Species richness & diversity in R



What is a community?

A biological community is an assemblage of populations of various species living close enough for potential interaction



Measuring Diversity

- Species richness is the total number of different species in the community
- Relative abundance is the proportion each species represents of the total individuals in the community
- Species diversity is an index that incorporates the number of species in an area and also their relative abundance





Community 1 A: 25% B: 25% C: 25% D: 25% opyright © 2008 Pearson Education, Inc., publishing as Pearson Benjamin Cummings. Community 2 A: 80% B: 5% C: 5% D: 10%

Two communities can have the same species richness but a different relative abundance and hence will have different species diversity.

Diversity at different scales



- 1.) Alpha diversity –the diversity at a single point
- 2.) Beta diversity the diversity in a habitat
- 3.) Gamma diversity the diversity in a landscape
- When measuring diversity or species richness, it is a good idea to control for the number of individuals and the amount of effort expended for sampling

Rarefaction Curves



- In ecology, rarefaction is a technique to standardize and compare species richness computed from samples of different sizes.
- The issue that arrives when sampling various species in a community is that the larger the number of individuals sampled, the more species that will be found.
 - Sampling curves generally rise very quickly at first and then level off towards an asymptote as fewer new species are found per unit of individuals collected.



Figure 2

Species richness



- Species richness is the number of species in a given area.
 - When you report this, you mention where and when you counted the species.
- Let's take a look at the *dune* dataset.
 - library(vegan)
 - data(dune)
- What are the variables?



What do the variable names mean?



How many species are there?

- Download and install the *BiodiversityR* package
- Iibrary(BiodiversityR)
- Diversity.1 <- diversityresult(dune, index = 'richness')</p>
- Diversity.1



Calculate the total number of species by site

- Diversity.2 <- diversityresult(dune, index = 'richness', method = 's')</p>
 - The *method* = 's' calculates total species richness by site
- Diversity.2



Aggregating sites by management

• data(dune.env)



- dune.env includes information soil thickness, amount of moisture, management, use, and amount of manure.
- Let's compare species richness by management type
- Diversity.4 <- diversitycomp(dune, y = dune.env, factor1 = 'Management', index = 'richness', method = 'all')

Diversity.4

Species-area curves

- A species-area curve is a relationship between the area of a habitat, or of part of a habitat, and the number of species found within that area.
- Larger areas tend to contain larger numbers of species, and empirically, the relative numbers seem to follow systematic mathematical relationships



Graphical example



Species-area Relationship on Log-log Axes

Species-area Relationship on Arithmetic Axes



Constructing species accumulation curves

- Species accumulation curves show the species richness for combinations of sites.
- These curves show the <u>average</u> pooled species richness.
- Accum.1 <accumresult(dune, method = 'exact')

Accum.1



Output

This is called a sample-based species accumulation curve



Plotting the result

accumplot(Accum.1)



Classic approach



- The classic approach to constructing species accumulation curves is by randomly selecting subsets and then obtaining the averages.
- Accum.2 <- accumresult(dune, method = 'random', permutations = 1000)
- Accum.2

Plot the result

accumplot(A ccum.2)



Comparing richness between samples



- Species accumulation curves are very useful for comparing species richness for subsets in the data when sample sizes of subsets are different.
- For example, in the *dune.env dataset*, you might want to compare richness according to different types of management activities
 - Management: a factor with levels: 'BF' (Biological farming), 'HF' (Hobby farming), 'NM' (Nature Conservation Management), and 'SF' (Standard Farming

Rarefaction curves - samples

 Accum.6 <accumcomp(dune, y = dune.env, factor = 'Management', method = 'exact')

 You will need to click on the graph to indicate where the legend should go



Rarefaction curves individuals

- In many cases, it is more informative to include information on the number of individuals you encountered.
- dune.env\$site.totals <apply(dune, 1, sum)

Accum.7 <accumcomp(dune, y = dune.env, factor = 'Management', scale = 'site.totals', method = 'exact', xlab = 'pooled individuals ')



Accum.7 output



A few more notes

- Accumulation curves can be either
 - Site-based accumulation curves; or
 - Individual-based accumulation curves
- The horizontal axis needs to be scaled by an average for all sites
 - This could be the average number of sites per site (i.e. 1 site/site), the average number of individuals per site, the average area per site, etc.
- Species richness depends upon sample size and sample size can be measured by different methods (# of sites, size of sample area, # of individuals), so different results can be obtained depending upon your choice of method

Calculating expected species richness



- There are several different methods to estimate species richness.
 - First-order Jacknife
 - Second-order Jacknife
 - Chao estimator
 - Bootstrap estimator
- Diversity.5 <- diversityresult(dune, index = 'jack1')</p>
- Diversity.6 <- diversityresult(dune, index = 'jack2')</p>
- Diversity.7 <- diversityresult(dune, index = 'chao')</p>
- Diversity.8 <- diversityresult(dune, index = 'boot')</p>
- cbind(Diversity.5, Diversity.6, Diversity.7, Diversity.8)

Output

There are between 31 –34 species present according to these estimators





Rank-abundance curves



- Rank-abundance curves are an easy way to begin investigating patterns of diversity
 - First, the total number of individuals is calculated for each species
 - Second, species are ranked from most abundant to least abundant.
 - Finally, a plot is constructed with the rank number on the x-axis and the abundance on the y-axis.
- RankAbund.1 <- rankabundance(dune)</p>

RankAbund.1

Rank-abundance curves



- The results are typically presented as a curve
- rankabunplot(RankAbund.1, scale = 'abundance')
- The wider the curve is on the x-axis, the higher the species richness
- A completely horizontal curve shows a completely evenly distributed system
- The steeper the curve, the less evenly species are distributed

Rank-abundance curve showing proportion

rankabunplot(R ankAbund.1, scale = 'proportion')



Modeling rank-abundance curves

- Niche apportionment models are mechanistic models used to explain relative species abundance distributions.
- These models describe how species break up resource pool in multi-dimensional space, determining the distribution of abundances of individuals among species.

Testing some common models

radfitresult(dune)



Support is strongest for the "preemption" model.

For more information about the models, look at the help file for *radfit* and Hubbell's (2001) book on unified neutral theory



Renyi diversity profile



- Renyi diversity profiles are easier to order from lowest to highest.
- The shape of the profile is an indication of the evenness.
 - A horizontal profile indicates that all species have the same evenness.
 - The less horizontal a profile is, the less evenly species are distributed.
- Renyi.1 <- renyiresult(dune)</p>
- Renyi.1

Plotting a Renyi diversity curve

renyiplot(Renyi.1)



Renyi evenness profiles

- The shape of the curve is typically influenced by evenness.
- You can compare evenness more directly by using Renyi evenness profiles.
- renyiplot(Renyi.1, evenness=TRUE)



Comparing evenness between sites



- Renyi.2 <- renyiresult(dune, method = 's')</pre>
- renyiplot(Renyi.2, evenness = TRUE)
- Alpha = 1 is the Shannon-Weiner diversity index
- Alpha = 2 is the log of the reciprocal of the Simpson diversity index

Comparing diversity between factors

 Renyi.3 <renyicomp(dune , y = dune.env, factor = 'Management', permutations = 100)



Comparing evenness between factors

Renyi.3a <-</p> renvicomp(dune, y = dune.env, factor = 'Management', evenness = TRUE, permutations = 100)

