Rarefaction Example

- Consider this dataset:

	sp1	sp2	sp3	sp4	sp5	sp6
sam1	6	1	0	9	0	1
sam2	138	5	2	260	3	19
sam3	115	7	12	325	1	43
sam4	125	3	4	190	4	27

- Where is diversity highest?
  - S
  - sam1 sam2 sam3 sam4
  - 4 6 6 6
  - Shannon
  - sam1 sam2 sam3 sam4
  - 1.0375911 0.9176461 0.9908044 1.0397044
- What about rarefied diversity?
- rarefy(community,sample=10)
- sam1 sam2 sam3 sam4
- 3.175905 2.576947 2.889674 2.842323

- Original matrix:

	sp1	sp2	sp3	sp4	sp5	sp6
sam1	6	1	0	9	0	1
sam2	138	5	2	260	3	19
sam3	115	7	12	325	1	43
sam4	125	3	4	190	4	27

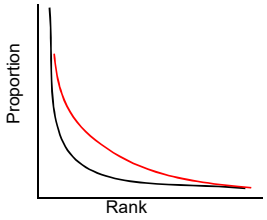
- Rarefied matrix
  - rrarefy(community,sample=10)

	sp1	sp2	sp3	sp4	sp5	sp6	Σ	S
sam1	3	1	0	5	0	1	10	4
sam2	3	0	0	7	0	0	10	2
sam3	1	0	0	6	1	2	10	4
sam4	3	0	0	7	0	0	10	2

- Repeated 1,000 times, the average S
  - sam1 sam2 sam3 sam4
  - 3.150 2.574 2.885 2.852

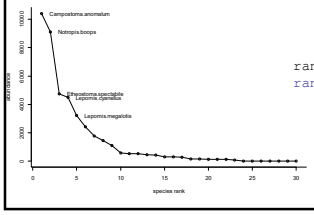
Species Abundance Curves

- Plot of rank abundance (x-axis) vs abundance or P_i (y-axis).
- More diverse communities lack numerically dominant species, flatter line.

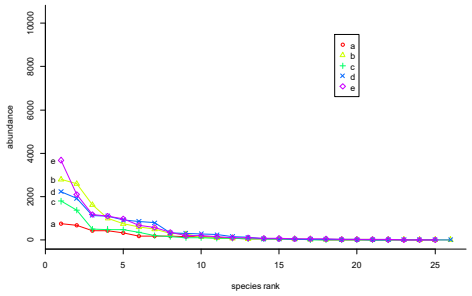


Species Abundance Curves

- Functions: rankabundance, rankabuncomp in the BiodiversityR package
- rankabundance(community)
  - Can use either raw abundance or proportion data
  - rankabuncomp allows for comparison among factors
  - rankabunplot will plot the results



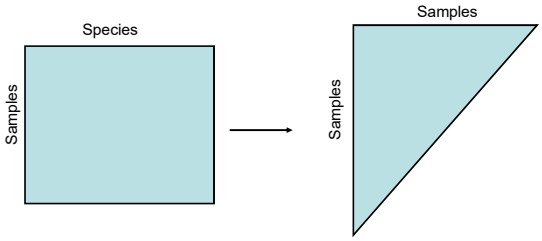

```
rank_data<-rankabundance(Brier_Ck)
rankabunplot(rank_data)
```




```
# Compare rank abundance among creeks or years
# THIS FUNCTION WILL WAIT FOR YOU TO CLICK ON THE GRAPH TO PLACE THE LEGEND
rank_data<-rankabuncomp(Brier_Ck,y=Brier_environmental,factor="year")
```

Community Similarity or Dissimilarity

- Community similarity indices quantify similarity among two samples.
- For a full community matrix do all possible pairwise comparisons among communities.



- Symmetrical vs. asymmetrical metrics
  - Are shared zeros indicators of actual similarity?
  - Community data typically uses asymmetric metric
- Qualitative vs. quantitative
  - Ordinal vs categorical, bionmical etc.
- Q mode vs. R mode
  - Q: Are actual objects being compared (question is how similar are A and B)
    - E.g.: how similar is community A and B
  - R: Are relationships or dependence of measures of interest (question is if A is correlated with B)
    - E.g. Is species X abundance correlated with temperature

Community Similarity or Dissimilarity

- Functions: **vegdist** (vegan package), **dsvdis** (labdsv package), **daisy** (cluster package), **designdist**(vegan)
- Very often raw abundance data can be used
  - Variable depending on properties of metric, look at how each is calculated
- Most are bound (0-1 range)
  - Conversion to similarity or dissimilarity
    - `sim_matrix<-vegdist(Brier_Ck)`
    - `dsim_matrix<-1-sim_matrix`

Quantitative Indices of Similarity (0-1.0)

$$Ruzicka(PSI) = \sum_{i=1}^{s} \min P_i$$

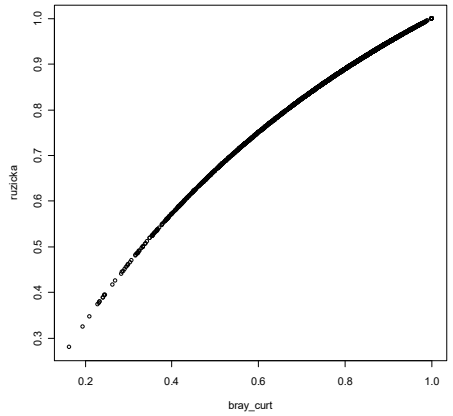
Where Pi = the proportion of the community composed of species i.

