

session_demonstration_script

February 19, 2023

1 Example code for using session.Session

Note: This notebook covers several relevant methods of the `Session` and `Stim` objects, detailing some of their arguments, as well. For more details, take a look at the docstring associated with a method of interest.

Import notes:

- Any python packages required by the codebase should be installed and available, if the required conda environment, installed from `osca.yml`, has been activated.
 - `util` is a [Github repo](#) of mine, and the correct branch `osca_mult` is automatically installed from `osca.yml`.
 - **Potential updates:** Errors internal to the codebase involving `util` code and occurring *after* new changes have been pulled from the `OpenScope_CA_Analysis` repo *may* be due to an update of the `osca_mult` branch of `util` that breaks backwards compatibility. Though I will try to avoid this, if running the notebook locally and an error occurs, make sure to check whether there are updates to the utility, and update your installation as needed, e.g., by running, from the command line: `pip install -U util-colleenjg`
-

1.1 1. Setup

1.1.1 Update logging and plot formatting

If you wish to use the same logging and formatting style as I do:

1.1.2 Data directory

The data directory should contain the session data, either in its **original format** or in **NWB format**.

* If in NWB format (production data, only), `datadir` should be a directory that contains the data in NWB format, at any depth.

* If using the data in its original format, `datadir` should specifically be the directory right before the data is split into `prod` (production) and `pilot` (pilot) data.

1.1.3 Running in a docker, or specifically in Binder

If the notebook is **running in a docker**, the dataset is downloaded in NWB format from the [Dandi archive](#) first, and the data directory is set accordingly.

In addition, if the notebook is **running specifically in Binder**, some analyses are slightly altered later, in order to reduce memory use.

If the notebook is **not running in a docker**, the dataset should be downloaded manually.

Be sure to download the dataset, if needed, and update ``datadir`` and ``datadir_nwb`` to point the correct location(s).

Currently they point to `../../data/OSCA` and `../../data/OSCA_NWB`, respectively.

1.1.4 Mouse dataframe

The mouse dataframe, contains the metadata for each session, including its 9-digit `sessid`, the `mouse_n`, `sess_n`, etc.

Mouse dataframe columns:

- * `sessid`: Unique session ID (9-digit)
- * `full_timestamp`: Full timestamp for the session (in UTC).
- * `mouse_n`: Mouse number
- * `mouseid`: Unique mouse ID (6-digit)
- * `date`: Recording date
- * `depth`: Recording depth (um)
- * `plane`: Recording plane (“dend” or “soma”)
- * `line`: Cell line (“L2/3-Cux2” or “L5-Rbp4”)
- * `runtype`: Type of session (“pilot” or “prod”). Only production data is available in NWB dataset.
- * `sess_n`: Session number
- * `nrois`: Number of valid ROIs (see *Note*)
- * `nrois_tracked`: Number of ROIs tracked across sessions (-1 for sessions with no tracking).
- * `nrois_all`: Same as `nrois`, but including bad (non valid) ROIs.
- * `nrois_allen`: Number of valid ROIs when using the `allen` segmentation for dendritic ROIs, instead of the `extr` segmentation (see *Note*).
- * `nrois_allen_all`: Same as `nrois_allen`, but including bad (non valid) ROIs.
- * `pass_fail`: Whether the session passed (P) or failed (F) quality control.
- * `all_files`: Whether all files are available for the session (original data format).
- * `any_files`: Whether any files are available for the session (original data format).
- * `incl`: Whether the session can be included in analyses (looser criterion than `pass_fail`).
- * `stim_seed`: Seed used to initialize stimuli for the session, during recording.
- * `notes`: Any notes on the session.

Note: The `allen` segmentations are used for all **somatic** data. The `extr` segmentations are preferred for all **dendritic** data. For this reason, the `allen` segmentation for **dendritic** data is **not included** in the NWB dataset. See **section 6** for details on `allen` and `extr` ROI mask types.

```
[6]:      sessid  full_timestamp  mouse_n  mouseid  sex  DOB  date  \
0    712483302             NaN         1    389778    F  20180323  20180621
1    712942208             NaN         1    389778    F  20180323  20180622
2    714893802             NaN         1    389778    F  20180323  20180627
3    715244457             NaN         1    389778    F  20180323  20180628
4    716425232             NaN         1    389778    F  20180323  20180702
..      ...              ...      ...      ...      ...      ...
78   833704570  20190307T163524        13    440889    F  20181212  20190307
```

79	834403597	20190308T164555	13	440889	F	20181212	20190308
80	836968429	20190314T152429	13	440889	F	20181212	20190314
81	837360280	20190315T152224	13	440889	F	20181212	20190315
82	838633305	20190318T232807	13	440889	F	20181212	20190318

	age_weeks	depth	plane	...	nrois_tracked	nrois_all	nrois_allen	\
0	12.857143	20	dend	...	-1	1468	232	
1	13.000000	375	soma	...	-1	78	62	
2	13.714286	20	dend	...	-1	-1	-1	
3	13.857143	20	dend	...	-1	949	458	
4	14.428571	375	soma	...	-1	79	56	
..	
78	12.142857	175	soma	...	147	251	224	
79	12.285714	175	soma	...	147	228	210	
80	13.142857	175	soma	...	-1	217	205	
81	13.285714	175	soma	...	-1	244	217	
82	13.714286	175	soma	...	-1	256	227	

	nrois_allen_all	pass_fail	all_files	any_files	incl	stim_seed	\
0	259	F	1	1	yes	103	
1	78	F	1	1	yes	103	
2	-1	F	0	1	no	103	
3	504	P	1	1	yes	103	
4	79	P	1	1	yes	103	
..	
78	251	P	1	1	yes	16745	
79	228	P	1	1	yes	10210	
80	217	P	1	1	yes	24253	
81	244	F	1	1	yes	19576	
82	256	F	1	1	no	30582	

	notes
0	dropped beh and eye tracking frames (7), stim ...
1	dropped beh and eye tracking frames (6), stim ...
2	missing 2P recordings and ROI traces
3	NaN
4	NaN
..	...
78	stim2twop alignment shifted corrected with 2nd...
79	dropped beh and eye tracking frames (6), stim ...
80	FOV shifted (poor alignment with previous sess...
81	z-drift (14 um)
82	laser wavelength incorrectly set to 800 nm (in...

