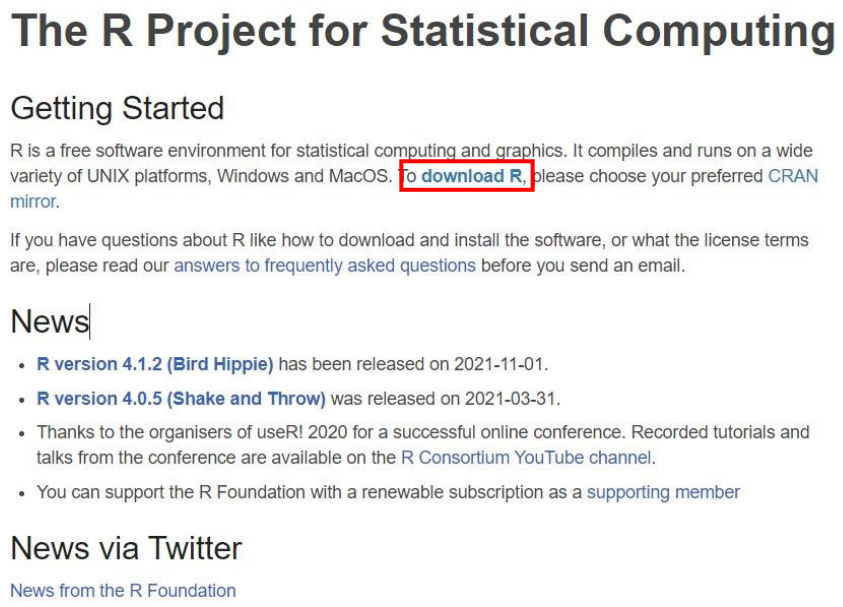
Guide to downloading R and RStudio

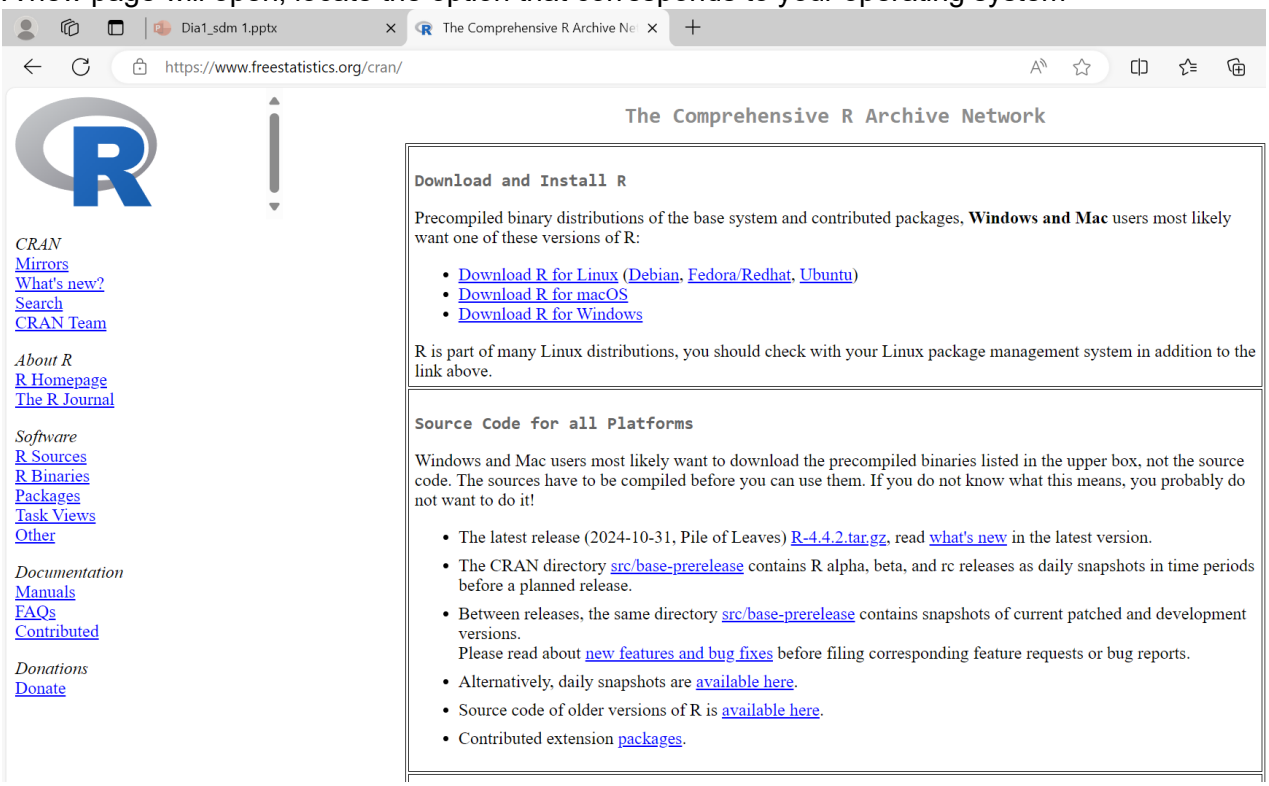
1. DOWNLOADING R

- Go to https://www.r-project.org/ and click on "download R" as shown in the figure below

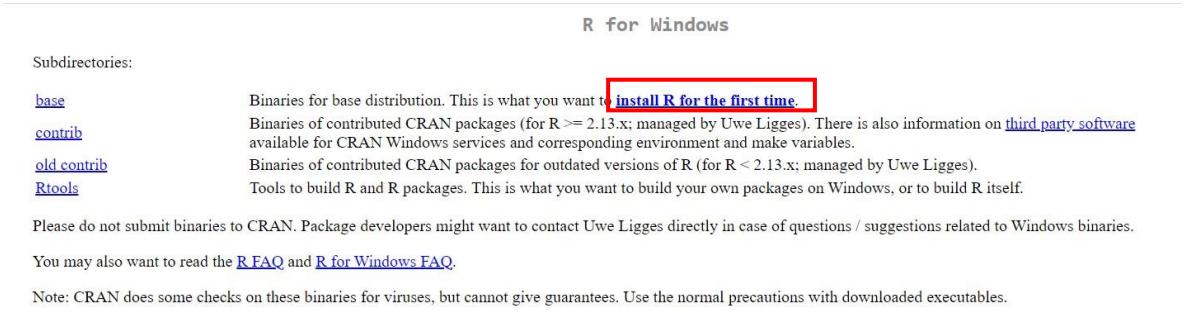


- A page with the following URL will open: https://cran.r-project.org/mirrors.html, where possible windows to download R are shown.

- A new page will open, locate the option that corresponds to your operating system



- When clicking on the appropriate option, a page will open showing the subdirectories: base, contrib, old contrib, and Rtools. Please click on "install R for the first time"



- A new page will open and show the file to download in "Download R 4.4.2 for Windows". Click and the file download will begin

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R-4.4.2 for Windows

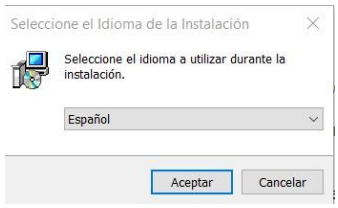
Download R-4.4.2 for Windows (83 megabytes, 64 bit)

