The goal of this task is to practice the basic elements of Bioconductor, Rmarkdown and github.

* Select a study from the Gene Expression Omnibus Database.
  + Provide its identifer GSEXXXX
* Make sure that you can find out
  + The Expression matrix
  + The experiment description
  + The experimental groups
    - Prepare a data frame with labels for each sample
* Fill in the information collected in the shared google sheet available in[the following link](https://docs.google.com/spreadsheets/d/1X2b307HliPHj0swaMiFO_3EeoZmWyHx0H4jtHpB_mUw/edit?usp=sharing)
* Download the data
  + Directly through the browser
* In order to do the analyses create an RStudio project in a folder and put it under version control using github
* Prepare a report in Rmarkdown where you must provide at least three pieces of information.
  + A description of the study that generated the data
  + Information on the experimental design used (groups, types of comparisons etc)
  + A brief description of the data
    - Numerical summaries
    - Univariate plots (e.g. Boxplots)
    - Other plots?
* You must do the previous step three times
  + First, do it using the R objects (data matrix, targets, information) created from the files downloaded from GEO.
  + Next, create an ExpressionSet using these objects, following the guidelines provided in the lab: "Practical-Bioconductor-Classes.pdf" and "Practical-Bioconductor-Classes.R". Repeat the previous descriptive analysis steps using the data from the ExpressionSet.
  + Last, use the geoQUERY package to download the data in a single instruction. Check that with this instruction yo ubtain the same expressionSet object that
* Once you are done, render the document ("knit" it to create an html file).
* Commit your changes and push them to your project's repository.
* Provide a link to your github repository both in your document and through github classroom (when asked by the instructor).