

Guide for using EMG scripts

Edited by Maxime Lemieux. Scripts were developed to analyze EMG data for the laboratory of Professor Frédéric Bretzner at Université Laval – Centre de recherche du CHU de Québec.

Analysis of EMG response to 10 ms photostimulations at rest

Step 1. Export data from Spike2

The structure was planned to analysis of multiple time period (ctl, wk1, wk3, wk7), percentage of maximal laser intensity (int65), pulse duration (dur010) and number of pulses (e.g., fsin for single, f010 for 10 Hz and f100 for 100 Hz). The format and number of character is important to make the database.

Step 2. Extract response to each photostimulation

Run script RestAnalysis.m

To test, use 'MRF17232_rest_ctl_int65_dur010_fsin.mat'.

The output is a file called Database_17232.

Step 3. Extract response to each photostimulation

Gather all output files in a single folder and run the following scripts for number of motor units and duration

Rest_LTA_Dur.m

Rest_LTA_MUnb.m

Results:

Array	Description
Dblist2	List of mice ID #
Data_Succ	Success rate (%) Col 1 – pre-SCI Col 2 – wk1 Col 3 – wk7
Data_MUnb	Col 1 – mean Col 2 – S.D. Col 3 - C.V.
Data_pval	Mann-Whitney test Col 1 – wk1 vs. pre-SCI Col 2 – wk7 vs pre-SCI

Analysis of EMG response to 10 ms photostimulations during locomotion

Note: to test step 1-3, use the following file Gi17230_ctl_loco_int60_dur010.mat

Step 1. Export Data from Spike2

4 channels of hi-passed filtered EMGs (RTA, RGL, LTA, LGL) exported from Spike2

4 channels of events (RTA_units, etc...) of spikes extracted from filtered EMGs

Stim timebase

Four files for time periods (ctl, wk1, wk3, wk7)

Step 2. LocoAnalysis.m

Prepare the database for responses to photostimulation.

Set a line 1 the ID of the mouse (*). Export file as '*_stimtb.mat'.

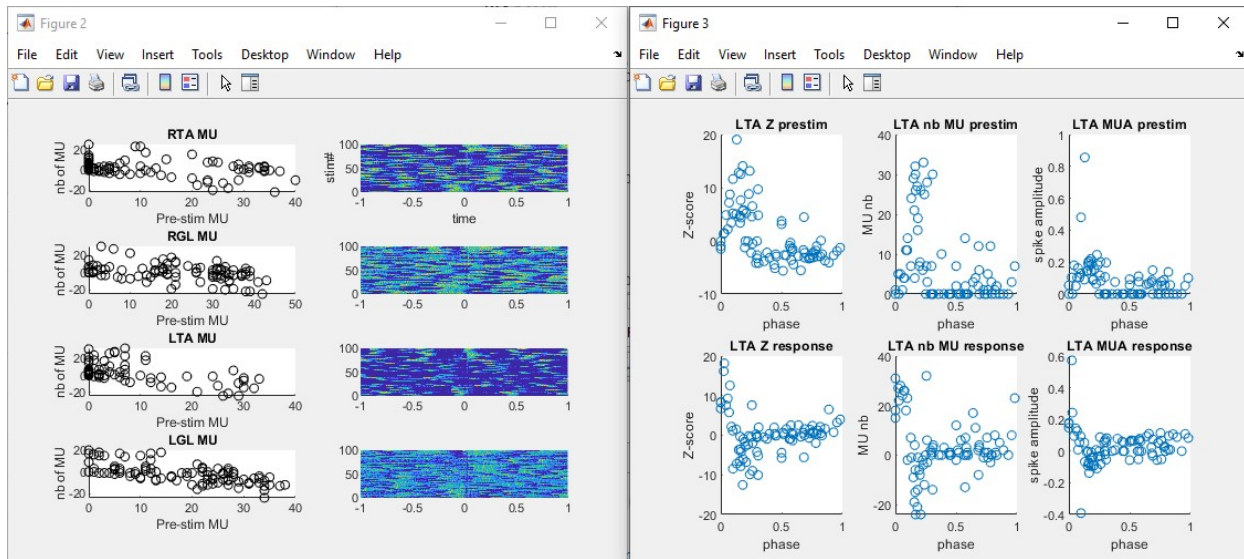
Step 3. LocoAnalysis2

Set at line 1 the ID and line 2 the timepoint.

Analyze the motor unit density, amplitude and Z-transformed in response to photostimulation. Evaluate the parameter in a time window (default is 50 ms) before and after photostimulation. Response is computed as the difference between after and before.

Note: This step usually lasts less than 5 minutes. However, some file can take 2-3 hours depending on the length and number of motor spikes on all channels.

Example of visualization



Step 4. LocoTool STATS

To test stats, unzip folder Gi17230_resp and place scripts in the folder.

Prepare data for stats. Data can be used for boxplot at this stage.

