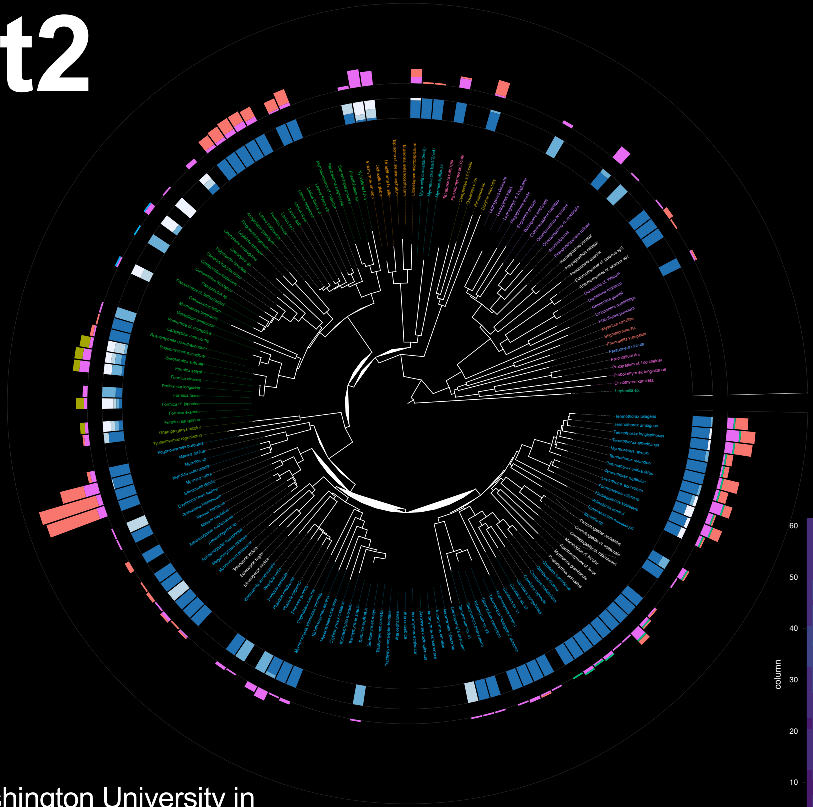
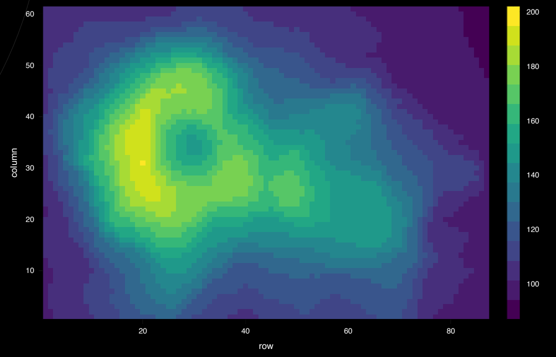
Evomics 2023

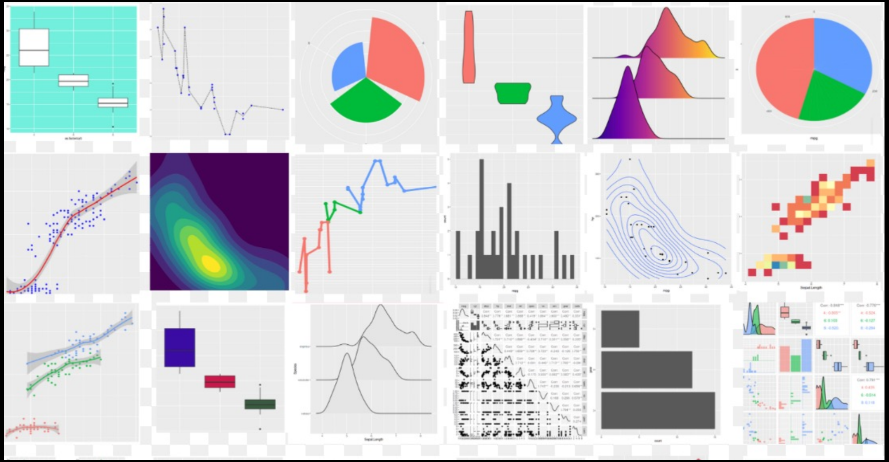
& ggplot2





Special thanks to Dr Scott Handley and Washington University in
St. Louis, Bernard Becker Medical Library, Research Computing for contributing their slides and
teaching materials to this session.

