

Windows installation of Connectivity Graphs

The connectivity graphs notebook provides access to information on individual neuron populations as per SCKAN and ApiNATOMY models. The *connectivity_graph.ipynb* allows visualisation of the individual neuron connections and the related anatomical features. The repository containing relevant files can be found below:

<https://github.com/keeran97/connectivity-graph.git>

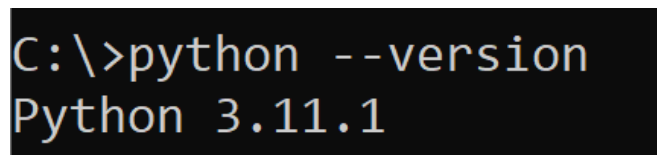
The jupyter notebook can be installed using various command interpreters – e.g. [PowerShell](#), [WSL](#) etc. In this case, the notebook was installed using the [Windows Command Prompt](#).

Requirements

Python

- If not already present, download and install Python as per the [official instructions](#).
- Be sure to select the 'Add Python to PATH' option.
- The installation can be tested with

python --version



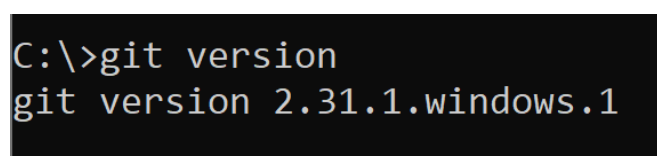
```
C:\>python --version
Python 3.11.1
```

Figure 1: Testing the installation/presence of Python. Note the version may vary with machine.

GitHub

- Download and install Git as per the [official instructions](#).
- Test the installation of Git.
- For more information on using Git refer to this [Git Cheat Sheet](#).

git version



```
C:\>git version
git version 2.31.1.windows.1
```

Figure 2: Testing the installation of Git via the version command. Note the version may vary with machine.

Poetry

- Poetry can be downloaded via the command below.

```
python -m pip install poetry
```

Installation

1. Having installed the requirements, clone the [connectivity-graph repository](https://github.com/keeran97/connectivity-graph).

```
git clone https://github.com/keeran97/connectivity-graph.git
```

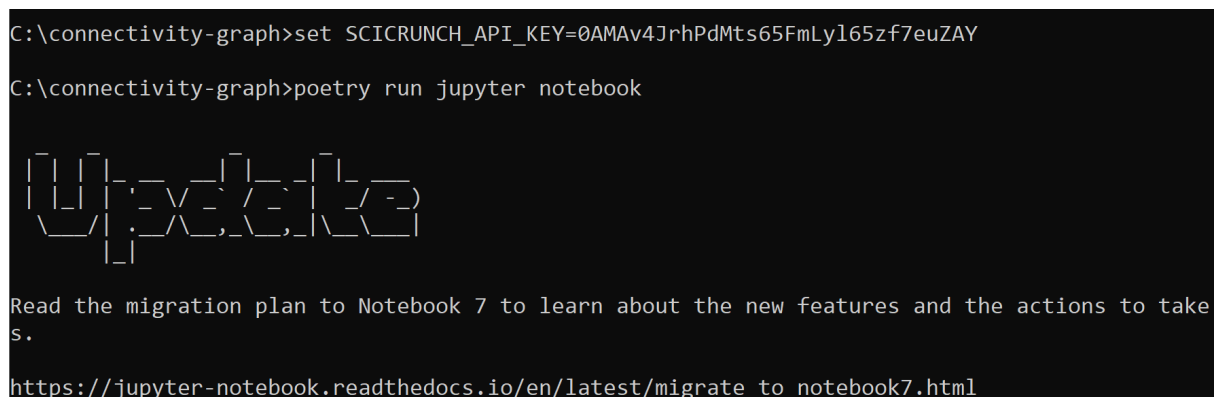
2. Navigate to the connectivity-graph notebook directory and install poetry†.

```
poetry install
```

3. A SciCrunch key will need to be set in order to access SCKAN. For more information on obtaining a SciCrunch API Key follow these [instructions](#).

Note that setting a variable will differ depending on what interpreter is being used. Figure 3 shows setting the SciCrunch key using a Windows Command Prompt.

```
set SCICRUNCH_API_KEY= *A valid SciCrunch API Key*
```



```
C:\connectivity-graph>set SCICRUNCH_API_KEY=0AMAv4JrhPdMts65FmLy165zf7euZAY
C:\connectivity-graph>poetry run jupyter notebook

Jupyter Notebook

Read the migration plan to Notebook 7 to learn about the new features and the actions to take
s.
https://jupyter-notebook.readthedocs.io/en/latest/migrate_to_notebook7.html
```

Figure 3: Setting the SciCrunch API Key in a Windows Command Prompt. This must be done before activating the Jupyter Notebook.