[83 rows x 24 columns]

1.2 2. Basics of initializing a Session object

Sessions can be initialized with their 9-digit `sessid`:

or with their `mouse_n`, `sess_n` and `runtype`:

1.2.1 Data format is identified automatically

During initialization, the code looks first for the session data in NWB format. If it doesn't find it, it looks for the data in its original format. If neither are found, an error is thrown.

1.2.2 Loading the data after initialization.

After creating the session, you must run `self.extract_info()`. This wasn't amalgamated into the `__init__` to reduce the amount of information needed to just create a session object.

1.2.3 Loading ROI/running/pupil info

You can load this information when you call `self.extract_info()` or manually later by calling `self.load_roi_info()`, `self.load_run_data()` and `self.load_pup_data()`.

Loading stimulus and alignment info...

Loading ROI trace info...

Loading running info...

Loading pupil info...

1.2.4 Stimulus dataframe

The stimulus dataframe, stored under `sess.stim_df`, details the stimulus feature for each segment of the presentation.

A **segment** is the minimal subdivision of the stimulus presentation: **0.3 sec** for the Gabor stimulus, and **1s** for the visual flow, and grayscale stimuli.

If a feature **does not apply** to certain segments (e.g., `gabor_number` for visual flow stimulus segments), the values for those segments will be `None`, `NaN` or `[]`, depending on the column's datatype.

Missing columns: Note that a few columns are missing, since the session was loaded with `full_table=False`. * `"gabor_orientations"`: Specific orientation of each Gabor patch, for each segment. * `"square_locations_x"`: Specific x location of each visual flow square, at **each frame** of each segment. * `"square_locations_y"`: Specific y location of each visual flow square, at **each frame** of each segment.

This is primarily to save memory, when loading a session, as this information is not typically needed. To load all columns, re-run `sess.extract_info()` with `full_table=True`. Data that is already loaded will not be re-loaded.

```
[10]:      stimulus_type stimulus_template_name  unexpected gabor_frame \
0      grayscale      grayscale      NaN
1      gabors      gabors      0.0      A
2      gabors      gabors      0.0      B
3      gabors      gabors      0.0      C
```

4	gabors	gabors	0.0	D
...
8839	visflow	visflow_right	0.0	
8840	visflow	visflow_right	0.0	
8841	visflow	visflow_right	1.0	
8842	visflow	visflow_right	1.0	
8843	grayscale	grayscale	NaN	

	gabor_kappa	gabor_mean_orientation	gabor_number	\
0	NaN	NaN	NaN	
1	16.0	0.0	30.0	
2	16.0	0.0	30.0	
3	16.0	0.0	30.0	
4	16.0	0.0	30.0	
...	
8839	NaN	NaN	NaN	
8840	NaN	NaN	NaN	
8841	NaN	NaN	NaN	
8842	NaN	NaN	NaN	
8843	NaN	NaN	NaN	

	gabor_locations_x	\
0	[]	
1	[-314.2481536790383, 726.6351926350328, -609.4...	
2	[278.93714376420894, -895.0169462360316, 830.4...	
3	[-694.2565883378384, 458.8415680953749, -472.6...	
4	[-631.2261180219028, -600.2310528361336, -887...	
...	...	
8839	[]	
8840	[]	
8841	[]	
8842	[]	
8843	[]	

	gabor_locations_y	\
0	[]	
1	[519.3985635606798, 429.54112277826425, 482.75...	
2	[-62.92603512701612, -329.96944361291634, -332...	
3	[162.5089263895926, 433.50619201931613, 567.71...	
4	[-21.003509639097615, -271.4924294875755, 555...	
...	...	
8839	[]	
8840	[]	
8841	[]	
8842	[]	
8843	[]	

	gabor_sizes	...	\
0		[]	...
1	[237, 382, 341, 269, 332, 300, 256, 322, 252,
2	[355, 245, 207, 246, 209, 371, 209, 400, 214,
3	[270, 274, 369, 230, 364, 205, 360, 315, 396,
4	[228, 332, 237, 248, 346, 308, 333, 277, 232,
...	
8839		[]	...
8840		[]	...
8841		[]	...
8842		[]	...
8843		[]	...

	square_proportion_flipped	start_frame_stim	stop_frame_stim	\
0	NaN	0	1800	
1	NaN	1800	1818	
2	NaN	1818	1836	
3	NaN	1836	1854	
4	NaN	1854	1872	
...	
8839	0.00	249960	250020	
8840	0.00	250020	250080	
8841	0.25	250080	250140	
8842	0.25	250140	250200	
8843	NaN	250200	251999	

	num_frames_stim	start_frame_twop	stop_frame_twop	num_frames_twop	\
0	1800	143	1046	903	
1	18	1046	1055	9	
2	18	1055	1064	9	
3	18	1064	1073	9	
4	18	1073	1082	9	
...	
8839	60	125551	125581	30	
8840	60	125581	125611	30	
8841	60	125611	125641	30	
8842	60	125641	125672	31	
8843	1799	125672	126575	903	

	start_time_sec	stop_time_sec	duration_sec
0	14.30646	44.332150	30.025690
1	44.33215	44.639380	0.307230
2	44.63938	44.939040	0.299660
3	44.93904	45.232430	0.293390
4	45.23243	45.526750	0.294320
...
8839	4183.68954	4184.690500	1.000960

8840	4184.69050	4185.691070	1.000570
8841	4185.69107	4186.692190	1.001120
8842	4186.69219	4187.690570	0.998380
8843	4187.69057	4217.673903	29.983333

[8844 rows x 24 columns]

1.2.5 Stimulus objects

Once `sess.extract_info()` is run, each Session object also contains Stim objects.

These come in one of three subclasses: `Gabors`, `Visflow`, `Grayscr`, and can be accessed with: `sess.stims`, `sess.gabors`, `sess.visflow`, `sess.grayscr`.

