Title of dataset:
Baseline and driven activity of p-type and ampullary electroreceptor afferents of the weakly electric fish A*pteronotus leptorhynchus*

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Brief description of dataset:
Datasets contain raw and derived data as are used in Grewe et al., 2017 (below). Data originates from semi-intracellular recordings of electroreceptor afferents. The whole dataset is split into two folders: (I) data recorded in p-type electroreceptor afferents, and (II) data recorded in ampullary electroreceptor afferents. The datasets contain spontaneous (baseline) activity and/or neuronal responses to white noise stimuli.

Keywords:
electroreceptors, action potentials, weakly electric fish, white noise, active electrosensory system, passive electrosensory system, baseline activity, Apteronotus leptorhynchus

Original publication (citation and doi, if available) / other References:
J. Grewe, A. Kruscha, B. Lindner, and J. Benda; Synchronous spikes are necessary but not sufficient for a synchrony code in populations of spiking neurons; PNAS; 2017
DOI: 10.1073/pnas.1615561114

Brief description of each file or set of files:
The data is stored in NIX[1] files. The *p-unit* folder contains recordings from p-type afferents (so called p-units) and the *ampullary* folder those recordings made in ampullary afferents. The basic structure of the files is the same for both cell types.

The following information is contained within the files:
1. Baseline activity; data_arrays with the "baseline" prefix
2. Stimulus driven activity; data_arrays with the "stimspikes" prefix. The name codes some information about the stimulus condition and the trial number
    a) contrast: the intensity of the stimulus given relative (contrast) to the strength of the EOD
    b) cutoff: the upper cutoff frequency of the white noise stimulus
    c) trial: the stimulus repetition
3. Stimulus waveform; stored in data_arrays with names like "stimspikes_contrast_2.5_cutoff_150_stimulus"
4. Derived data like coherence and power spectra of the responses can be found in data arrays with respective suffixes. For more details on the analyses see the referenced paper.
5. Metadata containing information about the recorded cell, subject, etc. can be found in the metadata section of the file.

[1] https://github.com/g-node/nix
[2] https://github.com/g-node/nixpy

Additional information (if any):

Files can be opened and read using standard hdf5 libaries supplied for python, java or matlab or. The recommended way, however, is to open the files with the NIX[2] libraries. The code snippet below shows how to read the raw data of the baseline activity from the files using the python nix library (nixio, can be installed via pip).

```python
import nixio as nix
import matplotlib.pyplot as plt

f = nix.File.open('2012-03-23-ad.nix', nix.FileMode.ReadOnly)
b = f.blocks[0]
pot = b.data_arrays['baseline membrane voltage']
potential = pot[:]
dim = pot.dimensions[0]
time = dim.axis(len(data))

plt.plot(time, potential)
plt.xlabel(dim.label + ' [' + dim.unit + ']')
plt.ylabel(pot.label + ' [' + pot.unit + ']')
plt.xlim([0, 0.01])
plt.show()
```

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