Setup

The labs of the Sequential Decision course are Jupyter notebooks, in Python. There are two ways to run them: on your laptop (sections 1 to 4, 15 to 20 minutes, done once), or online with Google Colab, without installing anything (section 5).

1. Get the course files

Download the setup archive from the course page and unzip it. You get a folder `sequential-decision/` that contains:

- this page;
- the folder `seqlearn/`, the Python package used in the labs: do not move it, the notebooks read it from the folder they are in;
- `environment.yml` and `check_install.py`, used below.

The notebook of each lab is downloaded separately, from the line of its session on the course page: save it **in this folder**, next to `seqlearn/`. Each notebook also has a `-colab` version for Google Colab (section 5). The first ones are `lab00.ipynb` (session 1, optional warm-up on Python, numpy and matplotlib) and `lab01-02.ipynb` (Labs 1 and 2).

When a lab needs a new version of `seqlearn`, the course page says so: download the setup archive again and replace the folder `seqlearn/` with the new one. Your notebooks are not modified.

Open a terminal **in this folder**:

- Windows: open the folder in the file explorer, right-click in it and choose "Open in Terminal". With option A below, use the "Miniforge Prompt" from the Start menu instead, and move to the folder with `cd path\to\sequential-decision`.
- macOS: open the application Terminal, type `cd` (with a space), drag the folder onto the window and press Enter.
- Linux: open a terminal and `cd` to the folder.

The command `ls` (macOS, Linux) or `dir` (Windows) must list `environment.yml` and `seqlearn`.

2. Create the environment

A virtual environment is a separate copy of Python with its own packages. It keeps the packages of this course apart from the rest of your machine. Choose one of the two options.

Option A: Miniforge (recommended if Python is not installed)

1. Download and run the Miniforge installer for your system from https://github.com/conda-forge/miniforge. Keep the default choices.
2. Open a new terminal (on Windows, the "Miniforge Prompt") in the course folder.
3. Create the environment, then activate it:

```
conda env create -f environment.yml
conda activate esiee-sequential
```

The prompt of the terminal now starts with `(esiee-sequential)`.

Option B: an existing Python (3.11 or later)

Check the version with `python --version` (or `python3 --version`). Then create the environment in the course folder, activate it and install the packages.

macOS and Linux:

```
python3 -m venv .venv
source .venv/bin/activate
pip install numpy matplotlib jupyterlab ipywidgets
```

Windows:

```
python -m venv .venv
.venv\Scripts\activate
pip install numpy matplotlib jupyterlab ipywidgets
```

The prompt of the terminal now starts with `(.venv)`.

3. Check the installation

In the same terminal, in the course folder, with the environment activated:

```
python check_install.py
```

The last line must be `Installation OK.`

4. Start Jupyter

```
jupyter lab
```

A page opens in your browser. In the file list on the left, open `lab01-02.ipynb`, or `lab00.ipynb` first if Python or numpy is new to you. To stop Jupyter, press `Ctrl+C` twice in the terminal.

You can also open the notebooks with VS Code (extensions "Python" and "Jupyter"): open the course folder, then choose the environment `esiee-sequential` or `.venv` with "Select Kernel", at the top right of the notebook.

At each session, open a terminal in the course folder, activate the environment and start Jupyter. Nothing needs to be installed again.

```
conda activate esiee-sequential     (option A)
source .venv/bin/activate           (option B, macOS and Linux)
.venv\Scripts\activate              (option B, Windows)
jupyter lab
```

5. Without installation: Google Colab

Go to https://colab.research.google.com (a Google account is required), choose File > Upload notebook, and select the `-colab` version of the lab, for instance `lab03-colab.ipynb`. The first cells of the notebook, in the section "Framework", write the `seqlearn` package on the Colab machine: run them first, and again after each reconnection. Download your notebook at the end of the session (File > Download > Download .ipynb), since Colab does not keep it on your laptop.

Common problems

- **`conda` is not recognized** (Windows). Use the "Miniforge Prompt" from the Start menu, not the default terminal.
- **`python` is not recognized**, or the version is older than 3.11. Use option A, or Google Colab.
- **"Running scripts is disabled on this system"** when activating `.venv` (Windows PowerShell). Run `Set-ExecutionPolicy -Scope CurrentUser RemoteSigned`, then activate again, or use the "Command Prompt" instead of PowerShell.
- **`ModuleNotFoundError: No module named 'seqlearn'`**. The folder `seqlearn/` must be next to the notebook, and Jupyter (or `check_install.py`) must be started from the course folder. Save the notebooks in the course folder, not in your downloads folder.

- `ModuleNotFoundError: No module named 'seqlearn.challenge'` (or another part of `seqlearn`). The folder `seqlearn/` is older than the notebook: download the setup archive again and replace `seqlearn/`.
- `ModuleNotFoundError: No module named 'numpy'` in a notebook. The notebook does not use the course environment. Close Jupyter, activate the environment in the terminal (its name must appear in the prompt), and start `jupyter lab` again from this terminal.
- **The sliders of Lab 3 do not appear** ("ipywidgets is missing"). The environment was created before Lab 3: run `conda install -n esiee-sequential -c conda-forge ipywidgets` (option A) or `pip install ipywidgets` in the activated `.venv` (option B), then restart Jupyter.
- **The command hangs or fails behind the school network.** Try again on another network (phone hotspot): the installation downloads about 300 MB. Meanwhile, use Google Colab.