## #### Species Information Database Query, Distribution Maps - Access to the R package of the Global Flora and Trait Database

library(devtools)

library("GIFT")

library("dplyr")

library(ggplot2)

library("sf")

library("rnaturalearth")

library("rnaturalearthdata")

library("tidyr")

library("patchwork")

anemone\_lookup <- GIFT\_species\_lookup(genus = "Anemone", epithet = "nemorosa")

kable(anemone\_lookup, "html") %>%

kable\_styling(full\_width = FALSE)

#############download of checklists of western\_mediterranean

ex\_meta <- GIFT\_checklists(taxon\_name = "Angiospermae",

shp = western\_mediterranean,

overlap = "centroid\_inside",

list\_set\_only = TRUE)

medit <- GIFT\_checklists(taxon\_name = "Angiospermae",

complete\_taxon = TRUE,

floristic\_group = "native",

complete\_floristic = TRUE,

geo\_type = "All",

shp = western\_mediterranean,

overlap = "centroid\_inside",

remove\_overlap = FALSE,

taxonomic\_group = TRUE) # this argument adds two

########################################trait extraction

trait\_meta <- GIFT\_traits\_meta()

trait\_meta[which(trait\_meta$Trait1 == "Leaf size"), ]

lsize <- GIFT\_traits(trait\_IDs = c("4.4.3"), agreement = 0.66,

bias\_ref = FALSE, bias\_deriv = FALSE)

lsize\_raw <- GIFT\_traits\_raw(trait\_IDs = c("4.4.3"))

as.numeric(lsize\_raw[which(lsize\_raw$work\_species == "Robinia pseudoacacia"),

"trait\_value"])

as.numeric(lsize[which(lsize$work\_species == "Robinia pseudoacacia"),

"trait\_value\_4.4.3"])

###Seed mass####1 grain weight, unit g

trait\_meta[which(trait\_meta$Trait1 == "Seed mass"), ]

seed <- GIFT\_traits(trait\_IDs = c("3.2.3"), agreement = 0.66,

bias\_ref = FALSE, bias\_deriv = FALSE)

seed\_raw <- GIFT\_traits\_raw(trait\_IDs = c("3.2.3"))

as.numeric(seed[which(seed$work\_species == "Rhapis excelsa"), ###平均值

"trait\_value\_3.2.3"])

######Plant height

trait\_meta[which(trait\_meta$Trait1 == "Plant height"), ]

height <- GIFT\_traits(trait\_IDs = c("1.6.2"), agreement = 0.66,

bias\_ref = FALSE, bias\_deriv = FALSE)

height\_raw <- GIFT\_traits\_raw(trait\_IDs = c("1.6.2"))

# Raw values

as.numeric(height\_raw[which(height\_raw$work\_species == "Fagus sylvatica"),

"trait\_value"])

# Aggregated value

as.numeric(height[which(height$work\_species == "Fagus sylvatica"),

"trait\_value\_1.6.2"])

## ###############Trait comparison

library(MASS)

library(plyr)

aa <- read.csv ("trait箱线.csv",header=T)

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(Seed, na.rm=TRUE),

sd = sd(Seed,na.rm=TRUE),

n = sum(!is.na(Seed)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.6, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Seed dry mass" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20),legend.text=element\_text(size=25))

P1<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P1

aa <- read.csv ("trait箱线.csv",header=T)

aa <- read.csv ("trait箱线-菊科.csv",header=T)

aa <- read.csv ("trait箱线-苋科.csv",header=T)

aa <- read.csv ("trait箱线-十字蝶.csv",header=T)

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(abundance1, na.rm=TRUE),

sd = sd(abundance1,na.rm=TRUE),

n = sum(!is.na(abundance1)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Abundance in spring" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P1<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P1

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(abundance2, na.rm=TRUE),

sd = sd(abundance2,na.rm=TRUE),

n = sum(!is.na(abundance2)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Abundance in summer" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P2<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P2

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(coverage1, na.rm=TRUE),

sd = sd(coverage1,na.rm=TRUE),

n = sum(!is.na(coverage1)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Coverage in spring" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P3<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P3

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(coverage2, na.rm=TRUE),

sd = sd(coverage2,na.rm=TRUE),

n = sum(!is.na(coverage2)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Coverage in summer" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P4<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P4

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(frequency1, na.rm=TRUE),

sd = sd(frequency1,na.rm=TRUE),

n = sum(!is.na(frequency1)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Frequency in spring" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P5<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P5

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(frequency2, na.rm=TRUE),

sd = sd(frequency2,na.rm=TRUE),

n = sum(!is.na(frequency2)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Frequency in summer" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P6<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P6

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(Height, na.rm=TRUE),

sd = sd(Height,na.rm=TRUE),

n = sum(!is.na(Height)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Height" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P7<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P7

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(Leaf, na.rm=TRUE),

sd = sd(Leaf,na.rm=TRUE),

n = sum(!is.na(Leaf)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Leaf size" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P8<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P8

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(Dinflores, na.rm=TRUE),

sd = sd(Dinflores,na.rm=TRUE),

n = sum(!is.na(Dinflores)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Inflorescence diameter/length" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P9<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P9

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(Ninflores, na.rm=TRUE),

sd = sd(Ninflores,na.rm=TRUE),

n = sum(!is.na(Ninflores)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Number of florets per inflorescence" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P10<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P10

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(Dflower, na.rm=TRUE),

sd = sd(Dflower,na.rm=TRUE),

n = sum(!is.na(Dflower)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Flower diameter" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P11<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P11

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(Lfruit, na.rm=TRUE),

sd = sd(Lfruit,na.rm=TRUE),

n = sum(!is.na(Lfruit)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Fruit length" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P12<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P12

ca <- ddply(aa, c("origin"), summarise,

meanb = mean(Seed, na.rm=TRUE),

sd = sd(Seed,na.rm=TRUE),

n = sum(!is.na(Seed)),

se = sd/sqrt(n))

ca

P <- ggplot(ca, mapping =aes(origin, meanb,color=origin,fill=origin)) +

geom\_errorbar(aes(ymin=meanb-se, ymax=meanb+se),

width=0.5, size=1.2, position=position\_dodge(0.3)) +

geom\_line(position=position\_dodge(0.6),size=2,col= "#45818e") +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Seed dry mass" )+

theme(axis.title = element\_text(size=22),######坐标轴字体大小

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )

P13<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P13

pdf("Figtrait箱线.pdf",width=27.3,height=9.3)

ggarrange(P1,P2,P3,P4,P5, P6,P7,P8, P9,P10,P11,P12,P13,

ncol=7, nrow=2)

dev.off()

###

aa <- read.csv ("trait箱线-功能数.csv",header=T)

P <- ggplot(aa, aes(x = origin, y = funcN, color = origin)) +

geom\_boxplot(size = 1.6) + theme(panel.grid=element\_blank() )+ theme\_bw()+ theme(axis.title = element\_text(size=19),

axis.text = element\_text(size=14),legend.text=element\_text(size=14),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Species type", y="Function number")

P1<- P+scale\_color\_manual(values =c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+scale\_fill\_manual(values = c(anative="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))

P1

my\_com <- list(c ("anative","exotic"),c("anative","exotic.in"),c("exotic","exotic.in"))

compare\_means(abundance1 ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(abundance2 ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(coverage1 ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(coverage2 ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(frequency1 ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(frequency2 ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(Height ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(Leaf ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(Dinflores ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(Ninflores ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(Dflower ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(Lfruit ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(Seed ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

compare\_means(funcN ~ origin,data= aa, method= "wilcox.test", paired= FALSE)

ggplot(aa, mapping =aes(origin, abundance2)) + geom\_boxplot(width = 0.6, size= 0.7) +

geom\_point(position=position\_dodge(0.6),size=4.2)+ theme\_bw()+labs(x="Species type", y="Leaf size" )+

theme(axis.title = element\_text(size=22),

axis.text = element\_text(size=20))+theme(panel.grid=element\_blank(),legend.position = "No" )+

geom\_signif(comparisons = my\_com, step\_increase = 0.04,

map\_signif\_level = T,

test=wilcox.test,size=1,

textsize=5)

library(ggplot2)

library(reshape2)

aa <- read.csv ("trait箱线.csv",header=T)

ggplot(aa,aes(Lfruit))+

geom\_histogram(aes(y=..count..),

binwidth = 10,fill="#f8ed83")+

scale\_x\_continuous(limits = c(0,240))+ theme\_bw() +theme(panel.grid=element\_blank() )

########################################################upset plot

library(UpSetR)#

library(ggplot2)

library(ComplexUpset)

sets <- read.csv ("upset.csv",header=T)

library(ggpattern)

P<- upset(sets,genres,name = "Blossom time",

width\_ratio = 0.1,height\_ratio =0.6, annotations = list(

'Ninflores'=ggplot(mapping = aes(y = Ninflores)) +

geom\_boxplot(alpha=0.5,na.rm = T)+theme (axis.title = element\_text(size=20),

axis.text = element\_text(size=18))+theme(panel.grid=element\_blank() ),

'Dinflores'=ggplot(mapping = aes(y = Dinflores)) +

geom\_boxplot(alpha=0.5,na.rm = T)+theme (axis.title = element\_text(size=20),

axis.text = element\_text(size=18))+theme(panel.grid=element\_blank() ),

'Dflower'=ggplot(mapping = aes(y = Dflower)) +

geom\_boxplot(alpha=0.5,na.rm = T)+theme (axis.title = element\_text(size=20),

axis.text = element\_text(size=18))+theme(panel.grid=element\_blank() ),

'Tinflores'=(

ggplot(mapping=aes(fill=Tinflores, pattern=Tinflores))

+ geom\_bar(stat='count',position='fill' )+ scale\_y\_continuous(labels=scales::percent\_format())

+ geom\_bar\_pattern(aes(pattern=Tinflores,pattern\_angle= Tinflores),fill= "white",color="black",pattern\_spacing=0.03)

+theme (axis.title = element\_text(size=20),

axis.text = element\_text(size=18))+theme(panel.grid=element\_blank())

+ ylab('Inflorescence type'))

),

sort\_sets = FALSE,sort\_intersections\_by =c('degree', 'cardinality'), base\_annotations = list(

"intersection size" = intersection\_size(

counts = F,

mapping = aes(fill=origin)

)

+ scale\_fill\_manual(values = c(native="#24325f",exotic = "#f0c929",exotic.in = "#82491e"))+theme (axis.title = element\_text(size=20),

axis.text = element\_text(size=18))+theme(panel.grid=element\_blank())

)

)

P +theme (axis.title = element\_text(size=20),

axis.text = element\_text(size=18))

**################For qualitative traits, mosaic charts were used for comparison**

library(vcd)

library(gnm)

library(vcdExtra)

library(MASS)

install.packages("vcdExtra",type="binary")

b <- read.csv ("mosaic.csv",header=T)

art <- xtabs(~ origin + type, data = b)

art <- xtabs(~ origin + habit, data = b)

art <- xtabs(~ origin + Monocotyledons, data = b)

art <- xtabs(~ origin + NitrogenFixer, data = b)

art <- xtabs(~ origin + Leafphenology, data = b)

art <- xtabs(~ origin + Leafcompoundness, data = b)

art <- xtabs(~ origin + Leafshape, data = b)

art <- xtabs(~ origin + Leafmargin, data = b)

art <- xtabs(~ origin + Fperiod, data = b)

art <- xtabs(~ origin + Tinflores, data = b)

art <- xtabs(~ origin + Fcolor, data = b)

art <- xtabs(~ origin + Fsymmetry, data = b)

art <- xtabs(~ origin + Fshape, data = b)

art <- xtabs(~ origin + fruittype, data = b)

art <- xtabs(~ origin + Pollination, data = b)

art <- xtabs(~ origin + Dispersal, data = b)

b <- read.csv ("mosaic-function.csv",header=T)

art <- xtabs(~ origin + func, data = b)

art

mosaic(art, gp = shading\_Friendly)

mosaic(art, gp = shading\_max)

## ############ Phylogenetic tree

library(phytools)

library(caper)

library(rotl)

devtools::install\_github("jinyizju/V.PhyloMaker")

devtools::install\_github("helixcn/plantlist")

library(V.PhyloMaker)

library(plantlist)

library(picante)

example <- read.csv("species list.csv")

# generate the phylogeny presented in Figure 1a

tree.a <- phylo.maker(sp.list=example, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

write.tree(tree.a$scenario.3,"Figure.1a.tre")

# generate the phylogeny presented in Figure 1b

rel <- bind.relative(sp.list=example, tree=GBOTB.extended, nodes=nodes.info.1 )

tree.b <- phylo.maker(sp.list=rel$species.list, tree=rel$phylo,nodes=rel$nodes.info, scenarios="S3")

write.tree(tree.b$scenario.3,"Figure.1b.tre")

tree.a

tree.aa <- tree.a$scenario.3

tree.aa

###The phylogenetic signal was assessed using the λ metric, calculated the λ metric of species RFR using the phylosig function in the R package phytools

