MICB 475 Meeting #8 Agenda
2023-11-16
Emily to take minutes

1. **Review Plots (at bottom of agenda)**
   a. Are they publication ready?
   b. Any feedback on how they are looking?

2. **Confirm that birth-mode was controlled for correctly in analysis**
   a. For alpha diversity

```
# Linear Regression Significance Tests
high_alphadiv <- estimate_richness(high_BMI_phyloseq_rare)
high_samp_dat <- sample_data(high_BMI_phyloseq_rare)
high_samp_dat_bmi <- data.frame(high_samp_dat, high_alphadiv)

linear_test_result_high<- summary(glm(Shannon ~ feed + baby_delivery, data=high_samp_dat_bmi))$coefficients
print(linear_test_result_high)
```

   b. For beta diversity: was not addressed in bray-curtis or weighted unifrac analysis, but was in permanova analysis with the code:

```
all_BMI_data_wu <- data.frame(sample_data(all_BMI_phyloseq_rare_new))
adonis2(distance_unifrac ~ mom_bmi_label*feed + baby_delivery, data=all_BMI_data_wu)
```
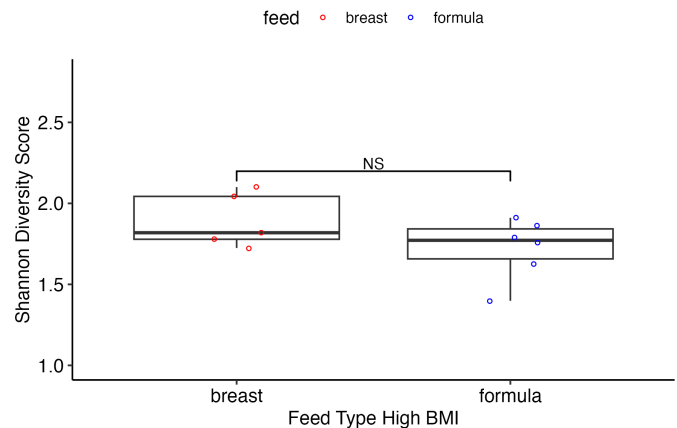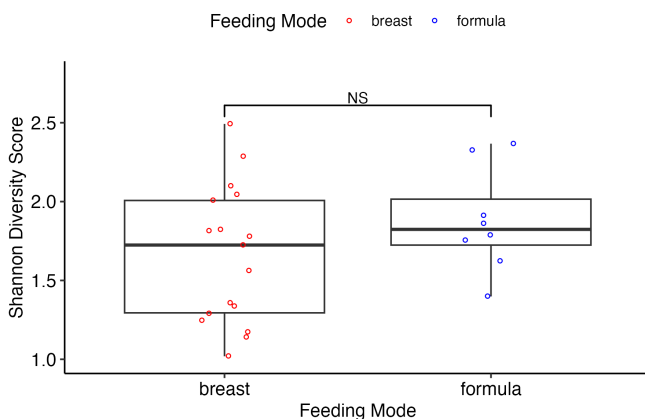
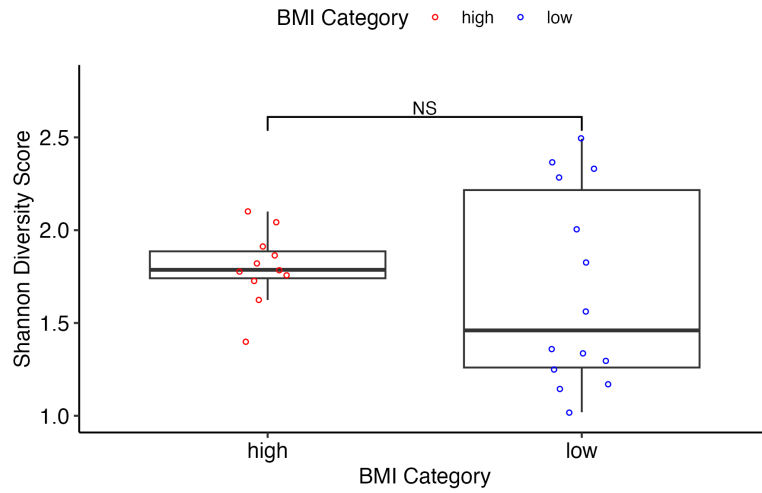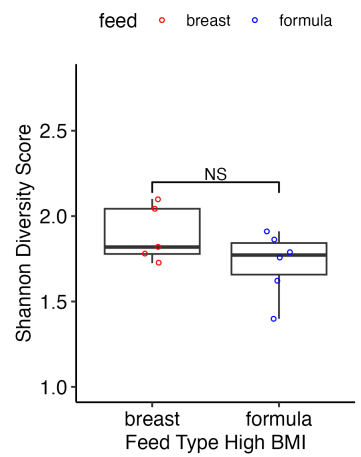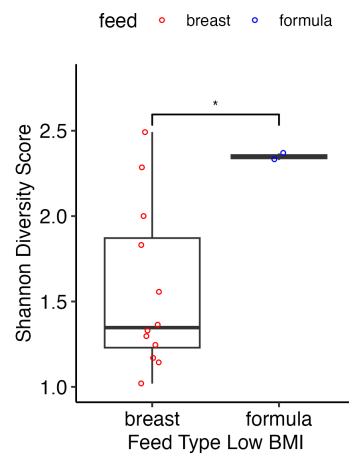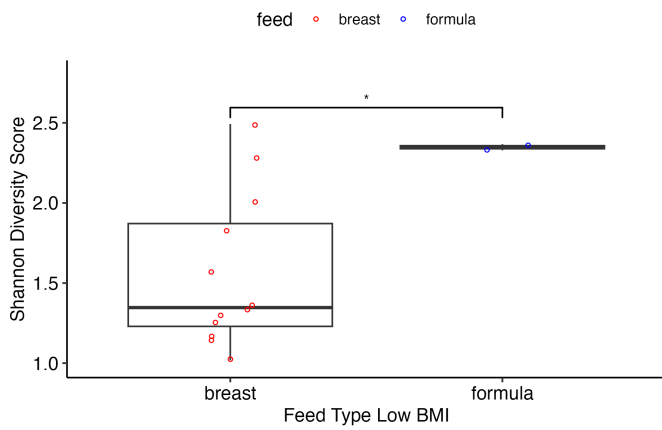   c. Do we have to control for birth mode for our DESeq analysis?

