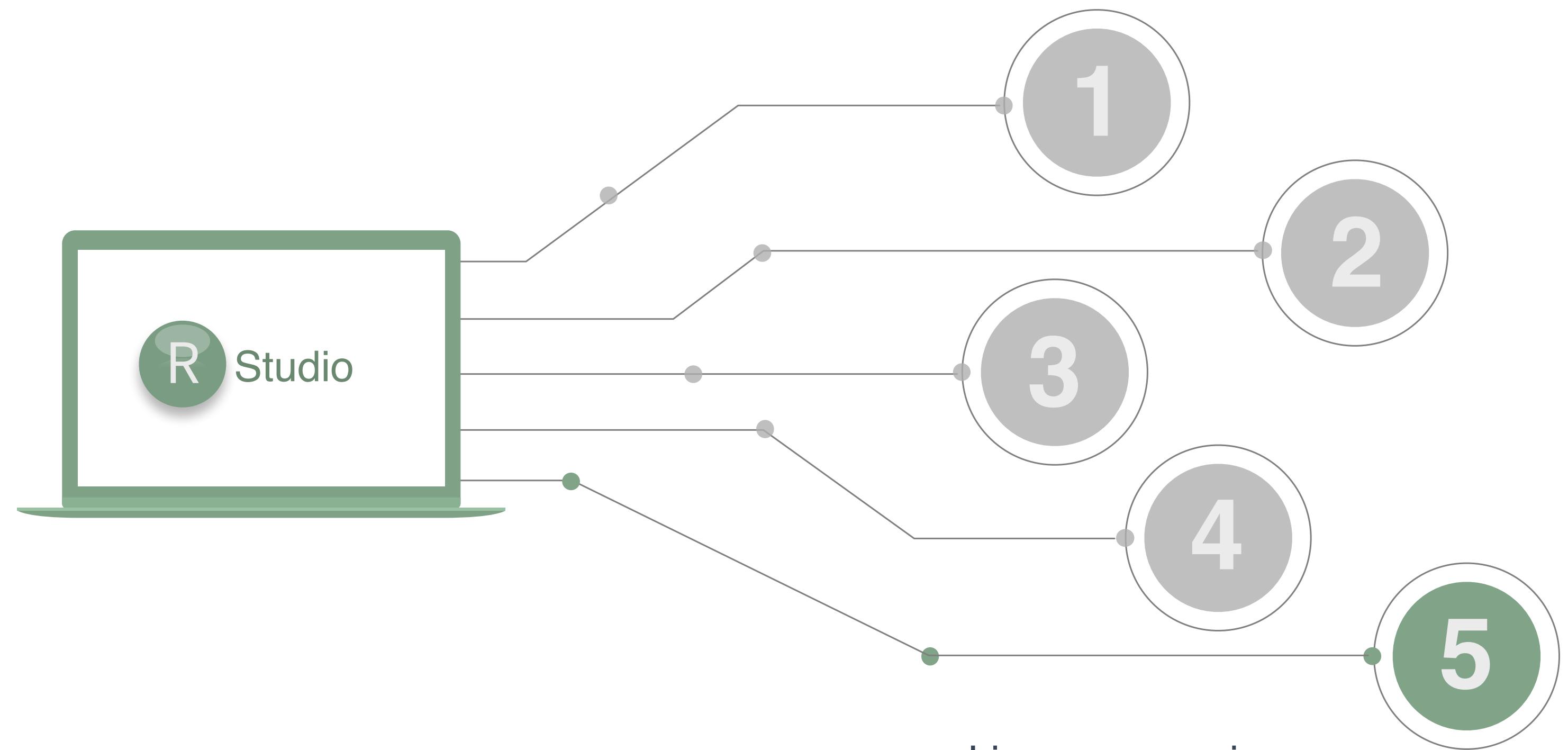
```
my.data <- mutate(my.data, x = factor(x))  
my.data$z <- as.numeric(my.data$z)
```

GET
STARTED

REGRESSION
MODELS

TESTS/
COMPARISONS

VARIABLES

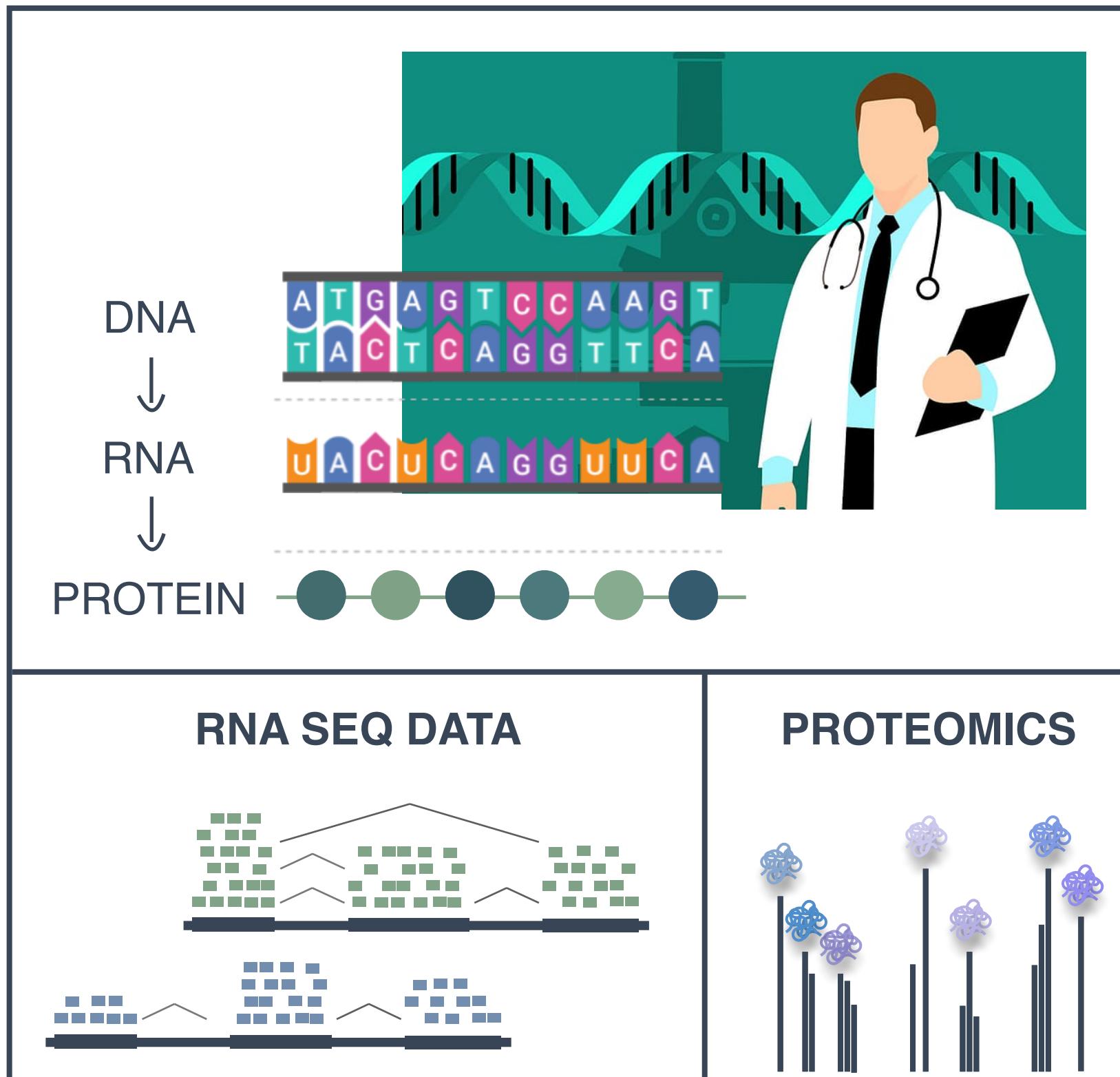


- Linear regression
- Summary Statistics
- ANOVA
- Logistic regression
- Clustering
- Correlation