Alternatively, the API Key can be permanently added to the environment by following these [instructions](#).

4. Activate the Jupyter notebook†.

```
poetry run jupyter notebook
```

The jupyter notebook should open in a web browser, as seen in Figure 5.

```
C:\connectivity-graph>poetry run jupyter notebook

Read the migration plan to Notebook 7 to learn about the new features and the actions to take if you are using extensions.
https://jupyter-notebook.readthedocs.io/en/latest/migrate_to_notebook7.html

Please note that updating to Notebook 7 might break some of your extensions.

[I 10:08:59.321 NotebookApp] Serving notebooks from local directory: C:\connectivity-graph
[I 10:08:59.321 NotebookApp] Jupyter Notebook 6.5.4 is running at:
[I 10:08:59.321 NotebookApp] http://localhost:8888/?token=dfbf66493429e7e858a47600fe90eff58d7f711f9548f9d1
[I 10:08:59.336 NotebookApp] or http://127.0.0.1:8888/?token=dfbf66493429e7e858a47600fe90eff58d7f711f9548f9d1
[I 10:08:59.336 NotebookApp] Use Control-C to stop this server and shut down all kernels (twice to skip confirmation).
[C 10:08:59.522 NotebookApp]

To access the notebook, open this file in a browser:
file:///C:/Users/bbal372/AppData/Roaming/jupyter/runtime/nbserver-17012-open.html
Or copy and paste one of these URLs:
http://localhost:8888/?token=dfbf66493429e7e858a47600fe90eff58d7f711f9548f9d1
or http://127.0.0.1:8888/?token=dfbf66493429e7e858a47600fe90eff58d7f711f9548f9d1
0.02s - Debugger warning: It seems that frozen modules are being used, which may
0.00s - make the debugger miss breakpoints. Please pass -Xfrozen_modules=off
0.00s - to python to disable frozen modules.
0.00s - Note: Debugging will proceed. Set PYDEVD_DISABLE_FILE_VALIDATION=1 to disable this validation.
```

Figure 4: Activating the Jupyter notebook. A web browser should open, as shown in Figure 5.

[†] **NOTE:** If steps 2 & 4 fail, Python may need to be invoked.

python -m poetry install

python -m poetry run jupyter notebook

Usage

1. Once successfully installed, start the Jupyter Notebook.

NOTE: If the browser doesn't automatically open, the Notebook can be accessed via the URL, as seen in Figure 3.

2. Navigate to and open the *connectivity_graph.ipynb* notebook.



Figure 5: Opening the connectivity-graph jupyter notebook. The *connectivity_graph.ipynb* file visualises individual neuron populations.

3. Neuron populations can be visualised by running the notebook. The first part of the notebook imports and loads the appropriate packages. The latter part, shown in Figure 6, visualises the neuron population.

ApiNATOMY Models

The different populations can be visualised by changing the *entity* attribute of the Jupyter Notebook, highlighted in Figure 5.

```
In [4]: from pprint import pprint  
entity = 'ilxtr:neuron-type-keast-4'  
(knowledge, graph) = display_connectivity_for_entity(production, entity)  
pprint(knowledge)
```

Figure 6: Changing the entity field (highlighted in the red box) in the jupyter notebook allows visualisation of the different neuron populations.

Table 1 displays the different IDs that can be used. The 'X' represents the path ID. For more information on the different ApiNATOMY models and their neuron populations, refer to the documentation below.

