Instructions: Graphing here can be done using packages and commands we used in lab – artistic embellishments are optional and not required. Data sets are available from the course web site's schedule for this week: https://sciences.ucf.edu/biology/d4lab/methods-1

Your answer to each question should include (a) a graph or statistical result and (b) a sentence or two that clearly answers the question, based on the graph.

Remember to provide your code, and submit your answers as a pdf.

Questions below use the speciespH.txt data set, which represents an experiment in forest plots to test the effect of pH changes on soil micro-arthropod communities (mites, collembolans, ants, etc. - see this NRCS web site for what these look like). Random plots were either untreated (*mid*), or had pH reduced (sulfuric acid additions, like acid rain; *low*), or had pH increased (baking soda additions; high). Samples of plots were collected identically and yielded collective microathropod biomass (g/L) and species richness.

- Make histograms and QQ normality plots to compare distributions for each of Low, Mid, and High pH treatments and for both Biomass & Species variables. Do Biomass and Species look normally distributed? Do they look like they have homogeneous variance? [2 pts]
- 2. Conduct Shapiro-Wilk tests on Biomass and again on Species. Explain your results and how these results compare to your visual interpretations from Question #1 above. [2 pts]
- 3. Now evaluate homogeneity of variance among treatments for Biomass and for Species. Explain your result in English. [2 pts]
- 4. Now transform Biomass and Species, and re-evaluate normality and homogeneity of variance Can you get Species and Biomass to meet both statistical assumptions? If yes, explain what worked. If not, explain what failed. **[4 pts]**