

session_demonstration_script

November 26, 2021

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:

- These packages should be present if installing the conda environment from `osca.yml`.
- `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, check whether there are updates to the utility, if an error occurs, and consider updating your installation, e.g., by running, from the command line:
`pip install -U util-colleenjg`

```
[1]: import sys
from pathlib import Path

from matplotlib import pyplot as plt
import numpy as np
import pandas as pd

sys.path.extend([".", ".."])
from analysis import session
from sess_util import sess_gen_util, sess_plot_util
from util import gen_util, logger_util, plot_util
```

1.1 Plot formatting

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

```
[2]: plot_util.linclab_plt_defaults()
```

1.2 Set paths to main data directory and the mouse dataframe

1.2.1 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.

```
[3]: datadir = Path("../", "../", "data", "OSCA")
```

1.2.2 Mouse dataframe

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

```
[4]: mouse_df = pd.read_csv(Path("../", "mouse_df.csv"))
```

Mouse dataframe columns:

- * **sessid**: Unique session ID (9-digit)
- * **dandi_session_id**: Dandiset session ID for data in NWB format.
- * **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.

```
[5]: mouse_df
```

```
[5]:      sessid dandi_session_id  mouse_n  mouseid      date  depth plane  \
0    712483302                NaN        1   389778  20180621    20  dend
1    712942208                NaN        1   389778  20180622   375  soma
2    714893802                NaN        1   389778  20180627    20  dend
3    715244457                NaN        1   389778  20180628    20  dend
4    716425232                NaN        1   389778  20180702   375  soma
..      ...                ...      ...      ...      ...      ...
78   833704570                NaN       13   440889  20190307   175  soma
79   834403597  20190314T152429       13   440889  20190308   175  soma
80   836968429  20190314T152429       13   440889  20190314   175  soma
81   837360280  20190315T152224       13   440889  20190315   175  soma
82   838633305                NaN       13   440889  20190318   175  soma
```

```
      line runtype  sess_n  ...  nrois_tracked  nrois_all  nrois_allen  \
0    L5-Rbp4  pilot      1  ...           -1        1468        232
1    L5-Rbp4  pilot      2  ...           -1         78         62
2    L5-Rbp4  pilot      3  ...           -1         -1         -1
3    L5-Rbp4  pilot      4  ...           -1        949        458
4    L5-Rbp4  pilot      5  ...           -1         79         56
..      ...      ...      ...      ...      ...      ...
78   L23-Cux2  prod       2  ...          147        251        224
79   L23-Cux2  prod       3  ...          147        228        210
80   L23-Cux2  prod       4  ...           -1        217        205
81   L23-Cux2  prod       5  ...           -1        244        217
82   L23-Cux2  prod       6  ...           -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 set to 800 um

```

```
[83 rows x 21 columns]
```

1.3 1. Basics of initializing a Session object

Sessions can be initialized with their 9-digit sessid:

```
[6]: sess = session.Session(764704289, datadir=datadir, mouse_df=mouse_df)
```

or with their mouse_n, sess_n and runtime:

```
[7]: sess = session.Session(mouse_n=6, sess_n=1, runtime="prod", datadir=datadir,
    ↪ mouse_df=mouse_df)
```

1.3.1 Data format is identified automatically

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

1.3.2 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.

1.3.3 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()`.

```
[8]: sess.extract_info(full_table=False, roi=True, run=True, pupil=True)
```

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

```
Loading ROI trace info...
```

```
Loading running info...
```

```
WARNING: Session 764704289: 211 dropped running frames (~0.1%) (in pre-
processing).
```

```
Loading pupil info...
```

1.3.4 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 grayscreen 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.

```
[9]: sess.stim_df
```

```
[9]:      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      1.0
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     135.0     30.0
2     16.0     135.0     30.0
3     16.0     135.0     30.0
4     16.0     135.0     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  [-957.5664595131418, -573.877007228148, 789.96...
2  [-628.4848961265818, 341.7183469416823, 321.20...
3  [683.6508663589163, -890.7309000633387, -754.8...
4  [579.5453003762645, -499.8681800025132, -951.1...
...
```

