

Alpha diversity statistical analysis

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A) 16S rRNA alpha diversity statistical analysis

1. Shannon diversity Index

```
#Load libraries
library(tidyverse)
library(lme4)
library(MuMIn)
library(performance)
library(datawizard)
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")
```

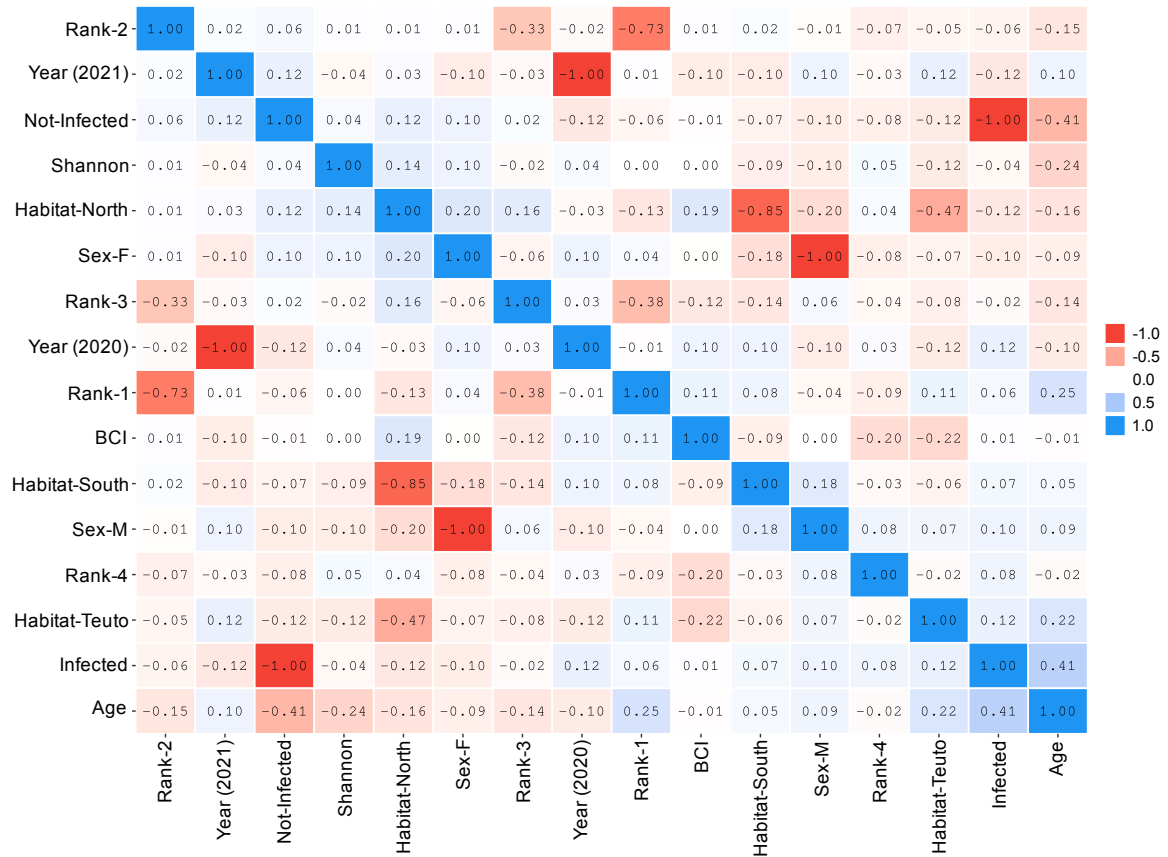
1.1 Check correlation between variables

```
#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)
```

Correlation 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)
```

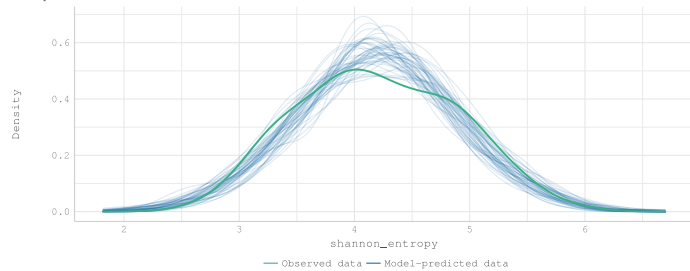
1.3 Check Normality

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

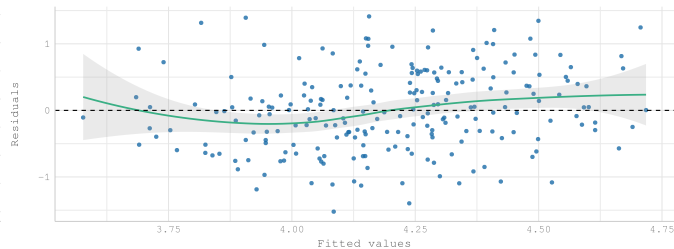
1.4 Model Diagnostics

