1 NeoDash User Manual

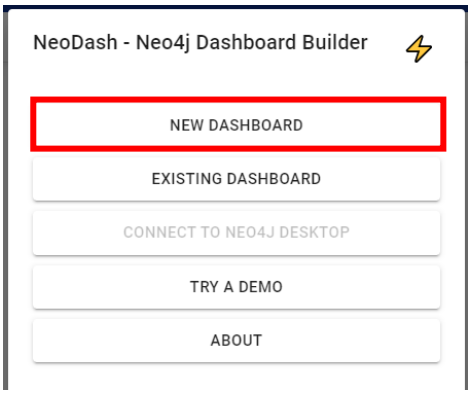
1.1 Loading NeoDash Dashboard File in Web Browser

1. Download the “dashboard.json” using the following link.

   Use right mouse click → Save as… → save the file.

2. Open NeoDash in a web browser.

3. Click on “NEW DASHBOARD”.



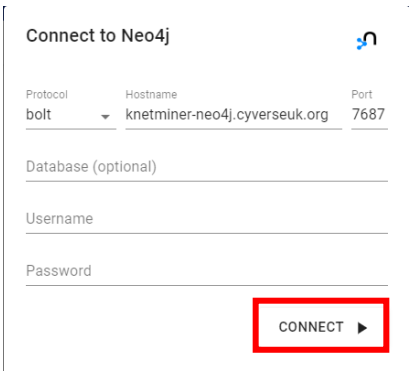
4. Fill the following details as follows:

   a. Protocol: Choose “bolt” from the drop-down menu

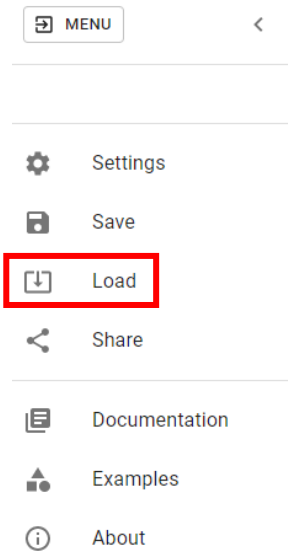
   b. Hostname: knetminer-neo4j.cyverseuk.org

   c. Port: 7687

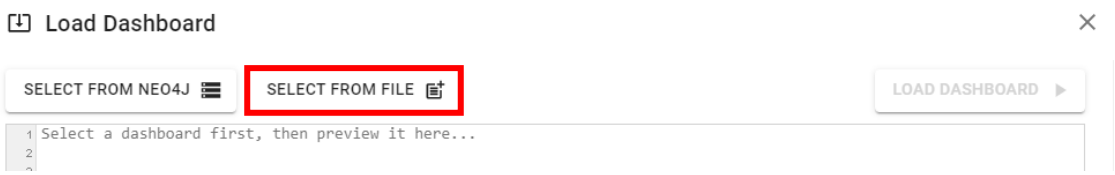
      And click “CONNECT”



5. Click the 3 dashes on the top left side  and click on “Load” from the menu.



6. Click “SELECT FROM FILE”, choose the “dashboard.json” file and click “open”.



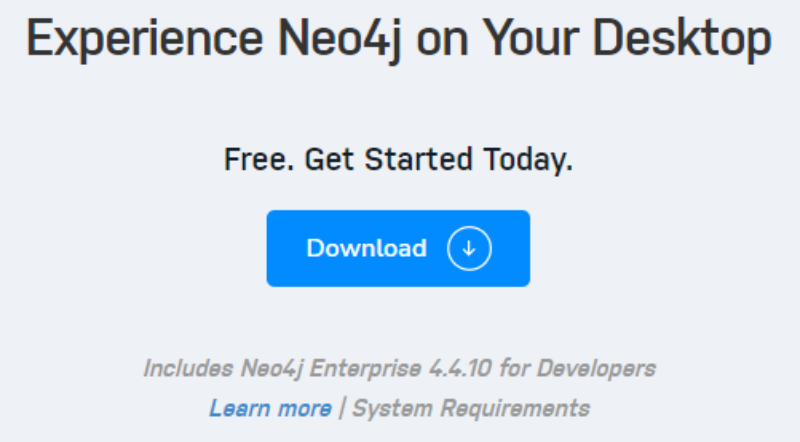
7. Then click on “LOAD DASHBOARD”.