8839	[]
8840	[]
8841	[]
8842	[]
8843	[]

	gabor_locations_y \
0	[]
1	[-523.4450587378464, 22.61763399099607, -287.1...
2	[-122.57399381760757, -198.4686150995812, 203...
3	[-270.11244158601005, 574.7874674037628, -168...
4	[322.1656471050667, 97.49426011674268, 244.289...
...	...
8839	[]
8840	[]
8841	[]
8842	[]
8843	[]

	gabor_sizes ... \
0	[] ...
1	[293, 392, 392, 323, 280, 396, 316, 363, 226,
2	[313, 319, 262, 228, 400, 210, 264, 218, 308,
3	[396, 212, 277, 210, 390, 329, 406, 317, 358,
4	[326, 244, 208, 212, 251, 242, 341, 299, 406,
...
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	0.25	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	125552	125582	30
8840	60	125582	125612	30
8841	60	125612	125642	30
8842	60	125642	125672	30
8843	1799	125672	126575	903

	start_time_sec	stop_time_sec	duration_sec
0	14.277090	44.301717	30.024627
1	44.301717	44.602241	0.300524
2	44.602241	44.902563	0.300322
3	44.902563	45.202768	0.300204
4	45.202768	45.503007	0.300240
...
8839	4183.741890	4184.742721	1.000831
8840	4184.742721	4185.743529	1.000808
8841	4185.743529	4186.744364	1.000835
8842	4186.744364	4187.745223	1.000860
8843	4187.745223	4217.728557	29.983333

[8844 rows x 24 columns]

1.3.5 Stimulus objects

Once `sess.extract_info()`, each Session object now 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`.

```
[10]: print(f"number of rois      : {sess.get_nrois()}")
      print(f"mouse number    : {sess.mouse_n}")
      print(f"mouse ID       : {sess.mouseid}")
      print(f"gabor object     : {sess.gabors}")
      print(f"2p frames per sec    : {sess.twop_fps:.2f}")
      print(f"stimulus frames per sec: {sess.stim_fps:.2f}")
```

```
number of rois      : 628
mouse number        : 6
mouse ID            : 413663
gabor object        : Gabors (stimulus from session 764704289)
2p frames per sec   : 30.08
stimulus frames per sec: 59.95
```

1.4 2. Retrieving data of interest

1.4.1 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).

```
[11]: gab_seg_ns = sess.gabors.get_segs_by_criteria(gabk=16, gabfr=3, unexp=1,
        ↪by="seg")
```

1.4.2 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.

```
[12]: pre = 1.0
      post = 1.0
      twop_fr_ns = sess.gabors.get_fr_by_seg(gab_seg_ns, start=True, ch_fl=[pre,
        ↪post], fr_type="twop")["start_frame_twop"]
      stim_fr_ns = sess.gabors.get_fr_by_seg(gab_seg_ns, start=True, ch_fl=[pre,
        ↪post], fr_type="stim")["start_frame_stim"]
```

1.4.3 Retrieving the data of interest

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

```
[13]: roi_data_df = sess.gabors.get_roi_data(twop_fr_ns, pre, post, scale=True)
      run_data_df = sess.gabors.get_run_data(stim_fr_ns, pre, post, scale=True)
      pup_data_df = sess.gabors.get_pup_diam_data(twop_fr_ns, pre, post, scale=True)
```

1.4.4 Retrieving data statistics of interest

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

```
[14]: roi_stats_df = sess.gabors.get_roi_stats_df(
        twop_fr_ns, pre, post, integ=True, stats="mean", error="sem", byroi=False
    )
```

```
[15]: roi_stats_df
```

```
[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  0.026752
          error_SEM    0.000911

```

1.4.5 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]: roi_data_df
```

```

[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   -0.009556
          -0.966102   -0.644810
          -0.932203   -0.214521
          -0.898305   -0.116127
          -0.864407   -0.318214
...
643  95           0.864407    0.050568
          0.898305    0.445153
          0.932203    0.108850
          0.966102    0.116475
          1.000000    0.213779

```

```
[3617280 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.)

```

[17]: roi_data = gen_util.reshape_df_data(roi_data_df, squeeze_cols=True)
print("ROI data shape: {} ROIs x {} sequences x {} time values".
      ↪format(*roi_data.shape))

