File Arrangement in OSF Data:

ExtraCellInfo.mat

Saline_day0\
- Rat S\
  - Events_bsl.mat
  - Events_vi.mat
  - spikeStruct_CM.mat
  - sua_CM.mat
- Rat T\ ...
- Rat U\ ...
- Rat V\ ...

Psilocybin_03mg\
- Rat S\ ...
- Rat T\ ...
- Rat U\ ...
- Rat V\ ...

Psilocybin_1mg\
- Rat S\ ...
- Rat T\ ...
- Rat U\ ...
- Rat V\ ...

SpikeDataTutorial_Update.m

File description:

The ExtraCellInfo.mat contains:
BRKey: A cell array containing the numeric registration indices for the different brain regions are:

'1' 'Other'

'2' 'Dorsal Peduncular Cortex'

'3' 'Infralimbic Cortex'

'4' 'Prelimbic Cortex'

'5' 'Cingulate Cortex'

'6' 'Secondary Motor Cortex'

We consider only the Infralimbic, Prelimbic and Cingulate cortices to address mPFC in the rats.

CLKey: A cell array containing the numeric registration indices for the different cell types are:

'1' 'Pyramidal Cell'

'2' 'Narrow Interneuron'

'3' 'Wide Interneuron'

We consider all the cell types.

UnitReg: A cell array with rows for rats and columns for drugs. The first four rows are for the Rats S, T, U, and V, and the columns are Saline, Psilocybin_03mg, Psilocybin_1mg. Each entry contains a matrix with rows as the recorded single units and 9 columns:

ClusterID	Peak Channel	Y coord.	Brain Region	Cell Type	Stability (rest)	Stability (active)	FR change (rest)	FR change (active)
…	…	…	…	…	…	…	…	…

UnitRegKey contains the feature labels of the columns as shown above. The cluster IDs are all single unit activities (sua), and represent distinct neurons recorded by Neuropixels. We only used sua for all the following analyses.

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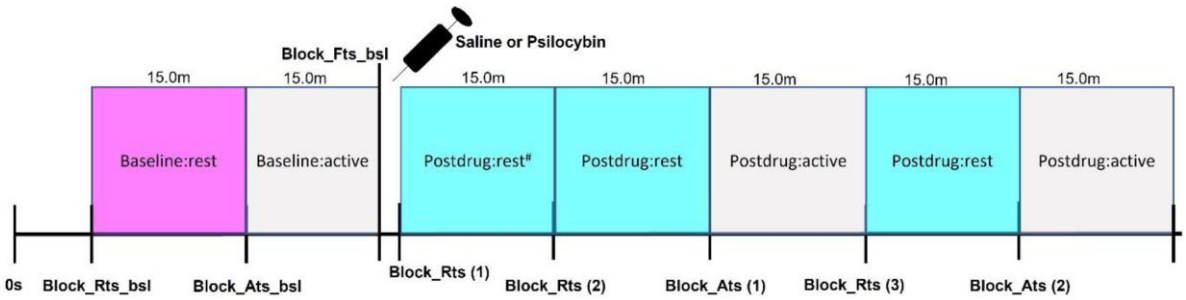
1. The schema of a single trial of recording:



Each Rat folder within a Drug folder contains:

Events_bsl.mat has three values of timestamps:

> block_Rts_bsl marks the beginning of baseline resting phase. block_Ats_bsl marks the end of baseline resting phase and the beginning of the active phase. block_Fts_bsl marks the end of baseline pre-drug phase. All values are in seconds.

Events_vi.mat has two lists of timestamps:

> block_Rts lists the start timepoints of postdrug resting phase 1, resting phase 2 and resting phase 3. block_Ats lists the start timepoints of postdrug active phase 1 and active phase 2. All values are in seconds.

spikeStruct_CM.mat has a dictionary named sp. It has multiple entries. Two dictionary entries, sp.clu and sp.st are of relevance here.

> sp.clu is a sequence of cluster IDs arranged based on their spiking instance in forward time. sp.st is list of spike times in seconds and is of the same length as sp.clu list.

sua_CM.mat contains 4 entries.

> sua is a vector list of all the recorded units which are purely single unit activities.
>
> CL is also a vector of the same length as sua and informs about which type of neuron is a sua id. The numeric entries are the same as mentioned above in CLkey.
>
> CLinfo contains the information about numeric indexing of the cell types, just like CLkey above.

peakch is a vector of the same length as sua and CL, and informs about which electrode was closest to the sua ID while recording.

SpikeDataTutorial_Update.m provides the descriptions of the various files just like above and also a working example to plot the rastergram of a single neuron spiking (single unit activity) during the 15min. long predrug resting period in a rat.

