**­­Microbial Diversity and Ecology Lab, Fall 2020**

**Week 10 Lab 17/18: Phyloseq Part 2**

**Due**: Friday October 30, 11:59 pm

**Task**: upload this document in the assignment on WyoCourse; Week 10 Lab 17/18 Phyloseq Part2, with your answers embedded and rename the file by adding your last name at the end of the file name, e.g. Week10\_lab17/18\_Phyloseq2\_Assignment\_vanDiepen. Please save your file as a Word document.

**Points**: 2.0

**Objective**: In this tutorial you will continue with phyloseq. You will make pretty graphs and calculate p-values for various beta diversity metrics based on the work you did in week 9 when you looked at alpha diversity. Let’s continue the fun!!

**Instructions:** Open the latest version of the Rmd file “Phyloseq\_final” which you saved at the end of the week 9, starting at ~ line 197 and refer back to this document when you are ready to answer a question or complete one of the exercises.

First thing to do would be to load the environment that you saved at the end of the Week 9 tutorial (named something like vanDiepen\_phyloseq\_Env2.Rdata.

Then, also load the following packages to be able to do the analyses below: phyloseq, ggplot2, psych.

Exercise 16 (~Line 214): What distance metrics are supported by the distance() function? What benefit would using Bray-Curtis over Jaccard provide?

Answer:

Exercise 17 (Line ~225): Add a title to this graph and center it above the graph. Make the title descriptive. Use Google to find out how to do this. Try something like "Add title ggplot". Save the plot and put it in your handout here:

Bonus: Can you color the points so high grazing is grey and no grazing is green?

Exercise 18 (~Line 238): Create the same graph but for class level instead, save the plot and put a copy of it in your handout.

Answer:

Exercise 19 (Line ~246): Load the Vegan package. Record your code in the handout.

Answer:

Exercise 20 (~Line 262): Search "metaMDS"" in the help search bar. Within the help page titled "vegan::metaMDS"" look at the available options. What does the "k=" argument do? What about the "previous.best=T" argument? Provide a brief explanation in your lab handout here:

Exercise 21 (~281): Look at the help page for the ordiplot() function. What does the "type=" argument mean? We have points as the type in this function. Re-run the function changing the type argument to one of the other options. Can you think of the advantages of having a figure with points instead of text? What about the other way around? Provide a brief answer here.

Answer:

Exercise 22 (~312): Look at the Adonis help page. What format does the data have to be in? Record this in your handout. What format does the parDist() function require? Do you understand you must convert the table to a data.matrix first then run the distance function?

Answer:

Copy the output from your adonis analysis to your lab handout here. Were any of the variables significant?

Answer:

Exercise 23 (~332): View the "sd" object. Make sure it looks right. What is the pH of site CLEX1\_5? Record this in your handout.

Answer:

Exercise 24 (~340): Look in the upper right pane in your environment tab to see what type of object "e" is? Using the "$" operator look at what is contained in the "e" object. Record some this in your handout.

Answer:

Exercise 25 (~Line344): Search google for other options for ggplot based graphs. What would you use instead of geom\_boxplot? Record at least two in your handout.

Answer:

Exercise 26 (~Line 363): Save two graphs: One with the legend and one without. Include them in your handout.

Answer:

Exercise 27 (~Line 374): Alter the annotate code to have your letters at the same y coordinate above each bar. Include a copy of your graph in the lab handout.

Answer: