# Chance’s Second Thesis Chapter: Understand Thermal Niche from Consumption TPCs

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**HOW TO READ THIS DOCUMENT:** This document contains the stats and modeling for my second chapter of my thesis. The document is split into 7 different sections.

* Study introduction – contains questions, hypothesis, predictions, experimental design, and methods
* Data processing (inclusive vs censoring model) – explains how I cleaned up the data for the models.
* Basic information on dataset
* Binary Model: alive vs dead
* Acclimation modeling
* The big question: Are there differences in consumption rate across temperature and species. This section is split into two sections
  + Period checking – testing for differences across time blocks
  + Temperature and species – modeling the overall model
* Extras!

**Study Introduction**

**Question:** Is there thermal niche overlap or complementary in consumption among the predatory crabs of the Gulf of Maine?

**Hypothesis:** There is thermal niche complementary between the crab predators.

**Null Hypothesis:** There is thermal niche overlap between the crab predators.

**Predictions:**

* Prediction 1: The Asian shore crab will have the highest consumption TPC/thermal niche compared to green crabs and cancer crabs. Followed by green crabs having the second highest TPC/thermal niche. Meanwhile, cancer crabs (*Cancer borealis* preferred, but *Cancer irroratus* backup - more on this later)
* Prediction 2:There is no difference in consumption TPC between green crabs, Asian shore crabs, and cancer crabs.
* Prediction 3: There is some overlap between 2 of the species, but not the last one.

**Experimental Design:**

2 Systems (2 possible temperatures at a time), 5 temperature regimes (minimum to map out a TPC), 3 species, 6 repetitions. We can only fit 18 individuals in each system.

6 reps \* 3 species \* 5 temperature regimes \* 2 temporal blocks = 180 crabs

**Methods**

Crabs were collected and brought into GMS via SCUBA, intertidally, or trapping. Only males with 2 or less missing legs were used in the study. Upon entry into the lab, crabs were weight and carapace length was measured. Crabs were placed into 5 gallon buckets in a wet table with a recirculating seawater system. Each were supplied with a water line and air line. There were two wet tables for one system which was set to one temperature treatment. The temperature treatments were 18, 20, 22, 24, and 26 degrees Celcius.

Crabs were fed 3 times a week with clam and squid in an alternating pattern. Crabs were acclimated for the trial temperature for two weeks and fed an additional 3 times for the feeding trial.

## 

## **Data Processing**

We need to clean up the data first to use it. What I did…

NOTE: “feeding points” refer to a measurement of feeding. Therefore we have multiple feeding points from a single individual crab.

* Removed feeding points that used mussels and mackerel. We fed two days total of mussels and mackerel to find out that it was too difficult to measure accurately. Afterwards, we switched to Clam and Squid in an alternating pattern
* I then removed those who molted (removed as in removed all feeding points that individual contributed to the dataset) as molting has been shown in the literature to affect feeding rate.
* I removed the first week and first period of feeding from Trial 18 and 22 since they were fed two days in a row (accidentally + understanding methods). They still had 3 weeks of feeding (2 weeks of acclimation similar to the other trials).
* I removed feeding points for those who ate everything that we fed them. This is because it’s possible they could have eaten more and the point becomes inaccurate.
* Very rarely (around 4-5 times total), food would be found floating in the bucket after waiting the feeding period. I have removed these feeding points as well because the crab couldn’t get to the food and eat for the feeding period and therefore the point cannot be trusted
* The rest of the code is marking individuals if they’ve eaten or not, still eaten, making extra variables so that further analyses are easier.

We have some decisions to make, but we’ll boil it down to the all-inclusive model vs the censoring model

Inclusive model:

-Add in all those who died as zeros and even beyond after they died they remain as 0’s.

-Also keep in replacement data.

-Keep crabs who died as is in the data set

Censoring model:

-Remove feeding points from all those who died and those who were replacement.

-Turn all the feeding points of those who did not eat to 0

-Remove dead individual

Inclusive model:

-Includes all those who died, data points after they’ve died becomes 0

-Induces those that were replaced as well

-We had an extra cancer crab replacement at the time when CI44 died, so we replaced the crab before the trial started, hence removal of the extra individuals. I renamed all the replacements to have the original replaced crab ID and “R” to note that it was a replacement therefore, CI44 R is really just CI44. Which I changed below.

inclusive <- all  
  
inclusive$proportion.eaten <- inclusive$amount.eaten / inclusive$WW  
inclusive <- subset(inclusive, !is.na(inclusive$proportion.eaten))  
  
inclusive <- subset(inclusive, inclusive$ID != "CI44")  
inclusive$ID <- ifelse(inclusive$ID == "CI44 R", "CI44", inclusive$ID)

Censor model:

-Removes those who died completely and those who were used to be replaced.

-Sets those who didn’t eat to 0 (for feeding points)

censor <- all  
  
censor$amount.eaten <- ifelse(grepl("DE", censor$Notes.x, fixed = TRUE), 0, censor$amount.eaten)  
censor$amount.eaten <- ifelse(censor$amount.eaten < 0, 0, censor$amount.eaten)  
  
censor <- censor[is.na(censor$Date.x) | !(censor$ID %in% deathMeta$ID),]  
  
  
censor <- censor %>% filter(!grepl("DI", Notes.x))  
censor <- censor %>% filter(!grepl("ADDI", Notes.x))  
censor <- censor %>% filter(!grepl("RE", Notes.x))  
censor <- censor %>% filter(!grepl("molted", Notes.x))  
  
censor$proportion.eaten <- censor$amount.eaten / censor$WW  
censor <- subset(censor, !is.na(censor$proportion.eaten))

### 

### **Basic information on the dataset (Post Data Modifications)**

Inclusive on top, Censor on the bottom. Number of Individuals

|  | 18 | 20 | 22 | 24 | 26 |
| --- | --- | --- | --- | --- | --- |
| CI | 12 | 14 | 13 | 16 | 14 |
| CM | 12 | 11 | 10 | 12 | 12 |
| HS | 12 | 10 | 11 | 11 | 8 |
|  |  |  |  |  |  |
| CI | 12 | 10 | 7 | 7 | 7 |
| CM | 12 | 11 | 9 | 12 | 11 |
| HS | 12 | 10 | 11 | 10 | 8 |

Inclusive on top, Censor on the bottom. Number of Feeding Points

|  | 18 | 20 | 22 | 24 | 26 |
| --- | --- | --- | --- | --- | --- |
| CI | 89 | 117 | 99 | 131 | 117 |
| CM | 85 | 95 | 81 | 100 | 97 |
| HS | 82 | 90 | 81 | 99 | 67 |
|  |  |  |  |  |  |
| CI | 89 | 90 | 56 | 62 | 63 |
| CM | 85 | 95 | 72 | 100 | 88 |
| HS | 82 | 90 | 81 | 89 | 67 |

### 

### **The Binary Model: Dead vs Alive**

### **Question:** Are there differences in the number of alive/dead individuals as temperature increases? Which species out of the three is this relationship the strongest?

**Exploratory Graphs:**

-I added the extras on the master data frame which contains all individuals who were ever in the systems that are included in the project

-I then created two exploratory graphs to represent how the data looks in general

- NOTE - a good model should show that there is a decrease in alive individuals as temperature increases for the Rock Crab. Green crabs and shore crabs should remain relatively flat (no increase death with temperatures)

**Model Selection:**

-To account for the separated data, I will use a bias reduced GLM. Following code from: <https://bscheng.com/2016/12/11/modeling-completely-separated-data-in-r/>

-I then fit the model to an all mod (all explanatory variables added with interactions). Then dredged the model to see which model is the “best”

-The best model came back as one that included temperature and Species (all explanatory variables); however, without interactions

-Best model <- dead ~ Temperature (numeric) + Species (factor)

**Dead or alive RESULTS (binary model):**

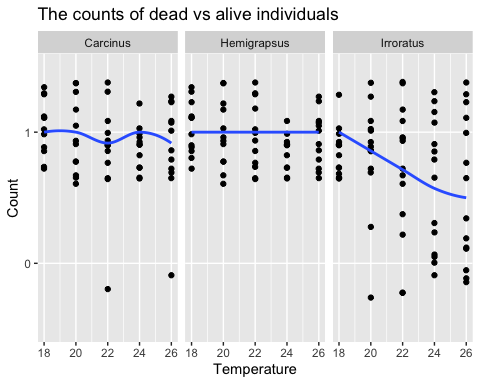
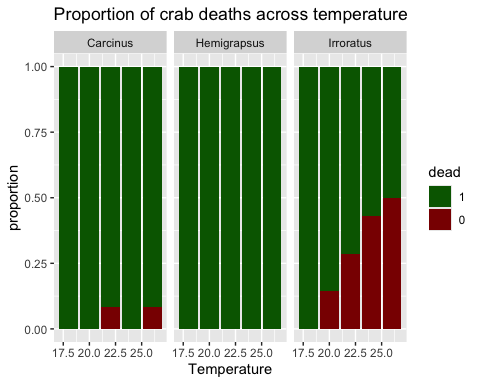
-This best model summary tells us there are differences in the INTERCEPTS between green crabs/shore crabs and rock crabs. The model also indicates that there is a slope that is negative for ALL species. This is because we did not include an interaction (including an interaction makes the model find no differences and AIC finds no interaction model a worse one)

-Since it seems obvious that rock crabs are doing worse than green crabs and shore crabs (a little disappointed it didn’t pick it up), I modeled with just rock crab data

-I modeled just rock crab data and found that there was a significantly negative slope as temperature increases.

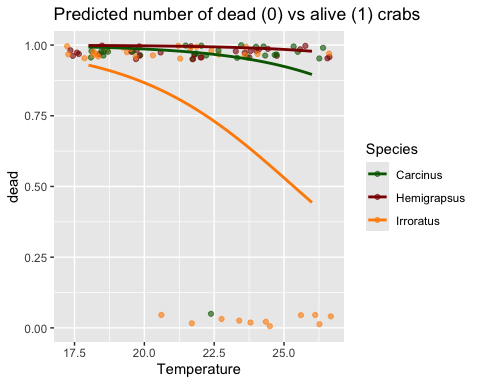
**Summary:**

I modeled dead and alive crabs using a bias reduced GLM. After dredging the best model was a full additive model (temperature and species); however, the model dictates all species have the same slope (decrease of alive individuals across temperature) and therefore I modeled just rock crabs to see a negative slope (decrease in alive individuals)



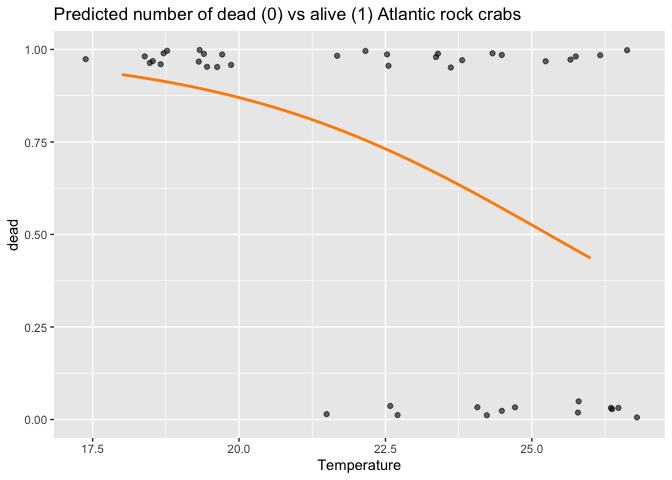
After the exploratory graphs, we should have a model that suggests no change across species and an increase in rock crab deaths as temperature increases. I’ll try dredging the full model with Temperature and species. This is the best model summary output.

##   
## Call:  
## brglm(formula = dead ~ Temperature + Species, family = binomial,   
## data = master, na.action = "na.fail")  
##   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 11.2559 2.6607 4.230 2.33e-05 \*\*\*  
## Temperature -0.3501 0.1066 -3.284 0.00102 \*\*   
## SpeciesHemigrapsus 1.6474 1.5722 1.048 0.29470   
## SpeciesIrroratus -2.3808 0.7277 -3.272 0.00107 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 119.507 on 188 degrees of freedom  
## Residual deviance: 86.896 on 185 degrees of freedom  
## Penalized deviance: 79.82214   
## AIC: 94.896



That model doesn’t really describe that the shore crab and green crab rate are 0. The general temperature variable is across the whole data set and not species specific. I can tell based off the raw data that there are only two death points for green crabs and zero for shore crab. Therefore it might not be necessary to model them. Instead, here I’ll just model rock crabs. The following is the best rock crab model summary and the predicted values

##   
## Call:  
## brglm(formula = dead ~ Temperature, family = binomial, data = holddf,   
## na.action = "na.fail")  
##   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 9.0887 2.7284 3.331 0.000865 \*\*\*  
## Temperature -0.3594 0.1171 -3.069 0.002144 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 74.654 on 69 degrees of freedom  
## Residual deviance: 69.280 on 68 degrees of freedom  
## Penalized deviance: 62.52653   
## AIC: 73.28



### **Acclimation: Are there differences in proportion eaten across week number for each species, temperature regime and time block?**

**Background:** Before we test if the amount consumed has differences among species and temperature, we need to understand if these differences are due to acclimation or the actual baseline for that temperature. This section divides the proportion consumed by week number (there were 3 weeks for each trial) and compares them within species and temperature treatment to test if there were any acclimation effects after the two-week acclimation period.

#### **Exploratory Graphs:**

-I started by graphing what we would expect the acclimation models to suggest.

-If acclimation worked, we should expect an increase or decrease in the first week to the second then it should hit a flat line (indicating no change in consumption) going from week 2 to 3. That would indicate 2 weeks of acclimation is sufficient for measuring consumption

-I summarized the mean and standard error for each species, temperature and period then graphed the proportion consumed over week number to test if the acclimation worked. I also compared these graphs between the censor model and inclusive model

-I found very little differences (visually) between the inclusive and censor model

-It seems like there are very little differences between all weeks for rock crabs and green crabs; however, we do see some differences in shore crabs between the week numbers. Hopefully our model reflects this.

#### **Modeling Acclimation:**

-Each species was modeled separately as we are only interested in if the acclimation time was sufficient (i.e. consumption rate is stable after two weeks of acclimation)

-Further, each temperature was modeled independently of each other because we do not care about differences among different temperature treatments.

-I started by graphing out response variables for each species. Green crabs and shore crabs seem to be relatively normal while rock crabs have some potential weirdness.

-For each species, I tested which model worked best for temperature treatment 18 and then applied that model to the rest of the temperature treatments and checked for fit

#### **Model Fitting:**

-Green crabs: Their response variable was mainly normal, so I started by using a GLM with a family of gaussian. After checking the diagnostics, the models seem to be a good fit across all temperature treatments

-Shore crabs: The previous steps were repeated and I found the model fit was ok for all the temperature treatments (family = gaussian)

-Rock crabs: The typically normal GLM did not fit well for these crabs. I tried other models such as Gamma; however, found poor fit in all. Even transforming the data did not work. I then decided to model it with zero-inflation as I noticed in the graphs there was a large group surrounding zero. Modeling with zero-inflation provided a strong fit for all temperature treatments; however, for temperature treatment 20 I fitted a zero-inflated gaussian model rather than a Gamma model (which are the rest) since the distribution of the response variable was normal and the model was a better fit then a Gamma for 20 C temperature treatment.

#### **Pairwise comparisons (RESULTS FOR ACCLIMATION):**

-I then made pairwise comparisons between each week number for all species and temperature treatments.

-Reminder: We are looking for differences between week number 2 and 3. If there are no differences this will indicate consumption has flattened and stablized. If not, then feeding may potentially continue to increase or decrease.

Green crabs: No differences between any groups

Shore crabs: some temperature treatments have differences between groups (importantly between week 2 and 3). The only temperature treatments where we see differences between week 2 and 3 are temperature treatments 22C and 24C

Additional note for shore crabs: Both differences between week 2 and 3 for temperature treatments 22 C and 24 C are always decrease from week 2 to 3 (week 3 is always smaller amount) - as noted before this may be a saturation effect. Crabs are eating more than enough and therefore will opt out of feeding more in future feedings.

Rock crabs: No differences between week 2 and 3 for all temperature treatments, but some have differences between week 1 and 3

**Summary:**

I first made exploratory graphs, then modeled each species and temperature treatment separately. I used GLMs for shore and green crabs while I used zero-inflated models for rock crabs. All models fit well and the only difference between week 2 and 3 consumption rate lies within temperature treatment 22C and 24 C for shore crabs.

