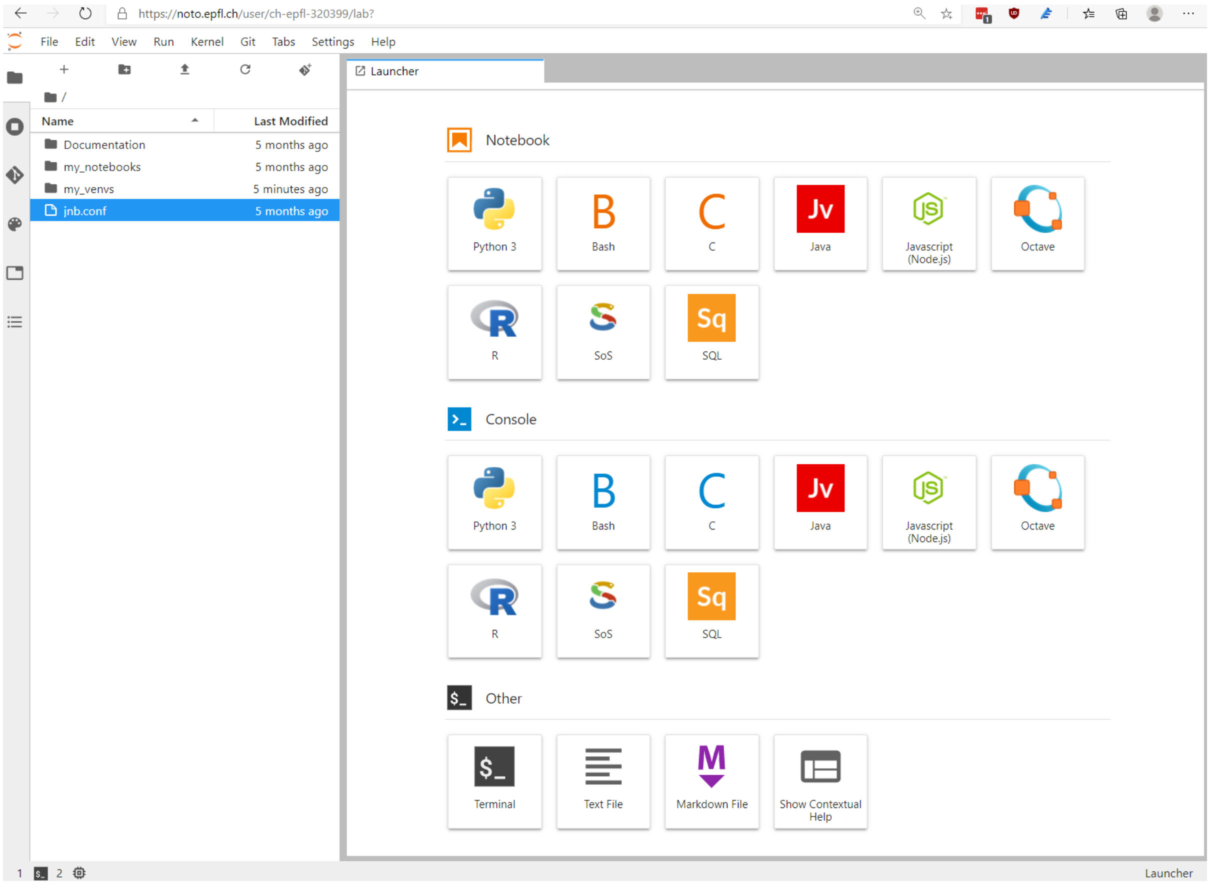
Install and running BIOGEME, a cross-platform solution using https://noto.epfl.ch

Noto is a single use Jupyter notebook webserver hosted on epfl. It is a suitable alternative if you cannot successfully set up biogeme/python on your local computer.

First, go to https://noto.epfl.ch



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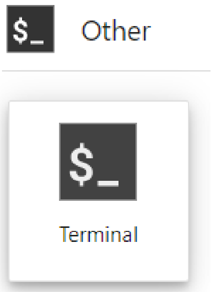
Documentation	5 months ago
my_notebooks	5 months ago
my_venvs	5 minutes ago
jnb.conf	5 months ago

This is the welcome page for a jupyter server hosted on epfl servers for you to use.

