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1  set.seed(2024) #For reproducibility
2  # Abelisaurid Maxilla evolution
3  #Packages
4  library(geomorph)
5  library(ape)
6  library(mvMORPH)
7  library(RRPP)
8  library(geiger)
9  library(phytools)
10 library(paleotree)
11 library(strap)
12 library(geoscale)
13 library(bayou)
14 library(Claddis)
15 library(dplyr)
16 library(disparity)
17 library(ggplot2)
18 library(nlme)
19 library(paleoTS)
20 library(fBasics)
21 library(MuMIn)
22 library(MASS)
23 library(vegan)
24 library(ggpubr)
25 library(rgl)
26 library(geometry)
27 library(webshot2)
28 library(surface)
29 #Geometric-Morphometric data and phylogenetic tree----
30 setwd() #Enter your working directory
31 Abelis<-readland.tps(file = "Supplementary_data_2.tps",readcurves = T) #Lanmark data
32 Abelis<-estimate.missing(A=Abelis,method="TPS") #Estimate missing landmarks
33 # we prepared semi landmarks to slide
34 lineasemi1 <- c(3,7:10,4)
35 lineasemi2 <- c(2,11:15,6)
36 lineasemi3 <- c(4,1:19,5)
37 lineasemi<-cbind(lineasemi1,lineasemi2,lineasemi3)
38 curve1<-matrix(0, nrow=4, ncol=3)
39 for(i in 1:nrow(curve1)){curve1[i,]<-c(lineasemi[i],lineasemi[i+1],lineasemi[i+2])}
40 #Procrustes analysis
41 Abelis_gpa<-gpagen(A=Abelis,curves = curve1)
42
43 #Species names of landmark data
44 species <- c("Abelisaurus","Allosaurus","Aucasaurus","Carnotaurus","Ceratosaurus",
45 "Dilophosaurus","Ekrixinatosaurus","Herrerasaurus","Limusaurus","Llukalkan",
46 "Majungasaurus","Masiakasaurus","Noasaurus","Skorpiovenator","Spectrovenator",
47 "Rugops","Syntarsus")
48
49 #Calibrated tree
50 AbeliPhy<-read.tree(file = "abelis_fully_resolved_tree_cal3_calibration.tre")
51 #We drop de taxa that have not maxilla
52 windows()
53 plot(AbeliPhy)
54 pr.species<-c("Berberosaurus","Genyodectes",
55 "Eoabelisaurus","Rajasaurus",
56 "Elaphrosaurus",
57 "Indosaurus","Arcovenator",
58 "Ilokelesia","Viavenator",
59 "Niebla","Huinculsaurus",
60 "Vespersaurus","Velocisaurus",
61 "Laevisuchus","MNNTig6",
62 "CCG20011","Xenotarsosaurus",
63 "MPM99","AbeliLaColonia")
64 nodes<-sapply(pr.species,grep,x=AbeliPhy$tip.label)
65
66 AbeliPhy<-drop.tip(AbeliPhy,pr.species)
67
68 AbeliPhy$edge.length[AbeliPhy$edge.length == 0] <- 0.01

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65 windows()
66 plotTree(AbeliPhy, fsize=0.6, lwd=1,
67          ftype="i")
68 # Now we can conduct Phylogenetic comparative analysis
69
70 #Evolution model without hyphotesis(SURFACE)----
71 #All taxa clade
72 Abelis_Phy_Coords<-geomorph.data.frame(coords=Abelis_gpa$coords, size=Abelis_gpa$Csize,
73 Phy = AbeliPhy)
74 Abelis_PhyPCA<-gm.prcomp(A=Abelis_Phy_Coords$coords, phy =Abelis_Phy_Coords$Phy, GLS=
75 TRUE)
76 #Dilophosaurus clade
77 #pr.species<-c("Herrerasaurus", "Syntarsus")
78 nodes<-sapply(pr.species, grep, x=AbeliPhy$tip.label)
79
80 AbeliPhy<-drop.tip(AbeliPhy, pr.species)
