

Bio 682
Quantitative Biology

Homework Assignment Part Deux:

We have been talking about measures of diversity in class: species richness (S), species evenness (E), and Shannon (information theoretic) diversity (H'), and Simpson's D in class. These measures, and total sample abundance are not independent of each other – each describes a different aspect of the allocation of abundance into species and samples, and each affects our perceptions of what “diversity” means. This part of the homework will involve using PC-ORD to calculate information about the diversity of the samples you entered in Part One.

A. Richness. Pull your data file into PC-ORD where you can find it. Choose **SUMMARY** from the menu bar, and then **SPECIES-AREA CURVES** to look at how species accumulate as you add samples. Add a descriptive title for the output and click on “OK” to run the routine. The results will show up in the “Result.txt” box in the lower right of the window. Print the Results.txt box (**File | Print | Result.txt**) and examine the output. How many species did you encounter in all 20 samples? How many are likely to be in the area, based on 1st order jackknife extrapolations? If you wanted to get, on average, 80% of the species likely to be in the whole of Bristol Channel (e.g. the Jackknife number) how many samples would you have to take? Choose **Graph | Species-area curves** to look at a prettier version of the graph in the Results.txt box, (plus curves representing +/- 2 standard deviations) based on multiple samples. You can use the Options menu to delete the graph of average dissimilarity.

B. Diversity. Next, examine the richness and diversity of your samples and how these measures are related. Again, choose **SUMMARY**, then **ROW AND COLUMN SUMMARY**, then within that choose **ONLY ROWS** Sites (or choose Both Rows and Columns, but here you're really only interested in sample attributes). Give a descriptive name for your output, then click OK. The results will appear in the Result.txt box in the lower right hand corner again (you will be asked about the contents of the Result.txt from the richness question above, -- discard it or save it as a .txt file for later). You'll see information about the sites themselves (first table), along with information about the matrix overall (second table: size, % empty cells, etc.).

Print out the results file (**File | Print | Result.txt**) and examine the information in the first table. Which site has the highest diversity as measured by S? by E? by H' ? by D? Do these differ? Use the cut-and-paste function in Windows to paste that table into a spreadsheet, and parse the table into columns (in Excel, select the length of the pasted data table, choose **Data | Text to columns**, in Lotus 1-2-3, choose **Range | parse**). Now that the columns of total N (= “Sum”), S, E, and H' are separate, use your spreadsheet's graphing function (or other graphing program) to examine several pairwise plots of these numbers (e.g., S vs. N, H' vs. S....). Print several of the graphs. In two or three sentences, describe what each graph says about these measures of diversity and their interrelationships.

Return to the data table and square-root transform the numbers of individuals to get a measure of biomass (in general, the number of individuals in these zooplankton decreases as the square of individual mass, so the total biomass per species is a linearly related to the square root of total numbers). Does this change your conclusions about which samples are the most diverse?