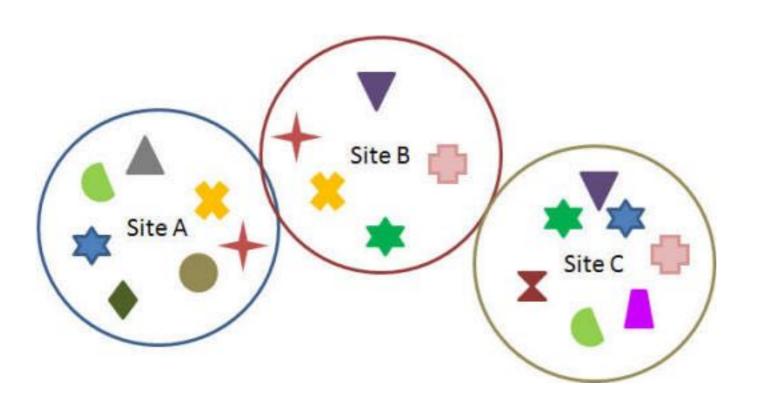
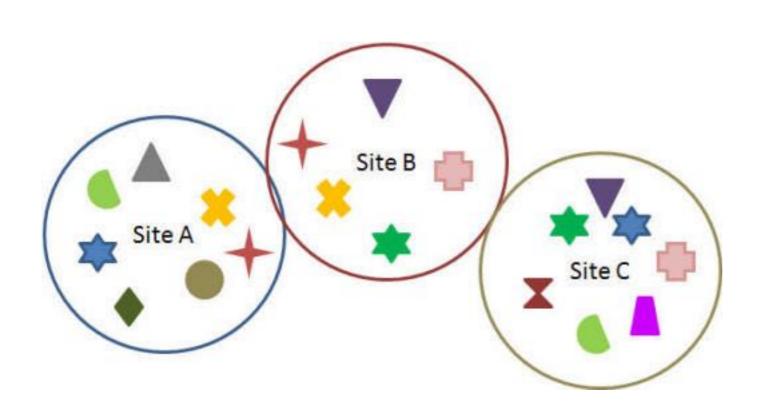
# Statistical Analysis of Amplicon Data

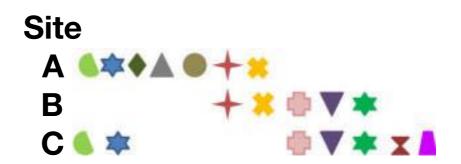
Part 2 February 22, 2019

#### Useful Reference

 GUide to STatistical Analysis in Microbial Ecology (GUSTA ME)!: <a href="https://mb3is.megx.net/gustame">https://mb3is.megx.net/gustame</a>

