Lab 2 R Source Code

Code:

```r
1  #
2  # Shawn Schwartz, 2019
3  # EEB C174 UCLA Spring 2019
4  # Lab 2 HW - Bat Testes
5  #
6
7  #clean up workspace
8  rm(list=ls())
9
10 #includes
11 library(phytools)
12 library(dplyr)
13
14 #directories
15 wd_path <- "~/Developer/EEB-C174-Labs/Lab2"
16 setwd(wd_path)
17 output_path <- "output/"
18 resources_path <- "resources/"
19
20 #### Import Data ####
21 bat_tree <- read.tree(paste0(resources_path, "bat_tree.tre"))
22 bat_traits <- read.csv(paste0(resources_path, "batTraits.csv"))
23
24 #### Clean Up Datasets ####
25 rownames(bat_traits) <- bat_traits$Species
26 cbind(rownames(bat_traits), bat_tree$tip.label) #check order
27 bat_traits <- bat_traits[match(bat_tree$tip.label, rownames(bat_
       traits)), ]
28 cbind(rownames(bat_traits), bat_tree$tip.label) #confirm matching
       order
29
30 #### Naive Analysis of Trait Data ####
31 trait_bodymass <- bat_traits$Body.mass..g.
32 trait_bodymass
33
34 trait_groupsize <- bat_traits$Group.size
35 trait_groupsize
36
```

```r
37  trait_testesmass <- bat_traits$Testes.mass..g.
38  trait_testesmass
39
40  ##compute relative traits
41  ###testes mass adjusted for body mass
42  relative_testes <- trait_testesmass/trait_bodymass
43  relative_testes
44
45  plot(trait_bodymass, relative_testes)
46
47  ##transform trait data with natural log
48  ln_trait_bodymass <- log(trait_bodymass)
49  ln_trait_bodymass
50
51  ln_trait_testesmass <- log(relative_testes)
52  ln_trait_testesmass
53
54  ln_trait_groupsize <- log(trait_groupsize)
55  ln_trait_groupsize
56
57  plot(ln_trait_bodymass, ln_trait_testesmass)
58  plot(ln_trait_groupsize, ln_trait_testesmass)
59
60  ##fit a linear model to the ln(data)
61  fit <- lm(ln_trait_testesmass ~ ln_trait_bodymass)
62  plot(ln_trait_bodymass, ln_trait_testesmass, xlab = "ln(Body Mass)
      ", ylab = "ln(Relative Testes Mass)")
63  abline(fit)
64
65  summary(fit)
66  lm_fit_summary <- capture.output(print(summary(fit)))
67  writeLines(lm_fit_summary, con = file(paste(output_path, "lm_
      summary_fit.txt")))
68
69  group_fit <- lm(ln_trait_testesmass ~ ln_trait_groupsize)
70  summary(group_fit)
71  lm_group_fit_summary <- capture.output(print(summary(group_fit)))
72  writeLines(lm_group_fit_summary, con = file(paste(output_path, "lm
      _summary_group_fit.txt")))
73
74  #### Analysis with PICs ####
75  PIC_ln_trait_bodymass <- pic(ln_trait_bodymass, bat_tree)
```

```r
76  PIC_ln_trait_testesmass <- pic(ln_trait_testesmass, bat_tree)
77  PIC_fit <- lm(PIC_ln_trait_testesmass ~ PIC_ln_trait_bodymass - 1)
        #-1 to remove intercept
78  plot(PIC_ln_trait_bodymass, PIC_ln_trait_testesmass, xlab = "
        Contrasts in ln(Body Mass)", ylab = "Contrasts in ln(Relative
        Testes Mass)")
79  abline(PIC_fit)
80
81  summary(PIC_fit)
82  lm_PIC_fit_summary <- capture.output(print(summary(PIC_fit)))
83  writeLines(lm_PIC_fit_summary, con = file(paste(output_path, "lm_
        summary_PIC_fit.txt")))
84
85  PIC_ln_trait_groupsize <- pic(ln_trait_groupsize, bat_tree)
86  PIC_group_fit <- lm(PIC_ln_trait_testesmass ~ PIC_ln_trait_
        groupsize - 1)
87  summary(PIC_group_fit)
88  lm_PIC_group_fit_summary <- capture.output(print(summary(PIC_group
        _fit)))