```
check_model(model_shannon)
```

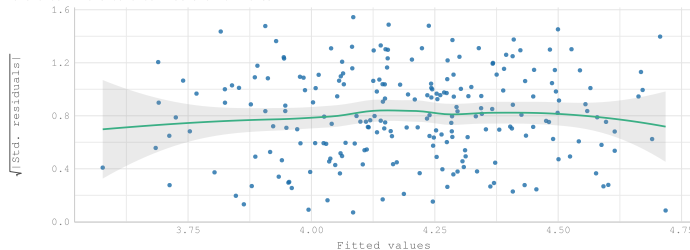
Posterior Predictive Check
Model-predicted lines should resemble observed data line



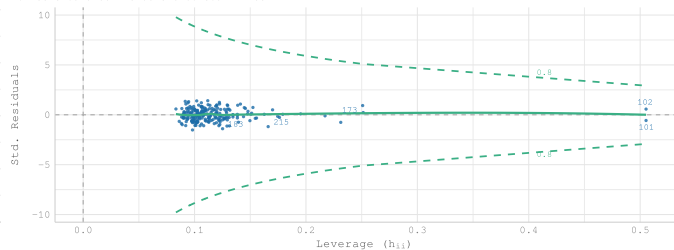
Linearity
Reference line should be flat and horizontal



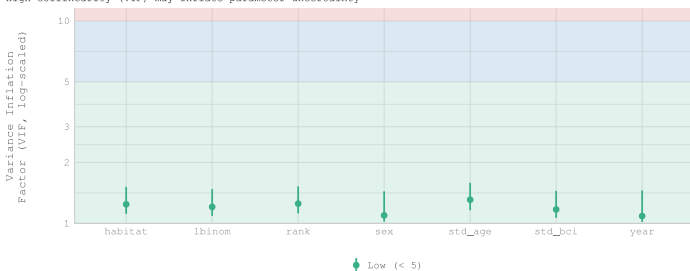
Homogeneity of Variance
Reference line should be flat and horizontal



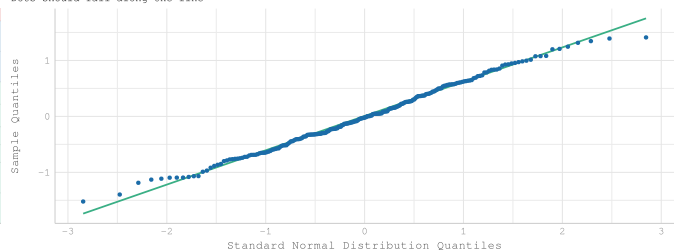
Influential Observations
Points should be inside the contour lines



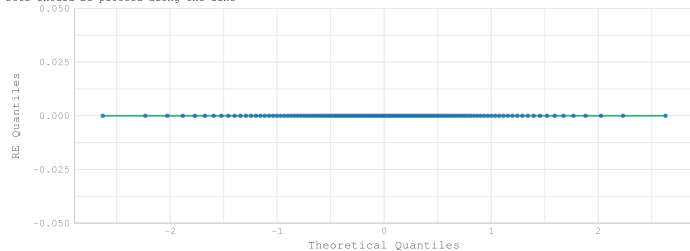
Collinearity
High collinearity (VIF) may inflate parameter uncertainty



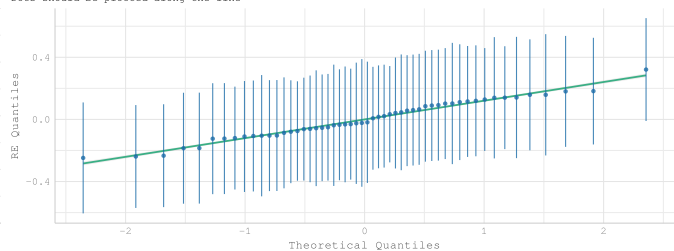
Normality of Residuals
Dots should fall along the line



Normality of Random Effects (ring_number:nest)
Dots should be plotted along the line



Normality of Random Effects (nest)
Dots should be plotted along the line



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
-2.38433	-0.63636	-0.03356	0.65990	2.21304

Random effects:

Groups	Name	Variance	Std.Dev.
ring_number:nest	(Intercept)	0.00000	0.0000
nest	(Intercept)	0.04932	0.2221
Residual		0.40710	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

```
rank2      -0.0925053    0.0964370    -0.959
rank3      -0.1613338    0.1423461    -1.133
rank4       0.2139437    0.5077520     0.421
sexM       -0.1144732    0.0963586    -1.188
year2021    0.0683771    0.1981118     0.345
habitatsoth -0.1657539    0.1744792    -0.950
habitatteuto -0.2976098    0.2869742    -1.037
lbinom1     0.0787340    0.1036844     0.759
```

Correlation of Fixed Effects:

```
(Intr) std_ag std_b_ rank2 rank3 rank4 sexM yr2021 hbtst hbtstt
std_age      0.143
std_bci     -0.087  0.023
rank2       -0.404  0.196  0.101
rank3       -0.246  0.216  0.210  0.378
rank4       -0.025  0.112  0.240  0.132  0.167
sexM        -0.388 -0.043 -0.088 -0.035 -0.146 -0.138
year2021    -0.177 -0.106  0.100 -0.028  0.029  0.041 -0.138
habitatsoth -0.143 -0.013  0.156  0.048  0.168  0.094 -0.207  0.134
habitatteut -0.087 -0.137  0.239  0.074  0.114  0.077 -0.082 -0.086  0.124
lbinom1     -0.521 -0.371 -0.036 -0.032 -0.079 -0.082 -0.043  0.142 -0.038 -0.065
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')
```

1.6 Significance values

```
> Anova(model_shannon)

Analysis of Deviance Table (Type II Wald chisquare tests)

