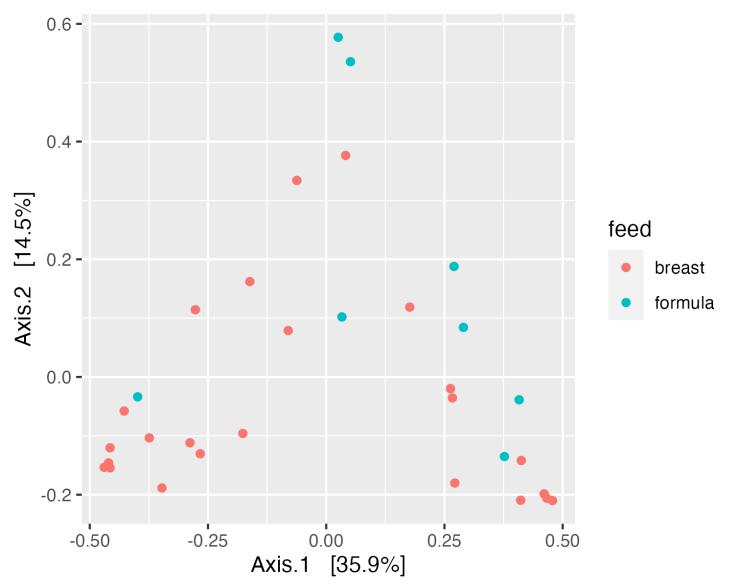
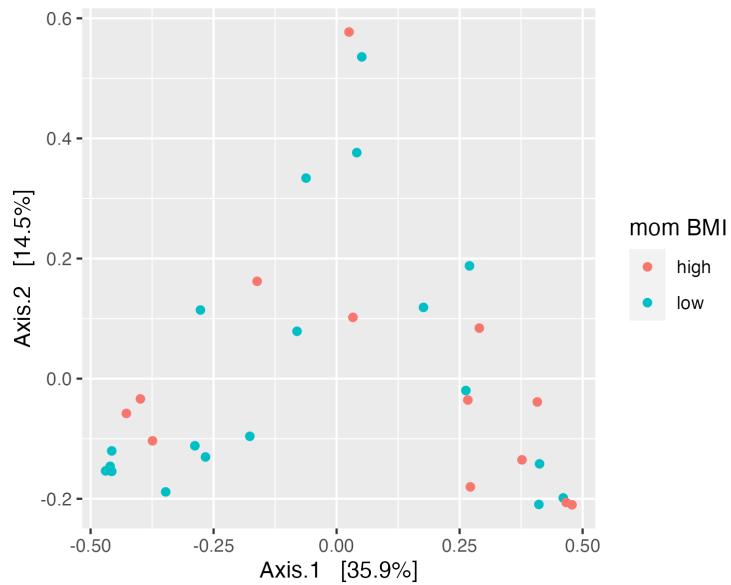