Start by activating a Terminal command line:

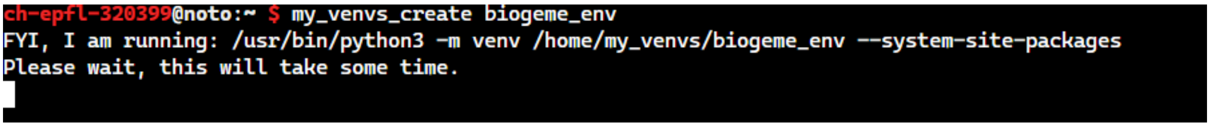


click this

It will take you to a terminal screen. You will need to do the following steps to set up your noto environment to have biogeme working.

```
Welcome to Jupyter!
ch-epfl-320399@noto:~ $
```

Type: `my_venvs_create biogeme_env`

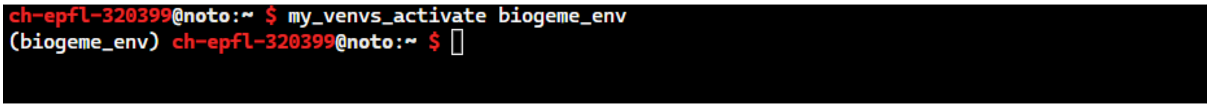


```
ch-epfl-320399@noto:~ $ my_venvs_create biogeme_env
FYI, I am running: /usr/bin/python3 -m venv /home/my_venvs/biogeme_env --system-site-packages
Please wait, this will take some time.
```

A Python virtual environment is created that will host the biogeme installation and the required libraries. You only need to do this installation once, except if the virtual environment is removed, more on that later.

Once it is done, activate the virtual environment:

`my_venvs_activate biogeme_env`

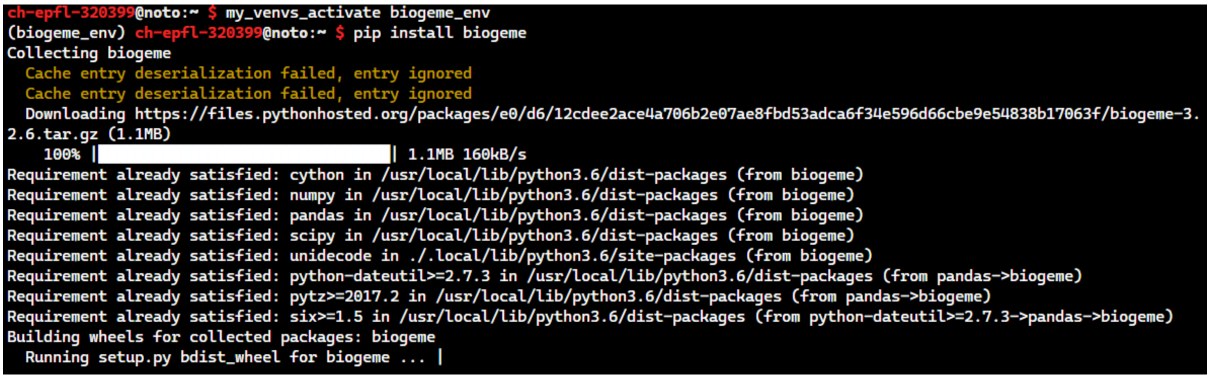


```
ch-epfl-320399@noto:~ $ my_venvs_activate biogeme_env
(biogeme_env) ch-epfl-320399@noto:~ $ 
```

You will have `(your_env_name) ch-epfl-xxxx@noto:~ $` in front of your command line, to indicate that you are in a virtual environment.