— Statistics in R
EXERCISE 5

BIOINFORMATICS IN R

HIGH THROUGHPUT DATA



BIOINFORMATIC ANALYSIS

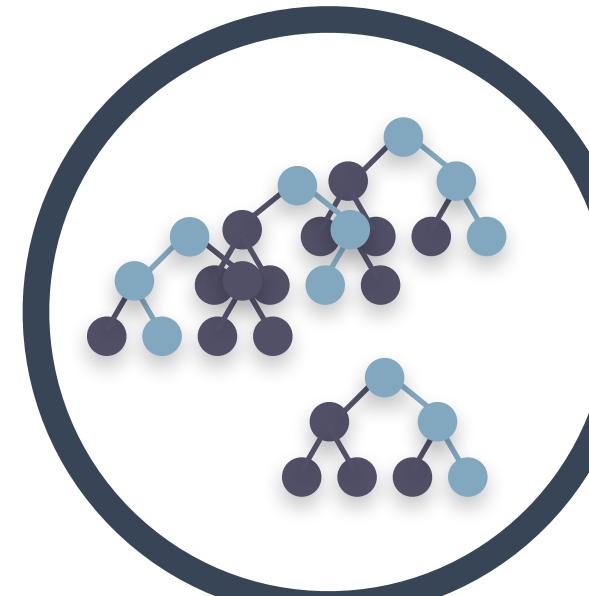
DIMENSIONALITY REDUCTION



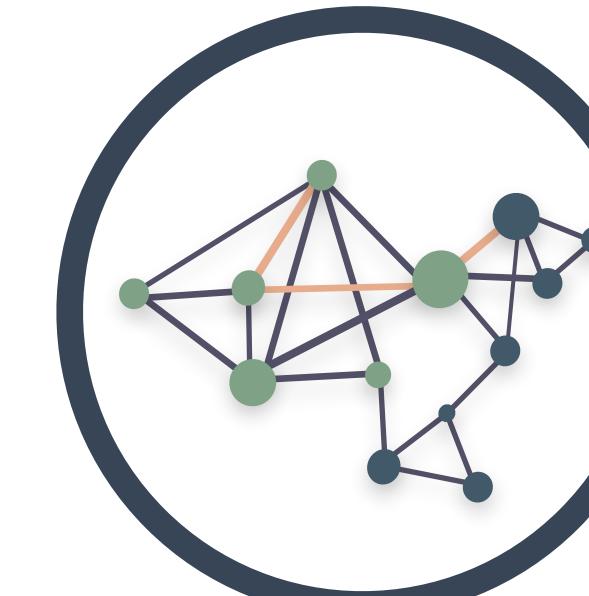
CLUSTERING



MACHINE LEARNING



NETWORK ANALYSIS



THE TOP OF THE R ICEBERG



STATISTICAL ANALYSIS

Statistical models (linear, generalized, mixed, ...)

Statistical tests (t-test, chisq, anova, ...)

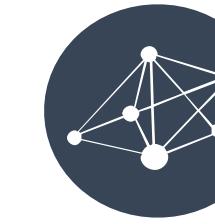
Survival analysis (Cox, Kaplan meier)



DATA MANGEMENT



EASY PLOTTING



BIOINFORMATIC ANALYSIS

— FROM EXCEL TO R

WANT MO-R-E?



The Section for Biostatistics offers a number statistics-oriented R courses:

Spring

[Basic Statistics for Health Researchers \(Danish course\)](#)

ECTS: 9,0

[Epidemiological methods in medical research](#)

ECTS: 7

[Advanced topics in health research B](#)

ECTS: 2,8

[Statistical methods in bioinformatics](#)

ECTS: 3,5

[Statistical analysis of survival data](#)

ECTS: 4,9

<https://publichealth.ku.dk/about-the-department/biostat/>

[Programming and statistical modelling in R](#)

ECTS: 1,6

[Bayesian methods in biomedical research](#)

ECTS: 2,4

[Psychometric validation of patient reported outcome measures](#)

ECTS: 2,5

[Introduction to validation of patient reported outcome measures](#)

[Causal inference I](#)

ECTS: 2,5

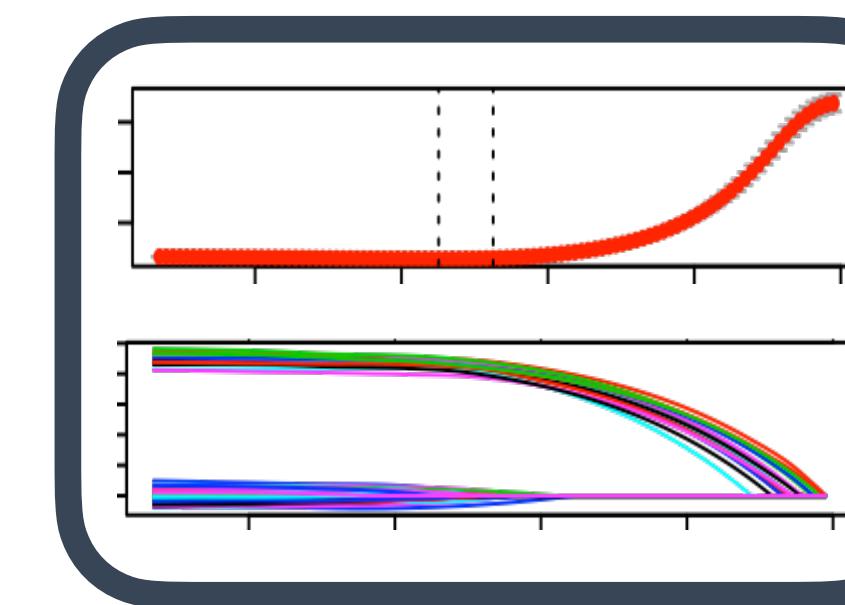
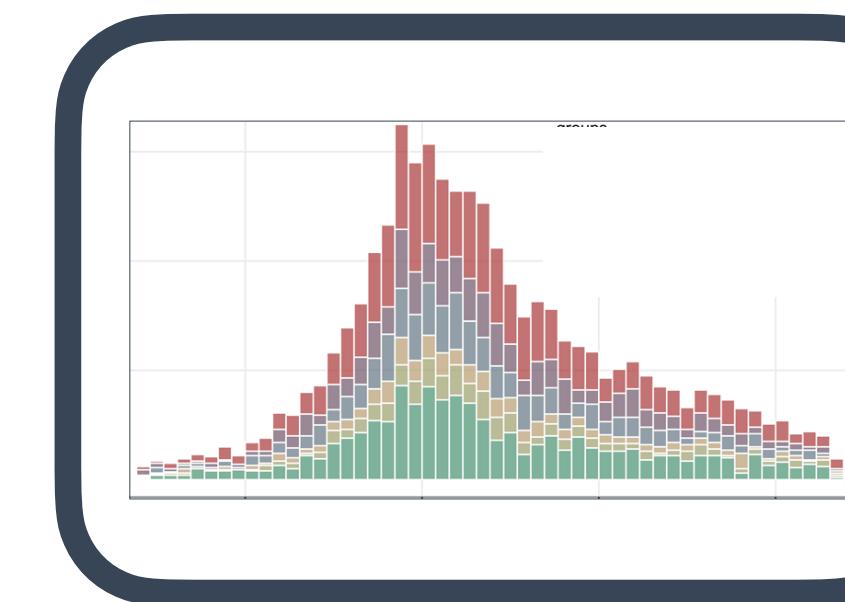
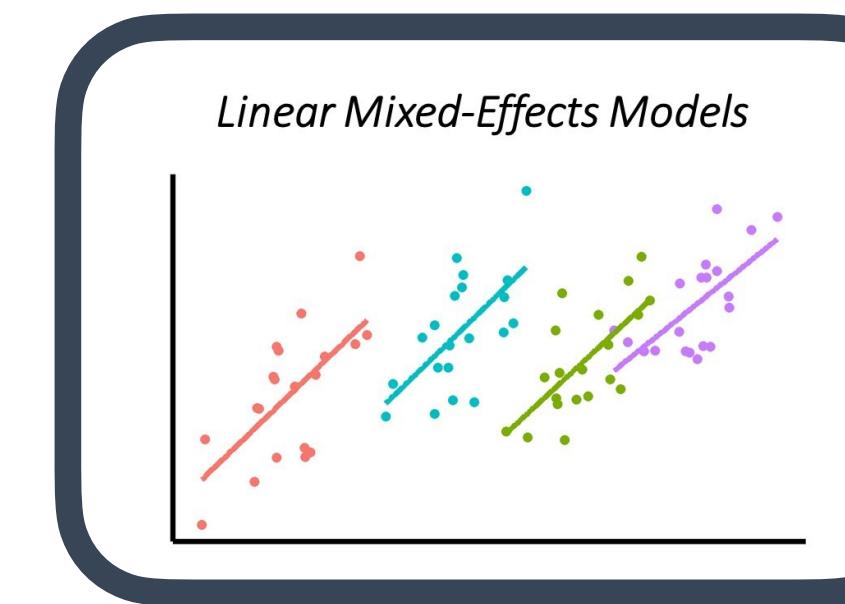
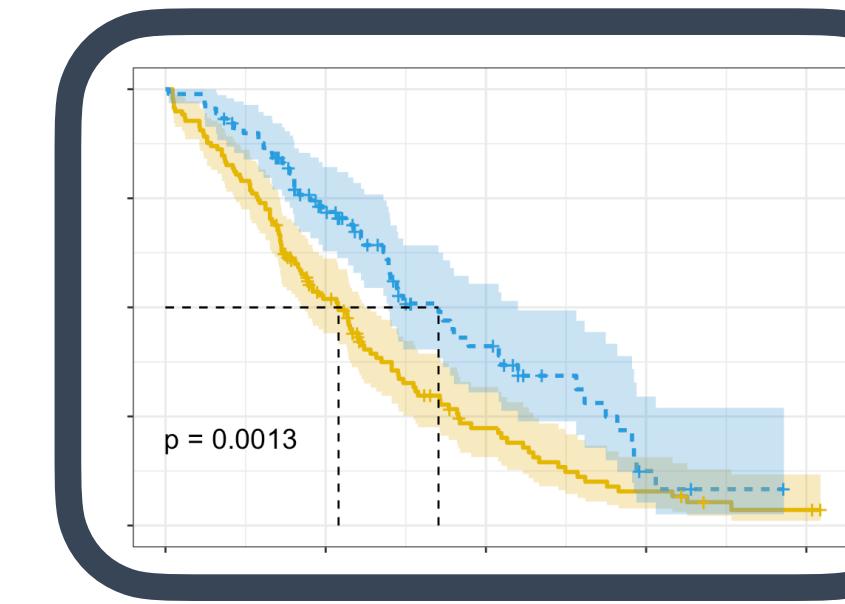
[Use of the statistical software R](#)

