

WILD6770
Spring 2008

Productivity-Diversity Assignment (due Feb. 19)

As the review papers on productivity-diversity relationships show, despite tremendous interest in patterns of species richness across gradients of productivity, generalization remains difficult. One problem has been finding comparable datasets. Often species richness is measured in plots of different sizes in different locations, or different methods are used to estimate productivity.

The "Nutrient Network" is a new approach to solving these problems. At more than 40 sites around the globe, researchers have implemented a standardized experiment to test productivity-diversity relationships (among other things). You can read about the project here:
<http://web.science.oregonstate.edu/~seabloom/nutnet/>.

We will use pre-treatment data from 11 sites (the ones that have already submitted data) to test the productivity-diversity relationship. Information about the sites is in the NutNet_sites.xls spreadsheet. In addition, you will find two data files attached, one for biomass and one for cover. Ask me if you do not understand some of the column names in these files.

Your assignment is relatively simple: produce a series of scatter plots showing the relationship between plot-level biomass on the x-axis (a measure of productivity) and plot-level species richness on the y-axis.

1. One figure should show data for all plots at all sites (many points on the graph).
2. The next figure should just show the mean plot-level richness plotted against mean biomass for each site (11 points on the graph).
3. Finally, repeat these two figures using data for just native species, and again for just exotic species.

I give you some R tips on how to do this below.

Discuss how your results compare to the published productivity-diversity literature. If they differ, can you explain why? Are the patterns different for natives and exotics? Why might this be?

Here is some pseudo code for the steps you will need to script:

1. Import the cover and biomass data into R
2. Calculate the species richness of each plot using the aggregate() function. For example, if "cover" is the name of the data frame containing the cover data:

```
richness=aggregate(cover$rich,by=list("site"=cover
    $site,"block"=cover$block,"plot"=cover$plot,
    "subplot"=cover$subplot),FUN=sum)
names(richness)[5]="S"
```
3. Calculate the total biomass of each plot, again using aggregate
4. Merge the richness and biomass data using merge()
5. Now you should be able to graph the plot-level data
6. Calculate site-level richness and biomass using aggregate() again
7. Now you should be able to graph the site-level data
8. To repeat for just natives or exotics, use the subset() function to create a new data frame, then go back to step 3