## load data from Mahler et al. (2010)

data(anoletree)

data(anole.data)

## run phylogenetic PCA

pca<-phyl.pca(anoletree,anole.data)

print(pca)

## plot results

plot(pca)

biplot(pca)

anoletree

anole.data

##Computes phylogenetic signal using two different methods

trait <- read.csv("trait.csv",row.names = 1) ###row.names=1

trait

ln.Seed<-log(setNames(trait$Seed,

rownames(trait)))

ln.Height<-log(setNames(trait$Height,

rownames(trait)))

ln.Leaf<-log(setNames(trait$Leafsize,

rownames(trait)))

ln.Nflorets<-log(setNames(trait$Nflorets,

rownames(trait)))

ln.Dinflor<-log(setNames(trait$Dinflor,

rownames(trait)))

ln.Dflower<-log(setNames(trait$Dflower,

rownames(trait)))

ln.Lfruit<-log(setNames(trait$Lfruit,

rownames(trait)))

ln.freq<-log(setNames(trait$freq,

rownames(trait)))

ln.abund<-log(setNames(trait$abund,

rownames(trait)))

ln.cover<-log(setNames(trait$cover,

rownames(trait)))

## compute phylogenetic signal lambda##

lambda.Seed<-phylosig(tree.aa,ln.Seed,

method="lambda",test=TRUE)

print(lambda.Seed)

plot(lambda.Seed)

lambda.Height<-phylosig(tree.aa,ln.Height,

method="lambda",test=TRUE)

print(lambda.Height)

plot(lambda.Height)

lambda.Leaf<-phylosig(tree.aa,ln.Leaf,

method="lambda",test=TRUE)

print(lambda.Leaf)

plot(lambda.Leaf)

lambda.Nflorets<-phylosig(tree.aa,ln.Nflorets,

method="lambda",test=TRUE)

print(lambda.Nflorets)

plot(lambda.Nflorets)

lambda.Dinflor<-phylosig(tree.aa,ln.Dinflor,

method="lambda",test=TRUE)

print(lambda.Dinflor)

plot(lambda.Dinflor)

lambda.Dflower<-phylosig(tree.aa,ln.Dflower,

method="lambda",test=TRUE)

print(lambda.Dflower)

plot(lambda.Dflower)

lambda.Lfruit<-phylosig(tree.aa,ln.Lfruit,

method="lambda",test=TRUE)

print(lambda.Lfruit)

plot(lambda.Lfruit)

lambda.freq<-phylosig(tree.aa,ln.freq,

method="lambda",test=TRUE)

print(lambda.freq)

plot(lambda.freq)

lambda.abund<-phylosig(tree.aa,ln.abund,

method="lambda",test=TRUE)

print(lambda.abund)

plot(lambda.abund)

lambda.cover<-phylosig(tree.aa,ln.cover,

method="lambda",test=TRUE)

print(lambda.cover)

plot(lambda.cover)

tree <- read.csv("species list-seed.csv")

tree <- read.csv("species list-leaf.csv")

tree <- read.csv("species list-Nflor.csv")

tree <- read.csv("species list-Dinflor.csv")

tree <- read.csv("species list-Dflower.csv")

tree <- read.csv("species list-Lfruit.csv")

# generate the phylogeny presented in Figure 1a

tree.b <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.bb <- tree.b$scenario.3

tree.bb

#####

trait <- read.csv("trait-seed.csv",row.names = 1)

ln.seed<-log(setNames(trait$Seed,

rownames(trait)))

lambda.seed<-phylosig(tree.bb,ln.seed,

method="lambda",test=TRUE)

print(lambda.seed)

trait <- read.csv("trait-leaf.csv",row.names = 1)

ln.Leaf<-log(setNames(trait$Leafsize,

rownames(trait)))

lambda.Leaf<-phylosig(tree.bb,ln.Leaf,

method="lambda",test=TRUE)

print(lambda.Leaf)

trait <- read.csv("trait-Nflor.csv",row.names = 1)

ln.Nflor<-log(setNames(trait$Nflorets,

rownames(trait)))

lambda.Nflor<-phylosig(tree.bb,ln.Nflor,

method="lambda",test=TRUE)

print(lambda.Nflor)

trait <- read.csv("trait-Dinflor.csv",row.names = 1)

ln.Dinflor<-log(setNames(trait$Dinflor,

rownames(trait)))

lambda.Dinflor<-phylosig(tree.bb,ln.Dinflor,

method="lambda",test=TRUE)

print(lambda.Dinflor)

trait <- read.csv("trait-Dflower.csv",row.names = 1)

ln.Dflor<-log(setNames(trait$Dflower,

rownames(trait)))

lambda.Dflor<-phylosig(tree.bb,ln.Dflor,

method="lambda",test=TRUE)

print(lambda.Dflor)

trait <- read.csv("trait-Lfruit.csv",row.names = 1)

ln.Lfruit<-log(setNames(trait$Lfruit,

rownames(trait)))

lambda.Lfruit<-phylosig(tree.bb,ln.Lfruit,

method="lambda",test=TRUE)

print(lambda.Lfruit)

## ####### library(phylosignal) The relationship between trait and evolutionary tree

library(phylosignal)

library(ape)

library(phylobase)

#### Asteraceae

tree <- read.csv("species list-Asteraceae.csv")

tree.c <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.cc <- tree.c$scenario.3

tree.cc

traitA <- read.csv("trait-Aster.csv",row.names = 1)

traitA

### Example using a tree of class 'phylo4'

tree.cc <- as(tree.cc, "phylo4")

tree.cc

## using 'merge.data'

?phylo4d

Aster<- (matchData <- phylo4d(tree.cc, tip.data=traitA, merge.data=TRUE))

Aster

barplot.phylo4d(Aster)

phyloSignal(Aster)

Height.cg <- phyloCorrelogram(Aster, trait = "Height")

Leafsize.cg <- phyloCorrelogram(Aster,

trait = "Leafsize")

Dflower.cg <- phyloCorrelogram(Aster, trait = "Dflower")

freq.cg <- phyloCorrelogram(Aster, trait = "freq")

abund.cg <- phyloCorrelogram(Aster, trait = "abund")

cover.cg <- phyloCorrelogram(Aster, trait = "cover")

plot(Height.cg)

plot(Leafsize.cg)

plot(Dflower.cg)

plot(freq.cg)

plot(abund.cg)

plot(cover.cg)

### compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Aster, trait = "Height",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "Height",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###

local.i <- lipaMoran(Aster, trait = "Leafsize",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "Leafsize",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###

local.i <- lipaMoran(Aster, trait = "Dflower",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "Dflower",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###

local.i <- lipaMoran(Aster, trait = "freq",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "freq",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###

local.i <- lipaMoran(Aster, trait = "abund",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "abund",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###

local.i <- lipaMoran(Aster, trait = "cover",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "cover",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

##############

tree <- read.csv("species list-Asterseed.csv")

tree <- read.csv("species list-AsterNflor.csv")

tree <- read.csv("species list-AsterDinflor.csv")

tree <- read.csv("species list-AsterLfruit.csv")

tree.c <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.cc <- tree.c$scenario.3

tree.cc

traitA <- read.csv("trait-Asterseed.csv",row.names = 1)

traitA <- read.csv("trait-AsterNflor.csv",row.names = 1)

traitA <- read.csv("trait-AsterDinflor.csv",row.names = 1)

traitA <- read.csv("trait-AsterLfruit.csv",row.names = 1)

traitA

### Example using a tree of class 'phylo4'

tree.cc <- as(tree.cc, "phylo4")

tree.cc

## using 'merge.data'

Aster<- (matchData <- phylo4d(tree.cc, tip.data=traitA, merge.data=TRUE))

Aster

barplot.phylo4d(Aster)

phyloSignal(Aster)

### compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Aster, trait = "Seed",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "Seed",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

### compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Aster, trait = "Nflorets",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "Nflorets",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

## compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Aster, trait = "Dinflor",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "Dinflor",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Aster, trait = "Lfruit",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Aster, trait = "Lfruit",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

#############Amaranthaceae et al.

tree <- read.csv("species list-Amaranthaceae.csv")

tree.c <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.cc <- tree.c$scenario.3

tree.cc

traitA <- read.csv("trait-Amaranthaceae.csv",row.names = 1)

traitA

### using a tree of class 'phylo4'

tree.cc <- as(tree.cc, "phylo4")

tree.cc

## using 'merge.data'

Amaran<- (matchData <- phylo4d(tree.cc, tip.data=traitA, merge.data=TRUE))

Amaran

barplot.phylo4d(Amaran)

phyloSignal(Amaran)

### compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Amaran, trait = "Seed",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "Seed",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

### compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Amaran, trait = "Height",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "Height",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(Amaran, trait = "Leafsize",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "Leafsize",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(Amaran, trait = "Dflower",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "Dflower",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(Amaran, trait = "freq",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "freq",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(Amaran, trait = "abund",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "abund",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(Amaran, trait = "cover",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "cover",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

tree <- read.csv("species list-AmaranNflorets.csv")

tree <- read.csv("species list-AmaranDinflor.csv")

tree <- read.csv("species list-AmaranLfruit.csv")

tree.c <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.cc <- tree.c$scenario.3

tree.cc

traitA <- read.csv("trait-AmaranNflorets.csv",row.names = 1)

traitA <- read.csv("trait-AmaranDinflor.csv",row.names = 1)

traitA <- read.csv("trait-AmaranLfruit.csv",row.names = 1)

traitA

### Example using a tree of class 'phylo4'

tree.cc <- as(tree.cc, "phylo4")

tree.cc

## using 'merge.data'

Amaran<- (matchData <- phylo4d(tree.cc, tip.data=traitA, merge.data=TRUE))

Amaran

###画图compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Amaran, trait = "Nflorets",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "Nflorets",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Amaran, trait = "Dinflor",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "Dinflor",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Amaran, trait = "Lfruit",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Amaran, trait = "Lfruit",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

#################### Fabaceae and Brassicaceae

tree <- read.csv("species list-FabBra.csv")

tree.c <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.cc <- tree.c$scenario.3

tree.cc

traitA <- read.csv("trait-FabBra.csv",row.names = 1)

traitA

### using a tree of class 'phylo4'

tree.cc <- as(tree.cc, "phylo4")

tree.cc

## using 'merge.data'

FabBra<- (matchData <- phylo4d(tree.cc, tip.data=traitA, merge.data=TRUE))

FabBra

barplot.phylo4d(FabBra)

phyloSignal(FabBra)

### compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(FabBra, trait = "Height",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "Height",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(FabBra, trait = "Leafsize",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "Leafsize",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(FabBra, trait = "Dflower",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "Dflower",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(FabBra, trait = "Nflorets",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "Nflorets",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(FabBra, trait = "Lfruit",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "Lfruit",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(FabBra, trait = "freq",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "freq",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(FabBra, trait = "abund",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "abund",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

local.i <- lipaMoran(FabBra, trait = "cover",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "cover",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

##############################

tree <- read.csv("species list-FabBraDin.csv")

tree <- read.csv("species list-FabBraSeed.csv")

tree.c <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.cc <- tree.c$scenario.3

tree.cc

traitA <- read.csv("trait-FabBraDin.csv",row.names = 1)

traitA <- read.csv("trait-FabBraSeed.csv",row.names = 1)

traitA

### Example using a tree of class 'phylo4'

tree.cc <- as(tree.cc, "phylo4")

tree.cc

## using 'merge.data'

FabBra<- (matchData <- phylo4d(tree.cc, tip.data=traitA, merge.data=TRUE))

FabBra

###画图compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(FabBra, trait = "Dinflor",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "Dinflor",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

### compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(FabBra, trait = "Seed",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(FabBra, trait = "Seed",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col) ##导出3.665X4 少了3个物种的距离

#################### Poaceae

tree <- read.csv("species list-Poa.csv")

tree.c <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.cc <- tree.c$scenario.3

tree.cc

traitA <- read.csv("trait-Poa.csv",row.names = 1)

traitA

### using a tree of class 'phylo4'

tree.cc <- as(tree.cc, "phylo4")

tree.cc

## using 'merge.data'

Poa<- (matchData <- phylo4d(tree.cc, tip.data=traitA, merge.data=TRUE))

Poa

barplot.phylo4d(Poa)

phyloSignal(Poa)

###画图compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Poa, trait = "Height",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "Height",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(Poa, trait = "Leafsize",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "Leafsize",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(Poa, trait = "Dflower",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "Dflower",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(Poa, trait = "Nflorets",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "Nflorets",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(Poa, trait = "Lfruit",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "Lfruit",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(Poa, trait = "freq",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "freq",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(Poa, trait = "abund",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "abund",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(Poa, trait = "cover",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "cover",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

###画图

local.i <- lipaMoran(Poa, trait = "Dinflor",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "Dinflor",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col)

