

# 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](mailto: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**.



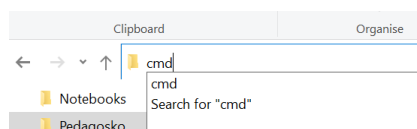
#### 2) Install git


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/BioMed2425/
```

### 5) Go into the downloaded folder

```
> cd BioMed2425
```

### 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.

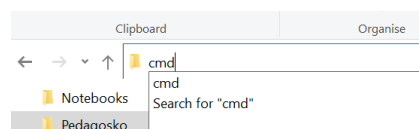
### 2) Install *git*


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 workshop, you can remove it with

```
> conda deactivate
```

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

```
> jupyter kernelspec uninstall metabolic
```