

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(jttools)

#Load dataset
metadata <- readRDS("metadata-rarefied.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,"metadata-rarefied.rds")
```

1.1 Model Shannon

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

1.2 Check Normality

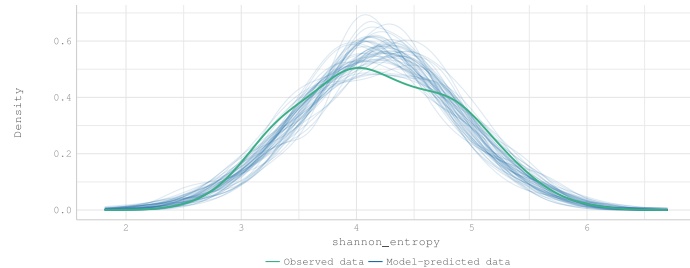
```
> check_normality(model_shannon)
OK: residuals appear as normally distributed (p = 0.394).
```

1.3 Model Diagnostics

```
check_model(model_shannon)
```

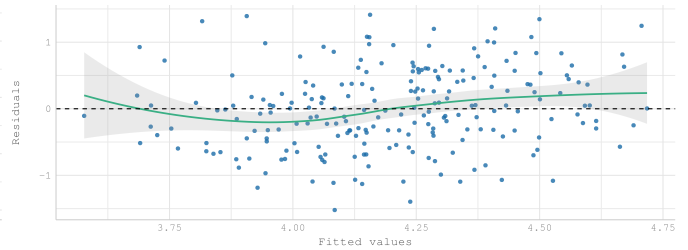
Posterior Predictive Check

Model-predicted lines should resemble observed data line



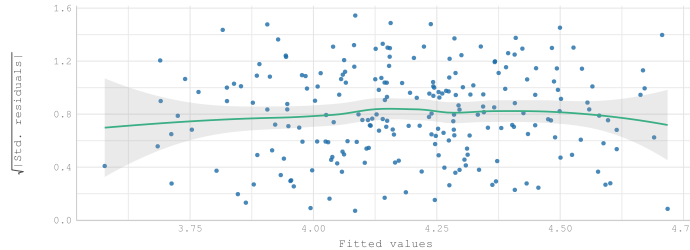
Linearity

Reference line should be flat and horizontal



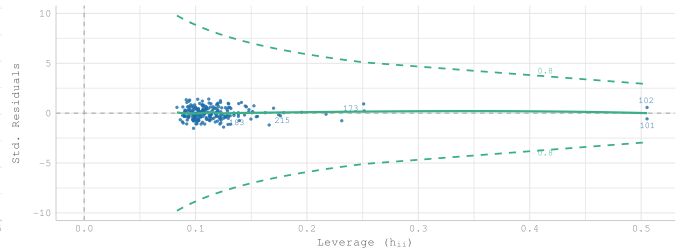
Homogeneity of Variance

Reference line should be flat and horizontal



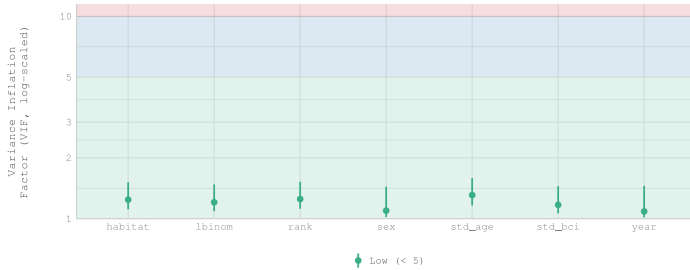
Influential Observations

Points should be inside the contour lines



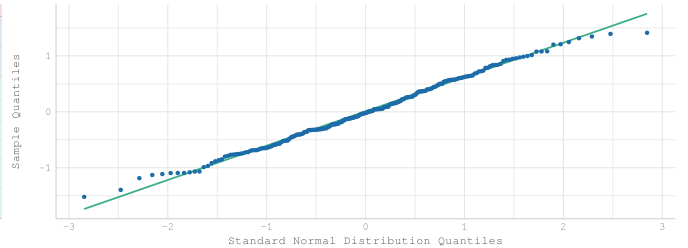
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



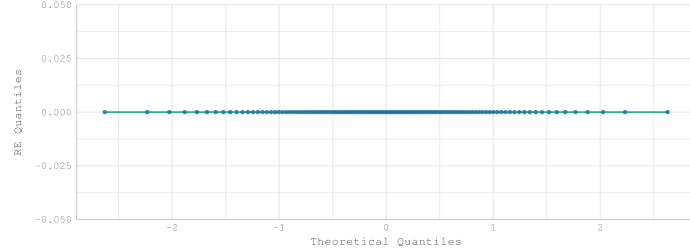
Normality of Residuals

Dots should fall along the line



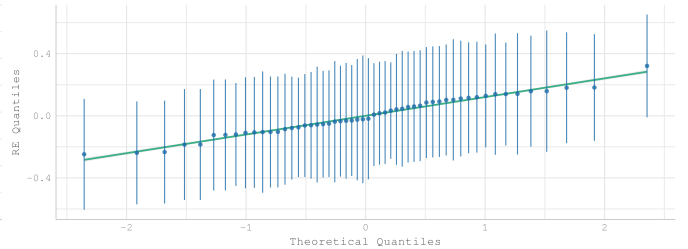
Normality of Random Effects (ring_number:nest)

Dots should be plotted along the line



Normality of Random Effects (nest)

Dots should be plotted along the line



1.4 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
habitatouth	-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	hbttst	hbtttt
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')

1.5 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
```

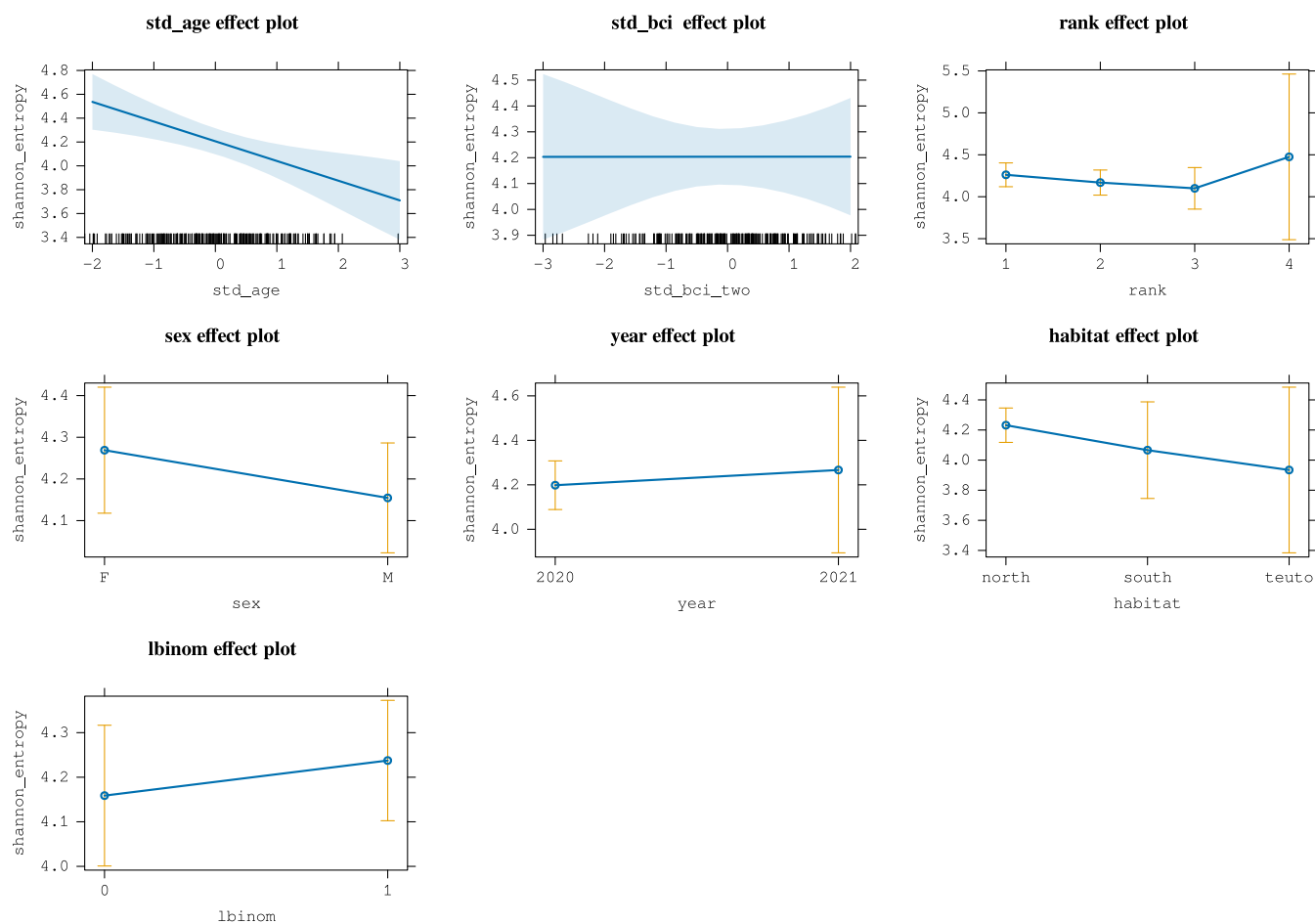
1.6 Marginal and conditional R-squared

```
r.squaredGLMM(model_shannon)

      R2m      R2c
[1,] 0.0758452 0.1757042
```