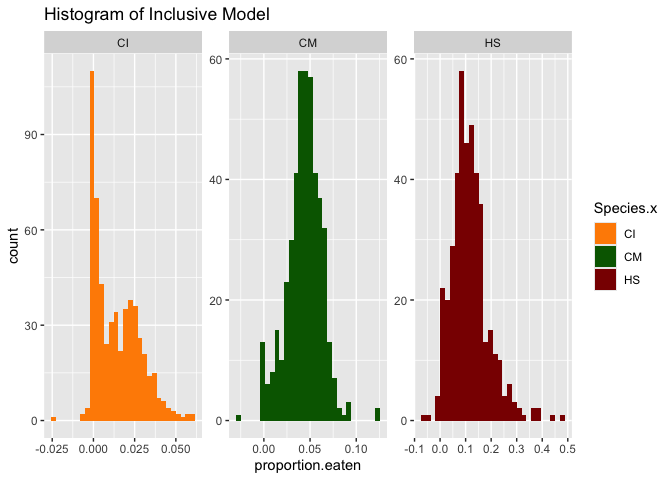
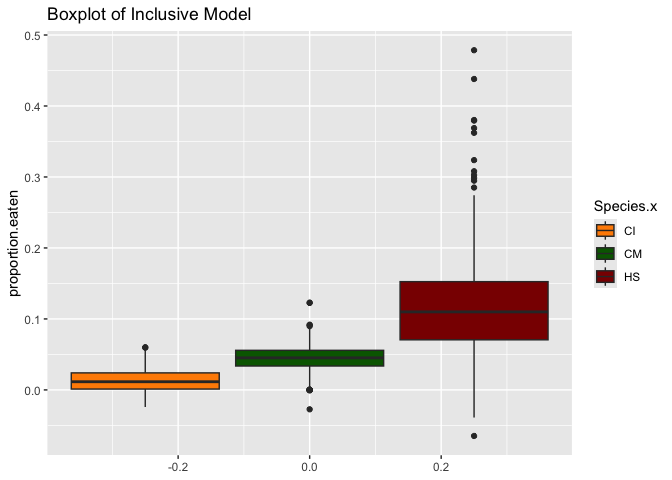
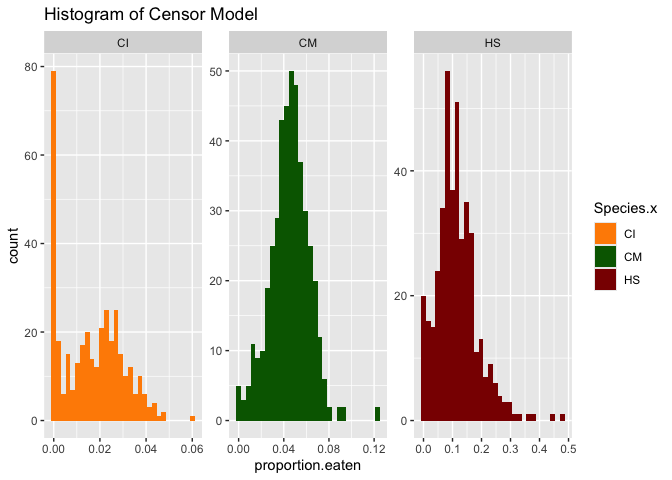
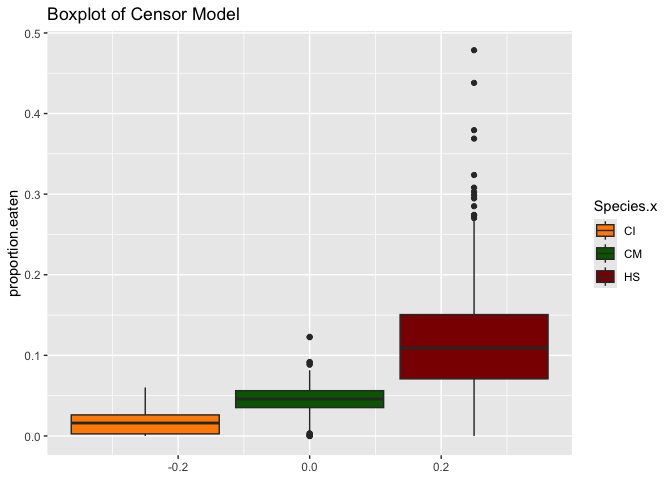
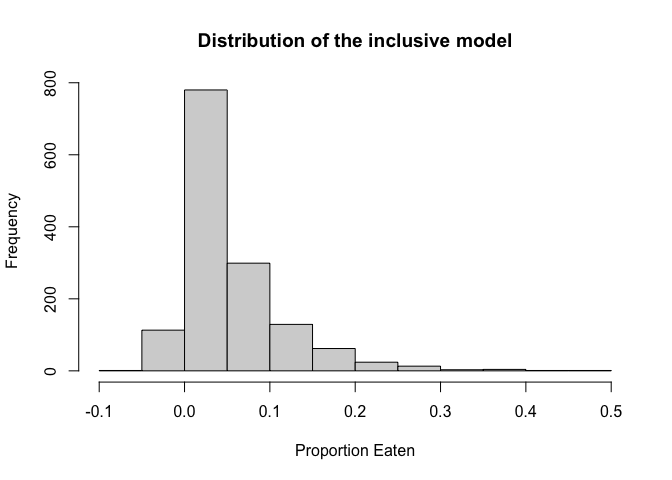
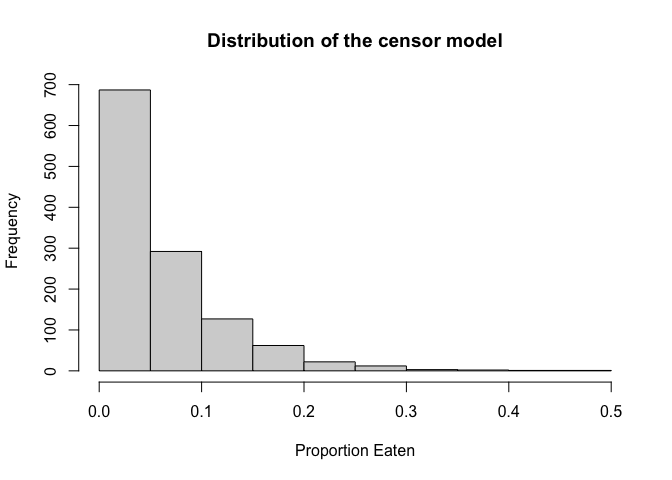
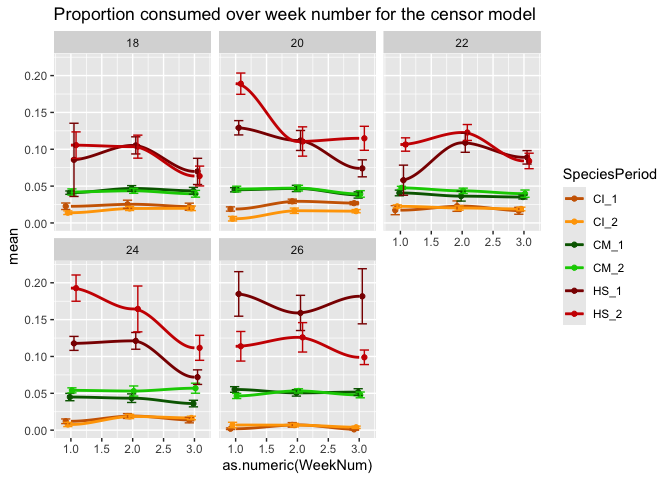
**HOW TO READ THIS SECTION:** Summarized methods and results are located above here in text. If you want to look at diagnostic plots and summary outputs/pairwise comparisons (which are summed here as well). The order is as follows:

-Exploratory graphs (first glance at data and distributions)

-Each species and their specific temperature treatment diagnostic plots and summary output. Starting with…

* Green crabs at 18 C through green crabs at 26 C
* Shore crabs at 18 C through shore crabs at 26 C
* Rock crabs at 18 C through rock crabs at 26 C

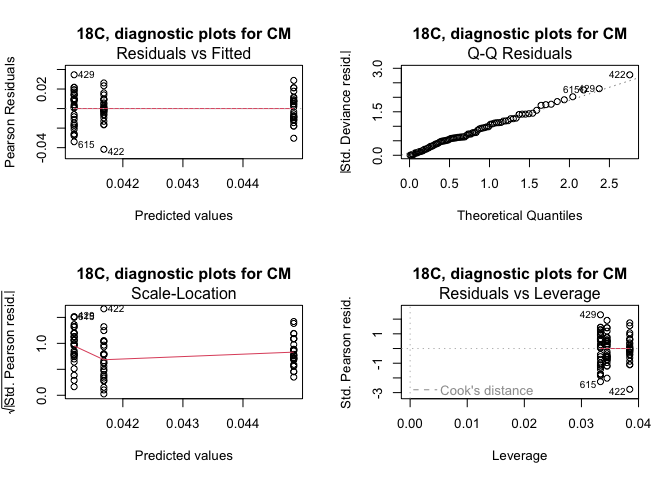
-Each diagnostic plot is the best fitting model for that species in that temperature treatment. The model is used to determine differences between week number to understand if the acclimation period worked. Those without week number differences did not include pairwise comparisons (as they would all be the same anyways). Those with differences also have pairwise comparisons added under the plots to see which weeks differed.



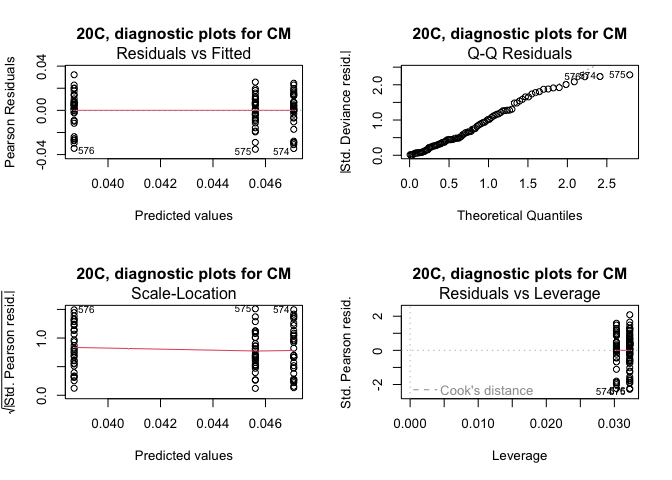
Both models look similar so I’ll do analysis exploration with the censor model and compare towards the end.

I’ll be modeling each species independently since I am interested in how each species responds on their own and not differences between other species (I want to know if acclimation worked or not so it doesn’t involve other species) Further, I want to understand how each week number differs WITHIN temperature. Therefore, it is probably best to model each temperature on their own NOTE: Temperature is being taken as a factor here since we only care about within temperature treatments! I’ll only be using the censor model since it lacks negatives and it’s easier to handle. Also, preliminary graphs suggests data is very similar and both aren’t needed for all comparisons (I will compare final models) Week number will be used as a factor since we care about direct differences between week 1 and 3 not just if it increases across the weeks We’ll use a GLM and add, Week number as the only explanatory variable. We’ll model specific temperatures and species on their own.

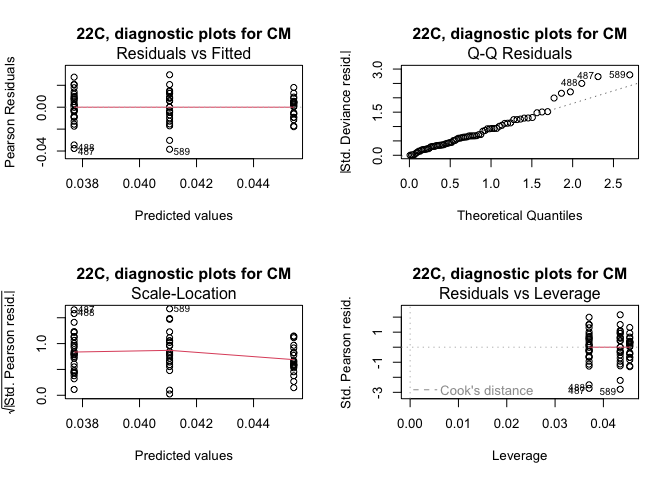
Let’s begin with green crabs since they are normal and “easier” to handle. In this next section, you’ll see the diagnostic plots and then the following is the model summary (to parse differences).



