

Statistical dataset documentation

Table of Contents

Overview	1
Index and trace file columns.....	2
Manual pupil keyframes table.....	4
Plaque 3D distance table and z-stacks	5
Source data	6

Overview

The statistical export dataset contains traces of astrocytic Ca^{2+} activity in the field-of-view (FOV) as well as within astrocytic subcompartments, locomotion-traces, pupil tracking and time segmentation data based on animal behavior. All traces are resampled to 30 samples per sec. except pupil traces (see below). The dataset is the final data as it was used for statistical analysis in the publication. It contains both full traces from trials, and sub-segments from time periods where the mouse showed a specific behaviour.

The folder *Additional tables* contains manually measured pupil diameters from recordings where these were recorded. Data was added at key frames (in the other frames values are represented by NaNs). The data can be linked with two-photon microscopy data through the column `ts_name`.

Source data contains the raw data used to generate the statistical dataset. The image recordings (time series and z-stacks) use the Bruker Prairie file format, but with tiffs converted to HDF5. The data can be loaded using the [Begonia analysis library](#) from GliaLab, but the version of HDF5 used is not compatible with ImageJ. Begonia can however read and convert these files into formats compatible with ImageJ.

Other source data are in CSV, AVI and standard image formats. These outputs were generated on a GliaLab custom recording rig built in LabView, but should be readable by most scripts as they rely on typical file types.

Index and trace file columns

The files are generated using CSV-export in the GliaLab processing library [Begonia](#). Documentation on the multi-modality table structure used to collate and segment the data can be [found at this link](#), and the specific method used to export data [can be found here](#).

The “ArcSwe data export v3.1.1 to statisticians” folder:

- “Full”: Astrocytic Ca²⁺ signal traces from the FOV and cellular compartments of the relevant data types for full 300 second trials (not segmented by behaviour)
- “Full-rois”: Same, but for individual regions-of-interests
- “Run” and “Still” folders contain the same structure and data as “Full” and “Full-rois”, but only for segments classified as running or quiet wakefulness.

The folders contains two types of files:

- Index.csv (single file per folder): an index of the traces including metadata of the recording and animal characteristics such as genotype
- Traces 1,...n (multiple files): files containing 500 columns each where a column contains an individual trace with a data point on each row

Select columns (not in order) in index.csv:

Name	Description
entity	Name of the two-photon recording (“TSeries name”, otherwise known as <code>ts_name</code> in some of our datasets and scripts).
ts_name	Same as <i>entity</i> . Included in tables to enable easy join-operations with other tables that might not use “entity” to indicate the recording name.
trace_file	Name of file in the same directory containing the trace
trace_name	Column name within the trace file
quality_category	“OK” indicates the data looks good and can be included in analysis without reservation.
category	The type of data a single trace contains: raw: speed_da_sec: speed of mouse on running wheel in degrees pr. second bh: run / stil; categorical data indicating when the mouse is running/still roa comp: active fraction: Known in publication as “ROA density”. How much of the observed area shows calcium indicator activity (1 = all) roa comp: new events: new events per frame: used to calculate ROA frequency
seg_category	When segmented, the category of the time segment: run.strict: the running state as defined in the publication. still.strict: behavioral quiescence as defined in the publication Asterisk (*) indicates not segmented (i.e. full trace length)
trace_length	Length of trace in data points

ca_compartment	If trace is from compartment or FOV-trace, this contains information about which. AE: not in use, AS: astrocyte soma, FOV: field-of-view; Gp: astrocyte processes, Ca: astrocyte endfoot towards capillary, "CH1" indicates the color channel of the recording. In this publication we only use channel 1 (green).
roi_type	If trace is from individual regions-of-interests (RoI), this contains the type of RoI. Like with compartments: AE: Not used. AS: Astrocyte soma Ca: Astrocyte capillary endfeet Gp: Astrocyte processes Xg: Not used.
start_frame	Start point of the segment within the full recording
end_frame	End point
mouse_geno	Mouse genotype.
mouse_name	Name of the mouse used.
mouse_name_short	Name of mouse as used in the publication graphs. Short format for easy use in graphs.
ts_optzoom	Optical zoom setting of the microscope. 4 or 2.5.
ts_dx	Microns pr. pixels on the x-axis.
ts_dy	Microns pr. pixels on the y-axis.
ts_stage_z_um	Approximate depth from dura mater in micrometer. Not always exact, and the plane could be at somewhat different depths. This variance is not quantified.
ts_hotfixed_dt	Some recordings had a wrong setting in the microscope causing it to average two and two frames. Old versions of the processing code did not account for this, and a correction was applied to the delta-time parameter to ensure the code executed. This flag indicates the fix was applied.

Manual pupil keyframes table

Manual keyframes are used to interpolate the pupil size changes. Keyframe values are recorded at timepoints where the size is about to change and when it has complete a change. Values in between are interpolated for analysis.

Name	Unit	Description
event_type	puff/run	Flag indicating if the time segment pertains to the mid-trial air-puff or a spontaneous run (see publication)
time_s	sec	The time the segment starts within the full recording
frame	int	Frames from segment start
x, y, w, h	pixel	Pupil box coordinates
blink	yes/no	Indicates if the mouse blinking at the time point
boundbox_x, y, w, h	pixel	Area covering the mouse eye from corner to corner. As the height of the eye opening changes, the width is the most reliable axis. The height covers the eye at least to its widest opening.

Plaque 3D distance table and z-stacks

The additional data directory contains a CSV file with distances from region-of-interest centers to the nearest plaque signal point in 3D space. This data is calculated from volumetric z-stack recordings, and is relative to this recordings coordinate system.

This data was not fully obtainable for all recordings (see publication methods section for details). In the cases where a z-stack was obtained that could be used to plot 3D-distances, the z-stack is included in the recording folder. Since a z-stack is used for multiple imaging planes, they are duplicated between recordings.

Source data

Included alongside the tables are the 2-photon microscope recordings and directories with additional instrument outputs. The data is processed using the [Begonia library](#), and this Matlab library can be used to read the image files. Raw data for mouse running wheel and pupil tracking is also provided in paired “riddata” directories.

An recordings index table is also provided that links the same data that is described in the previous sections to individual recordings.

The 2-photon image recordings in this dataset have been motion corrected with [NoRMCorre library](#) using rigid transformation, but are otherwise unchanged.