The the Stim object `stim`, the Session object can be accessed with `stim.sess`.

```
number of rois      : 90
mouse number       : 4
mouse ID           : 411771
gabor object       : Gabors (stimulus from session 760260459)
2p frames per sec  : 30.08
stimulus frames per sec: 59.95
```

1.3 3. Retrieving data of interest

1.3.1 Identifying stimulus segments of interest

From a Session's Stim, you can get a list of segments that fit a specific criterion, e.g. **U segments** (unexpected, 3rd Gabor frame).

1.3.2 Identifying frame numbers of interest, to index the data

Then, you can retrieve the exact frame numbers that match these segments.

Specifically, you can access: * `twop` frame numbers, which index the two-photon data and pupil data, and * `stim` frame numbers, which index the running data.

Note: When retrieving the frame numbers, specifying `ch_fl` (check flanks) ensures that only frame numbers whose flanks are within the recording are returned. In other words, any frame number too close to the start or end of the recording (based on `pre/post` values), will be dropped.

1.3.3 Retrieving the data of interest

You can now get the **ROI / running / pupil data** corresponding to these reference frames and the specified `pre / post` periods (in sec).

1.3.4 Retrieving data statistics of interest

You can also directly obtain statistics on the data of interest.

```
[15]: datatype          roi_traces
      bad_rois_removed    yes
      scaled              no
      baseline            no
      integrated          yes
      smoothing           no
      fluorescence        dff
      general ROIs sequences
      stats    None stat_mean    0.062516
              error_SEM    0.017370
```

1.3.5 Using hierarchical dataframes

Data and statistics are returned in a hierarchical dataframe with **columns** and **indices**.

This has the advantage of allowing metadata to be stored in dummy columns, however extracting data from these dataframes can be tricky, syntactically.

```
[16]: datatype          roi_traces
      bad_rois_removed    yes
      scaled              yes
      baseline            no
      integrated          no
      smoothing           no
      fluorescence        dff
      ROIs sequences time_values
0    0          -1.000000   -0.338172
      -0.966102    0.155122
      -0.932203    0.150821
      -0.898305    0.053135
      -0.864407   -0.100729
...
102  81          0.864407    0.297796
      0.898305   -0.031714
      0.932203    0.339743
      0.966102    0.524661
      1.000000   -0.289968
```

```
[442800 rows x 1 columns]
```

To **extract a numpy array** with the correct dimensions from a hierarchical dataframe, you can use the following utility function: `gen_util.reshape_df_data()`.

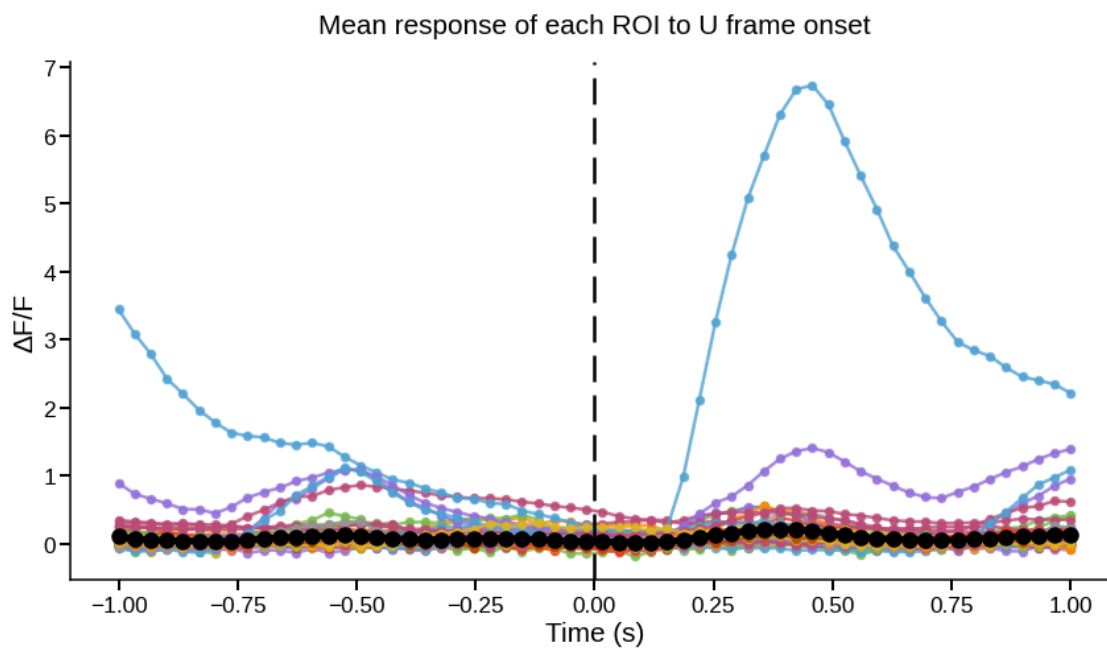
Here, each index level, then column level is turned into a new axis, **i.e. ROIs x sequences x time_values** (In this case, `squeeze_cols` is set to `True` to prevent each dummy column from becoming its own axis.)

