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Supplementary Material for article by Stowasser et al.

ERG Analysis – Matlab Scripts, User Guide

1. Introductions

The scripts ***ERGAnalysis_SinglePulses.m*** and ***ERGAnalysis_Flicker.m*** assist in analyzing ERG data by finding data points that are useful for the data analysis such as analyzing on-transients, maximal photoreceptor responses, off-transients, baseline recovery and finding the critical flicker fusion frequency. The text in the PDF file needs to be pasted into MATLAB .m files. Make sure that this process does not add new lines into the code. In order to apply any of the scripts, recorded data first needs to be exported with the recording software (in our case AD Instruments) into MATLAB format, and then loaded into MATLAB (The MathWorks Inc.). The scripts generate several figures and save all settings and analyzed data automatically as a ***.mat*** file within a result folder that is automatically generated by the scripts.

The script ***ERGAnalysis_SinglePulses.m*** assists in analyzing individual ERG responses. Typically these result from stimulating the eye with relatively long lasting and clearly separated light pulses in which concurrent stimuli arrive after the response has recovered from previous stimuli. To use this script you can record as many responses as you like within each 'data block'. The script ***ERGAnalysis_Flicker.m*** assist in analyzing ERG responses to relatively high frequency pulses and assists in finding the critical flicker fusion frequency. To be able to use this script, record each stimulus train as separate 'data block' (stop the recording after each train and start the recording again before the next stimulus train).

Both programs will find important points, the specific meanings of which vary between species and stimulus conditions. Note that in not all cases all computed points are meaningful. For example, some points are designed to find on and off transients that are observed in flies but often are absent from other recordings. Therefore it is important that the user carefully evaluates his/her data to determine which of the points are most meaningful for the desired analysis.

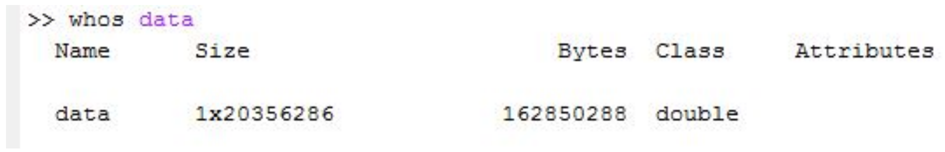
2. Load the data into MATLAB

First, export the recorded data in MATLAB format (.mat) using the recording software and load the data into MATLAB, for instance by simply dragging the file into the MATLAB workspace window or command line window.

3. Necessary variables and accepted data formats

After loading the data, there should be several variables available in the workspace window of MATLAB, not all of which however are needed for this analysis. You can use the following command in the command line to check the format of a variable: >> whos VariableName

An example of the command line that you then will see is:



```
>> whos data
  Name      Size                    Bytes  Class     Attributes

  data      1x20356286          162850288  double
```

List of necessary variables and their formats:

Name	Size	Class	
data	1xN	double	N is the total number of data points that were collected in the trial ***data*** contains the stimulus and recording data of all blocks
datastart	2xN	double	N is the number of data blocks, the first row contains the start indices of the response data blocks the second row contains start indices of the stimulus data blocks
dataend	2xN	double	has the same format as ***datastart*** but holds the data ending indices of the response and stimulus data blocks

samplerate	2xN	double	has the same format as ***datastart*** but holds the sample rates

4. <u>**How to initiate and run the scripts**</u>

The programs are organized to analyze each 'data block' individually. To do so first open either script in MATLAB and scroll to the section entitled 'Initiation'. This section contains several variables that you can change to adjust the program to your need. To get started you need to assign the correct block number to variable ***blocknumber*.** You find this variable under: 'a'. This variable defines which block (recording sequence) is analyzed. A list and description of all variables that you might want to adjust is below. Finally run the script by clicking on the green triangular 'run' symbol of the editor window. Note that you can run the script multiple times without reloading your raw data.

a. ***blocknumber***: determines which recording sequence is being analyzed.

b. ***savedata***: if this variable is set to ***false*** then the data will not be saved, while if it is set to ***true***, all data will be saved.

c. ***stim.scale***: determines how big the binary stimulus is displayed on the figures.
stim.shift: determines where (relative to the response) the stimulus is displayed.
In both scripts these variables are needed in step 3.2. Change these variables if you need to adjust the appearance of the stimulus in the figures.

d. ***response.w_smooth***: In both scripts this variable is needed in step 4 and determines the window size that is used for a moving average to smooth the raw data (***response.raw*)** and compute ***response.smoothed***. The larger the window size, the stronger the data is smoothed. NOTE: You will lose information if the window size is too large.

e. ***point_1.w_average***: is the number of data points that are averaged.
In ***ERGAnalysis_singlePulses.m*** in step 6.1 it determines how many data points of ***response.smoothed*** will be averaged just before <u>each</u> stimulus onset to compute <u>each</u> ***point_1.average*** of **point 1** .
In ***ERGAnalysis_Flicker.m*** in step 6.1.1. and 6.1.2 it determines how many data points of ***response.smoothed*** will be averaged just before <u>the first</u> stimulus onset to compute the <u>first</u> ***point_1.average*** of **point 1**.

f. These variables are needed in ***ERGAnalysis_singlePulse.m*** in step 6.3. to compute **point 3a**, **point 3b** and **point 3c**.
point_3a.w_average, point_3b.w_avergae and ***point_3c.w_average:*** number of data points of ***response.smoothed*** that are averaged to compute ***point_3a.average, point_3b.average*** and ***point_3c.average*** respectively.
point_3b.skip: In step 6.3.c it determines how many data points will be skipped after stimulus onset to compute **point 3b*.*** This variable allows the program to find the most negative point in the sustained ERG response, even if there is a more negative point tightly following the onset of the stimulus onset.

g. These variables are needed in both scripts in step 6.4 to compute **point 4**
point_4.window: In ***ERGAnalysis_singlePulses.m*** the variable determines the number of data points that will be included after the end of the stimulus when searching for **point 4** (minimum response value of ***response.smoothed***) after <u>each</u> stimulus offset. In ***ERGAnalysis_Flicker.m*** this variable only applies to <u>the last</u> stimulus offset. This point is useful if there is a negative transient signal after the stimulus is terminated.
point_4.w_average: This variable determines how many data points of ***response.smoothed*** will be averaged to compute ***point_4.average***.

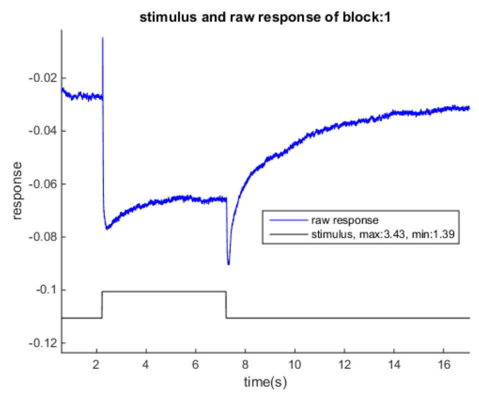
h. ***point_5.window***: In both scripts this variable is needed in step 6.5 to compute **point 5**. In ***ERGAnalysis_singlePulses.m*** the variable determines the number of data points that will be included after the end of the stimulus when searching for **point 5** after <u>each</u> stimulus offset. In ***ERGAnalysis_Flicker.m*** this variables only applies to <u>the last</u> stimulus offset.

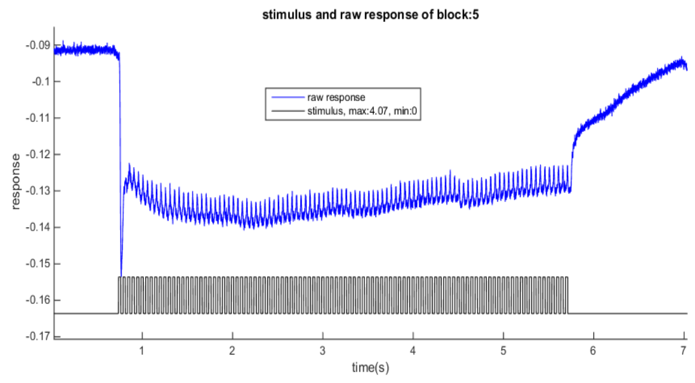
This point is useful if there is a positive transient signal after the stimulus is terminated.

5. Data analysis output

The scripts generate several figures and store these figures with all data in a result directory which is called: "results_block_N" where N is the block number.

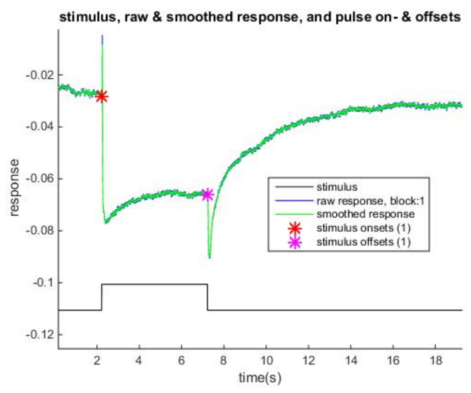
5.1. figure_rawdata: rawdata

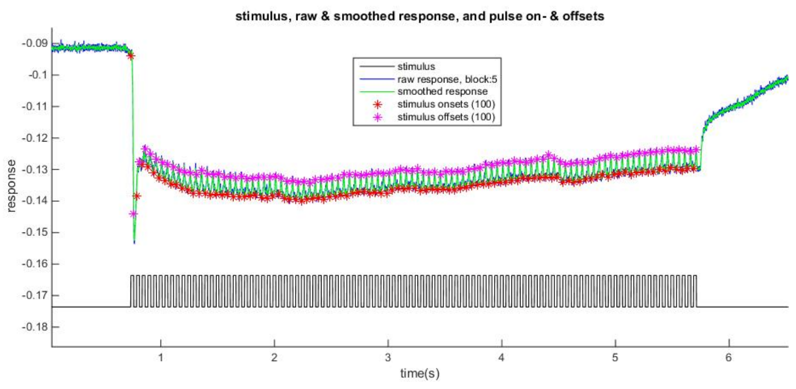




The first figure that is generated shows the raw data of the response (***response.raw***) and plots the stimulus (***stim.plot***) below it. The figure on the left is an example generated with the script ***ERGAnalysis_SinglePulses.m*** and the one on the right is an example generated with the script ***ERGAnalysis_Flicker.m***. The figure legend indicates the maximum and minimum values that were used in the stimulus.

