

Modelling of Biological Processes - Installation instructions

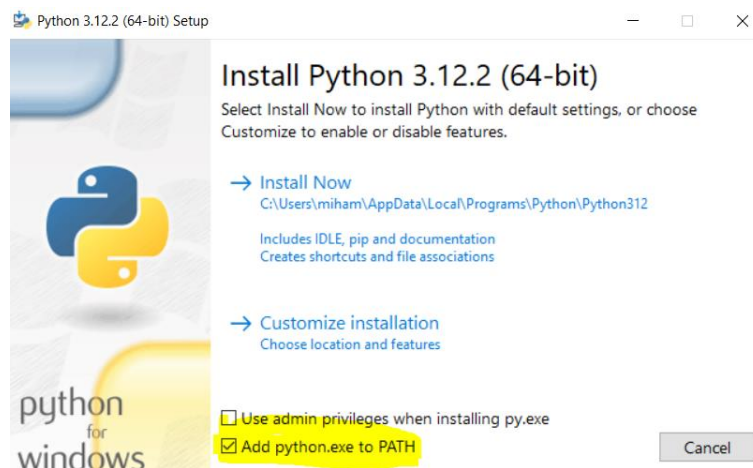
This document describes two options to install the programming environment for the workshop. The easier option (**option 1**) is to install Python and all the required libraries within it. The other option (**option 2**) is installing a virtual environment through Python and Anaconda.

Please contact me if you encounter any problems (miha.moskon@fri.uni-lj.si).

Option 1: Installation in Python

1) Install Python

You can download python from <https://www.python.org/>. Download and run the installation file. During the install, **select the option Add python.exe to PATH**.



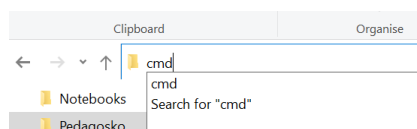
2) Install git


You can download git from <https://git-scm.com/>. Run the installation after download.

3) Open the console in your working directory

In Windows:

Option 1: Open the working directory (the folder in which you will be saving workshop files) in your file explorer. Write `cmd` in the address bar and press enter.



Option 2: Click on start menu  and write `cmd`. Change the folder into your working directory using the command `cd`.

All the following steps contain commands to be typed into the console.

4) Download the files for the workshop

```
> git clone https://github.com/mmoskon/BioMed2324/
```

5) Go into the downloaded folder

```
> cd BioMed2324
```

6) Install the required packages

```
> pip install -r requirements.txt
```

7) Run the Jupyter Lab / Notebook

You can use either Jupyter Lab:

```
> jupyter lab
```

or Jupyter Notebook:

```
> jupyter notebook
```

Your default browser will open an interface to work with IPython Notebook (.ipynb) files.

Option 2: installation within a virtual environment in Anaconda

1) Install *Anaconda*

Download Anaconda from <https://www.anaconda.com/>. Run the installation after the download.

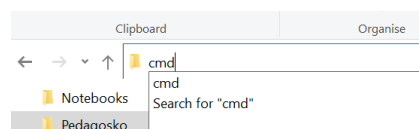
2) Install *git*


Download git from <https://git-scm.com/>. Run the installation after the download.

3) Open the console in your working directory

In Windows:

Option 1: Open the working directory in your file explorer. Write *cmd* in the address bar and press enter.



Option 2: Click on start menu  and write *cmd*. Change the folder into your working directory using the command *cd*.

4) All the following steps contain commands to be typed into the console. Download the files for the workshop

```
> git clone https://github.com/mmoskon/BioMed2324/
```

5) Go into the downloaded folder

```
> cd BioMed2324
```

6) Install the virtual environment

```
> conda create --name metabolic python=3.12.2
```

7) Activate the virtual environment

```
> conda activate metabolic
```

8) Install the required packages

```
> pip install -r requirements.txt
```

9) Install the virtual environment in *Jupyter*

```
> python -m ipykernel install --user --name=metabolic
```

10) Run the Jupyter Lab / Notebook

One option is to use Jupyter lab

```
> jupyter lab
```

You can also use Jupyter Notebook

```
> jupyter notebook
```

Your default browser will open an interface to work with IPython Notebook (ipynb) files.

11) Remove the virtual environment

If you will not be using the created virtual environment after the worksop, you can remove it with

```
> conda deactivate
```

```
> conda remove --name metabolic --all
```

```
> jupyter kernelspec uninstall metabolic
```