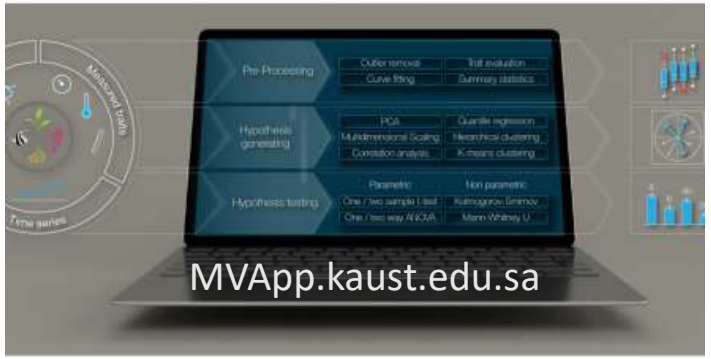
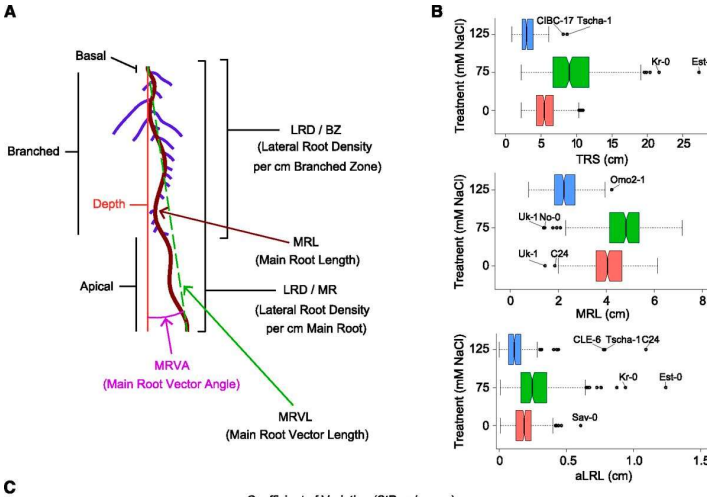
Magdalena Julkowska
@mmjulkowska
PostDoc at Salt Lab, KAUST, KSA

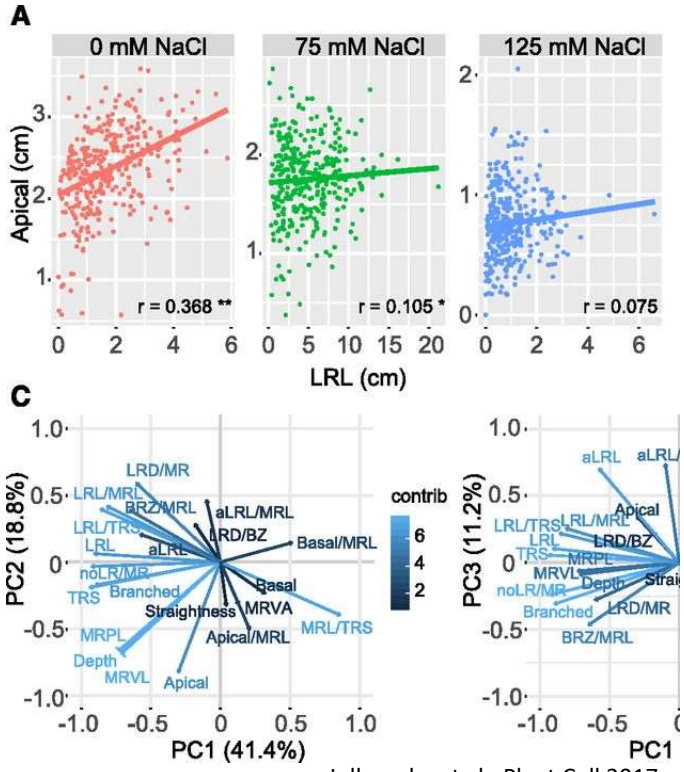
Plantae Seminar
21st of May, 2019

Data visualization:
Optimizing data exploration and illustrative storytelling

Joy Of Bubbles is a piece of digital artwork by Cristian Ilies Vasile , 2013







Julkowska et al., Plant Cell 2017

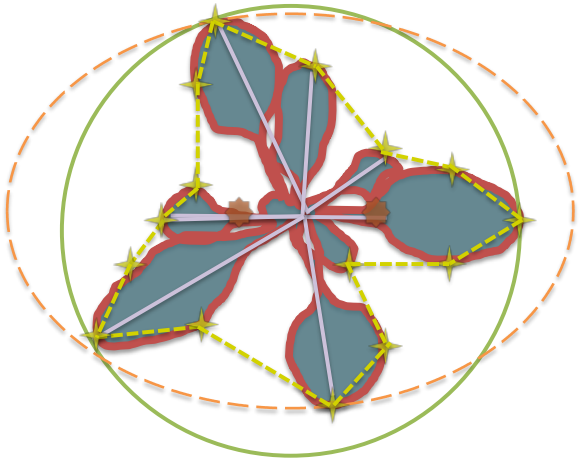
Julkowska et al., daily challenges 2019

My (hi)story of data visualization

Example high-throughput data output

RGB traits = 8

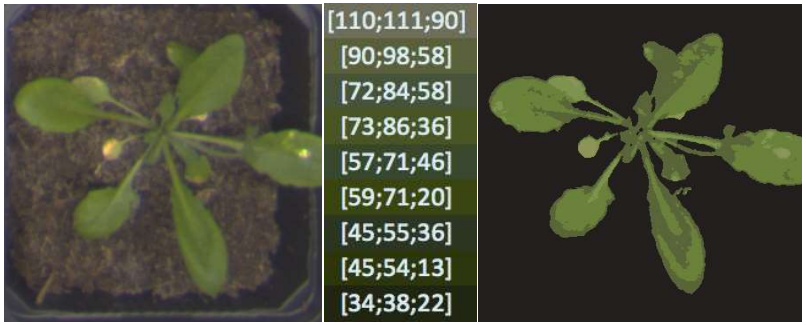
Area
Perimeter
Roundness
Compactness
Isotropy
Rotational mass symmetry
Eccentricity
Slenderness of leaves



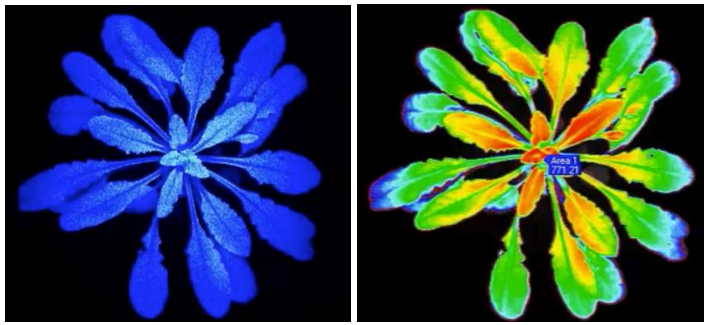
Fluorescence parameters = 17

F_o	minimal fluorescence (dark adapted)
F_m	maximal fluorescence (dark adapted)
F_o'	minimal fluorescence (light adapted)
F_m'	maximal fluorescence (light adapted)
F_t	instantaneous fluorescence level at time (t)
F_v	variable fluorescence (dark adapted)
F_p	peak fluorescence in the initial Kautsky effect
F_v/F_m	maximal PSII quantum yield (dark adapted)
ΦP	actual PSII quantum yield (light adapted)
F_v'/F_m'	maximal PSII quantum yield (light adapted)
qP	coefficient of photochemical quenching
ΦNO	quantum yield of non-photochemical dissipation
ΦNPQ	quantum yield of non-photochemical quenching
NPQ	non-photochemical quenching for PSII heat loss
PQ	photochemical quenching
qN	ChlF quenched by non-photochemical processes
Rfd	ratio of fluorescence decay

Greenness hues = 9



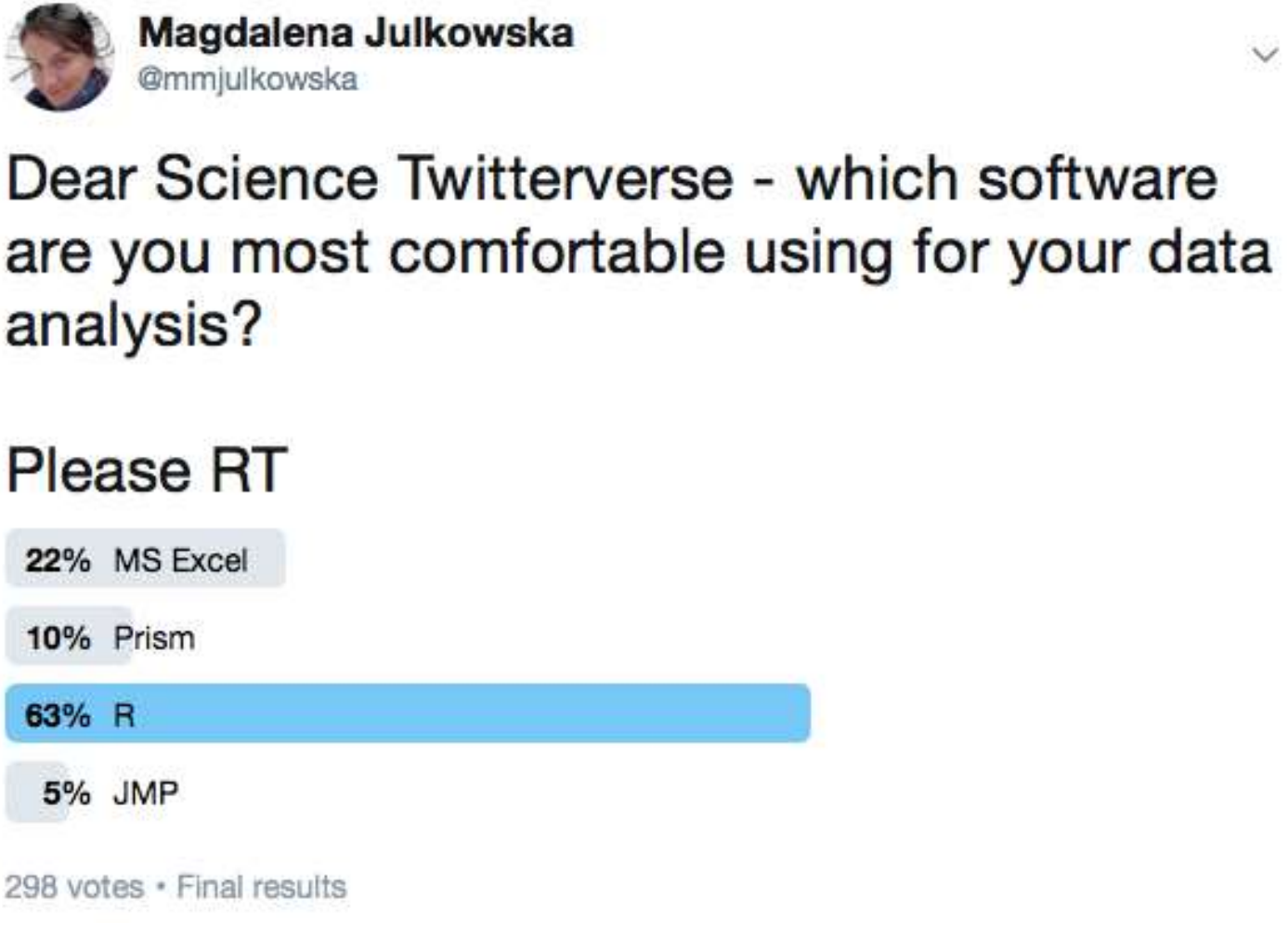
Original image | Greenness hues | Colour segmentation



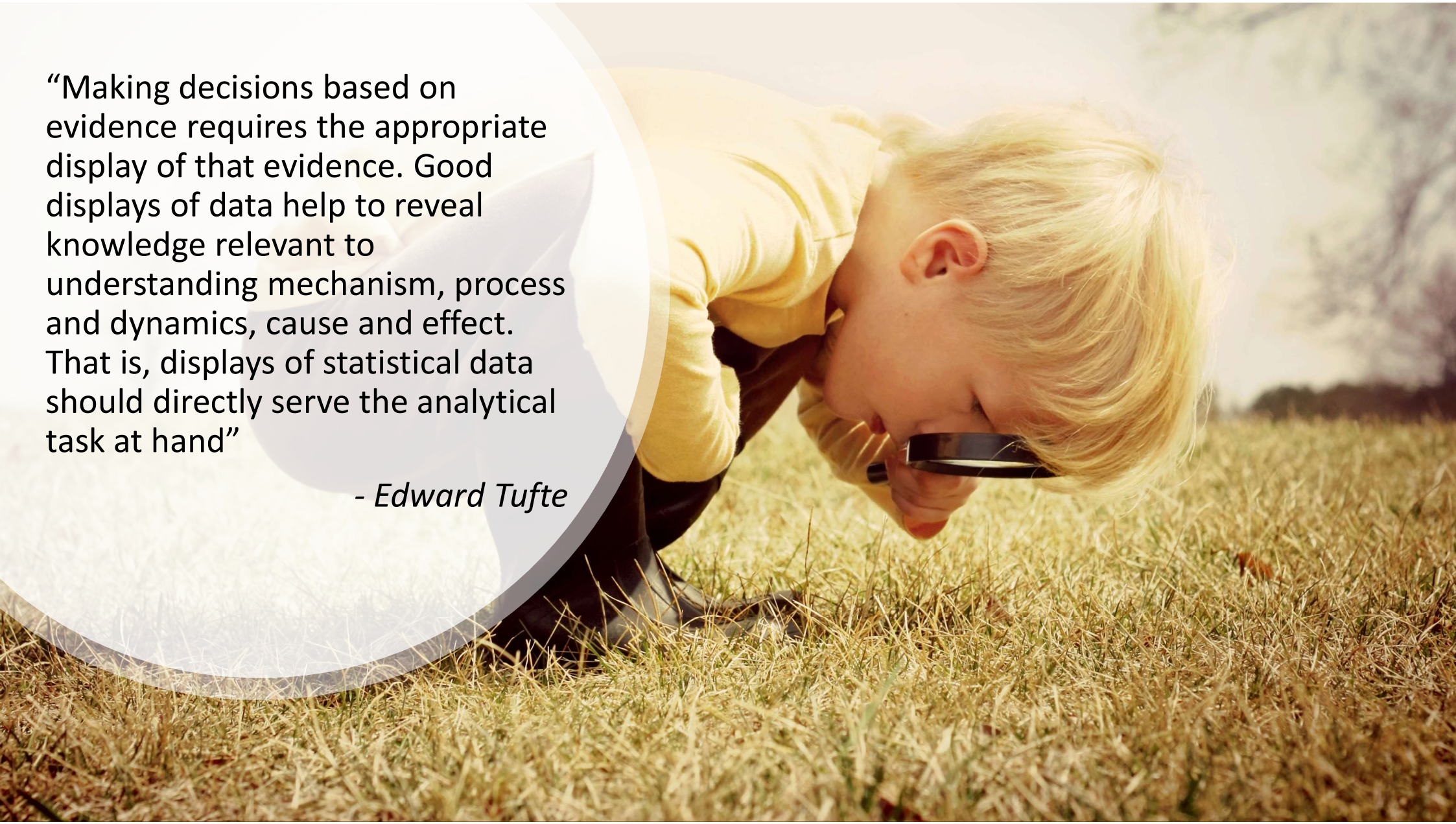
F_o – minimum fluorescence | F_m – maximum fluorescence

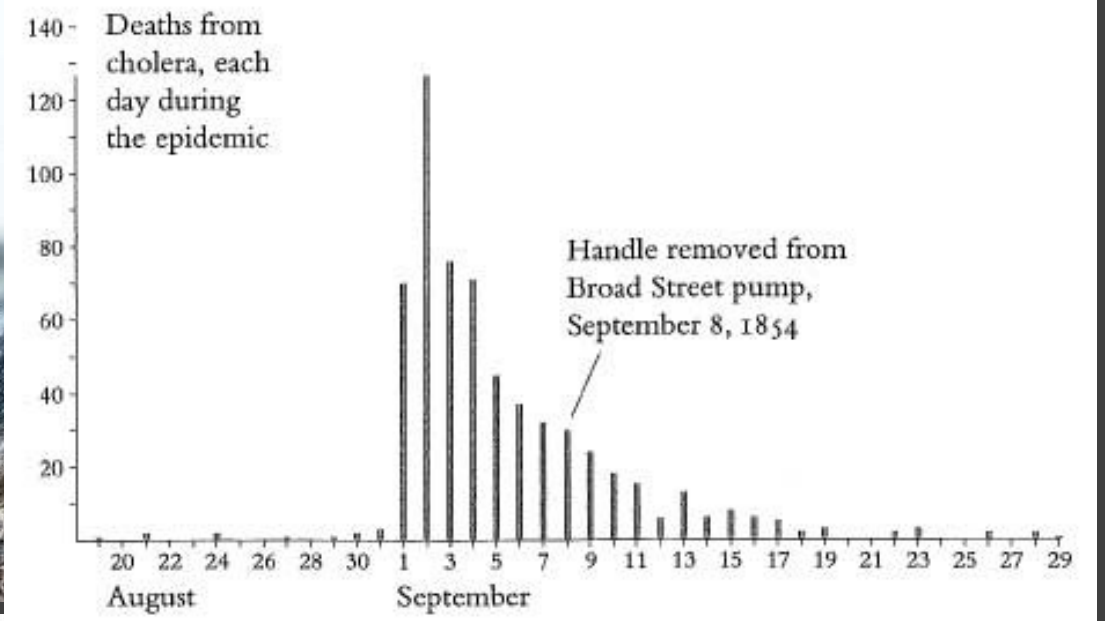
Example high-throughput data output

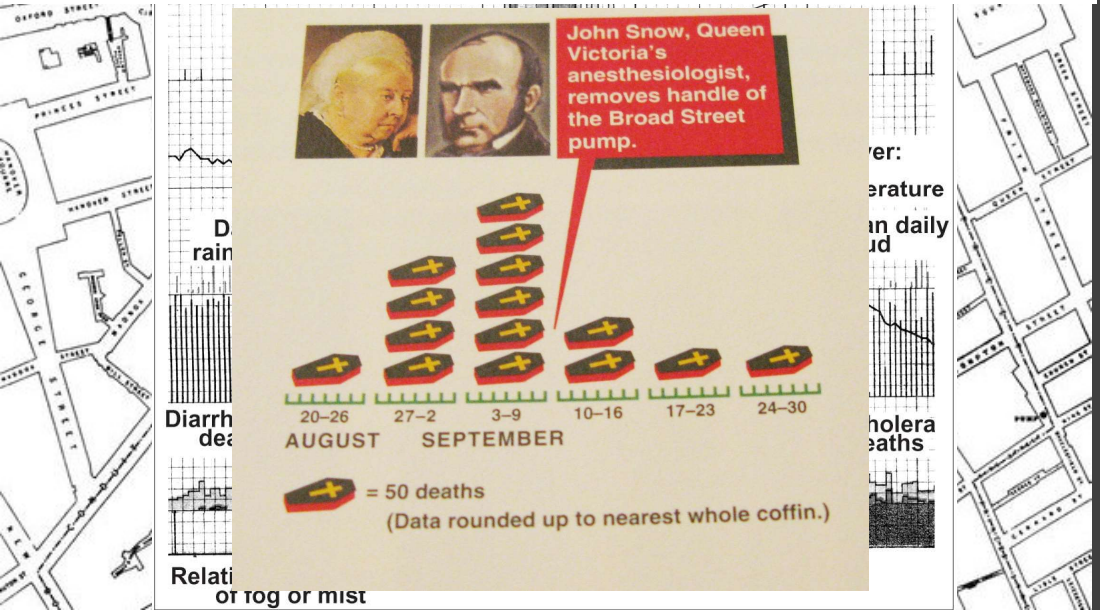
8 + 9 +




“Although we often hear that data speak for themselves, their voices can be soft and sly”
- Mostellet, Fienberg & Rouke
Beginning Statistics with Data Analysis


“Making decisions based on evidence requires the appropriate display of that evidence. Good displays of data help to reveal knowledge relevant to understanding mechanism, process and dynamics, cause and effect. That is, displays of statistical data should directly serve the analytical task at hand”
- Edward Tufte



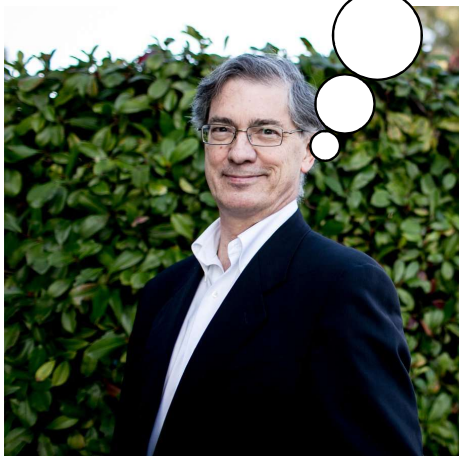


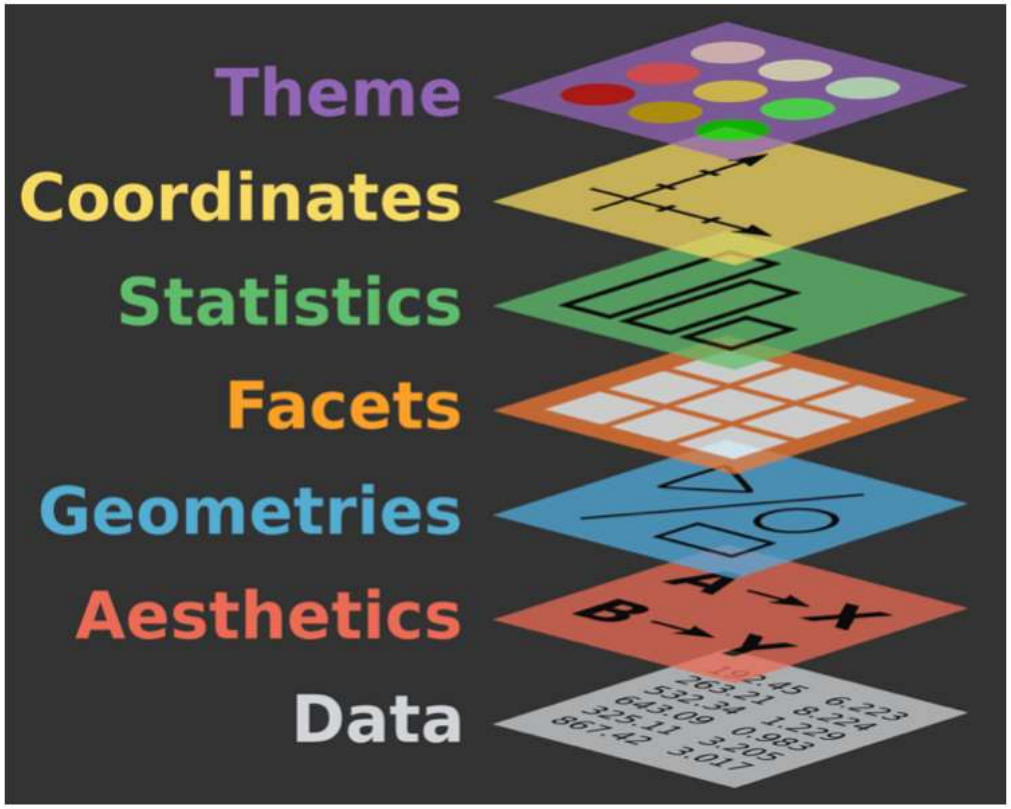
Visualization of cholera saves the day… or does it?

