CEFET/RJ

R-Basics

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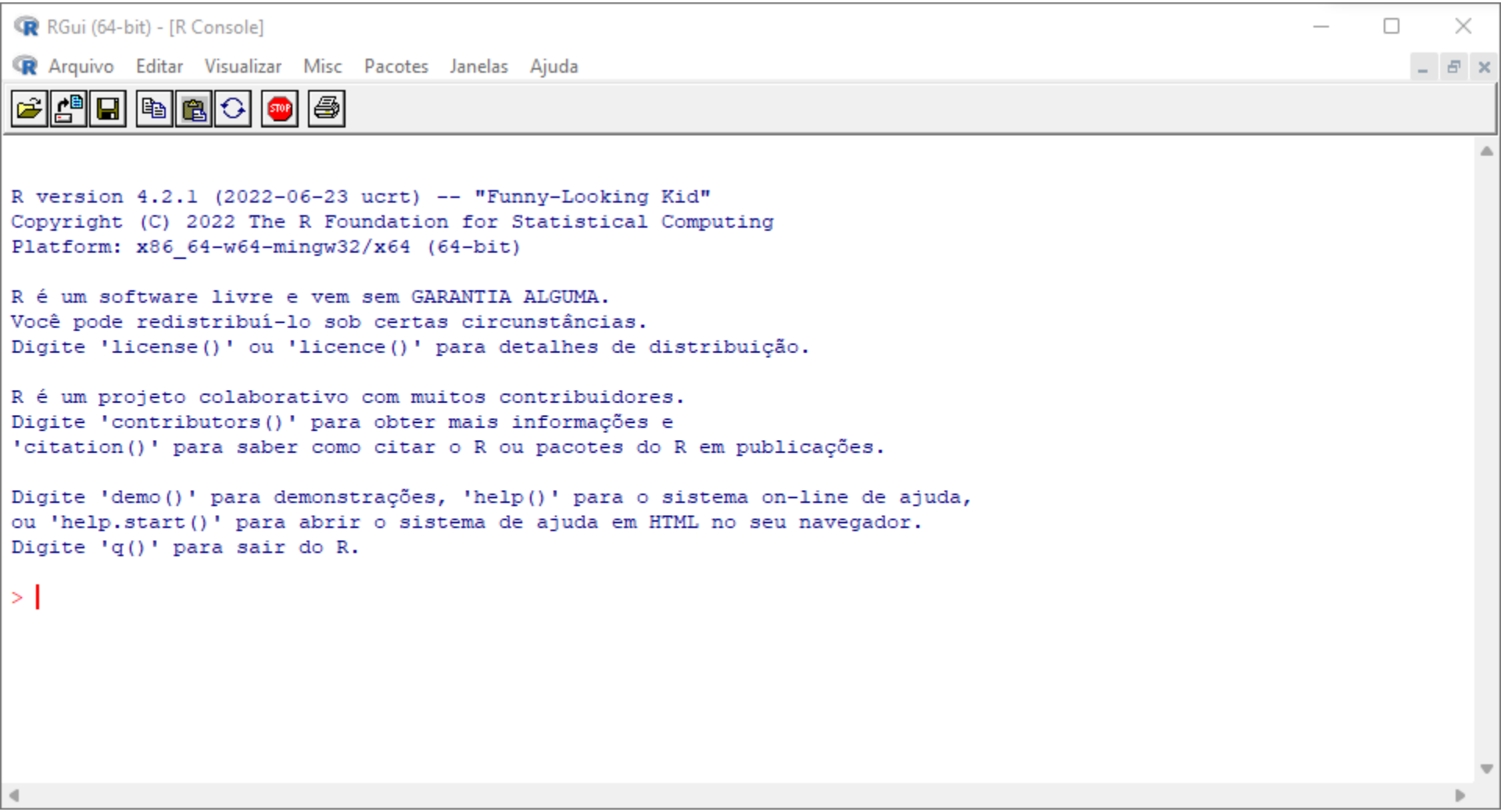
Introduction to R