##############################

tree <- read.csv("species list-PoaSeed.csv")

tree.c <- phylo.maker(sp.list=tree, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S3")

tree.cc <- tree.c$scenario.3 ######转化成可用的正常的phylo树格式

tree.cc

traitA <- read.csv("trait-PoaSeed.csv",row.names = 1)

traitA

### Example using a tree of class 'phylo4'

tree.cc <- as(tree.cc, "phylo4")

tree.cc

## using 'merge.data'

Poa<- (matchData <- phylo4d(tree.cc, tip.data=traitA, merge.data=TRUE))

Poa

###画图compute local Moran’s I for each species to detect hotspots of autocorrelation in Height, leafsize...

local.i <- lipaMoran(Poa, trait = "Seed",

prox.phylo = "nNodes",

as.p4d = TRUE)

points.col <- lipaMoran(Poa, trait = "Seed",

prox.phylo = "nNodes")$p.value

points.col <- ifelse(points.col < 0.05, "red", "#24325f")

dotplot.phylo4d(local.i, dot.col = points.col) ##导出3.955X4

## ########### Logistic regression

dd <- read.csv ("逻辑回归-native春季.csv",header=T)

dd <- read.csv ("逻辑回归-native夏季.csv",header=T)

#数据标准化 Z-score

dd<-scale(dd)

write.csv(dd,"逻辑回归夏.csv")

dd <- read.csv ("逻辑回归春.csv",header=T)

dd <- read.csv ("逻辑回归夏.csv",header=T)

model <- glm(RE~RN,family = "binomial",data = dd)

model <- glm(RE~FDN,family = "binomial",data = dd)

model <- glm(RE~CoverageN,family = "binomial",data = dd)

model <- glm(RE~HeightN,family = "binomial",data = dd)

model <- glm(RE~LeafSN,family = "binomial",data = dd)

model <- glm(RE~InDN,family = "binomial",data = dd)

model <- glm(RE~InNN,family = "binomial",data = dd)

model <- glm(RE~FlowerDN,family = "binomial",data = dd)

model <- glm(RE~FruitLN,family = "binomial",data = dd)

model <- glm(RE~SeedN,family = "binomial",data = dd)

summary(model)

glm.logodd <- predict(model,newdata = dd)

head(glm.logodd)

head(exp(glm.logodd))

#P（y=1/X)

glm.pro <- predict(model,newdata = dd,type = "response")

head(glm.pro)

model.predict<- ifelse(glm.pro>0.5,1,0)

head(model.predict)

table(dd$RE,model.predict)

dd$pro\_hat <- glm.pro

dd$random\_data <- runif(dd$RN)

library(data.table)

roc\_data<- reshape2::melt(dd[,c(1,22,23)],id.vars="RE",variable.name = "class",value.name ="response")

library(plotROC)

ggroc <- ggplot(roc\_data, aes(d=RE, m=response, color=class)) +

geom\_roc() +

scale\_color\_discrete(name = "class", labels = c("logit", "Random")) +

geom\_abline() +scale\_color\_manual(values = c("#ff829a", "#0000ff"))+theme\_bw()+theme(panel.grid=element\_blank())

ggroc

## ################Species correlation net -ggraph

library(tidygraph)

library(ggplot2)

library(ggraph)

library(ggrepel)

#####edges

library(corrplot)

library(psych)

cc <- read.csv ("correlation物种夏.csv", header=T)

corr\_matrix <- corr.test(cc, method = 'spearman')

corr\_matrix$r

corr\_matrix$p

corr<-corr\_matrix$r

corrP<-corr\_matrix$p

write.table(corr ,"corr.csv")

write.table(corrP ,"corrP.csv")

rm(list = ls())

nodes<- read.csv ("nodes夏.csv",header=T)

edges<- read.csv ("edges夏.csv",header=T)

graph <- tbl\_graph(nodes = nodes, edges = edges, directed = F)

PP<-ggraph(graph, layout = 'linear', circular = T) +

geom\_edge\_fan(aes(color = correlation, width = width),strength=3) +

scale\_edge\_width(range = c(1.5,2.5)) +

scale\_edge\_color\_manual(values = c('#FFA2A4','#C9DBED')) +

geom\_node\_point(aes(size = Abundance,fill=Cluster),shape=21) +

scale\_fill\_manual(values = c('#3A76A9','#D13021','#FDBF7B','#804B23','#81D8DD')) +

scale\_size(range = c(8,20)) +

geom\_node\_point(aes(color=Origin),size=3.1) + geom\_node\_label(aes(label = species,colour=Origin),

repel = TRUE,position = position\_nudge\_repel(x = c(0.1, 0.15, -0.1, -0.15),y = c(0.1, 0.15, -0.1, -0.15)),angle=1,size=3.5,fontface="italic",alpha=0.85) +

theme\_graph()

PP

PP<-PP+ scale\_fill\_rickandmorty()+ scale\_color\_jco()

PP

###导出PDF12.5改成16

pdf("CCor.pdf",width=16,height=11)

print(PP)

dev.off()

## #########The influence of focal species on community richness

aa <- read.delim("clipboard",header=T)

G <-ggplot(aa, mapping =aes(abund,Rplot,color=origin, shape=cluster) )+geom\_point(size=1.6,alpha=0.75,color="darkgrey")+

geom\_smooth(se=TRUE,size=1.5,alpha=0.35)+

theme\_bw() +theme(panel.grid=element\_blank() )+ facet\_grid(.~ spe)

G <- G + scale\_fill\_rickandmorty()+ scale\_color\_rickandmorty()

G

aa <- read.delim("clipboard",header=T)

G1 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#f0c929")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.35, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values ="#f0c929")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Cardamine flexuosa")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G1

aa <- read.delim("clipboard",header=T)

G2 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=15,alpha=0.75,color="#f0c929")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.35, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#f0c929")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Tradescantia fiumiensis")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G2

aa <- read.delim("clipboard",header=T)

G3 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#f0c929")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.35, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#f0c929")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Trifolium repens")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G3

aa <- read.delim("clipboard",header=T)

G4 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#f0c929")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.35, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#f0c929")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Veronica persica")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G4

aa <- read.delim("clipboard",header=T)

G5 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Alternanthera philoxeroides")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G5

aa <- read.delim("clipboard",header=T)

G6 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Erigeron canadensis")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G6

aa <- read.delim("clipboard",header=T)

G7 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Erigeron sumatrensis")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G7

aa <- read.delim("clipboard",header=T)

G8 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=15,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Oxalis martiana")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G8

aa <- read.delim("clipboard",header=T)

G9 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Oxalis corniculata")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G9

aa <- read.delim("clipboard",header=T)

G10 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Phragmites australis")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G10

aa <- read.delim("clipboard",header=T)

G11 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Polygonum posumbu")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G11

aa <- read.delim("clipboard",header=T)

G12 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=15,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Polygonum runcinatum var. sinense")+theme(plot.title= element\_text(size=13.1,face="italic",hjust=0.8,vjust=-8))

G12

aa <- read.delim("clipboard",header=T)

G13 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Stellaria media")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G13

aa <- read.delim("clipboard",header=T)

G14 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Youngia japonica")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G14

pdf("Fig典型物种.pdf",width=24,height=6)

ggarrange(G1,G2,G3,G4,G5,G6,G7,G8,G9,G10,G11,G12,G13,G14,

ncol=7, nrow=2)

dev.off()

######################summer

aa <- read.delim("clipboard",header=T)

G1 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=15,alpha=0.75,color="#f0c929")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.35, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#f0c929")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Crassocephalum crepidioides")+theme(plot.title= element\_text(size=14.3,face="italic",hjust=0.8,vjust=-8))

G1

aa <- read.delim("clipboard",header=T)

G2 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#f0c929")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.35, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#f0c929")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Galinsoga parviflora")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G2

aa <- read.delim("clipboard",header=T)

G3 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=15,alpha=0.75,color="#f0c929")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.35, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#f0c929")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Talinum paniculatum")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G3

aa <- read.delim("clipboard",header=T)

G4 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.35, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Alternanthera philoxeroides")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G4

aa <- read.delim("clipboard",header=T)

G5 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Bidens pilosa")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G5

aa <- read.delim("clipboard",header=T)

G6 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Erigeron canadensis")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G6

aa <- read.delim("clipboard",header=T)

G7 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=15,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Ipomoea purpurea")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G7

aa <- read.delim("clipboard",header=T)

G8 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#82491e")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#82491e")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Symphyotrichum subulatum")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G8

aa <- read.delim("clipboard",header=T)

G9 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Artemisia argyi")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G9

aa <- read.delim("clipboard",header=T)

G10 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Broussonetia papyrifera")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G10

aa <- read.delim("clipboard",header=T)

G11 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Digitaria sanguinalis")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G11

aa <- read.delim("clipboard",header=T)

G12 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Humulus scandens")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G12

aa <- read.delim("clipboard",header=T)

G13 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=17,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Polygonum posumbu")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G13

aa <- read.delim("clipboard",header=T)

G14 <-ggplot(aa, mapping =aes(abund,Rplot) )+geom\_point(size=3, shape=16,alpha=0.75,color="#24325f")+

geom\_smooth(se=FALSE,size=1.3,alpha=0.3, color="black")+

theme\_bw() +theme(panel.grid=element\_blank() )+ scale\_color\_manual(values = "#24325f")+ theme(axis.title = element\_text(size=16),

axis.text = element\_text(size=15),legend.text=element\_text(size=15),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Abundance in community",

y="Species richness of community") + ggtitle ("Setaria viridis")+theme(plot.title= element\_text(size=15,face="italic",hjust=0.8,vjust=-8))

G14

######

pdf("Fig典型物种夏.pdf",width=24,height=6)

ggarrange(G1,G2,G3,G4,G5,G6,G7,G8,G9,G10,G11,G12,G13,G14,

ncol=7, nrow=2)

dev.off()

#########

aa <- read.delim("clipboard",header=T)

GGT<-ggplot(aa, aes(x = spes, y = Rplot, color = origin)) +

geom\_boxplot(size = 0.9, varwidth = FALSE) + theme\_grey() + theme(axis.title = element\_text(size=14),

axis.text = element\_text(size=11),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Typical species",

y="Species richness of community") + theme(legend.position = 'none')

GGT<- GGT + scale\_fill\_rickandmorty()+ scale\_color\_rickandmorty()

GGT <- GGT+ geom\_signif(comparisons = list(c("1Tri.rep","2Eri.can"),c("1Tri.rep","3Pol.pos"),c("2Eri.can","3Oxa.cor"),

c("1Tra.fiu","3Oxa.cor"),c("1Tri.rep","1Tra.fiu"),

c("3Pol.pos","3Oxa.cor")),

test = t.test,textsize = 7,vjust=0.7,

y\_position = c(26,27.5,29,24.5,21.5,26),

tip\_length = c(c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05)),

size=0.5,color="black", map\_signif\_level = T)

GGT

aa <- read.delim("clipboard",header=T)

GGT2<-ggplot(aa, aes(x = spes, y = Rplot, color = origin)) +

geom\_boxplot(size = 0.9, varwidth = FALSE) + theme\_grey() + theme(axis.title = element\_text(size=14),

axis.text = element\_text(size=11),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Typical species",

y="Species richness of community") + theme(legend.position = 'none')

GGT2<- GGT2 + scale\_fill\_rickandmorty()+ scale\_color\_rickandmorty()

GGT2 <- GGT2+ geom\_signif(comparisons = list(c("1Gal.par","2Ipo.pur"),c("1Gal.par","3Pol.pos"),

c("1Gal.par","2Bid.pil"),c("3Pol.pos","3Dig.san")),

test = t.test,textsize = 7,vjust=0.7,

y\_position = c(26,27.5,24.5,26),

tip\_length = c(c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05),c(0.05,0.05)),

size=0.5,color="black", map\_signif\_level = T)

GGT2

######

pdf("Fig典型物种22.pdf",width=19.4,height=3.4)

ggarrange(GGT,GGT2,

ncol=2, nrow=1)

dev.off()

## ############### diversity comparison box plot

library(GGally)

library(ggplot2)

library(ggsci)

aa=read.delim("clipboard",header=T)

A <- ggplot(aa, aes(x = MHT, y = R, color = origin)) +

geom\_boxplot(size = 1.3) + facet\_grid(~season)+ theme\_grey()+ theme(axis.title = element\_text(size=19),

axis.text = element\_text(size=14),legend.text=element\_text(size=14),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

x="Microhabitat type", y="Species richness")

A <- A + scale\_color\_rickandmorty()

A

###导出PDF

pdf("MHT箱图.pdf",width=24,height=5.3)

print(A)

dev.off()

library( agricolae )

df <- read.delim("clipboard",header=T)

fit <- aov(R~MHT, data = df)

print(duncan.test(fit, "MHT", alpha=0.05))