- Cholera outbreak in London, August 1854
- John Snow puts the data in spatial context to identify strong relationship between Broadstreet Pump and deaths by cholera
  - ✓ Place the data in appropriate context to asses cause and effect
  - ✓ Make quantitative comparisons – compared with what?
- Be careful with
  - ➢ Individual vs rate representation
  - ➢ Aggregation by time

Grammar of graphics

"framework which follows a layered approach to describe and construct visualizations or graphics in a structured manner."





Leland Wilkinson (1980) "The Grammar of Graphics"
https://www.springer.com/in/book/9780387245447

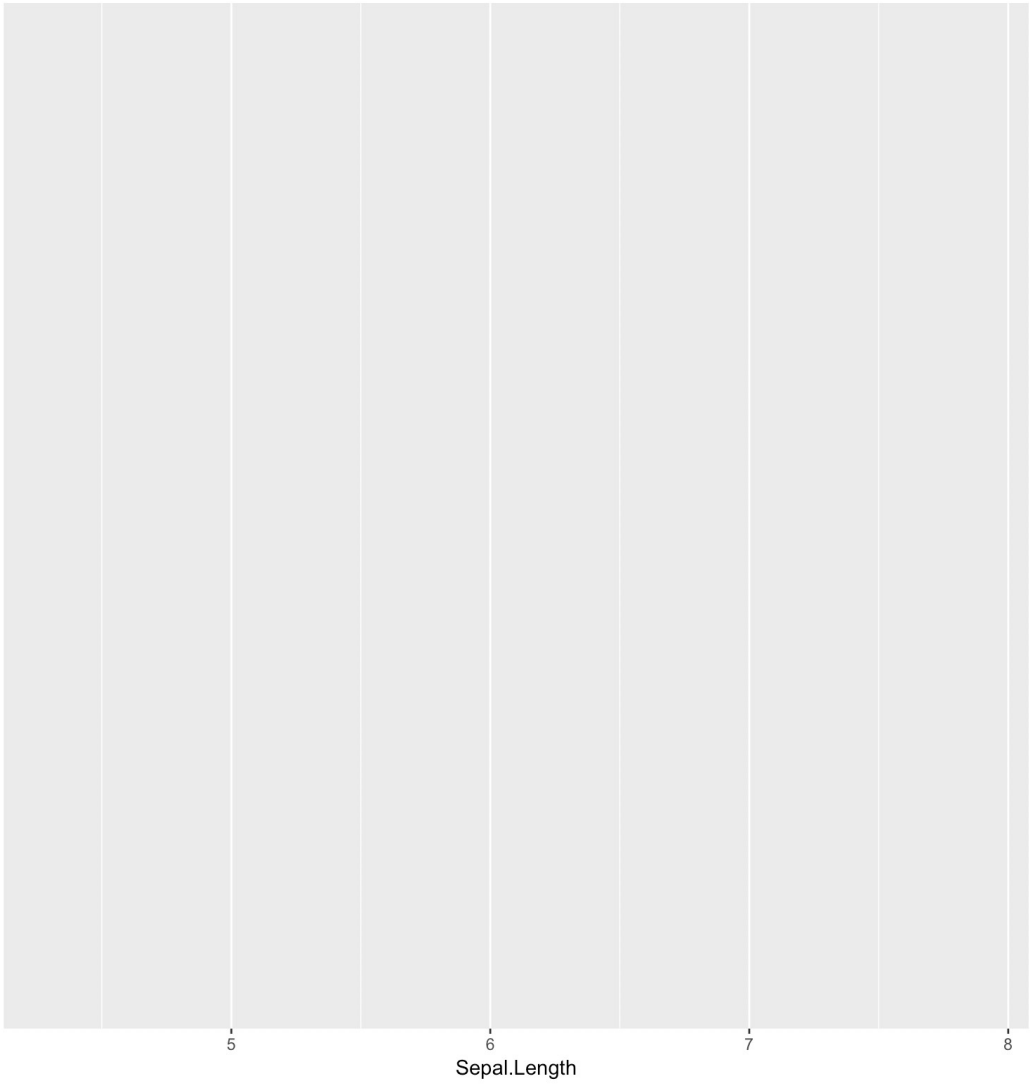
Grammar of Graphics using ggplot

```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris)
```


Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

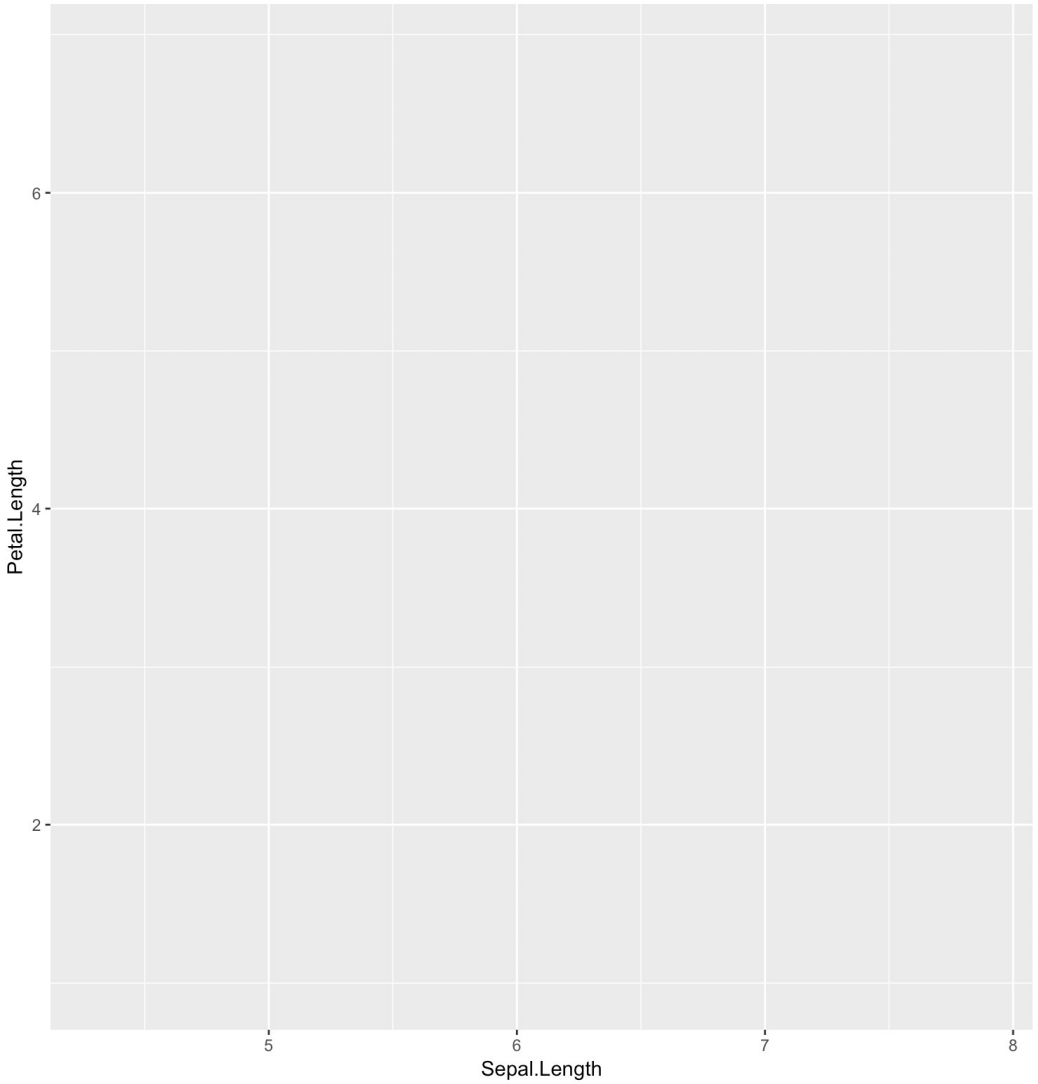
```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length)
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

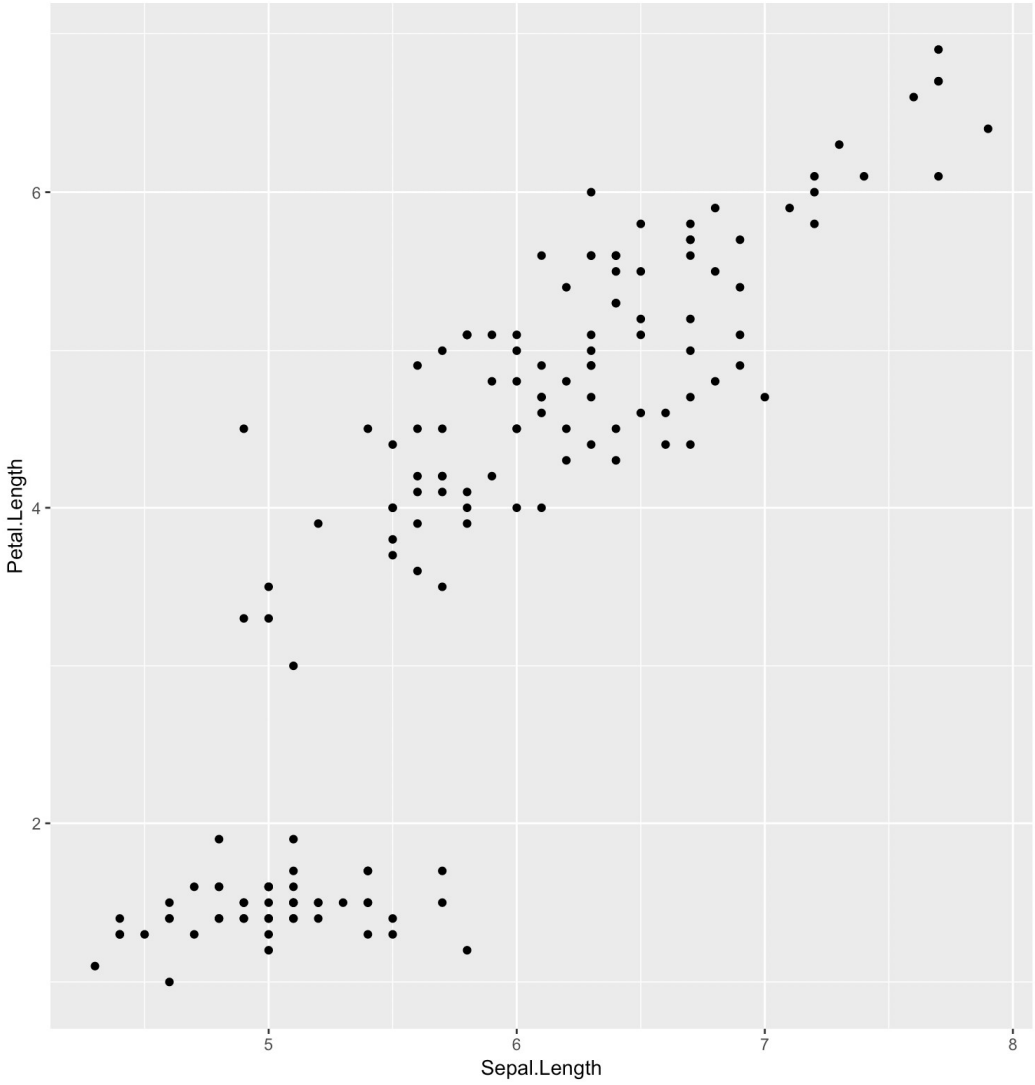
```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length) +
  aes(y= Petal.Length)
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

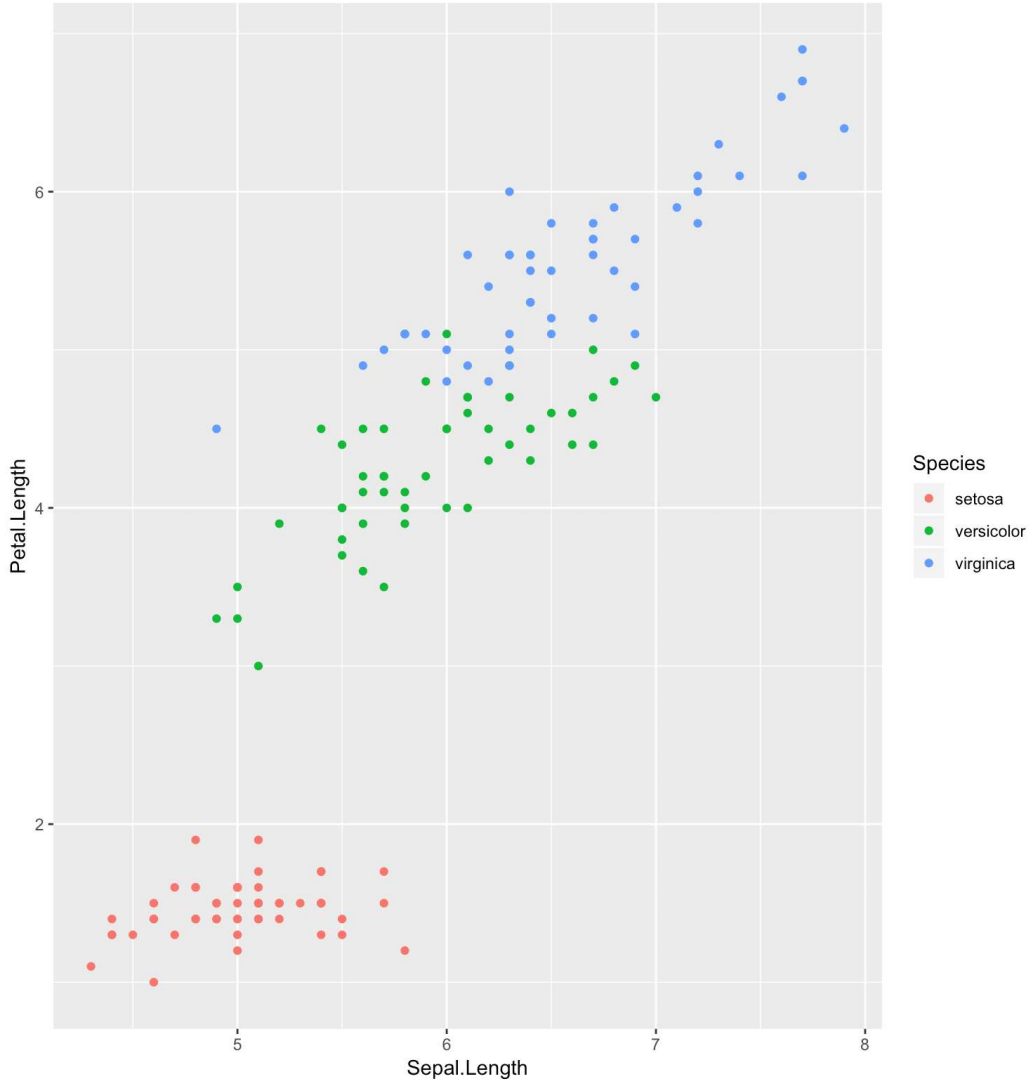
```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length) +
  aes(y= Petal.Length) +
  geom_point()
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

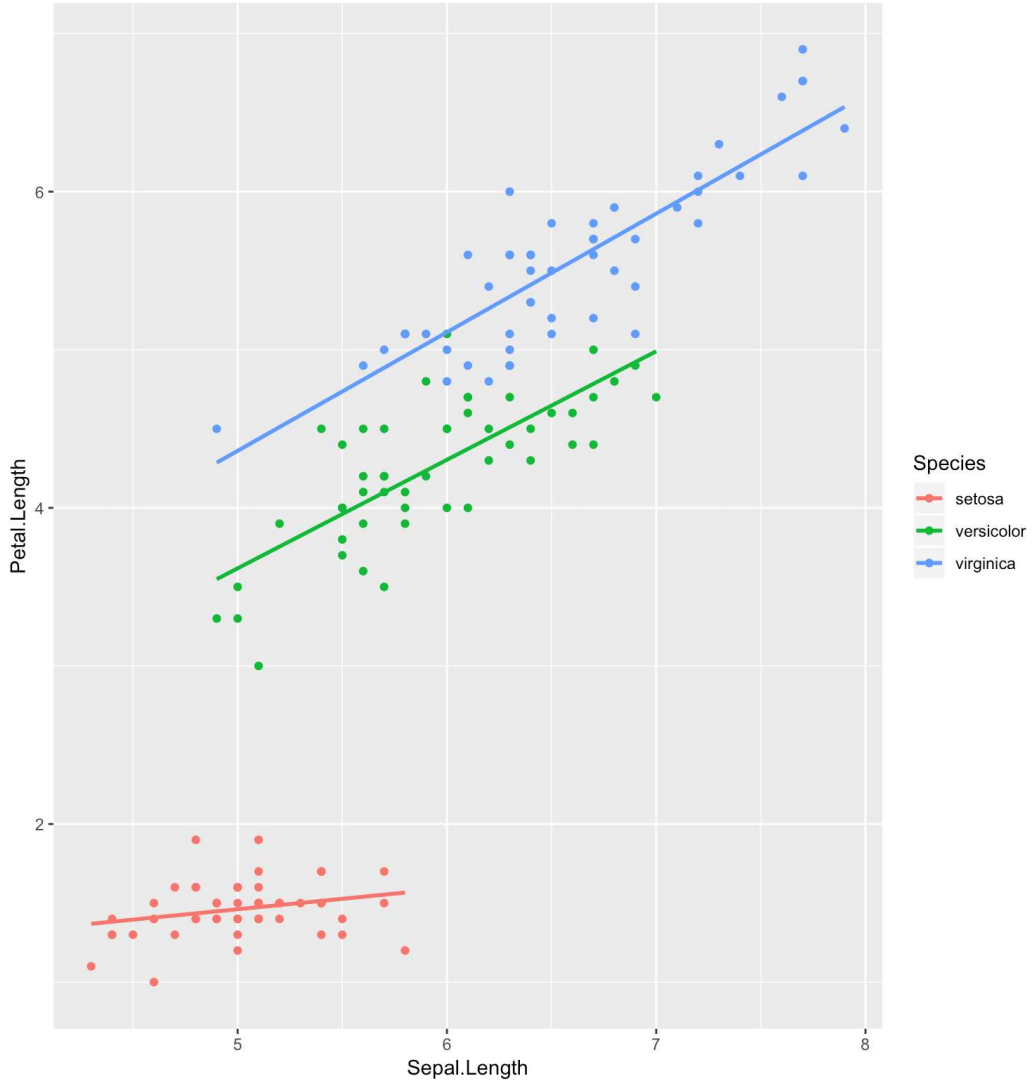
```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length) +
  aes(y= Petal.Length) +
  geom_point() +
  aes(col = Species)
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