- R is a programming language and free software environment for statistical computing
  - Supported by the R Foundation for Statistical Computing
- Created by Ross Ihaka and Robert Gentleman at Auckland University, New Zealand
- R was derived by S (Bell Laboratories - AT&T)
- R is a language broadly used by statisticians, data miners, and data scientists
- Current version 4.4

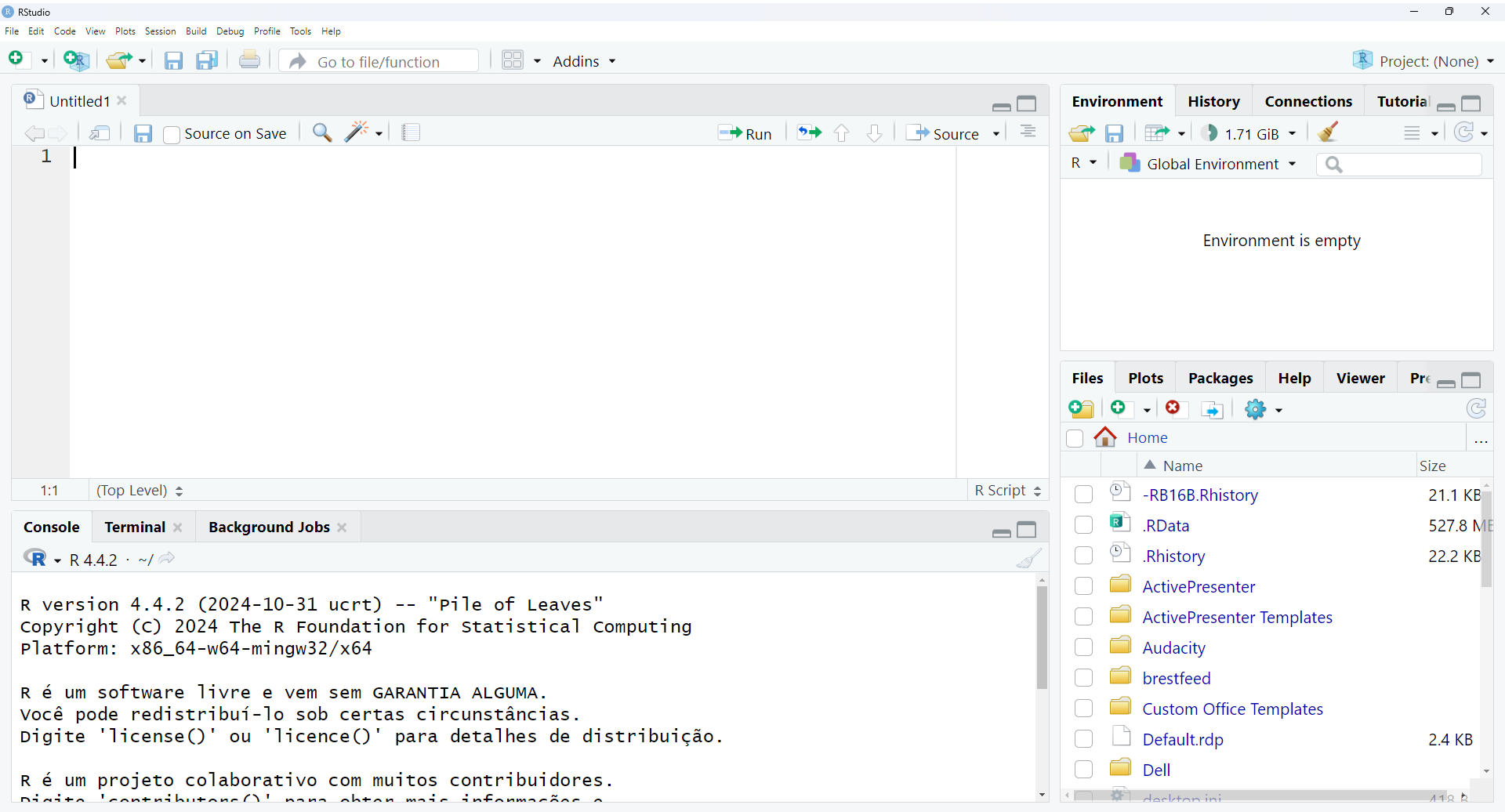
https://www.r-project.org/

R Console



Available for Windows, Mac, Linux

R Studio



Vantagens significativas: IDE com visualização de dados, depuração, criação de perfil
http://www.rstudio.com