README on the Windows binary distribution
New features in this version

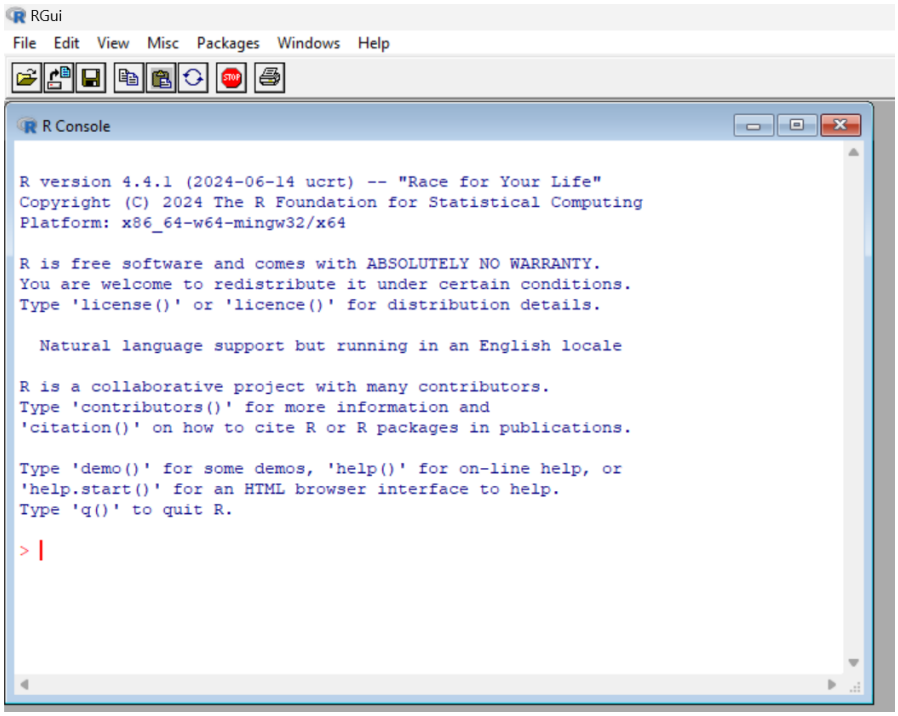
This build requires UCRT, which is part of Windows since Windows 10 and Windows Server 2016. On older systems, UCRT has to be installed manually from here.

If you want to double-check that the package you have downloaded matches the package distributed by CRAN, you can compare the md5sum of the .exe to the fingerprint on the master server.

- Download the file and install it by clicking Accept



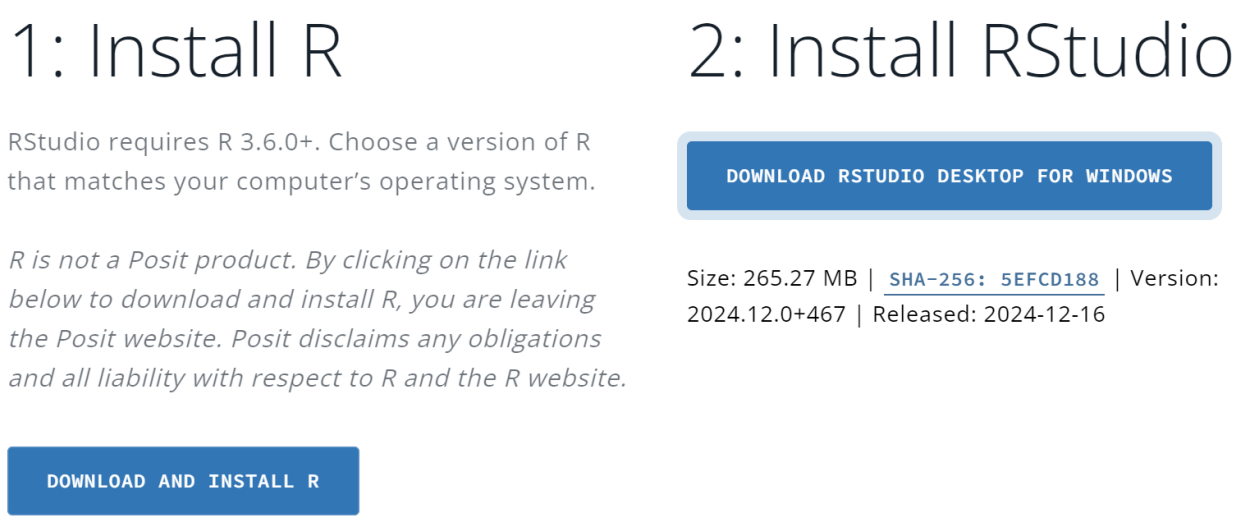
- When opening R, it will have the following appearance:



2. RSTUDIO DOWNLOADING

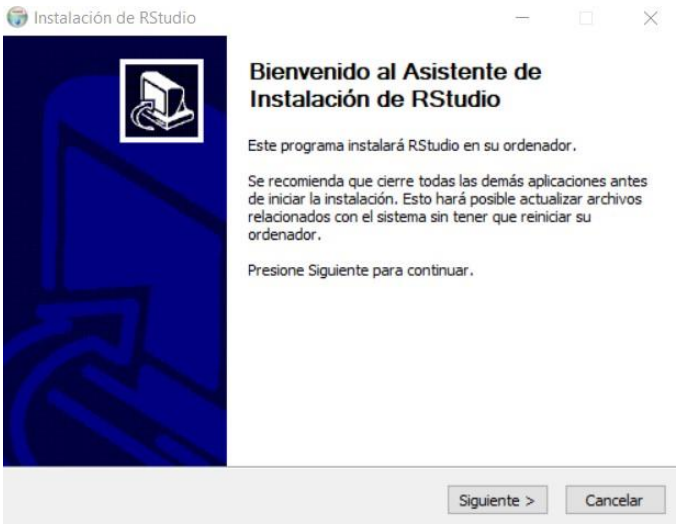
RStudio is an integrated development environment, that is, software that integrates various tools for agile script development such as editor, code indentation, development of new packages, etc.

- To download, go to https://posit.co/download/rstudio-desktop/ and explore the page

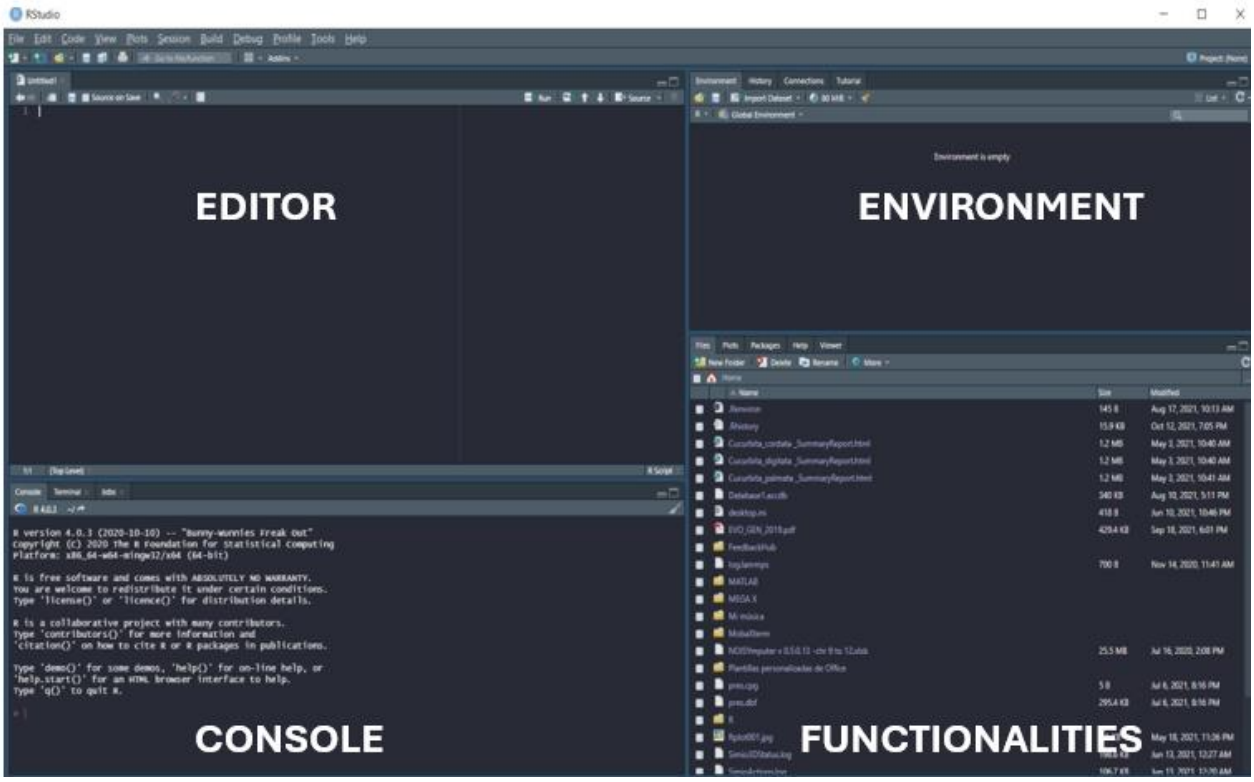


- Click on DOWNLOAD. This will download an installation file from the link https://download1.rstudio.org/electron/windows/RStudio-2024.12.0-467.exe

Para instalarlo, abra el archivo descargado y dé click en siguiente, una serie de ventanas se abrirá, por favor de click en siguiente o en aceptar.

