**Green-channel only imaging and matching cells across multiple sessions (Dark vs. Light, Transgenic vs. Virus, Pre- vs. Post-RW, etc.)**

-Mouse info is in **expt\_list\_tjw** for all except dark/light, which is in **exp\_list\_darklight\_actual\_tjw**

-Use **Day1\_ImageProcessing\_tjw**for session 1, stopping at the very end where it mentions red cells

-Use **Day23\_ImageProcessing\_tjw** for both sessions 2 and 3, matching each to the session 1 data

-If you would like to match session 3 to session 2, and session 2 has already been matched to session 1, you should use **Day23\_ImageProcessing\_tjw\_rematched**, which will use the shifted session 2 data

-if you have more than 3 sessions, just continue this process, using **Day23\_ImageProcessing\_tjw** or **\_rematched** as many times as needed

-Use **k\_and\_max\_newAvg\_vals** on each session from above to get k values, max df/f, and avg tuning curves for subsequent analyses

-The next step will vary based on project, but the idea is similar across all scripts 🡪 take the output from the multiple imaging sessions done above and identify tuned/matched cells across multiple sessions at the individual subject level, producing plots and saving data for pooling across subjects

-For dark/light:

-Use **new\_multi\_day\_darklight\_updatetjw** to take output from individual days done above and identify tuned/matched cells across experiment on an individual subject level

-Use **new\_darklight\_analysis\_update\_tjw** or **new\_darklight\_analysis\_update\_LM\_tjw**, depending on imaging area, to pool individual subject analyses from above to make group level observations

-Use **new\_pooled\_darklight\_regression** to analyze the above data via regression models, comparing both within and across imaging areas

-For TG/Virus:

-Use **new\_multi\_day\_TGvirus\_update\_tjw** to take output from individual days done above and identify tuned/matched cells across experiment on an individual subject level

-Use **new\_pooled\_TGvirus\_tjw** to pool individual subject data and make group analyses between TG and virus mice

-For running wheel (RW):

-These individual subject data have already been analyzed by the **new\_multi\_day\_TGvirus\_update\_tjw** script, as some of those mice were selected to take part in this additional experiment

-Use **new\_pooled\_RW\_tjw** to pool appropriate individual subject data and make comparisons from before and after the running wheel implementation

**Arc Project (KRAB): Red and green channel imaging and matching cells across multiple sessions**

-Mouse info is in **expt\_list\_arc**

-Use **Day1\_ImageProcessing\_tjw**for session 1, continuing to the end to complete the identification of red cells

-Use **Day23\_ImageProcessing\_red\_tjw** for sessions 2 and 3, matching each to session 1 data

-Use **k\_and\_max\_newAvg\_vals** on each session from above to get k values, max df/f, and avg tuning curves for subsequent analyses

-Use **new\_multi\_day\_redVgreen\_update\_tjw** to take the output from the multiple imaging sessions done above and identify tuned/matched cells across multiple sessions at the individual subject level, producing plots and saving data for pooling across subjects

-Use either **new\_pooled\_redVgreen\_tjw** or **new\_pooled\_redVgreen\_GLmice\_tjw**, depending on Arc Promoter/TJ LacZ mice or Arc Enhancer/Grace LacZ mice, respectively 🡪 this will take the individual subject multi-day data from above and pool it across subjects based on group (Arc/LacZ) and cell color (red/green) to produce many plots and a few variables for further comparisons across experiments

-Use **arc\_promVenhancer\_pooled\_tjw** for some comparisons across experimental groups for red cells only

-Use either **new\_pooled\_arc\_regression** or **new\_pooled\_arc\_regression\_GL**, , depending on Arc Promoter/TJ LacZ mice or Arc Enhancer/Grace LacZ mice, respectively, to use regression models to predict change in pref ori

**Classical conditioning, behavior only (no actual imaging)**

-These scripts are kept separately in the **class\_cond** folder

-The next steps will vary based on number of stimuli used (1 CS+ or 1CS+/1CS-)

-For only 1 stimulus (CS+)

-Mouse info is in **RC\_training\_sessions\_lists\_SJ\_tjw**

-Use **RC\_raw\_analysis\_shortened\_ver2\_tjw** for analysis and plotting

-For 2 stimuli (CS+/CS-)

-Mouse info is in **crpTrainDayList\_tjw**

-Use **crpBxOnlyOverview\_Carlo\_orig\_tjw** for analysis and plotting

**Phase reversing stimulus – 5 days**

-Mouse info is in **exp\_list\_phaserev\_tjw**

-For 1ori sessions (on days 1-5), use **phaserev\_ori\_tjw** (not matched across days – individual population of cells each day)

-Use **phaserev\_individuals\_tjw** for analysis and plotting

-Alternatively, use **phaserev\_ori\_match\_tjw**, **phaserev\_responsive\_cells**, and **multi\_day\_ori\_scatter\_phaserev\_tjw** if matching across days is desired

**Tips for multi-day imaging**

-Make sure the monitor for stimuli is at the same position each session before imaging by aligning the numbers marked on the tape in front of the monitor and on its stand

-Draw circles in Sharpie on the table around where the feet of the imaging rig stand 🡪 use this to approximate where to position the rig in subsequent sessions

-Be sure to mark your initials and the date you made the circles for reference

-Draw a line in Sharpie on the mouse’s headpost where the clamp is positioned 🡪 use this to approximate where to position the clamp on the mouse’s headpost in subsequent sessions

-When you take your day 1/session 1 snapshot, be sure that you are including some identifying vasculature (not just cells!) that can be referenced in the future 🡪 use the combination of vasculature and cells to match up subsequent snapshots the best you can

-Be sure to alert lab members that you are starting multi-day imaging so that no-one changes the 2p setup – otherwise it will be very difficult to find a matching imaging plane from before