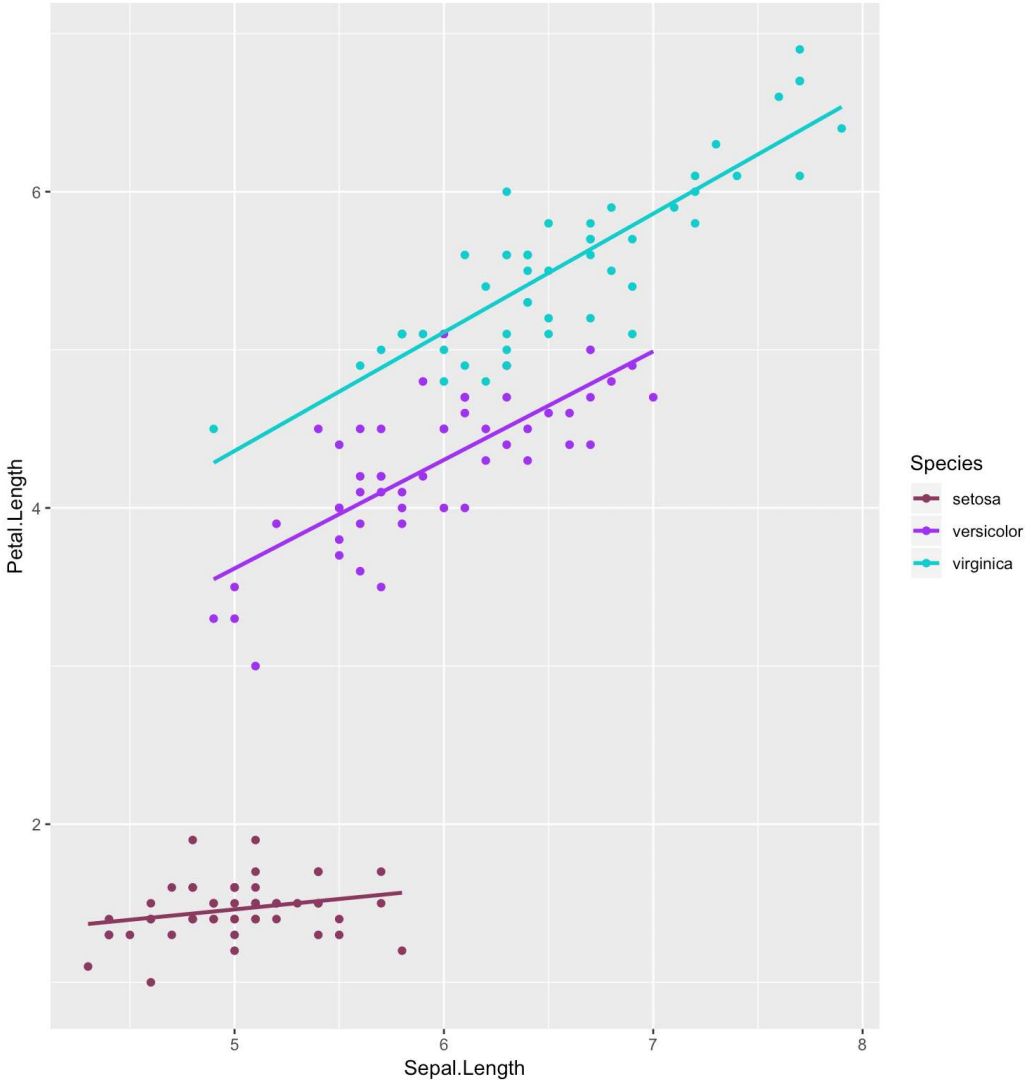
```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length) +
  aes(y= Petal.Length) +
  geom_point() +
  aes(col = Species) +
  geom_smooth(method = "lm", se = F)
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

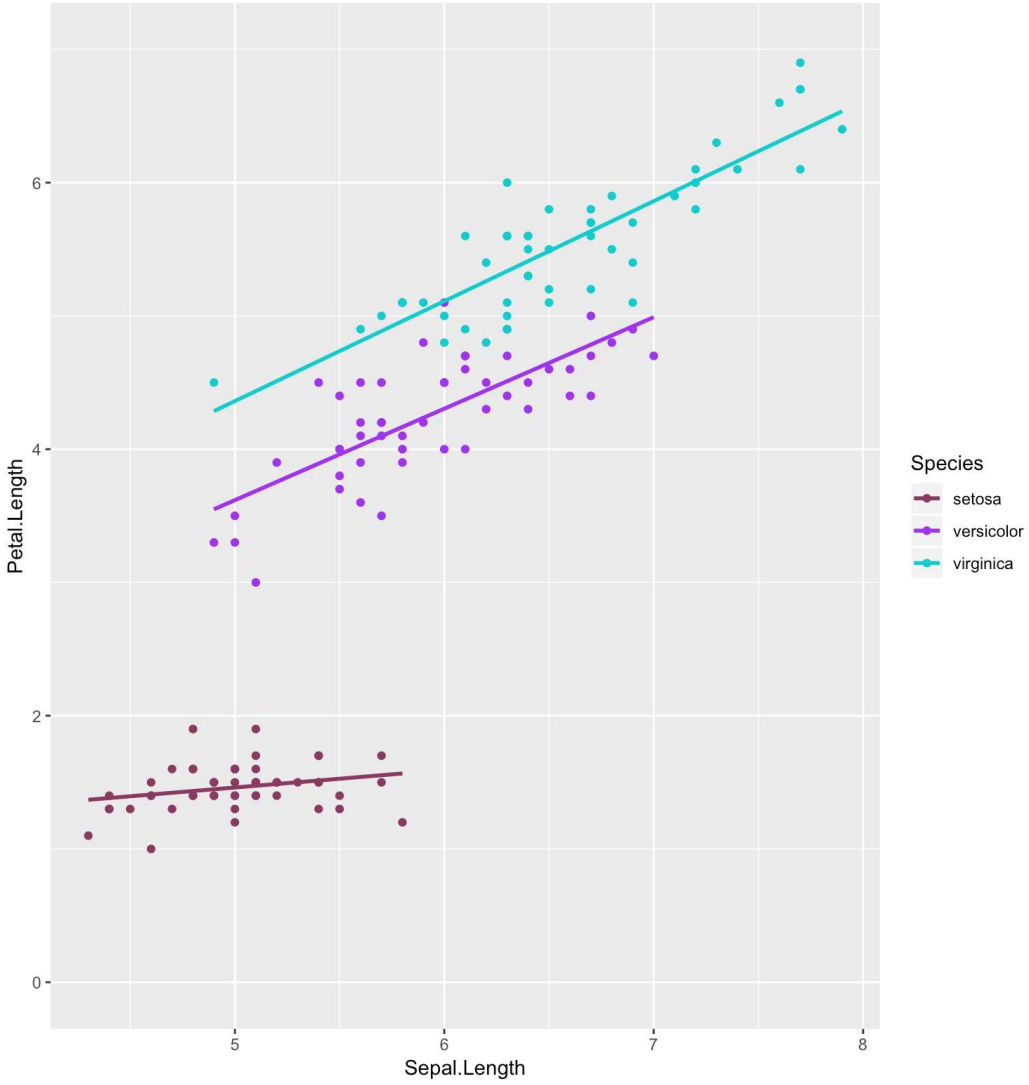
```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length) +
  aes(y= Petal.Length) +
  geom_point() +
  aes(col = Species) +
  geom_smooth(method = "lm", se = F) +
  scale_color_manual(values = c("hotpink4", "purple",
"cyan3"))
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

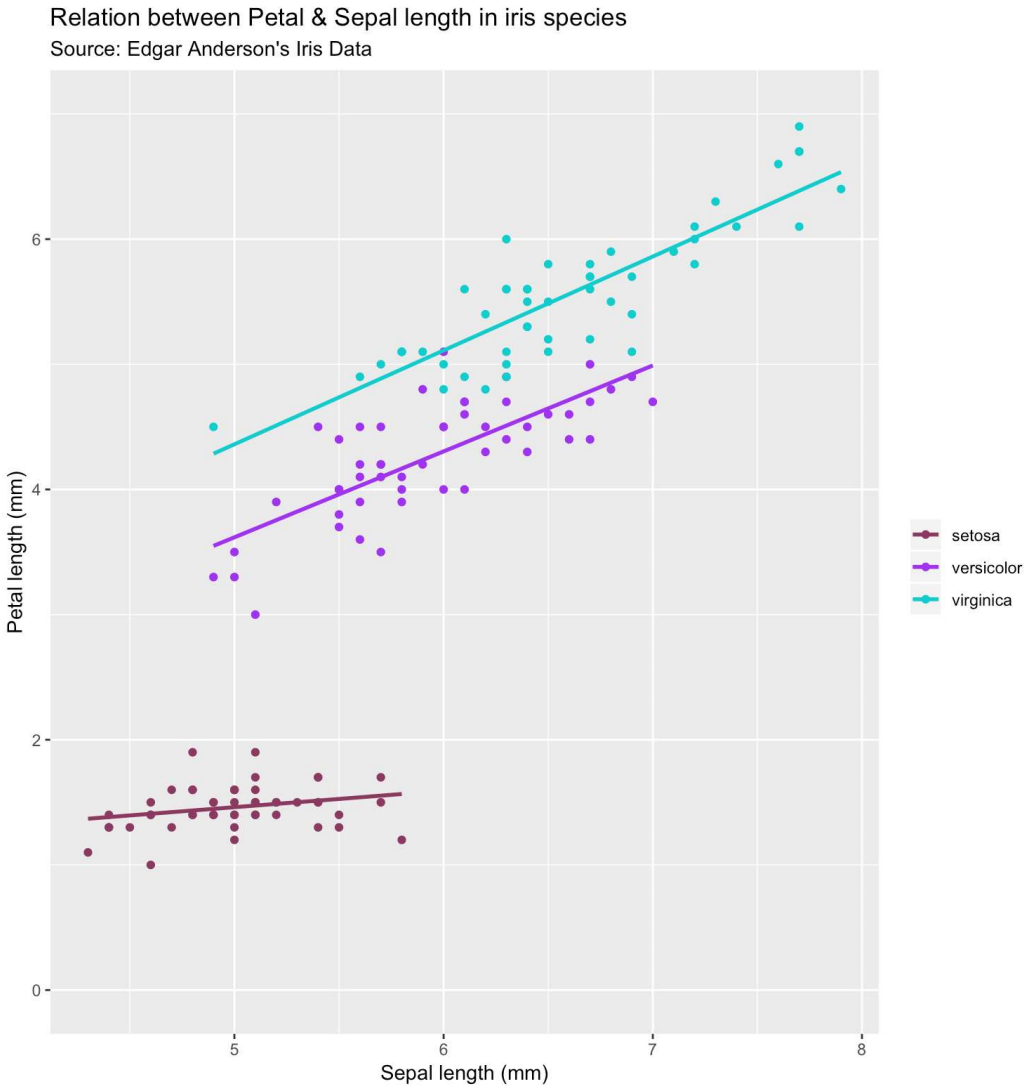
```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length) +
  aes(y= Petal.Length) +
  geom_point() +
  aes(col = Species) +
  geom_smooth(method = "lm", se = F) +
  scale_color_manual(values = c("hotpink4", "purple",
"cyan3")) +
  ylim(0,7)
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

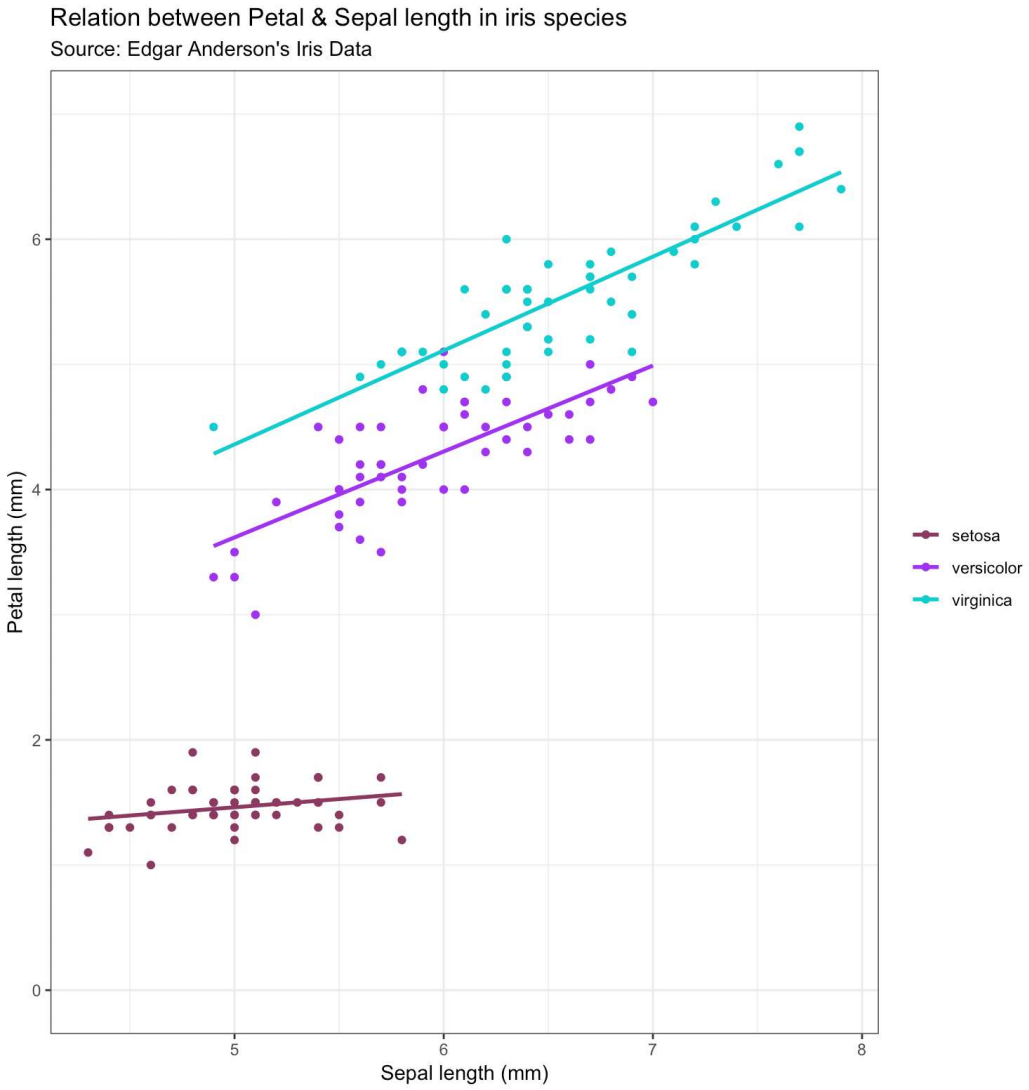
```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length) +
  aes(y= Petal.Length) +
  geom_point() +
  aes(col = Species) +
  geom_smooth(method = "lm", se = F) +
  scale_color_manual(values = c("hotpink4", "purple",
"cyan3")) +
  ylim(0,7) +
  labs(col="") +
  labs(title="Relation between Petal & Sepal length in iris
species") +
  labs(subtitle="Source: Edgar Anderson's Iris Data") +
  labs(x ="Sepal length (mm)") +
  labs(y ="Petal length (mm)")
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

```
# R-code:
library(ggplot2)
head(iris)

ggplot(data = iris) +
  aes(x = Sepal.Length) +
  aes(y= Petal.Length) +
  geom_point() +
  aes(col = Species) +
  geom_smooth(method = "lm", se = F) +
  scale_color_manual(values = c("hotpink4", "purple",
"cyan3")) +
  ylim(0,7) +
  labs(col="") +
  labs(title="Relation between Petal & Sepal length in iris
species") +
  labs(subtitle="Source: Edgar Anderson's Iris Data") +
  labs(x ="Sepal length (mm)") +
  labs(y ="Petal length (mm)") +
  theme_bw()
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

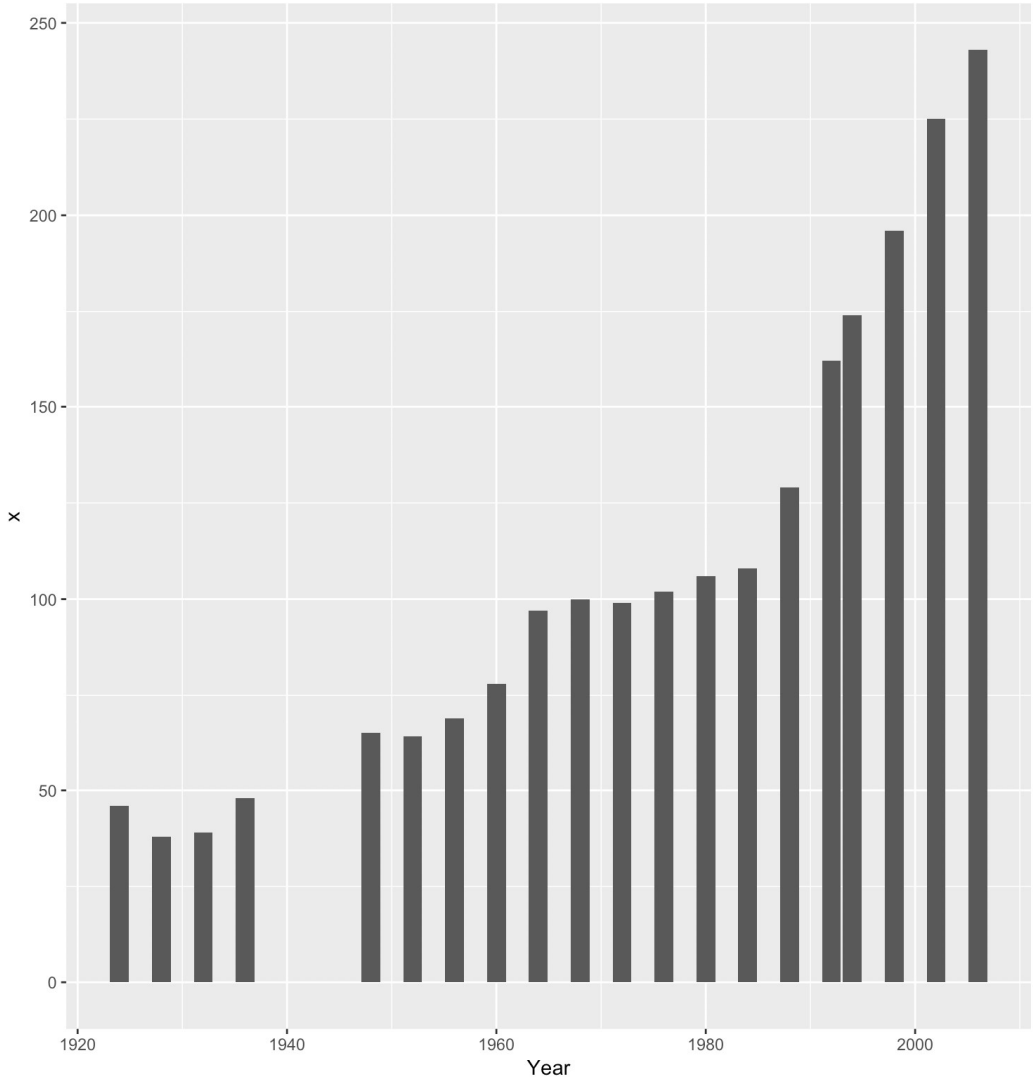
Grammar of Graphics using ggplot

```
# R-code:
library(ggplot2)

ggplot(data = medals2)
```


Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

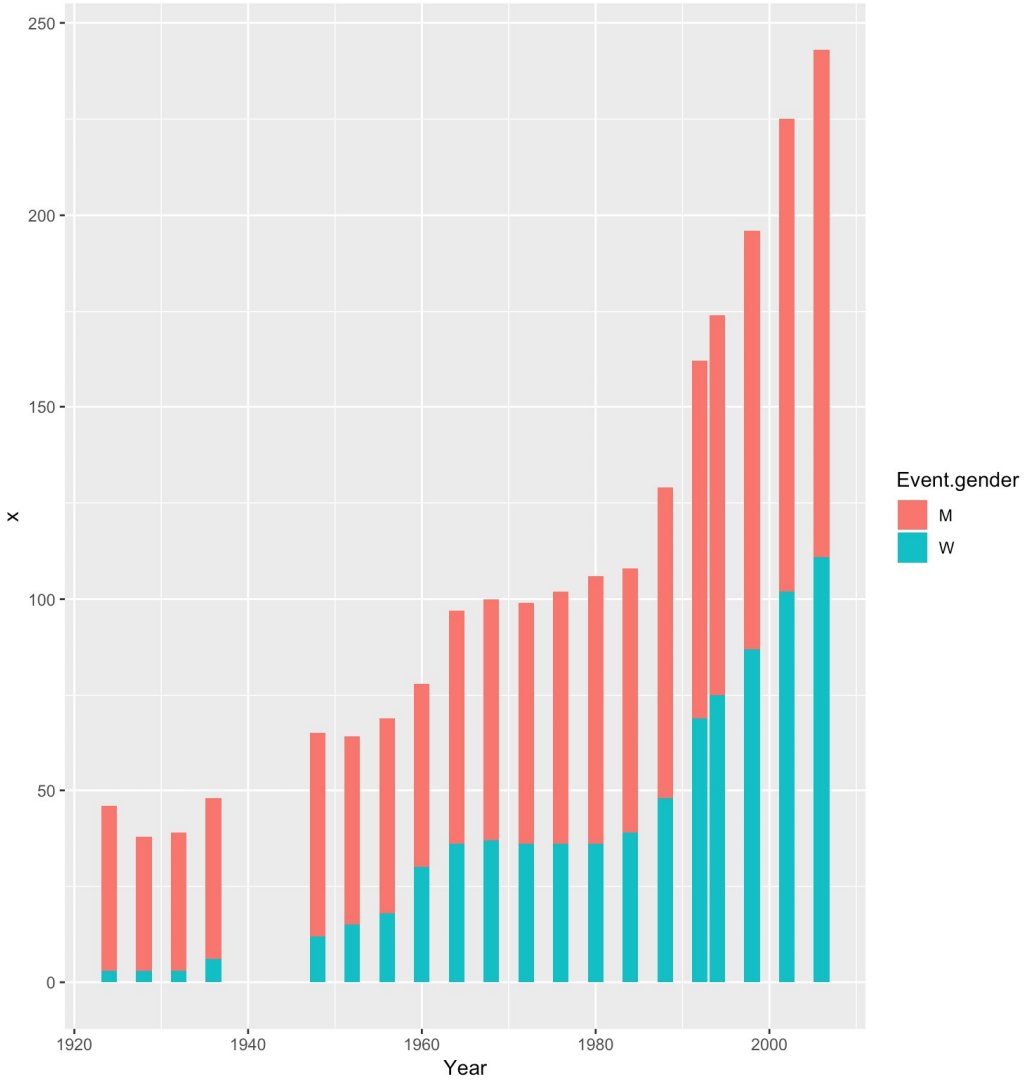
```
# R-code:
library(ggplot2)

ggplot(data = medals2)+
  aes(x = Year)+
  aes(y = x)+
  geom_bar(stat="identity")
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

```
# R-code:
library(ggplot2)

ggplot(data = medals2)+
  aes(x = Year)+
  aes(y = x)+
  geom_bar(stat="identity")+
  aes(fill = Event.gender)
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

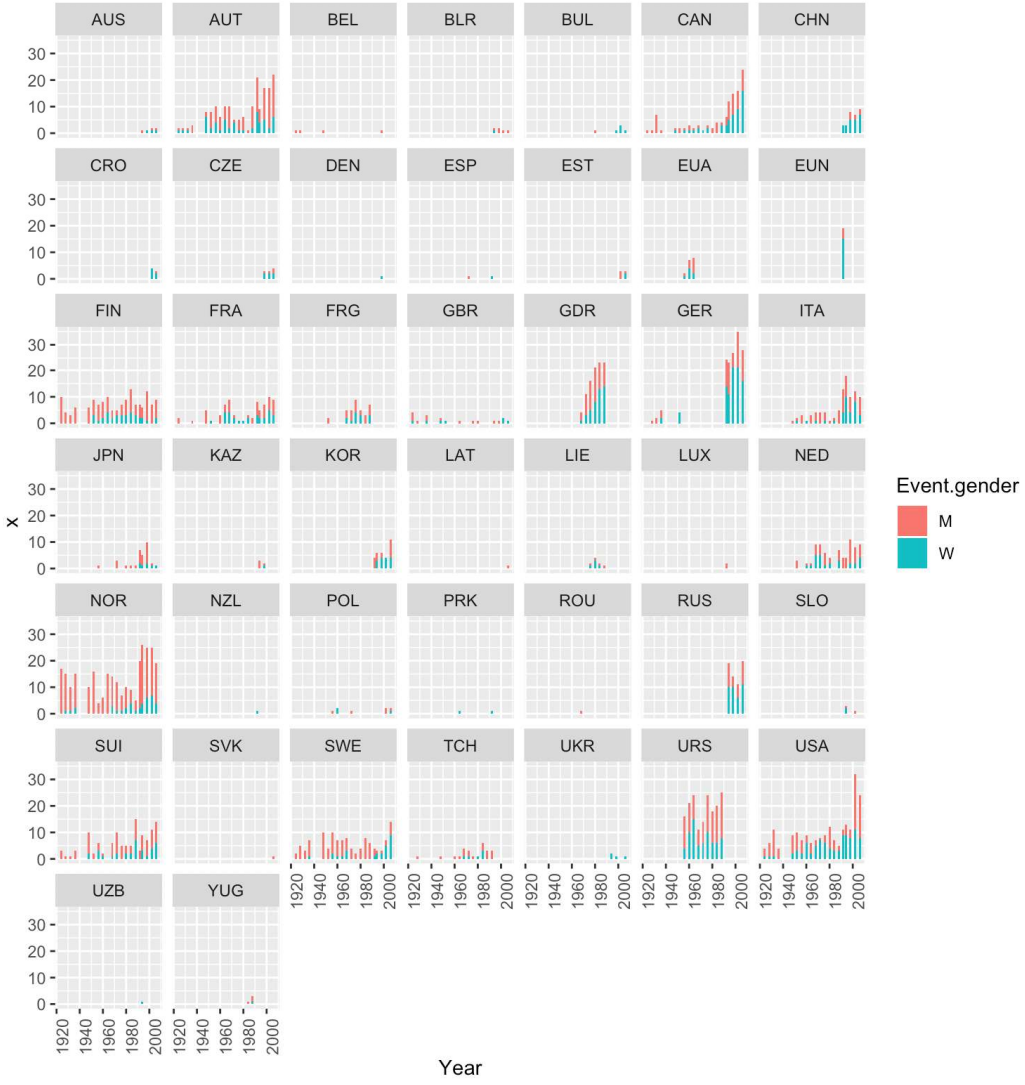
Grammar of Graphics using ggplot

