Programming Basics for Bio(techno)logical Data

This series is not meant to replace a formal programming course, and thus it will not cover programming theory or fundamentals. Rather, it is aims to introduce useful tools and techniques that can be applied for the preprocessing, analysis, and visualization of data, with a focus on bio(techno)logical data. Example workflows and relevant links are provided for each concept.

In this tutorial: You will learn how to: **1)** install Python and Python packages with miniConda, **2)** create and run a Jupyter Notebook in Visual Studio Code, and **3)** import those packages.

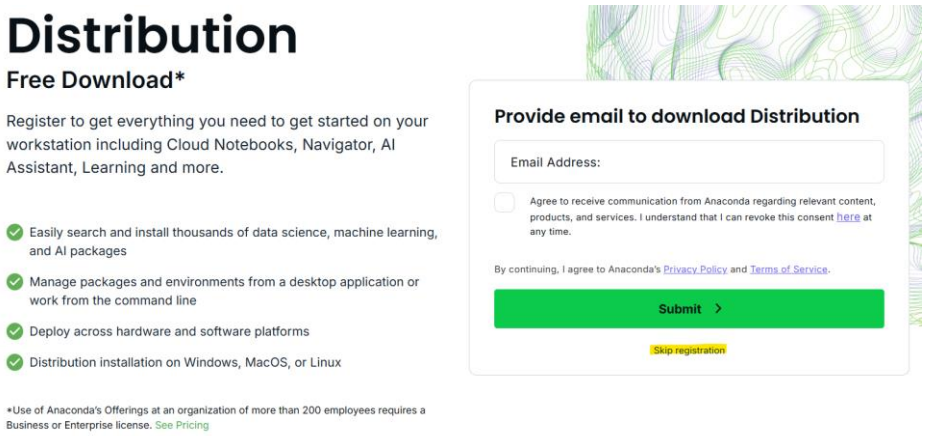
Note: All code will be bolded and in the font **`Courier New`**.

1. Install Python via miniConda

Python is like a toolbox that contains basic tools (commands) you can use to perform tasks on a computer. Out of the box, Python comes with simple tools like a calculator (for math) and a notepad (for handling text). Python packages (or libraries) are like extra tool sets you can add to your toolbox. If you need more advanced tools, you can download them and add (install) them to your toolbox. These packages can be stored in Python environments (like tools on a shelf). One of the biggest challenges in Python is the managing of these environments. Often, packages are not compatible with each other, or a package may require a specific version of another package. You can create different environments for different tasks which require different packages or different package versions. Python (and its additional packages), like any computer program, needs to be installed.

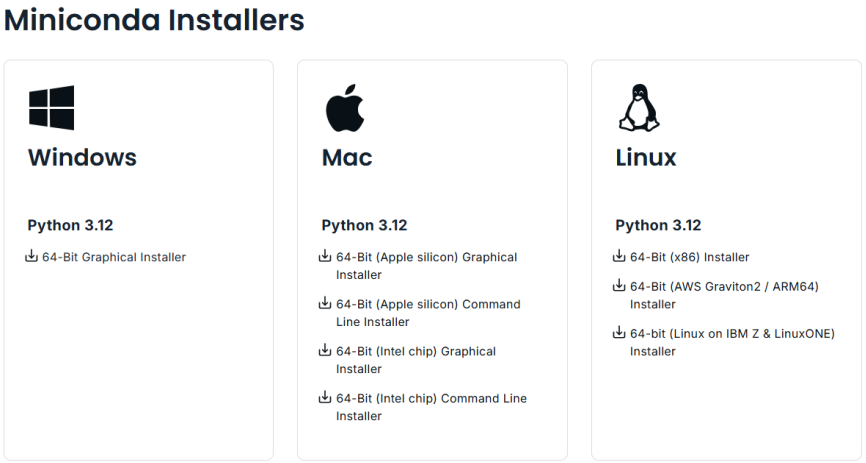
We will use **miniConda** to install Python and create environments where we store our packages. Note: **miniConda** not Anaconda.

