Environment configuration

This section is necessary only if you want to use your own computer to work with notebooks. As explained previously the simplest way to work with notebooks is to use the Jupyter Hub server at Institut Mines Telecom.

If you do not have Python or all the libraries that we will use already installed on your machine, we suggest that you use **Conda** installer. As explained on conda website: *"Conda is an open source package management system and environment management system for installing multiple versions of software packages and their dependencies and switching easily between them. It works on Linux, OS X and Windows, and was created for Python programs but can package and distribute any software"*. Thus, using Conda, you can create independent programming environments in which you install the packages you want without interfering with the rest of your system.

Conda is included in **Anaconda** and **Miniconda**.

You can get **Anaconda** for your platform here (install the python3 version). It will install many Python scientific libraries on your machine and should work fine. After installation you should have an Anaconda3 folder in your programs drop-down menu. Click on the Anaconda Navigator icon inside Anaconda3 and when the Anaconda Navigator opens, launch jupyter by clicking on the jupyter icon. You can get the files of the labs either by moving through directories in the web interface or by dragging and dropping the files into the files interface.

If you are running a Linux or Mac OSX operating system, to avoid installing many libraries that will not be useful for the labs of the MOOC, we propose that you use the **Miniconda** installer. It will enable you install simply the

minimal environment you will need for the labs, with Python 3, Numpy, Scipy, Matplotlib and Jupyter notebook environnements. You can also do it if you have a Windows operating system, but since we have experienced some difficulties with jupyter notebooks with this installation, it could be easier for Windows users to download Anaconda as explained above.

We have tested the following instructions on Linux and Mac OSX for installing and launching Python3 notebooks.

- 1) Download miniconda here (choose the Python 3 version of miniconda). Under Linux/Mac OSX, make the downloaded file executable by typing in the terminal

  > $ chmod +x path_to_downloaded_file/downloaded_file_name

  (Under windows, simply run the .exe downloaded file).

- 2) Install miniconda, following the instructions. This will create a miniconda3 folder under your home directory (Miniconda3 under Windows), unless you have specified another location during installation. This folder contains several subfolders.
- 3) Create an environement for the labs, including the packages that we will need:

  > $ conda create -n Lab numpy scipy matplotlib jupyter

  This can take a few minutes. Note that the conda command is located in subdirectory *miniconda3/bin* under Linux or Mac OSX and in subdirectory *Miniconda3\Scripts* under Windows (by default the miniconda directory is in your home directory as explained above). The Lab folder will be created in the subdirectory envs of your miniconda3 folder.

- 4) To activate the Python environment, under Linux or Mac OSX type in a terminal (the activate command is in the bin folder)

  > $ source activate Lab

  (under windows type *\> activate Lab* where the activate command is in the Scripts folder)

- 5) Download the notebooks of the MOOC and copy them in a folder you have created for the labs of the MOOC, say MOOC_LABS.
- 6) Go to your MOOC_LABS folder and launch jupyter notebooks:

  > $ jupyter notebook

In your browser, the files present in the current directory should appear in the jupyter interface. You can move into this directory and subdirectories and open .ipynb files by clicking on them.

You can edit the notebook by using the commands on top of the notebook page. You can also use shortcuts in the help section on top of the page. More information about jupyter notebooks is available at http://jupyter.org/.

You can close the notebooks using Ctrl+C in the terminal. Do not forget to save your work before closing notebooks (for safety, save it from time to time when working).

To deactivate your environment, in the terminal, type

> $ source deactivate Lab

(under Windows type *\> deactivate Lab*)

More information about how to use conda can be found here.