1. **No manipulation in the original data**
2. **Eusociality as a function of haplodiploidy**

phyloglm(formula = Eusociality ~ Haplodiploidy, data = data\_hap1,

phy = tree\_hap1, method = c("logistic\_MPLE"), boot = 1000)

AIC logLik Pen.logLik

88.30 -41.15 -40.18

Method: logistic\_MPLE

Mean tip height: 478.0884

Parameter estimate(s):

**alpha: 4.017898e-05**

bootstrap mean: 0.0005916906 (on log scale, then back transformed)

so possible upward bias.

bootstrap 95% CI: (3.834711e-05,0.1064465)

**Coefficients:**

**Estimate StdErr z.value lowerbootCI upperbootCI p.value**

**(Intercept) -0.717895 2.063069 -0.347974 -6.460932 -0.2148 0.7279**

**Haplodiploidy 0.264260 0.327687 0.806440 0.083845 4.3585 0.4200**

Note: Wald-type p-values for coefficients, conditional on alpha=4.017898e-05

Parametric bootstrap results based on 1000 fitted replicates

1. **Haplodiploidy as a function of eusociality**

phyloglm(formula = Haplodiploidy ~ Eusociality, data = data\_hap1,

phy = tree\_hap1, method = c("logistic\_MPLE"), boot = 1000)

AIC logLik Pen.logLik

124.02 -59.01 -58.23

Method: logistic\_MPLE

Mean tip height: 478.0884

Parameter estimate(s):

**alpha: 0.0001424529**

bootstrap mean: 0.0002349944 (on log scale, then back transformed)

so possible upward bias.

bootstrap 95% CI: (4.615564e-05,0.0157752)

**Coefficients:**

**Estimate StdErr z.value lowerbootCI upperbootCI p.value**

**(Intercept) 0.159431 1.881742 0.084725 -4.352963 0.4719 0.9325**

**Eusociality 0.124201 0.261549 0.474869 -0.086867 2.2004 0.6349**

Note: Wald-type p-values for coefficients, conditional on alpha=0.0001424529

Parametric bootstrap results based on 1000 fitted replicates

1. **Removing eusociality presence for aphids**

**(MPLE model)**

1. Eusociality as a function of haplodiploidy

phyloglm(formula = Eusociality ~ Haplodiploidy, data = data\_hap1\_pr,

phy = tree\_hap1\_pr, method = c("logistic\_MPLE"), boot = 1000)

AIC logLik Pen.logLik

75.06 -34.53 -33.99

Method: logistic\_MPLE

Mean tip height: 478.0884

Parameter estimate(s):

**alpha: 3.933114e-05**

bootstrap mean: 0.001048337 (on log scale, then back transformed)

so possible upward bias.

bootstrap 95% CI: (3.837474e-05,0.1082759)

**Coefficients:**

**Estimate StdErr z.value lowerbootCI upperbootCI p.value**

**(Intercept) -1.62811 2.60486 -0.62503 -7.60263 -0.3762 0.5320**

**Haplodiploidy 0.32380 0.57244 0.56566 0.14173 4.8268 0.5716**

**Note: Wald-type p-values for coefficients, conditional on alpha=3.933114e-05**

**Parametric bootstrap results based on 1000 fitted replicates**

1. Haplodiploidy as a function of eusociality

**(MPLE model)**

phyloglm(formula = Haplodiploidy ~ Eusociality, data = data\_hap1\_pr,

phy = tree\_hap1\_pr, method = c("logistic\_MPLE"), boot = 1000)

AIC logLik Pen.logLik

123.73 -58.87 -58.22

Method: logistic\_MPLE

Mean tip height: 478.0884

Parameter estimate(s):

**alpha: 0.0001338765**

bootstrap mean: 0.0002309817 (on log scale, then back transformed)

so possible upward bias.

bootstrap 95% CI: (4.50387e-05,0.01797132)

**Coefficients:**

**Estimate StdErr z.value lowerbootCI upperbootCI p.value**

**(Intercept) 0.22188 1.89395 0.11715 -4.48402 0.6000 0.9067**

**Eusociality 0.17101 0.30535 0.56006 -0.08869 2.4707 0.5754**

**Note: Wald-type p-values for coefficients, conditional on alpha=0.0001338765**

**Parametric bootstrap results based on 1000 fitted replicates**

1. **Removing eusociality presence for aphids and termites at the same time**
2. Eusociality as a function of a haplodiploidy