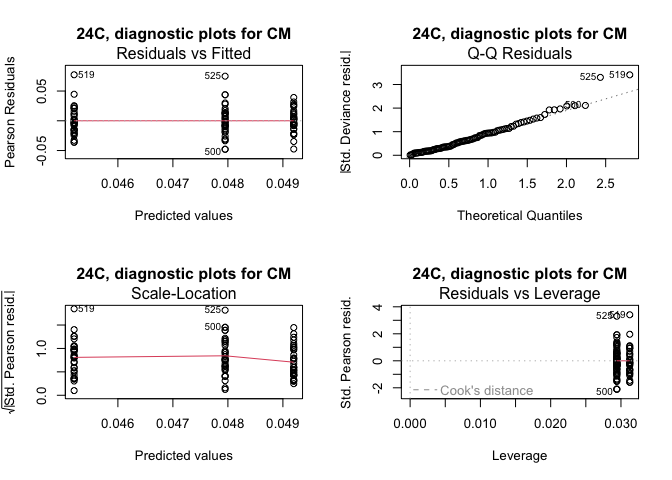
##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.0416836 0.0030046 13.873 <2e-16 \*\*\*  
## as.factor(WeekNum)2 0.0031616 0.0041378 0.764 0.447   
## as.factor(WeekNum)3 -0.0004948 0.0041051 -0.121 0.904   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.0002347242)  
##   
## Null deviance: 0.019475 on 84 degrees of freedom  
## Residual deviance: 0.019247 on 82 degrees of freedom  
## AIC: -464.19  
##   
## Number of Fisher Scoring iterations: 2



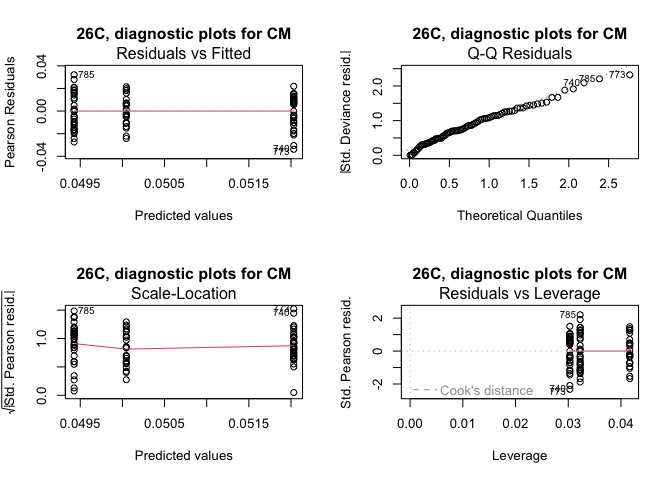
##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.045614 0.002818 16.189 <2e-16 \*\*\*  
## as.factor(WeekNum)2 0.001463 0.003924 0.373 0.7101   
## as.factor(WeekNum)3 -0.006905 0.003985 -1.733 0.0865 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.000246112)  
##   
## Null deviance: 0.023902 on 94 degrees of freedom  
## Residual deviance: 0.022642 on 92 degrees of freedom  
## AIC: -514.87  
##   
## Number of Fisher Scoring iterations: 2



##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.045410 0.002993 15.173 <2e-16 \*\*\*  
## as.factor(WeekNum)2 -0.004355 0.004186 -1.040 0.3018   
## as.factor(WeekNum)3 -0.007705 0.004032 -1.911 0.0602 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.0001970666)  
##   
## Null deviance: 0.014317 on 71 degrees of freedom  
## Residual deviance: 0.013598 on 69 degrees of freedom  
## AIC: -405.04  
##   
## Number of Fisher Scoring iterations: 2

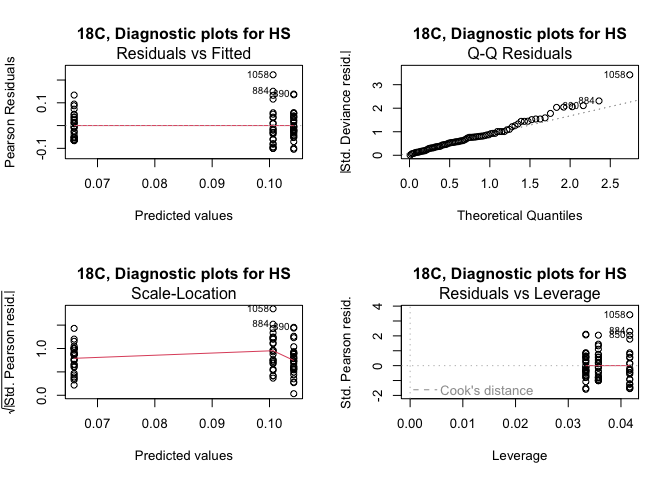


##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.049197 0.003953 12.447 <2e-16 \*\*\*  
## as.factor(WeekNum)2 -0.001248 0.005590 -0.223 0.824   
## as.factor(WeekNum)3 -0.003993 0.005677 -0.703 0.483   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.0005311926)  
##   
## Null deviance: 0.051799 on 99 degrees of freedom  
## Residual deviance: 0.051526 on 97 degrees of freedom  
## AIC: -465.3  
##   
## Number of Fisher Scoring iterations: 2



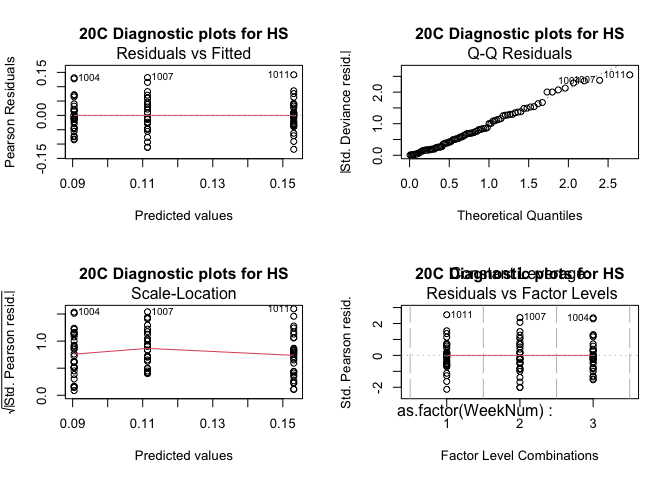
##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.0500460 0.0030191 16.576 <2e-16 \*\*\*  
## as.factor(WeekNum)2 0.0019866 0.0039679 0.501 0.618   
## as.factor(WeekNum)3 -0.0006187 0.0040214 -0.154 0.878   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.0002187617)  
##   
## Null deviance: 0.018712 on 87 degrees of freedom  
## Residual deviance: 0.018595 on 85 degrees of freedom  
## AIC: -486.94  
##   
## Number of Fisher Scoring iterations: 2

Next up is Shore crabs. Shore crabs had a semi normal shape…? Some skew, so I’ll try a GLM with normal distribution first and see how well the model does Again, I’ll model the temperatures separately as I only care about differences within treatment. Same format as previous however, those with differences will contain pairwise differences



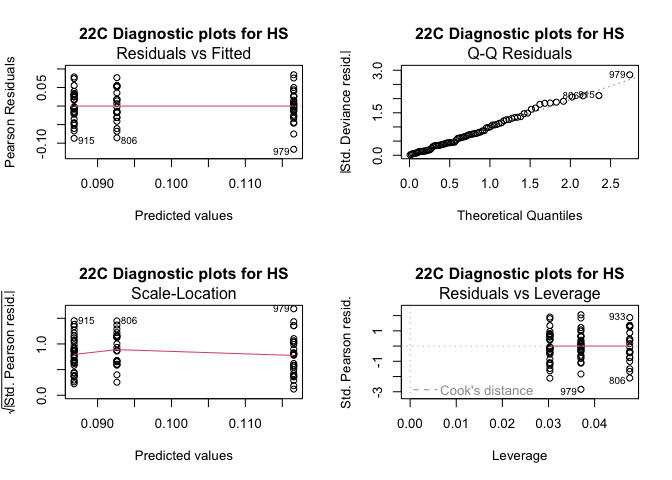
##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.100622 0.013610 7.393 1.31e-10 \*\*\*  
## as.factor(WeekNum)2 0.003609 0.018260 0.198 0.8438   
## as.factor(WeekNum)3 -0.034701 0.018547 -1.871 0.0651 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.004445653)  
##   
## Null deviance: 0.37622 on 81 degrees of freedom  
## Residual deviance: 0.35121 on 79 degrees of freedom  
## AIC: -206.45  
##   
## Number of Fisher Scoring iterations: 2

## contrast estimate SE df t.ratio p.value  
## WeekNum1 - WeekNum2 -0.00361 0.0183 79 -0.198 0.9787  
## WeekNum1 - WeekNum3 0.03470 0.0185 79 1.871 0.1539  
## WeekNum2 - WeekNum3 0.03831 0.0175 79 2.187 0.0797  
##   
## P value adjustment: tukey method for comparing a family of 3 estimates