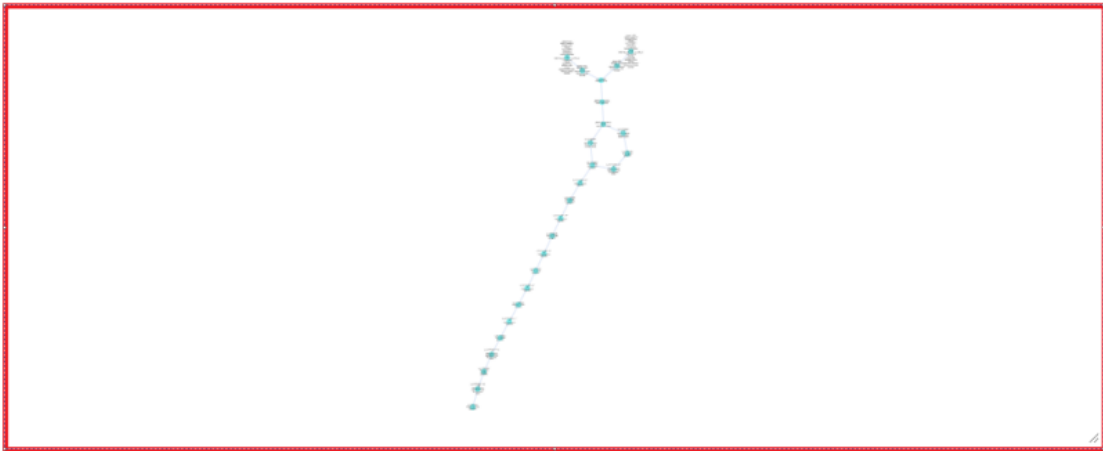
<https://scicrunch.org/sawg/about/SCKAN>

Model	Ilxtr ('X' represents path ID)	Path IDs
ApiNATOMY model of bronchomotor control	neuron-type-bromo-X	1, 2, 3, 4, 5, 6
ApiNATOMY model of the spleen	neuron-type-splen-X	1, 2, 3, 4, 5
ApiNATOMY model of the stomach	neuron-type-sstom-X	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13
Ardell-Armour model of the heart	neuron-type-aacar-X	1, 2i, 2m, 4, 5, 6, 7a, 7v, 8a, 8v, 9a, 9v, 10a, 10v, 11, 12, 13
Bolser-Lewis model of defensive breathing	neuron-type-bolew-unbranched-X	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29
Keast model of the bladder	neuron-type-keast-X	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20
SAWG model of the distal colon	neuron-type-sdcol-X	b, c, d, f, g, h, i, j, j', k, l, l', m, n, o, p, q

Table 1: The different ilxtr IDs for neuron populations.

```
In [4]: from pprint import pprint
```

```
entity = 'ilxtr:neuron-type-keast-4'  
(knowledge, graph) = display_connectivity_for_entity(production, entity)  
pprint(knowledge)
```



```
{'axons': [],  
 'connectivity': [[['ILX:0739296', []], ['ILX:0777092', []]],  
                  [['ILX:0739299', []], ['UBERON:0018675', []]],  
                  [['ILX:0789109', []], ['ILX:0793228', []]],  
                  [['ILX:0777086', []], ['ILX:0739295', []]],  
                  [['ILX:0793559', []], ['kblad:K100', ['UBERON:0001258']]],  
                  [['ILX:0777087', []], ['ILX:0789062', []]],  
                  [['ILX:0777089', []], ['ILX:0788315', []]],  
                  [['ILX:0789062', []], ['ILX:0777088', []]],  
                  [['ILX:0788315', []], ['ILX:0777090', []]],  
                  [['ILX:0739297', []], ['ILX:0739299', []]],  
                  [['UBERON:0018675', []], ['UBERON:0016508', []]],  
                  [['ILX:0793228', []], ['UBERON:0018675', []]],  
                  [['ILX:0777088', []], ['ILX:0786933', []]],  
                  [['ILX:0777093', []], ['ILX:0789109', []]],  
                  [['UBERON:0016508', []], ['ILX:0793559', []]],  
                  [['ILX:0777091', []], ['ILX:0739296', []]],  
                  [['ILX:0787009', []], ['ILX:0777086', []]],  
                  [['kblad:K100', ['UBERON:0001258']],  
                   ['kblad:K105',  
                    ['ILX:0793663',  
                     'kblad:ref_mat_KM_11_K100_3',  
                     'kblad:K100',  
                     'UBERON:0001258']]],  
                  [['kblad:K99', ['UBERON:0006082']],  
                   ['kblad:K106',  
                    ['ILX:0793664',  
                     'kblad:ref_mat_KM_11_K99_3',  
                     'kblad:K99',  
                     'UBERON:0006082']]],  
                  [['ILX:0793559', []], ['kblad:K99', ['UBERON:0006082']]],  
                  [['ILX:0739297', []], ['ILX:0777093', []]],  
                  [['ILX:0739295', []], ['ILX:0777087', []]],  
                  [['ILX:0786933', []], ['ILX:0777089', []]],  
                  [['ILX:0777090', []], ['ILX:0790472', []]]]
```

Figure 7: The section of the `connectivity_graph.ipynb` notebook that visualises neuron populations (highlighted by the red box).

The window that visualises the neuron population can be navigated by left-clicking and dragging, and scrolling to zoom in/out. Note that the window can be resized from the lower right corner.