Did Complex Song and Dance Co-Evolve With Brain Size in the Birds of Paradise (Aves: Paradisaeidae)?

2024-08-08

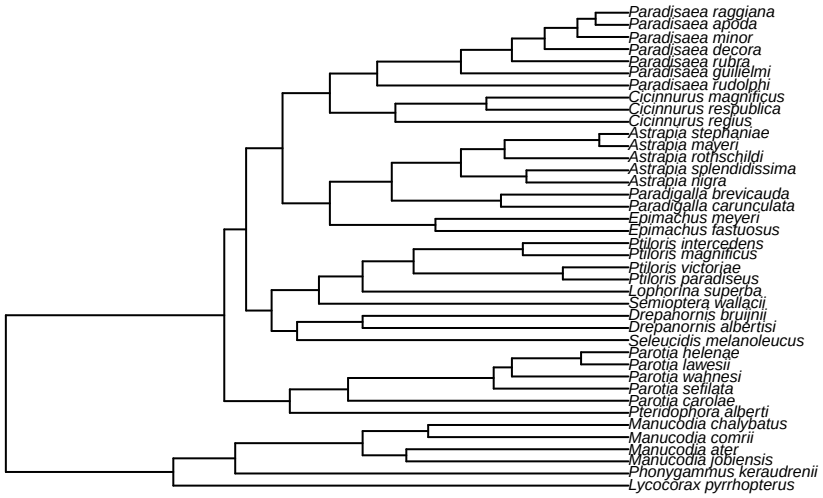
Code used to analyse the relationship between courtship display complexity and brain size in the birds of paradise

```
# First, load all the required packges and set the working directory
library(phytools) # Comparative methods
library(ggplot2) # Plotting
library(dplyr) # Data wrangling
library(caper) # PGLS
library(patchwork) # Combining plots
library(sensiPhy) # Model stability
library(ggrepel) # Annotating plots more flexibly
```

Part 1: Associations between complexity scores

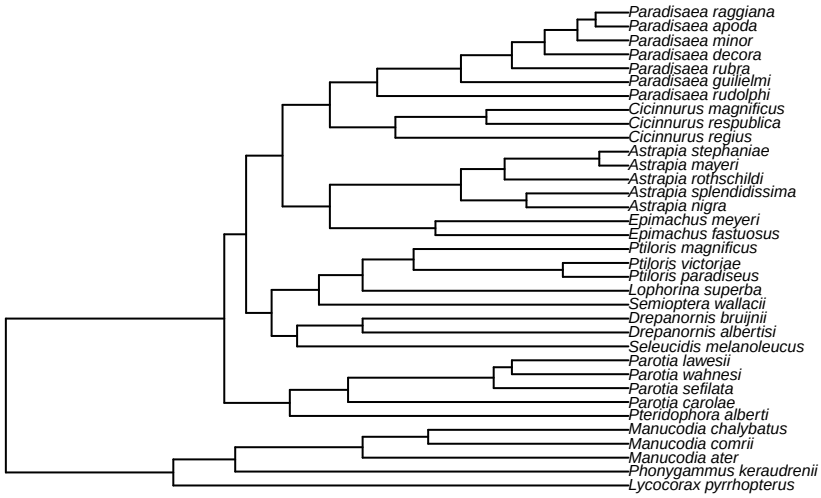
1.1. Prepare the dataframe and tree

```
# First, we'll import the bird of paradise phylogeny from Ligon et al. (2018)
tree <- read.nexus("Ligon.et.al._UltrametricTree") # Import the tree as .nexus
 # Quick look at the tree; this includes all species recognized by Irestedt et al. (2009)
plot(tree, cex = .5)
```



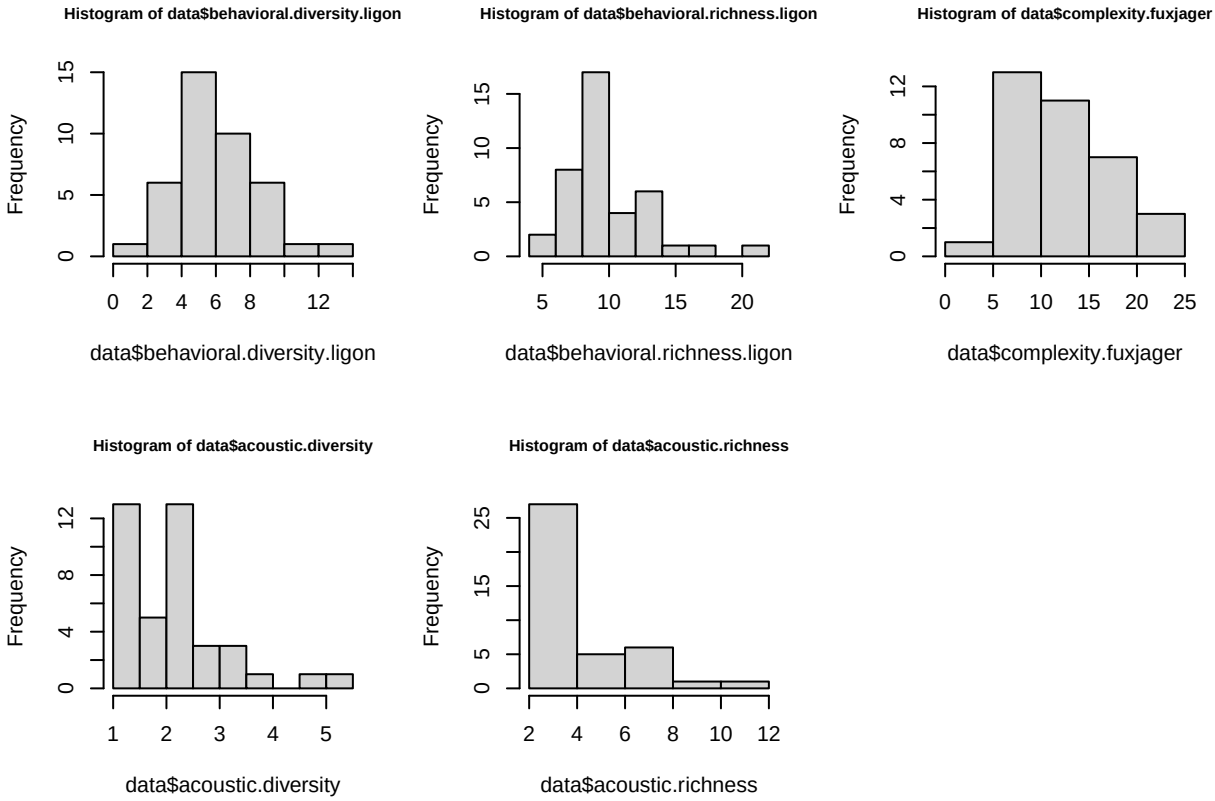

```
# We'll also load the full dataframe that includes complexity scores for all species
data <- read.csv("Paradisaeidae_Brain.Data.Full.csv")
str(data)
```

```r
# Some descriptive stats of brain size in the BoPs
data2 <- filter(data, ECV != "NA")
mean(data2$ECV)
(mean(data2$ECV)*1.036)/1000 # Conversion to mass (in g)
sd(data2$ECV)
(sd(data2$ECV)*1.036)/1000
max(data2$ECV)
(max(data2$ECV)*1.036)/1000
min(data2$ECV)
(min(data2$ECV)*1.036)/1000

# For behavioral complexity (Miles & Fuxjager, 2018),
# we don't have data for the following species;
missing.fuxjager <- c("Manucodia_jobiensis",
                      "Paradigalla_brevicauda",
                      "Paradigalla_carunculata",
                      "Parotia_helenae",
                      "Ptiloris_intercedens")

# We can drop these species from the tree used for analyses
# incorporating data from Miles & Fuxjager (2018)
tree.fuxjager <- drop.tip(tree, missing.fuxjager)
sum(table(tree.fuxjager$tip.label)) # this tree has 35 species
plot(tree.fuxjager, cex = .5) # Let's take a look
```




```r
# We can also drop these from the data frame
data.fuxjager <- filter(data, complexity.fuxjager != "NA")

# Let's first take a look at the distribution of all complexity scores
par(mfrow = c(2, 3))
hist(data$behavioral.diversity.ligon, cex.main = .75)
hist(data$behavioral.richness.ligon, cex.main = .75)
hist(data$complexity.fuxjager, cex.main = .75)
hist(data$acoustic.diversity, cex.main = .75)
hist(data$acoustic.richness, cex.main = .75)
# Acoustic complexity scores appear skewed, so may need to be transformed later on...

# Create comparative data set for caper for all species with
```

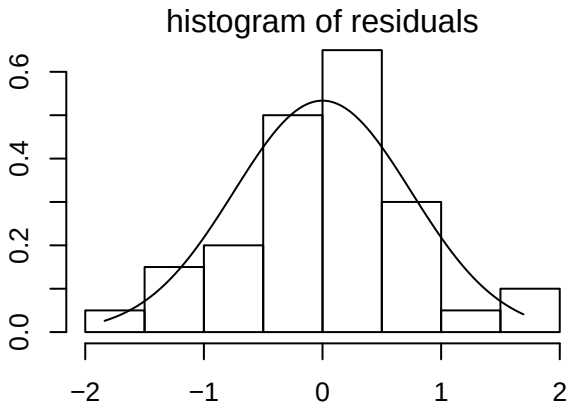
```
# complexity scores from Ligon et al. 2018
complexity_scores_1 <- comparative.data(phy = tree,
                                        data = data,
                                        names.col = species,
                                        vcv = TRUE,
                                        na.omit = FALSE,
                                        warn.dropped = TRUE)
# Create another comparative data set for caper for all species
# with complexity scores from Miles & Fuxjager 2018
complexity_scores_2 <- comparative.data(phy = tree.fuxjager,
                                        data = data.fuxjager,
                                        names.col = species,
                                        vcv = TRUE,
                                        na.omit = FALSE,
                                        warn.dropped = TRUE)
```

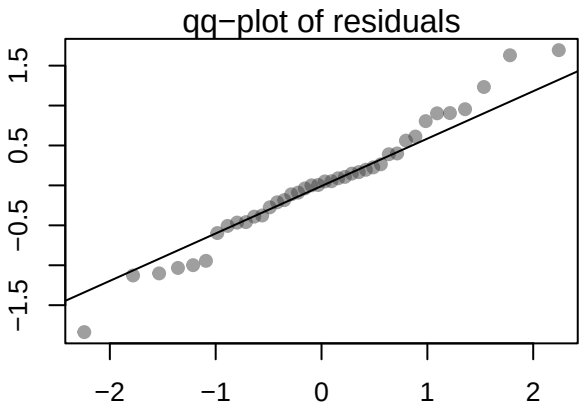


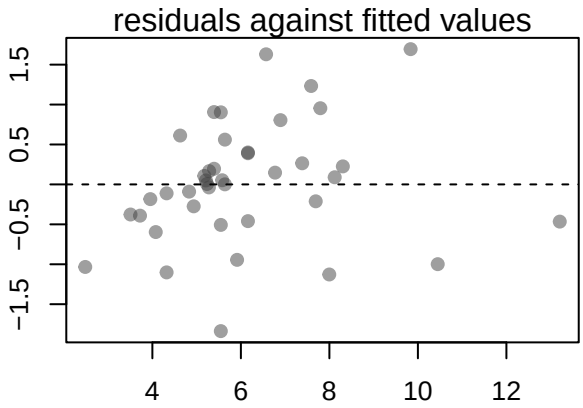
Now that we have all our complexity score data in the same place, we can see how they relate to one another.

1.2. Running PGLS models

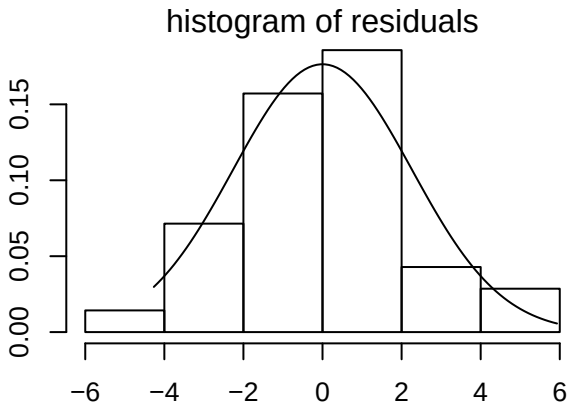
```
# Call the diagnostic functions
source("diagnostic_fcns.r")

# Fit a pgls model: diversity ~ richness [behavioural]
m1<- pgls(behavioral.diversity.ligon ~ behavioral.richness.ligon,
          data = complexity_scores_1, lambda = 1)
# Diagnostics
diagnostics.plot(m1)
```

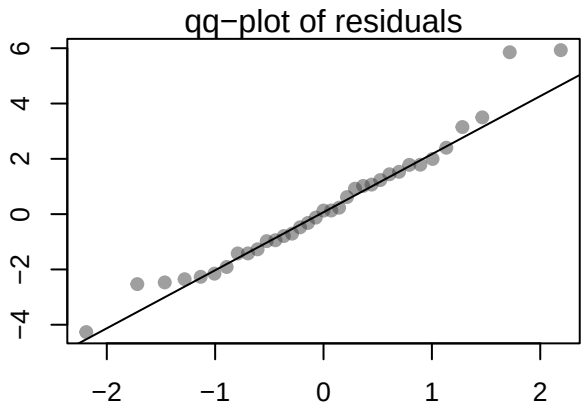


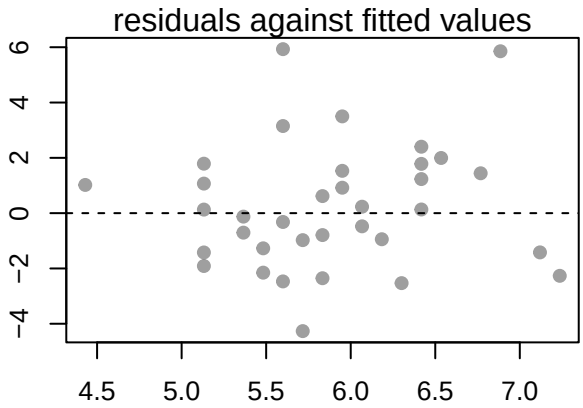




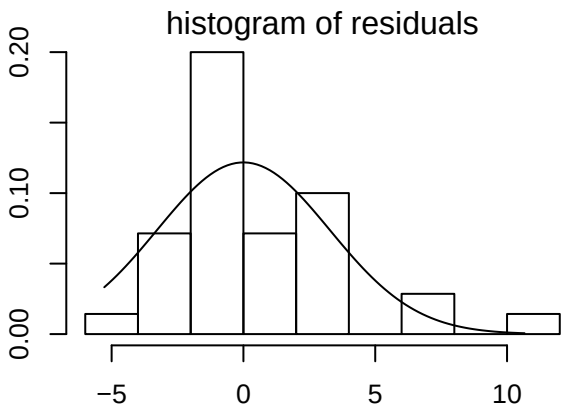

```r
# Inspect the output
summary(m1)
# Formal test of normality
res1 <- residuals(m1, phylo = TRUE)
shapiro.test(res1)

# Fit a pgls model: diversity ~ complexity
m2<- pgls(behavioral.diversity.ligon ~ complexity.fuxjager,
          data = complexity_scores_2, lambda = 1)
# Diagnostics
diagnostics.plot(m2)
```

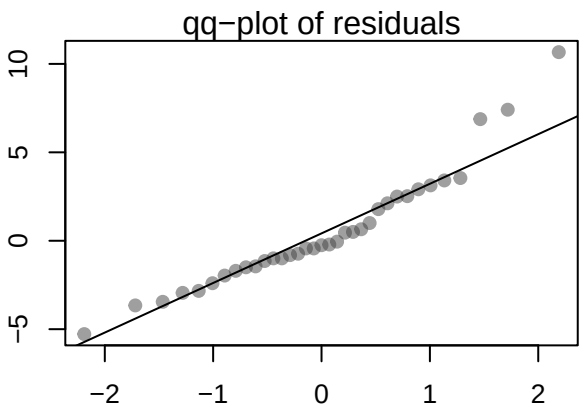


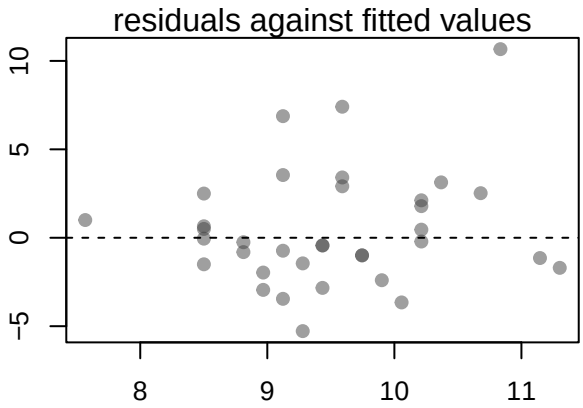




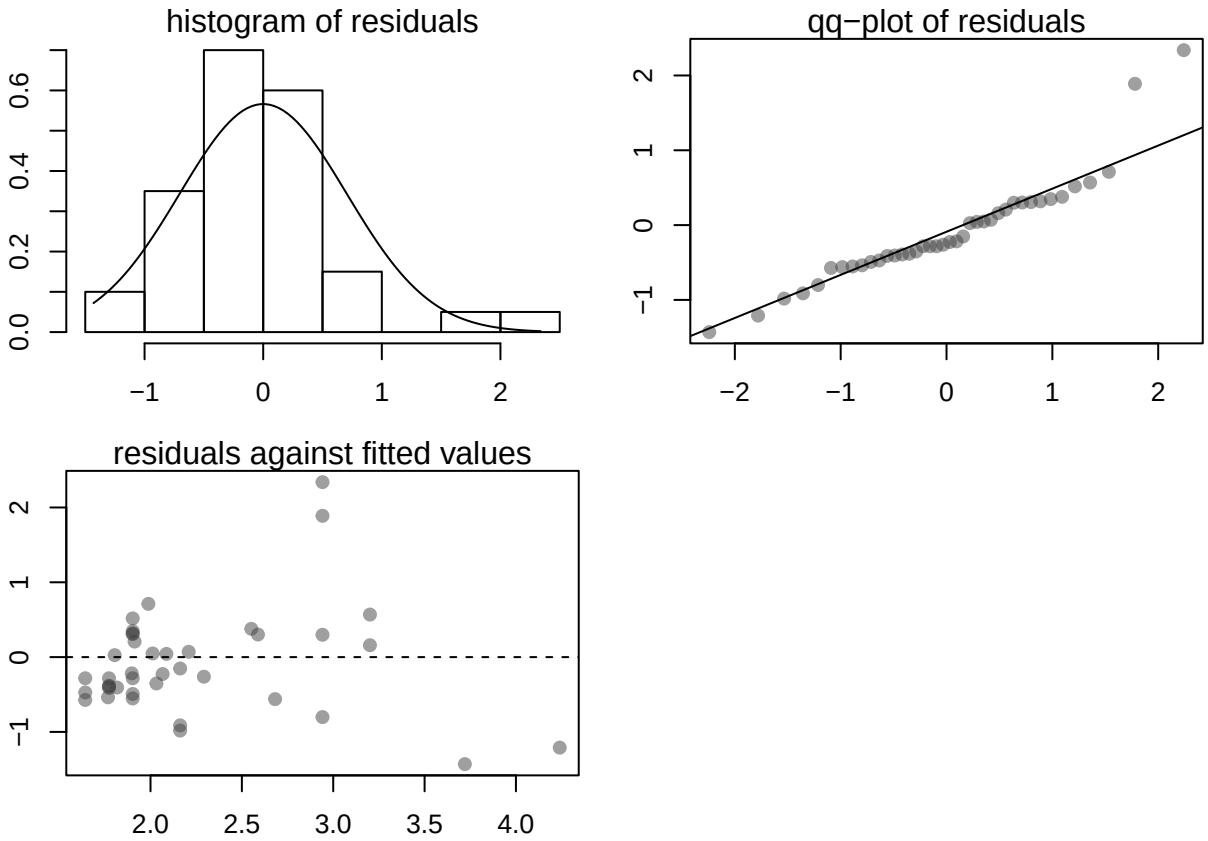

```r
# Inspect the output
summary(m2)
# Formal test of normality
res2 <- residuals(m2, phylo = TRUE)
shapiro.test(res2)

# Fit a pgls model: richness ~ complexity
m3<- pgls(behavioral.richness.ligon ~ complexity.fuxjager,
          data = complexity_scores_2, lambda = 1)
# Diagnostics
diagnostics.plot(m3)
```








```r
# Inspect the output
summary(m3)
# Formal test of normality
res3 <- residuals(m3, phylo = TRUE)
shapiro.test(res3)

# Fit a pgls model: diversity ~ richness [acoustic]
m4<- pgls(acoustic.diversity ~ acoustic.richness,
          data = complexity_scores_1, lambda = 1)
# Diagnostics
diagnostics.plot(m4)
```

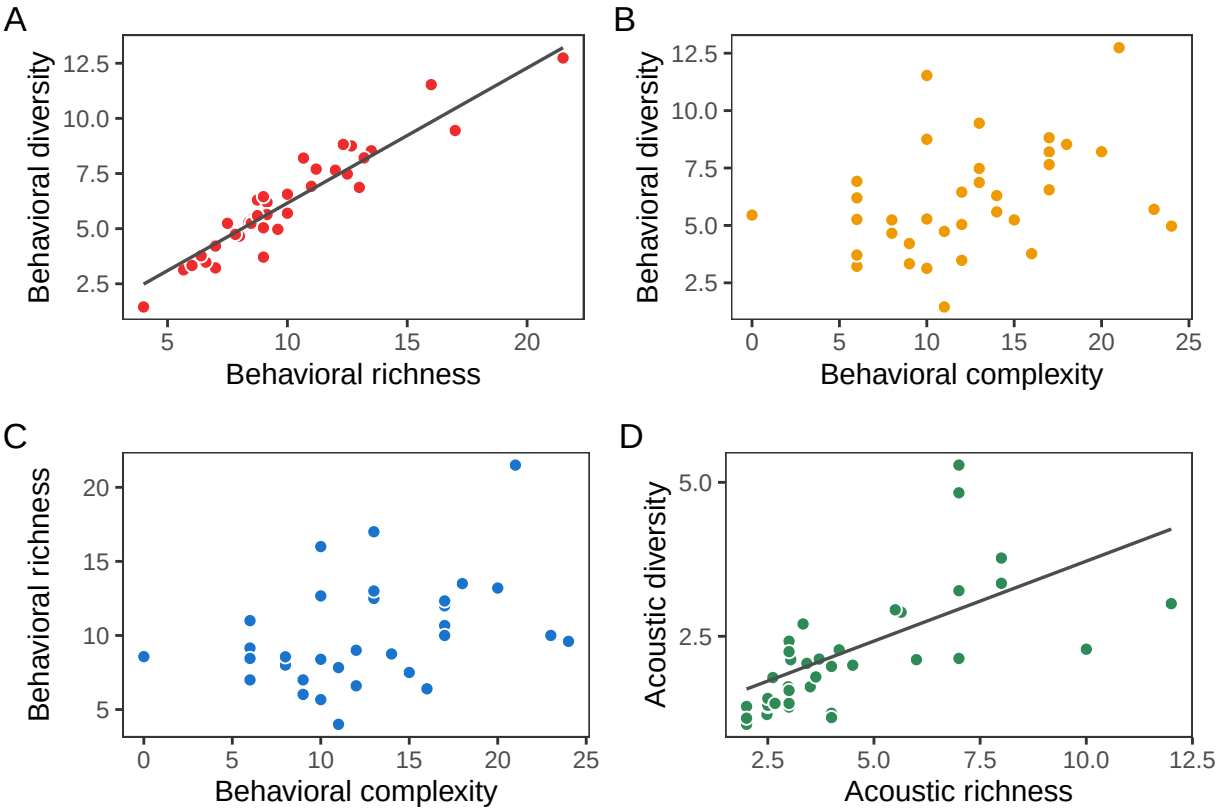



```
# Inspect the output
summary(m4)
# Formal test of normality
res4 <- residuals(m4, phylo = TRUE)
shapiro.test(res4)
```

1.3. Plotting associations between complexity scores

```
### Let's plot these results ###

# Model 1 #

# Predict values
m1.fit<- predict(m1, data)

# Create data frame for males with predicted values
df_predicted.m1 <- mutate(data, predicted = m1.fit)

p1 <- ggplot(data, aes(y = behavioral.diversity.ligon, x = behavioral.richness.ligon)) +
  geom_point(data = data, shape = 21, size = 2, alpha = 1,
             col = "white", fill = "firebrick2") +
  geom_line(data = df_predicted.m1, aes(y = predicted),
            color = "grey30", linetype = 1, linewidth = 0.6) +
  theme_bw() + ylab("Behavioral diversity") + xlab("Behavioral richness") +
  labs(colour = "Clade") +
  scale_y_continuous(breaks = c(2.5, 5, 7.5, 10, 12.5)) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
```

```r
# Model 2 #

p2 <- ggplot(data.fuxjager, aes(y = behavioral.diversity.ligon, x = complexity.fuxjager)) +
  geom_point(data.fuxjager = data, shape = 21, size = 2, alpha = 1,
             col = "white", fill = "orange2") +
  theme_bw() + ylab("Behavioral diversity") + xlab("Behavioral complexity") +
  labs(colour = "Clade") +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())

# Model 3 #

p3 <- ggplot(data.fuxjager, aes(y = behavioral.richness.ligon, x = complexity.fuxjager)) +
  geom_point(data.fuxjager = data, shape = 21, size = 2, alpha = 1,
             col = "white", fill = "dodgerblue3") +
  theme_bw() + ylab("Behavioral richness") + xlab("Behavioral complexity") +
  labs(colour = "Clade") +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())

# Model 4 #

# Predict values
m4.fit<- predict(m4, data)

# Create data frame for males with predicted values
df_predicted.m4 <- mutate(data, predicted = m4.fit)

p4 <-  ggplot(data, aes(y = acoustic.diversity, x = acoustic.richness)) +
  geom_point(data = data, shape = 21, size = 2, alpha = 1,
             col = "white", fill = "seagreen") +
  geom_line(data = df_predicted.m4, aes(y = predicted),
            color = "grey30", linetype = 1, linewidth = 0.6) +
  theme_bw() + ylab("Acoustic diversity") + xlab("Acoustic richness") +
  labs(colour = "Clade") +
  scale_y_continuous(breaks = c(2.5, 5, 7.5, 10, 12.5)) +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())

# Stitch plots together
combined <- (p1|p2)/(p3|p4) & theme(legend.position = "bottom")
combined + plot_layout(guides = "collect") + plot_annotation(tag_levels = 'A')
```



Part 2: Relative brain size and signal complexity scores

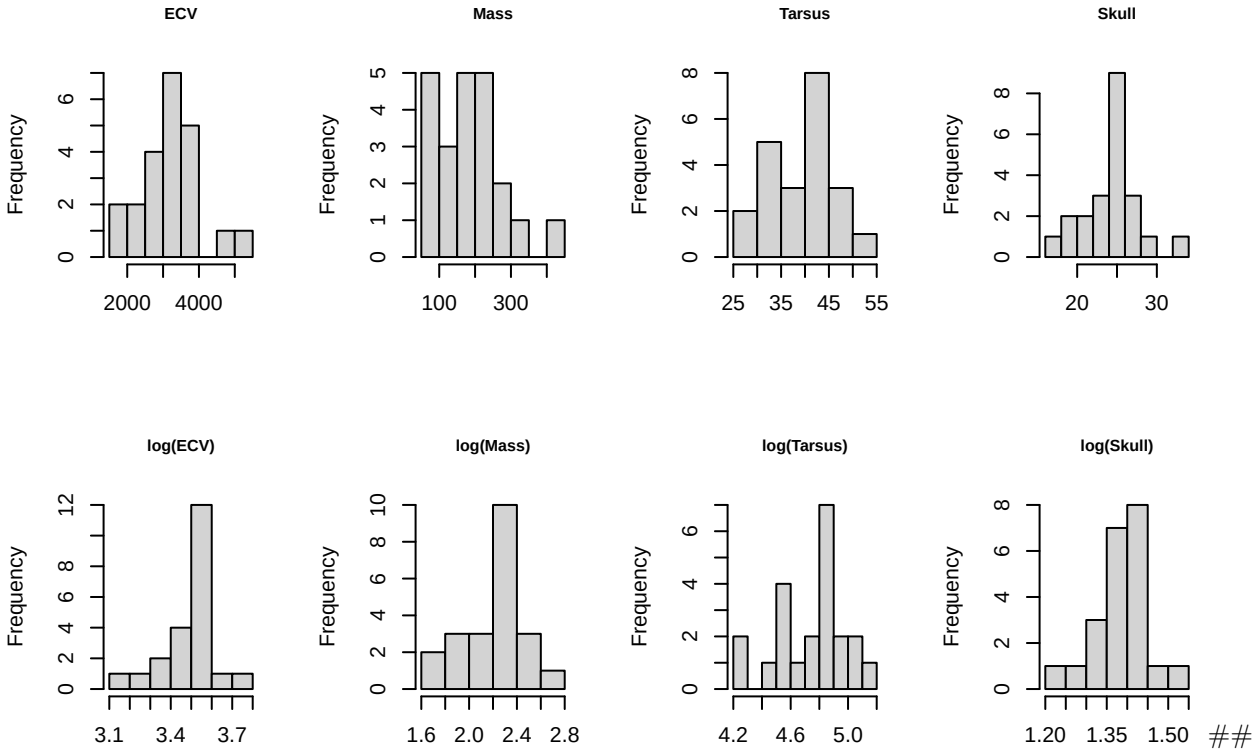
2.1. Importing data and tree again; starting with a fresh workspace

```
# Start with a fresh R environment
rm(list = ls())

# Import the tree
tree <- read.nexus("Ligon.et.al._UltrametricTree") # Import the tree as .nexus
# Import the data
data <- read.csv("Paradisaeidae_Brain.Data.csv") # Import the dataframe as .csv

# Let's take a quick look at the data
str(data, 4)
max(data$ECV) # Largest brain is Lycocorax pyrrhopterus with 5048.42 mm^3
min(data$ECV) # Smallest brain is Cicinnurus regius with 1557.87 mm^3
mean(data$ECV) # Our mean brain size is 3218.609 mm^3...
sd(data$ECV) # with a standard deviation of 896.6828 mm^3
```

2.2. Inspection of variables

```
# Log-transform body mass and brain mass
data$logECV <- log10(data$ECV)
data$logMass <- log10(data$body.mass)
data$logTarsus <- log10(data$tarsus.length^3)
data$logSkull <- log10(data$skull.length)
```

```
par(mfrow = c(2, 4))
hist(data$ECV, main = "ECV", cex.main = .75, xlab = NULL)
hist(data$body.mass, main = "Mass", cex.main = .75, xlab = NULL)
hist(data$tarsus.length, main = "Tarsus", cex.main = .75, xlab = NULL)
hist(data$skull.length, main = "Skull", cex.main = .75, xlab = NULL)
hist(data$logECV, main = "log(ECV)", cex.main = .75, xlab = NULL)
hist(data$logMass, main = "log(Mass)", cex.main = .75, xlab = NULL)
hist(data$logTarsus, main = "log(Tarsus)", cex.main = .75, xlab = NULL)
hist(data$logSkull, main = "log(Skull)", cex.main = .75, xlab = NULL)
```



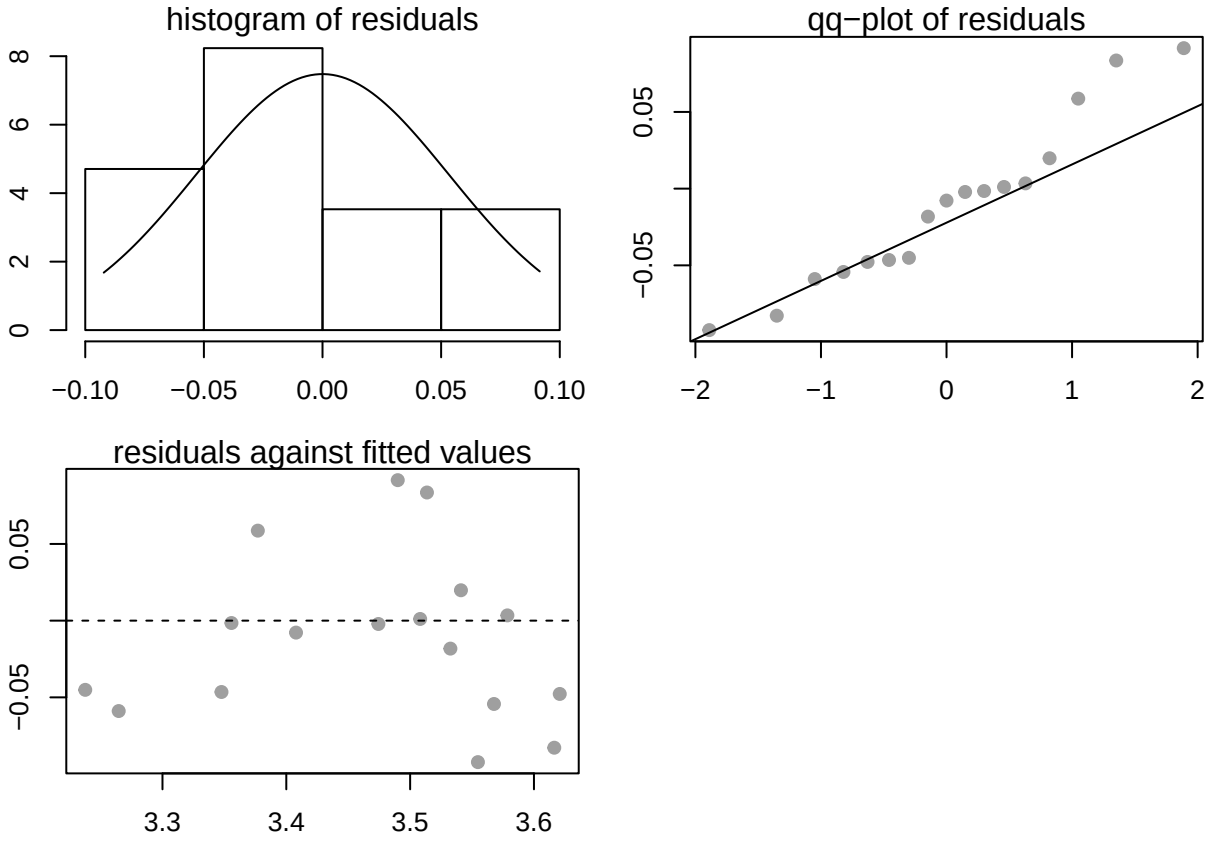
2.3. Preparing dataframes and trees with subsetted species

Now we have two data sets and two phylogenetic trees; one pair for all bird of paradise species, and another pair for only the core birds of paradise. We will use these two data sets to investigate any associations between brain size and behavioral complexity

2.4.1 PGLS models including body mass as a predictor

```
# Call the diagnostic functions
source("diagnostic_fcns.r")
# Call the custom sensitivity analysis script (from Mellor et al. 2021)
source("influ_phylm2_Paterno_et_al.R") # Use these functions for models with >1 predictor
source("summary_influ_phylm2_Paterno_et_al.R")
source("plot_influ_phylm2_Paterno_et_al.R")

############################
### Behavioral diversity ###
############################

# Fit pgls model
```

```
m1<- pgls(logECV ~ behavioral.diversity.ligon + logMass,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m1)
```

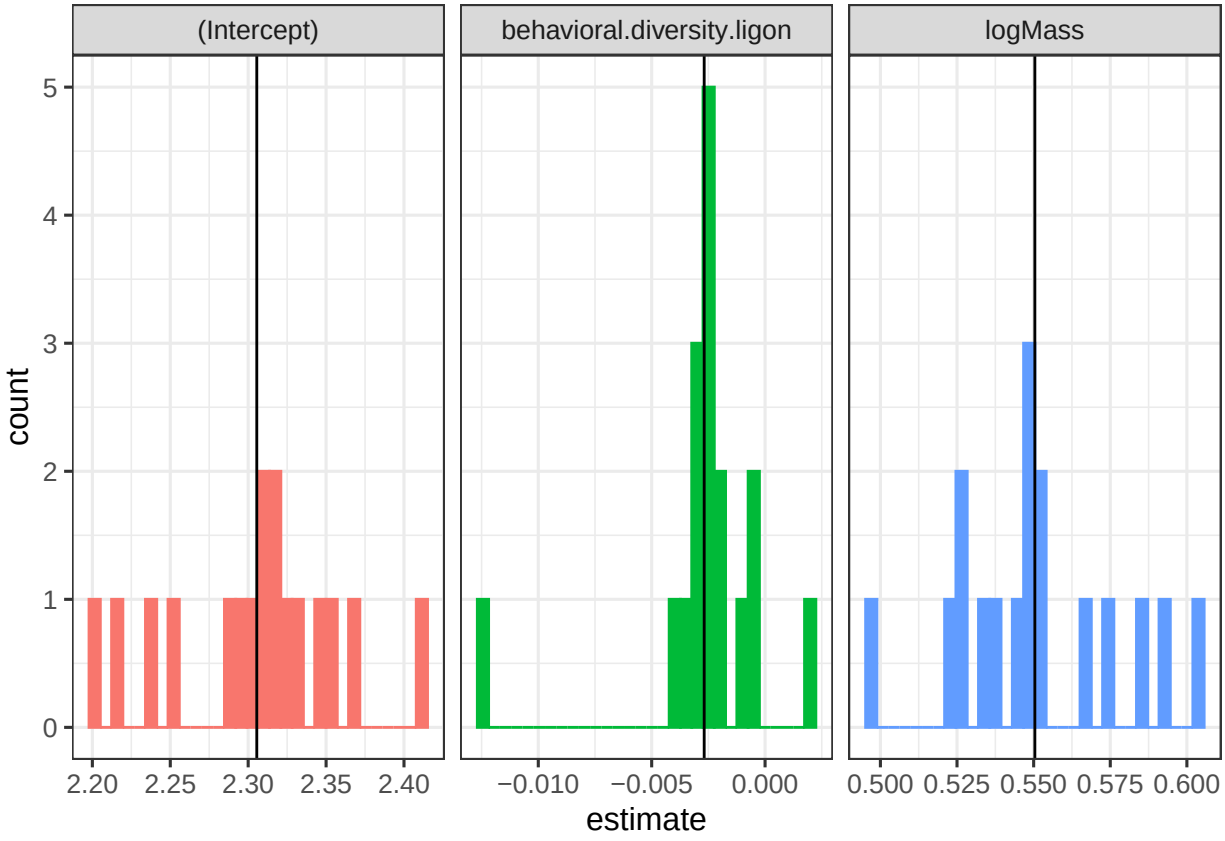



```
# Inspect the output
summary(m1)
# Formal test of normality
res1 <- residuals(m1, phylo = TRUE)
shapiro.test(res1)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m1 <- influ_phylm2(logECV ~ behavioral.diversity.ligon + logMass,
                         phy = comparative_data_poly$phy,
                         data = comparative_data_poly$data, model = "BM",
                         track = FALSE)
```