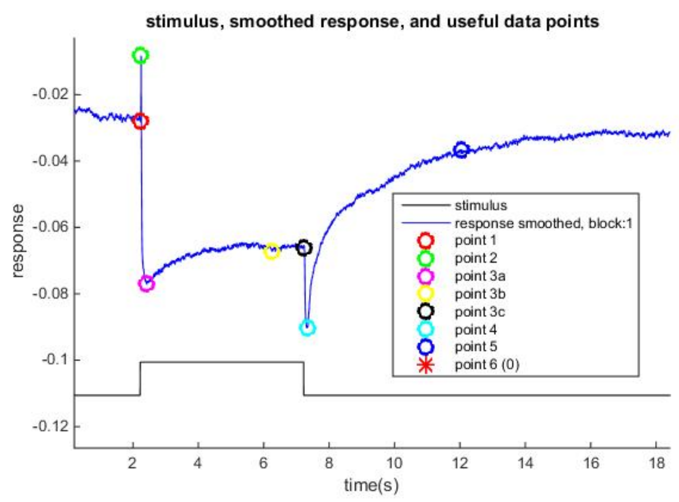
5.2 *figure_stim_onoff: smoothed data with stimulus on and offsets*





The second figure shows the original response (***response.raw)*** in blue, the smoothed response (***response.smoothed***) in green, the stimulus (***stim.plot***) in black and data points that mark the beginning and end of the stimulus as red and magenta stars respectively. The figure on the left shows an example generated by the script ***ERGAnalysis_SinglePulses.m*** and on the right is an example generated by the script ***ERGAnalysis_Flicker.m***. In order to better keep track of the stimuli, the number of onsets and offsets are indicated in the figure legend (in brackets).

5.3 figure_points: generated by ***ERGAnalysis_SinglePulses.m: points of interest***



This figure shows ***response.smoothed*** in blue***, stim.plot*** in black, and the points 1 through 6 in various colors (see figure legend).

point 1: is the average response value of ***response.smoothed*** just before the stimulus onset, ***point_1.w_average*** determined how many data points were averaged. We suggest using this value as the baseline value as it immediately precedes the onset of the stimulus.

point 2: is the maximum response value of ***response.smoothed*** between stimulus onset and offset. This point is useful to evaluate on-transients for species in which they exist (e.g. flies).

point 3a: is the average minimum response value of ***response.smoothed*** between stimulus onset and offset, ***point_3a.w_average*** determined how many data points were averaged. This point is potentially useful as the strongest response value (manifested as the most negative response) of the photoreceptor.

point 3b: is also an average minimum response value of ***response.smoothed*** between stimulus onset and offset, but this time it is possible to exclude a set number of points at the beginning of the sequence (as defined in ***point_3b.skip***), ***point_3b.average*** determined how many data points were averaged. This point can be used to evaluate the sustained photoreceptor response even if there is an overshoot at the beginning (as in our example).

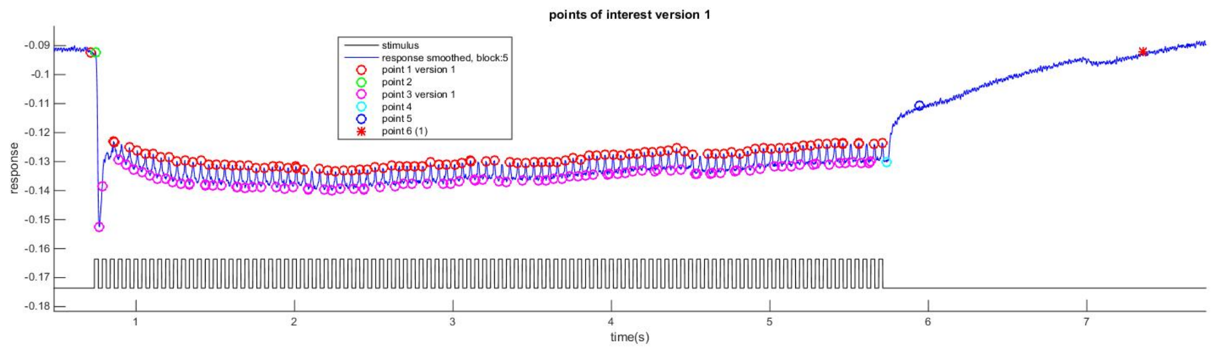
point 3c: is the average response value of ***response.smoothed*** at the time of the end of the stimulus. In some cases this is the most informative point to calculate the sustained photoreceptor points, ***point_3b.average*** determined how many data points were averaged. This point can also be used as the baseline for calculating off-transient sizes.

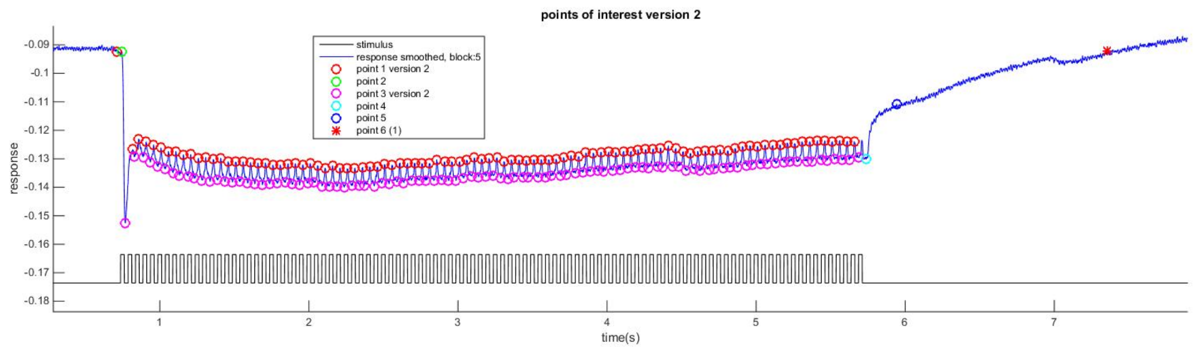
point 4: is the average minimum response value of ***response.smoothed*** within a specified time period (defined by ***point_4.window***) following the end of the stimulus. The variable ***point_4.w_average*** determined how many data points of ***response.smoothed*** were averaged for this point.

point 5: is the average maximum response value of ***response.smoothed*** within a window specified as for **point 4**. This point could be used to evaluate a transient positive signal that follows the end of the stimulus. The variable ***point_5.window*** determined how many data points after stimulus offset were included in the search and ***point_5.w_average*** determined how many data points were averaged.

point 6: indicates when the baseline value (***point_1.average***) is first recovered after the end of each stimulus. The number in brackets shows if the baseline was recovered and how often the baseline was recovered if the trace contains multiple stimuli. In our case, the baseline was not recovered so the number is zero and the point is absent from the graph. Had the baseline recovered, this number would be 1.

5.4 figure_points_v1 and ***figure_points_v2:*** generated by ***ERGAnalysis_Flicker.m: points of interest version 1/version 2***





These figures show the ***response.smoothed*** in green, the ***response.average*** in blue, the stimulus in black, and points 1 through 5 as described below. To assess if photoreceptors follow the stimulus it is necessary to evaluate the figures of both versions. As long as one of the two versions consistently displays points 1 and 3, photoreceptors tend to follow the stimulus. However if there are failures in both versions, then photoreceptors are starting to fail following the stimulus (as illustrated in Figure 10 of the manuscript).

point 1: the first data point of **point 1** is the average response value just before the beginning of the stimulus where ***point_1.w_average*** determined how many data points of ***response.smoothed*** were averaged. All following data points of **point 1** are maximum response values of ***response.smoothed*** (as specified below).

point 3: are minimum response values of ***response.smoothed***.

There are two versions in which **point 1** and **point 3** are found. One or the other version should find consistent values as long as the response continues to follow the stimulus. The two versions are necessary because due to a delay in photoreceptor response the stimulus end can precede the strongest response. Depending on the magnitude of this delay relative to the stimulus frequency, maximum/minimum responses occur either between the end of two consecutive stimuli or between the beginning of two consecutive stimuli. Version 1 searches for maximum responses between two consecutive stimulus ends and minimum responses between two consecutive stimulus beginnings. Version 2 does the opposite (it searches for maximum responses between two consecutive stimulus beginnings and minimum responses between two consecutive stimulus endings). In this example version 2 worked better than version 1, in which points are inconsistent. Note that flicker fusion data should be examined closely for instances in which photoreceptors start to skip stimuli. This can be done easily by zooming into the resulting figure.

point 2: is the maximum response value of ***response.smoothed*** between the first two stimulus onsets. This point is useful to calculate on transients if they exist.

point 4: is the average minimum response value within a window right after the end of the last stimulus. The variable ***point_4.window*** determines how many data points after stimulus offset are included in the search. The variable ***point_4.w_average*** determines how many data points of ***response.smoothed*** are averaged.

point 5: is the average maximum response value of ***response.smoothed*** within a window right after the end of the last stimulus. The variable point_5.w_average determines how many data points are averaged and the variable

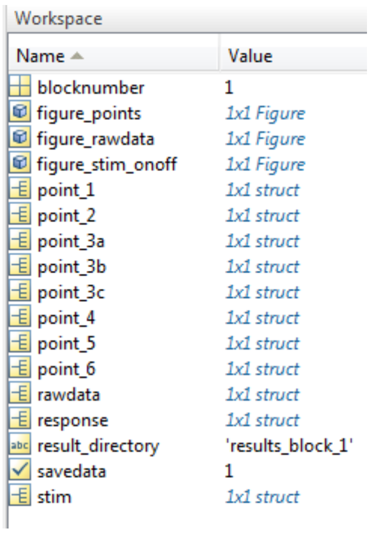
point_5.window determines how many data points are included in the search.

point 6: is the first time when ***point_1.v_1.average(1)*** (baseline) is reached after the ending of the stimulus. The number in the brackets indicates if the original baseline was reached again at the end of the recording (1: it was reached, 0: it was not reached).

