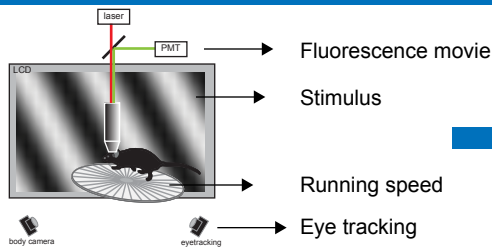


Allen Brain Observatory: Visual Coding 2P Dataset

Data from each imaging session is packaged in an NWB file



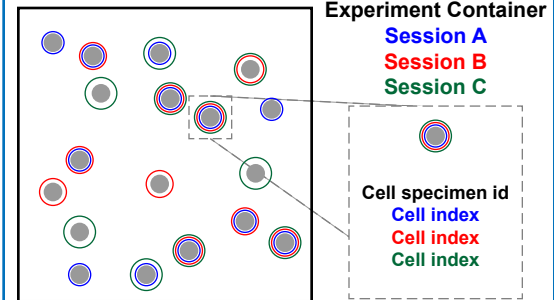
NWB File

Max projection
Segmented ROI masks
Raw fluorescence traces
Neuropil traces
Neuropil r values
Neuropil corrected traces
 $\Delta F/F$ traces
Cell specimen IDs

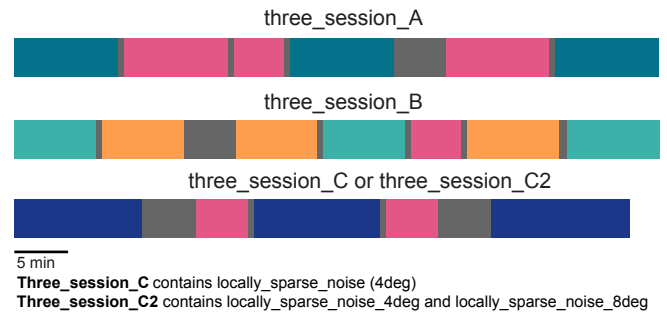
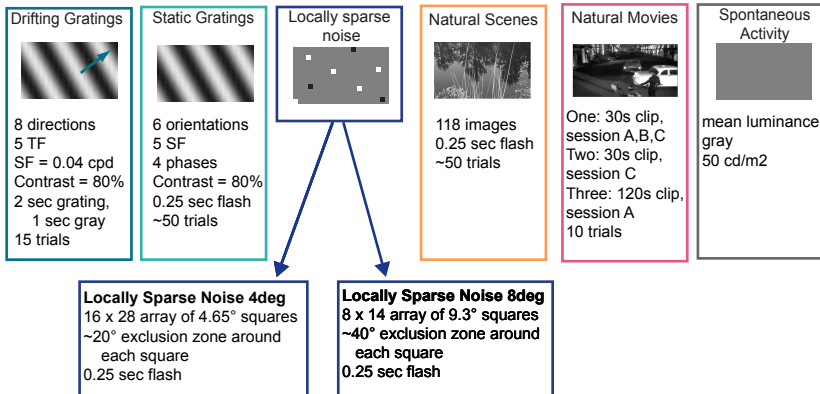
Stimulus tables
Stimulus templates
Pupil location
Pupil area
Running speed
Motion correction values
Meta data

Data is collected from each field-of-view across three ophys experiment sessions to create a single experiment container. Data from each ophys experiment session is in one NWB file. The experiment container ID links the three ophys experiment session for a given field of view. Segmented ROIs are matched across the three sessions, and given a unique cell specimen id.