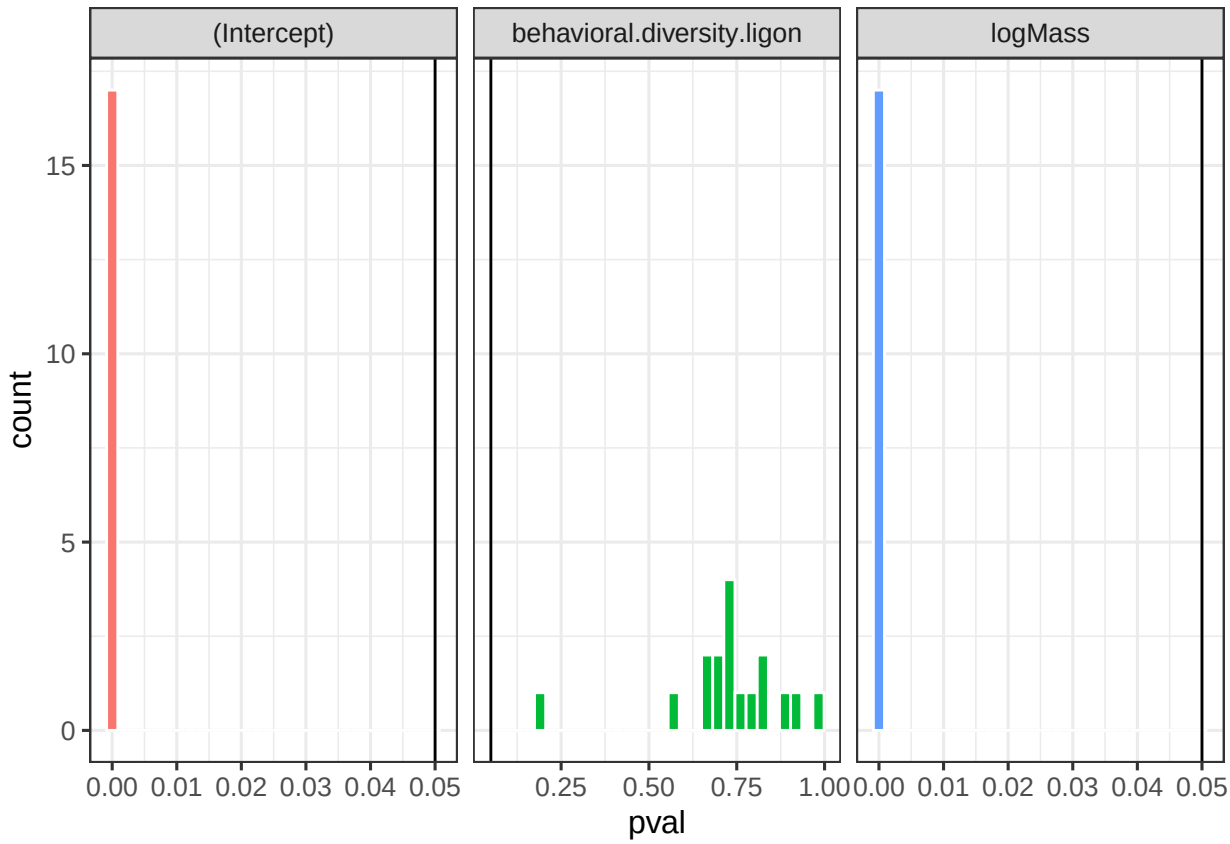
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m1$full.model.estimates
# test for influential species:
summary_influ2(sensi.m1)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m1)
```

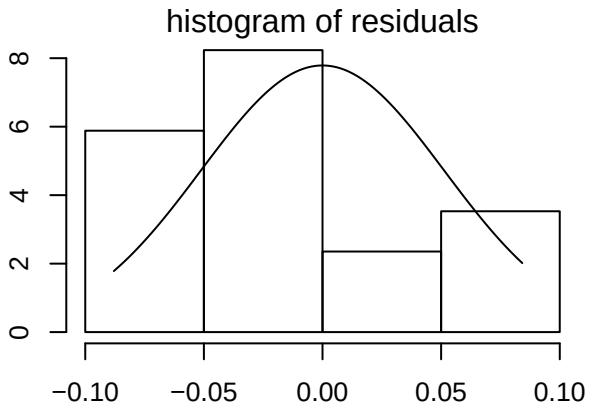
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

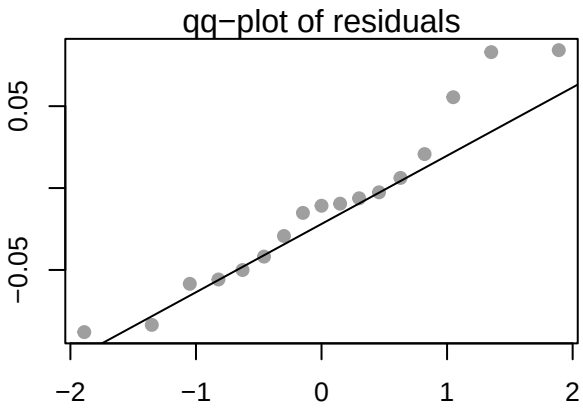


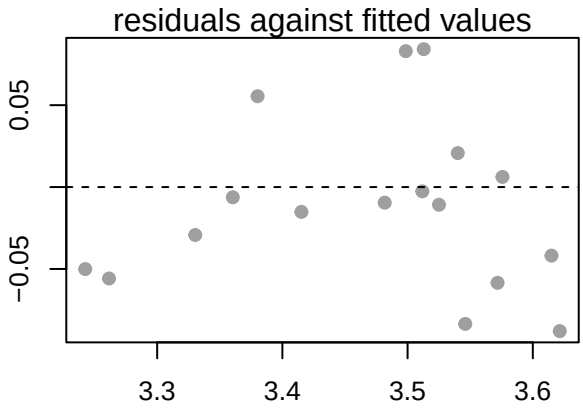

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m1$sensi.estimates

############################
### Behavioral richness ###
############################

# Fit pgls model
m2<- pgls(logECV ~ behavioral.richness.ligon + logMass,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m2)
```





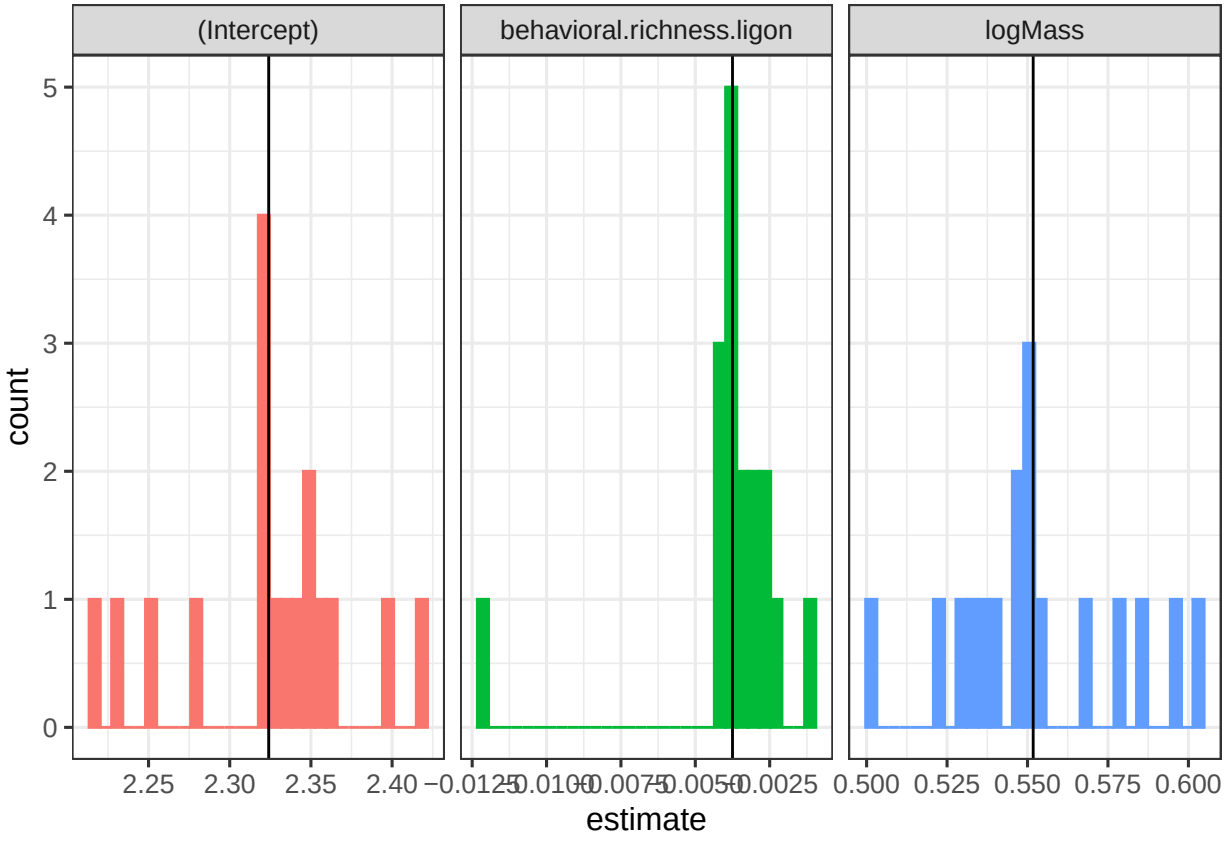



```
# Inspect the output
summary(m2)
# Formal test of normality
res2 <- residuals(m2, phylo = TRUE)
shapiro.test(res2)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m2 <- influ_phylm2(logECV ~ behavioral.richness.ligon + logMass,
                         phy = comparative_data_poly$phy,
                         data = comparative_data_poly$data, model = "BM",
                         track = FALSE)
```

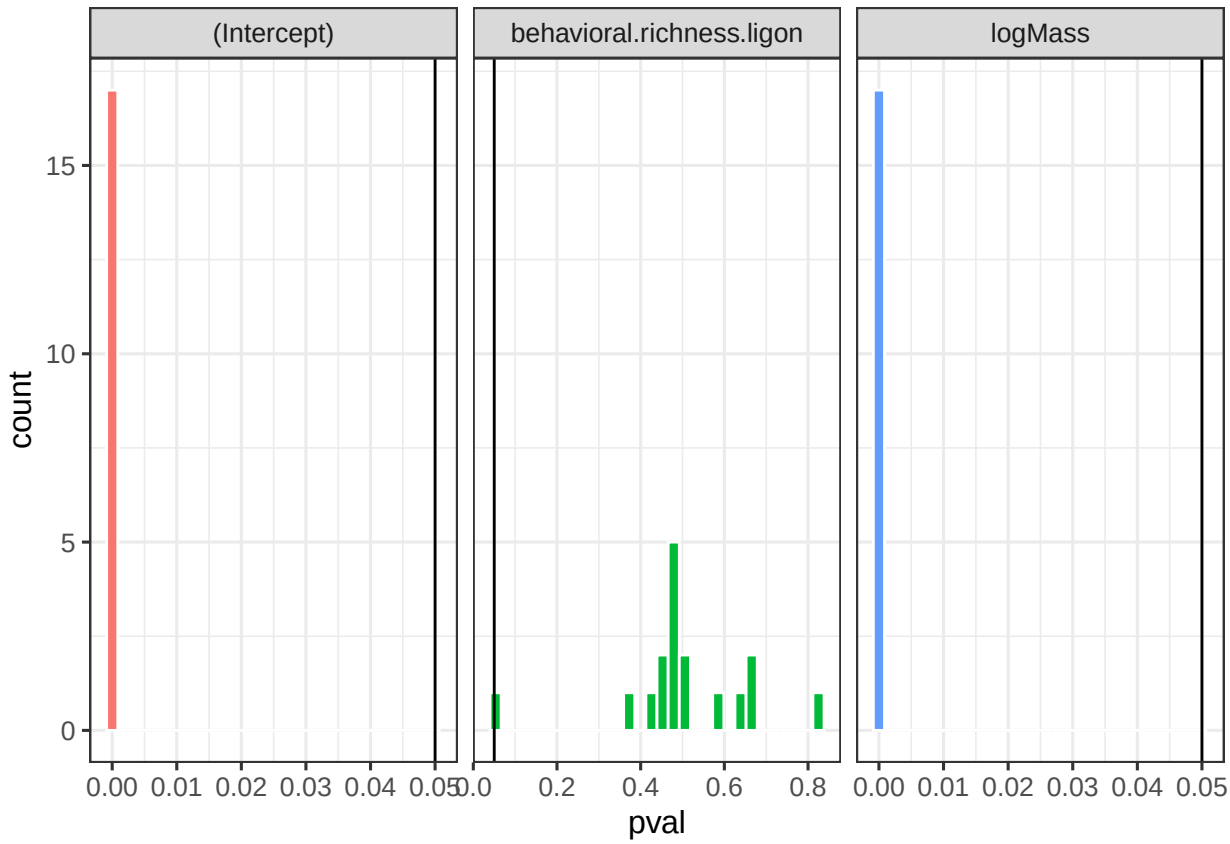
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m2$full.model.estimates
# test for influential species:
summary_influ2(sensi.m2)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m2)
```

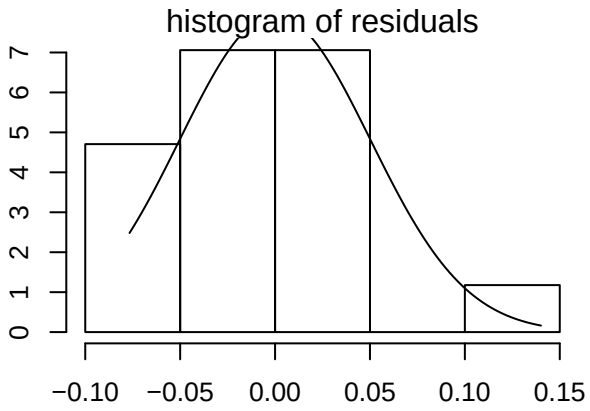
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

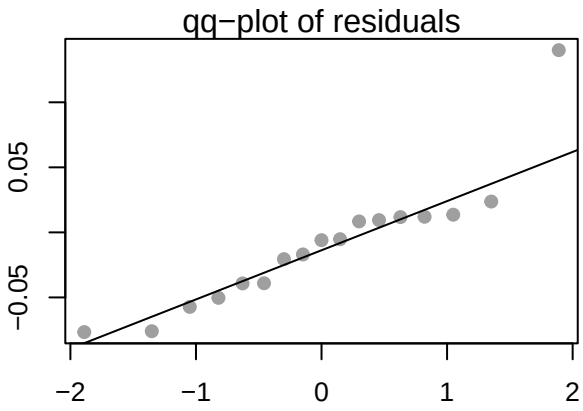


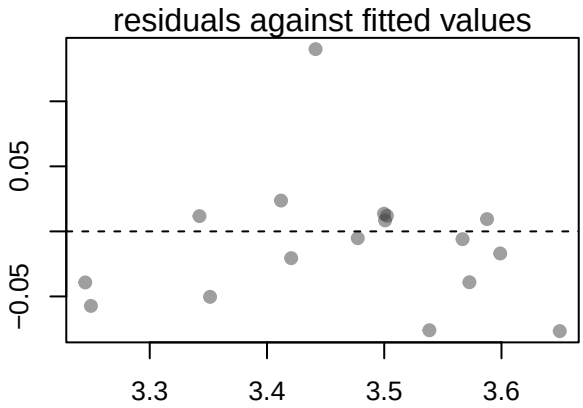

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m2$sensi.estimates

##############################
### Behavioral complexity ###
##############################

# Fit pgls model
m3<- pgls(logECV ~ complexity.fuxjager + logMass,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m3)
```





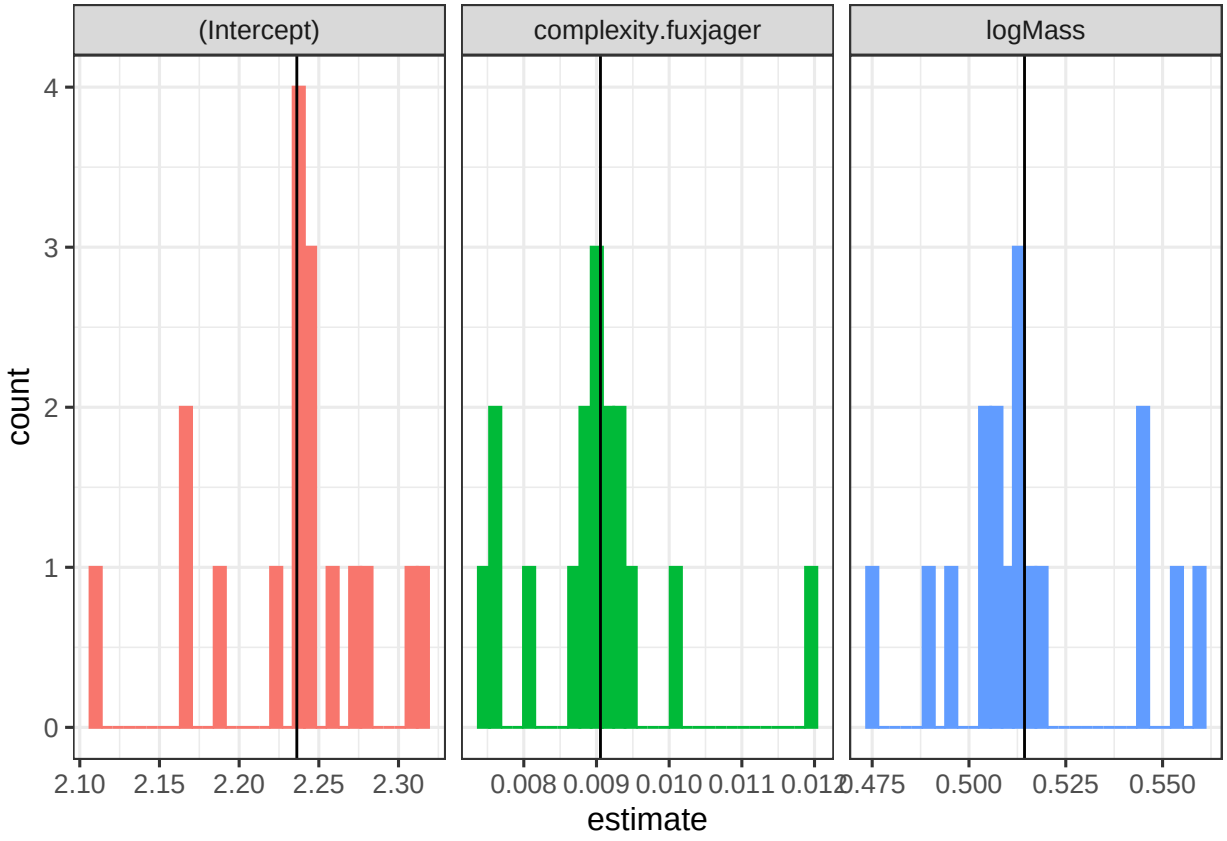



```
# Inspect the output
summary(m3)
# Formal test of normality
res3 <- residuals(m3, phylo = TRUE)
shapiro.test(res3)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m3 <- influ_phylm2(logECV ~ complexity.fuxjager + logMass,
                         phy = comparative_data_poly$phy,
                         data = comparative_data_poly$data, model = "BM",
                         track = FALSE)
```

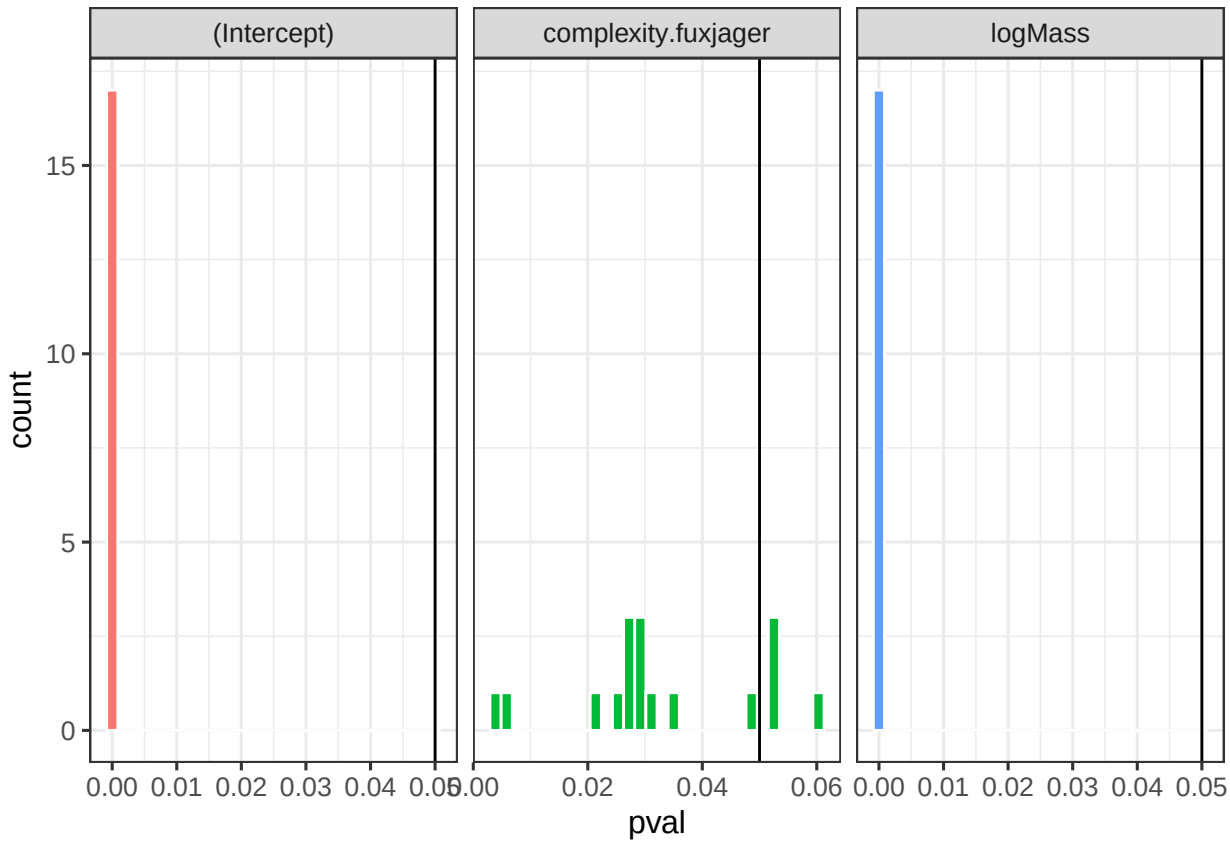
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m3$full.model.estimates
# test for influential species:
summary_influ2(sensi.m3)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m3)
```

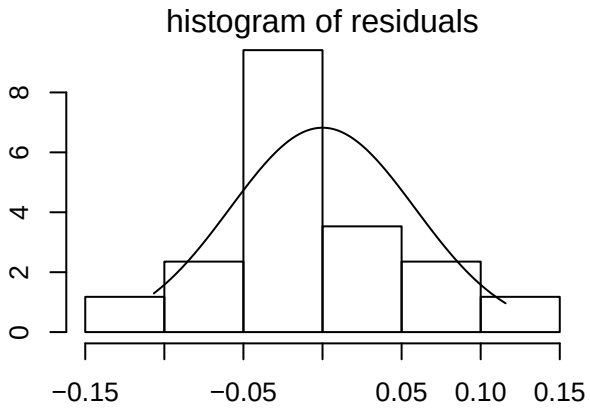
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

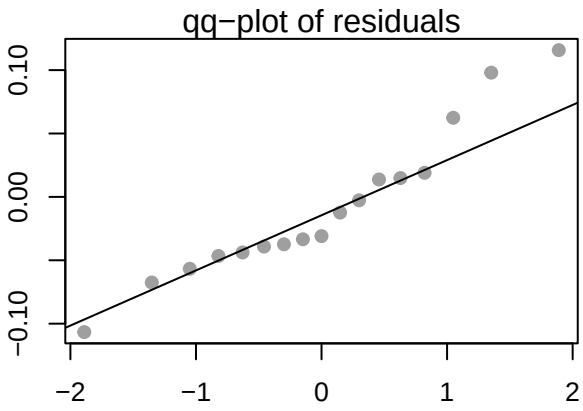


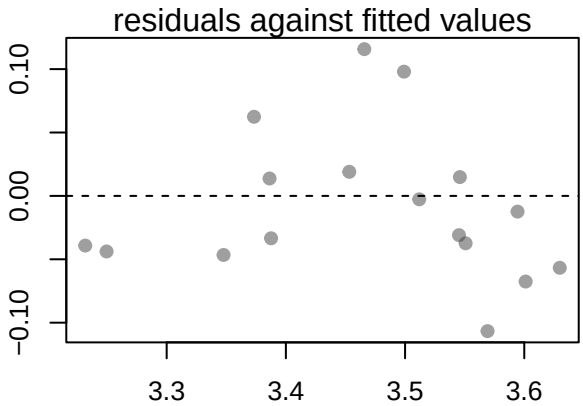

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m3$sensi.estimates

############################
### Acoustic diversity ###
############################

# Fit pgls model
m4<- pgls(logECV ~ acoustic.diversity.ligon + logMass,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m4)
```





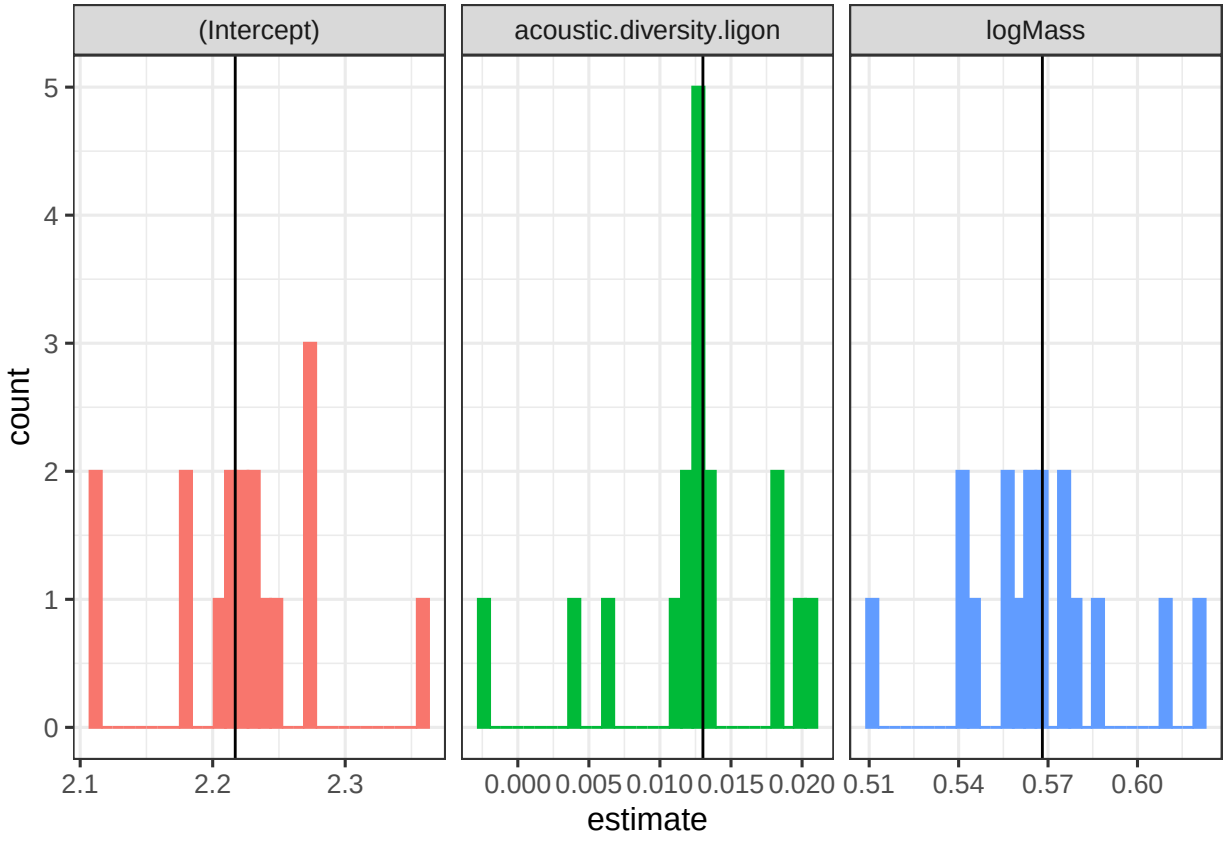



```
# Inspect the output
summary(m4)
# Formal test of normality
res4 <- residuals(m4, phylo = TRUE)
shapiro.test(res4)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m4 <- influ_phylm2(logECV ~ acoustic.diversity.ligon + logMass,
                         phy = comparative_data_poly$phy,
                         data = comparative_data_poly$data, model = "BM",
                         track = FALSE)
```

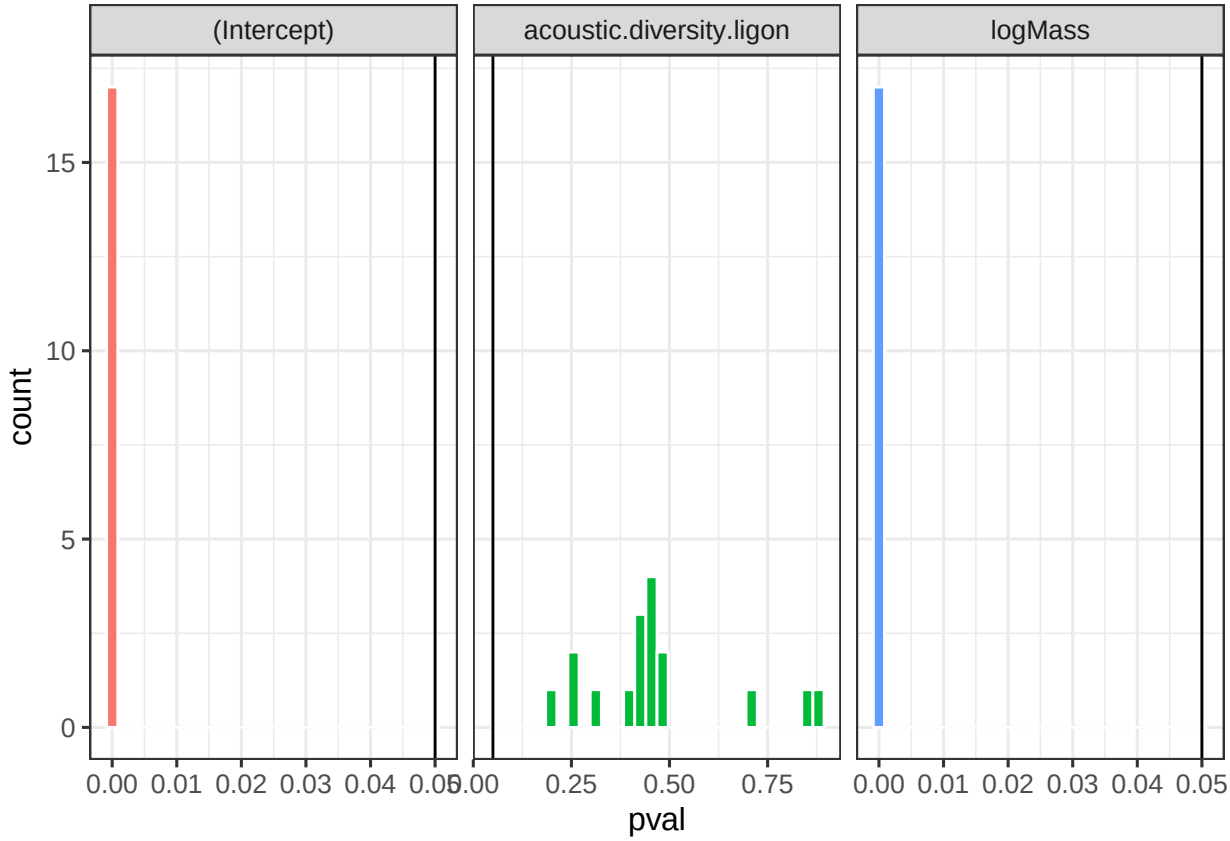
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m4$full.model.estimates
# test for influential species:
summary_influ2(sensi.m4)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m4)
```

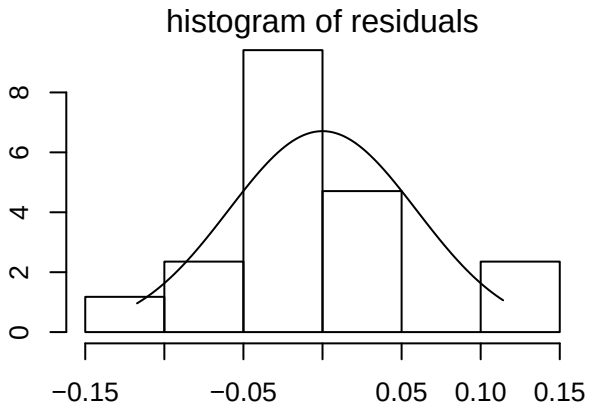
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

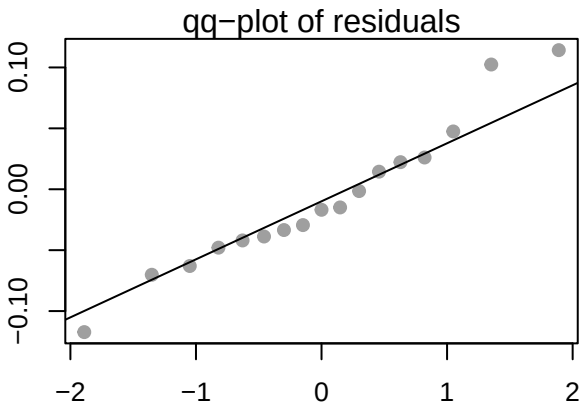


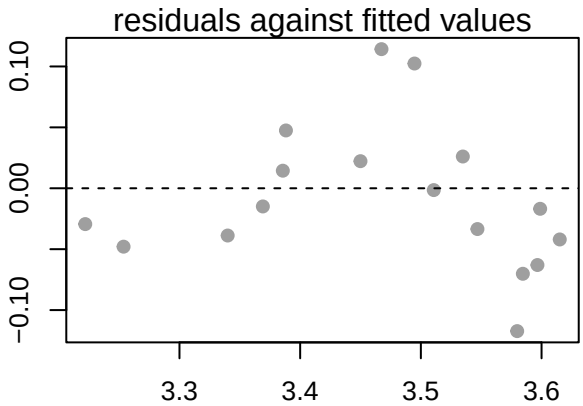

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m4$sensi.estimates

##########################
### Acoustic richness ###
##########################

# Fit pgls model
m5<- pgls(logECV ~ acoustic.richness.ligon + logMass,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m5)
```





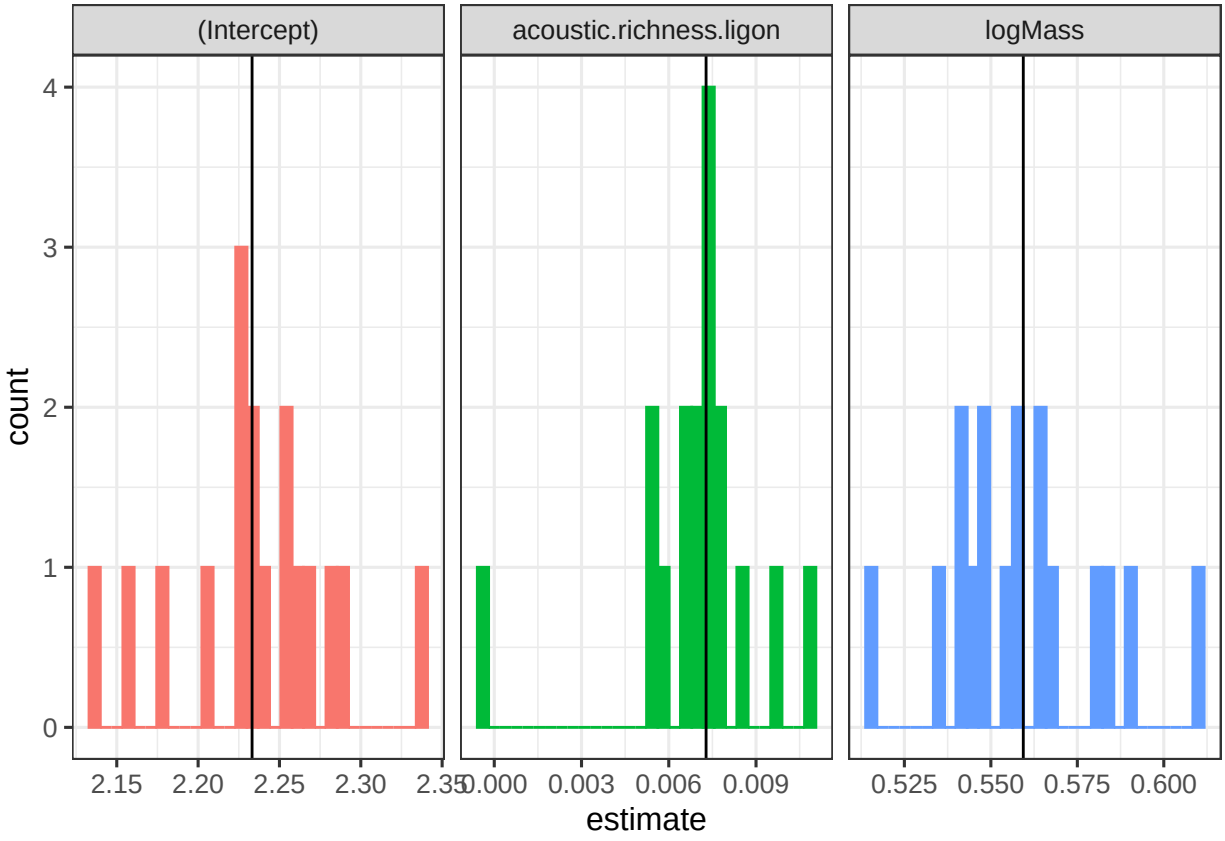



```
# Inspect the output
summary(m5)
# Formal test of normality
res5 <- residuals(m5, phylo = TRUE)
shapiro.test(res5)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m5 <- influ_phylm2(logECV ~ acoustic.richness.ligon + logMass,
                         phy = comparative_data_poly$phy,
                         data = comparative_data_poly$data, model = "BM",
                         track = FALSE)
```

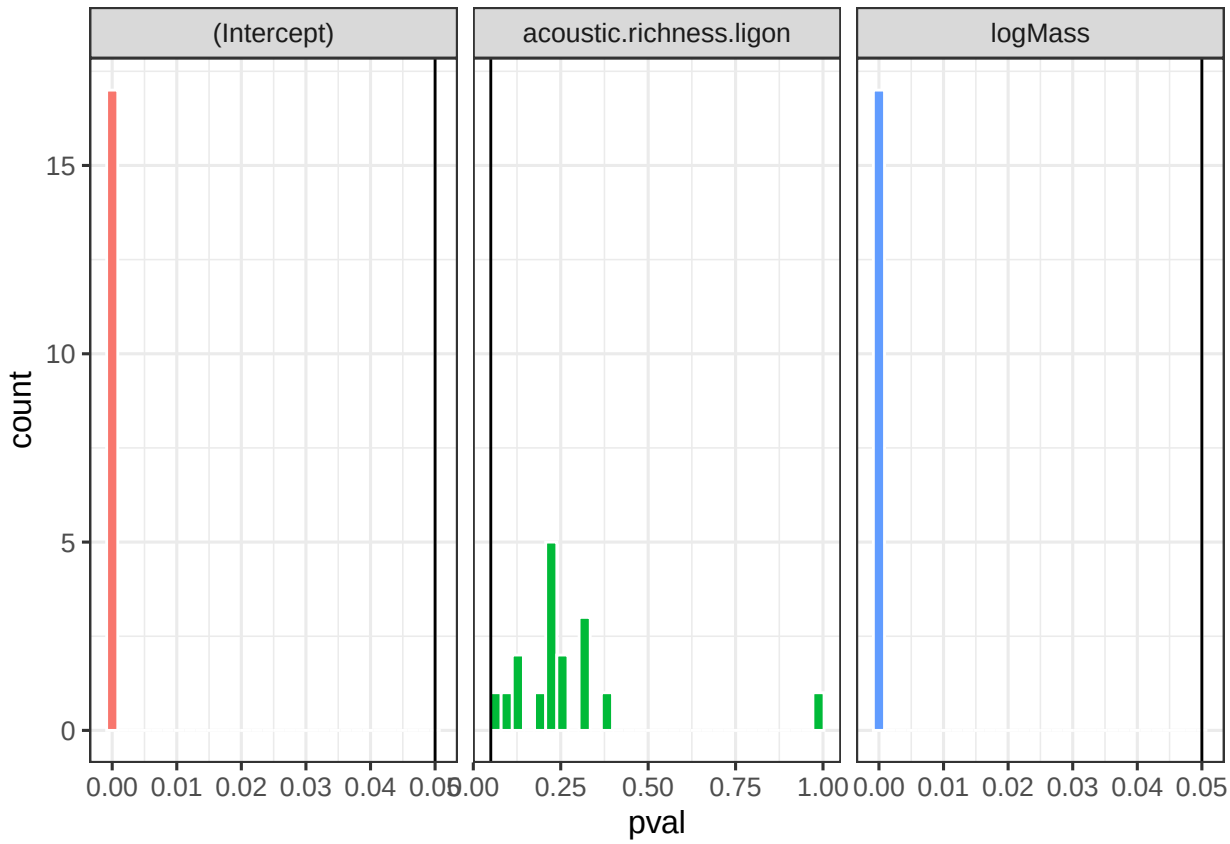
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m5$full.model.estimates
# test for influential species:
summary_influ2(sensi.m5)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m5)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



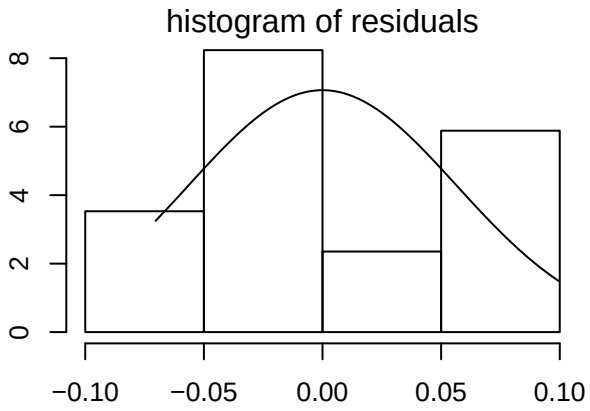

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

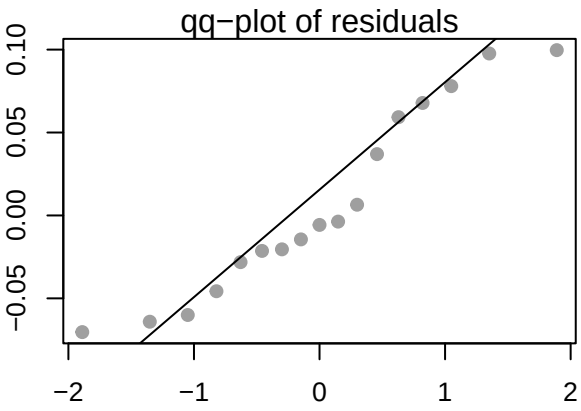


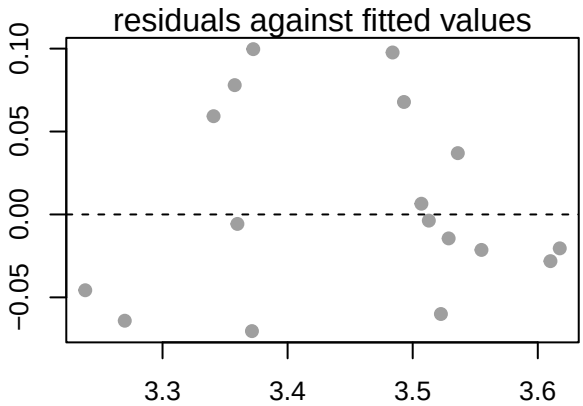

```
sensi.m5$sensi.estimates
```

2.4.2 Repeat analyses using tarsus cubed as a metric of body size

```
############################
### Behavioral diversity ###
############################

# Fit pgls model
m1.t<- pgls(logECV ~ behavioral.diversity.ligon + logTarsus,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m1.t)
```





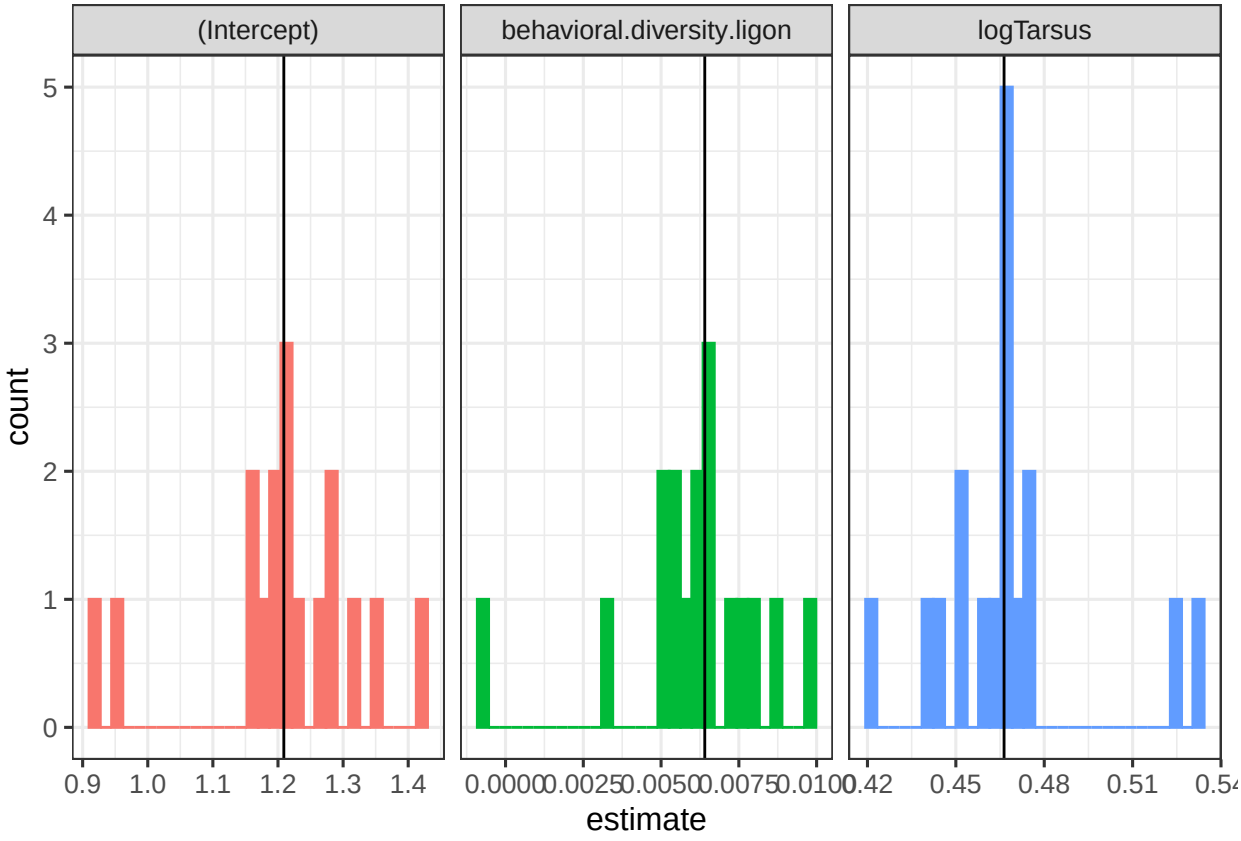



```
# Inspect the output
summary(m1.t)
# Formal test of normality
res1.t <- residuals(m1.t, phylo = TRUE)
shapiro.test(res1.t)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m1.t <- influ_phylm2(logECV ~ behavioral.diversity.ligon + logTarsus,
                           phy = comparative_data_poly$phy,
                           data = comparative_data_poly$data, model = "BM",
                           track = FALSE)
```

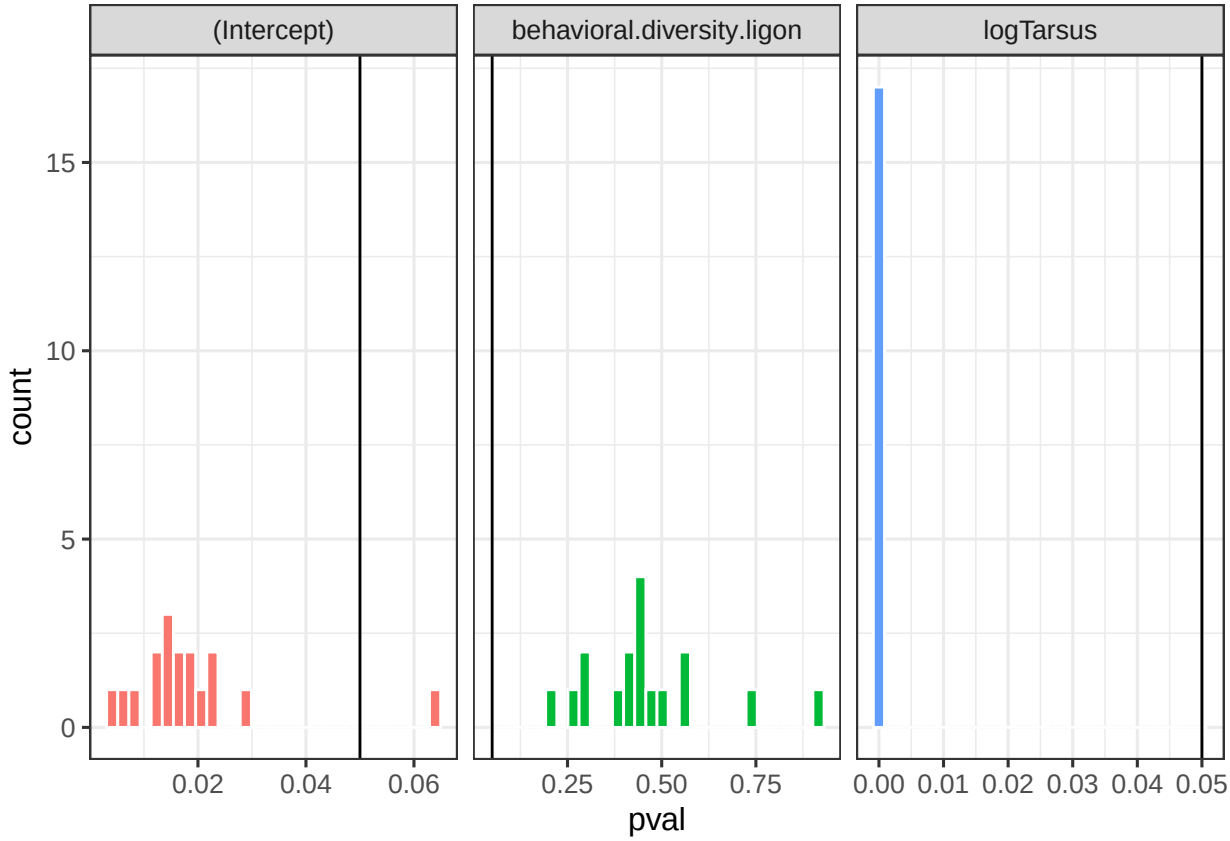
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m1.t$full.model.estimates
# test for influential species:
summary_influ2(sensi.m1.t)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m1.t)
```

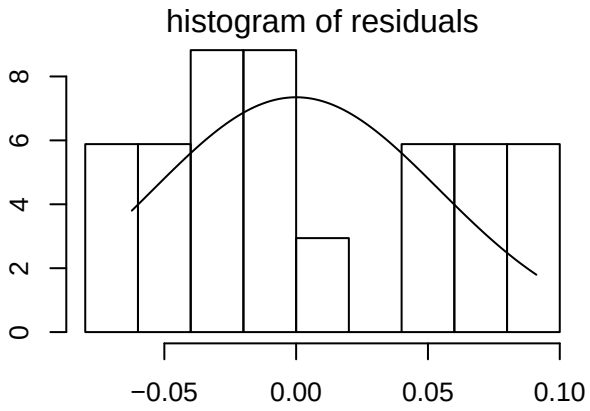
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

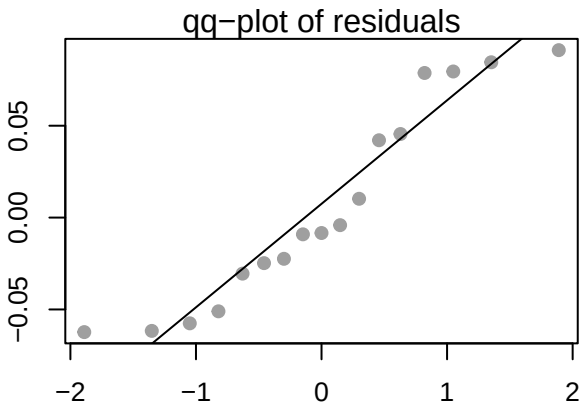


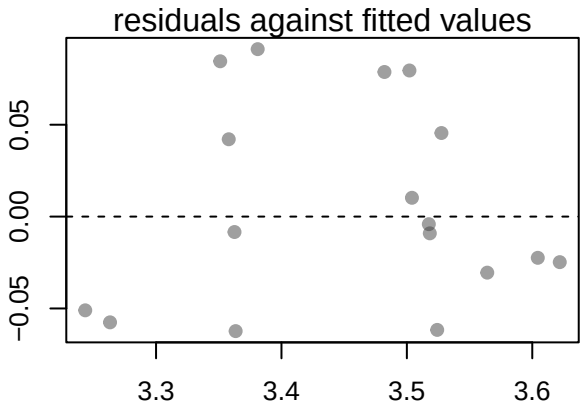

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m1.t$sensi.estimates

############################
### Behavioral richness ###
############################

# Fit pgls model
m2.t<- pgls(logECV ~ behavioral.richness.ligon + logTarsus,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m2.t)
```





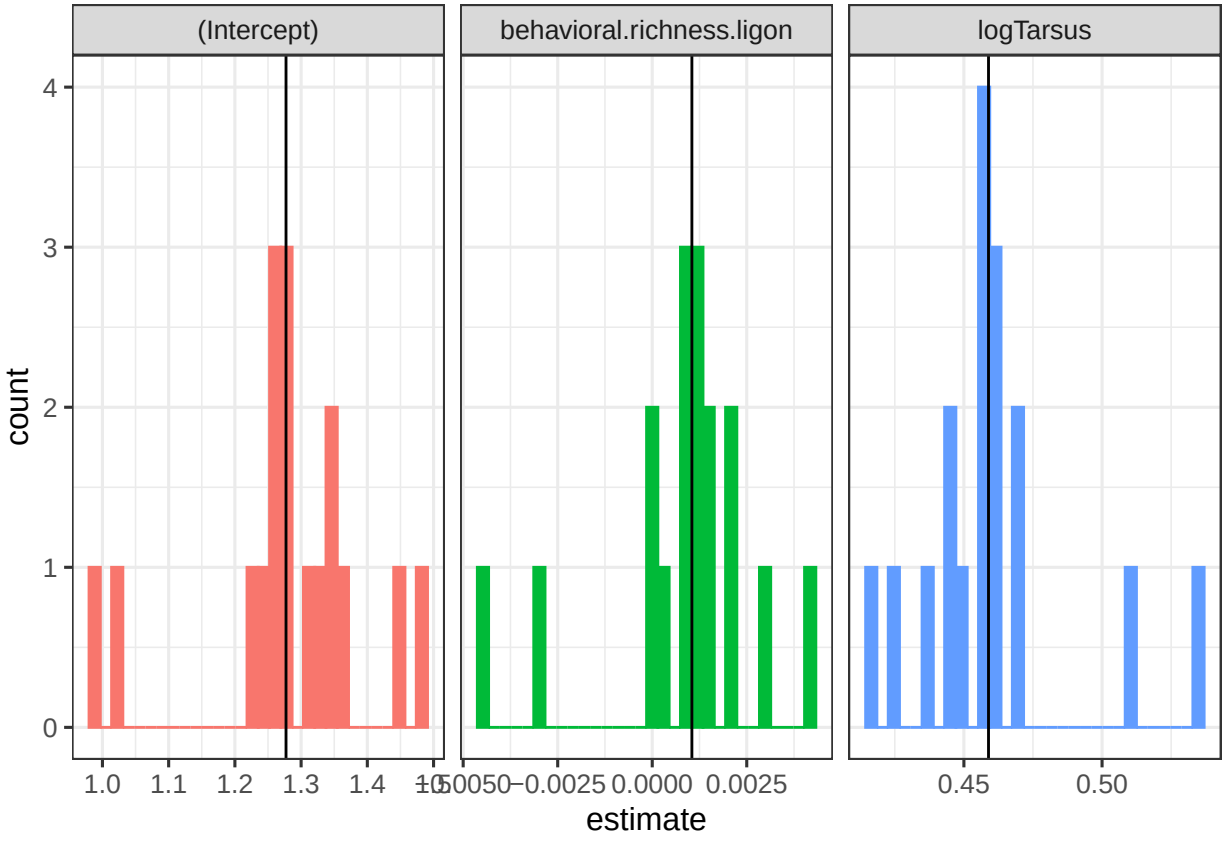



```
# Inspect the output
summary(m2.t)
# Formal test of normality
res2.t <- residuals(m2.t, phylo = TRUE)
shapiro.test(res2.t)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m2.t <- influ_phylm2(logECV ~ behavioral.richness.ligon + logTarsus,
                           phy = comparative_data_poly$phy,
                           data = comparative_data_poly$data, model = "BM",
                           track = FALSE)
```

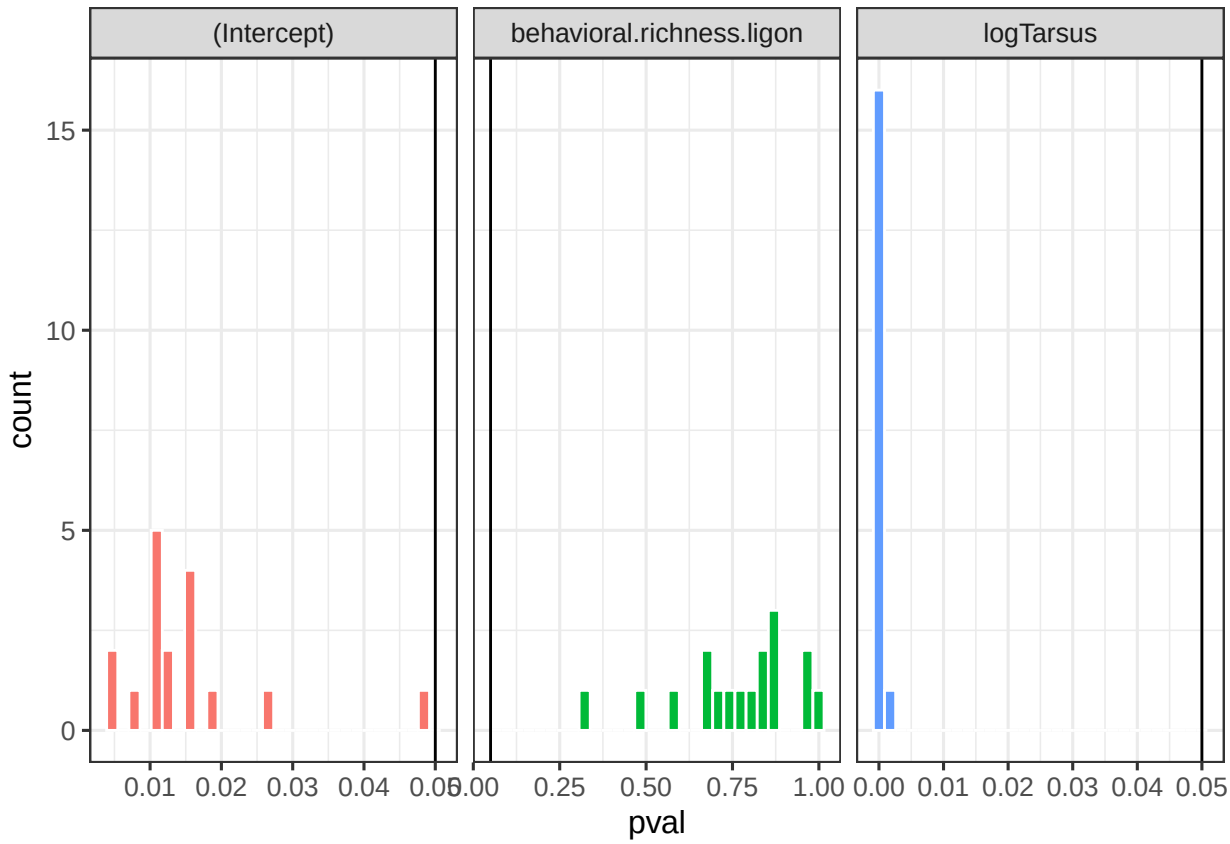
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m2.t$full.model.estimates
# test for influential species:
summary_influ2(sensi.m2.t)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m2.t)
```

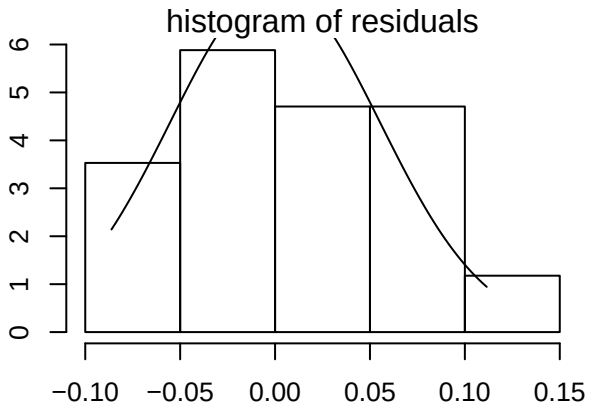
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

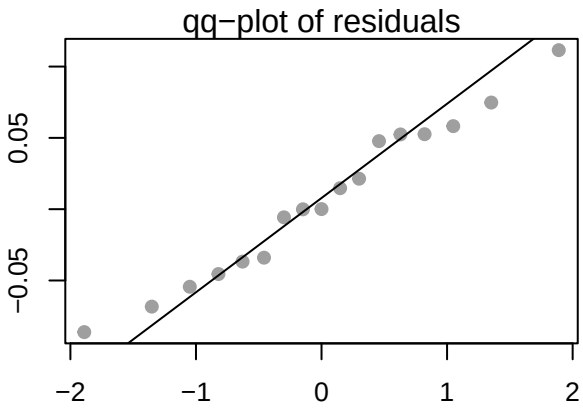


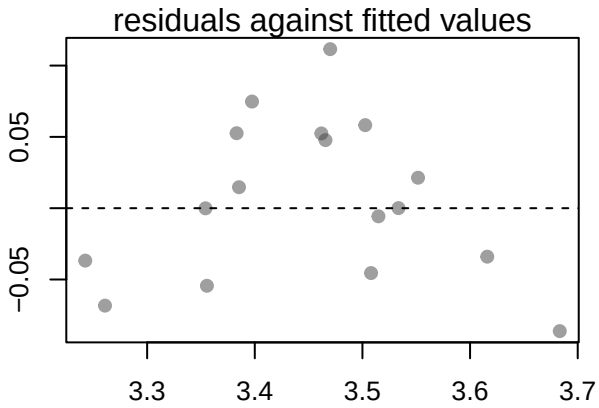

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m2.t$sensi.estimates

##############################
### Behavioral complexity ###
##############################

# Fit pgls model
m3.t<- pgls(logECV ~ complexity.fuxjager + logTarsus,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m3.t)
```





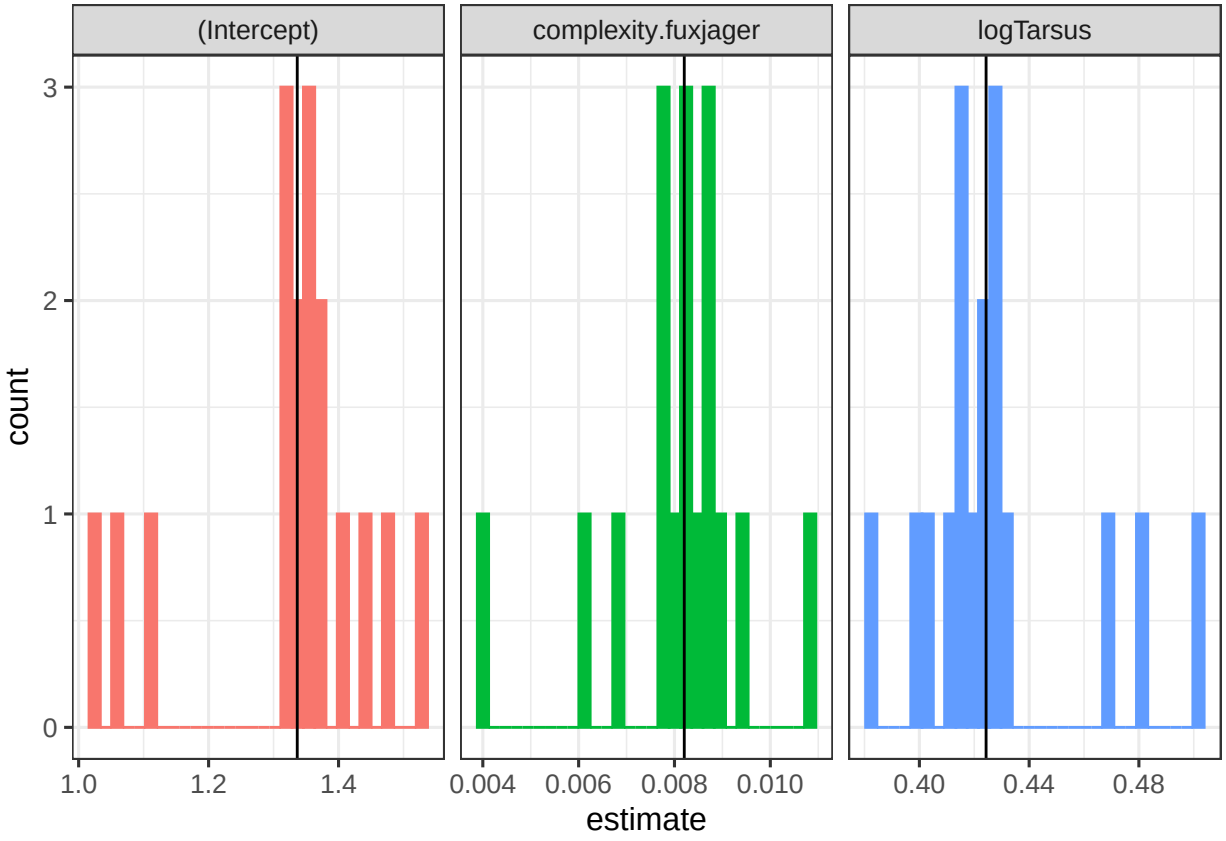



```
# Inspect the output
summary(m3.t)
# Formal test of normality
res3.t <- residuals(m3.t, phylo = TRUE)
shapiro.test(res3.t)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m3.t <- influ_phylm2(logECV ~ complexity.fuxjager + logTarsus,
                           phy = comparative_data_poly$phy,
                           data = comparative_data_poly$data, model = "BM",
                           track = FALSE)
```

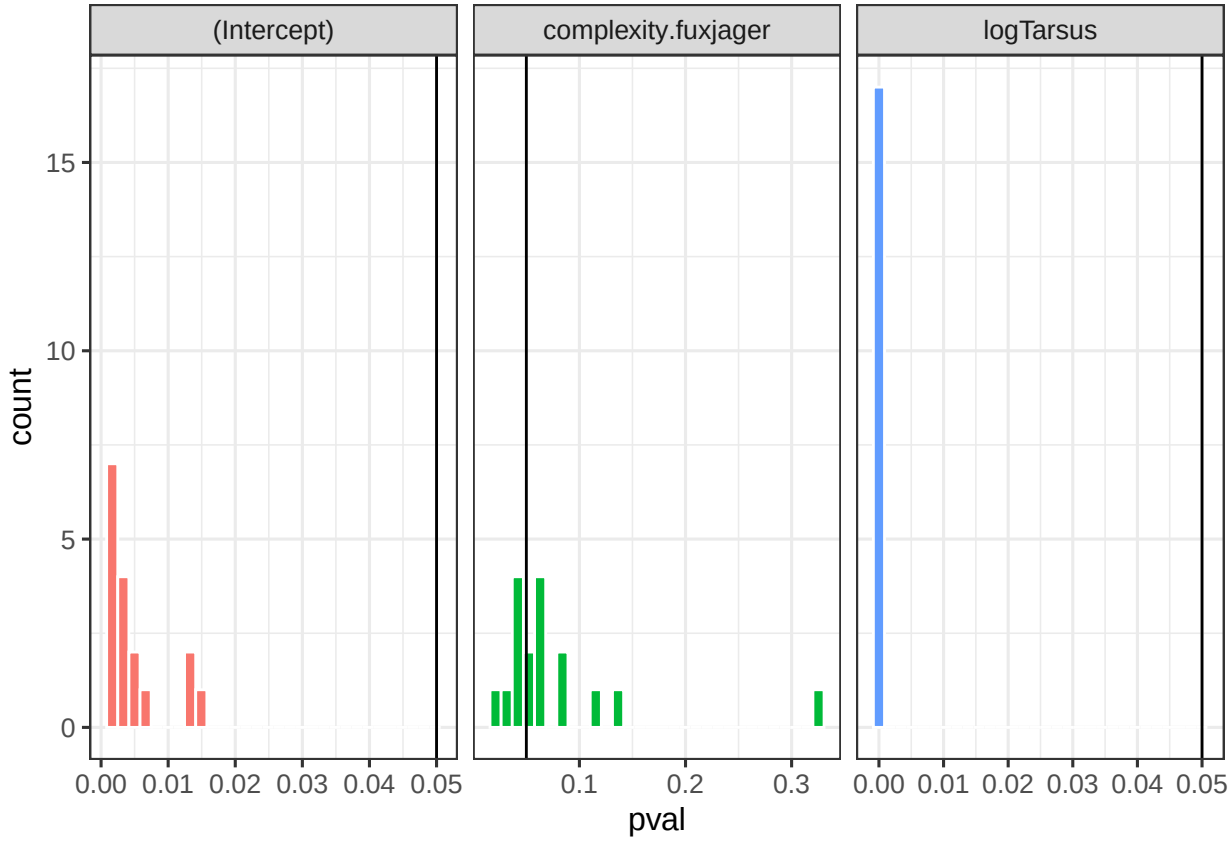
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m3.t$full.model.estimates
# test for influential species:
summary_influ2(sensi.m3.t)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m3.t)
```

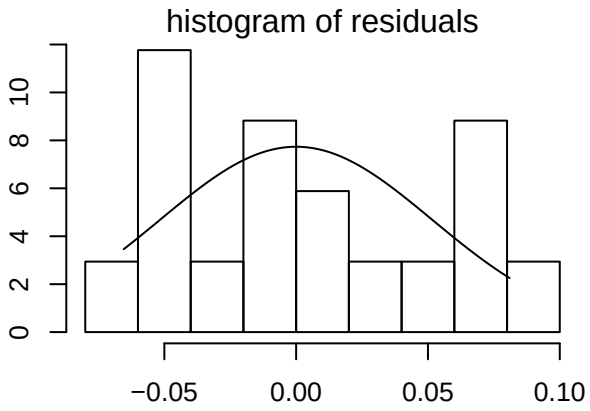
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

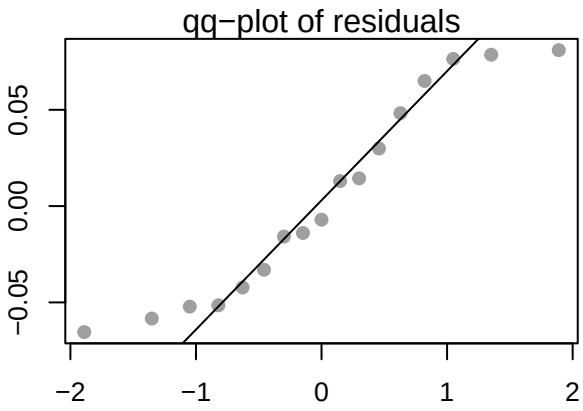


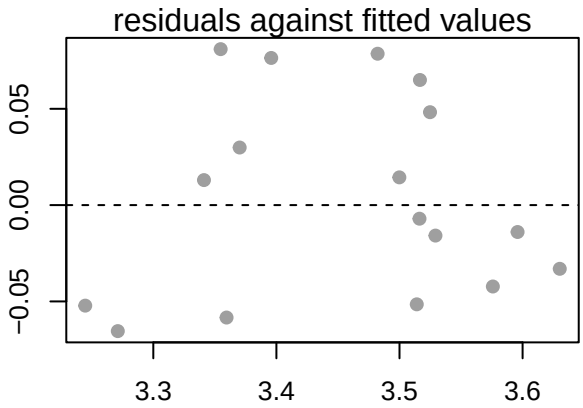

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m3.t$sensi.estimates

############################
### Acoustic diversity ###
############################

# Fit pgls model
m4.t<- pgls(logECV ~ acoustic.diversity.ligon + logTarsus,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m4.t)
```





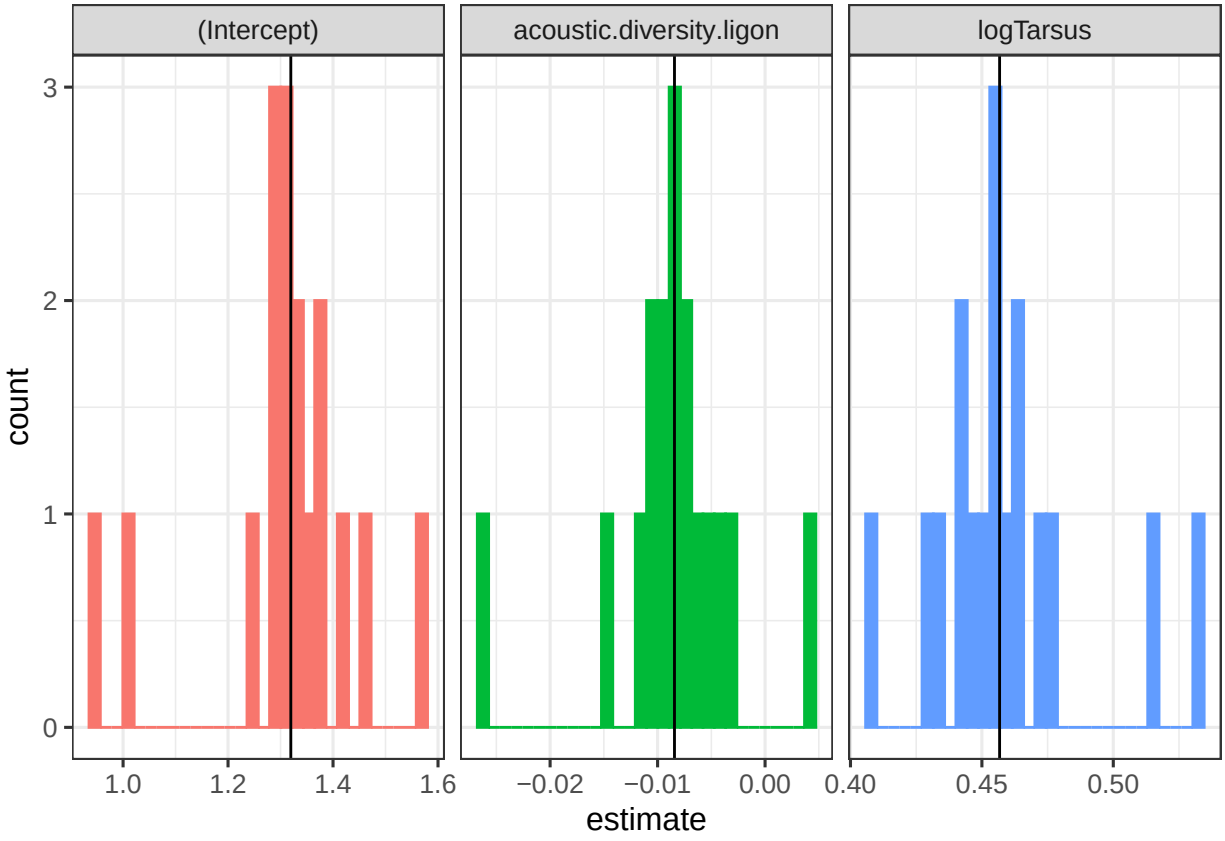



```
# Inspect the output
summary(m4.t)
# Formal test of normality
res4.t <- residuals(m4.t, phylo = TRUE)
shapiro.test(res4.t)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m4.t <- influ_phylm2(logECV ~ acoustic.diversity.ligon + logTarsus,
                           phy = comparative_data_poly$phy,
                           data = comparative_data_poly$data, model = "BM",
                           track = FALSE)
```

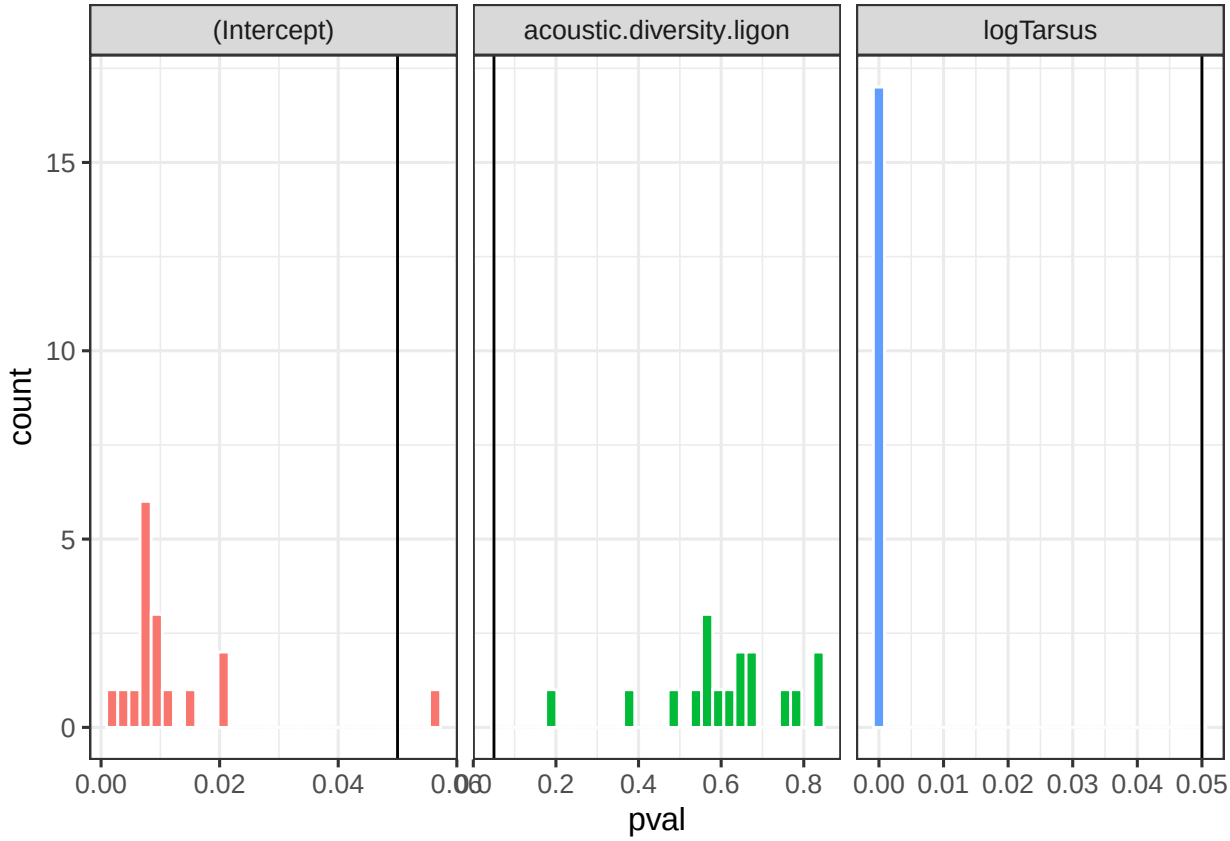
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m4.t$full.model.estimates
# test for influential species:
summary_influ2(sensi.m4.t)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m4.t)
```

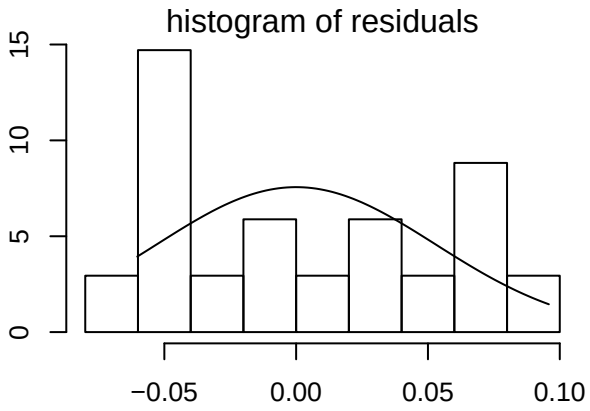
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

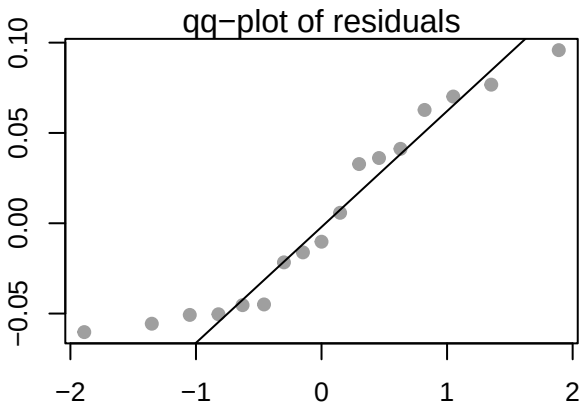


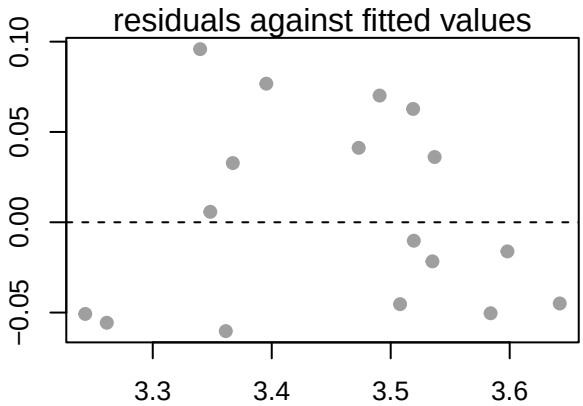

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m4.t$sensi.estimates

##########################
### Acoustic richness ###
##########################

# Fit pgls model
m5.t<- pgls(logECV ~ acoustic.richness.ligon + logTarsus,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m5.t)
```