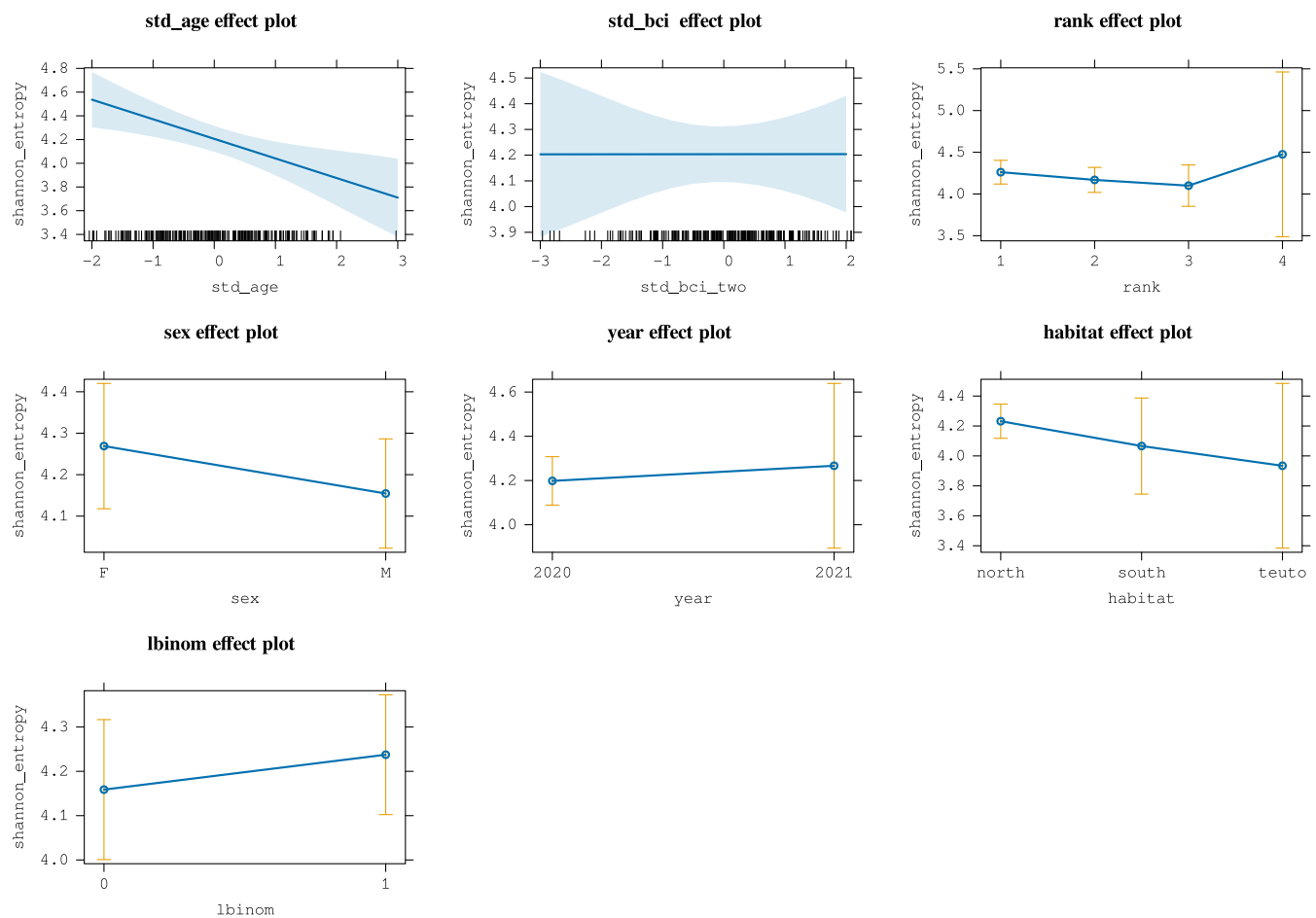
Response: shannon_entropy
          Chisq    Df Pr(>Chisq)
std_age      9.7564   1  0.001787 **
std_bci       0.0000   1  0.997383
rank         2.0552   3  0.561028
sex          1.4113   1  0.234836
year         0.1191   1  0.729986
habitat      1.7600   2  0.414783
lbinom       0.5766   1  0.447636
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

1.7 Marginal and conditional R-squared

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

1.8 Plot model effects

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



1.9 Significance of random effects

```
>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)

```
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).

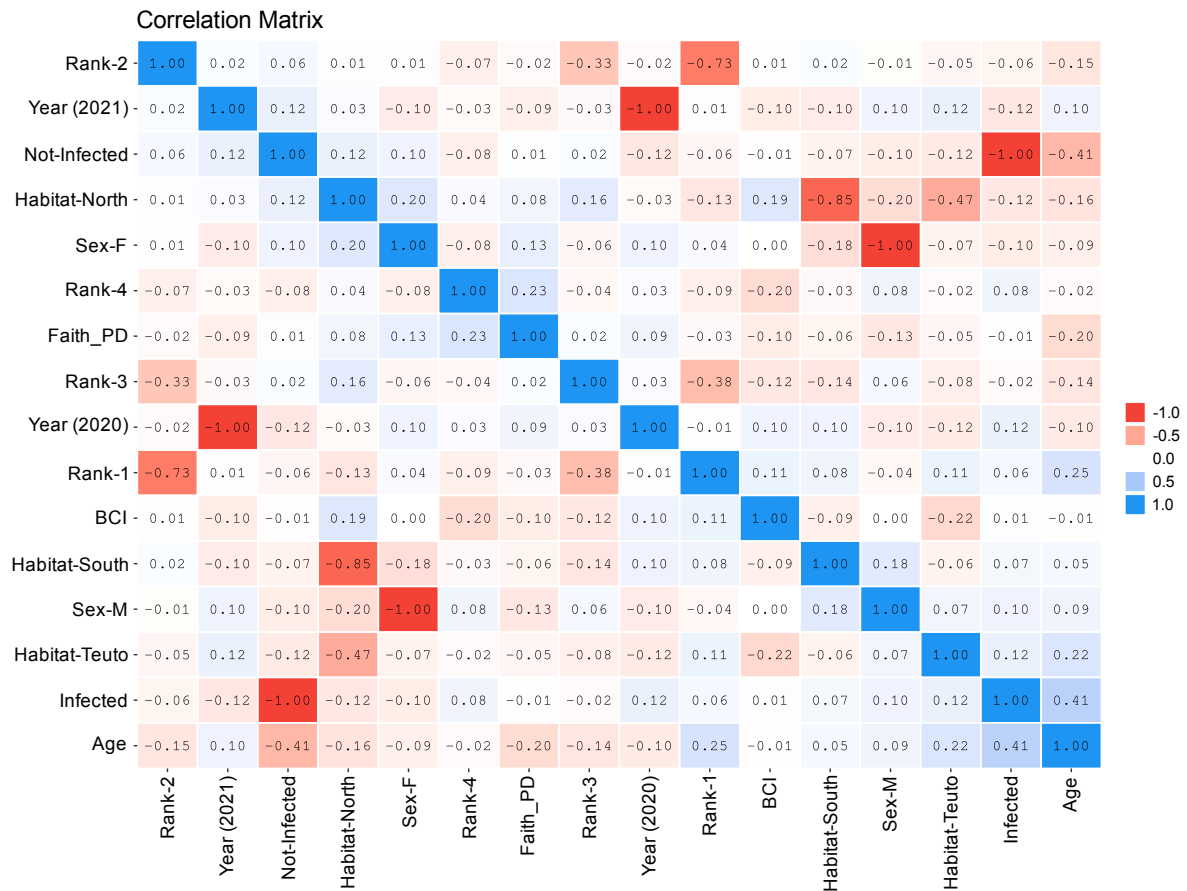
#Log transform faith
metadata$log_faith <- log10(metadata$faith_pd)
```

2.2 Check correlation between variables

