

董雷, 王静, 刘永刚, 赵志平, 米湘成, 郭柯 (2021) 太行山北段地区荆条灌丛和三裂绣线菊灌丛群落谱系结构. 生物多样性, 29 (1): 21–31. <http://www.biodiversity-science.net/CN/10.17520/biods.2020192>

附录 2 本研究所使用的 R 代码

Appendix 2 R codes used in this research

```
##计算  $\alpha$  多样性
sp_diversity <- read.csv("sp.csv",header=T)
names(sp_diversity)[1:3] <- c("plotname", "species", "abundance")
library(spaa)
library(vegan)
shrub.mat <- data2mat(sp_diversity)
Shannon <- diversity(shrub.mat, index = "shannon")
S <- specnumber(shrub.mat)
Pielou <- Shannon/log(S)
sr.all <- cbind(Shannon, Pielou)
write.csv(sr.all,"sprichness.csv")

##去除方差膨胀因子大于 10 的环境变量
df <- read.csv("environment.csv")
library(car)
vif(lm(nri~ala+mat+map+maxt+mint+maxp+minp+pet+aspect+slope+ai,data=df))
vif(lm(nri~ala+mat+map+maxt+mint+maxp+minp+pet+aspect+slope,data=df))
vif(lm(nri~ala+mat+map+mint+maxp+minp+pet+aspect+slope,data=df))
vif(lm(nri~ala+map+maxt+mint+maxp+minp+pet+aspect+slope,data=df))
vif(lm(nri~ala+map+mint+maxp+minp+pet+aspect+slope,data=df))
vif(lm(nri~ala+mint+maxp+minp+pet+aspect+slope,data=df))
vif(lm(nri~ala+mint+maxp+minp+aspect+slope,data=df))

#####
##构建谱系树
library("V.PhyloMaker")
species <- read.csv("splist.csv")
tree.a <- phylo.maker(sp.list=species, tree=GBOTB.extended, nodes=nodes.info.1, scenarios="S1")
phy <- tree.a$scenario.1
plot(phy)
write.tree(phy,"phy.tree")

##谱系信号检验
library(picante)
##性状数据
traits <- read.csv("traits.csv", header = TRUE, row.names = 1)
pairs(traits)
traits <- log10(traits)#对形状数据进行对数变换, 使数据更接近正态分布
pairs(traits)
multiPhylosignal(traits, multi2di(phy))

##样方数据预处理
library(vegan)
com <- read.csv(sample.csv)

#样方和谱系树重新匹配, 确保谱系树和样方中的物种一一对应
combined <- match.phylo.comm(phy, com)
phy <- combined$phy
comm <- combined$comm
#str(phy)

##计算 NRI
nri.weight <- ses.mpd(comm,cophenetic(phy),null.model="taxa.label",abundance.weighted = T)
nri.weight$NRI <- -nri.weight$mpd.obs.z#计算 NRI
write.csv(nri.weight,"NRI.csv")
```

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```
##荆条灌丛和三裂绣线菊灌丛  $\alpha$  多样性、谱系结构和谱系多样性比较
df <- read.csv("result.csv")
t.test(metadata$SR ~ df$community)
t.test(metadata$Shannon ~ df$community)
t.test(metadata$Pielou ~ df$community)
t.test(metadata$nri ~ df$community)

##群落整体与环境的多元回归
df2 <- as.data.frame( scale(df))
lm_all <- lm(nri~maxp+minp+cosasp+ala+slop+mint,data=df2)
summary(lm_all)
anova(lm_all)
round(coef (lm_all), 2)

##荆条灌丛与环境的多元回归
vitex <- subset(df2,community=="Vitex")
lm_vitex <- lm(nri~maxp+minp+cosasp+ala+slop+mint,data=vitex)
summary(lm_vitex)
anova(lm_vitex)
round(coef (lm_vitex), 2)

##三裂绣线菊灌丛与环境的多元回归
spiraea <- subset(df2,community=="Spiraea")
lm_spiraea <- lm(nri~maxp+minp+cosasp+ala+slop+mint,data=spiraea)
summary(lm_spiraea)
anova(lm_spiraea)
round(coef (lm_spiraea), 2)

#####
##谱系 PCPS 分析
library(PCPS)
res <- pcps(comm.p.dist)
summary(res, choices = c(1, 2))$scores
plot(res, display = "text", groups = c(rep("Clade-A", 5), rep("Clade-B", 7),
rep("Clade-C", 5),rep("Clade-D", 7),rep("Clade-E", 15)),cex=0.6)
```