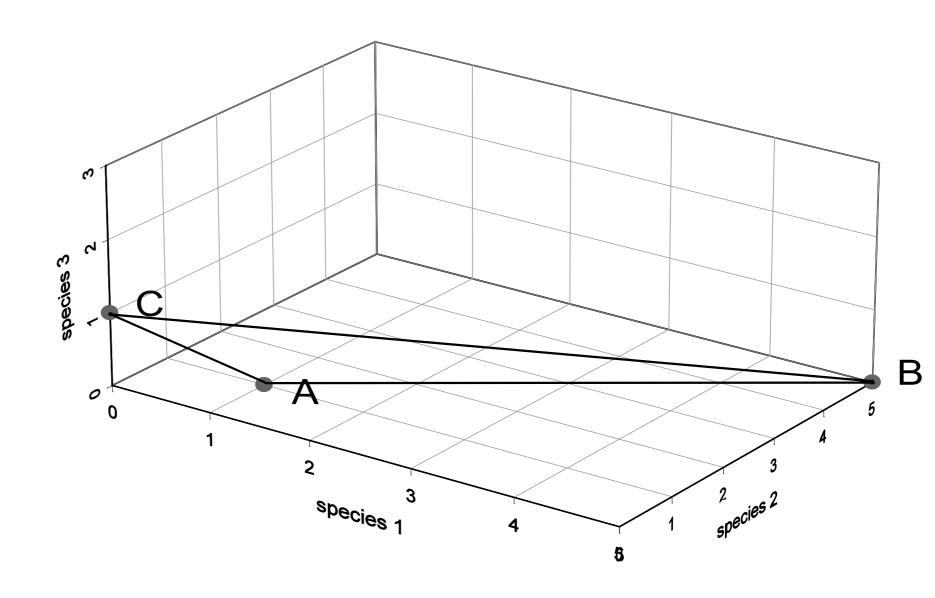






	Species			
	1	2	3	
Α	1	1	0	
В	5	5	0	
С	0	0	1	

	Species			
	1	2	3	
Α	1	1	0	
В	5	5	0	
С	0	0	1	

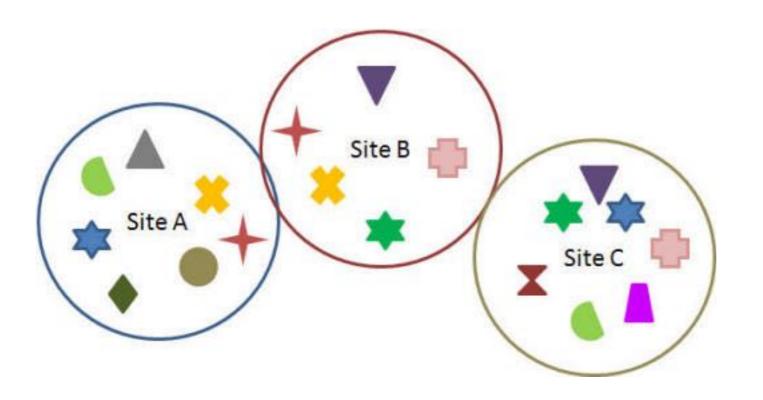


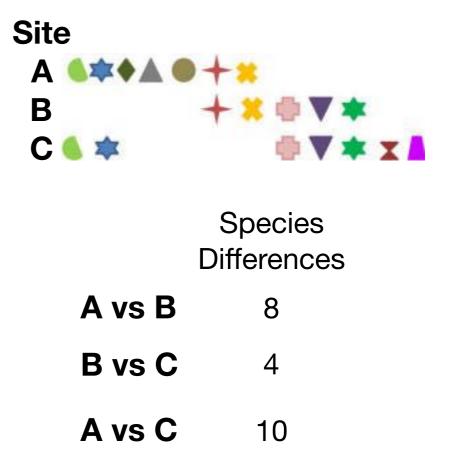
# Beta Diversity Metrics

- Number of Taxa
- Bray-Curtis Dissimilarity
- UniFrac
- etc

### Number of Taxa

How different are samples?





### **Bray-Curtis Dissimilarity**

$$D_{BC} = 1 - 2 \frac{\sum_{i=1}^{S} min(a_i, b_i)}{\sum_{i=1}^{S} a_i + b_i}$$

Where  $x_i$  is the abundance of species i in sample X

# **Bray-Curtis Dissimilarity**

$$D_{BC} = 1 - 2 \frac{\sum_{i=1}^{S} min(a_i, b_i)}{\sum_{i=1}^{S} a_i + b_i}$$

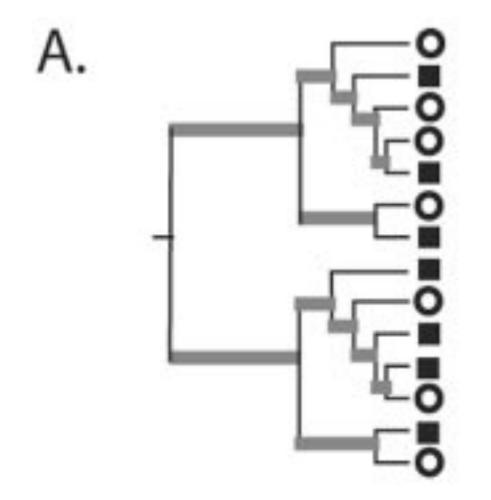
	Species			
	1	2	3	
Α	1	1	0	
В	5	5	0	
С	0	0	1	

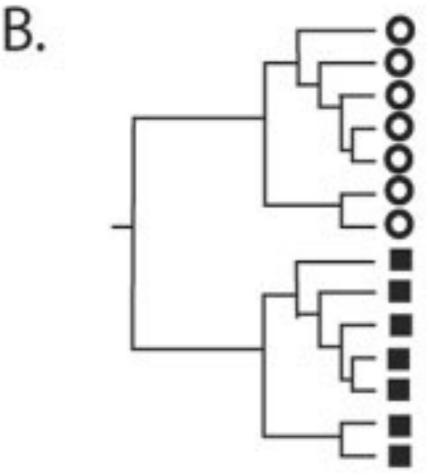
Where  $x_i$  is the abundance of species i in sample X