```
#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)
```



2.3 Model Faith PD

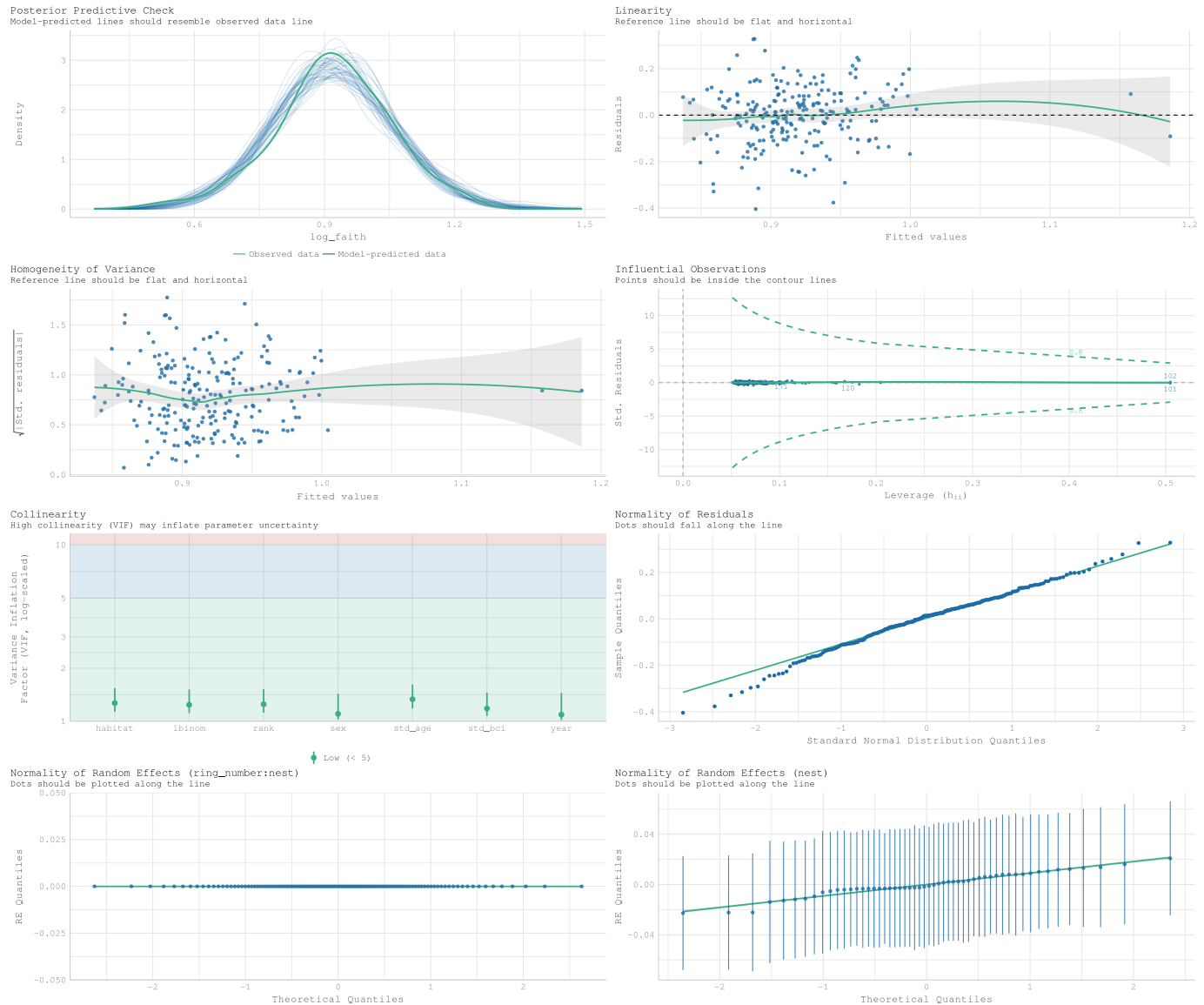
```
model_faith <- lmer(log_faith ~ std_age + std_bci + rank + sex + year + habitat + lbinom +
(1|nest/ring_number), data = metadata)
```

2.4 Check Normality

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

2.5 Model Diagnostics

```
check_model(model_faith)
```



2.6 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: -225.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.1497	-0.5645	0.1041	0.6145	2.5580

Random effects:

Groups	Name	Variance	Std.Dev.
ring_number:nest	(Intercept)	0.0000000	0.00000
nest	(Intercept)	0.0006666	0.02582
Residual		0.0164990	0.12845

```
Number of obs: 226, groups: ring_number:nest, 117; nest, 54
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	0.9407717	0.0199731	47.102
std_age	-0.0285771	0.0102204	-2.796
std_bci	-0.0067600	0.0097165	-0.696
rank2	-0.0189343	0.0192559	-0.983
rank3	-0.0154191	0.0279228	-0.552
rank4	0.2347500	0.0988584	2.375
sexM	-0.0360834	0.0186700	-1.933
year2021	-0.0134265	0.0354902	-0.378
habitatsoth	-0.0029790	0.0315251	-0.094
habitatteuto	0.0008674	0.0526736	0.016
lbinom1	0.0146748	0.0200224	0.733

Correlation of Fixed Effects:

	(Intr)	std_ag	std_b_	rank2	rank3	rank4	sexM	yr2021	hbttst	hbtttt
std_age	0.164									
std_bci	-0.079	0.018								
rank2	-0.428	0.188	0.090							
rank3	-0.280	0.200	0.210	0.374						
rank4	-0.027	0.097	0.246	0.127	0.155					
sexM	-0.394	-0.052	-0.097	-0.037	-0.137	-0.129				
year2021	-0.166	-0.115	0.105	-0.031	0.035	0.045	-0.148			
habitatsoth	-0.124	-0.011	0.172	0.049	0.187	0.104	-0.220	0.136		
habitatteut	-0.086	-0.142	0.251	0.076	0.125	0.087	-0.082	-0.071	0.130	
lbinom1	-0.525	-0.394	-0.043	-0.034	-0.070	-0.095	-0.049	0.152	-0.041	-0.063

optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')

