

Map-tools under Windows

Installation:

Python

- Download and run the installer [here](#), ticking the Add Python to the PATH box when the installation starts.

Git

- Download and run the installer [here](#), accepting all default options.

Poetry

- From the Windows' Start menu, run Git/Git CMD.
- Within the command window, verify Python and git have been installed by giving the commands:

```
git --version  
  
python --version
```

- You should see something like:

```
C:\Users\Dave>git --version  
git version 2.35.1.windows.2  
  
C:\Users\Dave>python --version  
Python 3.10.2
```

- Now run:

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

Map-tools

- Give the command:

```
git clone https://github.com/AnatomicMaps/map-tools.git
```

- followed by:

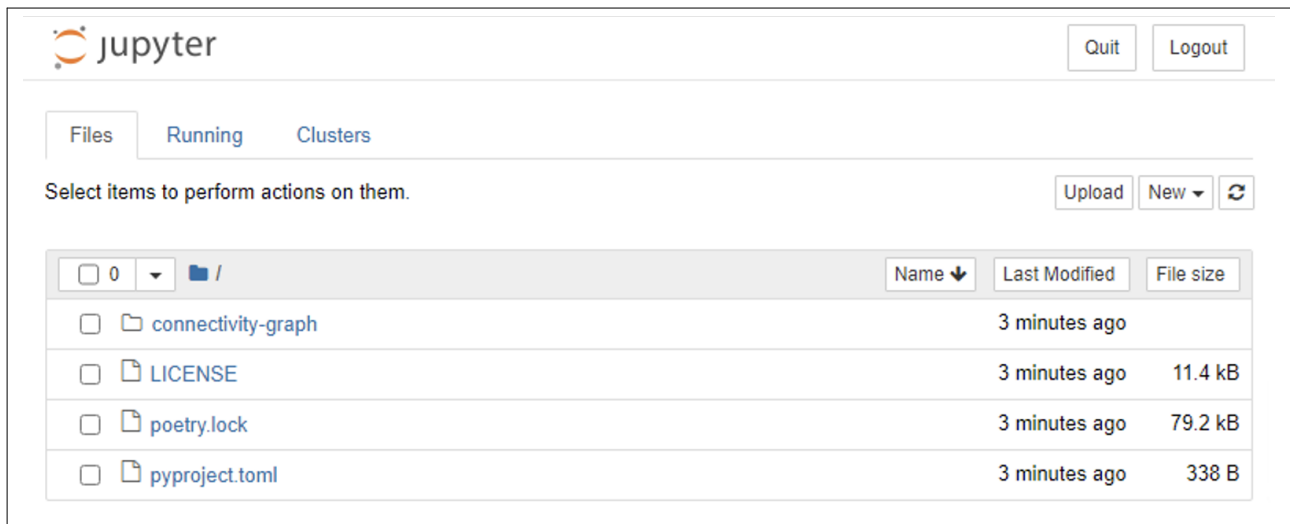
```
cd map-tools  
  
poetry install
```

Running


From the `Git` CMD prompt and in the `map-tools` directory (which is where you are after the above installation process) start the Jupyter notebook server with:

```
poetry run jupyter notebook
```

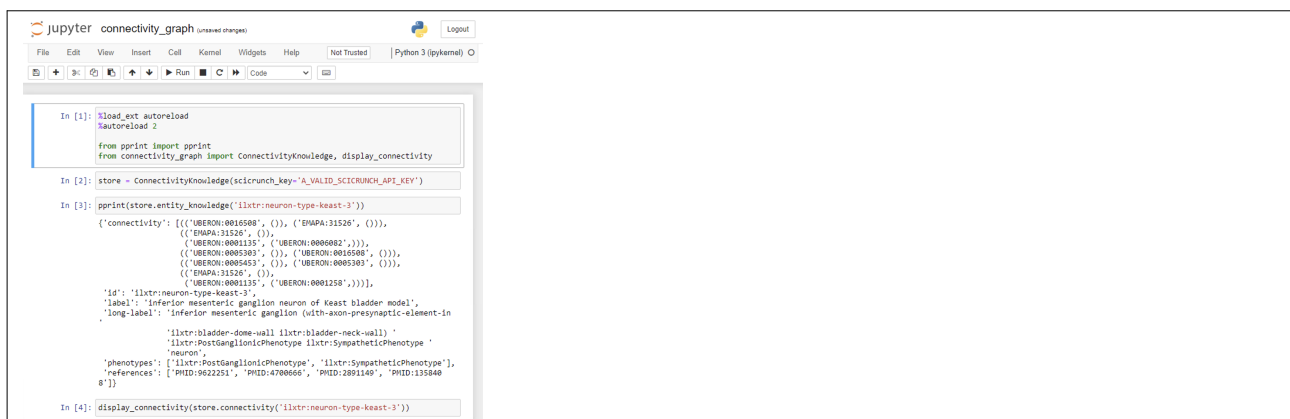
A browser window should open which should eventually show:



Click on `connectivity-graph` to get:



Click on `connectivity_graph.ipynb` to get:



Click **Run** in the toolbar to execute the code in the first cell to get:

```
jupyter connectivity_graph (unsaved changes) Logout
```

```
File Edit View Insert Cell Kernel Widgets Help Not Trusted Python 3 (ipykernel)
```

```
In [1]: %load_ext autoreload
        %autoreload 2

        from pprint import pprint
        from connectivity_graph import ConnectivityKnowledge, display_connectivity
```

```
In [2]: store = ConnectivityKnowledge(scicrunch_key='A_VALID_SCICRUNCH_API_KEY')
```

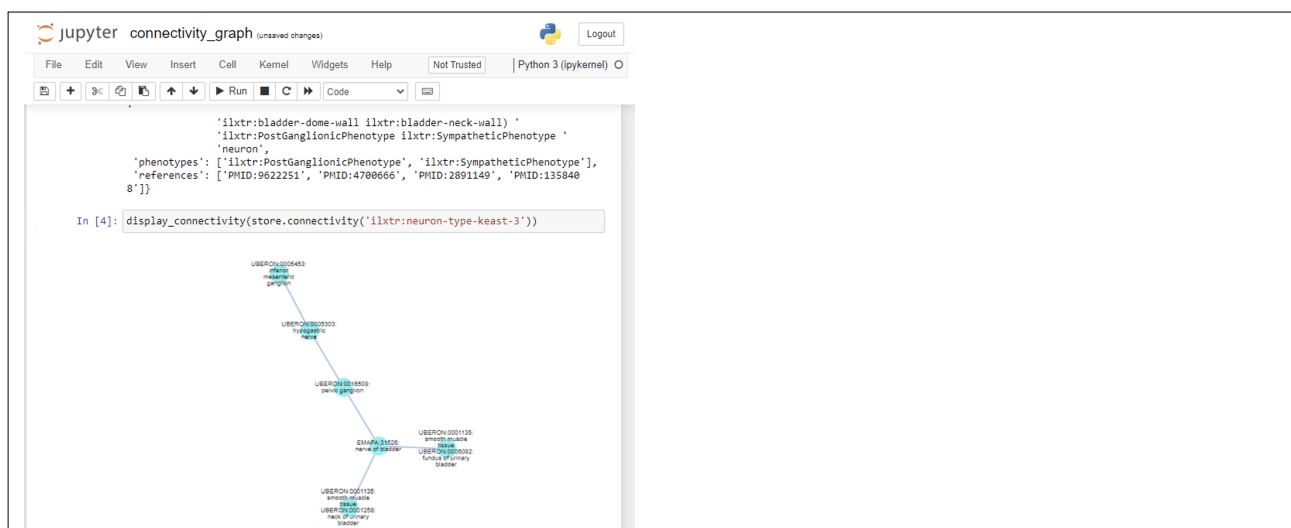
```
In [3]: pprint(store.entity_knowledge('ilxtr:neuron-type-keast-3'))

{'connectivity': [((('UBERON:0016508', ()), ('EMAPA:31526', ())),
                   (('EMAPA:31526', ()),
                    ('UBERON:0001135', ('UBERON:0006082',))),
                   (('UBERON:0005303', ()), ('UBERON:0016508', ())),
                   (('UBERON:0005453', ()), ('UBERON:0005303', ())),
                   (('EMAPA:31526', ()),
                    ('UBERON:0001135', ('UBERON:0001258',)))),
 'id': 'ilxtr:neuron-type-keast-3',
 'label': 'inferior mesenteric ganglion neuron of Keast bladder model',
 'long-label': 'inferior mesenteric ganglion (with-axon-presynaptic-element-in
                'ilxtr:bladder-dome-wall ilxtr:bladder-neck-wall) '
 'ilxtr:PostGanglionicPhenotype ilxtr:SympatheticPhenotype '
 'neuron',
 'phenotypes': ['ilxtr:PostGanglionicPhenotype', 'ilxtr:SympatheticPhenotype'],
 'references': ['PMID:9622251', 'PMID:4700666', 'PMID:2891149', 'PMID:135840
                8']}]
```

Replace `A_VALID_SCICRUNCH_API_KEY` with an actual API key for SciCrunch and click `Run` to execute code in this cell.

The cell number will briefly change to [*] to indicate that code is running and change back to a number when execution is complete. Click **Run** after a cell's code has finished to execute code in the following cell.

The result after the final two cells have been run should be like:



and:

```
models': 'ilxtr:neuron-type-aacar-12'},
{'id': 'ilxtr:neuron-type-aacar-12'},
{'id': 'ilxtr:neuron-type-aacar-10a',
 'models': 'ilxtr:neuron-type-aacar-10a'},
{'id': 'ilxtr:neuron-type-aacar-8v',
 'models': 'ilxtr:neuron-type-aacar-8v'},
{'id': 'ilxtr:neuron-type-aacar-2i',
 'models': 'ilxtr:neuron-type-aacar-2i'},
{'id': 'ilxtr:neuron-type-aacar-9v',
 'models': 'ilxtr:neuron-type-aacar-9v'},
{'id': 'ilxtr:neuron-type-aacar-6',
 'models': 'ilxtr:neuron-type-aacar-6'},
{'id': 'ilxtr:neuron-type-aacar-5',
 'models': 'ilxtr:neuron-type-aacar-5'},
{'id': 'ilxtr:neuron-type-aacar-7a',
 'models': 'ilxtr:neuron-type-aacar-7a'},
{'id': 'ilxtr:neuron-type-aacar-8a',
 'models': 'ilxtr:neuron-type-aacar-8a'}}]]
```

