# FlyGroomA Instructions

## Notes:

* Download FlyGroomA folder from GitHub.
* Before using, you should add FlyGroomA folder and all subfolders to your Matlab path. Make sure any old versions of grooming code is removed from Matlab path.

## Part 1 – Processing manual analysis files

The first step in the analysis is to convert the txt files from your manual grooming program into mat files.

1. At the Matlab command prompt, type compileGroomingData\_all
2. **Select Files:** Select all the txt files you want to process. These should be files that belong to the same genotype or condition.
3. **Name of Genotype/Condition:** enter a name for the genotype or condition.
4. **Time Range:** Enter the time range for analysis in seconds. If the analysis files have different durations, you should enter the minimum time range for all files.
5. **File Type Selection:** Choose Noldus or VCode
6. **Select behav\_params.csv** file to use. This file specifies which behaviors are included in the txt files. Names in behave\_params must exactly match names used for scoring.
7. **Output:** A mat file will be saved in the same folder as the text files.

## Part 2 – Analyzing grooming

* Type FlyGroomA at command prompt to launch.

## A. Launch FlyGroomA and add files to analyze

* 1. Add mat files to analyze. Click on a file will display behaviors in the mat file.
  2. Select the appropriate behav\_params.csv file. This should be the same one used to process the manual annotation text files. Button is red when no csv file loaded and green when loaded.
  3. Specify time range for plots.
  4. Select which genotypes to plot.
  5. Select which behaviors to plot.

## A screenshot of a computer Description automatically generatedB. Boxplots

1. **Grouping**: determines how data is grouped on plots
   1. Behavior: Each plot shows one behavior for each genotype
   2. Genotype: Each plot shows multiple behaviors for one genotype
2. **Control**: Specify which genotype should be treated as the control in statistical analyses (not yet implemented).
3. **Graph**: default is boxplot (bar plots to be added in future)
4. **Statistics**: Select parametric or non-parametric statistics (not yet implemented)
5. **Metric**: Select all metrics to plot
6. **Binning**: Default is to plot total time specified in time range. (Binning of specific time periods to be added)
7. **Export data to Excel**: Writes out data from each plot into an excel file. Excel file name will be Figure\_num\_Metric\_YearMonthDayHourMin.xls. For example, “Figure\_2\_Dur\_2404051222.xlsx” was from Figure 2 plot of Duration made on 4/5/24 at 12:22PM.
   1. Bout Frequency: number of bouts per minute
   2. Bout Duration: duration of bouts in seconds
   3. Percent time: % time performing behavior
   4. Total time: Cumulative time performing behavior.
8. **Plot**!

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## C. Histograms

* 1. **Plot stimulus:** When checked this will add a shaded bar to regions of histogram that correspond to stimulus on.
  2. **Color of stimulus:** Specify this as Red, Green, Blue values between 0-1. The adjacent circle will turn that color.
  3. **Frame rate:** Set this to the frame rate of the videos, if different from 30 frames per second (fps).
  4. **Smoothing:** The data in the histogram is smoothed with a running mean. This specifies the window of time over which to average the data. The default is 1 second, meaning the histogram will show the average fraction of flies performing a behavior in 1 second intervals.
  5. **Plot!**

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## D. Ethograms

1. Ethogram type: Currently, only plots “Compact” which creates a raster plot of selected behaviors. Each line is a separate fly. When multiple genotypes are selected, one ethogram per genotype is created.
2. Plot Stimulus: Check to add a shaded bar indicating stimulation times. Color can be specified by RGB.
3. A screenshot of a computer

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