Data From: Emerging experience-dependent dynamics in primary somatosensory cortex reflect behavioral adaptation

Waiblinger, Christian, The Wallace H. Coulter Department of Biomedical Engineering
McDonnell, Megan, The Wallace H. Coulter Department of Biomedical Engineering
Borden, Peter, The Wallace H. Coulter Department of Biomedical Engineering
Stanley, Garrett, The Wallace H. Coulter Department of Biomedical Engineering
christian.waiblinger@gatech.edu, garrett.stanley@bme.gatech.edu

In order to access the data and computer code that support the findings of this study, all files can be downloaded from Dryad. Files are compressed ZIP files (Windows 10) and need to be saved and extracted before access.

The main dataset contains GEVI (genetically encoded voltage imaging) data from primary somatosensory cortex (S1) and simultaneously recorded behavioral readouts (licks and whisker stimulation) in a Go-No-go detection task.

Open-source software was used for image data processing (MiCAM05-N256, Scimedia, Ltd). Psychometric data analysis and curve fits were performed using open-source software psignifit toolbox version 2.5.6 for MATLAB version 5 and up (Wichmann & Hill, 2001 a,b).

https://uni-tuebingen.de/en/fakultaeten/mathematisch-naturwissenschaftliche-fakultaet/fachbereiche/informatik/lehrstuehle/neuronale-informationsverarbeitung/research/software/psignifit/

MATLAB Download: https://github.com/wichmann-lab/psignifit/archive/master.zip

python Download: https://github.com/wichmann-lab/python-psignifit/archive/master.zip

All other analyses were performed with custom MATLAB programs. All provided data and code can be accessed with MATLAB. The dataset is structured as follows:

1. **GEVI_data:** Each folder corresponds to an animal (e.g. A_ID01, A_ID05, etc.). Within each animal folder, there are multiple folders for different stimulus conditions (e.g. "STIM1", "STIM2", etc. For lesions, e.g. "A_ID14_X_STIM1"). Within each stimulus condition are multiple days/sessions of imaging (e.g. Awake_04_03_s1.mat, etc.). These files can be loaded and accessed via MATLAB (see "code_files"). Note, due to exclusion of mice that did not express GEVI, animal ID's in the manuscript deviate from ID's from the original experiments. The updated ID's are described in a separate document, "Animal_IDs.xlsx".

2. **Behav_data:** These files contain processed psychometric data from each animal (for basic learning, e.g. "mouse05_learning.mat". For different stimulus distributions, e.g. "mouse05_range.mat". For lesions, e.g. "mouse14_lesion.mat"). In addition, this folder

contains group data/analysis/modeling results from multiple animals (e.g. *"M01_M05_M06_M07_M13_M14_Full.mat"*). All files can be loaded and accessed via MATLAB (see "Code_files").

3. **code_files:** This folder contains MATLAB programs for all analysis. Note, Psychometric data analysis and curve fits were performed using open-source software psignifit (see above link for download). The sub-folder "Code for figures" contains all necessary MATLAB code to re-produce the main figures of the manuscript. Within each code, loading files, data analysis/statistics and plotting procedures are described step-by-step.

4. **Histology:** This folder contains histology images (TIF files) that were used for the manuscript (Fig. 1 and Fig. 6). All other histology images are available from the corresponding author upon reasonable request.

For detailed questions about the data and computer code, please contact the corresponding author **garrett.stanley@bme.gatech.edu**