1. Install miniConda following the directions included on the conda website:
    a. https://www.anaconda.com/docs/getting-started/miniconda/install#windows-installation (instructions)
    b. https://www.anaconda.com/download?utm_source=anacondadocs&utm_medium=documentation&utm_campaign=download&utm_content=installwindows (link to the downloads)



Created By: Dr. Isabella Casini
Edited By: Justin Chitpin
Last Updated: 12.03.2025

c. You can choose to register but there is no need so you can click “Skip registration”.
d. Scroll down to find the **miniConda** installers and select the one for your operating system.

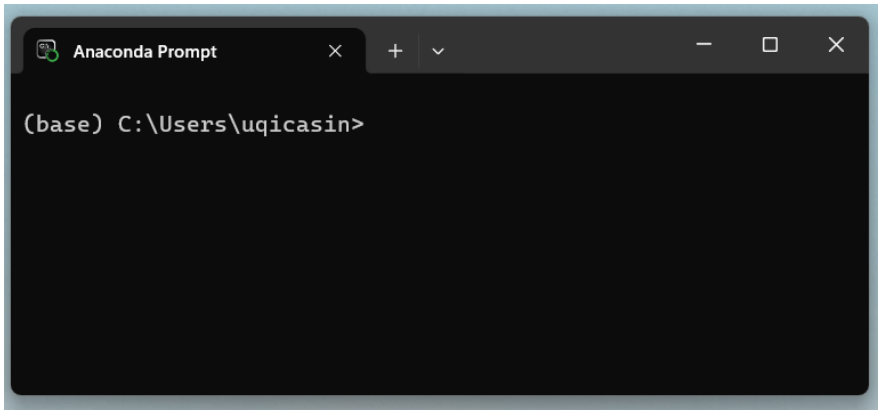


e. Run the installer (the executable file).
    i. Install miniConda only in a path **without spaces (not this** “C:\Users\Isa Casini\....”). If your username has a space in it, choose a different directory (*e.g.*, C:\).

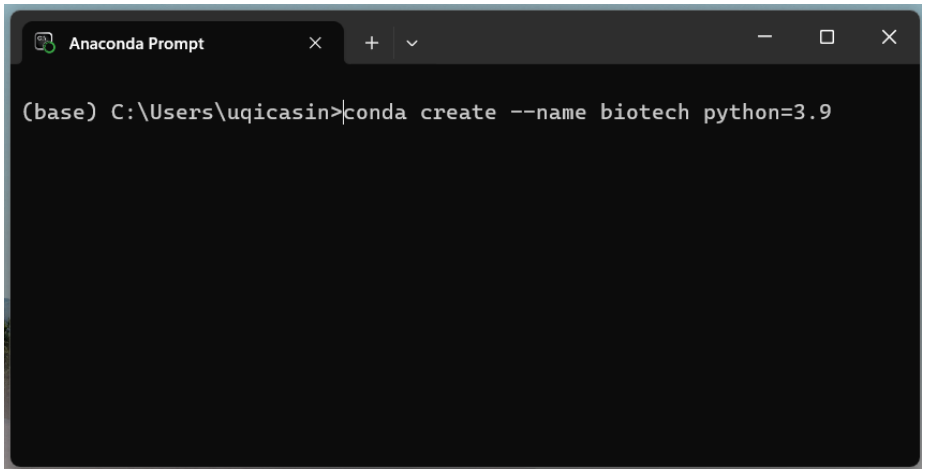
2. Confirm where Conda is installed.
    a. In my Windows installation: **C:\Users\uqicasin\AppData\Local\miniconda3**
    b. Note: AppData is a hidden folder

2. Create a Conda Environment

1. Open the **Anaconda Prompt**. The icon looks like this: 
    a. You should see the directory you’re in (**C:\Users\uqicasin**) and your Python base or starting environment (**base**) to the left.

