

# Microbiome workshop

September 2024

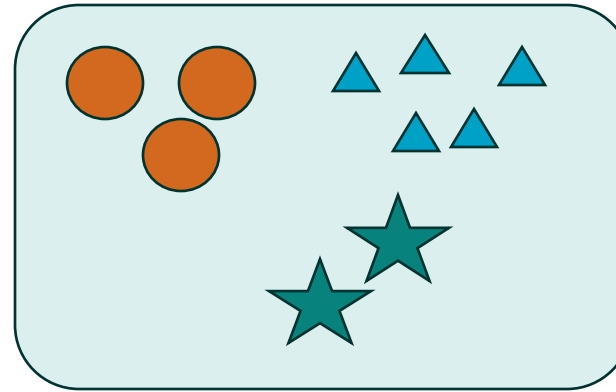


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# Beta-diversity analysis. Introduction

**Beta-diversity** measures the variation in microbial community composition between different samples

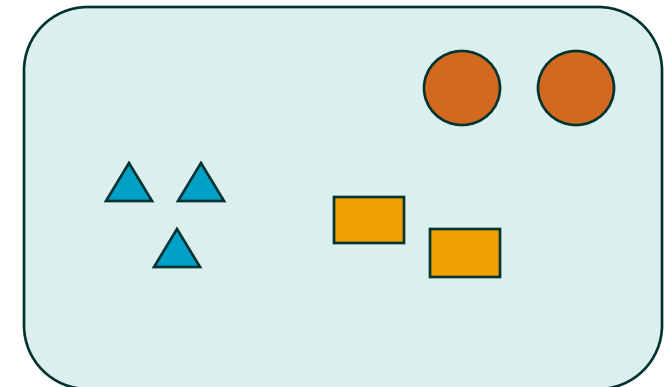
Sample 1




Alpha diversity = 3

$$\text{Beta diversity} = (3-2) + (3-2)$$

Sample 2



Alpha diversity = 3



## Methods to measure beta-diversity

**Bray-Curtis** - Measures the compositional dissimilarity between two samples based on the counts of species or OTUs/ASVs

**UniFrac** - Incorporates phylogenetic information to measure the distance between microbial communities

**Unweighted UniFrac** considers only the presence or absence of species, while **Weighted UniFrac** also accounts for the abundance of species.

**Jaccard** - Considers the presence or absence of species to measure similarity between samples



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# Data Requirements

## OTU/ASV Tables

Essential for calculating metrics like  
Bray-Curtis, Jaccard, and UniFrac

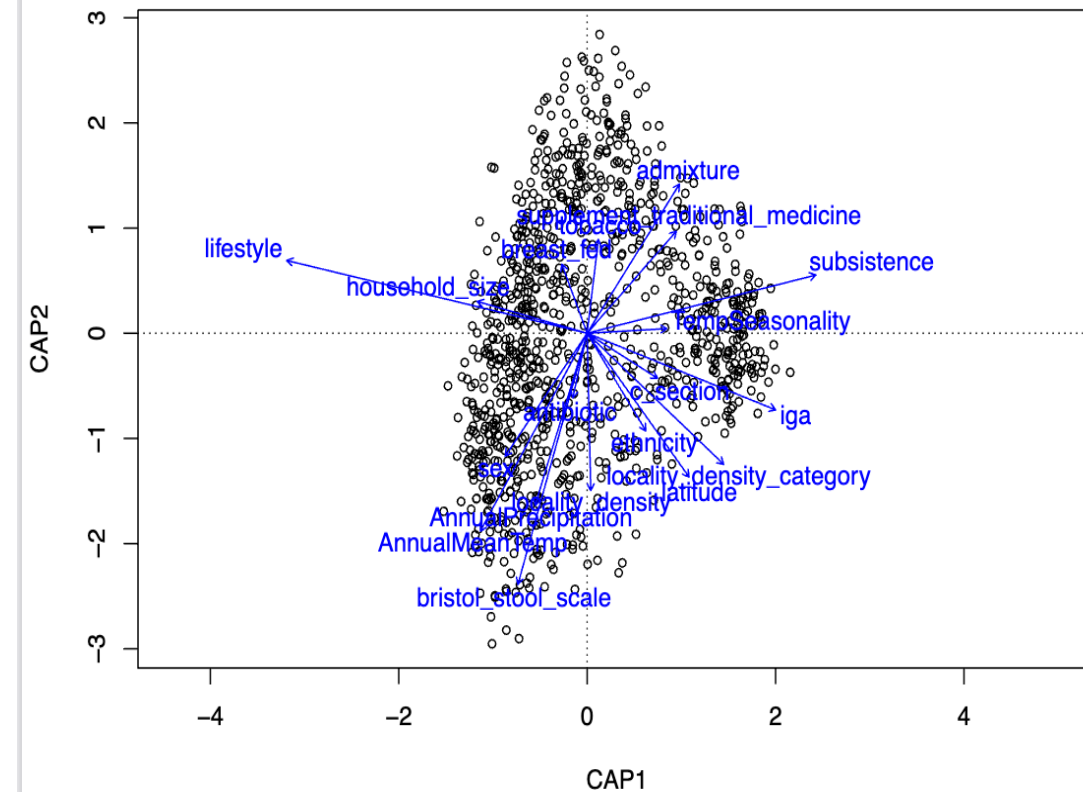
## Phylogenetic Trees

important for UniFrac distance

# How environmental variables influence the variation in community data ?

## Capscale R package - Canonical Analysis of Principal Coordinates

- Distance-Based Redundancy Analysis
- Stepwise analysis - identify the most important variables in a multivariate model
- Biplot - a visual interpretation of the ordination results, showing both the samples and the influence of environmental variables



# Test the significance of differences between groups

- **ADONIS/PERMANOVA**  
(Permutational Multivariate Analysis of Variance Using Distance Matrices)
- **ANOSIM**(Analysis of Similarities)
- Uses permutations (random reordering of the data) to test the null hypothesis that group differences are not significant.
- Ranks the distances and compares the ranks within groups to the ranks between groups

# Final result for all countries