1.7 Plot model effects

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



Repeatability Analysis

```
> rpts <- rpt(shannon_entropy ~ std_age + std_bci + rank + sex + year + habitat + (1|nest) +
(1|ring_number),
             grname = c("nest", "ring_number"), data = metadata,
             datatype = "Gaussian",adjusted = TRUE,
             nboot = 1000, npermut = 1000)

> summary(rpts)
```

Repeatability estimation using the lmm method

```
Call = rpt(formula = shannon_entropy ~ std_age + std_bci_two + rank + sex + year + habitat + (1
| nest) + (1 | ring_number), grname = c("nest", "ring_number"), data = metadata, datatype =
"Gaussian", nboot = 1000, npermut = 1000, adjusted = TRUE)
```

Data: 228 observations

nest (54 groups)

Repeatability estimation overview:

R	SE	2.5%	97.5%	P_permut	LRT_P
0.109	0.0618	0	0.224	0.017	0.028

Bootstrapping and Permutation test:

	N	Mean	Median	2.5%	97.5%
boot	1000	0.0940	9.14e-02	0	0.2237
permut	1000	0.0156	1.12e-12	0	0.0932

Likelihood ratio test:

```
logLik full model = -239.6265
logLik red. model = -241.4516
D = 3.65, df = 1, P = 0.028
```

ring_number (117 groups)

Repeatability estimation overview:

R	SE	2.5%	97.5%	P_permut	LRT_P
0	0.0633	0	0.219	1	0.5

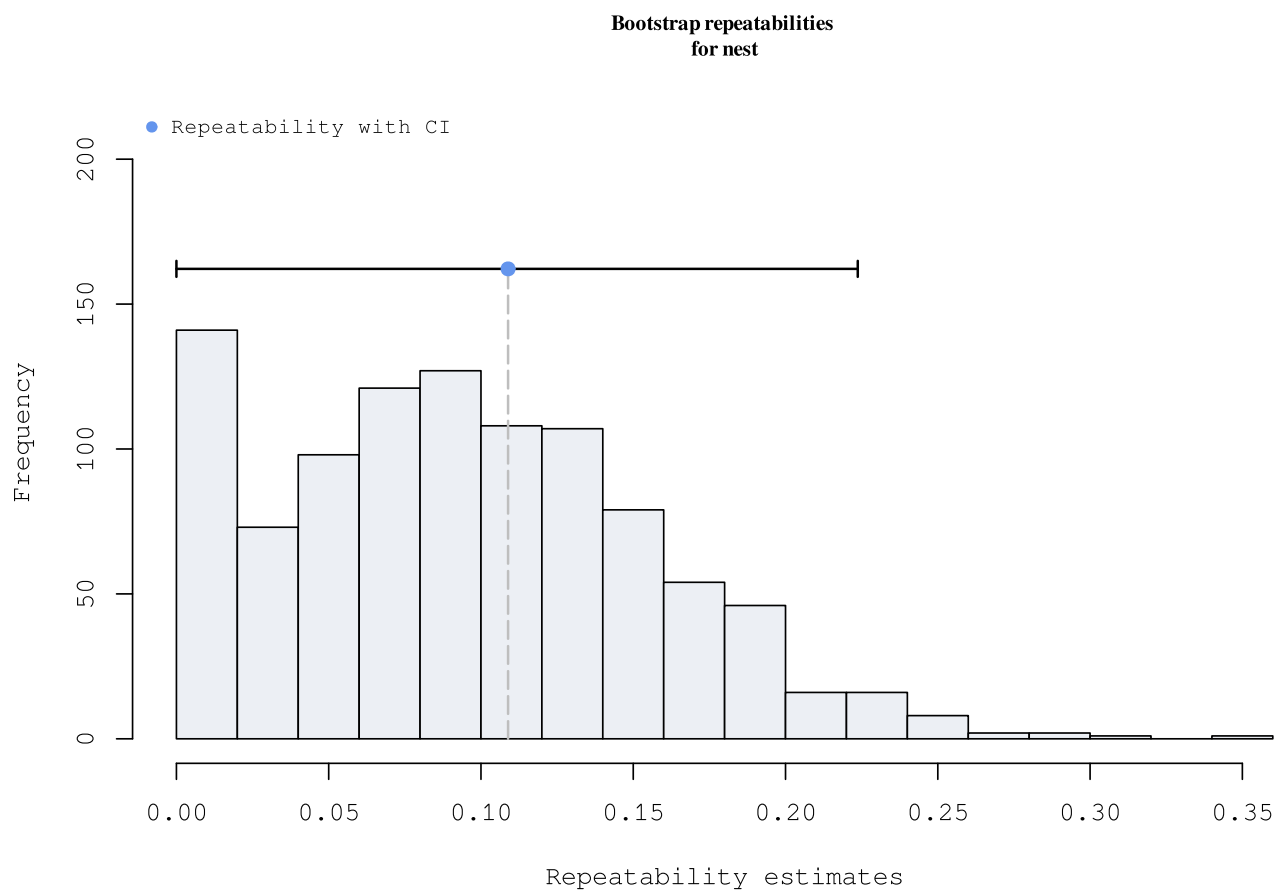
Bootstrapping and Permutation test:

	N	Mean	Median	2.5%	97.5%
boot	1000	0.0430	1.13e-08	0	0.219
permut	1000	0.0347	1.69e-11	0	0.175

