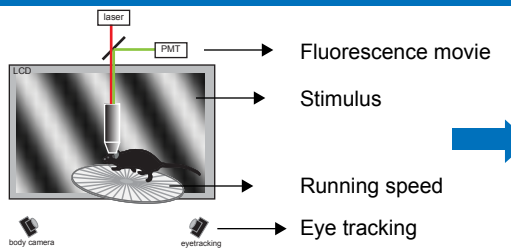
Allen Brain Observatory: Visual Coding 2P Dataset

Data from each imaging session is packaged in an NWB file

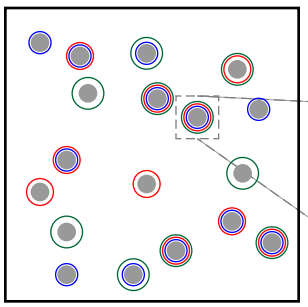


NWB File

Max projection	Stimulus tables
Segmented ROI masks	Stimulus templates
Raw fluroscencence traces	Pupil location
Neuropil traces	Pupil area
Neuropil r values	Running speed
Neuropil corrected traces	Motion correction values
ΔF/F traces	Meta data
Cell specimen IDs	

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

Drifting Gratings
8 directions
5 TF
SF = 0.04 cpd
Contrast = 80%
2 sec grating,
1 sec gray
15 trials

Static Gratings
6 orientations
5 SF
4 phases
Contrast = 80%
0.25 sec flash
~50 trials

Locally sparse noise

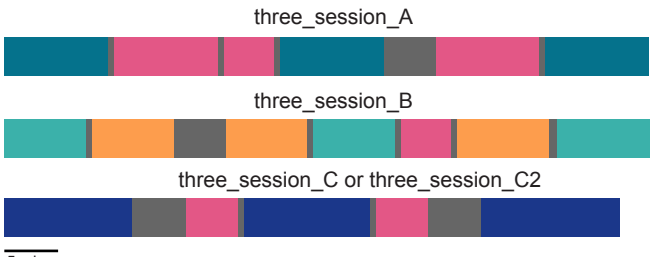
Natural Scenes
118 images
0.25 sec flash
~50 trials

Natural Movies
One: 30s clip, session A,B,C
Two: 30s clip, session C
Three: 120s clip, session A
10 trials

Spontaneous Activity
mean luminance gray
50 cd/m2

Locally Sparse Noise 4deg
16 x 28 array of 4.65° squares
~20° exclusion zone around each square
0.25 sec flash

Locally Sparse Noise 8deg
8 x 14 array of 9.3° squares
~40° exclusion zone around each square
0.25 sec flash



Three_session_C contains locally_sparse_noise (4deg)
Three_session_C2 contains locally_sparse_noise_4deg and locally_sparse_noise_8deg

Dataset October 2017

Cre line	Layers	VISp	VISpm	VISl	VISal	VISam	VISrl	total	color
Emx1-IRES-Cre; Camk2a-tTA; Ai93	2/3, 4, 5	2137 (7)	835 (4)	1872 (6)	1787 (7)	457 (3)	1946 (6)	9034 (33)	#9F9F9F
Cux2-CreERT2; Camk2a-tTA; Ai93	2/3, 4	5832 (16)	2890 (13)	3845 (13)	2648 (11)	1102 (6)	720 (6)	17037 (62)	#A92E66
Rorb-IRES2-Cre; Camk2a-tTA; Ai93	4	1339 (5)	436 (4)	1035 (5)	902 (5)	546 (6)	440 (2)	4698 (27)	#7841BE
Scnn1a-Tg3-Cre; Camk2a-tTA; Ai93	4	1873 (9)						1873 (9)	#4F63C2
Nr5a1-Cre; Camk2a-tTA; Ai93	4	668 (6)	331 (7)	405 (5)	165 (3)	165 (5)	1039 (3)	2773 (29)	#5BB0B0
Rbp4-Cre; Camk2a-tTA; Ai93	5	278 (3)	481 (5)	402 (5)	362 (4)	137 (3)	16 (1)	1676 (21)	#5CAD53
total		**12127 (46)**	**4973 (33)**	**7559 (34)**	**5864 (30)**	**2407 (23)**	**4161 (15)**	**37091 (181)**	

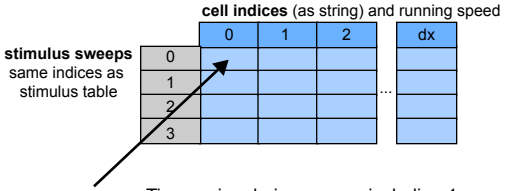
Next data release will be October 4, 2018

Cell specimens table metrics

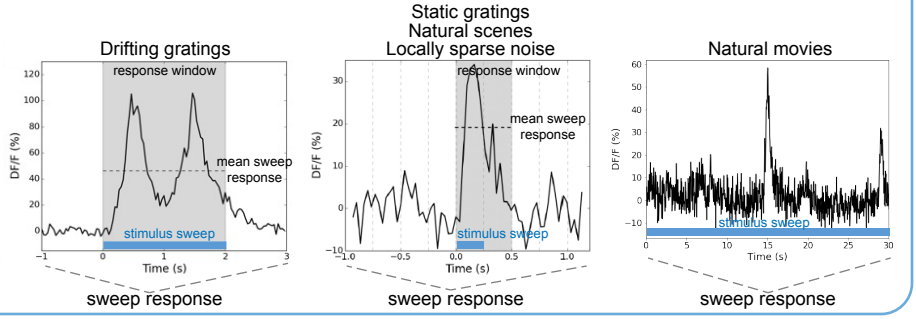
Preferred conditions	• Preferred direction • Preferred temporal frequency • Preferred orientation • Preferred spatial frequency • Preferred phase • Preferred image • Peak DFF
Selectivities	• Orientation selectivity • Direction selectivity • TF discrimination index • SF discrimination index • Image selectivity
Receptive field parameters	• RF center location, ON and OFF • RF area, ON and OFF • Overlap index • Centroid distance
Reliabilities	• Reliability: mean trial-to-trial correlation at preferred condition
Running modulation	• Ratio of mean response to preferred condition when mouse is running to when it is stationary
Statistical tests	• 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, or receptive field, array characterizing mean responses to different stimulus conditions, signal correlation and noise correlation matrices, representational similiarity matrices, and speed tuning arrays. The **Sweep Response** and **Mean Sweep Response** are DataFrames that summarize the fluorescence response to each stimulus sweep - each stimulus presentation.



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() #dxcm 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. This is different from visual behavior.

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