Protocol for using my matlab scripts for AP/AHP Iclamp analysis
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Apr 8 2024

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(SHRTable.frequency_Hz_);
wky_thresh = str2double(WKYTable.frequency_Hz_);
```