```

ROI data shape: 628 ROIs x 96 sequences x 60 time values

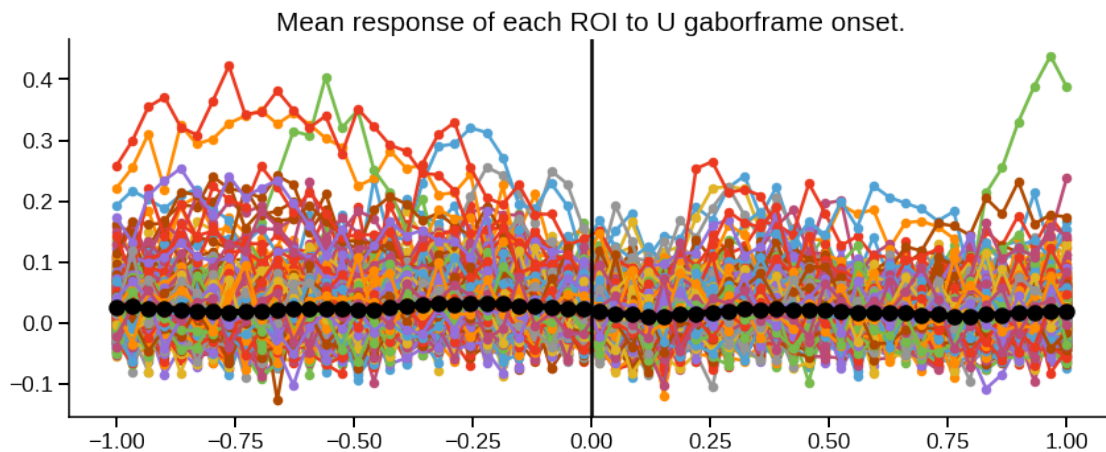
You can also retrieve the time stamps for each frame.

```
[18]: xran = roi_data_df.index.unique("time_values")
```

1.4.6 Visualizing the data

Finally, we can plot each ROIs mean activity across sequences, as well as a mean across ROIs.

```
[19]: fig, ax = plt.subplots(1, figsize=(12, 5))
_ = ax.plot(xran, np.mean(roi_data, axis=1).T, marker=".") # mean per ROI
_ = ax.plot(xran, np.mean(np.mean(roi_data, axis=1).T, axis=1),
            lw=5, c="k", marker="o") # mean across ROIs
_ = ax.axvline(0, c="k")
_ = ax.set_title("Mean response of each ROI to U gaborframe onset.")
```



1.4.7 The same steps apply for Visflow

```
[20]: visflow_seg_ns = sess.visflow.get_segs_by_criteria(visflow_size=128, unexp=1,
    ↪remconsec=True, by="seg")

pre = 1.0
post = 1.0
twop_fr_ns = sess.visflow.get_fr_by_seg(
    visflow_seg_ns, start=True, ch_fl=[pre, post],
    ↪fr_type="twop")["start_frame_twop"]
stim_fr_ns = sess.visflow.get_fr_by_seg(
    visflow_seg_ns, start=True, ch_fl=[pre, post],
    ↪fr_type="stim")["start_frame_stim"]

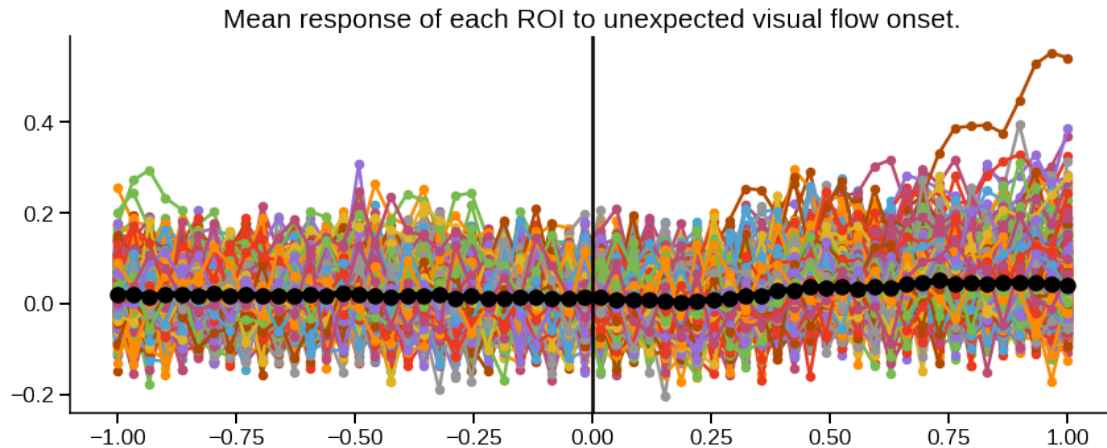
roi_data_df = sess.visflow.get_roi_data(twop_fr_ns, pre, post, scale=True)
```

```

roi_data = gen_util.reshape_df_data(roi_data_df, squeeze_cols=True)
xran = roi_data_df.index.unique("time_values")

fig, ax = plt.subplots(1, figsize=(12, 5))
_ = ax.plot(xran, np.mean(roi_data, axis=1).T, marker=".") # mean per ROI
_ = ax.plot(xran, np.mean(np.mean(roi_data, axis=1).T, axis=1),
            lw=5, c="k", marker="o") # mean across ROIs
_ = ax.axvline(0, c="k")
_ = ax.set_title("Mean response of each ROI to unexpected visual flow onset.")

