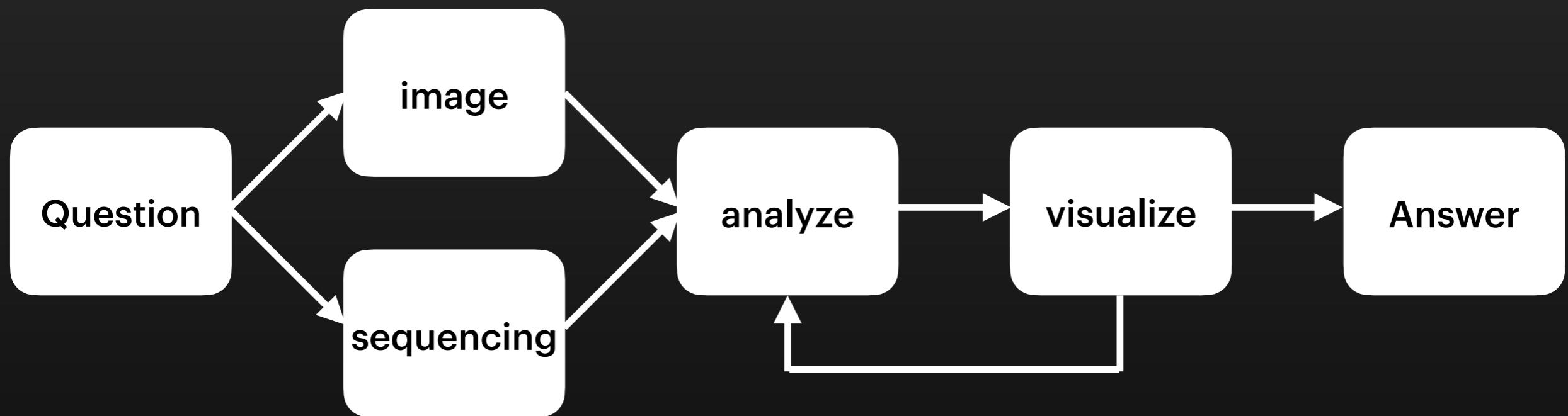


Interactive spatial-omics analysis

Kevin Yamauchi
ETH Zürich

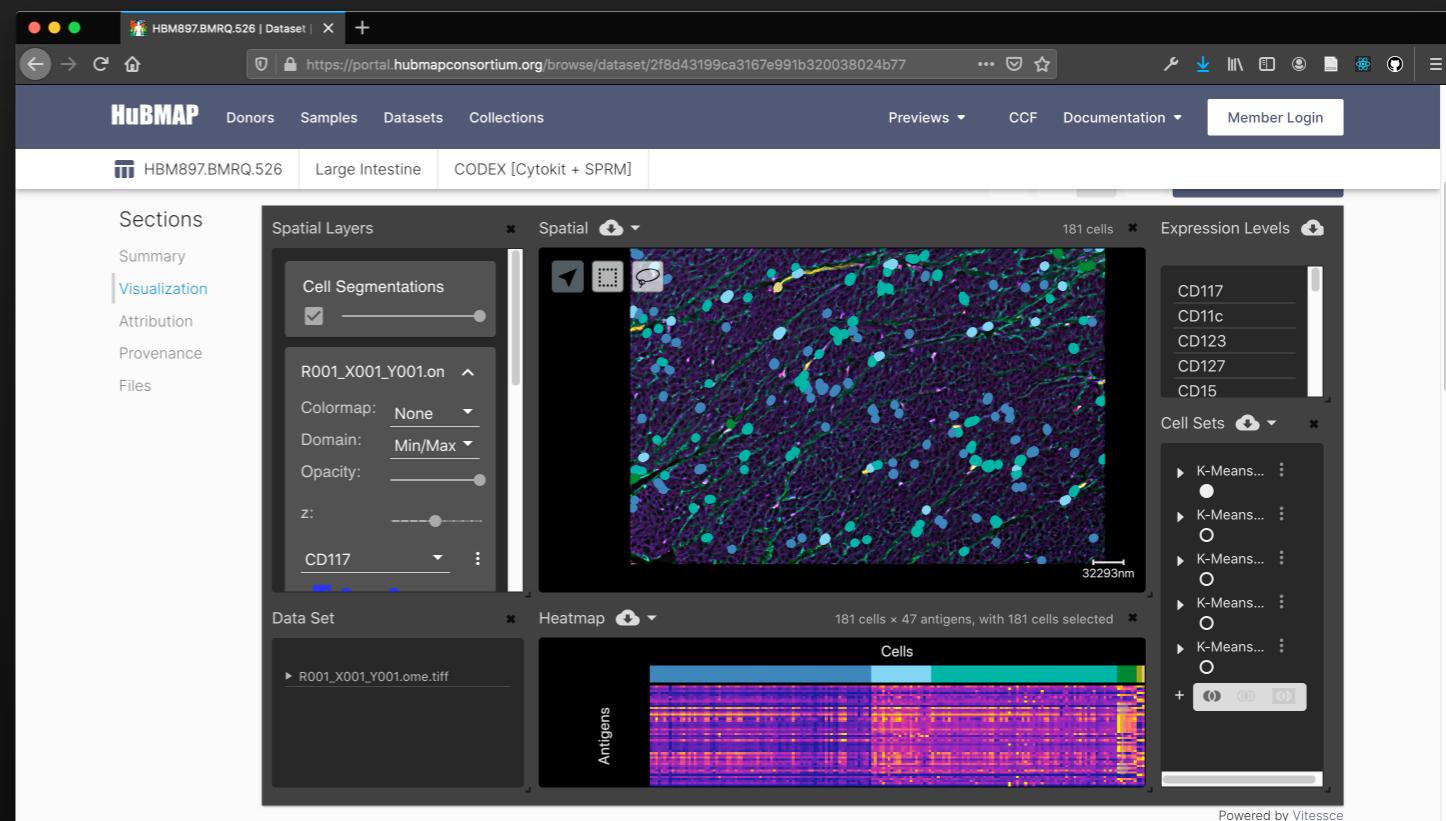
Interactive analysis of spatial-omics data



Vitessce is a performant, web-based spatial single cell sequencing exploration tool



- Client-side rendering
- Overlay annotations on images
- Good for exploration and viewing
- Cannot make annotations and use them in your analysis

