

Installing R packages into Anaconda Navigator

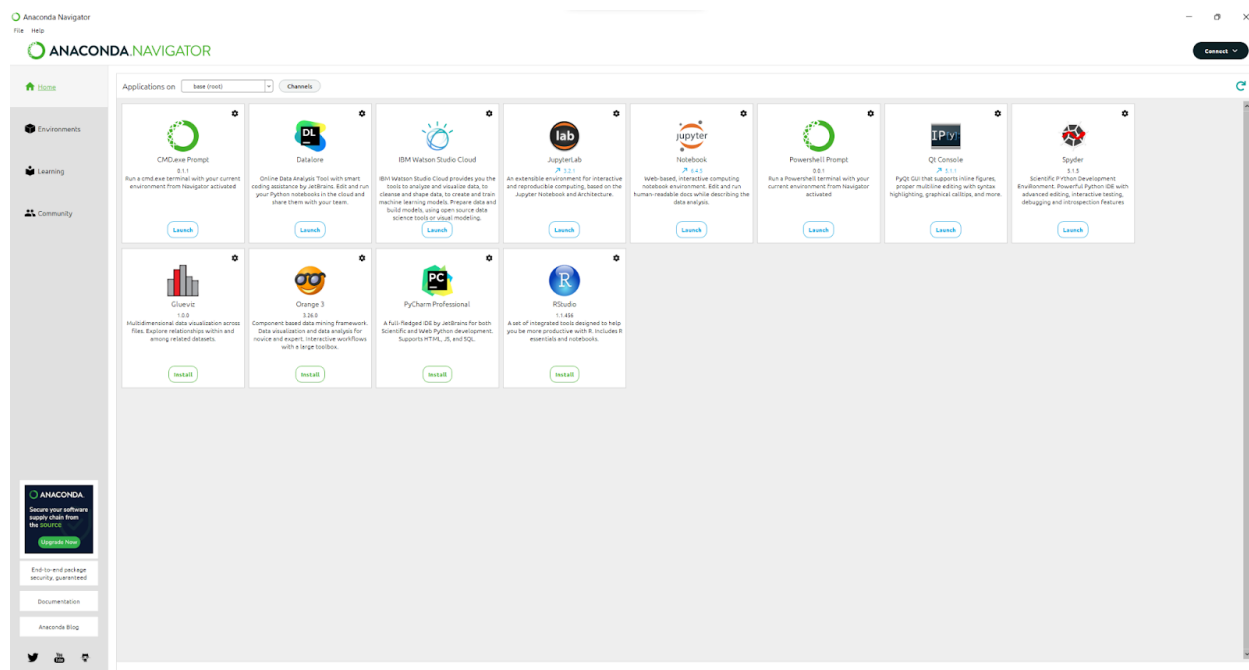
By Abzer Kelminal (abzer.shah@uni-tuebingen.de)

Anaconda is a desktop application that allows the user to launch common python programs without using the command line. <https://www.anaconda.com/>

To install Anaconda on different OS: Windows, MacOS, Linux [Anaconda | Anaconda Distribution](#)

Installation steps: <https://docs.anaconda.com/anaconda/install/windows/>

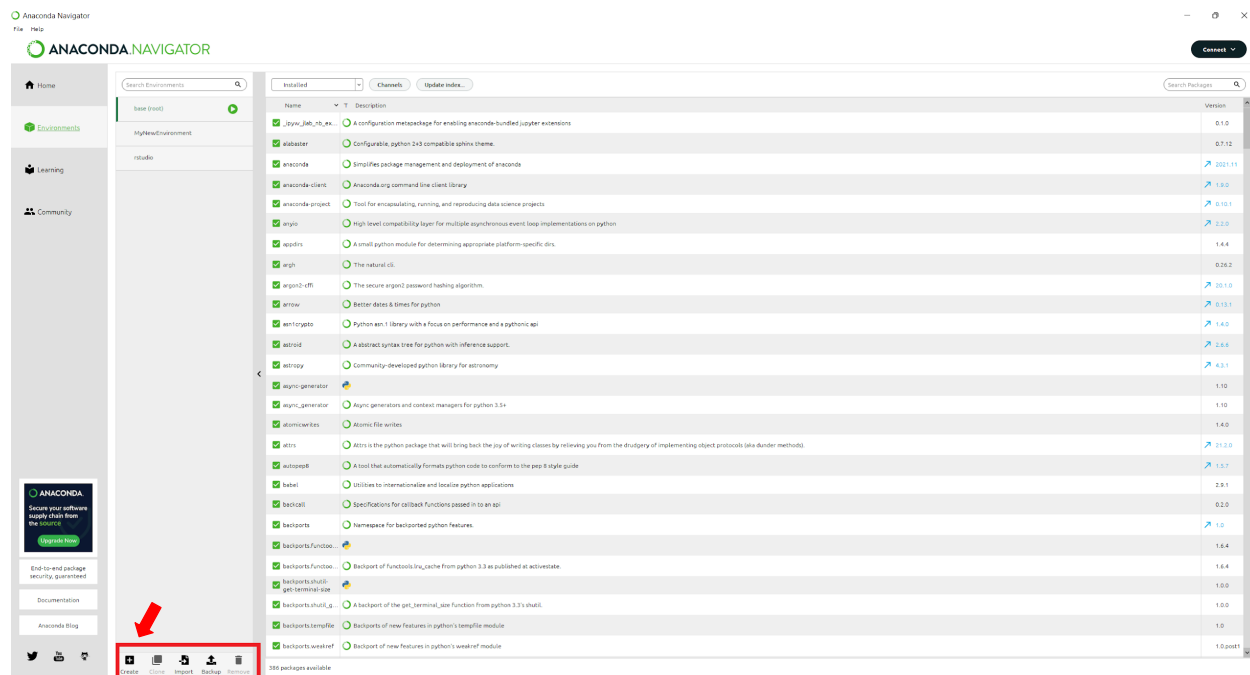
This is how the homepage of Anaconda looks like: You can launch Jupyter Notebooks directly from here.



