Software Setup

Folder structure for the course

 You should create a specific folder for this course under your user folder. Under Windows a typical location could be something like (the ellipsis represents possible intermediate folders):

```
C:/Users/your_user_folder/.../MasterBD/FMAD/
while for MacOS users you should use something like:
  /Users/your_user_folder/.../MasterBD/FMAD/
and finally for Linux it would be:
  /home/your_user_folder/.../MasterBD/FMAD/
```

- The folder that you have created will always be referred to in these notes as the Course Folder. In the above examples we named it FMAD but you can give it any name you want. As usual, it is a good idea to keep it short and meaningful (and free of spaces, unusual characters, etc.)
- We will be using Git and GitHub repositories for the Course Notes and Assignments. In particular, the following repository will be used to share all the common course material:

https://github.com/mbdfmad/fmad2223

In the next section we will tell you how to get a local copy of this repository to your computer. For the time being you can browse the contents of the repository, but do not download it yet! This repository will always be referred to in these notes as the Common Repository. Soon you will be also using your *personal repository* and it is important to get the distinction and name conventions right from the beginning.

Windows computers

Installing Git

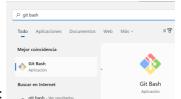
Important Note: If you already have a working and recent setup of Git (current version is 2.37), skip to the *Installing Anaconda Python* subsection.

 Install Git for Windows using this link. When asked about "Adjusting your PATH environment", select Git from the command line and also from 3rd-party



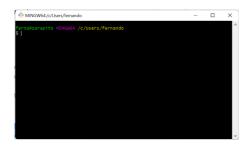
software. For all the rest of the setup it is ok to accept the defaults.

• When the Git setup is completed hit the Windows key and begin typing Git Bash.



You should see results like this:

Open the *Git Bash* application. A new *terminal* window will appear with a prompt waiting for your commands.



The details of the prompt (user and machine names) will be different in your case, of course. We will return here soon, but first we need a GitHub account.

Create a GitHub account

Important Note: even if you already have a GitHub account you need to have an account that is linked with your university email (the one ending in @alu.comillas.edu). You can create that account using this link. Make sure to log out first if you were already logged with a non-university-associated account. And we recommend reading this advice first.

Clone the common repository

Using the Git Bash terminal navigate to the Course Folder. You can get there using the cd command. Make sure that you have changed into the right folder before going further!! You can use the pwd command to check your current location. Ask for help if you run into trouble.

• In that folder run the following command:

```
git clone https://github.com/mbdfmad/fmad2223.git
```

Git will begin cloning (downloading) the contents of the repo to a folder named fmad2223 in your computer. The process looks like this (the number of cloned objects will surely be greater in your case):

```
MINOWGAL/Chaen/Gena/MAD

Carrailazaranito MINOWG4 - 

S cd FMAD/

Ternalazaranito MINOWG4 - 

S cd FMAD/

Ternalazaranito MINOWG4 - 

FMAD

To dia one https://ghubb.com/mbdfmad/fmad2223.git

To dia one https://ghubb.com/mbdfmad/fmad2223.git

Ternalte Enumerating Objects: 200, done.

Fmante: Enumerating Objects: 100% (20/20), done.

Fmante: Countring objects: 100% (20/20), done.

Fmante: Countring objects: 100% (20/20), 382, pack-reused 0

Racetving objects: 100% (20/20), 382, 37 KIB | 962,00 KIB/s, done.

Racelving deltas: 100% (20/20), 382,37 KIB | 962,00 KIB/s, done.
```

The fmad2223 folder will then be a subfolder of the *Course Folder*. You should consider this fmad2223 folder as a *read-only* folder. You will soon see how to update its contents as the course progresses, but **you are not expected to directly modify the contents of the fmad2223 folder** (and you shouldn't). You can *copy* any object from this folder (e.g. the code examples that we will provide) to other locations in your computer if you want to make changes. Finally, if you are a seasoned Git user you can opt for a fork of the repo instead of cloning it.

Keeping your local copy of the *common repository* updated.