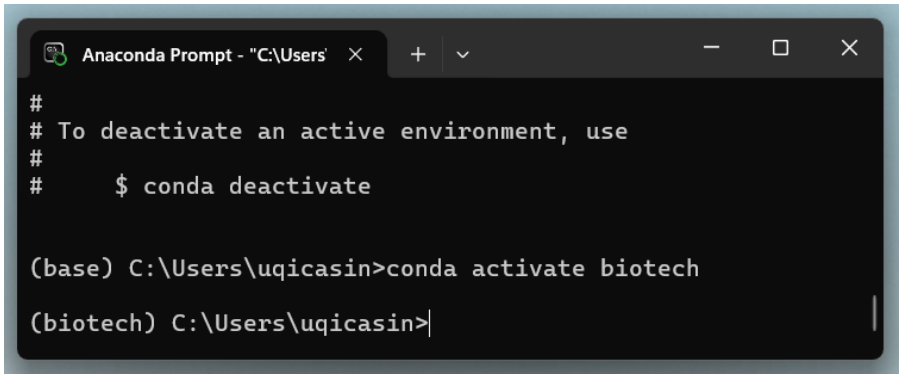


2. Create a new Python environment, called “biotech”: paste the following command and hit “**Enter**”.
    a. `conda create --name biotech python=3.9`



b. You will be asked the following question: “Proceed ([y]/n)?
   i. The default response is “y” or yes.
   ii. Type “**`y`**” and hit “**Enter**”

3. Activate your new environment: paste the following command and hit “**Enter**”.
   a. **`conda activate biotech`**
   b. You should see that your environment has changed from “base” to “biotech”.



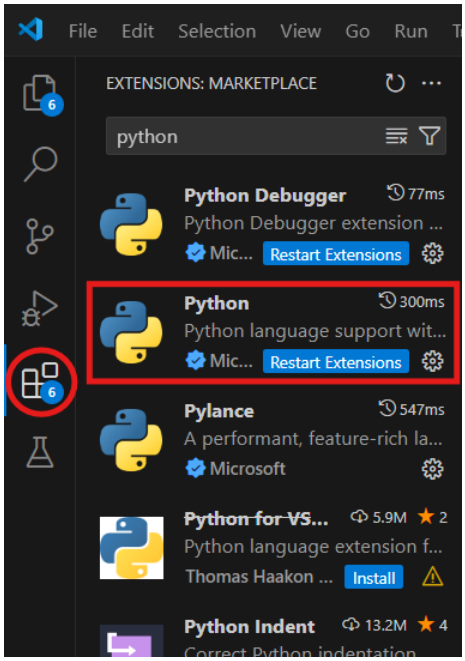
4. Install packages of interest (pandas, numpy, matplotlib, jupyter): paste the following commands and hit “**Enter**”.
   a. **`conda install pandas numpy matplotlib`**
   b. **`conda install jupyter`**
   c. You will be asked the following question: “Proceed ([y]/n)?
      i. The default response is “y” or yes.
      ii. Type “**`y`**” and hit “**Enter**”
   d. Note: additional packages will be automatically installed for our packages of interest to function.
5. Check that your packages were installed: paste the following command and hit “Enter”.
   a. **`conda list`**

6. Make sure your environment is visible through Jupyter Notebook: paste the following command and hit "**Enter**".
    a. `python -m ipykernel install --user --name biotech --display-name "Python(biotech)"`

3. Install an IDE: VSCode

An Integrated Development Environment (IDE) has tools for building, editing, debugging, and testing code. We will be using Visual Studio Code (VSCode) because it is free and commonly used. Other options include: Spyder, PyCharm, IDLE.