**(MPLE model)**

**Warning message (although not an error message)**

Graphical user interface, text, application, email

Description automatically generated

Call:

phyloglm(formula = Eusociality ~ Haplodiploidy, data = data\_hap2\_pr,

phy = tree\_hap2\_pr, method = c("logistic\_MPLE"), boot = 1000)

AIC logLik Pen.logLik

56.56 -25.28 -24.66

Method: logistic\_MPLE

Mean tip height: 478.0884

Parameter estimate(s):

**alpha: 0.09326454**

bootstrap mean: 0.002352795 (on log scale, then back transformed)

so possible downward bias.

bootstrap 95% CI: (3.898639e-05,0.1110988)

**Coefficients:**

**Estimate StdErr z.value lowerbootCI upperbootCI p.value**

**(Intercept) -7.33502 1.40111 -5.23513 -7.41192 -4.7489 1.649e-07 \*\*\***

**Haplodiploidy 4.90392 1.45238 3.37646 -0.41446 5.4071 0.0007342 \*\*\***

**---**

**Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1**

**Note: Wald-type p-values for coefficients, conditional on alpha=0.09326454**

**Parametric bootstrap results based on 1000 fitted replicates**

1. Haplodiploidy as a function of eusociality

**(MPLE model)**

Graphical user interface, text, application, email

Description automatically generated**Warning message (although not an error message)**

phyloglm(formula = Haplodiploidy ~ Eusociality, data = data\_hap2\_pr,

phy = tree\_hap2\_pr, method = c("logistic\_MPLE"), boot = 1000)

AIC logLik Pen.logLik

118.85 -56.42 -56.88

Method: logistic\_MPLE

Mean tip height: 478.0884

Parameter estimate(s):

**alpha: 0.0001471388**

bootstrap mean: 0.0002207654 (on log scale, then back transformed)

so possible upward bias.

bootstrap 95% CI: (4.816031e-05,0.001159775)

Coefficients:

**Estimate StdErr z.value lowerbootCI upperbootCI p.value**

**(Intercept) 0.0483880 1.8655727 0.0259373 -2.3903294 0.7118 0.9793**

**Eusociality 1.4079135 1.0827130 1.3003571 -0.0016357 3.6854 0.1935**

**Note: Wald-type p-values for coefficients, conditional on alpha=0.0001471388**

**Parametric bootstrap results based on 1000 fitted replicates**

1. **Removing haplodiploidy presence for Coleoptera, Diptera, Collembola, Hemiptera, and Phthiraptera.**
2. Eusociality as a function of haplodiploidy

**(MPLE model)**

phyloglm(formula = Eusociality ~ Haplodiploidy, data = data\_hap3\_pr,

phy = tree\_hap3\_pr, method = c("logistic\_MPLE"), boot = 1000)

AIC logLik Pen.logLik

86.82 -40.41 -39.72

Method: logistic\_MPLE

Mean tip height: 478.0884

Parameter estimate(s):

**alpha: 4.192998e-05**

bootstrap mean: 0.0006296398 (on log scale, then back transformed)

so possible upward bias.

bootstrap 95% CI: (3.836871e-05,0.104387)

**Coefficients:**

**Estimate StdErr z.value lowerbootCI upperbootCI p.value**

**(Intercept) -0.99523 2.17461 -0.45766 -6.59962 -0.2760 0.6472**

**Haplodiploidy 0.33494 0.45623 0.73415 0.14695 4.4561 0.4629**

**Note: Wald-type p-values for coefficients, conditional on alpha=4.192998e-05**

**Parametric bootstrap results based on 1000 fitted replicates**

1. Haplodiploidy as a function of eusociality

**(MPLE model)**

phyloglm(formula = Haplodiploidy ~ Eusociality, data = data\_hap3\_pr,

phy = tree\_hap3\_pr, method = c("logistic\_MPLE"), boot = 1000)

AIC logLik Pen.logLik

53.64 -23.82 -22.88

Method: logistic\_MPLE

Mean tip height: 478.0884

Parameter estimate(s):

**alpha: 4.281425e-05**

bootstrap mean: 9.639242e-05 (on log scale, then back transformed)

so possible upward bias.

bootstrap 95% CI: (3.846866e-05,0.002873909)

**Coefficients:**

**Estimate StdErr z.value lowerbootCI upperbootCI p.value**

**(Intercept) 0.0130500 1.9604442 0.0066567 -4.1596634 1.4191 0.9947**

**Eusociality 0.1203709 0.2268773 0.5305549 -0.0107104 2.1622 0.5957**

**Note: Wald-type p-values for coefficients, conditional on alpha=4.281425e-05**

**Parametric bootstrap results based on 1000 fitted replicates**