This will load the “KnetMiner Dashboard”.

8. To view the cypher query for each report, click on the 3 dots at the top right of each report box.

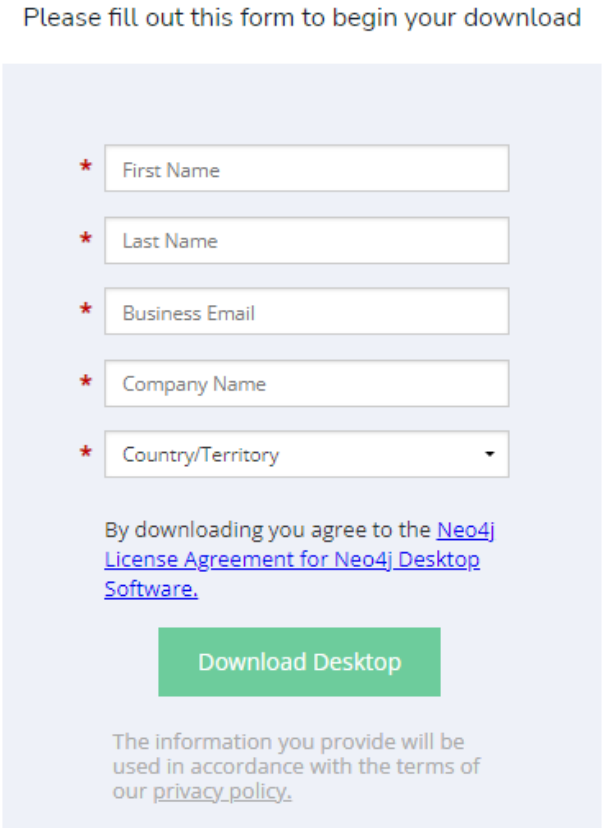
1.2 Loading NeoDash Dashboard File in Neo4j Desktop

1. Download Neo4j from the following link.

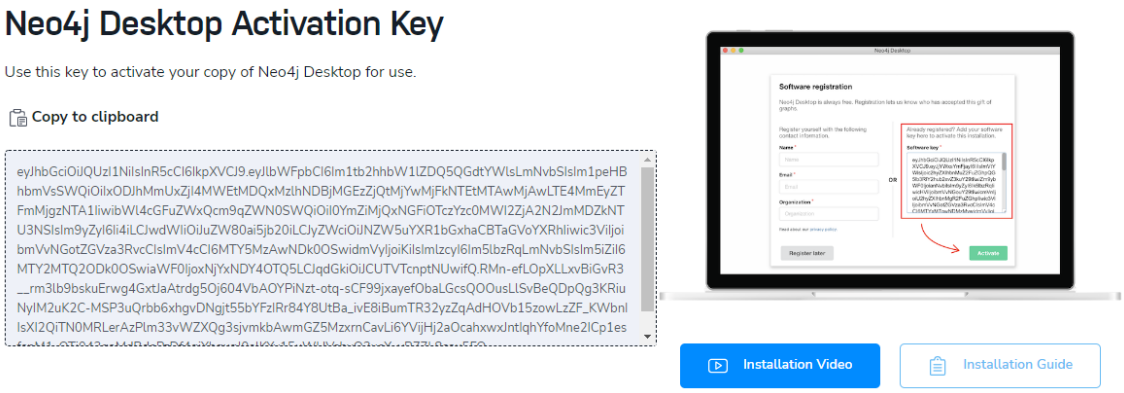


2. Fill the form with your name and email and choose a country. If you don't have a company name, you can just add dot "."

