'Unnamed: 0', Extra column that pandas created… ignore

'cell\_specimen\_id', Cell id! Use this to merge with your dataframe

'lifetime\_sparseness\_nm3', Lifetime sparseness for nm3. Lifetime sparseness is a metric from 0 to 1, where 0 means the cell responds to all stim conditions, 1 means it responds uniquely to only one condition. This is computed for all stimuli, this is the value for natural move 3

'responsive\_nm3', Boolean for responding to NM3

'reliability\_nm3', Response reliability – mean cross-trial correlation of response

'peak\_frame\_nm3', frame of NM3 that the cell has the largest response to (I think)

'lifetime\_sparseness\_nm1a',

'responsive\_nm1a',

'reliability\_nm1a',

'peak\_frame\_nm1a',

These are the same as above for the other movie presentations. And many of these apply to the other stimuli below as well

'lifetime\_sparseness\_nm1b', '

responsive\_nm1b',

'reliability\_nm1b',

'peak\_frame\_nm1b',

'lifetime\_sparseness\_nm2',

'responsive\_nm2',

'reliability\_nm2',

'peak\_frame\_nm2',

'lifetime\_sparseness\_nm1c',

'responsive\_nm1c',

'reliability\_nm1c',

'peak\_frame\_nm1c',

'experiment\_container\_id', Experiment container ID

'tld1\_name', This is the Cre line

'area', Visual Area

'imaging\_depth\_x', imaging depth – ignore these, there are several.

'depth\_range', Depth range – this is the thing to use for depth information

'type', E or I for excitatory or inhibitory

'pref\_ori\_dg', Preferred direction for DG stimulus

'pref\_tf\_dg', Preferred Temporal Frequency

'num\_pref\_trials\_dg', # significant trials for DG – used for responsive, also a form of reliability

'responsive\_dg', Boolean for responding to DG

'g\_osi\_dg', Orientation selectivity for DG

'g\_dsi\_dg', Direction selectivity for DG (I actually have a different metric for this… in a different dataframe. They are closely related, so if we see something here, it’ll map to the other one, but I like the other one better)

'tfdi\_dg', TF discrimination index. Ignore

'reliability\_dg', Reliability – same as for NM

'lifetime\_sparseness\_dg',

'fit\_tf\_dg', peak TF from curve fitting

'fit\_tf\_ind\_dg', index of peak TF from curve fitting

'tf\_low\_cutoff\_dg', from curve fitting – less relevant

'tf\_high\_cutoff\_dg', from curve fitting – less relevant

'run\_pval\_dg', p-value for running modulation of peak response to DG

'run\_resp\_dg', mean response to peak condition in running trials

'stat\_resp\_dg', mean response to peak condition in stationary trials

'run\_mod\_dg', Running modulation metric (run-stat)/stat (if enhanced)…see code. Probably less useful than just is it modulated or not from the pval above.

'peak\_blank\_dg', compares peak response to blank sweep - ignore

'all\_blank\_dg', compares mean of all responses to blank sweep - ignore

'imaging\_depth\_y', imaging depth – ignore these, there are several.

'pref\_ori\_sg', preferred orientation for SG

'pref\_sf\_sg', preferred spatial frequency for SG

'pref\_phase\_sg', preferred phase for SG

'num\_pref\_trials\_sg',

'responsive\_sg', Boolean for responsiveness

'g\_osi\_sg',

'sfdi\_sg', ignore – equivalent of the TFDI metric above

'reliability\_sg',

'lifetime\_sparseness\_sg',

'fit\_sf\_sg',

'fit\_sf\_ind\_sg',

'sf\_low\_cutoff\_sg', ignore

'sf\_high\_cutoff\_sg', ignore

'run\_pval\_sg', ignore – I think running modulation of SG and NS stimuli is too messy to think about.

'run\_mod\_sg',

'run\_resp\_sg',

'stat\_resp\_sg',

'imaging\_depth\_x.1', imaging depth – ignore these, there are several.

'pref\_image\_ns', preferred image for natural scenes

'num\_pref\_trials\_ns',

'responsive\_ns',

'image\_selectivity\_ns',

'reliability\_ns',

'lifetime\_sparseness\_ns',

'run\_pval\_ns', ignore – again, too messy

'run\_mod\_ns',

'run\_resp\_ns',

'stat\_resp\_ns',

'imaging\_depth\_y.1', imaging depth – ignore these, there are several.

‘in\_rl', Boolean for cells imaged in RL if they actually map inside the region borders. Only relevant for RL

'include', Boolean for inclusion based on in\_rl above

'cre\_depth', tuple of Cre and depth range useful for making visualizations

'percent\_trials\_dg',

'percent\_trials\_ns',

'speed', Hmmm… I don’t remember this!

'area\_off\_1', Area of largest OFF subfield

'area\_off\_2', Area of second OFF subfield

'area\_on\_1', Area of largest ON subfield

‘area\_on\_2', Area of second ON subfield

'chi', Chi square value for receptive field

'oeid', experiment id?

'overlap\_11', Overlap of Off\_1 and On\_1 subfields

'overlap\_12', Overlap of 1 and 2 (I forget if it’s Off\_1 or On\_1)

'overlap\_21', Overlap of 2 and 1 (this is the opposite of above)

'overlap\_22', Overlap of Off\_2 and On\_2 subfields

'lsn\_stimulus', name of which LSN stimulus was used

'total\_area', total RF area, taking all subfields and overlap into account

'responsive\_lsn', Boolean of whether cell has RF

'cv\_dg', Coefficient of variation for DG – a metric of reliability

'cv\_nm3',

'cv\_sg',

'cv\_ns',

'cv\_nm1a',

'cv\_nm1b',

'cv\_nm2',

'cv\_nm1c',

'cv\_lsn',

'responsive\_nmall', Boolean for whether cell is responsive to ANY of the NM from any session

'run\_stat\_dg',

'responsive\_rundg', Boolean for significant running modulation?

'run\_corr\_mean', Mean correlation of cell activity with running speed across all sessions

'run\_corr\_A\_lw', Correlation of cell activity with session A

'run\_corr\_B\_lw',

'run\_corr\_C\_lw',

responsive\_run', Not sure, let me check.

'dg\_all\_RidgeRegress\_CC', Not sure – from Gabe’s modeling stuff. Ignore

'cluster\_id' ID of response type cluster from platform paper. Worth looking at – but only a subset of cells have this.