OBJETIVO 2B - % DE ESPECIES MIGRATORIAS

Linear mixed model fit by REML ['lmerMod']

Formula: Prevalencia[as.factor(dados1$Especie)] ~ migrantes + (1 | Bioma) +

(1 | Localidade)

Data: dados1

REML criterion at convergence: -8.5

Scaled residuals:

Min 1Q Median 3Q Max

-1.32209 -0.81814 -0.08289 0.51242 3.03880

Random effects:

Groups Name Variance Std.Dev.

Localidade (Intercept) 1.340e-10 1.158e-05

Bioma (Intercept) 2.082e-04 1.443e-02

Residual 5.316e-02 2.306e-01

Number of obs: 261, groups: Localidade, 47; Bioma, 7

Fixed effects:

Estimate Std. Error t value

(Intercept) 0.302107 0.023591 12.806

migrantes -0.001396 0.001371 -1.018

Correlation of Fixed Effects:

(Intr)

migrantes -0.743

convergence code: 0

boundary (singular) fit: see ?isSingular

> parameters::p\_value(model)

Parameter p

1 (Intercept) 1.518430e-37

2 migrantes 3.084461e-01

% DE AVES MIGRATORIAS

> model <- lmer(Prevalencia[as.factor(dados1$Especie)]~abundance + RiquezadeHospedeiros + migrantes + n\_migrants + RiquezadeParasitos +

+ + (1|Totalsample) + (1|Temp) + (1|Prec) + (1|Bioma), dados1)

boundary (singular) fit: see ?isSingular

> summary(model)

Linear mixed model fit by REML ['lmerMod']

Formula:

Prevalencia[as.factor(dados1$Especie)] ~ abundance + RiquezadeHospedeiros +

migrantes + n\_migrants + RiquezadeParasitos + +(1 | Totalsample) +

(1 | Temp) + (1 | Prec) + (1 | Bioma)

Data: dados1

REML criterion at convergence: 38.8

Scaled residuals:

Min 1Q Median 3Q Max

-1.4205 -0.6965 -0.1904 0.5387 2.9474

Random effects:

Groups Name Variance Std.Dev.

Prec (Intercept) 0.00000 0.0000

Totalsample (Intercept) 0.00000 0.0000

Temp (Intercept) 0.00000 0.0000

Bioma (Intercept) 0.00000 0.0000

Residual 0.05613 0.2369

Number of obs: 224, groups: Prec, 44; Totalsample, 38; Temp, 35; Bioma, 7

Fixed effects:

Estimate Std. Error t value

(Intercept) 0.3352415 0.0514530 6.515

abundance -1.3637210 0.6790074 -2.008

RiquezadeHospedeiros 0.0003779 0.0009494 0.398

migrantes 0.0094743 0.0076503 1.238

n\_migrants 0.0004363 0.0003979 1.096

RiquezadeParasitos -0.0012881 0.0015183 -0.848

Correlation of Fixed Effects:

(Intr) abndnc RqzdHs mgrnts n\_mgrn

abundance -0.147

RiqzdHspdrs -0.612 0.028

migrantes -0.011 -0.946 -0.040

n\_migrants 0.186 0.032 0.159 -0.281

RiquzdPrsts -0.160 0.083 -0.595 0.048 -0.454

convergence code: 0

boundary (singular) fit: see ?isSingular

> (aov <- anova(model))

Analysis of Variance Table

Df Sum Sq Mean Sq F value

abundance 1 0.283921 0.283921 5.0587

RiquezadeHospedeiros 1 0.000463 0.000463 0.0083

migrantes 1 0.140389 0.140389 2.5013

n\_migrants 1 0.035779 0.035779 0.6375

RiquezadeParasitos 1 0.040396 0.040396 0.7197

> parameters::p\_value(model)

Parameter p

1 (Intercept) 7.245024e-11

2 abundance 4.460042e-02

3 RiquezadeHospedeiros 6.906092e-01

4 migrantes 2.155566e-01

5 n\_migrants 2.728912e-01

6 RiquezadeParasitos 3.962271e-01

> 4.460042e-02

[1] 0.04460042

PLASMODIUM

> model3 <- lmer(PrevalenceP[as.factor(dados1$Especie)]~abundance + RiquezadeHospedeiros + migrantes + n\_migrants + RiquezaP +

+ + (1|Totalsample) + (1|Temp) + (1|Prec) + (1|Bioma), dados1)

boundary (singular) fit: see ?isSingular

> summary(model3)

Linear mixed model fit by REML ['lmerMod']

Formula:

PrevalenceP[as.factor(dados1$Especie)] ~ abundance + RiquezadeHospedeiros +

migrantes + n\_migrants + RiquezaP + +(1 | Totalsample) +

(1 | Temp) + (1 | Prec) + (1 | Bioma)

Data: dados1

REML criterion at convergence: -444.5

Scaled residuals:

Min 1Q Median 3Q Max

-1.3169 -0.5191 -0.1324 0.1656 3.5519

Random effects:

Groups Name Variance Std.Dev.