Experiment Container



Diverse stimuli are presented across three imaging sessions



Dataset October 2018

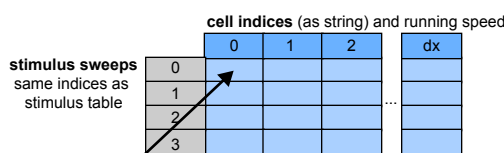
Cre line	Layers	E/I	F/S	VisP	VisI	VisAl	VisPm	VisAm	VisId	Total
Emx1-IRES-Cre; Camk2a-tTA; Ai93	2/3,4,5	exc	6f	3073 (10)	2098 (8)	1787 (7)	835 (4)	457 (3)	3011 (9)	11261 (41)
Slc17a7-IRES2-Cre; Camk2a-tTA; Ai93	2/3,4,5	exc	6f	4840 (17)	3230 (16)	374 (2)	1970 (15)	235 (2)	137 (2)	10786 (54)
Slc17a7-IRES2-Cre; Camk2a-tTA; Ai94	2/3,4,5	exc	6s	1419 (3)						1419 (3)
Cux2-CreERT2; Camk2a-tTA; Ai93	2/3, 4	exc	6f	5081 (16)	2792 (11)	3103 (13)	2361 (13)	1616 (11)	1829 (12)	16782 (76)
Rorb-IRES2-Cre; Camk2a-tTA; Ai93	4	exc	6f	2218 (8)	1191 (6)	1242 (6)	764 (7)	735 (8)	1464 (5)	7614 (40)
Sonn1a-Tg3-Cre; Camk2a-tTA; Ai93	4	exc	6f	1873 (9)						1873 (9)
Nr5a1-Cre; Camk2a-tTA; Ai93	4	exc	6f	578 (8)	421 (6)	220 (6)	331 (7)	171 (6)	1658 (6)	3379 (39)
Rbp4-Cre_KL100; Camk2a-tTA; Ai93	5	exc	6f	458 (7)	485 (7)	441 (6)	509 (6)	355 (8)	102 (4)	2350 (38)
Fezf2-CreER; Ai148 (cortico-thalamic)	5	exc	6f	407 (4)	981 (5)					1388 (9)
Tlx3-Cre_PL56; Ai148 (cortico-cortical)	5	exc	6f	1181 (6)	946 (3)					2127 (9)
Ntsr1-Cre_GN220; Ai148	6	exc	6f	573 (6)	719 (7)		581 (5)			1873 (18)
Sst-IRES-Cre; Ai148	4, 5	inh	6f	266 (17)	301 (15)	24 (1)	247 (14)		46 (2)	884 (49)
Vip-IRES-Cre; Ai148	2/3, 4	inh	6f	352 (17)	315 (17)		387 (16)			1054 (50)
Pvalb-IRES-Cre; Ai162	4, 5	inh	6s	322 (16)	139 (5)					461 (21)
Total				22641 (144)	13618 (106)	7191 (41)	7985 (87)	3569 (38)	8247 (40)	63251 (456)

Cell specimens table metrics

Preferred conditions	<ul style="list-style-type: none"> Preferred direction Preferred temporal frequency Preferred orientation Preferred spatial frequency Preferred phase Preferred image Peak DFF
Selectivities	<ul style="list-style-type: none"> Orientation selectivity Direction selectivity TF discrimination index SF discrimination index Image selectivity
Receptive field parameters	<ul style="list-style-type: none"> RF center location, ON and OFF RF area, ON and OFF Overlap index Centroid distance
Reliabilities	<ul style="list-style-type: none"> Reliability: mean trial-to-trial correlation at preferred condition
Running modulation	<ul style="list-style-type: none"> Ratio of mean response to preferred condition when mouse is running to when it is stationary
Statistical tests	<ul style="list-style-type: none"> P-value: ANOVA comparing all stimulus conditions Running modulation p-value: KS test comparing responses to preferred condition when mouse stationary with when mouse is running Chi value (LSN)

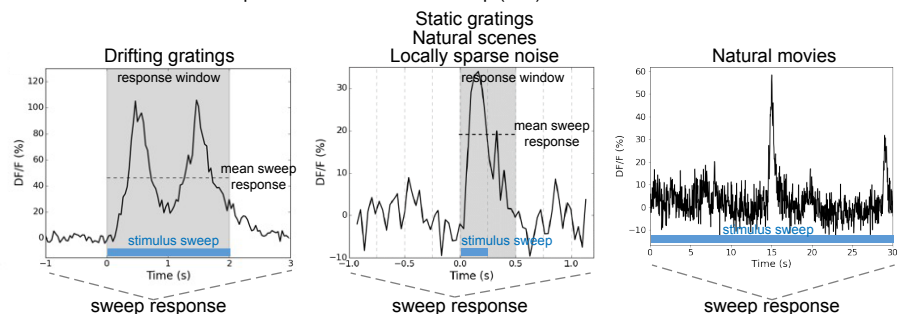
Analysis Object: Sweep Response and Mean Sweep Response

The analysis object contains several stimulus specific objects summarizing different aspects of the cellular and population responses to the stimulus. These include a response array characterizing the mean and s.e.m. of responses to each stimulus condition, signal correlation and noise correlation matrices, representational similarity matrices, and speed tuning arrays. The **Sweep Response** and **Mean Sweep Response** are DataFrames that summarize the fluorescence response to each stimulus sweep (trial).



