## EEB 698, Fall 2019: Some dissimilarity measures

Goal: one number quantifying dissimilarity in species composition between samples  $i$  and  $j$ 

Data:  $y_{ik}$  = abundance (perhaps 0,1) of species k in sample i, so rows = samples Where needed,  $Y_i$  is total abundance in sample  $i$ , and

 $p_{ik} = y_{ik}/Y_i$ , the proportional abundance for species k in sample i

Properties of dissimilarity measures:

1)  $d_{ij} \geq 0$ . No negative dissimilarities

2)  $d_{ij} = 0$  only when two samples are the same, as viewed by the dissimilarity For some: same abundance, i.e.  $y_{ik} = y_{jk}$  for all species  $(k)$ .

For others: same proportion, i.e.  $p_{ik} = p_{jk}$  for all species  $(k)$ .

3)  $d_{ij} = d_{ji}$ . Matrix is symmetric. Same dissim. when go from i to j or j to i.

Additional property that defines a distance (not just a dissimilarity): 4)  $d_{ik} \leq d_{ij} + d_{jk}$  for 3 samples, i, j and k. Triangle inequality

Measures that satisfy 1-4 are called metric; those that satisfy 1-3 are called semi-metric.

Why this can matter: if metric (4 satisfied), can put the 3 locations on a piece of paper so that distance between them is the dissimilarity. Impossible (triangle doesn't close) when semi-metric.

What about similarity? (large value  $\Rightarrow$  similar, 0 or close to 0 *Rightarrow* very different) Measures with a maximum value, e.g., Bray-Curtis, Morisita, Jaccard, Sorenson, similarity  $= 1$  - dissimilarity

Presence-absence data:  $y_{ik} = 0$  or 1 for all species and sites Usually written in terms of:

- a: number of species only in sample  $i$ , i.e. in  $i$  but not both
- b: number of species only in sample  $i$ , i.e. in  $i$  but not both
- c: number of species in both samples

Sorenson:

$$
d_{ij} = \frac{a+b}{a+b+2c} = \frac{(a+b)/2}{(A+B)/2}
$$
  
= 
$$
\frac{|y_{ik} - y_{jk}|}{Y_i + Y_j}
$$
, when *y*'s are 0 or 1.  
(So Sorenson is BC on presence/absence data)

 $A = a + c =$  total number species in i,  $B = b + c =$  total number species in j.

Jaccard:

$$
d_{ij} = \frac{a+b}{a+b+c}
$$

$$
= \frac{2S}{1+S}
$$

Continuous data:

Euclidean:

$$
d_{ij} = \sqrt{\sum_{k} (y_{ik} - y_{jk})^2}
$$

Manhattan:

$$
d_{ij} = \sum_{k} |y_{ik} - y_{jk}|
$$

Bray-Curtis:

$$
d_{ij} = \frac{\sum_{k} |y_{ik} - y_{jk}|}{\sum_{k} (y_{ik} + y_{jk})} = \frac{\sum_{k} |y_{ik} - y_{jk}|}{Y_{i} + Y_{j}}
$$

Canberra:

$$
d_{ij} = \frac{1}{\text{# non-zero entries}} \sum_{k} \left[ \frac{|y_{ik} - y_{jk}|}{y_{ik} + y_{jk}} \right]
$$

Bray-Curtis on proportional abundance, first compute  $p_{ik} = y_{ik}/Y_i$  for each sample:

$$
d_{ij} = \frac{\sum_{k} |p_{ik} - p_{jk}|}{\sum_{k} (p_{ik} + p_{jk})}
$$
  
= 
$$
\frac{1}{2} \sum_{k} |p_{ik} - p_{jk}|
$$

Morisita-Horn, computed using  $y$ 's,  $p$ 's computed "internally":

$$
d_{ij} = 1 - \frac{2 \sum_{k} (y_{ik}/Y_{i})(y_{jk}/Y_{j})}{\sum_{k} (y_{ik}/Y_{i})^{2} + \sum_{k} (y_{jk}/Y_{j})^{2}}
$$
  
= 
$$
1 - \frac{2 \sum_{k} p_{ik} p_{jk}}{\sum_{k} p_{ik}^{2} + \sum_{k} p_{jk}^{2}}
$$
  
= 
$$
\frac{\sum_{k} (p_{ik} - p_{jk})^{2}}{\sum_{k} p_{ik}^{2} + \sum_{k} p_{jk}^{2}}
$$