2.7 Significance values

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

Response: log_faith

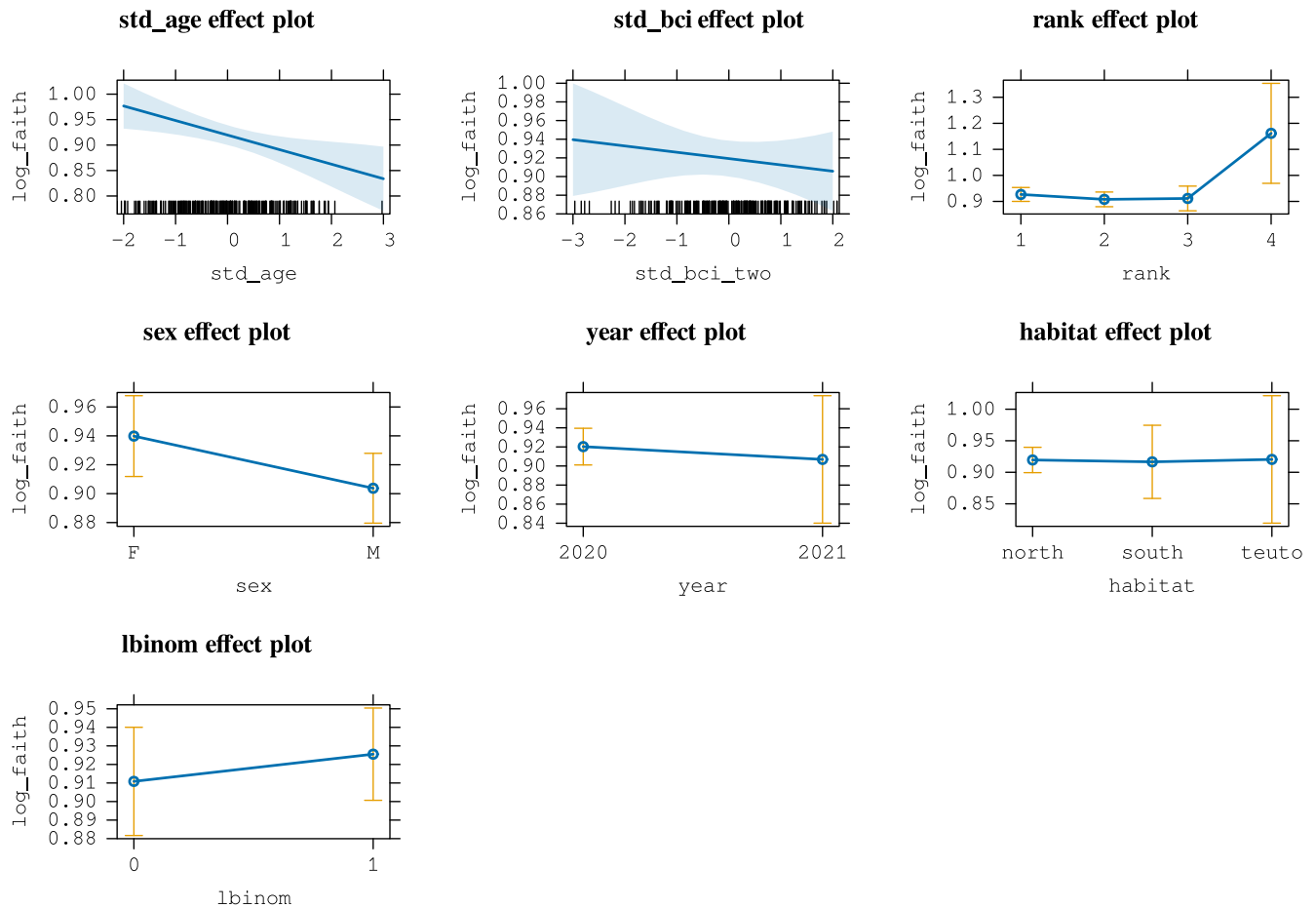
      Chisq  Df  Pr(>Chisq)
std_age   7.8181  1  0.005173 **
std_bci    0.4840  1  0.486605
rank      7.5620  3  0.055986 .
sex       3.7353  1  0.053274 .
year      0.1431  1  0.705197
habitat    0.0098  2  0.995125
lbinom    0.5372  1  0.463609
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2.8 Marginal and Conditional R-squared

```
> r.squaredGLMM(model_faith)
      R2m      R2c
[1,] 0.09268855 0.1279241
```

2.9 Plot model effects

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



2.10 Significance of random effects

```
> 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)
               npar logLik      AIC      LRT Df Pr(>Chisq)
<none>                14 112.74 -197.49
(1 | ring_number:nest)  13 112.74 -199.49 0.00000  1      1.0000
(1 | nest)              13 112.45 -198.91 0.58057  1      0.4461
```

B) 28S rRNA alpha diversity statistical analysis

1. Shannon diversity Index

```
#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

```
#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

```
> 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

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

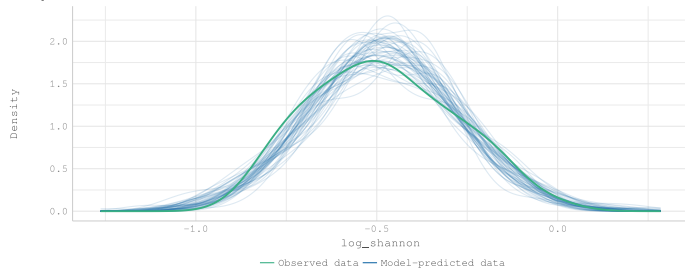
1.4. Check Normality

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

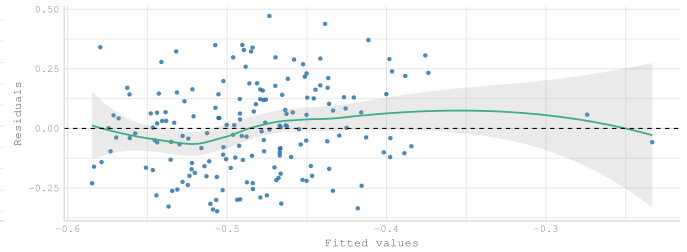
1.5. Model Diagnostics