5.2 Available Variables and the content of results.mat

After running the scripts or after loading ***results.mat*** into the workspace of MATLAB, there are a variety of variables available for further data analysis. To access the variables, simply double click on them. A variable window will then open. If the variable is a *struct* such as ***data***, it will show the content of the *struct* (such as a series of arrays). For any variable that is an array, or a single value such as ***blocknumber***, clicking it will display a spreadsheet that shows the values. You then can copy the values of the spreadsheet for instance into a program like Excel for further data analysis. The following section summarizes available variables and their meanings.

5.2.1 Available variables when running the script ERGAnalysis_SinglePulse.m



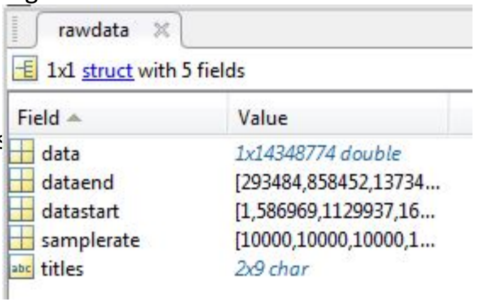
Workspace

Name	Value
blocknumber	1
figure_points	1x1 Figure
figure_rawdata	1x1 Figure
figure_stim_onoff	1x1 Figure
point_1	1x1 struct
point_2	1x1 struct
point_3a	1x1 struct
point_3b	1x1 struct
point_3c	1x1 struct
point_4	1x1 struct
point_5	1x1 struct
point_6	1x1 struct
rawdata	1x1 struct
response	1x1 struct
result_directory	'results_block_1'
savedata	1
stim	1x1 struct

blocknumber: is the number of the block that was analyzed
result_directory: is the name of the folder into which all files were saved
savedata: determines if the data is saved, 1 -> is saved, 0 -> is not saved

rawdata: is a *struct* that holds the raw data that was initially imported into MATLAB, as illustrated in the figure.

data: holds the raw recorded data
dataend: holds the block end indices
datastart: holds the block start indices
samplerate: holds the sample rates



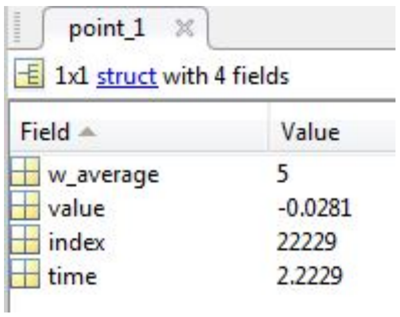
rawdata

1x1 struct with 5 fields

Field	Value
data	1x14348774 double
dataend	[293484,858452,13734...
datastart	[1,586969,1129937,16...
samplerate	[10000,10000,10000,1...
titles	2x9 char

point_1: is a *struct* that holds all variables of point 1.

w_average: is the number of data points that were averaged of ***response_smoothed*** before each stimulus onset to compute *value*
value: is the average response value of ***w_average*** data points before each stimulus onset
index: is the data index of ***value***
time: is the real time of ***value***



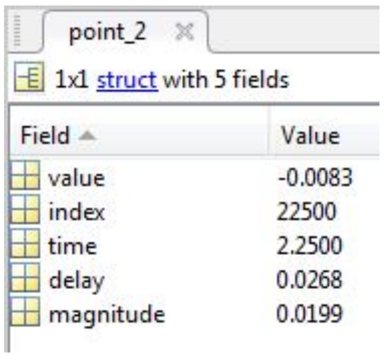
point_1

1x1 struct with 4 fields

Field	Value
w_average	5
value	-0.0281
index	22229
time	2.2229

point_2: is a *struct* that holds all data of point 2.

value: is the maximum value of ***response.smoothed*** between the stimulus on and offset.
time: is the real time of ***value***
index: is the data index of ***value***



point_2

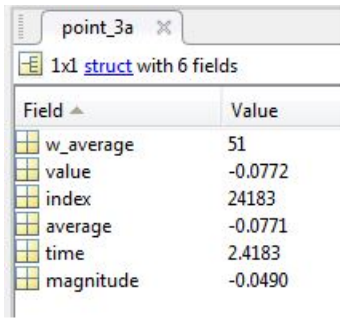
1x1 struct with 5 fields

Field	Value
value	-0.0083
index	22500
time	2.2500
delay	0.0268
magnitude	0.0199

delay: is the time between the first stimulus onset and ***time***

magnitude: is the difference between ***value*** (which is ***point_2.value***) and ***point_1.value*** of the same stimulus pulse. In many cases this directly describes the size of an on transient.

point_3a: is a *struct* that holds all data of **point 3a.**



point_3a

1x1 struct with 6 fields

Field	Value
w_average	51
value	-0.0772
index	24183
average	-0.0771
time	2.4183
magnitude	-0.0490

w_average: the number of data points of ***response.smoothed*** around ***index*** that are averaged to compute ***average***

value: is the minimum value of ***response.smoothed*** between stimulus on and offset

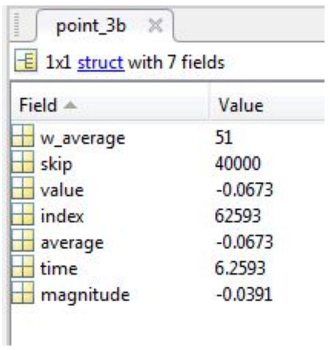
index: is the data index of ***value***

time: is the real time of ***value***

average: is the average of ***w_average*** data points of ***response.smoothed*** around ***index***

magnitude: is the difference between ***value*** (which is ***point_3a.value***) and ***point_1.value*** of the same stimulus pulse. In many cases this is a good description of the magnitude of the sustained photoreceptor response

point_3b: is a *struct* that holds all data of **point 3b.**



point_3b

1x1 struct with 7 fields

Field	Value
w_average	51
skip	40000
value	-0.0673
index	62593
average	-0.0673
time	6.2593
magnitude	-0.0391

w_average: the number of data points that are averaged as for **point 3a**

skip: is the number of data points that will be skipped after stimulus onset

value: is the minimum value of ***response.smoothed*** between ***skip*** data points after stimulus onset and stimulus offset.

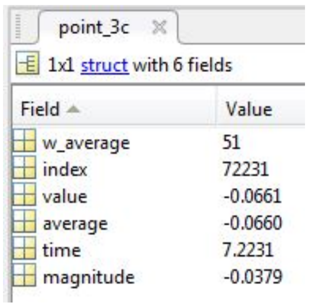
index: is the data index of ***value***

average: is the average response value of ***response.smoothed*** as for **point 3a**

time: is the real time of ***value***

magnitude: is the difference between ***value*** (which is ***point_3b.value***) and ***point_1.value*** of the same stimulus pulse. In many cases this is a good description of the magnitude of the sustained photoreceptor response

point_3c: is a *struct* that holds all data of **point 3c.**



point_3c

1x1 struct with 6 fields

Field	Value
w_average	51
index	72231
value	-0.0661
average	-0.0660
time	7.2231
magnitude	-0.0379

w_average: the number of data points that are averaged as for **point 3a**

index: is the data index of ***value***

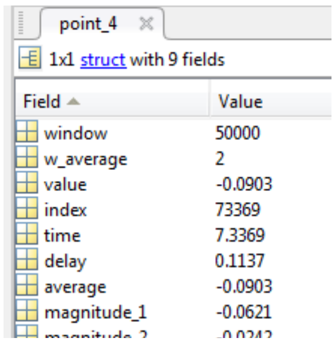
value: is the value of ***response.smoothed*** just before stimulus offset

average: is the average response value of ***response.smoothed*** as for **point 3a**

time: is the real time of ***value***

magnitude: is the difference between ***value*** (which is ***point_3c.value***) and ***point_1.value*** of the same stimulus pulse. In many cases this is a good description of the magnitude of the sustained photoreceptor response

point_4: is a *struct* that holds all data of **point 4**.



point_4

1x1 struct with 9 fields

Field	Value
window	50000
w_average	2
value	-0.0903
index	73369
time	7.3369
delay	0.1137
average	-0.0903
magnitude_1	-0.0621

window: is the number of data points that are included after stimulus offset

w_average: the number of data points that are averaged as for **point 3a**

value: is the minimum value of ***response.smoothed*** within a ***window*** of data points after stimulus offset.

index: is the data index of ***value***

time: is the real time of ***value***

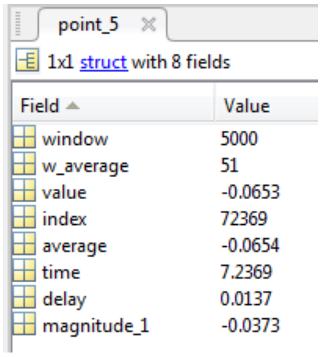
delay: is the time between stimulus offset and ***time***

average: is the average response value of ***response.smoothed*** as for **point 3a**

magnitude_1: is the difference between ***average*** (which is ***point_4.average***) and ***point_1.average*** of the same stimulus pulse**.** This describes the total change in magnitude between the baseline and the lowest point (frequently the off transient).

magnitude_2: is the difference between ***average*** (which is ***point_4.average***) and ***point_3c.average*** of the same stimulus pulse. This often is a good quantification of the off transient.

point_5: is a *struct* that holds all data of **point 5**.



point_5

1x1 struct with 8 fields

Field	Value
window	5000
w_average	51
value	-0.0653
index	72369
average	-0.0654
time	7.2369
delay	0.0137
magnitude_1	-0.0373

window: is the number of data points that are included after stimulus offset

w_average: the number of data points that are averaged as for **point 3a**

value: is the maximum value of ***response.smoothed*** within ***window*** data points after stimulus offset

index: is the data index of ***value***

average: is the average response value of ***response.smoothed*** as for **point 3a**

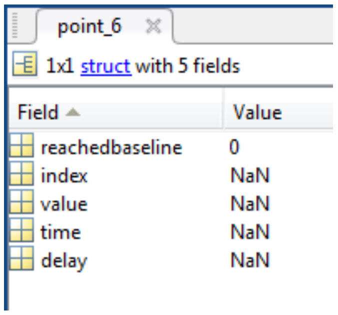
time: is the real time of ***value***

delay: is the time between the last stimulus offset and ***time***

magnitude_1: is the difference between ***average*** (which is ***point_5.average***) and ***point_1.average*** of the same stimulus pulse. This is useful to determine the magnitude between the innitial baseline reading and a maximum that occurs after the stimulus has terminated.

magnitude_2:is the difference between ***point_5.average*** and ***point_3c.average*** of the same stimulus pulse. This is useful to determine the magnitude between the end of the sustained photoreceptor response, and a maximum that occurs after the stimulus has terminated.

point_6: is a *struct* that holds all data of **point 6.** If this point does not exist, its variables (except for ***reachedbaseline***) will hold *NaN* (not a number)



point_6

1x1 struct with 5 fields

Field	Value
reachedbaseline	0
index	NaN
value	NaN
time	NaN
delay	NaN

reachedbaseline: indicates if and after how many stimuli ***point_1.value*** (baseline) was reached if the bock contains more than one stimulus.

