Documentation data retinal bipolar cell recordings

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1. General structure

The repository:

https://gin.g-node.org/gollischlab/Schreyer_and_Gollisch_2021_salamander_retinal_bipolar_cell_recordings

contains the voltage responses of bipolar cells to diverse light stimuli. The bipolar cells were recorded in the whole-mount salamander retinas with sharp electrodes. The data is part of the manuscript by Schreyer and Gollisch (2021) published in Neuron with the title: Nonlinear spatial integration in retinal bipolar cells shapes the encoding of artificial and natural stimuli. Details about the stimulus and analyses can be found in the manuscript. The repository contains 3 folders: spatiotemporalWhiteNoise, naturalMovies, and Spot, whose content is explained one by one in the following sections.

2. Spatiotemporal white noise stimulus

The folder contains the data for the spatiotemporal white noise stimulus and is composed of:

-Excel file: LogInfo_SpatioTemporalWhiteNoise.xlsx

-multiple *.mat files (the actual data)

-folder: code spatiotemporal white noise

The excel file is the guide for the *.mat files and contains:

-filename (of .mat file)

-cell ID, which is composed of the recording date, the retina number and cell number. For example, the .mat file: 155200029Comp (see below) is the response to the spatiotemporal white noise stimulus of cell 2 that was recorded on the 15.05.20 in the first retina:

Filename	Date	Retina Number	Cell Number	update rate (Hz)	pixel size	FrozenFrames	RunningFrames
155200029Comp	150520	1	2	10	12		
189010032Comp	180911	2	1	25	9	300	1500

- update rate: the update rate of the stimulus. For example, for file 155200029Comp the stimulus was updated every 0.1 s (100ms) -> 10 Hz

-pixel size: relevant for stimulus regeneration (see below). The OLED monitor was composed of 800x600 pixels (1 pixel=2.5μm). For the spatiotemporal white noise, the screen was subdivided into small squares (checkers), which were updated randomly to black or white at the stimulus update rate (see above). For example, for the file 155200029Comp, 12x12 monitor pixels were packed together into one square (checker).

-Frozen and Running Frames: some cells were recorded with a non-repeating binary white noise sequence (running frames) that was regularly interrupted with an identical sequence (frozen frames). For example, for the file 189010032Comp, the sequence was interrupted every 1500 frames (RunningFrames) by 300 frozen frames (FrozenFrames=300 frames).

The *.mat files contain per cell:

membPot: the preprocessed voltage signal. The voltage signal is downsampled to 1 millisecond resolution and de-trended with a high-pass filter (see Methods of the original paper). The numbers represent measured voltage values in mV. For example, membPot(1) is the measured voltage response at the first millisecond.

ttls_ms: pulses that mark the onset time of frames when the stimulus was updated. These frame times are given in milliseconds. This information is used to align the recorded voltage response to the timing of the stimulus.

**Folder: code spatiotemporal white noise**

Contains example code of how to analyze the voltage responses to white noise (linear-nonlinear model analysis). Start with:

BC_mainWhiteNoise.m -> which contains the overview over the individual functions to run

[STA_output]=BC_STA(loadData,filename,pixelSize,seed,Hz); -> for performing the response-weighted average for the voltage signal, analogous to the common calculation of the spike-triggered average (STA) for spiking neurons (Chichilnisky, 2001). You should get such a plot when running the code for filename:155200029Comp.mat (Cell2 in Retina 1, 150520). It shows the STA frame with the maximum response:

STA best frame, filename: 155200029Comp.mat
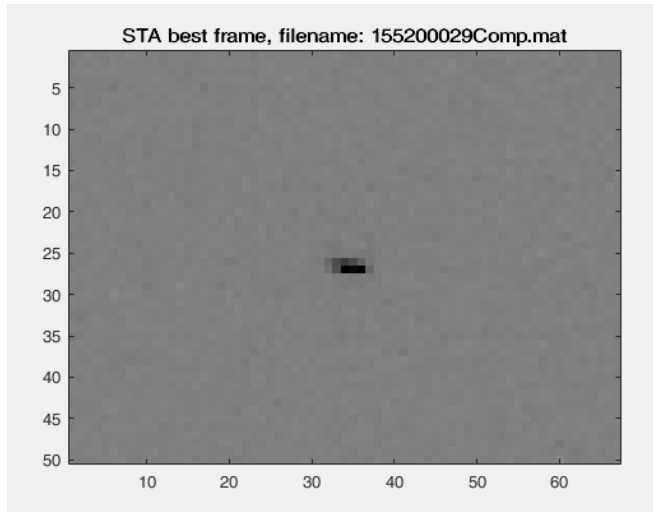
[NL_output]=BC_NL(STA_output)-> for performing the output nonlinearity. You should get such a plot when running the code for filename:155200029Comp.mat (Cell2 in Retina 1, 150520). It shows the output nonlinearity:

NL: filename: 155200029Comp.mat
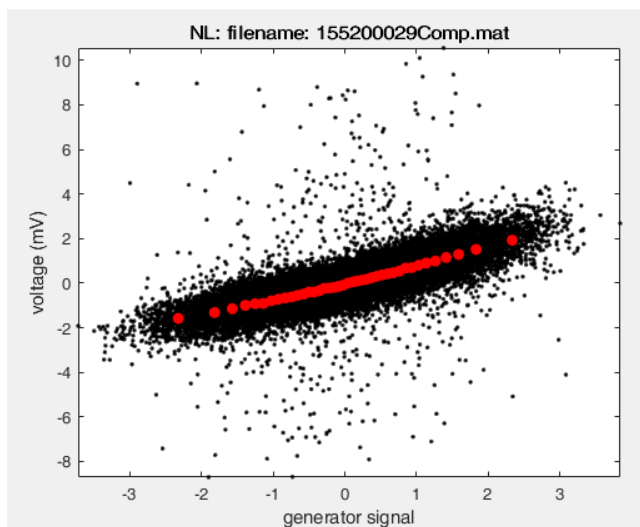
[pred_output]=BC_pred(STA_output) -> for performing the prediction. You should get such a plot when running the code for filename:155200029Comp.mat (Cell2 in Retina 1, 150520). It shows the LN model components and the prediction output:
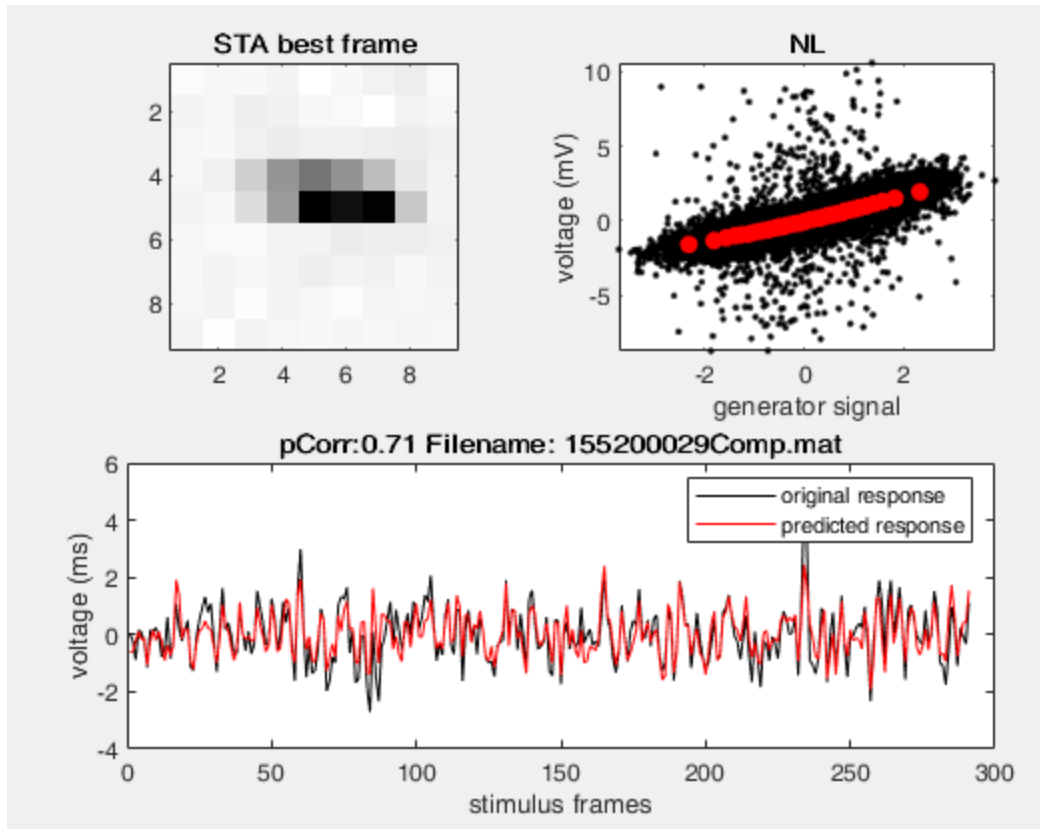
The stimulus can be reconstructed by the following functions:

https://github.com/gollischlab/RecreateWhiteNoiseStimuliWithMatlab

stimulus = recreateBinaryWhiteNoiseStimulus(Nx, Ny, Nframes, seed)

monitorXPixels=800; monitorYPixels=600;

Nx=ceil(monitorXPixels/pixelSize); Ny=ceil(monitorYPixels/pixelSize);

seed=-10000 (no frozen frames); seed frozen frames=-20000;

Nframes=length(ttls_ms)

Note: the stimulus values are drawn from the lower left corner.

