Introduction to R

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What is R?

R is a language and environment for statistical computing and graphics

R provides tools for statistical analysis and data visualisation

Pros

- Free (as in "free speech", but also as in "free beer")
- It runs on all platforms (Windows, Mac or Linux)
- Can be extended with packages
- Large community: easy to get help
- R supports fairly large datasets (assuming you have enough RAM)

Cons

- You have to learn how to use a scripting language
- R natively supports only fairly large datasets

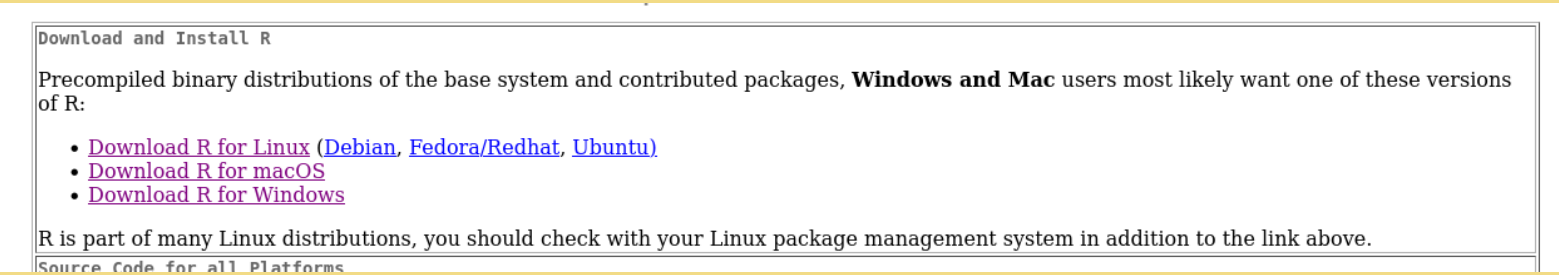

Aim: coding in R without being too scared

Installation

- Installing R
- Installing RStudio, the graphical interface

Installing R

Download R from the http://cran.mirror.garr.it/mirrors/CRAN/ web page and install it

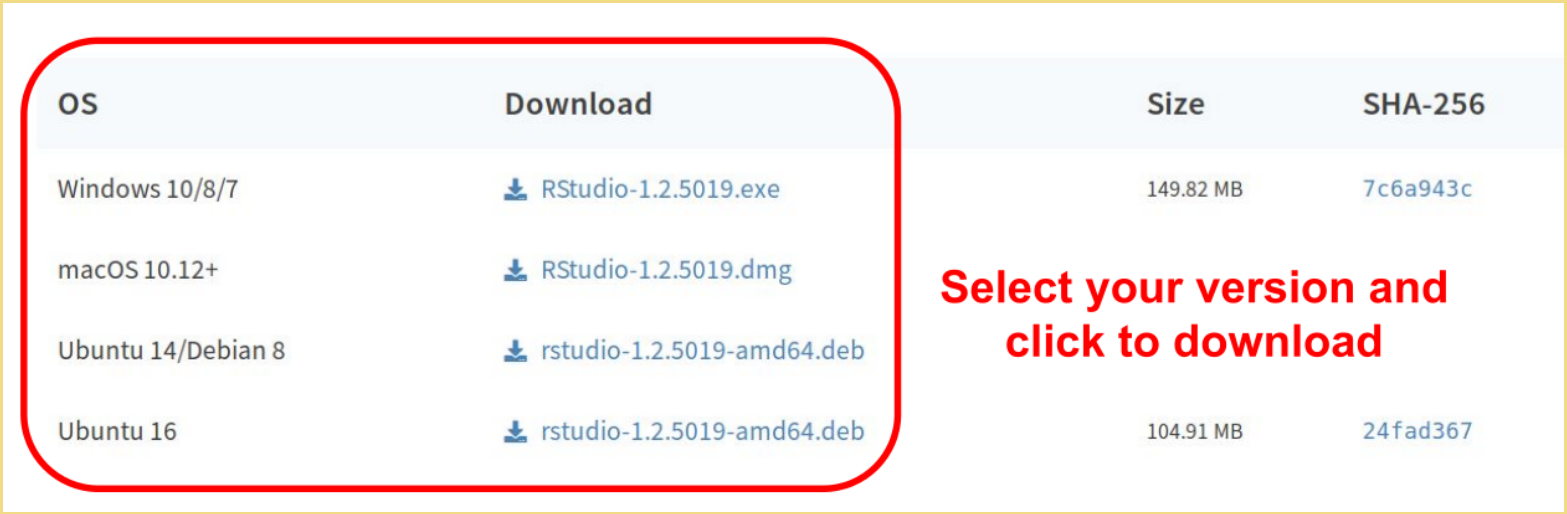


After the installation you should have two executable: *R_x86_64* and a *R_i386*

RStudio

For this course we will use **RStudio** . It is a graphical interface for R, that helps the programmer making it more user-friendly.

After installing R, download RStudio from https://www.rstudio.com/products/rstudio/download/#download



Plan

4 Lessons

- Introduction
- Basic functions
- Plotting
- Hypothesis testing

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1 Lesson

- Simulation of exam

Files

The *R* folder in the gdrive *bioinformatics_2021_2022* contains all the required material:

- *patric_redux.csv*, the table we will use for the lessons
- the course slides in pdf (including this one)
- the *R_commands.pdf*, a cheatsheet with the commands to use for the exam (it will be also provided during the exam)
- zip files for the lessons

The course material for R is also available online at https://tiagonardi.github.io/R_intro_2022/

Other resources

A complete cheatsheet for R is available at
https://github.com/rstudio/cheatsheets/blob/main/base-r.pdf