Juliet’s data from CaMPARI2 experiments, studying changes in neural activity in monocular visual cortex after monocular deprivation.

GOAL: Create a statistical model to study how much variance in my data can be explained by several different factors.

The data in CAMPRAT\_MD\_ex.mat is basically a huge list of fluorescence values from individual neurons, along with other information about each cell.

For these experiments, I virally injected CaMPARI2, a photoconvertible fluorescent protein, into each hemisphere of visual cortex of rats, performed monocular deprivation (which affects activity of visual cortex neurons differently in each hemisphere) a couple weeks later, then prepared acute brain slices of visual cortex of each animal some amount of days after the monocular deprivation. For each animal, I chose 2 brain slices per hemisphere (4 slices total per animal), and with each of those slices, I photoconverted the CAMPARI2 in the slice, and then took many images of the cells in the slice in the unconverted fluorescent channel (green) and the converted fluorescent channel (red). Afterwards, I can compute a red/green ratio number for each individual cell (i.e. fluorescence value of interest). I want to ask if red/green ratios are different between the two hemispheres in rats in various experimental groups. Here, I am mostly referring to which day after MD I’m performing the experiment as the different experimental groups.

Therefore, in each experimental group, for each cell, there are multiple sources of variability that could explain differences in red/green ratios across groups of cells: The major ones (I think) are 1) animal 2) slice 3) hemisphere (deprived or control) 4) cortical Layer.

These variables are all tracked in the .mat file, but the experimental group is listed in the matlab script that I use to analyze this data. The script lists groups of animal numbers by what experiment they were in.

Animals each have a unique number; slice numbers are unique WITHIN an animal, but not between animals. If you combine animal number and slice number, this would be a unique number though. Hemisphere is tracked in the ‘deprived’ column of the .mat file. 1 indicates the slice was from the deprived hemisphere, and 0 indicates it was from the control hemisphere. Cortical layer is either 2 for layer 2/3 or 5 for layer 5/6.

The CAMPARI\_MD\_analysis\_NBIO207A.m script (which is actually a function that just takes the .mat file provided) asks which experimental group you are interested in, and then plots the data in multiple ways, comparing control and deprived cells by animal and by slice, in cumulative distribution plots and violin plots.