R Packages

- Packages are collections of functions made available as libraries
  - Published in the CRAN Repository
    - Quality control
    - good documentation
  - Uploaded from a GitHub repository
    - Versions under development
- Currently have more than 22000 packages
  - https://cran.r-project.org/
- R has a very active community
  - Several researchers, professors, programmers, and statisticians
- DAL Packages: 7 pacotes
  - https://cran.r-project.org/web/packages/daltoolbox/index.html
  - https://cran.r-project.org/web/packages/harbinger/index.html
  - https://cran.r-project.org/web/packages/tspredit/index.html

https://www.r-project.org

R Package installation and loading

Package checking and instalation

```
if(!require(daltoolbox)) {
  install.packages("daltoolbox")
}
```

Package loading

```
library(daltoolbox)
```

Avoid unnecessary package loading

Variable definitions

Variable definition and assignment

```
weight <- 60
height = 1.75
subject <- "A"
healthy <- TRUE
```

Variable evaluation

```
weight
```

```
## [1] 60
```

A string is a sequence of characters. It is internally represented in double quotes.
It is enclosed inside single quotes('This is a string') or inside the double quotes("This is also a string").

Functions for variable conversion

```
weight <- as.integer(weight)
is.integer(weight)
```

```
## [1] TRUE
```

Family of functions as.* converts data types: Type “as.” and press space to see all them.

Vectors

definition

```
weight <- c(60, 72, 57, 90, 95, 72)
height <- c(1.75, 1.80, 1.65, 1.90, 1.74, 1.91)
subject <- c("A", "B", "C", "D", "E", "F")
```

evaluation

```
weight
```

```
## [1] 60 72 57 90 95 72
```

```
height
```

```
## [1] 1.75 1.80 1.65 1.90 1.74 1.91
```

```
subject
```

```
## [1] "A" "B" "C" "D" "E" "F"
```

Function c creates a vector from static values.
Function rep creates a vector of a particular size.

Iterations: for loop

from one to the length of weight

```
bmi <- 0
for (i in 1:length(weight)) {
  bmi[i] <- weight[i]/height[i]^2
}
```

evaluation of the bmi vector

```
bmi
```

```
## [1] 19.59184 22.22222 20.93664 24.93075 31.37799 19.73630
```

For loops: defined such that variable iterates over all elements of a vector.

Iterations: while loop

run while i is below or equal to the length of weight

```
bmi <- 0
i <- 1
while (i <= length(weight)) {
  bmi[i] <- weight[i]/height[i]^2
  i <- i + 1
}
```

```
bmi
```

```
## [1] 19.59184 22.22222 20.93664 24.93075 31.37799 19.73630
```

While loops: are executed while a condition is satisfied, it is expected that variables for condition evaluation are changed inside the loop.

Creating functions

name <- function(parameters) { body }

```
compute_bmi <- function(weight, height) {
  bmi <- weight/height^2
  return(bmi)
}
```

calling it

```
bmi <- compute_bmi(60, 1.75)
bmi
```

```
## [1] 19.59184
```

```
bmi <- compute_bmi(weight, height)
bmi
```

```
## [1] 19.59184 22.22222 20.93664 24.93075 31.37799 19.73630
```

Functions are defined with parameters and code assigned to a function name.
Functions should return a value.

