

## Lab 6 R Source Code

### Code:

```
1 #
2 # Shawn Schwartz , 2019
3 # EEB C174 UCLA Spring 2019
4 # Lab 6 HW – Diversity Dynamics of Labrids
5 #
6
7 rm(list=ls())
8
9 #imports
10 library(phytools)
11 library(geiger)
12 library(ape)
13 library(apTreeshape)
14
15 cwd <- "~/Developer/EEB-C174-Labs/Lab6"
16 resources_path <- "resources/"
17 output_path <- "output/"
18
19 setwd(cwd)
20
21 labrid_tree <- read.tree(paste0(resources_path,"Labridae.tre"))
22 plot(labrid_tree, type = "fan", show.tip.label = F)
23 plot(labrid_tree, cex = 0.3)
24
25 ##### Diversification Methods #####
26 #Turn phylo into tree shape
27 labrid_treeshape <- as.treeshape(labrid_tree)
28
29 ## run colless test ##
30 labrid_colless_test <- colless.test(tree = labrid_treeshape, model
    = "yule", alternative = "less", n.mc = 1000)
31 labrid_colless_test
32
33 ## gamma stat ##
34 makeTransparent <- function(someColor, alpha=10)
35 {
36   newColor <- col2rgb(someColor)
37   apply(newColor, 2, function(curcoldata)
```

```
38 {
39   rgb(red=curcoldata[1],
40       green=curcoldata[2],
41       blue=curcoldata[3],
42       alpha=alpha,
43       maxColorValue=255)
44 })
45 }
46 ltt.plot(labrid_tree, log = "y")
47 plotTree(labrid_tree, color = makeTransparent("blue", alpha = 50),
48         ftype = "off", add = TRUE, mar = par()$mar)
49 # sample 50% of the tree
50 half_num <- (length(labrid_tree$tip.label))/2
51 half_num <- half_num + .5
52 half_num
53 incomplete_labrid_tree <- drop.random(phy = labrid_tree, n = half_
54   num)
55 ltt.plot(incomplete_labrid_tree, log = "y")
56 plotTree(incomplete_labrid_tree, color = makeTransparent("blue",
57   alpha = 50), ftype = "off", add = TRUE, mar = par()$mar)
58
59 labrid_tree_gammastat <- gammaStat(labrid_tree)
60 incomplete_labrid_tree_gammastat <- gammaStat(incomplete_labrid_
61   tree)
62 labrid_tree_gammastat
63 incomplete_labrid_tree_gammastat
64
65 ## Get the age of the clade by finding the branching time at the
66   root.
67 age <- branching.times(labrid_tree)[1]
68
69 ## Manually specify total richness
70 richness <- 600
71 labrid_birth <- (log(richness) - log(2)) / age
72 labrid_birth
73
74 num_simulations <- 1000
75 gamma_null <- numeric(num_simulations)
76 # gamma_null will hold the simulated gamma values
77 # for the trees that have been pruned down
78 for (i in 1:num_simulations)
```

```
75 {
76   sim_labrid_tree <- sim.bdtree(b = labrid_birth, d = 0, stop = "
      taxa", n = richness)
77   prune <- drop.random(sim_labrid_tree, 136) #here we drop 136
      species randomly from the tree (i.e., ~40%)
78   gamma_null[i] <- gammaStat(prune)
79 }
80
81 hist(gamma_null, xlim = c(-3.5, 3.5))
82 arrows(x0 = labrid_tree_gammastat, y0 = 100, x1 = labrid_tree_
      gammastat, y1 = 0, col = "red", lwd = 2, xlab = "Null Gammas",
      main = "Incomplete Sampling")
83
84 mean(gamma_null)
85 sd(gamma_null)
86
87
88 #which of the null values is smaller (more negative) than the data
      ?
89 smallerNull <- gamma_null <= labrid_tree_gammastat
90 smallerNull
91 count <- sum(smallerNull)
92 count
93 mcr_pval <- (count + 1)/(num_simulations+1)
94 mcr_pval
95
96 ## MEDUSA: Investigating Rate Shifts ##
97 #Question: Have different Labridae traits evolved at different
      rates?
98 run1 <- medusa(phy = labrid_tree)
99 run1
100
101 shift_nodes <- run1$model$split.at
102 shift_nodes
103 plot(run1, show.tip.label = FALSE)
104 extracted_clade_1 <- extract.clade(phy = labrid_tree, node = shift
      _nodes[1])
105 extracted_clade_2 <- extract.clade(phy = labrid_tree, node = shift
      _nodes[2])
106 extracted_clade_3 <- extract.clade(phy = labrid_tree, node = shift
      _nodes[3])
107
```

```
108 plot(extracted_clade_1, cex = 0.2)
109     axisPhylo()
110
111 plot(extracted_clade_2, cex = 0.6)
112     axisPhylo()
113
114 plot(extracted_clade_3, cex = 0.3)
115     axisPhylo()
```