

Appendix B from T. Bell et al., “A Linear Model Method for Biodiversity–Ecosystem Functioning Experiments” (Am. Nat., vol. 174, no. 6, p. 836)

Analyses for the Random Partitions Design

These are instructions for conducting the analyses in the main article.¹ The analyses were conducted using R, version 2.8.1, which is available as a free download at <http://www.r-project.org>.

1. Set Up the Workspace

Clear the workspace

```
rm(list=ls())
```

Set the seed for random number so that results are reproducible

```
set.seed(13531)
```

2. Input the Experimental Design Defined in Figure 1 of the Manuscript

M = Subject

```
M=as.factor(c(1,3,4,7,8,9,13,14,15,16,17,18,2,5,6,10,11,12,19,20,21,22,23,24))
```

Q = Partitioned species pool

```
Q=as.factor(c(1,3,3,5,5,5,7,7,7,7,7,7,2,4,4,6,6,6,8,8,8,8,8,8))
```

R = Richness treated as a continuous variable

```
R=c(6,3,3,2,2,2,1,1,1,1,1,1,6,3,3,2,2,2,1,1,1,1,1,1)
```

```
R.fac=as.factor(R)
```

Sp.x = Presence/absence of species x

```
Sp.1=c(1,1,0,1,0,0,0,0,0,0,1,1,0,1,0,0,1,0,0,0,0,0,1,0)
```

```
Sp.2=c(1,0,1,1,0,0,0,0,1,0,0,0,1,0,1,0,0,1,0,0,0,0,0,1)
```

```
Sp.3=c(1,1,0,0,0,1,0,1,0,0,0,0,1,0,1,0,1,0,0,0,0,1,0,0)
```

```
Sp.4=c(1,0,1,0,1,0,1,0,0,0,0,0,1,1,0,0,1,0,0,0,1,0,0,0)
```

```
Sp.5=c(1,0,1,0,0,1,0,0,0,1,0,0,1,1,0,1,0,0,0,0,1,0,0,0)
```

```
Sp.6=c(1,1,0,0,1,0,0,0,0,0,1,0,1,1,0,1,0,0,1,0,0,0,0,0)
```

Combine the species into a single matrix (this is useful later)

```
Sp.matrix=matrix(ncol=6,nrow=length(Sp.1),c(Sp.1,Sp.2,Sp.3,Sp.4,Sp.5,Sp.6))
```

```
colnames(Sp.matrix)=paste("Sp.",1:6,sep="")
```

3. Ecosystem Function = Log Richness + Error (See Eq. [8])

Input the response variable

```
y.log=log10(R)+rnorm(length(R),mean=0,sd=1)
```

Reproduce figure A1

```
plot(y.log~R)
```

Model A in figure 2

```
lm1.1=lm(y.log~Q); anova(lm1.1)
```

¹ Code that appears in the *American Naturalist* has not been peer-reviewed, nor does the journal provide support.

```
lm1.2=lm(resid(lm1.1)~-1+M); anova(lm1.2)
```

Model B in figure 2

```
lm1.1=lm(y.log~R); anova(lm1.1)
lm1.2=lm(resid(lm1.1)~-1+Sp.1+Sp.2+Sp.3+Sp.4+Sp.5+Sp.6); anova(lm1.2)
lm1.3=lm(resid(lm1.2)~-1+R.fac); anova(lm1.3)
lm1.4=lm(resid(lm1.3)~-1+Q); anova(lm1.4)
lm1.5=lm(resid(lm1.4)~-1+M); anova(lm1.5)
```

Model C in figure 2

```
lm1.1=lm(y.log~ Sp.1+Sp.2+Sp.3+Sp.4+Sp.5+Sp.6); anova(lm1.1)
lm1.2=lm(resid(lm1.1)~-1+R); anova(lm1.2)
lm1.3=lm(resid(lm1.2)~-1+R.fac); anova(lm1.3)
lm1.4=lm(resid(lm1.3)~-1+Q); anova(lm1.4)
lm1.5=lm(resid(lm1.4)~-1+M); anova(lm1.5)
```