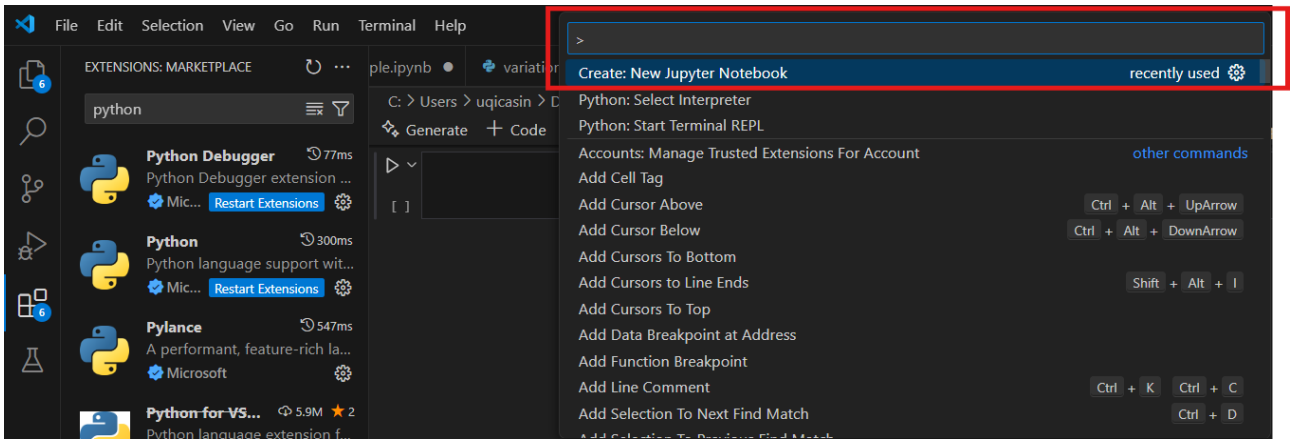
1. Install VSCode for your
    a. https://code.visualstudio.com/Download
2. Install the Python extension (if you have Python installed it may already be there).



    a. Search for the extension
    b. Click "**Install**"
3. Install the following extensions the same way as the previous step:
    a. Python Debugger
    b. Jupyter
    c. Data Wrangler
    d. XML
    e. Rainbow CSV
    f. Prettier - Code formatter

4. Testing Your Setup

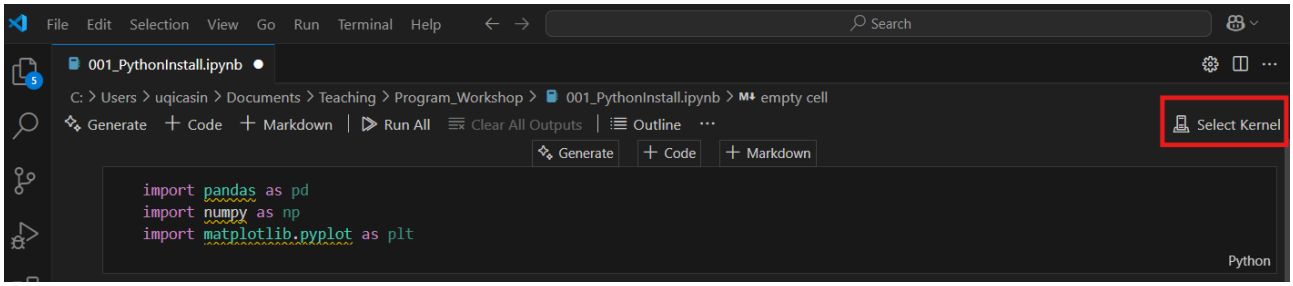
1. In VScode, create a new Jupyter Notebook file:
   a. Click into the search bar at the top of the VScode.
   b. Type "**ctrl**" and "**p**" simultaneously
   c. Then type and click: "**Create: New Jupyter Notebook**"