81
82 AbeliPhy$edge.length[AbeliPhy$edge.length == 0] <- 0.01
83 plot(AbeliPhy)
84
85 #procutes coordinates object
86 Abelis<-Abelis_gpa$coords[,c("Abelisaurus", "Aucasaurus", "Carnotaurus",
87 "Ekrixinatosaurus", "Majungasaurus", "Skorpiovenator", "Llukalkan", "Spectrovenator",
88 "Rugops", "Ceratosaurus", "Noasaurus", "Limusaurus", "Masiakasaurus", "Dilophosaurus",
89 "Allosaurus")]
90 #Phylogenetic Data frame
91 Abelis_Phy_Coords<-geomorph.data.frame(coords=Abelis, Phy = AbeliPhy)
92
93 Abelis_PhyPCA<-gm.prcomp(A=Abelis_Phy_Coords$coords, phy =Abelis_Phy_Coords$Phy, GLS=
94 TRUE)
95 #Removal estimated taxa analysis
96 pr.species<-c("Llukalkan", "Abelisaurus")
97 nodes<-sapply(pr.species, grep, x=AbeliPhy$tip.label)
98
99 AbeliPhy<-drop.tip(AbeliPhy, pr.species)
100
101 AbeliPhy$edge.length[AbeliPhy$edge.length == 0] <- 0.01
102 plot(AbeliPhy)
103
104 #We make a new procutes coordinates object
105 ##Without Herrerasaurus and Syntarsus
106 Abelis<-Abelis_gpa$coords[,c("Aucasaurus", "Carnotaurus", "Ekrixinatosaurus",
107 "Majungasaurus", "Skorpiovenator", "Spectrovenator", "Rugops", "Ceratosaurus", "Noasaurus",
108 "Limusaurus", "Masiakasaurus", "Dilophosaurus", "Allosaurus")]
109 #With Herrerasaurus and Syntarsus
110 Abelis<-Abelis_gpa$coords[,c("Aucasaurus", "Carnotaurus", "Ekrixinatosaurus",
111 "Majungasaurus", "Skorpiovenator", "Spectrovenator", "Rugops", "Ceratosaurus", "Noasaurus",
112 "Limusaurus", "Masiakasaurus", "Dilophosaurus", "Allosaurus", "Herrerasaurus", "Syntarsus"
113 )]
114
115 #Phylogenetic data frame
116 Abelis_Phy_Coords<-geomorph.data.frame(coords=Abelis, Phy = AbeliPhy)
117
118 #We have to calculate again the PhyloPCA
119 Abelis_PhyPCA<-gm.prcomp(A=Abelis_Phy_Coords$coords, phy =Abelis_Phy_Coords$Phy, GLS=
120 TRUE)
121
122 #Notice that first you have to choose one of the data sets above before you run
123 SURFACE analysis.
124 AbeliPhy<-nameNodes(AbeliPhy)
125 #Data transformation for SURFACE
126 data.dino<-data.frame(PC1_Phy=Abelis_PhyPCA$x[,1], PC2_Phy=Abelis_PhyPCA$x[,2], PC3_phy
127 =Abelis_PhyPCA$x[,3], PC4_Phy=Abelis_PhyPCA$x[,4])
128 olist<-convertTreeData(AbeliPhy, data.dino)
129 otree<-olist[[1]]
130 odata<-olist[[2]]
131 #We look for phenotypic optima
132 x<-surfaceForward(otree, odata, aic_threshold = 0, exclude = 0)
133 surfaceSummary(x)
134 k<-length(x)
135 #Plot of how many optima SURFACE fou

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122 windows()
123 surfaceTreePlot(AbeliPhy, x[[k]], labelshifts = T)
124 #Evolutionary trends, Phylogenetic signal and PGLS analysis----
125
126 #Ecological category whit Spectrovenator as Generalis sp (Prior Hypothesis)
127 eco<-c("Esp", "Gen", "Esp", "Esp", "Gen", "Gen", "Esp", "Gen", "Gen",
128        "Esp", "Esp", "Gen", "Gen", "Esp", "Gen", "Esp", "Gen")
129 #Ecological category whit Spectrovenator as specialis sp (Posterior hypothesis)