```
# R-code:
library(ggplot2)

ggplot(data = medals2)+
  aes(x = Year)+
  aes(y = x)+
  geom_bar(stat="identity")+
  aes(fill = Event.gender)+
  facet_wrap(~Country)
```

Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

```
# R-code:
library(ggplot2)

ggplot(data = medals2)+
  aes(x = Year)+
  aes(y = x)+
  geom_bar(stat="identity")+
  aes(fill = Event.gender)+
  facet_wrap(~Country)+
  labs(col="")+
  labs(title="Olympic medals between 1924 and 2006")+
  labs(subtitle="Source: IOC | olympic.org")+
  labs(x ="")+
  labs(y ="Number of medals")+
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
```



Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Grammar of Graphics using ggplot

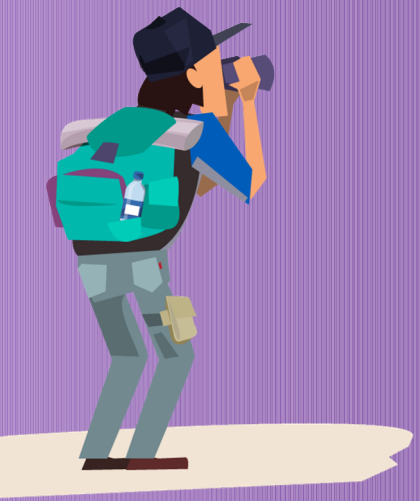
```
# R-code:
library(ggplot2)

ggplot(data = medals2)+
  aes(x = Year)+
  aes(y = x)+
  geom_bar(stat="identity")+
  aes(fill = Event.gender)+
  facet_wrap(~Country)+
  labs(col="")+
  labs(title="Olympic medals between 1924 and 2006")+
  labs(subtitle="Source: IOC | olympic.org")+
  labs(x ="")+
  labs(y ="Number of medals")+
  theme_bw()+
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
```

Inspired by Rladies ggplot2 flipbook
https://evamaerey.github.io/ggplot_flipbook/ggplot_flipbook_xaringan.html#232

Exploratory vs. confirmatory visualization

Exploratory questions:

+ Which traits change in response to heat stress?
+ How are my metabolites connected?

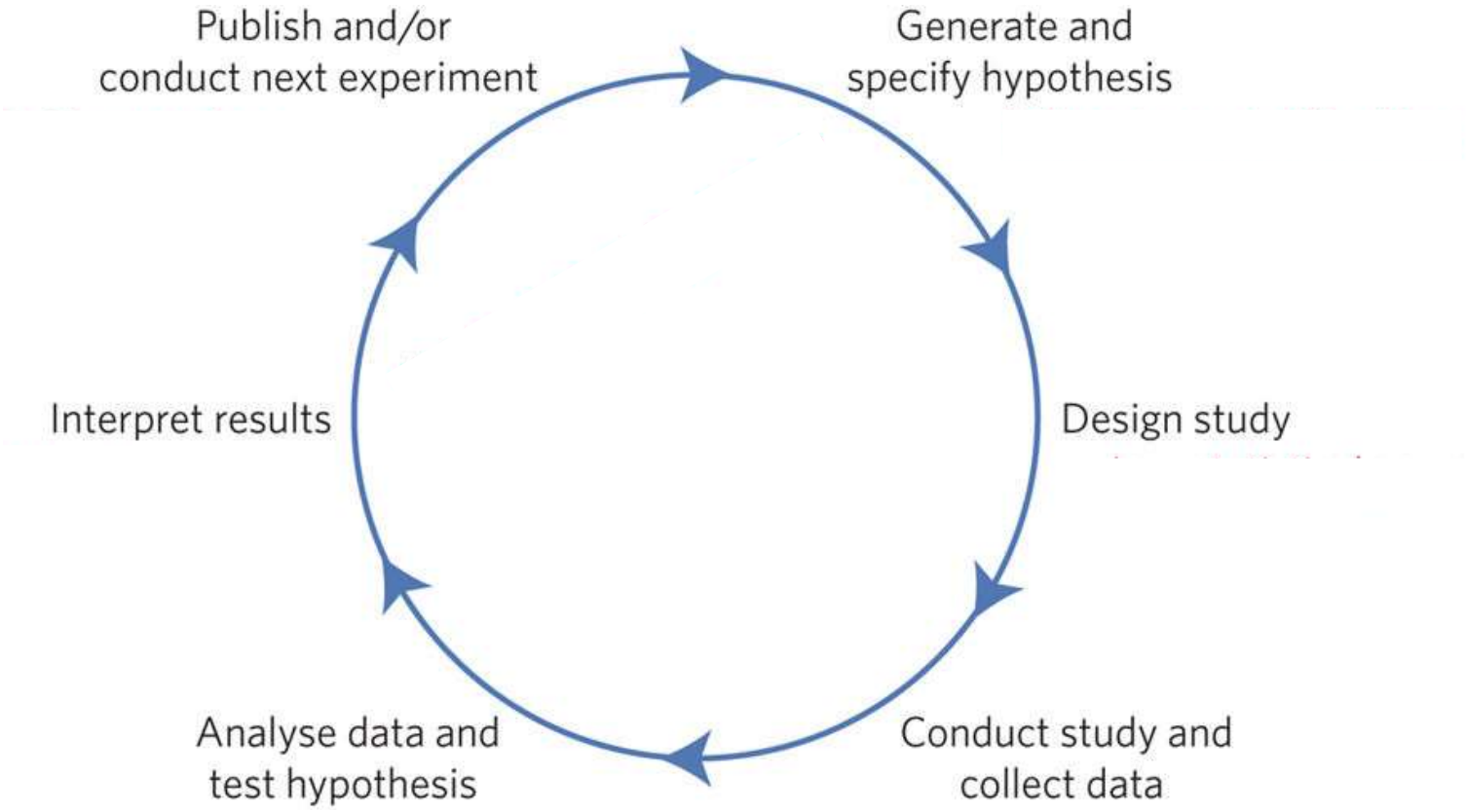


Confirmatory questions:

+ Is my gene affecting ion uptake?
+ Does my mutant accumulate less ABA?

Does my gene affects CO_2 accumulation?

Hypothesis after results are known (HARKing) is not OK!



Munafò, M. R., Nosek, B. A., Bishop, D. V. M., Button, K. S., Chambers, C. D., Sert, N. P. du, … Ioannidis, J. P. A. (2017). A manifesto for reproducible science. *Nature Human Behaviour*, *1*(1), s41562-016-0021-016. https://doi.org/10.1038/s41562-016-0021

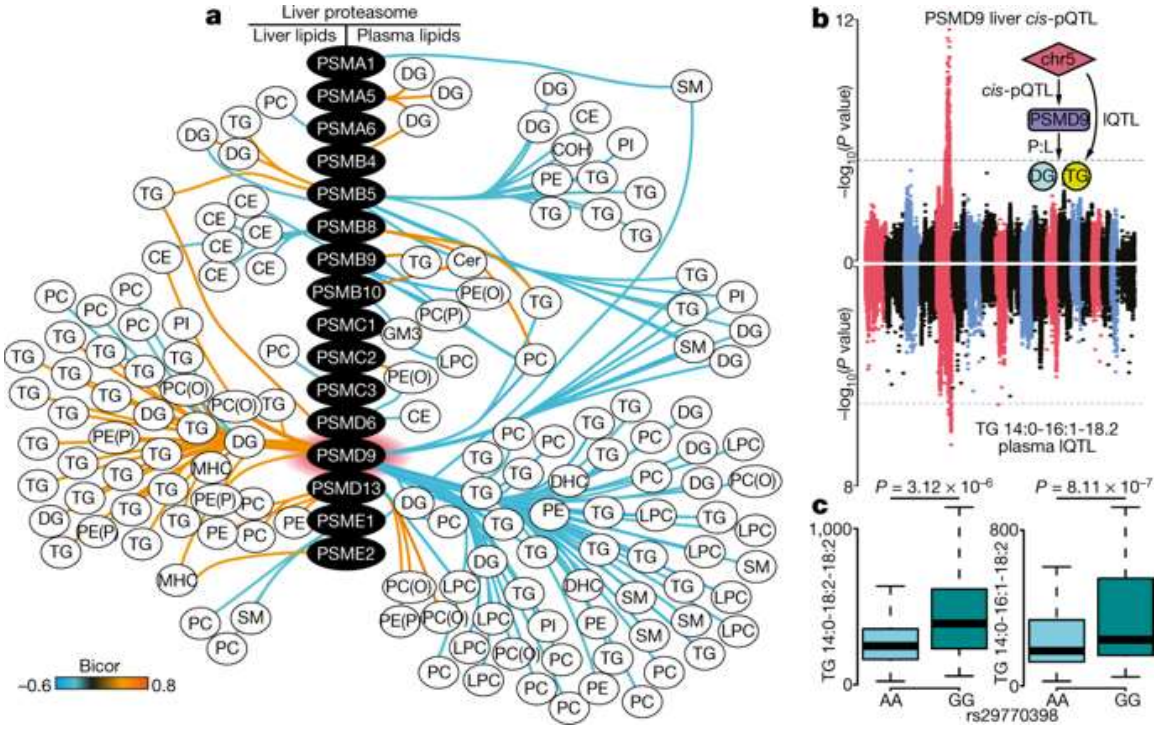
Exploratory visualization

- Comparing and interpreting the data
- Understanding the relationship between variables
- Experimenting with multiple ways to present and summarize your data
- Producing crude representations
- (Interactive)
- Not intended for final publication

Slide inspired by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

Illustrative visualization

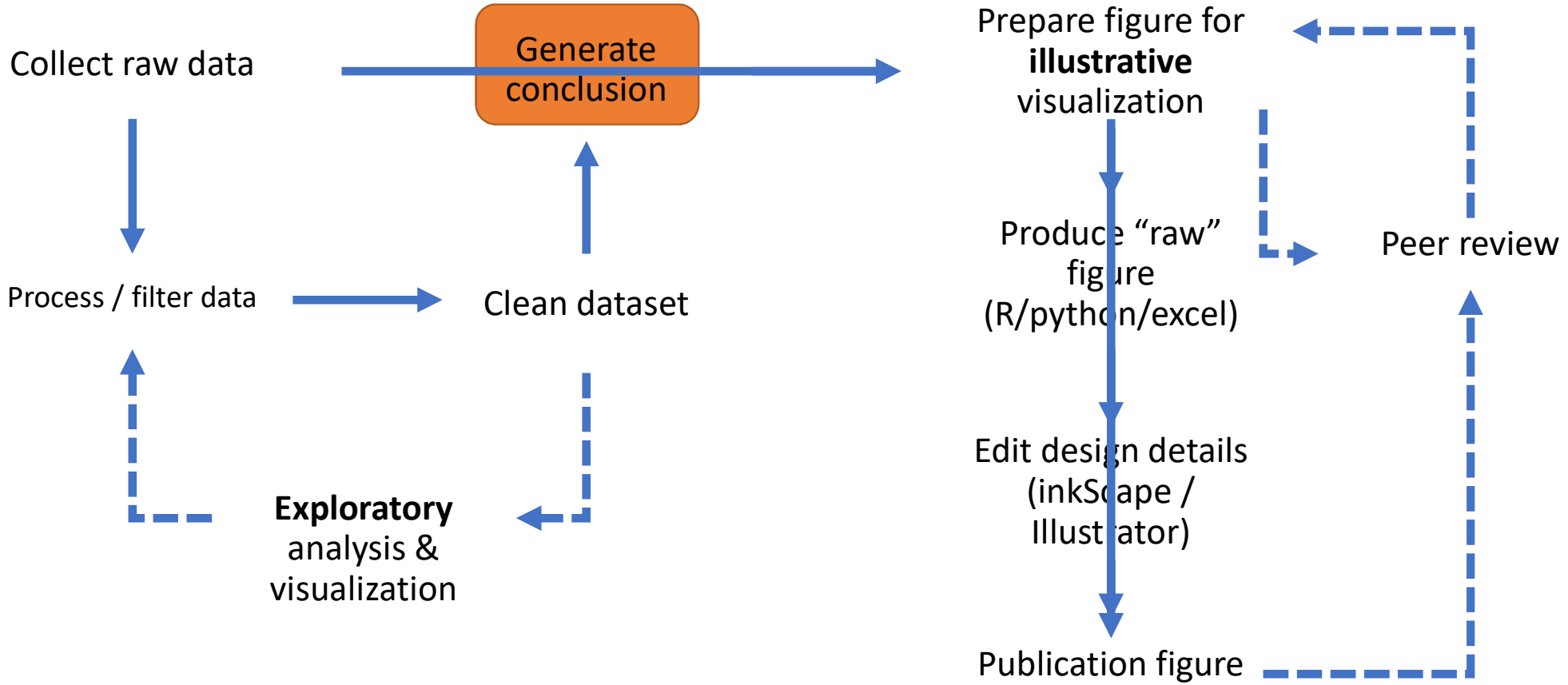
- Helps to convey special point
- Carefully chosen (sub)set of data
- Optimized presentation
- Allows reader to critically evaluate your data
- Used in papers



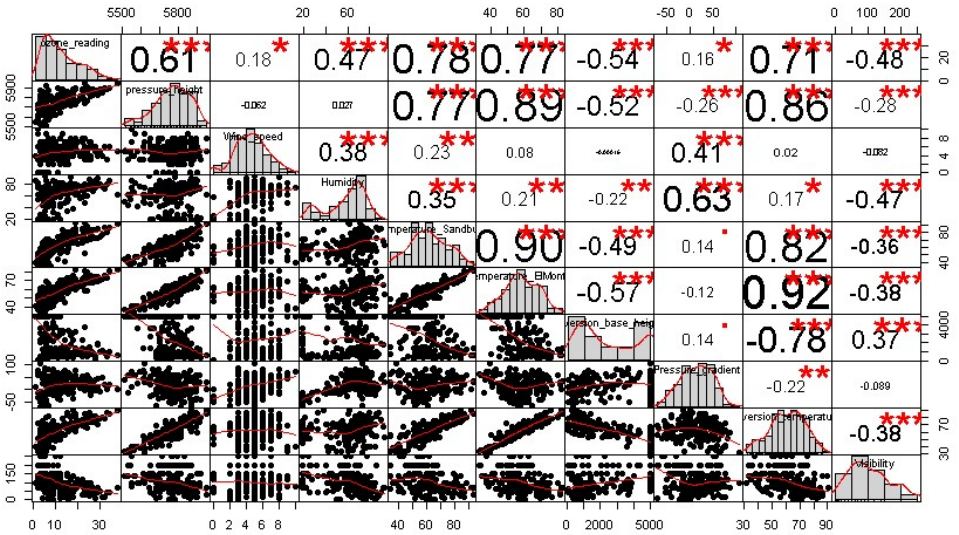
Parker et al., An integrative systems genetic analysis of mammalian lipid metabolism (2019) Nature

Slide inspired by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

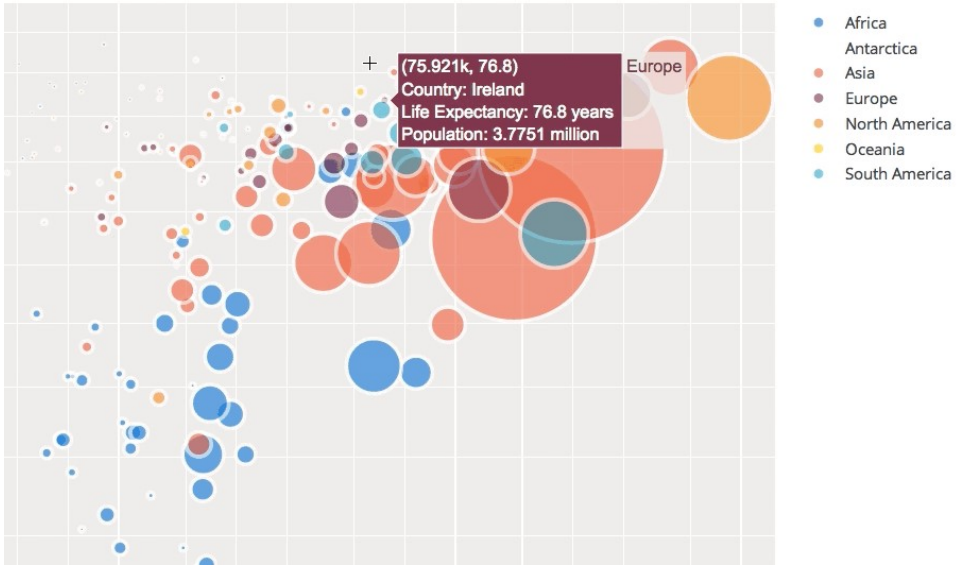
Exploratory data visualization process



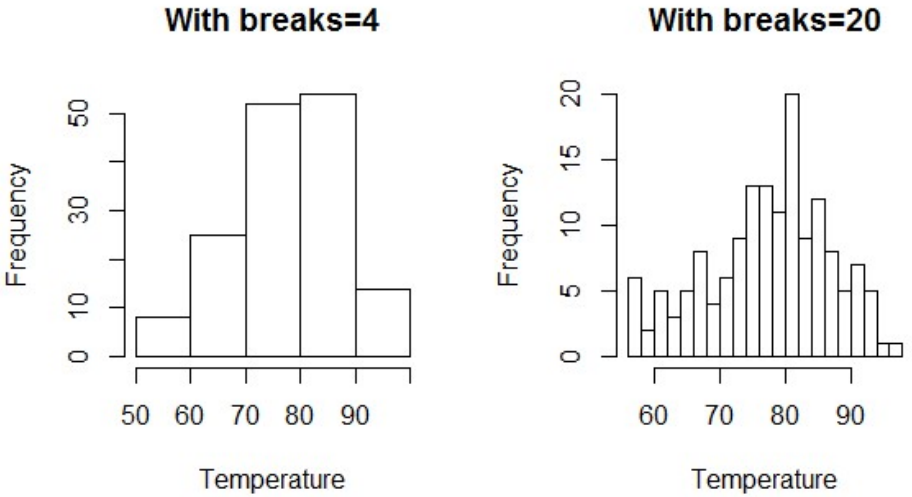
Slide by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**



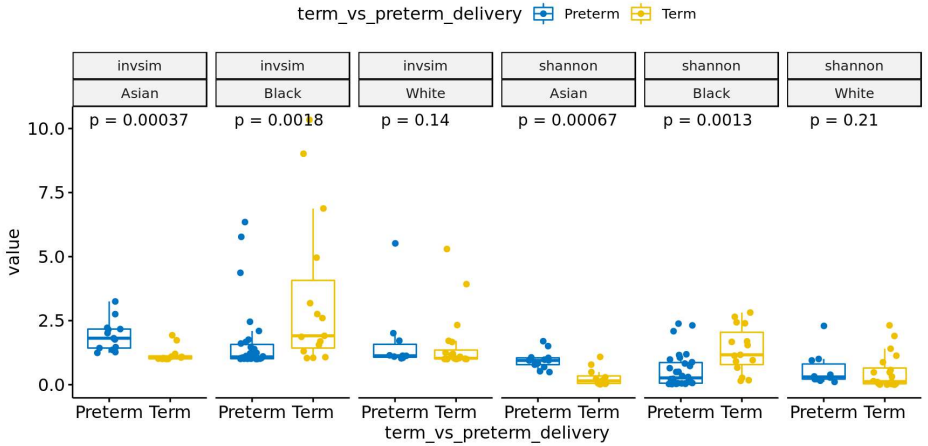
Correlogram to examine bi-variate relations



Interactive graphics (e.g. Plot.ly)



Histograms to examine data distribution

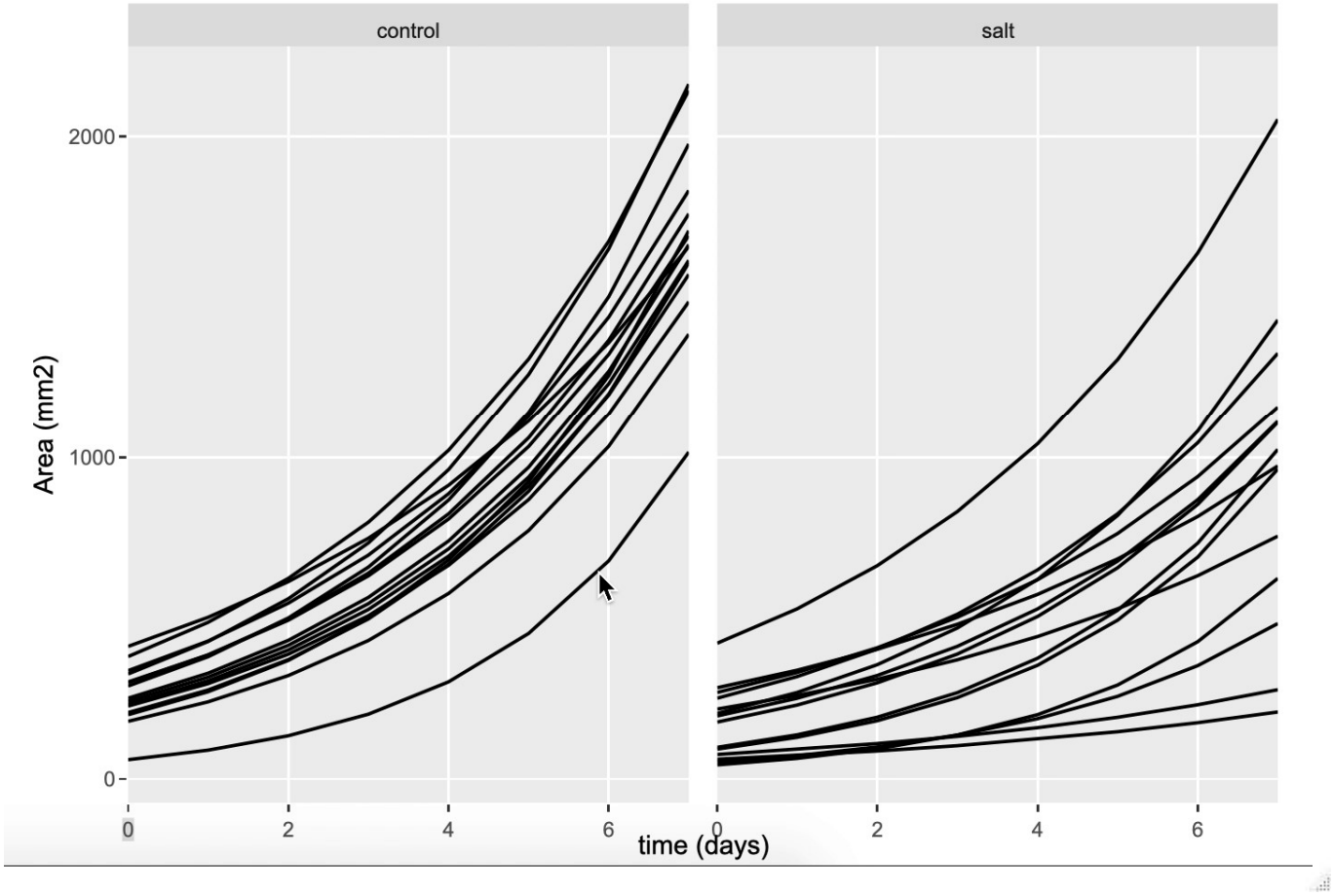


Multiple comparisons (e.g. ggpubr)

Slide inspired by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

Interactive libraries for efficient data exploration

