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http://www.r-phylo.org/wiki/HowTo/Table_of_Contentsを参照

install.packages("ape")
install.packages("geiger")

library(ape)

#upload tree and data file
geotree <- read.nexus("Geospiza.nex")
geodata <- read.table("Geospiza.txt")

#plot input tree (in three different formats)
plot(geotree)
plot(geotree, type="cladogram", use.edge.length=FALSE)
plot(geotree, type="fan")
#reroot tree with "fusca"
rerootedgeotree <- root(geotree, "fusca")

#use 'geiger' to check if all names in the tree file are present in the data file
library(geiger)
name.check(geotree, geodata)
#drop "olivacea" which lacks measurement data
geotree <- drop.tip(geotree, "olivacea")

#create data column for wing length and beak diameter
wingL <- geodata$wingL
beakD <- geodata$beakD
#attach names to wingL and beakD data so that they match those in the tree
names(wingL) <- row.names(geodata)
names(beakD) <- row.names(geodata)
#plot raw wingL and beakD data
plot(wingL, beakD)

#calculate phylogenetic independent contrasts using the 'pic' function
ContrastwingL <- pic(wingL, geotree)
ContrastbeakD <- pic(beakD, geotree)

#view wingL contrasts
ContrastwingL

#plot contrasts to the nodes in the tree
plot(geotree)
nodelabels(round(ContrastwingL, 3), adj=c(0, -0.5), frame="n")
nodelabels(round(ContrastbeakD, 3), adj=c(0, 1), frame="n")

#regress wingL conrasts against beakD contrasts
#'-1' is needed so that regression line runs through the origin
RegressBeakWing <- lm(ContrastbeakD~ContrastwingL -1)
#sumarize data, plot contrasts and show regression line
summary.lm(RegressBeakWing)
plot(ContrastwingL, ContrastbeakD)
abline(RegressBeakWing)

#below are commands for phylogenetic general least square analysis
#create data frame consisting of wingL and beakD
DF.geospiza <- data.frame(wingL,beakD,row.names=row.names(geodata))
#reorder rows in the data file to match the order in the tree
DF.geospiza <- DF.geospiza[geotree$tip.label,]
DF.geospiza #display data frame

#analysis of the data under the Brownian motion model
bm.geospiza<-corBrownian(phy=geotree)
bm.gls<-gls(wingL~beakD,correlation=bm.geospiza,data=DF.geospiza)
summary(bm.gls)

#analysis of the data using correlation factor alpha
#'10' donates alpha and can be any number from 0 to infinity
alpha.geospiza<-corMartins(10,phy=geotree)
alpha.gls<-gls(wingL~beakD,correlation=alpha.geospiza,data=DF.geospiza)
summary(alpha.gls)
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