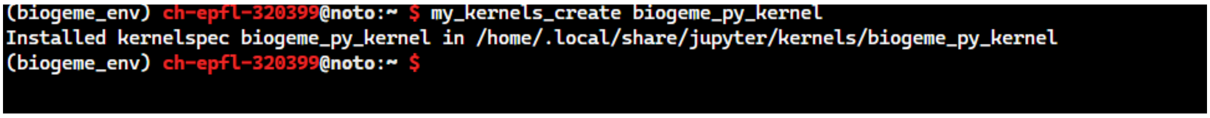
Installing BIOGEME

type `pip install biogeme` in the command line (in your virtual env)



```
ch-epfl-320399@noto:~ $ my_venvs_activate biogeme_env
(biogeme_env) ch-epfl-320399@noto:~ $ pip install biogeme
Collecting biogeme
  Cache entry deserialization failed, entry ignored
  Cache entry deserialization failed, entry ignored
  Downloading https://files.pythonhosted.org/packages/e0/d6/12cdee2ace4a706b2e07ae8fbd53adca6f34e596d66cbe9e54838b17063f/biogeme-3.
2.6.tar.gz (1.1MB)
    100% |████████████████████████████████| 1.1MB 160kB/s
Requirement already satisfied: cython in /usr/local/lib/python3.6/dist-packages (from biogeme)
Requirement already satisfied: numpy in /usr/local/lib/python3.6/dist-packages (from biogeme)
Requirement already satisfied: pandas in /usr/local/lib/python3.6/dist-packages (from biogeme)
Requirement already satisfied: scipy in /usr/local/lib/python3.6/dist-packages (from biogeme)
Requirement already satisfied: unidecode in ./.local/lib/python3.6/site-packages (from biogeme)
Requirement already satisfied: python-dateutil>=2.7.3 in /usr/local/lib/python3.6/dist-packages (from pandas->biogeme)
Requirement already satisfied: pytz>=2017.2 in /usr/local/lib/python3.6/dist-packages (from pandas->biogeme)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.6/dist-packages (from python-dateutil>=2.7.3->pandas->biogeme)
Building wheels for collected packages: biogeme
  Running setup.py bdist_wheel for biogeme ... |
```

Now, create a custom kernel for biogeme, type: `my_kernels_create biogeme_py_kernel` (you can use any name you want)

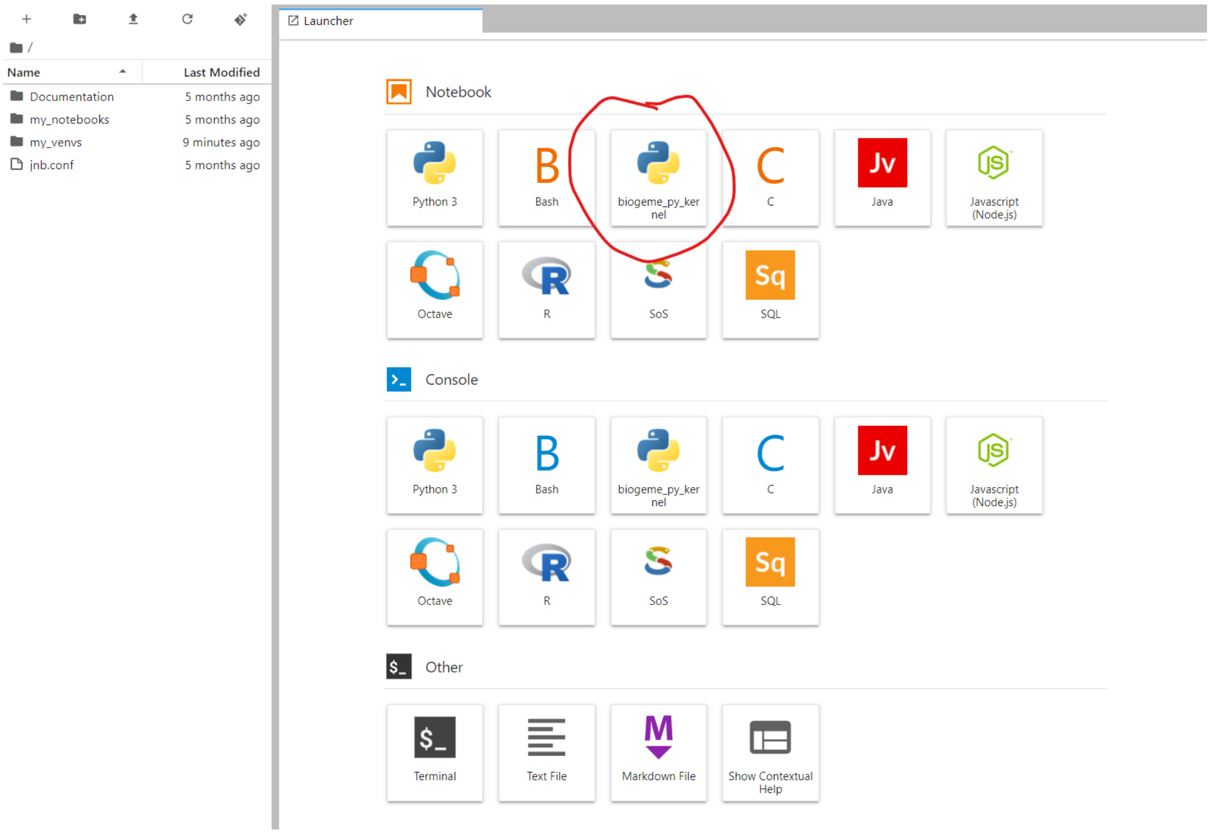


```
(biogeme_env) ch-epfl-320399@noto:~ $ my_kernels_create biogeme_py_kernel
Installed kernelspec biogeme_py_kernel in /home/.local/share/jupyter/kernels/biogeme_py_kernel
(biogeme_env) ch-epfl-320399@noto:~ $
```

