

Readme/log for Feb 23 2024

Matlab files

Sayaka (Saya) Minegishi
minegishis@brandeis.edu

2/23/2024

Description of each script that you can run

- “**CMA_batch_analysisFeb17.m**” –click on Run button to analyze all abf files in the same directory where this script & its function scripts are stored. Gives results for each file in tables.
- “**feb17_single.m**” – run analysis on an abf file of interest. Specify its file name after “filename1=”. Then hit Run.
- “**Feb23_batchEVOKED.m**” – click run to perform **batch-analysis** on the properties of the FIRST AP DETECTED IN EACH CELL (+freq in the trace). Creates a summary table. For evoked samples.
- “**Feb23_singleEVOKED.m**” – specify abf file, click run to perform single-cell analysis on the properties of the FIRST AP DETECTED IN THE ABF FILE (+freq in the trace). Creates a summary table. Used for analysis of evoked samples.

Log – what has been changed from Feb 20 files

- Created “**Feb23_batchEVOKED.m**”, a separate script to perform batch-analysis on the properties of the FIRST AP DETECTED IN A CELL. Creates a summary table.
- Created “**Feb23_singleEVOKED.m**”, the single-file analysis ver. Of Feb23_batchEVOKED.m.