**Eusociality as a function of haplodiploidy**

**MPLE regression**

Graphical user interface, text, application, email

Description automatically generated

**Method: logistic\_MPLE**

**Mean tip height: 478.0884**

**Parameter estimate(s):**

**alpha: 3.869352e-05**

bootstrap mean: 7.867767e-05 (on log scale, then back transformed)

so possible upward bias.

bootstrap 95% CI: (3.83349e-05,0.01300529)

**Coefficients:**

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

**(Intercept) -0.130857 1.766512 -0.074077 -5.802949 -0.1706 0.9409494**

**Haplodiploidy 4.621208 1.233112 3.747597 1.157240 9.4897 0.0001785**

(Intercept)

Haplodiploidy \*\*\*

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

Note: Wald-type p-values for coefficients, conditional on alpha=3.869352e-05

Parametric bootstrap results based on 1000 fitted replicates

**IG10 regression**

**(Non-convergence problem)**

Call:

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

phy = tree\_hap1\_pr, method = c("logistic\_IG10"), boot = 1000)

AIC logLik Pen.logLik

153.48 -73.74 -73.71

**Method: logistic\_IG10**

**Mean tip height: 478.0884**

**Parameter estimate(s):**

**alpha: 0.0003683895**

bootstrap mean: 0.0002445278 (on log scale, then back transformed)

so possible downward bias.

bootstrap 95% CI: (4.259296e-05,0.001970777)

**Coefficients:**

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

**(Intercept) -2.04640 2.67008 -0.76642 -2.04640 -2.0464 0.4434**

**Haplodiploidy 0.00000 0.36494 0.00000 0.00000 0.0000 1.0000**

Note: Wald-type p-values for coefficients, conditional on alpha=0.0003683895

Parametric bootstrap results based on 1000 fitted replicates