```
check_model(model_shannon) # normality of residuals identified by visual inspection
```

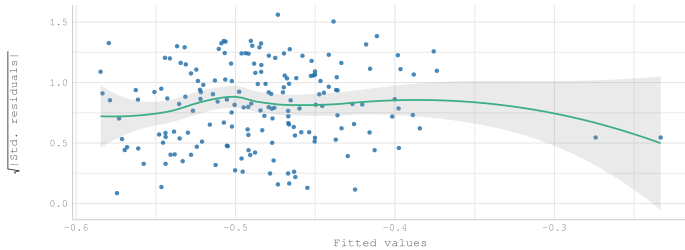
Posterior Predictive Check
Model-predicted lines should resemble observed data line



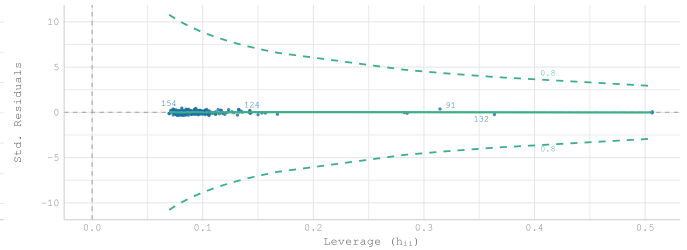
Linearity
Reference line should be flat and horizontal



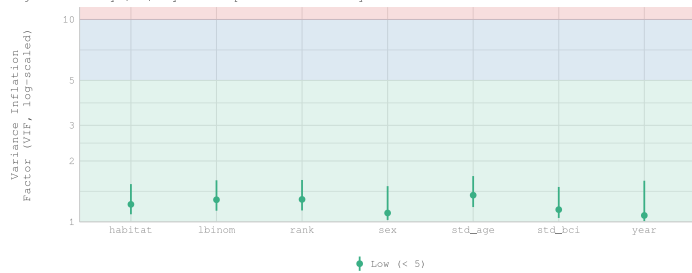
Homogeneity of Variance
Reference line should be flat and horizontal



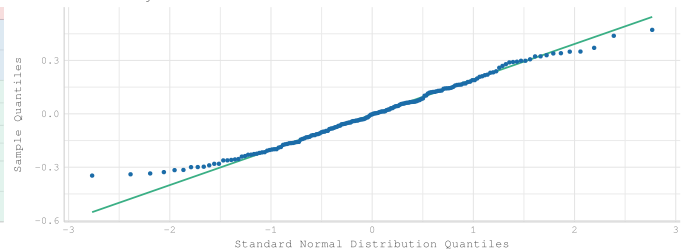
Influential Observations
Points should be inside the contour lines



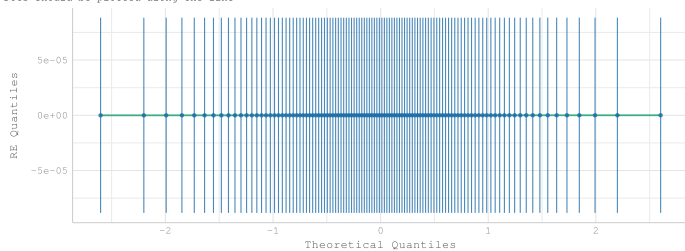
Collinearity
High collinearity (VIF) may inflate parameter uncertainty



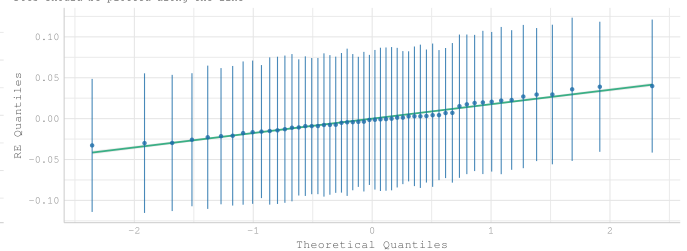
Normality of Residuals
Dots should fall along the line



Normality of Random Effects (ring_number: nest)
Dots should be plotted along the line



Normality of Random Effects (nest)
Dots should be plotted along the line



1.6. Model Summary

```
> 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
habitatsoth   0.068654    0.053602    1.281
habitatteuto  0.112459    0.108764    1.034
year2021      0.003454    0.061376    0.056
lbinom1       0.019645    0.034963    0.562

Correlation of Fixed Effects:
      (Intr) std_ag std_b_ sexM  rank2 rank3 rank4 hbtstst hbtsttt yr2021
std_age      0.186
std_bci      -0.023  0.002
sexM         -0.408 -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
habitatsoth  -0.111  0.047  0.138 -0.164  0.026  0.183  0.106
habitatteut  -0.123 -0.151  0.184  0.036  0.123  0.113  0.066  0.078
year2021     -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

```
> Anova(model_shannon)
Analysis of Deviance Table (Type II Wald chisquare 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
---
```

