**Ecol 8990**

**Assignment # 4**

**Due Wed Nov 1, 5 pm**

Note: The work should be individual. Use R Markdown to complete the assignment. The Markdown (.Rmd) file itself is part of the assignment.

**1-** The ‘Tree\_plot\_exercise.R’ file contains a modified version of the simulated tree growth dataset we used in class to compare the lm and lme approaches as random effects vary in size. I modified this version so that the entire dataframe is created within the script instead of importing the original .csv file with Species and Plot columns. In this version you can alter the total sample size (parameter N) in the dataset (the number of species and plots remain constant). Analyze the data using an *lme* model (with Plotfact as a random effect).

**2-** Now create a new dataframe with mean growth rate values per species per plot. Re-analize the data with Species as the fixed effect and Plotfact as the random effect, but at the level of plot rather than individual tree. How do the results change?

**3-** Now modify the code (using a loop) so that this exercise is repeated for different values of N (32, 64, 100, 150, 200). Store the resulting p-values from the two lme models (individual-level and plot-level) in vectors and then plot the relationship between N and these p-values as lines. Tip 1: you can obtain the p-value from the lme object with

anova(lme.mod)["Species", "p-value"]

Tip 2: look at the scripts I posted for class (“linear\_reg\_power.R” and “GLM\_vs\_OLS\_V2.R”) if you get stuck.

Does it matter whether we analyze the data at the individual level or plot level?

Please put a hard copy of the final Markdown .pdf or Word document in my mailbox, and email me the .Rmd file that generated the document.