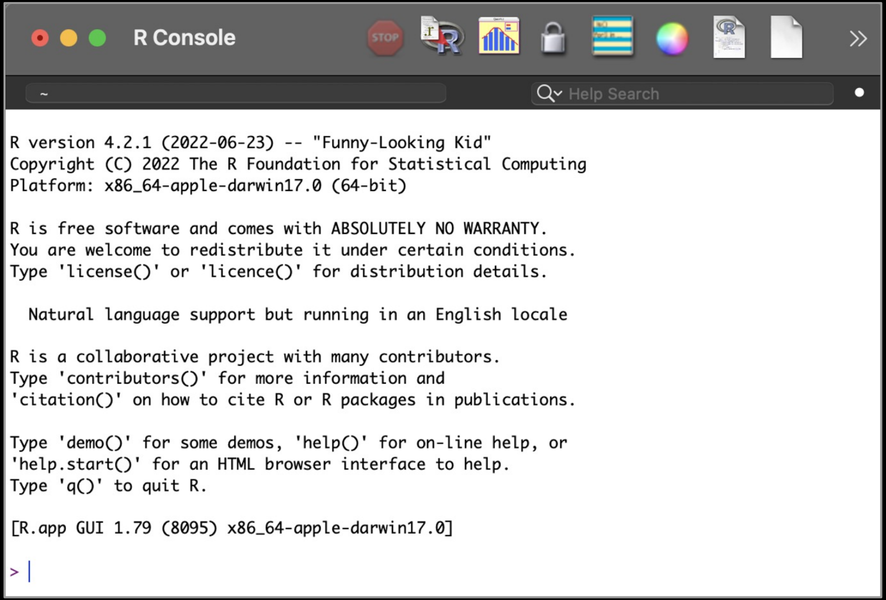
Outline



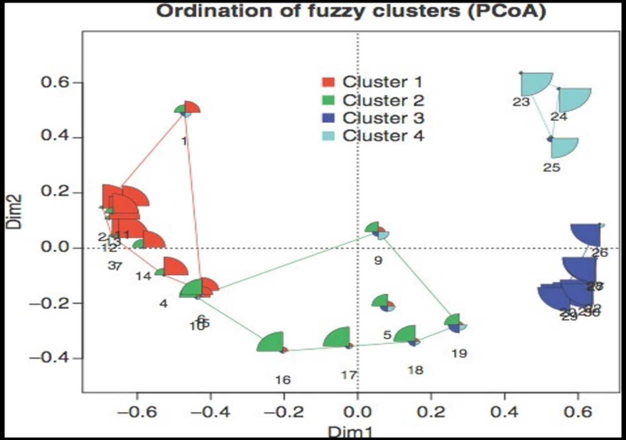
- **What is R**
  - Why is it useful?
  - What can be done with R?
  - RStudio
- **Installing packages**
- **General data structures**

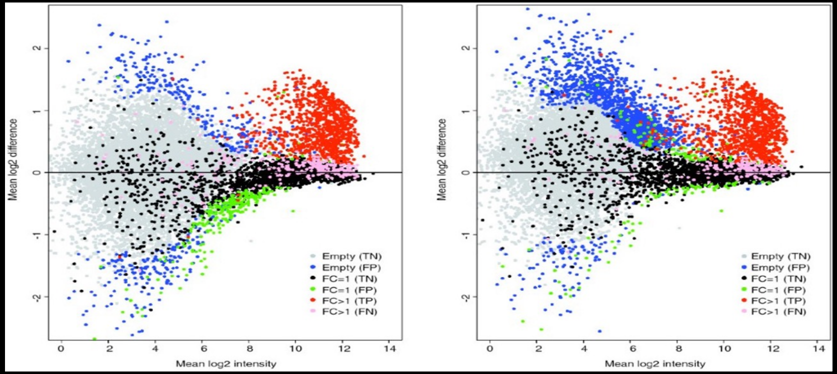
What is R?

A free software environment for statistical computing and graphics



```
R version 4.2.1 (2022-06-23) -- "Funny-Looking Kid"
Copyright (C) 2022 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin17.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[R.app GUI 1.79 (8095) x86_64-apple-darwin17.0]

> 
```





Why is R useful?

- **Open source**
- **Data management and manipulation**
  - Importing data in various formats (like text files, excel files, etc.)
  - Manipulating data (subsetting and filtering tables, merging, transposing, etc.)
- Cutting-edge **graphical data visualization**
- Support for rich **statistical simulation and modeling**
- Well established system of **packages and documentation**
- **Active development** and dedicated **community**

stack**overflow**

Why is R useful?

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→ Stay tuned for our lab session!

- Cutting-edge **graphical data visualization**

→ David Barnett (05/24) and Jim Whiting (05/25) sessions

- Support for rich **statistical simulation and modeling**
- Well established system of packages and documentation
- **Active development** and dedicated **community**

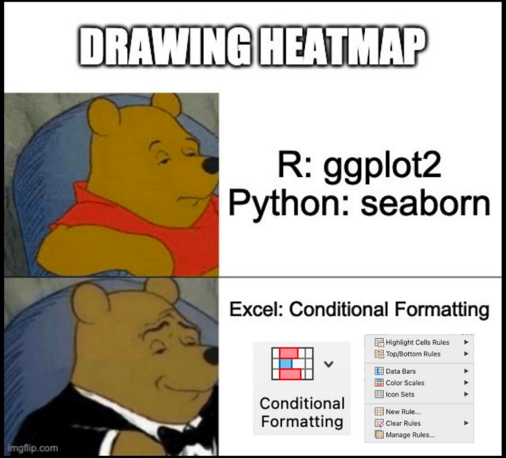
→ Next slides →

Where to learn more about R

- The R Project Homepage: http://www.r-project.org
- Quick R Homepage: http://www.statmethods.net
- Bioconductor: http://www.bioconductor.org
- An Introduction to R (long!): http://cran.r-project.org/doc/manuals/R-intro.html
- Guide to downloading and installing R and RStudio: https://rstudio-education.github.io/hopr/starting.html
- R Graph gallery (inspiration for R charts) https://r-graph-gallery.com
- Google - there are tons of tutorials, guides, demos, packages and more