ROI data shape: 90 ROIs x 82 sequences x 60 time values

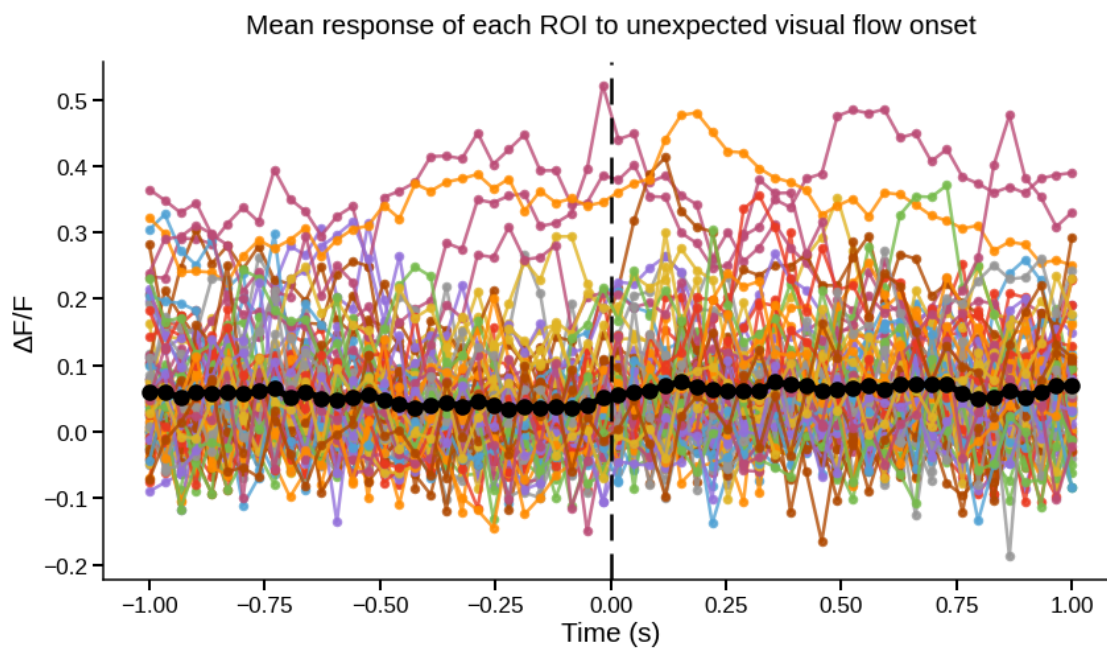
You can also retrieve the time stamps for each frame.

1.3.6 Visualizing the data

Finally, we can plot each ROI's mean activity across Gabor sequences, as well as a mean across ROIs.



1.3.7 The same steps apply to analysing the visual flow stimulus



1.4 4. Tracked ROIs

ROI tracking was performed on the production data.

At any point, it is possible to **restrict the data returned** to only the tracked ROIs, called `sess.set_only_tracked_rois(True)`.

Here, we retrieve the data, **integrated over each sequence**.

The dataframe returned contains data only for tracked ROIs.

```
[23]: datatype      roi_traces
      bad_rois_removed      yes
      scaled              yes
      baseline            no
      integrated          yes
      smoothing           no
      fluorescence       dff
      ROIs sequences
28    0                  0.101591
      1                  0.188843
      2                 -0.072082
      3                  0.685275
      4                  0.033439
...
22    27                  0.026887
      28                  0.523182
      29                 -0.039192
      30                 -0.059955
      31                  0.080472
```

```
[1504 rows x 1 columns]
```

1.4.1 Extracting tracked ROI data *correctly* (!)

Importantly, the ROIs are now sorted in their tracking order, which ensures that they are correctly aligned across sessions.

As a result, the “**ROIs**” index may no longer be in increasing order, like in this example.

ROI numbers, ordered for tracking:

```
28, 69, 90, 2, 55, 7, 5, 73, 101, 16, 93, 85, 84, 17, 15, 18, 29, 26, 13, 48, 1,
74, 25, 87, 72, 88, 89, 76, 0, 78, 67, 57, 62, 50, 42, 41, 43, 14, 32, 6, 45,
46, 98, 44, 27, 34, 22
```

Note that these **ROI numbers** are assigned for each session separately. Thus, e.g., ROI #28 from session 1 is most likely not the same neuron/dendrite as the ROI #28 from session 2, for the same mouse. For this reason, **the tracking ordering** is important: it allows ROI traces from different sessions to be lined up correctly with one another.

To ensure that the tracked ROI order is preserved when extracting the data, the safest option is to use the utility function introduced above, i.e. `gen_util.reshape_data_df()`. It will ensure that the order is preserved.

```
Tracked ROI data shape using the correct method, i.e.,
gen_util.reshape_df_data()
47 ROIs x 32 sequences
```

Do not use the `.unstack()` method for hierarchical dataframes!

Even though the `.unstack()` method is typically a convenient way to extract a 2D array from a hierarchical dataframe, it will cause major problems here. Specifically, `.unstack()` internally triggers a resorting of the hierarchical indices. Thus, using it will completely mess up the tracked ROI order.

```
Tracked ROI data shape using the wrong method, i.e., .unstack()
47 ROIs x 32 sequences
```

As you can see, the dimensions are still correct. However, the **ROI sorting is actually lost!**

For example, **ROI #5**, which should appear at index 6 in the array, is now at index 3.

```
Data for the tracked ROI at index 6, when using the correct method: i.e.,
gen_util.reshape_df_data()
0.005, 0.024, -0.050, -0.553, 0.629, -0.051, -0.057, 0.071, -0.003, -0.067 ...
```

```
Data for the tracked ROI at index 6, when using the wrong method: i.e.,
.unstack()
0.053, 0.191, 0.232, -0.004, -0.008, 0.060, 0.083, -0.031, 0.015, 0.024 ...
```

```
Data for the tracked ROI that should be at index 6 is instead at index 3,
when using the wrong method: i.e., .unstack()
0.005, 0.024, -0.050, -0.553, 0.629, -0.051, -0.057, 0.071, -0.003, -0.067 ...
```

1.4.2 Reset the session to start using all ROIs, again

1.5 5. Additional tips on indexing a hierarchical dataframe

```
[31]: scaled          yes
      baseline        no
      integrated      no
      smoothing       no
      fluorescence    dff
      ROIs sequences time_values
0      1          -1.0    -0.183646
      20          -1.0     0.013693
      21          -1.0   -0.091127
3      1          -1.0     0.221201
      20          -1.0     0.347209
      21          -1.0   -0.163844
```

5	1	-1.0	-0.243460
	20	-1.0	-0.422120
	21	-1.0	0.203985

1.6 6. Retrieving several Session objects, based on criteria

1.6.1 Identifying mice or session IDs to omit (pilot data only)

`sess_gen_util.all_omit()` allows keeping track of **which session IDs or mice must be left out**.

This actually **only applies to pilot data**, where some mice did not see all the stimuli of interest, and one session has incomplete data.