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

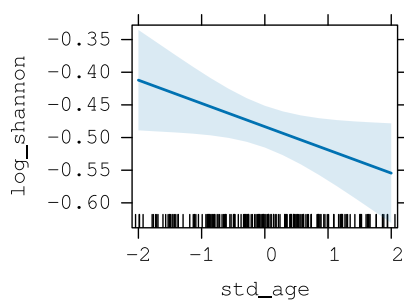
1.8. Marginal and conditional R-squared

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

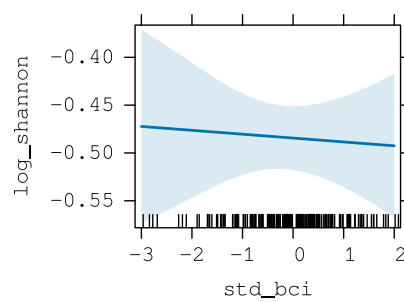
1.9. Plot model effects

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

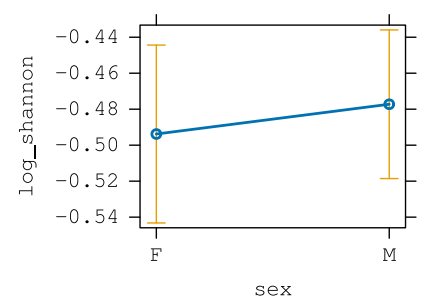
std_age effect plot



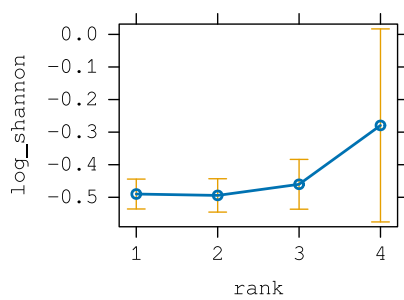
std_bci effect plot



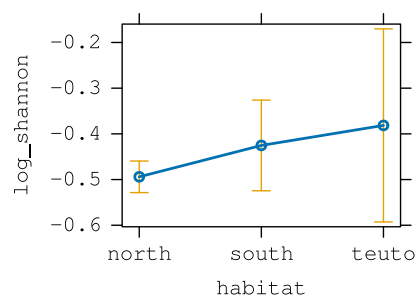
sex effect plot



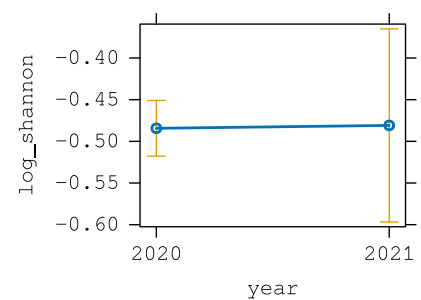
rank effect plot



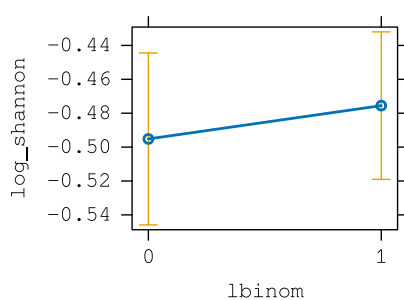
habitat effect plot



year effect plot



lbinom effect plot



1.10. Significance of random effects

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

Model:
log_shannon ~ std_age + std_bci + sex + rank + habitat + year + lbinom + (1 | ring_number:nest) + (1 | nest)
              npar logLik      AIC      LRT Df Pr(>Chisq)
<none>              14 14.434 -0.86813
(1 | ring_number:nest) 13 14.434 -2.86813 0.00000 1      1.0000
(1 | nest)             13 14.145 -2.28934 0.57879 1      0.4468
```

2. Faith phylogenetic diversity

2.1 Check correlation between variables

```
#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)

```
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

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

2.3. Check Normality

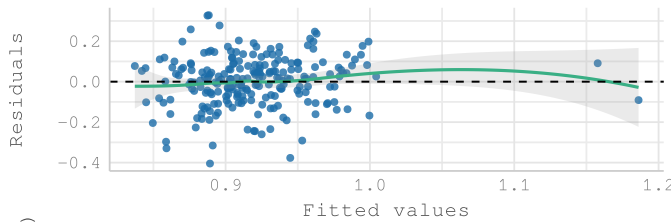
```
> check_normality(model_faith)
OK: residuals appear as normally distributed (p = 0.661).
```

2.4. Model Diagnostics

```
check_model(model_faith)
```

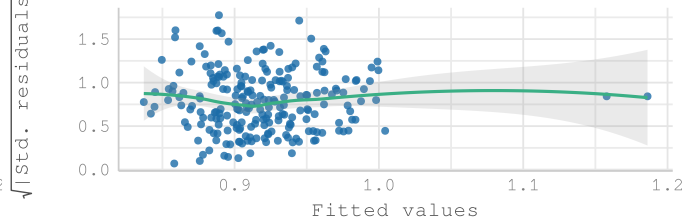
Linearity

Reference line should be flat and horizontal



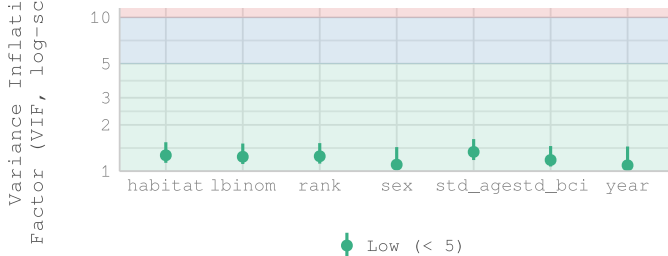
Homogeneity of Variance

Reference line should be flat and horizontal



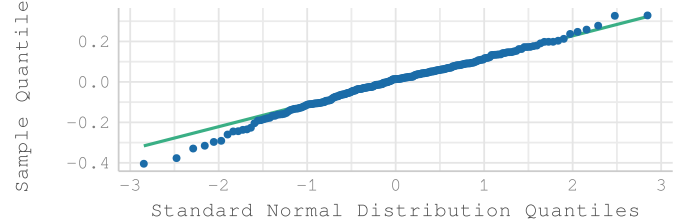
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



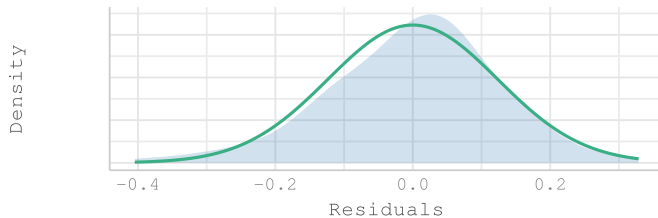
Normality of Residuals

Dots should fall along the line



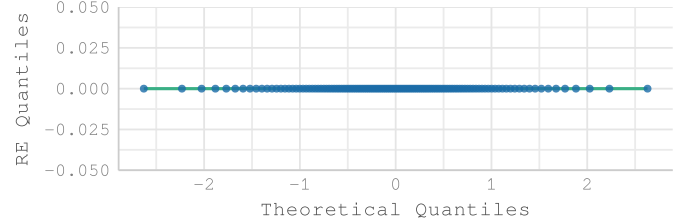
Normality of Residuals

Distribution should be close to the normal curve



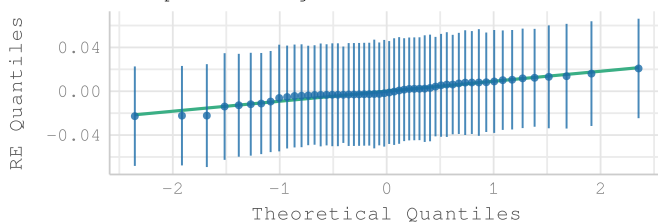
Normality of Random Effects (ring_number:nest)

Dots should be plotted along the line



Normality of Random Effects (nest)

Dots should be plotted along the line



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
-2.62275	-0.65997	0.01234	0.63677	2.32240

