

**Material suplementario 1.****Script modificado de Sidlauskas (2008) para R**

```
library(ape)
```

```
library(MASS)
```

```
library(geiger)
```

```
library(cluster)
```

```
library(phytools)
```

```
library("geomorph")
```

```
library("babette")
```

```
##### ANALYZE REAL DATA BRICKELLIA
```

```
#Barroetia y Brickellia
```

```
## define the taxa by clades
```

```
EG <- c("Carminatia_tenuiflora6193", "Ageratina_wrightii8813")
```

```
Barroetia <- c("Brickellia_subuligera8811",
```

```
             "Brickellia_sonorana8149", "Brickellia_pavonii8866",
```

```
             "Brickellia_laxiflora3070", "Brickellia_coixtlahuaca6145",
```

```
             "Brickellia_huahuapana705")
```

```
Kuhnia <- c("Brickellia_scoparia8857")
```

```
Coleosanthus <- c("Brickellia_pendula7057", "Brickellia_lemmonii2507",
```

```
                "Brickellia_secundiflora1839")
```

```
Brickellia <- c("Brickellia_grandiflora2688", "Brickellia_simplex1327",
```

```
              "Brickellia_monocephala19174")
```

```
Leptanthodium <- c("Brickellia_diffusa14650", "Brickellia_coulteri2836")
```

```
Microphyllae <- c("Brickellia_veronicifolia8812")
```

```
Gemmipedium <- c("Brickellia_spinulosa22722")
```

```
Phanerostylis <- c("Brickellia_pedunculosa8820", "Brickellia_problematica6784",
```

```
                 "Brickellia_coahuilensis2058")
```

```
Xerobrickellia <- c("Brickellia_cardiophylla6926",
```

```
                  "Brickellia_laciniata6869", "Brickellia_rhomboidea459")
```

```
A <- Xerobrickellia
B <- c(Phanerostylis, Gemmipedium, Microphyllae, Barroetea, Brickellia,
      Leptanthodium, Kuhnia, Coleosanthus)
C <- c(Phanerostylis, Gemmipedium, Microphyllae)
D <- c(Barroetea, Brickellia,
      Leptanthodium, Kuhnia, Coleosanthus)
E <- Barroetea
f <- c(Brickellia,
      Leptanthodium, Kuhnia, Coleosanthus)
G <- Leptanthodium
H <- c(Brickellia, Kuhnia, Coleosanthus)
I <- Brickellia
J <- c(Kuhnia, Coleosanthus)
## load and define phylogeny
characintrees <- ape::read.nexus("Mol/Brickell_partsinburn.nex.run1.tre")
characintrees %>% length()
characintrees <- characintrees[sample(1:9900, size = 1000, replace = FALSE)]
class(characintrees)
## define trees for just A
n = length(characintrees)
n
Atrees <- vector("list", n)
for (i in 1:n){
  Atrees[[i]] <- ape::drop.tip(phy = characintrees[[i]], c(EG, B))
  Atrees[[i]] <- compute.brlen(Atrees[[i]], 1)
}
## define trees for just B
Btrees <- vector("list", n)
for (i in 1:n){
  Btrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A))
```

```
Btrees[[i]] <- compute.brlen(Btrees[[i]],1)
}
## define trees for just C
Ctrees <- vector("list", n)
for (i in 1:n){
  Ctrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A, D))
  Ctrees[[i]] <- compute.brlen(Ctrees[[i]],1)
}
## define trees for just D
Dtrees <- vector("list", n)
for (i in 1:n){
  Dtrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A, C))
  Dtrees[[i]] <- compute.brlen(Dtrees[[i]],1)
}
## define trees for just E
Etrees <- vector("list", n)
for (i in 1:n){
  Etrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A, C, f))
  Etrees[[i]] <- compute.brlen(Etrees[[i]],1)
}
## define trees for just f
ftrees <- vector("list", n)