```
# R-code:
library(ggplot2)
library(plotly)

my_plot <- ggplot(data = done)+
  aes(x = time.day)+
  aes(y = Area)+
  aes(group = Plant_ID)+
  geom_line(stat="identity")+
  facet_grid(~treatment)+
  ylab("Area (mm2)")+
  xlab("time (days)")+
  theme(legend.position = "none")+
  ylim(0, 2900)

ggplotly(my_plot)
```



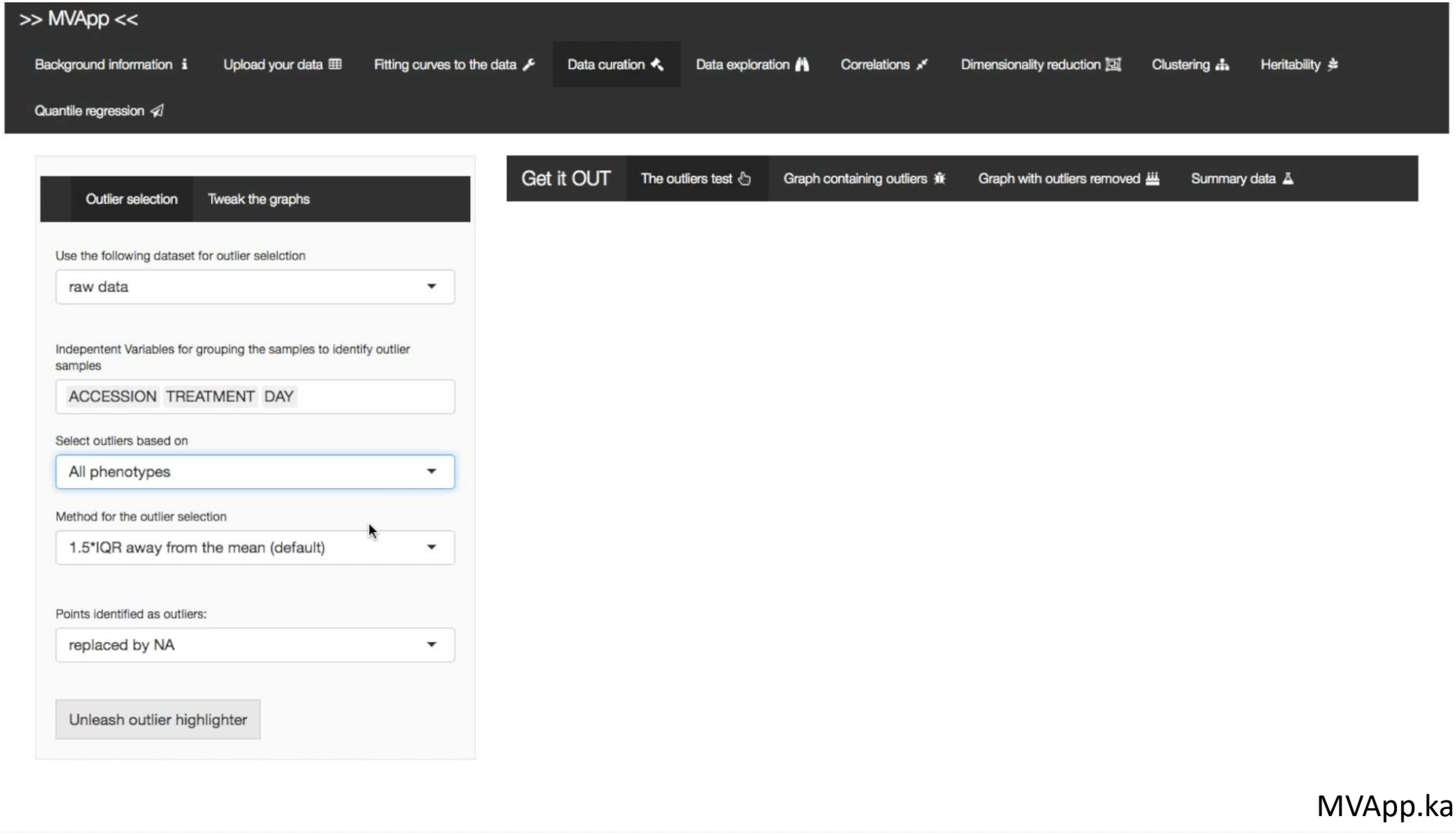
Other

MVApp - Multivariate analysis application for streamlined data analysis and curation

Magdalena M Julkowska, Stephanie Saade, Gaurav Agarwal, Ge Gao, Yveline Pailles, Mitchell J.L. Morton, Mariam Awlia, Mark Tester

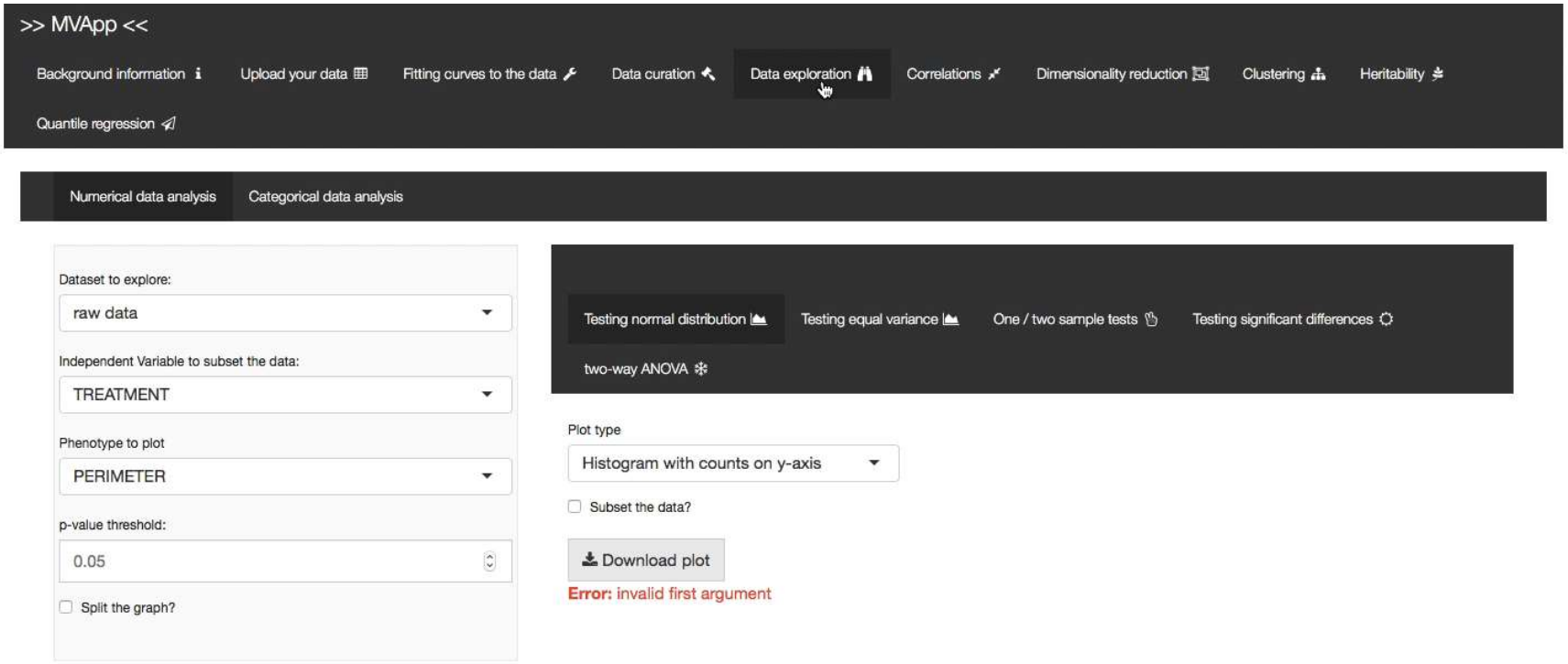
Published May 2019. DOI: https://doi.org/10.1104/pp.19.00235

MVApp >> outlier selection



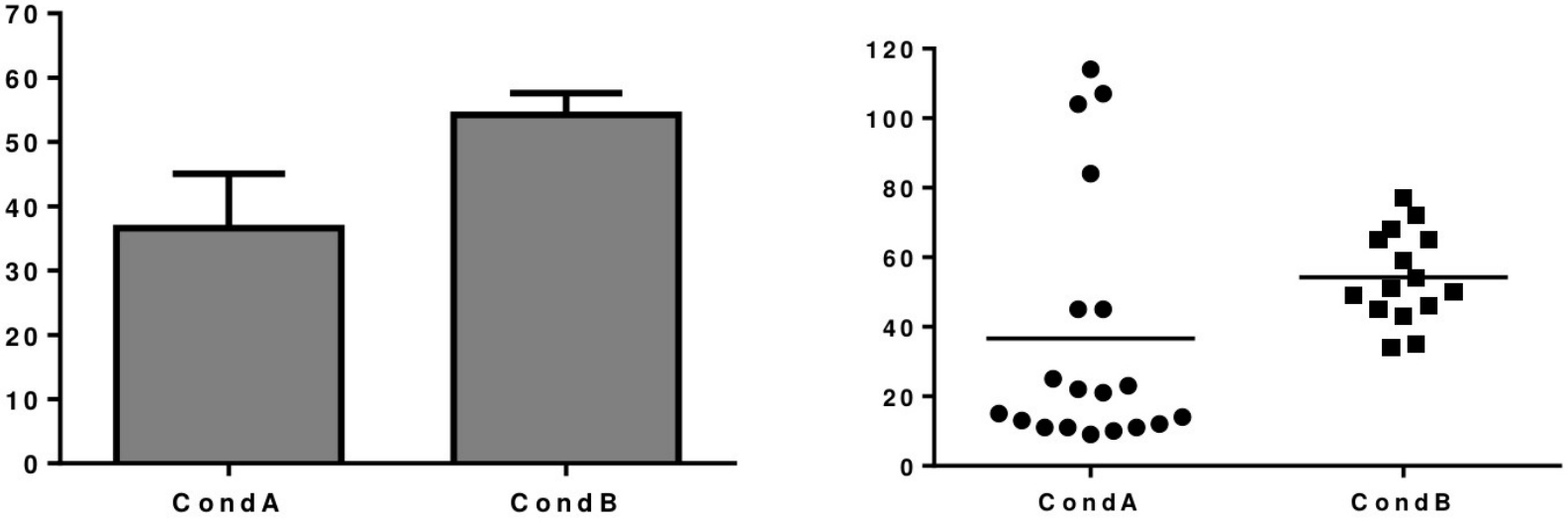
MVApp.kaust.edu.sa

MVApp >> hypothesis testing



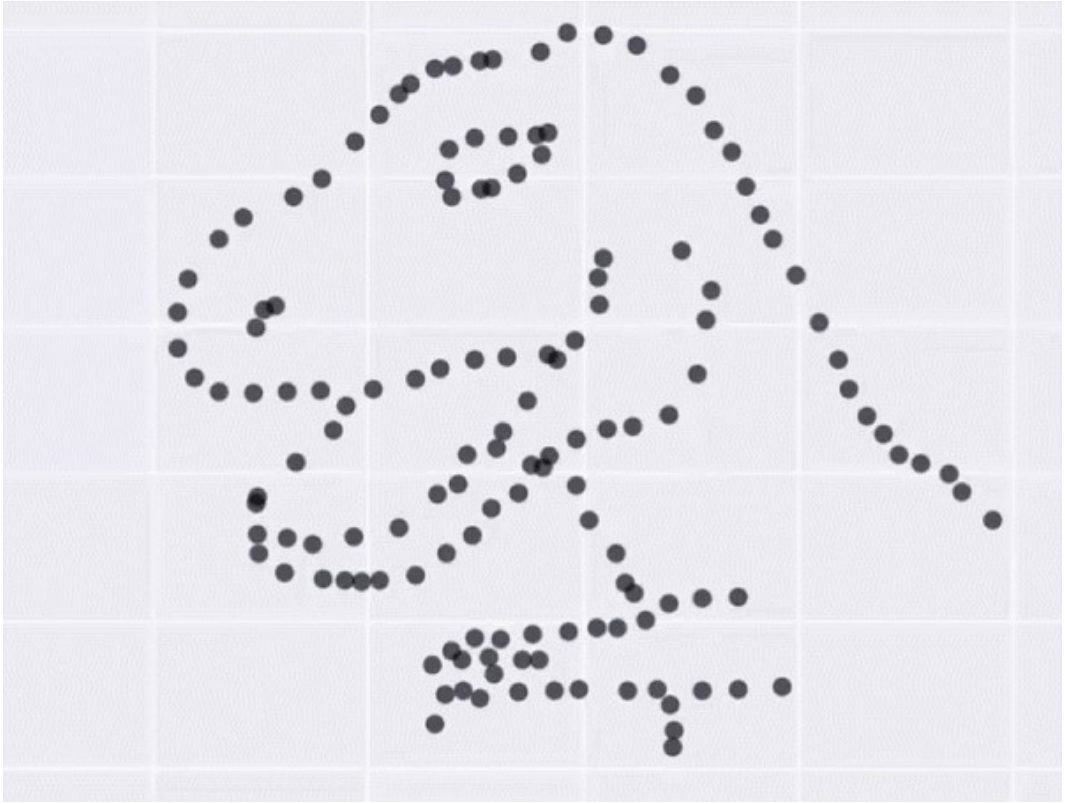
MVApp.kaust.edu.sa

Sins of confirmatory analysis:
#1 You can do better than a bar graph!



Sins of confirmatory analysis:
#1 You can do better than a bar graph!

X Mean	54.26
Y Mean	47.83
X SD	16.76
Y SD	26.93
Corr.	-0.06

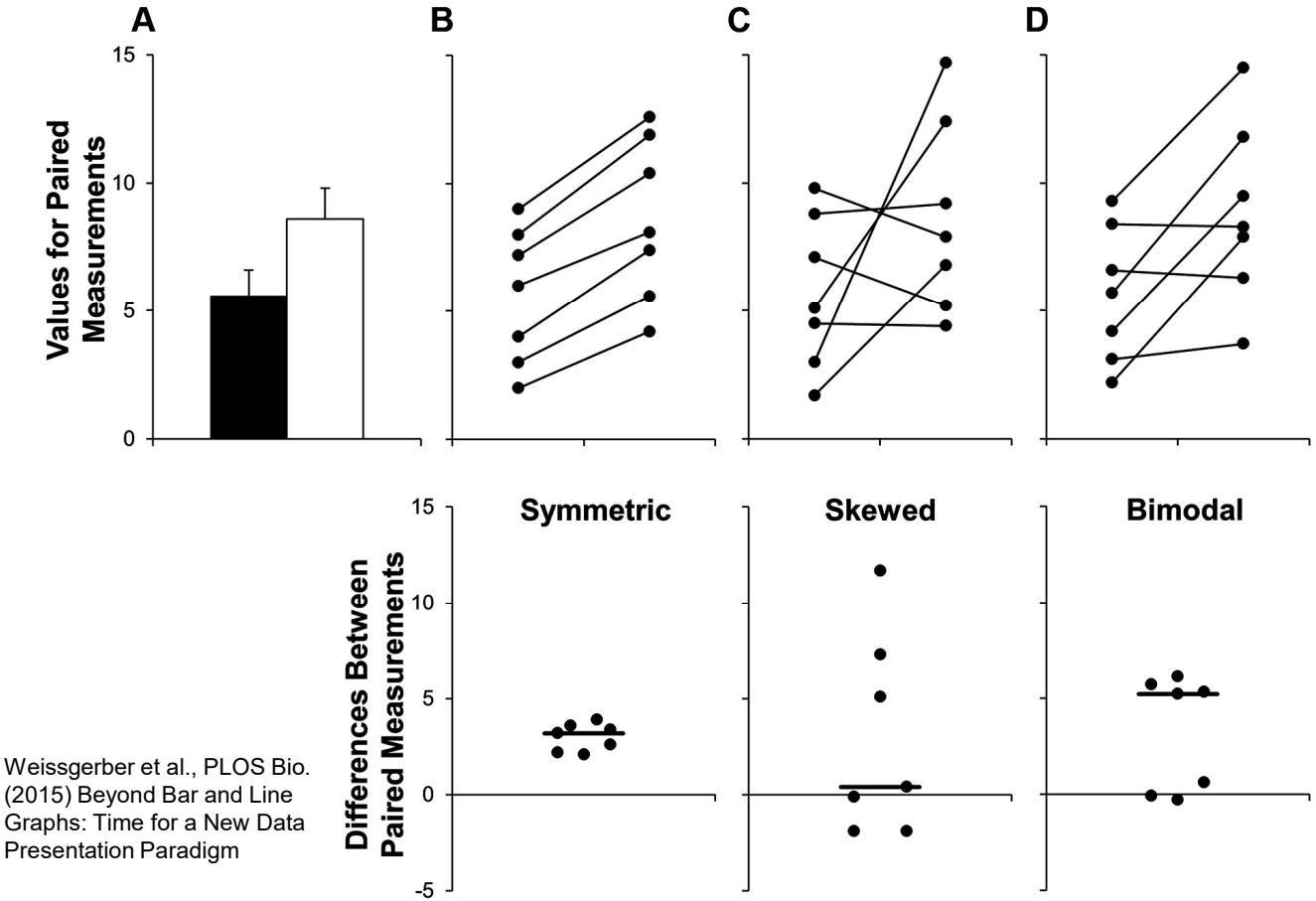


Same Stats, Different Graphs: Generating Datasets with Varied Appearance and Identical Statistics through Simulated Annealing

Sins of confirmatory analysis:
#1 You can do better than a bar graph!

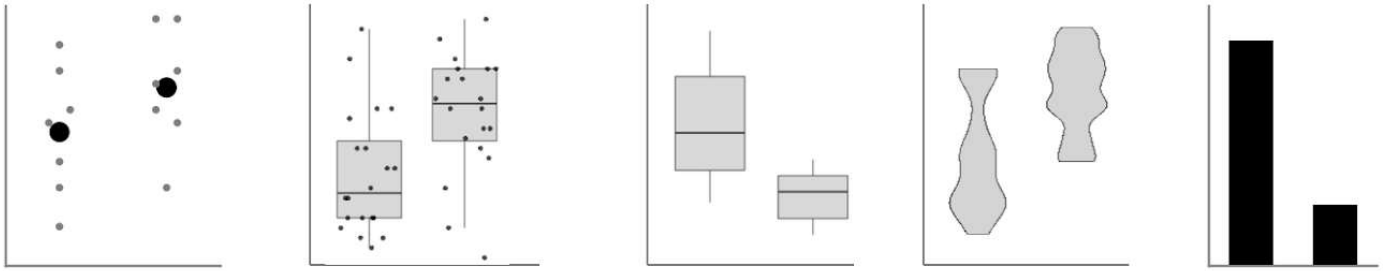
Alternatives to bar graphs allow you to better present:

- paired / non-paired samples
- distribution of your data points



Weissgerber et al., PLOS Bio. (2015) Beyond Bar and Line Graphs: Time for a New Data Presentation Paradigm

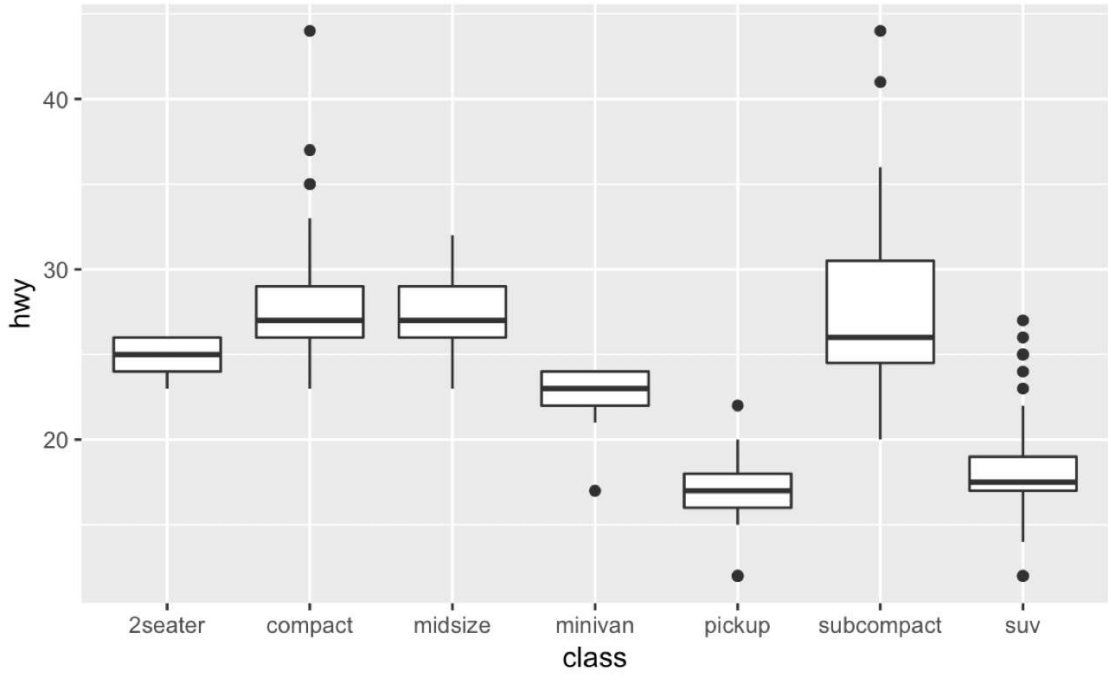
Bar graph alternatives



	Dotplot	**Boxplot with points**	**Boxplot**	**Violin plot (with or without points)**	**Bar graph**
Outcome variable	Continuous	Continuous	Continuous	Continuous	Counts & proportions
Sample size	Small	Medium	Large	Medium to Large	Any
Data distribution	Any	Any	Do not use for bimodal data	Any	N/A

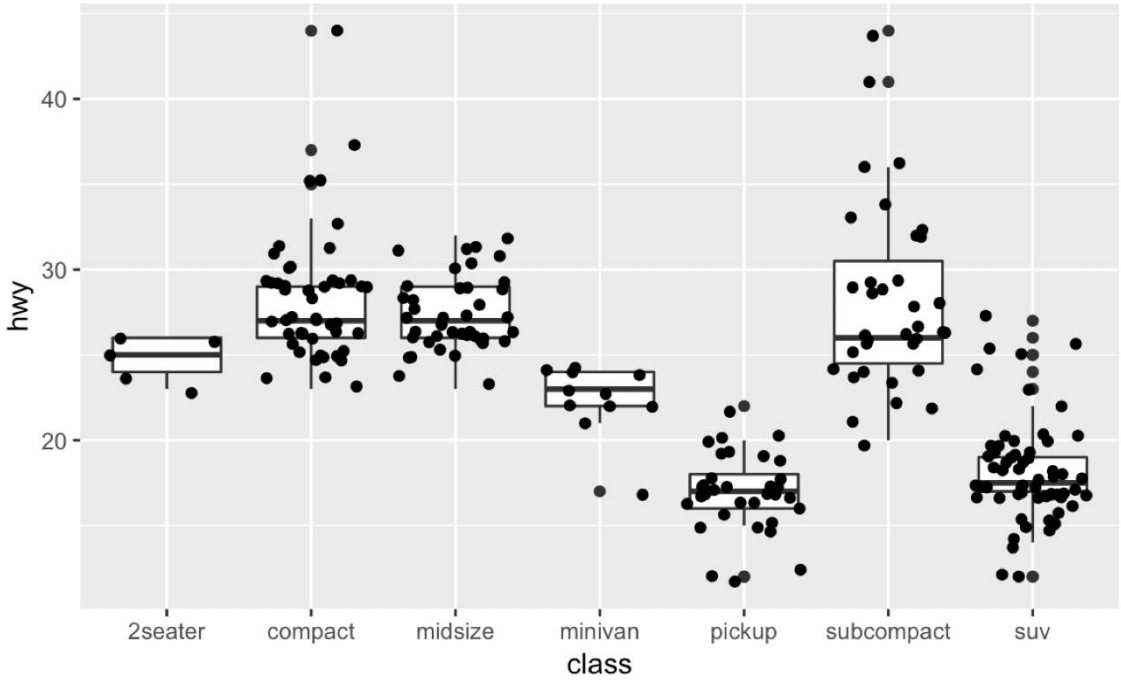
Making effective uni-variate plot