```



1.5 3. 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)`.

```
[21]: sess.set_only_tracked_rois(True)
```

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

```
[22]: tracked_roi_data_df = sess.visflow.get_roi_data(twop_fr_ns, pre, post,
↪scale=True, integ=True)
```

The dataframe returned contains data only for tracked ROIs.

```
[23]: tracked_roi_data_df
```

```
[23]: datatype      roi_traces
bad_rois_removed    yes
scaled              yes
baseline            no
integrated          yes
```

smoothing		no
fluorescence		dff
ROIs	sequences	
0	0	-0.077642
	1	0.002518
	2	-0.076000
	3	0.060652
	4	-0.000458
...		...
242	28	-0.069519
	29	0.043961
	30	0.051469
	31	-0.011017
	32	0.188034

[4488 rows x 1 columns]

1.5.1 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.

```
[24]: roi_ns_ordered = tracked_roi_data_df.index.unique("ROIs").to_numpy()
print(f"ROI numbers, ordered for tracking:\n{'', '.join([str(roi_n) for roi_n in
↪roi_ns_ordered])}")
```

ROI numbers, ordered for tracking:

0, 3, 5, 8, 9, 11, 23, 24, 32, 45, 49, 52, 53, 55, 64, 66, 67, 70, 75, 91, 111,
123, 155, 205, 213, 215, 218, 221, 222, 223, 225, 227, 228, 229, 230, 232, 234,
238, 240, 245, 246, 247, 251, 253, 254, 257, 264, 269, 270, 273, 294, 300, 308,
315, 336, 346, 347, 350, 371, 372, 373, 374, 376, 377, 378, 379, 381, 382, 383,
386, 389, 391, 392, 394, 398, 404, 406, 409, 413, 417, 428, 432, 434, 435, 446,
449, 453, 464, 482, 518, 523, 528, 529, 530, 531, 532, 533, 536, 538, 539, 540,
543, 547, 549, 552, 554, 555, 556, 557, 558, 562, 563, 565, 571, 572, 575, 579,
580, 582, 585, 596, 608, 625, 643, 63, 72, 85, 332, 405, 188, 129, 267, 486,
616, 1, 242

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.

```
[25]: tracked_roi_data = gen_util.reshape_df_data(tracked_roi_data_df,
↪squeeze_cols=True)
print("Tracked ROI data shape using the correct method, i.e., gen_util.
↪reshape_df_data()"
      "\n{} ROIs x {} sequences".format(*tracked_roi_data.shape))
```

Tracked ROI data shape using the correct method, i.e.,
gen_util.reshape_df_data()
136 ROIs x 33 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.

```
[26]: tracked_roi_data_wrong = tracked_roi_data_df.unstack().to_numpy()
print("Tracked ROI data shape using the wrong method, i.e., .unstack()"
      "\n{} ROIs x {} sequences".format(*tracked_roi_data_wrong.shape))
```

Tracked ROI data shape using the wrong method, i.e., .unstack()
136 ROIs x 33 sequences

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

For example, **ROI #8**, which should appear as index 3 in the array, is now at index 4.

```
[27]: roi_idx_3_data = tracked_roi_data[3, :10]
print(f"Data for tracked ROI at index 3, when using the correct method: i.e., ↵
      ↵gen_util.reshape_df_data()"
      f"\n{'', '.join([f'{{val:.3f}}' for val in roi_idx_3_data])}] ...")
```