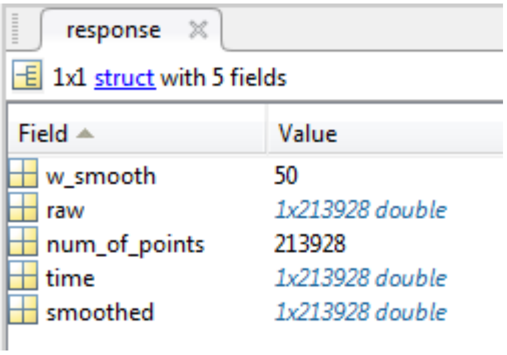
index: is the data index of ***value***

value: is the response value of ***response.smoothed*** for the first time when baseline was reached after each stimulus offset

time: is the real time of ***value***

delay: is the time between the last stimulus offset and ***time***

response: is a *struct* that holds all data that is related to the response traces.



response

1x1 struct with 5 fields

Field	Value
w_smooth	50
raw	*1x213928 double*
num_of_points	213928
time	*1x213928 double*
smoothed	*1x213928 double*

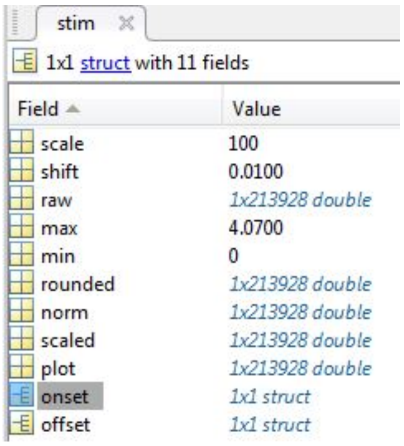
raw: holds the raw response data of the analyzed block

num_of_points: is the number of data points of the analyzed block

time: is the real time of the block

w_smooth: is the window size to compute ***smoothed***.
smoothed: is the moving average of ***raw***

stim: is a *struct* that holds all data that is related to the stimulus traces.



stim

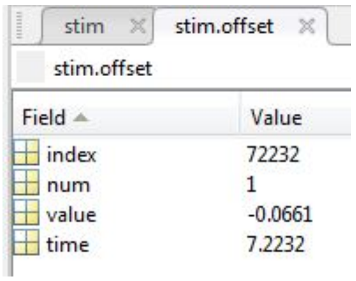
1x1 struct with 11 fields

Field	Value
scale	100
shift	0.0100
raw	1x213928 double
max	4.0700
min	0
rounded	1x213928 double
norm	1x213928 double
scaled	1x213928 double
plot	1x213928 double
onset	1x1 struct
offset	1x1 struct

raw: is the raw stimulus trace of the analyzed block
max: is the maximal stimulus value of the block
min: is the minimum stimulus value of the block
binary: is the stimulus in binary format
scale: defines by how much ***binary*** will be scaled to prepare the stimulus to be plotted
scaled: is the ***binary*** stimulus after scaling as defined by ***scale***
shift: defines by how much ***scaled*** is shifted relative to the minimum response value to plot the stimulus
plot: is ***scaled*** after shifting as defined by ***shift***

onset: is a *struct* that holds all stimulus onset data
offset: is a *struct* that holds all stimulus end (offset) data

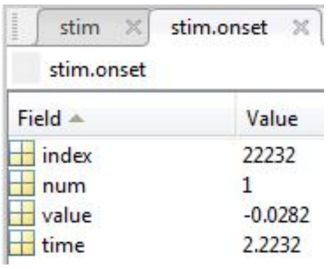
The *structs* ***onset*** and ***offset*** hold the variables:
index: are indices of all stimulus on/offsets
time: are the times of each **index**
num: is the number of stimulus on/offsets
value: is the value of ***response.smoothed*** at ***time***



stim | stim.offset

stim.offset

Field	Value
index	72232
num	1
value	-0.0661
time	7.2232



stim | stim.onset

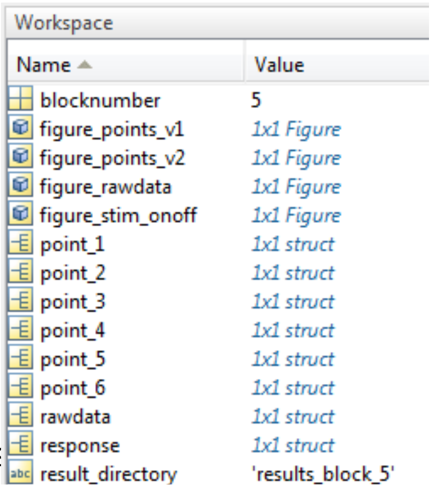
stim.onset

Field	Value
index	22232
num	1
value	-0.0282
time	2.2232

5.2.2 Available variables when running the script *ERGAnalysis_Flicker.m*

The following variables are exactly the same as when running the script ***ERGAnalysis_SinglePulses.m***:

blocknumber
result_directory
rawdata
response
savedata
stim



Workspace

Name	Value
blocknumber	5
figure_points_v1	1x1 Figure
figure_points_v2	1x1 Figure
figure_rawdata	1x1 Figure
figure_stim_onoff	1x1 Figure
point_1	1x1 struct
point_2	1x1 struct
point_3	1x1 struct
point_4	1x1 struct
point_5	1x1 struct
point_6	1x1 struct
rawdata	1x1 struct
response	1x1 struct
result_directory	'results_block_5'

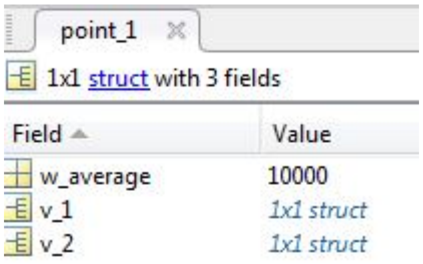
The following variables are somewhat different from the SinglePulses script described above:

point_1: is a *struct* that holds all data of all **point 1**.

w_average: number of data points of response_smoothed that were averaged before the first stimulus onset to compute value(1)

v_1: is a *struct* that holds all data of **point 1** version 1

v_2: is a *struct* that holds all data of **point 1** version 2



point_1

1x1 struct with 3 fields

Field	Value
w_average	10000
v_1	1x1 struct
v_2	1x1 struct

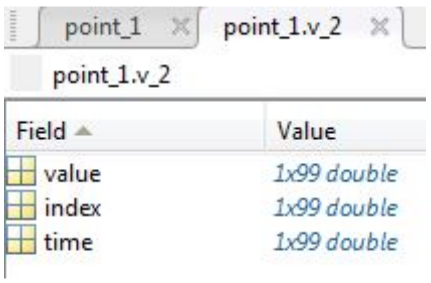
value: are response values of all **point 1**

index: are data indices of all ***value***

time: is the real time of all ***value***

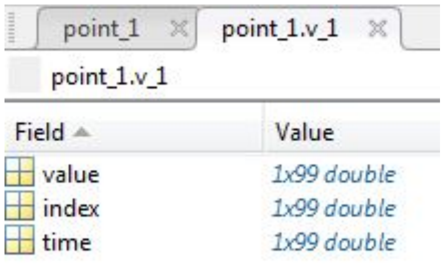
version 1: ***value(1),*** the first value within the array**,** is the average of ***w_average*** data points of ***response_smoothed*** just before the first stimulus onset. All other ***value*** are the maximum value of ***response.smoothed*** between two consecutive stimulus offsets.

version 2: ***value(1)***, the first value within the array, is the same as in version 1. All other ***value*** are the maximum value of ***response.smoothed*** between two consecutive stimulus onsets.



point_1.v_2

Field	Value
value	1x99 double
index	1x99 double
time	1x99 double



point_1.v_1

Field	Value
value	1x99 double
index	1x99 double
time	1x99 double

point_2: is a *struct* that holds all data of **point 2**.