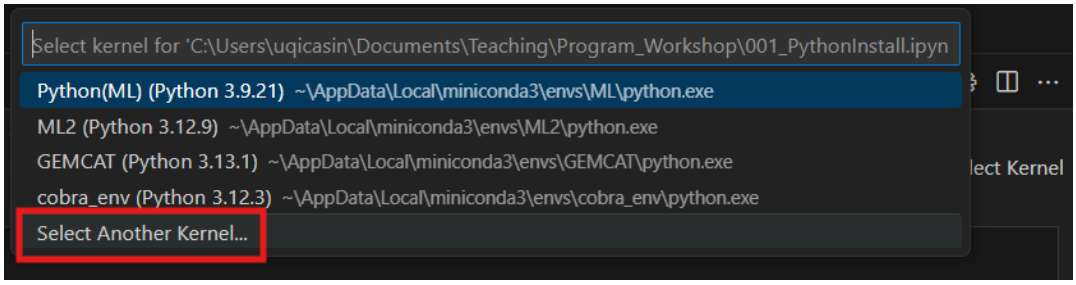
   d. Save your file (File → Save/Save as…)

2. Set the Kernel – we want to set the kernel to your conda environment we made (

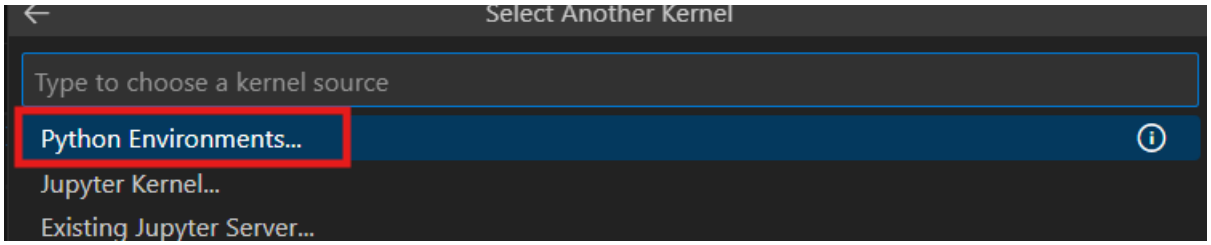
3. **Create a Conda** Environment):
   a. Click "Select Kernel".



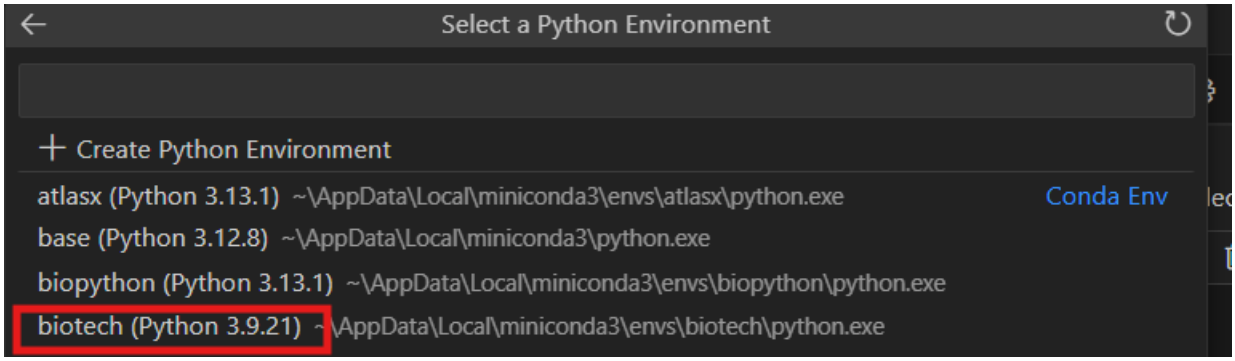
   b. Click "Select Another Kernel"



   c. Click "Python Environments…"



d. Click on the “biotech” environment



4. Type the following code into the first cell to import the packages with their “nicknames”:
   a. `import pandas as pd`
   b. `import numpy as np`
   c. `import matplotlib.pyplot as plt`
5. Execute (run) the first cell by clicking “**Shift**” and “**Enter**” simultaneously.
   a. You should see the set kernel and a green check mark if the cell executed without errors.