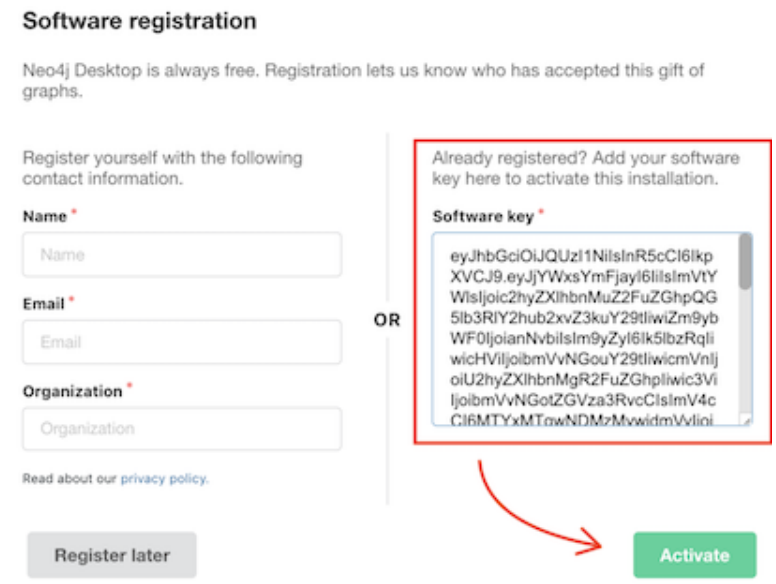
   Then click on "Download Desktop".