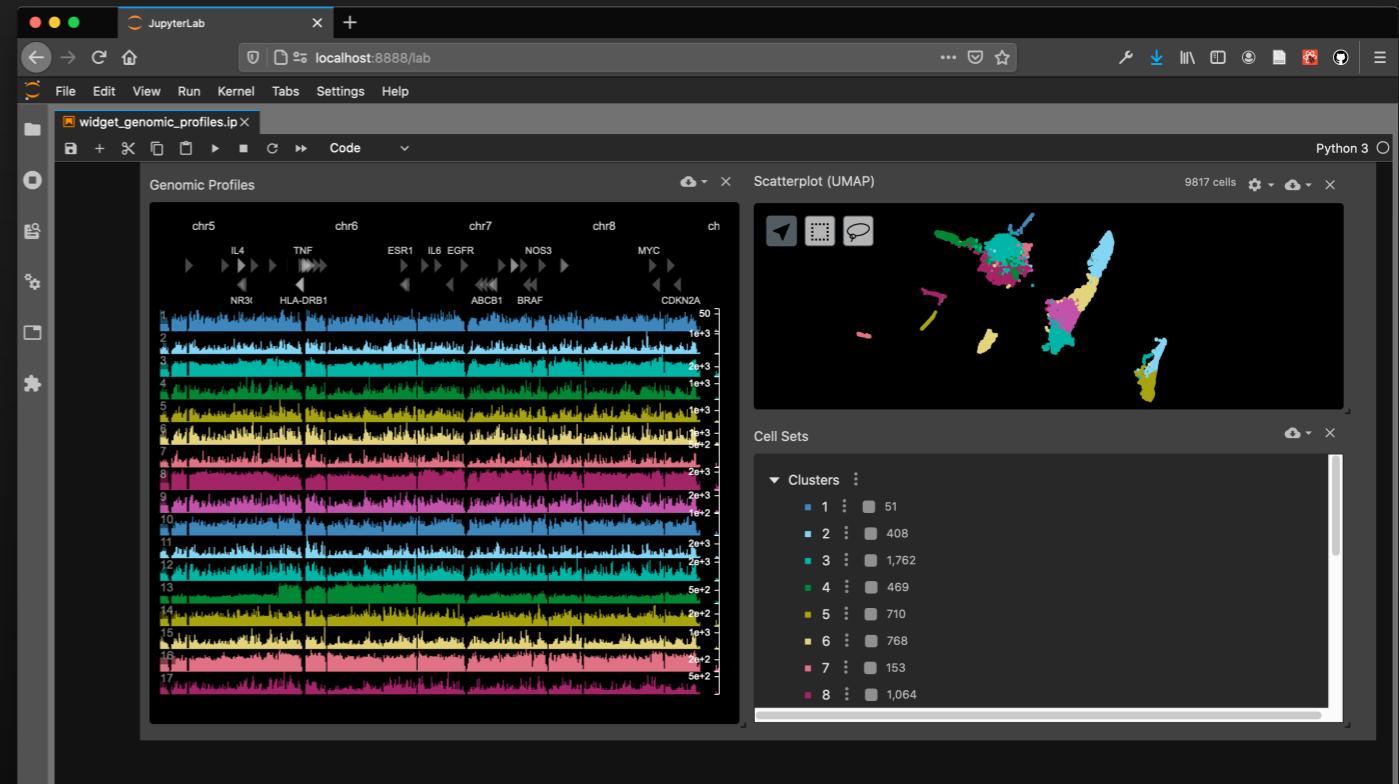


<http://vitessce.io/>

Vitessce is a performant, web-based spatial single cell sequencing exploration tool

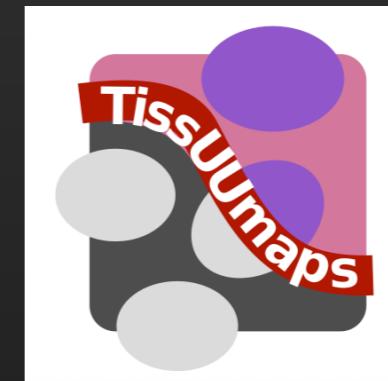


- Client-side rendering
- Overlay annotations on images
- Good for exploration and viewing
- Cannot make annotations and use them in your analysis
- Can be integrated into jupyter notebook and RStudio
- Rich data visualisations