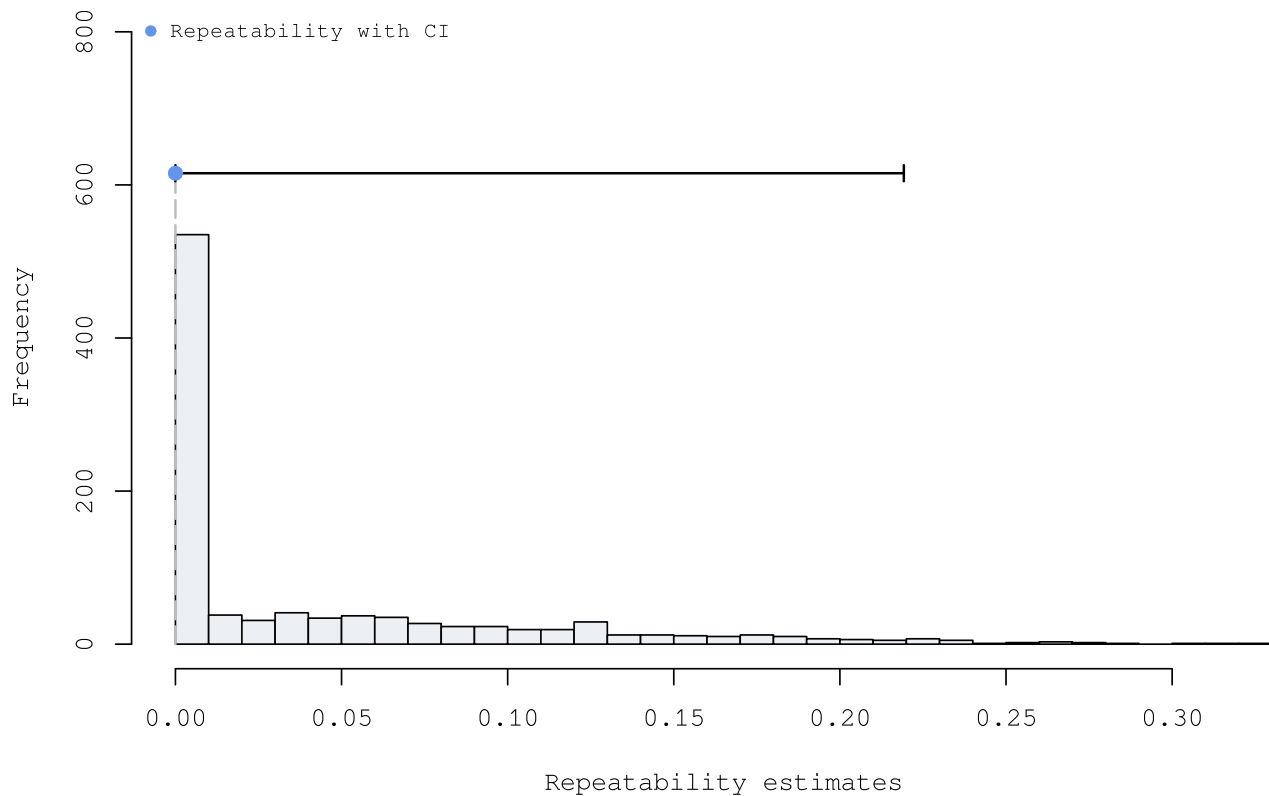
Likelihood ratio test:

```
logLik full model = -239.6265
logLik red. model = -239.6265
D = 2.27e-13, df = 1, P = 0.5
```

```
plot(rpts, grname="nest", type="boot", cex.main=0.8, col = "#ECEFF4")
plot(rpts, grname="ring_number", type="boot", cex.main=0.8, col = "#ECEFF4")
```



Bootstrap repeatabilities for ring_number



Faith phylogenetic diversity

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)  
Warning: Non-normality of residuals detected (p = 0.003).  
  
#Log transform faith  
metadata$log_faith <- log10(metadata$faith_pd)
```

2.1 Model Faith PD

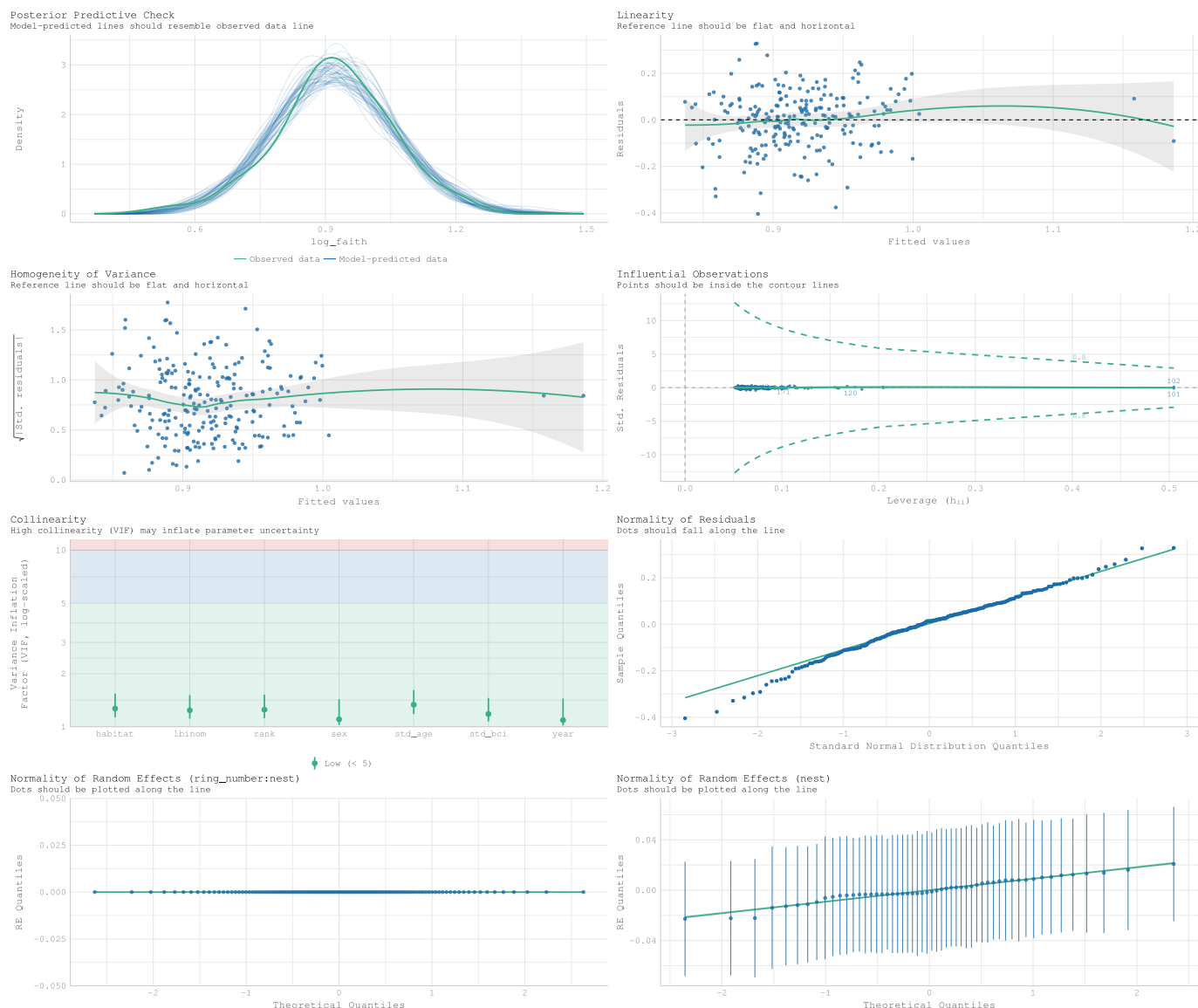
```
model_faith <- lmer(log_faith ~ std_age + std_bci + rank + sex + year + habitat + lbinom +  
(1|nest/ring_number), data = metadata)
```


2.2 Check Normality

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

2.3 Model Diagnostics

```
check_model(model_faith)
```



2.4 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
habitatouth	-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')

2.5 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
```