3. This will open a new page with the activation key.

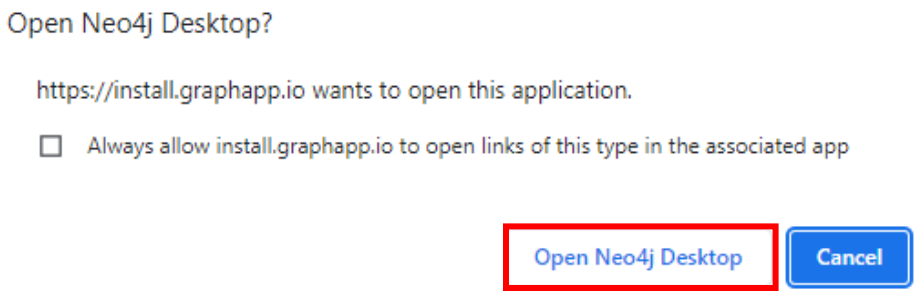


4. After installing Neo4j desktop, copy the activation key and paste it into “Software Key” and click “Activate”.

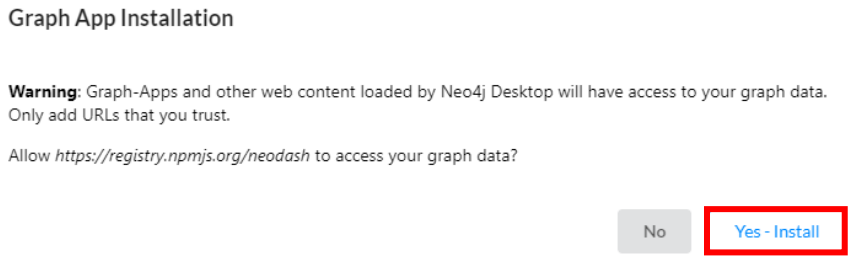


5. Install NeoDash from the following link.

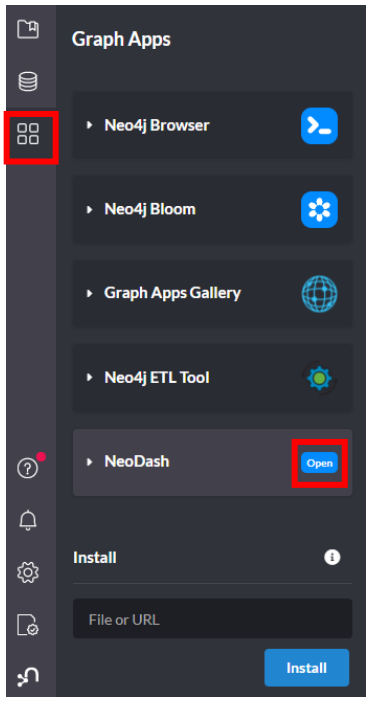
6. This will show a pop-up, click on “Open Neo4j Desktop”.



7. Neo4j will open and ask for confirmation.



8. Click on “Graphs App” button on the left. Then, hover over “NeoDash” and click “Open”.

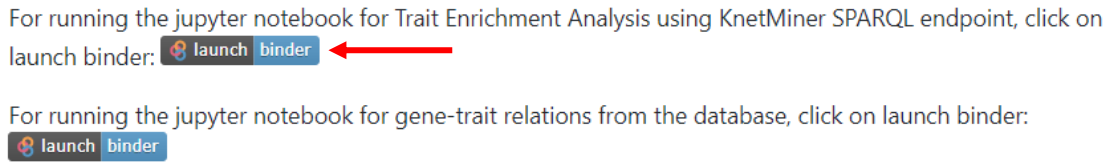


9. This will open a new window for NeoDash. Follow the same steps as section 1.1 to load the dashboard.

2 Jupyter Notebook User Manual

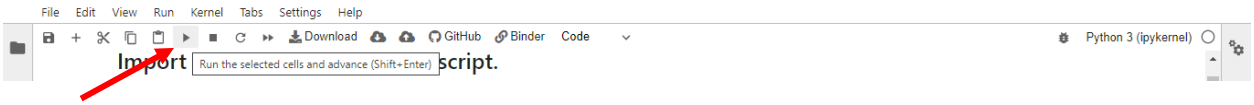
2.1 Launching Jupyter Notebook Using Binder

1. Open the GitHub page.
2. Scroll down to the README.md and click on the “launch binder” badge for the relevant Jupyter Notebook, either for trait enrichment analysis or for gene-trait relations file for all genes of a certain species.

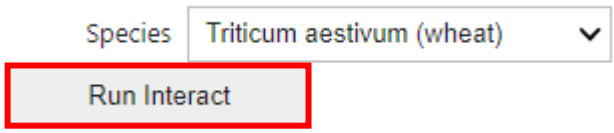


This will open the binder page, which will take some time to load the notebook.

3. In the notebook, click on each cell and run it from the play button above. **Note: it is important to run the cells in order.**



4. Some cells will show an interactive interface to choose from a list. Follow the instructions and after each choice, click on “Run Interact” button.



Notes:

1. The results tables can be downloaded via the download links (as below) or view all rows using the “View whole tables section”.

   Download gene-trait table CSV file

   Download trait enrichment table CSV file

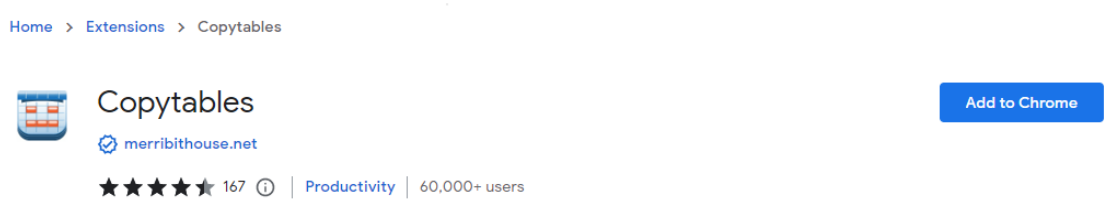
2. In the trait enrichment notebook, you can choose a trait or a gene to view the related genes or traits respectively.