130 ecoE<-c("Esp", "Gen", "Esp", "Esp", "Gen", "Gen", "Esp", "Gen", "Gen",
131         "Esp", "Esp", "Gen", "Gen", "Esp", "Esp", "Esp", "Gen")
132 #Phylogenetic Data frame (Prior Hypothesis)
133 #Notice that first we have to select what eco data we can run (change eco object in
134 #Ecologia groups)
135 Abelis_Phy_Coords<-geomorph.data.frame(coords=Abelis_gpa$coords, size=Abelis_gpa$Csize,
136   Phy = AbeliPhy, Ecologia=eco, Especie=species)
137 #Phylogenetic Data frame whit (Posterior hypothesis)
138 Abelis_Phy_Coords<-geomorph.data.frame(coords=Abelis_gpa$coords, size=Abelis_gpa$Csize,
139   Phy = AbeliPhy, Ecologia=ecoE, Especie=species)
140
141 #Phylo PCA
142 Abelis_PhyPCA<-gm.prcomp(A=Abelis_Phy_Coords$coords, phy =Abelis_Phy_Coords$Phy, GLS=
143 TRUE)
144 summary(Abelis_PhyPCA)
145 #PACA
146 Abelis_PaCA<-gm.prcomp(A=Abelis_Phy_Coords$coords, phy =Abelis_Phy_Coords$Phy, GLS=TRUE
147 , align.to.phy = TRUE, transform = FALSE)
148 #Levels of the factor to plot
149 gp <- as.factor(paste(Abelis_Phy_Coords$Ecologia))
150 levels(gp)
151 #Phylo PCA
152 windows()
153 plot(Abelis_PhyPCA, axis1=1, axis2= 2, phylo =TRUE, cex=2, pch= 19, col=gp, phylo.par=
154 list( tip.labels =TRUE, node.labels=FALSE, anc.states= FALSE, edge.color= "black",
155 edge.width= 1, tip.txt.cex =0.5, tip.txt.adj = c(-0.1, -0.1) ))
156
157 #PACA
158 windows()
159 plot(Abelis_PaCA, axis1=1, axis2= 2, phylo =TRUE, cex=2, pch= 19, col=gp, phylo.par=
160 list( tip.labels =TRUE, node.labels=FALSE, anc.states= F, edge.color= "black",
161 edge.width= 1, tip.txt.cex =0.5, tip.txt.adj = c(-0.1, -0.1) ))
162 dev.off()
163 physig.Abelis<-physignal.z(A= Abelis_Phy_Coords$coords, phy= Abelis_Phy_Coords$Phy,
164 iter = 100000)
165 summary(physig.Abelis)
166
167 #PGLS
168 #If we can run the PGLS analysis in Posterior hypothesis we have to change the
169 Ecologia in the data frame
170 #Procustes coordinates
171 Phy_eco<-procD.pgls(Abelis_Phy_Coords$coords~Abelis_Phy_Coords$Ecologia*
172 Abelis_Phy_Coords$size, phy = Abelis_Phy_Coords$Phy, SS.type = "II", iter = 999)
173 summary(Phy_eco)
174 #PGLS in Phylo PCA
175 Phy_eco<-procD.pgls(Abelis_PhyPCA$x[,1:4]~Abelis_Phy_Coords$Ecologia*Abelis_Phy_Coords
176 $size, phy = Abelis_Phy_Coords$Phy, SS.type = "II", iter = 999)
177 summary(Phy_eco)
178 #PGLS in PACA
179 Phy_eco<-procD.pgls(Abelis_PaCA$x[,1:4]~Abelis_Phy_Coords$Ecologia*Abelis_Phy_Coords$
180 size, phy = Abelis_Phy_Coords$Phy, SS.type = "II", iter = 999)
181 summary(Phy_eco)
182
183 #Phylogenetic Signal
184 #Procustes coordinates
185 physig.Abelis<-physignal.z(A= Abelis_Phy_Coords$coords, phy= Abelis_Phy_Coords$Phy,
186 iter = 100000)
187 summary(physig.Abelis)
188 #PhyloPCA
189 physig.Abelis<-physignal.z(A= Abelis_PhyPCA$x[,1:3], phy= Abelis_Phy_Coords$Phy, iter
190 = 100000)
191 #PACA
192 physig.Abelis<-physignal.z(A= Abelis_PaCA$x[,1:5], phy= Abelis_Phy_Coords$Phy, iter =