Data for tracked ROI at index 3, when using the correct method: i.e.,
gen_util.reshape_df_data()
0.032, -0.114, -0.035, -0.002, 0.032, -0.081, 0.004, -0.045, 0.046, 0.022 ...

```
[28]: roi_idx_3_data_wrong = tracked_roi_data_wrong[3, :10]
print(f"Data for tracked ROI at index 3, when using the wrong method: i.e., ↵
      ↵unstack()"
      f"\n{'', '.join([f'{{val:.3f}}' for val in roi_idx_3_data_wrong])}] ...")
```

Data for tracked ROI at index 3, when using the wrong method: i.e., .unstack()
-0.009, 0.013, 0.049, 0.026, -0.013, 0.741, -0.074, 0.004, 0.003, -0.035 ...

```
[29]: roi_idx_4_data_wrong = tracked_roi_data_wrong[4, :10]
print(f"Data for tracked ROI that should be at index 3 is instead at index 4,\n"
      "when using the wrong method: i.e., .unstack()"
      f"\n{'', '.join([f'{{val:.3f}}' for val in roi_idx_4_data_wrong])}] ...")
```

Data for tracked ROI that should be at index 3 is instead at index 4,
when using the wrong method: i.e., .unstack()
0.032, -0.114, -0.035, -0.002, 0.032, -0.081, 0.004, -0.045, 0.046, 0.022 ...

1.5.2 Reset the session to start using all ROIs, again

```
[30]: sess.set_only_tracked_rois(False)
```

1.6 4. Additional tips on indexing a hierarchical dataframe

```
[31]: # getting columns
roi_data_series = roi_data_df["roi_traces"]

# getting specific ROIs, from their IDs, e.g. (0, 3, 4)
roi_data_specific_rois = roi_data_df.loc([0, 3, 4])

# getting specific sequences (0, 3, 4) for all ROIs <- second order index, so
↳ requires a pandas slice
roi_data_specific_seqs = roi_data_df.loc[(pd.IndexSlice[:, [1, 20, 21]]), ]

# using both index and columns
roi_data_specific = roi_data_df.loc[(pd.IndexSlice[[0, 3, 4], [1, 20, 21]],
↳ -1)], ("roi_traces", "yes")]
roi_data_specific
```

```
[31]: scaled          yes
baseline            no
integrated          no
smoothing           no
fluorescence       dff
ROIs sequences time_values
0    1          -1.0    -0.114423
    20          -1.0    -0.502503
    21          -1.0    -0.020213
3    1          -1.0     0.647332
    20          -1.0     0.039799
    21          -1.0     0.066638
4    1          -1.0     0.339988
    20          -1.0     0.644120
    21          -1.0    -0.572354
```

1.7 5. Retrieving several Session objects, based on criteria

1.7.1 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.

```
[32]: omit_sess, omit_mice = sess_gen_util.all_omit(runtype="prod")
```

1.7.2 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

```
[33]: mouse_ns, sess_ns, sessids = sess_gen_util.get_sess_vals(
      mouse_df, ["mouse_n", "sess_n", "sessid"], sess_n=[1, 2, 3],
      ↪runtype="prod", plane="dend", omit_sess=omit_sess,
      omit_mice=omit_mice, unique=False)
```

```
[34]: print("\n".join([f"mouse {m:2}: {sid} (session {n})" for m, sid, n in
      ↪zip(mouse_ns, sessids, sess_ns)]))
```

```
mouse 6: 764704289 (session 1)
mouse 6: 765193831 (session 2)
mouse 6: 766502238 (session 3)
mouse 8: 777914830 (session 1)
mouse 8: 778864809 (session 2)
mouse 8: 779650018 (session 3)
mouse 9: 826187862 (session 1)
mouse 9: 826773996 (session 2)
mouse 9: 827833392 (session 3)
mouse 10: 826338612 (session 1)
mouse 10: 826819032 (session 2)
mouse 10: 828816509 (session 3)
mouse 11: 823453391 (session 1)
mouse 11: 824434038 (session 2)
mouse 11: 825180479 (session 3)
```

1.7.3 Loading the sessions

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

```
[35]: dend_sessions = sess_gen_util.init_sessions(
      sessids[:5], datadir, mouse_df, full_table=False, omit=True, runtype="prod",
      roi=True, run=True
    )

soma_sessions = sess_gen_util.init_sessions(
      [758519303], datadir, mouse_df, full_table=False, omit=True, runtype="prod",
      roi=True, run=True
    )
```

Creating session 764704289...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
WARNING: Session 764704289: 211 dropped running frames (~0.1%) (in pre-processing).
Finished creating session 764704289.