Steps:

1. Download the data folder from the OSF link. https://osf.io/t69ap/files/osfstorage#

2. Download and unzip the Metrics file in the Metrics_data directory on the github repository.

3. Copy and paste the Metrics.mat under every drug and rat folder in the unzipped file to the corresponding drug and rat folder in the downloaded OSF data.
   Metrics.mat contains all-numeric matrix data, metsua, with 15 columns. The first column is the cluster ID. Amongst the rest of the columns, col. 3 (presence ratio), col. 4 (ISI violations) and col. 6 (amplitude cutoff) were considered to select the cluster IDs with presence ratio <0.9, ISI violations <0.5, and amplitude cutoff <0.1. This can be done simply using AND selection operation on the matrix.

4. Extract the individual matrices for the drugs and rats in the cell array UnitReg under the ExtraCellInfo.mat and save them separately under the folders \Drugs\Rats (eg. \Saline\Rat S) as UnitReg.mat files. This will be helpful when running the data processing codes mentioned later.

5. Create folders ExtractdData\ and SpikeMatrix\ under all the Rats folder across all the Drugs folder. For instance, \Saline\Rat S\ ExtractdData\ and \Saline\Rat S\ SpikeMatrix\. Do it for all rats and drugs.

6. Note the path of the save data location in your local system. While running all the codes in the repository, do not miss to replace the MainPath at the top of the script with your local path.

7. Run BR_CT_spiketimes.m in the Data_processing directory on the repository.
   It saves the spike times of the single unit Cluster IDs belonging to a particular brain region (BR) and particular cell type (CT) by performing an AND selection operation for the brain region by its numeric index in Col. 4 and cell type by its numeric index in Col. 5. in the UnitReg.mat The script also performs another AND operation on top using the metsua, as mentioned above, to filter the units with chosen presence ratio, ISI violations, and amplitude cutoff. Therefore, for the total 9 combinations of 3 brain regions (Inf, Pre, and Cing) and 3 cell types (Py, NS, and WS), we can extract 9 distinct lists of cluster IDs. The outputs are saved in the folder ExtractdData\ as SpTm_BR_CT.mat

8. Now run State_BR_CT_spiketimes.m in the Data_processing directory.
   It further partitions the spike timings of the BR- and CT- based units for the different phases or rat's states within the trial. The output is saved in the ExtractdData\ as State_BR_CT.mat For instance, file 'Act_Base_Cing_NS.mat' has the spike timings of the narrow-spiking units from cingulate cortex during the predrug baseline active phase of the trial. The states in the saved files are denoted as:

Predrug Baseline phases:

Base_: resting phase, Act_Base_: active phase,

Postdrug phases:

Pstdrg1_: resting phase 1, Pstdrg2_: resting phase2, Pstdrg3_: resting phase 3

Act_Pstdrg1_: active phase 1, Act_Pstdrg2_: active phase 2

9. Next run SpkMatrix.m in the Data_processing directory.
   Using the extracted State_BR_CT.mat data in the ExtractdData\, it creates a time-binned spike matrix. Each row of the matrix would represent a unit belonging to a state X BR X CT and the columns represent time-bins with counts of spikes within those bins. For every combination of state X BR X CT, we create a spike matrix data with time bins of sizes 10ms and 20ms, by editing the dt variable withing the script. The outputs are saved in the folder SpkMatrix\ as State_BR_CT_dt10ms.mat and State_BR_CT_dt20ms.mat You can choose other time bins as well, and it will save the data in a similar way with new dt labels.

10. To compute MSD values, move to the Compute_MSD\ directory on the repository and run Compute_MSD.m. As always, take care of the MainPath and the dt value in the top two lines of the script. Next run the script PostdrgAveraging.m, and finally run the AdjustMSDdistribution.m.
    This will eventually give you a cell array data MSDs_RatPooled. The rows will be Saline, Psilocybin_03mg, and Psilocybin_1mg. The columns will be the states: Predrug Rest, Predrug Active, Postdrug Rest and Postdrug Active. In each cell, you will have a vector of MSDs, pooled across rats, for the networks of all neurons across brain regions and cell types in the individual rats.

11. To obtain unitwise LZ values, move to the Compute_LZ\ directory on the repository and run Compute_unitLZ.m. Take care of the MainPath and the dt value in the top two lines of the script. Next run UnitLZ.m scipt. Eventually, you will obtain an excel file UnitLZ.xls with Col. 1 Unit ID number, Col2. Drug, Col.3 Rat, Col. 4 State, Col. 5 Brain Region, Col. 6 Cell Type, and Col. 7 the LZ value.