Output: SortedData_*.mat

Arrays:

Parent array	Extension	Child array	
LOCO		.LEFT .RIGHT	Stimulation during locomotion
RESET		.LEFT .RIGHT	Stimulation causes a stop
STOP		.LEFT .RIGHT	Stimulation during a stops (for a least 1 sec)
SWING	_LEFT _RIGHT	.EXC .INH .FAIL .PROP	
STANCE	_LEFT _RIGHT	.EXC .INH .FAIL .PROP	
PRESW	_LEFT _RIGHT	_LEFT _RIGHT	
RESET	_LEFT _RIGHT		
STOP	_LEFT _RIGHT		

Inside each of these arrays:

Column#		muscle
1	Timepoint in the SCI timeline (0, 1, 3 and 7)	
2	Stimulation time in the spike2 file	
3	Phase of stim in relation to the current step cycle	
4	z-value prestim	LTA
5	MSD value prestim	
6	MSD response	
7	Amplitude response (averaged post-averaged pre)	
8	z-value prestim	LGL
9	MSD value prestim	
10	MSD response	
11	Amplitude response (averaged post-averaged pre)	

Step 5. Run statistics for the longitudinal analysis

Mann-Whitney are run to compare each timepoint after SCI with pre-SCI level. Fisher test are also run to check variability.

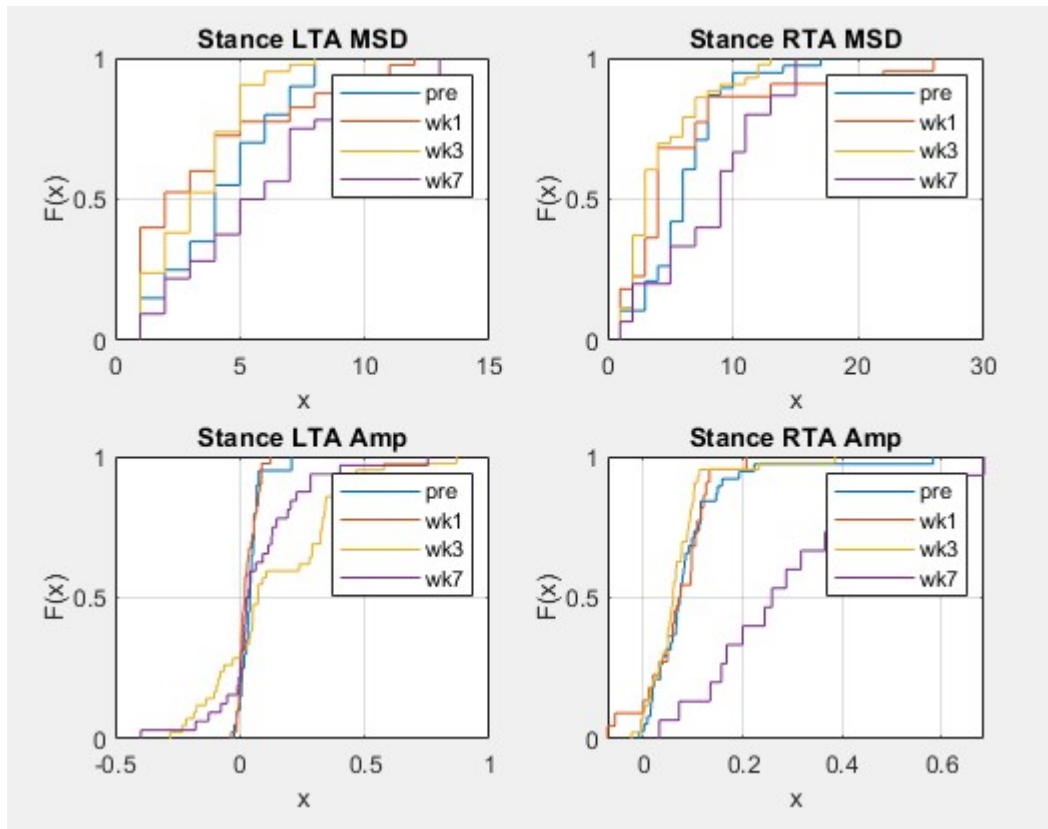
For excitatory activity in flexors during stance, run LocoTool_STATS_SWING.m

For excitatory activity in extensors during swing, run LocoTool_STATS_STANCE.m

For inhibitory activity in extensors, run LocoTool_STATS_STANCE.m

Results are printed in the command window. Mean, SD and CV are stored in MUD_LTA and MUA_LTA (same for _RTA, RGL and _LGL).

Example of visualization



Step 6. Pooled statistics

To test scripts, unzip folder Left medial MRF.

Analysis of EMG response to trains of photostimulations during locomotion

Unzip 17465_data to test.

Step 1. Export data from Spike 2

In spike 2, duplicate TA EMG, rectify and smooth the signal. Name the trace 'flexor'. Do the same for GL (rename extensor). In the 'Analysis' tab, select sub-menu 'Measurements' and 'Data channel', select the peak, onset and offset of the flexor burst. Name events 'peak', 'onburst' and 'offburst'.

Step 2. Extract data and run statistics

EMGBurstAnalysis_Train_FLEX.m (peak activity, uses Wilcoxon signed rank)

EMGBurstAnalysis_Train_EXT.m (integrated activity, uses Wilcoxon signed rank)

Data are stored in the arrays STATS_CTL and STATS_WK7