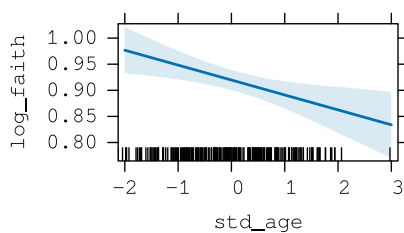
2.6 Marginal and Conditional R-squared

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

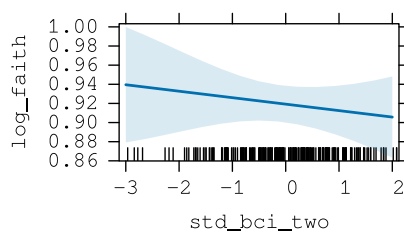
2.7 Plot model effects

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

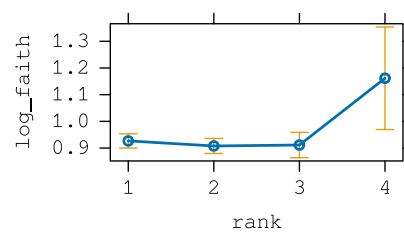
std_age effect plot



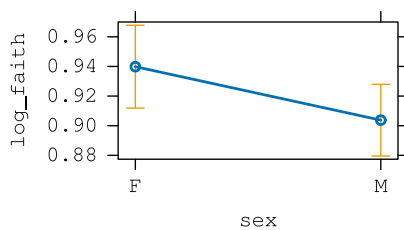
std_bci effect plot



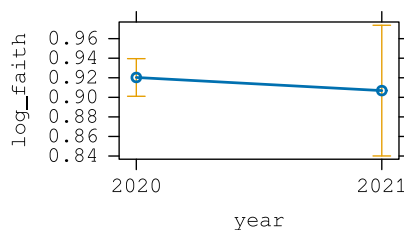
rank effect plot



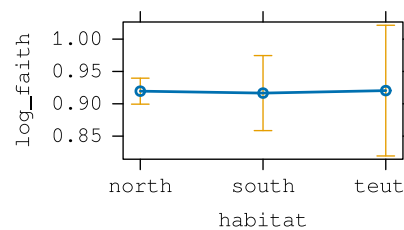
sex effect plot



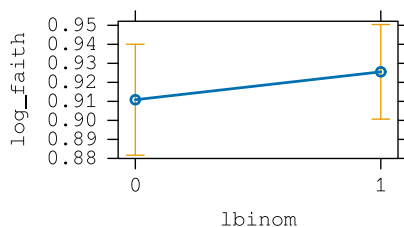
year effect plot



habitat effect plot



lbinom effect plot



2.8 Repeatability Analysis

```
> rpts2 <- rpt(log_faith ~ std_age + std_bci + rank + sex + year + habitat + (1|nest) +
(1|ring_number),
              grname = c("nest", "ring_number"), data = metadata,
              datatype = "Gaussian",adjusted = TRUE,
              nboot = 1000, npermut = 1000)

> summary(rpts2)
```

Repeatability estimation using the lmm method

```
Call = rpt(formula = log_faith ~ std_age + std_bci + rank + sex + year + habitat + (1 | nest) +
(1 | ring_number), grname = c("nest", "ring_number"), data = metadata, datatype = "Gaussian",
nboot = 1000, npermut = 1000, adjusted = TRUE)
```

Data: 228 observations

nest (54 groups)

Repeatability estimation overview:

	R	SE	2.5%	97.5%	P_permut	LRT_P
	0.0385	0.046	0	0.158	0.17	0.222

Bootstrapping and Permutation test:

	N	Mean	Median	2.5%	97.5%
boot	1000	0.0404	2.57e-02	0	0.1575
permut	1000	0.0167	2.04e-11	0	0.0987

Likelihood ratio test:

```
logLik full model = 117.2883
logLik red. model = 116.9959
D = 0.585, df = 1, P = 0.222
```

ring_number (117 groups)

Repeatability estimation overview:

	R	SE	2.5%	97.5%	P_permut	LRT_P
	0	0.0551	0	0.188	1	0.5

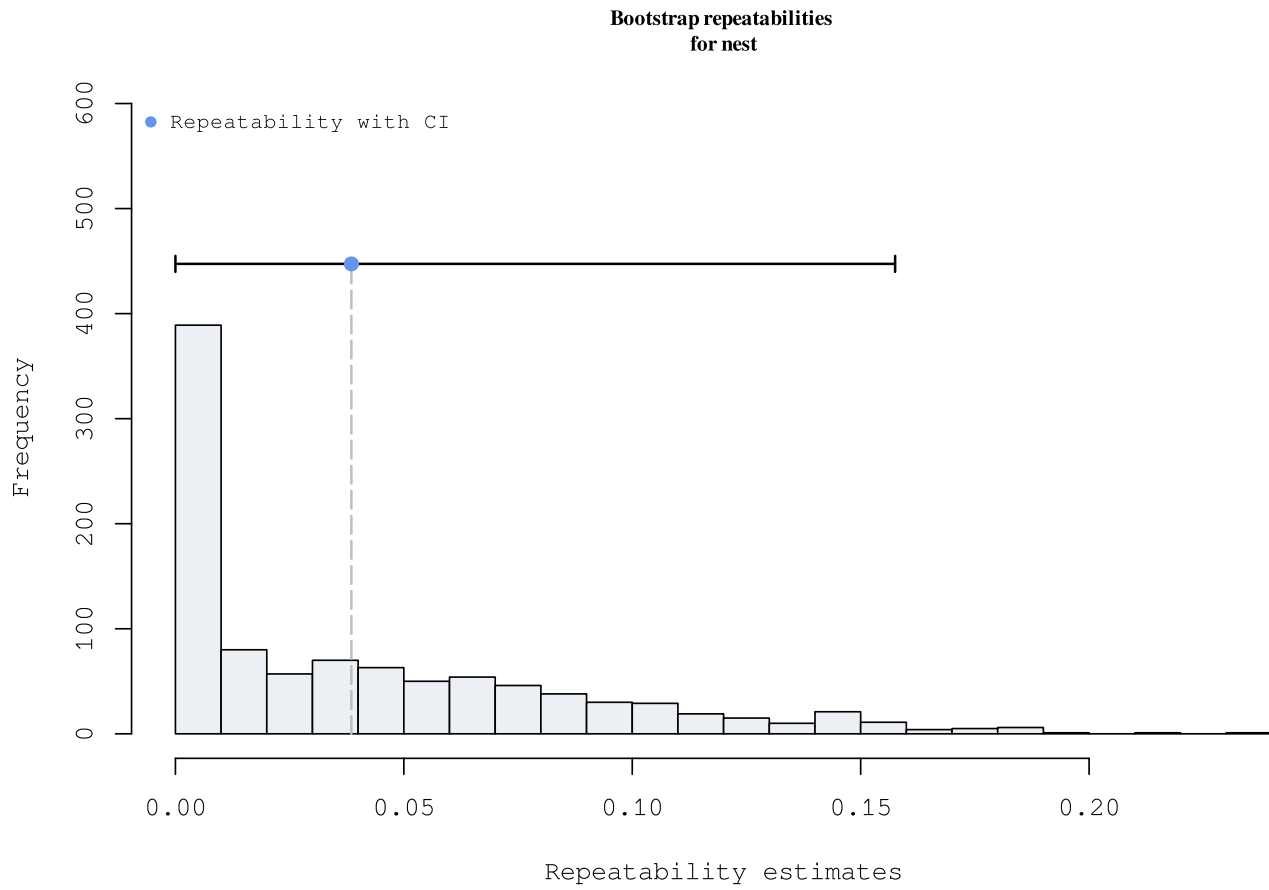
Bootstrapping and Permutation test:

	N	Mean	Median	2.5%	97.5%
boot	1000	0.0350	3.76e-11	0	0.188
permut	1000	0.0329	1.42e-12	0	0.192

