

APR 15, 2024

FibPho: Analysis Protocol

In 2 collections

Sasha Burwell¹

¹Duke University

ASAP Collaborative Research Network



Sasha Burwell **Duke University**

ABSTRACT

This protocol details the analysis of the fiber photometry data.





DOI:

dx.doi.org/10.17504/protocols.io. bp2l62nrzgqe/v1

Protocol Citation: Sasha Burwell 2024. FibPho: Analysis Protocol. protocols.io

https://dx.doi.org/10.17504/protoc ols.io.bp2l62nrzgqe/v1

License: This is an open access protocol distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working

Created: Apr 08, 2024

Last Modified: Apr 15, 2024

Apr 15 2024

PROTOCOL integer ID: 98224

Keywords: ASAPCRN

Analysis Protocol

1 Each animal has one folder per recording session generated by Synapse with all the fiber photometry recording data from that session. Make a copy of the

trialData.mat

generated by the behavior code from that same session and add it to the folder.

2 To analyze the fiber photometry signals time-locked to the behavioral trials, across multiple behavior sessions for one animal, run the MATLAB code

fibpho_averaging_acrossdays(Cohort, Mouse, Bank)

This saves a

Cohort_Mouse_allTrials_fibdat_dFF.mat

variable with the raw 415nm and 465nm signals and the calculated dF/F signal per behavior trial

3 Copy the

Cohort_Mouse_allTrials_fibdat_dFF.mat

variables from all mice in an experimental condition into one folder

4 Run the MATLAB code

fibpho_averaging_acrossMice

to combine and analyze trial-based fiber photometry signals across animals.

4.1 Modify the

"ExperimentalStage"

variable (line 39) to generate the data for the specific session/trials you are interested in.

- 4.2 This code calculates a mean dF/F signal per animal for the cue and reward time windows, and prints them to the command line.
- **4.3** This code also generates the across time waveform plots for visualization of mean and SEM, as in Figure 3 and Ext. Figure 4.
- 5 Use the MATLAB code

```
BootFitDifferencePlot
```

to analyze the difference between groups and generate Ext. Fig 4b.

5.1 X values = cue-burst sessions 6-10 (

```
ExperimentalStage = 'XCRIT'
).
```

5.2 Y values = reward-omission pause first 4 extinction trials (

```
ExperimentalStage = 'B1'
).
```

5.3 Exclude mice with recording signals too low to detect pauses (X < 1).

6 Use the MATLAB code

TwoGroupsMeanDiff

with the mean dF/F values of the included mice (calculated above) to generate the Gardner-Altman plots in Figure 3 and Ext. Figure 4