For the prod data, the lists are empty.

1.6.2 Retrieving mouse / session numbers and IDs that fit specific criteria

`sess_gen_util.get_sess_vals()` can be used to retrieve information for sessions that meet certain criteria.

e.g., **session number 1, 2 or 3, production, dendritic plane**

```
mouse 1: 758519303 (session 1)
mouse 1: 759189643 (session 2)
mouse 1: 759660390 (session 3)
mouse 3: 761624763 (session 1)
mouse 3: 761944562 (session 2)
mouse 3: 762250376 (session 3)
mouse 4: 760260459 (session 1)
mouse 4: 760659782 (session 2)
mouse 4: 761269197 (session 3)
mouse 7: 777496949 (session 1)
mouse 7: 778374308 (session 2)
mouse 7: 779152062 (session 3)
mouse 12: 826659257 (session 1)
mouse 12: 827300090 (session 2)
mouse 12: 828475005 (session 3)
mouse 13: 832883243 (session 1)
mouse 13: 833704570 (session 2)
mouse 13: 834403597 (session 3)
```

1.6.3 Loading the sessions

`sess_gen_util.init_sessions()` can be used to **initialize the sessions** and **extract the requested data**.

```
Creating session 758519303...
Loading stimulus and alignment info...
```

```
Loading ROI trace info...
Loading running info...
Finished creating session 758519303.
```

```
Creating session 759189643...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
Finished creating session 759189643.
```

```
Creating session 759660390...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
Finished creating session 759660390.
```

```
Creating session 764704289...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
Finished creating session 764704289.
```

1.6.4 Using the loaded sessions

Now, one can run through the sessions, and run whatever analysis is needed.

Note here that, when calling `stim.get_segs_by_criteria()`, **features that do not apply to the stimulus** (e.g., `gabfr` for the `visflow` stimulus) **are simply ignored**.

```
Session ID: 758519303 (mouse 1, session 1)
    visflow: 31 sequences
    gabors: 94 sequences
Session ID: 759189643 (mouse 1, session 2)
    visflow: 34 sequences
    gabors: 90 sequences
Session ID: 759660390 (mouse 1, session 3)
    visflow: 33 sequences
    gabors: 105 sequences
Session ID: 764704289 (mouse 6, session 1)
    visflow: 33 sequences
    gabors: 96 sequences
```

1.7 7. Retrieving ROI masks from a session

Boolean ROI masks can be obtained for each Session.

1.7.1 Dendritic mask types

For **dendritic sessions**, the Session is built to assume that **extr** (not **allen**) ROI data is to be used. This can be checked by checking `self.dend`. As long as `self.dend` is properly set, the correct ROI data and masks will be loaded.

The **allen** masks were extracted with a pipeline tailored to somatic ROIs, and are therefore not preferred for dendritic data.

In contrast, the **extr** masks were extracted with the EXTRACT pipeline, which specifically enables dendrite-shaped ROIs to be identified.

Note that, for this reason, *only the extr dendritic ROIs and masks* are included in the data in NWB formatted data.

Dendritic session, ROI type: **extr**

Somatic session, ROI type: **allen**

1.7.2 Loading masks

Masks can be loaded as follows, with dimensions: **ROI x height x width**, retrieving only masks for ROIs that are valid (when evaluated by their dF/F traces).

Notes: - **If sessions are set to use only tracked ROIs**, as described above, only masks for the tracked ROIs (sorted in the tracking order) will be returned. - If running this notebook in **Binder**, the dendritic masks will not loaded, as the memory requirements are too high (~2-3GB).

In most functions, by default, ROIs that are considered **bad (non valid)** are automatically removed (`rem_bad=True`).

Note that, **for the NWB data**, the *bad ROIs were removed altogether*.

These ROIs either:

- (1) **contain NaN/Infs values** or
- (2) **have been deemed too noisy**.

If, for whatever reason, **all masks are needed**, including those for the bad ROIs,

- (1) ensure that the session is currently set to return all ROI data, with `sess.only_tracked_rois(False)`, then
- (2) call `self.get_roi_masks(rem_bad=False)`.

Of course, as explained above, if using the NWB data, there are no bad ROIs.

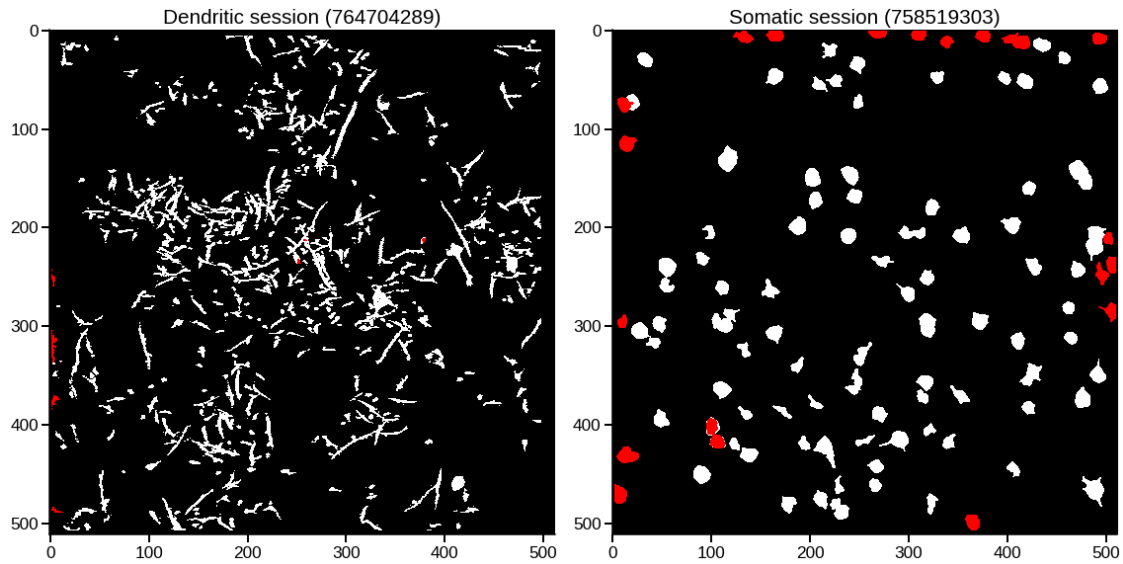
1.7.3 Bad ROIs

When using the data in its **original format**, one can get a list of bad ROIs, by using `self.get_bad_rois()`.