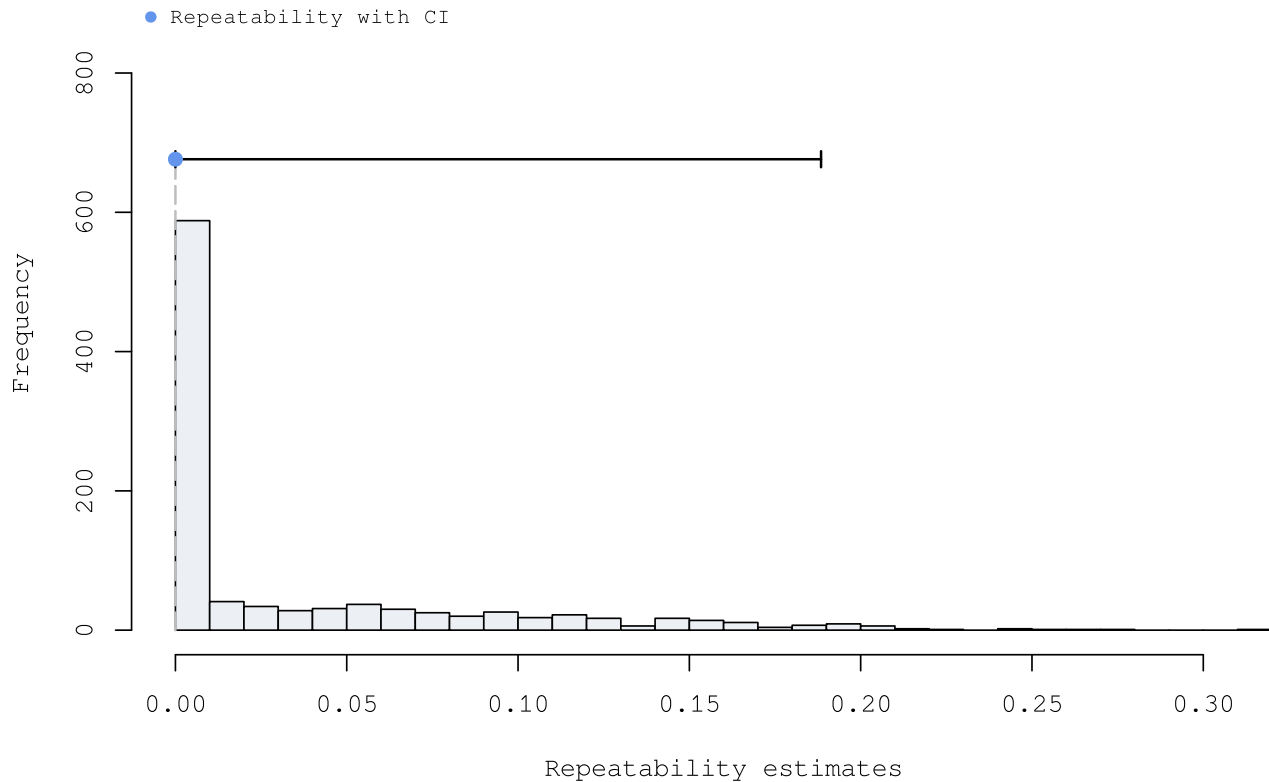
Likelihood ratio test:

```
logLik full model = 117.2883
logLik red. model = 117.2883
D = 2.27e-13, df = 1, P = 0.5
```

```
plot(rpts2, grname="nest", type="boot", cex.main=0.8, col = "#ECEFF4")  
plot(rpts2, grname="ring_number", type="boot", cex.main=0.8, col = "#ECEFF4")
```



Bootstrap repeatabilities for ring_number



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("metadata-rarefied.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,"metadata-rarefied.rds")

```

1.1. 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

```

1.2. Model Faith PD

```

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

```

1.3. Check Normality

```

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

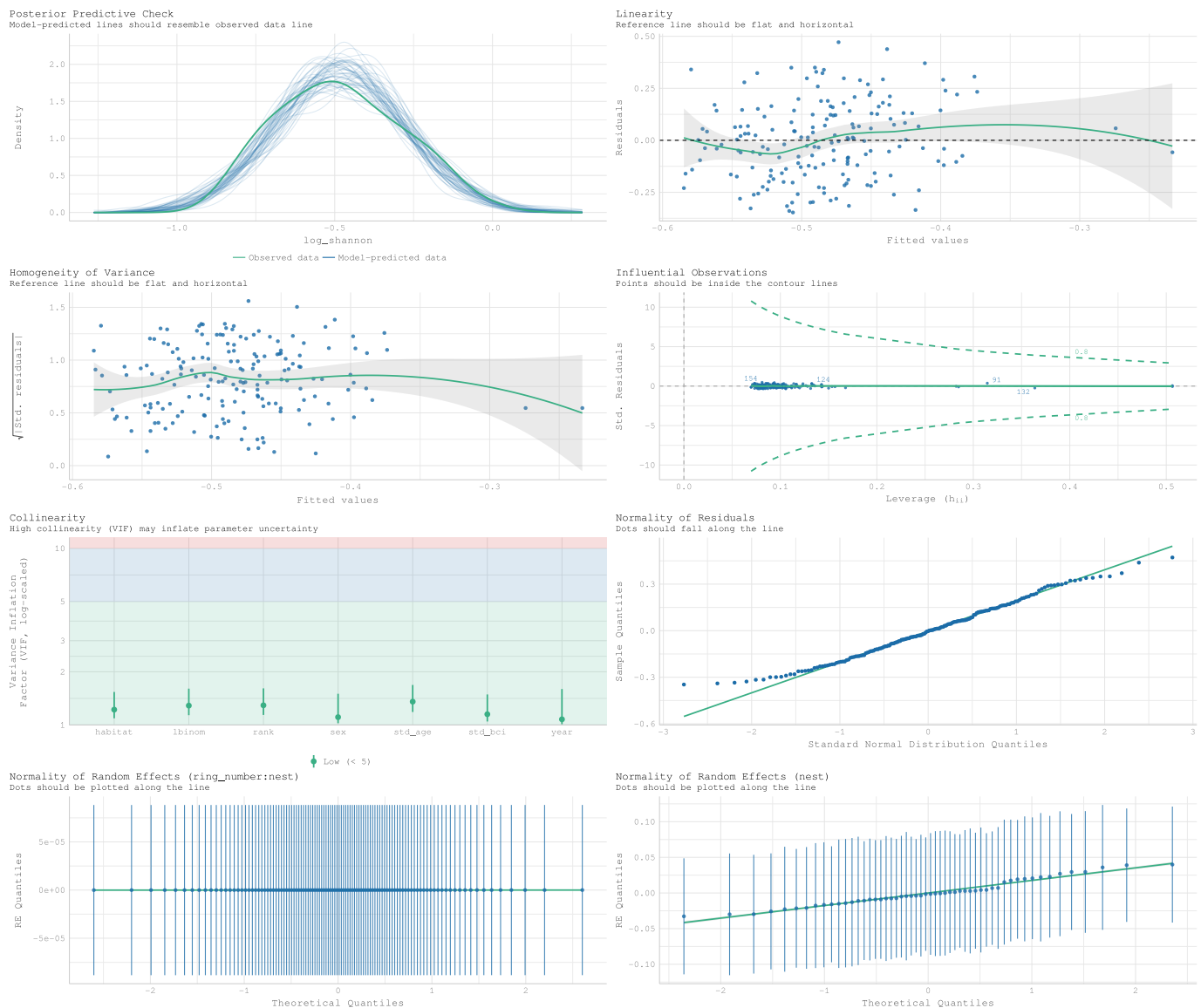
```

1.4. Model Diagnostics

```

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

```



1.5. 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
habitatouth	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	hbttst	hbtttt	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

1.6. 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
```

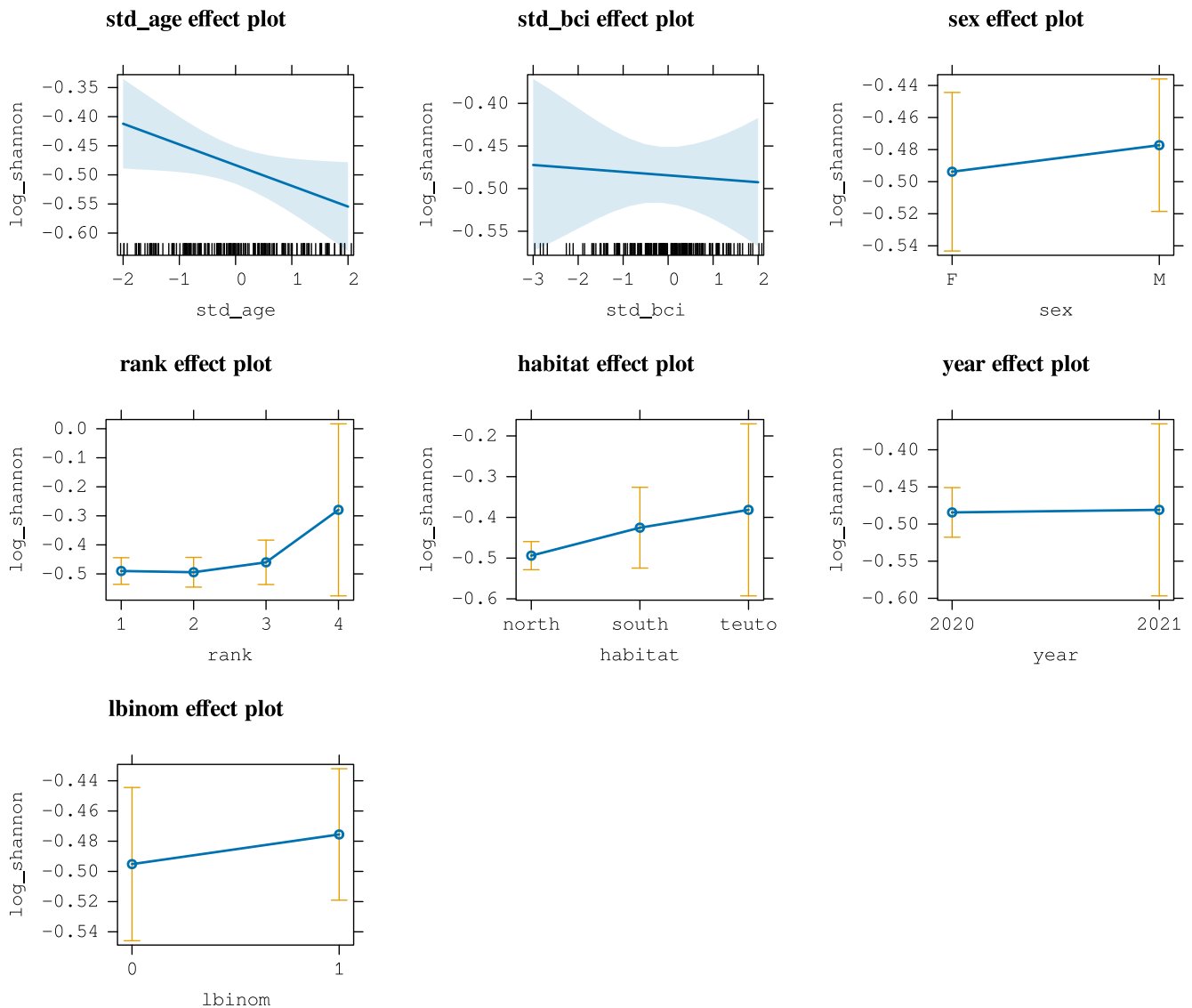
1.7. Marginal and conditional R-squared

