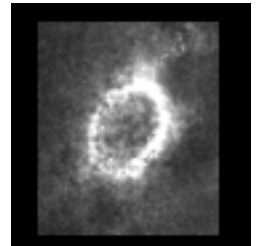
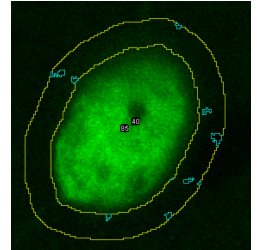


Project description

About the data:

There are two data folders.

- 1) The 'csv_results' folder contains the results from an image processing program called ImageJ. The program was given images of neurons with synapses around them and for each image it analyzed how many synapses are around a given neuron in a two micron ring (see upper image on the right). It counted the number of synapses as well as their size and how brightly the signal is they emit. Each row represents a different neuron.
- 2) The 'wfa_images' folder contains images of nets around neurons, called perineuronal nets (lower image on the right). These can be visualized with the chemical 'WFA'. Each mouse has its own folder, which contains images of such perineuronal nets.



Goal of this project:

The mice in this data were genetically modified. A gene was removed (knocked-out'). One goal of the project is to determine whether there are systematic differences in the synapses or perineuronal nets of the genetically modified mice ('knock-outs' or 'kos'), when compared to normal mice, referred to as 'wild-type' or 'wt'.

Another personal goal is for me to learn how to visualize and analyze this type of nested/hierarchical data. For example in the 'csv_results' folder, for each mouse there are multiple images and each image contains hundreds of neurons. This type of data is common in neuroscience, yet analyzing it is tricky. Finally, I would like to learn how to analyze images in python. I have been using ImageJ for some while now, but to really understand how to process images, you need to code it yourself.

Structure of the project:

The notebook contains three parts: 1) Data visualization 2) Statistical analysis 3) Image processing.