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100000)
177
178
179 #Disparity trough time analysis----
180 windows()
181 x<-dtl(AbeliPhy, Abelis_PhyPCA$x[,1:4], index="avg.sq",
182       mdi.range=c(0,1), nsim=10000, CI=0.95, plot=TRUE,
183       calculateMDIp=T)
184 #Evolutions models, comparing the Prior and Posterior hypothesis in all taxa clade
185 ----
186 #We mapped the ecological character in the tree with Spectrovenator as a Gen (Prior
187 hypothesis)
188 state<-as.vector(c(rep("ESP",8),rep("GEN",9)));names(state)<-AbeliPhy$tip.label
189 #We mapped the ecological character in the tree with Spectrovenator as a Esp
190 (Posterior Hypothesis)
191 state1<-as.vector(c(rep("ESP",9),rep("GEN",8)));names(state1)<-AbeliPhy$tip.label
192 #We create the Prior Hypothesis
193 treeAbeli<-make.simmap(AbeliPhy, state, model="ER", nsim=1)
194
195 plot(treeAbeli)
196 #We create the Posterior Hypothesis obtained by SURFACE
197 treeAbeli1<-make.simmap(AbeliPhy, state1, model="ER", nsim=1)
198 plot(treeAbeli1)
199
200 #The first four components of Phylo PCA explained the 90% of variance in data
201 OU1<-mvOU(treeAbeli, Abelis_PhyPCA$x[,1:4], model="OU1")
202 OUM<-mvOU(treeAbeli, Abelis_PhyPCA$x[,1:4], model="OUM") #Prior hypothesis
203 BM1<-mvBM(treeAbeli, Abelis_PhyPCA$x[,1:4], model="BM1")
204 BMM<-mvBM(treeAbeli, Abelis_PhyPCA$x[,1:4], model="BMM") #Prior hypothesis
205 EB<-mvEB(treeAbeli, Abelis_PhyPCA$x[,1:4], diagnostic=FALSE, echo=FALSE)
206 BMMS<-mvBM(treeAbeli1, Abelis_PhyPCA$x[,1:4], model="BMM") #Posterior hypothesis
207 OUMS<-mvOU(treeAbeli1, Abelis_PhyPCA$x[,1:4], model="OUM") #Posterior hypothesis
208
209 #AKAIKE criterion information, weight and Looklihood
210 AIC<-data.frame(AIC=c(OU1$AIC, OUM$AIC, BM1$AIC, BMM$AIC, EB$AIC, BMMS$AIC, OUMS$AIC))
211 LogLik<-data.frame(LogLik=c(OU1$LogLik, OUM$LogLik, BM1$LogLik, BMM$LogLik, EB$LogLik,
212 BMMS$LogLik, OUMS$LogLik))
213 results<-c(OU1$AIC, OUM$AIC, BM1$AIC, BMM$AIC, EB$AIC, BMMS$AIC, OUMS$AIC)
214 aicw(results)
215
216 #Evolutions models, comparing the Prior and Posterior hypothesis in Dilophosaurus
217 clade ----
218 #We drop Herrerasaurus and Syntarsus
219 pr.species<-c("Herrerasaurus", "Syntarsus")
220 nodes<-sapply(pr.species, grep, x=AbeliPhy$tip.label)
221
222 AbeliPhy<-drop.tip(AbeliPhy, pr.species)
223
224 AbeliPhy$edge.length[AbeliPhy$edge.length == 0] <- 0.01
225 plot(AbeliPhy)
226
227 #We make a new procutes coordinates object
228 Abelis<-Abelis_gpa$coords[,c("Abelisaurus", "Aucasaurus", "Carnotaurus",
229 "Ekrixinatosaurus", "Majungasaurus", "Skorpiovenator", "Llukalkan", "Spectrovenator",
230 "Rugops", "Ceratosaurus", "Noasaurus", "Limusaurus", "Masiakasaurus", "Dilophosaurus",
231 "Allosaurus")]
232 #Phylogenetic Data frame
233 Abelis_Phy_Coords<-geomorph.data.frame(coords=Abelis, Phy = AbeliPhy)
234