```
# R-code:
library(ggplot2)
library(ggbeeswarm)
library(RColorBrewer)
library(ggridges)
library(gapminder)

my_box_plot <- ggplot(data = mpg,
               aes(x = class, y = hwy))
               + geom_boxplot()

my_box_plot
```



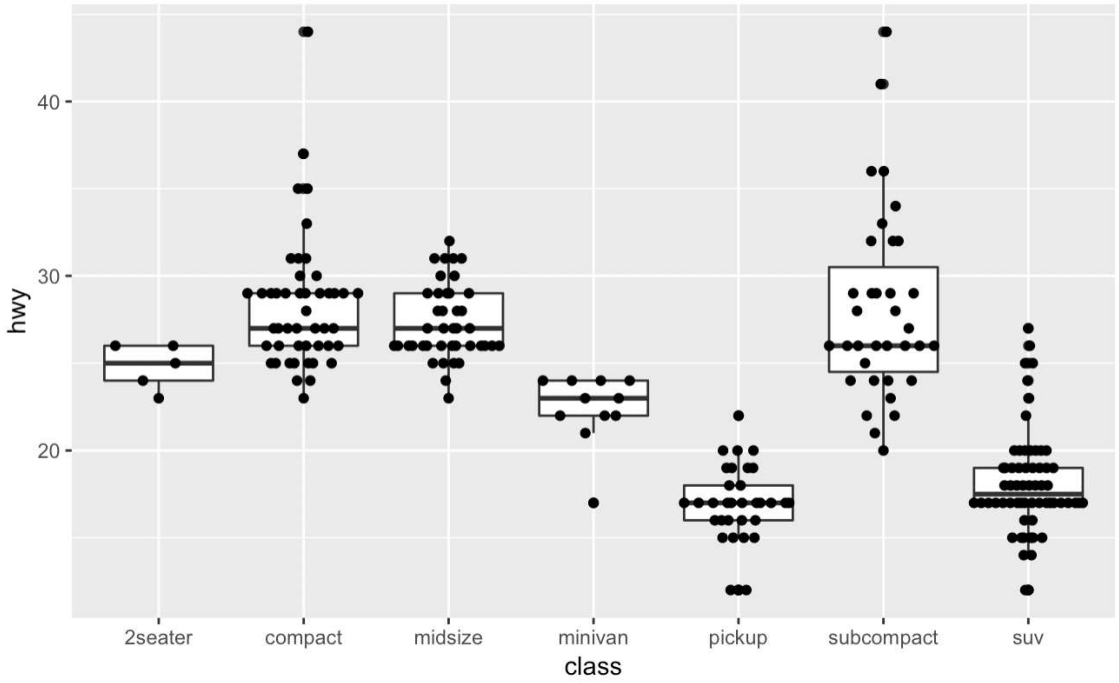
Making effective uni-variate plot

```
# R-code:
library(ggplot2)
library(ggbeeswarm)
library(RColorBrewer)
library(ggridges)
library(gapminder)

my_box_plot <- ggplot(data = mpg,
                aes(x = class, y = hwy))
                + geom_boxplot()
                + geom_jitter()

my_box_plot
```



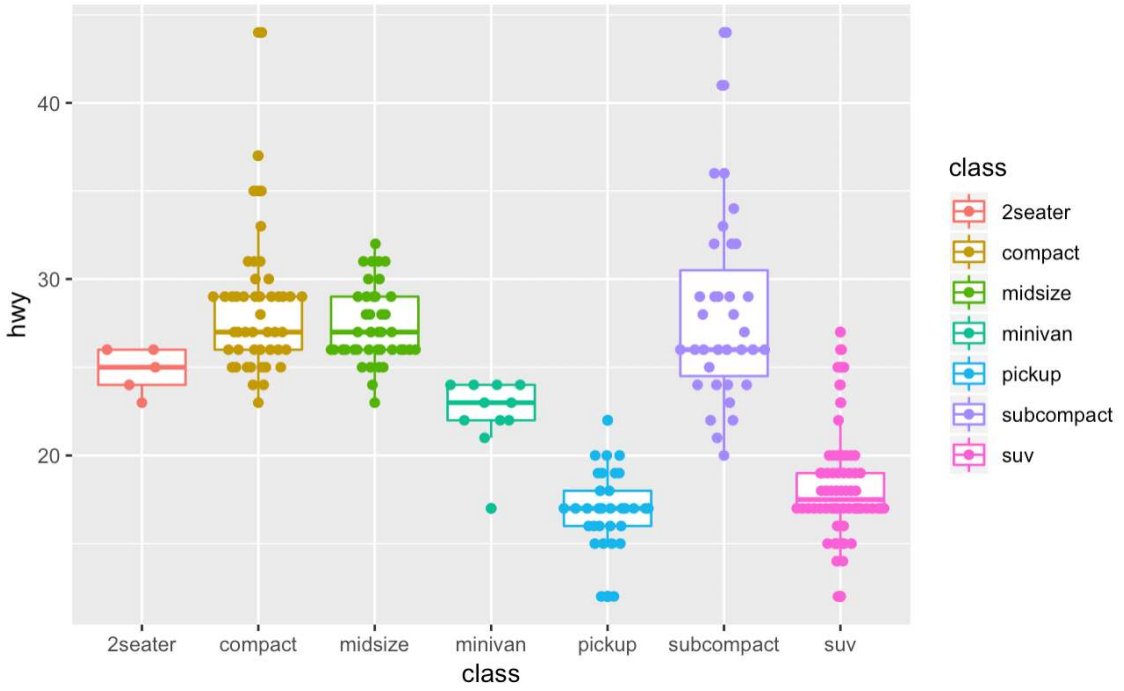
Making effective uni-variate plot

```
# R-code:
library(ggplot2)
library(ggbeeswarm)
library(RColorBrewer)
library(ggridges)
library(gapminder)

my_box_plot <- ggplot(data = mpg,
                aes(x = class, y = hwy))
                + geom_boxplot()
                + geom_quasirandom()

my_box_plot
```



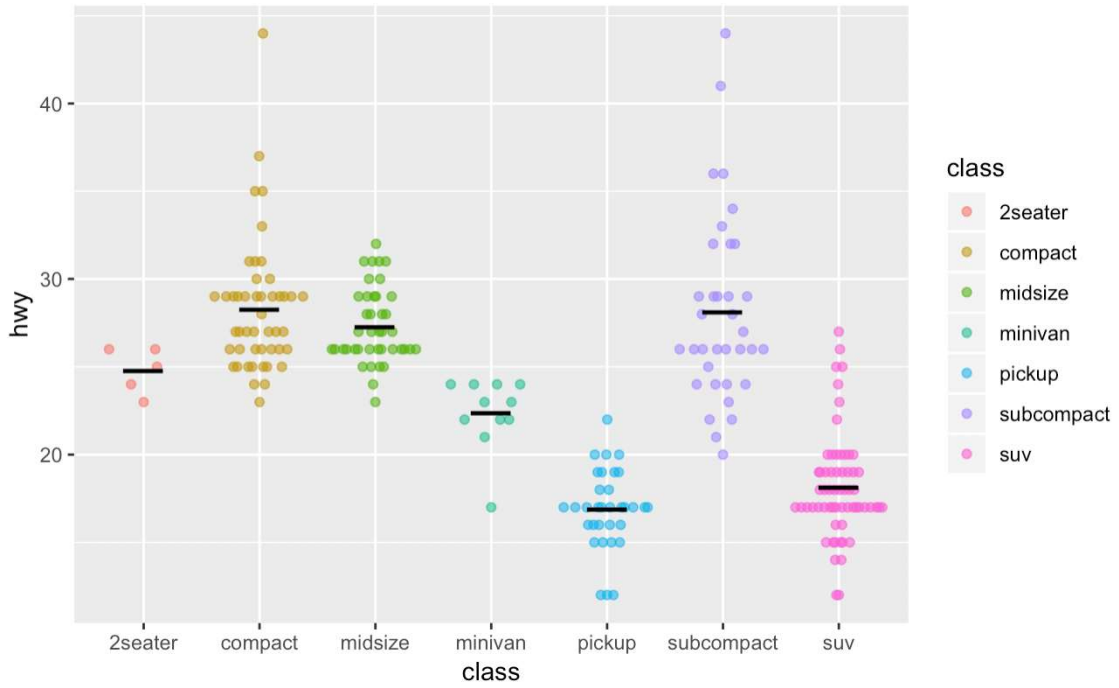
Making effective uni-variate plot

```
# R-code:
library(ggplot2)
library(ggbeeswarm)
library(RColorBrewer)
library(ggridges)
library(gapminder)

my_box_plot <- ggplot(data = mpg,
                aes(x = class, y = hwy, colour = class))
                + geom_boxplot()
                + geom_quasirandom()

my_box_plot
```



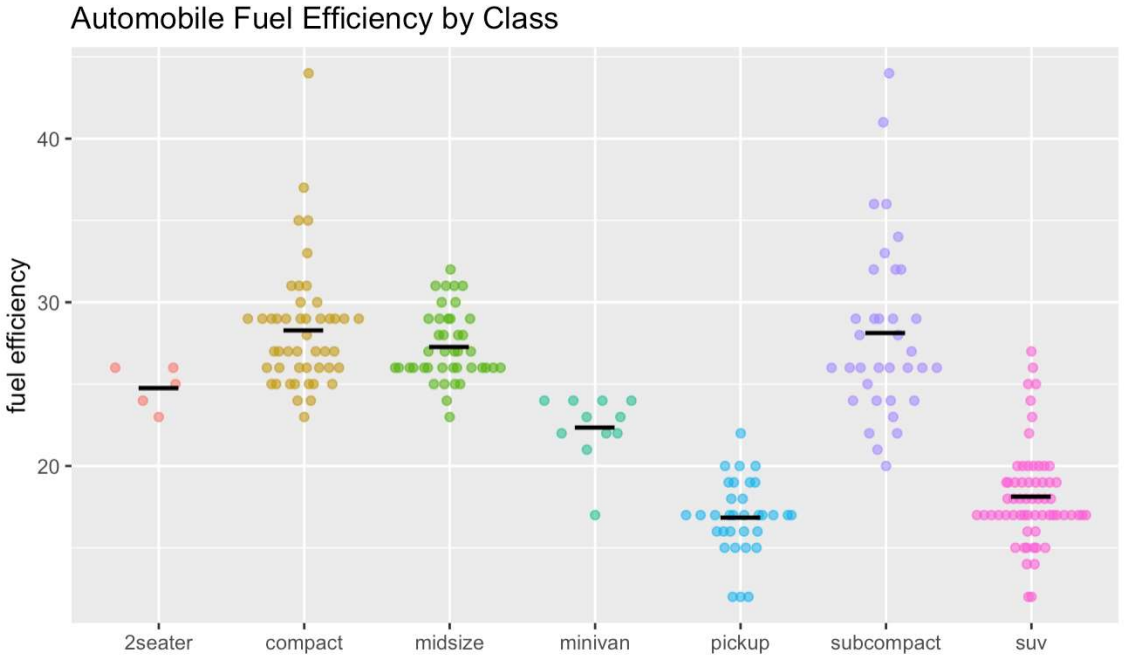
Making effective uni-variate plot

```
# R-code:
library(ggplot2)
library(ggbeeswarm)
library(RColorBrewer)
library(ggridges)
library(gapminder)

my_box_plot <- ggplot(data = mpg,
              aes(x = class, y = hwy, colour = class))
              + geom_quasirandom(alpha = 0.6)
               + stat_summary(fun.y=mean,
                           geom="point", shape=95, size=10,
                           color="black", fill="black")

my_box_plot
```



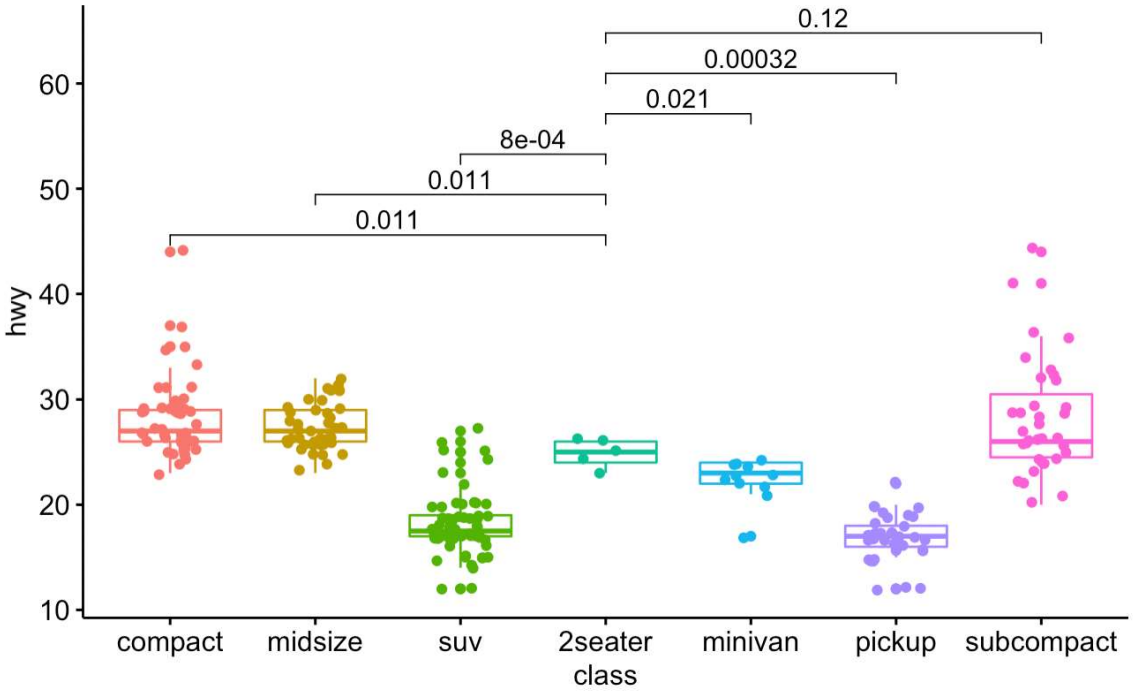
Making effective uni-variate plot

```
# R-code:
library(ggplot2)
library(ggbeeswarm)
library(RColorBrewer)
library(ggridges)
library(gapminder)

my_box_plot <- ggplot(data = mpg,
              aes(x = class, y = hwy, colour = class))
              + geom_quasirandom(alpha = 0.6)
               + stat_summary(fun.y=mean, geom="point",
                           shape=95, size=10, color="black",
                           fill="black")
               + labs(y = "fuel efficiency", x = "",
                           title = "Automobile Fuel Efficiency
                           by Class")
              + theme(legend.position = "none")

my_box_plot
```

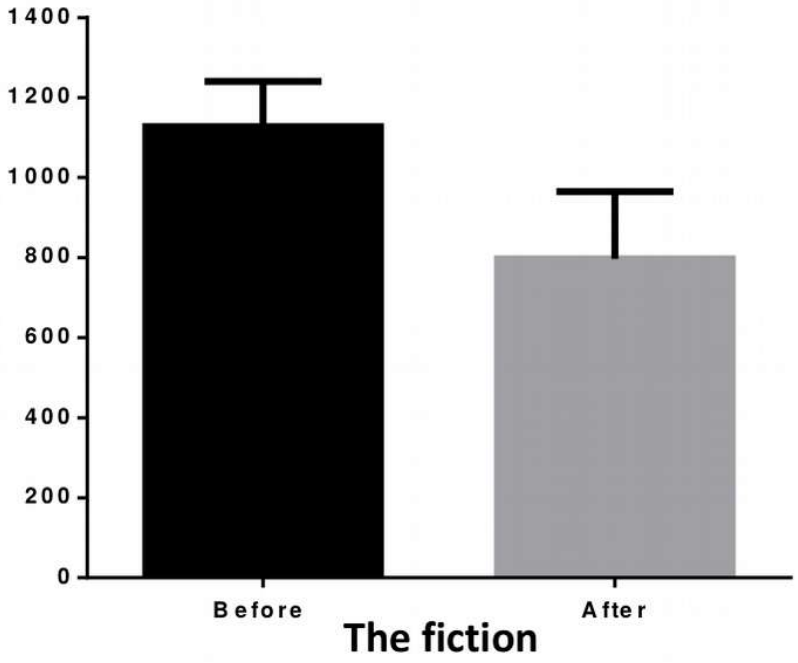


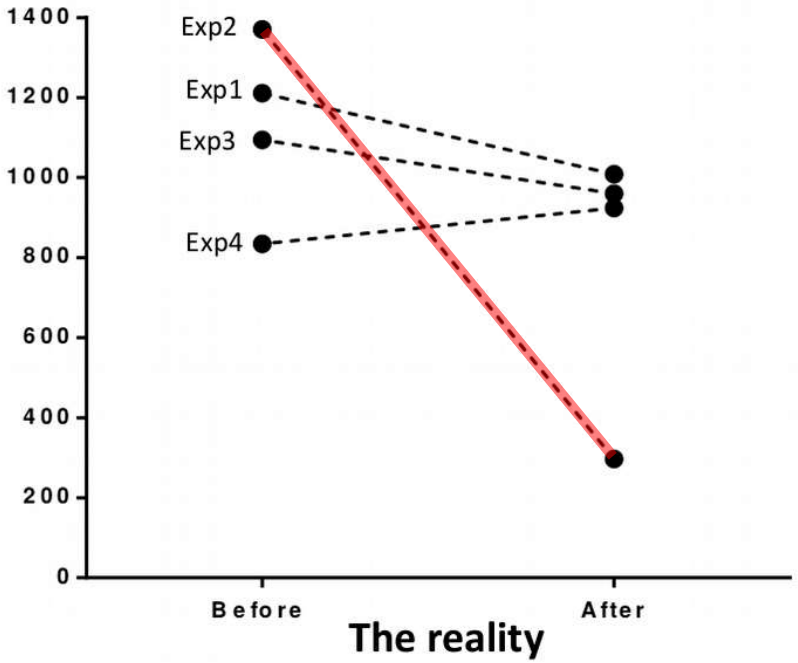
Making effective uni-variate plot

```
# R-code:
library(ggpubr)

my_comparisons <- list( c("2seater", "compact"),
c("2seater", "midsize"), c("2seater", "suv"),
c("2seater", "minivan"), c("2seater", "pickup"),
c("2seater", "subcompact"))

