ESCI upf.
School of International Studies

P1 | Basic tools for data visualization

Introduction

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Course overview

Theoretical sessions (20h)

T1 | Introduction (Guillaume Filion)

Part 1: Tools for data visualization (Marta Coronado)
T2.1 | Basic (`ggplot2`) - P1, P2
T2.2 | For bioinformatics - P3 (first assignment)
T3 | Dynamic and interactive (`plotly`, `shiny`) - P4, P5 (second assignment)

Part 2: Visualization concepts (Guillaume Filion)
T4 | Exploitation - P6
T5 | Exploration - P7
T6 | Advanced - P8

Course overview

Practical sessions (16h)

Part 1 | Tools for data visualization (Marta Coronado)

Sessions 1-3 | Basic tools for data visualization

Session 4-5 Interactive visualization

Part 2 | Visualization concepts (Guillaume Filion)

Sessions 6 | Principal component analysis

Sessions 7 | Co-inertia analysis

Sessions 8 | t-SNE

Evaluation

- **10% active participation**
  - Tools (Marta, 9 sessions)
    Individual submission at the end of each session
  - Concepts (Guillaume, 9 sessions)

- **40% group assignments** (minimum grade 4/10)
  - 4 assignments, each 10%

- **50% final exam** (minimum grade 4/10)

Practical session dynamics

Content (P1-P5)

- Introduction
- Exercises - complete and submit to aul@-ESCI
- Project (divided in to 2 assignments)

Interactive R documents

`R code` can be executed within RStudio!

```r
value ← 2
value + 3
```

```
## [1] 5
```

Important code will be highlited! 😉

```r
if (TRUE) {
  message("Very important!")
}
```

Get started!

Tools for data visualization

Exercise: show your tools!

1. Download the data in this file and, using any tool you like (e.g.: R, online tools, Microsoft Excel, etc.), represent the following:
   - A scatter plot of the variables x and y.
   - A bar plot of the counts of z.
2. Discuss with your partner the pros and cons of the chosen tool.

Type of tools

Two main types:

- Graphical user interface (GUI)

  Many examples: Perseus computational platform, Cytoscape, Blast2GO, Gephi, …

- Code-based

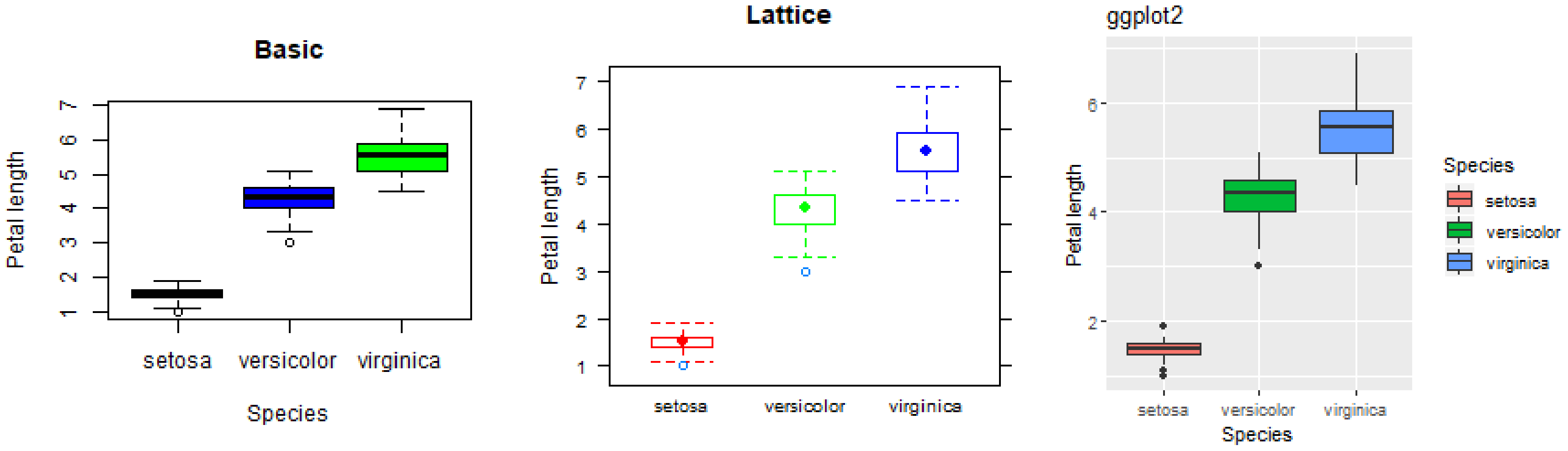
  R (and other computer languages)

