####One size does not fit all: variation in anatomical traits associated with emersion behavior in mudskippers (Gobiidae: Oxudercinae)

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## Read in phylogeny from McCraney et al. 2020

gobytreeM0<-read.tree("gobytree.txt")

## Read in and trim the phylogeny

tipstodrop<-gobytreeM0$tip.label[300:827]

pruned.phy<- drop.tip(gobytreeM0, tipstodrop)

tipstodrop2<-pruned.phy$tip.label[1:253]

pruned.phy2<- drop.tip(pruned.phy, tipstodrop2) # Mudskipper tree with outgroup.

tipstodrop4<-pruned.phy2$tip.label[34:46]

pruned.phy4<- drop.tip(pruned.phy2, tipstodrop4) # Mudskipper tree without outgroup.

savetips<-c(1,4,5,16,23,25,27,29,31)

tipstodrop5<-pruned.phy4$tip.label[-savetips]

pruned.phy5<- drop.tip(pruned.phy4, tipstodrop5) # target species only

## Read in the trait data:

mudtraitsphylo\_A<-as.data.frame(read.csv('Trait\_data\_A\_phylo.csv', header=TRUE))

row.names(mudtraitsphylo\_A)<-mudtraitsphylo\_A[,1]

traits\_A<-mudtraitsphylo\_A[,2:13] # remove species list

heattraits\_A<-as.matrix(traits\_A) # for heat map

## Phylogentic signal:

phylosig(pruned.phy5, heattraits\_A[,7], method="lambda") # Pagel’s λ

phylosig(pruned.phy5, heattraits\_A[,7], method="K") # Blomberg’s K

## Phylogenetic generalized least squares regression:

obj<-name.check(pruned.phy5, traits\_A)

obj

bm<-corBrownian(1, pruned.phy5)

gls(Emersiongroup ~ No..of.scale.layers, data= traits\_A, correlation=bm)

## PGLMM:

muddatdata<-traits\_A[-2]

binaryPGLMM(muddatdata$Dermal.bulge ~ muddatdata$Papilla, data = muddatdata,pruned.phy5)