#########correlation

library(ggpubr)

library(ggcorrplot)

library(ggsci)

library(GGally)

library(rstatix)

dd <- read.delim("clipboard",header=T) ###不能有缺失值.11.21允许有NA了！

pm <- ggpairs(dd,columns = 2:19, legend = c(1,1),

ggplot2::aes(color = season),

upper = list(continuous = wrap("cor",method ="spearman")) )+ theme\_bw()

pm <- pm + scale\_fill\_npg()+ scale\_color\_npg()+ theme\_bw() +theme(panel.grid=element\_blank() )

pm

pm <- ggpairs(dd,columns = 2:13,

upper = list(continuous = wrap("cor",method ="spearman")) )+ theme\_bw()

pm

## ##########correlation between native and exotic

library(psych)

library(ggplot2)

df<- read.delim("clipboard",header=T)

corr\_matrix <- corr.test(df, method = 'spearman')

cor<-corr\_matrix$r

p<-corr\_matrix$p #p

write.table(cor,"cor.csv")

write.table(p,"corp.csv")

data<- read.csv ("correlation.csv",header=T)

data

ggplot(data=data,aes(x=Exotic,y=Native))+

geom\_point(aes(size=`Cor`,

fill=`PPP`, color=`Sign`),

shape=22)+

scale\_fill\_manual(values = c("white", "#fa797b","#fcacad","#24325f","#5872c5"))+

scale\_color\_manual(values = c("#fa797b","#24325f"))+ facet\_grid(season~MHT)+

theme\_bw()+

theme(panel.grid.major= element\_blank(),

panel.grid.minor= element\_blank(),

plot.title = element\_text(hjust = 0.5, size = 12),

axis.text.y =element\_text(size = 12, color = "black"),

axis.text.x.top=element\_text(angle=90,hjust = 0,vjust = 0.1,

color = 'black',size = 12),

axis.ticks = element\_blank(),

legend.key.size = unit(0.15, "inches"))+

labs(x="",y=NULL)+

scale\_x\_discrete(position = 'top')

## ################Niche overlap and Network diagram

library(spaa)

library(vegan)

a=read.delim("clipboard",header=T)

nicheover<- niche.overlap(a,method = "levins")

nicheover<-as.matrix(nicheover)

write.csv(nicheover, "nicheover.csv")

class(nicheover)

nicheover2<- read.csv("nicheover.csv")

name=setdiff(colnames(nicheover2),c('spe'))

name

library(data.table)

nicheover2=reshape2::melt(nicheover2,id.vars='spe',measure.vars=name,variable.name="spe",vaalue.name="nicheover")

nicheover2

write.csv(nicheover2, "nicheover2.csv")

nicheover3<- read.csv("nicheover.csv")

name=setdiff(colnames(nicheover3),c('spe'))

name

library(data.table)

nicheover3=reshape2::melt(nicheover3,id.vars='spe',measure.vars=name,variable.name="spe",vaalue.name="nicheover")

nicheover3

write.csv(nicheover3, "nicheover3.csv")

library(tidyverse)

library(igraph)

library(ggraph)

library(tidygraph)

library(ggplot2)

library(ggsci)

nodes<-read.csv("nodes春总.csv",header=T)

edges<-read.csv("edges春总.csv",header=T)

nodes<-read.csv("nodes夏总.csv",header=T)

edges<-read.csv("edges夏总.csv",header=T)

nodes<-read.csv("nodesRW春.csv",header=T)

edges<-read.csv("edgesRW春.csv",header=T)

nodes<-read.csv("nodesRN春.csv",header=T)

edges<-read.csv("edgesRN春.csv",header=T)

nodes<-read.csv("nodesWV春.csv",header=T)

edges<-read.csv("edgesWV春.csv",header=T)

nodes<-read.csv("nodesFRV春.csv",header=T)

edges<-read.csv("edgesFRV春.csv",header=T)

nodes<-read.csv("nodesFRGP春.csv",header=T)

edges<-read.csv("edgesFRGP春.csv",header=T)

nodes<-read.csv("nodesFRGL春.csv",header=T)

edges<-read.csv("edgesFRGL春.csv",header=T)

nodes<-read.csv("nodesRW夏.csv",header=T)

edges<-read.csv("edgesRW夏.csv",header=T)

nodes<-read.csv("nodesRN夏.csv",header=T)

edges<-read.csv("edgesRN夏.csv",header=T)

nodes<-read.csv("nodesWV夏.csv",header=T)

edges<-read.csv("edgesWV夏.csv",header=T)

nodes<-read.csv("nodesFRV夏.csv",header=T)

edges<-read.csv("edgesFRV夏.csv",header=T)

nodes<-read.csv("nodesFRGP夏.csv",header=T)

edges<-read.csv("edgesFRGP夏.csv",header=T)

nodes<-read.csv("nodesFRGL夏.csv",header=T)

edges<-read.csv("edgesFRGL夏.csv",header=T)

###

net\_pc<-graph\_from\_data\_frame(

d=edges,vertices=nodes,

directed=TRUE)

?mutate

net\_pc

plot(net\_pc)

V(net\_pc)

V(net\_pc)$location

deg<-degree(net\_pc,mode="all")

deg

###春总度deg>125 夏总deg>124

graph\_gt <- as\_tbl\_graph(net\_pc) %>%

mutate(deg = centrality\_degree(mode='all'),

group=group\_infomap())

autograph(graph\_gt)

PP<-ggraph(graph\_gt, layout = 'kk') +

geom\_edge\_fan(aes(edge\_width=value),color="gray") +

geom\_node\_point(aes(size = deg,fill=factor(Origin),shape=factor(Cluster)))+

geom\_node\_text(aes(filter= deg> 124,label=name,color=factor(Origin)),size=4.7, repel = TRUE,fontface="italic")+

scale\_color\_discrete()+

scale\_edge\_width(range=c(0,2.6))+

theme\_graph() +

scale\_shape\_manual(values = c(D =21,G=24,O=22))+ scale\_fill\_rickandmorty()+

scale\_color\_manual(values = c(exotic ='#090900',exotic.in='#632d04',native='#0f1f52'))

PP

#### 春R-W度deg>55 RN-deg>77 WV-deg>77 FRV-deg>86 FRGP-deg>50 FRGL-deg>63，夏R-W度deg>57 RN-deg>60 WV-deg>66 FRV-deg>100 FRGP-deg>66 FRGL-deg>74

graph\_gt <- as\_tbl\_graph(net\_pc) %>%

mutate(deg = centrality\_degree(mode='all'),

group=group\_infomap())

autograph(graph\_gt)

PP<-ggraph(graph\_gt, layout = 'kk') +

geom\_edge\_fan(aes(edge\_width=value),color="gray") +

geom\_node\_point(aes(size = deg,fill=factor(Origin),shape=factor(Cluster)))+

geom\_node\_text(aes(filter= deg>74,label=name,color=factor(Origin)),size=6, repel = TRUE,fontface="italic")+

scale\_color\_discrete()+

scale\_edge\_width(range=c(0,2.6))+

theme\_graph() +

scale\_shape\_manual(values = c(D =21,G=24,O=22))+ scale\_fill\_rickandmorty()+

scale\_color\_manual(values = c(exotic ='#090900',exotic.in='#632d04',native='#0f1f52'))

PP

ggraph(graph\_gt, layout = 'kk') +

geom\_edge\_fan(aes(edge\_width=value),color="gray") +

geom\_node\_point(aes(size = deg,fill=factor(Origin)),shape=21)+

geom\_node\_text(aes(filter= deg>12,label=name),size=2.5)+

scale\_color\_discrete()+

scale\_edge\_width(range=c(0,2.6))+

guides(size=F,fill=F)+

theme\_graph()+

facet\_nodes(~Cluster) +

theme\_graph(foreground = 'steelblue', fg\_text\_colour = 'white')

############### Combined Box Diagram Typography by DOG originn is the source of the species that overlaps with it, and origin is the source of the species itself

aa=read.delim("clipboard",header=T)

P1<-ggplot(aa, aes(x = to, y = value, color= origin, fill= originn)) +

geom\_boxplot(size = 1.5) +theme(panel.grid=element\_blank() )+ theme\_bw()

P1<-P1+labs(x="Species", y="Niche overlap at plot level" )+

theme(axis.title = element\_text(size=35),

axis.text = element\_text(size=33))+theme(legend.position = "No" )+scale\_fill\_manual(values = c(native="#7086c4",exotic = "#fafd7c",exotic.in = "#b37648"))+

scale\_color\_manual(values =c(native="#24325f",exotic = "#f0c828",exotic.in = "#82491e"))

P1<-P1+scale\_y\_continuous(expand = c(0,0),limits= c(0,0.75))

P1

###保存PDF6X40 D加C

aa=read.delim("clipboard",header=T)

P1<-ggplot(aa, aes(x = to, y = value, color= origin, fill= originn)) +

geom\_boxplot(size = 1.5) +theme(panel.grid=element\_blank() )+ theme\_bw()

P1<-P1+labs(x="Species", y="Niche overlap at plot level" )+

theme(axis.title = element\_text(size=35),

axis.text = element\_text(size=33))+theme(legend.position = "No" )+scale\_fill\_manual(values = c(native="#7086c4",exotic = "#fafd7c",exotic.in = "#b37648"))+

scale\_color\_manual(values =c(native="#24325f",exotic = "#f0c828",exotic.in = "#82491e"))

P1<-P1+scale\_y\_continuous(expand = c(0,0),limits= c(0,1.5))

P1

**# Comparison of total box plots of niche overlap by species source type**

aa=read.delim("clipboard",header=T)

P1<-ggplot(aa, aes(x = type, y = value, color= type, fill= type)) +

geom\_boxplot(size = 1.5) +theme(panel.grid=element\_blank() )+ theme\_bw()

P1<-P1+labs(x="Species", y="Niche overlap at plot level" )+

theme(axis.title = element\_text(size=35),

axis.text = element\_text(size=33))+theme(legend.position = "No" )+scale\_fill\_manual(values = c(NN="#7086c4",NE="#fafd7c",NI="#b37648",EE = "#fafd7c",EI = "#b37648",II = "#b37648"))+

scale\_color\_manual(values =c(NN="#24325f",NE="#24325f",NI="#24325f",EE = "#f0c828",EI = "#f0c828",II = "#82491e"))

P1<-P1+scale\_y\_continuous(expand = c(0,0),limits= c(0,1.0))+facet\_grid(~Cluster)

P1

with(data=aa,

pairwise.wilcox.test(x=value,g=type,p.adjust.method = "holm")

**##################Functional diversity calculation**

library(FD)

trait<- read.csv ("FDNtrait-春.csv",header=T, row.names=1)

abun<- read.csv ("FDN样方矩阵-春.csv",header=T, row.names=1)

trait<- read.csv ("FDNtrait-夏.csv",header=T, row.names=1)

abun<- read.csv ("FDN样方矩阵-夏.csv",header=T, row.names=1)

trait

abun

ex3 <- dbFD(trait, abun,corr="lingoes")

ex3

write.table(ex3,"FD.csv")

## #############ggcoef\_model(): Model coefficients

library(GGally)

library(ggplot2)

library(broom.helpers)

library(psych)

library(ggpubr)

library(ggcorrplot)

library(ggsci)

library(rstatix)

bb <- read.csv ("ggcoefMHT.csv",header=T)

bb <- read.csv ("ggcoefMHT春.csv",header=T)

bb <- read.csv ("ggcoefMHT夏.csv",header=T)

mod\_simple1 <- glm(RE ~ MHT, family=poisson, data = bb)

mod\_simple2 <- lm(RN ~ MHT, data = bb)

mod\_simple3 <- lm(RRatio ~ MHT+RN+RE, data = bb)

mod\_simple4 <- lm(CoverageE ~ MHT, data = bb)

mod\_simple5 <- lm(CoverageN ~ MHT, data = bb)

mod\_simple6 <- lm(HeightE ~ MHT, data = bb)

mod\_simple7 <- lm(HeightN ~ MHT, data = bb)

mod\_simple8 <- lm(LeafSE ~ MHT, data = bb)

mod\_simple9 <- lm(LeafSN ~ MHT, data = bb)

mod\_simple10 <- lm(InDE ~ MHT, data = bb)

mod\_simple11 <- lm(InDN ~ MHT, data = bb)

mod\_simple12 <- lm(InNE ~ MHT, data = bb)

mod\_simple13 <- lm(InNN ~ MHT, data = bb)

mod\_simple14 <- lm(FlowerDE ~ MHT, data = bb)

mod\_simple15 <- lm(FlowerDN ~ MHT, data = bb)

mod\_simple16 <- lm(FruitLE ~ MHT, data = bb)

mod\_simple17 <- lm(FruitLN ~ MHT, data = bb)

mod\_simple18 <- lm(SeedE ~ MHT, data = bb)

mod\_simple19 <- lm(SeedN ~ MHT, data = bb)

mod\_simple20 <- lm(FDE ~ MHT, data = bb)

mod\_simple21 <- lm(FDN ~ MHT, data = bb)