Wide range…

❓ **Question**
What prons and cons do you think GUI tools have in comparison to code-based?

Visualization libraries in R

- `base`
- `grid`: `lattice` and `ggplot2`

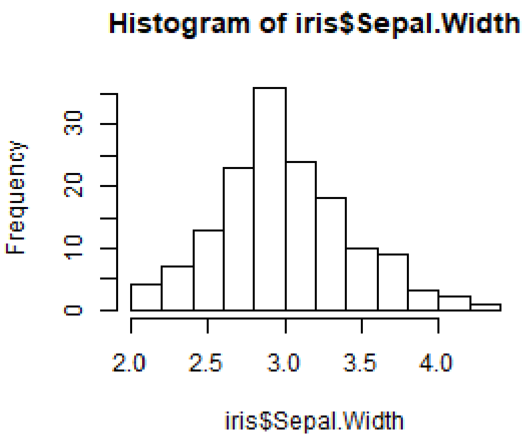


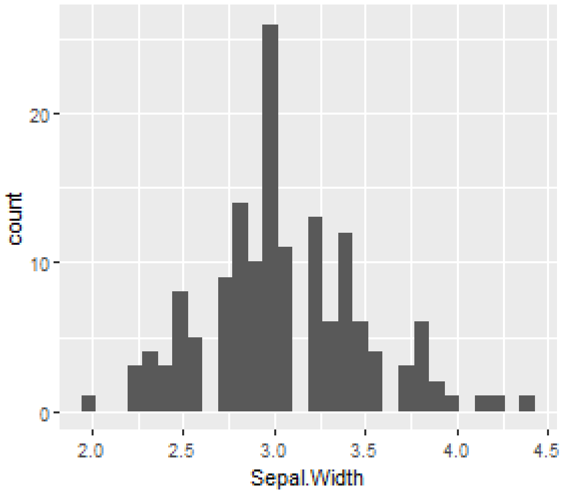
❓ Question
Describe the graphics. In your opinion, which do you think is the simplest? and the most complex? do you think the code to generate the figures reflect the complexity?

Visualization libraries in R

```
# base
hist(iris$Sepal.Width)

# ggplot2
ggplot(iris, aes(Sepal.Width)) +
  geom_histogram()
```

