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Using the intrinsic electrophysiological properties analysis program

(i.e. for I/V and I/F curves in current clamp)

**Step 1**

Create an excel spreadsheet that has the following columns. The first row should have the column names in it and each subsequent row should have the relevant data for 1 cell. See sampleTable.xlsx for an example. The order of the columns is irrelevant.

1. Folder - This is the name of the folder in which the data for a group of cells are stored. There is likely one folder per acquisition session. All of these folders should be contained in one folder for batch processing
2. mouseID – This is a user set field that is used as a label for the processed data
3. cellID – This is a user set field that is combined with the mouseID to label the data for a each cell
4. SweepStart – First acquisition number to process for the cell
5. SweepEnd – The last acquisition number to process for the cell
6. (Optional) CurrentPulse – A list of the current pulse amplitudes used for each cycle position. (see below for various options). If, for example, cycle positions 1, 2, and 3 correspond to amplitudes of -100, 0, and 100 pA, enter ‘-100, 0, 100’ in this field. Copy it down for all the cells acquired with the same cycle definition.
7. (Optional) – Any other columns containing relevant data can be added. These will be passed through to the final data analysis object for future use. They can be used to stored location of cells, genetic identity of cells, drugs applied, or anything else.

**Step 2**

Run phLoadFromExcel

1. Select the folder that contains all of the data folders listed in the ‘Folder’ column of the spreadsheet
2. Select the folder in which the output files will be stored. If the user does not want to save the output files, press ‘Cancel’

This function makes and sets a bunch of global variables called csTableNum csTableTxt csTableRaw csTableSize.

These store the numeric (csTableNum), text (csTableTxt), and all (csTableRaw) content of the spreadsheet.

csTableSize is set to [number\_of\_columns number\_of\_cells]

**Step 3**

Run phAnalyzeIntrinsicProperties(cellList, (optional\_param, optional\_param\_value)\*)

**cellList** is a numeric array of the indices of the cells to analyze. If set to [], all cells are analyzed. E.g. [1:5] to analyze the first 5 cells, 13 to analyze cell 13,   
[1 7 11] to analyze cells 1, 7, and 11 in the table. Since the table was a header row the cell 13, for example, would be found in row 14 of csTableRaw and the original excel spreadsheet.

**optional\_param, optional\_param\_value** are pairs of parameters and values. These are analyzed in eval statements and can be used to over ride any parameters used by the code. Some that are often used are (with defaults):

pulseAmplitudeMode=1 % see code line 55 for explanation of this parameter

pulseStart=1500 % when the variable current pulse starts (in ms)

pulseEnd=2500 % when the variable current pulse ends (in ms)

checkPulseSize=-50 % the amplitude of the standard RC check pulse (in pA)

checkPulseStart=200 % when the standard RC pulse check starts and ends

checkPulseEnd=500

maxRestSD=5; % max SD of the resting voltage to pass QC

minRm=50; % min Rm to pass QC

maxRm=1000; % max Rm to pass QC

maxVm=-50; % max Vm for inclusion and to pass QC

minVm=-90; % min Vm for inclusion and to pass QC

E.g.

phAnalyzeIntrinsicProperties(1:10)

% analyze cells 1-10

phAnalyzeIntrinsicProperties([1 10 12], ‘pulseAmplitudeMode’, 2)

% analyze cells 1, 10, and 12 and set pulseAmplitudeMode=2

phAnalyzeIntrinsicProperties([], ‘pulseAmplitudeMode’, 2, ‘maxRestSD‘, 3)

% analyze all cells and set pulseAmplitudeMode=2 and put a limit of 3 mv standard   
% deviation of the resting potential for traces to pass quality control

As each cell is analyzed the results f are stored in newCell and save to disk in a .mat file with the name ‘mouseID\_cellID.mat’

For each cell, a summary page is plotted and this is saved as a PDF with the name ‘mouseID\_cellID.pdf’

The data for each cell is also stored in the structure array csAllCells with csAllCells(1) corresponding to the results for cell 1, etc…

newCell.acq{trace#) (equivalently csAllCells(celL#).acq{trace#}) has the raw data object in it whereas the other fields are either numeric arrays with results of analysis, optional columns carried through from the excel table (gray in example below), or action potential analysis structures.