If the data is in **NWB format**, there should be **no bad ROIs**, as they have already been removed.

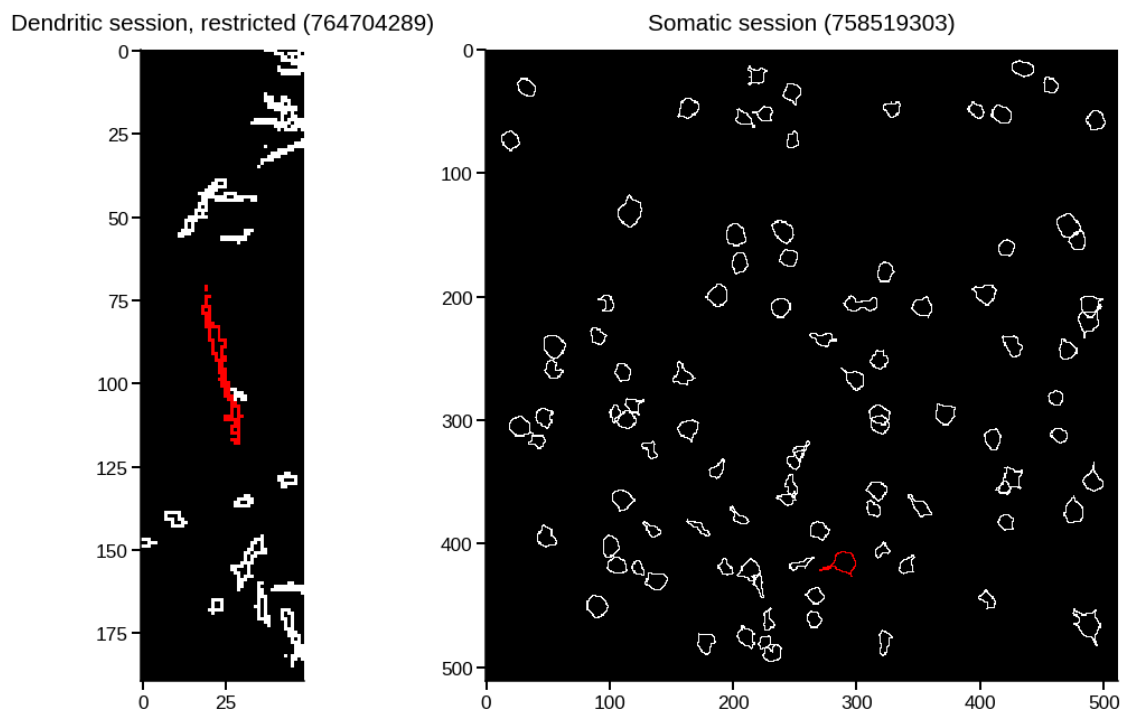
1.7.4 Visualizing ROI masks

`sess_plot_util.plot_ROIs()` can be used to visualize ROIs, where specific ROIs can be set to red using a `valid_mask`.



1.7.5 Visualizing ROI mask contours

`sess_plot_util.plot_ROI_contours()` can be used to visualize ROI contours, optionally restricted to around an ROI of interest.



1.8 8. Visualizing stimulus templates (NWB data only)

If using the NWB versions of the data, one should note that different NWB versions are available for each session, on the [Dandi archive](#).

The basic versions are the smallest ones (~130 MB to 1.7 GB each), and contain all the data needed for most analyses. In contrast, the versions with `+image` in the name also contain the stimulus templates, i.e. all unique stimulus frame images. They are typically ~1.5 GB larger than the corresponding basic versions.

We can load an example session: mouse 1, session 1, downloaded from the Dandi archive: [sub-408021_ses-758519303_behavior+ophys.nwb](#).

Be sure to download the file, and place it in the ``datadir_nwb`` directory:
`/media/colleen/LaCie/OtherBackups/CredAssign/OSCA_NWB.`

```
/home/colleen/Documents/PhD/OpenScope_CA_Analysis/analysis/session.py:278:  
UserWarning:
```

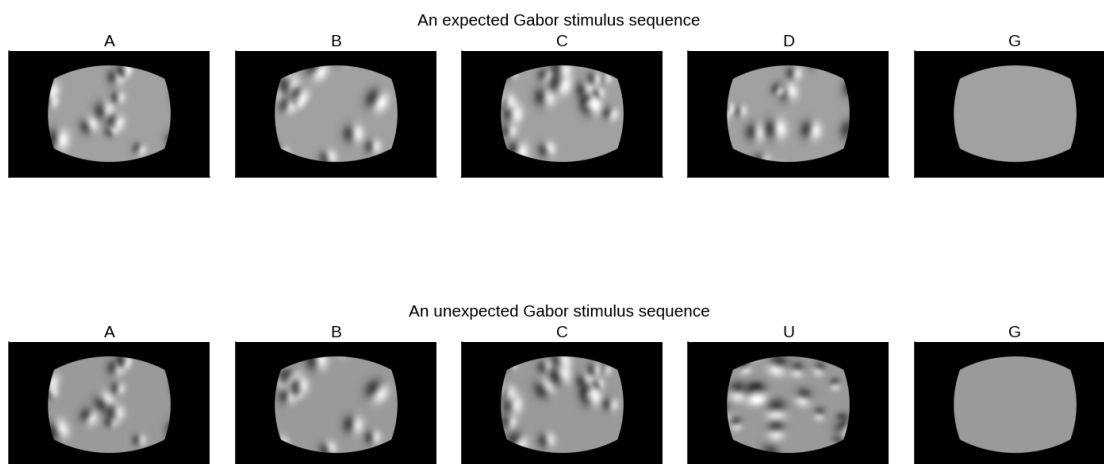
```
Several NWB files were found for this session. When loading data, the first file  
listed that contains the required data will be used.
```

```
Loading stimulus and alignment info...
```

As the warning indicates, the `Session` object has found both the basic version of the data for this session, and the version that also contains the stimulus template (`+image`) in the specified data directory. At any step where data must be loaded, the `Session` object will load it from the first listed version (alphabetically) that contains the required data.