3. You can view the network knowledge graphs that link them using the “View Network” link.

	Gene Accession	Gene Name	Evidence	Network URL
0	TRAESCS2A02G246300	AAO1	TM_1-0	View Network
1	TRAESCS4B02G200600	ABCG17	TM_0-1	View Network
2	TRAESCS3B02G404600	ABI5	TM_0-1	View Network
3	TRAESCS3B02G404600	ABI5	TM_1-0	View Network

4. To copy a list of genes from a table, you can use the [chrome extension Copytables].

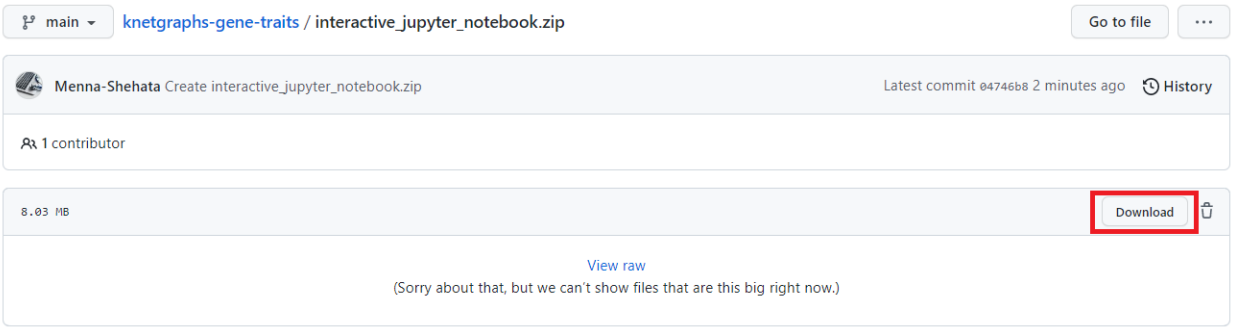
   (This extension works on other browsers as well)



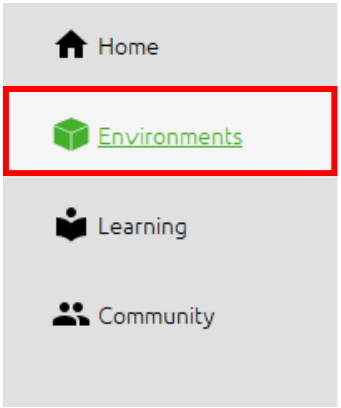
   Use Ctrl + Alt + left click on column heading

2.2 Using Jupyter Notebook on Local Computer

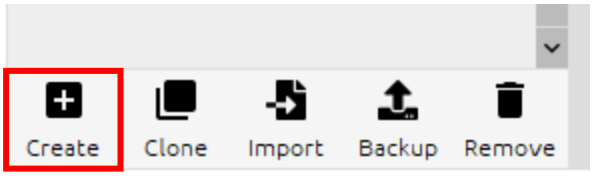
1. Download the zipped folder containing all the files using the GitHub Link. Click on Download.



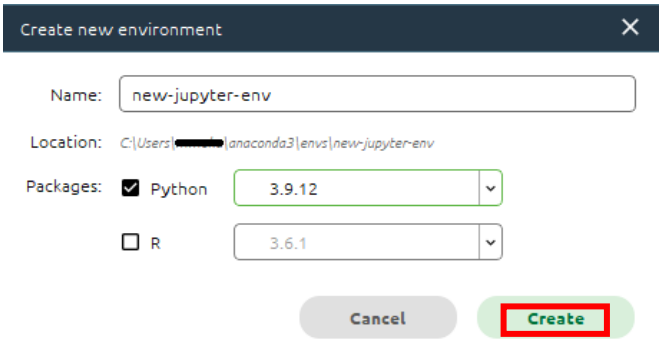
2. Copy all the files to the folder: Local Disk (C:) → Users → (your username).
3. Install Anaconda by choosing your operating system and following installation instructions.
4. Open “Anaconda Navigator” and click on “Environments” in the right panel.



