Lab 4 R Source Code

Code:

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1 #
2 # Shawn Schwartz, 2019
_3 # EEB C174 UCLA Spring 2019
 # Lab 4 HW - Evolution of Carnivoran Dentition and Body Size
  #
6
  #clean up workspace
  rm(list=ls())
  #includes
10
  library (phytools)
  library (geiger)
12
  library (phylolm)
13
14
  cwd <- "~/Developer/EEB-C174-Labs/Lab4"
15
  resources path <- "resources/"
16
  output path <- "output/"
17
18
  setwd (cwd)
19
20
  ##### Read in Tree and Trait Data #####
21
  carnivoran tree <- read.tree(paste0(resources path, "carnivoran
     tree.tre"))
  carnivoran trait <- read.csv(paste0(resources path, "carnivoran
     trait.csv"), header = TRUE, sep = ",")
  carnivoran SE <- read.csv(paste0(resources path, "carnivoran SE.csv
     "), header = TRUE, sep = ",")
  pdf(paste0(output path, "1 carnivoran trait.pdf"))
26
  plot (carnivoran tree, cex = 0.25)
27
    axisPhylo()
28
    add.scale.bar()
29
  dev.off()
30
31
  ##### Fit Models #####
  #c1: fit models to cross sectional shape of the upper canine
  C1 data <- carnivoran trait $C1
  names (C1 data) <- carnivoran trait $Taxa
```

```
C1 SE <- carnivoran SE$C1
  names (C1 SE) <- carnivoran SE$Taxa
37
38
  carniv fit c1.bm <- fitContinuous(phy = carnivoran tree, dat = C1
39
     data, SE = C1\_SE, model = c("BM")
  carniv fit c1.ou <- fitContinuous(phy = carnivoran tree, dat = C1
40
     data, SE = C1 SE, model = c("OU")
  carniv fit c1.eb <- fitContinuous(phy = carnivoran_tree, dat = C1_
41
     data, SE = C1 SE, model = c("EB")
  carniv fit c1. white <- fitContinuous (phy = carnivoran tree, dat =
42
     C1 data, SE = C1 SE, model = c("white"))
43
  #RLGA: fit models to the relative upper grinding area
  RLGA_data <- carnivoran trait$RLGA
  names (RLGA data) <- carnivoran trait $Taxa
  RLGA SE <- carnivoran SE$RLGA
47
  names (RLGA SE) <- carnivoran SE$Taxa
48
49
  carniv fit RLGA.bm <- fitContinuous(phy = carnivoran tree, dat =
     RLGA data, SE = RLGA SE, model = c("BM"))
  carniv fit RLGA.ou <- fitContinuous(phy = carnivoran tree, dat =
     RLGA data, SE = RLGA SE, model = c("OU"))
  carniv fit RLGA.eb <- fitContinuous(phy = carnivoran tree, dat =
     RLGA data, SE = RLGA SE, model = c("EB"))
  carniv fit RLGA. white <- fitContinuous (phy = carnivoran tree, dat
     = RLGA data, SE = RLGA SE, model = c("white"))
54
  #ln-cbrt-bodymass: fit models to the log cuberoot of body mass
  lncbrt bodymass data <- carnivoran trait$log cuberoot mass
56
  names (lncbrt bodymass data) <- carnivoran trait $Taxa
  lncbrt bodymass SE <- carnivoran SE$logMass
  names (Incbrt bodymass SE) <- carnivoran SE$Taxa
59
60
  carniv fit lncbrt bodymass.bm <- fitContinuous(phy = carnivoran_
     tree, dat = lncbrt bodymass data, SE = lncbrt bodymass SE, model
      = \mathbf{c} ( "BM" ) )
  carniv fit lncbrt bodymass.ou <- fitContinuous(phy = carnivoran
     tree, dat = lncbrt bodymass data, SE = lncbrt bodymass SE, model
      = \mathbf{c} ("OU")
  carniv fit lncbrt bodymass.eb <- fitContinuous(phy = carnivoran
     tree, dat = lncbrt bodymass data, SE = lncbrt bodymass SE, model
      = \mathbf{c} ("EB")
```

