

# Biodiversity Science BEF Module

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In this lab, we will explore some questions about biodiversity and its effects on ecosystem functioning. To do so, we will use data and scripts (with some modifications) kindly provided by Jake Grossman.

## Set up your data and your working directory

Set up a working directory and put the two data files in that directory. Tell R that this is the directory you will be using, and read in your data:

```
setwd("path/for/your/directory")
```

Install and load the following packages

```
library(agricolae)
```

Read in data from “Species richness and traits predict overyielding in stem growth in an early-successional tree diversity experiment” (Grossman et al. 2017; Ecology 98:2601-14)

```
df <- read.csv("Data/BEF_Lesson_Data.csv",header=T)
```

```
names(df)
```

“df” should now be a data frame with 9 columns and 140 rows. The rows are the 140 experimental plots in the FAB experiment. The columns are as follows:

```
dim(df)
```

1. Plot = an arbitrary index for each plot
2. SR = species richness of the plot (1, 2, 5, or 12 species)
3. Comp = a categorical code that is the same for plots with the same composition. M = monoculture, B = biculture, F = five-species, and T = 12-species
4. PSV = phylogenetic species variability (Helmus et al. 2007) - a metric of phylogenetic diversity independent of species richness
5. FDis = functional dispersion (Laliberte and Legendre 2010) - a metric of functional diversity independent of species richness
6. NBE = net biodiversity effect - observed biodiversity ( $d_Y$ ) minus expected biodiversity (based on monocultures (not give in this example)
7. CE = complementarity effects (Loreau and Hector 2001)  $CE + SE = NBE$ ; calculated using a script from Forest Isbell - UMN-Twin Cities
8. SE = selection effects (Loreau and Hector 2001) see above
9.  $d_Y$  = delta biomass, the average change in stem biomass of a tree in a given plot (kg)

Important - Note that there is no value for NBE, CE, and SE for monocultures since these can only be calculated for polycultures

## Exercise 1

### Question 1: does stem biomass yield depend on plot composition and richness?

First, set a color scheme to distinguish among composition by color and then, plot the data to see if there is a visible trend:

```
comp.cols <- c(rep("red", 12), rep("orange", 28), rep("yellow", 10), rep("green", 1))  
  
with(df, plot(Comp, d_Y, col = comp.cols))
```

Now, use a regression model to assess whether there is a difference:

```
m1 <- lm(d_Y ~ Comp, data = df)  
summary(m1)
```

```
anova(m1) # Use an ANOVA for categorical data
```

Since an ANOVA is significant, you can use a post-hoc test to gauge differences in composition:

```
m1.df <- HSD.test(m1, "Comp", group = TRUE, console = TRUE)
```

Wow, there is a lot of variability among plot compositions. But what if we summarize across this variability based on the number of species in the plot. Following the same steps as above:

```
with(df, plot(SR, d_Y)) #It's a little hard to assess the pattern graphically
```

```
m2 <- lm(d_Y ~ SR, data = df)  
summary(m2) #A linear model indicates "no"
```

```
anova(m2) #ANOVA confirms this.
```

Please answer the following questions:

1. Do plots of different composition vary in yield?
2. What about plots that vary in species richness/diversity?

### Question 2: does overyielding depend on plot composition and richness?

Keep in mind that instead of how much biomass a plot produces, the response variable is now that number MINUS what would be expected if each tree in the plot were growing in monoculture. So, this adjusts for the “innate” productivity of each species.

What about plots of different compositions?

```
with(df, plot(Comp, NBE, col = comp.cols))
```

```
m3 <- lm(NBE ~ Comp, data = df)  
summary(m3)
```

```
anova(m3)
```

```
m3.df <- HSD.test(m3, "Comp", group = TRUE, console = TRUE)
```

Interesting!

3. Which four plots have the highest overyielding according to the post-hoc test?

Given this, 4. what do you expect you’ll find when you assess the dependence of overyielding on species richness?

```
with(df, plot(SR, NBE)) #Note: it doesn't make sense to plot NBE of monocultures
```

```
m4 <- lm(NBE ~ SR, data = df)
summary(m4)
```

```
anova(m4)
```

```
m4.df <- HSD.test(m4, "SR", group = TRUE, console = TRUE)
```

Take a moment to compare the output of model 4 to that of model 2.

5. This helps explain the importance of monocultural controls in biodiversity experiments.

## Exercise 2

**Question 3: How do different levels of species richness compare in terms of complementarity and selection?**

The tools you use here should now feel familiar: first, analyze graphically; then make a linear model and assess it with ANOVA if the ANOVA is significant, use post-hoc testing

First, complementarity effects:

```
with(df, plot(SR, CE))
```

```
m5 <- lm(CE ~ SR, data = df)
summary(m5)
```

```
anova(m5)
```

```
m5.df <- HSD.test(m5, "SR", group = TRUE, console = TRUE)
```

Then, selection effects:

```
with(df, plot(SR, SE))
```

```
m6 <- lm(SE ~ SR, data = df)
summary(m6)
```

```
anova(m6)
```

```
m6.df <- HSD.test(m6, "SR", group = TRUE, console = TRUE)
```

You can even plot CE and SE together

```
with(df, plot(SR, CE, col = "blue"))
with(df, points(SR, SE, col = "red"))
abline(h = 0) #Just to make it easier to tell positive from negative
```

6. How do CE and SE compare to each other and NBE (overyielding)?

7. What does positive CE mean? What does negative CE mean?

8. What about positive and negative values of SE? (This can be confusing.)

**Question 4: Do you find evidence of transgressive overyielding?**

To ask this question, let's return to the plot from Question 1:

```
with(df, plot(SR, d_Y, ylim = c(-0.05, 0.25)))
#and add a horizontal line:
abline(h = 0)
```

**9. Are the least productive (or even average) polycultures more productive than the most productive monocultures?**

(If you are still unconvinced, you could code all monocultures as “0” and all polycultures as “1” and do a t-test...)

## Exercise 3

**Question 5: Which dimension of biodiversity - taxonomic (species richness), phylogenetic, or functional diversity best predicts overyielding in productivity in the FAB experiment?**

To address this question, we’ll see how much of the variability in overyielding (NBE) is explained by each dimension. For a univariate regression model, we can just use  $R^2$  from the linear model output to do model comparison.

```
m4 <- lm(NBE ~ SR, data = df)
summary(m4) #This is our old friend from question 2.
```

```
m7 <- lm(NBE ~ PSV, data = df)
summary(m7) # What about phylogenetic diversity?
```

```
m8 <- lm(NBE ~ FDis, data = df)
summary(m8) # Or functional diversity?
```

So, if you had to choose one, **10. which dimension of diversity would you say best predicts overyielding in stem growth?**

**11. What do you make of the differences in  $R^2$  values for each dimension?**

Optional: You can also do this analysis with CE or SE as the dependent variable.

## References

Grossman, J. J., Cavender-Bares, J., Hobbie, S. E., Reich, P. B., & Montgomery, R. A. (2017). Species richness and traits predict overyielding in stem growth in an early-successional tree diversity experiment. *Ecology*, 98(10), 2601–2614. doi:10.1002/ecy.1958