

# Explore Freeze-dried samples hellinger and CLR beta diversity

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## Introduction

I here use Hellinger transformed counts which puts more weight to common ASVs) and clr-transformed approach *for more information on clr, see Gloor et al. 2017 and Gloor's github tutorial ( [https://github.com/ggloor/CoDa\\_microbiome\\_tutorial/wiki/Part-1:-Exploratory-Compositional-PCA-biplot](https://github.com/ggloor/CoDa_microbiome_tutorial/wiki/Part-1:-Exploratory-Compositional-PCA-biplot) )* to explore beta diversity of freeze-dried and frozen samples.

## Hellinger

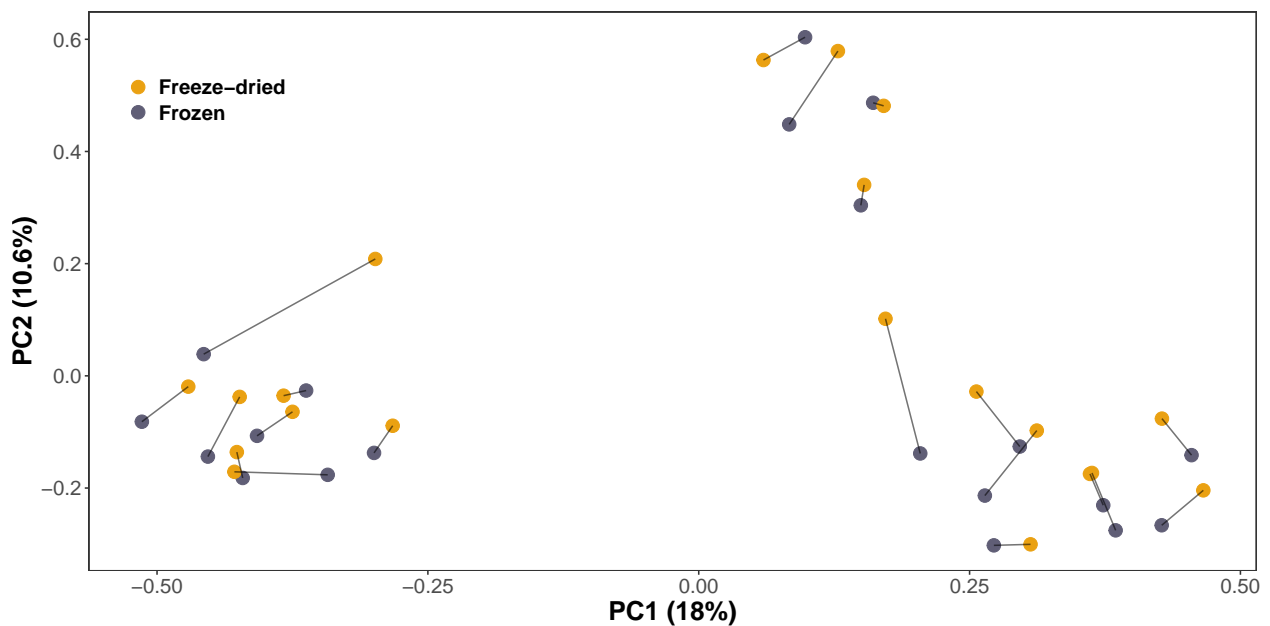


Figure 1: Figure 1. PCA Hellinger Transformed counts.

Permanovas hellinger

## CLR

I've calculatad clr using the compositions-package and adding the psuedocount **0.65** to each ASV/sample count.