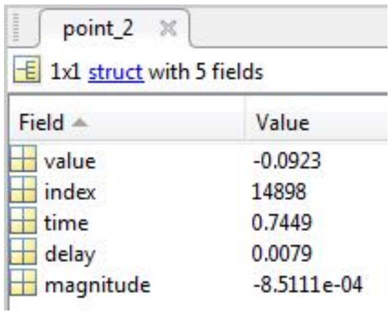
value: is the maximum value of ***response.smoothed*** between the first stimulus onset and the second stimulus offset.

index: is the data index of ***value***

time: is the real time of ***value***

delay: is the time between the first stimulus onset and ***time***

magnitude: is the difference between ***point_1.v_1.value(1)*** (baseline before stimulus onset)and ***value***



point_2

1x1 struct with 5 fields

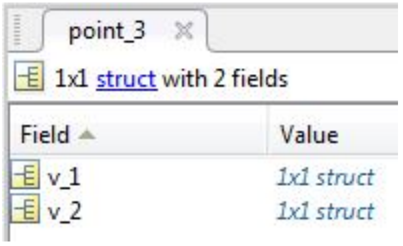
Field	Value
value	-0.0923
index	14898
time	0.7449
delay	0.0079
magnitude	-8.5111e-04

point_3: is a *struct* that holds all data of **point 3**

v_1: holds all data of **point 3** version 1

v_2: holds all data of **point 3** version 2

Each of the *structs* **v_1** and **v_2** holds the variables:



point_3

1x1 struct with 2 fields

Field	Value
v_1	1x1 struct
v_2	1x1 struct

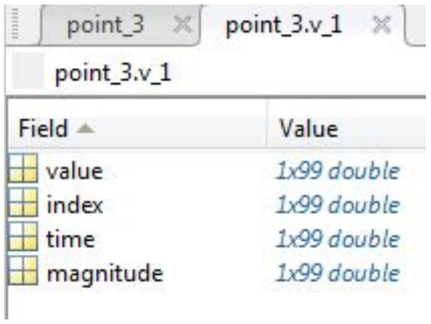
value: are the response values of ***response.smoothed*** of all **point 3**

index: is the data indices of all **value**

time: is the real time of all ***value***

magnitude: is the difference b/w ***value*** (*point_3.value*) and *point_1.value* of the same stimulus pulse and version. It is the difference b/w the maximal and minimal response value of each stimulus pulse.

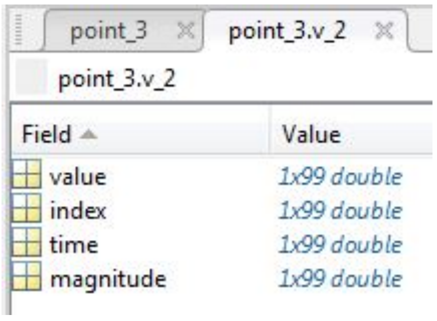
version 1: ***value*** are the minimum value of ***response.smoothed*** between two consecutive stimulus onsets.
version 2: ***value*** are the minimum value of ***response.average*** between two consecutive stimulus offsets.



point_3 | point_3.v_1

point_3.v_1

Field	Value
value	1x99 double
index	1x99 double
time	1x99 double
magnitude	1x99 double



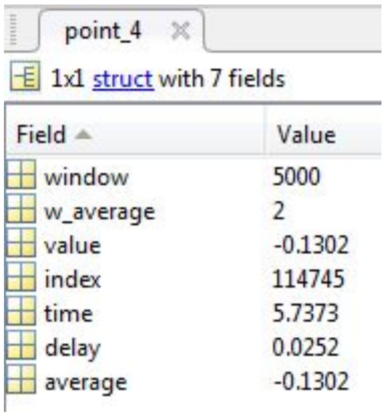
point_3 | point_3.v_2

point_3.v_2

Field	Value
value	1x99 double
index	1x99 double
time	1x99 double
magnitude	1x99 double

point_4: is a *struct* that holds all data of **point 4**.

window: number of data points that are included when searching for **point 4** right after the last stimulus offset
value: is the minimum value of ***response.smoothed*** within ***window*** data points after the last stimulus offset.
index: is the data index of ***value***
time: is the real time of ***value***
delay: is the time between the last stimulus offset and ***time***
w_average: is the number of data points of ***response.smoothed*** around ***index*** that are averaged to compute ***average***.
average: is the average of ***w_average*** data points of ***response.smoothed*** around ***index***



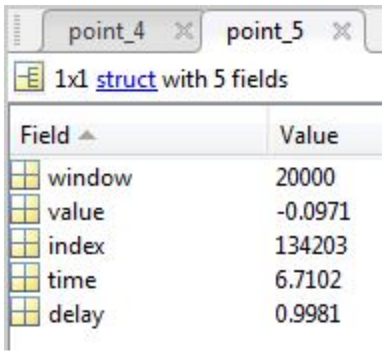
point_4

1x1 struct with 7 fields

Field	Value
window	5000
w_average	2
value	-0.1302
index	114745
time	5.7373
delay	0.0252
average	-0.1302

point_5: is a *struct* that holds all data of **point 5**.

window: is the number of data points that are included when searching for **point 5** right after the last stimulus offset
value: is the maximum value of ***response.average*** within ***window*** data points right after the last stimulus offset
index: is the data index of ***value***
time: is the real time of ***value***
delay: is the time between the last stimulus offset and ***time***



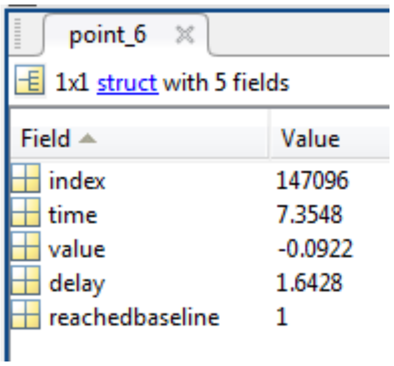
point_4 | point_5

1x1 struct with 5 fields

Field	Value
window	20000
value	-0.0971
index	134203
time	6.7102
delay	0.9981

point_6: is a *struct* that holds all data of **point 6.** If this point does not exist, its variables (except for ***reachedbaseline***) will hold *NaN* (not a number)

reachedbaseline: indicates if baseline (***point_1.v_1.value(1)***) was reached after the end of the stimulation
index: is the data index of ***value***
value: is the response value of ***response.smoothed*** for the first time



point_6

1x1 struct with 5 fields

Field	Value
index	147096
time	7.3548
value	-0.0922
delay	1.6428
reachedbaseline	1

when baseline was reached after the end of the stimulation

time: is the real time of ***value***

delay: is the time between the last stimulus offset and ***time***

6. Trouble shooting, the meaning of error messages that you might get

The scripts contain several error traps. These traps protect you from accidentally crashing the programs. The following explains the meaning of the error messages (in red) which will be displayed in the command window if one of these error traps terminated the script to keep it from crashing.

the number of stimulus onsets and offsets are not equal, check stimulus trace for artifacts
This error means that the number of stimulus beginnings and endings that were detected by the script is unequal. One reason for this could be that the recording was stopped before the end of the last stimulus. It could also be that the raw stimulus recording contains large artifacts so that the script falsely accepted one or multiple of these artifacts as a stimulus beginning or ending. If you get this error, look at your raw stimulus recording to find out what happened. If you stopped the recording before the ending of the last stimulus, you could remove your last incomplete response recording. If there are large artifacts, you need to find a way to remove these artifacts or you could use another stimulus recording if the recording was taken with the exact same timing (the time of the beginnings and endings of the stimulus must be exactly the same).

point_1.w_average precedes the beginning of the recording
This error means that ***point_1.w_average*** is too large.

point_3b.skip is too large
This error means that the variable ***point_3b.skip*** is too large. Choose a smaller value so that the starting point for searching for **point 3b** does not exceed the ending of the stimulus.

point_4.window is too large for pulse:N or point_4.window exceeds the end of the recording
If you get this error choose a smaller ***point_4.window*** so that the window within which the script searches for **point 4** will not exceed the beginning of the next stimulus or the ending of the recording.