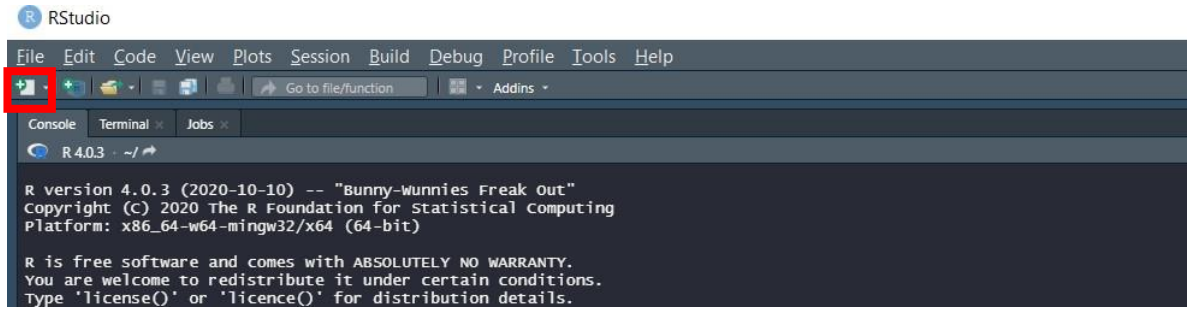
- 

Once RStudio is installed, when opening the program it will look like this. The program has four panels: editor, where the code to be run is written, in the console panel, functions and code are run, in the environment panel you will find the files that are in the computer's memory, and finally in the lower panel, there is a functionality panel where you will find various options to use alongside R such as files, graphics, help, or a viewer to visualize interactive graphics.



3. INSTALLING LIBRARIES FROM CRAN AND BIOCONDUCTOR

- Once you have R and RStudio installed, you can install packages, that is, the programs that run in R. For this, open RStudio and click on the icon , which will open a new text editor.



