Analyses:

Richness + diversity comparisons among treatment groups. This would take the form of a boxplot, with stats via a linear mixed effect model. Diversity estimates can be output from CNVRG and tossed into a boxplot – I’ve started playing around with this, but I do not understand the output of the calc-div function in CNVRG. See script “Alpha\_Diversity\_Calc\_16s”. This will need to be updated.

Ordination + permanova (once with soil and plant data combined and again for each dataset separately. Probably could pick a couple of these ordinations and pair them with the rich/div boxplot for a four-panel plot.  – See scripts “Ordination\_and\_Adonis16S” and “Ordination\_and\_AdonisITS”. This includes only the soil data for the three time points.

Differential relative abundance analysis (pairwise between all treatments) - make a table of how many taxa differ between treatment pairings. This is all automated more or less with CNVRG.  – See scripts “” and “”.

boxplot of weed cover and maybe another one of any plant performance metrics (ANOVA or linear mixed effect model for stats).  – I have this in the text currently. This includes enzyme activities.

Funguilds assignments and models of differential abundance – See script “Funguid\_Assignments”. We need to revisit how to assign differential abundance. Should we do this with the CNVRG package and then post hoc assign funguild assignments to those taxa that we can? What about if we summarize by the groups and then check to see if coarse level assignments revel differences?

Might include:

Bacterial/fungal families versus treatment (boxplot and could follow up with linear model, as above).

Summary statistics to say how many soil taxa were in the phyllosphere  - Eg., could make a Venn diagram, or a table to show which taxa were found in each treatment / substrate.