**Argrett Lab 5**

For this lab, we will continue working with the Cholla demography data, focusing on fitting a function for reproduction. Please turn in the code and output for the following (26 pts total):

1. Make a new variable for reproduction from the “Goodbuds\_t” variable, by assigning all plants that had > 0 buds a “1” for reproduction, and “0” if they did not produce any buds. There are many ways to do this. If you are having trouble with a good search term, try searching how to turn abundance/counts into presence-absence. Turn in just the code for this. (2 pts)

cholla$Reproduced <- ifelse(cholla$Goodbuds\_t>0, 1, 0)

1. Chart, scatter chart

   Description automatically generatedPreliminary visualizations for reproduction as a function of size. Please produce a plot that looks similar to the preliminary visualization that we did for survival. (4pts)

1. State the reproduction model fit using glm(). Turn in just the code for this (2pts)

reprod\_model <- glm(Reproduced ~ logvol\_t, family = "binomial", data=cholla)

1. Check model assumptions by making a qqplot with residuals from qresid(), making a residual~fitted plot to check for dispersion patterns, and calculate ss:df ratio to check for overdispersion (6 pts). Give your best judgement/interpretation of the output. Are model assumptions upheld? (2pts)

Chart, scatter chart

Description automatically generatedChart, line chart

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My calculation of ss:df ratio returns a value of 2.663986 which being higher than a value of 1 implies overdispersion meaning that we might not have the correct model for our underlying data. While this is of concern the assumptions of the model are still upheld due to the normal distribution of the residuals in the qqplot. The fitted residuals also look evenly distributed below and above qres = 0 which provides further evidence of our model assumptions being adequate.

1. Interpret the output of the reproduction glm model. How would you report these results? (2 pts for the glm output, 4 pts for results sentences)

Call:

glm(formula = Reproduced ~ logvol\_t, family = "binomial", data = cholla)

Deviance Residuals:

Min 1Q Median 3Q Max

-2.7367 -0.3561 -0.0543 -0.0001 4.3328

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -17.21378 0.52898 -32.54 <2e-16 \*\*\*

logvol\_t 1.53850 0.04783 32.16 <2e-16 \*\*\*

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 6776.9 on 6089 degrees of freedom

Residual deviance: 3317.8 on 6088 degrees of freedom

(700 observations deleted due to missingness)

AIC: 3321.8

Number of Fisher Scoring iterations: 7

Cholla size in year one was a decent indicator of reproductive ability (psuedo-R2 = 0.503). Fitted intercept was -17.21 (z = -32.54, df = 6088, P <2e-16) slope was 1.54 (z = 32.16, df = 6088, P < 2e-16), indicating that probability of reproduction increased with size.

1. Plot the fitted model on top of the observed data (2 pts).

Chart, line chart

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