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In vivo Ephys: Analysis Protocol

In 2 collections

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ABSTRACT

This protocol details the analysis procedures performed on the in vivo electrophysiology data post-spike sorting.

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Analysis Protocol

1 To plot the waveforms from one electrode of interest in the raw data (ex, Fig. 1c), run the Matlab code

```
plotRawTraces(electrode)
```

on the raw continuous data.

2 To analyze the sorted templates extracted from Spyking Circus,

2.1 Use the custom matlab code.

```
plotSpikes(chWithCell)
```

2.2 chWithCell = array of the electrode which has a cell for each template (ex [5 15 3]).

> **Note**
>
> Make sure this is in the order of the templates output by Spyking Circus.

2.3 Calculates and plots spike amplitude, cumulative spikes, and firing rate in Hz for all the templates saved.

3 From the resulting Templates_data structure, save each row as an individual dat variable.

i.e., for ch 15 in the above example:

```
load Templates_data;
dat = Templates_data(2, :); %row 2 is channel 15 data
save('mouse_date_ch15_data', 'dat');
```

4 Copy multiple channels into one folder for grouped analysis, and run

```
spikingAcrossCells
```

in this folder.

5 Referencing the control and experimental

```
allCells
```

data structures created from

```
spikingAcrossCells
```

, run

```
plotFeaturesAcrossTime
```

to generate the plots seen in the left of Fig. 1d, e, and f.

6 Use the features in the

```
allCells
```

data structure:

6.1 Calculate delta norm as (post-pre)/(post+pre) for each feature for each cell.

6.2 Input ddHTP values as

```
y1
```

and +HTP values as

```
y2
```

into the Matlab code

```
TwoGroupsMeanDiff
```

for statistical analysis and generating the plots seen in the right of Fib. 1d, e, and f.

6.3 Use GraphPad Prism to generate the plots in Ext. Fig 2d and h-l from the delta norm features.