- If you are used to auto syncing tools such as Dropbox, OneDrive, ICloud Drive and the like, you must keep in mind that **Git repos are not auto-syncing**. To keep the information in your repos updated you have to manually update them (both ways, from your computer to GitHub and viceversa).
- This will be very important for our workflow in the lectures of the course. So make sure to get it right, and ask for help soon if you need it. Every work session for this course will begin with the following ritual:
 - Open a Terminal (the Git Bash terminal or, see below, the Anaconda terminal are both ok).
 - Navigate to your local fmad2223 folder. Do not confuse this with the Course Folder.
 - Run git status to check that everything is ok.
 - Run git pull origin main. Depending on the update status of your local copy of the repo you will either download the new contents from the repo at GitHub or you will receive a message saying that you are Already up to date.

Don't worry too much, however. You cannot break anything, since you won't have write permissions for this GitHub repo. Worst case scenario, you can (backup

your local files and) delete the fmad2223 folder and clone it again to get the latest contents.

Setting up a local Git configuration for the Common Repository

• Using still the *Git Bash* terminal, change into the fmad2223 folder and set your local Git configuration with these commands (the first one is the folder change from the *Course Folder* to fmad2223):

```
cd fmad2223
git config --local user.name
'replace_this_with_your_GitHub_username'
git config --local user.email
'replace_this_with_your_university_email'
git config --global init.defaultBranch main
```

• By the way, if you are doing this setup for the first time, now you can close the *Git Bash* terminal window.

Installing Anaconda Python

Important Note: If you already have a working setup of Anaconda Python (with Python 3.8 or 3.9) then skip to the *Create a Conda Environment for the Course* subsection. If your Python version is older: get updated, people!

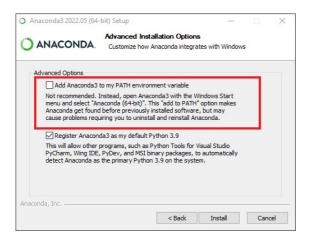
• Begin by navigating to the Anaconda Web Page:



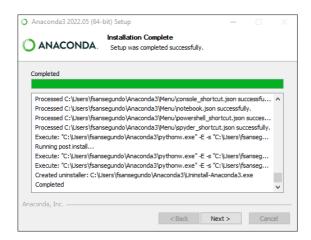
• Click the download link. When the download finishes, run the Anaconda Installer.



In the following setup dialogs you can (and probably should) accept all the
defaults. Be careful with this step! Unles you have a good reason not to, please
leave the first box unmarked, as illustrated here:



When setup is completed you will see something like this:



Click on *Next* and do the same in the final dialogs (consisting in software ads and tutorials, we suggest to skip all of them).

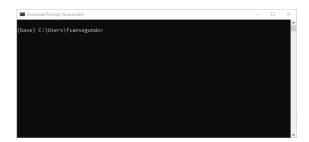
Create a Conda Environment for the Course

• A conda environment allows us to organize our work in projects, keeping each project dependencies isolated from the rest of your work. It is also the best way to avoid running into the potentially catastrophic situation in where you have several Python versions and they conflict to create a mess. We urge you to always use environments to organize your work in Python. You can learn more about the use of Conda environments in this link. And to learn more about environments in Python in general, you can check these two links:

- A Guide to Python's Virtual Environments
- The Definitive Guide to Conda Environments
- We will be using a Conda environment named fmad for this course. To create the environment we will use the *Anaconda Terminal (or Anaconda Prompt)*. Hit the Windows key and begin typing *Anaconda*. You should see results like this:



The Anaconda Navigator is a GUI interface to manage your Anaconda setup. Some people like it a lot, but we will be using mostly the (old school) terminal-based command-line approach. Thus, start the *Anaconda Prompt* and a window like this one will open:



This terminal window is where most of our *Python management* will occur (but not the actual coding!)