ECTS: 2,1

* These are screenshots. Go to the website and scroll down to ‘Teaching’



— TEASER STATISTICS in R



Survival Analysis

`survival`: <https://rviews.rstudio.com/2017/09/25/survival-analysis-with-r/>

`survminer`: <https://cran.r-project.org/web/packages/survminer/survminer.pdf>
(<https://rpkgs.datanovia.com/survminer/>)

Mixed-Effects Models

`lme4`: <https://cran.r-project.org/web/packages/lme4/vignettes/lmer.pdf>

<https://cran.microsoft.com/snapshot/2017-08-01/web/packages/sjPlot/vignettes/sjplmer.html>

`glmmTMB`: <https://cran.r-project.org/web/packages/glmmTMB/index.html>

Epidemiological Analysis

`Epi`: <https://cran.r-project.org/web/packages/Epi/index.html>

`pubh`: <https://rviews.rstudio.com/2020/03/05/covid-19-epidemiology-with-r/>

https://cran.r-project.org/web/packages/incidence/vignettes/customize_plot.html

<https://rviews.rstudio.com/2020/03/05/covid-19-epidemiology-with-r/>

Elastic-Net Regression

`glmnet`: <https://cran.r-project.org/web/packages/glmnet/glmnet.pdf>

`elasticnet`: <https://cran.r-project.org/web/packages/elasticnet/elasticnet.pdf>

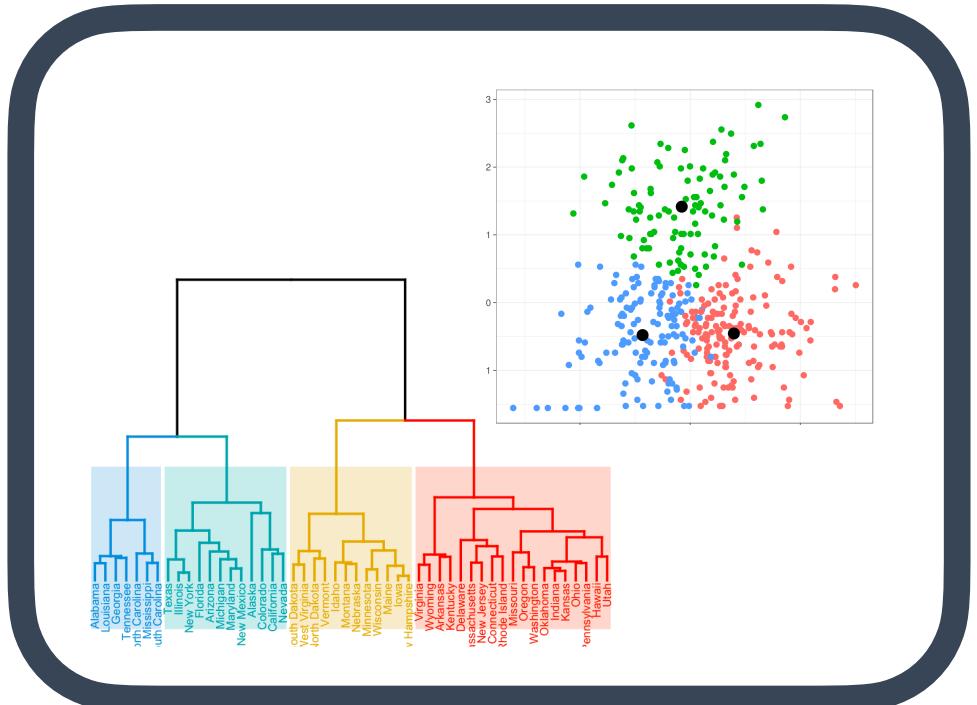
<https://www.datacamp.com/community/tutorials/tutorial-ridge-lasso-elastic-net>

TEASER

Machine Learning

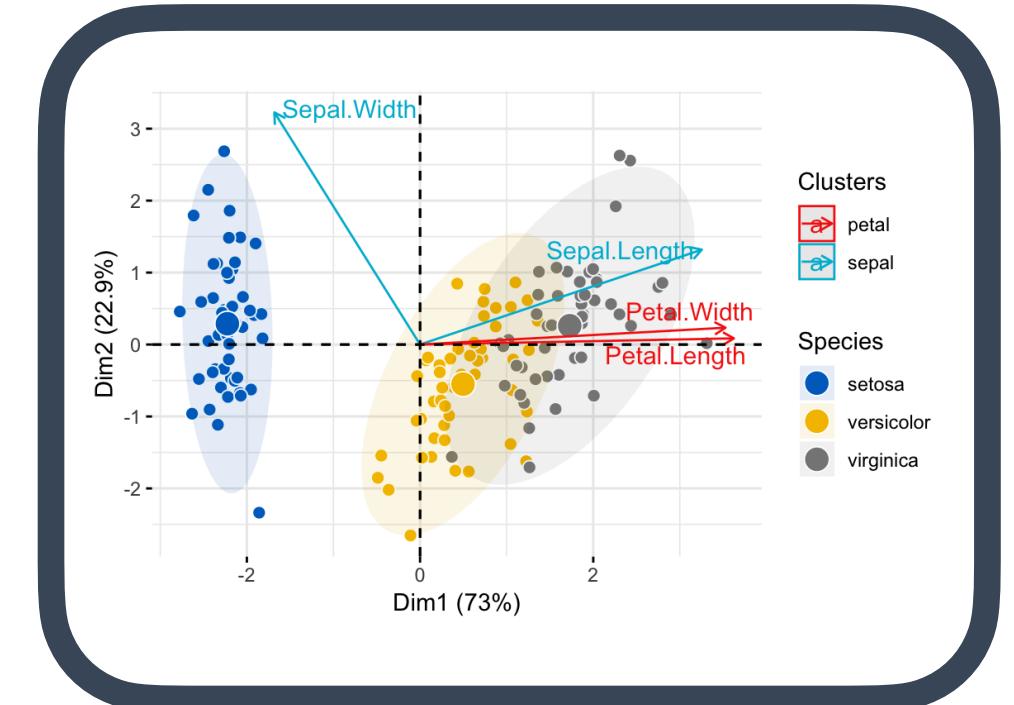
[https://lgatto.github.io/
IntroMachineLearningWithR/an-
introduction-to-machine-learning-
with-r.html](https://lgatto.github.io/IntroMachineLearningWithR/an-introduction-to-machine-learning-with-r.html)

