# Using the cellxgene browser

Shut down your jupyter lab.

In your command line prompt (within the docker container), type (replace <my\_path> with the path to your data directory):

cellxgene launch /root/host\_home/<my\_path>/data\_annotated.h5ad --port 8888 --host 0.0.0.0

Then, the cellxgene is starting up.

[cellxgene] Starting the CLI...

/opt/python/lib/python3.7/site-packages/anndata/\_core/anndata.py:21: FutureWarning: pandas.core.index is deprecated and will be removed in a future version. The public classes are available in the top-level namespace.

from pandas.core.index import RangeIndex

[cellxgene] Loading data from data\_processed.h5ad, this may take a while...

[cellxgene] Launching! Please go to http://0.0.0.0:8888 in your browser.

Copy the prompted URL to a browser window. (Under Windows, we experienced problems with the localhost path. If the cellxgene browser does not start, try replacing “0.0.0.0” with “localhost” or “127.0.0.1” in your browser window.)

Then, a pop-up window requests a file name for any personal data annotation file. Enter a name.

If you continue to experience issues with the browser or you used Google Colabs before, please have a look at the prepared cellxgene browsers:

3k PBMC single-cell RNA-seq data:

URL (accessible within the HMGU network): http://biocore.scidom.de:32837

Username: scanpy\_course

Password: 3k\_PBMC

Try the following things on:

1. Color the data by gene count.
2. Color the data by cell type annotation.
3. Examine the gene expression of your favourite gene.
4. Examine the gene expression of your second favourite gene.
5. Create a scatter plot of both genes (select “plot x” and “plot y” on the right-hand side).
6. Select only cells that express your favourite gene.
7. Deselect all cells.
8. Select only NK cells.
9. Select only NK cells which form are separate cluster and add the selection to ‘1:’ (top panel).
10. Select only NK cells which are adjacent to T cells and add the selection to ‘2:’ (top panel).
11. How many cells have you selected?
12. Run a differential expression test on the selected groups.
13. Look at the top 10 differentially expressed genes.
14. Change the 2D visualisation to a different embedding.
15. Use the lasso tool to select cells and display your favourite gene.
16. Keep the selection from the previous step and check the histogram plots in the right panel.
17. Explore.
18. More inspiration: <https://chanzuckerberg.github.io/cellxgene/posts/gallery>

You can also have a look at the cellxgene browser of a previous course (human brain single-nucleus RNA-seq data):

URL (accessible within the HMGU network): http://biocore.scidom.de:32815

Username: scanpy\_course

Password: sn\_brain