At this point, your new kernel is created. Now REFRESH your web browser and a new kernel will show on your welcome page. To go back to the welcome page, close all your notebooks and terminal or click the "+" on the top left corner

Starting a new kernel

Click on the kernel you have just created to start a biogeme kernel



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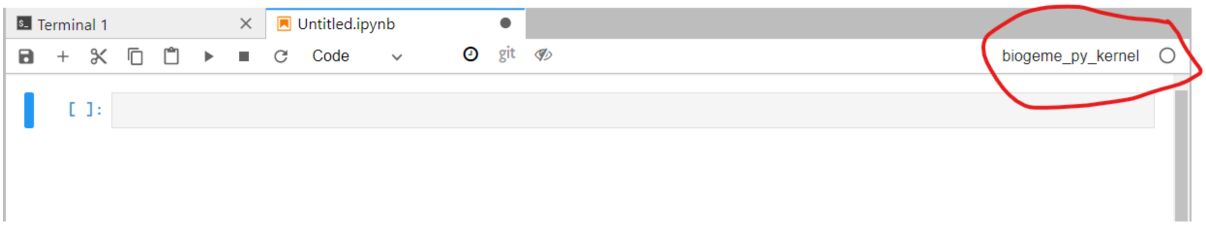
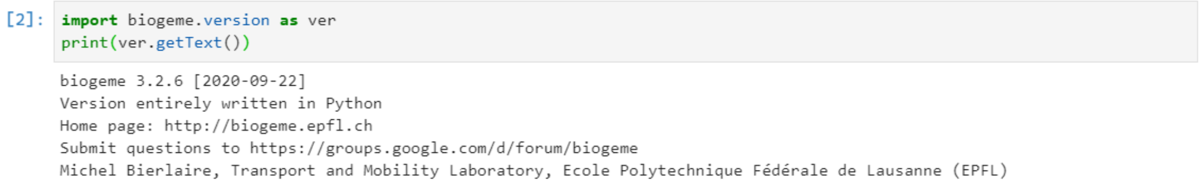
Name	Last Modified
Documentation	5 months ago
my_notebooks	5 months ago
my_venvs	9 minutes ago
jnb.conf	5 months ago

You will now see that the notebook is running in the "biogeme_py_kernel" Python environment, which means it has the biogeme package installed



Type:

```
import biogeme.version as ver
print(ver.getText())
```



```
[2]: import biogeme.version as ver
     print(ver.getText())

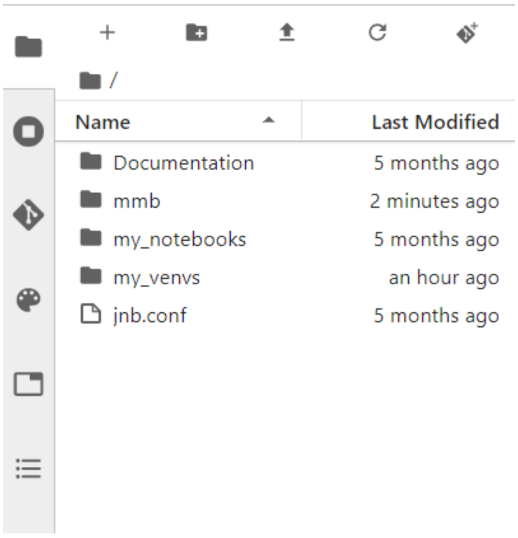
     biogeme 3.2.6 [2020-09-22]
     Version entirely written in Python
     Home page: http://biogeme.epfl.ch
     Submit questions to https://groups.google.com/d/forum/biogeme
     Michel Bierlaire, Transport and Mobility Laboratory, Ecole Polytechnique Fédérale de Lausanne (EPFL)
```

If you see the output above, you have successfully set up biogeme on noto!