point_5.window is too large for pulse:N or point_5.window exceeds end of recording
If you get this error choose a smaller ***point_5.window*** so that the window within which the script searches for **point 5** will not exceed the beginning of the next stimulus or the ending of the recording.

```
%---------------------------------------------------------------------


%                        ERG ANALYSIS Single Pulses


%---------------------------------------------------------------------

% This script assists in analyzing ERG responses to individual or low
% frequency light pulses. The script finds six points for each light pulse,
% makes three figures, and saves all data as described in the user guide.
% It can be applied after the data is exported and loaded into
% MATLAB as described in the user guide.

%--------------------------------------------------------------------
%                               INITIATION
%--------------------------------------------------------------------


%First, the script clears all data of a previous run except for the rawdata
if exist('point_1')
    clear -regexp ^point ^fig response stim blocknumber savedata;
end



%Next, there are several values that can be adjusted.
%Please see the user guide for detailed explanations.


%a. This variable defines which block is analyzed.
    blocknumber=1;
%b. If this variable is set to:
%     true: all data will be saved
%     false: data will not be saved
    savedata = true;
%c. These variables are needed in step 3.2 to optimally plot the stimulus.
    stim.scale = 100;% scales stim.binary
    stim.shift = 0.02;% shifts the stim.scaled
%d. This variable is needed in step 4.
    response.w_smooth=100; %window size for moving average
%e. This variable is needed in step 7.1
    point_1.w_average=5000; % number of averaged data points
%f. This variable is needed in step 7.3, 7.4, and 7.5
    point_3a.w_average = 51; % number of averaged data points
    point_3b.w_average = 51; % number of averaged data points
    point_3c.w_average = 51; % number of averaged data points
    point_3b.skip = 1000; % minimum number of data points that are between the
                         %onset of the stimulus and point 3b.
%g. This variables are needed in step 7.6
    point_4.window = 500;% window size
    point_4.w_average = 2;% number of averaged data points
%h. This variable is needed in step 7.7
    point_5.window = 1000;% window size
    point_5.w_average = 51;


%----------------------------------------------------------------------
%                      COMPUTATIONS DONE BY THE SCRIPT
%----------------------------------------------------------------------



% 1. It collects the relevant original data in a struct and clears
% all original data that is not needed



if exist('dataend') %collects the original data in a struct
    rawdata.data = data;
    rawdata.datastart = datastart;
    rawdata.dataend = dataend;
    rawdata.samplerate = samplerate;
    rawdata.titles = titles;
end



clear -regexp ^data ^com ^range ^unittext samplerate blocktimes titles...
firstsampleoffset tickrate;



%-----------------------------------------------------------------------
% 2. It extracts the raw data


% 2.1 This extracts the raw response data, the number of data points, and
%     real time of the block which is calculated from the sample rate
response.raw = rawdata.data(rawdata.datastart(1,blocknumber):rawdata.dataend(1,blocknumber));
response.num_of_points=length(response.raw);
response.time=(1:response.num_of_points)*(1/rawdata.samplerate(blocknumber));



% 2.2 This extracts the raw and the max and min stimulus
stim.raw=rawdata.data(rawdata.datastart(2,blocknumber):rawdata.dataend(2,blocknumber));
stim.max = max(round(stim.raw)); %maximum stimulus value of the block
stim.min = min(round(stim.raw)); %minimum stimulus value of the block



%------------------------------------------------------------------------
% 3. the stimulus is prepared so that we can easily find stimulus on and
%    offsets and it looks nice on the figures



% 3.1 It forces the stimulus to be full integers of either 0 or 1 (binary)
%     so that it will be easier to find stimulus on and offsets
%     NOTE: If the raw stimulus has large artifacts this might not work.
%           Check if the stimulus is in the figure raw_data.fig is a clean
%           square wave as expected. If not, then you need to find a way to
%           remove artifacts.
```

```
stim.binary=round(stim.raw*10);
stim.binary = stim.binary - min(stim.binary);
stim.binary=round(stim.binary/max(stim.binary));%stimulus in binary



% 3.2 It then prepares the stimulus for the figure.
stim.scaled = stim.binary/stim.scale; %scales the stimulus
stim.plot = stim.scaled +(min(response.raw)- stim.shift);% shifts it


%------------------------------------------------------------------------
% 4. the raw response data is then smoothed to remove noise. This is
%    done by computing the moving average. For that, we defined the
%    window size, which determines how strongly the data will be smoothed.
a = 1;
b = ones(1,response.w_smooth)/response.w_smooth;
response.smoothed=filter(b,a,response.raw); %smoothed response data
clear a b;


%------------------------------------------------------------------------
% 5. It finds stimulus on and offsets and related values



% 5.1 It finds the data index at which there is a stimulus on or offset
j = 1;
k = 1;
for i=1:response.num_of_points-1
    if stim.binary(i) < stim.binary(i+1)% finds stimulus onsets
        stim.onset.index(j)=i;
       j = j+1;
    elseif stim.binary(i)> stim.binary(i+1)% finds stimulus offsets
       stim.offset.index(k)=i;
       k = k+1;
    end
end
clear j k





% 5.2 it finds values that are related to stimulus onsets
stim.onset.num = length(stim.onset.index); % number of stimulus onsets
stim.onset.value = response.smoothed(stim.onset.index);%response values at stimulus onsets
stim.onset.time = response.time(stim.onset.index);% stimulus onset times



% 5.3 it finds values that are related to stimulus offsets
stim.offset.num = length(stim.offset.index);%number of stimulus offsets
stim.offset.value = response.smoothed(stim.offset.index);%response values at stimulus offsets
stim.offset.time = response.time(stim.offset.index);% stimulus offset times



    %error trap: in case the number of stimulus onsets is not to equal the
    % number of stimulus offsets. This can happen if the stimulus trace contains
    % very large artifacts or perhaps the recording was terminated before
    % the last stimulus offset. Check the raw stimulus trace and see what happened.



    if not(stim.offset.num == stim.onset.num)
        error('myApp:argChk', 'the number of stimulus onsets and offsets are not equal, check stimulus trace for artifacts');
    return; end;
    %end of error trap





%-----------------------------------------------------------------------
% 6. It extracts point 1 through point 5
point_6.reachedbaseline = 0;



for i=1:stim.onset.num



  % 6.1 point_1 is the response value just before each stimulus onset



       %Error trap: point_1.w_average precedes the beginning of the recording
       %or the ending of the previous stimulus
       if (stim.onset.index(i)-point_1.w_average<0)
         error('myApp:argChk', 'point_1.w_average precedes the beginning of the recording');
       return; end;



    point_1.average(i)=mean(response.smoothed((stim.onset.index(i)-point_1.w_average):(stim.onset.index(i))));
    point_1.index(i) = stim.onset.index(i)-round(point_1.w_average/2);
    point_1.time(i)= response.time(point_1.index(i));



  % 6.2 point_2 is the maximum response between stimulus on and offset.
    [point_2.value(i),J]=max(response.smoothed(stim.onset.index(i):stim.offset.index(i)));
    point_2.index(i)=stim.onset.index(i)+J;
    point_2.time(i)=response.time(point_2.index(i));
    point_2.delay(i)=response.time(J);
    point_2.magnitude(i)= point_2.value(i)- point_1.average(i);
    clear J;



   % 6.3.a point_3a is the minimum response value b/w stimulus on and offset
   [point_3a.value,J]=min(response.smoothed(stim.onset.index(i):stim.offset.index(i)));
    point_3a.index(i) = stim.onset.index(i)+J;
        i_begin = point_3a.index(i)-round(point_3a.w_average/2);
```

```
     i_end   = point_3a.index(i)+round(point_3a.w_average/2);
 point_3a.average(i) = mean(response.smoothed(i_begin:i_end));
 point_3a.time(i) = response.time(point_3a.index(i));
 point_3a.magnitude(i)=point_3a.average(i)- point_1.average(i);%
 clear i_begin i_end J;


% 6.3.b point_3b is the minimum response value b/w a certain number of
%     points after stimulus onset and stimulus offset
i_begin = stim.onset.index(i)+point_3b.skip;



    %Error trap: point_3b.skip exceedes stimulus offset, make it smaller
    if (i_begin >= stim.offset.index(i))
      error('myApp:argChk', 'point_3b.skip is too large');
    return; end;
    %end of error trap



[point_3b.value,J]=min(response.smoothed(i_begin:stim.offset.index(i)));
 point_3b.index(i) = stim.onset.index(i)+point_3b.skip+J;
     i_begin = point_3b.index(i)-round(point_3b.w_average/2);
     i_end   = point_3b.index(i)+round(point_3b.w_average/2);
 point_3b.average(i) = mean(response.smoothed(i_begin:i_end));
 point_3b.time(i) = response.time(point_3b.index(i));
 point_3b.magnitude(i)= point_3b.average(i)- point_1.average(i);
 clear i_begin i_end J;



% 6.3.c point_3c is the minimum response value just before stimulus offset
 point_3c.index(i) = stim.offset.index(i)-1;
 point_3c.value(i) = response.smoothed(point_3c.index(i)-1);
 point_3c.average(i)= mean(response.smoothed((point_3c.index(i)-point_3c.w_average):point_3c.index(i)));
 point_3c.time(i) = response.time(point_3c.index(i));
 point_3c.magnitude(i)=point_3c.average(i)- point_1.average(i);



% 6.4 point_4 is the minimum response value b/w the end of the stimulus
%     and a defined number of data points thereafter as defined
%     by point_4.window.



  %Error trap: point_4.window exceeds stimulus onset of the next pulse
  %            or the end of the recording
  if (i<stim.offset.num)
      if((stim.offset.index(i)+point_4.window)>stim.onset.index(i+1))
          error('myApp:argChk', strcat('point_4.window is too large for pulse:',num2str(i)));
  return; end; end;
  if((stim.offset.index(i)+point_4.window)>response.num_of_points)
         error('myApp:argChk', 'point_4.window exceeds the end of the recording');
  return; end;
 %end of error trap



[point_4.value(i),J]=min(response.smoothed(stim.offset.index(i):(stim.offset.index(i)+point_4.window)));
 point_4.index(i) = stim.offset.index(i)+J;
 point_4.time(i)=response.time(point_4.index(i));
 point_4.delay(i) = response.time(J);
     i_begin = point_4.index(i)-round(point_4.w_average/2);
     i_end   = point_4.index(i)+round(point_4.w_average/2);
 point_4.average(i) = mean(response.smoothed(i_begin:i_end));
 point_4.magnitude_1(i)=point_4.average(i)-point_1.average(i);
 point_4.magnitude_2(i)=point_4.average(i)-point_3c.average(i);
 clear i_begin i_end J;



% 6.5 point_5 is the maximal response value b/w the end of the stimulus
%     and a defined number of data points thereafter as defined
%     by point_5.window.



  %Error trap: point_5.window exceeds stimulus onset of the next pulse