Clustering



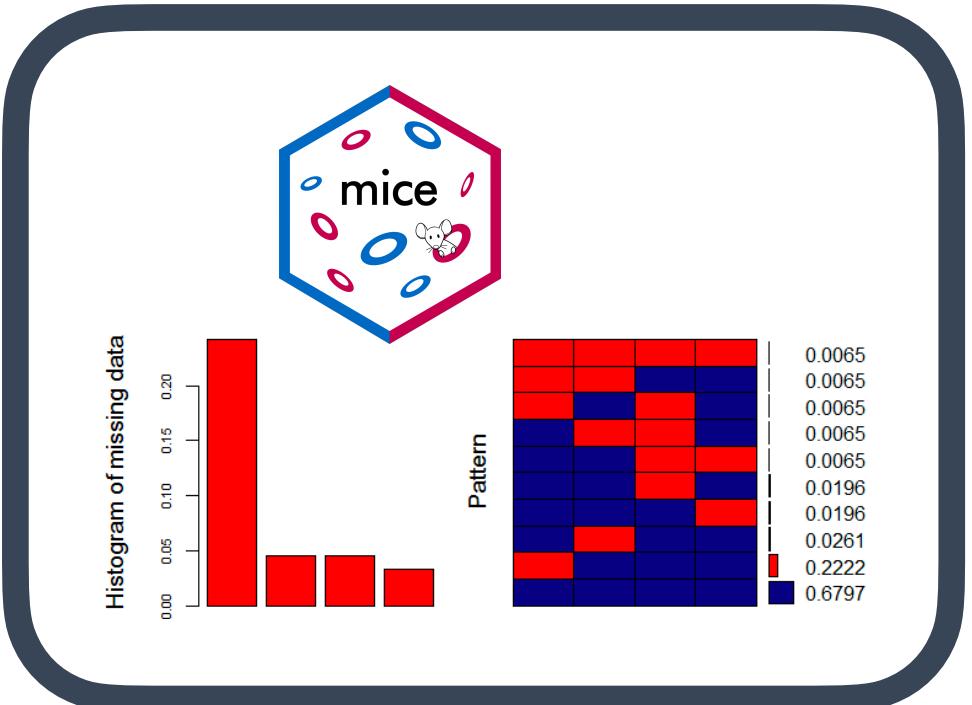
[https://statsandr.com/blog/clustering-
analysis-k-means-and-hierarchical-
clustering-by-hand-and-in-r/](https://statsandr.com/blog/clustering-analysis-k-means-and-hierarchical-clustering-by-hand-and-in-r/)

Feature Selection: PCA



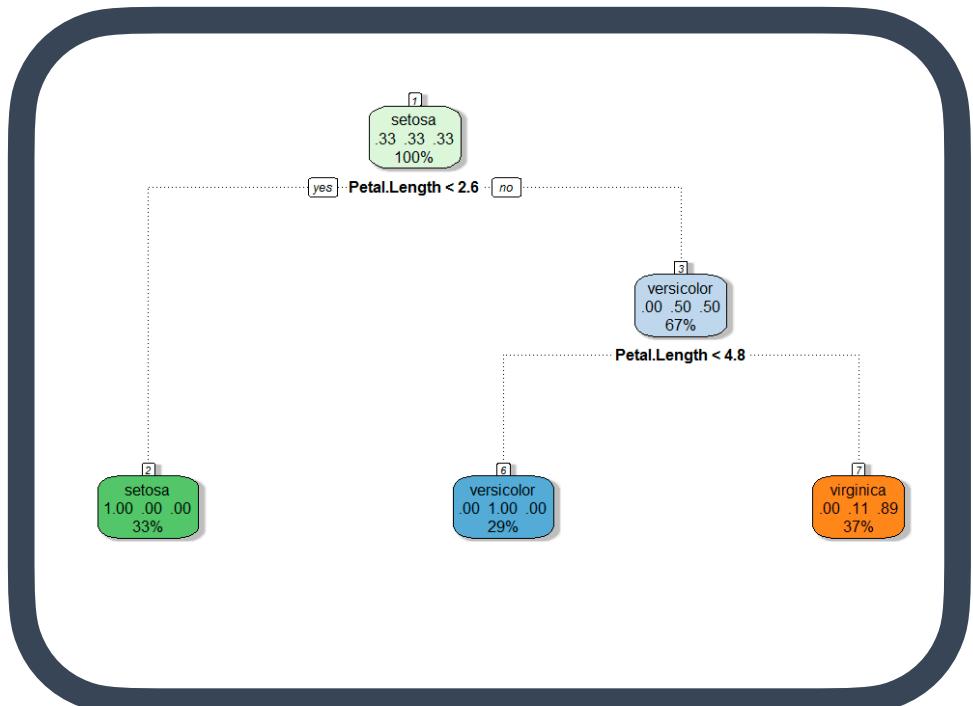
[https://bioconductor.org/packages/
release/bioc/vignettes/PCATools/inst/
doc/PCATools.html](https://bioconductor.org/packages/release/bioc/vignettes/PCATools/inst/doc/PCATools.html)

Missing Data



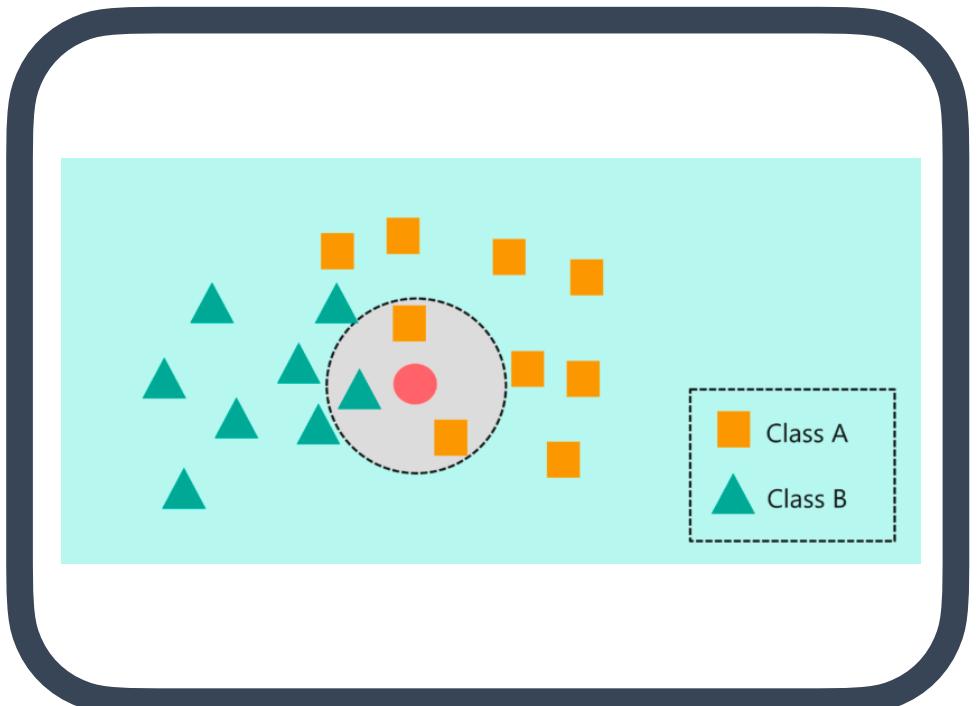
<https://amices.org/mice/>
[https://datascienceplus.com/imputing-
missing-data-with-r-mice-package/](https://datascienceplus.com/imputing-missing-data-with-r-mice-package/)