Creating session 765193831...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
WARNING: Session 765193831: 345 dropped running frames (~0.1%) (in pre-processing).
Finished creating session 765193831.

Creating session 766502238...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
WARNING: Session 766502238: 387 dropped running frames (~0.2%) (in pre-processing).
Finished creating session 766502238.

Creating session 777914830...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
WARNING: Session 777914830: 381 dropped running frames (~0.2%) (in pre-processing).
Finished creating session 777914830.

Creating session 778864809...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
WARNING: Session 778864809: 630 dropped running frames (~0.3%) (in pre-processing).
Finished creating session 778864809.

Creating session 758519303...
Loading stimulus and alignment info...
Loading ROI trace info...
Loading running info...
WARNING: Session 758519303: 175 dropped running frames (~0.1%) (in pre-processing).
Finished creating session 758519303.

1.7.4 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.

```
[36]: for sess in dend_sessions + soma_sessions:
      print(f"Session ID: {sess.sessid} (mouse {sess.mouse_n}, session {sess.
      ↪sess_n})")
      for stimtype in ["visflow", "gabors"]:
          stim = sess.get_stim(stimtype)
          segs = stim.get_segs_by_criteria(
              visflow_size=128, unexp=1, gabk=16, gabfr=3, by="seg",
              remconsec=(stimtype == "visflow")
          )
          print(f"    {stimtype}: {len(segs)} sequences")
```

```
Session ID: 764704289 (mouse 6, session 1)
    visflow: 33 sequences
    gabors: 96 sequences
Session ID: 765193831 (mouse 6, session 2)
    visflow: 34 sequences
    gabors: 98 sequences
Session ID: 766502238 (mouse 6, session 3)
    visflow: 29 sequences
    gabors: 94 sequences
Session ID: 777914830 (mouse 8, session 1)
    visflow: 32 sequences
    gabors: 83 sequences
Session ID: 778864809 (mouse 8, session 2)
    visflow: 29 sequences
    gabors: 88 sequences
Session ID: 758519303 (mouse 1, session 1)
    visflow: 31 sequences
    gabors: 94 sequences
```

1.8 6. Retrieving ROI masks from session.

Boolean ROI masks can be obtained for each Session.

1.8.1 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.

```
[37]: dend_sess = dend_sessions[0]
      print(f"Dendritic session, ROI type: {dend_sess.dend}")

      soma_sess = soma_sessions[0]
      print(f"Somatic session, ROI type: {soma_sess.dend}")
```

```
Dendritic session, ROI type: extr
```

```
Somatic session, ROI type: allen
```

1.8.2 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).

Note that **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.

```
[38]: dend_mask = dend_sess.get_roi_masks()
      soma_mask = soma_sess.get_roi_masks()
```

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.

```
[39]: dend_sess.set_only_tracked_rois(False)
      soma_sess.set_only_tracked_rois(False)

      dend_mask_all = dend_sess.get_roi_masks(rem_bad=False)
      soma_mask_all = soma_sess.get_roi_masks(rem_bad=False)
```

1.8.3 Bad ROIs

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

```
[40]: dend_nan_masks = np.asarray(dend_sess.get_bad_rois(fluor="dff"))
soma_nan_masks = np.asarray(soma_sess.get_bad_rois(fluor="dff"))

dend_valid = np.ones(len(dend_mask_all))
dend_valid[dend_nan_masks] = 0

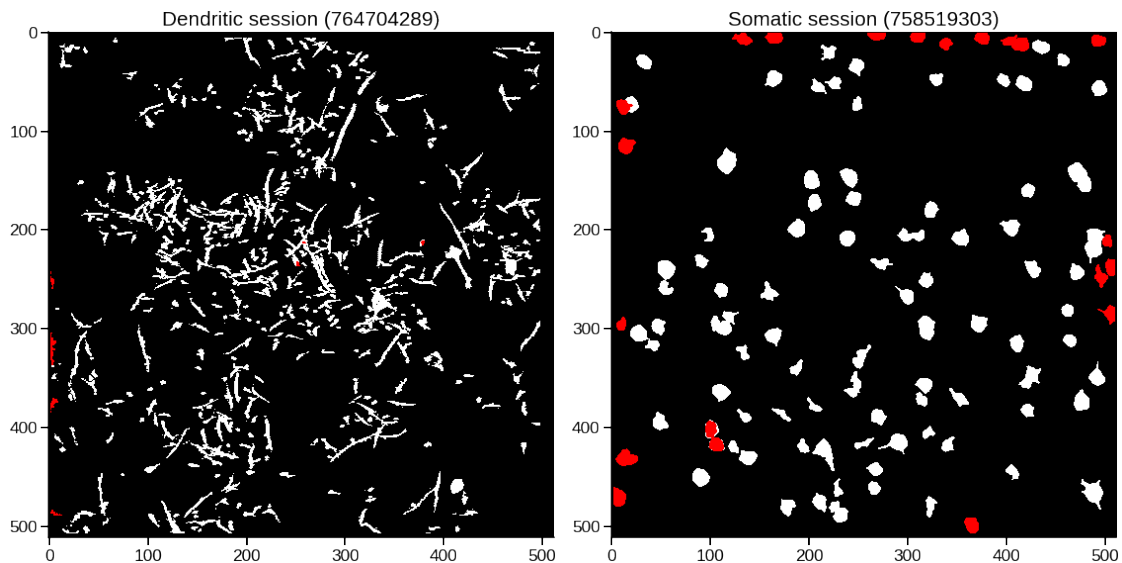
soma_valid = np.ones(len(soma_mask_all))
soma_valid[soma_nan_masks] = 0
```