# plot the graph
stat_graph
stat_graph <- ggboxplot(data = mpg, x = "class",
                                    y = "hwy", color = "class",
                                    add = "jitter")
                        + theme(legend.position = "none")
                        +
stat_compare_means(comparisons =
my_comparisons)


stat_graph
```



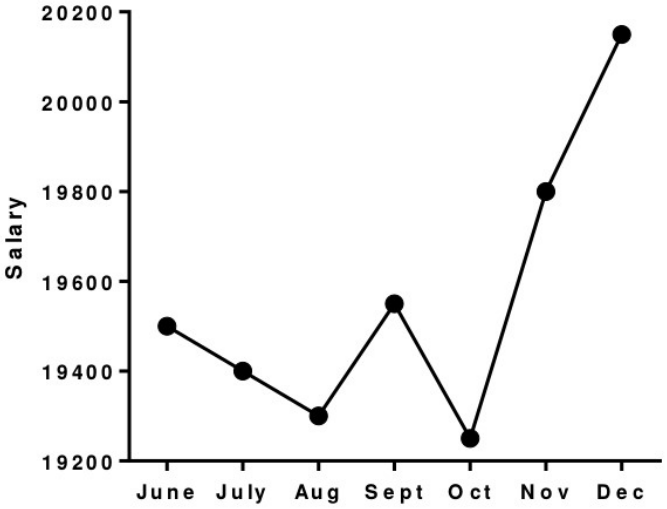
Sins of confirmatory analysis:
#2 Choosing the “most representative” experiment

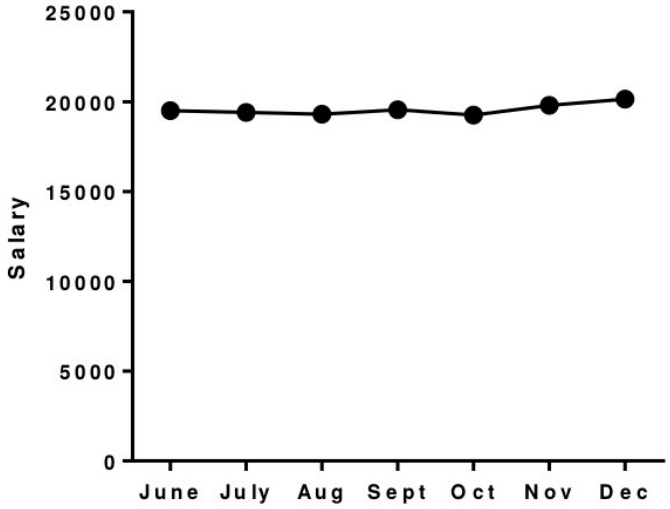




Slide inspired by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

Sins of confirmatory analysis:
#3 Choosing the wrong scale



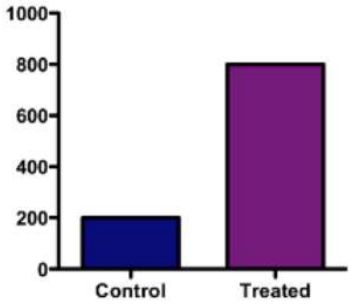


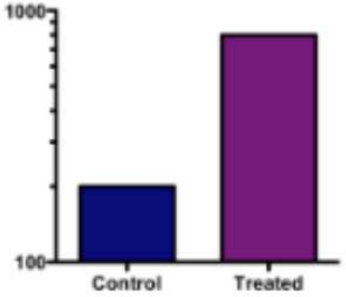
Slide inspired by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

Sins of confirmatory analysis:
#3 Choosing the wrong scale

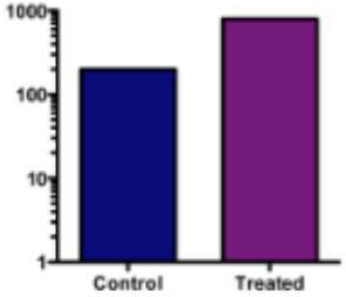
Log axis exaggerate differences between groups or minimize them

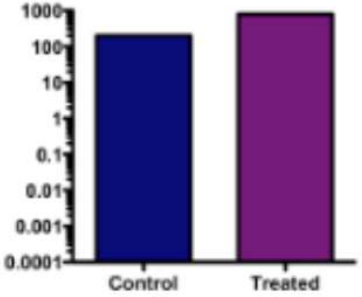
Linear





Logarithmic

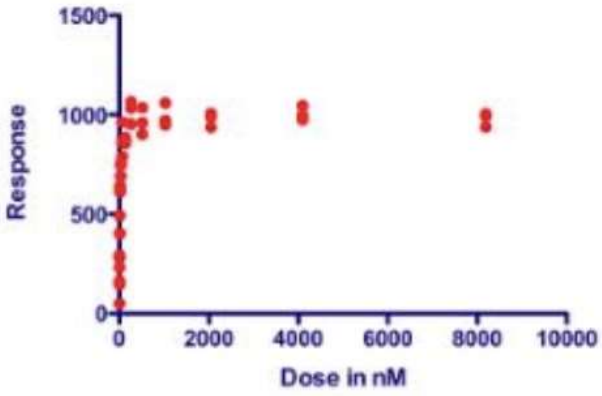


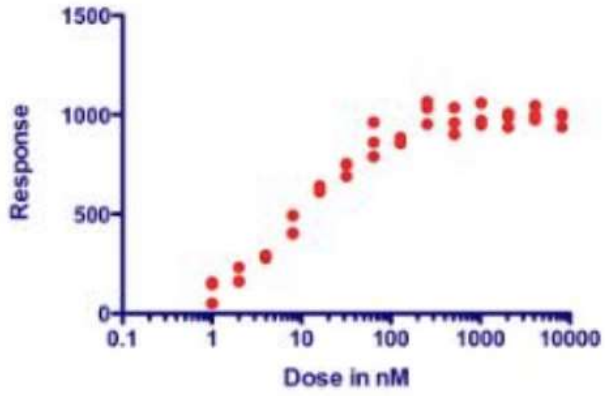


Slide inspired by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

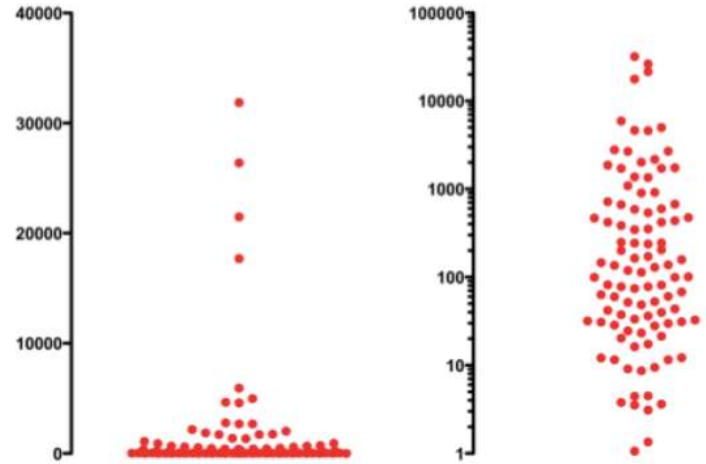
Use logarithmic scales OK for

- Logarithmically spaced values





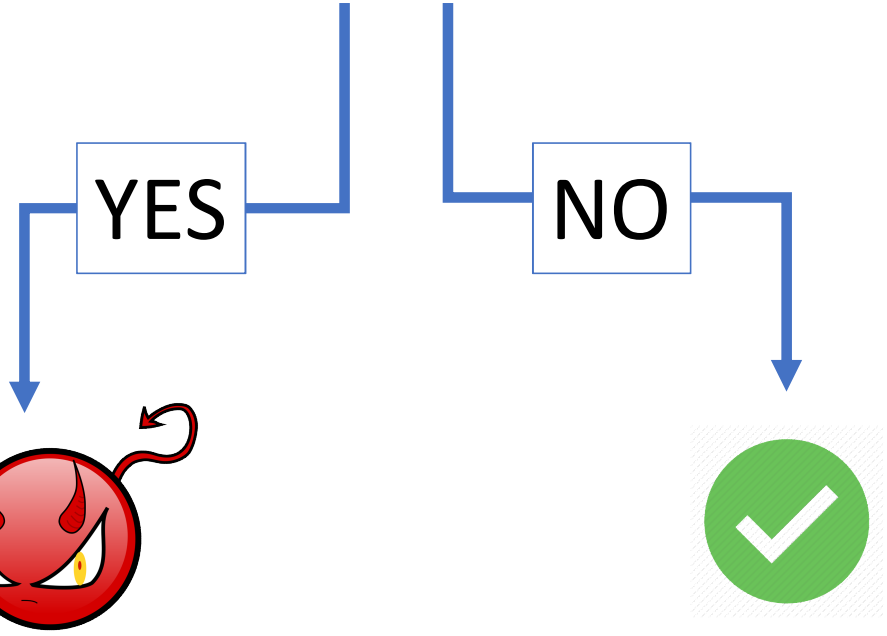
- Log-normal data



Slide inspired by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

Is my plot ethical?

Would a reader come to a different conclusion if they could see the details of the data which were omitted from the plot?



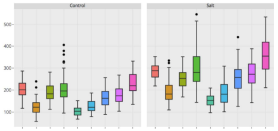
Slide inspired by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

What would you like to show?

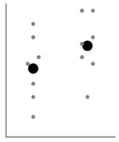
Comparison

Among items

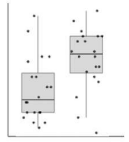
faceting over multiple conditions



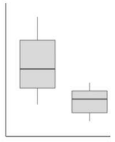
dot plot



box plot



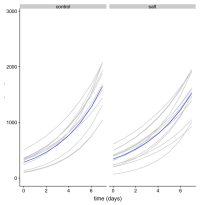
violin plot



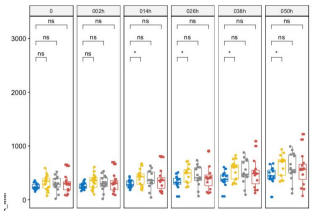
bar graph

Over time

line graph



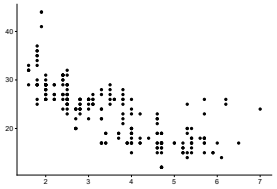
facetted plot



Relationship

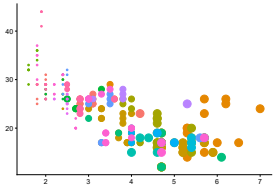
2 variables

scatter plot



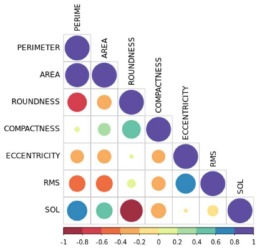
3-4 variables

bubble chart



> 4 variables

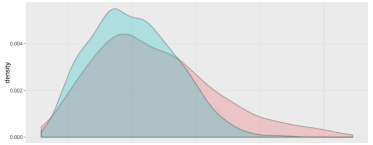
correlation heatmap



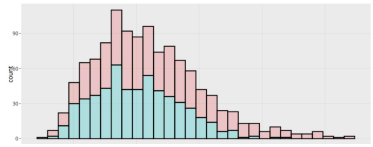
Distribution

1 variable

density histogram

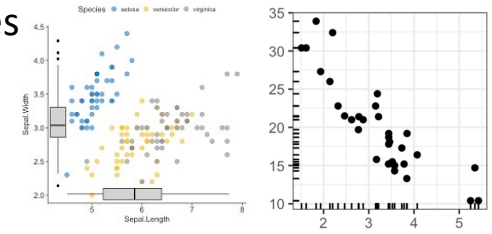


stacked count histogram



2 variables

scatter plot with rugs / box plot

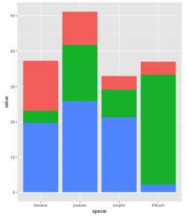


Composition

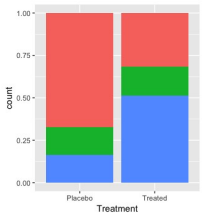
Among items

stacked column chart

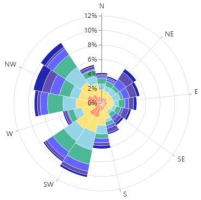
absolute



% of total

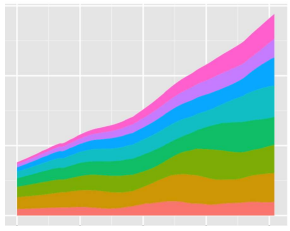


stacked radial bar chart



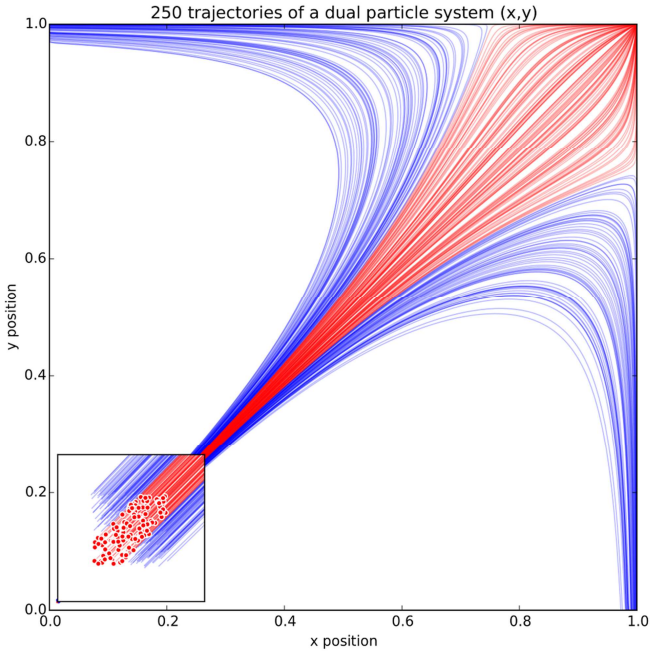
Over time

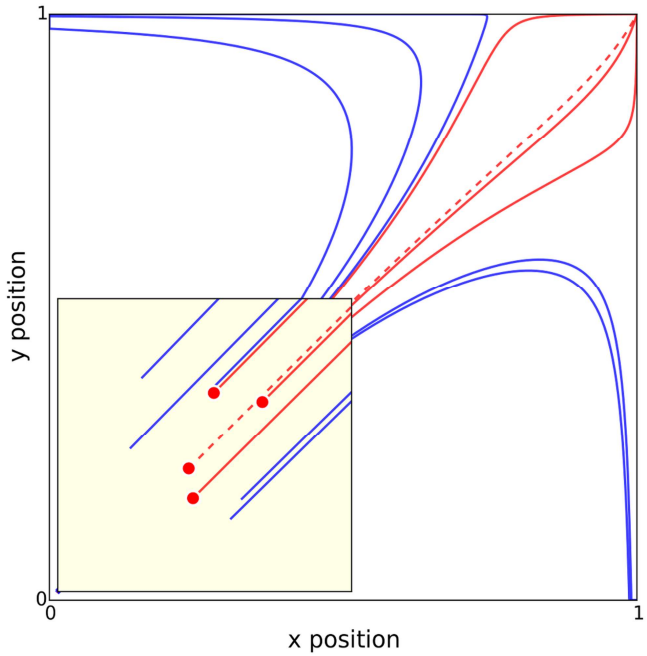
stacked area chart



10 rules for better figures

1. Know your audience
2. Identify your message
3. Adapt the figure to support medium

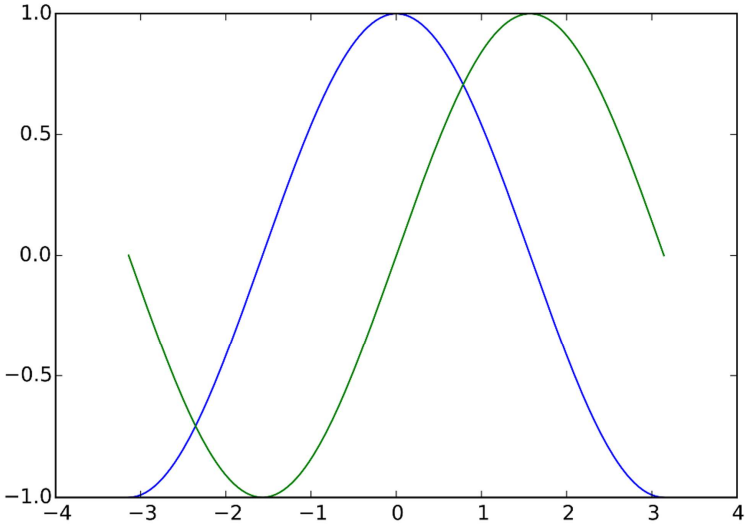


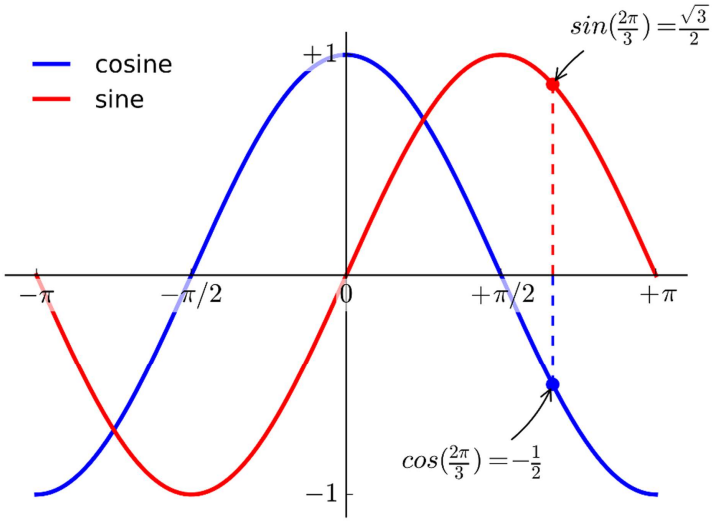


Rougier et al., PLOS Computational Biol. (2014) Ten Simple Rules for Better Figures

10 rules for better figures

1. Know your audience
2. Identify your message
3. Adapt the figure to support medium
4. Captions are NOT optional
5. Do not trust the defaults



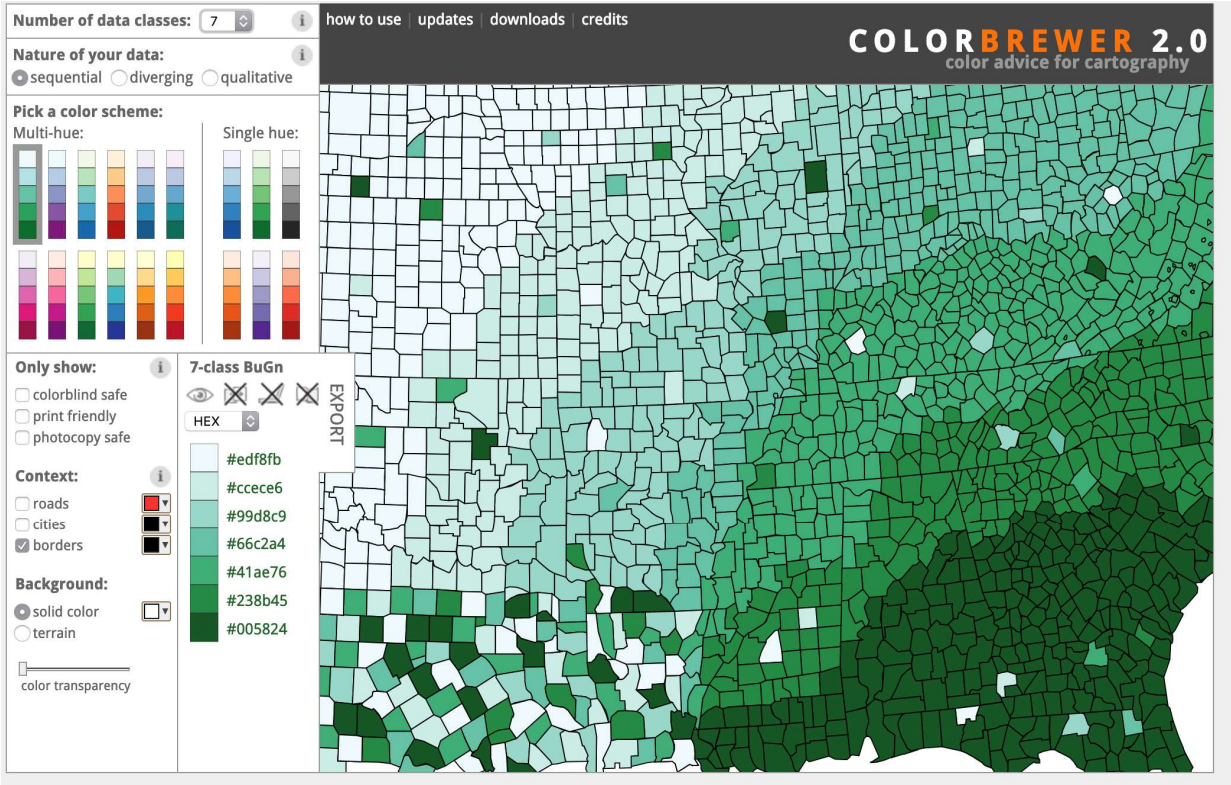


Rougier et al., PLOS Computational Biol. (2014) Ten Simple Rules for Better Figures

10 rules for better figures

1. Know your audience
2. Identify your message
3. Adapt the figure to support medium
4. Captions are NOT optional
5. Do not trust the defaults
6. Use color effectively

http://colorbrewer2.org/



Rougier et al., PLOS Computational Biol. (2014) Ten Simple Rules for Better Figures

10 rules for better figures

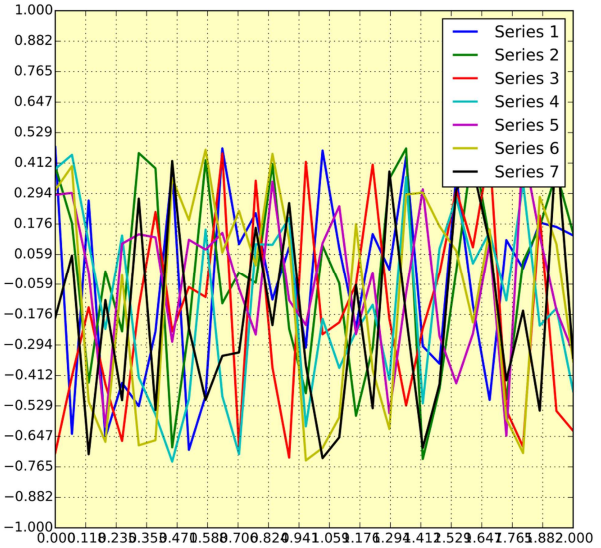
SimDaltonism

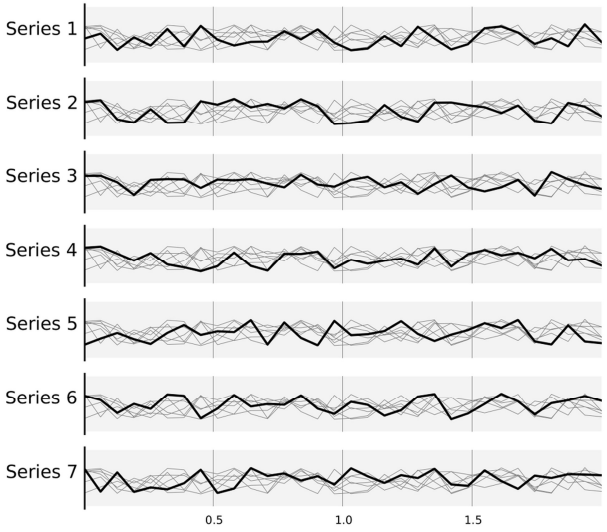
1. Know your audience
2. Identify your message
3. Adapt the figure to support medium
4. Captions are NOT optional
5. Do not trust the defaults
6. Use color effectively

Rougier et al., PLOS Computational Biol. (2014) Ten Simple Rules for Better Figures

10 rules for better figures

1. Know your audience
2. Identify your message
3. Adapt the figure to support medium
4. Captions are NOT optional
5. Do not trust the defaults
6. Use color effectively
7. Do not mislead the reader
8. Avoid “chart junk”





Rougier et al., PLOS Computational Biol. (2014) Ten Simple Rules for Better Figures

10 rules for better figures

1. Know your audience
2. Identify your message
3. Adapt the figure to support medium
4. Captions are NOT optional
5. Do not trust the defaults
6. Use color effectively
7. Do not mislead the reader
8. Avoid “chart junk”
9. Message > beauty
10. Use the right tools

Rougier et al., PLOS Computational Biol. (2014) Ten Simple Rules for Better Figures

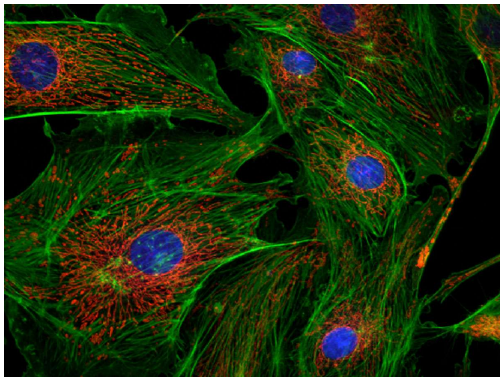
Combining elements into figure

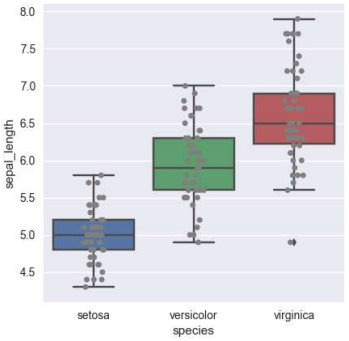
Have an idea of what your final figure will look like:

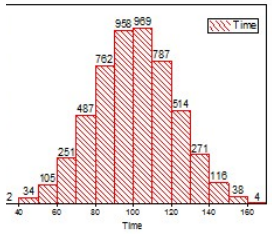
- What message are you trying to convey?
- How does each figure contribute to that message?
- Identify what is essential / supporting information
- Be consistent with color codes et al.

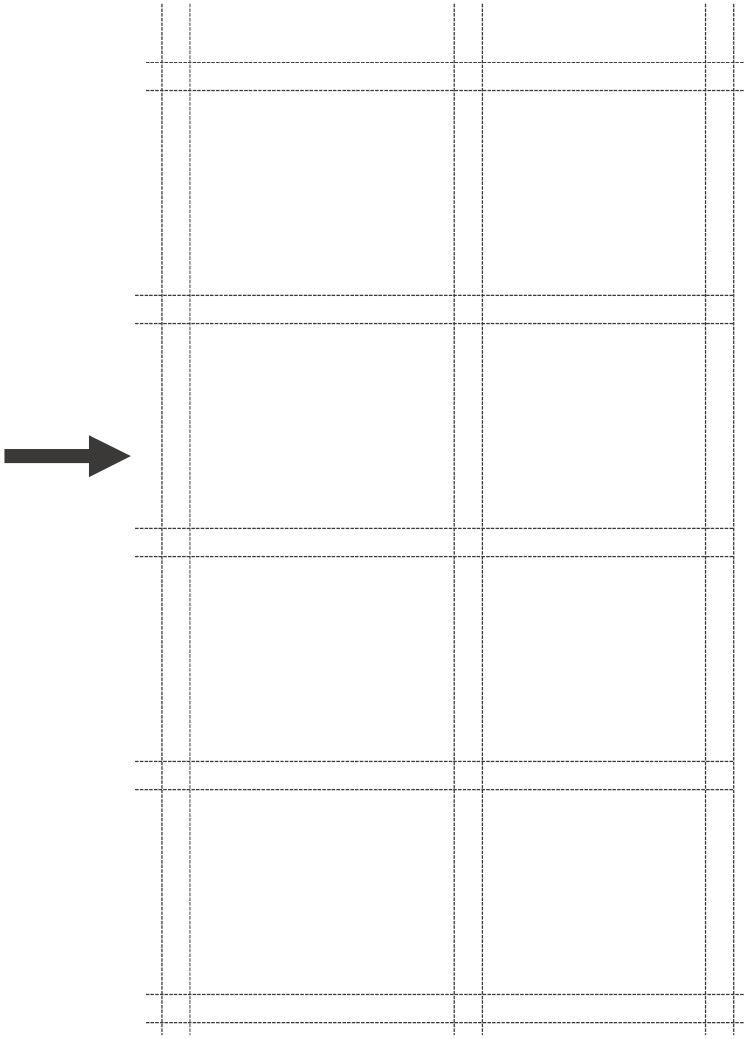
