Information you need to take into concideration before doing the Bioinformatic course for Biomedical Research

We will do part of the Hands-on exercise using the RStudio environment. For that reason, you will need to have access to RStudio (and R) in your computers. There are two ways of achieving it. Choose **one** of them:

1. Set up RStudio with Docker

- You will have to **install Docker** following one of these options, depending on your operating system:
  - If you have Windows: look at 'Steps_to_install_docker_on_Windows.docx'.
  - If you have Linux or Mac: look at 'Steps_to_install_docker_on_Linux_or_Mac.docx'.
- Once you have Docker installed, you can download an image with the RStudio server set up. In order to do that, it is important to enter to the folder where you want to work (we highly recommend you avoid folders with paths containing special characters such as spaces, accents or any special symbols). Once in the folder, you can access the terminal easily with right-click (and choosing the terminal). A terminal will open.
  1. At this point, you have to make sure that you have the file 'run_docker_base_HandsOnRstudioServer.sh' in the folder you are located. So, in the terminal you should write:
     ```
     pwd
     ```
     The working directory will be printed. It should be the one where you have your course material (let's call it '/path/to/course').
  2. Then, you should create a folder in this path called 'bioinfo'.
  3. Now, open the file 'run_docker_base_HandsOnRstudioServer.sh' and substitute '/path/to/course' with your working directory path (remember to save the changes). Note that if you are working on Windows your path will start with 'c:', 'e:' or similar. Then, you have to eliminate the ':' from the path and start the path with double slash. For example, if it starts with 'c:' you will have to write:
     ```
     localdir=//c/path/to/course/bioinfo
     ```
  4. Once done that, execute in the terminal the following command:
     ```
     bash run_docker_base_HandsOnRstudioServer.sh
     ```
 With that, you will have your RStudio Server set at your local host. If you have to re-run the 'run_docker_base_HandsOnRstudioServer.sh' script (e.g. because you have had problems mounting the folder). You should stop the container and delete it using these commands:
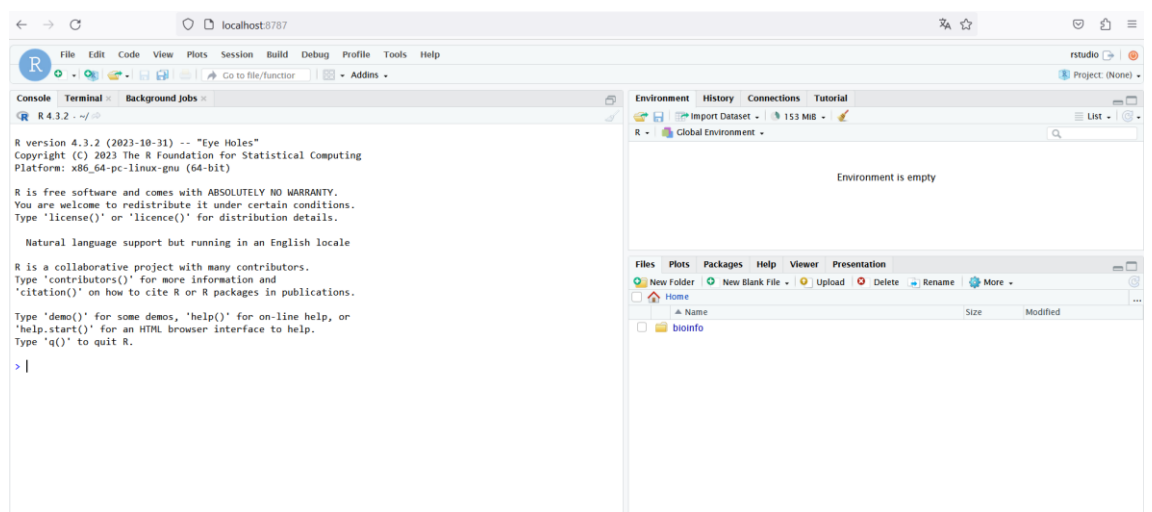 ```
  docker stop base_HandsOn_RStudio
  docker rm base_HandsOn_RStudio
  ```
  Then you can go back to step 4.
  If you want to ensure that you have your RStudio server set up, go to the specified port in the localhost (localhost:8787) and write the user name (rstudio) and password (bioinfo).
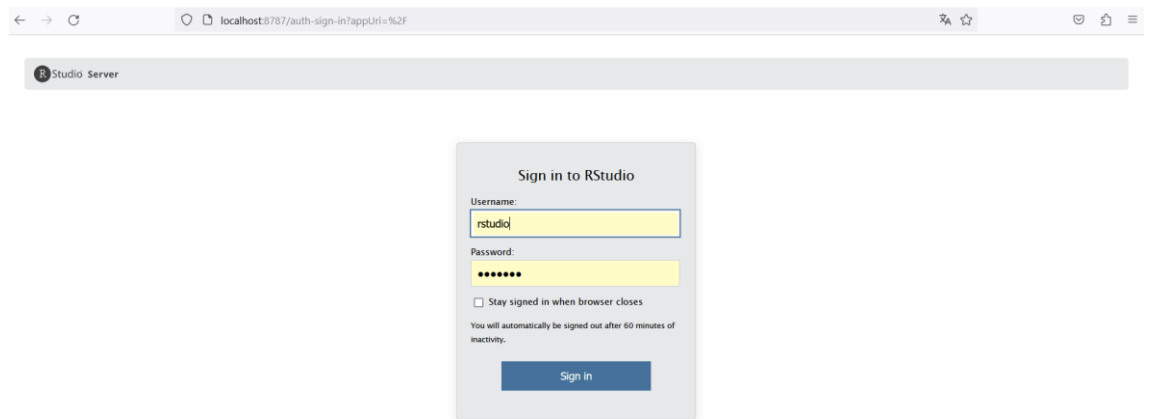
Click into 'Sign in'. The RStudio server should open:



Ensure you have your 'bioinfo' folder correctly mounted. It should appear in the right-lower pane. By going inside it, you should be able to access all the content you have locally in this folder.

## 2. Download R and RStudio and install the necessary files

You will need to follow the instructions available in this link: https://rstudio-education.github.io/hopr/starting.html

If you choose this option, you will need to manually install some packages. The necessary instruction (which you will have to execute in RStudio console) are:

```
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(version = "3.18")


BiocManager::install("GEOquery")
BiocManager::install("Rsubread")
BiocManager::install("edgeR")
BiocManager::install("limma")
BiocManager::install("pheatmap")
BiocManager::install("clusterProfiler")
```

```r
BiocManager::install("enrichplot")
BiocManager::install("org.Mm.eg.db")
BiocManager::install("AnnotationDbi")
BiocManager::install("DOSE")
BiocManager::install("ReactomePA")
```