### **Bray-Curtis Dissimilarity**

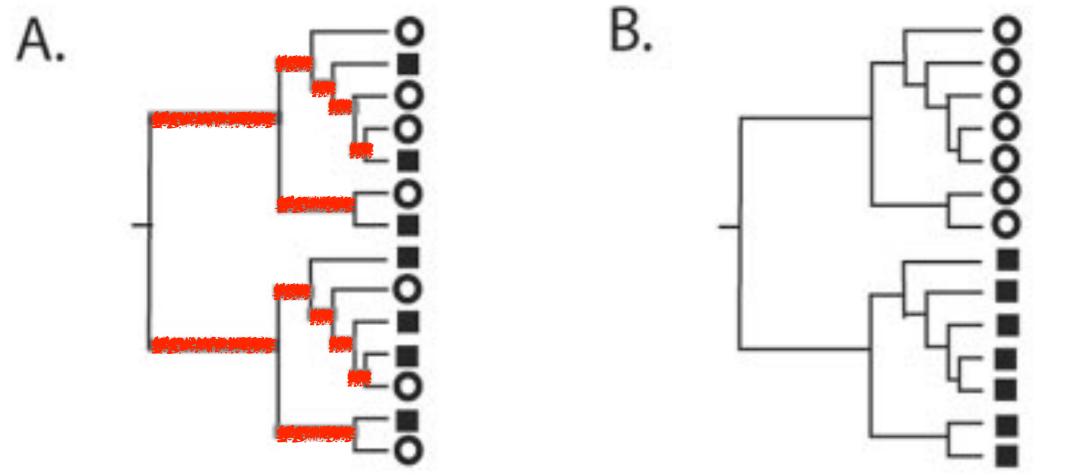
```
housing foodstuffs alcohol other services
     640
              328
                    147
                          169
                                 196
2
    1800
             484 515 2291
                                 912
     640
            328 147 169
                                 196
           3280
    6400
                    1470 1690
                                1960
```

 The phylogenetic distance between sets of taxa in a phylogenetic tree as the fraction of the branch length of the tree that leads to descendants from either one environment or the other, but not both.

