

Modelling of Biological Processes

Installation instructions

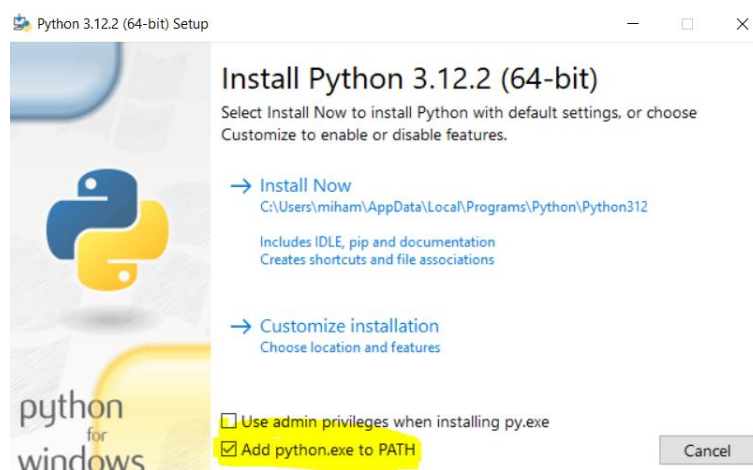
This document describes two options to install the programming environment for the workshop. An easier option (**option 1**) is to install Python and all the required libraries within it. If you have already been working with Python and Anaconda, you can also install a virtual environment as described in **option 2**.

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, please **selected the option Add python.exe to PATH**.



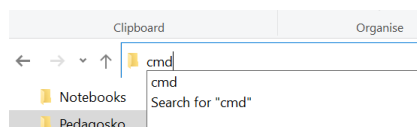
2) Install git


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 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) Download the files for the workshop

In the console you should write

```
> 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

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.

Option 2: installation within a virtual environment in Anaconda

1) Install *Anaconda*

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

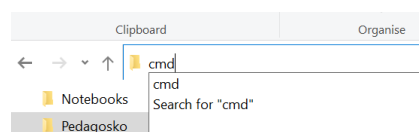
2) Install *git*


You can 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) Download the files for the workshop

In the console you should write

```
> 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 workshop, you can remove it with

```
> conda deactivate
```

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

```
> jupyter kernelspec uninstall metabolic
```