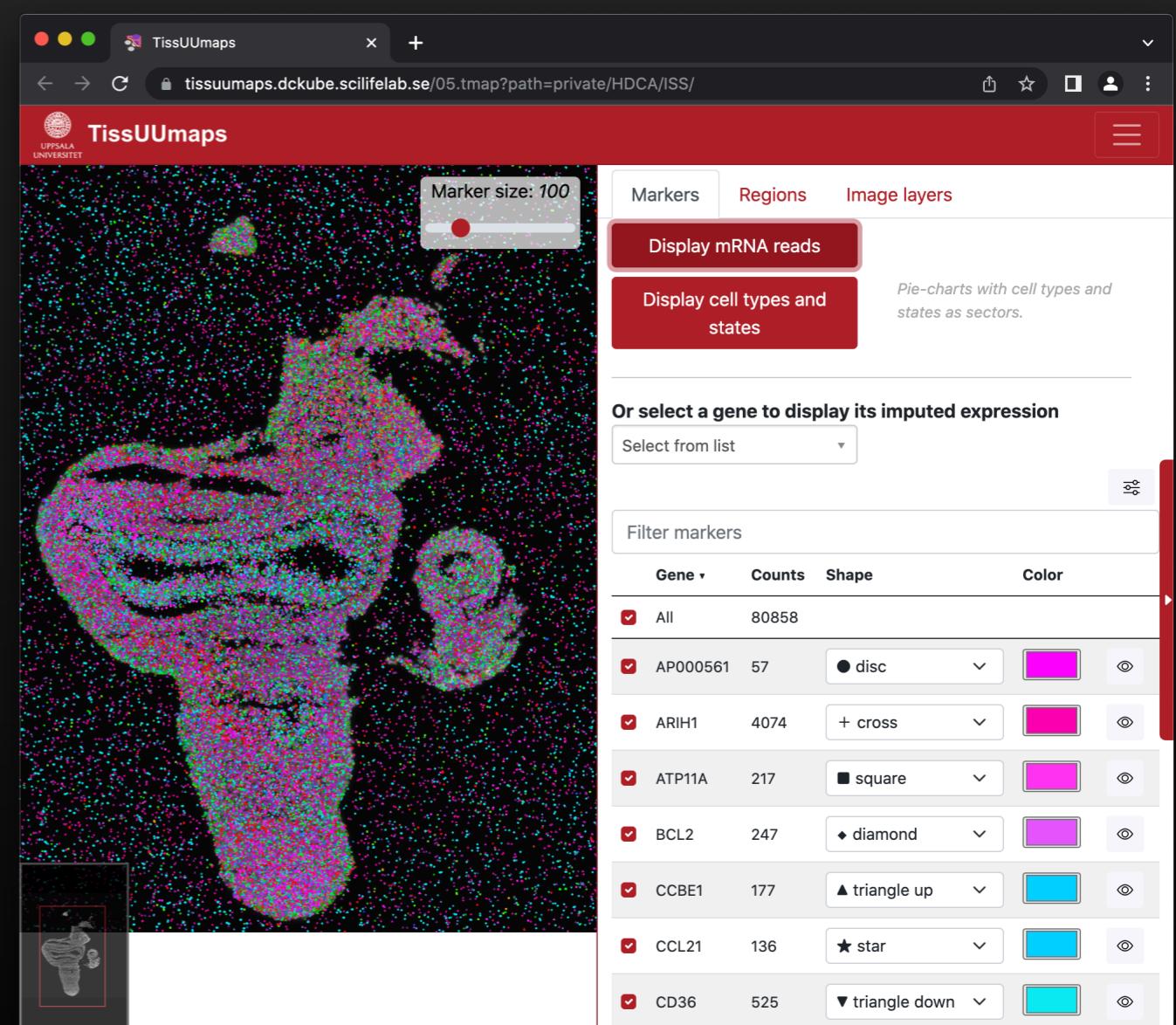


<http://vitessce.io/>

TissUUmaps is a browser-based tool for exploration of spot-based spatial-omics data



- Performant 2D rendering
- Overlay annotations on images
- Good for exploration and viewing
- Cannot make annotations and use them in your analysis
- Plugins for extending visualizations
- Gallery of many published datasets: <https://tissuumaps.github.io/gallery/>



<https://tissuumaps.github.io/>



napari

n-dimensional data viewer in python
open-source, community-developed

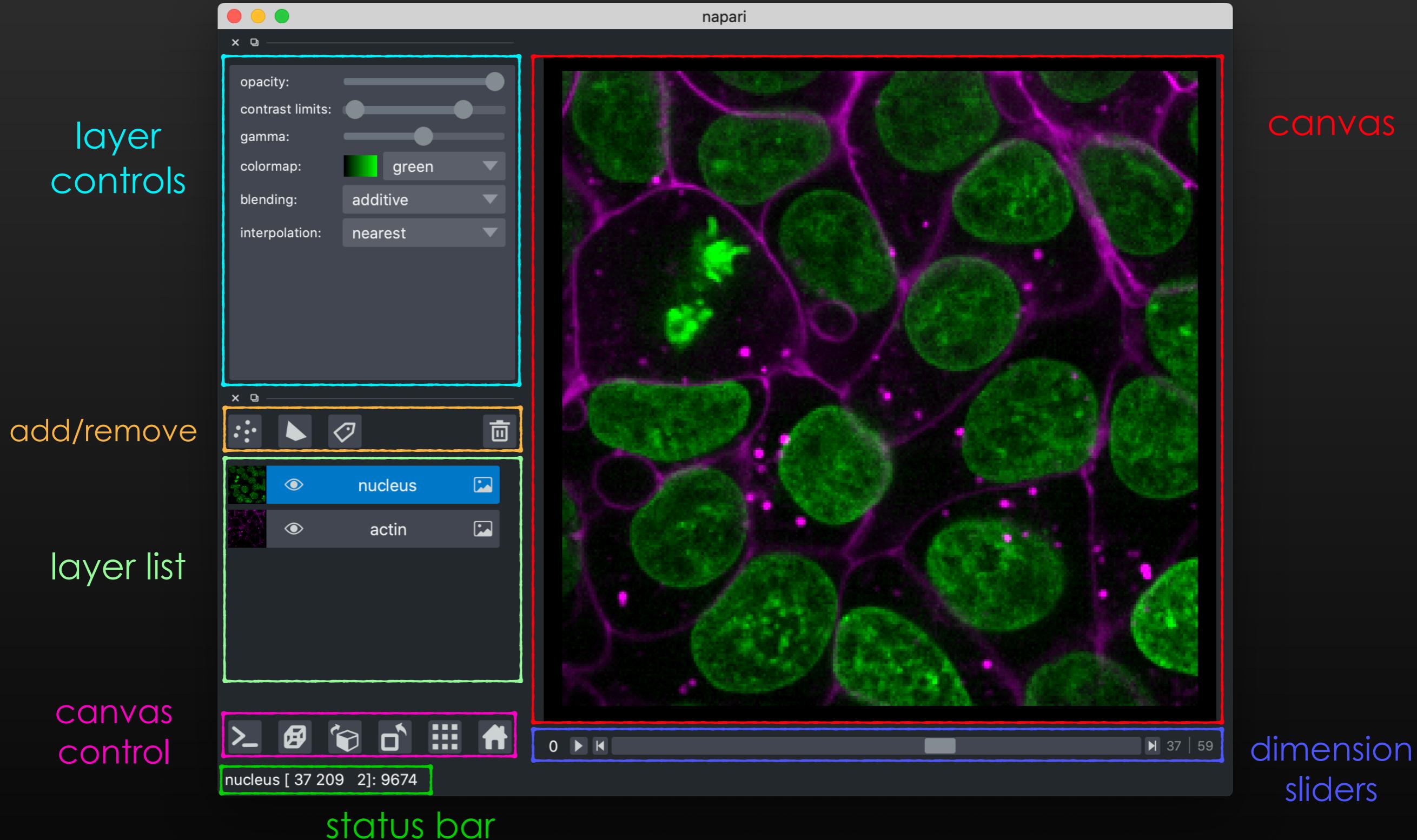
motivation:

- Provide fast (GPU-powered) visualization of n-dimensional images and datasets
- Integrate well with existing scientific python ecosystem
- Interactive analysis workflows
- Support arbitrarily large data (too large for memory, possibly remote)
- Extensible, customizable
- Inclusive, community-driven