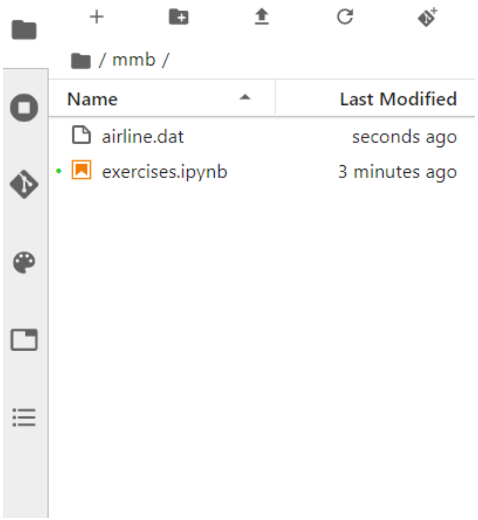
Note: noto is not a “google drive”, your work is saved on the EPFL server, but you may lose your work if the noto server is reset/corrupted on the server side (not in our control). ALWAYS SAVE YOUR WORK ON YOUR LOCAL COMPUTER (just in case)!

For information on how to use python/biogeme on Jupyter refer to https://jupyterlab.readthedocs.io/en/stable/

Hints: It is a good idea to organize your course folder to store your scripts/data/exercises. Create a folder e.g. “mmb” in the main noto directory:



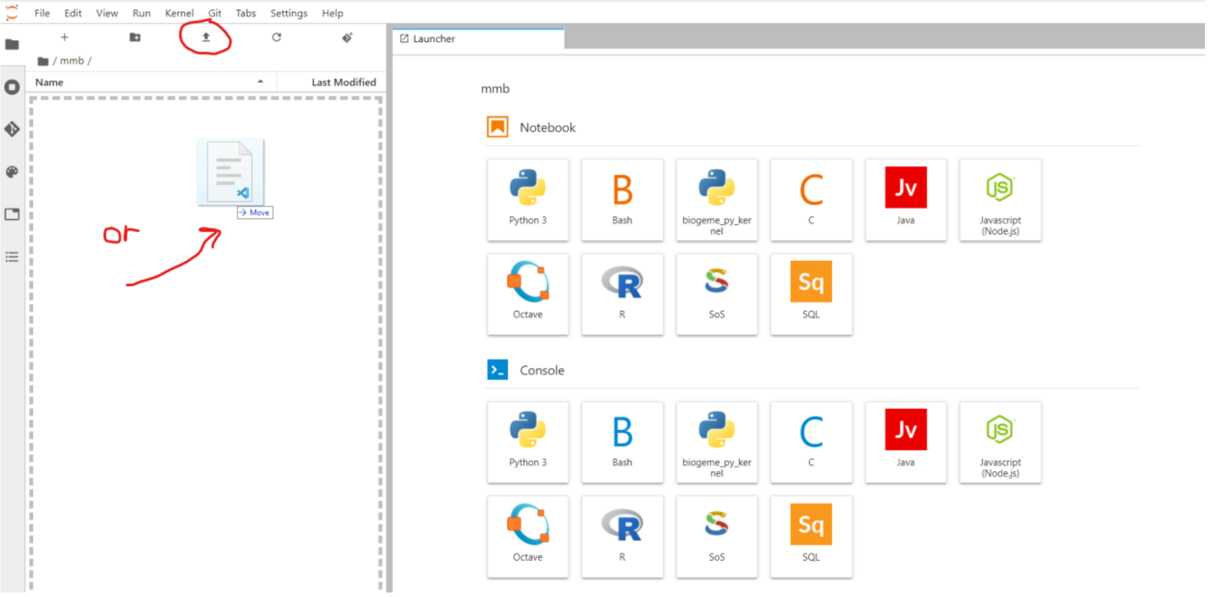
Name	Last Modified
Documentation	5 months ago
mmb	2 minutes ago
my_notebooks	5 months ago
my_venvs	an hour ago
jnb.conf	5 months ago