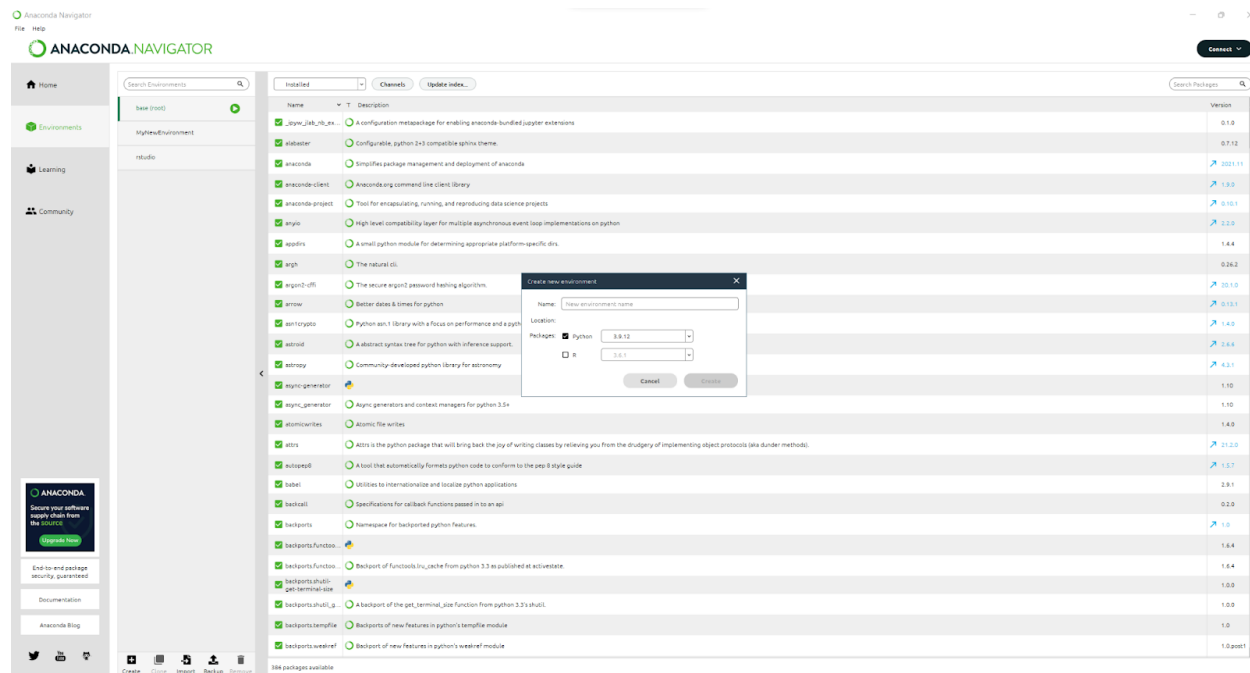
Anaconda, by default, works with Python kernels. In order to run Jupyter notebooks using R code, we need to install R Kernels onto our Anaconda environment.

To install R Kernels:

- 1) Go to the environment and click on 'create' shown on the lower right end of the page



- 2) A new dialog box would open as shown below. Select the R packages and provide a name for the new environment. After a while, the environment would be created.



The screenshot shows a JupyterLab environment with a notebook titled "Metabolomics_MultivariateDataAnalysis". The notebook content includes a title "Multivariate analyses for untargeted metabolomics data" and a byline "By M Ernst". The text describes a workflow for analyzing untargeted metabolomics data using PCA and MDS. A red box highlights the "R" icon in the top right corner of the JupyterLab interface, with a red arrow pointing to it.