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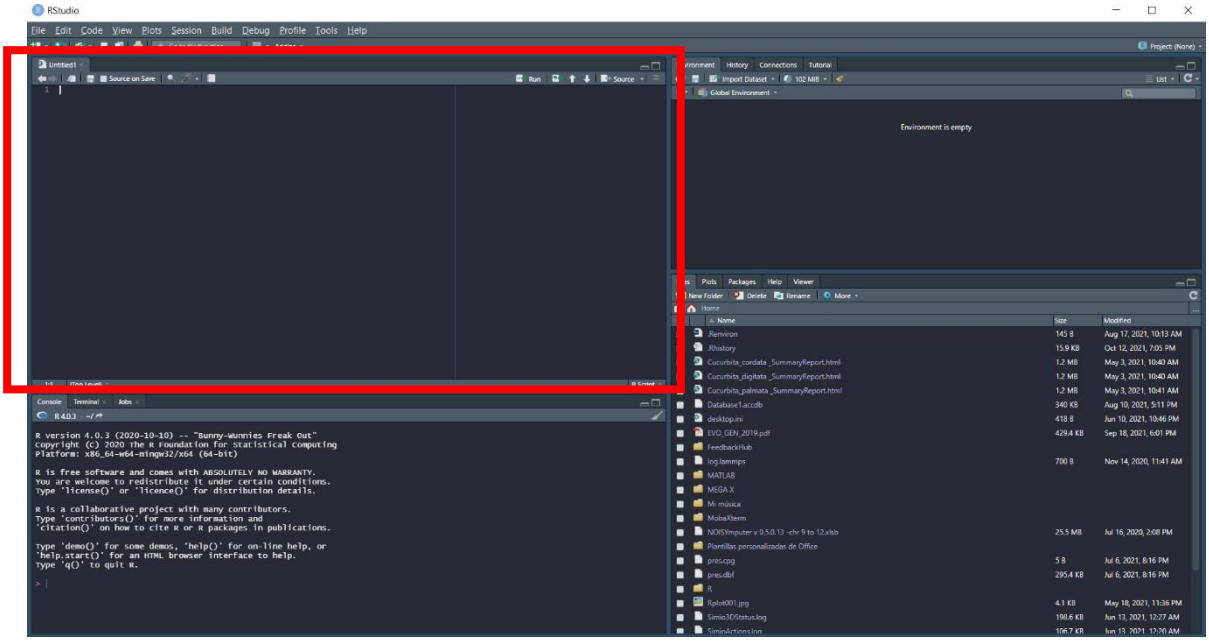
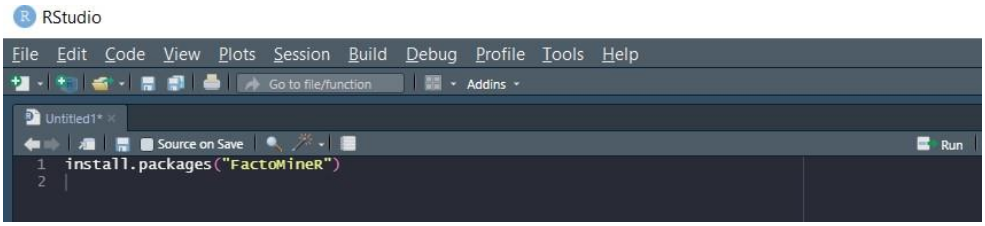
- The new editor will look like this: :



- To install packages, you must know which repository contains the desired package. The two most important repositories are CRAN and Bioconductor, however packages can also be installed from GitHub. To install a package from CRAN, write install.packages("PACKAGE NAME"), for example, install.packages("FactoMineR") and click RUN or if you prefer using the keyboard, use CTRL + ENTER:



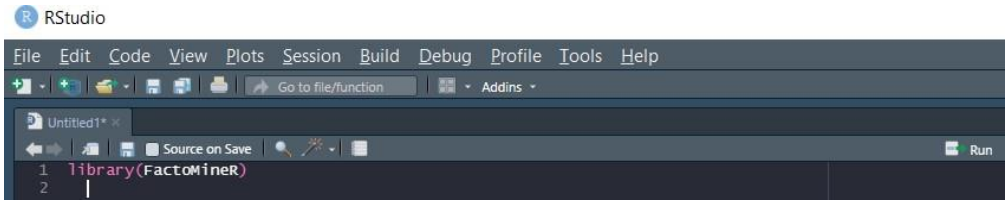
- An installation message will appear showing that the package was installed

```
> install.packages("FactoMineR")
Installing package into 'C:/Users/cami_/Documents/R/win-library/4.0'
(as 'lib' is unspecified)
trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.0/FactoMineR_2.4.zip'
Content type 'application/zip' length 3758758 bytes (3.6 MB)
downloaded 3.6 MB

package 'FactoMineR' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
        C:\Users\cami_\AppData\Local\Temp\RtmpERgsPi\downloaded_packages
> |
```

- To use the package, library("PACKAGE NAME"), for example, to use the FactoMineR package, use library(FactoMineR) and click RUN again



- To install from Bioconductor, go to the Bioconductor package page, https://bioconductor.org/packages/release/bioc/html/methylKit.html. In this case, instead of using the install.packages function, you will use the following instructions:

```
if (!requireNamespace("BiocManager", quietly = TRUE))    install.packages("BiocManager")

BiocManager::install("methylKit")
```

4. INSTALLATION OF LIBRARIES FROM GITHUB

- To install R packages from GitHub, you must install the devtools package and use the following instruction which details the GitHub repository from where the package will be downloaded, for example GapAnalysis

```
library(devtools)
remotes::install_github("ccsosa/GapAnalysis")
```