Part II

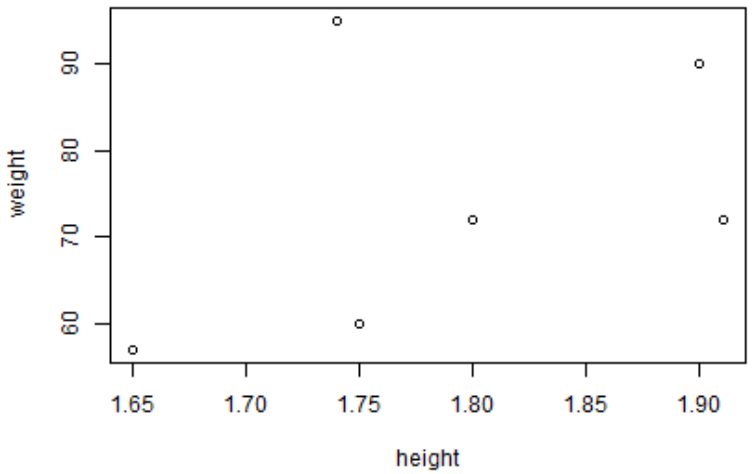
Plotting basic graphics

defining variables

```
weight <- c(60, 72, 57, 90, 95, 72)
height <- c(1.75, 1.80, 1.65, 1.90, 1.74, 1.91)
bmi <- weight/height^2
```

scatter plots

```
plot(height, weight)
```



The plot function is the basic plot function in R. The first parameter is the x-axis observations. In contrast, the second one is the y-axis observations.

All functions in R CRAN packages have help with examples

```
?base::plot
```

plot.default {graphics} R Documentation

The Default Scatterplot Function

Description

Draw a scatter plot with decorations such as axes and titles in the active graphics window.

Usage

```
## Default S3 method:
plot(x, y = NULL, type = "p",  xlim = NULL, ylim = NULL,
     log = "", main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
     ann = par("ann"), axes = TRUE, frame.plot = axes,
     panel.first = NULL, panel.last = NULL, asp = NA,
     xgap.axis = NA, ygap.axis = NA,
     ...)
```

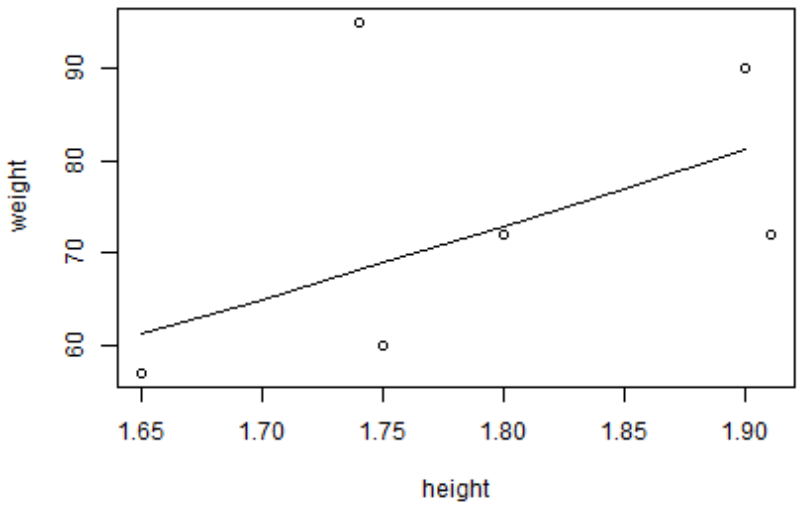
Arguments

`x, y`	the `x` and `y` arguments provide the x and y coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function `xy.coords` for details. If supplied separately, they must be of the same length.
`type`	1-character string giving the type of plot desired. The following values are possible, for details, see

All functions in R contain help documentation with example code available.

Canvas for plotting is still active until a new plot

```
plot(height, weight)
hh = c(1.65, 1.70, 1.75, 1.80, 1.85, 1.90)
lines(hh, 22.5 * hh^2)
```



Canvas is active until the following plot. Lines add added the current scatter plot.

Factors

- Factors are variables in R that refer to categorical data
- Factors in R are stored as a vector of integer values with a corresponding set of character values to use when the factor is displayed
- Both numeric and character variables can be made into factors, but a factor's levels are always character values

The factors can be either sorted (ordinal) or unsorted (categorical).

