**CRCNS.org spe-2 data description**
Version 0.6 (Oct 11, 2018)

Polytrode extracellular recordings with paired juxtacellular recordings

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## Summary

Simultaneous extracellular and juxtacellular recordings were obtained from the cortex of ketamine-anesthetized rats (spontaneous activity). Extracellular recordings were carried either using polytrodes with 32 or 128 electrodes arranged in dense arrays.

Twenty-two neurons were recorded with a distance less than 200 $\mu$m between the juxtacellular pipette tip and the closest extracellular electrode. For each paired-recording, we provide the extracellular recording and the corresponding juxtacellular recording.

Detailed information about the dataset is described in:

Neto, J. P., Lopes, G., Frazão, J., Nogueira, J., Lacerda, P., Baião, P., … Kampff, A. R. (2016). Validating silicon polytrodes with paired juxtacellular recordings: method and dataset. *Journal of Neurophysiology*, *116*(2), 892–903. http://doi.org/10.1152/jn.00103.2016.

Moreover, we have a repository containing the code used in the above publication:

https://github.com/georgedimitriadis/themeaningofbrain/tree/master/ExperimentSpecificCode/_2015_Paired_Recordings_JN/Joana_Neto

## Conditions for using the data

If you publish any work using the data, please cite the publication above (Neto et. al, 2016) and also the dataset:

Joana P. Neto, Gonçalo Lopes, João Frazão, Joana Nogueira, Pedro Lacerda, Pedro Baião, Arno Aarts, Alexandru Andrei, Silke Musa, Elvira Fortunato, Pedro Barquinha, and Adam R. Kampff (2018); Polytrode extracellular recordings with paired juxtacellular recordings. CRCNS.org
http://dx.doi.org/10.6080/K0CC0XW0

## Methods

Methods are fully described in Neto et al., 2016.

## Data files organization

The data folder is organised in a directory structure by paired-recording. Each directory titled 'xxxx_xx_xx_Pair_x_x', corresponds to a paired-recording. Following a stable juxtacellular recording we were sometimes able to move the extracellular probe or the pipette and obtain another recording configuration/distance for the same neuron.

Each directory contains the following files:

- xxxx_xx_xx_Pair_x_x_ReadMe.docx – recording parameters (e.g., number of channels (i.e., electrodes), datatype, sampling frequency, gain, conversion of values from bits to Volts, …) for each paired-recording.
- amplifierxxxx-xx-xxTxx_xx_xx.bin – extracellular recording from a silicon polytrode with 32 or 128 electrodes (frequency band from 0.1 to 7500 Hz).
- adcxxxx-xx-xxTxx_xx_xx.bin – juxtacellular recording from the juxtacellular micropipette (frequency band from 300 to 7500 Hz).
- xxxx_xx_xx_Pair_x_x_Software.docx – Python code to load the extracellular and juxtacellular recordings.
- xxxx_xx_xx_Pair_x_x.pdf - this is a pdf document with summary information for each paired-recording.
- xxxx_xx_xx_Pair_x_x_MapElectrodes.pdf - scheme with the geometry of the recorded extracellular electrodes in the polytrodes.

The docs folder contains:

- DataSummary.xlsx - an excel table with metadata (e.g., the micropipette tip and closest extracellular channel's spatial location, estimated distance between the two, number of spikes recorded in juxtacellular, average peak-peak amplitude of the extracellular spike in the closest channel, …) on each paired-recording.

**Data format**

- xxxx_xx_xx_Pair_x_x_ReadMe.docx – Paired-recording parameters. These parameters include sampling frequency in Hz (Sampling_frequency), number of extracellular electrodes (Probe_numChannels), datatype of extracellular recording (Probe_dtype), number of ADC inputs (Juxta_numChannels), datatype of juxtacellular recording (Juxta_dtype), ADC input used for the juxtacellular recording (Juxta_ADC_used_channel), juxtacellular recording gain (Juxta_Gain), conversion of values from bits to Volts (Probe_y_digitization, Probe_voltage_step_size, Juxta_y_digitization and Juxta_y_range), distance between the micropipette tip and the closest extracellular electrode (distance_min), closest electrode number (Probe_closest_electrode) and location in the polytrode of the extracellular coordinates ($X_{Extra}$, $Y_{Extra}$ and $Z_{Extra}$).

