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$tip.label%in%row.names(t
  response_variables\$CIENTIFIC_NAME<-gsub(" ","_",response_variables\$CIENTIFIC_NAME)
  rv<-filter(response_variables,SCIENTIFIC_NAME%in%tree_plotting$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$tip.label)
  dd<-data.frame(urb=exploiter2)
  dd$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))]</pre>
  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
##
     2075 -1034
##
## Raw residuals:
       Min
           1Q Median
                                3Q
                                       Max
## -10.076 2.175 3.320
                             4.521
                                     8.684
##
## Mean tip height: 123.4092
## Parameter estimate(s) using ML:
## sigma2: 0.267161
## Coefficients:
                                 StdErr t.value
                     Estimate
                                                 p.value
                    -8.485350 2.961122 -2.8656 0.004356 **
## (Intercept)
## log10(body_size) 1.701696 0.350295 4.8579 1.637e-06 ***
## clutch_size
                     0.624461 0.059007 10.5829 < 2.2e-16 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

```
library(phylosignal)
  library(phylobase)
  dd$body_size<-log10(dd$body_size)</pre>
  out<-phylo4d(tree_plotting_2,tip.data=dd)</pre>
  phyloSignal(out)
## $stat
##
                                                  K.star
                   Cmean
                                  Ι
                                             K
                                                            Lambda
## urb
              0.2456731 0.03417581 0.08672169 0.1097742 0.3552770
## body_size 0.8352878 0.12286859 3.60640652 1.2864414 0.9961203
## clutch_size 0.6328941 0.11811881 0.37816393 0.2431154 0.9570027
## $pvalue
                               K K.star Lambda
##
               Cmean
                         I
              0.001 0.001 0.075 0.063 0.001
## urb
## body_size 0.001 0.001 0.001 0.001 0.001
```

clutch_size 0.001 0.001 0.001 0.001 0.001