Factors

Factors are used to handle categorical data.

```
pain <- c(0,3,2,2,1)
fpain <- factor(pain,levels=0:3, ordered=TRUE)
fpain
```

```
## [1] 0 3 2 2 1
## Levels: 0 < 1 < 2 < 3
```

Levels provide correspondence between numerical values and categorical labels

```
levels(fpain) <- c("none","mild","medium","severe")
fpain
```

```
## [1] none   severe medium medium mild
## Levels: none < mild < medium < severe
```

Example of ordered factor indicating the level of pain for patients.

Using the function cut

- Consider the height variable
  - Persons lower than 1.5 m are small
  - Persons greater than 1.9 m are tall
  - Persons in between are medium
  - Convert the height variable into a factor with small, medium, tall

```
lev <- cut(height, breaks=c(0, 1.5, 1.9, .Machine$double.xmax), ordered=TRUE)
lev
```

```
## [1] (1.5,1.9]      (1.5,1.9]      (1.5,1.9]      (1.5,1.9]      (1.5,1.9]      (1.9,1.8e+308]
## Levels: (0,1.5] < (1.5,1.9] < (1.9,1.8e+308]
```

```
levels(lev) <- c("short", "medium", "tall")
lev
```

```
## [1] medium medium medium medium medium tall
## Levels: short < medium < tall
```

Matrix

Matrices can be filled from vectors or data frames.

```
x <- 1:9
x
```

```
## [1] 1 2 3 4 5 6 7 8 9
```

Converting a vector to matrix

```
dim(x) <- c(3,3)
x
```

```
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
```

Matrix is a two-dimensional data structure in R programming.
Dimensions of a vector can be changed to transform it into a matrix.

Matrix manipulation

Matrix manipulation

Converting a vector to a matrix by row

```
x <- matrix(1:9,nrow=3,byrow=TRUE)
x
```

```
##      [,1] [,2] [,3]
## [1,]    1    2    3
## [2,]    4    5    6
## [3,]    7    8    9
```

transposing a matrix

```
x <- t(x)
x
```

```
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
```

The conversion of a vector into a matrix can be defined in a row-based filling.
A matrix can be transposed using function t.

Lists

- Lists are the R objects which contain elements of different types, such as numbers, strings, vectors, matrix, data frame, and another list inside it
- A list can also contain a matrix or a function as its elements
- A list is created using the list() function
- List manipulation
  - Slicing a list []
  - Accessing an element inside a list [[]]

Creating a list

Lists are used to work with "objects"

```
a <- c(5260,5470,5640,6180,6390,6515,6805,7515,7515,8230,8770)
b <- c(3910,4220,3885,5160,5645,4680,5265,5975,6790,6900,7335)

mybag <- list(a, b, 0, "a")
mybag
```

```
## [[1]]
##  [1] 5260 5470 5640 6180 6390 6515 6805 7515 7515 8230 8770
##
## [[2]]
##  [1] 3910 4220 3885 5160 5645 4680 5265 5975 6790 6900 7335
##
## [[3]]
## [1] 0
##
## [[4]]
## [1] "a"
```

Lists can contain anything, including lists. To add a new item, use an empty position.

Adding elements into a list

```
n <- length(mybag)
mybag[[n+1]] <- "b"
mybag
```

```
## [[1]]
##  [1] 5260 5470 5640 6180 6390 6515 6805 7515 7515 8230 8770
##
## [[2]]
##  [1] 3910 4220 3885 5160 5645 4680 5265 5975 6790 6900 7335
##
## [[3]]
## [1] 0
##
## [[4]]
## [1] "a"
##
## [[5]]
## [1] "b"
```

Accessing a new position increase the size of the list

List slicing

```
slice <- mybag[1]
slice
```

```
## [[1]]
##  [1] 5260 5470 5640 6180 6390 6515 6805 7515 7515 8230 8770
```

```
is.list(slice)
```

```
## [1] TRUE
```

Lists accessed by single brackets return sublists.

