Manual

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This manual provides information about the analysis code accompanying the manuscript by Khani and Gollisch (2021): "Linear and nonlinear chromatic integration in the mouse retina". The code is provided as a MATLAB function Analyze_Chromatic_Integration_Stimulus that contains a few sub-functions inside. This code requires the following files to work:

- Frametimes file: This is a text file with the time stamps for specific frames of the chromatic integration stimulus. The time values are in seconds and they represent any change that happened on the screen. This includes the change in color/contrast of the screen after certain period of background illumination (onset of the stimulus) and change at the offset of the stimulus when the color/contrast is set to mean intensity (background) value.
- Spiketimes file: Spike times of spike sorted units. The values are in second and each individual value represent the time of a detected spike from a recorded ganglion cell.
- Stimulusparameters file: This is a text file that shows the exact parameters used for each specific version of the chromatic integration stimulus that was presented during each experimental session.
- Stimuli-names file: This is a text that contains the list of the stimulus names. This is used to ensure correct loading of the frametimes and stimulus parameters files.

Examples of the data format required to run the Analyze_Chromatic_Integration_Stimulus function is provided in example cells 1 to 7 folders available at the github repository:

https://github.com/gollischlab/ChromaticIntegrationAnalysis

Beyond these example cells, it is possible to run the Analyze_Chromatic_Integration_Stimulus function with the accompanying data from any of the recorded cells used in the manuscript, available at the public data repository at following link:

https://gin.g-node.org/gollischlab/Khani_and_Gollisch_2021_RGC_spike_trains_chromatic_integration

The function Analyze_Chromatic_Integration_Stimulus operates by first loading the required text files in MATLAB using the select_example_cell sub-function. The output of the select_example_cell() sub-function is then used by the ci_parameters() sub-function. The ci_parameters() function sets the list of parameters needed for the analysis of the chromatic integration stimulus. Additionally this function calculates the indices for the order of the stimulus presentation (see below). This is necessary to get the correct order of contrasts presented to the retina, since the contrast orders are randomized in the chromatic integration stimulus using Fisher-Yates random permutation algorithm [1]. The calculation of the indices for the contrast orders is done by the sub-function fisher_Yates_shuffle_order(). The output of this function is then used to re-organize the list of calculated rasters and PSTHs calculated as part of the ci_analysis() function. Once all the parameters for the analysis is set by the

ci_parameters(), they are fed into the ci_analysis() function. This is the main analysis function and it calls two sub-functions: 1- spikes_per_frametimes() and 2-reorder_contrast_spikes().

1- spikes_per_frametimes(): this sub-function calculates raster values for each contrast presented during the recording. It groups the spikes happened between the onset and offset of the stimulus. It additionally create a raster file for the background stimulus presented before the onset of each stimulus. Since a pulse from the frametimes appears at the onset of the stimulus and another pulse at the onset of the background illumination after the stimulus (offset), every other value of the frametimes shows the onset of the stimulus (to get the stimulus onset use: 2:2:numel(frametimes)). Once the frametimes corresponding to the onset of each stimulus is selected, the next frametimes after those belong to the offset of the stimulus. To get the spikes that happened during the last 500 before the onset of the stimulus, one needs to search for those spikes happened between 500 ms before the onset of the stimulus and the onset of the stimulus. These operations are the main part of the spikes_per_frametimes() function. The assigned spikes per stimulus presentation from this function are then fed into the reorder_contrast_spikes() function.
2- reorder_contrast_spikes(): this sub-function first reorders all the grouped spikes in way that all the spikes belong to same contrast combination are grouped together. The order is defined from the output of the fisher_Yates_shuffle_order() function. Once the spikes are ordered correctly, a PSTH (per-stimulus time histogram) is generated from all the trials of each contrast combination presented to the retina. The chromatic integration stimulus that was used in the manuscript contained contrast combinations that is categorized into two sets of green-On-UV-Off and green-Off-UV-On. The green-On-UV-Off set consists of 11 different combinations, ranging from 20% green and 0% UV to 0% green and -20% UV in steps of -2% for both colors. The green-Off-UV-On set contains the contrast-reversed combinations. The presented contrast values of the two set were as follows:

   green-On-UV-Off =

Green contrasts:	[20	18	16	14	12	10	8	6	4	2	0]
UV contrasts:	[0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20]

   green-Off-UV-On =

Green contrasts:	[-20	-18	-16	-14	-12	-10	-8	-6	-4	-2	0]
UV contrasts:	[0	2	4	6	8	10	12	14	16	18	20]

   As a result 22 contrast combinations were presented and the function reorder_contrast_spikes() generates 22 PSTHs, one per contrast combination. Additionally, this function returns 22 PSTHs for the responses to background light before the onset of each stimulus combination. These PSTHs are the used by the plot_chromatic_integration() function.

In the last part of the Analyze_Chromatic_Integration_Stimulus function, the calculated rasters and PSTHs are used by the plot_chromatic_integration() sub-function to make a chromatic integration curve and also series of PSTHs for each stimulus contrast combination. The generation and plotting of chromatic integration curve is done by the plot_chromatic_integration_curves() sub-function and the plotting of all the 22 PSTHs are done by the plot_chromatic_integration_psths() sub-function. These functions use series of plotting modules to create the output plot that is displayed on the screen. These plotting modules are: stairsfun(), barfun(), shadefun(), scalebarfun() and datascalefun().

References

[1] Fisher RA, Yates F. Statistical tables for biological, agricultural and medical research. Oliver and Boyd (1948).