R for Biologists

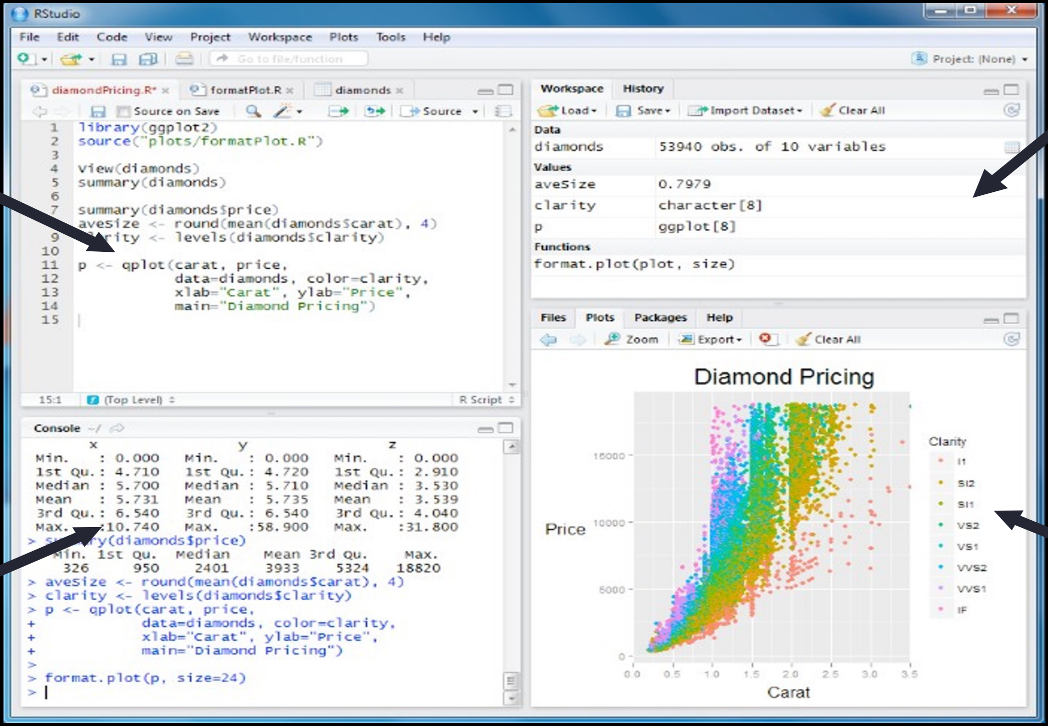
- **Bioconductor (http://bioconductor.org)**
  - 2,140 packages (05-27-2022):
    - Variant detection: coding changes, PolyPhen database
    - Annotation: pathway analysis, access GO, KEGG, NCBI and many others
    - High-throughput assays: flow cytometry, mass spec
    - Transcription factor binding detection
- **Phylogenetics and Evolution** (http://cran.r-project.org/web/views/Phylogenetics.html)
  - Ancestral State Reconstruction
  - Phylogenetic Inference
  - Trait Evolution
- **Ecology** (http://cran.r-project.org/web/views/Environmetrics.html)
  - Ordination
  - Cluster Analysis
  - Ecological Theory
  - Population Dynamics
  - Spatial Data Analysis



R Studio

Enter commands here

Workspace data



```r
library(ggplot2)
source("plots/formatPlot.R")

view(diamonds)
summary(diamonds)

summary(diamonds$price)
avesize <- round(mean(diamonds$carat), 4)
clarity <- levels(diamonds$clarity)

p <- qplot(carat, price,
           data=diamonds, color=clarity,
           xlab="Carat", ylab="Price",
           main="Diamond Pricing")

```

Data

diamonds 53940 obs. of 10 variables

Values

aveSize 0.7979

clarity character[8]

p ggplot[8]