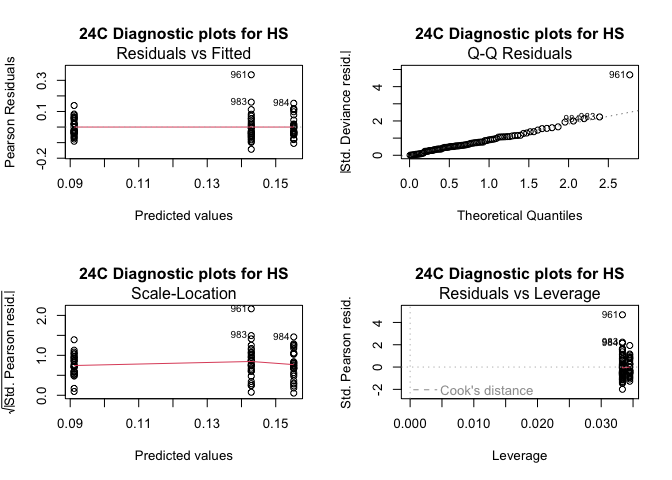
##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.15311 0.01032 14.833 < 2e-16 \*\*\*  
## as.factor(WeekNum)2 -0.04174 0.01460 -2.859 0.00531 \*\*   
## as.factor(WeekNum)3 -0.06269 0.01460 -4.294 4.54e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.003196736)  
##   
## Null deviance: 0.33923 on 89 degrees of freedom  
## Residual deviance: 0.27812 on 87 degrees of freedom  
## AIC: -256.75  
##   
## Number of Fisher Scoring iterations: 2

## contrast estimate SE df t.ratio p.value  
## WeekNum1 - WeekNum2 0.0417 0.0146 87 2.859 0.0146  
## WeekNum1 - WeekNum3 0.0627 0.0146 87 4.294 0.0001  
## WeekNum2 - WeekNum3 0.0209 0.0146 87 1.435 0.3277  
##   
## P value adjustment: tukey method for comparing a family of 3 estimates



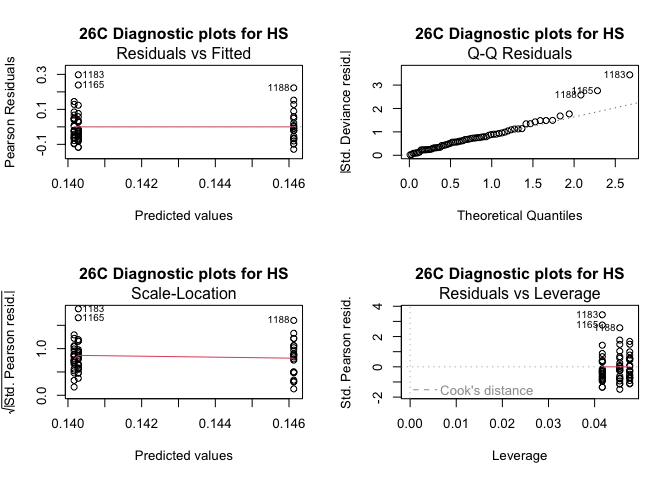
##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.092615 0.009129 10.145 6.65e-16 \*\*\*  
## as.factor(WeekNum)2 0.023937 0.012172 1.967 0.0528 .   
## as.factor(WeekNum)3 -0.005791 0.011678 -0.496 0.6214   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.001750149)  
##   
## Null deviance: 0.15053 on 80 degrees of freedom  
## Residual deviance: 0.13651 on 78 degrees of freedom  
## AIC: -279.38  
##   
## Number of Fisher Scoring iterations: 2

## contrast estimate SE df t.ratio p.value  
## WeekNum1 - WeekNum2 -0.02394 0.0122 78 -1.967 0.1274  
## WeekNum1 - WeekNum3 0.00579 0.0117 78 0.496 0.8735  
## WeekNum2 - WeekNum3 0.02973 0.0109 78 2.738 0.0207  
##   
## P value adjustment: tukey method for comparing a family of 3 estimates



##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.15526 0.01330 11.675 < 2e-16 \*\*\*  
## as.factor(WeekNum)2 -0.01240 0.01881 -0.659 0.51137   
## as.factor(WeekNum)3 -0.06411 0.01897 -3.380 0.00109 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.005305301)  
##   
## Null deviance: 0.52413 on 88 degrees of freedom  
## Residual deviance: 0.45626 on 86 degrees of freedom  
## AIC: -208.76  
##   
## Number of Fisher Scoring iterations: 2

## contrast estimate SE df t.ratio p.value  
## WeekNum1 - WeekNum2 0.0124 0.0188 86 0.659 0.7875  
## WeekNum1 - WeekNum3 0.0641 0.0190 86 3.380 0.0031  
## WeekNum2 - WeekNum3 0.0517 0.0190 86 2.726 0.0210  
##   
## P value adjustment: tukey method for comparing a family of 3 estimates

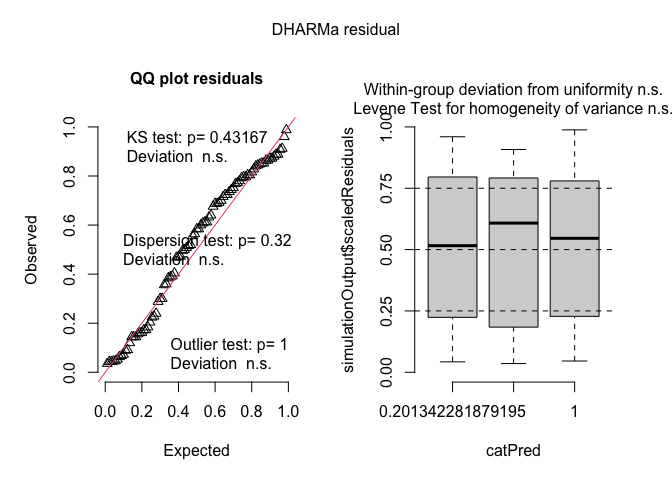


##   
## Call:  
## glm(formula = proportion.eaten ~ as.factor(WeekNum), data = censorsub)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.146129 0.018860 7.748 8.97e-11 \*\*\*  
## as.factor(WeekNum)2 -0.005962 0.026988 -0.221 0.826   
## as.factor(WeekNum)3 -0.005849 0.026111 -0.224 0.823   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.007825413)  
##   
## Null deviance: 0.50134 on 66 degrees of freedom  
## Residual deviance: 0.50083 on 64 degrees of freedom  
## AIC: -129.91  
##   
## Number of Fisher Scoring iterations: 2

## contrast estimate SE df t.ratio p.value  
## WeekNum1 - WeekNum2 0.005962 0.0270 64 0.221 0.9735  
## WeekNum1 - WeekNum3 0.005849 0.0261 64 0.224 0.9727  
## WeekNum2 - WeekNum3 -0.000113 0.0264 64 -0.004 1.0000  
##   
## P value adjustment: tukey method for comparing a family of 3 estimates

Same deal for rock crabs, I used simulated residuals from the DHARMa package as diagnostic plots since we’re using zero-inflated models now.

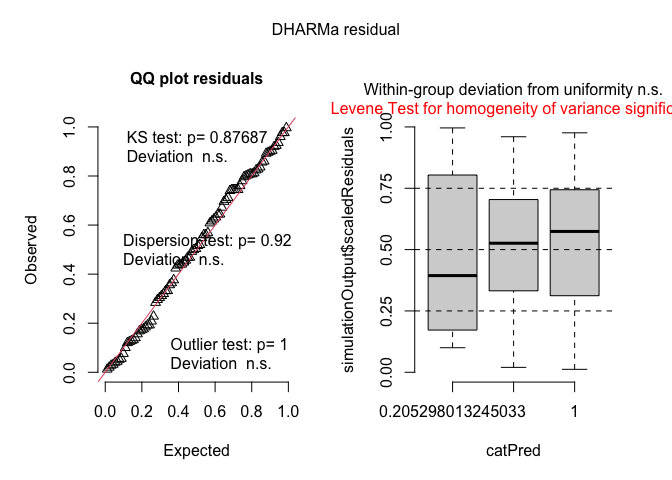
## 18C Diagnostic plots for CI



## Family: Gamma ( inverse )  
## Formula: proportion.eaten ~ as.factor(WeekNum)  
## Zero inflation: ~as.factor(WeekNum)  
## Data: censorsub  
##   
## AIC BIC logLik -2\*log(L) df.resid   
## -354.0 -336.6 184.0 -368.0 82   
##   
##   
## Dispersion estimate for Gamma family (sigma^2): 0.366   
##   
## Conditional model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 46.078 5.812 7.928 2.22e-15 \*\*\*  
## as.factor(WeekNum)2 -5.020 7.525 -0.667 0.505   
## as.factor(WeekNum)3 -5.859 7.580 -0.773 0.439   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Zero-inflation model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.3437 0.4584 -2.931 0.00338 \*\*  
## as.factor(WeekNum)2 -0.8535 0.7619 -1.120 0.26263   
## as.factor(WeekNum)3 -0.2657 0.6709 -0.396 0.69209   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## contrast estimate SE df z.ratio p.value  
## WeekNum1 - WeekNum2 5.020 7.52 Inf 0.667 0.7826  
## WeekNum1 - WeekNum3 5.859 7.58 Inf 0.773 0.7196  
## WeekNum2 - WeekNum3 0.839 6.82 Inf 0.123 0.9917  
##   
## Note: contrasts are still on the inverse scale. Consider using  
## regrid() if you want contrasts of back-transformed estimates.   
## P value adjustment: tukey method for comparing a family of 3 estimates