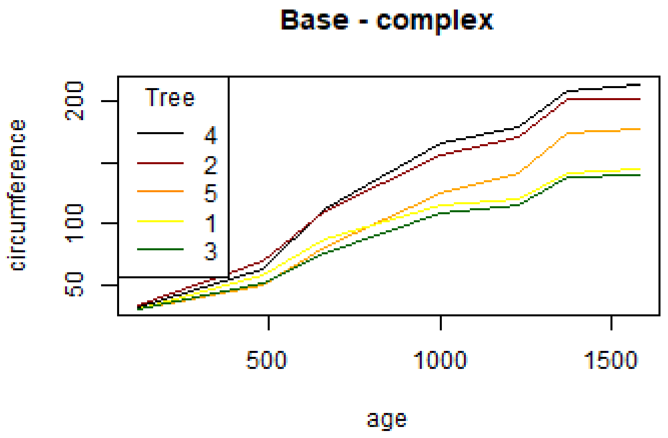


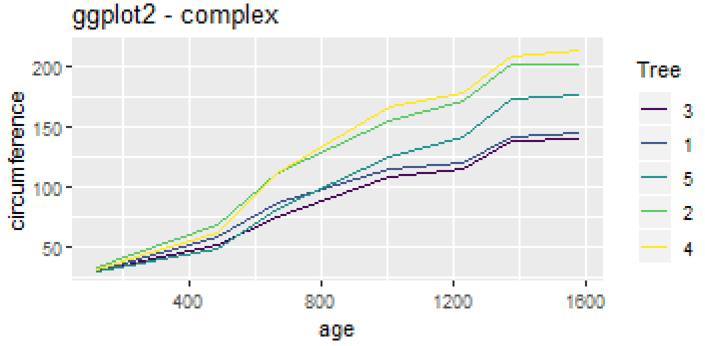


Visualization libraries in R

```
# base
plot(circumference ~ age,
     data=Orange[Orange$Tree %in% "4", ], type =
     main = "Base - complex")
points(circumference ~ age, col="darkred",
       data=Orange[Orange$Tree %in% "2", ], type
points(circumference ~ age, col="orange",
       data=Orange[Orange$Tree %in% "5", ], type
points(circumference ~ age, col="yellow",
       data=Orange[Orange$Tree %in% "1", ], type
points(circumference ~ age, col="darkgreen",
       data=Orange[Orange$Tree %in% "3", ], type
legend("topleft",
       c("4", "2", "5", "1", "3"), title="Tree",
       col=c("black", "darkred", "darkorange", '
       lty=c(1, 1, 1, 1, 1))
```

```
# ggplot2
ggplot(Orange, aes(age, circumference,
       colour = Tree)) + geom_line() +
       labs(title = "ggplot2 - complex")
```





Visualization libraries in R

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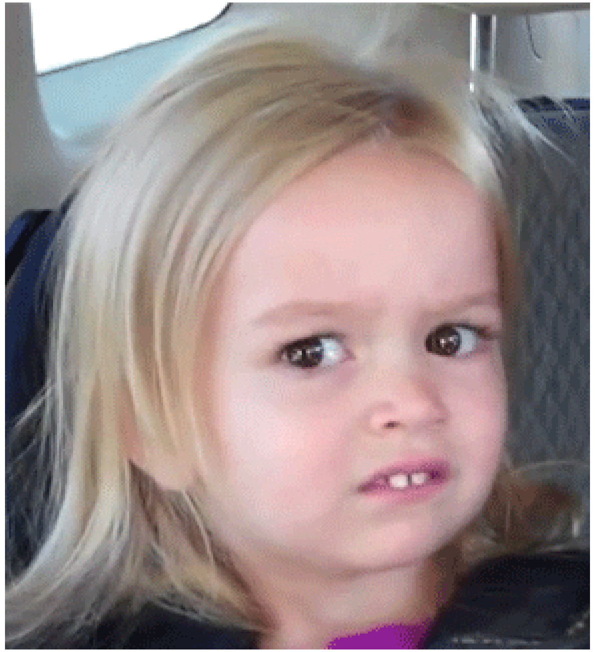
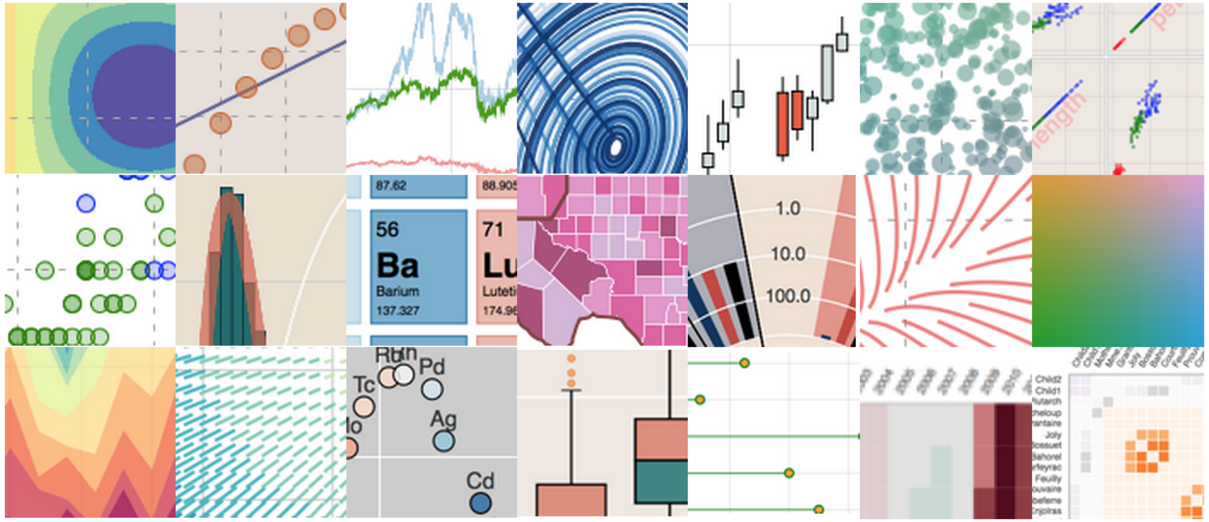


