### Alpha diversity statistical analysis

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<td>1.4. Check Normality</td>
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<td>2.4. Model Diagnostics</td>
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</tr>
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<td></td>
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<td>2.7. Marginal and Conditional R-squared</td>
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<td></td>
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<tr>
<td>2.9. Significance of random effects</td>
<td></td>
</tr>
</tbody>
</table>
A) 16S rRNA alpha diversity statistical analysis

1. Shannon diversity Index

```r
# Load libraries
library(tidyverse)
library(lme4)
library(MuMIn)
library(performance)
library(car)
library(effects)
library(ggpubr)
library(jtools)
library(correlation)
library(lmerTest)

# Load dataset
metadata <- readRDS("16S_metadata.rds")

# Calculate age and body condition index
metadata$bci_two <- resid(glm(weight ~ log10(wing) + sex, gaussian, metadata, na.action="na.exclude")) # calculate body condition
metadata$std_bci <- scale(metadata$bci_two) # scale bci values

metadata$age_days <- buteo_age(df = metadata, wing = "wing", sex = TRUE, unit = c("cm"), .plot = F, decimals = 2,.show_model = T)$fit
metadata$std_age <- scale(metadata$age_days) # scale age values

saveRDS(metadata,"16S_metadata.rds")
```

1.1 Check correlation between variables

```r
# Check correlation between variables from the model
test_cor_data <- metadata[, c("habitat", "rank", "year", "lbinom", "sex", "std_age", "std_bci_two", "shannon_entropy")]

correl <- correlation(test_cor_data, include_factors = TRUE)
correl <- cor_sort(as.matrix(correl)) # as matrix

# Plot matrix
corr_matrix <- visualisation_recipe(corr)
plot(corr_matrix)
```
1.2 Model Shannon

```
model_shannon <- lmer(shannon_entropy ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1|nest/ring_number), data = metadata)
```

1.3 Check Normality

```
> check_normality(model_shannon)
OK: residuals appear as normally distributed (p = 0.394).
```

1.4 Model Diagnostics

```
check_model(model_shannon)
```
1.5 Model Summary

> summary(model_shannon_final)

Linear mixed model fit by REML ['lmerMod']
Formula: shannon_entropy ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1 | nest/ring_number)
Data: metadata

REML criterion at convergence: 475.7

Scaled residuals:
  Min     1Q    Median     3Q    Max
-2.3843 -0.6363 -0.0336  0.6599  2.2130

Random effects:
  Groups     Name   Variance Std.Dev.
  ring_number:nest (Intercept)  0.000000  0.0000
  nest            (Intercept)  0.049320  0.2221
  Residual            0.407100  0.6380
Number of obs: 226, groups: ring_number:nest, 117; nest, 54

Fixed effects:
  Estimate Std. Error   t value
  (Intercept)  4.3068106  0.1058171  40.701
  std_age     -0.1652697  0.0529112  -3.124
  std_bci     0.0001679  0.0511950   0.003
1.6 Significance values

```r
> Anova(model_shannon)

Analysis of Deviance Table (Type II Wald chisquare tests)

Response: shannon_entropy

                     Chisq Df  Pr(>Chisq)
std_age             9.7564  1 0.001787 **
std_bci             0.0000  1 0.997383
rank2               2.0552  3 0.561028
rank3               0.1191  1 0.729986
rank4               1.7600  2 0.414783
sexM                0.5766  1 0.447636
yr2021              0.1191  1 0.729986
habitatsoth         1.7600  2 0.414783
habitatteuto        0.5766  1 0.447636
lbinom1             0.5766  1 0.447636
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

1.7 Marginal and conditional R-squared

```r
r.squaredGLMM(model_shannon)
R2m  R2c
[1,] 0.0758452 0.1757042
```

1.8 Plot model effects

```r
plot(allEffects(model_shannon))
```
1.9 Significance of random effects

```r
> ranova(model_shannon)
ANOVA-like table for random-effects: Single term deletions

Model: shannon_entropy ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1 | ring_number:nest) + (1 | nest)
npar logLik  AIC  LRT Df Pr(>Chisq)
<none> 14 -237.86 503.71
(1 | ring_number:nest) 13 -237.86 501.71 0.0000 1 1.00000
(1 | nest) 13 -239.56 505.12 3.4089 1 0.06485 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

2. Faith phylogenetic diversity

2.1 Log transform Faith

(model residuals not normal distributed)

```r
model_faith <- lmer(faith_pd ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1|nest/ring_number), data = metadata)
>
check_normality(model_faith)
Warning: Non-normality of residuals detected (p = 0.003).

#Log transform faith
metadata$log_faith <- log10(metadata$faith_pd)
```
2.2 Check correlation between variables

```r
#check correlation between variables from the model
test_cor_data <- metadata[, c("habitat", "rank", "year", "lbinom", "sex", "std_age", "std_bci_two", "faith_pd")]

correl <- correlation(test_cor_data, include_factors = TRUE)
correl <- cor_sort(as.matrix(correl)) # as matrix

# Plot matrix
corr_matrix <- visualisation_recipe(correl)
plot(corr_matrix)
```

### Correlation Matrix

<table>
<thead>
<tr>
<th></th>
<th>Year (2021)</th>
<th>Not-Infected</th>
<th>Habitat-North</th>
<th>Sex-F</th>
<th>Rank-4</th>
<th>Faith_PD</th>
<th>Rank-3</th>
<th>Year (2020)</th>
<th>Habitat-South</th>
<th>Sex-M</th>
<th>Habitat-Teuto</th>
<th>Infected</th>
<th>Age</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rank-2</td>
<td>1.00</td>
<td>0.02</td>
<td>0.06</td>
<td>0.01</td>
<td>0.08</td>
<td>-0.07</td>
<td>-0.02</td>
<td>-0.33</td>
<td>-0.67</td>
<td>-0.73</td>
<td>0.01</td>
<td>0.02</td>
<td>-0.01</td>
</tr>
<tr>
<td>Year (2021)</td>
<td>0.02</td>
<td>1.00</td>
<td>0.12</td>
<td>0.03</td>
<td>-0.10</td>
<td>-0.03</td>
<td>-0.09</td>
<td>-0.03</td>
<td>-1.50</td>
<td>0.01</td>
<td>-0.10</td>
<td>0.10</td>
<td>0.12</td>
</tr>
<tr>
<td>Not-Infected</td>
<td>0.24</td>
<td>0.12</td>
<td>1.00</td>
<td>0.12</td>
<td>0.10</td>
<td>-0.28</td>
<td>0.01</td>
<td>0.02</td>
<td>-0.12</td>
<td>-0.06</td>
<td>-0.11</td>
<td>-0.07</td>
<td>0.10</td>
</tr>
<tr>
<td>Habitat-North</td>
<td>0.01</td>
<td>0.03</td>
<td>0.12</td>
<td>1.00</td>
<td>0.20</td>
<td>0.04</td>
<td>0.08</td>
<td>0.16</td>
<td>-0.03</td>
<td>-0.13</td>
<td>0.19</td>
<td>-0.63</td>
<td>-0.20</td>
</tr>
<tr>
<td>Sex-F</td>
<td>-0.07</td>
<td>-0.03</td>
<td>-0.08</td>
<td>0.04</td>
<td>0.08</td>
<td>-0.04</td>
<td>0.03</td>
<td>-0.09</td>
<td>0.20</td>
<td>0.03</td>
<td>0.08</td>
<td>-0.02</td>
<td>-0.02</td>
</tr>
<tr>
<td>Rank-4</td>
<td>-0.02</td>
<td>-0.09</td>
<td>0.01</td>
<td>0.08</td>
<td>0.13</td>
<td>0.23</td>
<td>1.00</td>
<td>0.02</td>
<td>-0.09</td>
<td>0.03</td>
<td>-0.10</td>
<td>0.06</td>
<td>0.05</td>
</tr>
<tr>
<td>Faith_PD</td>
<td>-0.33</td>
<td>-0.03</td>
<td>0.02</td>
<td>0.16</td>
<td>-0.06</td>
<td>-0.04</td>
<td>0.02</td>
<td>1.03</td>
<td>0.03</td>
<td>-0.38</td>
<td>-0.12</td>
<td>-0.15</td>
<td>0.06</td>
</tr>
<tr>
<td>Rank-3</td>
<td>-0.02</td>
<td>-0.10</td>
<td>-0.12</td>
<td>-0.03</td>
<td>0.10</td>
<td>0.03</td>
<td>0.09</td>
<td>0.03</td>
<td>-0.01</td>
<td>0.10</td>
<td>0.10</td>
<td>-0.10</td>
<td>0.12</td>
</tr>
<tr>
<td>Year (2020)</td>
<td>-0.02</td>
<td>-0.10</td>
<td>-0.12</td>
<td>-0.03</td>
<td>0.10</td>
<td>0.03</td>
<td>0.09</td>
<td>0.03</td>
<td>-0.01</td>
<td>0.10</td>
<td>0.10</td>
<td>-0.10</td>
<td>0.12</td>
</tr>
<tr>
<td>Rank-1</td>
<td>-0.73</td>
<td>0.01</td>
<td>-0.04</td>
<td>0.13</td>
<td>0.04</td>
<td>-0.03</td>
<td>-0.03</td>
<td>0.38</td>
<td>-0.01</td>
<td>1.65</td>
<td>0.11</td>
<td>0.08</td>
<td>0.04</td>
</tr>
<tr>
<td>BCI</td>
<td>0.01</td>
<td>-0.10</td>
<td>-0.01</td>
<td>0.19</td>
<td>0.00</td>
<td>-0.20</td>
<td>-0.10</td>
<td>-0.12</td>
<td>0.10</td>
<td>0.11</td>
<td>1.55</td>
<td>-0.09</td>
<td>0.00</td>
</tr>
<tr>
<td>Habitat-South</td>
<td>0.02</td>
<td>-0.16</td>
<td>-0.07</td>
<td>-0.05</td>
<td>-0.18</td>
<td>-0.03</td>
<td>-0.06</td>
<td>-0.14</td>
<td>0.10</td>
<td>0.08</td>
<td>0.09</td>
<td>1.04</td>
<td>0.14</td>
</tr>
<tr>
<td>Sex-M</td>
<td>-0.01</td>
<td>0.10</td>
<td>-0.10</td>
<td>-0.20</td>
<td>-1.44</td>
<td>0.08</td>
<td>-0.13</td>
<td>0.04</td>
<td>-0.10</td>
<td>-0.04</td>
<td>0.00</td>
<td>1.40</td>
<td>0.07</td>
</tr>
<tr>
<td>Habitat-Teuto</td>
<td>-0.05</td>
<td>0.12</td>
<td>-0.12</td>
<td>0.47</td>
<td>-0.07</td>
<td>-0.02</td>
<td>-0.05</td>
<td>-0.08</td>
<td>0.12</td>
<td>0.11</td>
<td>-0.02</td>
<td>1.06</td>
<td>0.11</td>
</tr>
<tr>
<td>Infected</td>
<td>-0.04</td>
<td>-0.12</td>
<td>-1.44</td>
<td>-0.12</td>
<td>-0.10</td>
<td>0.08</td>
<td>-0.01</td>
<td>-0.02</td>
<td>0.12</td>
<td>0.06</td>
<td>0.01</td>
<td>0.07</td>
<td>0.10</td>
</tr>
<tr>
<td>Age</td>
<td>0.15</td>
<td>0.10</td>
<td>-0.01</td>
<td>-0.14</td>
<td>-0.69</td>
<td>-0.02</td>
<td>-0.20</td>
<td>-0.14</td>
<td>0.25</td>
<td>0.05</td>
<td>0.09</td>
<td>0.22</td>
<td>0.41</td>
</tr>
</tbody>
</table>

2.3 Model Faith PD

```r
model_faith <- lmer(log_faith ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1|nest/ring_number), data = metadata)
```

2.4 Check Normality

```r
> check_normality(model_faith)
OK: residuals appear as normally distributed (p = 0.081).
```
2.5 Model Diagnostics

```r
check_model(model_faith)
```

![Model diagnostics plots](image)

2.6 Model Summary

```r
> summary(model_faith)

Linear mixed model fit by REML ['lmerMod']
Formula: log_faith ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1 | nest/ring_number)
Data: metadata

REML criterion at convergence: -225.5

Scaled residuals:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>1Q</th>
<th>Median</th>
<th>3Q</th>
<th>Max</th>
</tr>
</thead>
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<tr>
<td></td>
<td>-3.1497</td>
<td>-0.5645</td>
<td>0.1041</td>
<td>0.6145</td>
<td>2.5580</td>
</tr>
</tbody>
</table>

Random effects:

<table>
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<th>Groups</th>
<th>Name</th>
<th>Variance</th>
<th>Std.Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>ring_number:nest (Intercept)</td>
<td>0.00000000</td>
<td>0.000000</td>
</tr>
<tr>
<td></td>
<td>nest (Intercept)</td>
<td>0.00066667</td>
<td>0.025820</td>
</tr>
<tr>
<td></td>
<td>Residual</td>
<td>0.01649900</td>
<td>0.128450</td>
</tr>
</tbody>
</table>
2.7 Significance values

<table>
<thead>
<tr>
<th>Response: log_faith</th>
<th>Chisq</th>
<th>Df</th>
<th>Pr(&gt;Chisq)</th>
</tr>
</thead>
<tbody>
<tr>
<td>std_age</td>
<td>7.8181</td>
<td>1</td>
<td>0.005173 **</td>
</tr>
<tr>
<td>std_bci</td>
<td>0.4840</td>
<td>1</td>
<td>0.486605</td>
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<tr>
<td>rank</td>
<td>7.5620</td>
<td>3</td>
<td>0.055986</td>
</tr>
<tr>
<td>sex</td>
<td>3.7353</td>
<td>1</td>
<td>0.053274</td>
</tr>
<tr>
<td>year</td>
<td>0.1431</td>
<td>1</td>
<td>0.705197</td>
</tr>
<tr>
<td>habitat</td>
<td>0.0098</td>
<td>2</td>
<td>0.995125</td>
</tr>
<tr>
<td>lbinom</td>
<td>0.5372</td>
<td>1</td>
<td>0.463609</td>
</tr>
</tbody>
</table>

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2.8 Marginal and Conditional R-squared

<table>
<thead>
<tr>
<th>R2m</th>
<th>R2c</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.09268855</td>
<td>0.1279241</td>
</tr>
</tbody>
</table>
2.9 Plot model effects

```r
plot(allEffects(model_faith))
```

<table>
<thead>
<tr>
<th>Effect</th>
<th>Plot</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>std_age</code></td>
<td><img src="image" alt="plot" /></td>
</tr>
<tr>
<td><code>std_bci</code></td>
<td><img src="image" alt="plot" /></td>
</tr>
<tr>
<td><code>rank</code></td>
<td><img src="image" alt="plot" /></td>
</tr>
<tr>
<td><code>sex</code></td>
<td><img src="image" alt="plot" /></td>
</tr>
<tr>
<td><code>year</code></td>
<td><img src="image" alt="plot" /></td>
</tr>
<tr>
<td><code>habitat</code></td>
<td><img src="image" alt="plot" /></td>
</tr>
<tr>
<td><code>lbinom</code></td>
<td><img src="image" alt="plot" /></td>
</tr>
</tbody>
</table>

2.10 Significance of random effects

```r
> ranova(model_faith)
boundary (singular) fit: see help('isSingular')
ANOVA-like table for random-effects: Single term deletions

Model:
log_faith ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1 | ring_number:nest) + (1 | nest)

<table>
<thead>
<tr>
<th></th>
<th>logLik</th>
<th>AIC</th>
<th>LRT</th>
<th>Df</th>
<th>Pr(&gt;Chi2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;none&gt;</td>
<td>112.74</td>
<td>-197.49</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(1</td>
<td>ring_number:nest)</td>
<td>112.74</td>
<td>-199.49</td>
<td>0.00000</td>
<td>1</td>
</tr>
<tr>
<td>(1</td>
<td>nest)</td>
<td>112.45</td>
<td>-198.91</td>
<td>0.58057</td>
<td>1</td>
</tr>
</tbody>
</table>
```

B) 28S rRNA alpha diversity statistical analysis
1. Shannon diversity Index

```r
# Load libraries
library(tidyverse)
library(lme4)
library(MuMIn)
library(performance)
library(datawizard)
library(car)
library(effects)
library(ggpubr)
library(multcomp)
library(jtools)

# Load dataset
metadata <- readRDS("28S_metadata.rds")

# Calculate age and body condition index
metadata$bci_two <- resid(glm(weight ~ log10(wing) + sex, gaussian, metadata, na.action="na.exclude")) # calculate body condition
metadata$std_bci <- scale(metadata$bci_two) # scale bci values

metadata$age_days <- buteo_age(df = metadata, wing = "wing", sex = TRUE, unit = c("cm"), .plot = F, decimals = 2, .show_model = T)$fit
metadata$std_age <- scale(metadata$age_days) # scale age values

saveRDS(metadata,"28S_metadata.rds")
```

1.1 Check correlation between variables

```r
# Check correlation between variables from the model

test_cor_data <- metadata[, c("habitat", "rank", "year", "lbinom", "sex", "std_age", "std_bci_two", "shannon_entropy")]

correl <- correlation(test_cor_data, include_factors = TRUE)
correl <- cor_sort(as.matrix(correl)) # as matrix

# Plot matrix

corr_matrix <- visualisation_recipe(correl)
plot(corr_matrix)
```

1.2. Transform Shannon

```r
> model_shannon <- lmer(shannon_entropy ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1|nest/ring_number), data = metadata)

> check_normality(model_shannon)
Warning: Non-normality of residuals detected (p < .001).

# Reflect and log transform shannon
metadata$log_shannon <- log10(max(metadata$shannon_entropy+1) - metadata$shannon_entropy)

# Data reflection changes direction of relationships
metadata$log_shannon <- -metadata$log_shannon # change directions of relationships again
```
1.3. Model Faith PD

```r
model_shannon <- lmer(log_shannon ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1|nest/ring_number), data = metadata)
```

1.4. Check Normality

```r
check_normality(model_shannon_final prev)
Warning: Non-normality of residuals detected (p = 0.046). # residuals still not normal distributed
```

1.5. Model Diagnostics

```r
check_model(model_shannon) # normality of residuals identified by visual inspection
```
1.6. Model Summary

```r
> summary(model_shannon)
Linear mixed model fit by REML ['lmerMod']
Formula: log_shannon ~ std_age + std_bci + sex + rank + habitat + year + lbinom + (1 | nest/ring_number)
   Data: metadata

REML criterion at convergence: -28.9

Scaled residuals:
     Min  1Q Median  3Q Max
-1.7910 -0.7103 -0.0168 0.6698 2.4352

Random effects:
  Groups     Name       Variance     Std.Dev.
   ring_number:nest (Intercept) 2.032e-09 4.508e-05
     nest (Intercept) 2.236e-03 4.729e-02
   Residual               3.754e-02 1.938e-01
Number of obs: 177, groups: ring_number:nest, 108; nest, 54

Fixed effects:
                  Estimate Std. Error t value
       (Intercept) -0.520591  0.034071  -15.280
      std_age     -0.035594  0.017628   -2.019
     std_bci     -0.004052  0.016615   -0.244
        sexM      0.016542  0.032398    0.511
         rank2    -0.004258  0.033979  -0.125
         rank3     0.029871  0.045397    0.658
         rank4     0.210610  0.152755    1.379
     habitat:south 0.068654  0.053602    1.281
    habitat:teuto 0.112459  0.108764    1.034
     year:2021   -0.003454  0.061376   -0.056
      lbinom1    -0.019645  0.034963   -0.562

Correlation of Fixed Effects:
                            (Intr) std_ag std_b std_bci   rank2   rank3  rank4 habitat:s  habitat:teu year:2021 lbinom1
       std_age         0.186
     std_bci    -0.023  0.002
       sexM      -0.048 -0.103 -0.112
     rank2      -0.426 0.143  0.086  0.062
     rank3      -0.265 0.231  0.206 -0.101  0.372
     rank4      -0.014 0.114  0.251 -0.136  0.123  0.178
 habitat:south -0.111  0.047  0.133  0.164  0.026  0.183  0.106
 habitat:teuto -0.123  0.151  0.184  0.036  0.123  0.113  0.066  0.078
     year:2021   -0.109  0.060  0.095 -0.155 -0.078  0.009  0.049  0.125 -0.091
      lbinom1    -0.504 -0.398 -0.024 -0.099  0.032 -0.120 -0.105 -0.079 -0.070  0.107
```

1.7. Significance values

```r
> Anova(model_shannon)
Analysis of Deviance Table (Type II Wald chi-square tests)

Response: log_shannon

             Chisq Df Pr(>Chisq)
    std_age  4.0769 1   0.04347 *
    std_bci  0.0595 1   0.80735
        sex  0.2607 1   0.60965
        rank 2.3064 3   0.51129
    habitat 2.5173 2   0.28404
     year  0.0032 1   0.95512
      lbinom 0.3157 1   0.57421
---
```
1.8. Marginal and conditional R-squared

```r
> r.squaredGLMM(model_shannon)
     R2m    R2c
(1,) 0.05739074 0.1103858
```

1.9. Plot model effects

```r
plot(allEffects(model_shannon))
```

1.10. Significance of random effects
2. Faith phylogenetic diversity

2.1 Check correlation between variables

```r
#check correlation between variables from the model
test_cor_data <- metadata[, c("habitat", "rank", "year", "lbinom", "sex", "std_age", "std_bci_two", "faith_pd")]
correl <- correlation(test_cor_data, include_factors = TRUE)
correl <- cor_sort(as.matrix(correl)) # as matrix

#Plot matrix
corr_matrix <- visualisation_recipe(correl)
plot(corr_matrix)
```

2.2 Log transform Faith

(model residuals not normal distributed)

```r
model_faith <- lmer(faith_pd ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1 | nest/ring_number),
data = metadata)

> check_normality(model_faith_final_lbinom)
Warning: Non-normality of residuals detected (p < .001).

# Log transform faith
metadata$log_faith <- log10(metadata$faith_pd)
```

2.2. Model Faith PD

```r
model_faith <- lmer(log_faith ~ std_age + std_bci + rank + sex + year + habitat + lbinom + (1 | nest/ring_number), data = metadata)
```
2.3. Check Normality

```
> check_normality(model_faith)
OK: residuals appear as normally distributed (p = 0.661).
```

2.4. Model Diagnostics

```
check_model(model_faith)
```

2.5. Model Summary

```
> summary(model_faith)

Linear mixed model fit by REML ['lmerMod']
Formula: log_faith ~ std_age + std_bci + rank + sex + year + habitat +  
        lbinom + (1 | nest/ring_number)
Data: metadata

REML criterion at convergence: -10

Scaled residuals:
    Min     1Q Median     3Q    Max
-2.6227 -0.6599  0.0123  0.6367  2.3224
```
### Random effects:

<table>
<thead>
<tr>
<th>Groups</th>
<th>Name</th>
<th>Variance</th>
<th>Std.Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>ring_number:nest</td>
<td>(Intercept)</td>
<td>0.00000</td>
<td>0.0000</td>
</tr>
<tr>
<td>nest</td>
<td>(Intercept)</td>
<td>0.00000</td>
<td>0.0000</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>0.04422</td>
<td>0.2103</td>
</tr>
</tbody>
</table>

Number of obs: 177, groups: ring_number:nest, 108; nest, 54

### Fixed effects:

<table>
<thead>
<tr>
<th>Estimate</th>
<th>Std. Error</th>
<th>t value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>0.403635</td>
<td>11.476</td>
</tr>
<tr>
<td>std_age</td>
<td>-0.020558</td>
<td>-1.113</td>
</tr>
<tr>
<td>std_bci</td>
<td>-0.019744</td>
<td>-1.152</td>
</tr>
<tr>
<td>rank2</td>
<td>0.007209</td>
<td>0.198</td>
</tr>
<tr>
<td>rank3</td>
<td>-0.014333</td>
<td>-0.298</td>
</tr>
<tr>
<td>rank4</td>
<td>0.315343</td>
<td>1.987</td>
</tr>
<tr>
<td>sexM</td>
<td>0.008349</td>
<td>0.246</td>
</tr>
<tr>
<td>year2021</td>
<td>0.004901</td>
<td>0.081</td>
</tr>
<tr>
<td>habitat:south</td>
<td>0.094678</td>
<td>1.765</td>
</tr>
<tr>
<td>habitat:teuto</td>
<td>0.219712</td>
<td>1.944</td>
</tr>
<tr>
<td>lbinom1</td>
<td>0.043000</td>
<td>1.173</td>
</tr>
</tbody>
</table>

Correlation of Fixed Effects:

```
      (Intr) std_ag std_b_ rank2 rank3 sexM yr2021 hbtst hbtttt
std_age   0.205            
std_bci   -0.013 -0.006    
rank2     -0.443 0.137 0.072 
rank3     -0.293 0.224 0.204 0.372 
rank4     -0.014 0.101 0.266 0.125 0.165 
sexM      -0.414 -0.117 -0.111 -0.065 -0.093 -0.128 
year2021  -0.098 -0.065 0.096 -0.083 0.007 0.049 -0.153 
habitatsoth -0.095 0.048 0.147 0.025 0.196 0.112 -0.169 0.123 
habitatteuto -0.125 -0.151 0.184 0.127 0.119 0.073 0.042 -0.085 0.078 
lbinom1   -0.504 -0.418 -0.036 0.030 -0.116 -0.118 -0.099 0.111 -0.087 -0.070 
optimizer (nloptwrap) convergence code: 0 (OK) 
boundary (singular) fit: see help('isSingular')
```

## 2.6. Significance values

```r
> Anova(model_faith_final)
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: log_faith

<table>
<thead>
<tr>
<th></th>
<th>Chisq</th>
<th>Df</th>
<th>Pr(&gt;Chisq)</th>
</tr>
</thead>
<tbody>
<tr>
<td>std_age</td>
<td>1.2377</td>
<td>1</td>
<td>0.26591</td>
</tr>
<tr>
<td>std_bci</td>
<td>1.3281</td>
<td>1</td>
<td>0.24914</td>
</tr>
<tr>
<td>rank</td>
<td>4.3856</td>
<td>3</td>
<td>0.22272</td>
</tr>
<tr>
<td>sex</td>
<td>0.0607</td>
<td>1</td>
<td>0.80540</td>
</tr>
<tr>
<td>year</td>
<td>0.0065</td>
<td>1</td>
<td>0.93569</td>
</tr>
<tr>
<td>habitat</td>
<td>6.3988</td>
<td>2</td>
<td>0.04079 *</td>
</tr>
<tr>
<td>lbinom</td>
<td>1.3759</td>
<td>1</td>
<td>0.24081</td>
</tr>
</tbody>
</table>

---
Signif. codes:  < 0.001 ***  0.001 **  0.01 *  0.05 .  0.1   1
```
2.6.1. Multiple comparison test for "Habitat"

```r
> library(multcomp)

> multicomp <- glht(model_faith, linfct = mcp(habitat="Tukey")) #multicomparsion for linear models

> confint(glht(model_faith_final_lbinom, mcp(habitat="Tukey")))

Simultaneous Confidence Intervals

Multiple Comparisons of Means: Tukey Contrasts

Fit: lmer(formula = log_faith ~ std_age + std_bci + rank + sex +
year + habitat + lbinom + (1 | nest/ring_number), data = metadata)

Quantile = 2.3042
95% family-wise confidence level

Linear Hypotheses:

<table>
<thead>
<tr>
<th>Estimate</th>
<th>lwr</th>
<th>upr</th>
</tr>
</thead>
<tbody>
<tr>
<td>south - north == 0</td>
<td>0.09468</td>
<td>-0.02890</td>
</tr>
<tr>
<td>teuto - north == 0</td>
<td>0.21971</td>
<td>-0.04067</td>
</tr>
<tr>
<td>teuto - south == 0</td>
<td>0.12503</td>
<td>-0.15431</td>
</tr>
</tbody>
</table>

> summary(multicomp, test = adjusted("holm"))

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: lmer(formula = log_faith ~ std_age + std_bci_two + rank + sex +
year + habitat + lbinom + (1 | nest/ring_number), data = metadata)

Linear Hypotheses:

| Estimate | Std. Error | z value | Pr(>|z|) |
|----------|------------|---------|---------|
| south - north == 0 | 0.09468 | 0.05363 | 1.765 | 0.116 |
| teuto - north == 0 | 0.21971 | 0.11300 | 1.944 | 0.116 |
| teuto - south == 0 | 0.12503 | 0.12123 | 1.031 | 0.302 |

(Adjusted p values reported -- BH method)

2.7. Marginal and Conditional R-squared

```r
> r.squaredGLMM(model_faith)

    R2m   R2c
[1,] 0.09305071 0.09305071

2.8. Plot model effects

```r
plot(allEffects(model_faith))
```
2.9. Significance of random effects

```r
> lmerTest::ranova(model_faith_final_lbinom)
boundary (singular) fit: see help('isSingular')
boundary (singular) fit: see help('isSingular')
ANOVA-like table for random-effects: Single term deletions

Model:
log_faith ~ std_age + std_bci_two + rank + sex + year + habitat + lbinom + (1 | ring_number:nest) + (1 | nest)
npar logLik      AIC     LRT Df Pr(>Chisq)
<none>           14 5.0039 17.992
(1 | ring_number:nest) 13 5.0039 15.992 0  1  1
(1 | nest)         13 5.0039 15.992 0  1  1
```