Creating lists with attributes

They are properties on the list

```
mybag <- list(x=a, y=b, const=0, lit="a")
mybag
```

```
## $x
##  [1] 5260 5470 5640 6180 6390 6515 6805 7515 7515 8230 8770
##
## $y
##  [1] 3910 4220 3885 5160 5645 4680 5265 5975 6790 6900 7335
##
## $const
## [1] 0
##
## $lit
## [1] "a"
```

Elements of lists can be named. It can be understood as an attribute of an object.

Adding, accessing, and removing elements

Adding, accessing, and removing elements

```
mybag$c <- mybag$x - mybag$y
mybag$const <- NULL
mybag$lit <- NULL
mybag
```

```
## $x
##  [1] 5260 5470 5640 6180 6390 6515 6805 7515 7515 8230 8770
##
## $y
##  [1] 3910 4220 3885 5160 5645 4680 5265 5975 6790 6900 7335
##
## $c
##  [1] 1350 1250 1755 1020  745 1835 1540 1540  725 1330 1435
```

Operator $ is used to access the attribute of a list.

Part III

Data frames

Data frames (tables) provide support for structured data.

```
a <- c(5260,5470,5640,6180,6390,6515,6805,7515,7515,8230,8770)
b <- c(3910,4220,3885,5160,5645,4680,5265,5975,6790,6900,7335)
```

```
data <- data.frame(A=a, B=b)
head(data)
```

```
##      A    B
## 1 5260 3910
## 2 5470 4220
## 3 5640 3885
## 4 6180 5160
## 5 6390 5645
## 6 6515 4680
```

A data frame is a table where each column corresponds to attributes, and each row corresponds to a tuple (object)

Adding a column in a data frame

```
data$c <- data$A + data$B
head(data)
```

```
##      A    B     c
## 1 5260 3910  9170
## 2 5470 4220  9690
## 3 5640 3885  9525
## 4 6180 5160 11340
## 5 6390 5645 12035
## 6 6515 4680 11195
```

A data frame is a table where each column corresponds to attributes, and each row corresponds to a tuple (object)

Removing a column of a data frame

```
data$A <- NULL
head(data)
```

```
##      B     c
## 1 3910  9170
## 2 4220  9690
## 3 3885  9525
## 4 5160 11340
## 5 5645 12035
## 6 4680 11195
```

Each column has a name. Novel columns can be added by assigning a value to them. Operator $ is used to access the column of a table.

Reading a csv file

There are many functions for reading CSV, Excel, and RData formats.

```
wine = read.table(
    "http://archive.ics.uci.edu/ml/machine-learning-databases/wine/wine.data",
                  header = TRUE, sep = ",")
  colnames(wine) <- c('Type', 'Alcohol', 'Malic', 'Ash',
                      'Alcalinity', 'Magnesium', 'Phenols',
                      'Flavanoids', 'Nonflavanoids',
                      'Proanthocyanins', 'Color', 'Hue',
                      'Dilution', 'Proline')
head(wine)
```

```
##   Type Alcohol Malic  Ash Alcalinity Magnesium Phenols Flavanoids Nonflavanoids Proanthocyanins Color  H
## 1    1   13.20  1.78 2.14       11.2       100    2.65       2.76          0.26             1.28  4.38 1.
## 2    1   13.16  2.36 2.67       18.6       101    2.80       3.24          0.30             2.81  5.68 1.
## 3    1   14.37  1.95 2.50       16.8       113    3.85       3.49          0.24             2.18  7.80 0.
## 4    1   13.24  2.59 2.87       21.0       118    2.80       2.69          0.39             1.82  4.32 1.
## 5    1   14.20  1.76 2.45       15.2       112    3.27       3.39          0.34             1.97  6.75 1.
## 6    1   14.39  1.87 2.45       14.6        96    2.50       2.52          0.30             1.98  5.25 1.
```

Try to view this file: http://archive.ics.uci.edu/ml/machine-learning-databases/wine/wine.data

Saving and loading Rdata files

saving a data frame

```
save(wine, file="wine.RData")
```

removing a data frame from memory

```
rm(wine)
```

loading it

```
load("wine.RData")
head(wine, 3)
```

```
##   Type Alcohol Malic  Ash Alcalinity Magnesium Phenols Flavanoids Nonflavanoids Proanthocyanins Color  H
## 1    1   13.20  1.78 2.14       11.2       100    2.65       2.76          0.26            1.28  4.38 1.
## 2    1   13.16  2.36 2.67       18.6       101    2.80       3.24          0.30            2.81  5.68 1.
## 3    1   14.37  1.95 2.50       16.8       113    3.85       3.49          0.24            2.18  7.80 0.
##   Dilution Proline
## 1     3.40    1050
## 2     3.17    1185
## 3     3.45    1480
```

R has some functions to save and load variables as a binary file.

