**Recording Data**

1. Open ‘oscillations.vi’ located on the scope PC’s desktop.
2. Set oscillation frequency (Hz) and amplitude (m)
   1. Make sure to right click and ‘set value to default’ for each change
3. After trapping beads, click play to run through individual trial or continuous play to run multiple trials.
4. The stage will continue oscillating until ‘stop oscillating’ AND ‘stop recording’ are clicked.
5. A prompt requesting a save name after each trial will appear.
   1. Naming convention must be: ‘FREQUENCY’ \_ ‘TRIAL NUMBER’ (always include .0 if whole number)
      1. 3.0\_6 – This name implies the run was done at 3 Hz and is the 6th trial.
      2. Matlab will use the frequency and trial number for analysis.

**Analyzing Data**

1. This code uses trap stiffness values saved in the ‘trapSTIFFNESS2’ function. So if new values have been recorded, adjust them there before analyzing data.
2. Following data collection, place all trials within ‘VE\_analysis/TESTS/’ folder
   1. Make sure to clear out previous trials, as Matlab will evaluate all files within this folder
3. Type ‘analyzeVE(‘x’)’ from the command line (replace ‘x’ with ‘y’ if oscillations done in y-direction)
4. Matlab will process all the data sets and request manual confirmation of each set before finalizing the data.
   1. 5 trials at a time will be displayed (3 rows: top=mirror trap, middle=fixed trap, bottom=stage). The frequency\_trial and mirror/fixed/stage are the title for each plot for reference.
   2. Visually confirm that the signal for each trial is clean: bead was held through entire process, no ‘hiccups’ in stage motion, etc.
   3. If all 5 trials are acceptable, press the space bar
   4. If any/multiple trials are flawed, press the number which corresponds to the trials position on the screen (1-5, so for the left-most trial, press 1. Right most trial press 5. Middle trial press 3…). If multiple are flawed, just press the number representing each trial in succession. When all errant trials have been noted, press the space bar.
      1. For example, if the second and last trials on screen appear flawed, hit ‘2’ then ‘5’ then space bar.
   5. Following the space bar, the next 5 trials will be displayed until all trials have been run through.
   6. The majority of trials will have a flat ‘tail’ at the end where the stage is no longer oscillating but still recording. This will be removed automatically from every trial, so can ignore.
5. For each trial which was noted as flawed, the program will allow the user to crop the set, selecting a region which is acceptable.
   1. 3 plots will be displayed. The left-most is mirror trap signal, right-most is fixed trap, and middle is the stage. To select the region to analyze, click first where to start then second where to end ON THE STAGE (MIDDLE) PLOT.
   2. If the data set is totally unusable, you may select the entire range. The error on the fit will be extremely high and the analysis will automatically remove the set itself.
6. The code will then proceed to fit each set and calculate G’, G’’, eta and will save all data to a .mat file, titled VE\_Data-‘Current date/time’.mat.

**Interpreting the output data**

* Two variable are saved
  + Fin\_fixed and fin\_mirror
    - The two sets are identical EXCEPT gP, gPP, n are calculated using either the fixed or mirror data, respectively (and then also the organized data at the bottom of the cell).
* Data from every trial will be shown
  + Except for the high error sets, which are removed
* Name - frequency in Hz
* Trial - trial number
* ampPSD - the amplitude of the mirror trap (Volts)
* ampPSD2 - the amplitude of the fixed trap (Volts)
* ampStage – amplitude of the stage (Volts)
* phasePSD, phasePSD2, phaseStage – phase of the fit (degrees)
* Period – (Recording frequency)/(this period) yields frequency in Hz
* Start – start point for fit, typically starts at point 2 (first point often gives problems) unless manually selected to start elsewhere (when looking for flawed sets)
* End – end point for fit, point at which stage stops oscillating (unless manually adjusted for flawed sets)
* diffPSD, diffPSD2, diffStage – normalized error for fits to data. Values less than 1 imply great fits, anything above 1 becomes questionable (used to remove problem sets). Terrible fits usually in the 40-50 range (for normalized error).
* gP – G’ for this trial
* gPP – G’’ for this trial
* n – eta for this trial
* The mean and standard deviation across all trials (for a given frequency) are evaluated below the last trial (MEAN and STDEV are noted in column 1)
* Additionally, all the MEAN and STDEV data are organized at the bottom of the cell (columns 1-7)
  + Column 1 is the ANGULAR frequency
  + Column 2 is G’ and column 3 its stdev
  + Column 4 is G’’ and column 5 its stdev
  + Column 6 is eta, and column 7 its stdev
  + This organizing of all the data makes it VERY SIMPLE for plotting in origin. Can simply copy this chunk of data over and plot each of these values against angular frequency with error.
  + Remember, this organized data is unique to the trap. Can plot/compare the data from the two traps.