In that prompt execute the command

conda create --name fmad

and after some moments something like this should happen

For the time being ignore the warning about updating Conda it it appears (we will deal with it in the next step) and just answer *y* and hit *Enter*. A successful environment creation looks like:

```
Proceed ([y]/n)? y

Preparing transaction: done
Verifying transaction: done
Executing transaction: done
#
# To activate this environment, use
#
# $ conda activate fmad
#
# To deactivate an active environment, use
#
# $ conda deactivate

(base) C:\Users\fsansegundo>
```

Update conda

 To update conda (if the warning appeared in the previous step) run this command:

```
conda update -n base -c defaults conda
```

As the following picture illustrates conda will present you with a summary of the update operation. Answer *y* and hit *Enter*.

```
| Meancode Pennyl (Peaconda): conda ental - name fend manyo - conda update - n base - c defaults conda
| Cilustria | Cilustri
```

Then conda will download the required software to autoupdate. The expected result looks like this:

Activate the environment

• When we created the fmad environment in a previous step, Conda showed us the activation command:

```
conda activate fmad
```

Run this command now. This will activate the newly created environment fmad. Note that the name of the active environment appears in parenthesis at the beginning of the prompt line:



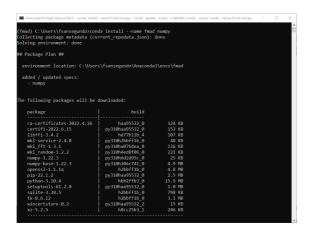
Make sure that the environment is correctly activated before proceeding!! If you have any problem ask for help.

Install the first library

 The first library that we will install is NumPy, which provides the foundation for much of the work we will doing in this course. We will discuss NumPy in coming sessions of the course. But to use it we first need to install it in our fmad environment. Execute this command now:

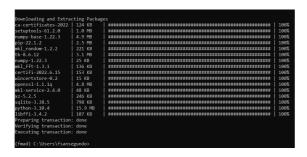
```
conda install --name fmad numpy
```

A summary of the libraries that need to be downloaded for the NumPy setup will appear



followed by a rather lengthy list of the libraries about to be installed (in most cases these two lists are almost equal)

Answer yes to make the setup begin and wait patiently while NumPy and all of its requirements are downloaded and installed. The process should end like this:



Install aditional libraries

- NumPy is just the first of the libraries that we will use in the course, but many others will also come into play. To name a few of the most relevant:
 - NumPy
 - Pandas
 - MatPlotLib
 - Scikit-Learn

Take a few moments to visit the homepage for each of these libraries.

Exercise: install all these libraries to the fmad environment. To install several libraries you don't need to repeat conda install for each library; you can use a single install command and separate the names of the libraries with a space.

Install the Jupyter Notebook & Jupyter Lab

• In this course we will talk to Python using the onterface provided by *Jupyter Notebooks*. The Jupyter Project provides a general purpose development environment which is well suited for Python (but not limited to it). It will play a

central role in our work with Python, but it installs (to the fmad environment) just like any other library.

```
conda install --name fmad jupyter
```

 When the setup ends execute the following two commands in order. The first one changes your current directory to your user folder in Windows. The second command opens the Jupyter Notebook in your default Web Browser:

```
cd %HOMEPATH%
jupyter notebook &
```

Like this:

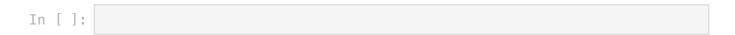


Note: We recommend to always start Jupyter from a folder high enough in your folder structure: you won't be able to easily move up from the starting point later. Make sure, however, that you are at the very least, at the *Course folder* level.

In a few moments your default *Web Browser* will open to a new page that shows the entry point for the running Jupyter server that we have just started:



You can use that page to navigate your folder structure until you get to the *Course Folder*. Once you are seeing the contents of that folder,



MacOS computers

 MacOS includes a system version of Python. We will not be using that version but we need to make sure that it does not interfere with our work and that the basic functioning of your computer is not affected. Always keep recent backups of your data before any complex setup like this!

•

Linux computers

• Most recent versions of Linux already come

```
In [1]: pip install nbconvert[webpdf]
    zsh:1: no matches found: nbconvert[webpdf]
In []:
```