Exporting data.frame into csv file

```
write.table(wine, file="wine.csv", row.names=FALSE, quote = FALSE, sep = ",")
```

Try to see the wine.csv

Part IV

Pipelines

The operator |> creates a pipeline.

The first parameter of the next invoked function receives the data from the pipeline.

Library *dplyr* contains a set of functions that support relational algebra operations.

```
flight_data <- read.table(text = "Year Quarter Flights Delays
                      2016 1 11 6
                      2016 2 12 5
                      2016 3 13 3
                      2016 4 12 5
                      2017 1 10 4
                      2017 2 9 3
                      2017 3 11 4
                      2017 4 25 15
                      2018 1 14 3
                      2018 2 12 5
                      2018 3 13 3
                      2018 4 15 4",
                      header = TRUE,sep = "")
```

Displaying the data frame

```
head(flight_data)
```

```
##   Year Quarter Flights Delays
## 1 2016       1      11      6
## 2 2016       2      12      5
## 3 2016       3      13      3
## 4 2016       4      12      5
## 5 2017       1      10      4
## 6 2017       2       9      3
```

Basic Query

```
library(dplyr)
```

```
result <- flight_data |>
   filter(Delays > 5) |>
   select(Year, Quarter, Flights)
head(result)
```

```
##   Year Quarter Flights
## 1 2016       1      11
## 2 2017       4      25
```

Aggregated query

```
result <- flight_data |>
   group_by(Year) |>
   summarize(mean = mean(Flights), sd = sd(Flights))
head(result)
```

```
## # A tibble: 3 x 3
##    Year  mean    sd
##   <int> <dbl> <dbl>
## 1  2016  12   0.816
## 2  2017  13.8 7.54
## 3  2018  13.5 1.29
```

Tables join

Store table

```
stores <- data.frame(
  city = c("Rio de Janeiro", "Sao Paulo", "Paris", "New York", "Tokyo"),
  value = c(10, 12, 20, 25, 18))
head(stores)
```

```
##             city value
## 1 Rio de Janeiro    10
## 2      Sao Paulo    12
## 3          Paris    20
## 4       New York    25
## 5          Tokyo    18
```

Division table

```
divisions <- data.frame(
  city = c("Rio de Janeiro", "Sao Paulo", "Paris", "New York", "Tokyo"),
  country = c("Brazil", "Brazil", "France", "US", "Japan"))
head(divisions)
```

```
##             city country
## 1 Rio de Janeiro  Brazil
## 2      Sao Paulo  Brazil
## 3          Paris  France
## 4       New York      US
## 5          Tokyo   Japan
```

Merge function

The function *merge* can be used to join data frames. It can be used to produce inner, left, right, and outer joins.

```
stdiv <- merge(stores, divisions, by.x="city", by.y="city")
head(stdiv)
```

```
##             city value country
## 1       New York    25      US
## 2          Paris    20  France
## 3 Rio de Janeiro    10  Brazil
## 4      Sao Paulo    12  Brazil
## 5          Tokyo    18   Japan
```

Aggregating merged data frame

```
result <- stdiv |> group_by(country) |>
   summarize(count = n(), amount = sum(value))
head(result)
```

```
## # A tibble: 4 × 3
##   country count amount
##   <chr>   <int>  <dbl>
## 1 Brazil      2     22
## 2 France      1     20
## 3 Japan       1     18
## 4 US          1     25
```