Random Forest



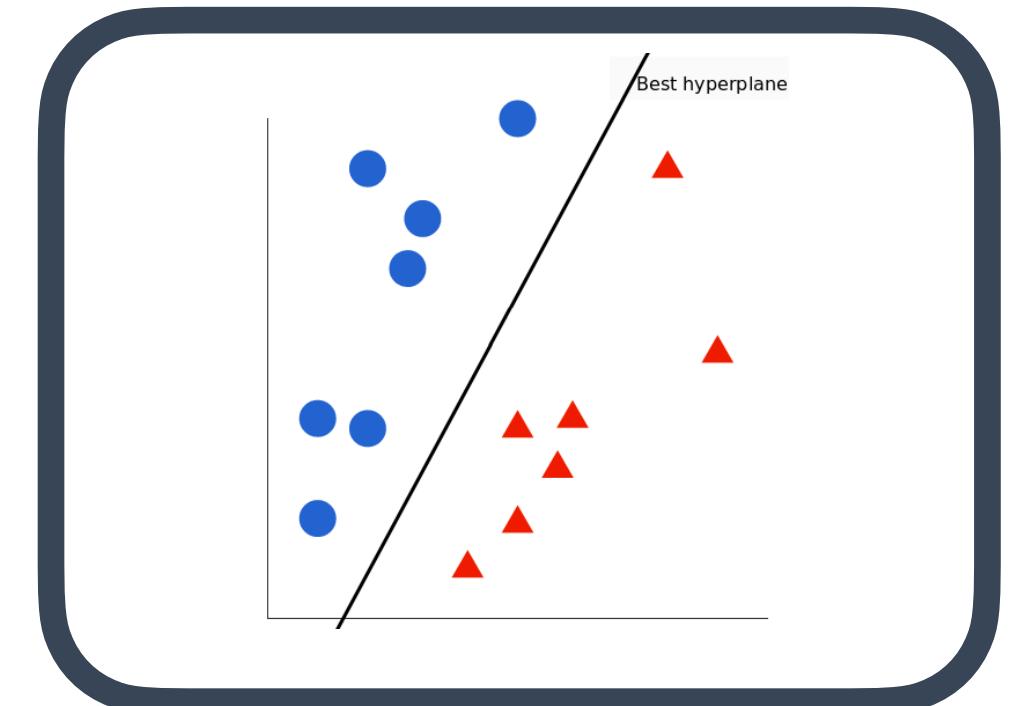
[https://www.blopig.com/blog/
2017/04/a-very-basic-introduction-to-
random-forests-using-r/](https://www.blopig.com/blog/2017/04/a-very-basic-introduction-to-random-forests-using-r/)

kNN



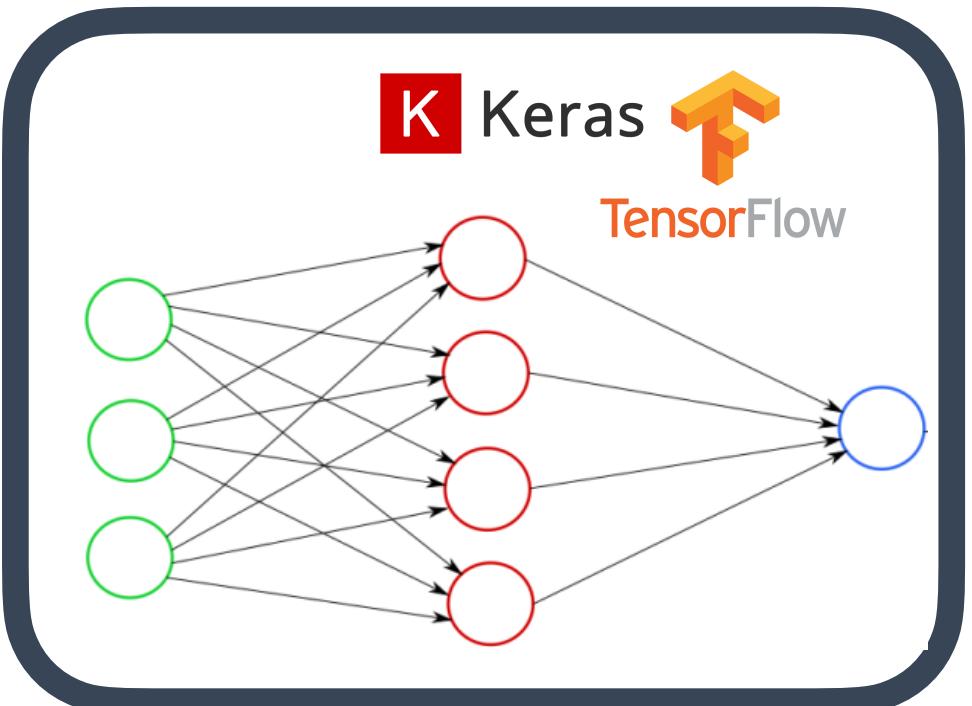
[https://www.edureka.co/blog/knn-
algorithm-in-r/](https://www.edureka.co/blog/knn-algorithm-in-r/)

SVM



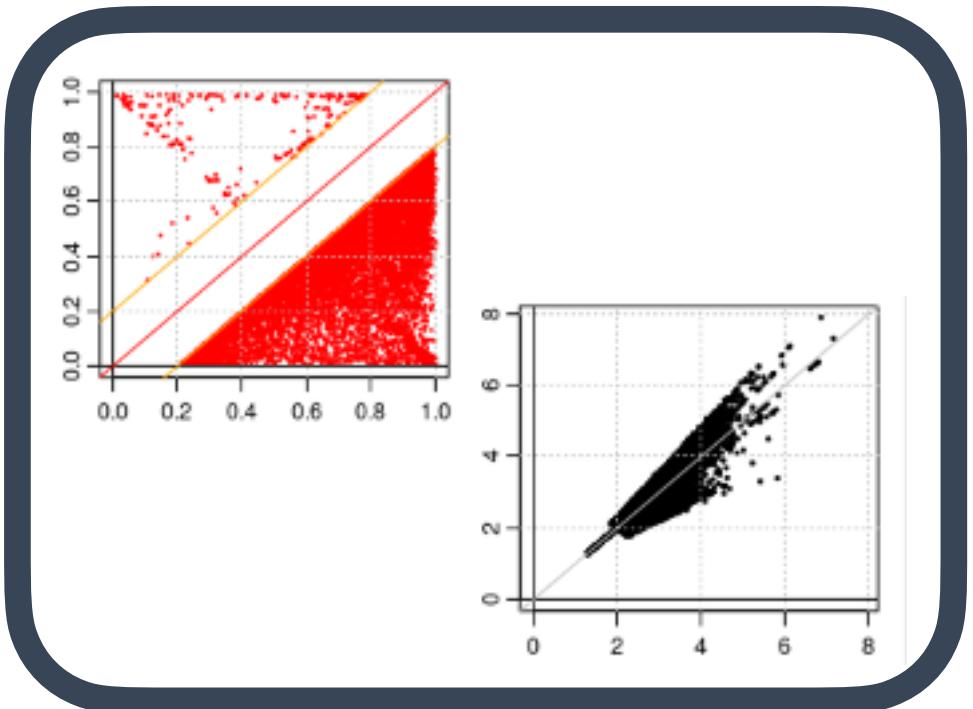
[https://cran.r-project.org/web/packages/
e1071/vignettes/svmdoc.pdf](https://cran.r-project.org/web/packages/e1071/vignettes/svmdoc.pdf)

Neural Networks



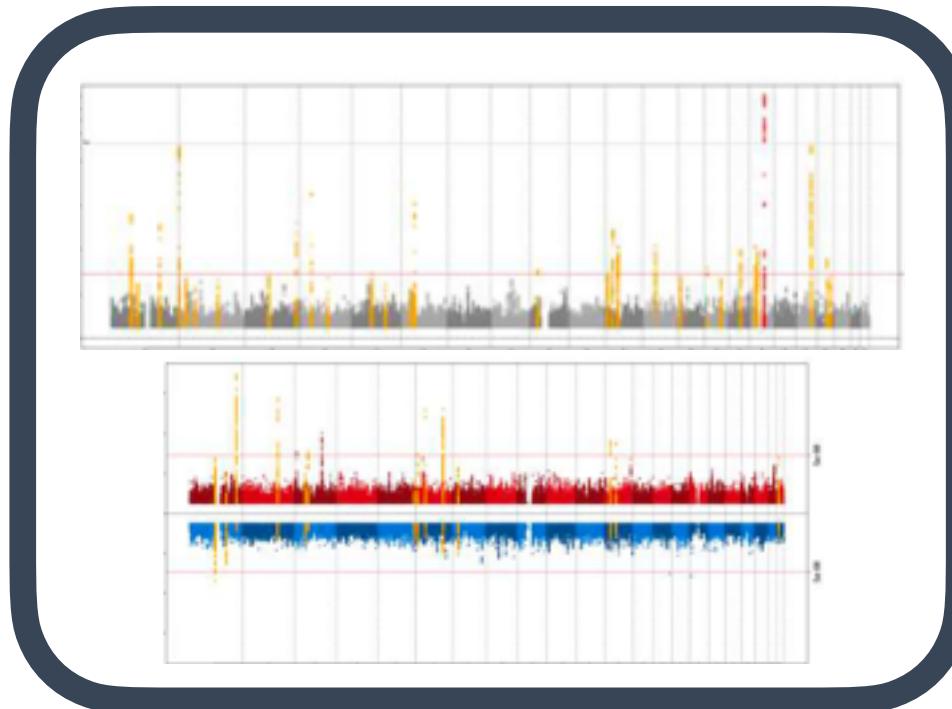
<https://keras.rstudio.com/>
<https://tensorflow.rstudio.com/>