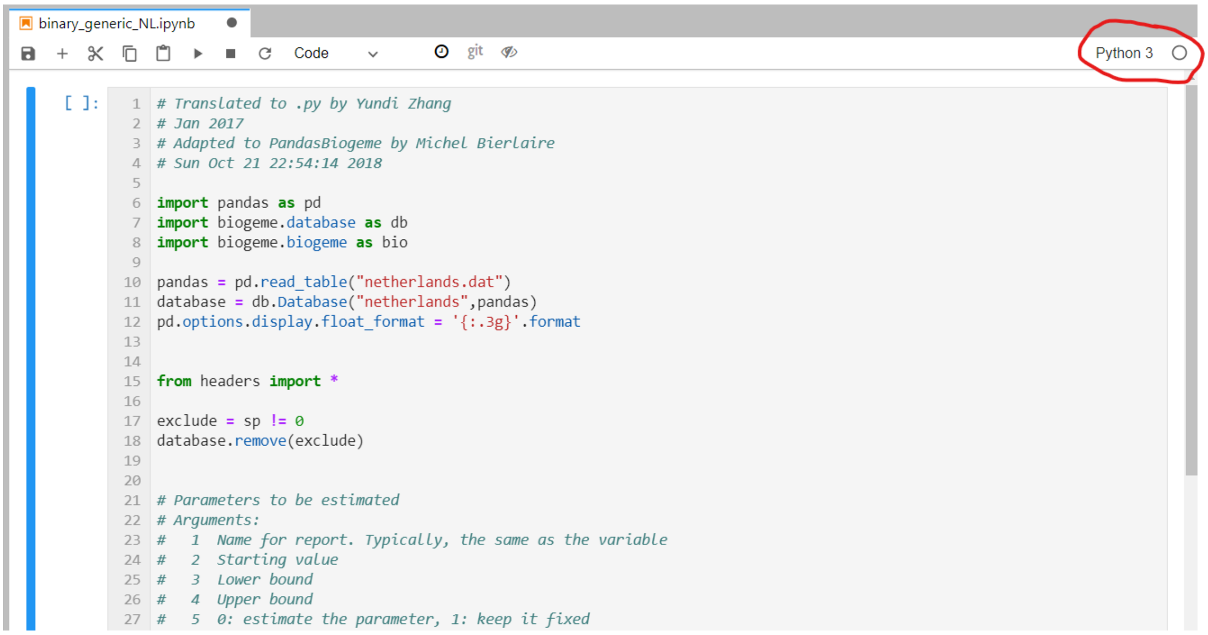
Name	Last Modified
airline.dat	seconds ago
exercises.ipynb	3 minutes ago

Importing your .ipynb files into noto

Running biogeme on your .ipynb files in noto can be done by dragging your files into the directory panel or by the upload button on the top right