Prec (Intercept) 1.084e-12 1.041e-06

Totalsample (Intercept) 2.611e-04 1.616e-02

Temp (Intercept) 4.213e-05 6.491e-03

Bioma (Intercept) 0.000e+00 0.000e+00

Residual 5.904e-03 7.684e-02

Number of obs: 224, groups: Prec, 44; Totalsample, 38; Temp, 35; Bioma, 7

Fixed effects:

Estimate Std. Error t value

(Intercept) 5.850e-02 1.787e-02 3.274

abundance -4.045e-01 2.304e-01 -1.755

RiquezadeHospedeiros 1.726e-04 3.047e-04 0.566

migrantes 6.212e-03 2.582e-03 2.405

n\_migrants -1.106e-05 1.223e-04 -0.090

RiquezaP -3.390e-04 6.299e-04 -0.538

Correlation of Fixed Effects:

(Intr) abndnc RqzdHs mgrnts n\_mgrn

abundance -0.165

RiqzdHspdrs -0.594 -0.022

migrantes 0.015 -0.951 0.042

n\_migrants 0.109 0.089 -0.121 -0.298

RiquezaP -0.201 0.175 -0.543 -0.089 -0.026

convergence code: 0

boundary (singular) fit: see ?isSingular

> (aov <- anova(model3))

Analysis of Variance Table

Df Sum Sq Mean Sq F value

abundance 1 0.058561 0.058561 9.9182

RiquezadeHospedeiros 1 0.001259 0.001259 0.2133

migrantes 1 0.035438 0.035438 6.0020

n\_migrants 1 0.000064 0.000064 0.0109

RiquezaP 1 0.001711 0.001711 0.2897

> parameters::p\_value(model3)

Parameter p

1 (Intercept) 0.001060068

2 abundance 0.079190335

3 RiquezadeHospedeiros 0.571099389

4 migrantes 0.016152797

5 n\_migrants 0.927968792

6 RiquezaP 0.590385428

HAEMOPROTEUS

> model4 <- lmer(PrevalenceH[as.factor(dados1$Especie)]~abundance + RiquezadeHospedeiros + migrantes + n\_migrants + RiquezaH +

+ + (1|Totalsample) + (1|Temp) + (1|Prec) + (1|Bioma), dados1)

boundary (singular) fit: see ?isSingular

> summary(model4)

Linear mixed model fit by REML ['lmerMod']

Formula:

PrevalenceH[as.factor(dados1$Especie)] ~ abundance + RiquezadeHospedeiros +

migrantes + n\_migrants + RiquezaH + +(1 | Totalsample) +

(1 | Temp) + (1 | Prec) + (1 | Bioma)

Data: dados1

REML criterion at convergence: -740.3

Scaled residuals:

Min 1Q Median 3Q Max

-2.16881 -0.52810 -0.02676 0.81232 2.68461

Random effects:

Groups Name Variance Std.Dev.

Prec (Intercept) 0.000000 0.00000

Totalsample (Intercept) 0.000000 0.00000

Temp (Intercept) 0.000000 0.00000

Bioma (Intercept) 0.000000 0.00000

Residual 0.001589 0.03987

Number of obs: 224, groups: Prec, 44; Totalsample, 38; Temp, 35; Bioma, 7

Fixed effects:

Estimate Std. Error t value

(Intercept) 8.194e-02 8.606e-03 9.521

abundance -1.099e-01 1.143e-01 -0.961

RiquezadeHospedeiros -1.084e-04 1.596e-04 -0.679

migrantes 6.245e-05 1.286e-03 0.049

n\_migrants 9.437e-06 7.734e-05 0.122

RiquezaH 1.145e-03 7.011e-04 1.632

Correlation of Fixed Effects:

(Intr) abndnc RqzdHs mgrnts n\_mgrn

abundance -0.124

RiqzdHspdrs -0.781 0.024

migrantes -0.006 -0.952 -0.001

n\_migrants 0.025 0.004 0.282 -0.213

RiquezaH 0.116 0.089 -0.594 -0.018 -0.636

convergence code: 0

boundary (singular) fit: see ?isSingular

> (aov <- anova(model4))

Analysis of Variance Table

Df Sum Sq Mean Sq F value

abundance 1 0.0194438 0.0194438 12.2348

RiquezadeHospedeiros 1 0.0006451 0.0006451 0.4059

migrantes 1 0.0004630 0.0004630 0.2913

n\_migrants 1 0.0035951 0.0035951 2.2622

RiquezaH 1 0.0042352 0.0042352 2.6649

> parameters::p\_value(model4)

Parameter p

1 (Intercept) 1.708860e-21

2 abundance 3.365182e-01

3 RiquezadeHospedeiros 4.972263e-01

4 migrantes 9.612724e-01

5 n\_migrants 9.028750e-01

6 RiquezaH 1.025821e-01

> 3.365182e-01

[1] 0.3365182