GWAS - QC & Data Harmonization



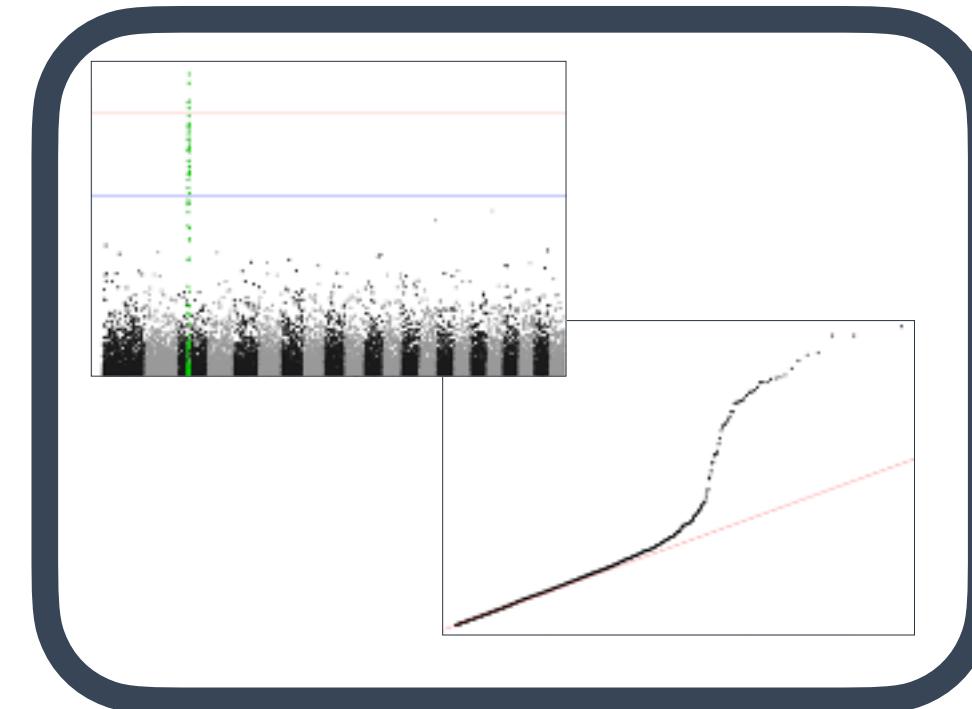
EasyQC: <https://www.uni-regensburg.de/medizin/epidemiologie-praeventivmedizin/genetische-epidemiologie/software/>

GWAS Data Management & Plots



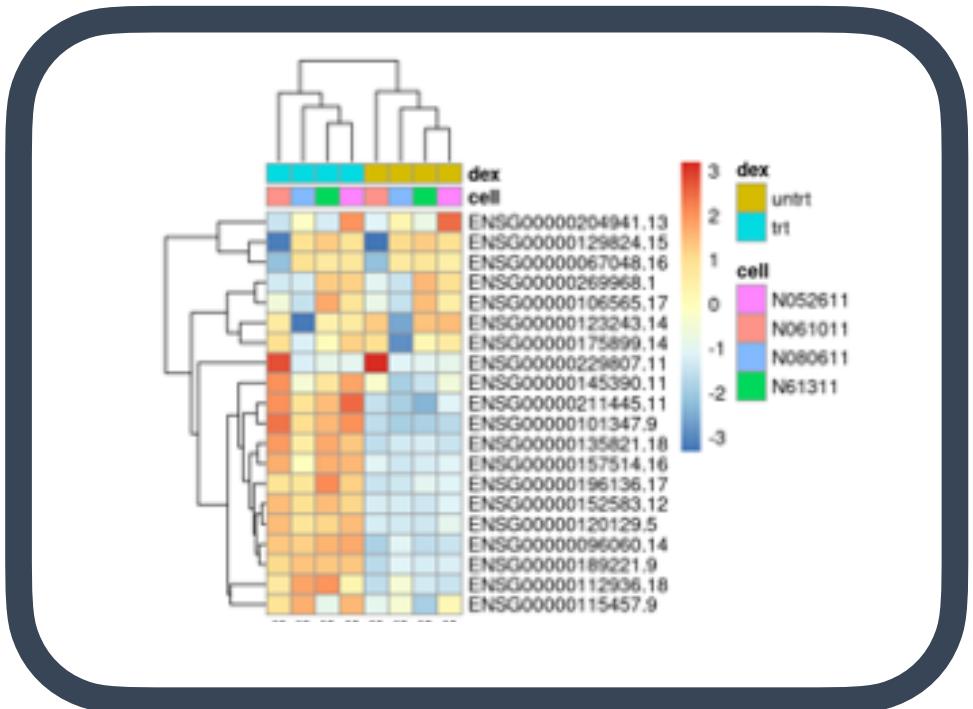
EasyStrata: <https://www.uni-regensburg.de/medizin/epidemiologie-praeventivmedizin/genetische-epidemiologie/software/>

More Plotting...



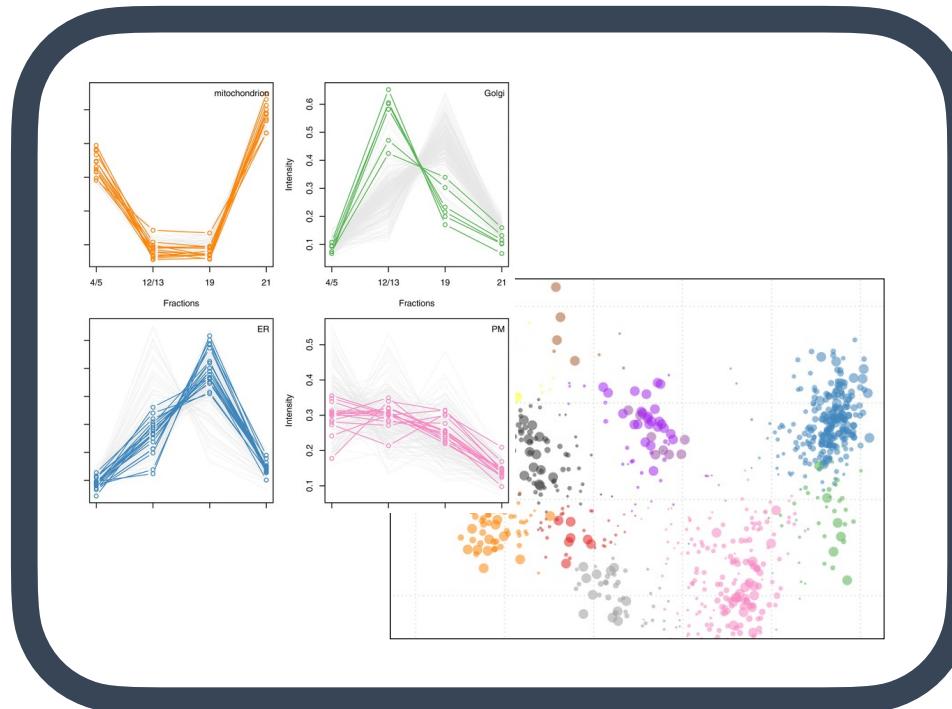
Manhattan and QQ plots: <https://cran.r-project.org/web/packages/qqman/vignettes/qqman.html>