89  writeLines(lm_PIC_group_fit_summary, con = file(paste(output_path,
        "lm_summary_PIC_group_fit.txt")))
90
91  #### Generate 2D Phylomorphospace ####
92  ln_traits <- cbind(ln_trait_bodymass, ln_trait_testesmass)
93  rownames(ln_traits) <- bat_traits$Species
94  pdf(paste0(output_path,"bat_testes_phylomorphospace.pdf"))
95    phylomorphospace(tree = bat_tree, ln_traits, xlab = "ln(Body
        Mass)", ylab = "ln(Relative Testes Mass)")
96  dev.off()
97
98  ln_traits_group <- cbind(ln_trait_groupsize, ln_trait_testesmass)
99  rownames(ln_traits_group) <- bat_traits$Species
100 pdf(paste0(output_path,"bat_testes_phylomorphospace_groupsize.pdf"
        ))
101   phylomorphospace(tree = bat_tree, ln_traits_group, xlab = "ln(
        Group Size)", ylab = "ln(Relative Testes Mass)")
102 dev.off()
103
104 #### Prepare Plots for Report ####
105 pdf(paste0(output_path,"bat_fit_analyses_GROUP_combined.pdf"))
106   par(mfrow = c(1,2))
107   #Plotting Naive Analysis
```

```
108    plot(ln_trait_groupsize, ln_trait_testesmass, xlab = "ln(Group
           Size)", ylab = "ln(Relative Testes Mass)", main = "Naive
           Analysis")
109    abline(fit)
110
111    #Plotting Analysis using PICs
112    plot(PIC_ln_trait_groupsize, PIC_ln_trait_testesmass, xlab = "
           PICs for ln(Group Size)", ylab = "PICs for ln(Relative Testes
           Mass)", main = "Analysis using PICs")
113    abline(PIC_fit)
114 dev.off()
115
116 pdf(paste0(output_path,"bat_fit_analyses_GROUP_separate.pdf"))
117    #Plotting Naive Analysis
118    plot(ln_trait_groupsize, ln_trait_testesmass, xlab = "ln(Group
           Size)", ylab = "ln(Relative Testes Mass)", main = "Naive
           Analysis")
119    abline(fit)
120
121    #Plotting Analysis using PICs
122    plot(PIC_ln_trait_groupsize, PIC_ln_trait_testesmass, xlab = "
           PICs for ln(Group Size)", ylab = "PICs for ln(Relative Testes
           Mass)", main = "Analysis using PICs")
123    abline(PIC_fit)
124 dev.off()
125
126 pdf(paste0(output_path,"bat_fit_analyses_separate.pdf"))
127    plot(ln_trait_bodymass, ln_trait_testesmass, xlab = "ln(Body
           Mass)", ylab = "ln(Relative Testes Mass)", main = "Naive
           Analysis")
128    abline(fit)
129
130    #Plotting Analysis using PICs
131    plot(PIC_ln_trait_bodymass, PIC_ln_trait_testesmass, xlab = "
           PICs for ln(Body Mass)", ylab = "PICs for ln(Relative Testes
           Mass)", main = "Analysis using PICs")
132    abline(PIC_fit)
133 dev.off()
134
135 pdf(paste0(output_path,"bat_fit_analyses_combined.pdf"))
136    par(mfrow = c(1,2))
137    #Plotting Naive Analysis
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138    plot(ln_trait_bodymass, ln_trait_testesmass, xlab = "ln(Body
         Mass)", ylab = "ln(Relative Testes Mass)", main = "Naive
         Analysis")
139    abline(fit)
140
141    #Plotting Analysis using PICs
142    plot(PIC_ln_trait_bodymass, PIC_ln_trait_testesmass, xlab = "
         PICs for ln(Body Mass)", ylab = "PICs for ln(Relative Testes
         Mass)", main = "Analysis using PICs")
143    abline(PIC_fit)
144 dev.off()
145
146 #### Get the Bat Tree ####
147 ladder_bat_tree <- ladderize(bat_tree)
148 pdf(paste0(output_path,"bat_tree_visual.pdf"))
149    plot(ladder_bat_tree, cex = 0.6)
150 dev.off()
```