Open your imported .ipynb file and change the kernel to the biogeme kernel that you have created



```
# Translated to .py by Yundi Zhang
# Jan 2017
# Adapted to PandasBiogeme by Michel Bierlaire
# Sun Oct 21 22:54:14 2018

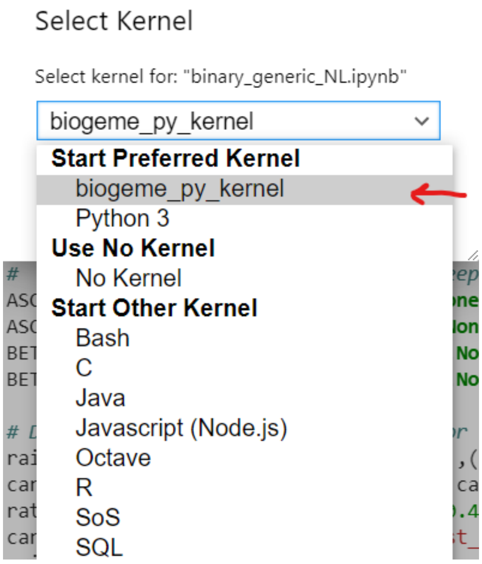
import pandas as pd
import biogeme.database as db
import biogeme.biogeme as bio

pandas = pd.read_table("netherlands.dat")
database = db.Database("netherlands",pandas)
pd.options.display.float_format = '{:.3g}'.format


from headers import *

exclude = sp != 0
database.remove(exclude)

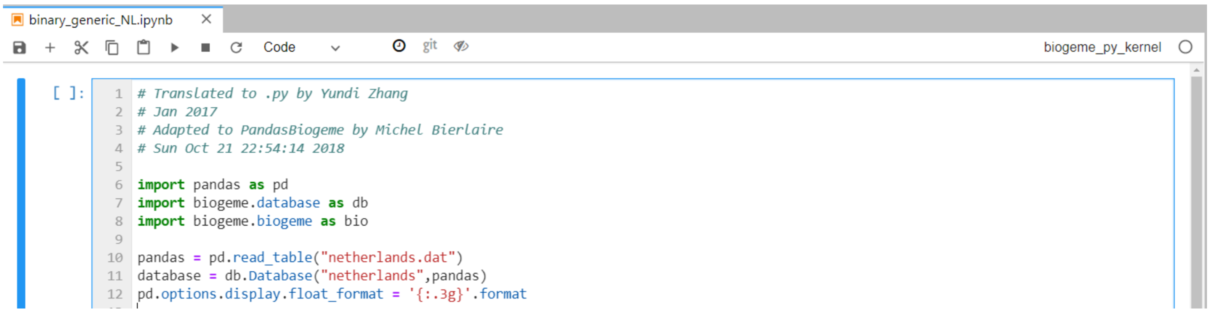

# Parameters to be estimated
# Arguments:
#   1  Name for report. Typically, the same as the variable
#   2  Starting value
#   3  Lower bound
#   4  Upper bound
#   5  0: estimate the parameter, 1: keep it fixed
```



Select Kernel

Select kernel for: "binary_generic_NL.ipynb"

biogeme_py_kernel



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import pandas as pd
import biogeme.database as db
import biogeme.biogeme as bio

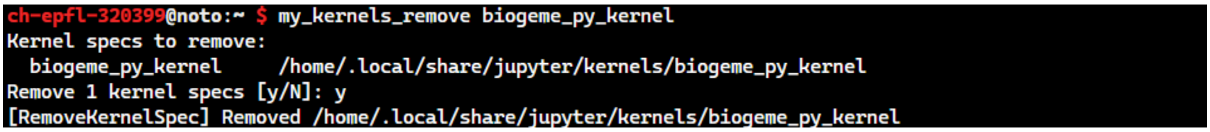
pandas = pd.read_table("netherlands.dat")
database = db.Database("netherlands",pandas)
pd.options.display.float_format = '{:.3g}'.format
```

It should display the right kernel which links the notebook to the correct Python virtual env with biogeme installed.

Other helpful commands

To remove kernel (in case you want to restart everything, this won’t remove your files), in terminal:

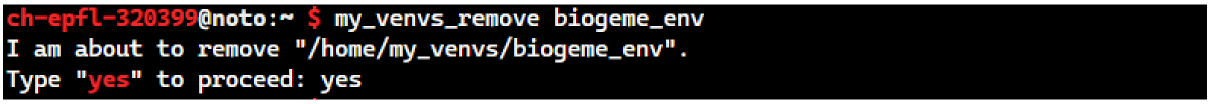
`my_kernels_remove the_name_of_your_kernel`



```
ch-epfl-320399@noto:~ $ my_kernels_remove biogeme_py_kernel
Kernel specs to remove:
  biogeme_py_kernel     /home/.local/share/jupyter/kernels/biogeme_py_kernel
Remove 1 kernel specs [y/N]: y
[RemoveKernelSpec] Removed /home/.local/share/jupyter/kernels/biogeme_py_kernel
```

To remove your virtual environment:

`my_venvs_remove the_name_of_your_venv`



```
ch-epfl-320399@noto:~ $ my_venvs_remove biogeme_env
I am about to remove "/home/my_venvs/biogeme_env".
Type "yes" to proceed: yes
```