Functions

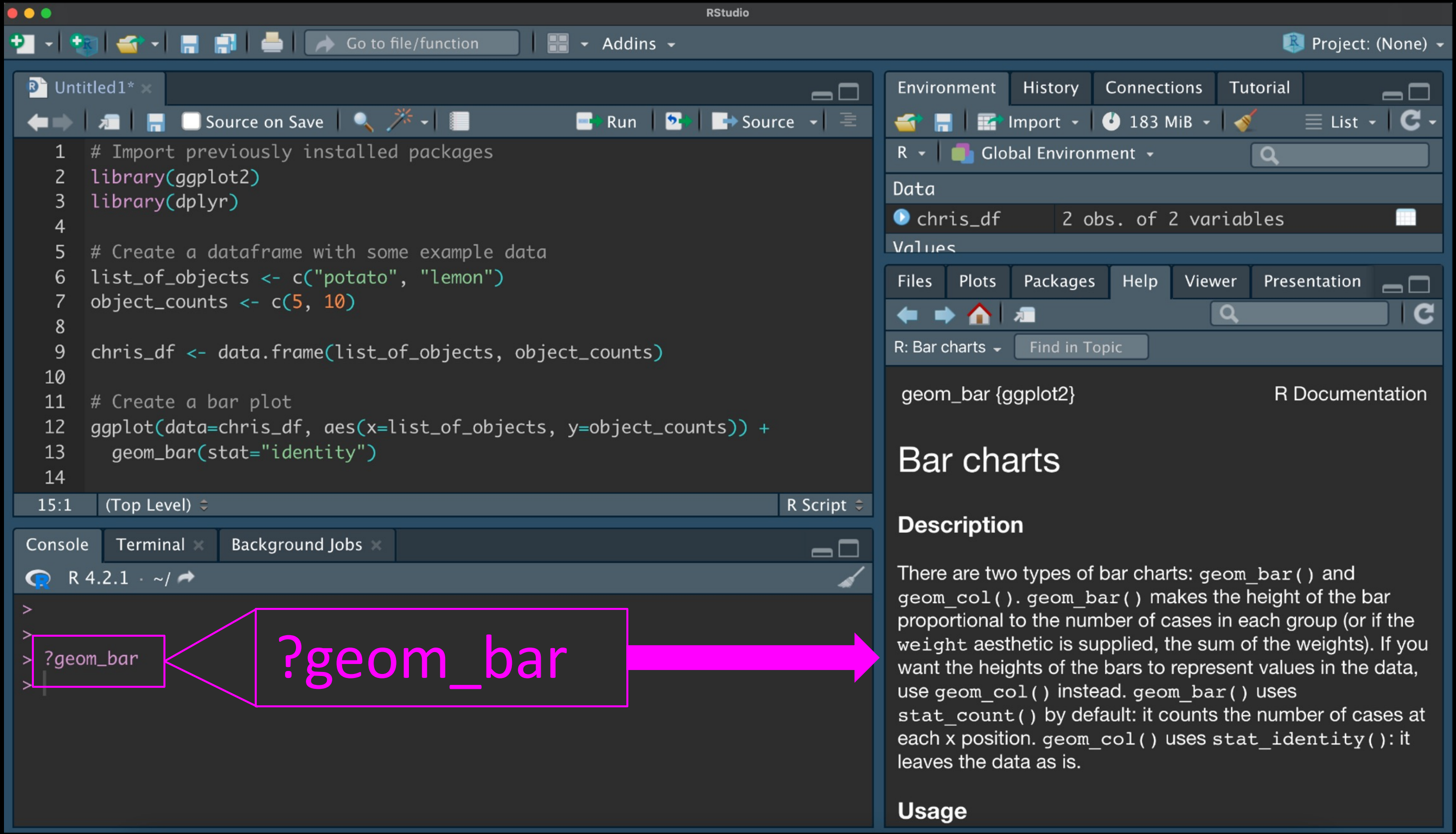
format.plot(plot, size)

```
       x               y               z
 Min.   : 0.000   Min.   : 0.000   Min.   : 0.000
 1st Qu.: 4.710   1st Qu.: 4.720   1st Qu.: 2.910
 Median : 5.700   Median : 5.710   Median : 3.530
 Mean   : 5.731   Mean   : 5.735   Mean   : 3.539
 3rd Qu.: 6.540   3rd Qu.: 6.540   3rd Qu.: 4.040
 Max.   :10.740   Max.   :58.900   Max.   :31.800
> summary(diamonds$price)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    326     950    2401    3933    5324   18820
> aveSize <- round(mean(diamonds$carat), 4)
> clarity <- levels(diamonds$clarity)
> p <- qplot(carat, price,
+            data=diamonds, color=clarity,
+            xlab="Carat", ylab="Price",
+            main="Diamond Pricing")
>
> format.plot(p, size=24)
> |
```

View results here

Help and Plots viewer

Handy R Studio tricks



```r
# Import previously installed packages
library(ggplot2)
library(dplyr)

# Create a dataframe with some example data
list_of_objects <- c("potato", "lemon")
object_counts <- c(5, 10)

chris_df <- data.frame(list_of_objects, object_counts)

# Create a bar plot
ggplot(data=chris_df, aes(x=list_of_objects, y=object_counts)) +
  geom_bar(stat="identity")

```

```
>
>
> ?geom_bar
>
```

?geom_bar

geom_bar {ggplot2} R Documentation

Bar charts

Description

There are two types of bar charts: `geom_bar()` and `geom_col()`. `geom_bar()` makes the height of the bar proportional to the number of cases in each group (or if the `weight` aesthetic is supplied, the sum of the weights). If you want the heights of the bars to represent values in the data, use `geom_col()` instead. `geom_bar()` uses `stat_count()` by default: it counts the number of cases at each x position. `geom_col()` uses `stat_identity()`: it leaves the data as is.