```
> r.squaredGLMM(model_shannon)
```

	R2m	R2c
[1,]	0.05739074	0.1103858

1.8. Plot model effects

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



1.9. Repeatability Analysis

```
> rpts <- rpt(shannon_entropy ~ std_age + std_bci + rank + sex + year + habitat + (1|nest) +
(1|ring_number),
  grname = c("nest", "ring_number"), data = metadata,
  datatype = "Gaussian", adjusted = TRUE,
  nboot = 1000, npermut = 1000)

> summary(rpts)

Repeatability estimation using the lmm method

Call = rpt(formula = log_shannon ~ std_age + std_bci + rank + sex + year + habitat + (1 | nest)
+ (1 | ring_number), grname = c("nest", "ring_number"), data = metadata, datatype = "Gaussian",
nboot = 1000, npermut = 1000, adjusted = TRUE)

Data: 179 observations
```

```
nest (54 groups)
```

```
Repeatability estimation overview:
```

R	SE	2.5%	97.5%	P_permut	LRT_P
0.0701	0.0643	0	0.217	0.108	0.18

```
Bootstrapping and Permutation test:
```

	N	Mean	Median	2.5%	97.5%
boot	1000	0.0634	5.07e-02	0	0.217
permut	1000	0.0210	6.95e-12	0	0.123

```
Likelihood ratio test:
```

```
logLik full model = 16.23022
```

```
logLik red. model = 15.81233
```

```
D = 0.836, df = 1, P = 0.18
```

```
ring_number (109 groups)
```

```
Repeatability estimation overview:
```

R	SE	2.5%	97.5%	P_permut	LRT_P
0	0.0745	0	0.243	1	1

```
Bootstrapping and Permutation test:
```

	N	Mean	Median	2.5%	97.5%
boot	1000	0.0486	3.10e-11	0	0.243
permut	1000	0.0396	1.42e-12	0	0.233

```
Likelihood ratio test:
```

```
logLik full model = 16.23022
```

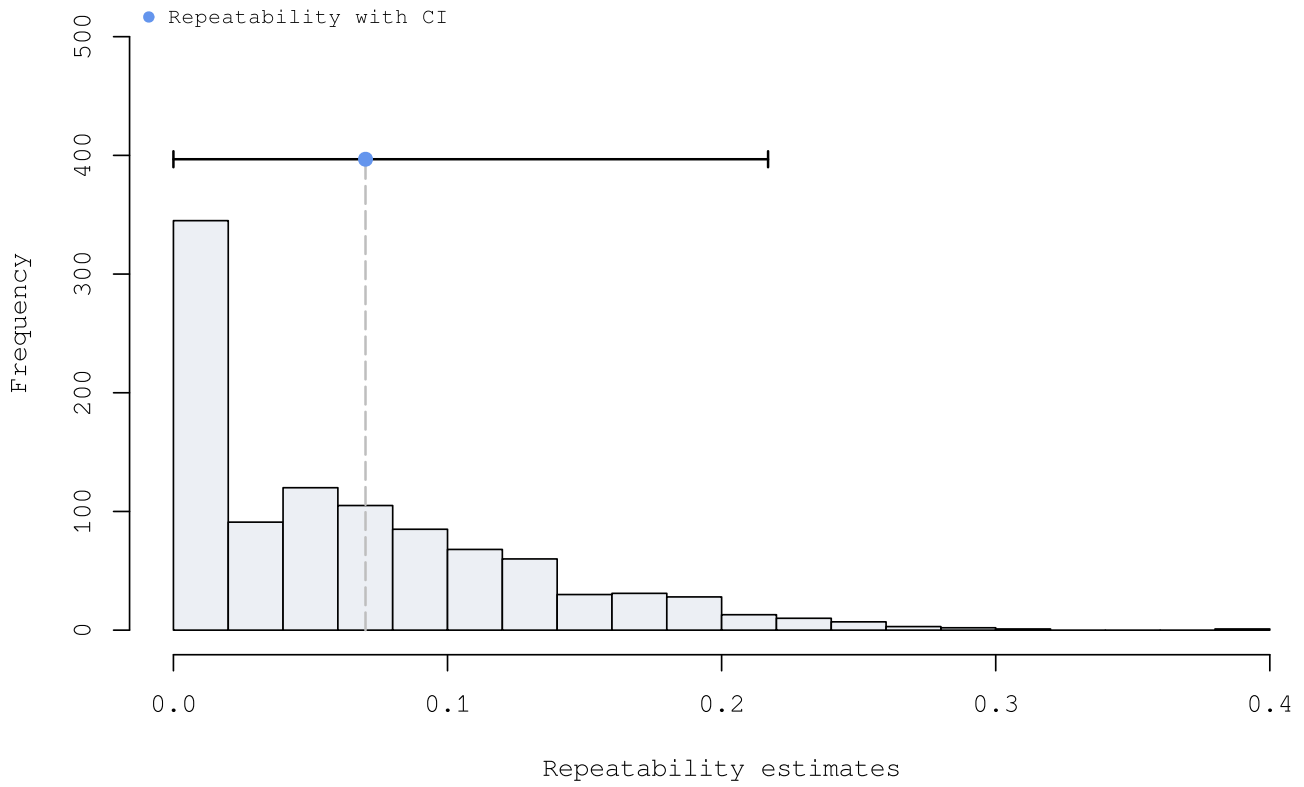
```
logLik red. model = 16.23022
```