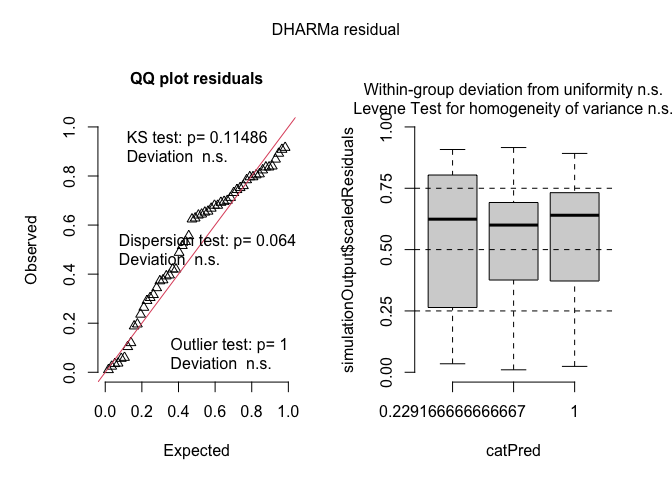
## 20C Diagnostic plots for CI



## Family: gaussian ( identity )  
## Formula: proportion.eaten ~ as.factor(WeekNum)  
## Zero inflation: ~as.factor(WeekNum)  
## Data: censorsub  
##   
## AIC BIC logLik -2\*log(L) df.resid   
## -523.4 -505.9 268.7 -537.4 83   
##   
##   
## Dispersion estimate for gaussian family (sigma^2): 0.000149   
##   
## Conditional model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.013659 0.002231 6.122 9.27e-10 \*\*\*  
## as.factor(WeekNum)2 0.010578 0.003156 3.352 0.000802 \*\*\*  
## as.factor(WeekNum)3 0.008834 0.003156 2.800 0.005117 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Zero-inflation model:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) -21.131 7133.061 -0.003 0.998  
## as.factor(WeekNum)2 -1.848 19390.793 0.000 1.000  
## as.factor(WeekNum)3 -1.814 18977.045 0.000 1.000

## contrast estimate SE df t.ratio p.value  
## WeekNum1 - WeekNum2 -0.01058 0.00316 83 -3.352 0.0034  
## WeekNum1 - WeekNum3 -0.00883 0.00316 83 -2.800 0.0173  
## WeekNum2 - WeekNum3 0.00174 0.00316 83 0.553 0.8454  
##   
## P value adjustment: tukey method for comparing a family of 3 estimates

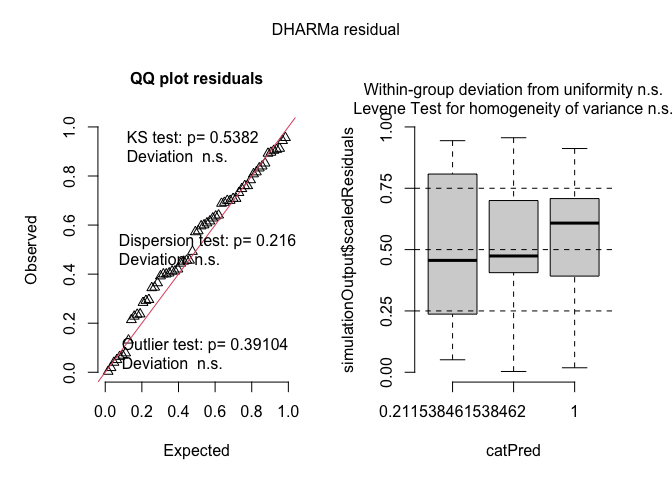
## 22C Diagnostic plots for CI



## Family: Gamma ( inverse )  
## Formula: proportion.eaten ~ as.factor(WeekNum)  
## Zero inflation: ~as.factor(WeekNum)  
## Data: censorsub  
##   
## AIC BIC logLik -2\*log(L) df.resid   
## -279.0 -264.8 146.5 -293.0 49   
##   
##   
## Dispersion estimate for Gamma family (sigma^2): 0.343   
##   
## Conditional model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 45.3992 6.4455 7.043 1.87e-12 \*\*\*  
## as.factor(WeekNum)2 -0.6557 9.1881 -0.071 0.943   
## as.factor(WeekNum)3 5.1697 9.3629 0.552 0.581   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Zero-inflation model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.83321 1.02899 -2.753 0.0059 \*\*  
## as.factor(WeekNum)2 0.06062 1.45648 0.042 0.9668   
## as.factor(WeekNum)3 0.58192 1.26943 0.458 0.6467   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## contrast estimate SE df z.ratio p.value  
## WeekNum1 - WeekNum2 0.656 9.19 Inf 0.071 0.9972  
## WeekNum1 - WeekNum3 -5.170 9.36 Inf -0.552 0.8454  
## WeekNum2 - WeekNum3 -5.825 9.43 Inf -0.618 0.8105  
##   
## Note: contrasts are still on the inverse scale. Consider using  
## regrid() if you want contrasts of back-transformed estimates.   
## P value adjustment: tukey method for comparing a family of 3 estimates

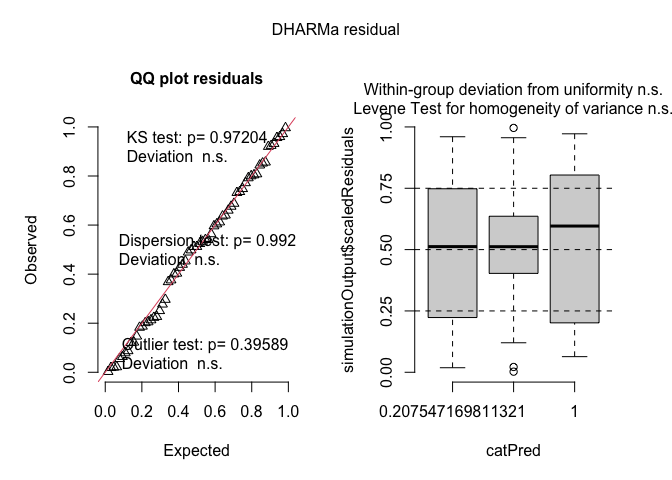
## 24C Diagnostic plots for CI



## Family: Gamma ( inverse )  
## Formula: proportion.eaten ~ as.factor(WeekNum)  
## Zero inflation: ~as.factor(WeekNum)  
## Data: censorsub  
##   
## AIC BIC logLik -2\*log(L) df.resid   
## -271.5 -256.6 142.8 -285.5 55   
##   
##   
## Dispersion estimate for Gamma family (sigma^2): 0.343   
##   
## Conditional model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 64.84 10.53 6.157 7.4e-10 \*\*\*  
## as.factor(WeekNum)2 -14.28 12.44 -1.148 0.251   
## as.factor(WeekNum)3 -6.28 13.27 -0.473 0.636   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Zero-inflation model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.4855 0.4494 -1.080 0.2799   
## as.factor(WeekNum)2 -2.5102 1.1189 -2.244 0.0249 \*  
## as.factor(WeekNum)3 -1.7117 0.8703 -1.967 0.0492 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## contrast estimate SE df z.ratio p.value  
## WeekNum1 - WeekNum2 14.28 12.4 Inf 1.148 0.4844  
## WeekNum1 - WeekNum3 6.28 13.3 Inf 0.473 0.8840  
## WeekNum2 - WeekNum3 -8.00 10.4 Inf -0.766 0.7239  
##   
## Note: contrasts are still on the inverse scale. Consider using  
## regrid() if you want contrasts of back-transformed estimates.   
## P value adjustment: tukey method for comparing a family of 3 estimates

## 26C Diagnostic plots for CI



## Family: Gamma ( inverse )  
## Formula: proportion.eaten ~ as.factor(WeekNum)  
## Zero inflation: ~as.factor(WeekNum)  
## Data: censorsub  
##   
## AIC BIC logLik -2\*log(L) df.resid   
## -109.6 -94.6 61.8 -123.6 56   
##   
##   
## Dispersion estimate for Gamma family (sigma^2): 0.795   
##   
## Conditional model:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 99.40 28.02 3.547 0.000389 \*\*\*  
## as.factor(WeekNum)2 -23.81 34.61 -0.688 0.491491   
## as.factor(WeekNum)3 45.07 53.46 0.843 0.399198   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Zero-inflation model:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 0.09531 0.43693 0.218 0.827  
## as.factor(WeekNum)2 -0.19062 0.61791 -0.308 0.758  
## as.factor(WeekNum)3 0.39020 0.62676 0.623 0.534

## contrast estimate SE df z.ratio p.value  
## WeekNum1 - WeekNum2 23.8 34.6 Inf 0.688 0.7705  
## WeekNum1 - WeekNum3 -45.1 53.5 Inf -0.843 0.6762  
## WeekNum2 - WeekNum3 -68.9 49.9 Inf -1.382 0.3506  
##   
## Note: contrasts are still on the inverse scale. Consider using  
## regrid() if you want contrasts of back-transformed estimates.   
## P value adjustment: tukey method for comparing a family of 3 estimates

### 

### **Period Checking : Are there differences in consumption rate across different species and temperature?**

#### **Background:** We need to check if the periods (time block one vs time block two) are different because if they are we should add it to the model. If they aren’t different then there would be no need to add periods to the model.

#### **Exploratory/Fitting the model:**

-I began by seeing if there were differences between periods for proportion consumed within each species and temperature treatments

-I fit different models for each species and temperature similar to what I did for finding acclimation effects. I only cared about within differences temperature treatment for a specific species which is why I did so.

-Period difference model <- (Proportion consumed ~ Period, data = specific\_species\_and\_temperature\_treatment)

To understand if there were differences between periods, I first created a histogram graph of the distribution from the data to determine which model I should I use. I then created the model and tested the fit. If the model didn’t fit well, I then used an alternative model and created a summary output. I began with rock crabs.