for (i in 1:n){
  ftrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A, C, E))
  ftrees[[i]] <- compute.brlen(ftrees[[i]],1)
}
## define trees for just G
Gtrees <- vector("list", n)
for (i in 1:n){
```

```
Gtrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A, C, E, H))
Gtrees[[i]] <- compute.brLen(Gtrees[[i]],1)
}
## define trees for just H
Htrees <- vector("list", n)
for (i in 1:n){
  Htrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A, C, E, G))
  Htrees[[i]] <- compute.brLen(Htrees[[i]],1)
}
## define trees for just I
Itrees <- vector("list", n)
for (i in 1:n){
  Itrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A, C, E, G, J))
  Itrees[[i]] <- compute.brLen(Itrees[[i]],1)
}
## define trees for just J
Jtrees <- vector("list", n)
for (i in 1:n){
  Jtrees[[i]] <- drop.tip(characintrees[[i]], c(EG, A, C, E, G, I))
  Jtrees[[i]] <- compute.brLen(Jtrees[[i]],1)
}
## load and define relative warp table for both groups
#in this case the PC are the warps, we used the first 4
#because explain almost 92% of variance
M_Brickcoord <- readland.tps("E:/M_B_ALL.tps",specID = "ID", readcurves = TRUE)
dimnames(M_Brickcoord)
sliders = rbind(define.sliders(c(3:27)), define.sliders(c(28:52)))
Y.gpa.M.all <- gpagen(M_Brickcoord, curves = sliders %>% as.matrix(),
  ProcD = TRUE)
```

```
geomorph::gm.prcomp(Y.gpa.M.all$coords) -> PCAmean_Brickellia
```

```
PCAmean_Brickellia
```

```
PCAmean_Brickellia$x
```

```
warps <- read.table ("PCAM_Brick.txt")
```

```
Awarps <- warps[Atrees[[1]]$tip, ]
```

```
Bwarps <- warps[Btrees[[1]]$tip, ]
```

```
Cwarps <- warps[Ctrees[[1]]$tip, ]
```

```
Dwarps <- warps[Dtrees[[1]]$tip, ]
```

```
Ewarps <- warps[Etrees[[1]]$tip, ]
```

```
fwarps <- warps[ftrees[[1]]$tip, ]
```

```
Gwarps <- warps[Gtrees[[1]]$tip, ]
```

```
Hwarps <- warps[Htrees[[1]]$tip, ]
```

```
Iwarps <- warps[Itrees[[1]]$tip, ]
```

```
Jwarps <- warps[Jtrees[[1]]$tip, ]
```

```
Awarps <- Awarps*100
```

```
Bwarps <- Bwarps*100
```

```
Cwarps <- Cwarps*100
```

```
Dwarps <- Dwarps*100
```

```
Ewarps <- Ewarps*100
```

```
fwarps <- fwarps*100
```

```
Gwarps <- Gwarps*100
```

```
Hwarps <- Hwarps*100
```

```
Iwarps <- Iwarps*100
```

```
Jwarps <- Jwarps*100
```

```
## CONDUCT PHYLOMORPHOSPACE ANALYSIS FOR A
```

```
Answer <- vector("list", n)
```

```
for (i in 1:n) {Answer[[i]]<-phylomorpho(Atrees[[i]],  
                                     Awarps)  
}
```

```
save(Aanswer, file="FullAphyloM.rda")
```

```
Aanswer[[1]]
```

```
## CONDUCT PHYLOMORPHOSPACE ANALYSIS FOR B
```

```
Banswer <- vector("list", n)
```

```
for (i in 1:n) {Banswer[[i]]<-phylomorpho(Btrees[[i]],  
                                     Bwarps)  
}
```

```
save(Banswer, file="FullBphyloM.rda")
```

```
Banswer[[1]]
```

```
## CONDUCT PHYLOMORPHOSPACE ANALYSIS FOR C
```

```
Canswer <- vector("list", n)
```

```
for (i in 1:n) {Canswer[[i]]<-phylomorpho(Ctrees[[i]],  
                                     Cwarps)  
}
```

```
save(Canswer, file="FullCphyloM.rda")
```

```
Canswer[[1]]
```

```
## CONDUCT PHYLOMORPHOSPACE ANALYSIS FOR D
```

```
Danswer <- vector("list", n)
```

```
for (i in 1:n) {Danswer[[i]]<-phylomorphy(Dtrees[[i]],