1.8.4 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`.

```
[41]: fig, ax = plt.subplots(1, 2, figsize=(16, 9))
sess_plot_util.plot_ROIs(ax[0], dend_mask_all, valid_mask=dend_valid)
_ = ax[0].set_title(f"Dendritic session ({dend_sess.sessid})")

sess_plot_util.plot_ROIs(ax[1], soma_mask_all, valid_mask=soma_valid)
_ = ax[1].set_title(f"Somatic session ({soma_sess.sessid})")
```



1.8.5 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.

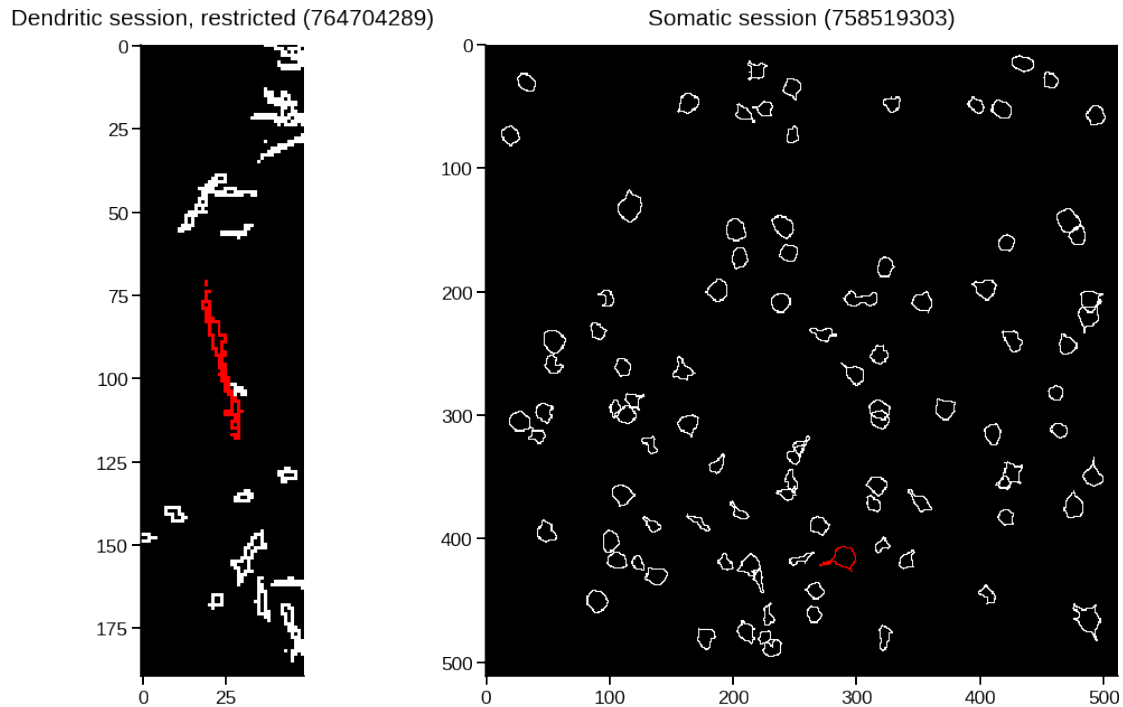
```
[42]: fig, ax = plt.subplots(1, 2, figsize=(16, 9))
sess_plot_util.plot_ROI_contours(ax[0], dend_mask, outlier=490, restrict=True)
```

```

_ = ax[0].set_title(f"Dendritic session, restricted ({dend_sess.sessid})", y=1.02)
↪02)

sess_plot_util.plot_ROI_contours(ax[1], soma_mask, outlier=30)
_ = ax[1].set_title(f"Somatic session ({soma_sess.sessid})", y=1.02)