% Examples of data structures

>> newCell

newCell =

Folder: 20160415

mouseID: 'SP8'

cellID: 1

Rin: 650

Cm: 18

SweepStart: 1

SweepEnd: 40

ML: 128

DV: 111

amp: 0

Injection: 'C'

Notes: NaN

CurrentPulse: '-100, -75, -50, -25, 10, 20, 30, 40, 50, 60, 70, 80, 90,…'

CurrentPulseID: 1

QC: 1

acqRate: 10

firstOnly: 1

acq: {1x40 cell}

acqNum: [1x40 double]

cycleName: {1x40 cell}

cyclePosition: [1x40 double]

pulsePattern: [1x40 double]

extraGain: [1x40 double]

pulseList: [1x17 double]

pulseListFirst: [17x2 double]

restMode: [1x40 double]

restMean: [1x40 double]

restMax: [1x40 double]

restMin: [1x40 double]

restSD: [1x40 double]

pulseRm: [1x40 double]

pulseV: [1x40 double]

nAP: [1x40 double]

traceQC: [1x40 logical]

sagV: [1x40 double]

reboundV: [1x40 double]

reboundAP: [1x40 double]

pulseAHP: [1x40 double]

postAP: {1x40 cell}

pulseAP: {1x40 cell}

checkPulseRend: [1x40 double]

checkPulseRpeak: [1x40 double]

checkPulseTau: [1x40 double]

pulseI: [1x40 double]

restMedian: [1x40 double]

checkPulseRpeakMean: 578.1116

checkPulseRendMean: 561.2954

checkPulseTauMean: 31.6586

>> round(newCell.restMedian(1:10)) % resting potential for first 10 trials

ans =

-58 -59 -59 -60 -59 -61 -58 -61 -61 -62

>> newCell.pulseI(1:10) % the current amplitudes of the first 10 pulses

ans =

-100 -75 -50 -25 10 20 30 40 50 60

>> newCell.pulseV(1:10) % the plateau potential reached in the first 10 pulses

ans =

NaN -98 -90 -79 -49 -46 -38 -35 -45 -35

NOTE – the first pulseV entry has a value of NAN because that trace failed QC

>> newCell.nAP(1:10) % numbers of action potentials in the first 10 pulses

ans =

NaN 0 0 0 0 0 0 5 9 11

>> newCell.pulseAP{10} % Get the AP parameters for trial 10 (in which there were 11 APs)

ans =

nAP: 11

AP\_peak\_V: [1x11 double]

AP\_peak\_time: [1x11 double]

AP\_AHP\_V: [1x11 double]

AP\_thresh\_V: [1x11 double]

AP\_thresh\_time: [1x11 double]

AP\_HW\_V: [1x11 double]

AP\_0W: [1x11 double]

AP\_HW: [1x11 double]

AP\_max\_dVdT: [1x11 double]

>> round(newCell.pulseAP{10}.AP\_peak\_V) % rounded peak voltage of all the APs in trial 10

ans =

21 22 19 22 22 21 22 21 23 23 14

>> newCell.pulseAP{10}.AP\_HW % Half width (at voltage midway from threshold to peak)

ans =

Columns 1 through 8 (% omitted last 3 here for brevity)

0.5810 0.5640 0.5828 0.5673 0.5817 0.5850 0.5683 0.5901

>> newCell.pulseAP{10}.AP\_0W % Width at 0 mV

ans =

Columns 1 through 8 (% omitted last 3 here for brevity)

0.5679 0.5662 0.5613 0.5666 0.5738 0.5777 0.5717 0.5723