                                     Dwarps)
}
save(Danswer, file="FullDphyloM.rda")
Danswer[[1]]

## CONDUCT PHYLORPHOSPACE ANALYSIS FOR E
Eanswer <- vector("list", n)

for (i in 1:n) {Eanswer[[i]]<-phylomorphy(Etrees[[i]],
                                     Ewarps)
}
save(Eanswer, file="FullEphyloM.rda")
Eanswer[[1]]

## CONDUCT PHYLORPHOSPACE ANALYSIS FOR F
fanswer <- vector("list", n)

for (i in 1:n) {fanswer[[i]]<-phylomorphy(ftrees[[i]],
                                     fwarps)
}
save(fanswer, file="FullfphyloM.rda")
fanswer[[1]]

## CONDUCT PHYLORPHOSPACE ANALYSIS FOR G
Ganswer <- vector("list", n)

for (i in 1:n) {Ganswer[[i]]<-phylomorphy(Gtrees[[i]],
                                     Gwarps)
```

```
}  
save(Ganswer, file="FullGphyloM.rda")  
Ganswer[[1]]  
  
## CONDUCT PHYLOMORPHOSPACE ANALYSIS FOR H  
Hanswer <- vector("list", n)  
  
for (i in 1:n) {Hanswer[[i]]<-phylomorphy(Htrees[[i]],  
                                     Hwarps)  
}  
save(Hanswer, file="FullHphyloM.rda")  
Hanswer[[1]]  
  
## CONDUCT PHYLOMORPHOSPACE ANALYSIS FOR I  
Ianswer <- vector("list", n)  
  
for (i in 1:n) {Ianswer[[i]]<-phylomorphy(Itrees[[i]],  
                                     Iwarps)  
}  
save(Ianswer, file="FullIphyloM.rda")  
Ianswer[[1]]  
  
## CALCULATE PHYLOMORPHOSPACE STATS FOR A  
load(file="FullAphyloM.rda")  
n  
Aresults <- matrix(0, nrow=n, ncol=12)  
for (i in 1:n) {Aresults[i, ] <- phylomorphostats(Aanswer[[i]],  
                                               Atrees[[i]],  
                                               Awarps)
```



```
}  
save(Aresults, file="FullASTATS1.rda")  
  
colnames(Bresults)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")  
  
Aresults  
  
## CALCULATE PHYLOMORPHOSPACE STATS FOR B  
  
load(file="FullBphyloM.rda")  
  
n  
  
Bresults <- matrix(0, nrow=n, ncol=12)  
  
for (i in 1:n) {Bresults[i, ] <- phylomorphostats(Banswer[[i]],  
          Btrees[[i]],  
          Bwarps)  
}  
  
save(Bresults, file="FullBSTATS1.rda")  
  
colnames(Bresults)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")  
  
Bresults  
  
## CALCULATE PHYLOMORPHOSPACE STATS FOR C  
  
load(file="FullCphyloM.rda")  
  
n  
  
Cresults <- matrix(0, nrow=n, ncol=12)  
  
for (i in 1:n) {Cresults[i, ] <- phylomorphostats(Canswer[[i]],  
          Ctrees[[i]],  
          Cwarps)  
}  
  
save(Cresults, file="FullCSTATS1.rda")  
  
colnames(Cresults)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")  
  
Cresults  
  
## CALCULATE PHYLOMORPHOSPACE STATS FOR D
```

```
load(file="FullDphyloM.rda")

n

Dresults <- matrix(0, nrow=n, ncol=12)

for (i in 1:n) {Dresults[i, ] <- phylomorphostats(Danswer[[i]],
                                             Dtrees[[i]],
                                             Dwarps)
}

save(Dresults, file="FullDSTATS1.rda")

colnames(Dresults) <- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")

Dresults

## CALCULATE PHYLOMORPHOSPACE STATS FOR E

load(file="FullEphyloM.rda")

n

Eresults <- matrix(0, nrow=n, ncol=12)

for (i in 1:n) {Eresults[i, ] <- phylomorphostats(Eanswer[[i]],
                                             Etrees[[i]],