Sweep response: Time series during sweep, including 1 second before and after stimulus presentation.

Mean sweep response: Mean of the time series during response window (no mean sweep response for natural movies)



Allen SDK: Brain Observatory Cache

Brain Observatory Cache

```
In [ ]: from allensdk.core.brain_observatory_cache import BrainObservatoryCache
        boc = BrainObservatoryCache(manifest_file=manifest_file)
```

Useful arguments

```
In [7]: boc.get_all_cre_lines()
```

```
Out[7]: [u'Cux2-CreERT2',
         u'Emx1-IRES-Cre',
         u'Nr5a1-Cre',
         u'Rbp4-Cre_KL100',
         u'Rorb-IRES2-Cre',
         u'Scnn1a-Tg3-Cre']
```

```
In [5]: boc.get_all_targeted_structures()
```

```
Out[5]: [u'VISal', u'VISam', u'VISl', u'VISp', u'VISpm', u'VISrl']
```

```
In [8]: boc.get_all_stimuli()
```

```
Out[8]: ['drifting_gratings',
         'locally_sparse_noise',
         'locally_sparse_noise_4deg',
         'locally_sparse_noise_8deg',
         'natural_movie_one',
         'natural_movie_three',
         'natural_movie_two',
         'natural_scenes',
         'spontaneous',
         'static_gratings']
```

Find data

Returns a list of experiment containers selected on arguments provided. Arguments are passed as a list.

```
In [ ]: boc.get_experiment_containers(file_name=None, ids=None, targeted_structures=None, imaging_depths=None,
                                     cre_lines=None, transgenic_lines=None, include_failed=False, simple=True)
```

Returns a list of ophys experiment sessions selected on arguments provided. Arguments are passed as a list.

```
In [ ]: boc.get_ophys_experiments(file_name=None, ids=None, experiment_container_ids=None, targeted_structures=None,
                                  imaging_depths=None, cre_lines=None, transgenic_lines=None, stimuli=None, session_types=None,
                                  cell_specimen_ids=None, include_failed=False, require_eye_tracking=False, simple=True)
```

Accessing data from the NWB file

Accesses data in NWB file for one ophys experiment session

```
In [ ]: data_set = boc.get_ophys_experiment_data(ophys_experiment_id)
```

```
In [ ]: time_stamps, dff_traces = data_set.get_dff_traces() #dff shape: number cells X number timestamps
```

```
In [ ]: running_speed, time_stamps = data_set.get_running_speed() #dxcn units: cm/s
```

```
In [ ]: time_stamps, pupil_location = data_set.get_pupil_location(as_spherical=True) #pupil_position shape: number timestampsX2
                                              #pupil_position units: degrees
```

```
In [ ]: time_stamps, pupil_size = data_set.get_pupil_size()
```

```
In [ ]: stimulus_table = data_set.get_stimulus_table('natural_scenes')
```

```
In [ ]: stimulus_template = data_set.get_stimulus_template('natural_scenes')
```

Note: the timestamps returned in all visual coding 2P sdk functions are identical. All data is aligned to the 2-photon acquisition frames.

Accessing data in the analysis object

Two methods to access the analysis object. This object is specific for an imaging session and a stimulus. It contains, among other things, the sweep response dataframe, the mean sweep response dataframe, and the response array.

The first method requires access to the analysis file (eg. on AWS):

```
In [ ]: ns = boc.get_ophys_experiment_analysis(ophys_experiment_id=session_id, stimulus_type='natural_scenes')
```

The second method runs the analysis on the data_set object (see box above). It takes a few minutes to run:

```
In [ ]: from allensdk.brain_observatory.natural_scenes import NaturalScenes
        ns = NaturalScenes(data_set)
```

More Information

SDK Installation: <http://alleninstitute.github.io/AllenSDK/install.html>

SDK Tutorials: <http://observatory.brain-map.org/visualcoding/sdk/index>

Experiment Documentation: <http://help.brain-map.org/display/observatory/Documentation>

Discussion Forum: <http://community.brain-map.org>

pip install allensdk