```
carniv fit lncbrt bodymass. white <- fitContinuous (phy = carnivoran
     tree, dat = lncbrt bodymass data, SE = lncbrt bodymass SE,
     model = c("white"))
65
  ##### Compare Results Using AIC #####
  c1.data <- c(carniv fit c1.bm\sopt\saic, carniv fit c1.ou\sopt\saic,
     carniv fit c1.eb$opt$aic, carniv fit c1.white$opt$aic)
  rlga.data <- c(carniv fit RLGA.bm$opt$aic, carniv fit RLGA.ou$opt$
     aic, carniv fit RLGA.eb$opt$aic, carniv fit RLGA.white$opt$aic)
  lncbrt.data <- c(carniv fit lncbrt bodymass.bm$opt$aic, carniv fit
     lncbrt bodymass.ou$opt$aic, carniv fit lncbrt bodymass.eb$opt$
     aic, carniv fit lncbrt bodymass.white sopt saic)
  AICresults <- rbind(c1.data, rlga.data, lncbrt.data)
  colnames (AICresults) <- c ("Brownian Motion", "Ornstein Uhlenbeck",
      "Early Burst", "White noise")
  AICresults
72
73
  write.csv(AICresults, file = paste0(output path, "AICresults.csv"))
74
75
  #transform AIC values into Akaike weights
76
  ##which can be interpreted as conditional probabilities for each
     model
  AICw c1 vals <- aicw(c1.data)
  AICw rlga vals <- aicw (rlga.data)
  AICw lncbrt vals <- aicw(lncbrt.data)
80
  write.csv(AICw c1 vals, file = paste0(output path, "AICw c1 vals.
82
     csv"))
  write.csv(AICw rlga vals, file = paste0(output path, "AICw rlga
83
     vals.csv"))
  write.csv(AICw lncbrt vals, file = paste0(output path, "AICw lncbrt
84
     vals.csv"))
85
  pdf(paste0(output path, "c1 AICw barplot.pdf"))
86
    barplot (AICw_c1_vals[,3], names.arg = c("Brownian Motion", "
87
       Ornstein Uhlenbeck", "Early Burst", "White noise"), ylim = c
       (0,1), main = "Cross Sectional Shape of Upper Canine", cex.
       names = 0.7
    abline (h = 1, lty = "dashed")
88
  dev. off()
89
  pdf(paste0(output path, "rlga AICw barplot.pdf"))
```

```
barplot (AICw rlga vals [,3], names.arg = c("Brownian Motion", "
92
        Ornstein Uhlenbeck", "Early Burst", "White noise"), ylim = c
        (0,1), main = "Relative Upper Grinding Area", cex.names = 0.7)
     abline (h = 1, lty = "dashed")
93
   dev.off()
95
   pdf(paste0(output_path, "lncbrt AICw barplot.pdf"))
96
     barplot (AICw lncbrt vals [,3], names.arg = c("Brownian Motion", "
97
        Ornstein Uhlenbeck", "Early Burst", "White noise"), ylim = c
        (0,1), main = "Log Cuberoot of Body Mass", cex.names = 0.7)
     abline (h = 1, lty = "dashed")
98
   dev.off()
99
100
  #### Disparity Through Time Plots ####
101
   pdf(paste0(output path, "c1 dtt plot.pdf"))
102
     c1.dtt <- dtt (phy = carnivoran tree, data = C1 data, nsim = 100,
103
         index = c("avg.sq"), plot = TRUE)
     title ("Cross Sectional Shape of Upper Canine")
104
   dev.off()
105
106
  pdf(paste0(output_path, "rlga_dtt_plot.pdf"))
107
     rlga.dtt <- dtt(phy = carnivoran tree, data = RLGA data, nsim =
108
        100, index = c("avg.sq"), plot = TRUE)
     title ("Relative Upper Grinding Area")
109
   dev. off()
110
   pdf(paste0(output path, "lncbrt dtt plot.pdf"))
112
     lncbrt.dtt <- dtt(phy = carnivoran tree, data = lncbrt bodymass
113
        data, nsim = 100, index = c("avg.sq"), plot = TRUE
     title ("Log Cuberoot of Body Mass")
114
  dev.off()
```