```



1.9 7. 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.

```
[43]: print(f"{sess}{gen_util.create_attribute_str(sess)}")
```

Session (758519303)

Public properties:
`self.align_pkl`

```
self.all_files
self.any_files
self.behav_video_h5
self.correct_data_h5
self.date
self.dend
self.depth
self.dir
self.drop_tol
self.expcdir
self.expid
self.gabors
self.grayscr
self.home
self.line
self.max_proj
self.max_proj_png
self.mouse_df
self.mouse_dir
self.mouse_n
self.mouseid
self.n_stims
self.notes
self.nwb
self.only_tracked_rois
self.pass_fail
self.plane
self.procdir
self.pup_data_h5
self.pup_video_h5
self.roi_extract_json
self.roi_facts_df
self.roi_mask_file
self.roi_masks
self.roi_names
self.roi_objectlist
self.roi_trace_dff_h5
self.roi_trace_h5
self.run_data
self.runtype
self.segid
self.sess_n
self.sessid
self.stim2twopfr
self.stim_df
self.stim_fps
self.stim_pk1
self.stim_seed
```

```

self.stim_sync_h5
self.stims
self.stimtypes
self.time_sync_h5
self.tot_stim_fr
self.tot_twop_fr
self.tracked_rois
self.twop2stimfr
self.twop_fps
self.visflow
self.zstack_h5

```

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_nrois()
self.get_plateau_roi_traces()
self.get_pup_data()
self.get_roi_masks()
self.get_roi_seqs()
self.get_roi_trace_path()
self.get_roi_traces()
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()

```

```
[44]: print(f"{sess.gabors}-{gen_util.create_attribute_str(sess.gabors)}")
```

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_par_by_frame()
self.get_stim_par_by_seg()

```

```
[45]: print(f"{sess.visflow}-{gen_util.create_attribute_str(sess.visflow)}")
```

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()

```

```
[46]: print(f"{sess.grayscr}{gen_util.create_attribute_str(sess.grayscr)}")
```

Grayscr (session 758519303)

```

Public properties:
    self.sess

```


Public methods:

```
self.get_all_fr()
self.get_start_fr()
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.

```
[47]: print(f"{sess}{gen_util.create_property_str(sess, max_length=40)}")
```

Session (758519303)

Public property values:

```
self.all_files: True
self.any_files: True
self.date: 20180926
self.dend: allen
self.depth: 175
self.drop_tol: 0.0003
self.expid: 759038671
self.gabors: Gabors (stimulus from session 758519303)
self.grayscr: Grayscr (session 758519303)
self.home: ../../data/OSCA
self.line: L23-Cux2
self.mouse_dir: True
self.mouse_n: 1
self.mouseid: 408021
self.n_stims: 2
self.notes: nan
self.nwb: False
self.only_tracked_rois: False
self.pass_fail: P
self.plane: soma
self.roi_mask_file: None
self.runtype: prod
self.segid: 759205610
self.sess_n: 1
self.sessid: 758519303
self.stim_fps: 59.95049782968851
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: 30.078378454283577
```

```
[48]: print(f"{sess.gabors}{gen_util.create_property_str(sess.gabors,↵
↵max_length=40)}")
```

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: 59.95049782968851
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]
```

```
[49]: print(f"{sess.visflow}{gen_util.create_property_str(sess.visflow,↵
↵max_length=40)}")
```

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: 59.95049782968851
```

```
self.stimtype: visflow
self.unexp_max_s: 4
self.unexp_min_s: 2
self.win_size: [1920, 1200]
```

```
[50]: print(f"{sess.grayscr}{gen_util.create_property_str(sess.grayscr,↵
↵max_length=40)}")
```

Grayscr (session 758519303)

Public property values:

self.ssess: Session (758519303)

```
[ ]:
```