235 #We have to perform a new Phylo PCA
236 Abelis_PhyPCA<-gm.prcomp(A=Abelis_Phy_Coords$coords, phy = Abelis_Phy_Coords$Phy, GLS=
237 TRUE)
238
239 #We mapped the ecological character in the tree with Spectrovenator as a Gen (Prior
240 Hypothesis)
241 state<-as.vector(c(rep("ESP",8),rep("GEN",7)));names(state)<-AbeliPhy$tip.label
242 #We mapped the ecological character in the tree with Spectrovenator as a Esp
243 (Posterior Hypothesis)
244 state1<-as.vector(c(rep("ESP",9),rep("GEN",6)));names(state1)<-AbeliPhy$tip.label
245 #We create the Prior Hypothesis
246 treeAbeli<-make.simmap(AbeliPhy, state, model="ER", nsim=1)

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235
236 plot(treeAbeli)
237 #We create the Posterior Hypothesis
238 treeAbeli1<-make.simmap(AbeliPhy, state1, model="ER", nsim=1)
239 plot(treeAbeli1)
240 #The first two components
241 OU1<-mvOU(treeAbeli, Abelis_PhyPCA$x[,1:4], model="OU1")
242 #Prior Hypothesis
243 OUM<-mvOU(treeAbeli, Abelis_PhyPCA$x[,1:4], model="OUM")
244 BM1<-mvBM(treeAbeli, Abelis_PhyPCA$x[,1:4], model="BM1")
245 #Prior Hypothesis
246 BMM<-mvBM(treeAbeli, Abelis_PhyPCA$x[,1:4], model="BMM")
247 EB<-mvEB(treeAbeli, Abelis_PhyPCA$x[,1:4], diagnostic=FALSE, echo=FALSE)
248 #Posterior Hypothesis
249 BMMS<-mvBM(treeAbeli1, Abelis_PhyPCA$x[,1:4], model="BMM")
250 #Posterior Hypothesis
251 OUMS<-mvOU(treeAbeli1, Abelis_PhyPCA$x[,1:4], model="OUM")
252
253 #AKAIKE criterion information, weight and Looklihood
254 AIC<-data.frame(AIC=c(OU1$AIC, OUM$AIC, BM1$AIC, BMM$AIC, EB$AIC, BMMS$AIC, OUMS$AIC))
255 LogLike<-data.frame(LogLik=c(OU1$LogLik, OUM$LogLik, BM1$LogLik, BMM$LogLik, EB$LogLik,
256 BMMS$LogLik, OUMS$LogLik))
257 results<-c(OU1$AIC, OUM$AIC, BM1$AIC, BMM$AIC, EB$AIC, BMMS$AIC, OUMS$AIC)
258 aicw(results)
259
260 #removal estimated taxa analysis----
261 #Notice that if you want to run this section in all taxa clade you will need re run
the all taxa clade
262 pr.species<-c("Llukalkan", "Abelisaurus")
263 nodes<-sapply(pr.species, grep, x=AbeliPhy$tip.label)
264
265 AbeliPhy<-drop.tip(AbeliPhy, pr.species)
266
267 AbeliPhy$edge.length[AbeliPhy$edge.length == 0] <- 0.01
268 plot(AbeliPhy)
269
270 #We make a new procutes coordinates object
271 ##Without Herrerasaurus and Syntarsus
272 Abelis<-Abelis_gpa$coords[,c("Aucasaurus", "Carnotaurus", "Ekrixinatosaurus",
273 "Majungasaurus", "Skorpiovenator", "Spectrovenator", "Rugops", "Ceratosaurus", "Noasaurus",
274 "Limusaurus", "Masiakasaurus", "Dilophosaurus", "Allosaurus")]
275
276 #With Herrerasaurus and Syntarsus
277 Abelis<-Abelis_gpa$coords[,c("Aucasaurus", "Carnotaurus", "Ekrixinatosaurus",
278 "Majungasaurus", "Skorpiovenator", "Spectrovenator", "Rugops", "Ceratosaurus", "Noasaurus",
279 "Limusaurus", "Masiakasaurus", "Dilophosaurus", "Allosaurus", "Herrerasaurus", "Syntarsus"
280 )]
281
282 #Phylogenetic data frame
