**Analysis using *analyzepatch***

**1. History**

The Matlab program *analyzepatch* (version 1.0, released March 2021) can be used for analyzing data obtained using the program *patchclamp*, which was described in a different document on this site.

The analyses provided by the program are \*basic\* analyses – things like f-I curves, measurement of a neuron’s passive properties, LTP curves, impedance curves. Anything more specialized requires additional scripting in Matlab or exporting the data to another analysis program (like Origin or Excel).

**2. Getting started**

**Requirements**

Software: (1) Matlab R2020b or later. (2) Matlab’s Signal Processing Toolbox, version 8.5 or later.

Hardware: The software will run on Windows, Mac, and Linux machines.

**Installation**

The program *analyzepatch* consists of a set of M-files written in Matlab. As such, the program works *within* the Matlab environment and does not require a formal installation.

The latest code will always be available on the GitHub site: <https://github.com/nsdesai/patchclamp>. (A nearly up-to-date version will also be on the TEAMS site of the LCSMS.)

Simply download the patchclamp folder to your hard disk. You can put the folder anywhere, but the most sensible place is within the Matlab folder, which you will find in the Documents folder (assuming you’ve already installed Matlab).

Then, let Matlab know where to find these files by adding the folder to its path. For example, type these two lines at the Matlab command line:

>> addpath('C:\Users\niraj\Documents\MATLAB\patchclamp')

>> savepath

Of course, you should substitute the name of your own file path (unless your name happens to be “niraj”).

If any of this confuses you, go here: <https://www.mathworks.com/help/matlab/search-path.html?s_tid=CRUX_lftnav>. Read the topics “What is the MATLAB Search Path?” and “Change Folders on the Search Path.”

**3. Opening the program**

To open the program, type this at the Matlab command line: analyzepatch.

This will open the main *analyzepatch* GUI.

Graphical user interface, application

Description automatically generated

Press the button **change directory** at top right and select the folder containing the data to be analyzed.

The list box below the button will then fill with the names of data files (i.e., MAT files with names like “experiment001trial001.mat”). You can choose which file or files to analyze in the usual Windows way: left click to select an item, use the shift or CTRL keys to select multiple items.

Then, using the checkboxes immediately below, select the channels to analyze.

The panel at lower left controls the analysis. It has four tabs: **display**, **analysis**, **fitting**, and **saving**.

**4. Display subpanel**

Graphical user interface, application

Description automatically generated

The button **display** will display saved data into the **analysis** window at right.

The **replace** checkbox allows you to decide whether whatever is already displayed in the **analysis** window will be cleared or not before plotting something new.

The **autoscale** checkbox allows you to decide whether the program auto scales the axes of the **analysis** window.

If the toggle switch is on **individual**, then individual traces will be displayed. If it is on **average**, then the traces will be averaged before display.

The arrow keys on either side of the **display** button allow you to navigate between different traces in a file. For example, say that the data file contains the responses to a family of current steps and the response to the first step is currently displayed. The right arrow will then plot the response to the next step in the sequence.

A data file may contain multiple sweeps (episodes). For example, if the file contains the response to a family of 10 current steps (say, -100 to +100 in increments of 20), then there will be 10 sweeps. You can specify which sweeps to display using the **first** and **last** fields. If the former is 3 and the latter is 7, then sweeps 3-7 will be displayed. Alternatively, pressing the button **first sweep** will set both fields to 1, so that only the first sweep will be displayed, and pressing the button **all sweeps** will result in all saved sweeps being displayed.

The checkbox **baseline subtract** determines whether data traces will be baseline subtracted before display. If yes, then the baseline to be subtracted will be the mean value between t = start and t = start + delta, where **start** and **delta** are specified in their respective fields.

Pressing the button **stimuli** will open a separate figure in which the output stimuli for displayed responses can be seen.

**5. Analysis subpanel**

Graphical user interface, application

Description automatically generated

Pressing the button **analyze** starts the analysis, the results of which will be displayed in the axes to the right. If the **replace** checkbox is checked, the axes will be cleared before display the new analysis results.

As in the **display** subpanel, one can select the range of sweeps (episodes) to analyze using the fields and buttons just below the **analyze** button.

If one wishes to confine the analysis to only a part of a full sweep, then one can do so by specifying **range** start and stop. For example, specifying start = 500 and stop = 1500 means that only the stretch of data between 500 msec and 1500 msec will be analyzed. If the **full** switch is on, then the whole range will be analyzed regardless of how start and stop are set.

The type of analysis to perform can be specified through the **analysis type** pulldown menu.

Graphical user interface, application

Description automatically generated

Pushing the button **parameters** opens a GUI in which the parameters to be used in the analysis (e.g., how spike threshold is defined) can be defined.

Graphical user interface, application

Description automatically generated

**6. Fitting subpanel**

The **fitting** subpanel allows you to fit simple functions (lines, exponentials) to pieces of data.

Graphical user interface, application

Description automatically generated

First press the **place data cursors** and then left click on the desired trace to place at least two data cursors (which can later be cleared using **clear data** cursors).

Then press one of the four buttons in the middle (**average**, **linear**, **exponential**, **linear**) to run the fitting process.

The numerical results will appear in the textbox at the bottom.

**7. Saving subpanel**

Analyses can be saved using the **saving** subpanel.

Graphical user interface, application

Description automatically generated

The names of the plotted traces will show up in the **traces** list box. Select one by left clicking over it; select others by doing the same with the shift or CTRL key pressed.

Choose the **file format** in which to save the analyses: Matlab, Excel, or ASCII.

The files will be saved to the folder displayed in the **directory** field. You can change the folder by pressing **change directory** and using the dialog window that then opens up.