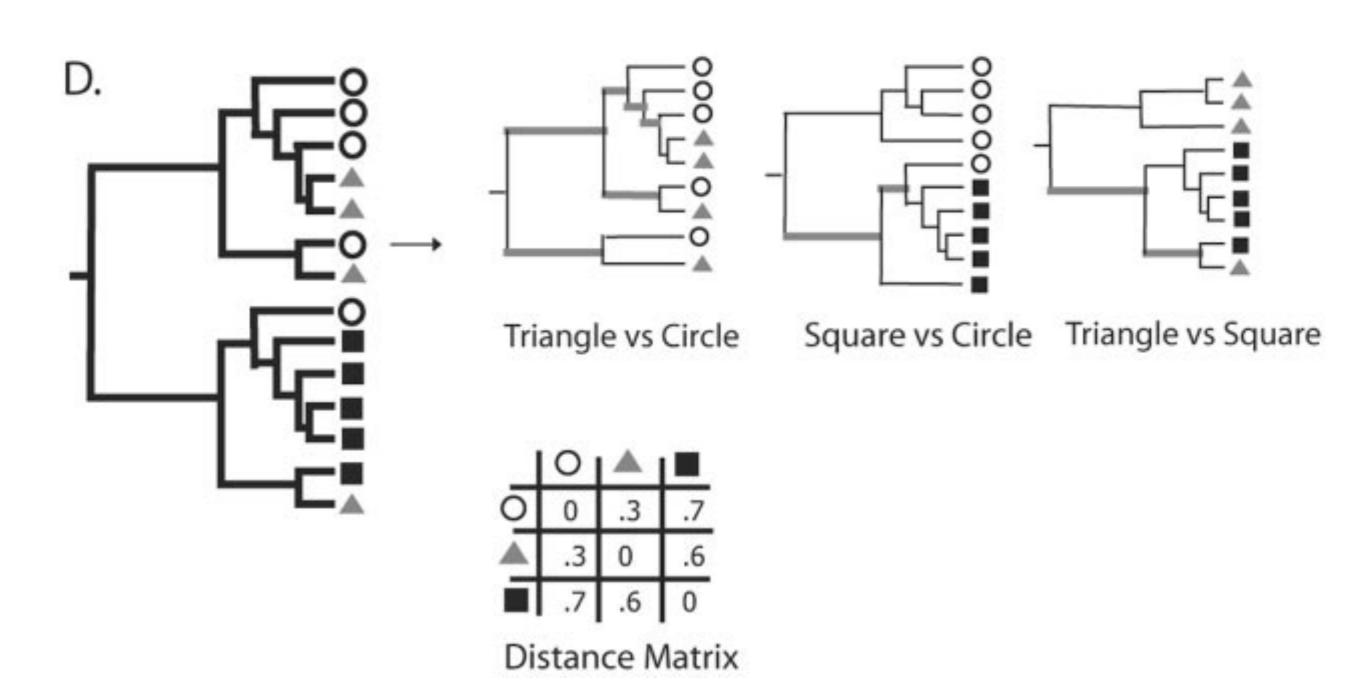




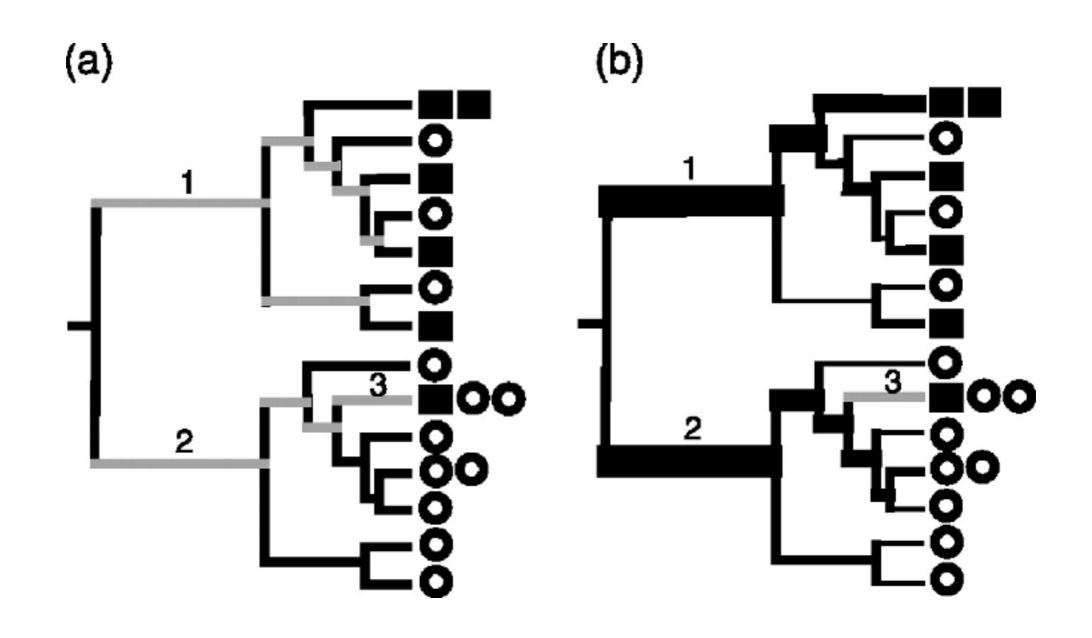
- 1. Label branches leading to taxa from both samples "shared"
- 2. Label branches leading to taxa which appears only in one sample "unshared".
- 3. Unifrac is the fraction of total branch length which is unshared. Alternatively, (the sum of "unshared" branch lengths)/(the sum of all tree branch lengths



- Label branches leading to taxa from both samples "shared"
- 2. Label branches leading to taxa which appears only in one sample "unshared".
- Unifrac is the fraction of total branch length which is unshared. Alternatively, (the sum of "unshared" branch lengths)/ (the sum of all tree branch lengths)



# Weighted UniFrac



# UniFrac: Unweighted vs Weighted

- Unweighted UniFrac
  - Qualitative
  - Sensitive to differences in overall community structure
  - Strongly influenced by differences in rare (low abundance) taxa
- Weighted UniFrac
  - Quantitative
  - Sensitive to differences in high abundance taxa

#### Generalized UniFrac

- Sensitive to differences in moderately abundant taxa
- Maintains ability to detect differences in high and low abundance taxa