Usage

Can add a "?" before a function and open this help information viewer

R Markdown Cheat Sheet

learn more at rmarkdown.rstudio.com

rmarkdown 0.2.50 Updated: 8/14

RStudio

1. Workflow

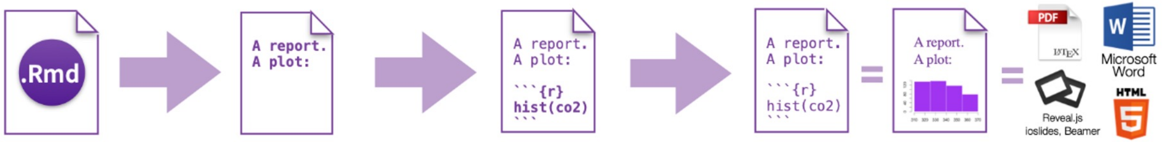
R Markdown is a format for writing reproducible, dynamic reports with R. Use it to embed R code and results into slideshows, pdfs, html documents, Word files and more. To make a report:

i. Open - Open a file that uses the .Rmd extension.

ii. Write - Write content with the easy to use R Markdown syntax

iii. Embed - Embed R code that creates output to include in the report

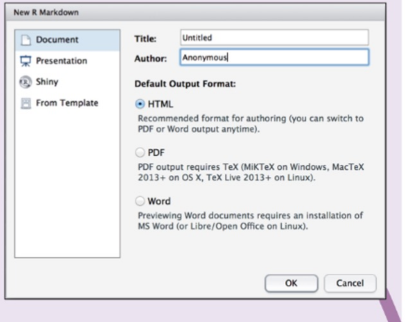
iv. Render - Replace R code with its output and transform the report into a slideshow, pdf, html or ms Word file.



2. Open File

Start by saving a text file with the extension .Rmd, or open an RStudio Rmd template

- In the menu bar, click
  File ▸ New File ▸ R Markdown…
- A window will open. Select the class of output you would like to make with your .Rmd file
- Select the specific type of output to make with the radio buttons (you can change this later)
- Click OK



Title: Untitled
Author: Anonymous

Default Output Format:

● HTML
Recommended format for authoring (you can switch to PDF or Word output anytime).

○ PDF
PDF output requires TeX (MiKTeX on Windows, MacTeX 2013+ on OS X, TeX Live 2013+ on Linux).

○ Word
Previewing Word documents requires an installation of MS Word (or Libre/Open Office on Linux).

4. Choose Output

Write a YAML header that explains what type of document to build from your R Markdown file.

YAML

A YAML header is a set of key: value pairs at the start of your file. Begin and end the header

```
---
title: "Untitled"
author: "Anonymous"
output: html_document
---

This is the start of my
```

The RStudio template writes the YAML header

3. Markdown

Next, write your report in plain text. Use markdown syntax to describe how to format text in the final report.

syntax	becomes
`Plain text`	Plain text
`End a line with two spaces to start a new paragraph.`	End a line with two spaces to start a new paragraph.
`*italics* and _italics_`	*italics* and *italics*
`**bold** and __bold__`	**bold** and **bold**
`superscript^2^`	superscript^2
`~~strikethrough~~`	~~strikethrough~~
`[link](www.rstudio.com)`	link
`# Header 1`	Header 1
`## Header 2`	Header 2
`### Header 3`	Header 3
`#### Header 4`	Header 4
`##### Header 5`	Header 5
`###### Header 6`	Header 6
`endash: --`	endash: –
`emdash: ---`	emdash: —
`ellipsis: ...`	ellipsis: …
`inline equation: $A = \pi*r^{2}$`	inline equation: $A = \pi * r^2$
`image: ![](path/to/smallorb.png)`	image:
`horizontal rule (or slide break):`	horizontal rule (or slide break):
`***`	

R installing packages

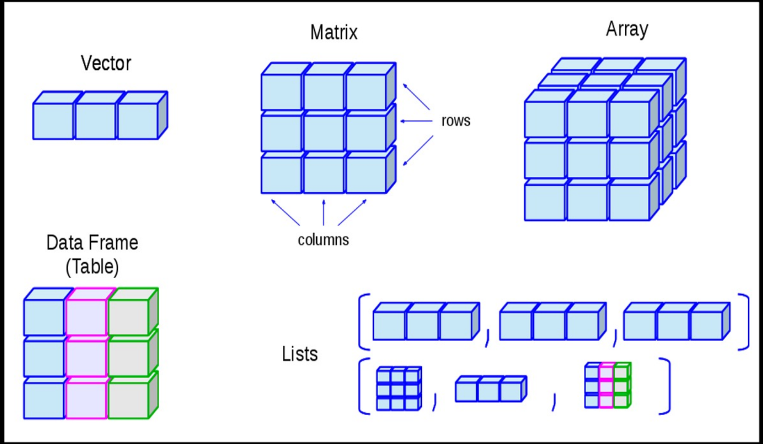
- **Bioconductor** (http://bioconductor.org)
  - BiocManager::install(“Package Name”)
- CRAN install (https://cran.r-project.org/web/packages/)
  - install.packages(“Package Name”)
- **GitHub install**
  - devtools::install_github(“Package Name”)
  - remotes::install_github(“Package Name”)

Images sourced from https://www.wikihow.com/Change-a-Light-Bulb

```
Warning in install.packages :
  package ‘memer’ is not available
 (for R version 3.6.1)
> library("memer")
Error in library("memer") : there
 is no package called ‘memer’
> |
```

General data structures

- **Vector** - ordered collection of data
  vector_1 <- c(2, 3, 4, 10)
  vector_2 <- c(“potato”, “lemonade”, “avocado”)
- **Matrix** - 2D collection of vectors with same data type
- **Array** - multiple dimension collection of vectors
- **Dataframe** - matrix-like with multiple data types (like an excel table with text and numbers)
- **Lists** - ordered collection of objects but can contain other lists or vectors inside it



http://venus.ifca.unican.es/Rintro/dataStruct.html

But..

which dataset should we use to do all these things?