- amplifierxxxx-xx-xxTxx_xx_xx.bin - binary, 16-bit resolution. In the binary file the samples storage order is in column-major. The datatype is variable, check the Probe_dtype for each paired-recording. No preprocessing has been performed on this data. The signal was sampled at 30 kHz.

- adcxxxx-xx-xxTxx_xx_xx.bin - Binary, 16-bit resolution. In the binary file the samples storage order is in column-major. The datatype is variable, check the Juxta_dtype for each paired-recording. No preprocessing has been performed on this data. Simultaneous recording of extracellular and juxtacellular electrodes used the Open Ephys (http://www.open-ephys.org) acquisition board, where one of the 8 ADC inputs is used for the juxtacellular recording. The signal was sampled at 30 kHz.

- xxxx_xx_xx_Pair_x_x_Software.docx – the Python code enables to load the extracellular and juxtacellular recordings and to reshape data. For the extracellular recording the data can be reshaped as *m* rows (channels) x *n* columns (samples) by knowing the number of channels (Probe_numChannels) and datatype (Probe_dtype). For the juxtacellular recording the data can also be reshaped as *m* rows (channels) x *n* columns (samples) by knowing the number of channels (Juxta_numChannels) and datatype (Juxta_dtype). In this recording we need to select the ADC input used for the juxtacellular recording and generate an 1D array (1 channel x samples) that contains the micropipette recording. The number of samples in extracellular and juxtacellular should be the same. Both extracellular and juxtacellular data can be converted in Volts. For each paired-recording retrieve information from 'xxxx_xx_xx_Pair_x_x _ReadMe.docx'.

- xxxx_xx_xx_Pair_x_x.pdf - This is a pdf document with summary information for each paired-recording. In that page, we show: (A) juxtacellular action potentials overlaid, time-locked to the maximum positive peak, with the average spike waveform superimposed, (B) the waveform averages for all the extracellular electrodes aligned on the juxtacellular spike peak (juxtacellular triggered average (JTA)), (C) extracellular dense polytrode array with a span of 275 $\mu$m along the shank axis, (D) spatial distribution of the amplitude for each channel's extracellular JTA waveform. The peak-to-peak amplitude within a time window (+/- 1 ms) surrounding the juxtacellular event was measured and the indicated color code was used to display and interpolate these amplitudes throughout the probe shaft, (E) the waveform averages for all the extracellular electrodes are spatially arranged. The closest electrode is marked with a red (*). The extracellular JTA time courses for each electrode are colored in the same way as in (B).

- xxxx_xx_xx_Pair_x_x_MapElectrodes.pdf – layout of polytrode electrodes array, which shows the electrodes' number correspondent to the recording order.

- DataSummary.xlxs - This is an excel spreadsheet with one row per paired-recording. For each paired-recording, a range of metadata is provided (specified by column headers). The distance designates the distance between the micropipette tip and the closest electrode on the extracellular probe. The error report uncertainty in distance estimate. The P2P amplitude is the maximum peak-to-peak amplitude of the JTAs across all extracellular channels for each paired recording. AP from bregma indicates the anterior-posterior distance relative to bregma for each pair. The depth is the distance from the brain surface to the cell recorded. This value is calculated by $Z_{juxta} – Z_{juxta\ insertion}$. The ADC channel column specifies which ADC channel was used to record juxtacellular activity and the ADC gain represents the amplification factor. Both are important parameters to load the juxtacellular recording. The Juxta threshold column indicates the threshold used for spike detection and the Juxta spikes indicates the corresponding number of detected spikes in the recording. The X, Y and $Z_{Extra}$ and X, Y and $Z_{Juxta}$ are the coordinates from the extracellular polytrode (position depicted in the ReadMe file) and from the pipette tip, respectively. These values are relative to the 'zeroing' point that is usually centered at the craniotomy and 1 to 4 mm above the tissue.

## How to get started

Inside each directory 'xxxx_xx_xx_Pair_x_x' the reader can find instructions in 'xxxx_xx_xx_Pair_x_x_Software.docx' on how to load data in Python, and in 'xxxx_xx_xx_Pair_x_x_Read Me.docx' he can retrieve for each paired-recording the parameters needed, so reading it is recommended.

## How to get help

You can get help with the dataset by posting any questions on the forum at CRCNS.org, or through direct email contact to joanasneto@gmail.com or adam.kampff@gmail.com.

## Change history

Version 0.6 (Oct 11, 2018) – Initial version.