#

mod\_simple1 <- lm(RE ~ MHT+RN, data = bb)

mod\_simple2 <- lm(RN ~ MHT+RE, data = bb)

mod\_simple3 <- lm(RRatio ~ MHT+RN+RE, data = bb)

mod\_simple4 <- lm(CoverageE ~ MHT+RN+RE, data = bb)

mod\_simple5 <- lm(CoverageN ~ MHT+RN+RE, data = bb)

mod\_simple6 <- lm(HeightE ~ MHT+RN+RE, data = bb)

mod\_simple7 <- lm(HeightN ~ MHT+RN+RE, data = bb)

mod\_simple8 <- lm(LeafSE ~ MHT+RN+RE, data = bb)

mod\_simple9 <- lm(LeafSN ~ MHT+RN+RE, data = bb)

mod\_simple10 <- lm(InDE ~ MHT+RN+RE, data = bb)

mod\_simple11 <- lm(InDN ~ MHT+RN+RE, data = bb)

mod\_simple12 <- lm(InNE ~ MHT+RN+RE, data = bb)

mod\_simple13 <- lm(InNN ~ MHT+RN+RE, data = bb)

mod\_simple14 <- lm(FlowerDE ~ MHT+RN+RE, data = bb)

mod\_simple15 <- lm(FlowerDN ~ MHT+RN+RE, data = bb)

mod\_simple16 <- lm(FruitLE ~ MHT+RN+RE, data = bb)

mod\_simple17 <- lm(FruitLN ~ MHT+RN+RE, data = bb)

mod\_simple18 <- lm(SeedE ~ MHT+RN+RE, data = bb)

mod\_simple19 <- lm(SeedN ~ MHT+RN+RE, data = bb)

mod\_simple20 <- lm(FDE ~ MHT+RN+RE, data = bb)

mod\_simple21 <- lm(FDN ~ MHT+RN+RE, data = bb)

?ggcoef\_compare

my\_models1 <- list(

"Richness-N" = mod\_simple2,"Richness-E" = mod\_simple1)

my\_models2 <- list(

"Coverage-N" = mod\_simple5,"Coverage-E" = mod\_simple4 )

my\_models3 <- list(

"Height-N" = mod\_simple7,"Height-E" = mod\_simple6)

my\_models4 <- list(

"Leafsize-N" = mod\_simple9,"Leafsize-E" = mod\_simple8)

my\_models5 <- list(

"InD-N" = mod\_simple11,"InD-E" = mod\_simple10)

my\_models6 <- list(

"InN-N" = mod\_simple13,"InN-E" = mod\_simple12)

my\_models7 <- list(

"FlowerD-N" = mod\_simple15,"FlowerD-E" = mod\_simple14)

my\_models8 <- list(

"FruitL-N" = mod\_simple17,"FruitL-E" = mod\_simple16)

my\_models9 <- list(

"Seed-N" = mod\_simple19, "Seed-E" = mod\_simple18)

my\_models10 <- list(

"FDN" = mod\_simple21,"FDE" = mod\_simple20)

my\_models11 <- list(

"RatioE" = mod\_simple3)

##spring

P1<- ggcoef\_compare(my\_models1, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P1<- P1+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P1

P2<- ggcoef\_compare(my\_models2, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P2<- P2+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P2

P3<- ggcoef\_compare(my\_models3, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P3<- P3+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P3

P4<- ggcoef\_compare(my\_models4, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P4<- P4+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P4

P5<- ggcoef\_compare(my\_models5, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P5<- P5+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P5

P6<- ggcoef\_compare(my\_models6, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P6<- P6+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P6

P7<- ggcoef\_compare(my\_models7, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P7<- P7+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P7

P8<- ggcoef\_compare(my\_models8, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P8<- P8+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P8

P9<- ggcoef\_compare(my\_models9, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P9<- P9+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P9

P10<- ggcoef\_compare(my\_models10, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P10<- P10+ scale\_fill\_manual(values = c("#24325f","#fa797b"))+

scale\_color\_manual(values = c("#24325f","#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P10

P11<- ggcoef\_compare(my\_models11, type = "dodged",point\_size =2,

point\_stroke =2,errorbar\_height = 0.2)

P11<- P11+ scale\_fill\_manual(values = c("#fa797b"))+

scale\_color\_manual(values = c("#fa797b"))+

theme(axis.title = element\_text(size=17),

axis.text = element\_text(size=14),legend.text=element\_text(size=11),legend.key.size = unit(0.5, "cm"))

P11

##

pdf("Fig1111春改.pdf",width=16,height=13.2)

ggarrange(P1,P2,P3,P4,P5,P6,P7,P8,P9,P10,P11,

ncol=4, nrow=3)

dev.off()

## ######Nneutral community model

library(Hmisc)

library(minpack.lm)

library(stats4)

#spp

spp<-read.csv("SPP春总.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP夏总.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP春FRV.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP春L.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP春GP.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP春R-NS.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP春R-W.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP春W-V.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP夏FRV.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP夏L.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP夏GP.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP夏R-NS.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP夏R-W.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-read.csv("SPP夏W-V.csv",head=T,stringsAsFactors=F,row.names=1)

spp<-t(spp)

N <- mean(apply(spp, 1, sum))

p.m <- apply(spp, 2, mean)

p.m <- p.m[p.m != 0]

p <- p.m/N

spp.bi <- 1\*(spp>0)

freq <- apply(spp.bi, 2, mean)

freq <- freq[freq != 0]

C <- merge(p, freq, by=0)

C <- C[order(C[,2]),]

C <- as.data.frame(C)

C.0 <- C[!(apply(C, 1, function(y) any(y == 0))),]

p <- C.0[,2]

freq <- C.0[,3]

names(p) <- C.0[,1]

names(freq) <- C.0[,1]

d = 1/N

m.fit <- nlsLM(freq ~ pbeta(d, N\*m\*p, N\*m\*(1 -p), lower.tail=FALSE),start=list(m=0.1))

m.fit

m.ci <- confint(m.fit, 'm', level=0.95)

freq.pred <- pbeta(d, N\*coef(m.fit)\*p, N\*coef(m.fit)\*(1 -p), lower.tail=FALSE)

pred.ci <- binconf(freq.pred\*nrow(spp), nrow(spp), alpha=0.05, method="wilson", return.df=TRUE)

Rsqr <- 1 - (sum((freq - freq.pred)^2))/(sum((freq - mean(freq))^2))

Rsqr

# Output 3 statistical outcome data tables, including the average relative abundance (p.csv), occurrence frequency (freq.csv), and predicted occurrence frequency (freq.pred.csv) for each species or taxa

write.csv(p, file = "p.csv")

write.csv(freq, file = "freq.csv")

write.csv(freq.pred, file = "freq.pred.csv")

# Mapping charts

library(grid)

bacnlsALL <-data.frame(p,freq,freq.pred,pred.ci[,2:3])

write.csv(bacnlsALL, file = "bacnlsALL.csv")

inter.col<-rep('#646464',nrow(bacnlsALL))

inter.col[bacnlsALL$freq <= bacnlsALL$Lower]<-'#1b8977'#

inter.col[bacnlsALL$freq >= bacnlsALL$Upper]<-'#ff758f'#

grid.newpage()

pushViewport(viewport(h=0.7,w=0.7))

pushViewport(dataViewport(xData=range(log10(bacnlsALL$p)), yData=c(0,0.7),extension=c(0.02,0)))

grid.rect()

grid.points(log10(bacnlsALL$p), bacnlsALL$freq,pch=20,gp=gpar(col=inter.col,cex=1,alpha=0.9))

grid.yaxis(gp=gpar(fontsize=17))

grid.xaxis(gp=gpar(fontsize=17))

grid.lines(log10(bacnlsALL$p),bacnlsALL$freq.pred,gp=gpar(col='blue',lwd=2),default='native')

grid.lines(log10(bacnlsALL$p),bacnlsALL$Lower ,gp=gpar(col='#004ff4',lwd=2,lty=2),default='native')

grid.lines(log10(bacnlsALL$p),bacnlsALL$Upper,gp=gpar(col='#004ff4',lwd=2,lty=2),default='native')

draw.text <- function(just, i, j) {

grid.text(paste("Rsqr=",round(Rsqr,3),"\n","m=",round(coef(m.fit,3))), x=x[j], y=y[i], just=just)

}

x <- unit(1:4/5, "npc")

y <- unit(1:4/5, "npc")

draw.text(c("centre", "bottom"), 4, 1)

##导出PDF5X5

#############

library(ggplot2)

df=read.delim("clipboard",header=T)

ggplot(df,aes(group1,value))+geom\_col(aes(color=group1,fill=group2),size=0.8)+facet\_grid(~MHT)+

scale\_fill\_manual(values = c("#f0c929", "#82491e","#24325f"))+theme\_bw()+theme(panel.grid=element\_blank() )+

scale\_color\_manual(values = c("#1b8977", "#646464","#ff758f"))

#####

df=read.delim("clipboard",header=T)

ggplot(df,aes(group1,value))+geom\_col(aes(fill=group2,width=0.8))+

scale\_fill\_manual(values = c("#f4d75f", "#82491e","#495888"))+theme\_bw()+theme(panel.grid=element\_blank() )+ theme(axis.title = element\_text(size=34),

axis.text = element\_text(size=33),legend.text=element\_text(size=33),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

y="Species number")

###PDF5.2X5.9 FRV5.2X6.1

df=read.delim("clipboard",header=T)

ggplot(df,aes(group1,Species))+

geom\_col(aes(color=group1),size=2.5,fill=NA)+

scale\_color\_manual(values = c("#1b8977", "#646464","#ff758f"))+theme\_bw()+theme(panel.grid=element\_blank() )+ theme(axis.title = element\_text(size=34),

axis.text = element\_text(size=33),legend.text=element\_text(size=33),legend.key.size = unit(0.5, "cm"))+

labs(title ="",

y="Species number")

###PDF5.3X5.5 FRV5.3X5.7

## ##Calculate the sum of total abundance and total coverage of species in different squares, and trait data

library(reshape)

a=read.delim("clipboard",header=T)

a$fre=1

a.abund=tapply(a$abund,list(a$plot,a$season,a$origin),sum);a.abund=melt(a.abund);a.abund.sum=tapply(a.abund$value,a.abund$X1,function(x)sum(x,na.rm = T))

a.coverage=tapply(a$coverage,list(a$plot,a$season,a$origin),sum);a.coverage=melt(a.coverage)

a.HeightXa=tapply(a$HeightXa,list(a$plot,a$season,a$origin),sum);a.HeightXa=melt(a.HeightXa)

a.LeafSXa=tapply(a$LeafSXa,list(a$plot,a$season,a$origin),sum);a.LeafSXa=melt(a.LeafSXa)

a.InDXa=tapply(a$InDXa,list(a$plot,a$season,a$origin),sum);a.InDXa=melt(a.InDXa)

a.InNXa=tapply(a$InNXa,list(a$plot,a$season,a$origin),sum);a.InNXa=melt(a.InNXa)

a.FlowerDXa=tapply(a$FlowerDXa,list(a$plot,a$season,a$origin),sum);a.FlowerDXa=melt(a.FlowerDXa)

a.FruitLXa=tapply(a$FruitLXa,list(a$plot,a$season,a$origin),sum);a.FruitLXa=melt(a.FruitLXa)

a.SeedXa=tapply(a$SeedXa,list(a$plot,a$season,a$origin),sum);a.SeedXa=melt(a.SeedXa)

write.table(a.abund,"a.abund.csv")

write.table(a.coverage,"a.coverage.csv")

write.table(a.HeightXa,"a.HeightXa.csv")

write.table(a.LeafSXa,"a.LeafSXa.csv")

write.table(a.InDXa,"a.InDXa.csv")

write.table(a.InNXa,"a.InNXa.csv")

write.table(a.FlowerDXa,"a.FlowerDXa.csv")

write.table(a.FruitLXa,"a.FruitLXa.csv")

write.table(a.SeedXa,"a.SeedXa.csv")

## #################SEM

library(piecewiseSEM)

install.packages("piecewiseSEM")##

#Box-Cox transformation

aa <- read.csv ("SEM-exoticspring.csv",header=T)

aa=read.delim("clipboard",header=T)

library(MASS)##Box-Cox transformation

library(moments)

MODEL1<-lm(CoverageE ~ RE+RRatio+ shdi, data =aa)

boxcox(MODEL1,plotit=T

boxcox(MODEL1,plotit=T,lambda= seq(-0.2,0.2,by=0.1))

befor.model<-lm(CoverageE ~ RE+RRatio+ shdi, data =aa)

summary(befor.model)

after.model<-lm((CoverageE^(0.01)-1)/0.01 ~ RE+RRatio+ shdi, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$CoverageE,be.res,main="before")

plot(aa$CoverageE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

CoverEbox<-(aa$CoverageE^(0.01)-1)/0.01

CoverEbox

write.csv(CoverEbox,"CoverEbox.csv")