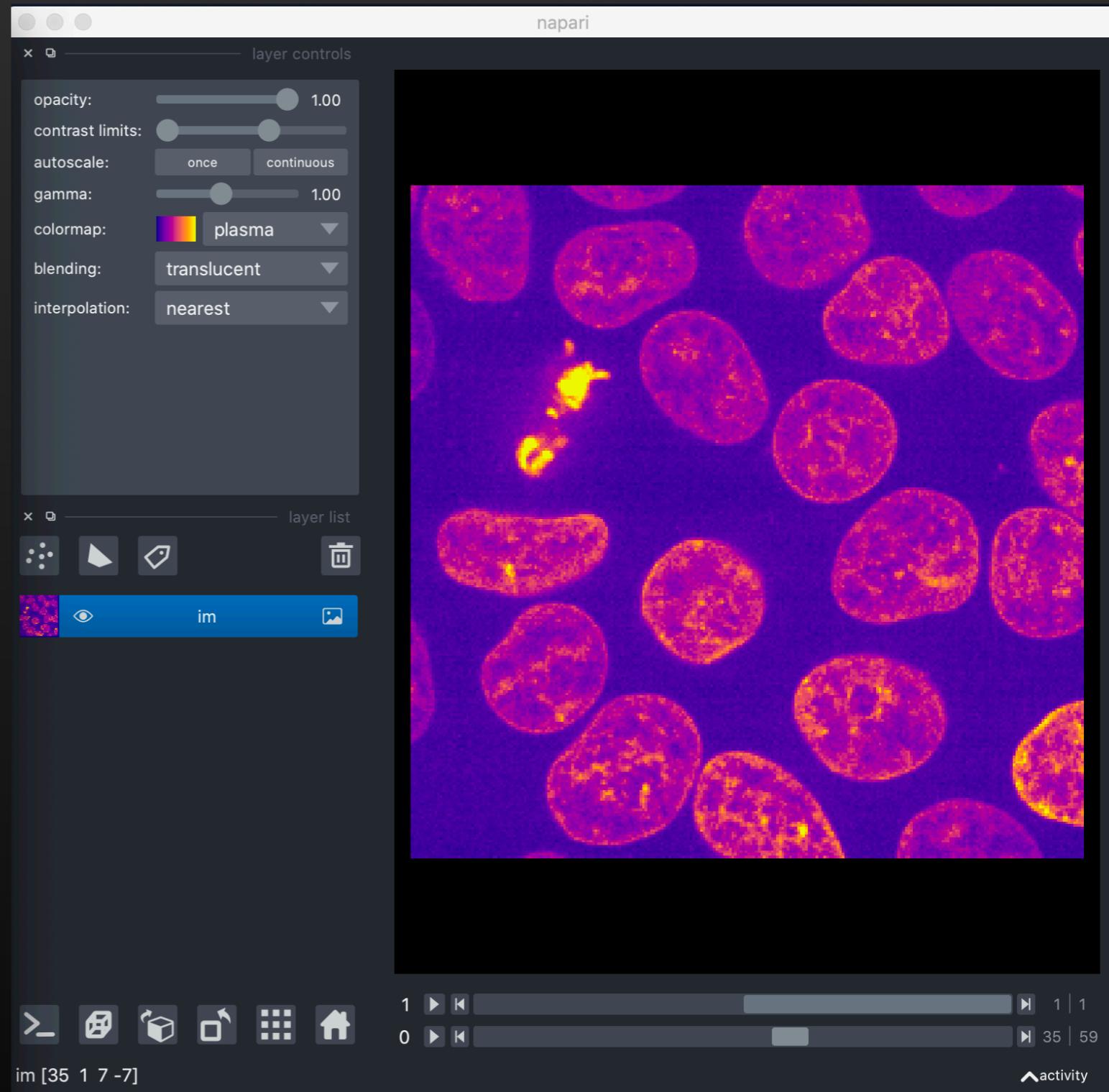
giant shoulders →



the napari viewer



napari supports interactive and scriptable analysis



napari supports interactive and scriptable analysis

The image shows a Jupyter Notebook interface on the left and a napari viewer window on the right.

Jupyter Notebook:

- In [1]:**

```
import napari
```
- In [4]:**

```
from skimage import data
im = data.cells3d()
viewer = napari.view_image(im);
```

napari Viewer:

- The viewer displays a 3D volume of cells colored with a plasma colormap.
- The **layer controls** panel on the left shows settings for opacity (1.00), contrast limits, autoscale (set to once), gamma (1.00), colormap (plasma), blending (translucent), and interpolation (nearest).
- The **layer list** panel shows a single layer named **im**.
- The bottom status bar shows **im [35 1 7 -7]**.
- The bottom navigation bar includes icons for zoom, rotate, and other viewer controls.
- The bottom right corner shows activity counts: 1 | 1 for the top row and 0 | 35 | 59 for the bottom row.

napari supports interactive and scriptable analysis

The image shows a Jupyter Notebook interface on the left and a napari viewer window on the right.

Jupyter Notebook:

- In [1]:**

```
import napari
```
- In [4]:**

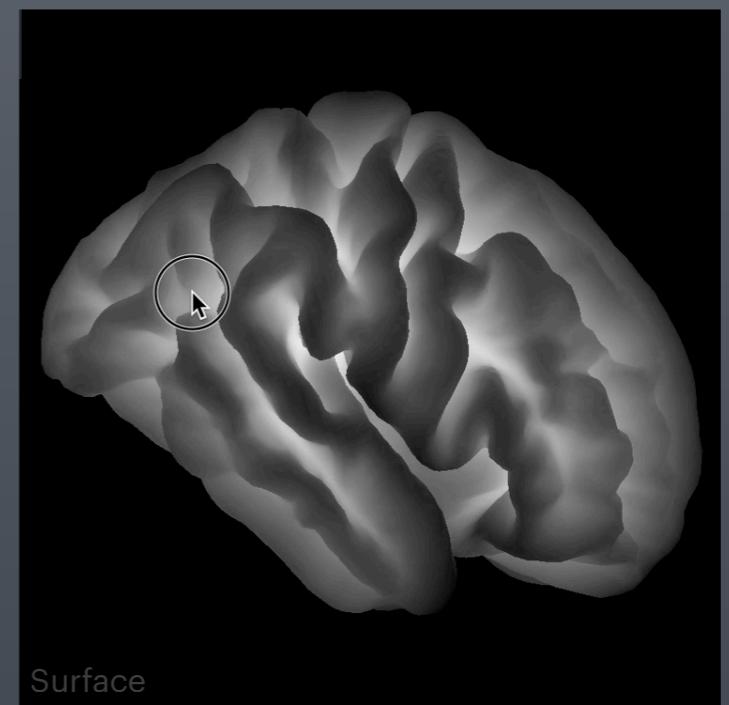
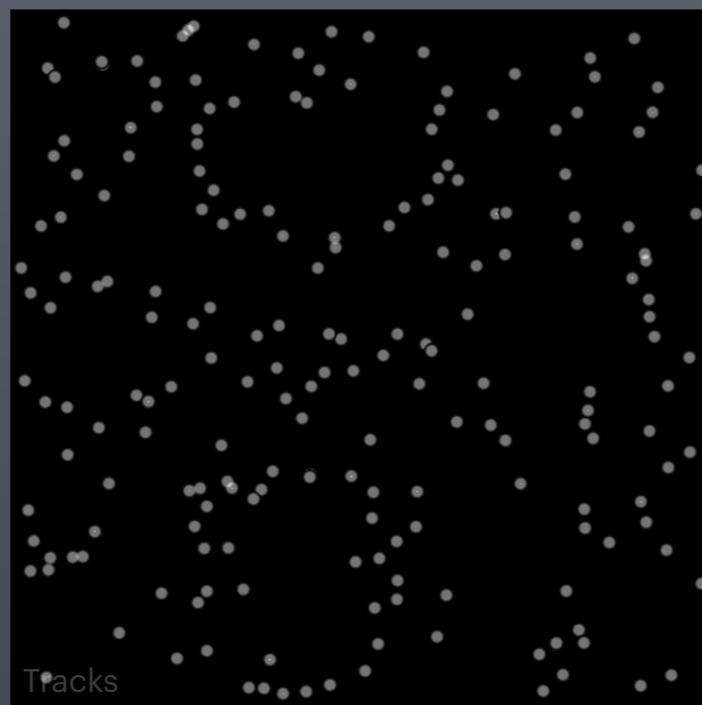
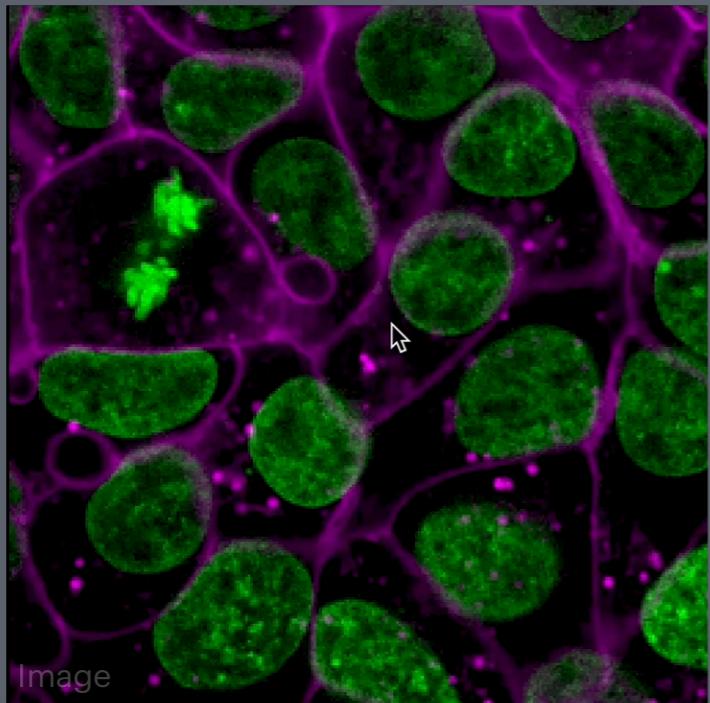
```
from skimage import data
im = data.cells3d()
viewer = napari.view_image(im);
```
- In [6]:**

```
from skimage import filters
blurred = filters.gaussian(im, sigma=3)
viewer.add_image(blurred);
```

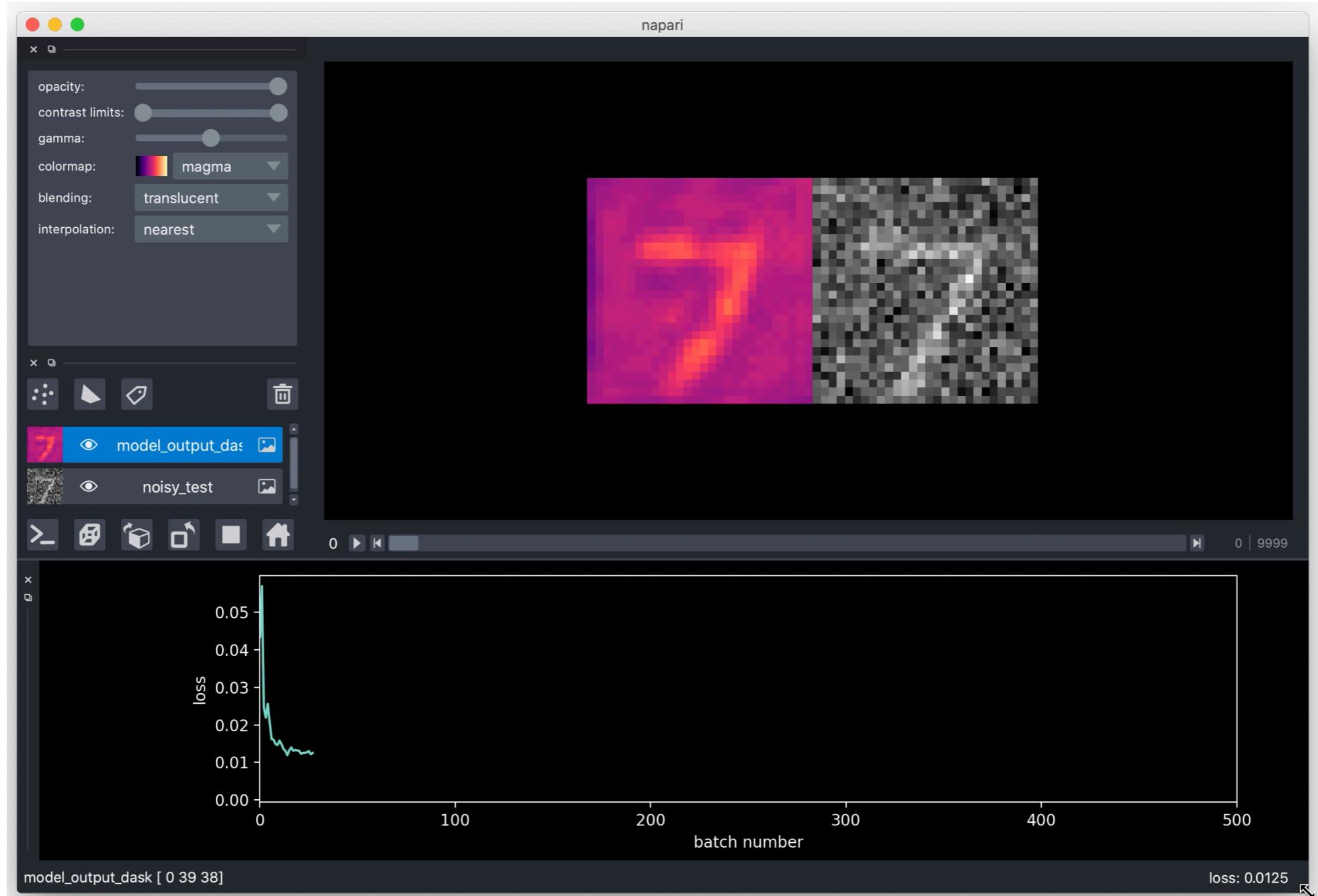
napari Viewer:

- The viewer displays a heatmap of blurred cells.
- The **layer controls** panel on the left shows settings for opacity (1.00), contrast limits, autoscale (set to once), gamma (1.00), colormap (plasma), blending (translucent), and interpolation (nearest).
- The **layer list** panel shows two layers: **blurred** (selected) and **im**.
- The bottom status bar shows the layer name **im [35 1 7 -7]**.
- The bottom navigation bar includes icons for zoom, rotate, and other viewer controls.

Layers: representations for different data types



napari integrates with the scientific python ecosystem



Example by Juan Nunez-Iglesias

Noise2Self method by Batson & Royer, 2019



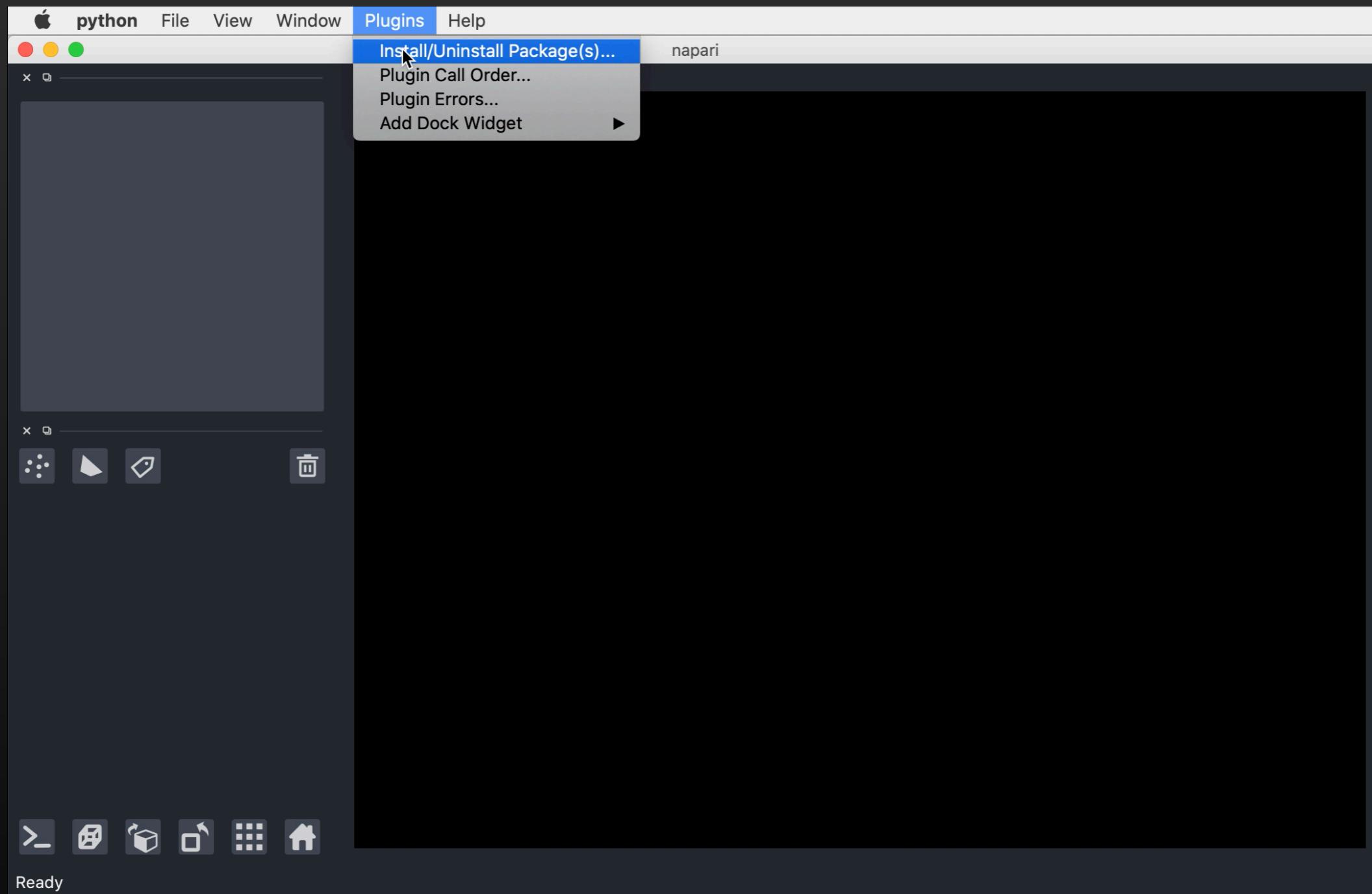
scikit-image
image processing in python



PyTorch

matplotlib

Built-in plugin installer

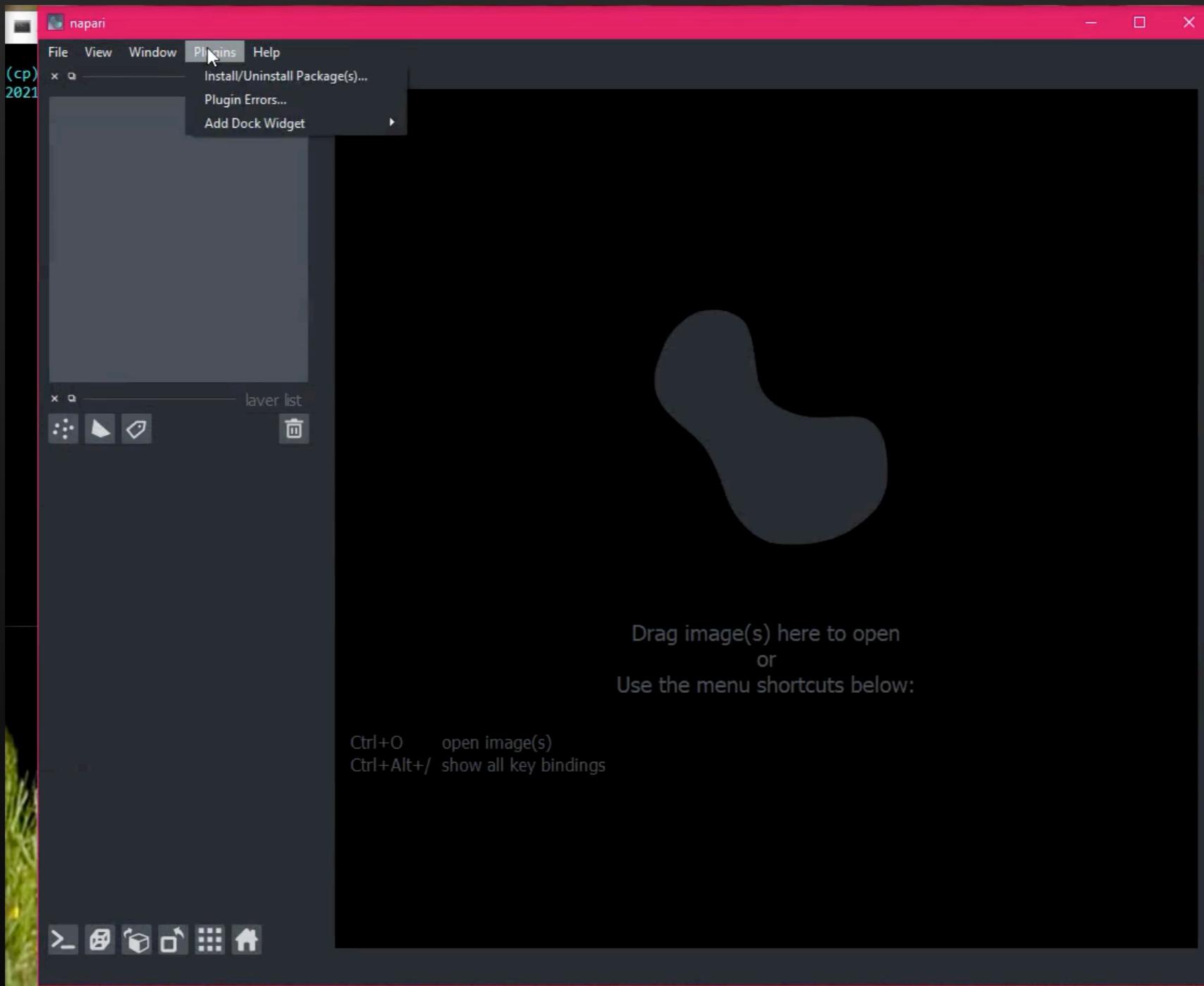


Plugins integrate analysis workflows into napari

cellpose-napari

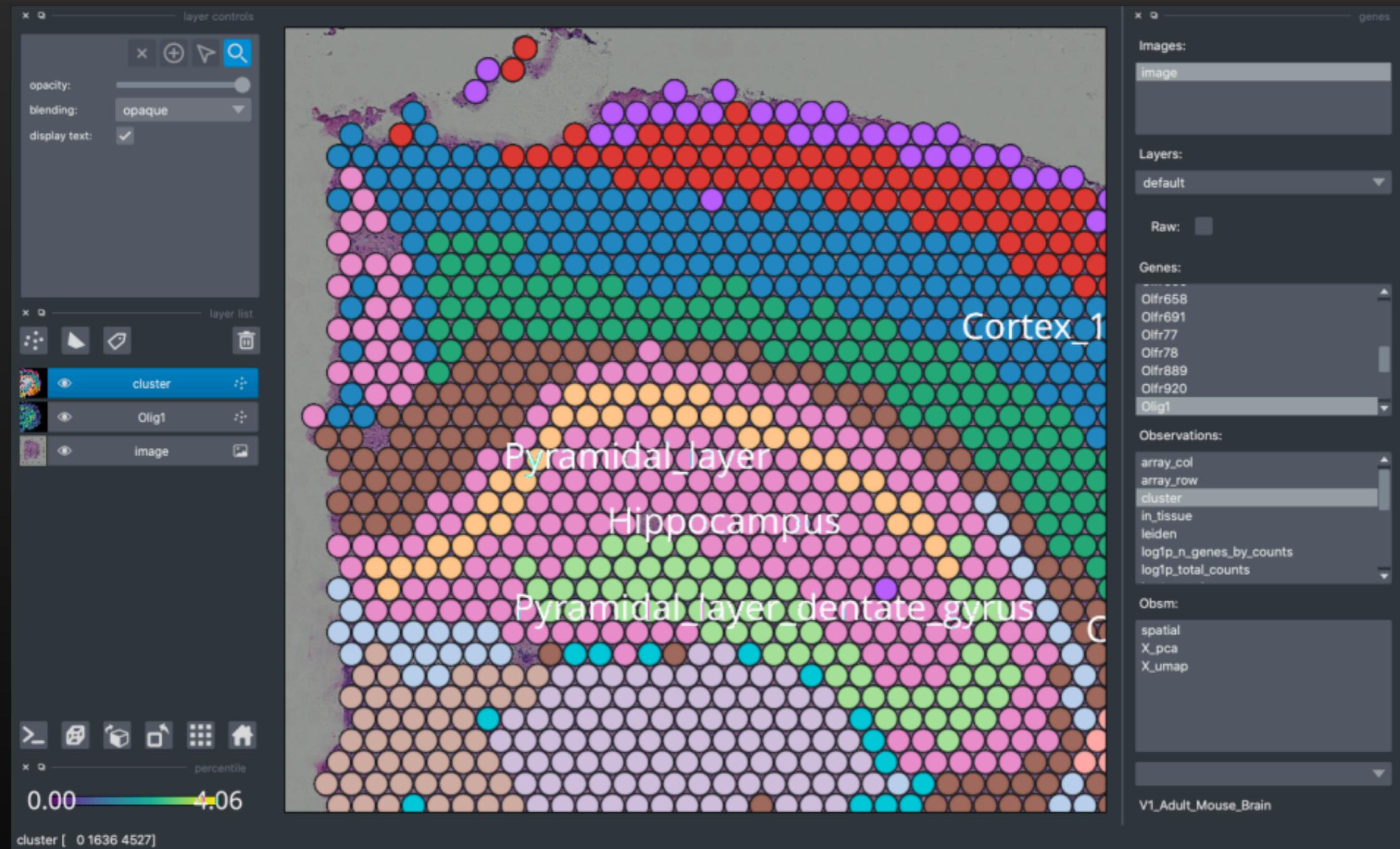
Deep neural network cell & nucleus segmentation