283 Abelis_Phy_Coords<-geomorph.data.frame(coords=Abelis, Phy = AbeliPhy)
284
285 #We have to calculate again the PhyloPCA
286 Abelis_PhyPCA<-gm.prcomp(A=Abelis_Phy_Coords$coords, phy =Abelis_Phy_Coords$Phy, GLS=
TRUE)
287
288 #We mapped the ecological character in the tree with Spectrovenator as a Gen (Prior
Hypothesis)
289 state<-as.vector(c(rep("ESP", 6), rep("GEN", 9)));names(state)<-AbeliPhy$tip.label
290 #We mapped the ecological character in the tree with Spectrovenator as a Esp (Prior
Hypothesis)
291 state1<-as.vector(c(rep("ESP", 7), rep("GEN", 8)));names(state1)<-AbeliPhy$tip.label
292 #We create the Prior ypothesis
293 treeAbeli<-make.simmap(AbeliPhy, state, model="ER", nsim=1)
294
295 plot(treeAbeli)
296 #We create the posterior hypothesis
297 treeAbeli1<-make.simmap(AbeliPhy, state1, model="ER", nsim=1)
298 plot(treeAbeli1)
299 #Evolutions models
300 #The first two components
301 OU1<-mvOU(treeAbeli, Abelis_PhyPCA$x[,1:4], model="OU1")
302 #Prior hypothesis

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296 OUM<-mvOU(treeAbeli, Abelis_PhyPCA$x[,1:4], model="OUM")
297 BM1<-mvBM(treeAbeli, Abelis_PhyPCA$x[,1:4], model="BM1")
298 #Prior Hypothesis
299 BMM<-mvBM(treeAbeli, Abelis_PhyPCA$x[,1:4], model="BMM")
300 EB<-mvEB(treeAbeli, Abelis_PhyPCA$x[,1:4], diagnostic=FALSE, echo=FALSE)
301 #Posterior Hypothesis
302 BMMS<-mvBM(treeAbeli1, Abelis_PhyPCA$x[,1:4], model="BMM")
303 #Posterior Hypothesis
304 OUMS<-mvOU(treeAbeli1, Abelis_PhyPCA$x[,1:4], model="OUM")
305 #AKAIKE criterion information, weight and Looklihood
306 AIC<-data.frame(AIC=c(OU1$AIC, OUM$AIC, BM1$AIC, BMM$AIC, EB$AIC, BMMS$AIC, OUMS$AIC))
307 LogLike<-data.frame(LogLik=c(OU1$LogLik, OUM$LogLik, BM1$LogLik, BMM$LogLik, EB$LogLik,
BMMS$LogLik, OUMS$LogLik))
308 results<-c(OU1$AIC, OUM$AIC, BM1$AIC, BMM$AIC, EB$AIC, BMMS$AIC, OUMS$AIC)
309 aicw(results)
310 #Morphological changes----
311 #Links between landmarks
312 s<-c(1,16,17,18,5,5,6,14,13,12,11,2,2,3,7,8,9,4)
313 d<-c(16,17,18,19,19,6,15,15,14,13,12,11,3,7,8,9,10,10)
314 x<-cbind(s,d)
315 PCAMAX1<-PCA$shapes$shapes.comp1$max
316 PCAMIN1<-PCA$shapes$shapes.comp1$min
317 PCAMAX2<-PCA$shapes$shapes.comp2$max
318 PCAMIN2<-PCA$shapes$shapes.comp2$min
319 PCAMEAN<-mshape(PCA$shapes$shapes.comp1)
320
321 #Mean shape
322 plotRefToTarget(M1=PCAMEAN,M2=PCAMEAN,method = "TPS",links = z)
323 dev.off()
324 #Phylo PC 1 maximum shape
325 plotRefToTarget(M1=PCAMAX1,M2=PCAMEAN,method = "TPS",links = x)
326
327 #Phylo PC 1 minimum shape
328 plotRefToTarget(M1=Abelis_PhyPCA$shapes$shapes.comp2$min,M2=mshape(Abelis_PhyPCA$
shapes$shapes.comp1),method = "TPS",links = x)
329 #Phylo PC 2 maximum shape
330 plotRefToTarget(M1=PCAMAX2,M2=PCAMEAN,method = "TPS",links = x)
331 #Phylo PC 2 minimu shape
332 plotRefToTarget(M1=PCAMIN2,M2=PCAMEAN,method = "TPS",links = x)
333
334
335

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