MODEL2<-lm(RE ~ shdi+InS, data =aa)

boxcox(MODEL2,plotit=T)

boxcox(MODEL2,plotit=T,lambda= seq(-1,0,by=0.1))

befor.model<-lm(RE ~ shdi+InS, data =aa)

summary(befor.model)

after.model<-lm((RE^(-0.48)-1)/(-0.48) ~ shdi+InS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$RE,be.res,main="before")

plot(aa$RE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

REbox<-(aa$RE^(-0.48)-1)/(-0.48)

REbox

write.csv(CoverEbox,"CoverEbox.csv")

aa$RE

MODEL3<-lm(RRatio ~ RE+shdi+InS+prd, data =aa)

boxcox(MODEL3,plotit=T)

boxcox(MODEL3,plotit=T,lambda= seq(-1,0,by=0.1))

befor.model<-lm(RRatio ~ RE+shdi+InS+prd, data =aa)

summary(befor.model)

after.model<-lm((RRatio^(-0.26)-1)/(-0.26) ~ RE+shdi+InS+prd, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$RRatio,be.res,main="before")

plot(aa$RRatio,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

RRatiobox<-(aa$RRatio^(-0.26)-1)/(-0.26)

RRatiobox

write.csv(RRatiobox,"box.csv")

aa$RRatio

MODEL4<-lm(HeightE ~ RE+ RRatiobox+shdi, data =aa)

boxcox(MODEL4,plotit=T)

boxcox(MODEL4,plotit=T,lambda= seq(-1,0,by=0.1))

befor.model<-lm(HeightE ~ RE+ RRatiobox+shdi, data =aa)

summary(befor.model)

after.model<-lm((HeightE^(-0.01)-1)/(-0.01) ~ RE+ RRatiobox+shdi, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$HeightE,be.res,main="before")

plot(aa$HeightE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

HeightEbox<-(aa$HeightE^(-0.01)-1)/(-0.01)

HeightEbox

write.csv(HeightEbox,"box.csv")

MODEL5<-lm(LeafSE ~ RE+RRatiobox+ shdi, data =aa)

boxcox(MODEL5,plotit=T)

boxcox(MODEL5,plotit=T,lambda= seq(0.2,0.5,by=0.1))

befor.model<-lm(LeafSE ~ RE+ RRatiobox+shdi, data =aa)

summary(befor.model)

after.model<-lm((LeafSE^(0.33)-1)/(0.33) ~ RE+ RRatiobox+shdi, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$LeafSE,be.res,main="before")

plot(aa$LeafSE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

LeafSEbox<-(aa$LeafSE^(0.33)-1)/(0.33)

LeafSEbox

write.csv(LeafSEbox,"box.csv")

MODEL6<-lm(InDE ~ RE+ RRatiobox + shdi, data =aa)

boxcox(MODEL6,plotit=T)

boxcox(MODEL6,plotit=T,lambda= seq(-0.2,0.5,by=0.1))

befor.model<-lm(InDE ~ RE+ RRatiobox + shdi, data =aa)

summary(befor.model)

after.model<-lm((InDE^(-0.04)-1)/(-0.04) ~ RE+ RRatiobox+shdi, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$InDE,be.res,main="before")

plot(aa$InDE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

InDEbox<-(aa$InDE^(-0.04)-1)/(-0.04)

InDEbox

write.csv(InDEbox,"box.csv")

MODEL7<-lm(InNE ~ RE+ RRatiobox + shdi+pdInS, data =aa)

boxcox(MODEL7,plotit=T)

boxcox(MODEL7,plotit=T,lambda= seq(-0.2,0.5,by=0.1))

befor.model<-lm(InNE ~ RE+ RRatiobox + shdi+pdInS, data =aa)

summary(befor.model)

after.model<-lm((InNE^(0.08)-1)/(0.08) ~ RE+ RRatiobox + shdi+pdInS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$InNE,be.res,main="before")

plot(aa$InNE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

InNEbox<-(aa$InNE^(0.08)-1)/(0.08)

InNEbox

write.csv(InNEbox,"box.csv")

MODEL8<-lm(FlowerDE ~ RE+ RRatiobox+CrO+ shdi, data =aa)

boxcox(MODEL8,plotit=T)

boxcox(MODEL8,plotit=T,lambda= seq(-0.5,0.5,by=0.1))

befor.model<-lm(FlowerDE ~ RE+ RRatiobox+CrO+ shdi, data =aa)

summary(befor.model)

after.model<-lm((FlowerDE^(-0.18)-1)/(-0.18) ~ RE+ RRatiobox+CrO+ shdi, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$FlowerDE,be.res,main="before")

plot(aa$FlowerDE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

FlowerDEbox<-(aa$FlowerDE^(-0.18)-1)/(-0.18)

FlowerDEbox

write.csv(FlowerDEbox,"box.csv")

MODEL9<-lm(FruitLE ~ RE+ RRatiobox+ shdi, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(-0.5,0.5,by=0.1))

befor.model<-lm(FruitLE ~ RE+ RRatiobox+ shdi, data =aa)

summary(befor.model)

after.model<-lm((FruitLE^(0.21)-1)/(0.21) ~ RE+ RRatiobox+ shdi, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$FruitLE,be.res,main="before")

plot(aa$FruitLE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

FruitLEbox<-(aa$FruitLE^(0.21)-1)/(0.21)

FruitLEbox

write.csv(FruitLEbox,"box.csv")

MODEL9<-lm(SeedE ~ RE+ RRatiobox, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(-0.5,0.5,by=0.1))

befor.model<-lm(SeedE ~ RE+ RRatiobox, data =aa)

summary(befor.model)

after.model<-lm((SeedE^(-0.25)-1)/(-0.25) ~ RE+ RRatiobox, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$SeedE,be.res,main="before")

plot(aa$SeedE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

SeedEbox<-(aa$SeedE^(-0.25)-1)/(-0.25)

SeedEbox

write.csv(SeedEbox,"box.csv")

######################SEM was performed with the converted data from box

aa <- read.csv ("SEM-exoticspring.csv",header=T)

library(piecewiseSEM)

mod1 <- psem(

lm(CoverEbox ~ RE+RRatiobox, data =aa),

glm(RE ~ shdi+InS, family=poisson, data =aa),

lm(RRatiobox~ RE+shdi+InS+prd, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

mod1 <- psem(

lm(HeightEbox ~ RE+ RRatiobox+shdi, data =aa),

glm(RE ~ shdi+InS, family=poisson, data =aa),

lm(RRatiobox~ RE+shdi+InS+prd, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(LeafSEbox ~ RE+RRatiobox+ shdi, data =aa),

glm(RE ~ shdi+InS, family=poisson, data =aa),

lm(RRatiobox ~ RE+shdi+InS+prd, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##花朵分别展开

aa <- read.csv ("SEM-exoticspring.csv",header=T)

mod1 <- psem(

lm(InDEbox ~ RE+ RRatiobox + shdi, data =aa),

glm(RE ~ shdi+InS, family=poisson, data =aa),

lm(RRatiobox ~ RE+shdi+InS+prd, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(InNEbox ~ RE+ RRatiobox + shdi+pdInS, data =aa),

glm(RE ~ shdi+InS, family=poisson, data =aa),

lm(RRatiobox ~ RE+shdi+InS+prd, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(FlowerDEbox ~ RE+ RRatiobox+CrO+prd, data =aa),

glm(RE ~ shdi+InS, family=poisson, data =aa),

lm(RRatiobox ~ RE+shdi+InS+prd, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(FruitLEbox ~ RE+ RRatiobox+ shdi+prd, data =aa),

glm(RE ~ shdi+InS, family=poisson, data =aa),

lm(RRatiobox ~ RE+shdi+InS+prd, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(SeedEbox ~ RE+ RRatiobox+shdi+prd, data =aa),

glm(RE ~ shdi+InS, family=poisson, data =aa),

lm(RRatiobox ~ RE+shdi+InS+prd, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

########################native species

aa <- read.csv ("SEM-nativespring.csv",header=T)

#Box-Cox transformation

library(MASS)

library(moments)

MODEL1<-lm(CoverageN ~ RN+RRatio+shapeCrO+shapeWa, data =aa)

boxcox(MODEL1,plotit=T)

boxcox(MODEL1,plotit=T,lambda= seq(0.2,0.7,by=0.1))

befor.model<-lm(CoverageN ~ RN+RRatio+shapeCrO+shapeWa, data =aa)

summary(befor.model)

after.model<-lm((CoverageN^(0.48)-1)/0.48 ~ RN+RRatio+shapeCrO+shapeWa, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$CoverageN,be.res,main="before")

plot(aa$CoverageN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

CoverNbox<-(aa$CoverageN^(0.48)-1)/0.48

CoverNbox

write.csv(CoverNbox,"box.csv")

MODEL2<-lm(RN ~ RRatio+shapeWa+pdGrE, data =aa)

boxcox(MODEL2,plotit=T)

boxcox(MODEL2,plotit=T,lambda= seq(0.2,0.9,by=0.1))

befor.model<-lm(RN ~ RRatio+shapeWa+pdGrE, data =aa)

summary(befor.model)

after.model<-lm((RN^(0.36)-1)/(0.36) ~ RRatio+shapeWa+pdGrE, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$RN,be.res,main="before")

plot(aa$RN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

RNbox<-(aa$RN^(0.36)-1)/(0.36)

RNbox

write.csv(RNbox,"box.csv")

MODEL3<-lm(HeightN ~ RNbox+ RRatio+pdReS, data =aa)

boxcox(MODEL3,plotit=T)

boxcox(MODEL3,plotit=T,lambda= seq(0,0.5,by=0.1))

befor.model<-lm(HeightN ~ RNbox+ RRatio+pdReS, data =aa)

summary(befor.model)

after.model<-lm((HeightN^(0.14)-1)/(0.14) ~ RNbox+ RRatio+pdReS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$HeightN,be.res,main="before")

plot(aa$HeightN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

HeightNbox<-(aa$HeightN^(0.14)-1)/(0.14)

HeightNbox

write.csv(HeightNbox,"box.csv")

MODEL5<-lm(LeafSN ~ RNbox+RRatio+ ReS+GrE+CrO+UcN, data =aa)

boxcox(MODEL5,plotit=T)

boxcox(MODEL5,plotit=T,lambda= seq(-0.5,0,by=0.1))

befor.model<-lm(LeafSN ~ RNbox+RRatio+ ReS+GrE+CrO+UcN, data =aa)

summary(befor.model)

after.model<-lm((LeafSN^(-0.12)-1)/(-0.12) ~ RNbox+RRatio+ ReS+GrE+CrO+UcN, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$LeafSN,be.res,main="before")

plot(aa$LeafSN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

LeafSNbox<-(aa$LeafSN^(-0.12)-1)/(-0.12)

LeafSNbox

write.csv(LeafSNbox,"box.csv")

MODEL6<-lm(InDN ~ RNbox+ RRatio + shapeWa + pdGrE + ReS, data =aa)

boxcox(MODEL6,plotit=T)

boxcox(MODEL6,plotit=T,lambda= seq(-0.2,0.5,by=0.1))

befor.model<-lm(InDN ~ RNbox+ RRatio + shapeWa + pdGrE + ReS, data =aa)

summary(befor.model)

after.model<-lm((InDN^(0.16)-1)/(0.16) ~ RNbox+ RRatio + shapeWa + pdGrE + ReS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$InDN,be.res,main="before")

plot(aa$InDN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

InDNbox<-(aa$InDN^(0.16)-1)/(0.16)

InDNbox

write.csv(InDNbox,"box.csv")

MODEL7<-lm(InNN ~ RNbox+RRatio +pdReS, data =aa)

boxcox(MODEL7,plotit=T)

boxcox(MODEL7,plotit=T,lambda= seq(-0.12,0.5,by=0.1))

befor.model<-lm(InNN ~ RNbox+RRatio +pdReS, data =aa)

summary(befor.model)

after.model<-lm((InNN^(-0.05)-1)/(-0.05) ~ RNbox+RRatio +pdReS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$InNN,be.res,main="before")

plot(aa$InNN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

InNNbox<-(aa$InNN^(-0.05)-1)/(-0.05)

InNNbox

write.csv(InNNbox,"box.csv")

MODEL8<-lm(FlowerDN ~ RNbox+ RRatio+ shapeCrO, data =aa)

boxcox(MODEL8,plotit=T)

boxcox(MODEL8,plotit=T,lambda= seq(-0.5,0.5,by=0.1))

befor.model<-lm(FlowerDN ~ RNbox+ RRatio+ shapeCrO, data =aa)

summary(befor.model)

after.model<-lm((FlowerDN^(0.1)-1)/(0.1) ~ RNbox+ RRatio+ shapeCrO, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$FlowerDN,be.res,main="before")

plot(aa$FlowerDN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

FlowerDNbox<-(aa$FlowerDN^(0.1)-1)/(0.1)

FlowerDNbox

write.csv(FlowerDNbox,"box.csv")

