

## Protocol for using the Matlab scripts for AP/AHP Iclamp analysis

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### **First step - Cloning the repository:**

Go to MATLAB, start a new Project from Git, enter the url for my github server in the blank box to create the project.

**Note:** I cloned my Iclamp analysis repository as a separate Project in matlab, so the code below applies specifically for Projects cloned from a Git repository. If your cloned folder is stored elsewhere you have to modify analysis\_dir and dirname in Apr8\_batchEVOKED.m to match it. If your cloned folder is stored in 'Matlab/Tools', you can just uncomment the commented code above and delete the alternative code.

### **Jason Luther Output Comparisons:**

Note: It's not clear which traces Jason used to obtain his data (which is stored in 'AP HAP rnl all cells.xlsx'). So for each cell, I picked files at random that had 2 spikes in one sweep.

1. Open a file from a particular cell in Clampfit, and confirm that the file has more than 2 spikes in a sweep.
2. Clone the iclamp AP&AHP analysis repository from my github:  
[https://github.com/sayakaminegishi/AP\\_AHP\\_Analysis\\_Iclamp\\_SayaMinegishi](https://github.com/sayakaminegishi/AP_AHP_Analysis_Iclamp_SayaMinegishi)
3. Store the file in a separate folder within the 'data' folder in my package.
4. On a separate matlab script, run:  

```
Apr8_batchEVOKED("folder_name_for_target_cell", "exceldocname.xlsx")
```

This runs a batch-analysis on all abf files stored in the folder folder\_name\_for\_target\_cell within the 'data' folder, and stores the results of AP/AHP analysis in exceldocname.xlsx, which will be created within the 'analyses' folder.
5. The table will show the properties of the first AP detected in the cell, at the first sweep that has at least 2 spikes.

### **Obtaining WKY/SHR AP&AHP properties from first AP in the first sweep with 2 spikes:**

1. Clone my github repo:  
[https://github.com/sayakaminegishi/AP\\_AHP\\_Analysis\\_Iclamp\\_SayaMinegishi](https://github.com/sayakaminegishi/AP_AHP_Analysis_Iclamp_SayaMinegishi)
2. Store all WKY abf files in the 'wky' folder within the 'data' folder, and all SHR abf files in the 'shr' folder.
3. Open a separate Matlab script, write at the top:  

```
newpath = "/Users/sayakaminegishi/MATLAB";  
userpath(newpath)
```

Where 'newpath' specifies the path for your MATLAB application.
4. To get the average of each WKY AP&AHP property, run, on a separate script:  

```
Apr8_batchEVOKED("wky", "WKYevoked_apr12.xlsx")
```

Where "WKYevoked\_apr12.xlsx" is the name of the excel file that contains the output information. This is stored in the 'analyses' folder.

5. For SHR analysis, run: `Apr8_batchEVOKED("shr", "SHRevoked_apr12.xlsx")`

### **T Tests comparing first AP properties between strains:**

The below instructions show you how to run t-tests to determine any difference in AP property values between SHR and WKY strains.

#### **For AP and AHP evoked analysis:**

1. Create one folder for WKY files, another folder for SHR abf files. Download all files from Apr 8 scripts on Github into each folder.
2. Run `Apr8_batchEVOKED.m` in each folder, after making sure that the name of the excel doc and the injected current steps are what you want.
3. Make a new folder to store the two Excel tables generated in part 2.
4. From `Apr_8_tests&analysis` folder on github, download all matlab files.
5. Run `Apr3_analyzeFirstAP_tTest.m` first to see whether there is ANY difference in means between the strains for each AP property of interest.
6. For AP properties that gave a significant difference in step 5, test in which direction (e.g. SHR>WKY) this difference occurs using a one-sided t test in `significant_onesided.m` and entering the property of interest after 'tablename.'. For example for frequency, say:

```
shr_thresh= str2double(SHRTTable.frequency_Hz_);  
wky_thresh = str2double(WKYTable.frequency_Hz_);
```