```
D = -1.51e-12, df = 1, P = 1
```

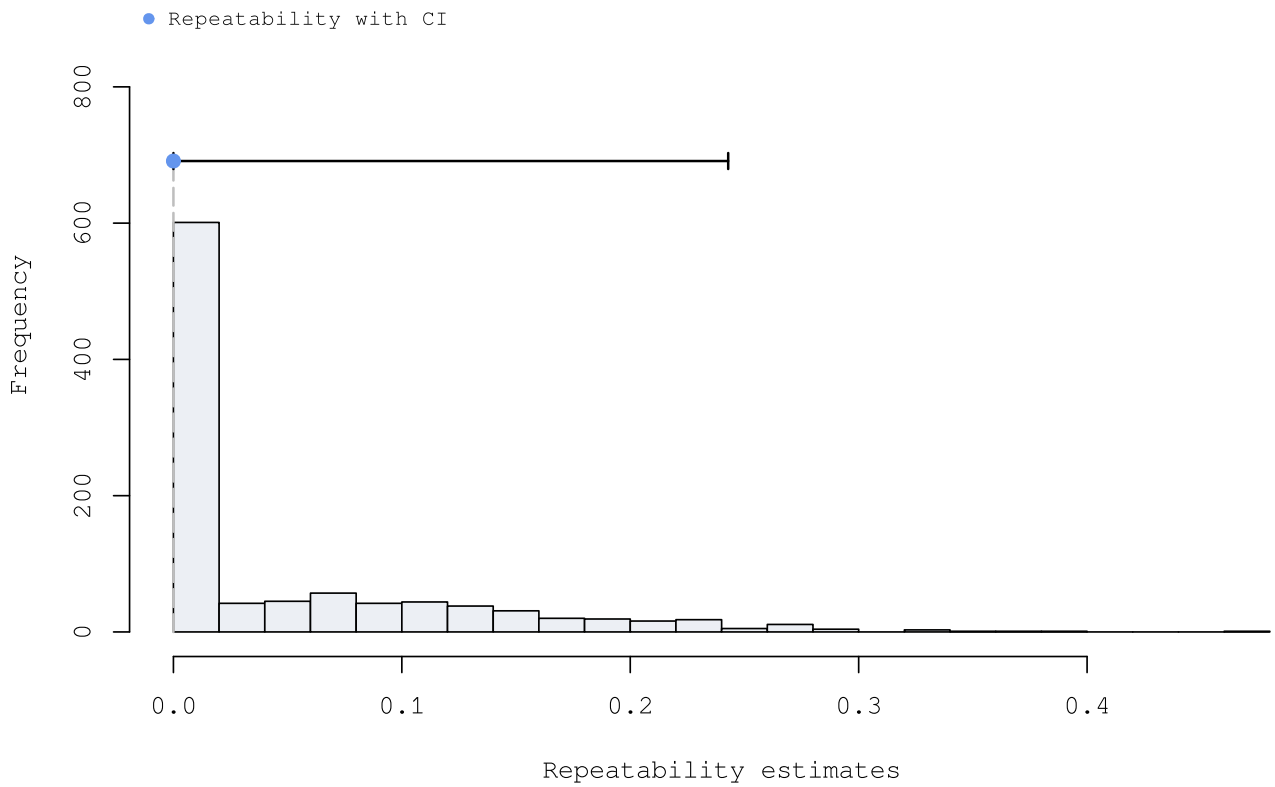
```
plot(rpts, grname="nest", type="boot", cex.main=0.8, col = "#ECEFF4")
```

```
plot(rpts, grname="ring_number", type="boot", cex.main=0.8, col = "#ECEFF4")
```

**Bootstrap repeatabilities
for nest**



**Bootstrap repeatabilities
for ring_number**



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_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

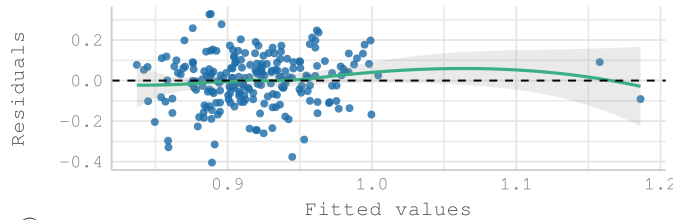
```
> check_normality(model_faith)  
OK: residuals appear as normally distributed (p = 0.661).
```

2.4. Model Diagnostics

```
check_model(model_faith)
```

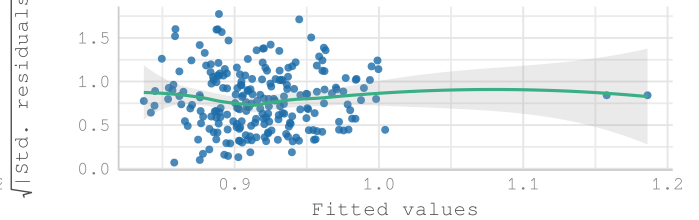
Linearity

Reference line should be flat and horizontal



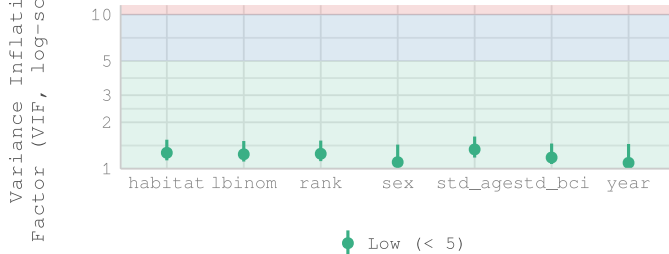
Homogeneity of Variance

Reference line should be flat and horizontal



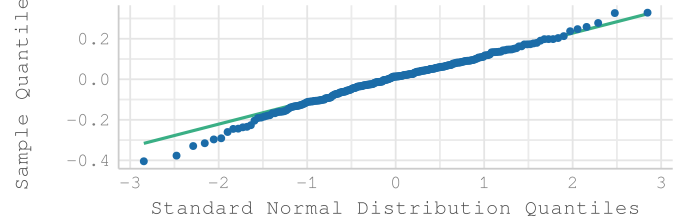
Linearity

High collinearity (VIF) may inflate parameter uncertainty



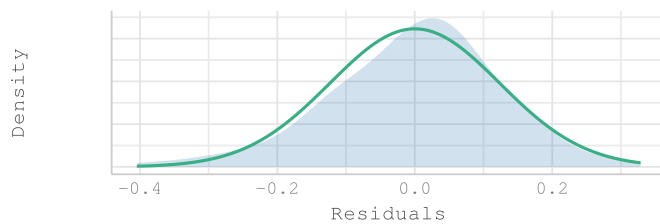
Normality of Residuals

Dots should fall along the line



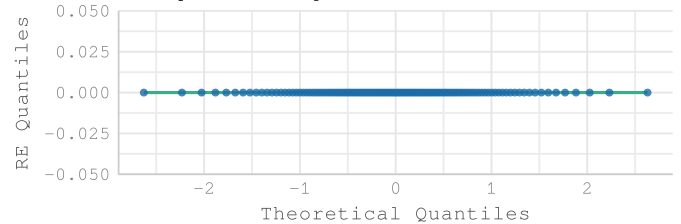
Normality of Residuals

Distribution should be close to the normal curve



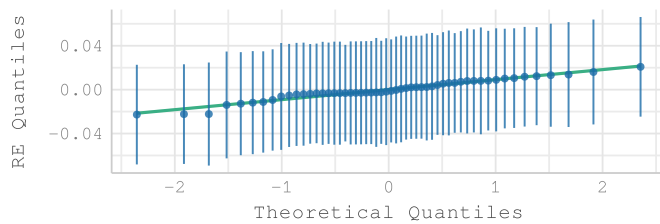
Normality of Random Effects (ring_number:nest)

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)	0.00000	0.0000
nest	(Intercept)	0.00000	0.0000
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
habitatouth	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

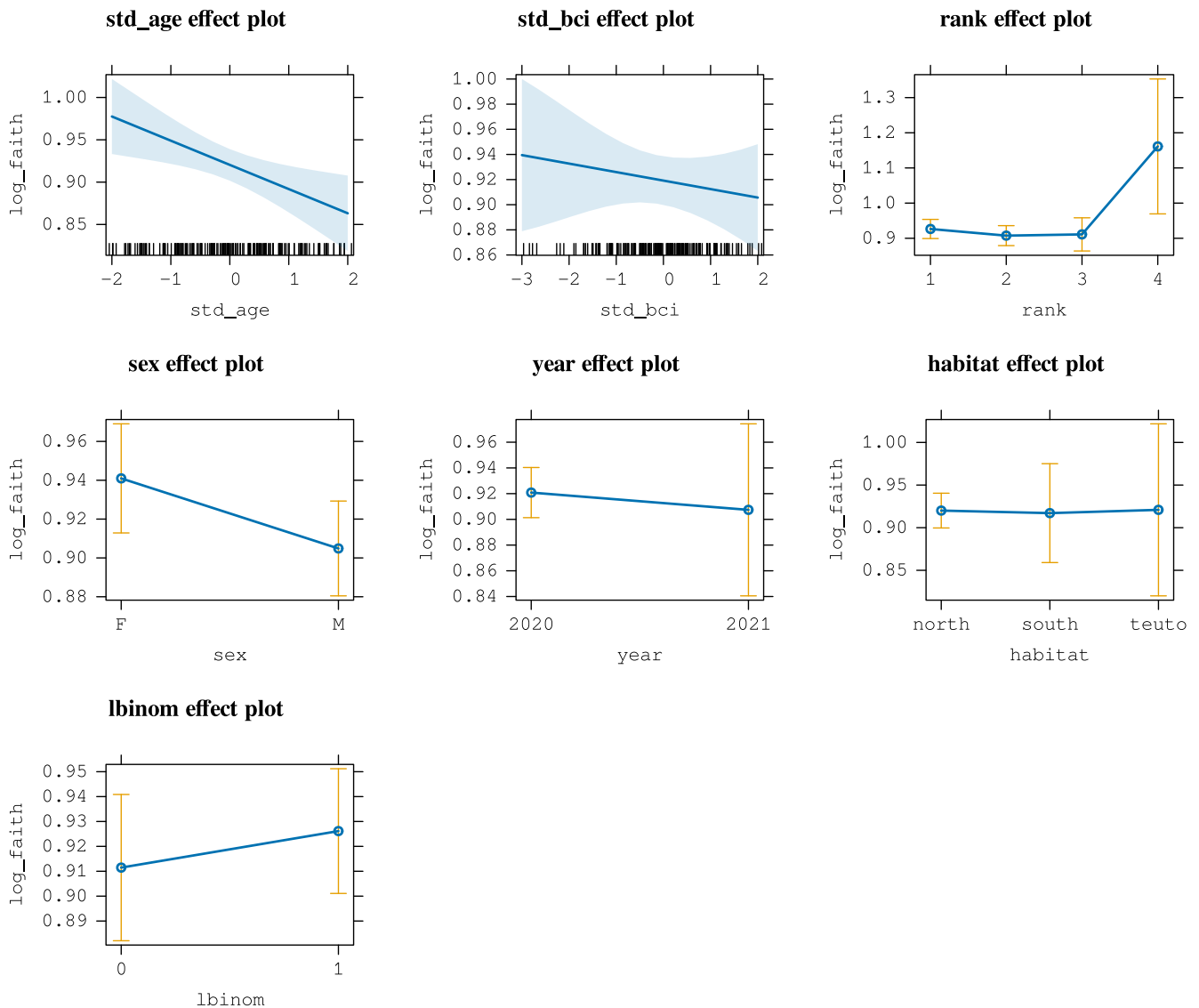
```
(Adjusted p values reported -- BH method)
```

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))
```