Meeting #6 Agenda

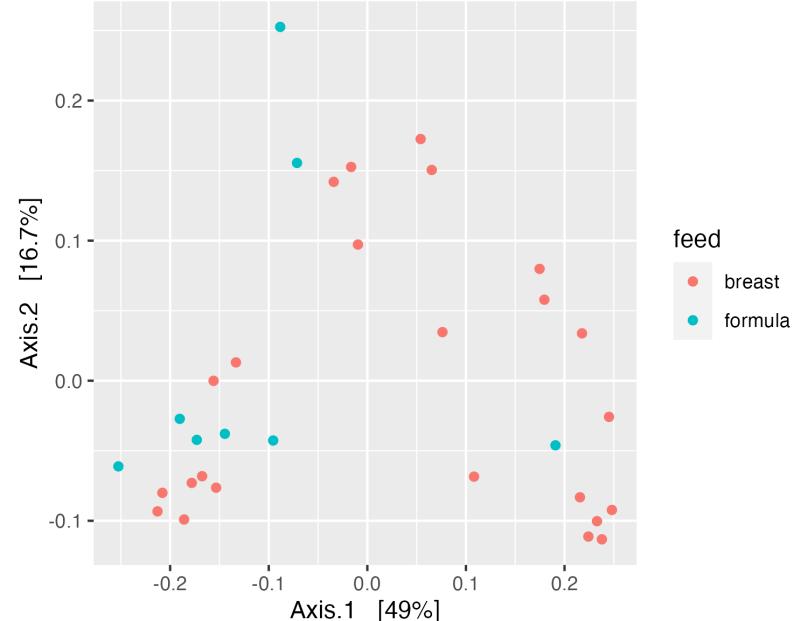
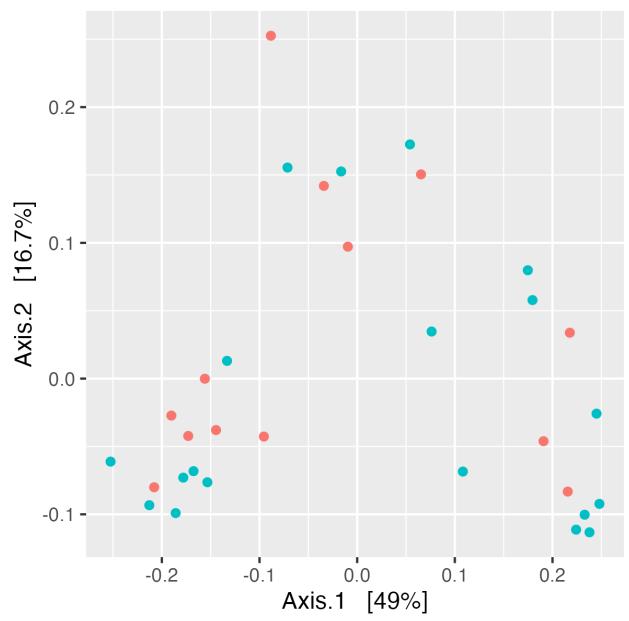
1. Want to remove NA from DESEQ plot on x axis (mixed in with genus names; attempt to filter out genus from phyloseq didn't solve the problem)
2. PiCRUST analysis - what's our input? We found some sources saying biom / some saying qza. → not quite sure where to progress
3. Show Avril our data!

Beta Diversity plots:

Bray Curtis Analyses:



Weighted unifrac Analyses:



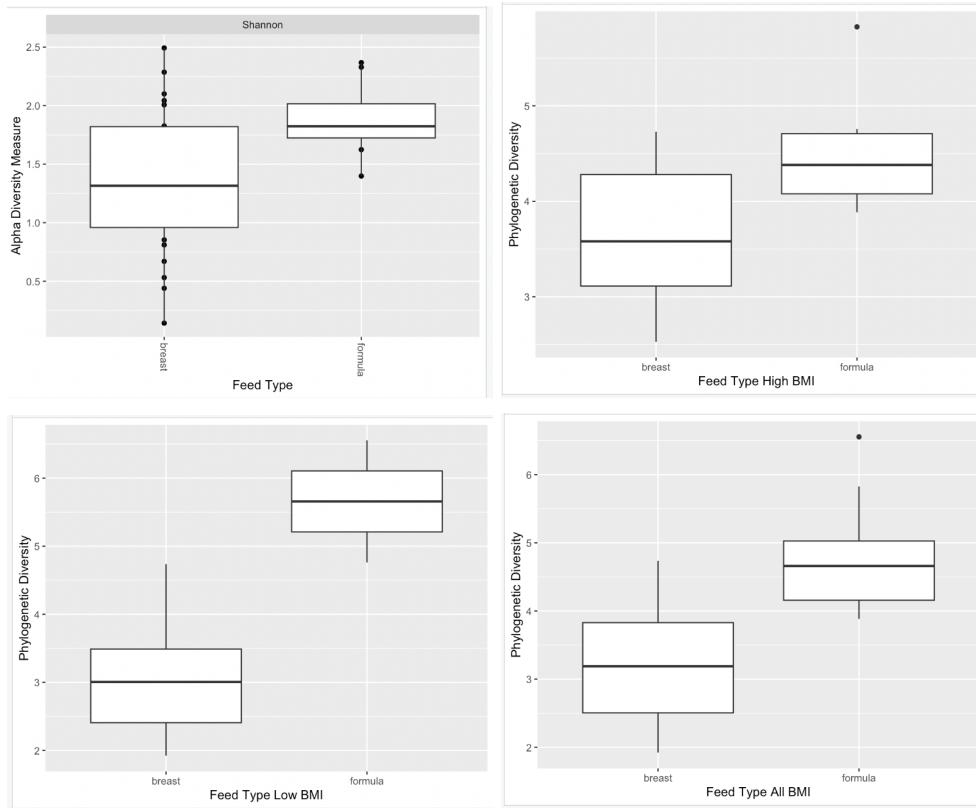
Permanova analysis:

Bray curtis:

```
# results:  
# Df SumOfSqs R2 F Pr(>F)  
# mom_bmi_label 1 0.3142 0.03259 1.0263 0.358  
# feed 1 0.5287 0.05484 1.7271 0.086 .  
# mom_bmi_label:feed 1 0.2261 0.02345 0.7386 0.636  
# Residual 28 8.5713 0.88911 |  
# Total 31 9.6403 1.00000  
  
# No significant results :(
```

Weighted unifrac:

```
# results:  
# Df SumOfSqs R2 F Pr(>F)  
# mom_bmi_label 1 0.05750 0.03054 0.9909 0.378  
# feed 1 0.15466 0.08216 2.6654 0.047 *  
# mom_bmi_label:feed 1 0.04563 0.02424 0.7864 0.516  
# Residual 28 1.62467 0.86306  
# Total 31 1.88245 1.00000  
  
# Significant result for feed
```



Significance:

High Feed:

Wilcoxon rank sum test with continuity correction

data: Observed by feed

W = 8, p-value = 0.07295

alternative hypothesis: true location shift is not equal to 0

Low Feed:

Wilcoxon rank sum test with continuity correction

data: Observed by feed

W = 0.5, p-value = 0.033

alternative hypothesis: true location shift is not equal to 0

All Feed:

Wilcoxon rank sum test with continuity correction

data: Observed by feed

W = 20, p-value = 0.0009956

alternative hypothesis: true location shift is not equal to 0

Shannon vs Feed for All BMI

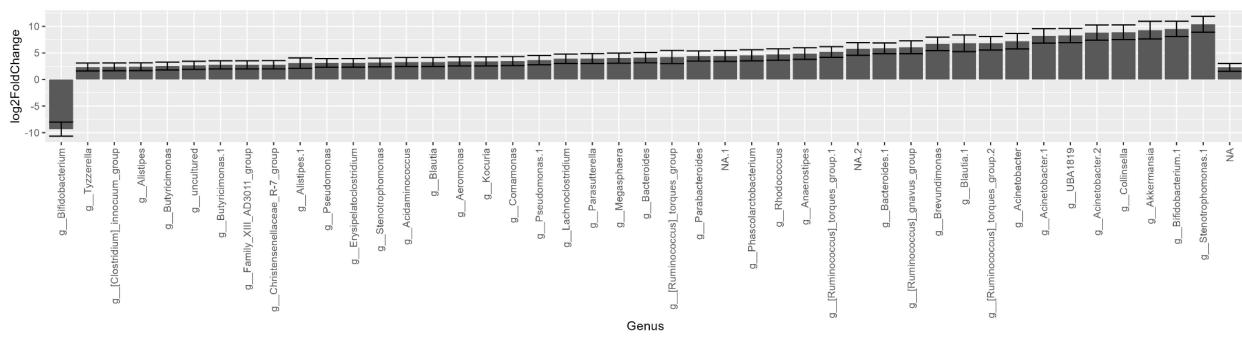
Kruskal-Wallis rank sum test

data: Shannon by feed

Kruskal-Wallis chi-squared = 4.7348, df = 1, p-value = 0.02956

Deseq Plots:

Low BMI



High BMI