MODEL9<-lm(FruitLN ~ RNbox+ RRatio, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(-0.5,0,by=0.1))

befor.model<-lm(FruitLN ~ RNbox+ RRatio, data =aa)

summary(befor.model)

after.model<-lm((FruitLN^(-0.11)-1)/(-0.11) ~ RNbox+ RRatio, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$FruitLN,be.res,main="before")

plot(aa$FruitLN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

FruitLNbox<-(aa$FruitLN^(-0.11)-1)/(-0.11)

FruitLNbox

write.csv(FruitLNbox,"box.csv")

MODEL9<-lm(SeedN ~ RNbox+ RRatio, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(-0.3,0,by=0.1))

befor.model<-lm(SeedN ~ RNbox+ RRatio, data =aa)

summary(befor.model)

after.model<-lm((SeedN^(-0.12)-1)/(-0.12) ~ RNbox+ RRatio, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$SeedN,be.res,main="before")

plot(aa$SeedN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

SeedNbox<-(aa$SeedN^(-0.12)-1)/(-0.12)

SeedNbox

write.csv(SeedNbox,"box.csv")

MODEL9<-lm(RRatio ~RN+RE, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(-0.3,0,by=0.1))

befor.model<-lm(SeedN ~ RNbox+ RRatio, data =aa)

summary(befor.model)

after.model<-lm((SeedN^(-0.12)-1)/(-0.12) ~ RNbox+ RRatio, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$SeedN,be.res,main="before")

plot(aa$SeedN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

SeedNbox<-(aa$SeedN^(-0.12)-1)/(-0.12)

SeedNbox

write.csv(SeedNbox,"box.csv")

############# sem

aa <- read.csv ("SEM-nativespring.csv",header=T)

aa <- read.csv ("SEM-nativesummer.csv",header=T)

###Richness与比例的关系

mod1 <- psem(

lm(RRatio ~RNbox+RE, data =aa),

lm(RE ~ RNbox, data =aa),

data =aa)

summary(mod1)

plot(mod1)

mod1 <- psem(

lm(CoverNbox ~ RNbox+RRatio+shapeCrO+shapeWa+pdGrE, data =aa),

lm(RNbox ~ RRatio+shapeWa+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(HeightNbox ~ RNbox+ RRatio+pdReS, data =aa),

lm(RNbox ~ RRatio+shapeWa+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

###

mod1 <- psem(

lm(LeafSNbox ~ RNbox+RRatio+ ReS+GrE, data =aa),

lm(RNbox ~ RRatio+shapeWa+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(InDNbox ~ RNbox+ RRatio + shapeWa + pdGrE + ReS, data =aa),

lm(RNbox ~ RRatio+shapeWa+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(InNNbox ~ RNbox+RRatio +pdReS+shapeWa, data =aa),

lm(RNbox ~ RRatio+shapeWa+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(FlowerDNbox ~ RNbox+ RRatio+ shapeCrO, data =aa),

lm(RNbox ~ RRatio+shapeWa+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(FruitLNbox ~ RNbox+ RRatio+pdGrE, data =aa),

lm(RNbox ~ RRatio+shapeWa+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(SeedNbox ~ RNbox+ RRatio+shapeWa, data =aa),

lm(RNbox ~ RRatio+shapeWa+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

#####################summer

aa <- read.csv ("SEM-exoticsummer.csv",header=T)

#Box-Cox

library(MASS)

library(moments)

MODEL1<-lm(CoverageE ~ RE+RRatio+pdReS, data =aa)

boxcox(MODEL1,plotit=T)

boxcox(MODEL1,plotit=T,lambda= seq(0,0.5,by=0.1))

befor.model<-lm(CoverageE ~ RE+RRatio+pdReS, data =aa)

summary(befor.model)

after.model<-lm((CoverageE^(0.16)-1)/0.16 ~ RE+RRatio+pdReS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$CoverageE,be.res,main="before")

plot(aa$CoverageE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

CoverEbox<-(aa$CoverageE^(0.16)-1)/0.16

CoverEbox

write.csv(CoverEbox,"box.csv")

MODEL2<-lm(RE ~ CrO+pdGrE+pdReS, data =aa)

boxcox(MODEL2,plotit=T)

boxcox(MODEL2,plotit=T,lambda= seq(0,0.4,by=0.1))

befor.model<-lm(RE ~ CrO+pdGrE+pdReS, data =aa)

summary(befor.model)

after.model<-lm((RE^(0.15)-1)/(0.15) ~ CrO+pdGrE+pdReS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$RE,be.res,main="before")

plot(aa$RE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

MODEL3<-lm(RRatio ~ RE+ReS+CrO+pdReS+pdGrE, data =aa)

boxcox(MODEL3,plotit=T)

boxcox(MODEL3,plotit=T,lambda= seq(0,0.4,by=0.1))

befor.model<-lm(RRatio ~ RE+ReS+CrO+pdReS+pdGrE, data =aa)

summary(befor.model)

after.model<-lm((RRatio^(0.11)-1)/(0.11) ~ RE+ReS+CrO+pdReS+pdGrE, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$RRatio,be.res,main="before")

plot(aa$RRatio,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

RRatiobox<-(aa$RRatio^(0.11)-1)/(0.11)

RRatiobox

write.csv(RRatiobox,"box.csv")

aa$RRatio

MODEL4<-lm(HeightE ~ RE+ RRatiobox+pdReS, data =aa)

boxcox(MODEL4,plotit=T)

boxcox(MODEL4,plotit=T,lambda= seq(0.3,0.7,by=0.1))

befor.model<-lm(HeightE ~ RE+ RRatiobox+pdReS, data =aa)

summary(befor.model)

after.model<-lm((HeightE^(0.52)-1)/(0.52) ~ RE+ RRatiobox+pdReS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$HeightE,be.res,main="before")

plot(aa$HeightE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

HeightEbox<-(aa$HeightE^(0.52)-1)/(0.52)

HeightEbox

write.csv(HeightEbox,"box.csv")

MODEL5<-lm(LeafSE ~ RE+RRatiobox+ ReS+CrO , data =aa)

boxcox(MODEL5,plotit=T)

boxcox(MODEL5,plotit=T,lambda= seq(-0.4,0,by=0.1))

befor.model<-lm(LeafSE ~ RE+RRatiobox+ ReS+CrO , data =aa)

summary(befor.model)

after.model<-lm((LeafSE^(-0.125)-1)/(-0.125) ~ RE+RRatiobox+ ReS+CrO, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$LeafSE,be.res,main="before")

plot(aa$LeafSE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

LeafSEbox<-(aa$LeafSE^(-0.125)-1)/(-0.125)

LeafSEbox

write.csv(LeafSEbox,"box.csv")

MODEL6<-lm(InDE ~ RE+ RRatiobox + shdi, data =aa)

boxcox(MODEL6,plotit=T)

boxcox(MODEL6,plotit=T,lambda= seq(0.2,0.5,by=0.1))

befor.model<-lm(InDE ~ RE+ RRatiobox + shdi, data =aa)

summary(befor.model)

after.model<-lm((InDE^(0.36)-1)/(0.36) ~ RE+ RRatiobox + shdi, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$InDE,be.res,main="before")

plot(aa$InDE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

InDEbox<-(aa$InDE^(0.36)-1)/(0.36)

InDEbox

write.csv(InDEbox,"box.csv")

MODEL7<-lm(InNE ~ RE+ RRatiobox +GrE, data =aa)

boxcox(MODEL7,plotit=T)

boxcox(MODEL7,plotit=T,lambda= seq(-0.2,0.5,by=0.1))

befor.model<-lm(InNE ~ RE+ RRatiobox +GrE, data =aa)

summary(befor.model)

after.model<-lm((InNE^(0.04)-1)/(0.04) ~ RE+ RRatiobox +GrE, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$InNE,be.res,main="before")

plot(aa$InNE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

InNEbox<-(aa$InNE^(0.04)-1)/(0.04)

InNEbox

write.csv(InNEbox,"box.csv")

MODEL8<-lm(FlowerDE ~ RE+ RRatiobox+InS, data =aa)

boxcox(MODEL8,plotit=T)

boxcox(MODEL8,plotit=T,lambda= seq(-0.5,0.5,by=0.1))

befor.model<-lm(FlowerDE ~ RE+ RRatiobox+InS, data =aa)

summary(befor.model)

after.model<-lm((FlowerDE^(-0.1)-1)/(-0.1) ~ RE+ RRatiobox+InS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$FlowerDE,be.res,main="before")

plot(aa$FlowerDE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

FlowerDEbox<-(aa$FlowerDE^(-0.1)-1)/(-0.1)

FlowerDEbox

write.csv(FlowerDEbox,"box.csv")

MODEL9<-lm(FruitLE ~ RE+ RRatiobox+shapeCrO+pdReS, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(0.2,0.5,by=0.1))

befor.model<-lm(FruitLE ~ RE+ RRatiobox+shapeCrO+pdReS, data =aa)

summary(befor.model)

after.model<-lm((FruitLE^(0.325)-1)/(0.325) ~ RE+ RRatiobox+shapeCrO+pdReS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$FruitLE,be.res,main="before")

plot(aa$FruitLE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

FruitLEbox<-(aa$FruitLE^(0.325)-1)/(0.325)

FruitLEbox

write.csv(FruitLEbox,"box.csv")

MODEL9<-lm(SeedE ~ RE+ RRatiobox+UcN, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(-0.5,0.5,by=0.1))

befor.model<-lm(SeedE ~ RE+ RRatiobox+UcN, data =aa)

summary(befor.model)

after.model<-lm((SeedE^(-0.2)-1)/(-0.2) ~ RE+ RRatiobox+UcN, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$SeedE,be.res,main="before")

plot(aa$SeedE,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

SeedEbox<-(aa$SeedE^(-0.2)-1)/(-0.2)

SeedEbox

write.csv(SeedEbox,"box.csv")

######## SEM

aa <- read.csv ("SEM-exoticsummer.csv",header=T)

mod1 <- psem(

lm(CoverEbox ~ RE+RRatiobox+pdReS, data =aa),

glm(RE ~ pdGrE+pdReS,family=poisson, data =aa),

lm(RRatiobox ~ RE+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(HeightEbox ~ RE+ RRatiobox+pdReS, data =aa),

glm(RE ~ pdGrE+pdReS,family=poisson, data =aa),

lm(RRatiobox ~ RE+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(LeafSEbox ~ RE+RRatiobox+ ReS , data =aa),

glm(RE ~ pdGrE+pdReS, family=poisson, data =aa),

lm(RRatiobox ~ RE+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

mod1 <- psem(

lm(InDEbox ~ RE+ RRatiobox+GrE+pdReS, data =aa),

glm(RE ~ pdGrE+pdReS,family=poisson, data =aa),

lm(RRatiobox ~ RE+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(InNEbox ~ RE+ RRatiobox+GrE+pdGrE+pdReS, data =aa),

glm(RE ~ pdGrE+pdReS,family=poisson, data =aa),

lm(RRatiobox ~ RE+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(FlowerDEbox ~RE+ RRatiobox +InS, data =aa),

glm(RE ~ pdGrE+pdReS,family=poisson, data =aa),

lm(RRatiobox ~ RE+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

glm(FruitLEbox ~ RE+ RRatiobox +shapeCrO, data =aa),

glm(RE ~ pdGrE+pdReS,family=poisson, data =aa),

lm(RRatiobox ~ RE+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(SeedEbox ~ RE+ RRatiobox+UcN+pdReS, data =aa),

glm(RE ~ pdGrE+pdReS,family=poisson, data =aa),

lm(RRatiobox ~ RE+pdGrE, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

###########################################native species

aa <- read.csv ("SEM-nativesummer.csv",header=T)

#Box-Cox transformation

library(MASS)

library(moments)

MODEL1<-lm(CoverageN ~ RN+RRatio+CrO+shapeCrO+pdReS, data =aa)

boxcox(MODEL1,plotit=T)

boxcox(MODEL1,plotit=T,lambda= seq(0.4,0.7,by=0.1))

befor.model<-lm(CoverageN ~ RN+RRatio+CrO+shapeCrO+pdReS, data =aa)

summary(befor.model)

after.model<-lm((CoverageN^(0.58)-1)/0.58 ~ RN+RRatio+CrO+shapeCrO+pdReS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$CoverageN,be.res,main="before")

plot(aa$CoverageN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

CoverNbox<-(aa$CoverageN^(0.58)-1)/0.58

CoverNbox

write.csv(CoverNbox,"box.csv")

MODEL2<-lm(RN ~ RRatio+prd+PuU+CoM, data =aa)

boxcox(MODEL2,plotit=T)

boxcox(MODEL2,plotit=T,lambda= seq(0.2,0.6,by=0.1))

befor.model<-lm(RN ~ RRatio+prd+PuU+CoM, data =aa)

summary(befor.model)

after.model<-lm((RN^(0.365)-1)/(0.365) ~ RRatio+prd+PuU+CoM, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$RN,be.res,main="before")

plot(aa$RN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

RNbox<-(aa$RN^(0.365)-1)/(0.365)

