**Workflow Overview:**

1. Behavior data comes in as a .dat file. We use groupAllTrialsOneStruct.m to convert and save the .dat file to a .mat file. This new .mat file will contain all the trials as structs within a cell array (trials) and an overview struct (header) that contains a general view of the behavior settings used.
2. Spike data comes in as a .nev file. This singular .nev file will contain he entire days’ worth of spike data spanning GaborRF, RFMap, and MTCAN/MTNAN.
3. Sorted spike data (.nev) will be converted to a .mat file with 3 columns (channel, event, timestamp). Channel column will contain units as well, for instance if channel 1 has two units, they will be labelled as 1A, 1B in the column.
4. spikeToBehavior.m script will then add each trials corresponding spikeData (across each channel and unit) as a struct to the trial’s struct. This script has to align the spike data appropriately.