

Team Activity Instructions

Step 1: fill in the following OTU table (on the board).

Communities are in columns, taxa (OTUs) in rows.

	A	B	C	D	E
OTU1 (orange)					
OTU2 (yellow)					
OTU3 (red)					
OTU4 (brown)					
OTU5 (green)					
OTU6 (blue)					

Step 2. In your teams, use these data to calculate the Bray-Curtis dissimilarity between each community A-E. Perform calculation “by hand” using a calculator or spreadsheet (but not an existing shortcut function e.g. in R or another program). Place calculated values into a resemblance matrix. The equation for calculating Bray-Curtis:

$$D_{jk} = \frac{\sum |(x_{ij} - x_{ik})|}{\sum (x_{ij} + x_{ik})}$$

Where, i is species (taxa or OTUs) and j and k are communities (sites or samples).

	A	B	C	D
B				
C				
D				
E				

Step 3. Arrange samples in 2-dimensional space based on Bray-Curtis dissimilarities. Use the board or a piece of paper to construct the ordination

In creating the ordination, let’s review how Bray and Curtis (1957) proposed to make the multi-dimensional arrangement See sections “the Ordination Method” and “Axis Construction”.

Quote below from p 330, emphasis added:

“This technique depends upon the selection of a pair of **reference stands** for the determination of stand positions on any one axis. [...] those stands which are furthest apart will be more accurate for judging interstand distance than those which are in close proximity. [...] The choice of reference stands should be, therefore, of those stands which are furthest apart and as a consequence, have the greatest sensitivity to over-all compositional change.”

And for Axis 2, quote from, p 331:

“Two new reference stands are selected which are in close proximity on the x axis, but which are nevertheless separated by a great interstand distance”

For the first, axis:

Select reference points (communities).

Arrange all other points in a straight line between the references, representing their differences from the references.

For the second axis:

Chose two communities on the first axis line that are in close proximity and yet have the largest distance between them by the resemblance calculation. Allow these two to serve as “references” for the range of axis 2. Arrange all other samples at their original Axis 1 position, but in reference to their resemblance to the new references on Axis 2.

Step 4. Check your ordination with the provided key. How well did you do? Can you understand what errors were made and why?