Gene Expression Analysis



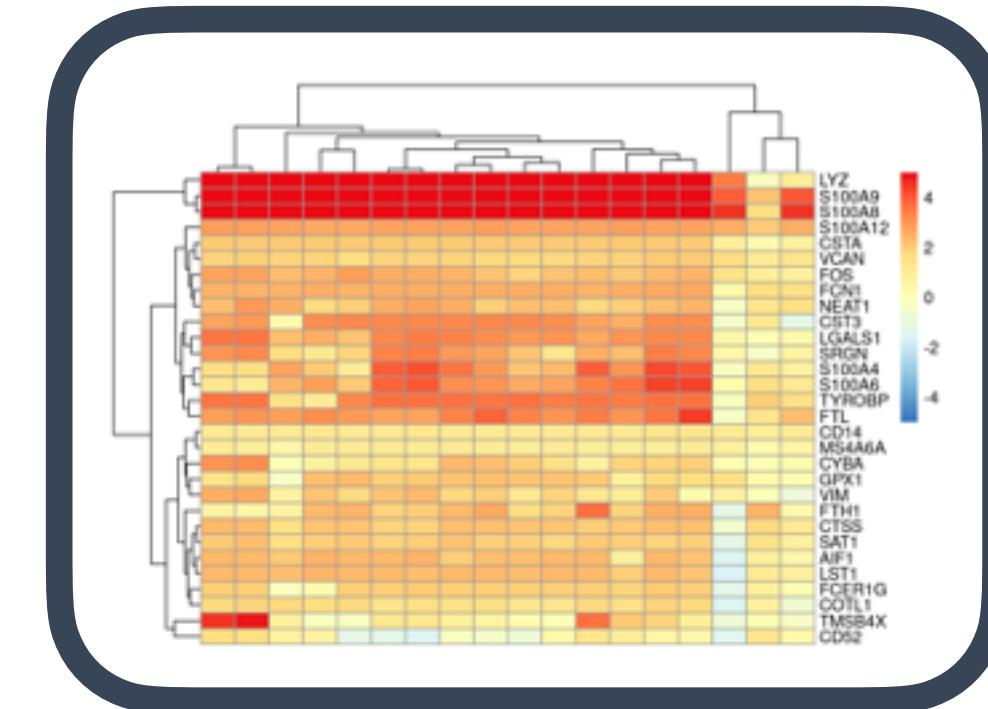
DESeq2, limma, EdgeR, etc.: http://www.bioconductor.org/packages/release/BiocViews.html#_RNASeq

Proteomics Analysis



RforProteomics: http://www.bioconductor.org/packages/release/BiocViews.html#_Proteomics

