

Jin-Sheng He, Xiangping Wang, Dan F. B. Flynn, Liang Wang, Bernhard Schmid, and Jingyun Fang. 2009. Taxonomic, phylogenetic, and environmental trade-offs between leaf productivity and persistence. *Ecology* 90:2779–2791.

## **Appendix B. R and Genstat code used in the the analyses**

### **1. Correlations between two leaf traits for the population data, site means, species means, and residuals after fitting sites and species (Table 2 and Fig. 3).**

#### **#population data**

```
#use only records that have data for both LogLMA and LogAmass  
sub=subset(trait, trait$LogLMA!="NA") # trait: the population data  
sub=subset(sub, sub$LogAmass!="NA")
```

```
x=sub$LogLMA; y=sub$LogAmass  
cor.test(x, y) #Pearson correlation
```

```
library(smatr) #SMA slope and elevation  
line.cis(y, x, method=1)
```

#### **#site means:**

```
sub=subset(sitemean, sitemean$LogLMA!="NA") # sitemean: the site means data  
sub=subset(sub, sub$LogAmass!="NA")
```

```
x=sub$LogLMA; y=sub$LogAmass  
cor.test(x, y)  
line.cis(y, x, method=1)
```

#### **#species means:**

```
sub=subset(speciesmean, speciesmean$LogLMA!="NA") # speciesmean: the species means  
data  
sub=subset(sub, sub$LogAmass!="NA")
```

```
x=sub$LogLMA; y=sub$LogAmass  
cor.test(x, y)  
line.cis(y, x, method=1)
```

#### **#residual correlation:**

```
sub=subset(trait, trait$LogLMA!="NA"); sub=subset(sub, sub$LogAmass!="NA")
```

```
#calculating residual correlation  
x=resid(lm(LogLMA~Species+Site,data=sub))  
y=resid(lm(LogAmass~Species+Site,data=sub))  
cor.test(x, y)  
line.cis(y, x, method=1)
```

### **2. Analysis of covariance (Table 3 and Appendix C)**

```
#use only records that have data for both LogLMA and LogAmass  
sub=subset(trait, trait$LogLMA!="NA")  
sub=subset(sub, sub$LogAmass!="NA")
```

```
#Calculating the sum of squares for LogLMA and LogAmass:  
aov.d=anova(lm(LogLMA~MAT+MAP+AET+VPD+BD10+log(SOC10)+log(TN10)+Veget  
ation+Site+Funcgr+Leg+Family+Genus+Species,data=sub))
```

```
aov.d=anova(lm(LogAmass~MAT+MAP+AET+VPD+BD10+log(SOC10)+log(TN10)+Vegetation+Site+Funcgr+Leg+Family+Genus+Species,data=sub))
```

```
write.table(aov.d,"clipboard",sep="\t",col.names=NA)#Paste the ANOVA table to Excel
```

```
#Calculating the sum of squares for LogLMA+LogAmass:
```

```
sum=sub$LogLMA+sub$LogAmass
```

```
aov.d=anova(lm(sum~MAT+MAP+AET+VPD+BD10+log(SOC10)+log(TN10)+Vegetation+Site+Funcgr+Leg+Family+Genus+Species,data=sub))
```

```
write.table(aov.d,"clipboard",sep="\t",col.names=NA)
```

```
#The subsequent analysis was done manually in Excel.
```

### 3. REML-covariance-analysis (Appendix D)

Genstat code (Payne, R. W., P. W. Lane, P. G. N. Digby, S. A. Harding, P. K. Leech, G. W. Morgan, et al. 1993. Genstat 5, Release 3, Reference manual. Clarendon Press, Oxford.):

```
calculate sum=LogLMA+LogAmass
```

```
for Y=LogLMA,LogAmass,sum
```

```
  vcomp constr=pos :reml Y          "total"
```

```
  vcomp random=SI;constr=pos :reml Y    "site"
```

```
  vcomp [fixed=SP] random=SI;constr=pos :reml Y    "site | species"
```

```
  vcomp random=SP;constr=pos :reml Y    "species"
```

```
  vcomp [fixed=SI] random=SP;constr=pos :reml Y    "species | site"
```

```
  vcomp [fixed=SI+SP];constr=pos :reml Y
```

```
endfor
```

"Further models were fitted in which SI or SP were decomposed into contrasts and

'residual' SI or SP, e.g.

```
vcomp [fixed=MAT+MAP+AET+VPD+BD10+SOC10+TN10] random=SI;c=pos :reml Y"
```

"The subsequent analysis was done manually in Excel as explained at the end of the R code given above."