Other visualization libraries

(Outside our scope)

- Python
  - `matplotlib`, `seaborn`
  - `Bokeh`, `pygal`
- Java: `Processing`
- Javascript: `D3.js`



Basic R knowledge

Installing a package

```r
# Download and install a package from CRAN
install.packages("ggplot2")

# Download and install a package from GitHub (you need the devtools library installed)
devtools::install_github("yihui/xaringan")
```

Loading a package

```r
# Load the library to the current session
library("ggplot2")
library("xaringan")
```

Loading data

```r
# Loading a tab-separated file with a header
data <- read.table("data.txt", header = TRUE, sep = "\t")
```

Data types and structures

Main data types (other will not be discussed: *complex* and *raw*):

- **Logical**: can only take on two values: true (`TRUE`, `T`) or false (`FALSE`, `F`)
- **Numeric**: real or decimal (`2`, `15.5`)
- **Integer**: `2L` (the `L` tells R to store this as an integer)
- **Character**: any type of character or number (`"a"`, `"swc"`, `"2"`)

ℹ To know the data type, you can use the `class()` function.

```
type_list <- list(TRUE, 1.2, 10L, "a")
sapply(type_list, class)
```

```
## [1] "logical"   "numeric"   "integer"   "character"
```

Data types and structures

Elements of the previous data types may be combined to form data structures. Main structures:

- **Vector**: collection of elements that holds data of a single data type
- **Matrix**: vector with dimensions (the number of rows and columns)
- **Factor**: to deal with categorical variables
- **List**: a special type of vector where each element can be a different type
- **Data Frame** ★: a special type of list where every element of the list has same length

```r
# A vector x of mode numeric
x <- c(1, 2, 3)

# A vector y of mode logical
y <- c(TRUE, TRUE, FALSE, FALSE)

# A vector z of mode character
z <- c("Sarah", "Tracy", "Jon")
```

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```
matrix22 <- matrix(
  c(1, 2, 3, 4),
  nrow = 2,
  ncol = 2)
matrix22
```

```
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
```

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```
factor_vector <- as.factor(c("rna", "dna", "dna", "rna"))
factor_vector
```

```
## [1] rna dna dna rna
## Levels: dna rna
```

```
str(factor_vector)
```

```
##  Factor w/ 2 levels "dna","rna": 2 1 1 2
```

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```
x ← list(1, "a", TRUE, 1+4i)
x
```

