Modèles statistiques en santé - M2 SNS -Let's start

Exercice 1 - Github beginners

Est-ce que git marche sur les machines de la salle de TD?

Step 0: First we need to install Git. Visit https://git-scm.com/downloads, download the package for your system and install.

After you install Git, the 'git' command should be available to you in the terminal :

Step 1: Let's say you have started with a hobby mini project and wrote a simple script in a file greeter.py. You can use Spyder or vscode as a Python editor.

```
def main():
   print("Ehlo World!")
main()
```

On branch main

Now you would like to save it in a Git repository.

Step 2: Move to the folder where greeter.py is located and create an empty Git repository using a command git init.

```
$ git init
Initialized empty Git repository in /Users/vmonbet/BIOSTATS/TP/TP0
$ ls -a
.
.git
To check the status of your repo, issue
$ git status
```

```
No commits yet
Untracked files:
  (use "git add <file>..." to include in what will be committed)
    greeter.py
Step 3: Let's tell Git to track our greeter py file and add it to the list for the next commit.
$ git add greeter.py
$ git status
On branch main
No commits yet
Changes to be committed:
  (use "git rm --cached <file>..." to unstage)
new file:
            greeter.py
Now the current version of the greeter.py is staged for commit and we can add it to our
repository.
$ git commit -m "Initial version of greeter function."
$ git status
[main (root-commit) 86474e9] Initial version of greeter function.
Step 4: In the greeter script we have a typo, so we change the text "Ehlo World!" to "Hello
BioStatistics!". We must save the file in our text editor so the changes are written to disk,
before we proceed!
$ git status
On branch main
Changes not staged for commit:
  (use "git add <file>..." to update what will be committed)
  (use "git restore <file>..." to discard changes in working directory)
modified:
            greeter.py
$ git commit -a -m "Hello text update."
[main dca6083] Hello text update.
1 file changed, 1 insertion(+), 1 deletion(-)
$ git status
On branch master
nothing to commit, working tree clean
```

```
as follows:
def main():
  student = input("Please enter your name: ")
  print(f"Dear {student}, we are happy to have you in the BioStistics track!")
main()
Again, add the file to stage and commit it to the repo.
$ git status
On branch master
Changes not staged for commit:
  (use "git add <file>..." to update what will be committed)
  (use "git restore <file>..." to discard changes in working directory)
    modified:
                greeter.py
no changes added to commit (use "git add" and/or "git commit -a")
$ git commit -a -m "Personal update."
[master 29710cc] Personal update.
 1 file changed, 3 insertions(+), 1 deletion(-)
$ git status
On branch master
nothing to commit, working tree clean
Step 6: Now our project has some history,
$ git log
commit 6f1e32e19aebab631a1728f984527c81fbea2d3c (HEAD -> main)
Author: Valerie Monbet <valerie.monbet@univ-rennes.fr>
Date:
        Sun Aug 10 12:46:51 2025 +0200
    Personal update.
commit_dca608385f2d75958afa36a7b20630447a656ed2
Author: Valerie Monbet <valerie.monbet@univ-rennes.fr>
Date:
        Sun Aug 10 12:42:41 2025 +0200
    Hello text update.
commit 86474e907f4a5d4cb652bb1a5871c635cbbdbe02
Author: Valerie Monbet <vmonbet@RT7F232XKJ.local>
Date: Sun Aug 10 12:27:47 2025 +0200
```

Step 5: We would now like to provide a more personal script, so we change the greeter.py

Initial version of greeter function.

Exercice 2 - Start your first project In this project, we will study liver steatosis. For that, we use a mice model as described in [Martin et al., 2025].

- 1. Create a directory for the project. THe directory will contains a least a paper, a dataset and some python codes. You can create sub-directories for a better reproducible research.
- 2. Download the dataset David and the compagnion paper.
- 3. Start writing a python code for
 - (a) Read the data (use pandas.read_csv)
 - (b) Remove lines with missing data (use pandas.dropna)
 - (c) Identiy the numbre of samples, the number of treatment groups, the number of samples per treatment groups
 - (d) Compute descriptive statistics for the observed variables as in Table 1 in [?]. See https://pandas.pydata.org/docs/dev/user_guide/style.html for table vizualisation.
- 4. Let's tell Git to track the files (paper, dataset and code(s)).

Références

[Martin et al., 2025] Martin, D., Monbet, V., Leroyer, P., Oliviero, N., Turlin, B., Salim, Z., Fautrel, A., Ropert, M., Sire, O., and Loréal, O. (2025). Sequential integration of multimodal data from serum improves the predictive performance of hepatic lipid accumulation in mice.