Tutorial

This is a brief tutorial to access the *in vivo* imaging data from the paper:
Bocchio M*, Gouny C*, Angulo-Garcia D, Toulat T, Quiroli E, Baude A, Cossart R. *Hippocampal hub neurons maintain distinct connectivity throughout their lifetime*. Nature Communications (accepted for publication). Pre-print on BioRxiv: https://doi.org/10.1101/813923

The NWB format

Each recording is saved in a Neurodata Without Borders (NWB) file containing calcium imaging movie, detected ROIs, filtered DF/F traces, inferred spikes and locomotion epochs.

For more information on the NWB format: https://www.nwb.org/how-to-use/

The NWB file can be opened using APIs for MATLAB (MatNWB) and Python (PyNWB). It can also be accessed using HDF5 viewer.

Details on the NWB schema can be found here: https://nwb-schema.readthedocs.io/en/stable/

Organisation of the file

The file was compiled in MATLAB using the MatNWB API (NWB version 2.2.2) following the Calcium Imaging tutorial available here, with some modifications.

Metadata

Metadata with the details on the imaging experiment are included in the file (e.g. details on the mouse, virus used, experimenter, etc.). Details on the mouse can be found in the `general_subject` group.

Raw data

The calcium imaging movie (motion-corrected using NORMCorre) can be found in:
`acquisition` → `TwoPhotonSeries`

Processed data

ROIs (detected using CaImAn) are stored as masks in:
`processing` → `ophys` → `nwbdatainterface` → `ImageSegmentation` → `planesegmentation` → `PlaneSegmentation`

Filtered DF/F traces can be found in:
`processing` → `ophys` → `nwbdatainterface` → `Fluorescence` → `roiresponseseries` → `RoiResponseSeries`

Inferred spikes (deconvolution using CaImAn constrained FOOPSI algorithm) are stored in:
`analysis` → `deconvolution`

Locomotion epochs are as a logical array in:
`processing` → `behavior` → `nwbdatainterface` → `TimeSeries`

Here is an example code to load the data from one calcium movie in MATLAB using MatNWB:

```
filename = 'Dlx1-2-GFP_jRGECO1a_05_20200211.nwb';

read_nwb = nwbRead(filename);

 % load raw movie
movie = read_nwb.acquisition.get('TwoPhotonSeries').data.load;

% load image masks (ROIs)
rois = read_nwb.processing.get('ophys'). ...
    nwbdatainterface.get('ImageSegmentation'). ...
    planesegmentation.get('PlaneSegmentation'). ...
    image_mask.data.load;

% load df/f traces
df_f_traces =
read_nwb.processing.get('ophys').nwbdatainterface.get('Fluorescence')...
    .roiresponseseries.get('RoiResponseSeries').data.load;

% load spike count array (from deconvolution)
spikenums =
read_nwb.analysis.get('deconvolution').nwbdatainterface.get('TimeSeries').data.lo
ad;

% load locomotion epochs (treadmill sensor)
mvmEpochsLogic =
read_nwb.processing.get('behavior').nwbdatainterface.get('TimeSeries').data.load;
mvmEpochsIndex = find (mvmEpochsLogic == 1);
restEpochsLogic = ~mvmEpochsLogic;
restEpochsIndex = find (restEpochsLogic == 1);
```

Analyses included in the paper can be reproduced using the following MATLAB code available on GitLab.

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