```
## [[1]]
## [1] 1
##
## [[2]]
## [1] "a"
##
## [[3]]
## [1] TRUE
##
## [[4]]
## [1] 1+4i
```

Data types and structures

Elements of the previous data types may be combined to form data structures. Main structures:

- **Vector**: collection of elements that holds data of a single data type
- **Matrix**: vector with dimensions (the number of rows and columns)
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- **List**: a special type of vector where each element can be a different type
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```r
dat ← data.frame(id = letters[1:10], x = 1:10, y = 11:20)
dat
```

```
##    id  x  y
## 1   a  1 11
## 2   b  2 12
## 3   c  3 13
## 4   d  4 14
## 5   e  5 15
## 6   f  6 16
## 7   g  7 17
## 8   h  8 18
## 9   i  9 19
## 10  j 10 20
```

Tidy data

Data frames with one observation per row and one variable per column.

```
not_tidy
```

```
##      maker cyl  hp carb
## 1 Delorian   4 160    4
## 2   Fantom   2  80    2
```

```
tidy
```

```
##      maker metric value
## 1 Delorian    cyl     4
## 2   Fantom    cyl   160
## 3 Delorian     hp     4
## 4   Fantom     hp     2
## 5 Delorian   carb    80
## 6   Fantom   carb     2
```

Tidy data

There are useful `packages::functions` to change from wide to long format:

```
reshape2::melt(
    not_tidy,
    id.vars= "maker",
    variable.name = "metric",
    value.name = "score"
    )

tidyr::gather(
    not_tidy,
    - maker,
    key = "metric",
    value = "score"
    )
```

Getting help

- `?read.table`, `?str`, `?as.factor`
- Press F1 (in RStudio)
- Stack Overflow (`R`, `ggplot2`)
- Ask your classmates or your teacher

Exercise: describe a data set

Read the file in this link, ensure it has a tidy and long format and indicate the data type of each variable.

Practice

Introduction to `ggplot2`

- Open the document `P1_exercises.Rmd` in RStudio and complete the exercises.
- Upload the completed document to Aul@-ESCI at the end of the session.

Project

Group project

The project has 3 differents parts (A, B and C) divided in two big assignments.

- You will deliver the 3 parts separately to get feedback before submitting the final version
- Each part must be submitted before next practical session
- The first assignment will contain parts A and B
- The second assignment will contain part C
- ~15 minutes in the end of each class devoted to discuss your problems

Final assignment dates:

- Parts A and B: 18 october
- Part C: 1 november

Project

Group project

Part A

- **1.** Create groups of ~4 people
- **2.** Choose a data set with the following requirements
  - Tabular format (txt, csv, tsv...)
  - More than 80 observations
  - At least 6 variables
  - At least 2 discrete and 3 continuous variables
  - Data with biological meaning
  - Different from the ones chosen by other groups

Project

Group project

- **3.** Describe your data set:
  - Where and why was the information collected?
  - Which is the meaning of each variable?
  - Do the variables have unit? Which one?
  - Does the data set have a long format?
- **4.** Write the code to:
  - Read it into R
  - Reshape the data if necessary into long format
  - Check the variable classes and update them if necessary

Write 3 and 4 in an `R Markdown` document and **submit it before next practical session** (one per group).

ℹ If you need help formatting the R Markdown, check the R Markdown cheatsheet available in Aul@-ESCI or ask me.

Data sets from research articles

- "Whole-genome landscapes of major melanoma subtypes" (e.g., Table S1)
- "Zika virus evolution and spread in the Americas" (Table S2)
- "Great ape genetic diversity and population history" (Table S1 or S3)
- "Transcriptome and genome sequencing uncovers functional variation in humans". Table with cis eQTLs in EUR (description)
- "Signatures of Archaic Adaptive Introgression in Present-Day Human Populations" (Table S3)
- "The evolutionary history of dogs in the Americas" (Table S1)
- "Ancient genomes document multiple waves of migration in Southeast Asian prehistory" (Table S1)