3. **Next steps:**
   a. Oral presentation: Dec 5-7
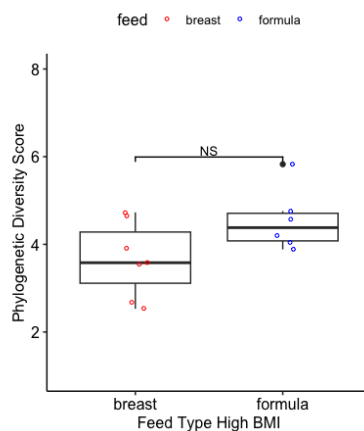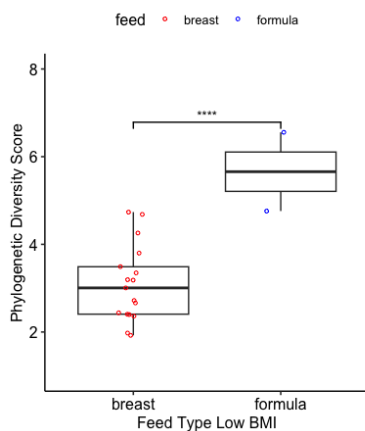   b. Draft manuscript: Dec 10

Alpha Diversity Plots
Shannon Diversity
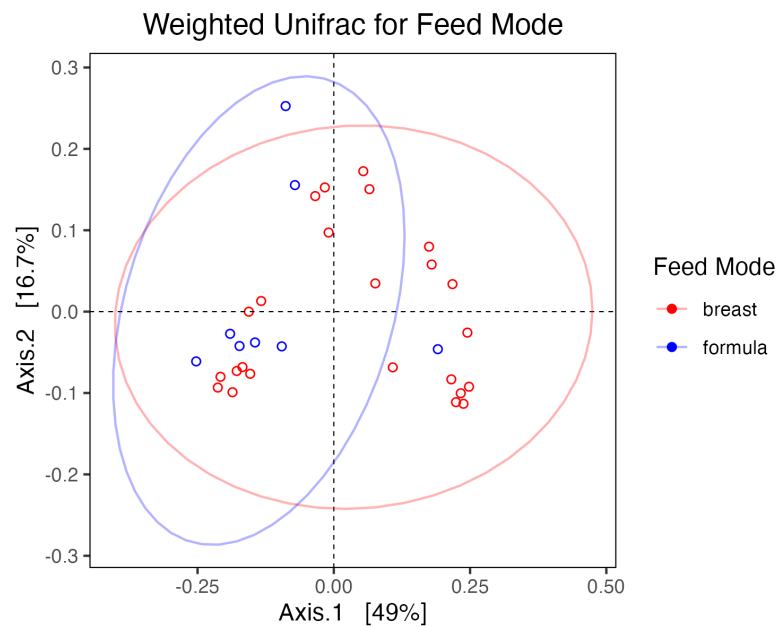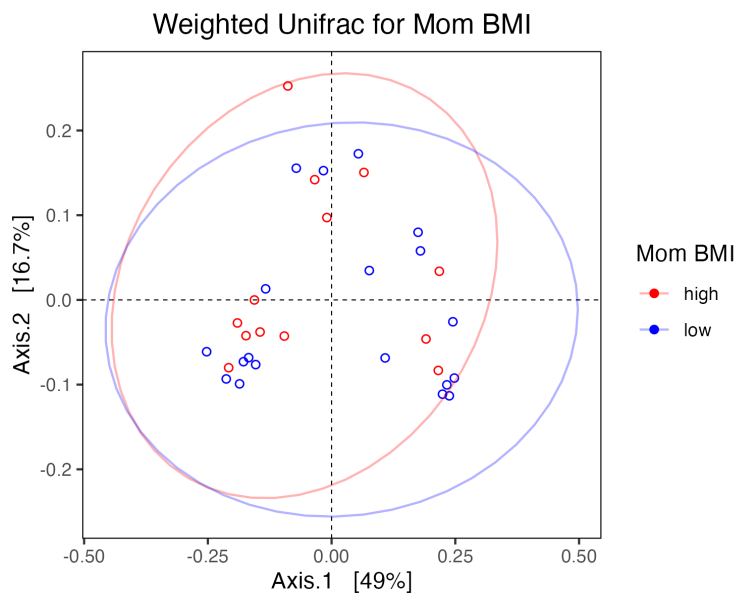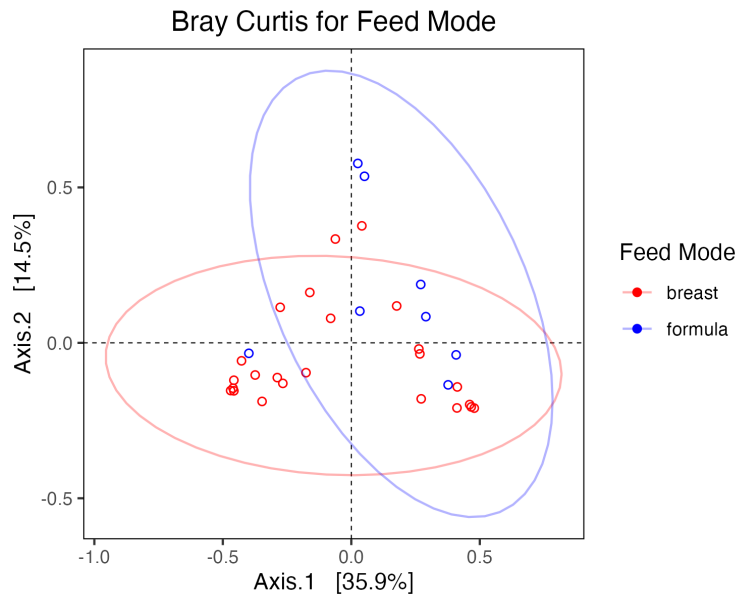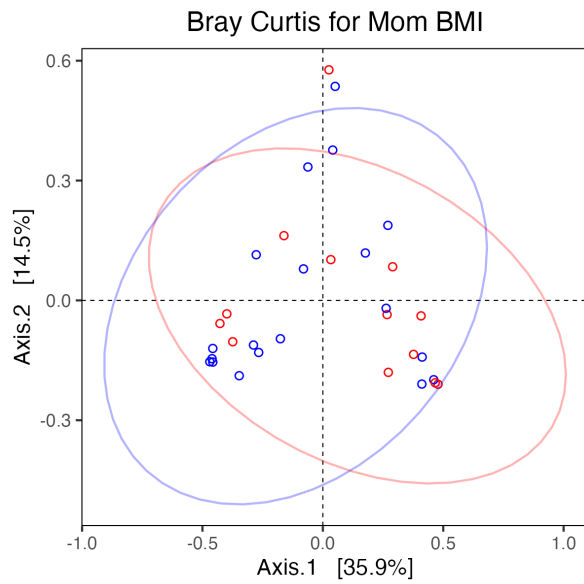
Phylogenetic Diversity:

1. Discussion regarding the linear model significance results meaning. "Feedformula = P<0.05). Does this indicate that there is a significance between breast and formula feed?

PICRUST2:

1. What input files do we need to use in R studio to visualize results?

Beta Diversity Graphs:

DESeq graphs:

DESeq Analysis of Low BMI Moms

DESeq Analysis of High BMI Moms