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1  set.seed(2024) #For reproducibility
2  # Abelisaurid Maxilla evolution
3
4  #Packages
5  library(geomorph)
6  library(ape)
7  library(mvMORPH)
8  library(RRPP)
9  library(geiger)
10 library(phytools)
11 library(paleotree)
12 library(strap)
13 library(geoscale)
14 library(bayou)
15 library(Claddis)
16 library(dplyr)
17 library(dispRity)
18 library(ggplot2)
19 library(nlme)
20 library(paleoTS)
21 library(fBasics)
22 library(MuMIn)
23 library(MASS)
24 library(vegan)
25 library(ggpubr)
26 library(rgl)
27 library(geometry)
28 library(webshot2)
29 library(surface)
30 #Notice that before to run simulation analysis you will need to run first the objects
    (Geometric morphometric data, Phylogenetic tree and Phylo PCA) in an especific data
    sets ("All taxa clade", "Dilophosaurus clade" and removed estimated taxa analysis) in
    Macroevolutionary analysis to then build the interval confidence.
31 #The BMM model was always the best model, but was different between Hypothesis in
    data sets, so that you must change the treeabeli (Prior hypothesis) for treeabeli1
    (Posterior hypothesis) phylogenetic tree if you want to build the confidence
    interval.
32
33
34 BMM90<-mvBM(treeAbeli1, Abelis_PhyPCA$x[,1:4], model="BMM")
35 simul4<-mvSIM(treeAbeli,nsim=500,param = BMM90)
36 #Fitting the best model to all data set simulated
37 results<-lapply(simul4,function(x){
38     mvBM(treeAbeli,x,model="BMM",method="rpf", echo=FALSE,diagnostic=FALSE)
39 })
40 sigma_simul_Esp_PC1<-sapply(results,function(x){x$sigma[1,1,"ESP"]})
41 sigma_simul_Esp_PC2<-sapply(results,function(x){x$sigma[2,2,"ESP"]})
42 sigma_simul_Esp_PC3<-sapply(results,function(x){x$sigma[3,3,"ESP"]})
43 sigma_simul_Esp_PC4<-sapply(results,function(x){x$sigma[4,4,"ESP"]})
44
45
46 sigma_simul_Gen_PC1<-sapply(results,function(x){x$sigma[1,1,"GEN"]})
47 sigma_simul_Gen_PC2<-sapply(results,function(x){x$sigma[2,2,"GEN"]})
48 sigma_simul_Gen_PC3<-sapply(results,function(x){x$sigma[3,3,"GEN"]})
49 sigma_simul_Gen_PC4<-sapply(results,function(x){x$sigma[4,4,"GEN"]})
50
51 #Create a confidence interval
52 ###PhyloPC1 for specialist hunters
53 ICEsp1<-quantile(sigma_simul_Esp_PC1,c(0.025,0.975))
54 #PhyloPC2 for specialist hunters
55 ICEsp2<-quantile(sigma_simul_Esp_PC2,c(0.025,0.975))
56 #PhyloPC3 for specialist hunters
57 ICEsp3<-quantile(sigma_simul_Esp_PC3,c(0.025,0.975))
58 #PhyloPC4 for specialist hunters
59 ICEsp4<-quantile(sigma_simul_Esp_PC4,c(0.025,0.975))
60 #PhyloPC1 for generalist hunters
61 ICGen1<-quantile(sigma_simul_Gen_PC1,c(0.025,0.975))
62 #PhyloPC2 for generalist hunters
63 ICGen2<-quantile(sigma_simul_Gen_PC2,c(0.025,0.975))
64 #PhyloPC3 for generalist hunters
65 ICGen3<-quantile(sigma_simul_Gen_PC3,c(0.025,0.975))

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66 #PhyloPC4 for generalist hunters
67 ICGen4<-quantile(sigma_simul_Gen_PC4,c(0.025,0.975))
68
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