Zool 421 Lab Deliverable (20 pts) Name:

Mammal Microbiome R online module

Refer back to “Step 6: On your own” in the Mammal Microbiome Tutorial Document. You will perform the same data analysis you did in the tutorial on a subsetted portion of the larger data set. You will subset the data by one of the 6 years (2013, 2014, 2015, 2017, 2018, or 2019) and perform diversity analysis on only the samples from that year.

1. Attach the figure output from **Step 7A: Alpha Diversity** (Plotting a Shannon value boxplot for samples group by location and colored by year). Include figure caption and title.
2. Attach the final output graph from **Step 7B: Beta Diversity** (plot the ordination with samples colored by location) in the Microbiome Tutorial. Add figure caption and title.
3. Attach the final output graph from **Step 8A: Taxonomy** (Create an Initial basic plot of taxonomy grouped by location and identifying all bacterial families)in the Microbiome Tutorial. Add figure caption and title.
4. Attach the final output graph from **Step 8B: Taxonomy** (Plot top10 families)in the Microbiome Tutorial. Add figure caption and title.

**Discussion Questions**

1. Which Region (E vs. W) had a higher Shannon’s Diversity value? What does a higher value indicate?
2. Did the moose appear to have significant differences in beta diversity when grouped by location? Explain why you think they or don’t appear to differ. What does bray-curtis test for? Explain your answer.