3. Natural movies

The folder contains the data for the natural movies and is composed of (same structure as spatiotemporal white noise):

-Excel file: LogInfo_NaturalMovies.xlsx

-multiple *.mat files (the actual data)

-folder: code natural movies

The excel file is the guide for the *.mat files:

The excel file has the same structure as for spatiotemporal white noise:

-filename (of .mat file)

-The cell ID (composed of the recording date, the retina number and cell number). The cell ID is the same for natural movies and spatiotemporal white noise and has to be used to find the corresponding files. For example, the .mat file: 16d200016Comp (see below) contains the response of the cell 5 to the movie that was recorded on the 161219 in the second retina. The corresponding response to the spatiotemporal white noise is found in LogInfo_SpatioTemporalWhiteNoise.xlsx and is file 16d200015Comp:

Filename	Date	Retina Number	Cell Number	update rate (Hz)	Movie
16d200016Comp	161219	2	5	25	4

- update rate: the update rate of the movie (same as for spatiotemporal white noise)

-movie: the "CatCam" movie number used (see below for stimulus regeneration)

-start and end frame: start and end frame of the movie (see below for stimulus regeneration)

The *.mat files contain per cell:

membPot: the preprocessed voltage signal, same as for the spatiotemporal white noise.

ttls_ms: the pulses (frames) when the stimulus was updated, same as for the spatiotemporal white noise stimulus.


Folder: code natural movies

Contains example code of how to analyze the voltage responses to natural movies.

BC_mainNaturalMovies.m -> which contains the overview over the individual functions to run

[movieSignal]=BC_getNaturalMovies(pixelSize);-> for regenerating the movie intensity values.

[naturalMovie_output]=BC_predNaturalMovies(loadData,filename,movieSignal,STA_output,NL_output,Hz) -> for performing the prediction. You should get such a plot when running the code for filename: 16d200016Comp.mat (Cell5 in Retina 2, 161220). It shows the average response of the cell to the movie and the prediction trace with the LN-model:
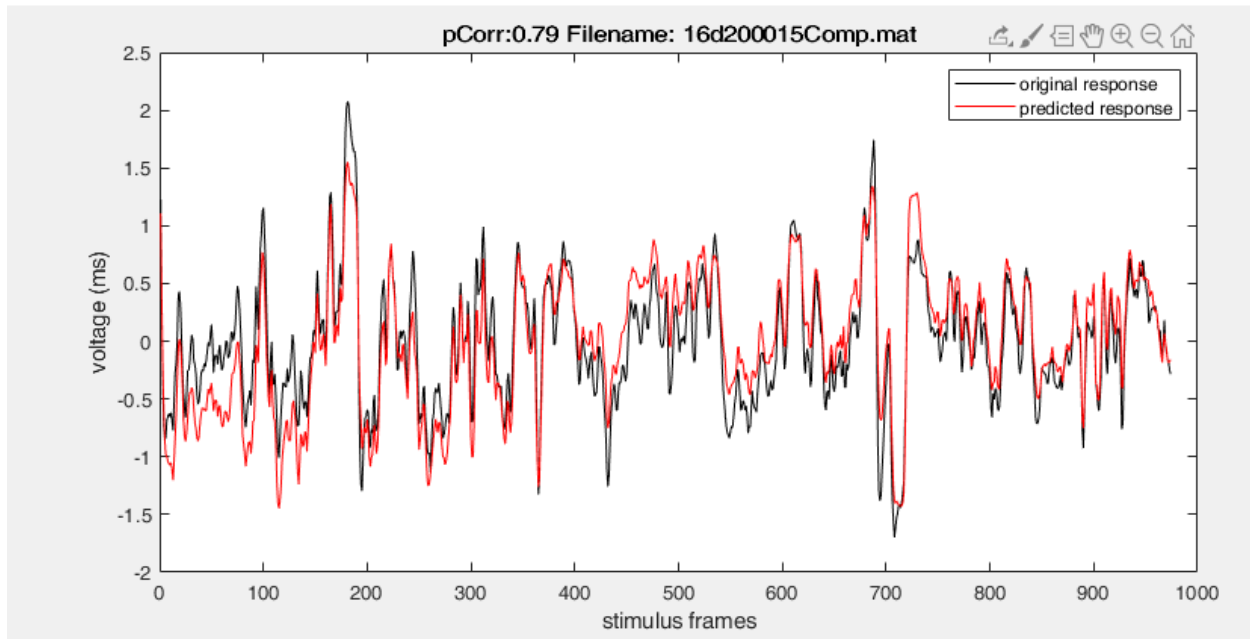
Regeneration of the movie intensity values:

The movie can be regenerated with the following function:

[movieSignal]=BC_getNaturalMovies(pixelSize);-> pixelSize is found in the corresponding excel file

We used the natural movies from the "CatCam" database (Betsch et al., 2004), which can be downloaded here (each frame of the movie is a .tiff file):

https://zenodo.org/record/46481

The tiff-file number used for each file can be found in the column "movie" in LogInfo_NaturalMovies.xlsx. Some movies were shortened/cut in time and in the excel columns "start and end frame" you find the starting and ending frame for each corresponding movie. For example, for file 16d200016Comp the movie 4 started with the first frame and ended at frame/image 998.

Note: the movie is drawn from the upper left corner (different from the spatiotemporal white noise), so the filter of the spatiotemporal white noise has to be adapted to the movie for convolution. Furthermore, the light intensity of the movie was scaled to the same mean intensity as for white noise stimulus. Additionally, the original dimension of the movie is: 320x240. For the projection on the retina, the movie pixels were upsampled (by 3x3) and cropped to the 800x600 pixels of the OLED (see Methods). The red rectangle in the left image below marks roughly how the unsampled image (960x720) is cut, the right image shows the cropped image with an 800x600 pixel dimension.
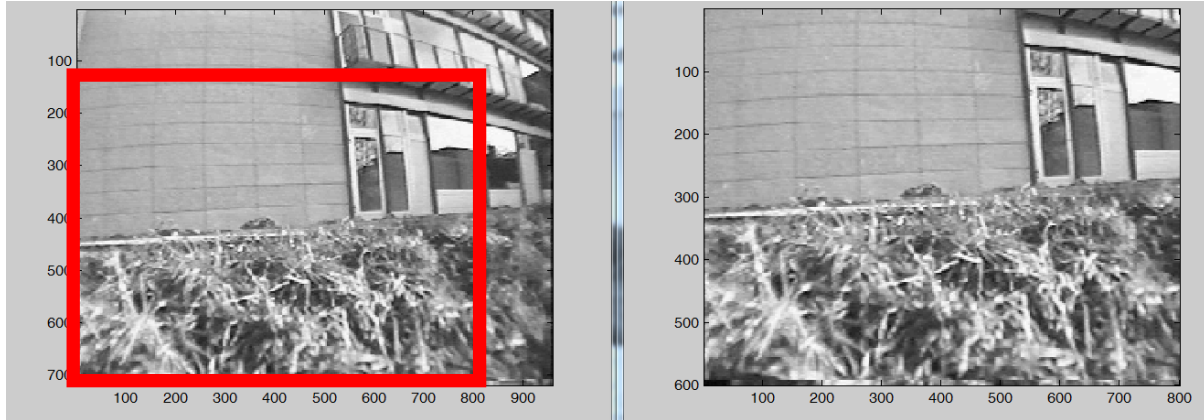
Image example from "CatCam" database (Betsch et al., 2004)

4. Spots

The folder contains the data for the spot stimuli and is composed of (see also spatiotemporal white noise section):

-Excel file: LogInfo_PatternedSpot.xlsx -> described in section a

-Excel file: LogInfo_UniformSpot.xlsx -> described in section b

-multiple *.mat files (the actual data)

-folder: functions patterned spot

-folder: functions uniform spot

a. Patterned Spot

The excel file: LogInfo_PatternedSpot.xlsx has the same structure as for the other stimuli (see e.g. natural movie section):

-filename (of .mat file) for the patterned spot stimulus

-The cell ID (composed of the recording date, the retina number and cell number). See natural movie chapter for an example.

-update rate: the update rate of the reversing pattern spot, the spot was reversed at 1 Hz for 4s.

-stimulus version: two patterned spot versions were shown (see below regeneration of the patterned spot).

-start and end frames: start and end frames of the corresponding spot patterns. The spot was divided into two halves ->1/2 spot, into four quarters -> 1/4 spot, into checkerboard layouts with squares of 25μm (->25 μm spot) or 10μm (->10 μm spot), see below for stimulus regeneration.

The *.mat files contain per cell:

membPot: the preprocessed voltage signal, downsampled to a 1ms resolution (not detrended).

ttls_ms: the pulses (frames) when the stimulus was updated, same logic as for the spatiotemporal white noise stimulus. At every contrast reversal (100%, see Methods), a pulse was recorded (~every 500ms; one full cycle ~1000ms). The starting and end pulse-index of each patterned spot can be found in the corresponding excel column. A gray screen of 4 s was shown between the different patterned spots, from which the baseline response can be computed. To compute the baseline response (as described in the Method), the membrane potential 1200-1000 ms before the starting pulse can be taken.

uniformTraceAVG: the baseline subtracted averaged response trace to the uniform spot for spot version 1 (see below).

Folder: functions patterned spot

Contains example code of how to analyze the voltage responses to patterned spot stimuli

Regeneration of the patterned spot:

The patterned spots were always presented over the receptive field center of the cells (see Methods). Two versions of the patterned spot were shown (see Methods):

The first version: starts with the split-spot, the spot divided into 4 quarters and the spot divided into subfields of 25μm. In the corresponding excel column the starting and end frame-index of each of the spots is given. The starting frame directly starts from the second trial, the first reversal (trial, 1s) is excluded from the analysis (see Methods).

In the patterned spot version 1, the responses to the reversing uniform spot was recorded in a different spot-module at a fixed set of spot diameters (50-500μm) (see Methods). For simplification, we directly provide for the cells recorded in the spot version 1 the baseline subtracted averaged response trace to the uniform spot (variable uniformTraceAVG).

The second version: starts by showing the uniform spot, the split-spot, the spot divided into 4 quarters, the spot divided into subfields of 25μm and the spot divided into subfields of 10μm. In the corresponding excel column the starting and end frame-index of each of the spots is given. The starting frame directly starts from the second trial (first second is excluded).

b. Uniform Spot

The excel file: LogInfo_UniformSpot.xlsx has the same structure as for the other stimuli (see e.g. natural movie section):

-filename (of .mat file) for the uniform spot stimulus

-The cell ID (composed of the recording date, the retina number and cell number). See natural movie chapter for an example.

-spot duration: the presentation length of each spot in milliseconds (~500ms)

-gray duration: the gray screen duration between spots (~1000ms)

-contrast: whether black spots were shown =0 or white spots =1

-stimulus version: four uniform spot version were shown (see "Regeneration of the uniform spot" below)

-start and end black spot and start and end white spot: the starting and end frames of the black and white spots. This is relevant for stimulus version 3, where the black and white spots were recorded in the same file (see below).

The *.mat files contain per cell:

membPot: the preprocessed voltage signal, downsampled to 1 ms resolution (not detrended).

ttls_ms: the pulses (frames) when the stimulus changed (see above).

Folder: functions uniform spot

Contains example code of how to analyze the voltage responses to uniform spot stimuli

Regeneration of the uniform spot:

The regeneration of the randomized spot diameters can be found in the function regenerationUniformSpotSizes.m. Four versions of the uniform spot were shown:

Version 1: 13 diameter sizes were used and presented at random order. Here, the black and white contrast were recorded in two separate files. The two corresponding files for each cell can be found in the excel file (contrast column). The first pulse is the gray screen (~1 s), the second pulse marks the appearance of the spot (1 trial), the third pulse is again the gray screen, the fourth pulse the appearance of a new spot etc.. For each trial, we subtracted the average baseline membrane potential measured over the 200 ms prior to the spot.

Version 2: Same as version 1 except that 11 diameter sizes were used.

Version 3: 11 diameter sizes were used and presented at random order (as for version 2). Here, however, the black and white spots were recorded in the same file. First, all black spots were presented and then all the white spots. The excel columns start and end of the black and white spot give the frame index of the start and end of the corresponding spot contrast. The pulses have the same order as for version 1 and 2: the first pulse is the gray screen (~1 s), the second pulse marks the appearance of the spot (1 trial) etc.

Version 4: 6 diameter sizes were presented at fixed order (50, 100, 200, 300, 400, 500 μm). The spots were presented without an interval of background illumination between the spot sizes. The spots reversed contrast (100%) at 1 Hz for 4s, with different spot sizes separated by background illumination of 4 s, which was used for computing the baseline membrane potential.

References

Betsch, B.Y., Einhäuser, W., Körding, K.P., and König, P. (2004). The world from a cat's perspective--statistics of natural videos, *Biol Cybern,* 90, 41-50.

Chichilnisky, E.J. (2001). A simple white noise analysis of neuronal light responses, *Network,* 12, 199-213.