1.8.1 Gabor sequence images

We can now identify the frame numbers for the **first Gabor sequence**, and **visualize** the corresponding stimulus images.



As we can see, whereas the Gabor patch orientations are consistent across frames in the expected sequence, they are rotated by 90° in the U frame of the unexpected sequence.

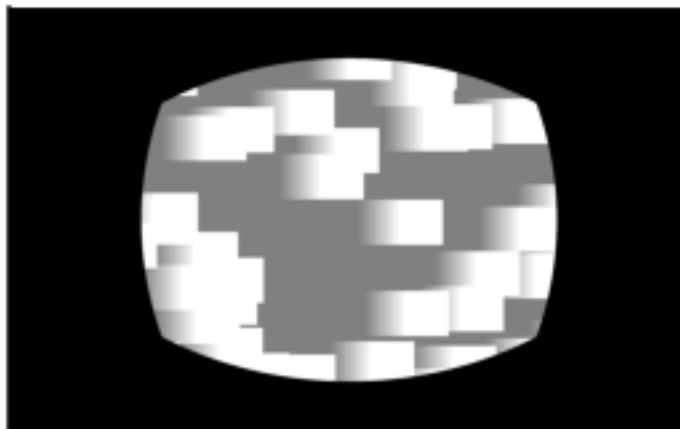
1.8.2 Warping

Note that the periphery of the images is masked in black. This is because, during the actual stimulus presentation, the images were presented on a **flat screen, and spherically warped**. This ensured that the apparent properties of the stimuli (size, speed, spatial frequency, etc.) were constant across the monitor, as seen from the mice's perspectives. The black masks overlayed on the unwarped stimuli stored in the NWB file, therefore, **mask the parts of the stimuli that were outside the edges of the screen, due to warping, and thus not visible** to the mice during the experiments.

1.8.3 Visual flow sequence images

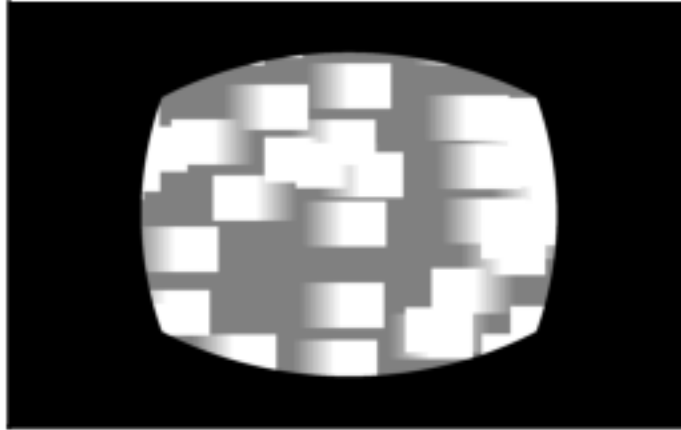
We can also visualize the **visual flow stimulus**. It is important to note that, whereas the Gabor images are static for each segment, the visual flow stimulus is in motion, and therefore changes at each frame. For this reason, we will simply identify the first visual flow segment in a sequence, and visualize the first few frames in that follow it.

An expected visual flow sequence



An unexpected visual flow sequence





We plot the first few frames in each sequence separately. We then also plot all the frames retained for each sequence, **overlayed in a graded way**, in order to visualize the squares **in motion**.

As we can see, in the **expected** sequence, all of the squares are moving rightward, uniformly. In contrast, in the **unexpected** sequence, although most squares are still moving rightward, ~25% of them are moving in the opposite direction, i.e., leftward.

1.8.4 Stimulus generating code and examples

This [repository](#) contains the code to generate these stimuli, as well as some example videos.

1.9 9. Last notes

There is much more to the codebase, and even to the `Session` and `Stim` objects, and almost all functions and methods are thoroughly documented.

When looking to implement a new analysis, consider checking to see whether relevant functions have already been implemented in:

- * `analysis/session.py`
- * `analysis/basic_analys.py`
- * `sess_util/sess_gen_util.py`

1.9.1 Methods/properties attached to `Session` and `Stim` objects.

```

Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
Loading pupil info...
Session (758519303)

```

```

Public properties:

```

```
self.DOB
self.age_weeks
self.all_files
self.any_files
self.date
self.dend
self.depth
self.drop_tol
self.gabors
self.grayscr
self.home
self.line
self.max_proj
self.mouse_df
self.mouse_n
self.mouseid
self.n_stims
self.notes
self.nwb
self.only_tracked_rois
self.pass_fail
self.plane
self.pup_data
self.pup_data_available
self.roi_facts_df
self.roi_masks
self.roi_names
self.run_data
self.runtype
self.sess_files
self.sess_n
self.sessid
self.sex
self.stim2twopfr
self.stim_df
self.stim_fps
self.stim_seed
self.stims
self.stimtypes
self.tot_stim_fr
self.tot_twop_fr
self.tracked_rois
self.twop2stimfr
self.twop_fps
self.visflow
```

Public methods:

```
self.check_flanks()
```

```

self.convert_frames()
self.data_loaded()
self.extract_info()
self.get_active_rois()
self.get_bad_rois()
self.get_fr_ran()
self.get_frames_timestamps()
self.get_local_nway_match_path()
self.get_nrois()
self.get_plateau_roi_traces()
self.get_pup_data()
self.get_registered_max_proj()
self.get_registered_roi_masks()
self.get_roi_masks()
self.get_roi_seqs()
self.get_roi_trace_path()
self.get_roi_traces()
self.get_roi_traces_by_ns()
self.get_run_velocity()
self.get_run_velocity_by_fr()
self.get_single_roi_trace()
self.get_stim()
self.load_pup_data()
self.load_roi_info()
self.load_run_data()
self.set_only_tracked_rois()