Single-Cell RNASeq



<https://cran.r-project.org/web/packages/e1071/vignettes/svmdoc.pdf>

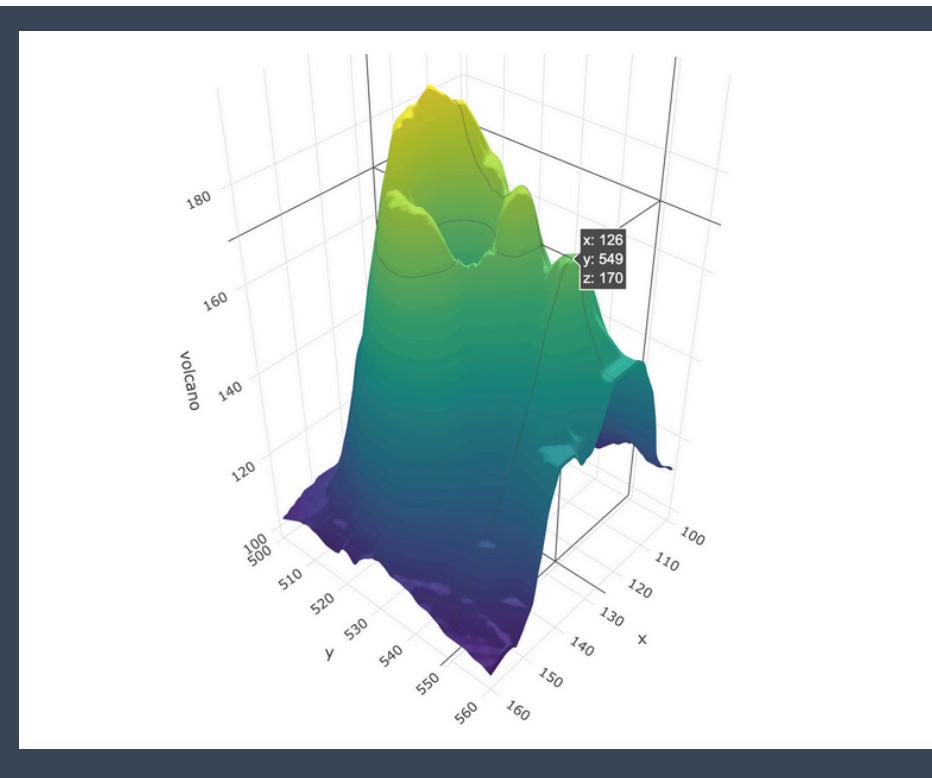
— TEASER Omics Data

<http://www.bioconductor.org/packages/release/BiocViews.html>

COOL STUFF IN R

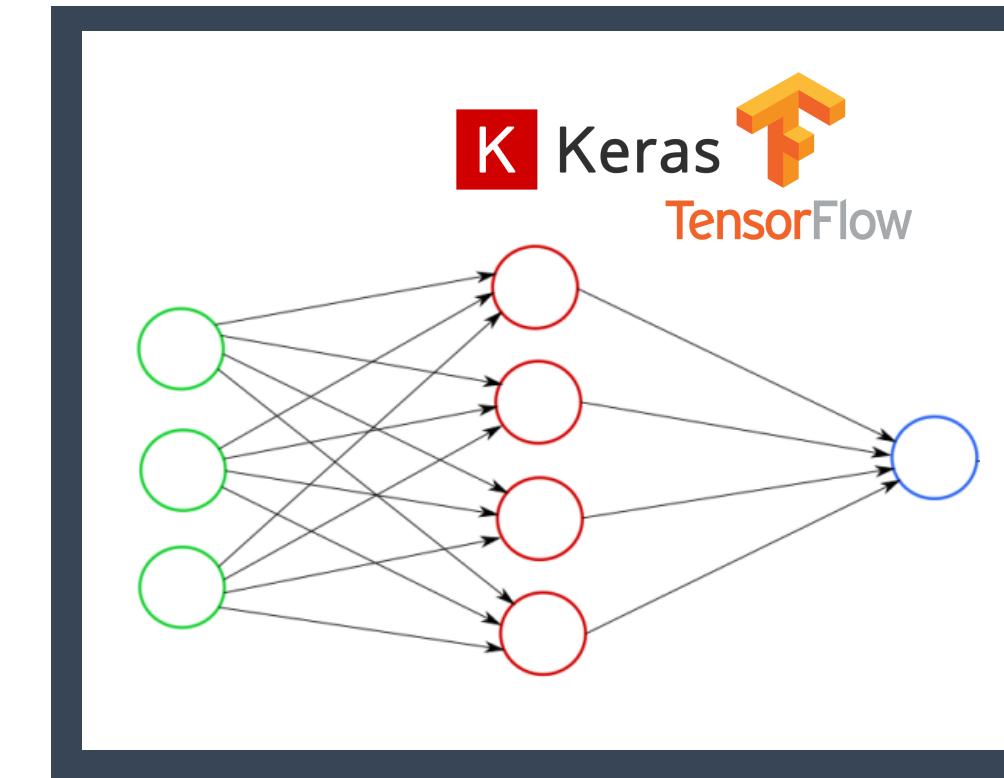
— FROM EXCEL TO R

PLOTTING IN 3D



<https://plotly-r.com/d-charts.html>

DEEP LEARNING



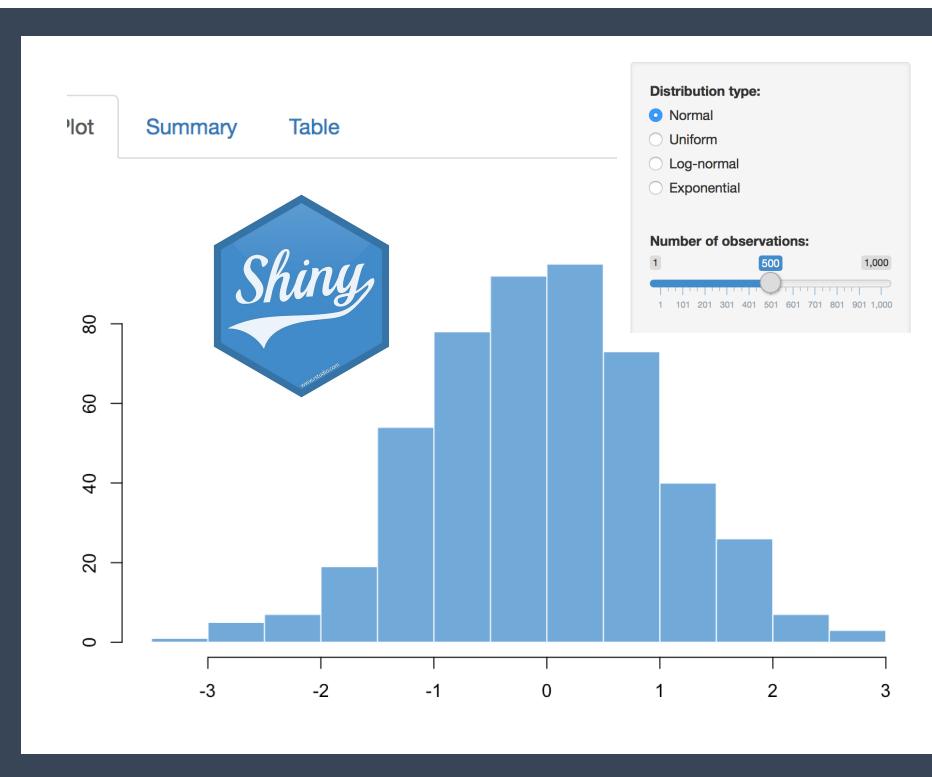
<https://keras.rstudio.com/>
<https://tensorflow.rstudio.com/>

BAYESIAN STATISTICS



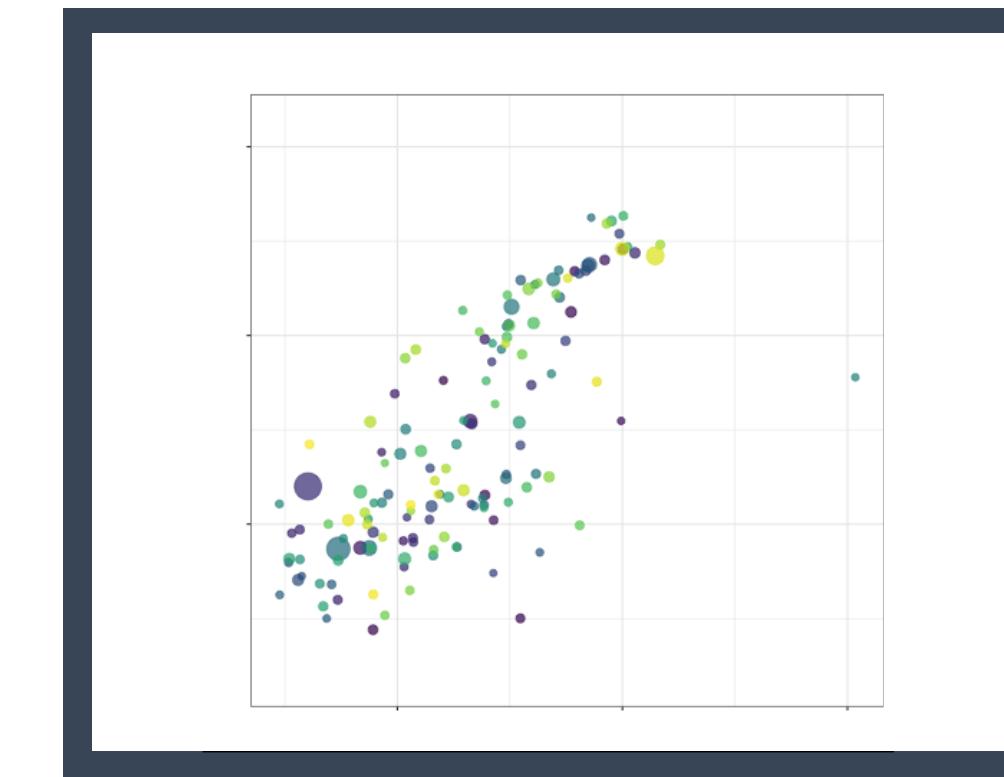
<https://mc-stan.org/users/interfaces/rstan>

WEBPAGE WITH R SHINY



<https://shiny.rstudio.com/>

INTERACTIVE PLOTS



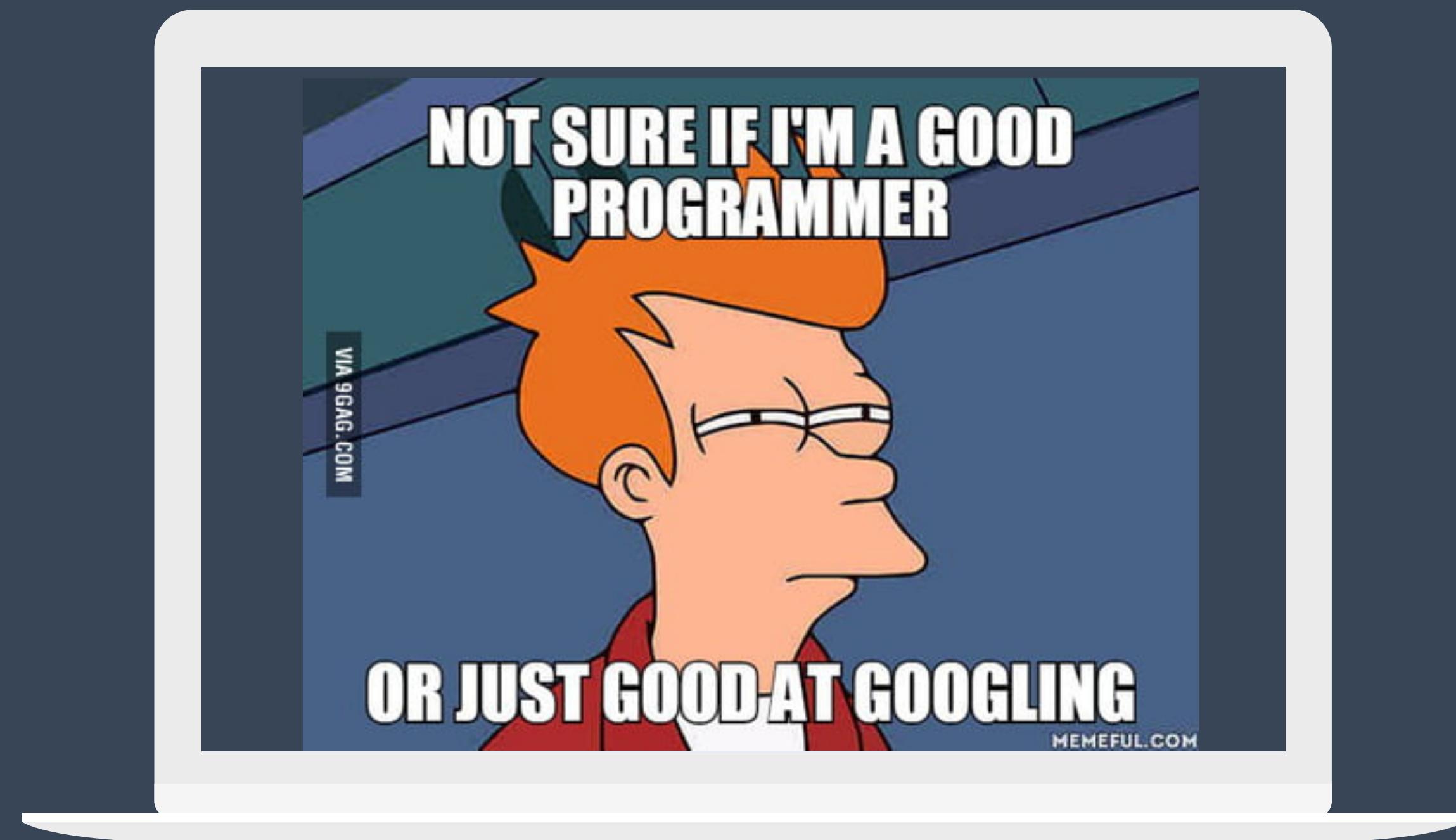
<https://gganimate.com/articles/gganimate.html>

MAIL AND MESSAGES



<https://github.com/briandconnelly/pushoverrr>

THANK YOU FOR LISTENING



This keynote presentation was created by Thilde Terkelsen,
Data Scientist, Center for Health Data Science, SUND, KU.
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