Arabidopsis thaliana* mutants *psbo1* and *psbo2

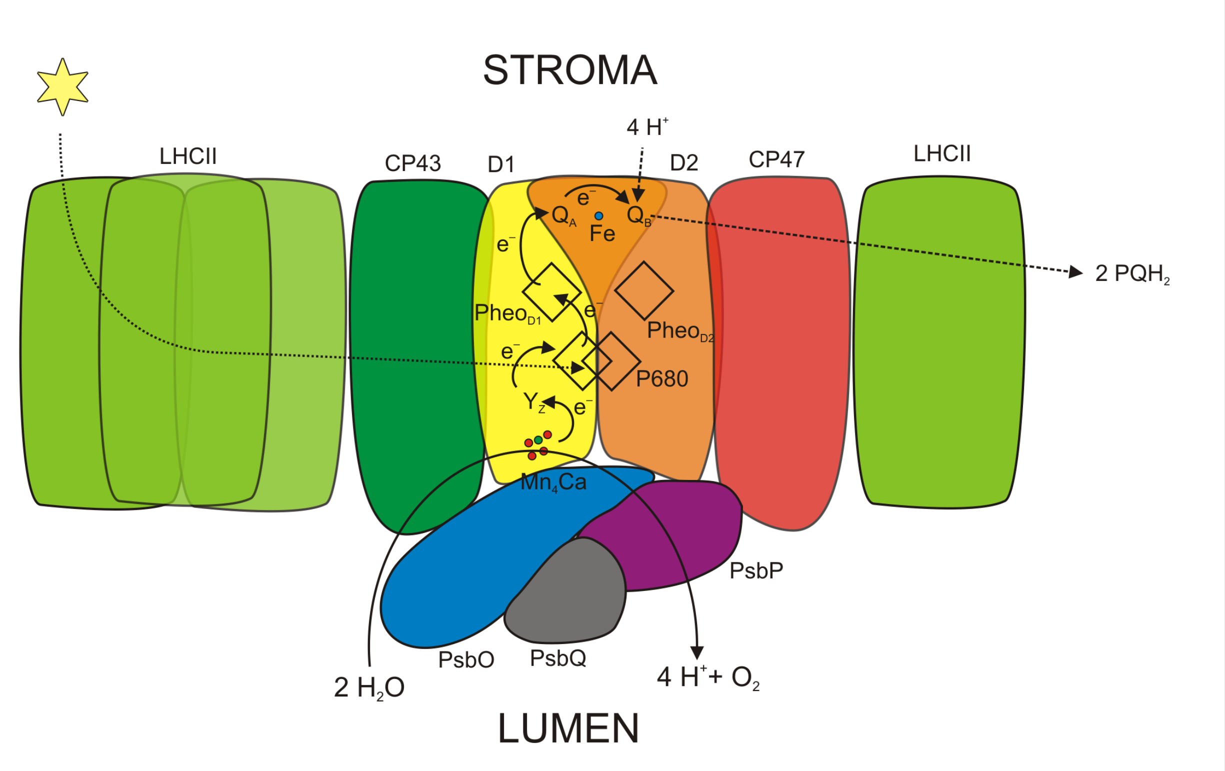
WT

psbo1

psbo2

PsbO protein

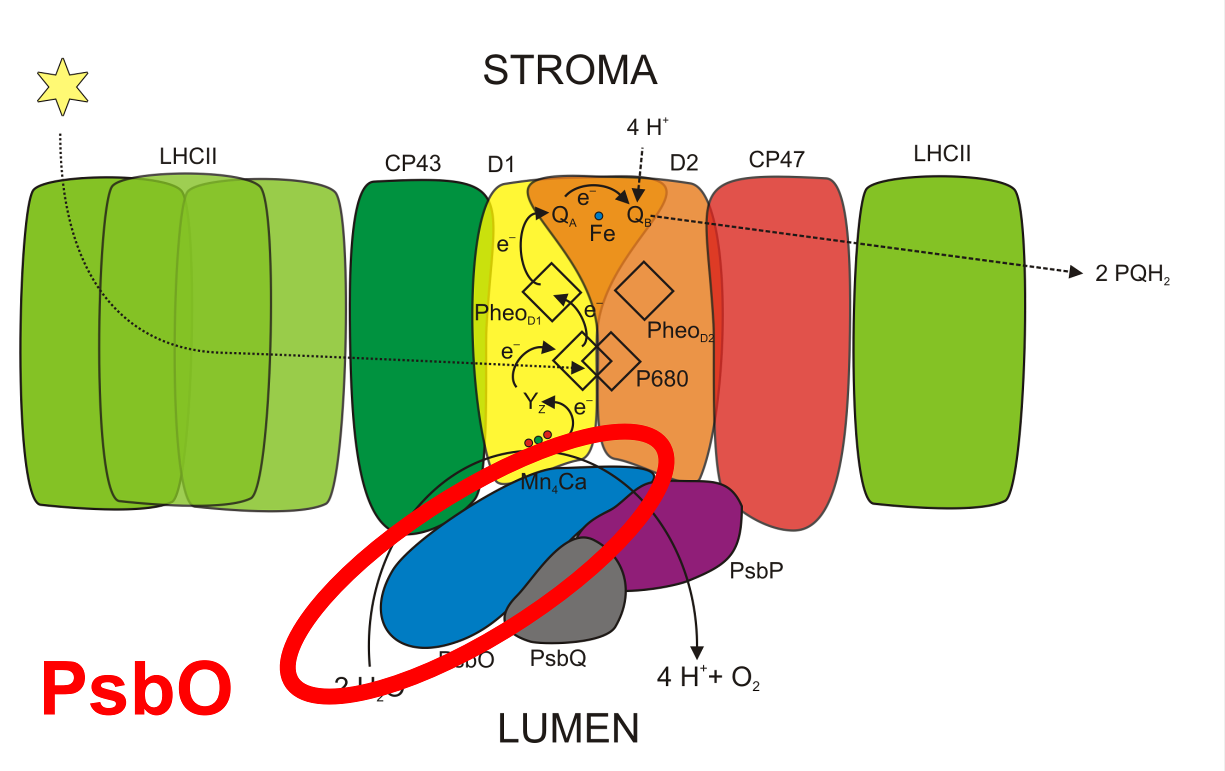
- Subunit of photosystem II
- Important for water splitting
- *Arabidopsis*: PsbO1 and PsbO2