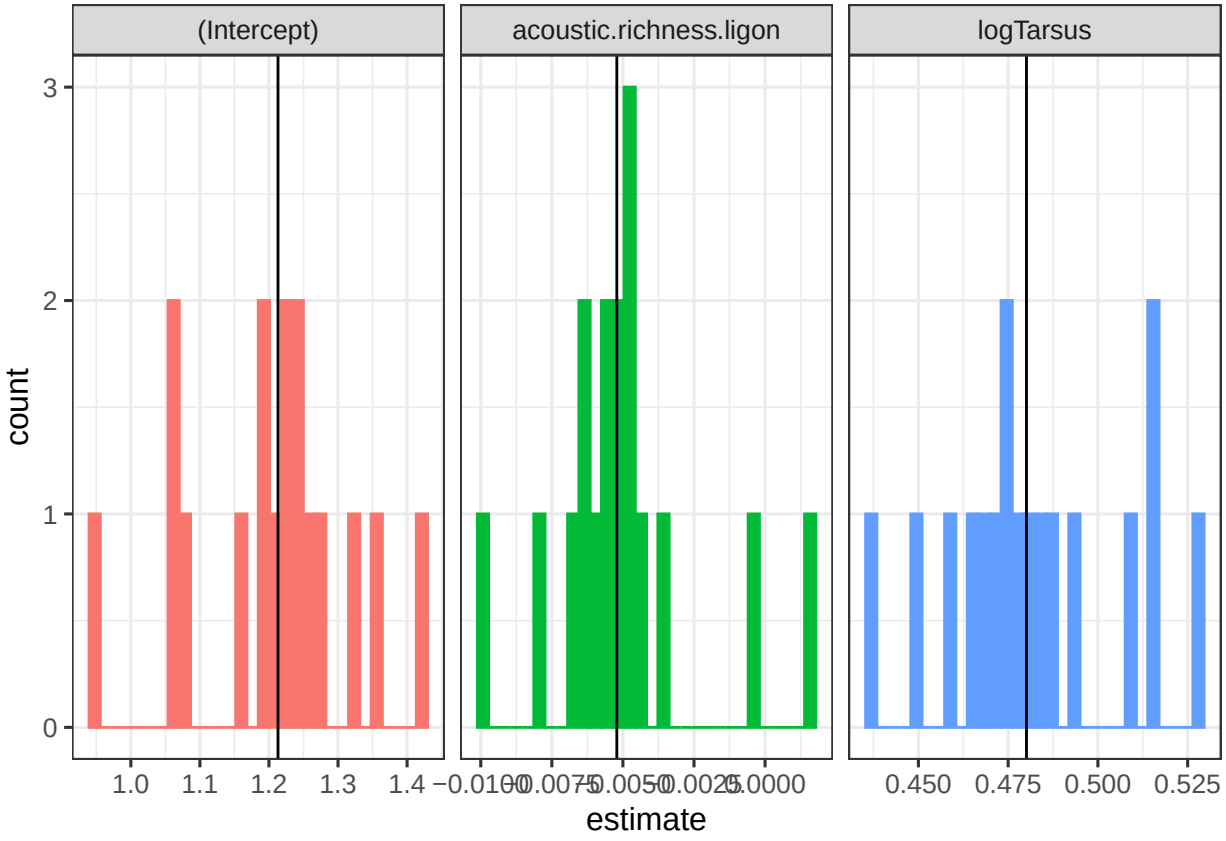



```
# Inspect the output
summary(m5.t)
# Formal test of normality
res5.t <- residuals(m5.t, phylo = TRUE)
shapiro.test(res5.t)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m5.t <- influ_phylm2(logECV ~ acoustic.richness.ligon + logTarsus,
                           phy = comparative_data_poly$phy,
                           data = comparative_data_poly$data, model = "BM",
                           track = FALSE)
```

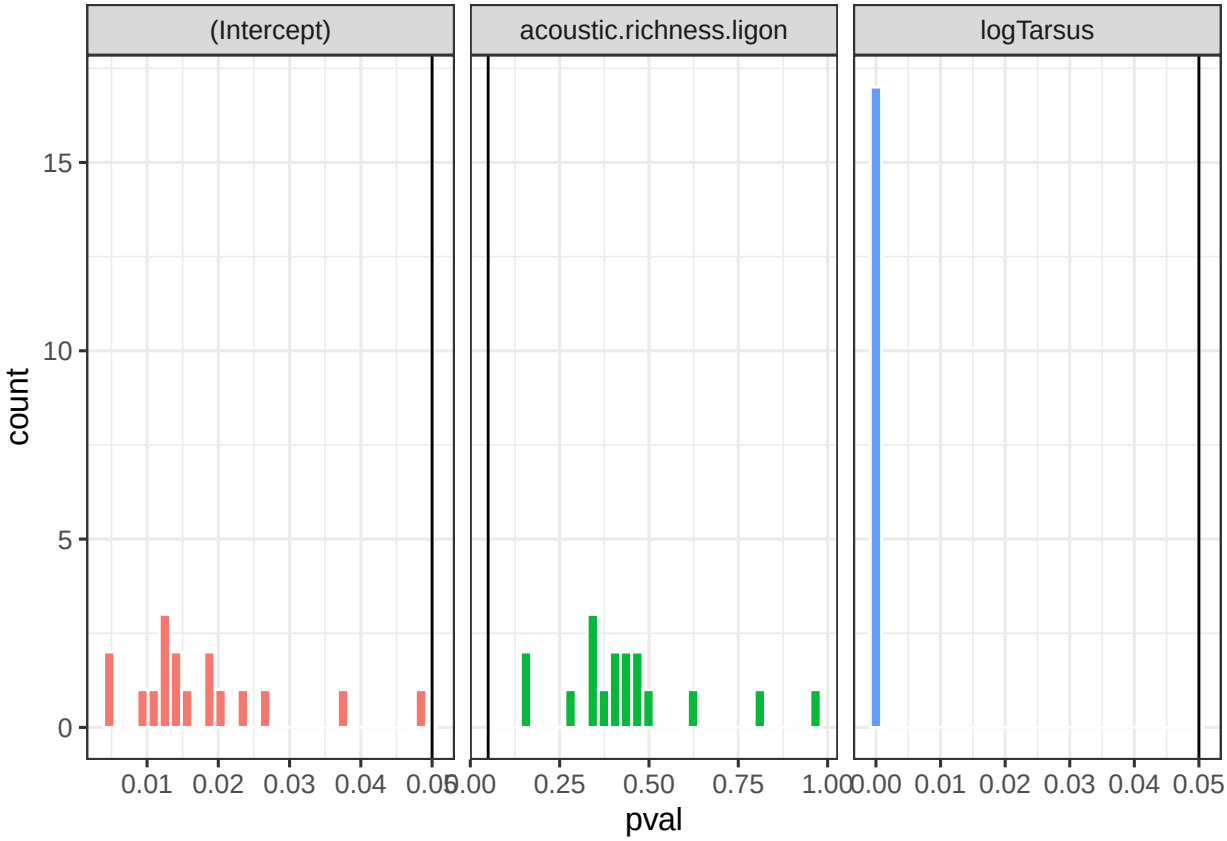
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m5.t$full.model.estimates
# test for influential species:
summary_influ2(sensi.m5.t)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.m5.t)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

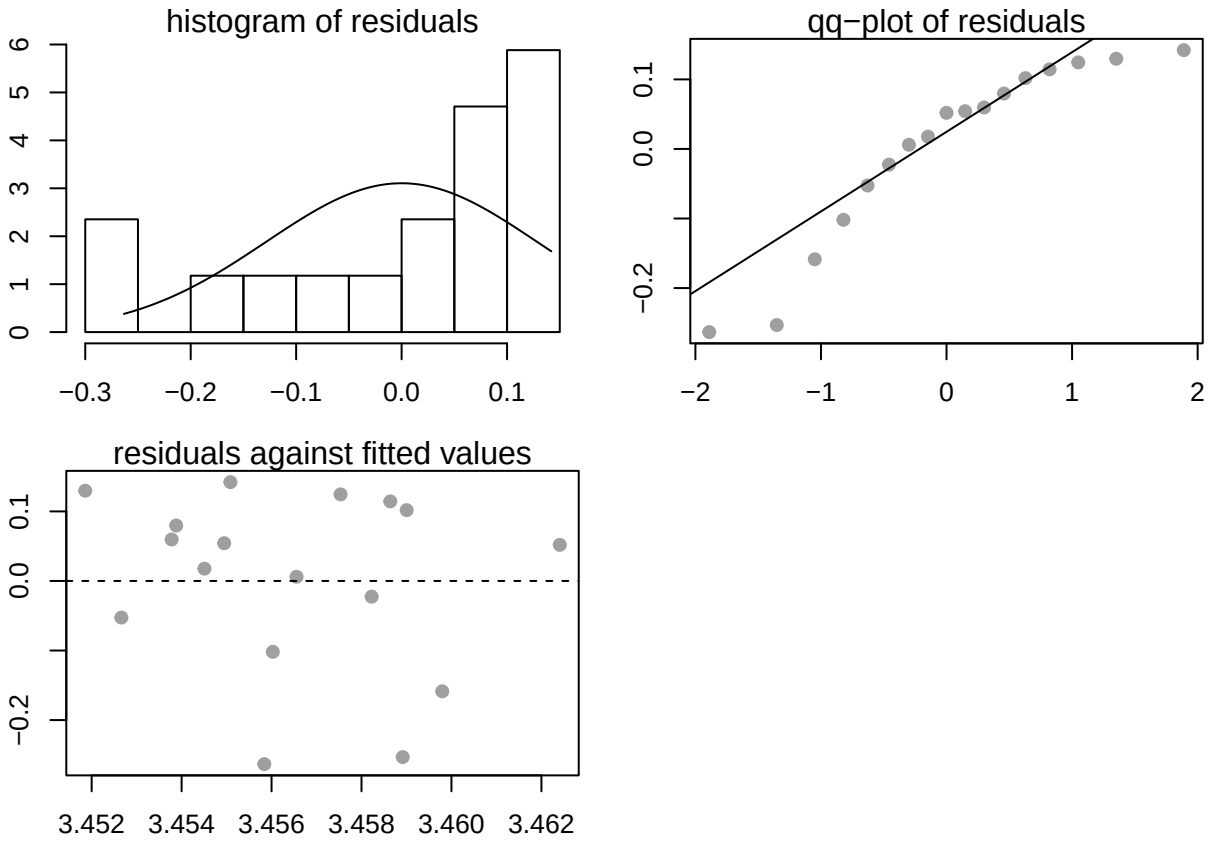



```
sensi.m5.t$sensi.estimates
```

We also want to run the same set of models without controlling for body size so we can test if any of these metrics correlate with absolute brain size.

2.5. PGLS models not including body mass as a predictor

```
############################
### Behavioral diversity ###
############################

# Note: Since the following models include only a single predictor, we can run both
# versions of the influ_phylm function, which show slightly different outputs.

# Fit pgls model
m6<- pgls(logECV ~ behavioral.diversity.ligon,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m6)
```



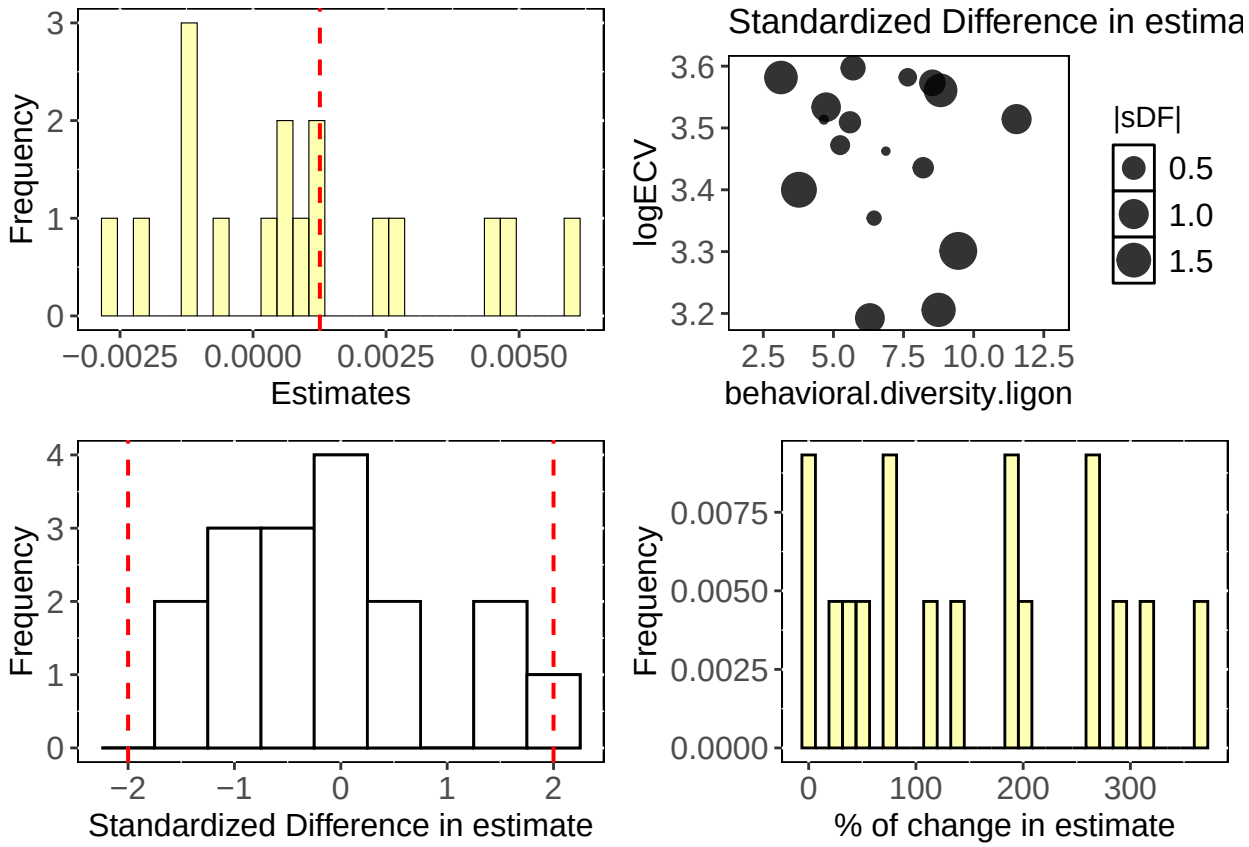

```
# Inspect the output
summary(m6)
# Formal test of normality
res6 <- residuals(m6, phylo = TRUE)
shapiro.test(res6)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m6 <- influ_phylm(logECV ~ behavioral.diversity.ligon,
                        phy = comparative_data_poly$phy,
                        data = comparative_data_poly$data, model = "BM",
                        track = FALSE)
```

```
## Used dataset has  17  species that match data and phylogeny
```

```
sensi.m6.2 <- influ_phylm2(logECV ~ behavioral.diversity.ligon,
                        phy = comparative_data_poly$phy,
                        data = comparative_data_poly$data, model = "BM",
                        track = FALSE)
```

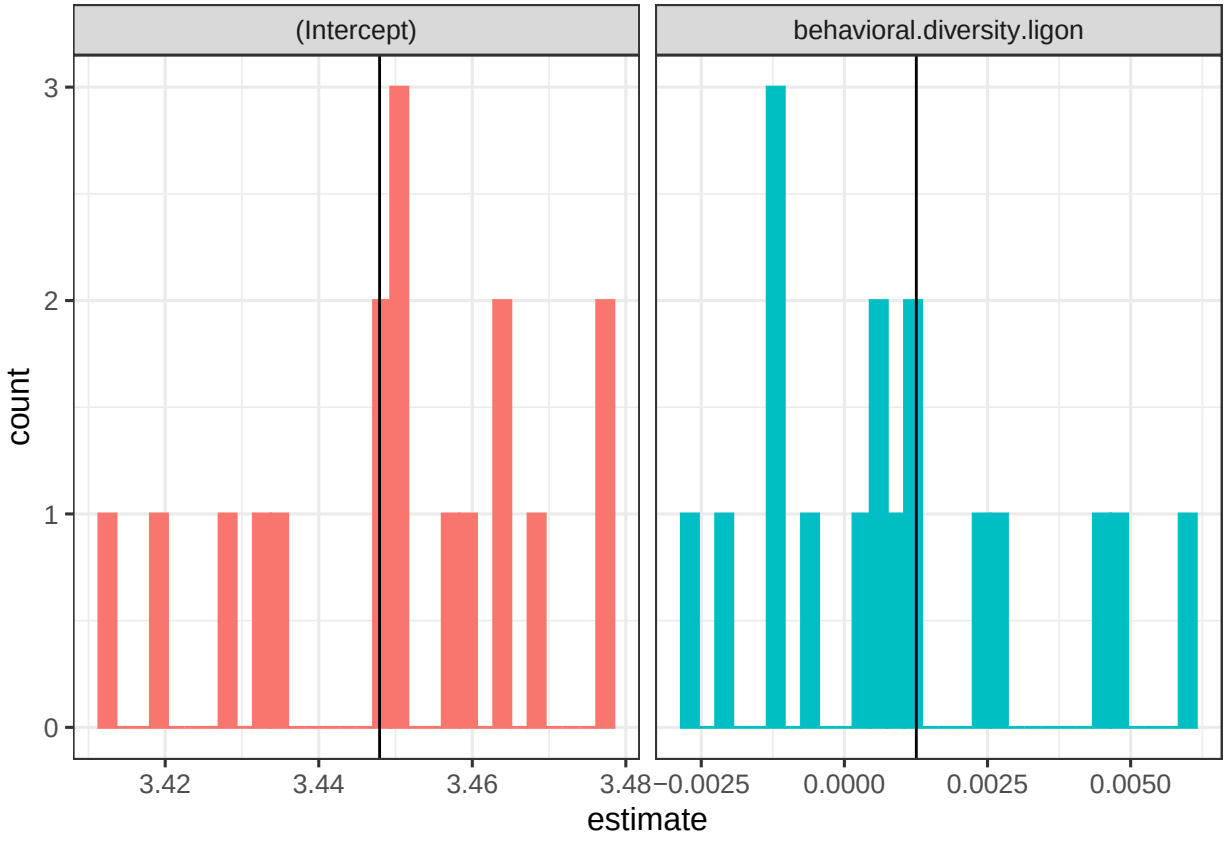
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m6$full.model.estimates
# test for influential species:
summary(sensi.m6)
# Visual sensitivity diagnostics
sensi_plot(sensi.m6)
```

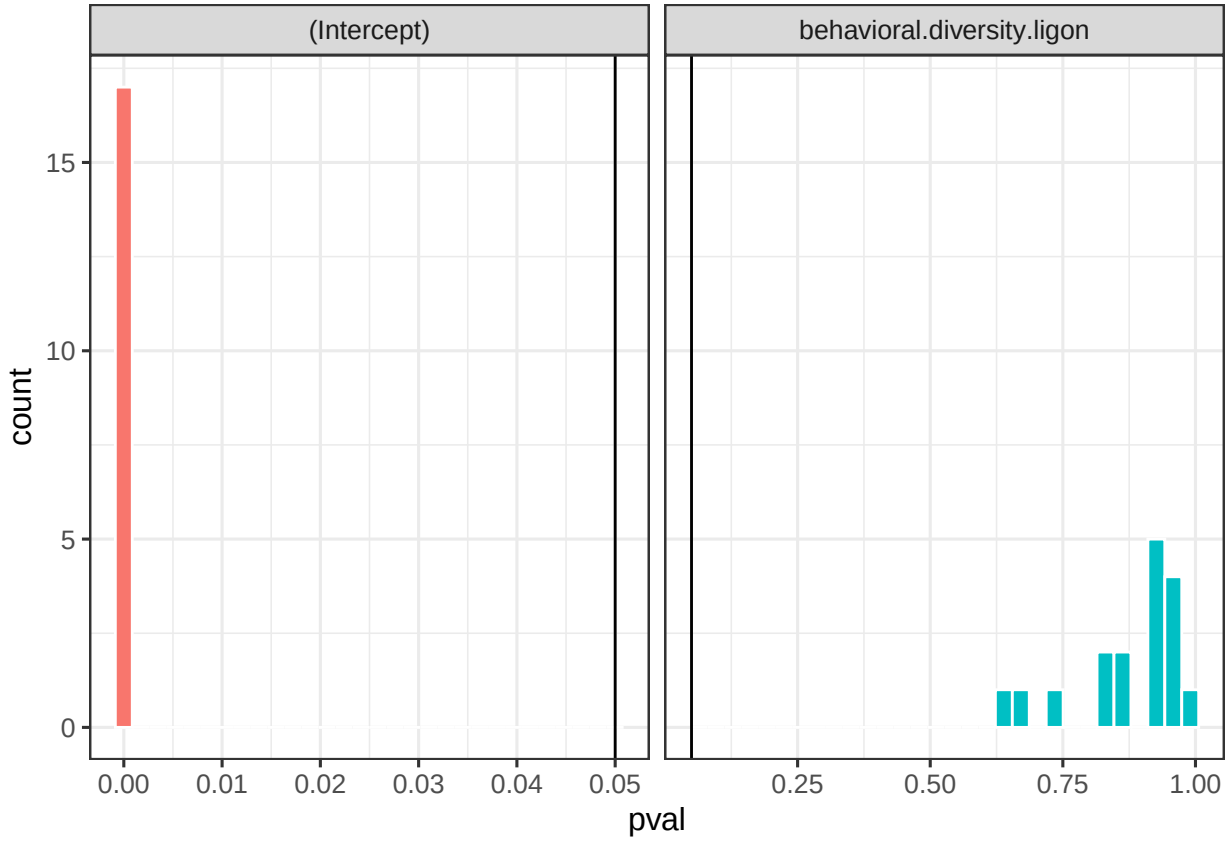



```
sensi_plot2(sensi.m6.2)
```

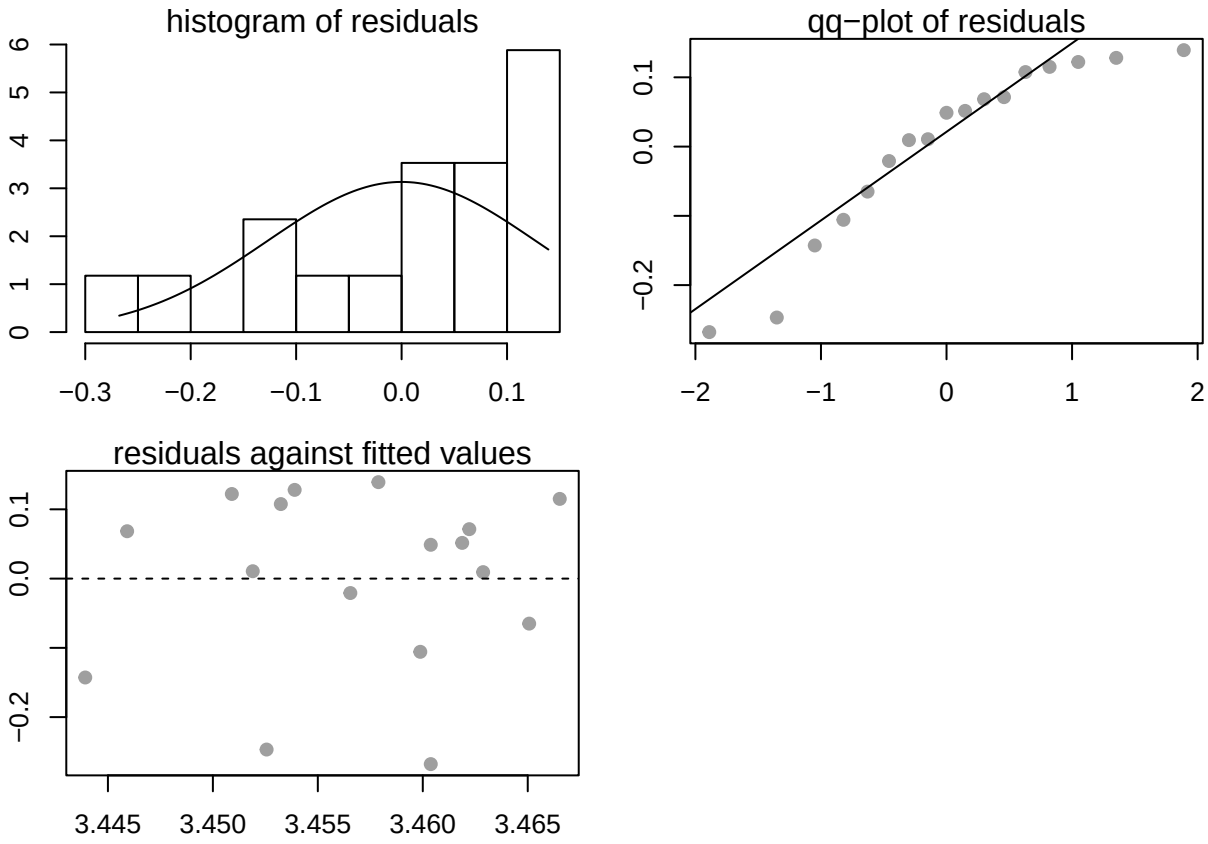
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m6$sensi.estimates

############################
### Behavioral richness ###
############################

# Fit pgls model
m7<- pgls(logECV ~ behavioral.richness.ligon,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m7)
```



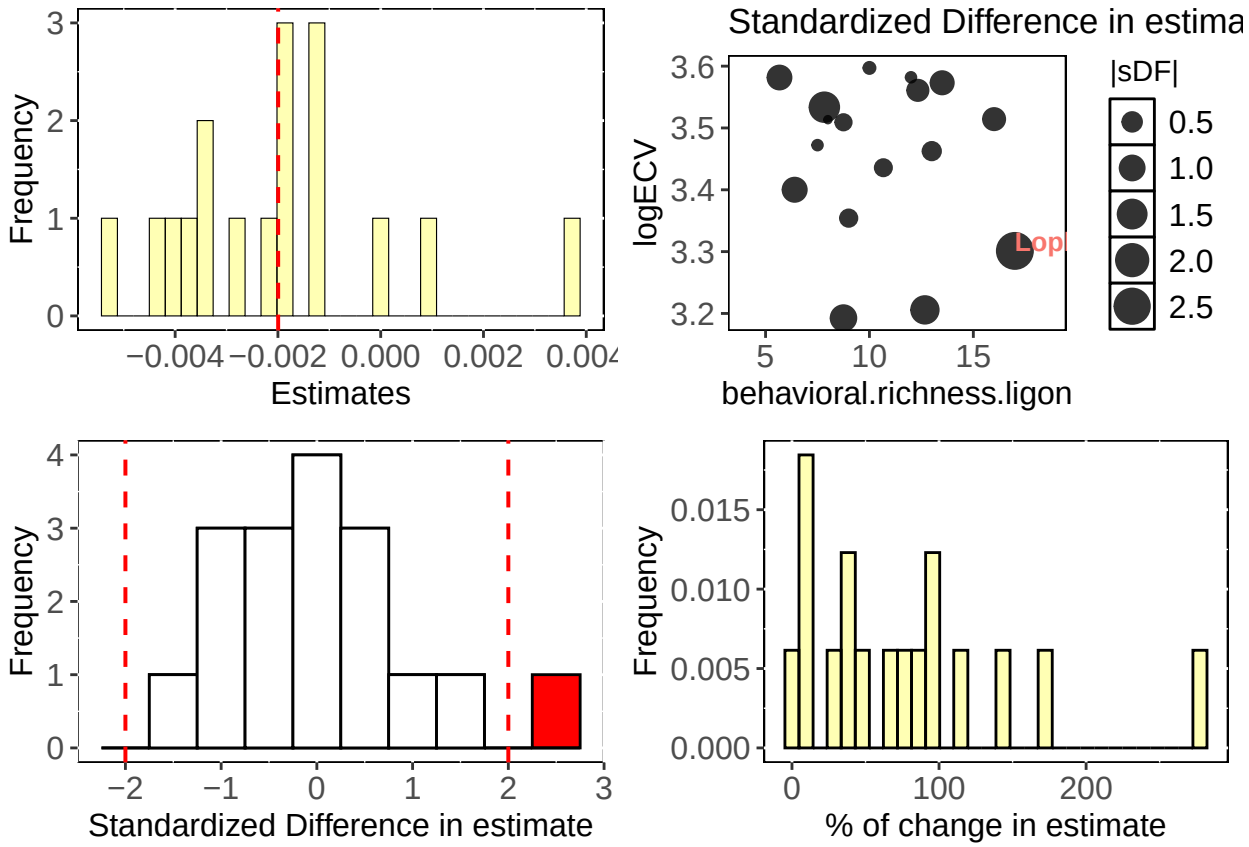

```
# Inspect the output
summary(m7)
# Formal test of normality
res7 <- residuals(m7, phylo = TRUE)
shapiro.test(res7)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m7 <- influ_phylm(logECV ~ behavioral.richness.ligon,
                        phy = comparative_data_poly$phy,
                        data = comparative_data_poly$data, model = "BM",
                        track = FALSE)
```

```
## Used dataset has  17  species that match data and phylogeny
```

```
sensi.m7.2 <- influ_phylm2(logECV ~ behavioral.richness.ligon,
                        phy = comparative_data_poly$phy,
                        data = comparative_data_poly$data, model = "BM",
                        track = FALSE)
```

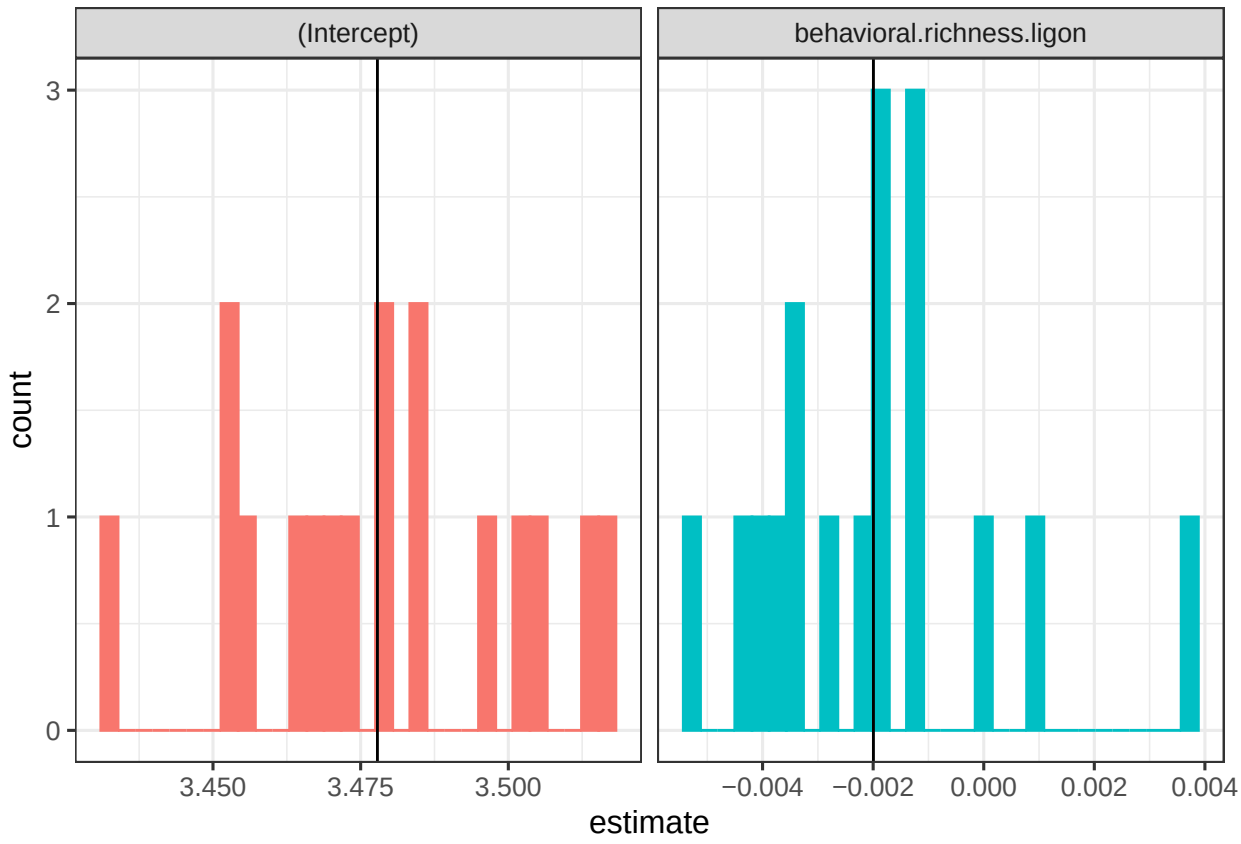
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m7$full.model.estimates
# test for influential species:
summary(sensi.m7)
summary_influ2(sensi.m7.2)$estimates
# Visual sensitivity diagnostics
sensi_plot(sensi.m7)
```

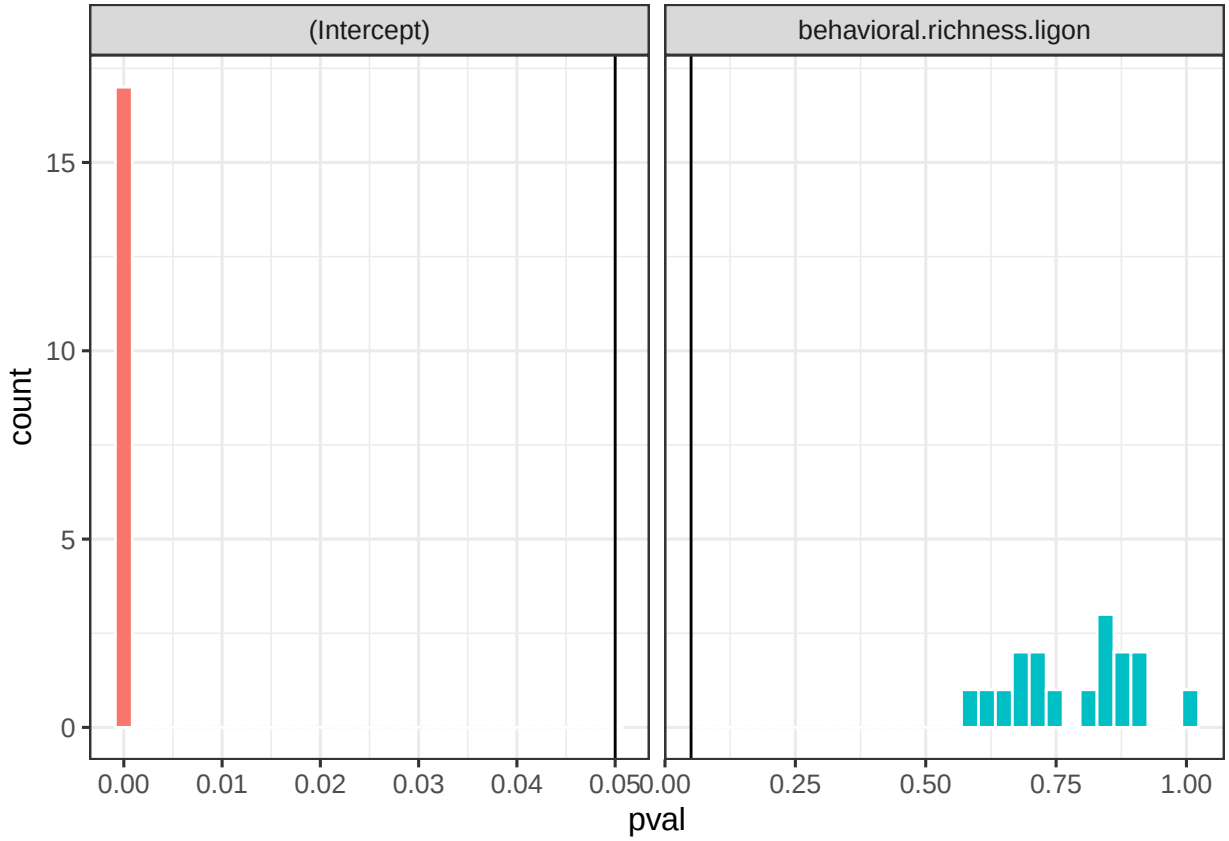



```
sensi_plot2(sensi.m7.2)
```

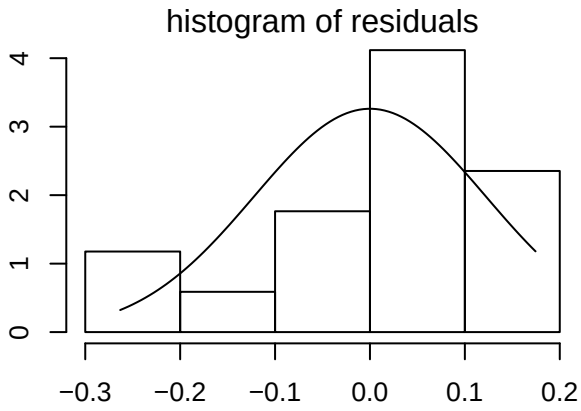
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

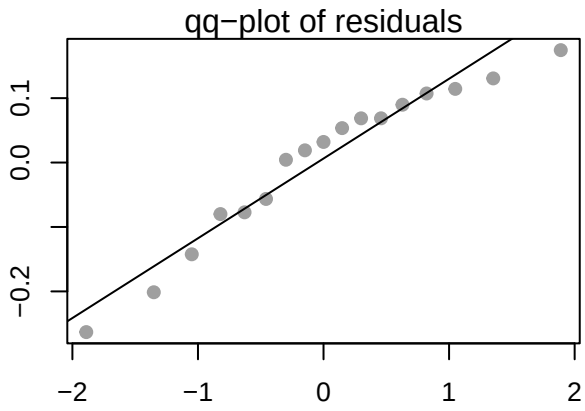


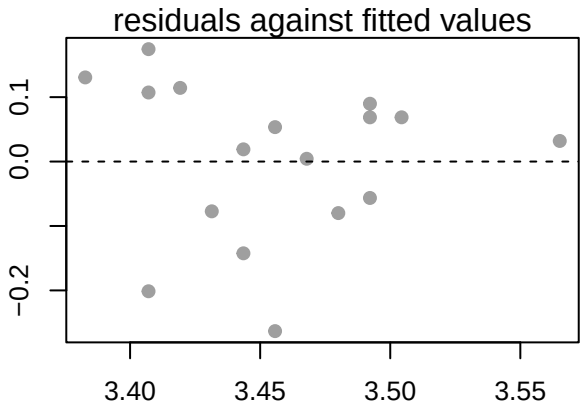

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m7$sensi.estimates

##############################
### Behavioral complexity ###
##############################

# Fit pgls model
m8<- pgls(logECV ~ complexity.fuxjager,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m8)
```







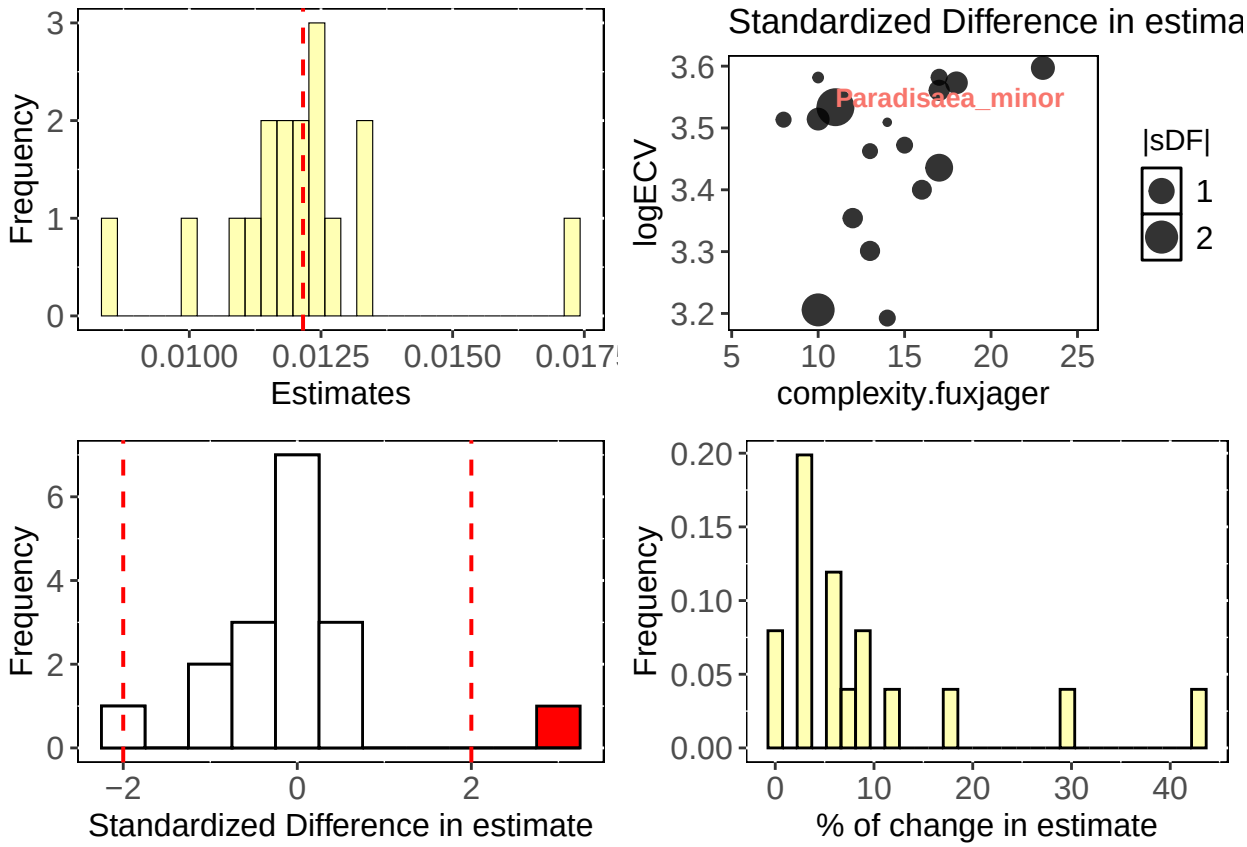

```
# Inspect the output
summary(m8)
# Formal test of normality
res8 <- residuals(m8, phylo = TRUE)
shapiro.test(res8)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m8 <- influ_phylm(logECV ~ complexity.fuxjager,
                        phy = comparative_data_poly$phy,
                        data = comparative_data_poly$data, model = "BM",
                        track = FALSE)
```

```
## Used dataset has  17  species that match data and phylogeny
```

```
sensi.m8.2 <- influ_phylm2(logECV ~ complexity.fuxjager,
                        phy = comparative_data_poly$phy,
                        data = comparative_data_poly$data, model = "BM",
                        track = FALSE)
```

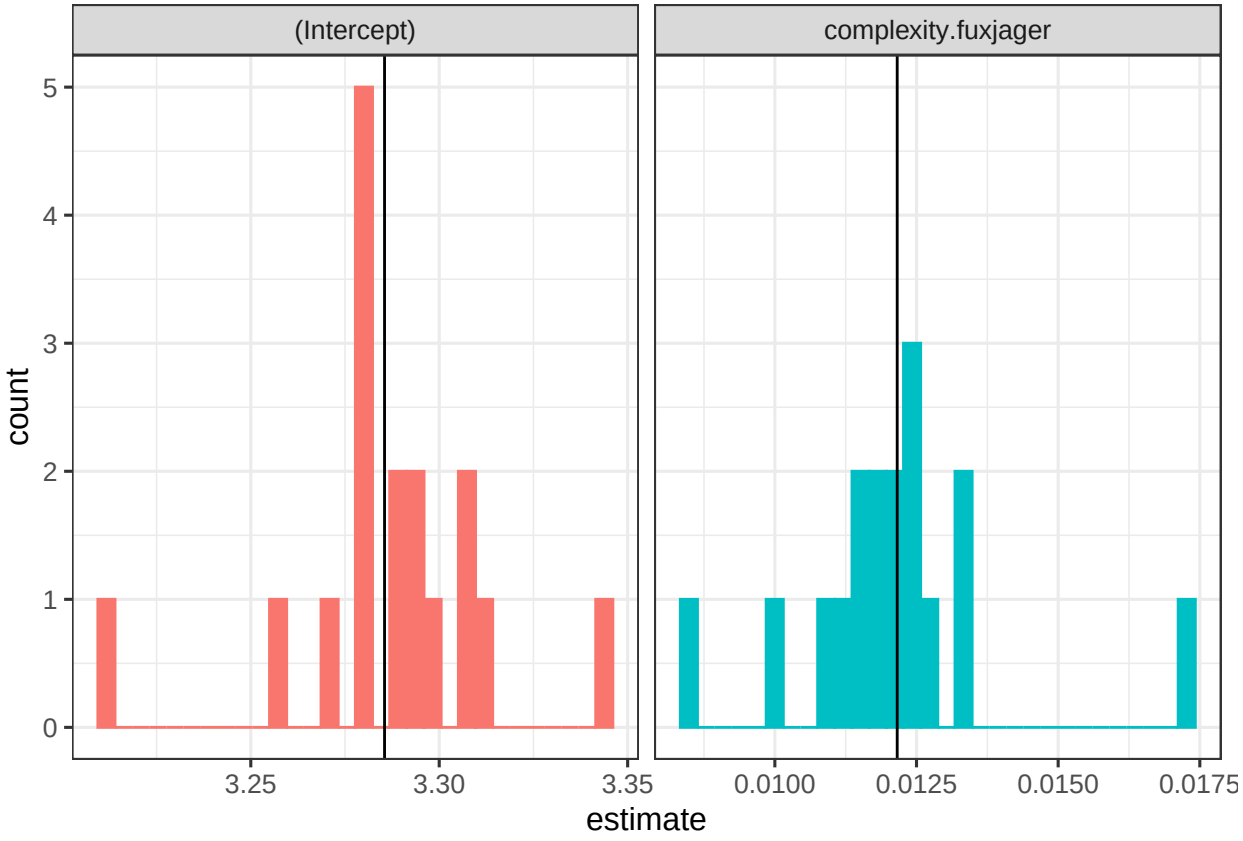
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m8$full.model.estimates
# test for influential species:
summary(sensi.m8)
summary_influ2(sensi.m8.2)$estimates
# Visual sensitivity diagnostics
sensi_plot(sensi.m8)
```

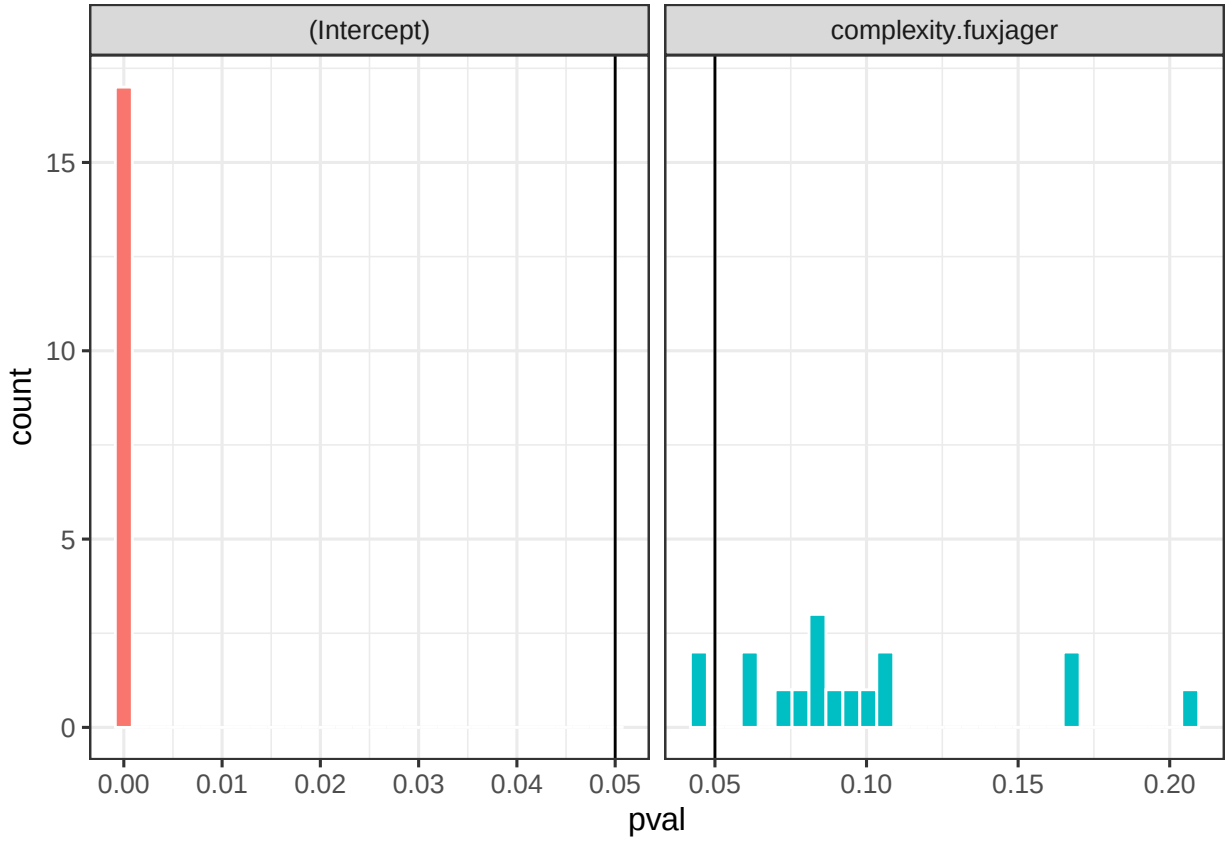



```
sensi_plot2(sensi.m8.2)
```

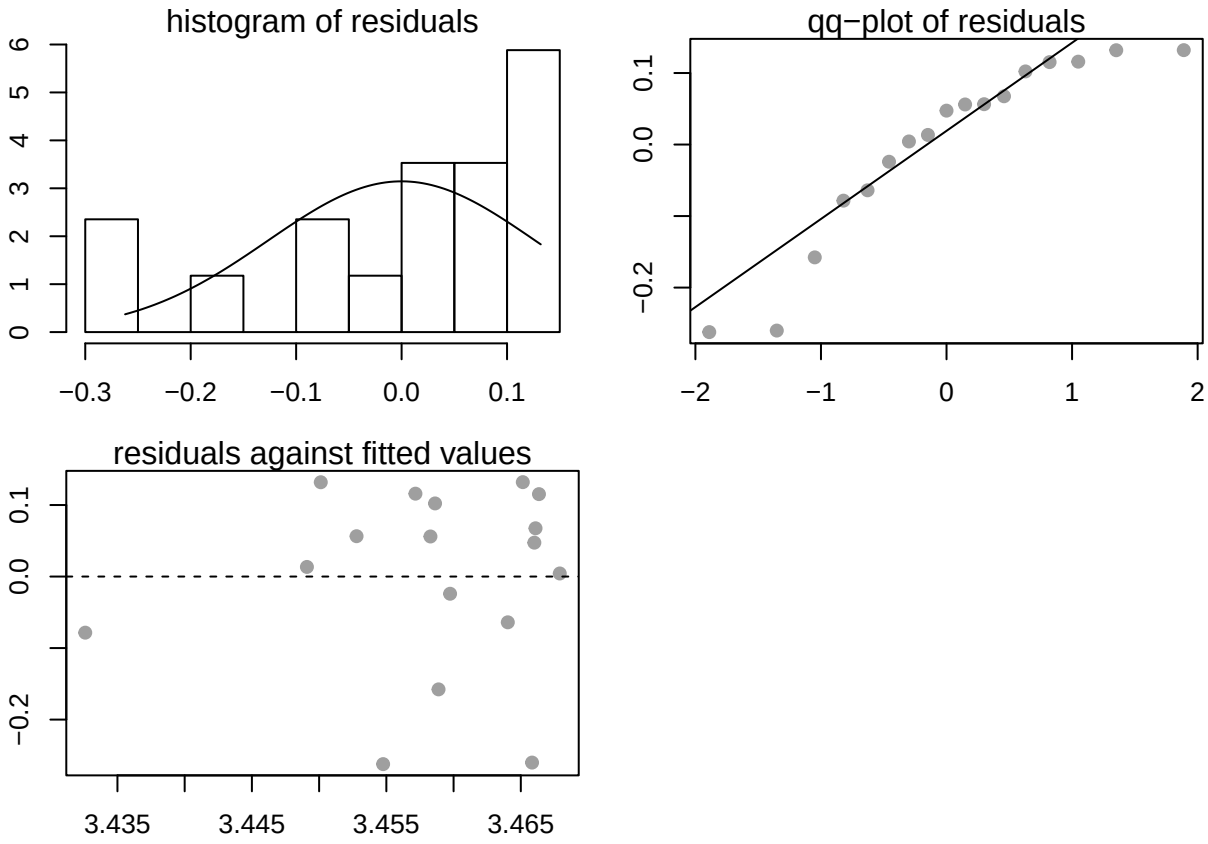
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m8$sensi.estimates

############################
### Acoustic diversity ###
############################

# Fit pgls model
m9<- pgls(logECV ~ acoustic.diversity.ligon,
          data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m9)
```



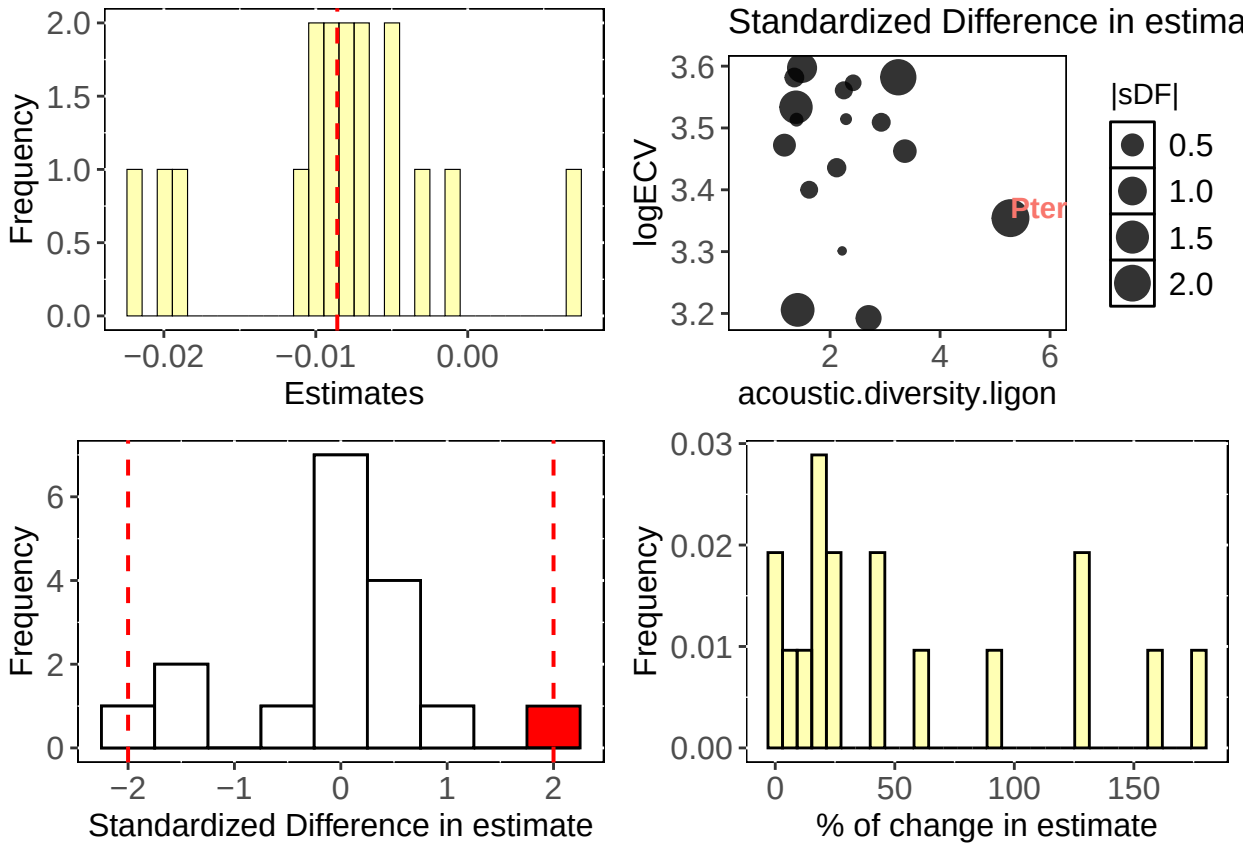

```
# Inspect the output
summary(m9)
# Formal test of normality
res9 <- residuals(m9, phylo = TRUE)
shapiro.test(res9)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m9 <- influ_phylm(logECV ~ acoustic.diversity.ligon,
                        phy = comparative_data_poly$phy,
                        data = comparative_data_poly$data, model = "BM",
                        track = FALSE)
```

```
## Used dataset has  17  species that match data and phylogeny
```

```
sensi.m9.2 <- influ_phylm2(logECV ~ acoustic.diversity.ligon,
                        phy = comparative_data_poly$phy,
                        data = comparative_data_poly$data, model = "BM",
                        track = FALSE)
```

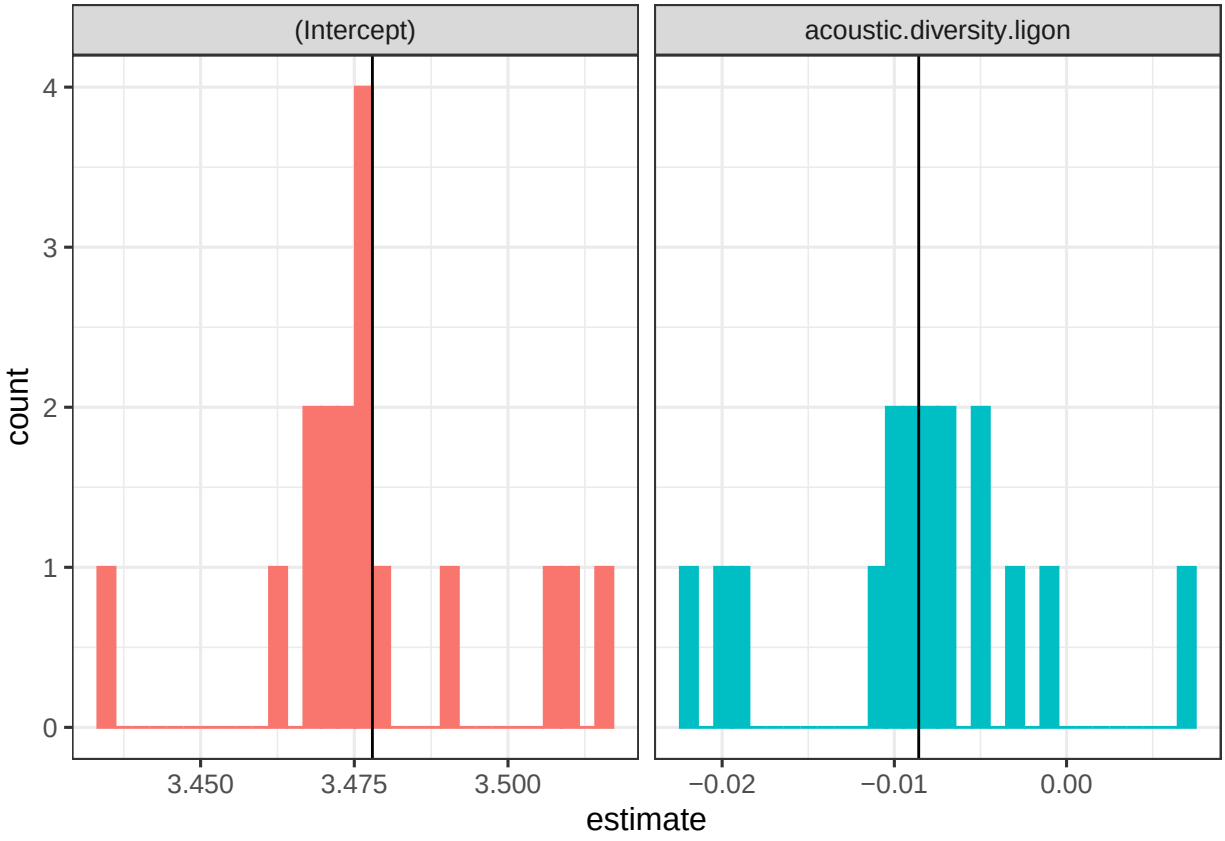
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m9$full.model.estimates
# test for influential species:
summary(sensi.m9)
# Visual sensitivity diagnostics
sensi_plot(sensi.m9)
```

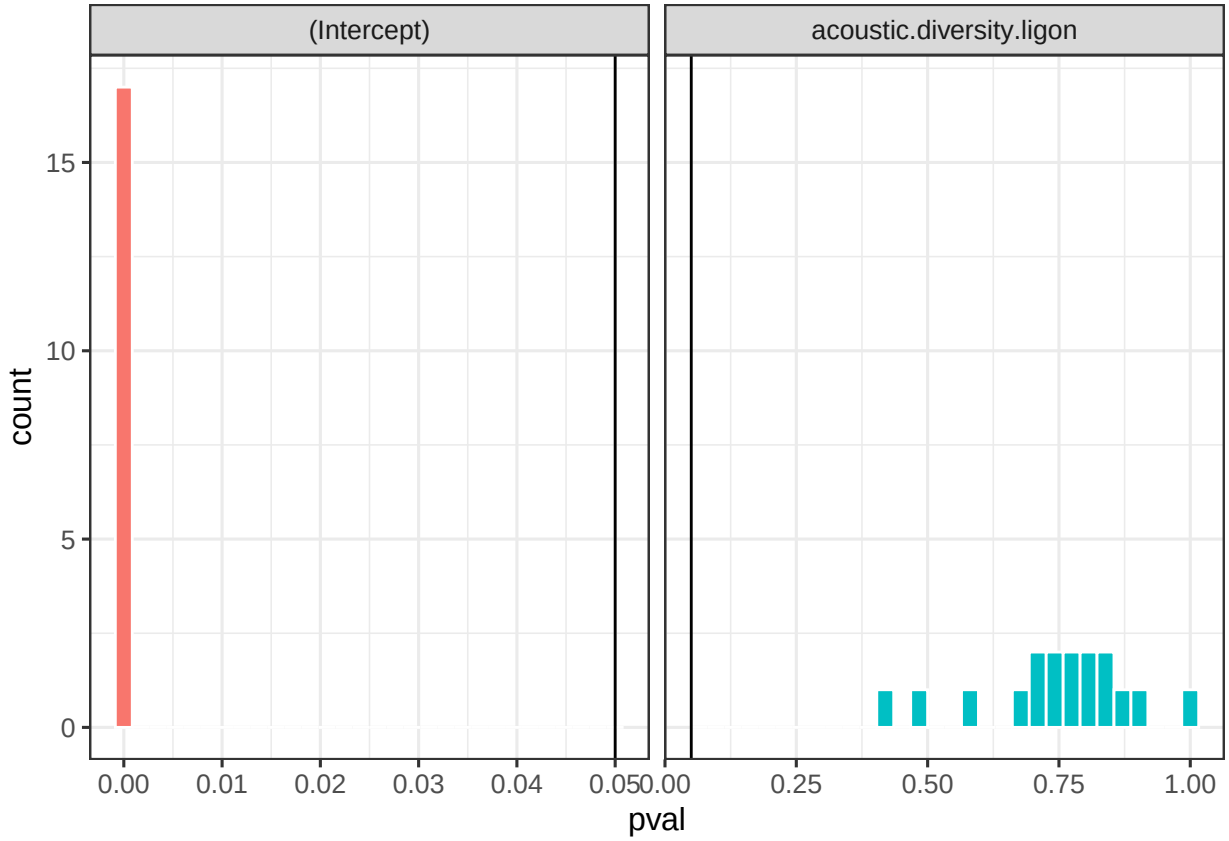



```
sensi_plot2(sensi.m9.2)
```

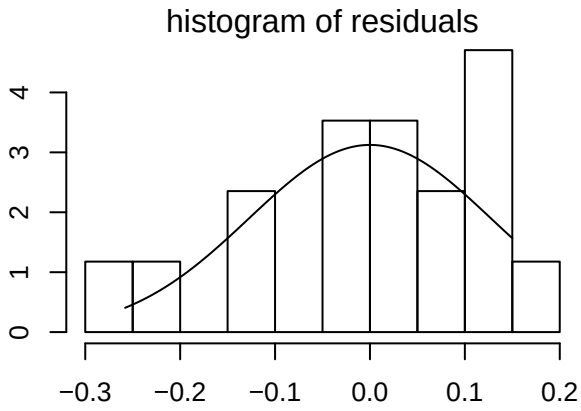
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

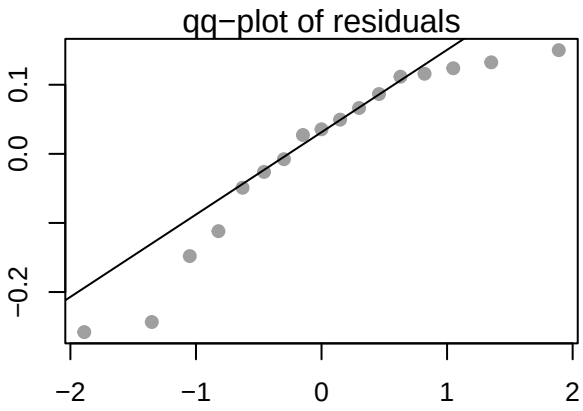


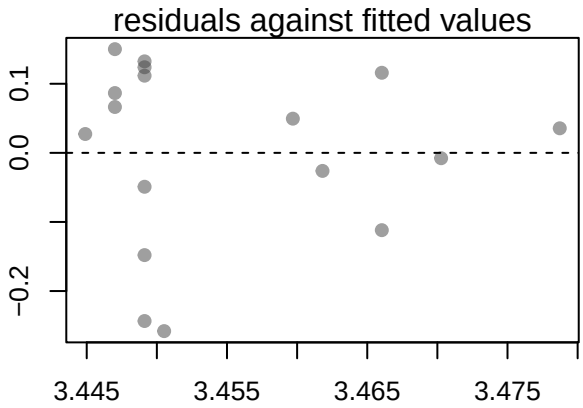

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
sensi.m9$sensi.estimates

##########################
### Acoustic richness ###
##########################

# Fit pgls model
m10<- pgls(logECV ~ acoustic.richness.ligon,
           data = comparative_data_poly, lambda = 1)
# Diagnostics
diagnostics.plot(m10)
```







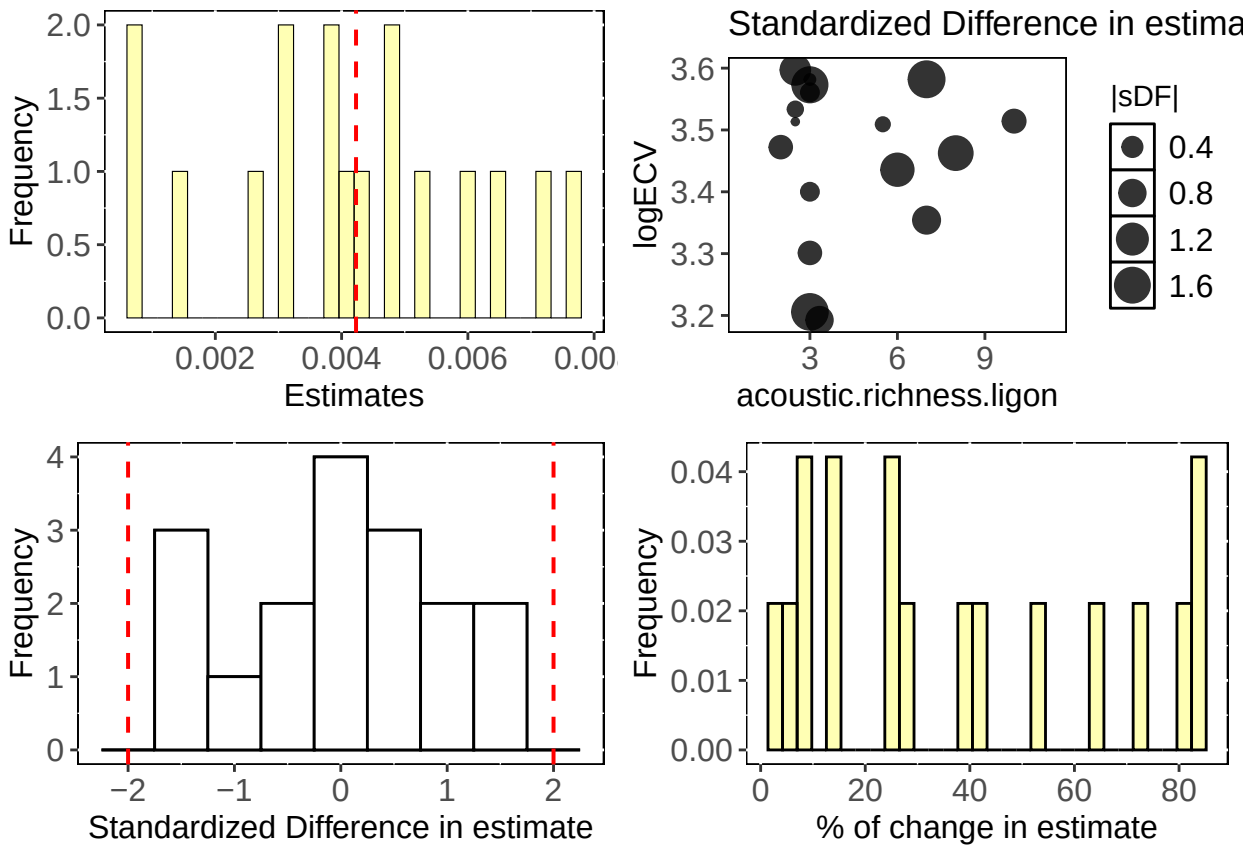

```
# Inspect the output
summary(m10)
# Formal test of normality
res10 <- residuals(m10, phylo = TRUE)
shapiro.test(res10)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m10 <- influ_phylm(logECV ~ acoustic.richness.ligon,
                         phy = comparative_data_poly$phy,
                         data = comparative_data_poly$data, model = "BM",
                         track = FALSE)
```

```
## Used dataset has  17  species that match data and phylogeny
```

```
sensi.m10.2 <- influ_phylm2(logECV ~ acoustic.richness.ligon,
                         phy = comparative_data_poly$phy,
                         data = comparative_data_poly$data, model = "BM",
                         track = FALSE)
```

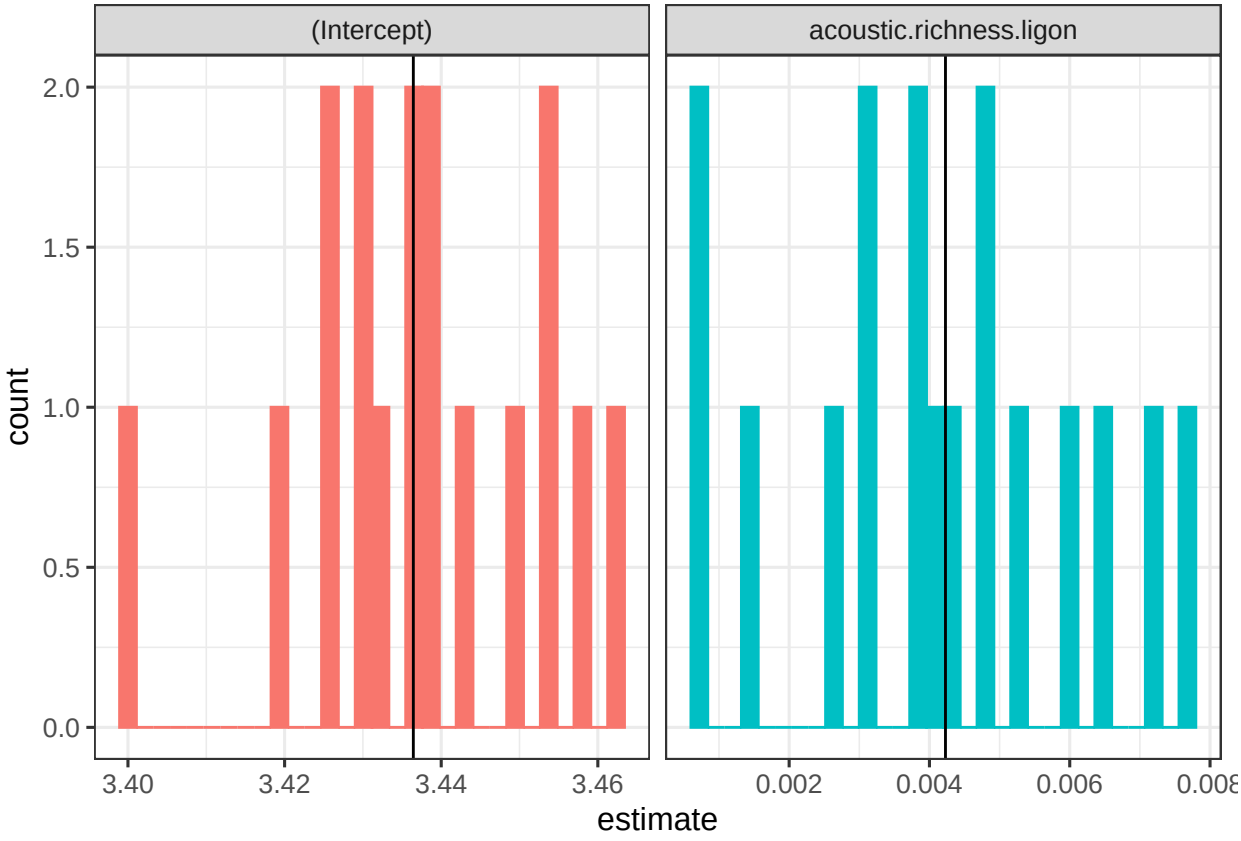
```
## Used dataset has  17  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m10$full.model.estimates
# test for influential species:
summary(sensi.m10)
# Visual sensitivity diagnostics
sensi_plot(sensi.m10)
```

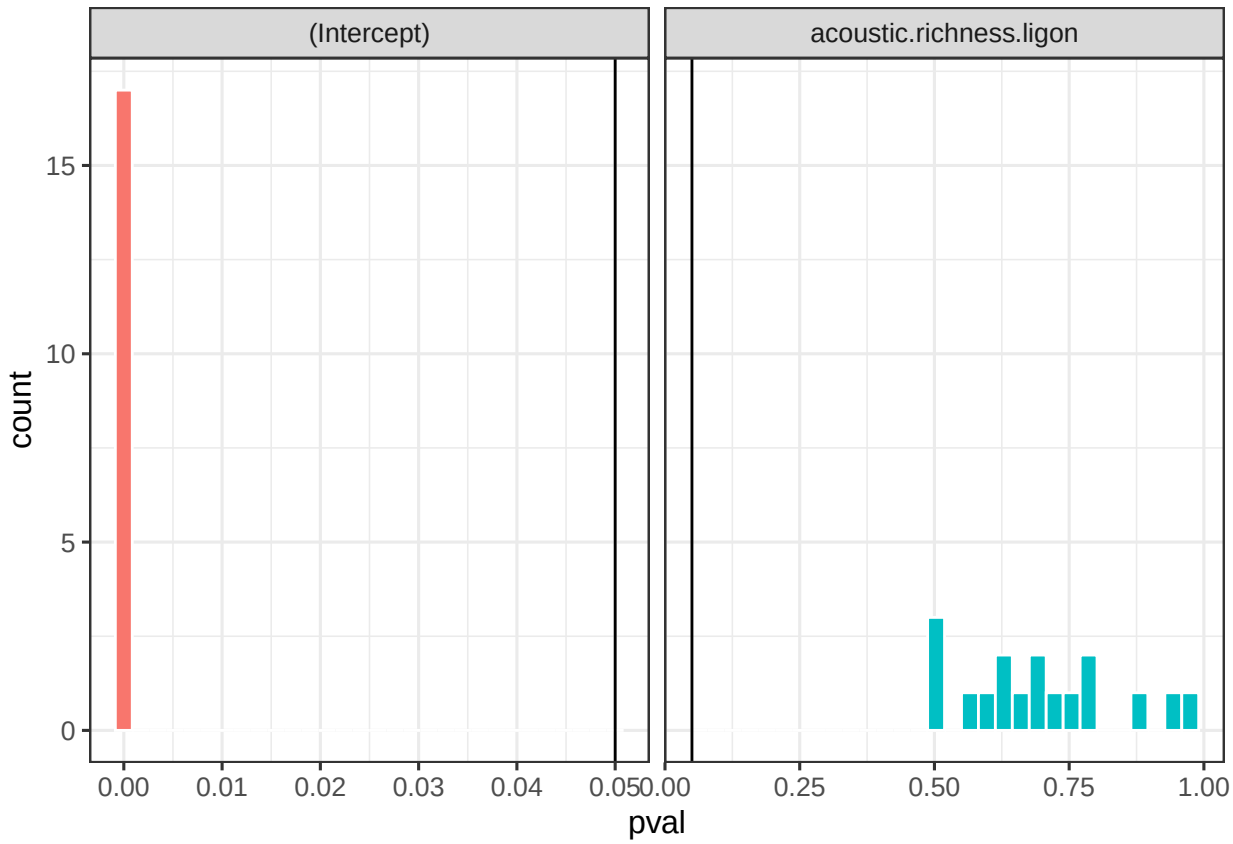



```
sensi_plot2(sensi.m10.2)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



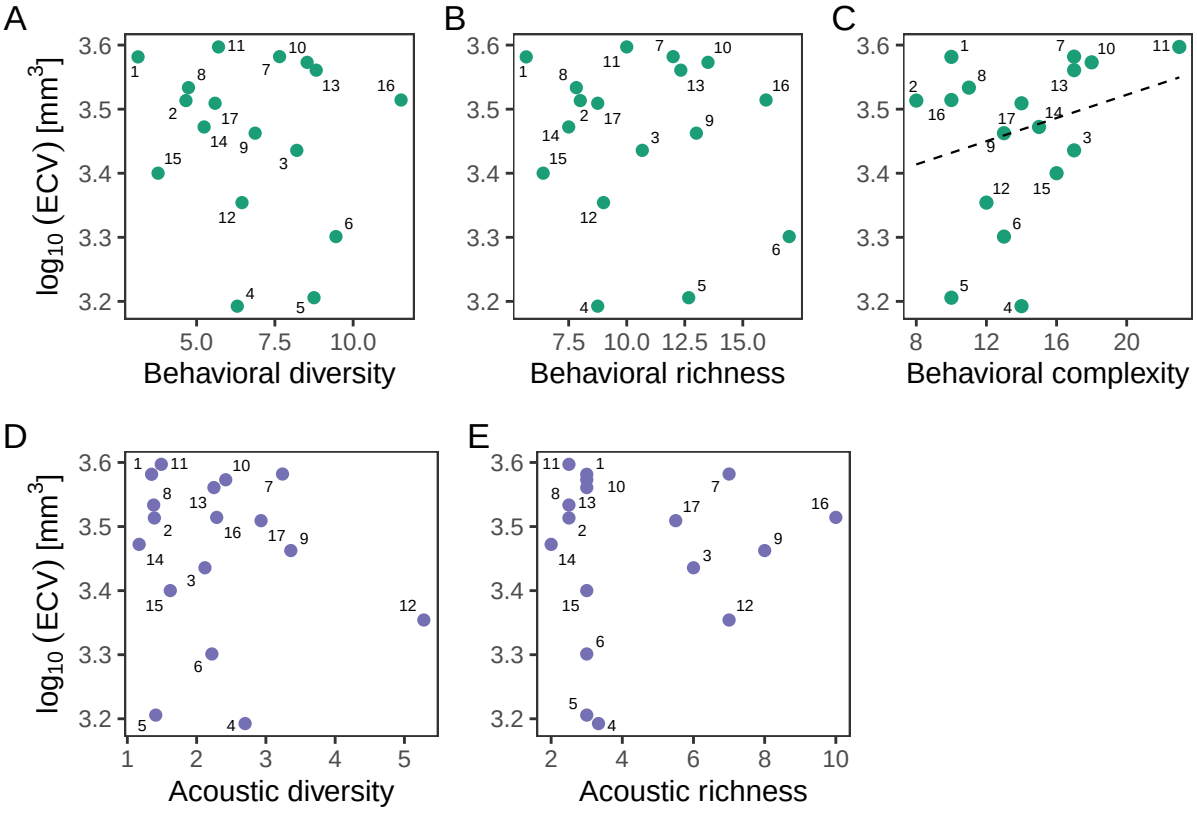

```
sensi.m10$sensi.estimates
```

2.6. Plotting

```
# Plot behavioral diversity
p1 <- ggplot(data.poly, aes(y = logECV, x = behavioral.diversity.ligon)) +
  geom_point(shape = 16, size = 2, alpha = 1, col = "#1B9E77") +
  theme_bw() +
  geom_text_repel(aes(label = species_number),
                  size = 2,
                  box.padding = 0.15,
                  point.padding = 0.15) +
  ylab(expression(log[10]~(ECV)~"["*mm^3*"]")) +
  xlab("Behavioral diversity") +
  labs(colour = "Clade") +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank())

# Plot behavioral richness
p2 <- ggplot(data.poly, aes(y = logECV, x = behavioral.richness.ligon)) +
  geom_point(shape = 16, size = 2, alpha = 1, col = "#1B9E77") +
  theme_bw() +
  geom_text_repel(aes(label = species_number),
                  size = 2,
                  box.padding = 0.15,
                  point.padding = 0.15) +
  ylab(NULL) +
```

```
#  ylab(expression(log[10]~(ECV)~"["*mm^3*"]")) +
  xlab("Behavioral richness") +
  labs(colour = "Clade") +
  scale_x_continuous(breaks = c(7.5, 10, 12.5, 15)) +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank())

# Plot behavioral complexity

# Generate predicted values while keeping logMass constant (e.g., at its mean)
mean_logMass <- mean(data.poly$logMass, na.rm = TRUE)

# Create a new data frame with the mean logMass for m3
data_for_prediction_m3 <- data.poly %>%
  mutate(logMass = mean_logMass)

# Predict values: Behavioral complexity for m3
m3.fit <- predict(m3, newdata = data_for_prediction_m3)

# Create data frame with predicted values for m3
df_predicted.m3 <- mutate(data_for_prediction_m3, predicted = m3.fit)

# We also want to highlight the species that, when dropped,
# result in a non-significant p-value
sp <- c("Cicinnurus_magnificus",
        "Cicinnurus_respublica",
        "Paradisaea_minor",
        "Parotia_lawesii")

# Plot the data, the model predictions, and the custom line
p3 <- ggplot(data.poly, aes(y = logECV, x = complexity.fuxjager)) +
  geom_point(col = "#1B9E77", shape = 16, size = 2, stroke = .75, alpha = 1) +
  geom_line(data = df_predicted.m3, aes(y = predicted),
            color = "black", linetype = 2, linewidth = 0.4) +
  geom_text_repel(aes(label = species_number),
                  size = 2,
                  box.padding = 0.15,
                  point.padding = 0.15) +
  theme_bw() +
  ylab(NULL) +
#  ylab(expression(log[10]~(ECV)~"["*mm^3*"]")) +
  xlab("Behavioral complexity") +
  labs(colour = "Clade") +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position = "none")

# Plot acoustic diversity
p4 <- ggplot(data.poly, aes(y = logECV, x = acoustic.diversity.ligon)) +
  geom_point(shape = 16, size = 2, alpha = 1, col = "#7570B3") +
  theme_bw() +
  geom_text_repel(aes(label = species_number),
                  size = 2,
```

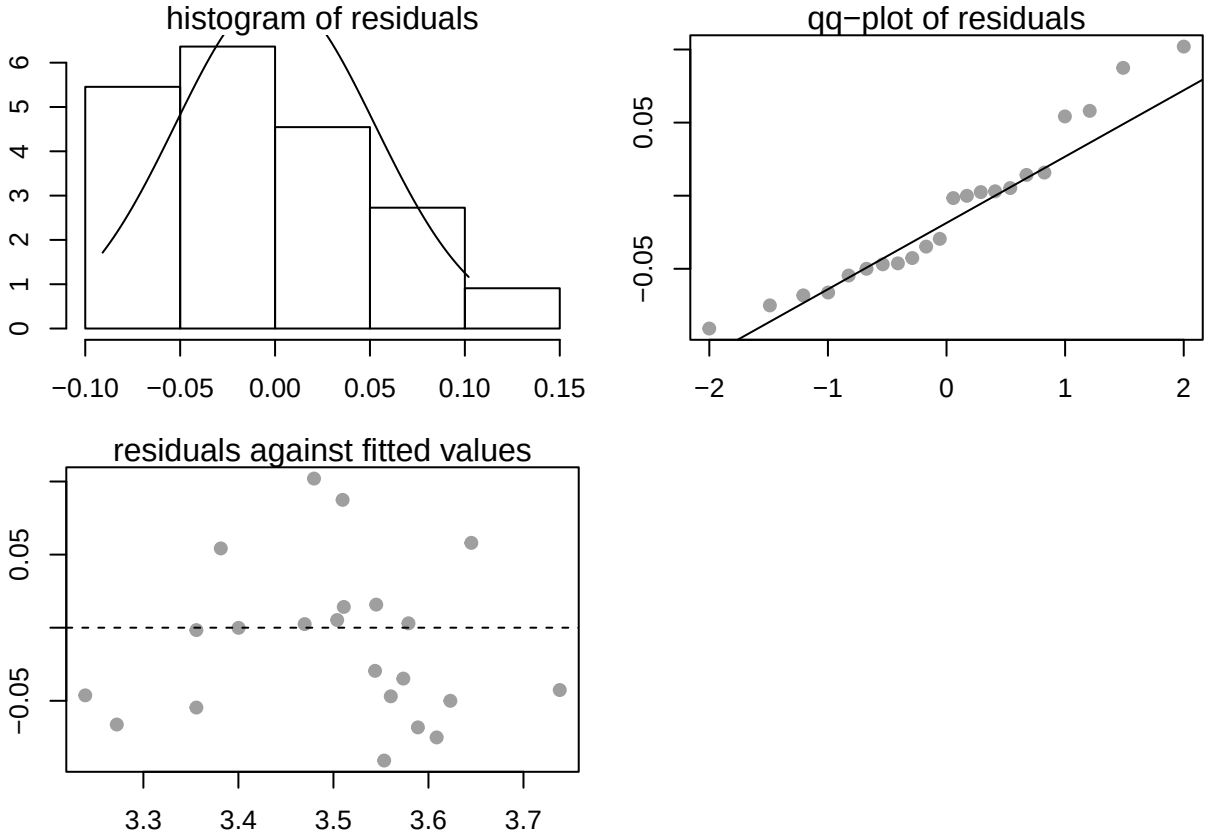
```
                  box.padding = 0.15,
                  point.padding = 0.15) +
  ylab(expression(log[10]~(ECV)~"["*mm^3*"]")) +
  xlab("Acoustic diversity") +
  labs(colour = "Clade") +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank())

# Plot acoustic richness
p5 <- ggplot(data.poly, aes(y = logECV, x = acoustic.richness.ligon)) +
  geom_point(shape = 16, size = 2, alpha = 1, col = "#7570B3") +
  theme_bw() +
  geom_text_repel(aes(label = species_number),
                  size = 2,
                  box.padding = 0.15,
                  point.padding = 0.15) +
  ylab(NULL) +
  xlab("Acoustic richness") +
  labs(colour = "Clade") +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank())

combined <- (p1|p2|p3)/(p4|p5|plot_spacer())
combined + plot_annotation(tag_levels = 'A')
```



Part 3: Testing for evolutionary grade shifts between BoP clades

3.1.1. Hypothesis-testing

```
# Fit a full model with a different intercept for both clades (mono vs poly)
m.full<- pgls(logECV ~ logMass + mating.system,
              data = comparative_data, lambda = 1)
# Diagnostics
diagnostics.plot(m.full)
```

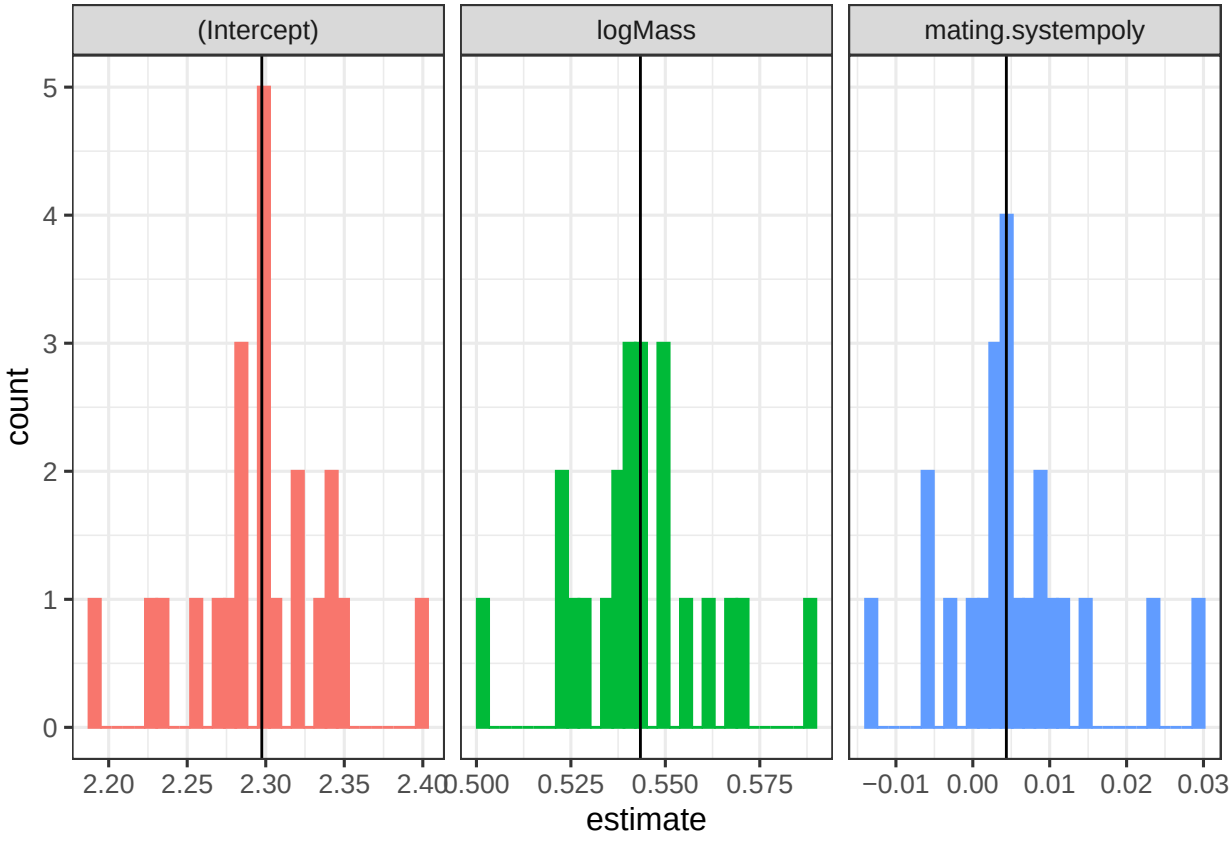



```
# Formal test of normality
res.full <- residuals(m.full, phylo = TRUE)
shapiro.test(res.full)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.mfull <- influ_phylm2(logECV ~ logMass + mating.system,
                            phy = comparative_data$phy,
                            data = comparative_data$data, model = "BM",
                            track = FALSE)
```

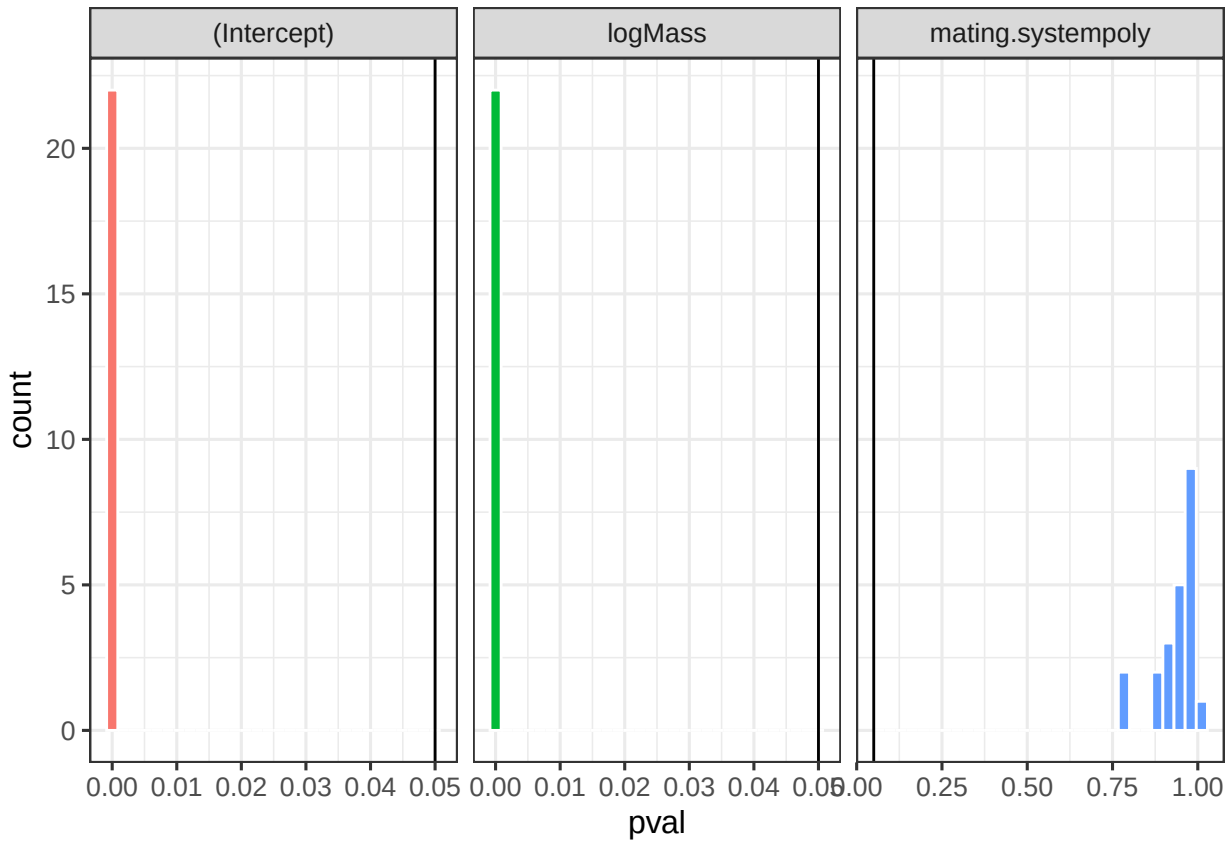
```
## Used dataset has  22  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.mfull$full.model.estimates
# test for influential species:
summary_influ2(sensi.mfull)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.mfull)
```

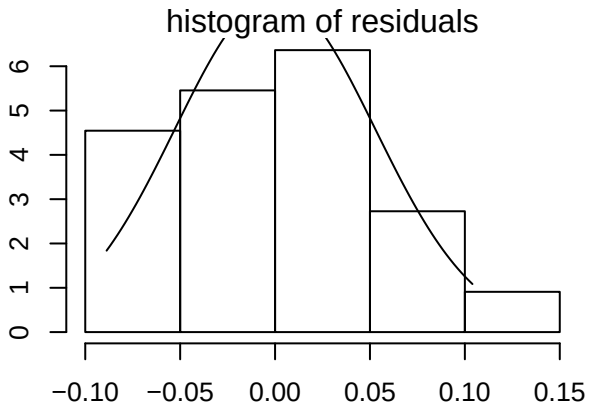
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

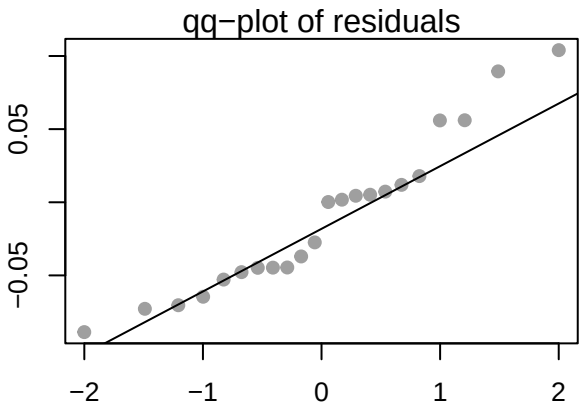


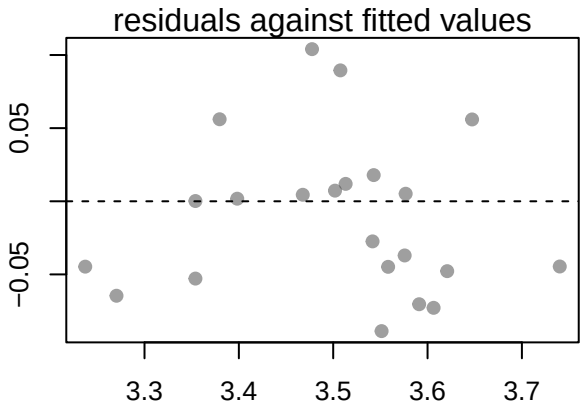

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
# Fit a null model without clade as a predictor
m.null<- pgls(logECV ~ logMass,
              data = comparative_data, lambda = 1)
# Diagnostics
diagnostics.plot(m.null)
```





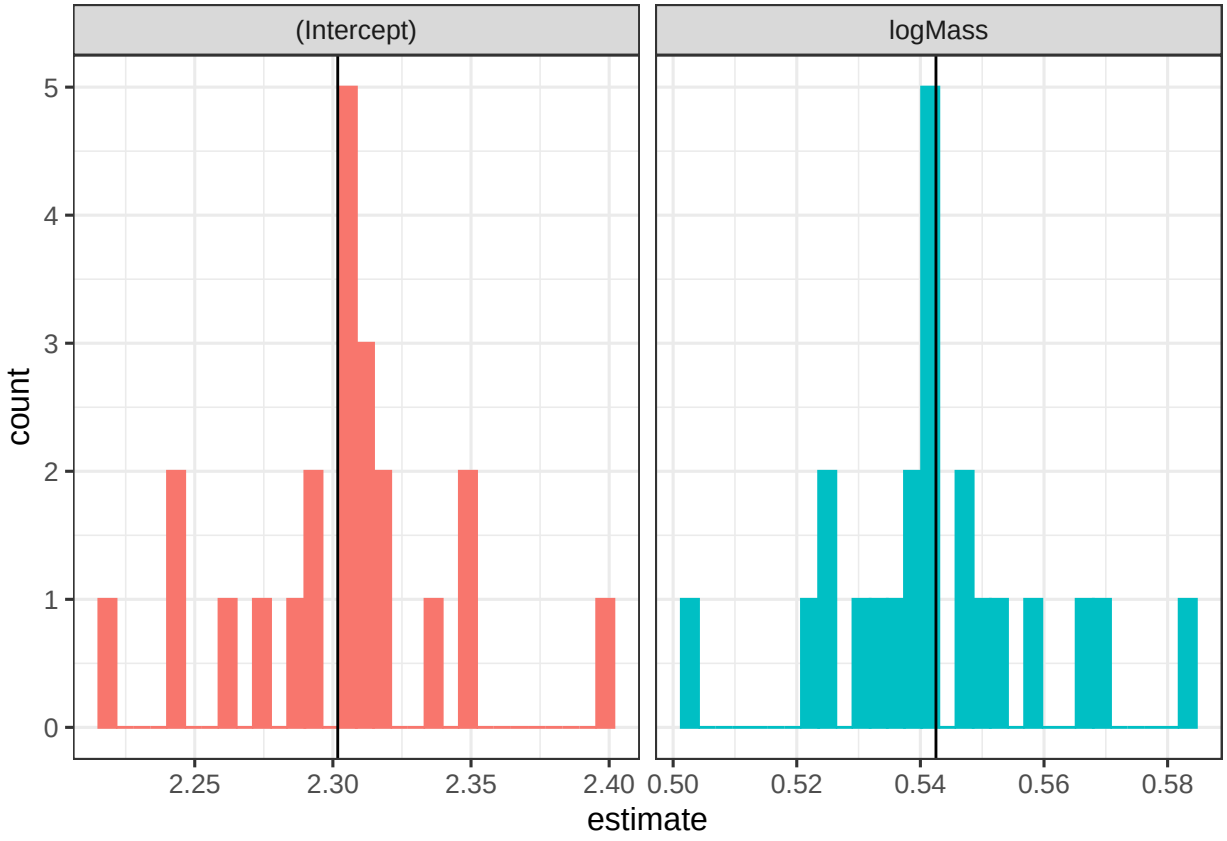



```
# Formal test of normality
res.null <- residuals(m.null, phylo = TRUE)
shapiro.test(res.null)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.mnull <- influ_phylm2(logECV ~ logMass,
                            phy = comparative_data$phy,
                            data = comparative_data$data, model = "BM",
                            track = FALSE)
```

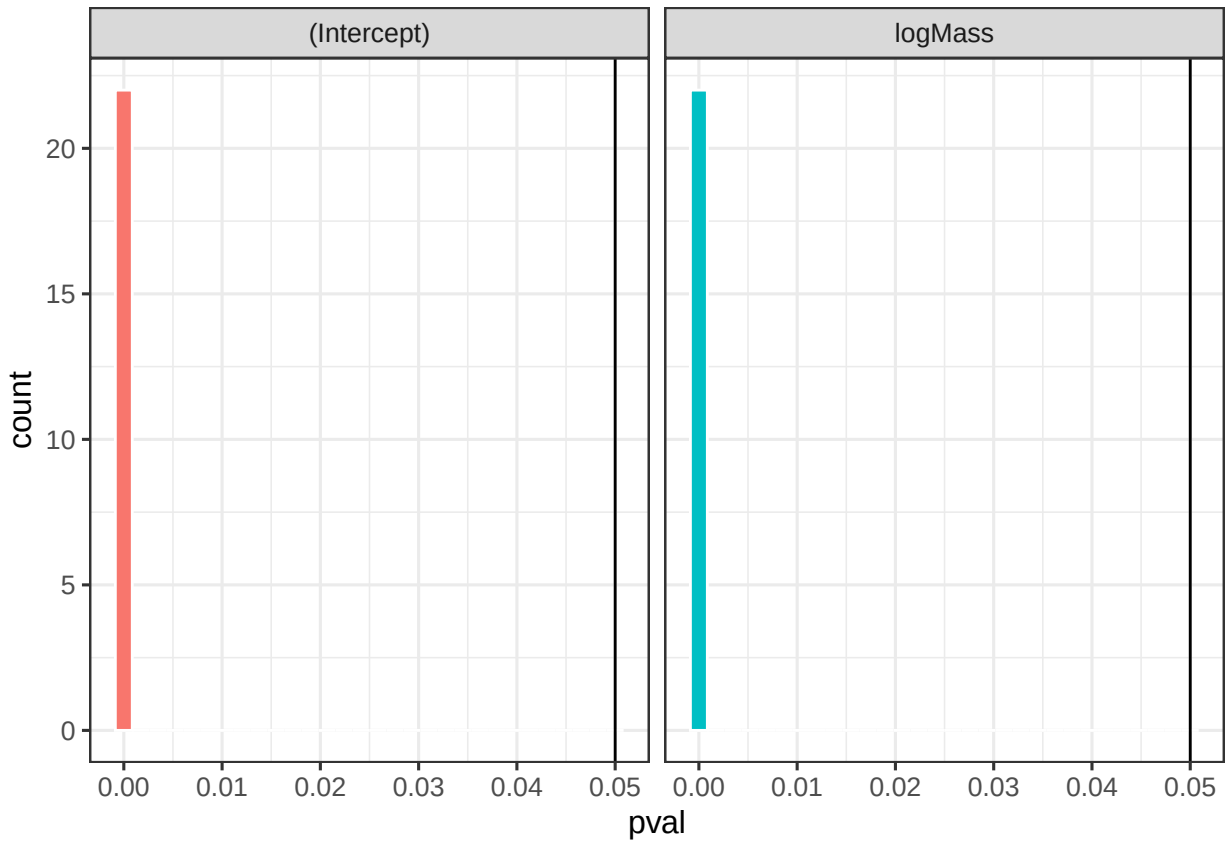
```
## Used dataset has  22  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.mnull$full.model.estimates
# test for influential species:
summary_influ2(sensi.mnull)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.mnull)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



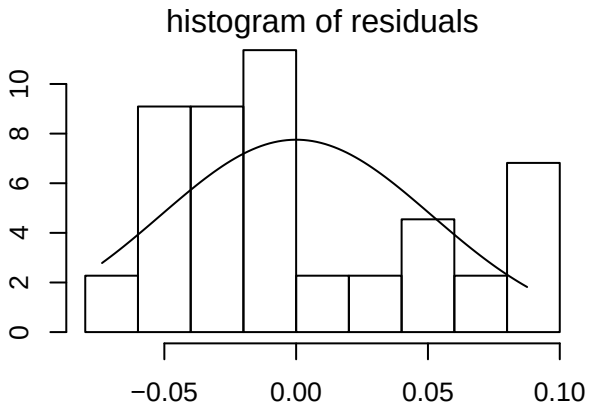

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

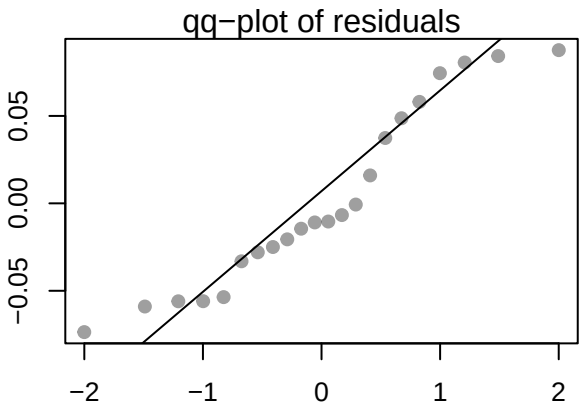


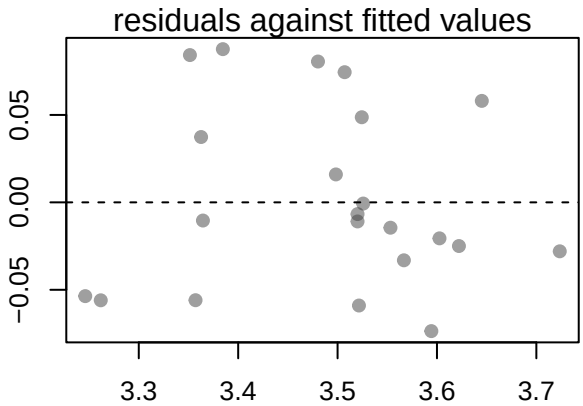

```
# Does including mating system as a model term improve the fit?
anova(m.null, m.full)
summary(m.null) # Nope
```

3.1.2. We can do the same using tarsus length cubed as a predictor

```
# Fit a full model with a different intercept for both clades (mono vs poly)
m.full.t<- pgls(logECV ~ logTarsus + mating.system,
              data = comparative_data, lambda = 1)
# Diagnostics
diagnostics.plot(m.full.t)
```





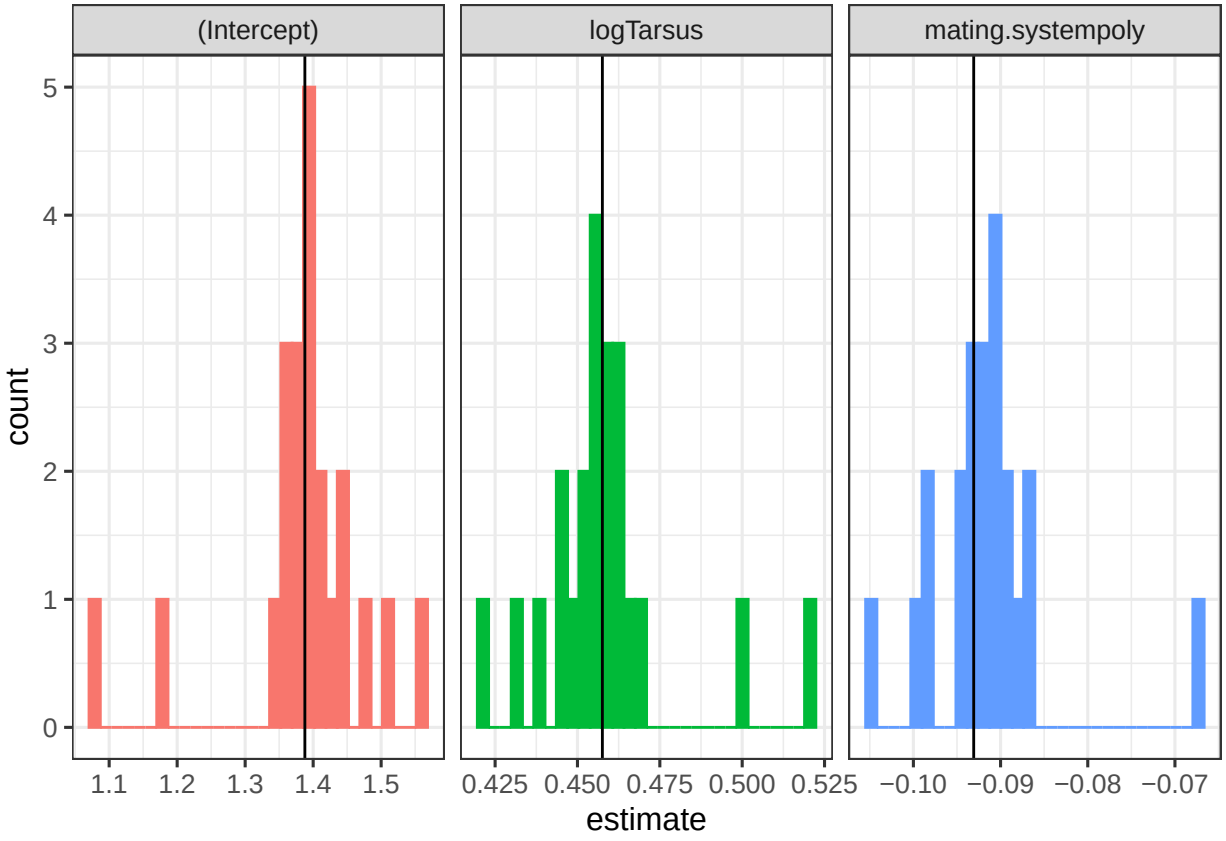



```
# Formal test of normality
res.full.t <- residuals(m.full.t, phylo = TRUE)
shapiro.test(res.full.t)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.mfull.t <- influ_phylm2(logECV ~ logTarsus + mating.system,
                              phy = comparative_data$phy,
                              data = comparative_data$data, model = "BM",
                              track = FALSE)
```

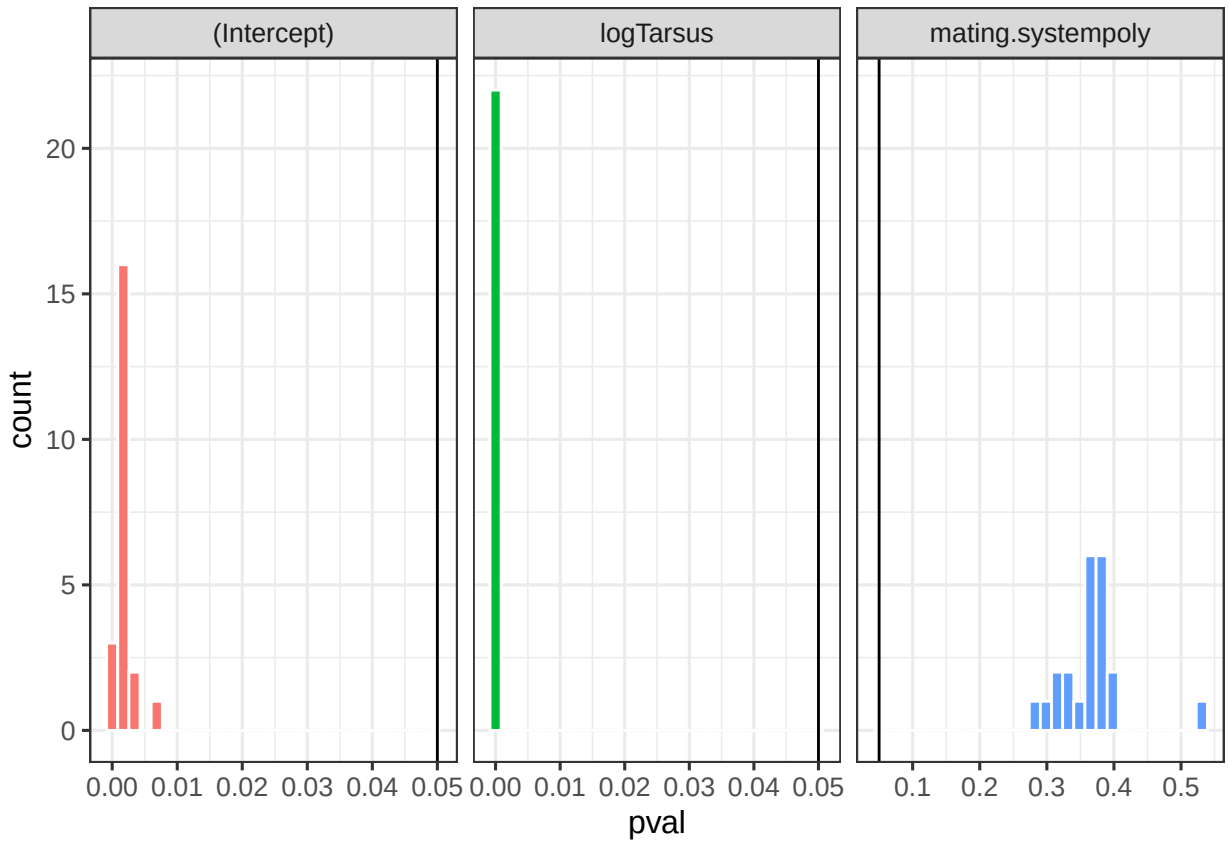
```
## Used dataset has  22  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.mfull.t$full.model.estimates
# test for influential species:
summary_influ2(sensi.mfull.t)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.mfull.t)
```

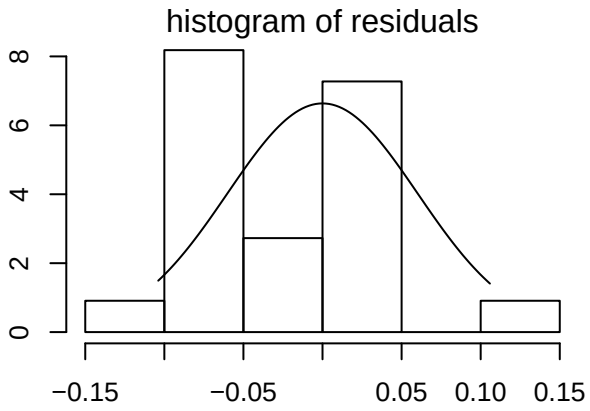
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

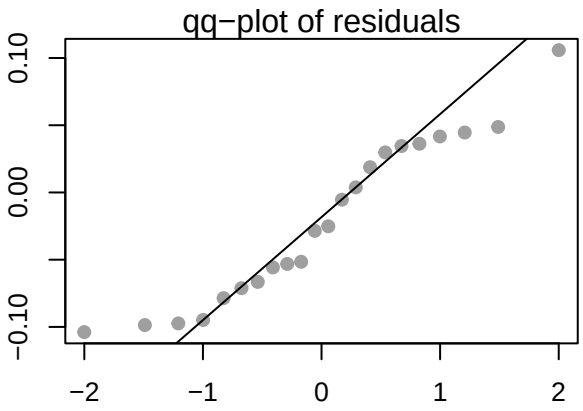


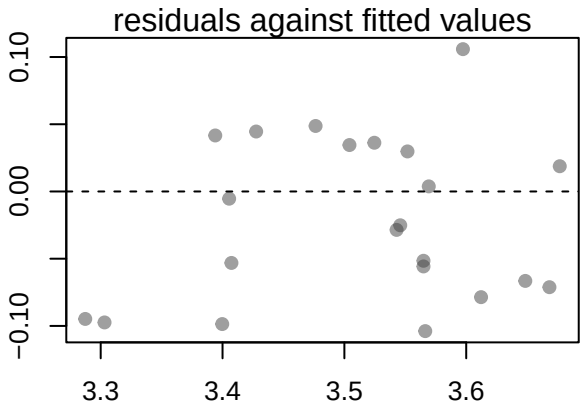

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
# Fit a null model without clade as a predictor
m.null.t<- pgls(logECV ~ logTarsus,
                data = comparative_data, lambda = 1)
# Diagnostics
diagnostics.plot(m.null.t)
```





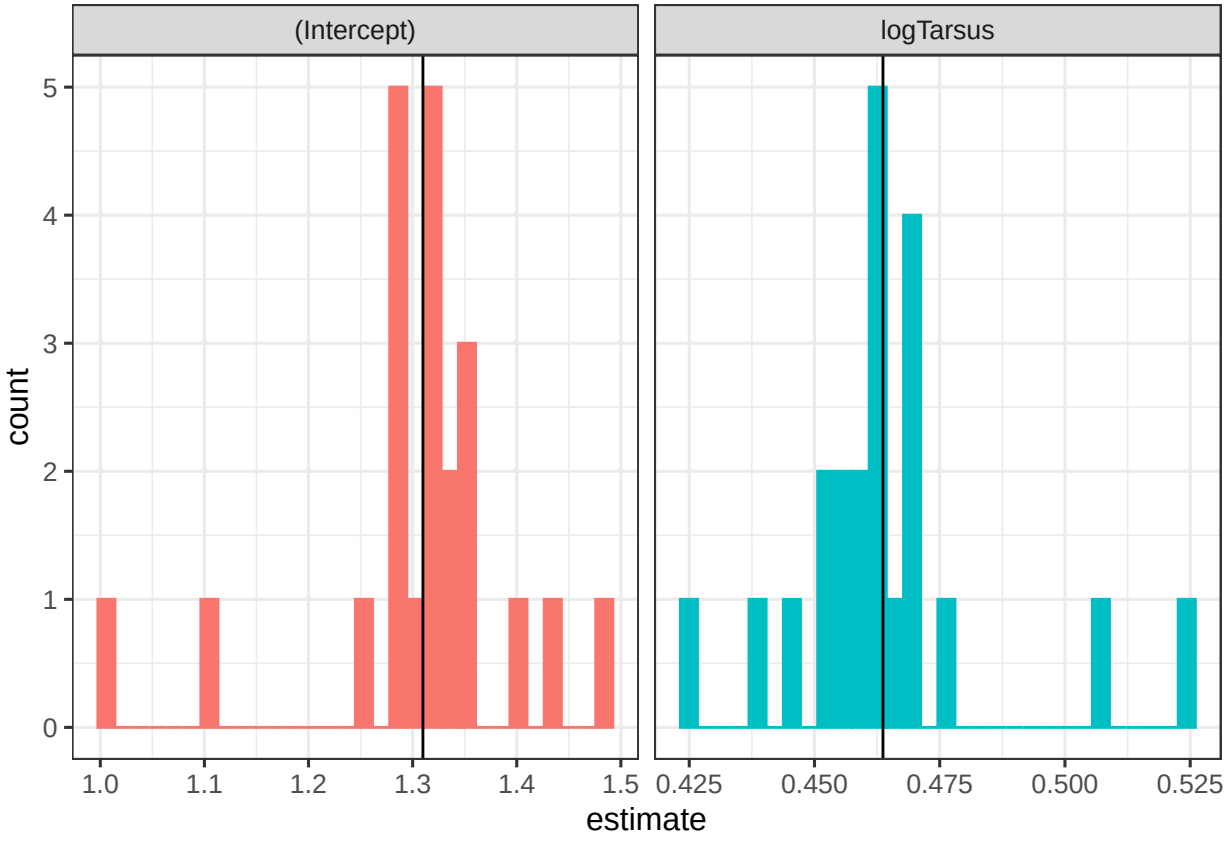



```
# Formal test of normality
res.null.t <- residuals(m.null.t, phylo = TRUE)
shapiro.test(res.null.t)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.mnull.t <- influ_phylm2(logECV ~ logTarsus,
                              phy = comparative_data$phy,
                              data = comparative_data$data, model = "BM",
                              track = FALSE)
```

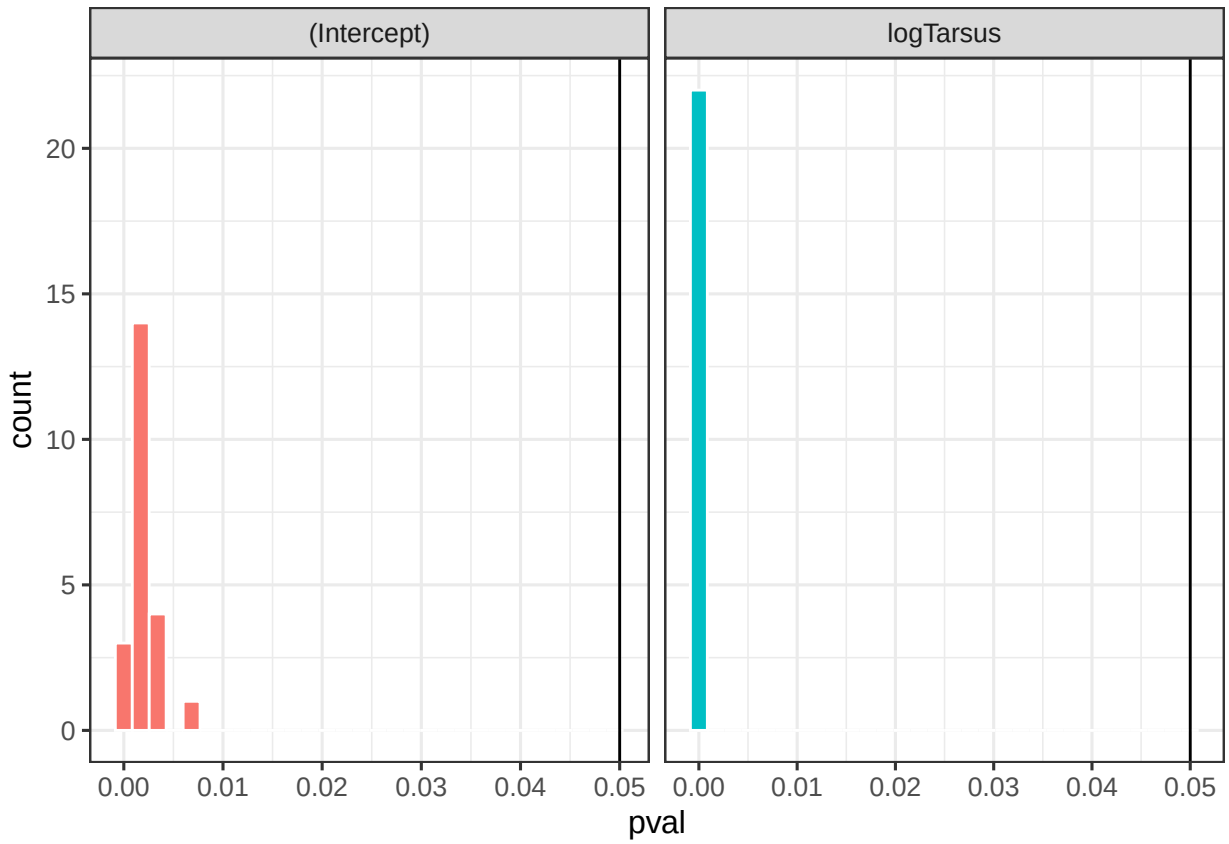
```
## Used dataset has  22  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.mnull.t$full.model.estimates
# test for influential species:
summary_influ2(sensi.mnull.t)$estimates
# Visual sensitivity diagnostics
sensi_plot2(sensi.mnull.t)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

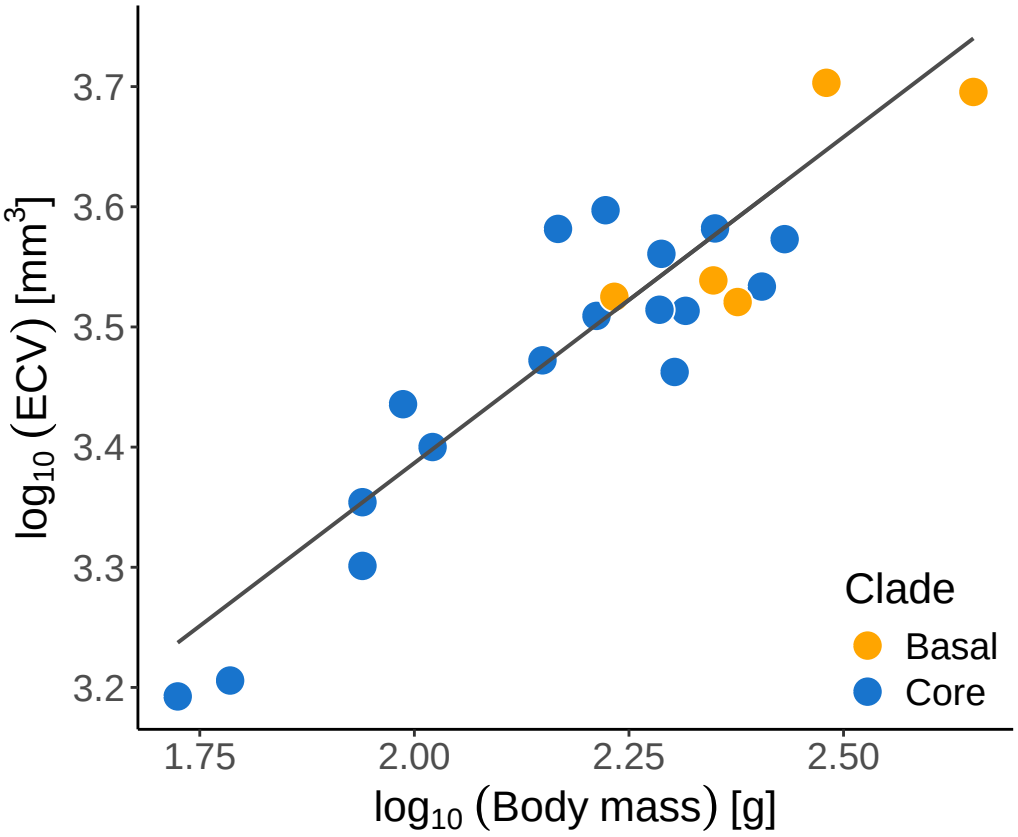



```
# Does including mating system as a model term improve the fit?
anova(m.null.t, m.full.t)
summary(m.null.t) # Nope
```

3.2. Plotting results

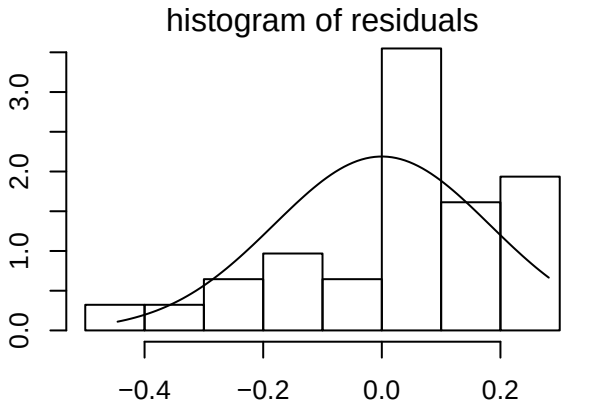
```
# Predict values
null.fit<- predict(m.null, data)

# Create data frame for males with predicted values
df_predicted.null <- mutate(data, predicted = null.fit)

p <- ggplot(data, aes(x = logMass, y = logECV, fill = mating.system)) +
  geom_point(shape = 21, size = 5, alpha = 1, col = "white") +
  geom_line(data = df_predicted.null, aes(y = null.fit),
            color = "grey30", linetype = 1, linewidth = 0.7) +
  scale_fill_manual(values = c("orange", "dodgerblue3"),
                    labels = c("Basal", "Core")) +  # Rename levels here
  theme_classic() +
  ylab(expression(log[10]~(ECV)~"["*mm^3*"]")) +
  xlab(expression(log[10]~(Body~mass)~"["*g*"]")) +
  theme(
    axis.text.x = element_text(size = 14),
    axis.text.y = element_text(size = 14),
    axis.title.x = element_text(size = 16),
    axis.title.y = element_text(size = 16),
    legend.title = element_text(size = 16),
```

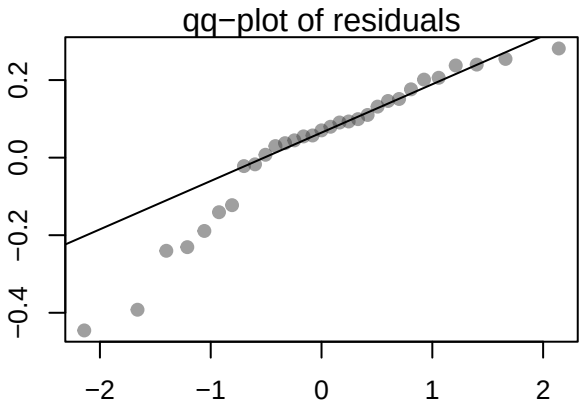
```
    legend.text = element_text(size = 14),
    legend.position = c(1, 0),
    legend.justification = c(1, 0),
    legend.background = element_blank()) +
  coord_fixed(ratio = 1.4) +
  scale_y_continuous(breaks = c(3.2, 3.3, 3.4, 3.5, 3.6, 3.7)) +
  theme(
    panel.grid.major = element_blank(),
    panel.grid.minor = element_blank()) +
  labs(fill = "Clade")

print(p)
```

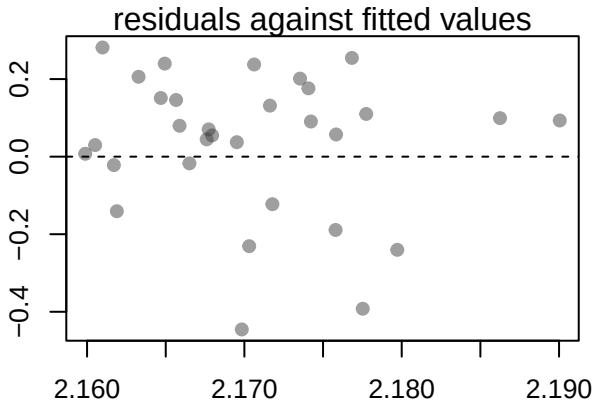



```
# For completeness, we also test whether body size predicts display complexity

# Start with a fresh R environment
rm(list = ls())

# Call other functions
source("diagnostic_fcns.r")
source("influ_phylm2_Paterno_et_al.R")
source("summary_influ_phylm2_Paterno_et_al.R")
source("plot_influ_phylm2_Paterno_et_al.R")

# Load the data again in the fresh environment
df <- read.csv("Paradisaeidae_Brain.Data.Full.csv")
# Load the tree
```

```r
tree <- read.nexus("Ligon.et.al._UltrametricTree")
# Only the core birds of paradise
df.poly <- filter(df, mating.system == "poly")

# First, run all models with body mass as a response variable

# New comparative data set:
comparative_df <- comparative.data(phy = tree,
                                   data = df.poly,
                                   names.col = species,
                                   vcv = TRUE,
                                   na.omit = FALSE,
                                   warn.dropped = TRUE)

# Fit model 1
m1 <- pgls(log10(bodymass.frith.g) ~ behavioral.diversity.ligon, data = comparative_df, lambda = 1)
# Diagnostics
diagnostics.plot(m1)
```



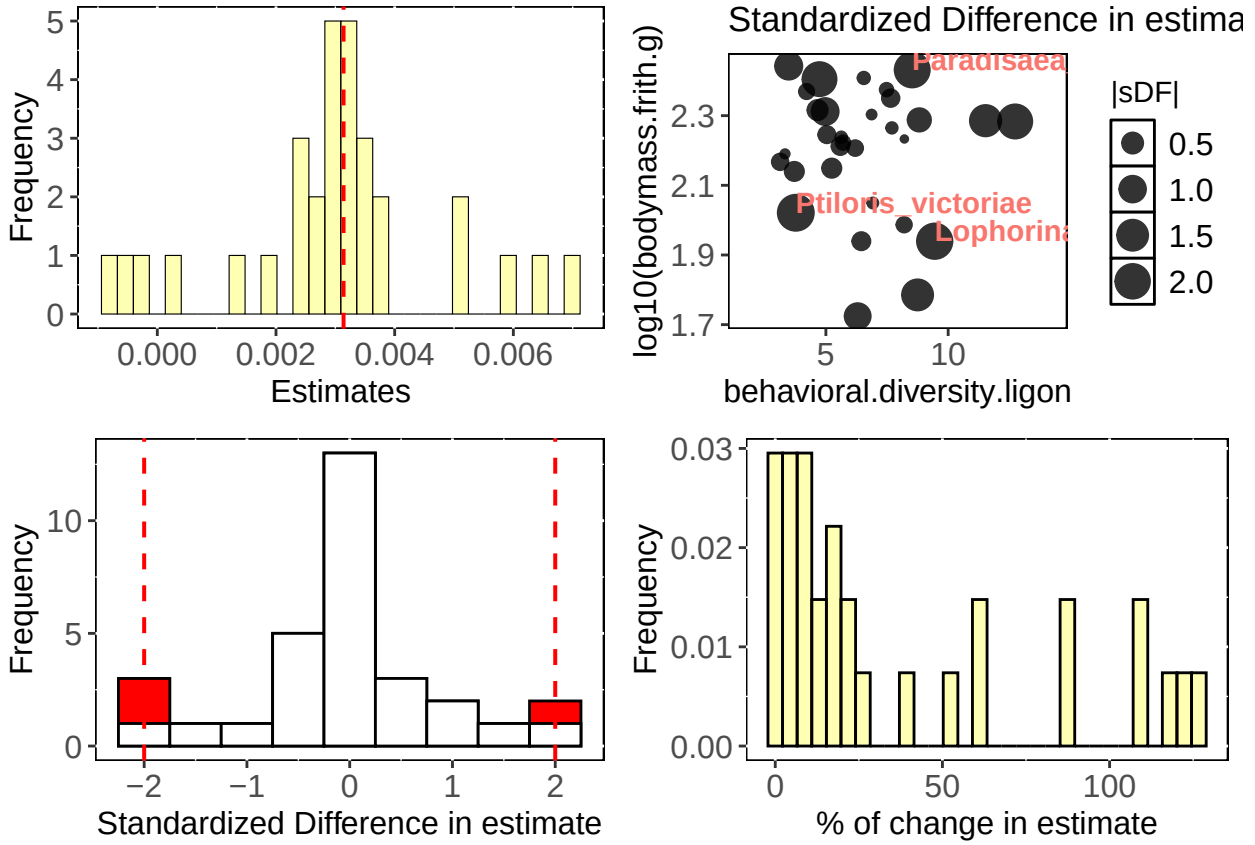




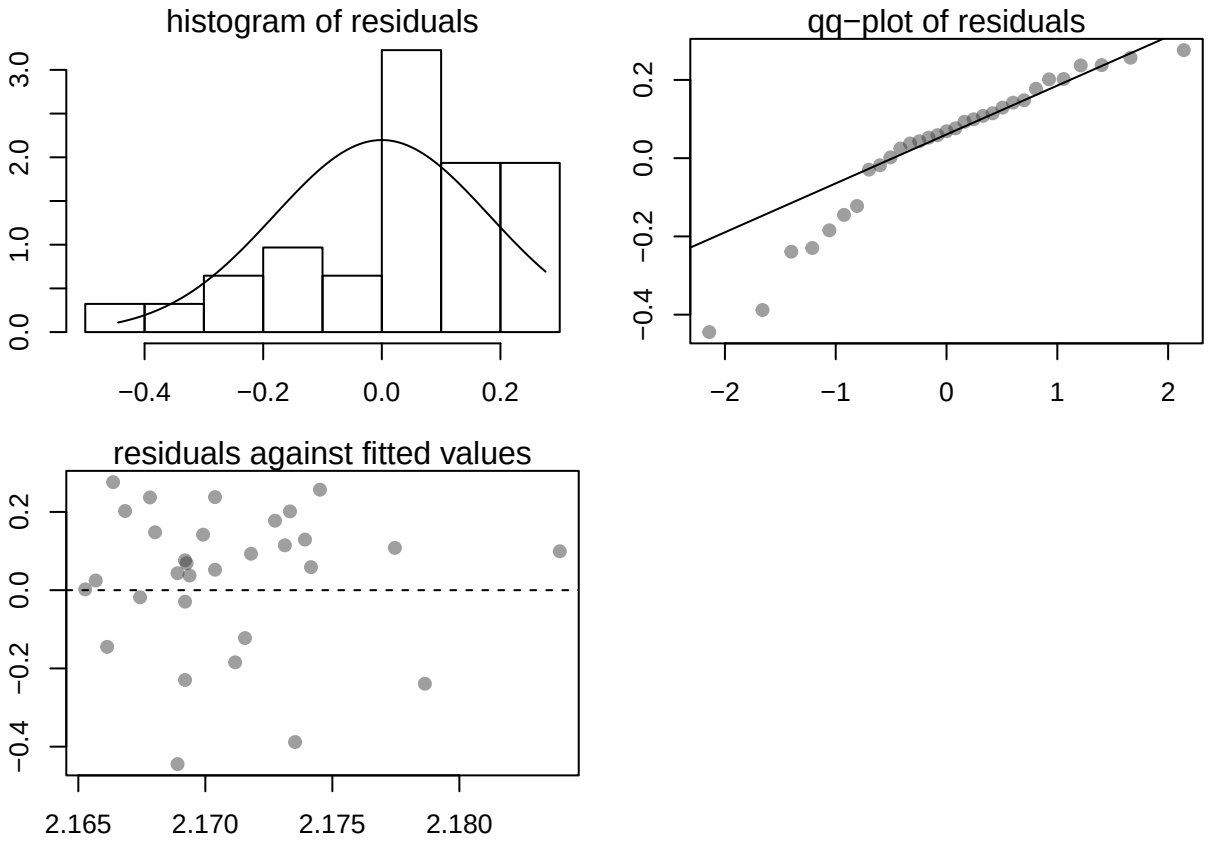

```r
# Formal test of normality
res.m1 <- residuals(m1, phylo = TRUE)
shapiro.test(res.m1)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m1 <- influ_phylm(log10(bodymass.frith.g) ~ behavioral.diversity.ligon,
                        phy = comparative_df$phy,
                        data = comparative_df$data, model = "BM",
                        track = FALSE)
```

```
## Used dataset has  31  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m1$full.model.estimates
# test for influential species:
summary(sensi.m1)
# Visual sensitivity diagnostics
sensi_plot(sensi.m1)
```



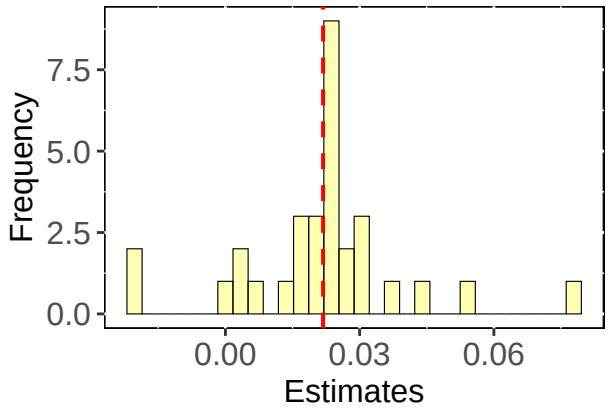

```
summary(m1)
nobs(m1)

# Fit model 2
m2<- pgls(log10(bodymass.frith.g) ~ behavioral.richness.ligon, data = comparative_df, lambda = 1)
# Diagnostics
diagnostics.plot(m2)
```

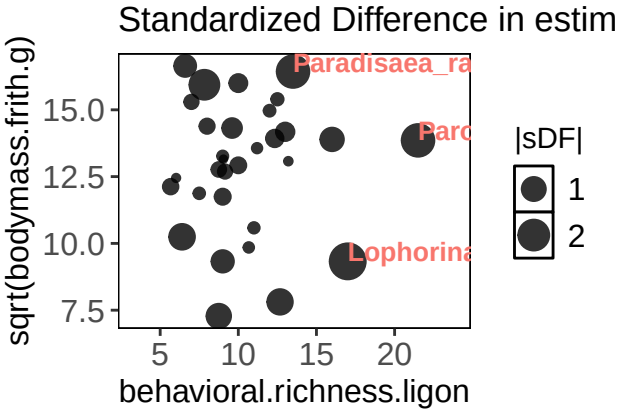


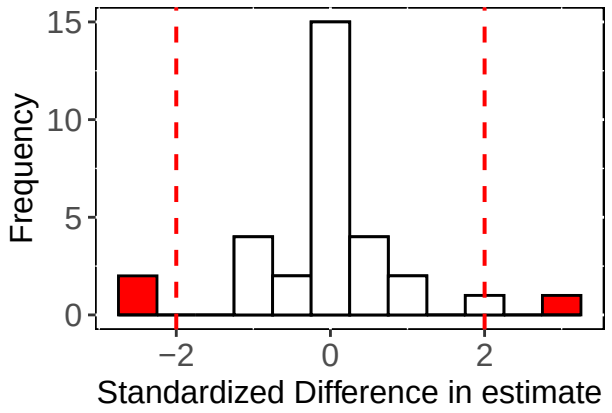

```
# Formal test of normality
res.m2 <- residuals(m2, phylo = TRUE)
shapiro.test(res.m2)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m2 <- influ_phylm(sqrt(bodymass.frith.g) ~ behavioral.richness.ligon,
                            phy = comparative_df$phy,
                            data = comparative_df$data, model = "BM",
                            track = FALSE)
```

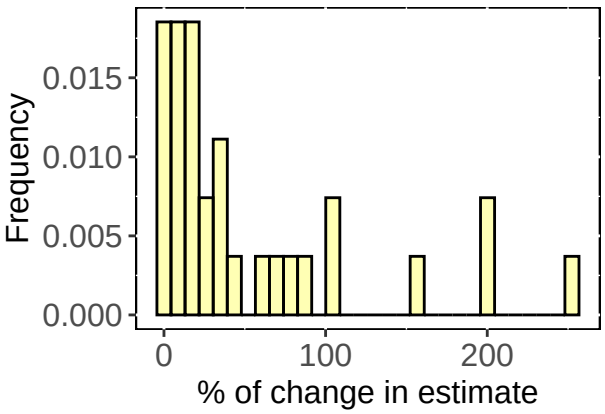
```
## Used dataset has  31  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m2$full.model.estimates
# test for influential species:
summary(sensi.m2)
# Visual sensitivity diagnostics
sensi_plot(sensi.m2)
```

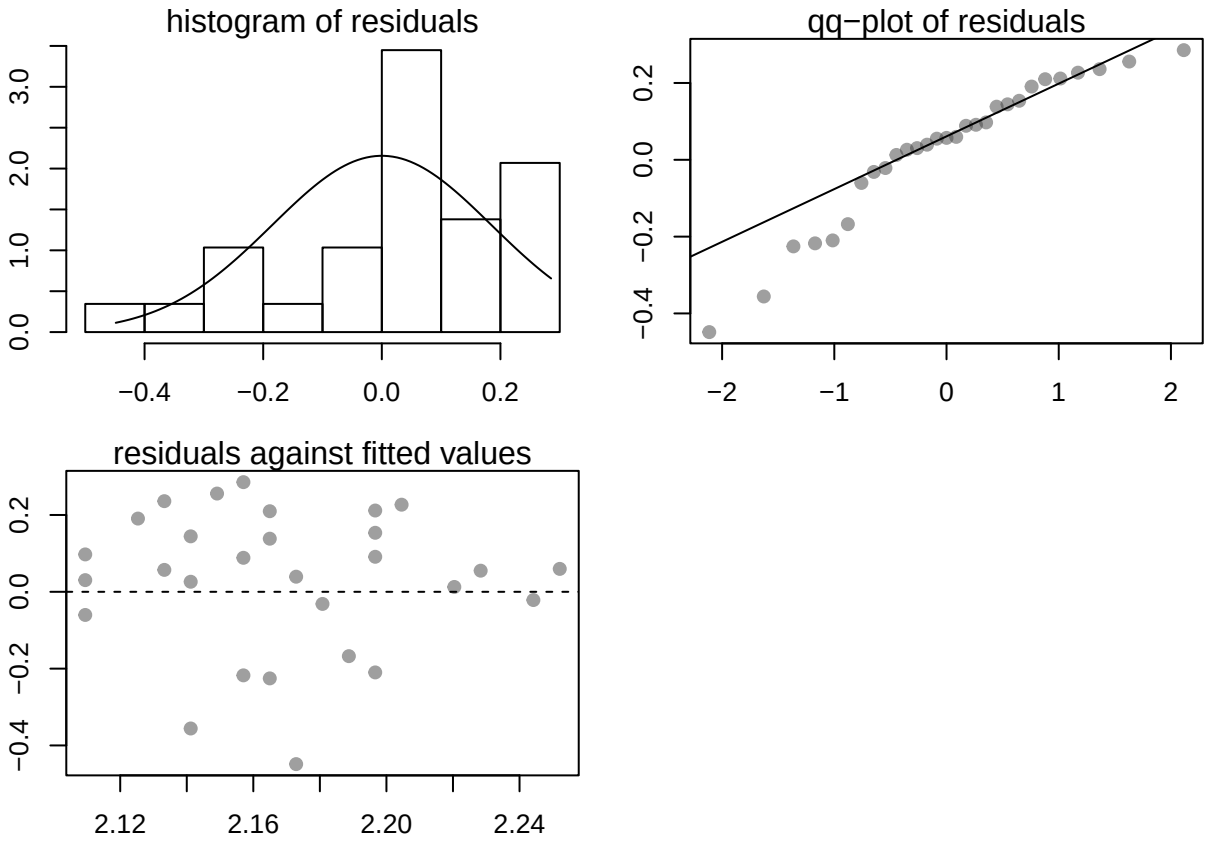








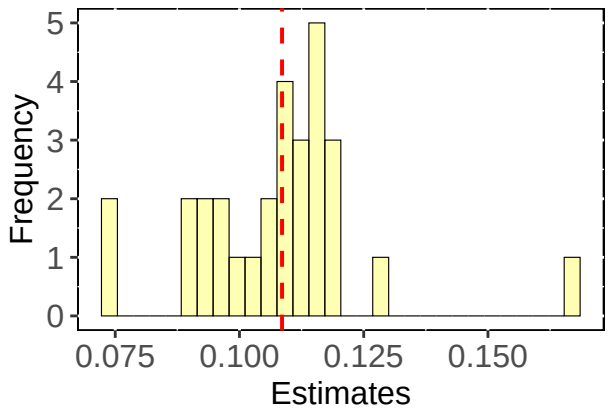

```r
summary(m2)

# Fit model 3
m3<- pgls(log10(bodymass.frith.g) ~ complexity.fuxjager, data = comparative_df, lambda = 1)
# Diagnostics
diagnostics.plot(m3)
```

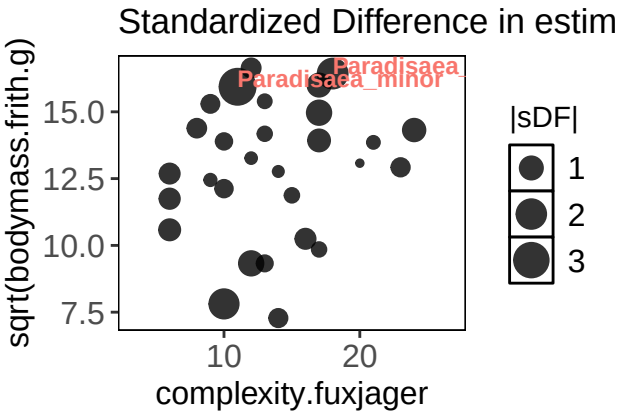


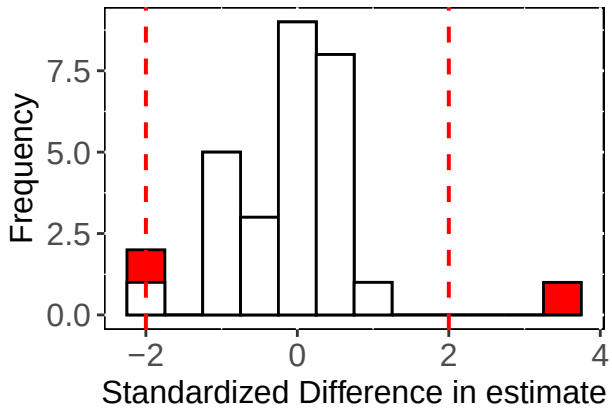

```
# Formal test of normality
res.m3 <- residuals(m3, phylo = TRUE)
shapiro.test(res.m3)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m3 <- influ_phylm(sqrt(bodymass.frith.g) ~ complexity.fuxjager,
                            phy = comparative_df$phy,
                            data = comparative_df$data, model = "BM",
                            track = FALSE)
```

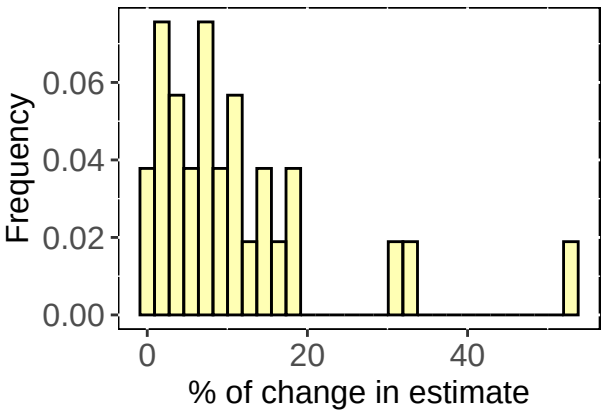
```
## Used dataset has  29  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m3$full.model.estimates
# test for influential species:
summary(sensi.m3)
# Visual sensitivity diagnostics
sensi_plot(sensi.m3)
```

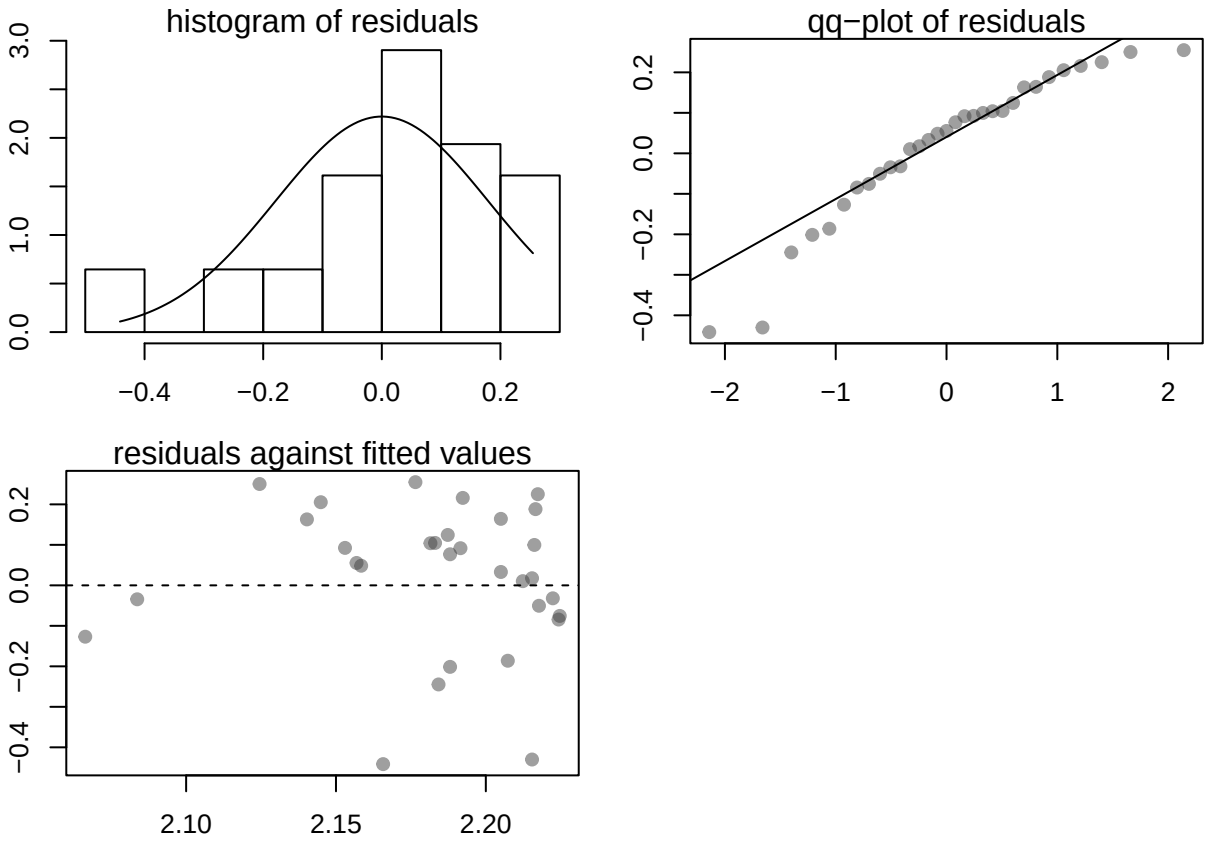








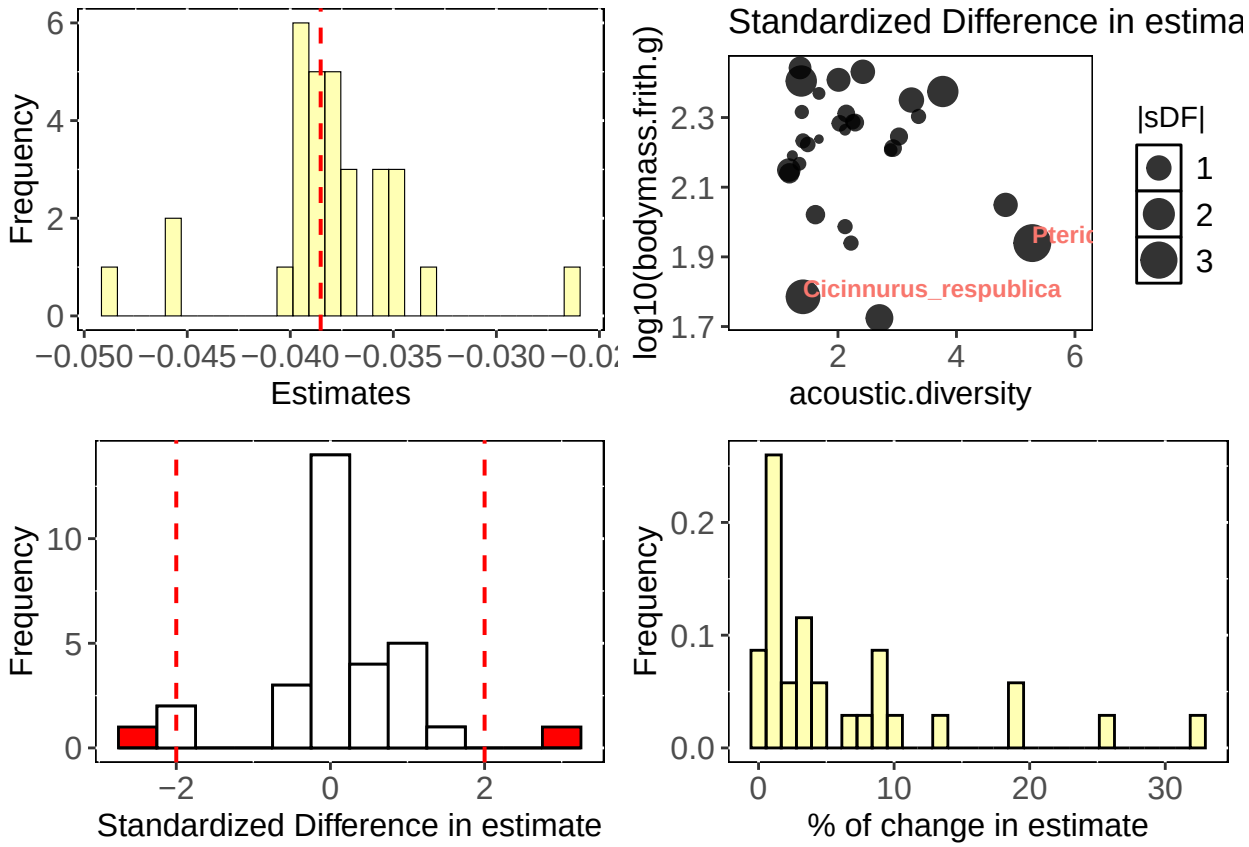

```
summary(m3)
nobs(m3)

# Fit model 4
m4<- pgls(log10(bodymass.frith.g) ~ acoustic.diversity, data = comparative_df, lambda = 1)
# Diagnostics
diagnostics.plot(m4)
```



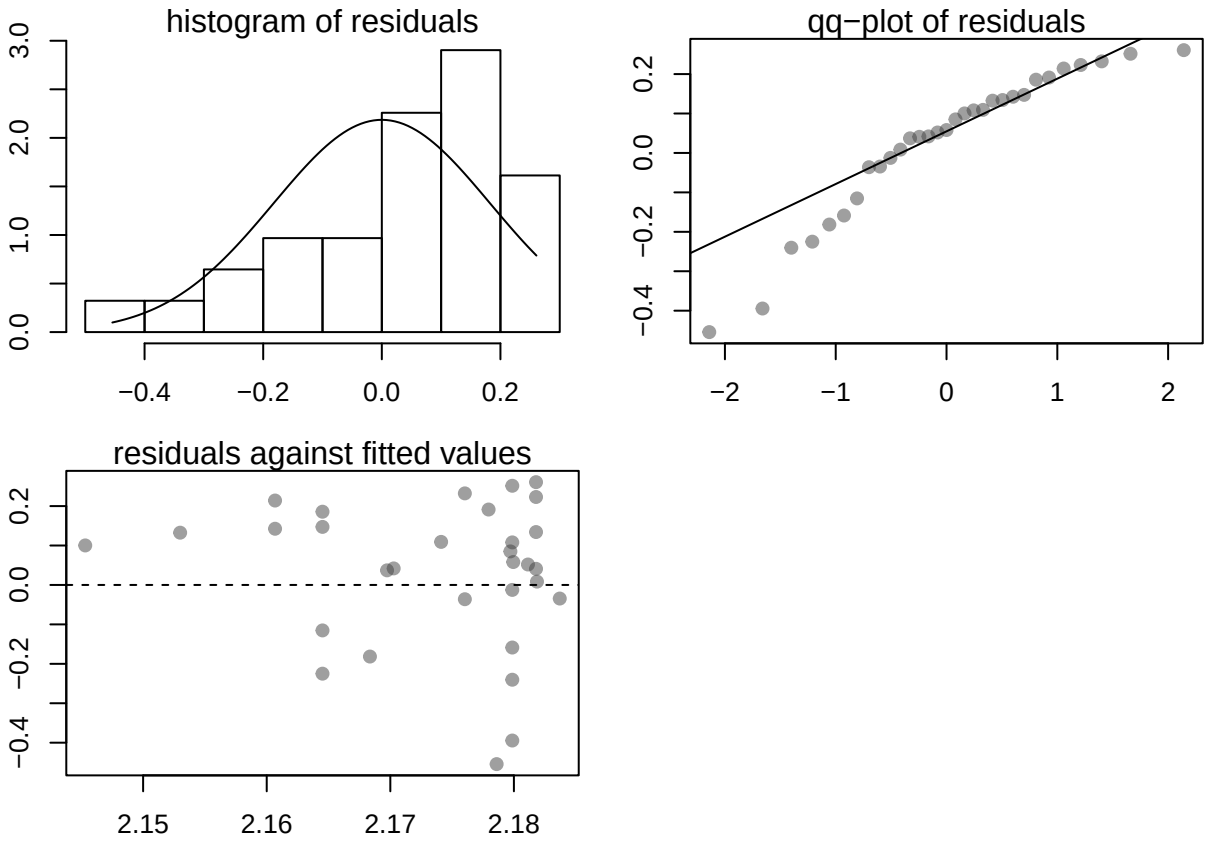

```
# Formal test of normality
res.m4 <- residuals(m4, phylo = TRUE)
shapiro.test(res.m4)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m4 <- influ_phylm(log10(bodymass.frith.g) ~ acoustic.diversity,
                            phy = comparative_df$phy,
                            data = comparative_df$data, model = "BM",
                            track = FALSE)
```

```
## Used dataset has  31  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m4$full.model.estimates
# test for influential species:
summary(sensi.m4)
# Visual sensitivity diagnostics
sensi_plot(sensi.m4)
```



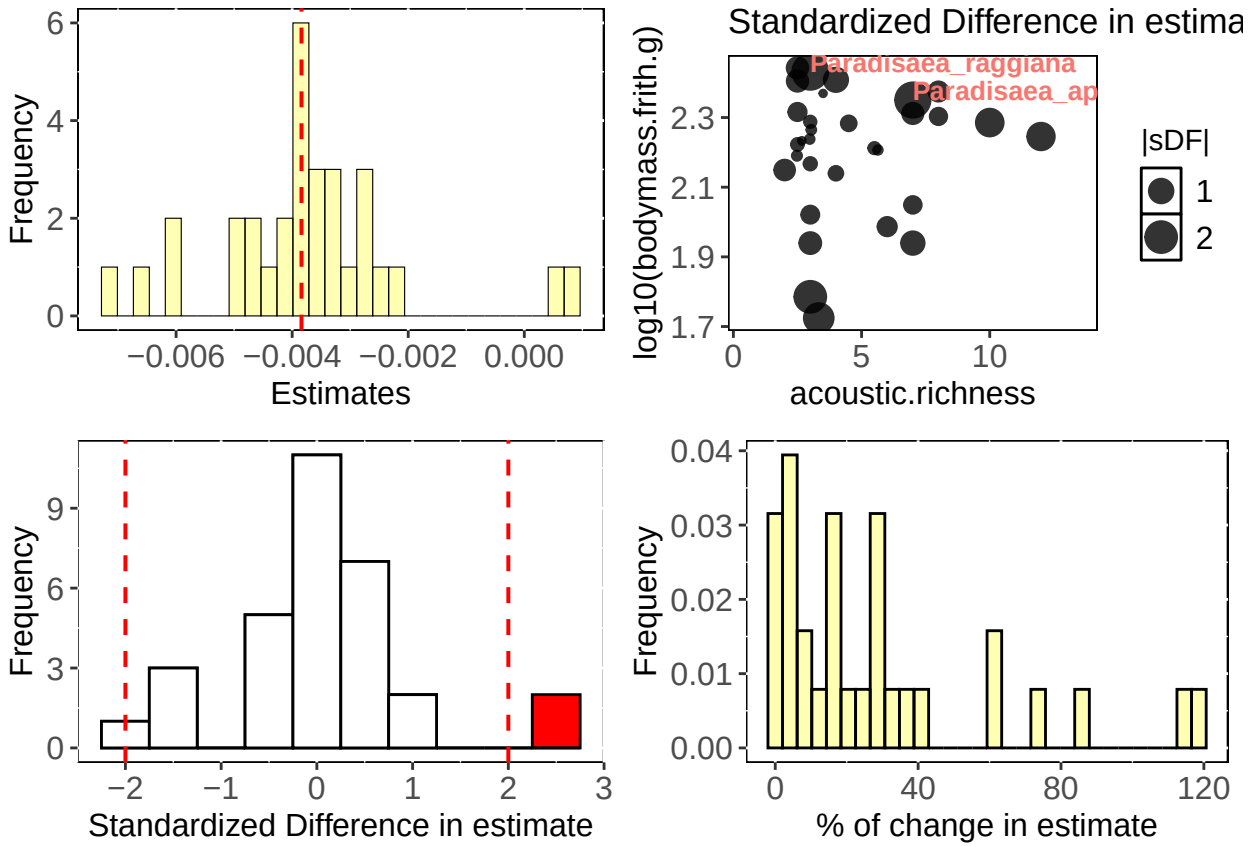

```
summary(m4)

# Fit model 5
m5<- pgls(log10(bodymass.frith.g) ~ acoustic.richness, data = comparative_df, lambda = 1)
# Diagnostics
diagnostics.plot(m5)
```



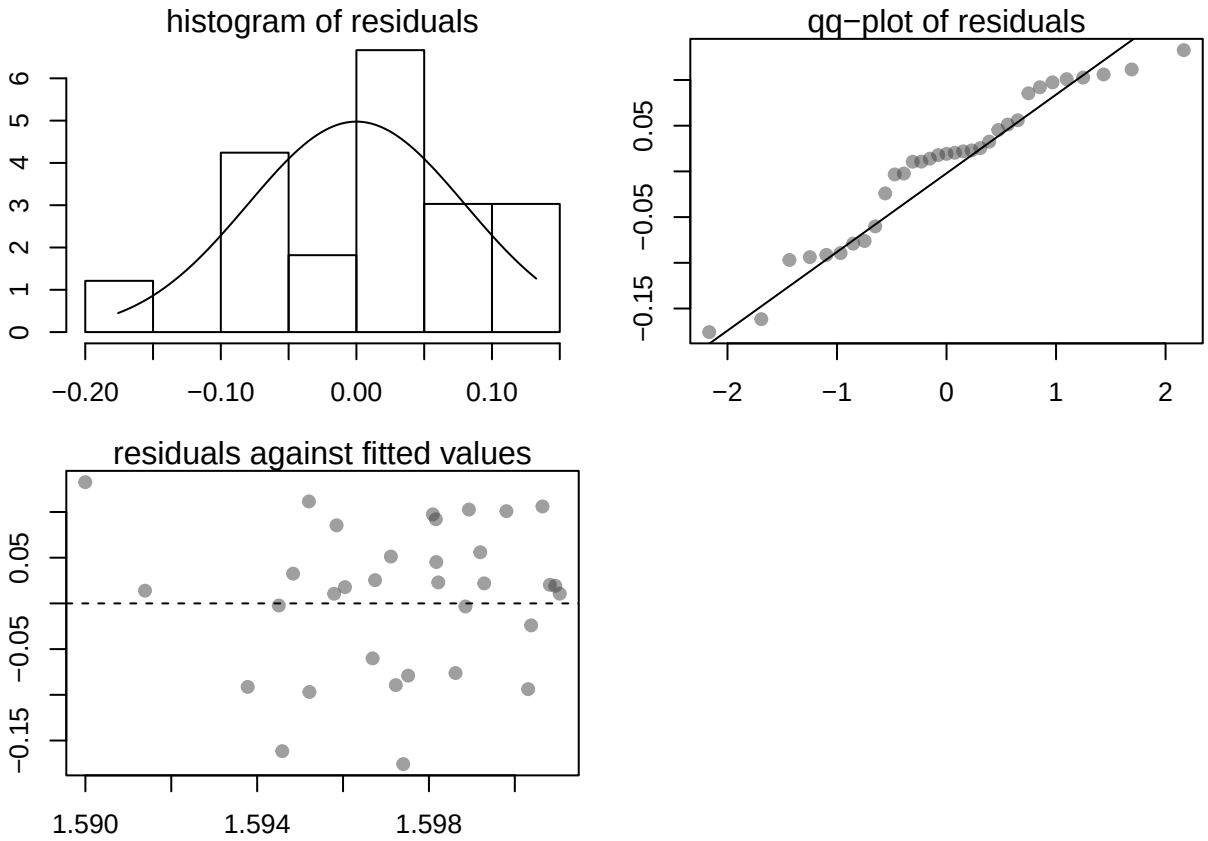

```
# Formal test of normality
res.m5 <- residuals(m5, phylo = TRUE)
shapiro.test(res.m5)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m5 <- influ_phylm(log10(bodymass.frith.g) ~ acoustic.richness,
                            phy = comparative_df$phy,
                            data = comparative_df$data, model = "BM",
                            track = FALSE)
```

```
## Used dataset has  31  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m5$full.model.estimates
# test for influential species:
summary(sensi.m5)
# Visual sensitivity diagnostics
sensi_plot(sensi.m5)
```



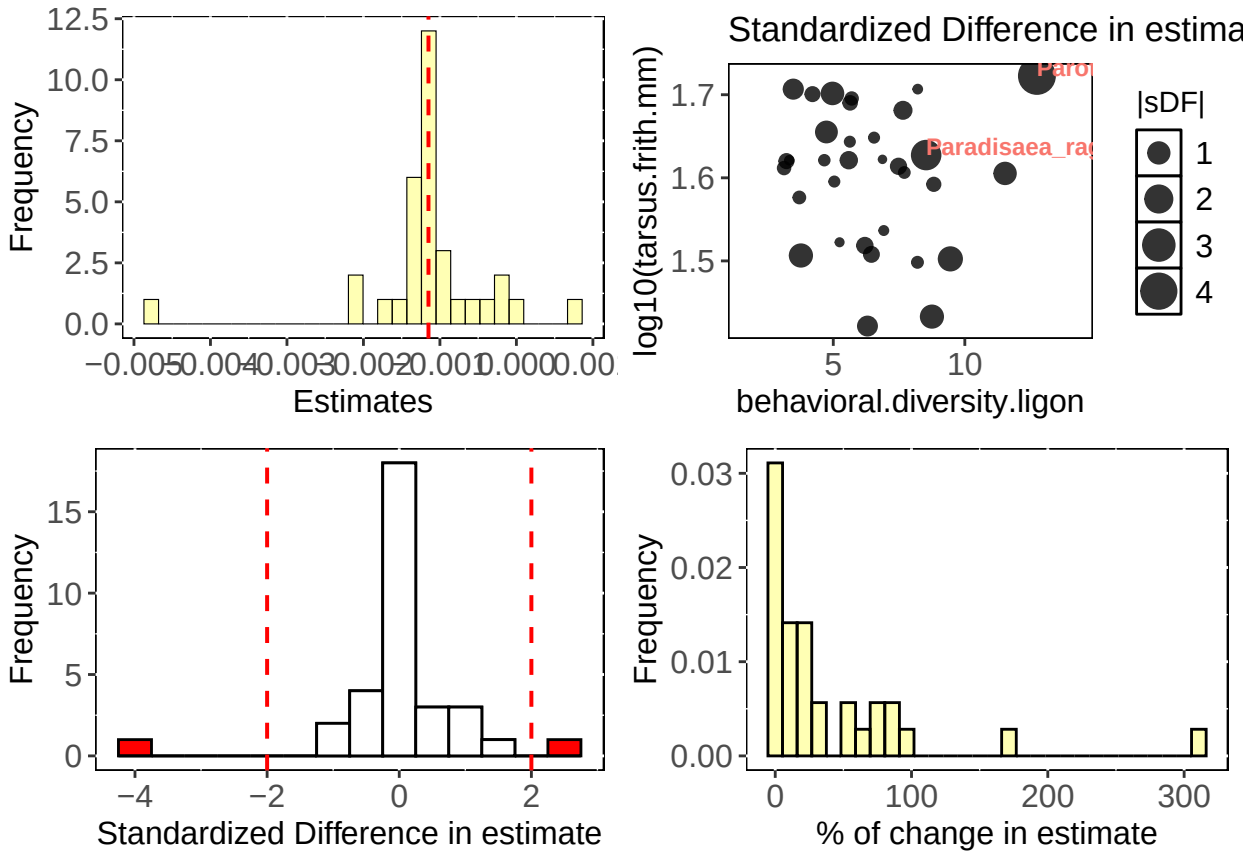

```
summary(m5)

# Fit model 6
m6<- pgls(log10(tarsus.frith.mm) ~ behavioral.diversity.ligon, data = comparative_df, lambda = 1)
# Diagnostics
diagnostics.plot(m6)
```



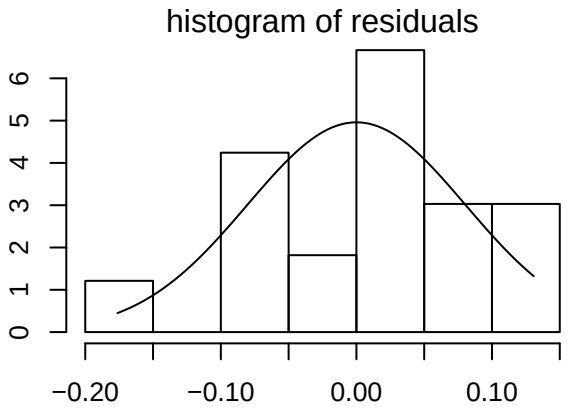

```
# Formal test of normality
res.m6 <- residuals(m6, phylo = TRUE)
shapiro.test(res.m6)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m6 <- influ_phylm(log10(tarsus.frith.mm) ~ behavioral.diversity.ligon,
                            phy = comparative_df$phy,
                            data = comparative_df$data, model = "BM",
                            track = FALSE)
```

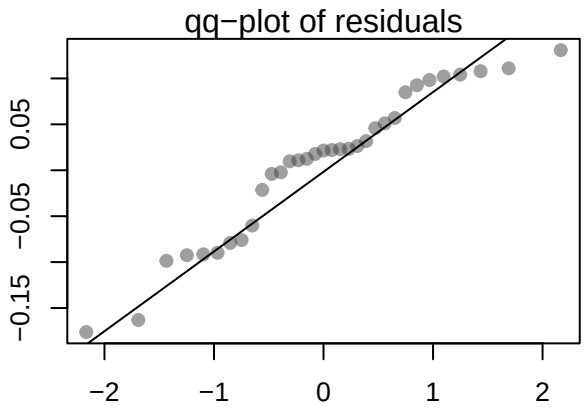
```
## Used dataset has  33  species that match data and phylogeny
```

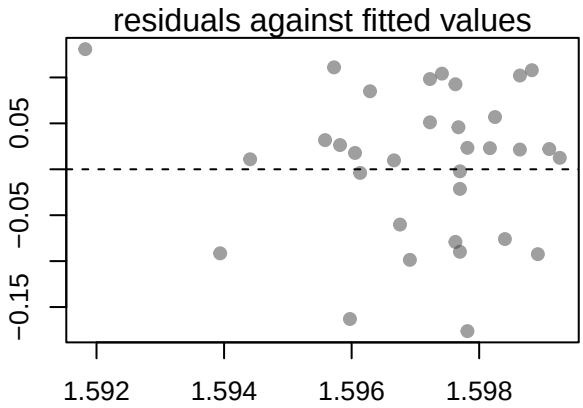
```
# Check full model estimates and compare to initial estimates:
sensi.m6$full.model.estimates
# test for influential species:
summary(sensi.m6)
# Visual sensitivity diagnostics
sensi_plot(sensi.m6)
```




```
summary(m6)
nobs(m6)

# Fit model 7
m7<- pgls(log10(tarsus.frith.mm) ~ behavioral.richness.ligon, data = comparative_df, lambda = 1)
# Diagnostics
diagnostics.plot(m7)
```



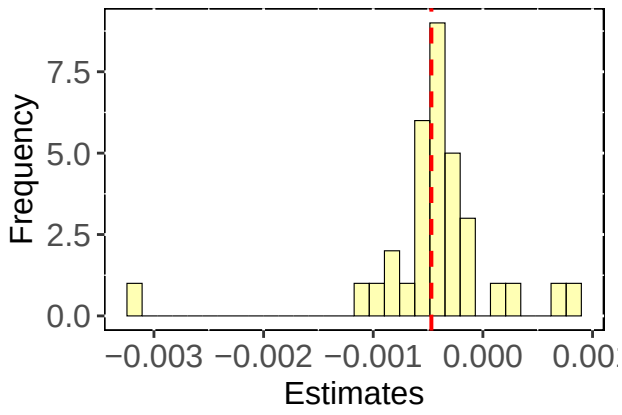


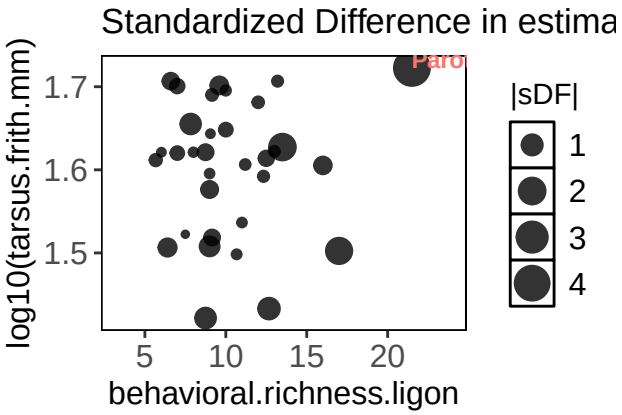


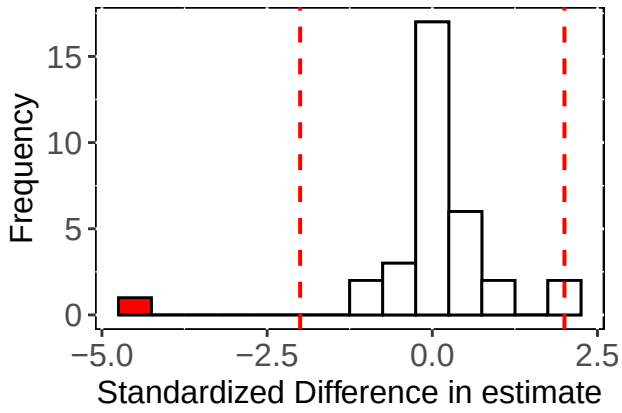

```
# Formal test of normality
res.m7 <- residuals(m7, phylo = TRUE)
shapiro.test(res.m7)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m7 <- influ_phylm(log10(tarsus.frith.mm) ~ behavioral.richness.ligon,
                            phy = comparative_df$phy,
                            data = comparative_df$data, model = "BM",
                            track = FALSE)
```

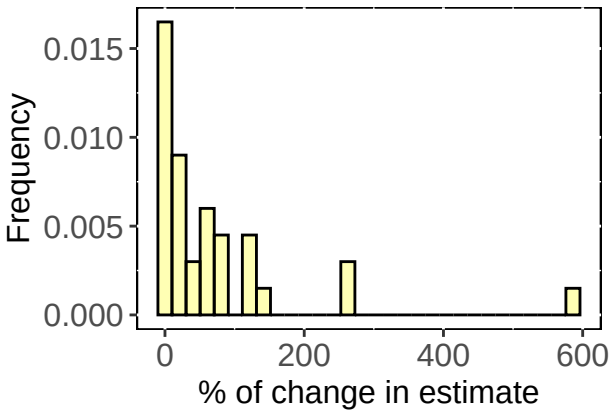
```
## Used dataset has  33  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m7$full.model.estimates
# test for influential species:
summary(sensi.m7)
# Visual sensitivity diagnostics
sensi_plot(sensi.m7)
```

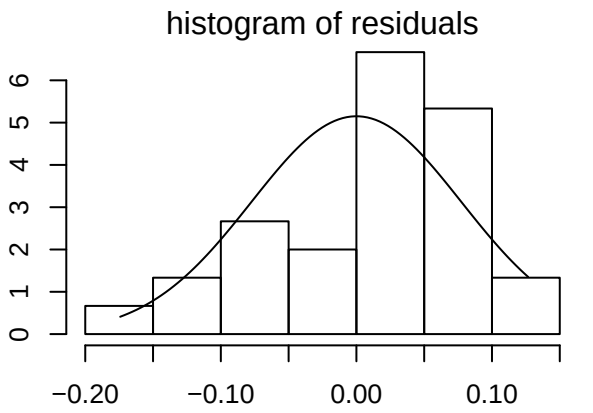


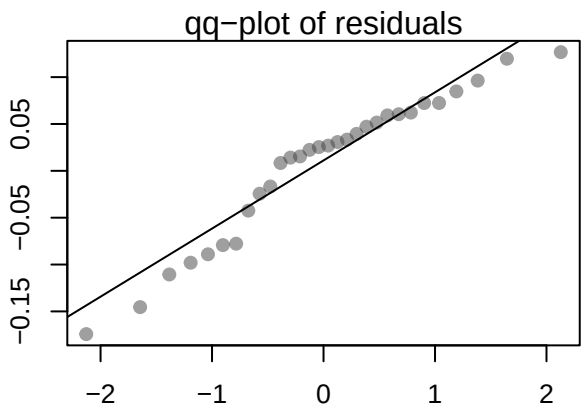


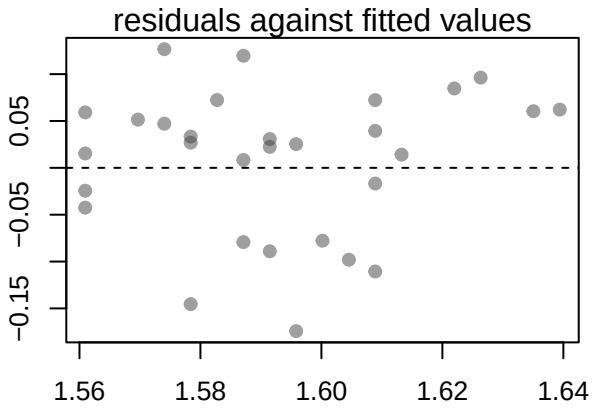





```r
summary(m7)

# Fit model 8
m8<- pgls(log10(tarsus.frith.mm) ~ complexity.fuxjager, data = comparative_df, lambda = 1)
# Diagnostics
diagnostics.plot(m8)
```



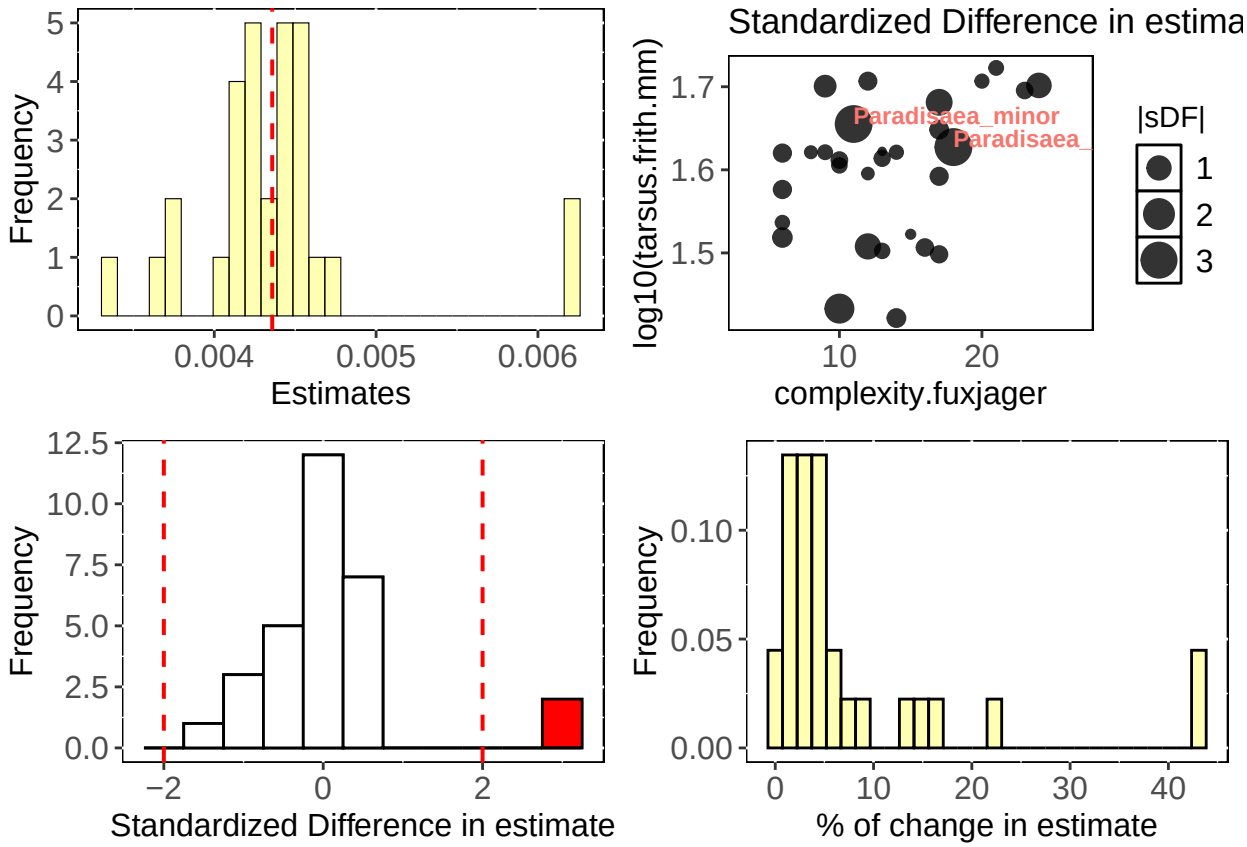




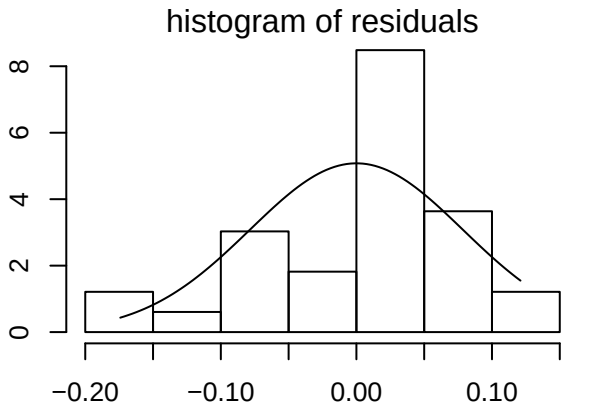

```
# Formal test of normality
res.m8 <- residuals(m8, phylo = TRUE)
shapiro.test(res.m8)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m8 <- influ_phylm(log10(tarsus.frith.mm) ~ complexity.fuxjager,
                            phy = comparative_df$phy,
                            data = comparative_df$data, model = "BM",
                            track = FALSE)
```

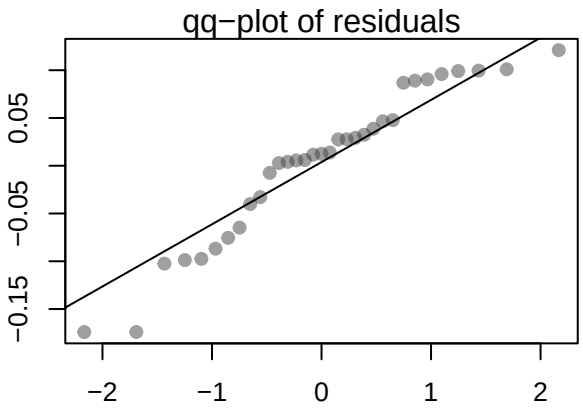
```
## Used dataset has  30  species that match data and phylogeny
```

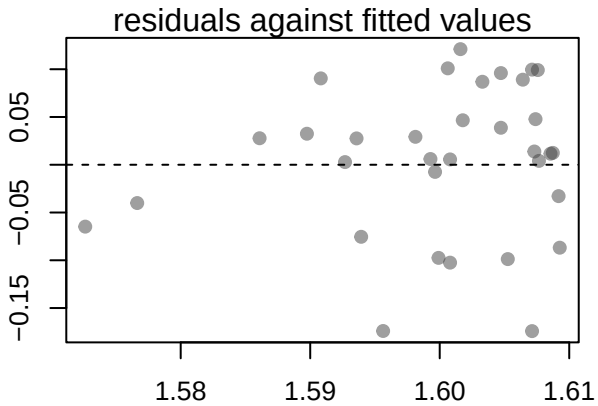
```
# Check full model estimates and compare to initial estimates:
sensi.m8$full.model.estimates
# test for influential species:
summary(sensi.m8)
# Visual sensitivity diagnostics
sensi_plot(sensi.m8)
```




```
summary(m8)
nobs(m8)

# Fit model 9
m9<- pgls(log10(tarsus.frith.mm) ~ acoustic.diversity, data = comparative_df, lambda = 1)
diagnostics.plot(m9)
```



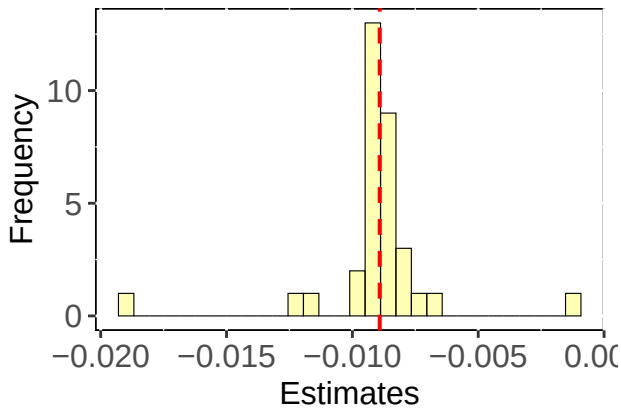


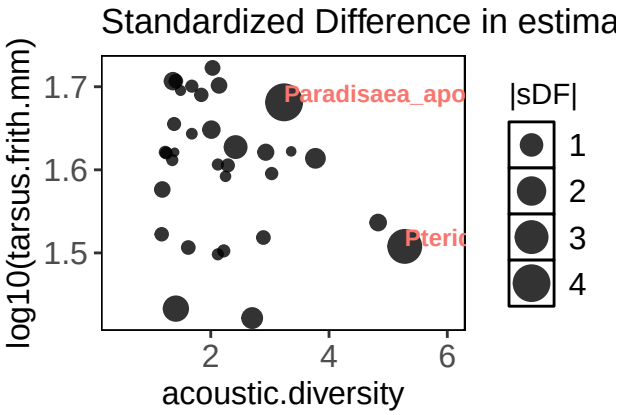


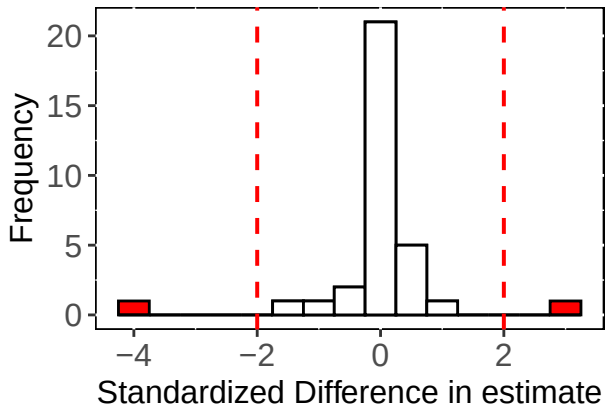

```
# Formal test of normality
res.m9 <- residuals(m9, phylo = TRUE)
shapiro.test(res.m9)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m9 <- influ_phylm(log10(tarsus.frith.mm) ~ acoustic.diversity,
                            phy = comparative_df$phy,
                            data = comparative_df$data, model = "BM",
                            track = FALSE)
```

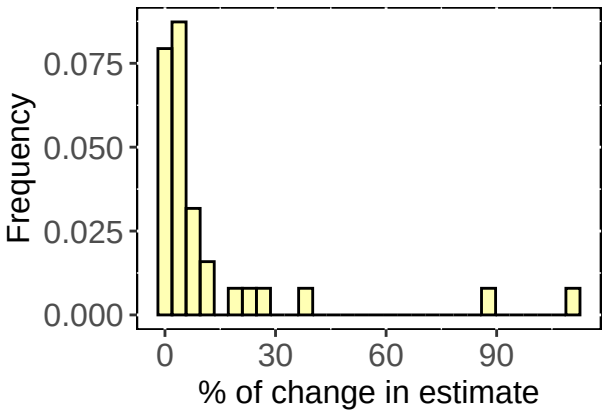
```
## Used dataset has  33  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m9$full.model.estimates
# test for influential species:
summary(sensi.m9)
# Visual sensitivity diagnostics
sensi_plot(sensi.m9)
```

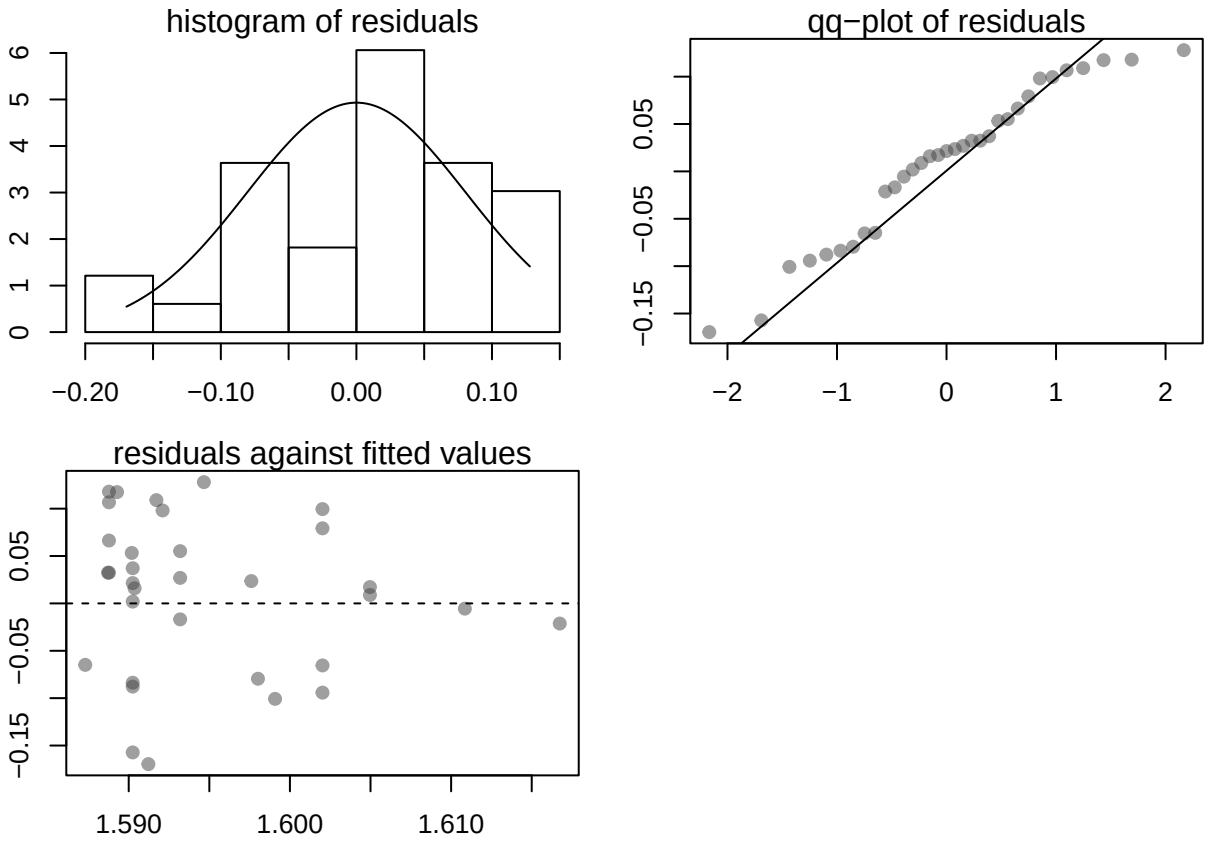








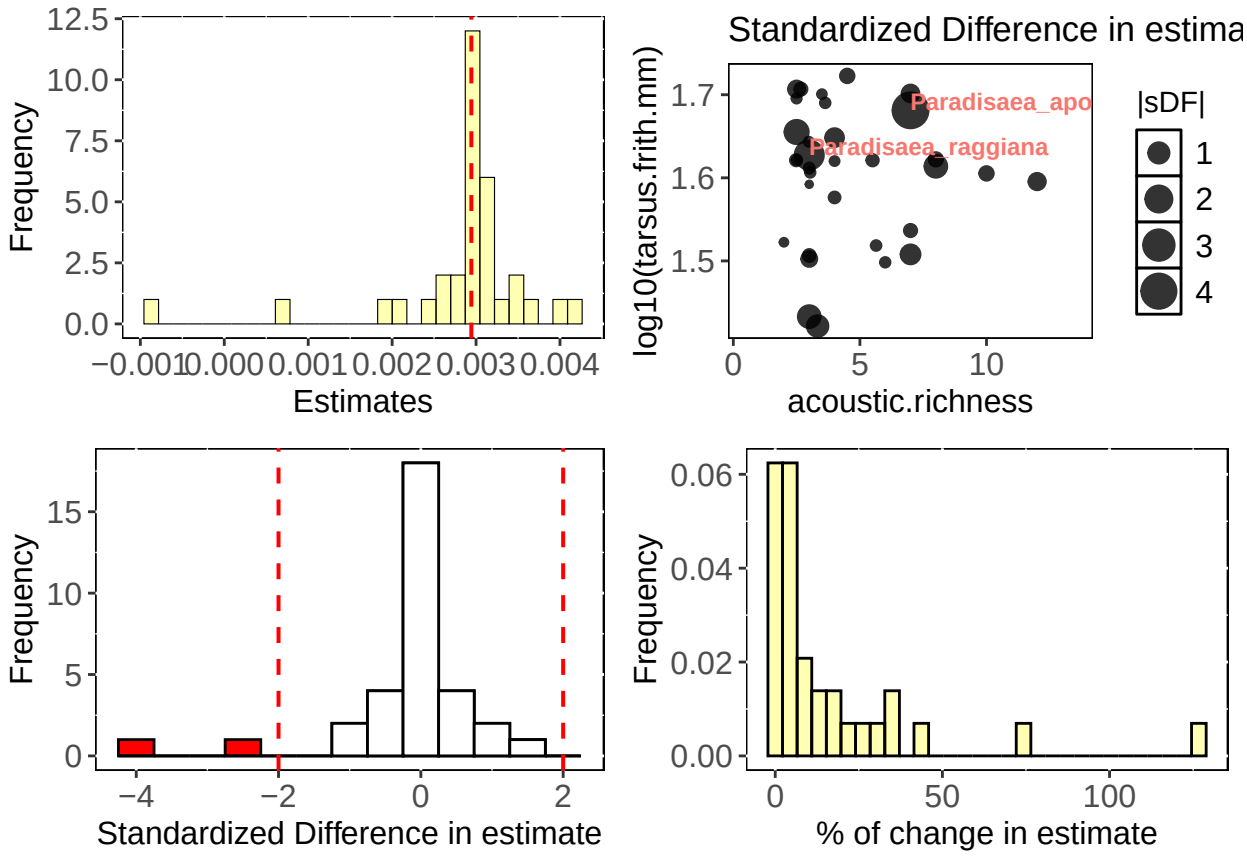

```
summary(m9)

# Fit model 10
m10<- pgls(log10(tarsus.frith.mm) ~ acoustic.richness, data = comparative_df, lambda = 1)
diagnostics.plot(m10)
```




```
# Formal test of normality
res.m10 <- residuals(m10, phylo = TRUE)
shapiro.test(res.m10)
# Phylogenetic sensitivity test using the sensiPhy package
sensi.m10 <- influ_phylm(log10(tarsus.frith.mm) ~ acoustic.richness,
                         phy = comparative_df$phy,
                         data = comparative_df$data, model = "BM",
                         track = FALSE)
```

```
## Used dataset has  33  species that match data and phylogeny
```

```
# Check full model estimates and compare to initial estimates:
sensi.m10$full.model.estimates
# test for influential species:
summary(sensi.m10)
# Visual sensitivity diagnostics
sensi_plot(sensi.m10)
```




```
summary(m10)
```

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