4. Incorporating Ecological Mechanisms

4.1 Calculate the Values of Ecosystem Functioning (y) for Each of the Four Scenarios Described in the Text

Scenario 1

```
sp.effects=1/6
y.1=rowSums(sp.effects*Sp.matrix)
```

Scenario 2

```
sp.effects2=(1:6)^2/91
y.2=rowSums(matrix(rep(sp.effects2,length(M)),ncol=6,nrow=length(Sp.1),
  byrow=T)*Sp.matrix)
```

Scenario 3

```
y.3=Sp.matrix[,1]*Sp.matrix[,2]
```

Scenario 4

```
y.4=c(); for(i in 1:6){y.4=cbind(y.4,Sp.matrix[,i]*sp.effects2[i])}
y.4=apply(y.4,1,max)
```

4.2 Reproduce Figures 3 and 4

Note that plots below show all of the data. For clarity, the plots in the article contain only the data from partition 1 ($P = 1$).

Figure 3

```
layout(matrix(c(1,2,3,4),2,2,byrow=T))
plot(y.1~R); plot(y.2~R); plot(y.3~R); plot(y.4~R)
```

Figure 4

```
layout(matrix(c(1,2,3,4),2,2,byrow=T))
plot(resid(lm(y.1~R))~R,ylim=c(-0.5,0.5))
plot(resid(lm(y.2~R))~R,ylim=c(-0.5,0.5))
plot(resid(lm(y.3~R))~R,ylim=c(-0.5,0.5))
plot(resid(lm(y.4~R))~R,ylim=c(-0.5,0.5))
```

4.3 Conduct the Analyses (i.e., Reproduce Table 1)

For simplicity, define a function that conducts the analysis

```
rp.analysis=function(y){
  lm1=lm(y~R)
  lm2=lm(resid(lm1)~-1+Sp.1+Sp.2+Sp.3+Sp.4+Sp.5+Sp.6)
  lm3=lm(resid(lm2)~-1+R.fac)
  lm4=lm(resid(lm3)~-1+Q)
  lm5=lm(resid(lm4)~-1+M)
  return(list(coef(lm1),coef(lm2),coef(lm3),coef(lm4),coef(lm5)))
```

```
}  
Scenario 1  
rp.analysis(y.1)  
Scenario 2  
rp.analysis(y.2)  
Scenario 3  
rp.analysis(y.3)  
Scenario 4  
rp.analysis(y.4)
```

4.4 Vary the Interaction Strength (See Text from Scenario 3)

```
b12 = actual interaction strength between Sp.1 and Sp.2 from -5 to +5  
b12=seq(0,1,by=0.01)  
b12.R will hold the nonlinear richness coefficients from each simulation  
b12.R=c()  
Cycle through each value of b12 and conduct the analysis  
for(i in 1:length(b12)) {  
  y.b12=Sp.matrix[,1]*Sp.matrix[,2]*b12[i]  
  lm.b12=rp.analysis(y.b12)  
  b12.R=cbind(b12.R,sum(sqrt(lm.b12[[3]]^2)))  
}  
Reproduce figure A2  
plot(b12.R[1,]~b12)
```

4.5 Vary Frequency of Interaction (i.e., Degree of Niche Overlap; See Scenario 4, Fig. 5)

```
niche.R will hold the NLR coefficient from each simulation  
niche.R=c()  
sp.niche holds the species “competitive abilities”  
sp.niche=c()  
for(i in 1:6) {sp.niche=cbind(sp.niche,Sp.matrix[,i]*sp.effects2[i])}  
Cycle through each value of niche overlap  
for(j in 1:6) {  
  y.niche holds the level of ecosystem functioning  
  y.niche=matrix(0,ncol=1,nrow=nrow(sp.niche))  
  if(j<5) {y.niche=y.niche+apply(sp.niche[, (j+1):6],1,sum)}  
  if(j>1) {y.niche=y.niche+apply(sp.niche[,1:j],1,max)}  
  if(j==5) {y.niche=y.niche+sp.niche[, (j+1)]}  
  Construct the linear models  
  lm.niche=rp.analysis(y.niche)  
  Output the relevant coefficients  
  niche.R=cbind(niche.R,sum(sqrt(lm.niche[[3]]^2)))  
}  
Reproduce figure 5  
plot(niche.R[1,]~c(1:6),type="l")
```