Photosystem II

PsbO protein

- Subunit of photosystem II
- Important for water splitting
- *Arabidopsis*: PsbO1 and PsbO2



PsbO

Photosystem II

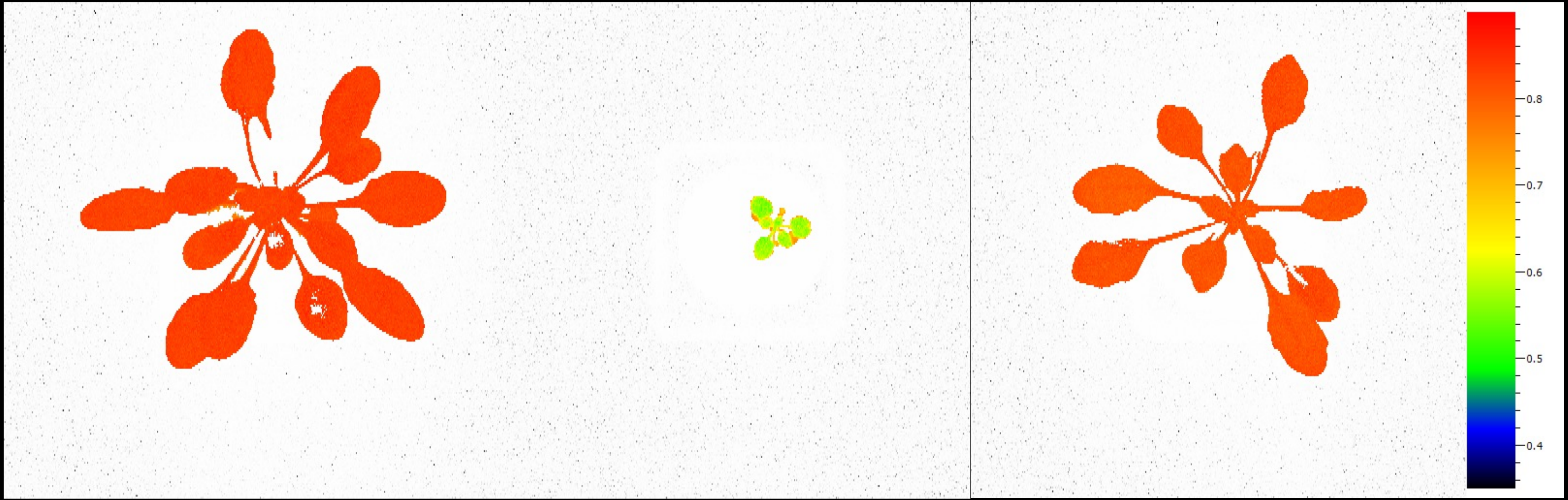
Experimental design

Control	Drought	Salt stress
WT	WT	WT
psbo1	*psbo1*	*psbo1*
psbo2	*psbo2*	*psbo2*
	- water	+ NaCl