RNbox

write.csv(RNbox,"box.csv")

MODEL3<-lm(HeightN ~ RNbox + RRatio+pdWa+shapeCrO, data =aa)

boxcox(MODEL3,plotit=T)

boxcox(MODEL3,plotit=T,lambda= seq(0,0.5,by=0.1))

befor.model<-lm(HeightN ~ RNbox + RRatio+pdWa+shapeCrO, data =aa)

summary(befor.model)

after.model<-lm((HeightN^(0.26)-1)/(0.26) ~ RNbox + RRatio+pdWa+shapeCrO, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$HeightN,be.res,main="before")

plot(aa$HeightN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

HeightNbox<-(aa$HeightN^(0.26)-1)/(0.26)

HeightNbox

write.csv(HeightNbox,"box.csv")

MODEL5<-lm(LeafSN ~ RNbox +RRatio+ ReS+CoM, data =aa)

boxcox(MODEL5,plotit=T)

boxcox(MODEL5,plotit=T,lambda= seq(-0.5,0,by=0.1))

befor.model<-lm(LeafSN ~ RNbox +RRatio+ ReS+CoM, data =aa)

summary(befor.model)

after.model<-lm((LeafSN^(-0.08)-1)/(-0.08) ~ RNbox +RRatio+ ReS+CoM, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$LeafSN,be.res,main="before")

plot(aa$LeafSN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

LeafSNbox<-(aa$LeafSN^(-0.08)-1)/(-0.08)

LeafSNbox

write.csv(LeafSNbox,"box.csv")

MODEL6<-lm(InDN ~ RNbox+ RRatio +pdReS+pdCrO, data =aa)

boxcox(MODEL6,plotit=T)

boxcox(MODEL6,plotit=T,lambda= seq(-0.2,0.5,by=0.1))

befor.model<-lm(InDN ~ RNbox+ RRatio +pdReS+pdCrO, data =aa)

summary(befor.model)

after.model<-lm((InDN^(0.32)-1)/(0.32) ~ RNbox+ RRatio +pdReS+pdCrO, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$InDN,be.res,main="before")

plot(aa$InDN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

InDNbox<-(aa$InDN^(0.32)-1)/(0.32)

InDNbox

write.csv(InDNbox,"box.csv")

MODEL7<-lm(InNN ~ RNbox+RRatio+pdCrO, data =aa)

boxcox(MODEL7,plotit=T)

boxcox(MODEL7,plotit=T,lambda= seq(-0.12,0.5,by=0.1))

befor.model<-lm(InNN ~ RNbox+RRatio+pdCrO, data =aa)

summary(befor.model)

after.model<-lm((InNN^(0.26)-1)/(0.26) ~ RNbox+RRatio+pdCrO, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$InNN,be.res,main="before")

plot(aa$InNN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

InNNbox<-(aa$InNN^(0.26)-1)/(0.26)

InNNbox

write.csv(InNNbox,"box.csv")

MODEL8<-lm(FlowerDN ~ RNbox+ RRatio+shapeInS, data =aa)

boxcox(MODEL8,plotit=T)

boxcox(MODEL8,plotit=T,lambda= seq(-0.5,0,by=0.1))

befor.model<-lm(FlowerDN ~ RNbox+ RRatio+shapeInS, data =aa)

summary(befor.model)

after.model<-lm((FlowerDN^(-0.175)-1)/(-0.175) ~ RNbox+ RRatio+shapeInS, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$FlowerDN,be.res,main="before")

plot(aa$FlowerDN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

FlowerDNbox<-(aa$FlowerDN^(-0.175)-1)/(-0.175)

FlowerDNbox

write.csv(FlowerDNbox,"box.csv")

MODEL9<-lm(FruitLN ~ RNbox+ RRatio+pdWa, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(-0.2,0,by=0.1))

befor.model<-lm(FruitLN ~ RNbox+ RRatio+pdWa, data =aa)

summary(befor.model)

after.model<-lm((FruitLN^(-0.05)-1)/(-0.05) ~ RNbox+ RRatio+pdWa, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$FruitLN,be.res,main="before")

plot(aa$FruitLN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

FruitLNbox<-(aa$FruitLN^(-0.05)-1)/(-0.05)

FruitLNbox

write.csv(FruitLNbox,"box.csv")

MODEL9<-lm(SeedN ~ RNbox+ RRatio+Wa, data =aa)

boxcox(MODEL9,plotit=T)

boxcox(MODEL9,plotit=T,lambda= seq(-0.3,0,by=0.1))

befor.model<-lm(SeedN ~ RNbox+ RRatio+Wa, data =aa)

summary(befor.model)

after.model<-lm((SeedN^(-0.06)-1)/(-0.06) ~ RNbox+ RRatio+Wa, data =aa)

summary(after.model)

be.res<-residuals(befor.model)

af.res<-residuals(after.model)

par(mfrow=c(2,2))

plot(aa$SeedN,be.res,main="before")

plot(aa$SeedN,af.res,main="after")

plot(befor.model,2)

plot(after.model,2)

SeedNbox<-(aa$SeedN^(-0.06)-1)/(-0.06)

SeedNbox

write.csv(SeedNbox,"box.csv")

aa <- read.csv ("SEM-nativesumme.csv",header=T)

mod1 <- psem(

lm(CoverNbox ~ RNbox +RRatio+CrO+shapeCrO+pdReS, data =aa),

lm(RNbox ~ RRatio+prd+PuU+CoM, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(HeightNbox ~ RNbox+ RRatio+pdWa+shapeCrO+CoM, data =aa),

lm(RNbox ~ RRatio+prd+PuU+CoM, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

###

mod1 <- psem(

lm(LeafSNbox ~ RNbox +RRatio+CoM+PuU, data =aa),

lm(RNbox ~ RRatio+prd+PuU+CoM, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(InDNbox ~ RNbox+ RRatio +pdReS+pdCrO, data =aa),

lm(RNbox ~ RRatio+prd+PuU+CoM, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(InNNbox ~ RNbox+RRatio+pdCrO, data =aa),

lm(RNbox ~ RRatio+prd+PuU+CoM, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(FlowerDNbox ~ RNbox+ RRatio+shapeInS++CoM , data =aa),

lm(RNbox ~ RRatio+prd+PuU+CoM, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(FruitLNbox ~ RNbox+ RRatio+pdWa, data =aa),

lm(RNbox ~ RRatio+prd+PuU+CoM, data =aa),

data =aa

)

summary(mod1)

plot(mod1)

##

mod1 <- psem(

lm(SeedN ~ RNbox+ RRatio+Wa, data =aa),

lm(RNbox ~ RRatio+prd+PuU+CoM , data =aa),

data =aa

)

summary(mod1)

plot(mod1)

## ########## Comparison of traits in spring and summer

library(tidyverse)

library(gghalves)

df<- read.delim("clipboard",header=T)

aa <- read.csv ("SScompa.csv",header=T)

ordercolors<-c("coral1","lightslateblue","olivedrab3","goldenrod1","lightgray")

ordercolors<-c("#e090c9","#4e6ca3","olivedrab3","goldenrod1","lightgray")

P1<-ggplot(data = df,

aes(x=season, y=value, fill=origin)) +

geom\_half\_violin(side = "r", color=NA, alpha=0.35) +

geom\_boxplot(side = "r", errorbar.draw = FALSE, width=0.2, linewidth=0.5) +

geom\_half\_point\_panel(side = "l", shape=21, size=1.6, color="white") +

scale\_fill\_manual(values = ordercolors) +

labs(y="Height (m)",x=NULL) +

theme\_classic() +

theme(legend.position = "bottom",

axis.title = element\_text(size = 16, color = "black"),

axis.text = element\_text(size=13, color = "black"))+facet\_grid(.~origin)

P1

df<- read.delim("clipboard",header=T)

P2<-ggplot(data = df,

aes(x=season, y=value, fill=origin)) +

geom\_half\_violin(side = "r", color=NA, alpha=0.35) +

geom\_boxplot(side = "r", errorbar.draw = FALSE, width=0.2, linewidth=0.5) +

geom\_half\_point\_panel(side = "l", shape=21, size=1.6, color="white") +

scale\_fill\_manual(values = ordercolors) +

labs(y="Leaf size (cm2)",x=NULL) +

theme\_classic() +

theme(legend.position = "bottom",

axis.title = element\_text(size = 16, color = "black"),

axis.text = element\_text(size=13, color = "black"))+facet\_grid(.~origin)

P2

df<- read.delim("clipboard",header=T)

P3<-ggplot(data = df,

aes(x=season, y=value, fill=origin)) +

geom\_half\_violin(side = "r", color=NA, alpha=0.35) +

geom\_boxplot(side = "r", errorbar.draw = FALSE, width=0.2, linewidth=0.5) +

geom\_half\_point\_panel(side = "l", shape=21, size=1.6, color="white") +

scale\_fill\_manual(values = ordercolors) +

labs(y="Inflorescence size (cm)",x=NULL) +

theme\_classic() +

theme(legend.position = "bottom",

axis.title = element\_text(size = 16, color = "black"),

axis.text = element\_text(size=13, color = "black"))+facet\_grid(.~origin)

P3

df<- read.delim("clipboard",header=T)

P4<-ggplot(data = df,

aes(x=season, y=value, fill=origin)) +

geom\_half\_violin(side = "r", color=NA, alpha=0.35) +

geom\_boxplot(side = "r", errorbar.draw = FALSE, width=0.2, linewidth=0.5) +

geom\_half\_point\_panel(side = "l", shape=21, size=1.6, color="white") +

scale\_fill\_manual(values = ordercolors) +

labs(y="Number of florets",x=NULL) +

theme\_classic() +

theme(legend.position = "bottom",

axis.title = element\_text(size = 16, color = "black"),

axis.text = element\_text(size=13, color = "black"))+facet\_grid(.~origin)

P4

df<- read.delim("clipboard",header=T)

P5<-ggplot(data = df,

aes(x=season, y=value, fill=origin)) +

geom\_half\_violin(side = "r", color=NA, alpha=0.35) +

geom\_boxplot(side = "r", errorbar.draw = FALSE, width=0.2, linewidth=0.5) +

geom\_half\_point\_panel(side = "l", shape=21, size=1.6, color="white") +

scale\_fill\_manual(values = ordercolors) +

labs(y="Flower size (cm)",x=NULL) +

theme\_classic() +

theme(legend.position = "bottom",

axis.title = element\_text(size = 16, color = "black"),

axis.text = element\_text(size=13, color = "black"))+facet\_grid(.~origin)

P5

df<- read.delim("clipboard",header=T)

P6<-ggplot(data = df,

aes(x=season, y=value, fill=origin)) +

geom\_half\_violin(side = "r", color=NA, alpha=0.35) +

geom\_boxplot(side = "r", errorbar.draw = FALSE, width=0.2, linewidth=0.5) +

geom\_half\_point\_panel(side = "l", shape=21, size=1.6, color="white") +

scale\_fill\_manual(values = ordercolors) +

labs(y="Fruit size (mm)",x=NULL) +

theme\_classic() +

theme(legend.position = "bottom",

axis.title = element\_text(size = 16, color = "black"),

axis.text = element\_text(size=13, color = "black"))+facet\_grid(.~origin)

P6

df<- read.delim("clipboard",header=T)

P7<-ggplot(data = df,

aes(x=season, y=value, fill=origin)) +

geom\_half\_violin(side = "r", color=NA, alpha=0.35) +

geom\_boxplot(side = "r", errorbar.draw = FALSE, width=0.2, linewidth=0.5) +

geom\_half\_point\_panel(side = "l", shape=21, size=1.6, color="white") +

scale\_fill\_manual(values = ordercolors) +

labs(y="Seed dry mass (g / 1000 seeds)",x=NULL) +

theme\_classic() +

theme(legend.position = "bottom",

axis.title = element\_text(size = 16, color = "black"),

axis.text = element\_text(size=13, color = "black"))+facet\_grid(.~origin)

P7

df<- read.delim("clipboard",header=T)

P8<-ggplot(data = df,

aes(x=season, y=value, fill=origin)) +

geom\_half\_violin(side = "r", color=NA, alpha=0.35) +

geom\_boxplot(side = "r", errorbar.draw = FALSE, width=0.2, linewidth=0.5) +

geom\_half\_point\_panel(side = "l", shape=21, size=1.6, color="white") +

scale\_fill\_manual(values = ordercolors) +

labs(y="Seed dry mass (g / 1000 seeds)",x=NULL) +

theme\_classic() +

theme(legend.position = "bottom",

axis.title = element\_text(size = 16, color = "black"),

axis.text = element\_text(size=13, color = "black"))+facet\_grid(.~origin)

P8

pdf("Fig4cc.pdf",width=20,height=3)

ggarrange(P1,P2,P3,P4,P5,P6,P7,

ncol=7, nrow=1)

dev.off()