                                             Ewarps)
}

save(Eresults, file="FullESTATS1.rda")

colnames(Eresults) <- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")

Eresults

## CALCULATE PHYLOMORPHOSPACE STATS FOR F

load(file="FullfphyloM.rda")

n

fresults <- matrix(0, nrow=n, ncol=12)

for (i in 1:n) {fresults[i, ] <- phylomorphostats(fanswer[[i]],
                                             ftrees[[i]],
                                             fwarps)
```

```
}  
save(fresults, file="FullfSTATS1.rda")  
  
colnames(fresults)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")  
  
fresults  
  
## CALCULATE PHYLOMORPHOSPACE STATS FOR G  
  
load(file="FullGphyloM.rda")  
  
n  
  
Gresults <- matrix(0, nrow=n, ncol=12)  
  
for (i in 1:n) {Gresults[i, ] <- phylomorphostats(Ganswer[[i]],  
Gtrees[[i]],  
Gwarps)  
}  
  
save(Gresults, file="FullGSTATS1.rda")  
  
colnames(Gresults)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")  
  
Gresults  
  
## CALCULATE PHYLOMORPHOSPACE STATS FOR H  
  
load(file="FullHphyloM.rda")  
  
n  
  
Hresults <- matrix(0, nrow=n, ncol=12)  
  
for (i in 1:n) {Hresults[i, ] <- phylomorphostats(Hanswer[[i]],  
Htrees[[i]],  
Hwarps)  
}  
  
save(Hresults, file="FullHSTATS1.rda")  
  
colnames(Hresults)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")  
  
Hresults  
  
## CALCULATE PHYLOMORPHOSPACE STATS FOR I
```

```
load(file="FullphyloM.rda")

n

lresults <- matrix(0, nrow=n, ncol=12)

for (i in 1:n) {lresults[i, ] <- phylomorphostats(lanswer[[i]],
                                               ltrees[[i]],
                                               lwarps)
}

save(lresults, file="FullISTATS1.rda")

colnames(lresults)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")

lresults

##### SIMULATE BRANCH LENGTHS AND CHARACTER EVOLUTION ON ACTUAL TREES

## designate variance-covariance matrix

PCAmatrix_Brickellia$d
round(PCAmatrix_Brickellia$d, 5)

vcv <- c(0.00792, 0, 0, 0, 0, 0.00189, 0, 0, 0, 0, 0.00077, 0, 0, 0, 0, 0.00056)

dim(vcv) <- c(4, 4)

## SET UP LISTS TO HOLD SIMULATION OUTPUT

trees <- vector("list", n)

ultratrees <- vector("list", n)

Atrees <- vector("list", n)

Asims <- vector("list", n)

Apms <- vector("list", n)

Astats <- matrix(0, n, 12)

Btrees <- vector("list", n)

Bsims <- vector("list", n)

Bpms <- vector("list", n)
```

```
Bstats <- matrix(0, n, 12)
Ctrees <- vector("list", n)
Csims <- vector("list", n)
Cpms <- vector("list", n)
Cstats <- matrix(0, n, 12)
Dtrees <- vector("list", n)
Dsims <- vector("list", n)
Dpms <- vector("list", n)
Dstats <- matrix(0, n, 12)
Etrees <- vector("list", n)
Esims <- vector("list", n)
Epms <- vector("list", n)
Estats <- matrix(0, n, 12)
ftrees <- vector("list", n)
fsims <- vector("list", n)
fpms <- vector("list", n)
fstats <- matrix(0, n, 12)

## drop outgroups from each tree
for (i in 1:n){

  trees[[i]] <- drop.tip(characintrees[[i]], c(EG))

## ultrametricize each tree using Schilling et al. 2015

for (i in 1:n) {
  lambda = 1.0141
  mu = 0.5707
```

```
ultratrees[[i]] <- ultrametricize.yr(trees[[i]], mu=mu, lambda=lambda, rho=0.4434)
}

## split trees into all clades (this case sections)

for (i in 1:n) {
