phylo_analyses

Everyone 3/22/2018

```
library(phylolm)
  trait<-data.frame(mean_body_size=traits$mean_body_size,clutch_size=traits$clutch_size)</pre>
  row.names(trait)<-row.names(traits)</pre>
  trait<-subset(trait,trait$mean_body_size!="NaN"&trait$clutch_size!="NaN")
  trait<-subset(trait,row.names(trait)%in%aus_bird_tree$tip.label)</pre>
  tree plotting <-drop.tip(aus bird tree, aus bird tree$tip.label[!aus bird tree$tip.label%in%row.names(t
  response_variables$SCIENTIFIC_NAME<-gsub(" ","_",response_variables$SCIENTIFIC_NAME)
  rv<-filter(response_variables, SCIENTIFIC_NAME%in%tree_plotting$tip.label)
  exploiter<-as.array(rv$exploiter)</pre>
  row.names(exploiter)<-rv$SCIENTIFIC_NAME</pre>
  exploiter2<-exploiter-mean(exploiter)
  tree_plotting_2<-drop.tip(tree_plotting, tree_plotting$tip.label[!tree_plotting$tip.label%in%row.names
  trait<-subset(trait,row.names(trait)%in%tree_plotting_2$tip.label)</pre>
  dd<-data.frame(urb=exploiter2)
  dd$body_size<-trait$mean_body_size[match(row.names(dd),row.names(trait))]
  dd$clutch size<-trait$clutch size[match(row.names(dd),row.names(trait))]
  summary(phylolm(urb~log10(body_size)+clutch_size,data=dd,phy=tree_plotting_2))
##
## Call:
## phylolm(formula = urb ~ log10(body_size) + clutch_size, data = dd,
       phy = tree_plotting_2)
##
##
##
      AIC logLik
##
     2100 -1046
##
## Raw residuals:
           1Q Median
                               3Q
                                      Max
      Min
## -10.133 2.043 3.371
                                     8.671
                            4.662
##
## Mean tip height: 123.4092
## Parameter estimate(s) using ML:
## sigma2: 0.278487
## Coefficients:
                                StdErr t.value
                    Estimate
                                                p.value
                   -8.368008 3.022570 -2.7685 0.005862 **
## (Intercept)
## log10(body_size) 1.604430 0.357640 4.4862
                                                 9.2e-06 ***
## clutch_size
                    ## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

```
library(phylosignal)
  library(phylobase)
  dd$body_size<-log10(dd$body_size)
  out<-phylo4d(tree_plotting_2,tip.data=dd)</pre>
  phyloSignal(out)
## $stat
##
                                                            Lambda
                   Cmean
                                  Ι
                                             K
                                                  K.star
## urb
              0.2560077 0.03539915 0.09641725 0.1213145 0.3838173
## body_size 0.8366279 0.12266909 3.62377562 1.2945208 0.9961014
## clutch_size 0.7006398 0.10983803 0.40268916 0.2649179 0.9587598
```