$$Bray - Curtis = \sum_{i=1}^{s} \frac{(x_{ij} - x_{ik})}{x_{ij} + x_{ik}}$$

Where x_{ij} = is the abundance of species i in community j

Both are bound
Typically log transform data

Bray-Curtis vs PSI distances for local fish community dataset



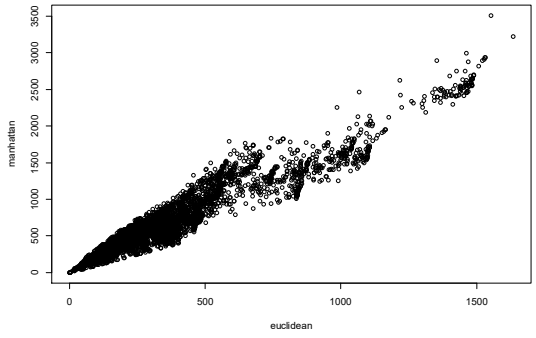
Quantitative Indices of Similarity (unbound)

$$Euclidian = \sqrt{\sum_{i=1}^{s} (x_{ij} - x_{ik})^2}$$

$$\textbf{\textit{Manhattan}} = = \sum_{i=1}^{s} \left| x_{ij} - x_{ik} \right|$$

Typically done without transformation. Some use presence/absence matrix with these metrics. No upper limit.

Euclidian vs Manhattan distances for local fish community dataset



Qualitative Indices of Similarity (0-1.0)

$$Steinhaus = 1 - \frac{a}{a+b+c}$$

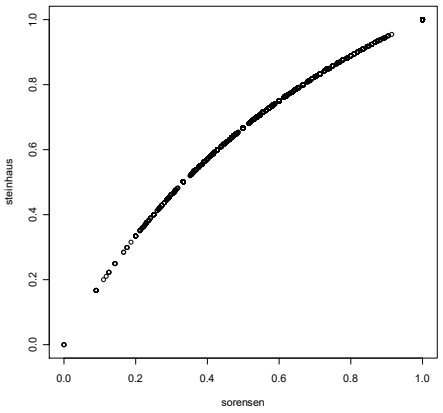
$$Sorensen = 1 - \frac{2a}{(2a+b+c)}$$

Where a = number of species in both communities, b= number of species unique to community 1, c = number of species unique to community 2

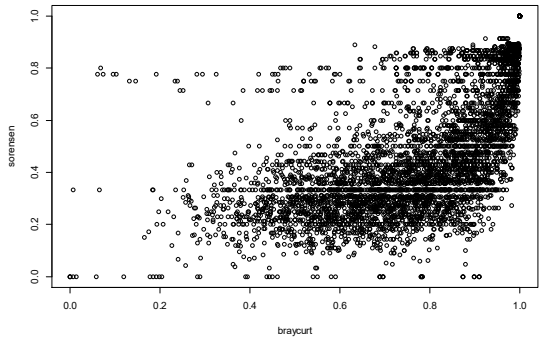
Both convert data to presence/absence.

Can be converted to dissimilarity by 1-Steinhaus or Sorensen.

Steinhaus vs Sorensen distances for local fish community dataset



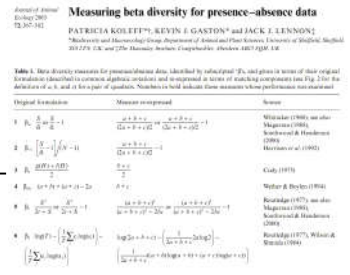
Bray-Curtis vs Sorensen distances for local fish community dataset



Defining your own function

- Function designdist in the vegan package allows you to define any similarity index.

```
designdist(community,method =
"(B+C)/2", abcd=TRUE)
```



Measuring beta diversity for presence–absence data

PATRICIA KOLEFF*†, KEVIN J. GASTON* and JACK J. LENNON‡

…review of 24 measures of beta diversity

Assignment

- We will be using the bee gut microbiome data from the paper read for class today. The data is available in datadryad:
- https://doi.org/10.5061/dryad.r02r1
- The data is presented in three files
  - Frequency of OTUs ("species") by library("samples")
  - Taxonomic information for each OTU (species)
  - Sample information (which treatment, etc.)
  - I did some filtering and processing to match what was written in the paper (eliminated mitochondria and chloroplasts, combined the "Naturals" groups etc.)
  - The processed data are given to you as
    - otu_table.csv – samples in rows by OTU in columns
    - sample_meta.csv – Factors for colony ID, Population, and Treatment

Assignment

- 1. Eliminate species (OTUs, the columns) with zero occurrences. What is the new total OTUs? Does that match what is in the paper?
- 2. Calculate the total OTUs per sample. What is the minimum of this among all the samples? Does this match what is in the paper?
- 3. Use the diversitycomp function to calculate species richness, Shannon diversity, and evenness for samples pooled (method="pooled") among treatments (factor1="Treatment").
- 4. Plot a species accumulation curve (random method) for the whole dataset. Use specaccum function.
- 5. Calculate a Bray-Curtis similarity matrix for the whole dataset. What is the mean Bray-Curtis dissimilarity?
- 6. Create a rarefied matrix using rrarefy, with the sample size set to the minimum total number of OTUs in a sample (item #2 above).
- 7. Repeat 3,4, and 5 above with the rarefied matrix. Discuss differences in your synthesis.