  %            or the end of the recording
  if (i<stim.offset.num)
      if((stim.offset.index(i)+point_5.window)>stim.onset.index(i+1))
          error('myApp:argChk', strcat('point_5.window is too large for pulse:',num2str(i)));
  return; end; end;
  if((stim.offset.index(i)+point_5.window)>response.num_of_points)
      error('myApp:argChk', 'point_5.window exceeds end of recording');
  return; end;
  %end of error trap



[point_5.value(i),J]=max(response.smoothed(stim.offset.index(i):(stim.offset.index(i)+point_5.window)));
 point_5.index(i) = stim.offset.index(i)+J;
     i_begin = point_5.index(i)-round(point_5.w_average/2);
     i_end   = point_5.index(i)+round(point_5.w_average/2);
 point_5.average(i) = mean(response.smoothed(i_begin:i_end));
 point_5.time(i)=response.time(point_5.index(i));
 point_5.delay(i) = response.time(J);
 point_5.magnitude_1(i)=point_5.average(i)-point_1.average(i);
 point_5.magnitude_2(i)=point_5.average(i)-point_3c.average(i);
 clear i_begin i_end J;


% 6.6 point_6 is the first time when baseline is reached after stimulus
% offset
J = find(response.smoothed(stim.offset.index(i):end)>=point_1.average(i));
if isempty(J)
    point_6.index(i) = NaN(1);
    point_6.value(i) = NaN(1);
    point_6.time(i) = NaN(1);
    point_6.delay(i) = NaN(1);
else
    point_6.index(i) = stim.offset.index(i)+J(1);
    point_6.time(i) = response.time(point_6.index(i));
    point_6.value(i) = response.smoothed(point_6.index(i));
```

```
       point_6.delay(i) = response.time(point_6.index(i)-stim.offset.index(i));
       point_6.reachedbaseline = point_6.reachedbaseline+1;



   end
   clear J;

end
clear i ;





%-------------------------------------------------------------------------
%                              MAKE FIGURES
%-------------------------------------------------------------------------






% It makes a figure of the smoothed and averaged response data, and
% point_1 through point_6
%figure_points = figure('numbertitle','off','name','points of interest');
title('stimulus, smoothed response, and useful data points');
xlabel('time(s)'); % x axis label
ylabel(strcat('response'));% y axis label
hold on;
plot(response.time,stim.plot,'black');
plot(response.time(response.w_smooth:end),response.smoothed(response.w_smooth:end),'b');
plot(point_1.time,point_1.average,'ro', 'markersize',9,'Linewidth',2);
plot(point_2.time, point_2.value,'go', 'markersize',9,'Linewidth',2);
plot(point_3a.time,point_3a.average,'mo','markersize',9,'Linewidth',2);
plot(point_3b.time,point_3b.average,'yo','markersize',9,'Linewidth',2);
plot(point_3c.time,point_3c.average,'ko','markersize',9,'Linewidth',2);
plot(point_4.time,point_4.average,'co','markersize',9,'Linewidth',2);
plot(point_5.time,point_5.average,'bo','markersize',9,'Linewidth',2);
plot(point_6.time,point_6.value,'r*','markersize',10,'Linewidth',1.5);
hold off;
legend ('stimulus',strcat('response smoothed, block:',num2str(blocknumber)),...
    'point 1', 'point 2','point 3a','point 3b','point 3c','point 4',...
    'point 5',strcat('point 6 (',num2str(point_6.reachedbaseline),')'));


% It makes a figure of the stimulus, raw response data, smoothed response
%
%
% data and stimulus on and offsets
figure_stim_onoff = figure('numbertitle','off','name','smoothed data with stimulus on and offsets');
title('stimulus, raw & smoothed response, and pulse on- & offsets');
xlabel('time(s)'); % x axis label
ylabel(strcat('response'));% y axis label
hold on;
plot(response.time,stim.plot,'black');
plot(response.time,response.raw,'b');
plot(response.time(response.w_smooth:end),response.smoothed(response.w_smooth:end),'g');
plot(stim.onset.time,stim.onset.value,'r*','markersize',10,'Linewidth',1.5);
plot(stim.offset.time, stim.offset.value,'m*','markersize',10,'Linewidth',1.5);
hold off


legend ('stimulus',strcat('raw response, block:',num2str(blocknumber)),...
    'smoothed response',...
    strcat('stimulus onsets (',num2str(stim.onset.num),')'),...
    strcat('stimulus offsets (',num2str(stim.offset.num),')'));



% It makes a figure of the stimulus and the raw response data
figure_rawdata = figure('numbertitle','off','name','rawdata');
title(strcat('stimulus and raw response of block:',...
    num2str(blocknumber)));
xlabel('time(s)'); % x axis label
ylabel('response');% y axis label
hold on
plot(response.time,response.raw,'b');
plot(response.time,stim.plot,'black');
hold off
legend ('raw response',strcat('stimulus, max:',...
    num2str(stim.max),', min:',num2str(stim.min)));


%---------------------------------------------------------------------------
%                            SAVES ALL DATA
%---------------------------------------------------------------------------


%It makes a directory into which all figures and results will be saved.
%The name of the directory is: results_block_N where N is the blocknumber



if savedata

    result_directory = strcat('results_block_',num2str(blocknumber));
    mkdir(result_directory);



%this saves all data that is in the workspace to a .m file.
    save(strcat(result_directory,'\results_block',num2str(blocknumber)));


end
```

```
%-----------------------------------------------------------------------
%                        ERG ANALYSIS Flicker
%-----------------------------------------------------------------------
% This script assists in analyzing ERG recordings when the eye was
% stimulated with light pulses of high frequency. It is recommended to be
% used when the frequency is too high to yield proper analysis with the
% single pulse script. The script finds five points, makes four figures,
% and saves all data as described in the user guide. The script can be
% applied after the data is exported and loaded into MATLAB as described
% in the user guide.

%----------------------------------------------------------------------
%                               INITIATION
%----------------------------------------------------------------------
%First, the script clears all data of a previous run except for the rawdata
if exist('point_1')
    clear -regexp ^point ^fig response stim blocknumber savedata;
end

%Next, there are several values that can be adjusted.
%Please see the user guide for detailed explanations.

%a. This variable defines which block is analyzed.
    blocknumber=5;
%b. If this variable is set to:
%      true: all data will be saved
%      false: no data will not be saved
    savedata = true;
%c. These variables are needed in step 3.2 to optimally plot the stimulus.
    stim.scale = 100;% scales stim.binary
    stim.shift = 0.02;% shifts the stim.scaled
%d. This variable is needed in step 4.
    response.w_smooth=50; %window size for moving average
%e. This variable is needed in step 7.1.1 and 7.1.2
    point_1.w_average=1000; % number of averaged data points
%g. These variables are needed in step 7.4
    point_4.window = 5000;% window size
    point_4.w_average = 2;% number of averaged data points
%h. This variable is needed in step 7.5
    point_5.window = 5000;% window size
    point_5.w_average = 51;
%-------------------------------------------------------------------------
%                     COMPUTATIONS DONE BY THE SCRIPT
%-------------------------------------------------------------------------

% 1. It collects the relevant original data in a struct and clears
% all original data that is not needed

if exist('dataend') %collects the original data in a struct
    rawdata.data = data;
    rawdata.datastart = datastart;
    rawdata.dataend = dataend;
    rawdata.samplerate = samplerate;
    rawdata.titles = titles;
end

clear -regexp ^data ^com ^range ^unittext samplerate blocktimes titles...
    firstsampleoffset tickrate;

%-------------------------------------------------------------------------
% 2. It extracts the raw data

% 2.1 This extracts the raw response data, the number of data points, and
%      real time of the block which is calculated from the sample rate
response.raw = rawdata.data(rawdata.datastart(1,blocknumber):rawdata.dataend(1,blocknumber));
response.num_of_points=length(response.raw);
response.time=(1:response.num_of_points)*(1/rawdata.samplerate(1));

% 2.2 This extracts the raw and the max and min stimulus
stim.raw=rawdata.data(rawdata.datastart(2,blocknumber):rawdata.dataend(2,blocknumber));
stim.max = max(round(stim.raw)); %maximum stimulus value of the block
stim.min = min(round(stim.raw)); %minimum stimulus value of the block

%-------------------------------------------------------------------------
% 3. the stimulus is prepared so that we can easily find stimulus on and
%    offsets and it looks nice on the figures

% 3.1 It forces the stimulus to be full integers of either 0 or 1 (binary)
%      so that it will be easier to find stimulus on and offsets
%      NOTE: If the raw stimulus has large artifacts this might not work.
%            Check if the stimulus in the figure raw_data.fig is a clean
%            square wave as expected. If not, then you need to find a way to
%            remove artifacts.
stim.binary=round(stim.raw*10);
stim.binary = stim.binary - min(stim.binary);
stim.binary=round(stim.binary/max(stim.binary));%stimulus in binary

% 3.2 It then prepares the stimulus for the figure.
stim.scaled = stim.binary/stim.scale; %scales the stimulus
stim.plot = stim.scaled +(min(response.raw)- stim.shift);% shifts it

%-------------------------------------------------------------------------
% 4. the raw response data is the smoothed to remove noise. This is
%    done by computing the moving average. For that, we defined the
%    window size, which determines how strongly the data will be smoothed.
a = 1;
b = ones(1,response.w_smooth)/response.w_smooth;
response.smoothed=filter(b,a,response.raw); %smoothed response data
clear a b;
```

```
%-----------------------------------------------------------------------
% 5. It finds stimulus on and offsets and related values

% 5.1 It finds the data index at which there is a stimulus on or offset
j = 1;
k = 1;
for i=1:response.num_of_points-1
    if stim.binary(i) < stim.binary(i+1)% finds stimulus onsets
        stim.onset.index(j)=i;
       j = j+1;
    elseif stim.binary(i)> stim.binary(i+1)% finds stimulus offsets
       stim.offset.index(k)=i;
       k = k+1;
    end
end
clear j k

% 5.2 it finds values that are related to stimulus onsets
stim.onset.num = length(stim.onset.index); % number of stimulus onsets
stim.onset.value = response.smoothed(stim.onset.index);%response values at stimulus onsets
stim.onset.time = response.time(stim.onset.index);% stimulus onset times

% 5.3 it finds values that are related to stimulus offsets
stim.offset.num = length(stim.offset.index);%number of stimulus offsets
stim.offset.value = response.smoothed(stim.offset.index);%response values at stimulus offsets
stim.offset.time = response.time(stim.offset.index);% stimulus offset times

    %error trap: in case the number of stimulus onsets is not equal to the
    % number of stimulus offsets. This can happen if the stimulus trace contains
    % very large artifacts or perhaps the recording was terminated before
    % the last stimulus offset. Check the raw stimulus trace and see what happened.

    if not(stim.offset.num == stim.onset.num)
        error('myApp:argChk', 'the number of stimulus onsets and offsets are not equal, check stimulus trace for artifacts');
