* \*eem\_list changes as you move down the program so if you need to fix something , you need to run through the program again
* Name everything
  + Set WD
  + Name project name
  + Name dilution
  + Select sample(s) for review
* Step1 :building libraries
  + Load packages
* Step2: load functions
  + Load functions
* Format data
  + Select project folder: Bradford Streams. Then raw data> run folder
  + Choose name: date it was analyzed
  + Creates an eem folder
    - First column is excitation wavelength
  + Spits out eems and abs data
* Select eems and abs data
* Eem\_list
* Create DG CSV
  + Create sheet
  + Open sheet to fill it in
  + Read in the edited DG sheet
  + DG should be greater than 1 if you are diluting
* Apply corrections to ABS Data
* FIX emission step size
* Double check min max
  + Check the min and max to see if it matches without set
* Subtract blank
  + Eem\_remove\_blank
* Inner filter effect
  + Will give you a warning- just ignore it
* Raman norm
  + Should start seeing changes in heat map
* Remove blanks
* Removing raman and rayliegh scatter
  + Loss of stripes
  + Error appears when you plot figure
* Remove rayliegh scatter band one
  + Change width is it intersects FDOM readings