Measurement – chlorophyl fluorescence

- Leaf rosette area
- F_V/F_M (QY_max) – maximum quantum yield of photosystem II

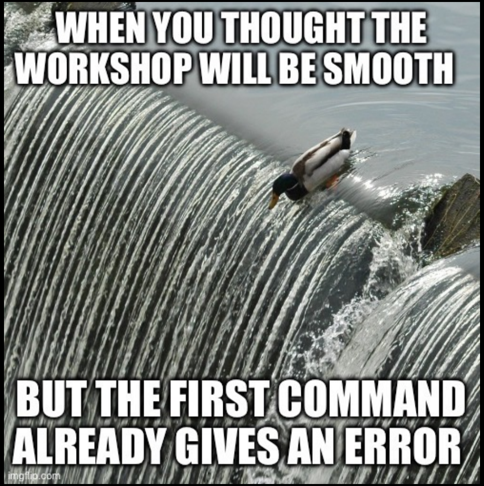
WT *psbo1* *psbo2*

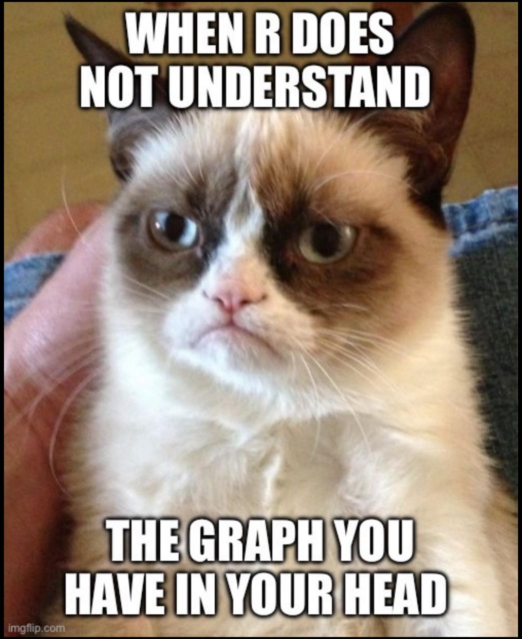


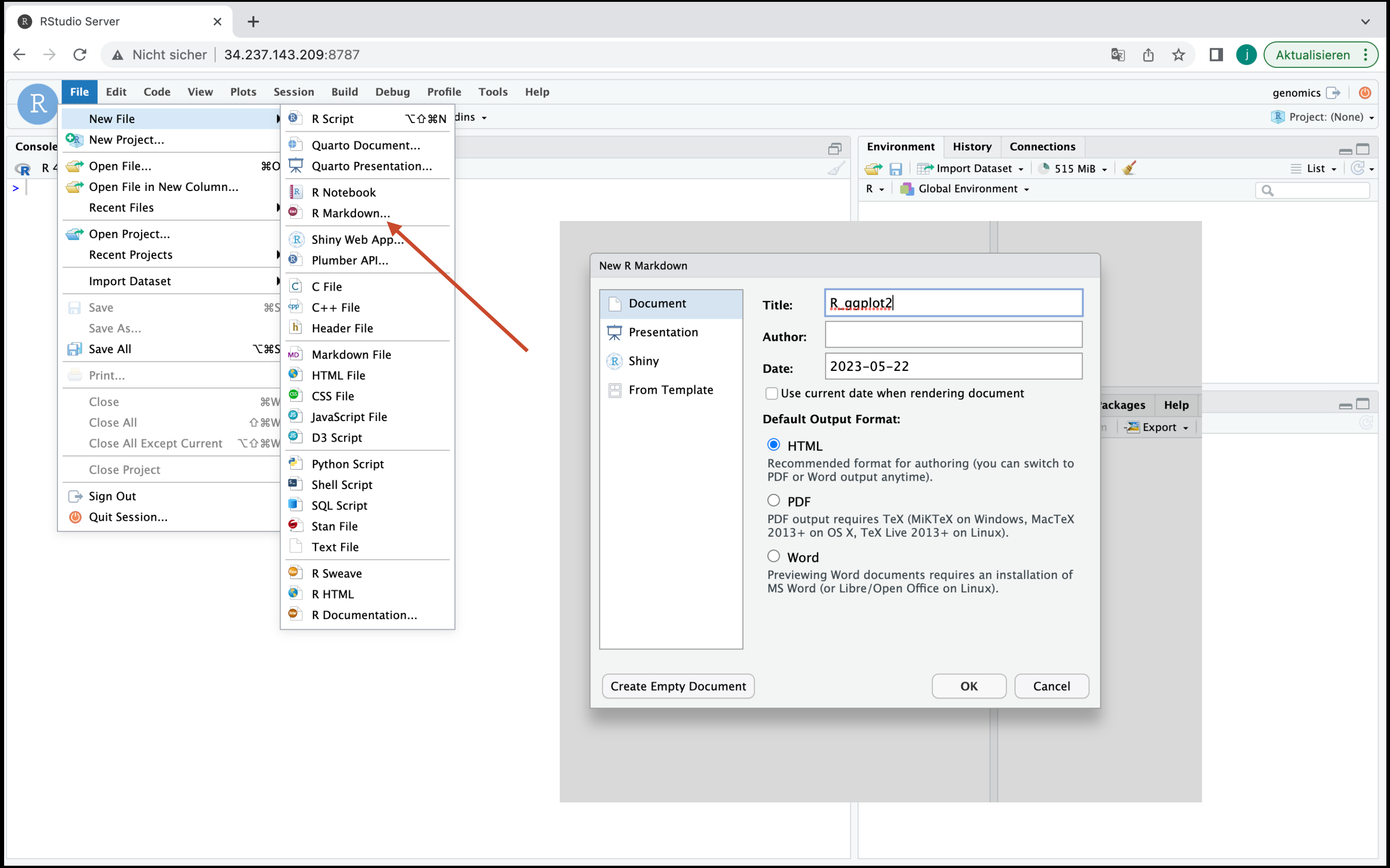
Yey!

Let‘s start the practical!

Open the Rstudio server by typing: <IP>:8787







Title: R_ggplot2

Author:

Date: 2023-05-22

☐ Use current date when rendering document

Default Output Format:

● HTML

Recommended format for authoring (you can switch to PDF or Word output anytime).

○ PDF

PDF output requires TeX (MiKTeX on Windows, MacTeX 2013+ on OS X, TeX Live 2013+ on Linux).

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