

# DOCUMENTING SUCCESSION OF THE RUMEN MICROBIAL COMMUNITY IN DAIRY CALVES



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## Introduction

Dairy cattle rely exclusively on the microbiota within their gastrointestinal tract for nutrient provisioning. The acquisition of a fully functioning gut microbiome early in life is therefore critical to survival of these animals. The establishment of a calf's gut microbiota has previously been characterized using proxies such as fecal sampling and destructive sampling methods, but it is unclear how accurate these methods are over time in the same animals. This study will address the gap in knowledge of microbial community succession through calf development as well as assess the use proxies.

Fecal proxies used to characterize the rumen microbiota of calves <1yr.

Dill-Mcfarland et. al. 2017

Destructive sampling used to characterize rumen microbiota of calves <9wks.

Dias et. al. 2018

Objective

Are proxies accurate over time within the same animals?

1.Dill-Mcfarland, K.A. et al. Sci Rep. 7:40864 (2017). 2.Dias, J. et al. Appl. Environ. Microbiol. 84(9):1 (2018)

## Methods

10 Calves  
Wk5-Wk17

Fecal (F)  
Rumen → Solids (RS)  
          → Liquid (RL)  
Buccal (O)



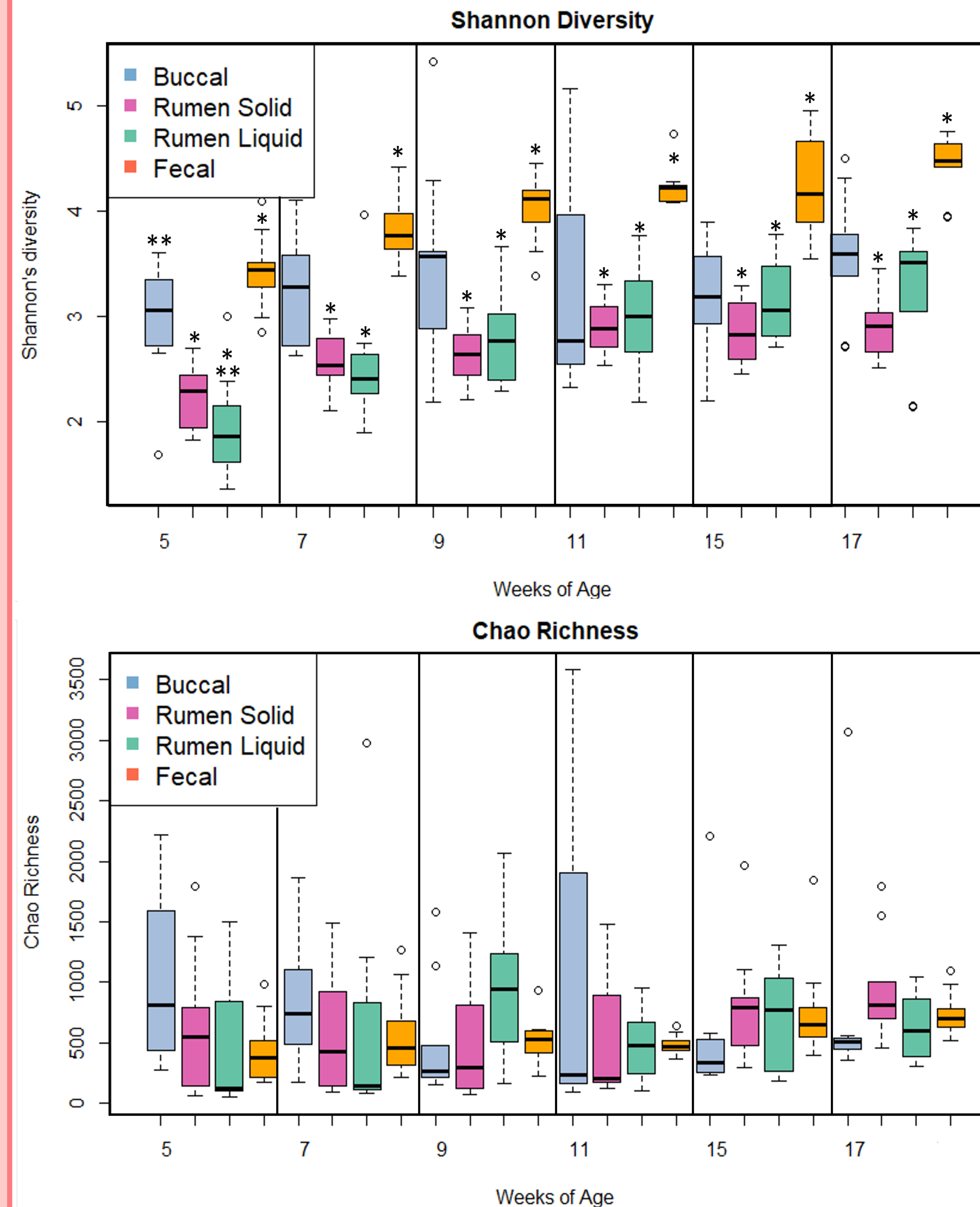
Analysis

DNA Extraction



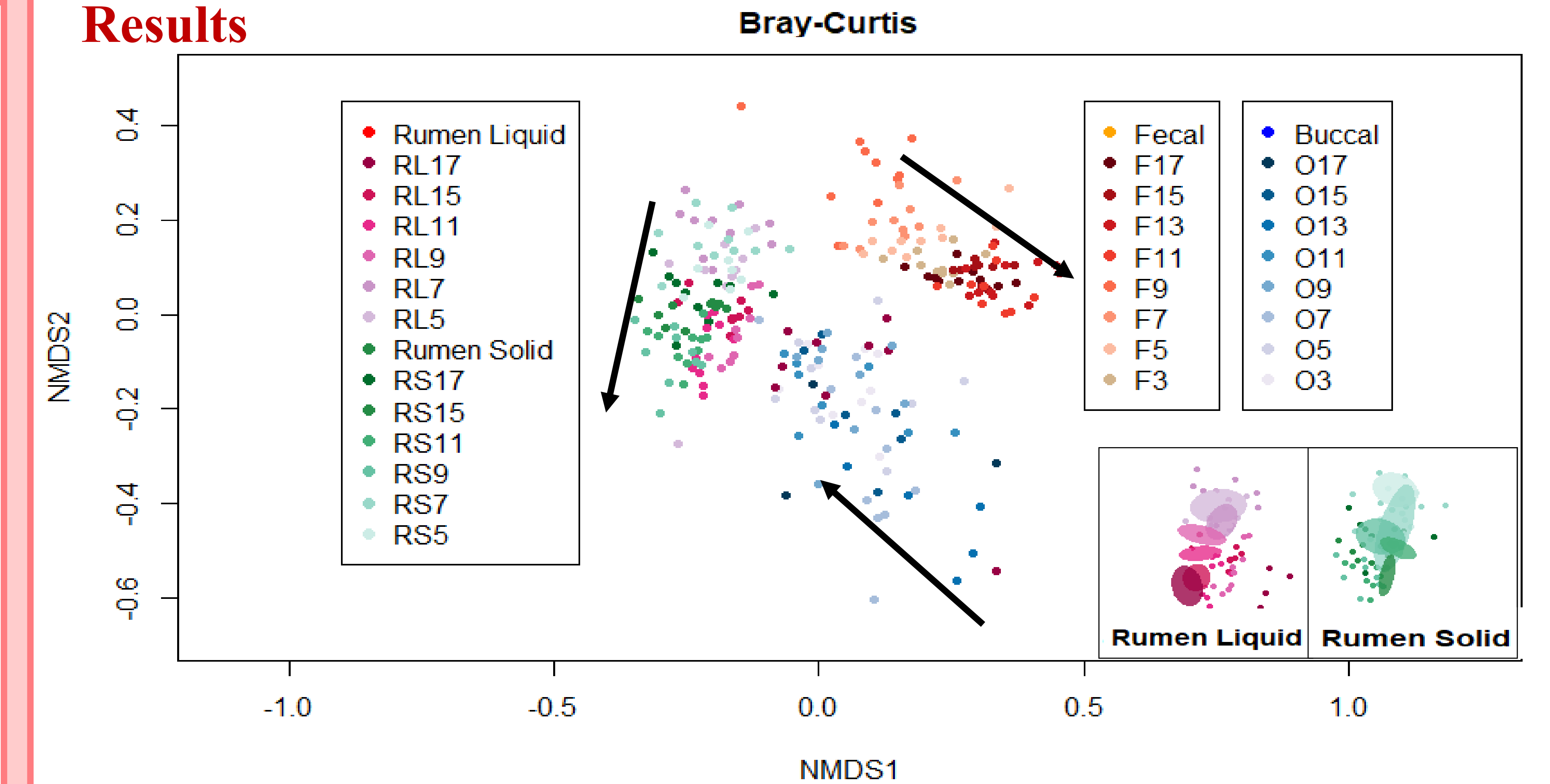
16SrRNA Illumina Sequencing

## Results



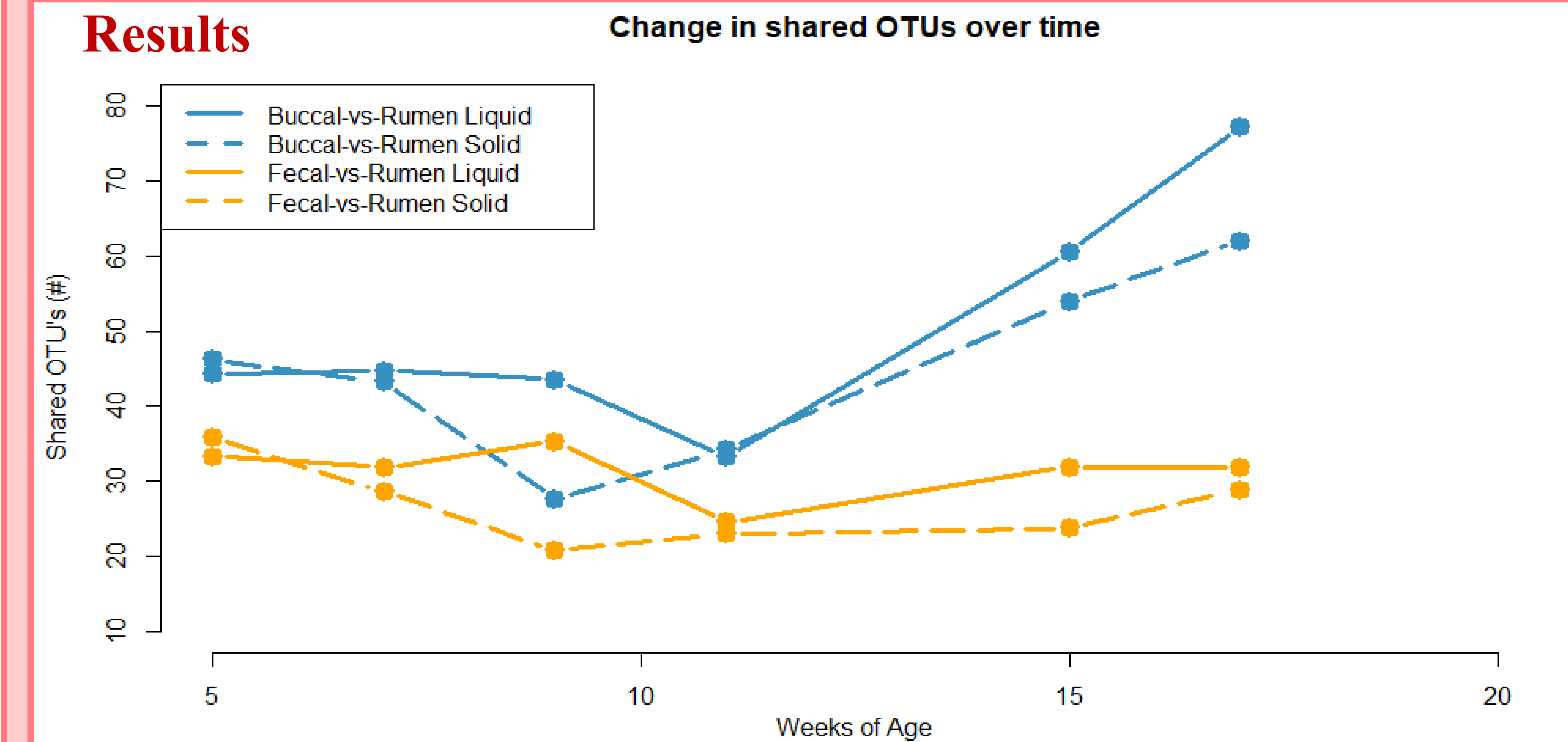
**Figure 1.** Box plot of sample diversity and richness by calf age of for all sample types. The bacterial community diversity in all fecal samples is significantly different from the rumen for all cases (p value <.005 (\*)) while buccal samples only statistically differ from the rumen in week 5 (p value <.005 (\*\*)). There is no significant difference in chao richness between any samples in the study.

## Results



**Figure 2.** Non-metric multidimensional scaling (NMDS) plot of samples types by age. Fecal samples resemble the rumen in early age but diverge as calves mature. Buccal samples are initially dissimilar to the rumen, but trend closer with age.

## Results



**Figure 3.** Line plot of the number of shared OTUs between sample types over time. Similar numbers of shared OTUs are found between different sample types in early age. As calves mature, the number of shared OTUs diverge. Buccal samples contain nearly double the amount of shared OTUs with the rumen than fecal at week 17.

## Acknowledgments

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## Conclusion

Fecal samples are more accurate proxies before rumen maturity.

- ❖ Alpha diversity and shared OTU counts are similar in early life
- ❖ Beta diversity shows fecal samples more closely resemble the rumen than buccal in early life

Buccal samples are more accurate proxies after rumination begins.

- ❖ Alpha diversity and shared OTU counts are more similar in buccal than fecal samples with time
- ❖ Beta diversity shows buccal samples more closely resembling the rumen with time