```

Random effects:
  Groups             Name                Variance Std.Dev.
ring_number:nest (Intercept) 0.000000  0.00000
nest              (Intercept) 0.000000  0.00000
Residual                                0.04422  0.2103
Number of obs: 177, groups: ring_number:nest, 108; nest, 54

Fixed effects:
              Estimate Std. Error t value
(Intercept)  0.403635  0.035173  11.476
std_age      -0.020558  0.018479  -1.113
std_bci      -0.019744  0.017132  -1.152
rank2         0.007209  0.036431   0.198
rank3        -0.014333  0.048106  -0.298
rank4         0.315343  0.158692   1.987
sexM          0.008349  0.033891   0.246
year2021      0.004901  0.060742   0.081
habitatsoth   0.094678  0.053631   1.765
habitatteuto  0.219712  0.113001   1.944
lbinom1       0.043000  0.036659   1.173

Correlation of Fixed Effects:
              (Intr) std_ag std_b_ rank2 rank3 rank4 sexM yr2021 hbttst 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
habitatteut   -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

```

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

Response: log_faith
              Chisq Df Pr(>Chisq)
std_age      1.2377  1  0.26591
std_bci      1.3281  1  0.24914
rank         4.3856  3  0.22272
sex          0.0607  1  0.80540
year         0.0065  1  0.93569
habitat      6.3988  2  0.04079 *
lbinom       1.3759  1  0.24081
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

2.6.1. Multiple comparison test for "Habitat"

```
> library(multcomp)

> multcomp <- glht(model_faith, linfct = mcp(habitat="Tukey")) #multicomparisson 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:

	Estimate	lwr	upr
south - north == 0	0.09468	-0.02890	0.21826
teuto - north == 0	0.21971	-0.04067	0.48009
teuto - south == 0	0.12503	-0.15431	0.40438

```
> summary(multcomp, 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

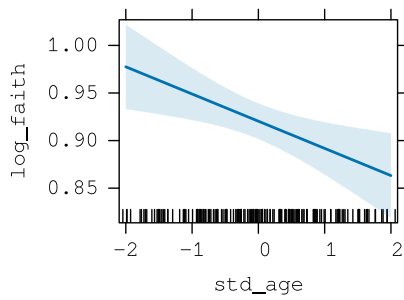
```
> r.squaredGLMM(model_faith)
```

	R2m	R2c
[1,]	0.09305071	0.09305071

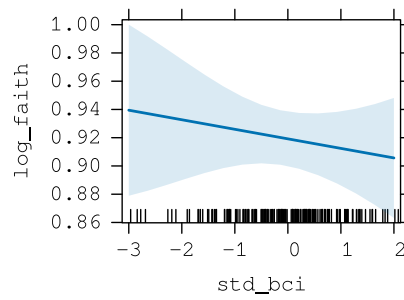
2.8. Plot model effects

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

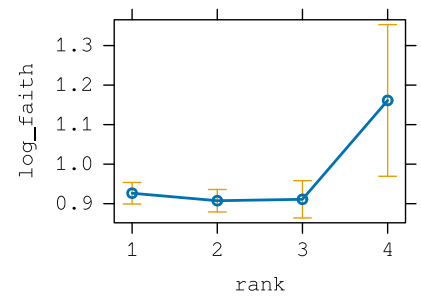
std_age effect plot



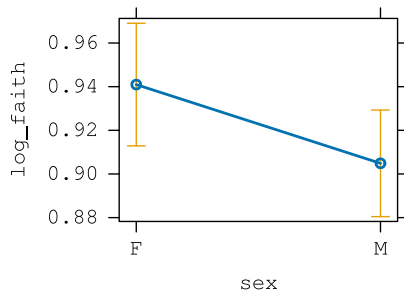
std_bci effect plot



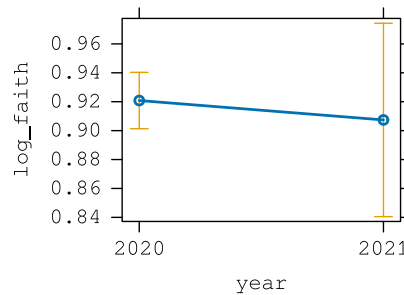
rank effect plot



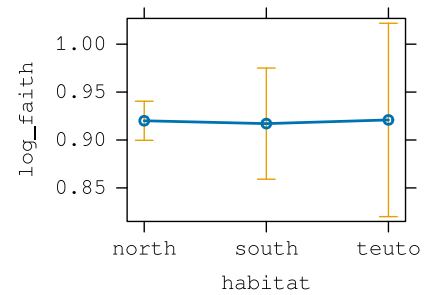
sex effect plot



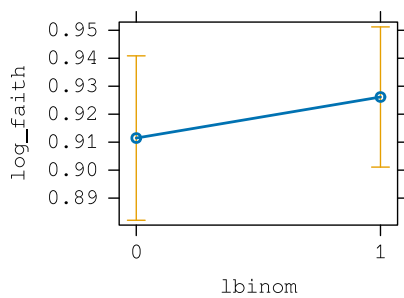
year effect plot



habitat effect plot



lbinom effect plot



2.9. Significance of random effects

```
> 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
```