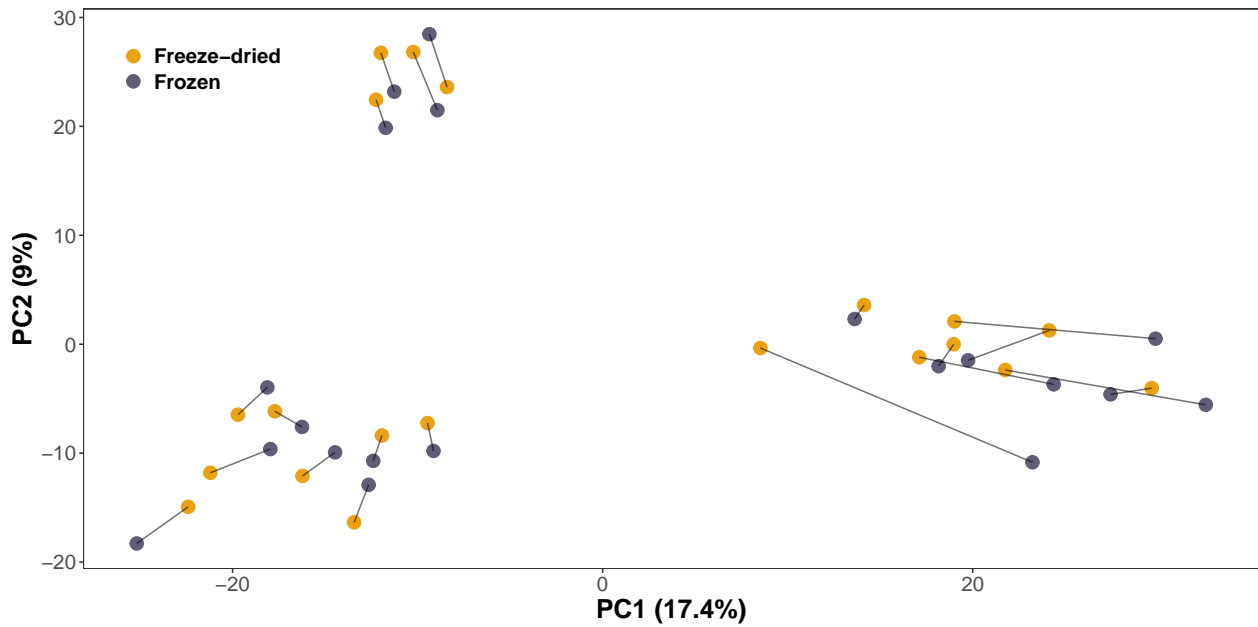


Figure 2: Fig 2. PCA on clr transformed counts.

Permanovas Aitchison/Euclidian distance of clr transformation

combine plots

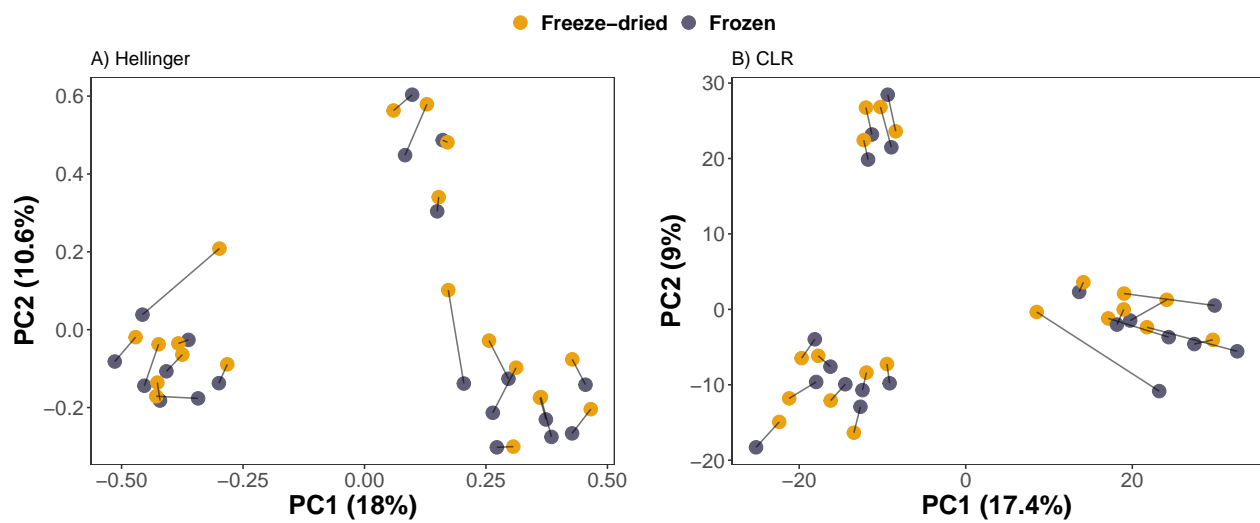


Figure 3: Figure 14. Combined PCA Hellinger and CLR.