    return; end;
    %end of error trap

%----------------------------------------------------------------------
% 6. Extracts point 1 through point 5

for i=1:stim.onset.num

   % finds relevant points around the first stimulus onset
   if(i==1)%
        % 6.1.1 point_1.v_1(1): first value is the response just before first stimulus begins

           %Error trap: point_1.w_average precides the beginning of the recording
           %or the ending of the previous stimulus
            if (stim.onset.index(i)-point_1.w_average<0)
               error('myApp:argChk', 'point_1.w_average precedes the beginning of the recording');
            return; end;

        point_1.v_1.value(1)= mean(response.smoothed((stim.onset.index(1)-point_1.w_average):(stim.onset.index(1))));
        point_1.v_1.index(1) = stim.onset.index(1)-round(point_1.w_average/2);
        point_1.v_1.time(1) = response.time(point_1.v_1.index(1));
        % 6.1.1 point_1.v_2(1): the first value is the response just before the first stimulus begins
        point_1.v_2.value(1) = point_1.v_1.value(1);
        point_1.v_2.index(1) = point_1.v_1.index(1);
        point_1.v_2.time(1) = point_1.v_1.time(1);

        % 6.2 point_2: maximum response value b/w the first stimulus
        %              beginning and second stimulus ending
        [point_2.value,R]= max(response.smoothed(stim.onset.index(1):stim.offset.index(2)));
        point_2.index =stim.onset.index(1)+R;
        point_2.time = response.time(point_2.index);
        point_2.delay =response.time(R);
        point_2.magnitude = point_2.value - point_1.v_1.value(1);
        clear R;

        % 6.3.1 point_3.v_1(1): is the first minimum response value version 1,
        %                       b/w the first two stimulus beginnings
        [point_3.v_1.value(1),R]=min(response.smoothed(stim.onset.index(1):stim.onset.index(2)));
        point_3.v_1.index(1) = stim.onset.index(1)+R;
        point_3.v_1.time(1) = response.time(point_3.v_1.index(1));
        point_3.v_1.magnitude(1)=point_3.v_1.value(1)- point_1.v_1.value(1);
        clear R;
        % 6.3.2 point_3.v_2(1): is the first minimum response value version 2,
        %                       b/w the first two stimulus endings
        [point_3.v_2.value(1),R]=min(response.smoothed(stim.offset.index(1):stim.offset.index(2)));
        point_3.v_2.index(1) = stim.offset.index(1)+R;
        point_3.v_2.time(1) = response.time(point_3.v_2.index(1));
        point_3.v_2.magnitude(1)=point_3.v_2.value(1)- point_1.v_2.value(1);
        clear R;

    % finds relevant data points after the last stimulus ends
    elseif (i == stim.onset.num)
    %   6.4 point_4: minimum response value after last stimulus ending

           %Error trap: point_4.window exceeds stimulus onset of the next pulse
           %            or the end of the recording
           if((stim.offset.index(i)+point_4.window)>response.num_of_points)
              error('myApp:argChk', 'point_4.window exceeds the end of the recording');
           return; end;
           %end of error trap

        [point_4.value,R]=min(response.smoothed(stim.offset.index(i):(stim.offset.index(i)+point_4.window)));
        point_4.index = stim.offset.index(i)+R;
        point_4.time = response.time(point_4.index);
        point_4.delay = response.time(R);
```

```
            i_begin = point_4.index-round(point_4.w_average/2);
            i_end = point_4.index+round(point_4.w_average/2);
        point_4.average = mean(response.smoothed(i_begin:i_end));
        point_4.magnitude_1 = point_4.average - point_1.v_1.value(1);
        clear R i_begin i_end;

    %   6.5 point_5: maximum response value after last stimulus ending
            %Error trap: point_5.window exceeds stimulus onset of the next pulse
            %            or the end of the recording
             if((stim.offset.index(i)+point_5.window)>response.num_of_points)
                 error('myApp:argChk', 'point_5.window exceeds end of recording');
             return; end;
             %end of error trap

         [point_5.value,R] = max(response.smoothed(stim.offset.index(i):(stim.offset.index(i)+point_5.window)));
         point_5.index = stim.offset.index(i)+R;
            i_begin = point_5.index - round(point_5.w_average/2);
            i_end   = point_5.index + round(point_5.w_average/2);
         point_5.average = mean(response.smoothed(i_begin:i_end));
         point_5.time = response.time(point_5.index);
         point_5.delay = response.time(R);
         point_5.magnitude_1 = point_5.average - point_1.v_1.value(1);
         clear i_begin i_end R;
    % 6.6 point_6 is the first time when baseline is reached after stimulus
    % offset
       J = find(response.smoothed(stim.offset.index(i):end)>=point_1.v_1.value(1));
       if isempty(J)
           point_6.index = NaN(1);
           point_6.value = NaN(1);
           point_6.time = NaN(1);
           point_6.delay = NaN(1);
           point_6.reachedbaseline = 0;
       else
           point_6.index = stim.offset.index(i)+J(1);
           point_6.time = response.time(point_6.index);
           point_6.value = response.smoothed(point_6.index);
           point_6.delay = response.time(point_6.index -stim.offset.index(i));
           point_6.reachedbaseline = 1;

       end
       clear J;



    % finds relevant data points between first and last stimulus
    else
       % 6.1.1 point_1.v_1: max response values b/w two consecutive stimulus beginnings
        [point_1.v_1.value(i),R] = max(response.smoothed(stim.offset.index(i):stim.offset.index(i+1)));
        point_1.v_1.index(i) = stim.offset.index(i)+R;
        point_1.v_1.time(i) = response.time(point_1.v_1.index(i));
       clear R;
       % 6.1.1 point_1.v_2: max response values b/w two consecutive stimulus endings
        [point_1.v_2.value(i),R] = max(response.smoothed(stim.onset.index(i):stim.onset.index(i+1)));
        point_1.v_2.index(i) = stim.onset.index(i)+R;
        point_1.v_2.time(i) = response.time(point_1.v_2.index(i));
       clear R;
       % 6.2.1 point_2.v_1: min response values b/w two consecutive stimulus beginnings
        [point_3.v_1.value(i),R]=min(response.smoothed(stim.onset.index(i):stim.onset.index(i+1)));
        point_3.v_1.index(i) = stim.onset.index(i)+R;
        point_3.v_1.time(i) = response.time(point_3.v_1.index(i));
        point_3.v_1.magnitude(i)=point_1.v_1.value(i)-point_3.v_1.value(i);
        clear R;
       % 6.2.2 point_2.v_2: min response values b/w two consecutive stimulus endings
        [point_3.v_2.value(i),R]=min(response.smoothed(stim.offset.index(i):stim.offset.index(i+1)));
        point_3.v_2.index(i) = stim.offset.index(i)+R;
        point_3.v_2.time(i) = response.time(point_3.v_2.index(i));
        point_3.v_2.magnitude(i)=point_1.v_2.value(i)-point_3.v_2.value(i);
       clear R;
   end
end
clear i;
%-------------------------------------------------------------------------
%                              MAKE FIGURES
%-------------------------------------------------------------------------
%It makes a figure of the smoothed and averaged response data and
%point_1 through point_4 version 2

figure_points_v2= figure('numbertitle','off','name','points of interest version 2');
title('points of interest version 2');
xlabel('time(s)'); % x axis label
ylabel(strcat('response'));% y axis label
hold on;
plot(response.time,stim.plot,'black');
plot(response.time(response.w_smooth:end),response.smoothed(response.w_smooth:end),'b');
plot(point_1.v_2.time,point_1.v_2.value,'ro','markersize',8,'Linewidth',1.5);
plot(point_2.time, point_2.value,'go','markersize',8,'Linewidth',1.5);
plot(point_3.v_2.time,point_3.v_2.value,'mo','markersize',8,'Linewidth',1.5);
plot(point_4.time,point_4.average,'co','markersize',8,'Linewidth',1.5);
plot(point_5.time,point_5.value,'bo','markersize',8,'Linewidth',1.5);
plot(point_6.time,point_6.value,'r*','markersize',8,'Linewidth',1.5);
hold off;
legend ('stimulus',strcat('response smoothed, block:',num2str(blocknumber)),...
    'point 1 version 2', 'point 2','point 3 version 2',...
    'point 4','point 5',strcat('point 6 (',num2str(point_6.reachedbaseline),')'));

%It makes a figure of the smoothed and averaged response data and
%point_1 through point_4 version 1
figure_points_v1= figure('numbertitle','off','name','points of interest version 1');
title('points of interest version 1');
```

```
xlabel('time(s)'); % x axis label
ylabel(strcat('response'));% y axis label
hold on;
plot(response.time,stim.plot,'black');
plot(response.time(response.w_smooth:end),response.smoothed(response.w_smooth:end),'b');
plot(point_1.v_1.time,point_1.v_1.value,'ro','markersize',8,'Linewidth',1.5 );
plot(point_2.time, point_2.value,'go','markersize',8,'Linewidth',1.5);
plot(point_3.v_1.time,point_3.v_1.value,'mo','markersize',8,'Linewidth',1.5);
plot(point_4.time,point_4.average,'co','markersize',8,'Linewidth',1.5);
plot(point_5.time,point_5.value,'bo','markersize',8,'Linewidth',1.5);
plot(point_6.time,point_6.value,'r*','markersize',8,'Linewidth',1.5);
hold off;
legend ('stimulus',strcat('response smoothed, block:',num2str(blocknumber)),...
    'point 1 version 1', 'point 2','point 3 version 1','point 4','point 5',...
    strcat('point 6 (',num2str(point_6.reachedbaseline),')'));

% It makes a figure of the stimulus, raw and smoothed response data, and
% stimulus on and offsets
figure_stim_onoff= figure('numbertitle','off','name','smoothed data with stimulus on and offsets');
title('stimulus, raw & smoothed response, and pulse on- & offsets');
xlabel('time(s)'); % x axis label
ylabel(strcat('response'));% y axis label
hold on;
plot(response.time,stim.plot,'black');
plot(response.time,response.raw,'b');
plot(response.time(response.w_smooth:end),response.smoothed(response.w_smooth:end),'g');
plot(stim.onset.time,stim.onset.value,'r*','markersize',7,'Linewidth',1);
plot(stim.offset.time, stim.offset.value,'m*','markersize',7,'Linewidth',1);
hold off
legend ('stimulus',strcat('raw response, block:',num2str(blocknumber)),...
    'smoothed response',...
    strcat('stimulus onsets (',num2str(stim.onset.num),')'),...
    strcat('stimulus offsets (',num2str(stim.offset.num),')'));

% It makes a figure of the stimulus and raw response data
figure_rawdata = figure('numbertitle','off','name','rawdata');
title(strcat('stimulus and raw response of block:',...
    num2str(blocknumber)));
xlabel('time(s)'); % x axis label
ylabel('response');% y axis label
hold on
plot(response.time,response.raw,'b');
plot(response.time,stim.plot,'black');
hold off
legend ('raw response',strcat('stimulus, max:',...
    num2str(stim.max),', min:',num2str(stim.min)));
%--------------------------------------------------------------------------
%                            SAVES ALL DATA
%--------------------------------------------------------------------------
%It makes a directory into which all figures and results will be saved.
%The name of the directory is: results_block_N where N is the blocknumber
if savedata

    result_directory = strcat('results_block_',num2str(blocknumber));
    mkdir(result_directory);

%this saves all data that is in the workspace to a .m file.
    save(strcat(result_directory,'\results_block',num2str(blocknumber)));
end

%end of script
```