  Atrees[[i]] <- drop.tip(ultratrees[[i]], B)
  Btrees[[i]] <- drop.tip(ultratrees[[i]], c(A))
  Ctrees[[i]] <- drop.tip(ultratrees[[i]], c(A, D))
  Dtrees[[i]] <- drop.tip(ultratrees[[i]], c(A, C))
  Etrees[[i]] <- drop.tip(ultratrees[[i]], c(A, C, f))
  ftrees[[i]] <- drop.tip(ultratrees[[i]], c(A, C, E))
}

## SIMULATE BROWNIAN EVOLUTION on each clade
#CLADE A
for (i in 1:(n)) {
  Asims[[i]] <- sim.char(Atrees[[i]], vcv, model = "BM")
}
Asims
save(Asims, file="Asims.rda")

## DISCARD BRANCH LENGTH INFO AND CALCULATE
#PHYLOMORPHSPACE FOR EACH SIMULATION on CLADE A
for (i in 1:(n)) {
  Atrees[[i]] <- compute.brLen(Atrees[[i]], 1)
  Apms[[i]] <- phylomorphy(Atrees[[i]], Asims[[i]][,1])
}
Apms
save(Apms, file="Apms.rda")
```

```
## CALCULATE PHYLOMORPHOSTATS FOR EACH SIMULATION on CLADE A
for (i in 1:(n)) {
  Astats[i, ] <- phylomorphostats(Apms[[i]],
                                Atrees[[i]],
                                Asims[[i]][,1])
}

colnames(Astats) <- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",
                    "ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")

Astats
save(Astats, file="Astats2.rda")

###REPEAT ALL FOR CLADE B
for (i in 1:(n)) {
  Bsims[[i]] <- sim.char(Btrees[[i]], vcv, model = "BM")
}

Bsims
save(Bsims, file="Bsims.rda")

## DISCARD BRANCH LENGTH INFO AND CALCULATE
#PHYLOMORPHOSPACE FOR EACH SIMULATION on CLADE B
for (i in 1:(n)) {
  Btrees[[i]] <- compute.brln(Btrees[[i]], 1)
  Bpms[[i]] <- phylomorphy(Btrees[[i]], Bsims[[i]][,1])
}

Bpms
save(Bpms, file="Bpms.rda")

## CALCULATE PHYLOMORPHOSTATS FOR EACH SIMULATION on CLADE B
for (i in 1:(n)) {
```

```
Bstats[i, ] <- phylomorphostats(Bpms[[i]],
                              Btrees[[i]],
                              Bsims[[i]][,1])
}

colnames(Bstats) <- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",
                    "ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")

Bstats
save(Bstats, file="Bstats2.rda")

###REPEAT ALL FOR CLADE C
for (i in 1:(n)) {
  Csims[[i]] <- sim.char(Ctrees[[i]], vcv, model = "BM")
}

Csims
save(Csims, file="Csims.rda")

## DISCARD BRANCH LENGTH INFO AND CALCULATE
## PHYLOMORPHOSPACE FOR EACH SIMULATION on CLADE C
for (i in 1:(n)) {
  Ctrees[[i]] <- compute.brln(Ctrees[[i]], 1)
  Cpms[[i]] <- phylomorphy(Ctrees[[i]], Csims[[i]][,1])
}

Cpms
save(Cpms, file="Cpms.rda")

## CALCULATE PHYLOMORPHOSTATS FOR EACH SIMULATION on CLADE C
for (i in 1:(n)) {
  Cstats[i, ] <- phylomorphostats(Cpms[[i]],
                                  Ctrees[[i]],
```



```
        Csims[[i]][,1])
    }

colnames(Cstats)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")

Cstats

save(Cstats, file="Cstats2.rda")

###REPEAT ALL FOR CLADE D
for (i in 1:(n)) {
  Dsims[[i]] <- sim.char(Dtrees[[i]], vcv, model = "BM")
}

Dsims

save(Dsims, file="Dsims.rda")

## DISCARD BRANCH LENGTH INFO AND CALCULATE
##PHYLOMORPHOSPACE FOR EACH SIMULATION on CLADE D
for (i in 1:(n)) {
  Dtrees[[i]]<- compute.brln(Dtrees[[i]], 1)
  Dpms[[i]] <- phylomorphy(Dtrees[[i]], Dsims[[i]][,1])
}

Dpms

save(Dpms, file="Dpms.rda")

## CALCULATE PHYLOMORPHOSTATS FOR EACH SIMULATION on CLADE D
for (i in 1:(n)) {
