

Tutorial 5/6 - Biodiversity & Ecosystem Function (Monday tutorial)

✓ Published

 Edit

 _

R Assignment 1: Biodiversity - Ecosystem Function

In Tutorials 5 and 6, we have been analysing different facets of biodiversity and how it relates to ecosystem function in experimental plant communities.

The four measures of biodiversity we calculated are:

1. Species richness
2. Ln-transformed species richness
3. Phylogenetic diversity using a phylogeny based on molecular substitutions (the original `phylogeny.phy` file from Tutorial 6)
4. Phylogenetic diversity with a phylogenetic tree that has been transformed to have branch lengths that reflect evolutionary time instead of molecular substitutions (the phylogeny created by the `chronomPL()` function from the `ape` library)

Instructions for these analyses can be found in the Tutorial 5 and 6 folders.

Questions to answer in your write-up:

Now that you have examined the biodiversity - ecosystem function relationship in these plant communities, please write up a written report that addresses the following:

1. Show your two plots of species richness plotted against above-ground biomass produced: one with raw species richness, another with ln-transformed species richness. These plots should include axes titles with appropriate units of measure and a line that describes the linear model outputs (i.e. the trend line for the data).

3 points

2. Describe the shape of the relationship between species richness and productivity. Also describe the linear model that generates this observed relationship. How does the observed relationship compare to the expected shape of the B-EF relationship? What mechanisms of the B-EF relationship does your model predict? How confident are you of this?

1 point

3. Discuss the likely ecological process(es) that you think shaped the observed richness-biomass relationship. Consider the alternative processes and how you might test your hypothesis for

which one caused the B-EF relationship.

1 point

4. Like Question 1, show two plots of our phylogenetic measure of biodiversity - phylogenetic diversity (PD) - plotted against average above-ground biomass. There should be one plot of PD calculated from the substitution-based phylogenetic tree and another from the time-calibrated phylogenetic tree from `chronomPL()`. Again, axes should be labelled with appropriate units with an overlaid line of best fit from the linear model.

3 points

5. Is the PD model you generated a better fit than the models with species richness? What did you initially predict would be a better fitting model? Did the model support your predictions?

1 point

6. How did transforming the branch lengths in the phylogenetic tree alter your model fitting results? Discuss why this phylogeny was better or worse in explaining the observed variation in above-ground biomass.

1 point

Your report should be between 500-800 words long (approximately 2 type-written pages). **Submit your written answers to the questions above AND your well-commented R code.**

This assignment is worth 10% of your final grade.

Points 10

Submitting a file upload

Due	For	Available from	Until
Feb 25 at 2pm	Everyone	-	-

+ [Rubric](#)