Notes for ACS Chem revision and Matlab analysis code

Raw data files are acquired using the LabView-based software, TarHeel Bob4, and University of Washington custom hardware for voltammetry experiments. Queries about hardware and software should be addressed to Dr Scott Ng-Evans ([ngevans@uw.edu](mailto:ngevans@uw.edu)).

Each 2-minute data file includes an accompanying .txt file containing the time of events as shown in the table below:

|  |  |
| --- | --- |
| Bit | TTL / Event |
| 0 | Cue (pellet trials) |
| 1 | Pellet (cued trials) |
| 2 | Nose poke |
| 3 | Cue (infusion trials) |
| 4 | Infusion (cued trials) |
| 5 | Pellet (uncued trials) |
| 6 | Infusion (uncued trials) |
| 7 | Dummy solenoid click |

Snips from raw data files centred around events of interest (+ / - 10 seconds) were made using CV\_BatchCutandSplice to split into five trial types as shown below.

|  |  |  |  |
| --- | --- | --- | --- |
| Trial type # | Trial type | Bit # | Save folder |
| 1 | Cued pellet | 0 | 01\_pelletcue |
| 2 | Cued infusion | 3 | 02\_infcue |
| 3 | Probe pellet | 5 | 03\_probepellet |
| 4 | Probe infusion | 6 | 04\_probeinf |
| 5 | Dummy | 7 | 05\_dummy |

Calibration matrices were made for each rat using dopamine transients evoked by cocaine+raclopride at the end of each recording session. Representative dopamine and pH CVs along with a calibration factor obtained before the recording session were passed to a Matlab script (CVMatrix) to generate ‘CVMatrix.txt’ and ConcMatrix.txt’.

The chemometrics batch process method on TarHeel was used to generate dopamine concentration values for all snips (CONC files; background at 5s).

Extract CONCs and associated files

1. Determine whether CB9 chemometrics was used and whether individual electrode calibrations exist for each rat.
2. If not (most likely) make CV and CONC matrices from cocaine files – place all files required for these in their own folder and use CV Matrix

Assemble data files in understandable data structure

Put raw data and snips into rat folders – include readme file with origin of data

Describe extraction of snips and conversion to concentration

Get appropriate behavioural files into new directory structure

Use allpvi and work out from here

1. Start new script that assumes all is in allpvi already

Scripts required:

CVMatrix

getcols

main.m

pvicols.m

nanmean.m

extractdata.m

noiseQa.m

trials.m

unpacked.m

voltdata\_history.m (to combine with main)

lineplot\_pvi.m

voltanalysis\_pvi.m

to make figures in publication

pvi\_reptraces\_PVI08.m

shadedErrorBar.m

for stats…

pvi\_avg\_stats

use new epochs to do stats in spss and remake bar graphs

TTLs

Use CV\_BatchCutandSplice to make