#### **Period Difference Results:**

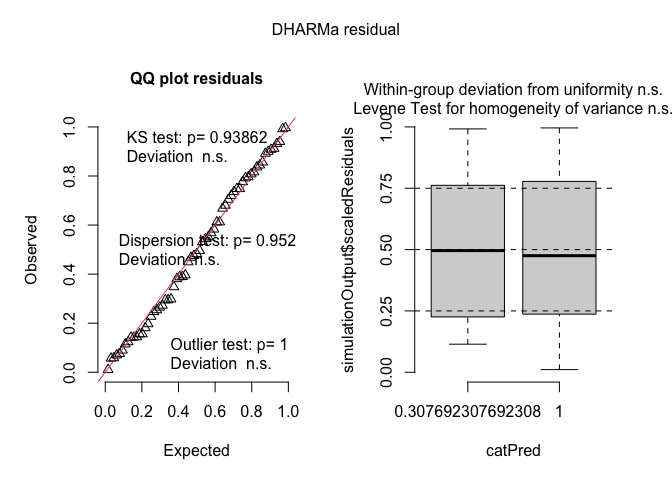
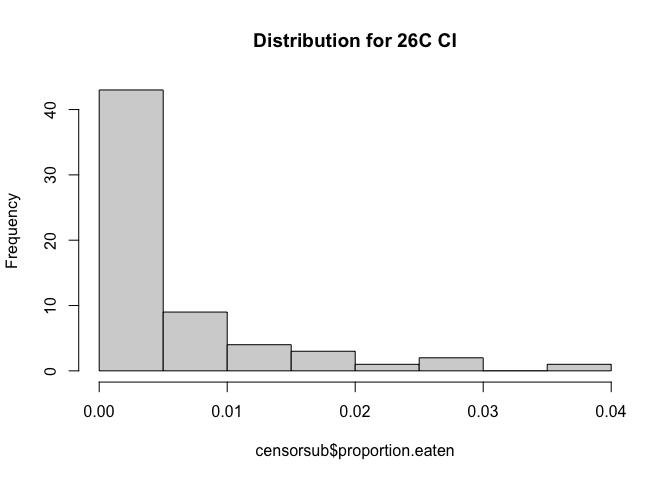
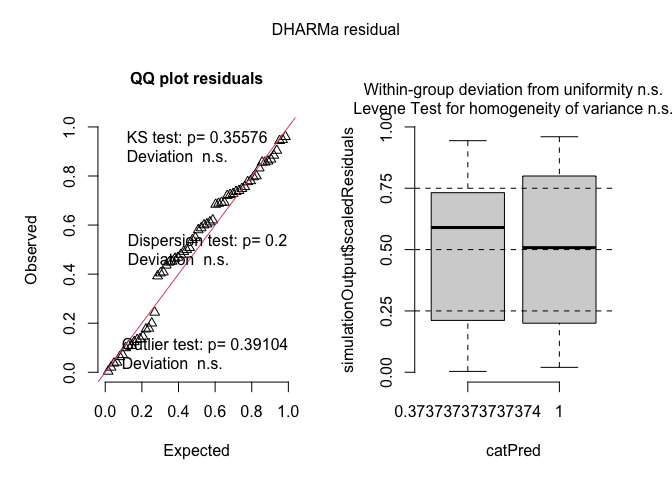
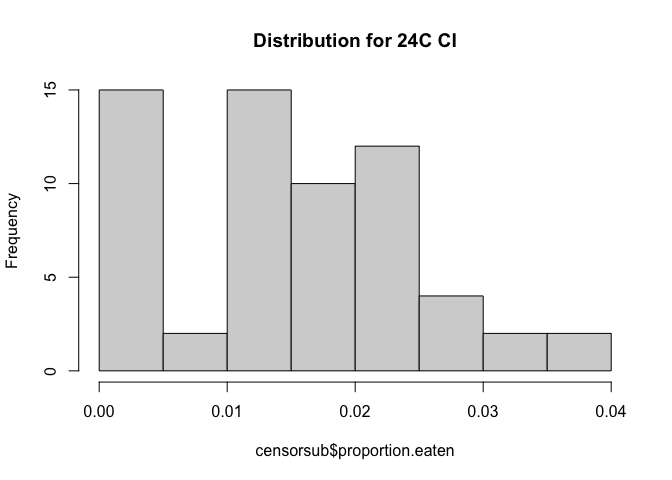
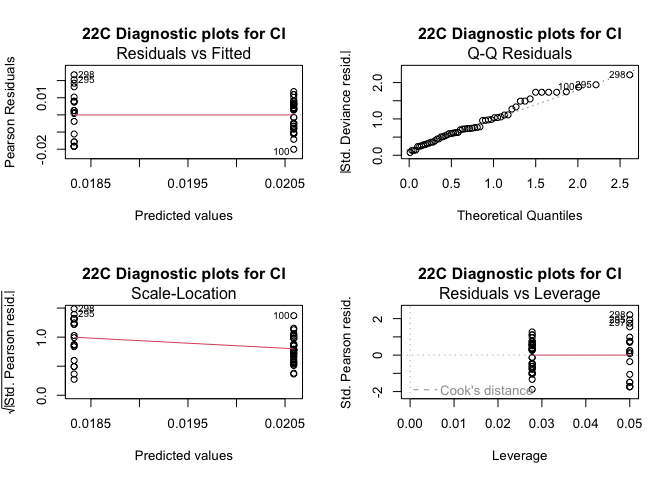
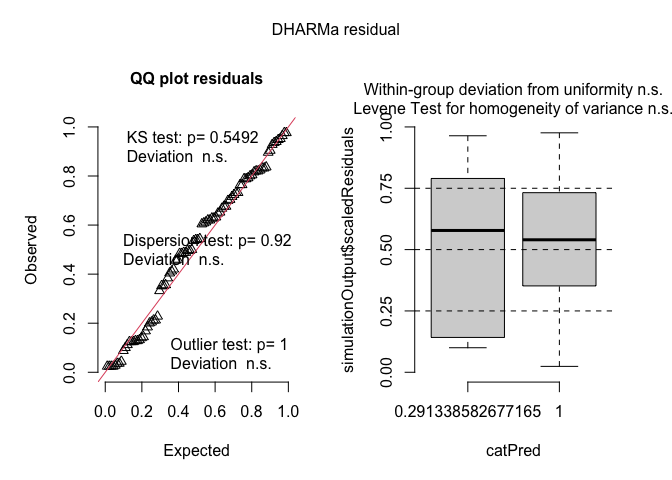
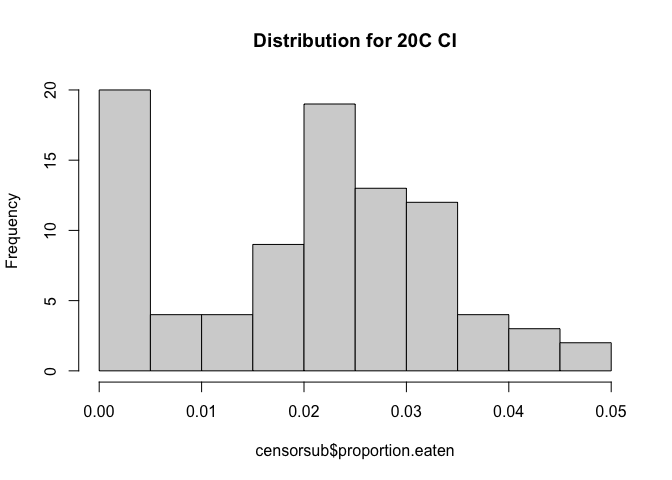
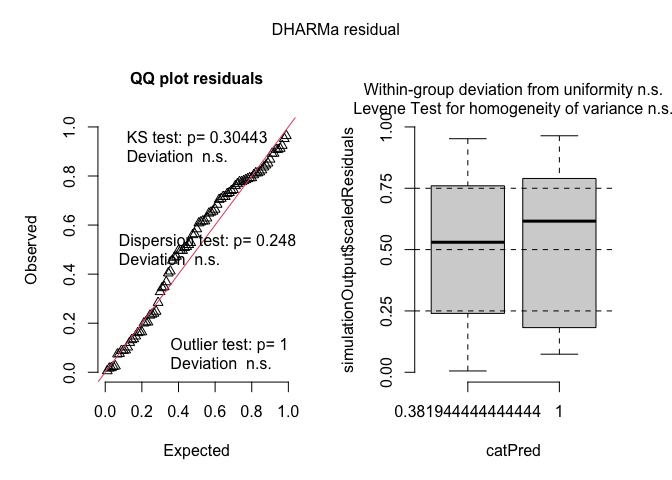
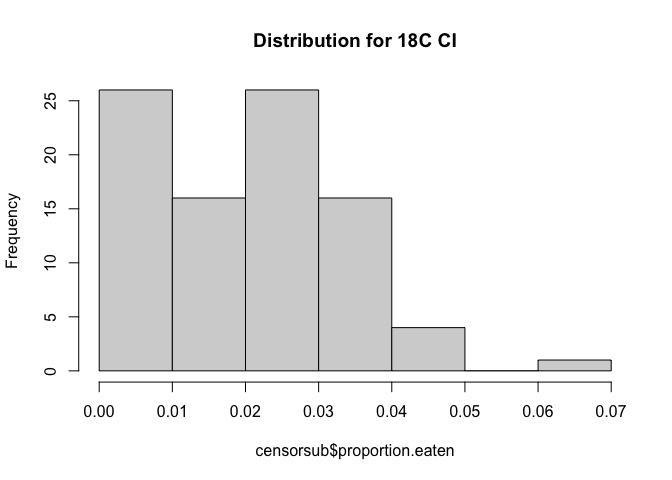
* For CI, the only temperature treatment where there were differences between periods was temperature treatment 20
* For CM, the only differences were in temperature treatment 24
* For HS, temperature treatment 20, 24, 26 had differences in periods

-Since there were differences between periods for some temperature treatments I added it to my models (unless AIC ranking told me Periods made the model worse)

