CRCNS.org alm-8 data description

Version 0.3 (July 29, 2022)

Data and simulations related to: Thalamus-driven functional populations in frontal cortex activity supports decision-making. Yang et al (2022) Nat Neurosci

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Summary

These experiments measure neuronal responses from the left hemisphere of premotor cortex (anterior lateral motor cortex, ALM) of adult mice performing pole location discrimination with a short-term memory. In a subset of the recordings, we inactivate activity of one of the brain regions providing inputs to ALM (ipsilateral S1/S2, contralateral ALM, and ipsilateral Thal_{ALM}) in some trials.

This dataset contains data from 9626 single units, 73 mice, 347 sessions. The dataset is described as "the primary dataset" in the paper below. The experiments (including experiment methods) are described in the paper.

Yang W, Tipparaju SL, Chen G, Li N, (2022). Thalamus-driven functional populations in frontal cortex activity supports decision-making. *Nat Neurosci*, in press.

How to download the data

The data can be downloaded from Zenodo at: <u>http://dx.doi.org/10.5281/zenodo.6846161</u>

The second dataset used in the paper can be downloaded also from Zenodo at <u>http://dx.doi.org/10.5281/zenodo.6713616</u>

How to cite the data

If you publish any work using the data, please cite the Yang et. al., (2022) publication above and also cite the dataset using the following:

Li N (2022); Data and simulations related to: Thalamus-driven functional populations in frontal cortex activity supports decision-making. Yang et al (2022) Nat Neurosci. http://dx.doi.org/10.5281/zenodo.6846161

Data analysis

The extracellular recording traces were band-pass filtered (300-6 kHz). Events that exceeded an amplitude threshold (4 standard deviations of the background) were subjected to manual spike sorting to extract single units. Spike widths were computed as the trough-to-peak interval in the mean spike waveform. Units with spike width < 0.35 ms were defined as fast-spiking (FS) neurons and units with spike widths > 0.45 ms as putative pyramidal neurons. Units with intermediate values (0.35 - 0.45 ms) were excluded. We concentrated our analyses on the putative pyramidal neurons.

File organization

.\Data_CompileData1_YangEtAl22.mat - contains the data (see variables below).

.\ scripts\ - contains analysis scripts that reproduces figures in the paper.

.\func\ - contains generic functions used by analysis scripts.

Data format

All variables in Data_CompileData1_YangEtAl22.mat are as below:

Time_cue_aligned neuron_PSTH_lick_left_correct neuron_PSTH_lick_left_error neuron_PSTH_lick_right_correct neuron_PSTH_lick_right_error neuron_info_activity_mode_w neuron_info_cell_type neuron_info_cell_type neuron_info_depth neuron_info_func_population neuron_info_mice_session neuron_info_photoinhibition neuron_info_tSNE_clusterID neuron_info_tSNE_coordinate neuron_spike_times

Below is a brief description of each variable

Time_cue_aligned

- Time stamp for the PSTHs. All data are time aligned to the 'go' cue onset time (in units of second), i.e. -2.6 s is onset of sample epoch, -1.3 s is the onset of the delay epoch, 0 s is the onset of response epoch.

neuron_PSTH_lick_left_correct% correctneuron_PSTH_lick_left_error% errneuron_PSTH_lick_right_correct% correctneuron_PSTH_lick_right_error% err

% correct trials % error trials % correct trials % error trials

- PSTHs of individual neurons. N x M matrix, N single units, M is down sampled PSTH with a bin size of 50 ms, trial types are organized by instructed trial type

neuron_spike_times

- Spike time information of individual neurons. N x 6 cell array, each row contains 1 single unit

Each entry contains spike times, K x 1 cell array: entries [spike times] for K trials. Trials are organized by trial type.

column1 - correct_lick_left_trials,

column2 - correct_lick_right_trials,

column3 - error_lick_left_trials,

column4 - error_lick_right_trials,

column5 - sample_delay_photoinhibition_lick_left_trials, -- correct and error combined; sample and delay combined

column6 - sample_delay_photoinhibition_lick_right_trials, -- correct and error combined; sample and delay combined

neuron_info_func_population

- Neuron assignment to 6 functional population. Each neuron is assigned to one population. units outside of these 6 profiles are assigned as NaN.

neuron_info_tSNE_coordinate

- Coordinates of all units in 2D tSNE space. Averaged PSTH was concatenated for licking left and licking right. Only PSTH from correct trials was included. Units with inconsistent PSTHs (Pearson's correlation between split data <0.5) were given zeros

neuron_info_tSNE_clusterID

- tSNE cluster ID for each unit

neuron_info_activity_mode_w

- unit weight to each activity mode

neuron_info_depth

- N x 1 vector, unit depth from manipulator readings

neuron info cell type

- N x 1 vector, 2 - FS, 1 - pyrmidal, 0 - unidentified, based on spike waveform width

neuron_info_connectivity

Photo-tagging experiments to test connectivity between 3 brain regions (left S1/S2, right ALM and left ALM thalamus) and left ALM
N x 3 vector, [S1/S2, cALM, ThalALM]; NaN if not tested, 0-unconnected, 1-connected

neuron_info_photoinhibition

- Photoinhibition experiments, tested only for a subset of neurons N x 1 vector, NaN-not tested; 1-S1/S2; 2-cALM; 3-ALM thalamus

neuron_info_mice_session

- N x 4 vector, [Mice, session, unit#, dataset#]
- Among dataset#, #5 is photoinhibition experiments, #6 is to photo-tagging experiments

How to get started

A collection of analyses scripts that reproduce figures in " Yang et al (2022)" is included in the folder "\scripts\"

demo_compute_activity_modes_independentTrials.m – plot t-SNE embedding and all the response profile clusters; plots PSTHs from an example cluster; plots neurons connected to S1/S2, cALM, Thal_{ALM} on the t-SNE.

demo_compute_tSNE_embedding.m – t-SNE embedding of neuronal response profiles (based on PSTH shape)

demo_compute_activity_modes.m – compute activity modes from neuronal population responses.

demo_compute_selectivity_vector_stability.m - analysis of selectivity vectors

To run a script (e.g. demo_compute_activity_modes_independentTrials.m):

- 1) open MATLAB
- 2) change current folder to the ".\ scripts\" folder
- 3) open the script & run.

Change history

No version number - Initial version matching initial version on Zenodo. Version 0.3 (July 29, 2022) - Changes for CRCNS.org: add title and "How to download data" section.