Hs Behavior Analyses 8-29-17

1. Process all high-speed movies to determine fish locations (centroid file) and change in pixels for every frame. Move **fastqc\_newdpixandcen.slurm** to data folder and change array and filename fields as necessary. For first run, array should span all videos, so 1-821. Code is currently hard-wired to use 821 movies because making image modes. Please contact if it’s not clear how to change it.

2. Run and repeat as necessary depending on dropouts. Use **motionqueuecheck.py** to generate list of dropouts.

3. Change **sectionsfile** as necessary to reflect experiment times. combo = start/stop.

4. Genotyping info:

Generate lists either using a matrix and **splitby…py** script, or manually input into a file called “**genotyping**” in the format Gene\_wt. Asterisks in this file denote genotypes to be included in pair-wise comparisons.

5. Run **makeinputgenoandfastqfiles.py** to generate **jobsubmission.sh** file with necessary fastqcs. Make sure that the folder contains your original run file (ie, finalnovembefile.txt).

6. Run **jobsubmission.sh**.

sbatch jobsubmission.sh

Make sure these files are in the same directory first:

**AnalyzedFish.py**

**EventSection.py**

**fileloading.py**

**Fish.py**

**processmotiondata.py**

**savedata.py**

**setupfishgraphing.py**

**statsandgraphs.py**

This step can take a few hours (>3).

Should generate outputfulldata\_<gene comparison> for each pairwise comparison.

7. Can run interactive session to sort statistics; load anaconda 4-3,

srun -p interact --pty --mem 6000 -t 0-1:00 /bin/bash

module load Anaconda/4.3.0-fasrc01

run lmmanalysissave.py

python ./lmmanalysisave.py

Should spit out “finalsorted\_<input>”