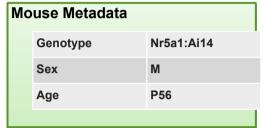
Allen Cell Types Database

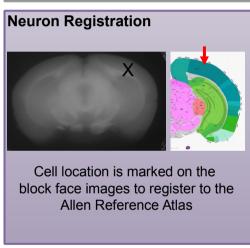
http://celltypes.brain-map.org/

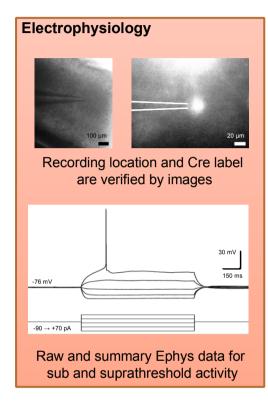
A multimodal database of single cell characterization to enable datadriven approaches to classification. Key features include: whole cell patch clamping, raw images and morphological reconstructions, a variety of abstract point models as well as biophysically detailed compartmental models, and single cell RNA sequencing data.

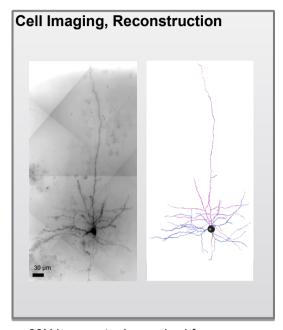
Single Cell Characterization: Electrophysiology & Morphology

A comprehensive dataset is acquired for each neuron. Here is an example of the multimodal data generation from one single experiment (Specimen 162961.04.02)



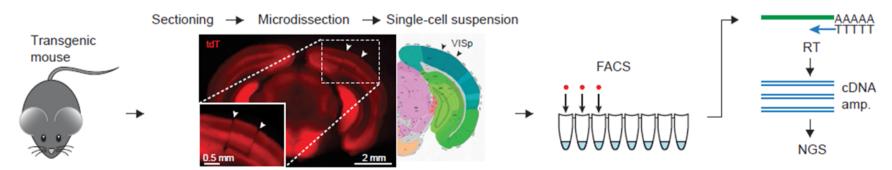






63X image stack acquired for every well-filled neuron. Reconstructions prioritized based on Ephys and fill.

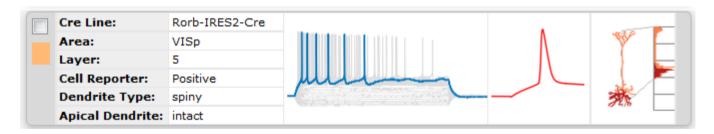
Transcriptomics: Isolating and profiling cells

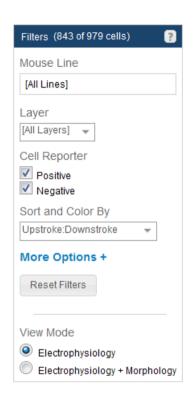


How to most effectively navigate and mine the Allen Cell Types Database

Electrophysiology & Morphology

- Search for cells of interest using the Filters panel (Cre line, layer, ephys or morphological features) on the website. Click here for more information on advanced search features.
- Clicking on a cell panel (see above) will take you to cell characterization data including stimuli, cell responses, models, links to download the NWB file for that experiment, as well as morphological images, reconstructions and features (when available).



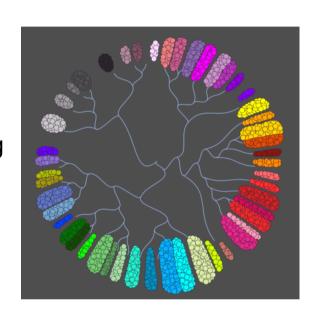


- Use the Allen SDK for sample code demonstrating how to download neuronal model parameters from the Allen Brain Atlas API and run your own simulations using stimuli from the Allen Cell Types Database or custom current injections:
 - Biophysical Models
 - Generalized LIF Models

How to most effectively navigate and mine the Allen Cell Types Database

Single Cell RNA Sequencing

- Prototype cell type classification was performed based on transcriptomics from single cells isolated from the primary visual cortex and is described here and here.
- Follow up studies are in progress and include RNA Sequencing from single cells isolated from the lateral geniculate complex, the primary visual cortex and from the anterior lateral motor area. From this page, you can download gene level FPKM values (as might be used in a heatmap display of gene expression for neurotransmitters) or access FPKM and TPM values for each sample.

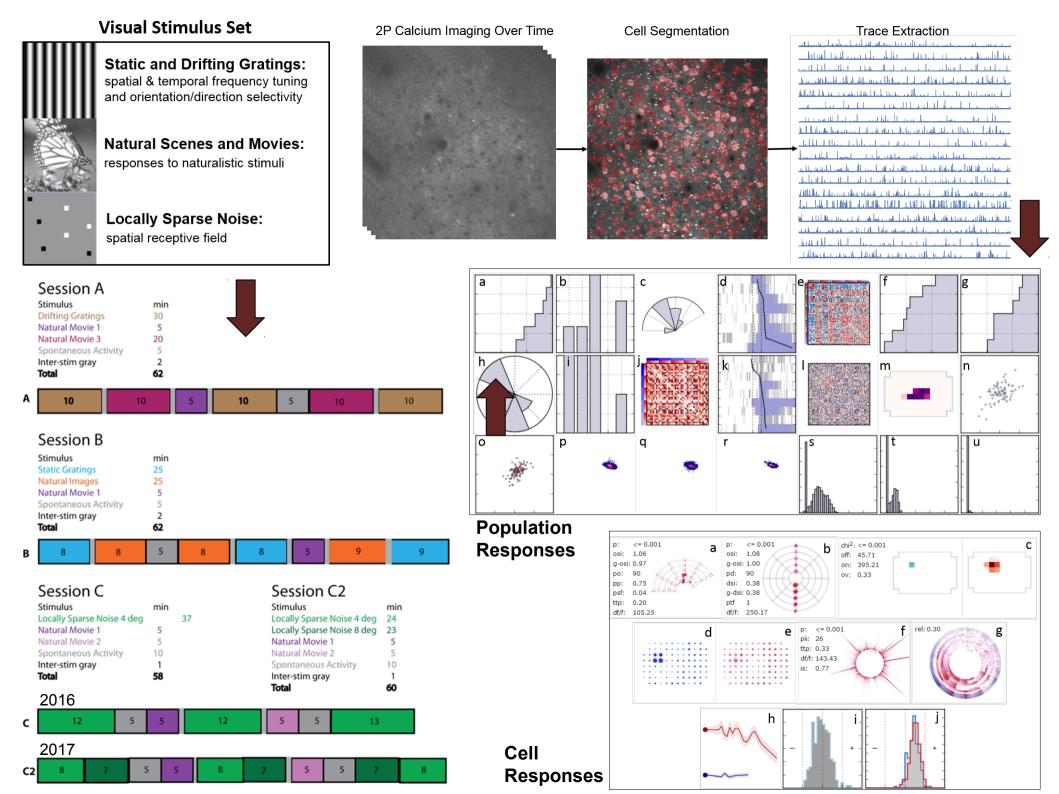


- What analyses can you perform?
 - Compare the transcriptome of your cell to identify similar cells
 - Identify marker genes of cell types
 - Look at expression patterns of functional categories of genes (i.e. ion channels, GPCRs etc.)

Allen Brain Observatory

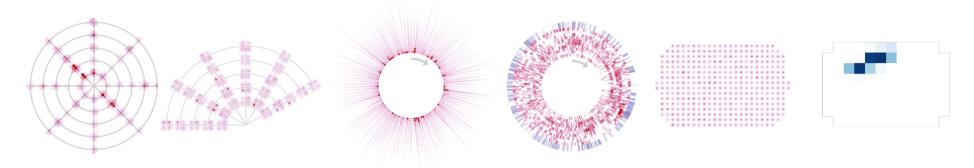
http://observatory.brain-map.org/visualcoding

The Allen Brain Observatory is an *in vivo* survey of physiological activity in the mouse visual cortex, featuring representations of visually evoked calcium responses from GCaMP6-expressing neurons in selected cortical layers, visual areas and Cre lines.



How to most effectively navigate and mine the Allen Brain Observatory – Visual Coding data set

Browse the Visual Stimuli (Drifting Gratings, Static Gratings, Natural Scenes,
Natural Movies & Locally Sparse Noise) from the website to understand each stimulus,
data analysis of the calcium responses, and the creation of the visualization.



- Browse or search for experiments (mouse line, area of visual cortex, depth) or for cells with desired responses. See Documentation and Online Help for more information.
- Download the computed features of a subset of cells (use the jupyter notebook located here) as a .csv file
- Use the AllenSDK to access the NWB files for any of these experiments: to compute your own metrics, work with the fluorescent traces or analyze the eye tracking data
- NWB file contents include: ROI masks, raw fluorescence for each ROI, $\Delta F/F$ for each ROI, running speed, eye tracking, motion correction (and more)