2017-10-06

Instructions for analyzing ephys sCRACM data on Matlab and plotting in R

1. Go to the 2017\_matlab\_ephys folder
2. Place in the new atf files of the newly patched cell in that folder
3. Open the the script “complied\_sCRACM\_afcorrect.m”
4. You need to change the filename to the one of the new atf file in (line 2)
5. You need to look at the grid picture and change the number in cellspot2 (line 10)
6. Depending on which layer the cell is in, change line 14. (it’s always “L2\_”for L2 or “L3\_”for L3.
7. If you run this, you will get a csv file and a PNG file.
8. Place both of these files into either the 2017\_10\_Het or 2017\_10\_HO depending on the genotype.
9. Once you have done this, open the 2017\_10\_Het or 2017\_10\_HO folder, run either “mapping\_csv\_Het.m” or “mapping\_csv\_HO.m”file (in each folder respectively).
10. You will get 1 output file with the following name: “Het15psCRACM\_avg.csv” or “HO15psCRACM\_avg.csv” in each of the respective folder.
11. Move each of the 2 files into the 2017\_R\_ephys folder. You will replace the old files with the same name in there.
12. Open the “cellid\_depth.csv” file in 2017\_R\_ephys folder with excel.
13. Add in the cellid number and depth and brain number. Notice that all the brains in 2017 are name as 2017A, B, etc… you need to add this information manually before you can use the R script in step 14.
14. Go to R studio, and open the R script, “2017\_10\_05\_ephys\_rcode\_vthresh\_14.R”
15. Set the working directory to the 2017\_R\_ephys folder
16. Run the R script file indicated on step 14.
17. The graphs will be visualized by typing p3a and p3b on the console.
18. The statistic will appear on the console output.

If you need to find any values in R, ask Monika to look over the script for you.