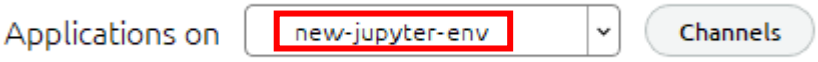
5. Below the list of environments, click on “Create”.



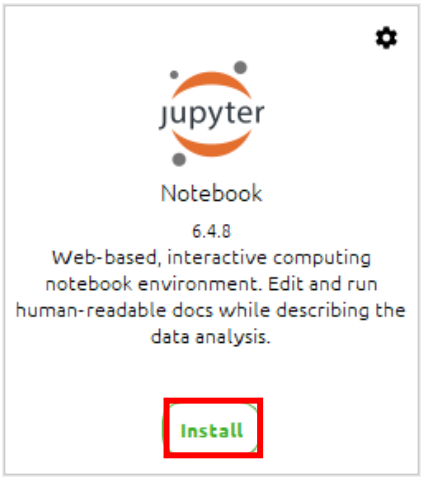
6. Give a name to the new environment, choose python 3.9 from the list and click “Create”. Note the location of the of the environment.



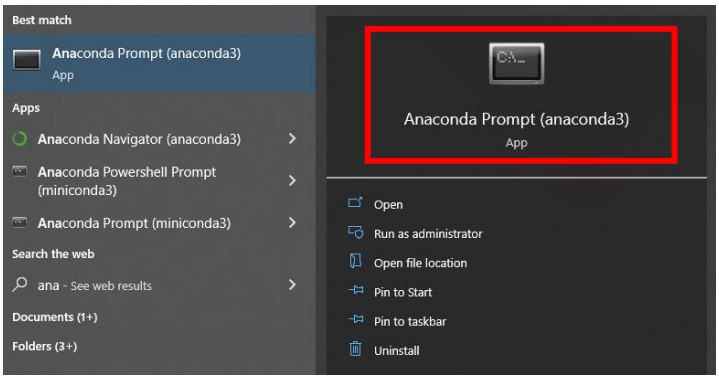
7. After the new environment is created, go back to “Home” from the right panel and choose the newly created environment from the list above.



8. From the application list, install “Jupyter Notebook”.



9. Search on the start menu for “Anaconda Prompt” and open it.



10. Type `conda env list` and copy the pathway to the jupyter environment

```
new-jupyter-env          C:\Users\[redacted]\anaconda3\envs\new-jupyter-env
```

11. Activate environment by typing `activate` and paste the pathway to the environment

```
activate C:\Users\[redacted]\anaconda3\envs\new-jupyter-env
```

Note, for macOS and Linux use: `source activate`

12. Install the libraries:

- Pandas: `conda install pandas`
- SPARQLWrapper: (use one of the following commands)

  ```
  conda install -c conda-forge sparqlwrapper
  conda install -c conda-forge/label/cf201901 sparqlwrapper
  conda install -c conda-forge/label/cf202003 sparqlwrapper
  ```

- SciPy: `conda install -c anaconda scipy`
- IPython widgets: `pip install ipywidgets`
- Activate the widgets:
  `jupyter nbextension enable --py widgetsnbextension`

13. To run the jupyter notebook, type: `jupyter notebook`

14. To deactivate the environment, type: `conda deactivate`

    Note, for macOS and Linux use: `source deactivate`

Notes:

```
C:\Users\[redacted]\anaconda3\envs\new-jupyter-env\lib\site-packages\scipy\__init__.py:146: UserWarning: A NumPy version >=1.16.5 an
d <1.23.0 is required for this version of SciPy (detected version 1.23.1
  warnings.warn(f"A NumPy version >={np_minversion} and <{np_maxversion}"
```

If you get the following error message for **NumPy**, use the following command on anaconda:

```
conda install -c conda-forge numpy=1.22.4
```