```

Gabors (stimulus from session 758519303)

Public properties:

```

self.all_gabfr
self.all_gabfr_mean_oris
self.block_params
self.deg_per_pix
self.exp_gabfr
self.exp_gabfr_mean_oris
self.exp_max_s
self.exp_min_s
self.kappas
self.n_patches
self.n_segs_per_seq
self.ori_ran
self.phase
self.seg_len_s
self.sess
self.sf
self.size_ran
self.stim_fps

```

```
self.stim_params
self.stimtype
self.unexp_gabfr
self.unexp_gabfr_mean_oris
self.unexp_max_s
self.unexp_min_s
self.win_size
```

Public methods:

```
self.get_A_frame_1s()
self.get_A_segs()
self.get_all_unexp_segs()
self.get_all_unexp_stim_fr()
self.get_fr_by_seg()
self.get_frames_by_criteria()
self.get_n_fr_by_seg()
self.get_pup_diam_data()
self.get_pup_diam_stats_df()
self.get_roi_data()
self.get_roi_stats_df()
self.get_run()
self.get_run_data()
self.get_run_stats_df()
self.get_segs_by_criteria()
self.get_segs_by_frame()
self.get_start_unexp_segs()
self.get_start_unexp_stim_fr_trans()
self.get_stats_df()
self.get_stim_beh_sub_df()
self.get_stim_df_by_criteria()
self.get_stim_images_by_frame()
self.get_stim_par_by_frame()
self.get_stim_par_by_seg()
```

Visflow (stimulus from session 758519303)

Public properties:

```
self.block_params
self.deg_per_pix
self.exp_max_s
self.exp_min_s
self.main_flow_dirs
self.n_squares
self.prop_flipped
self.seg_len_s
self.sess
self.speed
self.square_sizes
```

```
self.stim_fps
self.stim_params
self.stimtype
self.unexp_max_s
self.unexp_min_s
self.win_size
```

Public methods:

```
self.get_all_unexp_segs()
self.get_all_unexp_stim_fr()
self.get_dir_segs_exp()
self.get_fr_by_seg()
self.get_frames_by_criteria()
self.get_n_fr_by_seg()
self.get_pup_diam_data()
self.get_pup_diam_stats_df()
self.get_roi_data()
self.get_roi_stats_df()
self.get_run()
self.get_run_data()
self.get_run_stats_df()
self.get_segs_by_criteria()
self.get_segs_by_frame()
self.get_start_unexp_segs()
self.get_start_unexp_stim_fr_trans()
self.get_stats_df()
self.get_stim_beh_sub_df()
self.get_stim_df_by_criteria()
self.get_stim_images_by_frame()
```

Grayscr (session 758519303)

Public properties:

```
self.sess
self.stimtype
```

Public methods:

```
self.get_all_fr()
self.get_start_fr()
self.get_stim_images_by_frame()
self.get_stop_fr()
```

1.9.2 Example Session and Stim object property values.

Properties with long values (e.g., long dataframes, arrays, lists, strings) are omitted, for brevity.

Session (758519303)

Public property values:

```

self.DOB: 20180623
self.age_weeks: 13.5714285714286
self.all_files: True
self.any_files: True
self.date: 20180926
self.dend: extr
self.depth: 175
self.drop_tol: 0.0003
self.gabors: Gabors (stimulus from session 758519303)
self.grayscr: Grayscr (session 758519303)
self.line: L23-Cux2
self.mouse_n: 1
self.mouseid: 408021
self.n_stims: 2
self.notes: nan
self.nwb: True
self.only_tracked_rois: False
self.pass_fail: P
self.plane: soma
self.pup_data_available: True
self.runtype: prod
self.sess_n: 1
self.sessid: 758519303
self.sex: M
self.stim_fps: 59.951703429774675
self.stim_seed: 30587
self.stimtypes: ['gabors', 'visflow']
self.tot_stim_fr: 251999
self.tot_twop_fr: 126741
self.twop2stimfr: [nan nan nan ... nan nan nan]
self.twop_fps: 30.078983328254086

```

Gabors (stimulus from session 758519303)

Public property values:

```

self.all_gabfr: ['A', 'B', 'C', 'D', 'G', 'U']
self.all_gabfr_mean_oris: [0.0, 45.0, 90.0, 135.0, 180.0, 225.0]
self.deg_per_pix: 0.06251912565744862
self.exp_gabfr: ['A', 'B', 'C', 'D', 'G']
self.exp_gabfr_mean_oris: [0.0, 45.0, 90.0, 135.0]
self.exp_max_s: 90
self.exp_min_s: 30
self.kappas: [16]
self.n_patches: 30
self.n_segs_per_seq: 5
self.ori_ran: [0, 360]
self.phase: 0.25
self.seg_len_s: 0.3

```

```
self.sess: Session (758519303)
self.sf: 0.04
self.size_ran: [204, 408]
self.stim_fps: 59.951703429774675
self.stim_params: ['gabor_kappa']
self.stimtype: gabors
self.unexp_gabfr: ['U']
self.unexp_gabfr_mean_oris: [90.0, 135.0, 180.0, 225.0]
self.unexp_max_s: 6
self.unexp_min_s: 3
self.win_size: [1920, 1200]
```

Visflow (stimulus from session 758519303)

Public property values:

```
self.deg_per_pix: 0.06251912565744862
self.exp_max_s: 90
self.exp_min_s: 30
self.main_flow_dirs: ['left (nasal)', 'right (temp)']
self.n_squares: [105]
self.prop_flipped: 0.25
self.seg_len_s: 1
self.sess: Session (758519303)
self.speed: 799.7552664756905
self.square_sizes: [128]
self.stim_fps: 59.951703429774675
self.stimtype: visflow
self.unexp_max_s: 4
self.unexp_min_s: 2
self.win_size: [1920, 1200]
```

Grayscr (session 758519303)

Public property values:

```
self.sess: Session (758519303)
self.stimtype: grayscreen
```