2.9. Repeatability Analysis

```
> rpts2 <- rpt(log_faith ~ std_age + std_bci + rank + sex + year + habitat + (1|nest) +
(1|ring_number),
  grname = c("nest", "ring_number"), data = metadata,
  datatype = "Gaussian", adjusted = TRUE,
  nboot = 1000, npermut = 1000)
```

```
> summary(rpts2)
```

Repeatability estimation using the lmm method

```
Call = rpt(formula = log_faith ~ std_age + std_bci + rank + sex + year + habitat + (1 | nest) +
(1 | ring_number), grname = c("nest", "ring_number"), data = metadata, datatype = "Gaussian",
nboot = 1000, npermut = 1000, adjusted = TRUE)
```

Data: 179 observations

nest (54 groups)

Repeatability estimation overview:

R	SE	2.5%	97.5%	P_permut	LRT_P
0	0.0366	0	0.128	1	1

Bootstrapping and Permutation test:

	N	Mean	Median	2.5%	97.5%
boot	1000	0.0204	1.22e-14	0	0.128
permut	1000	0.0214	1.12e-13	0	0.145

Likelihood ratio test:

logLik full model = 6.67855

logLik red. model = 6.67855

D = 0, df = 1, P = 1

ring_number (109 groups)

Repeatability estimation overview:

R	SE	2.5%	97.5%	P_permut	LRT_P
0	0.0653	0	0.237	1	1

Bootstrapping and Permutation test:

	N	Mean	Median	2.5%	97.5%
boot	1000	0.0376	2.40e-13	0	0.237
permut	1000	0.0321	3.66e-17	0	0.223

Likelihood ratio test:

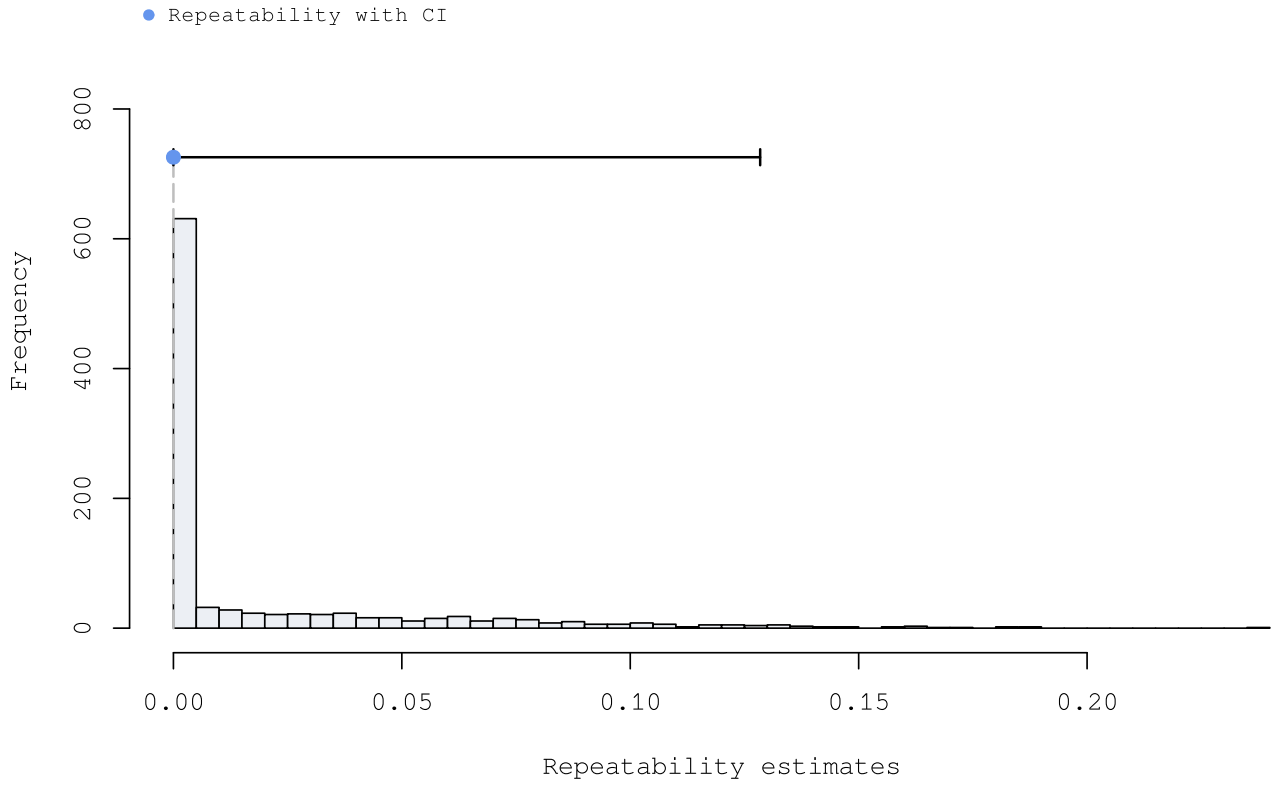
logLik full model = 6.67855

logLik red. model = 6.67855

D = 0, df = 1, P = 1

```
plot(rpts2, grname="nest", type="boot", cex.main=0.8, col = "#ECEFF4")
plot(rpts2, grname="ring_number", type="boot", cex.main=0.8, col = "#ECEFF4")
```

**Bootstrap repeatabilities
for nest**



**Bootstrap repeatabilities
for ring_number**