  Dstats[i, ] <- phylomorphostats(Dpms[[i]],
        Dtrees[[i]],
        Dsims[[i]][,1])
}
}
```

```
colnames(Dstats)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")
```

```
Dstats
```

```
save(Dstats, file="Dstats2.rda")
```

```
###REPEAT ALL FOR CLADE E
```

```
for (i in 1:(n)) {
```

```
  Esims[[i]] <- sim.char(Etrees[[i]], vcv, model = "BM")
```

```
}
```

```
Esims
```

```
save(Esims, file="Esims.rda")
```

```
## DISCARD BRANCH LENGTH INFO AND CALCULATE
```

```
#PHYLOMORPHOSPACE FOR EACH SIMULATION on CLADE E
```

```
for (i in 1:(n)) {
```

```
  Etrees[[i]]<- compute.brln(Etrees[[i]], 1)
```

```
  Epms[[i]] <- phylomorphy(Etrees[[i]], Esims[[i]][,1])
```

```
}
```

```
Epms
```

```
save(Epms, file="Epms.rda")
```

```
## CALCULATE PHYLOMORPHOSTATS FOR EACH SIMULATION on CLADE E
```

```
for (i in 1:(n)) {
```

```
  Estats[i, ] <- phylomorphostats(Epms[[i]],
```

```
    Etrees[[i]],
```

```
    Esims[[i]][,1])
```

```
}
```

```
colnames(Estats)<- c("mean.mbrlen", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")
```

Estats

```
save(Estats, file="Estats2.rda")
```

```
###REPEAT ALL FOR CLADE F
```

```
for (i in 1:(n)) {
```

```
  fsims[[i]] <- sim.char(ftrees[[i]], vcv, model = "BM")
```

```
}
```

```
fsims
```

```
save(fsims, file="fsims.rda")
```

```
## DISCARD BRANCH LENGTH INFO AND CALCULATE
```

```
#PHYLOMORPHOSPACE FOR EACH SIMULATION on CLADE F
```

```
for (i in 1:(n)) {
```

```
  ftrees[[i]]<- compute.brln(ftrees[[i]], 1)
```

```
  fpms[[i]] <- phylomorphy(ftrees[[i]], fsims[[i]][,1])
```

```
}
```

```
fpms
```

```
save(fpms, file="fpms.rda")
```

```
## CALCULATE PHYLOMORPHOSTATS FOR EACH SIMULATION on CLADE F
```

```
for (i in 1:(n)) {
```

```
  fstats[i, ] <- phylomorphostats(fpms[[i]],
```

```
    ftrees[[i]],
```

```
    fsims[[i]][,1])
```

```
}
```

```
colnames(fstats)<- c("mean.mbrln", "var", "tau", "sig", "variance", "volume", "sumvolume",  
"ldensity1", "ldensity2", "ldensity3", "brcor", "brsig")
```

```
fstats
```

```
save(fstats, file="fstats2.rda")
```

```
### CALCULATE STATISTICS COMPARING REAL CLADES TO SIMULATED CLADES
```

```
load(file="FullAphyloM.rda")
```

```
load(file="FullBphyloM.rda")
```

```
load(file="FullCphyloM.rda")
```

```
load(file="FullDphyloM.rda")
```

```
load(file="FullEphyloM.rda")
```

```
load(file="FullfphyloM.rda")
```

```
load(file="FullASTATS1.rda")
```

```
load(file="FullBkSTATS1.rda")
```

```
load(file="FullCSTATS1.rda")
```

```
load(file="FullDSTATS1.rda")
```

```
load(file="FullESTATS1.rda")
```

```
load(file="FullFSTATS1.rda")
```

```
## Calculate Stats for tests of scenario 1
```

```
## mean and SD
```

```
mean.ma1 <- mean(Aresults[,1]); mean.ma1
```

```
sd.ma1 <- sd(Aresults[,1]); sd.ma1
```

```
mean.mc2 <- mean(Bresults[,1]);mean.mc2
```

```
sd.mc2 <- sd(Bresults[,1]); sd.mc2
```

```
mean.ma3 <- mean(Cresults[,1]);mean.ma3
```

```
sd.ma3 <- sd(Cresults[,1]); sd.ma3
```

```
mean.mc4 <- mean(Dresults[,1]);mean.mc4
```

```
sd.mc4 <- sd(Dresults[,1]); sd.mc4
```

```
mean.ma5 <- mean(Eresults[,1]);mean.ma5
```

```
sd.ma5 <- sd(Eresults[,1]); sd.ma5
```

```
mean.mc6 <- mean(fresults[,1]); mean.mc6