Figure outlines can reduce time spent moving or resizing images

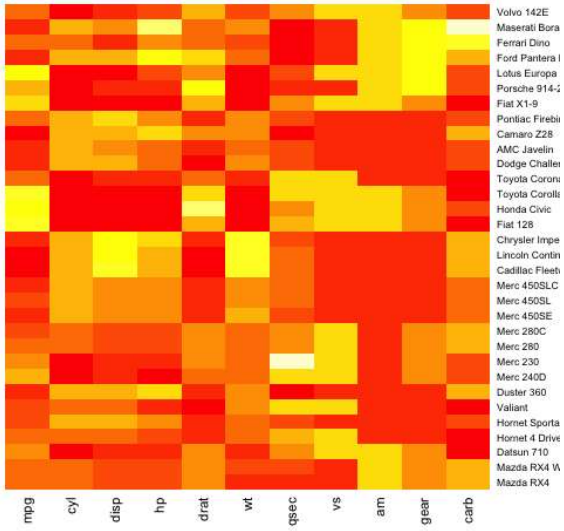
Use grids & alignments

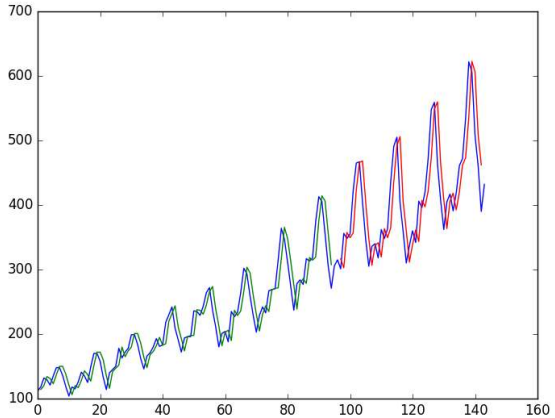










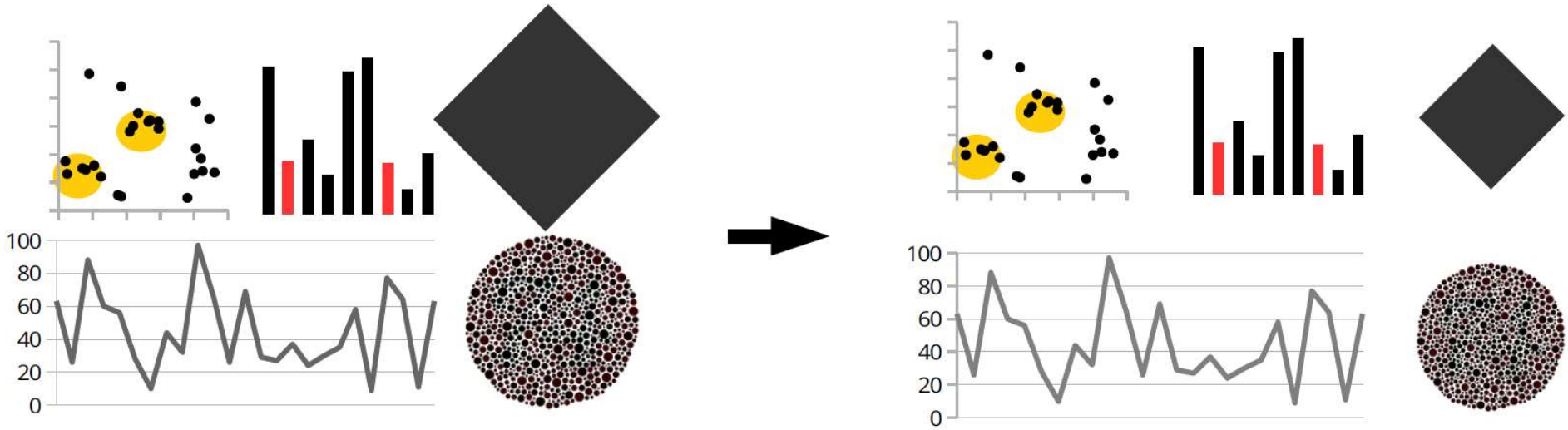


Slide inspired by Aiora Zabala, GitHub [bioinformatics-core-shared-training/**effective-figure-design**]

Visual weight & balance

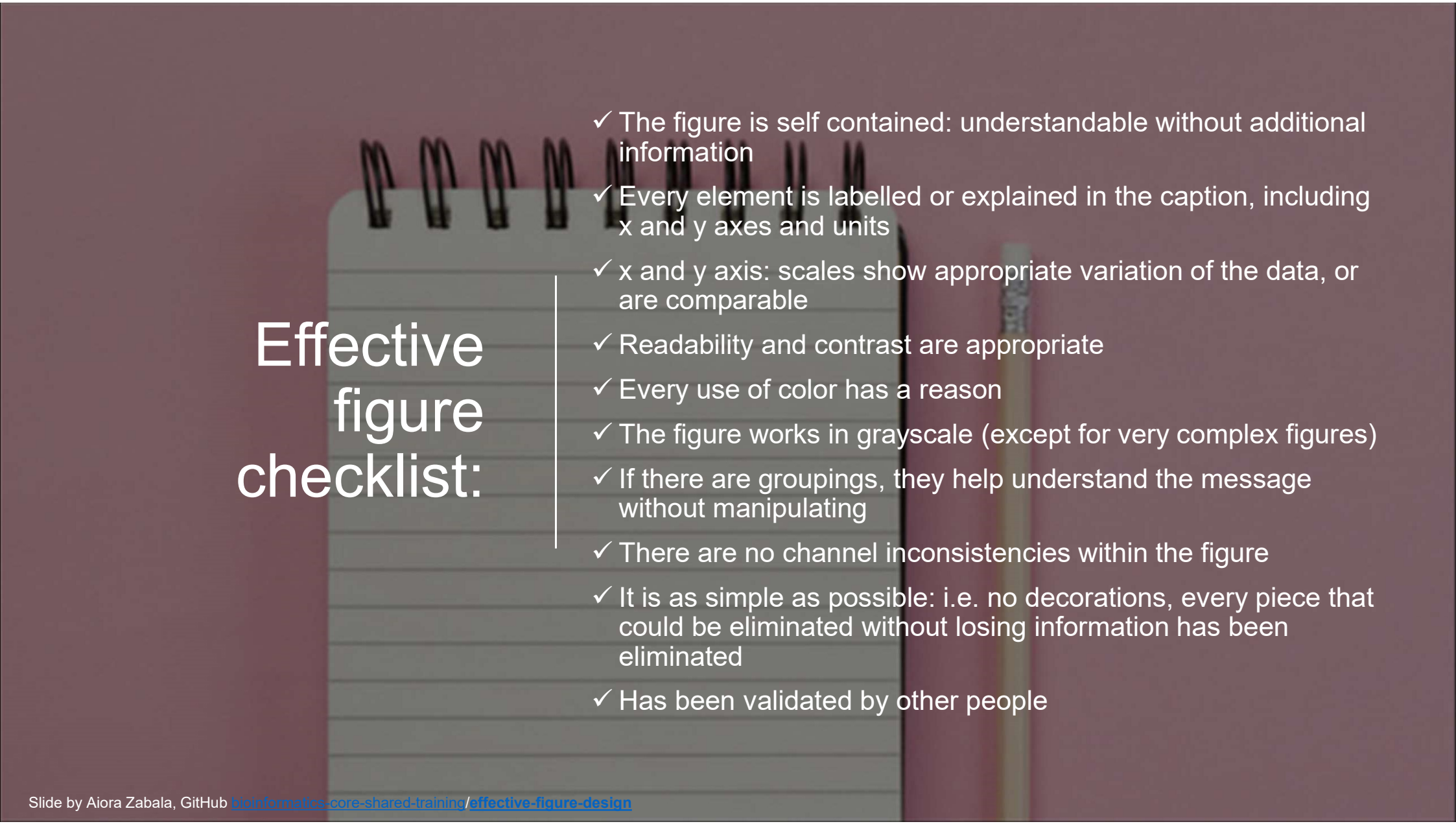
Visual weight & balance

Visual weight: A measure of how much an object on the page attracts and retains the attention of your viewer



? Which elements do you WANT to stand out in your figure?

Slide by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**



Effective figure checklist:

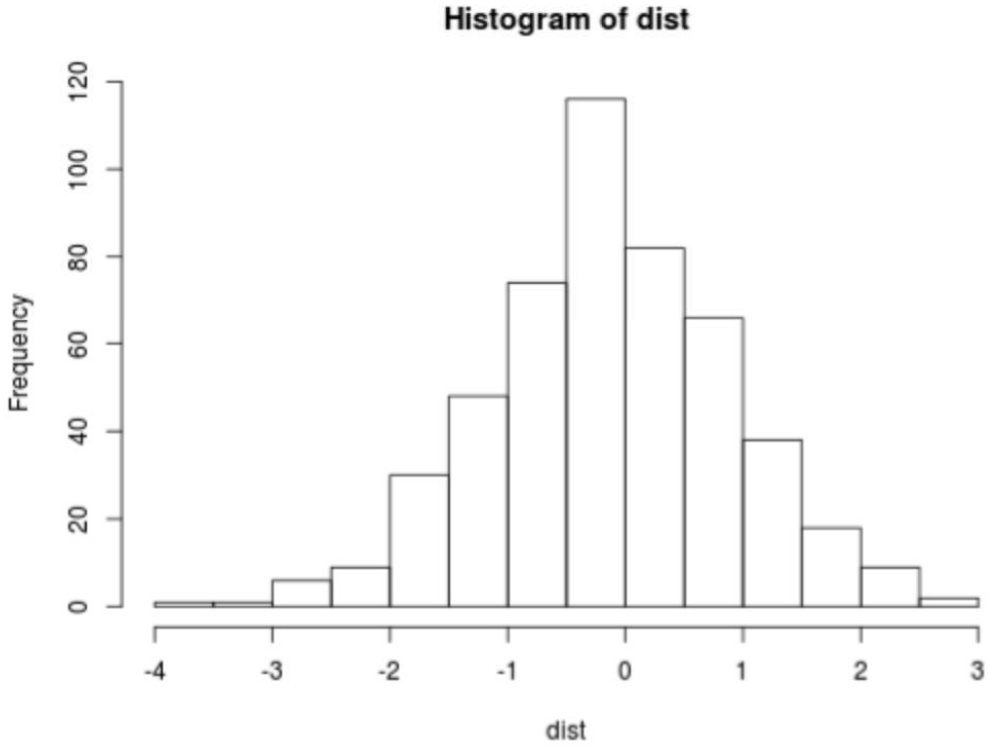
- ✓ The figure is self contained: understandable without additional information
- ✓ Every element is labelled or explained in the caption, including x and y axes and units
- ✓ x and y axis: scales show appropriate variation of the data, or are comparable
- ✓ Readability and contrast are appropriate
- ✓ Every use of color has a reason
- ✓ The figure works in grayscale (except for very complex figures)
- ✓ If there are groupings, they help understand the message without manipulating
- ✓ There are no channel inconsistencies within the figure
- ✓ It is as simple as possible: i.e. no decorations, every piece that could be eliminated without losing information has been eliminated
- ✓ Has been validated by other people

Slide by Aiora Zabala, GitHub bioinformatics-core-shared-training/**effective-figure-design**

Interactive apps for your supplemental data

- Shiny App - http://s

- Two files in folder '
  server.R >> F
  ui.R >> Mark
- Make sure your dir
  MyApp folder
- Run App by typing
  runApp("MyApp")
- Publish on GitHub ,



Interactive apps for your supplemental data

Not Secure | genseq-h0.science.uva.nl/shiny/App/Salt_NV_Root/

Salt_NV_Root App

Background Information | Explore the Phenotypes of Individual Accessions | Compare Individual Accessions | Explore the Correlations between Individual Traits | Cluster Analysis

About the App

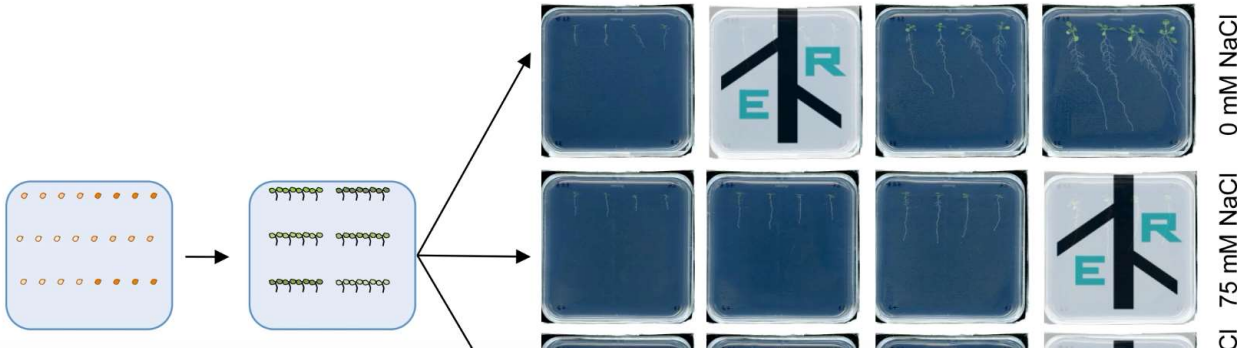
This Application was build to allow further exploration of the natural variation in Root System Architecture. The accompanying paper:

Genetic components of root architecture remodeling in response to salt
by Magdalena M. Julkowska Iko Koevoets, Selena Mol, Huub Hoefsloot, Richard Feron, Mark A. Tester, Joost J.B. Keurentjes, Arthur Korte, Michel A. Haring, Gert-Jan de Boer, Christa Testerink
Published in Plant cell, DOI:
https://doi.org/10.1105/tpc.16.00680

In this study we explore natural variation in RSA development under control and salt stress conditions by screening 347 Arabidopsis accessions of the HapMap population, and explore the association between the multi-trait phenotypes of root architecture and the genotype by using Genome Wide Association

Experimental Set-Up | Traits

The sterilized seeds were stratified in 0.1% agar at 4°C in the dark for 72 h and sown on square petri dishes (12 x 12 cm) containing 50 ml of control growth medium consisting of ½ Murashi-Skoog, 0.5% sucrose, 0.1% M.E.S. Monohydrate and 1% Daishin agar, pH 5.8 (KOH), dried for 1 h in a laminar flow. Plates were placed vertically at a 70° angle under long day conditions (21°C, 70% humidity, 16/8h light/dark cycle). Four days old seedlings were transferred to media supplemented with 0, 75 or 125 mM NaCl. Each plate contained four seedlings of two genotypes (two seedlings per genotype). Plates were placed in the growth chamber following a random design and scanned with Epson perfection V700 scanner at 200 dpi every other day until 8 days post transfer. The 8 days old seedlings grown in 0 mM NaCl were used for phenotyping of RSA in control conditions while for both salt stress conditions (75 and 125 mM NaCl) phenotypes of 12 days old seedlings were scored.



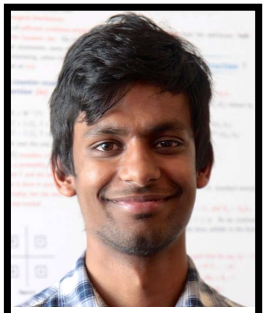
Take home:

- Present data in right context
- Exploratory or confirmatory analysis?
- Determine the right graph type
- Experiment with graph types and layering of aesthetics in your graph
  - > Most information
  - > Simplest representation
- Interactive apps for extending lifespan of your supplemental data
- Report & cite which (R / python / …) libraries you used to make your figure

Thank you / شكر

Guillaume Lobet
Jurlich / Louvain Uni.

KAUST



Gaurav Agarwal

Ge Gao

Stephanie Saade

Mitch Morton

Yveline Pailles

Mariam Awlia

@MVApp007

Useful resources

Short papers:

- Rolandi et al 2011. A Brief Guide to Designing Effective Figures for the Scientific Paper. Advanced Materials 23
- Rougier et al 2014. Ten Simple Rules for Better Figures. Plos Computational Biology 10:9

Design for scientists/ data:

- Carter. 2013. Designing science presentations – not just for figures, very clear
- Munzner. 2014. Visualization, analysis and design from a computer-graphics perspective
- Tufte. 2001. The visual display of quantitative information – from a theory-of-design perspective
- Meirelles. 2013. Design for information – advanced information visualizations (maps, time-space, flows)

Graphic design more generally:

- Krause. 2004. Design basics index – very concise and to the point
- Samara. 2014. Design elements: a graphic design manual – reference book
- Nature Points of View: http://blogs.nature.com/methagora/2013/07/data-visualization-points-of-view.html