Carsen Stringer (Janelia)



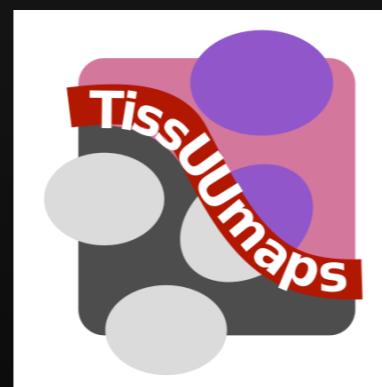
<https://github.com/MouseLand/cellpose-napari>

Visualization of spatial-omics analysis from squidpy



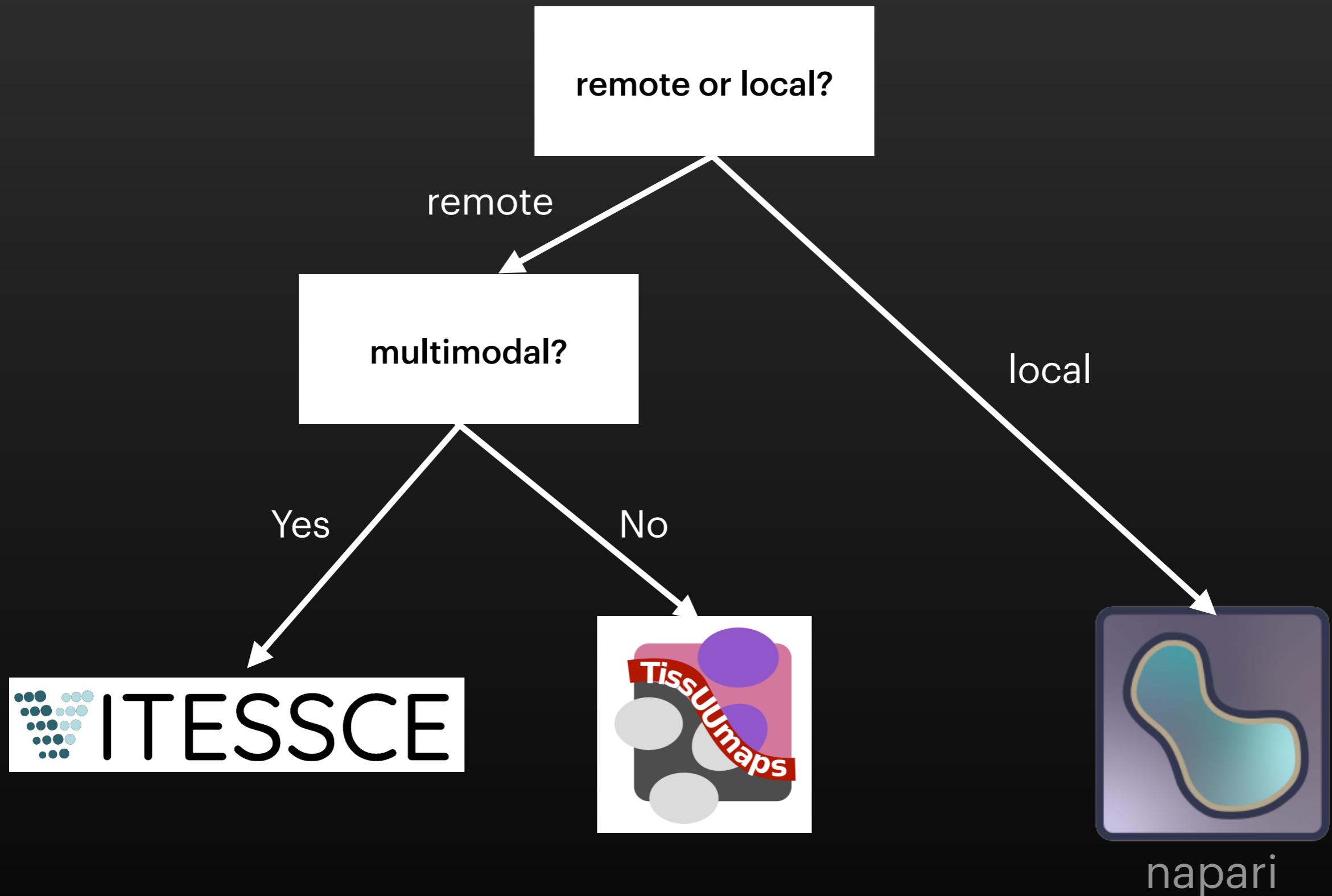
<https://github.com/theislab/squidpy>

Choosing a tool for interactive viewing/analysis



napari

Choosing a tool for interactive viewing/analysis



Conclusion and outlook

- There are both browser and desktop tools for viewing spatial omics data
- Tools for interactive analysis are very young, but are in development
- Many applications require some custom development, but the developers are friendly!
 - <https://image.sc/>
 - <https://napari.zulipchat.com/>
 - <https://github.com/theislab/squidpy>