```

```
sd.mc6 <- sd(fresults[,1]); sd.mc6
```

```
## MA/MB
```

```
n=length(Aanswer)
```

```
n
```

```
mratio1 <- vector("numeric", n)
```

```
for (i in 1:n){ mratio[[i]] <- Aresults[i,1]/Bresults[i,1]
```

```
}
```

```
mean.mratio1 <- mean(mratio)
```

```
sd.mratio1 <- sd(mratio)
```

```
## MC/MD
```

```
n=length(Aanswer)
```

```
n
```

```
mratio <- vector("numeric", n)
```

```
for (i in 1:n){ mratio[[i]] <- Cresults[i,1]/Dresults[i,1]
```

```
}
```

```
mean.mratio2 <- mean(mratio)
```

```
sd.mratio2 <- sd(mratio)
```

```
## ME/MF
```

```
n=length(Aanswer)
```

```
n
mratio <- vector("numeric", n)
for (i in 1:n){ mratio[[i]] <- Eresults[i,1]/fresults[i,1]
}
mean.mratio3 <- mean(mratio)
sd.mratio3 <- sd(mratio)

## Calculate Stats for tests of scenario 2

## mean and SD
mean.d1A <- mean(Aresults[,8]); mean.d1A
sd.d1A <- sd(Aresults[,8]); sd.d1A
mean.d1B <- mean(Bresults[,8]); mean.d1B
sd.d1B <- sd(Bresults[,8]); sd.d1B
mean.d1C <- mean(Cresults[,8]); mean.d1C
sd.d1C <- sd(Cresults[,8]); sd.d1C
mean.d1D <- mean(Dresults[,8]); mean.d1D
sd.d1D <- sd(Dresults[,8]); sd.d1D
mean.d1E <- mean(Eresults[,8]); mean.d1E
sd.d1E <- sd(Eresults[,8]); sd.d1E
mean.d1F <- mean(fresults[,8]); mean.d1F
sd.d1F <- sd(fresults[,8]); sd.d1F

mean.d2A <- mean(Aresults[,9]); mean.d2A
sd.d2A <- sd(Aresults[,9]); sd.d2A
mean.d2B <- mean(Bresults[,9]); mean.d2B
sd.d2B <- sd(Bresults[,9]); sd.d2B
mean.d2C <- mean(Cresults[,9]); mean.d2C
```

```
sd.d2C <- sd(Cresults[,9]); sd.d2C
mean.d2D <- mean(Dresults[,9]); mean.d2D
sd.d2D <- sd(Dresults[,9]); sd.d2D
mean.d2E <- mean(Eresults[,9]); mean.d2E
sd.d2E <- sd(Eresults[,9]); sd.d2E
mean.d2F <- mean(fresults[,9]); mean.d2F
sd.d2F <- sd(fresults[,9]); sd.d2F

## D1B/D1A
n=length(Aanswer)
d1ratio <- vector("numeric", n)
for (i in 1:n){ d1ratio[[i]] <- Bresults[i,8]/Aresults[i,8]
}

mean.d1ratio <- mean(d1ratio); mean.d1ratio
sd.d1ratio <- sd(d1ratio); sd.d1ratio

## D2B/D2A
n=length(Aanswer)
d2ratio <- vector("numeric", n)
for (i in 1:n){ d2ratio[[i]] <- Bresults[i,9]/Aresults[i,9]
}

mean.d2ratio <- mean(d2ratio); mean.d2ratio
sd.d2ratio <- sd(d2ratio); sd.d2ratio

## D1D/D1C
n=length(Aanswer)
d1ratio <- vector("numeric", n)
for (i in 1:n){ d1ratio[[i]] <- Dresults[i,8]/Cresults[i,8]
```

```
}

mean.d1ratio <- mean(d1ratio); mean.d1ratio
sd.d1ratio <- sd(d1ratio); sd.d1ratio

## D2D/D2C
n=length(Aanswer)
d2ratio <- vector("numeric", n)
for (i in 1:n){ d2ratio[[i]] <- Dresults[i,9]/Cresults[i,9]
}

mean.d2ratio <- mean(d2ratio); mean.d2ratio
sd.d2ratio <- sd(d2ratio); sd.d2ratio

## D1F/D1E
n=length(Aanswer)
d1ratio <- vector("numeric", n)
for (i in 1:n){ d1ratio[[i]] <- fresults[i,8]/Eresults[i,8]
}

mean.d1ratio <- mean(d1ratio); mean.d1ratio
sd.d1ratio <- sd(d1ratio); sd.d1ratio

## D2B/D2A
n=length(Aanswer)
d2ratio <- vector("numeric", n)
for (i in 1:n){ d2ratio[[i]] <- fresults[i,9]/Eresults[i,9]
}

mean.d2ratio <- mean(d2ratio); mean.d2ratio
sd.d2ratio <- sd(d2ratio); sd.d2ratio

## STATS BASED ON SIMULATED PHYLOMORPHOSPACES
```



```
load(file="Astats2.rda")
load(file="Bstats2.rda")
load(file="Cstats2.rda")
load(file="Dstats2.rda")
load(file="Estats2.rda")
load(file="fstats2.rda")