Part V

Statistical analysis

There are many statistical tests in R. One of the most used is the t-test. It checks if the mean of observations is not different from a theoretical value.

```
weight <- c(60, 72, 57, 90, 95, 72)
height <- c(1.75, 1.80, 1.65, 1.90, 1.74, 1.91)
bmi <- weight/height^2
```

```
t.test(bmi, mu=22.5)
```

```
##
##      One Sample t-test
##
## data:  bmi
## t = 0.34488, df = 5, p-value = 0.7442
## alternative hypothesis: true mean is not equal to 22.5
## 95 percent confidence interval:
##  18.41734 27.84791
## sample estimates:
## mean of x
##  23.13262
```

Test theoretical value of BMI equals to 22.5. Null hypothesis: no difference observed (p-value > 5%) Alternative hypothesis: they are different.
https://www.healthknowledge.org.uk/public-health-textbook/research-methods/1b-statistical-methods/parametric-nonparametric-tests

Python + R integration

Python code at retic.py

```
import pyreadr
import pandas

def add(x, y):
  return x + y

def read_rdata_mem(data):
  x = data["x"]
  print(x)
  y = data["y"]
  data["z"] = x + y
  return(data)
```

Library reticulate enables seamless integration with Python

```
library(reticulate)
source_python('https://raw.githubusercontent.com/eogasawara/analise-dados/refs/heads/main/python/retic.py')
x <- add(5, 10)
x
```

```
## [1] 15
```

Python + R dataset integration

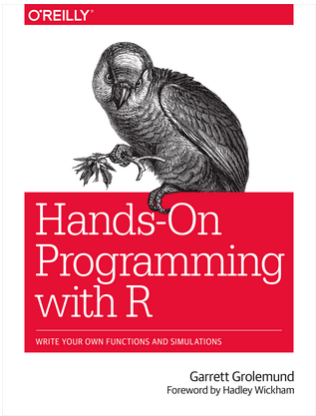
```
data <- data.frame(x = c(1:5), y=c(11:15))
dfm <- read_rdata_mem(data)
```

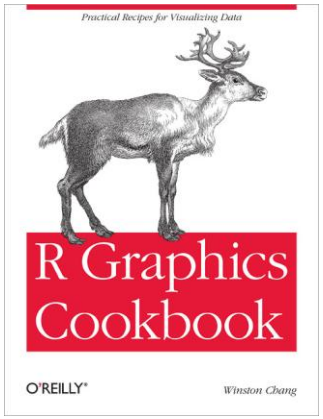
```
## 0    1
## 1    2
## 2    3
## 3    4
## 4    5
## Name: x, dtype: int32
```

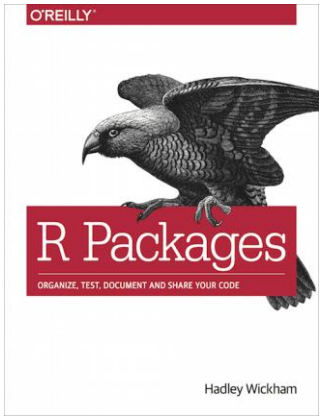
```
head(dfm)
```

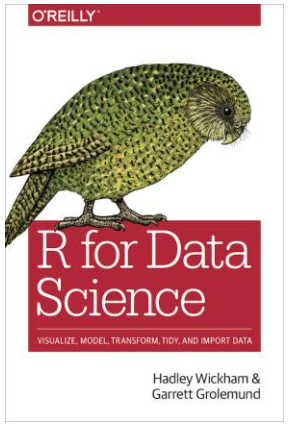
```
##   x  y  z
## 1 1 11 12
## 2 2 12 14
## 3 3 13 16
## 4 4 14 18
## 5 5 15 20
```

References









Hands-on Programming with R: https://rstudio-education.github.io/hopr/index.html
R Graphics Cookbook: https://r-graphics.org
R Packages: https://r-pkgs.org/index.html
R for Data Science: https://r4ds.had.co.nz

https://rstudio-education.github.io/hopr/basics.html

[1] G. Grolemund, 2014, Hands-On Programming with R: Write Your Own Functions and Simulations. O'Reilly Media, Inc.