###CLADES A vs B

## MORPHOMETRIC BRANCH LENGTH
msimratio1 <- Astats[,1]/Bstats[,1]
mean(msimratio1)
sd(msimratio1)
r = length(msimratio1)
r
mtest<-(msimratio1< mean.mratio1)
above = 0
below = 0
for (i in 1:r) {  if (mtest[[i]]==TRUE) below <- below+1
if (mtest[[i]]==FALSE) above <- above+1
}
MP <- above/r
MP

## LINEAGE DENSITY 1
d1simratio <- Bstats[,8]/Astats[,8]
mean(d1simratio)
r = length(d1simratio)
d1test<-(d1simratio<mean.d1ratio)
```

```
above = 0
below = 0
for (i in 1:r) {  if (d1test[[i]]==TRUE) below <- below+1
if (d1test[[i]]==FALSE) above <- above+1
}
D1P <- above/r
D1P
## LINEAGE DENSITY 2
d2simratio <- Bstats[,9]/Astats[,9]
mean(d2simratio)

r = length(d2simratio)
d2test<-(d2simratio<mean.d2ratio)
above = 0
below = 0
for (i in 1:r) {  if (d2test[[i]]==TRUE) below <- below+1
if (d2test[[i]]==FALSE) above <- above+1
}
D2P <- above/r
D2P

###CLADES C vs D
## MORPHOMETRIC BRANCH LENGTH
msimratio1 <- Cstats[,1]/Dstats[,1]
mean(msimratio1)
sd(msimratio1)
r = length(msimratio1)
r
mtest<-(msimratio1< mean.mratio2)
```

```
above = 0
below = 0
for (i in 1:r) {  if (mtest[[i]]==TRUE) below <- below+1
if (mtest[[i]]==FALSE) above <- above+1
}
MP <- above/r
MP
```

```
## LINEAGE DENSITY 1
d1simratio <- Dstats[,8]/Cstats[,8]
mean(d1simratio)
sd(d1simratio)
r = length(d1simratio)
d1test<-(d1simratio<mean.d1ratio)
above = 0
below = 0
for (i in 1:r) {  if (d1test[[i]]==TRUE) below <- below+1
if (d1test[[i]]==FALSE) above <- above+1
}
D1P <- above/r
D1P
```

```
## LINEAGE DENSITY 2
d2simratio <- Dstats[,9]/Cstats[,9]
mean(d2simratio)
sd(d2simratio)
r = length(d2simratio)
d2test<-(d2simratio<mean.d2ratio)
above = 0
below = 0
```

```
for (i in 1:r) { if (d2test[[i]]==TRUE) below <- below+1
if (d2test[[i]]==FALSE) above <- above+1
}
D2P <- above/r
D2P
```

```
###CLADES E vs F
```

```
## MORPHOMETRIC BRANCH LENGTH
```

```
msimratio1 <- Estats[,1]/fstats[,1]
```

```
mean(msimratio1)
```

```
sd(msimratio1)
```

```
r = length(msimratio1)
```

```
r
```

```
mttest<-(msimratio1< mean.mratio3)
```

```
above = 0
```

```
below = 0
```

```
for (i in 1:r) { if (mttest[[i]]==TRUE) below <- below+1
```

```
if (mttest[[i]]==FALSE) above <- above+1
```

```
}
```

```
MP <- above/r
```

```
MP
```

```
## LINEAGE DENSITY 1
```

```
d1simratio <- fstats[,8]/Estats[,8]
```

```
mean(d1simratio)
```

```
sd(d1simratio)
```

```
r = length(d1simratio)
```

```
d1test<-(d1simratio<mean.d1ratio)
```

```
above = 0
```

```
below = 0
for (i in 1:r) {  if (d1test[[i]]==TRUE) below <- below+1
if (d1test[[i]]==FALSE) above <- above+1
}
D1P <- above/r
D1P
## LINEAGE DENSITY 2
d2simratio <- fstats[,9]/Estats[,9]
mean(d2simratio)
sd(d2simratio)
r = length(d2simratio)
d2test<-(d2simratio<mean.d2ratio)
above = 0
below = 0
for (i in 1:r) {  if (d2test[[i]]==TRUE) below <- below+1
if (d2test[[i]]==FALSE) above <- above+1
}
D2P <- above/r
D2P
```

### Literatura citada

Sidlauskas B. 2008. Continuous and arrested morphological diversification in sister clades of characiform fishes: a phylomorphospace approach. *Evolution: International Journal of Organic Evolution* **62**: 3135-3156. DOI: <https://doi.org/10.1111/j.1558-5646.2008.00519.x>