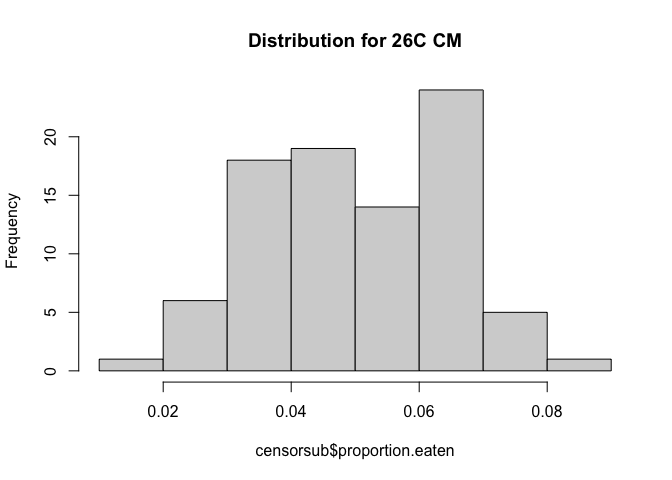
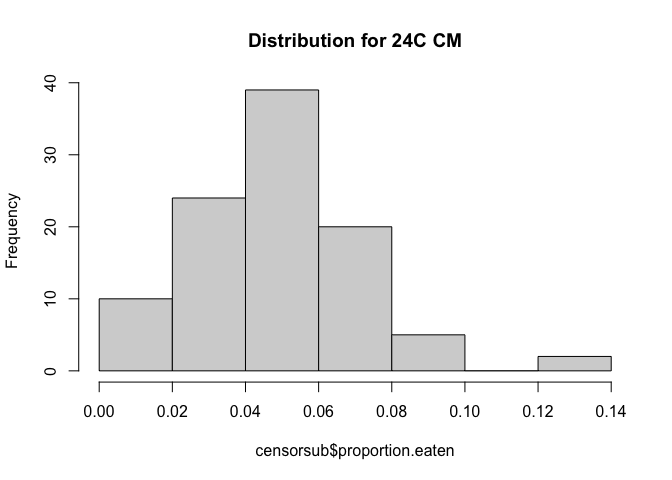
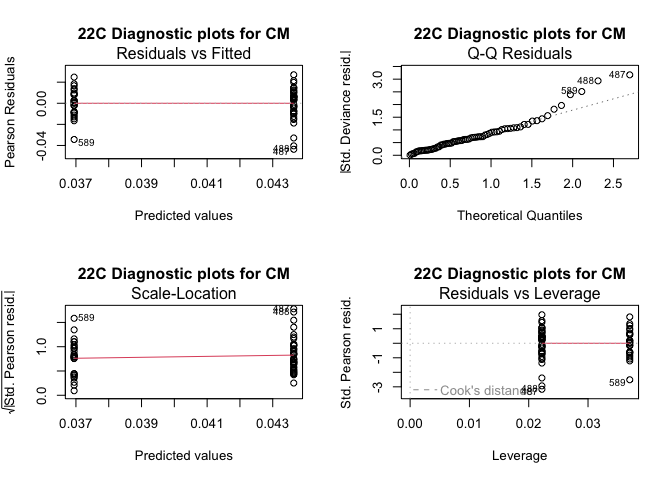
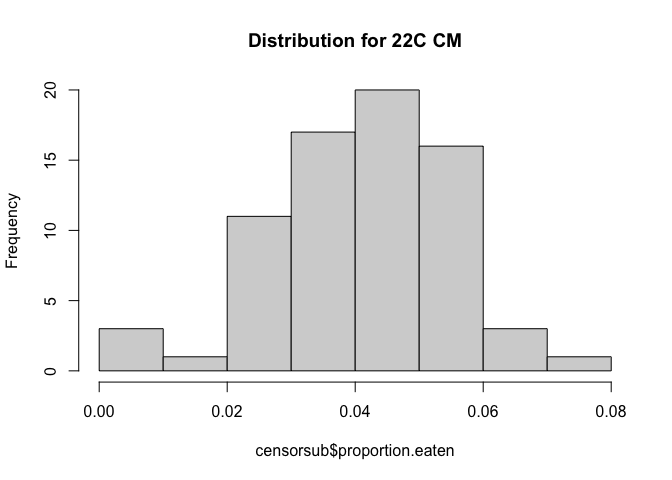
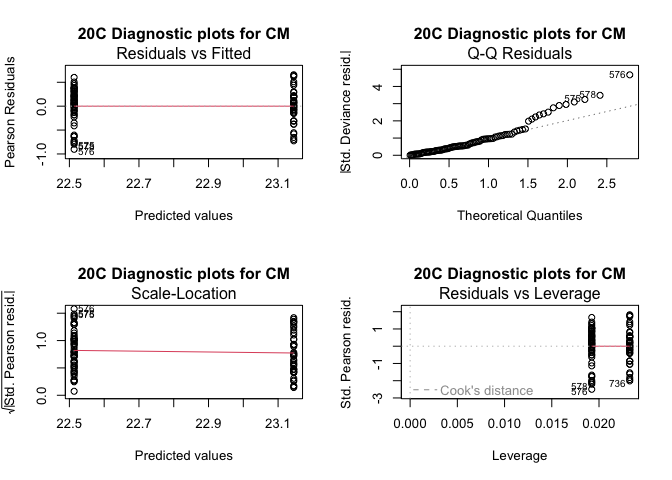
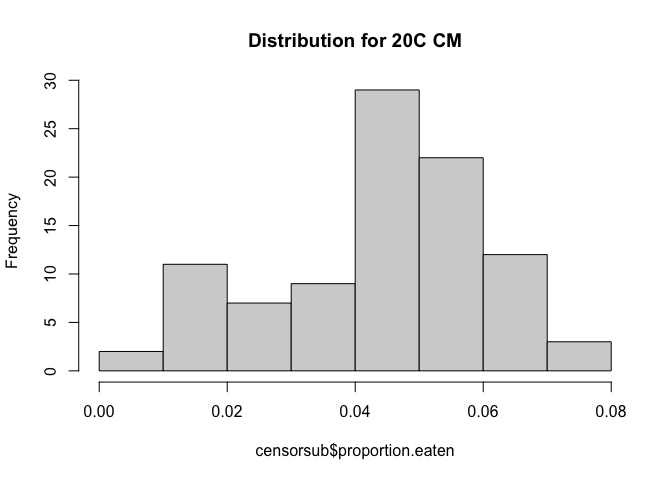
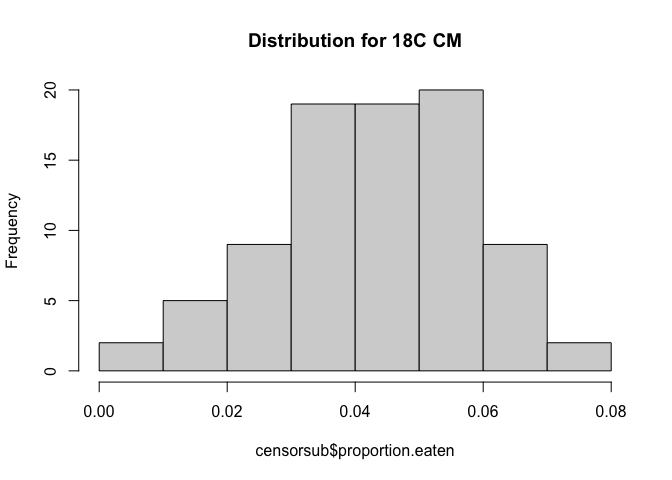
-The rest of the temperatures were not different between periods. Since there are differences between periods, I will add it to the model

**How to Read this Section:**

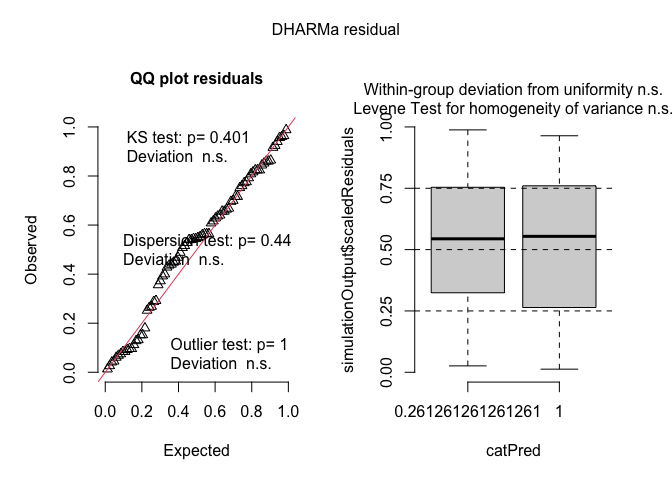
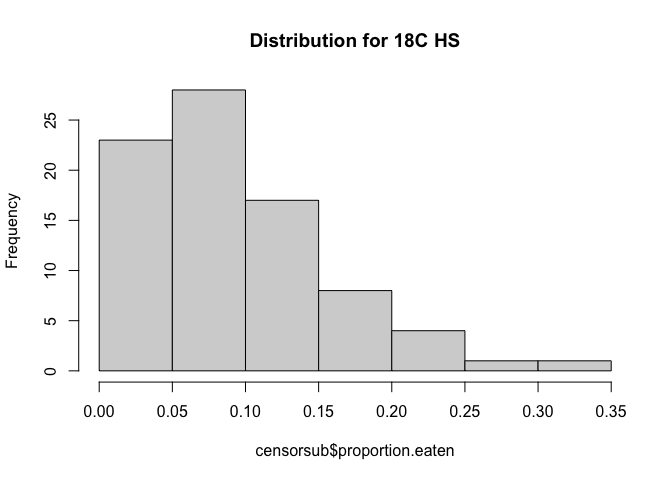
* Each distribution graph is related to a diagnostic plot (located directly underneath it)
* Each pair goes in order as such:
  + 18 C temperature treatment for rock crabs through 26 C for rock crabs
  + 18 C temperature treatment for green crabs through 26 C for green crabs
  + 18 C temperature treatment for shore crabs through 26 C for shore crabs
* The diagnostic plots are the best fitting model for that specific species and temperature.



Moving on to green crabs, which used normal GLMs

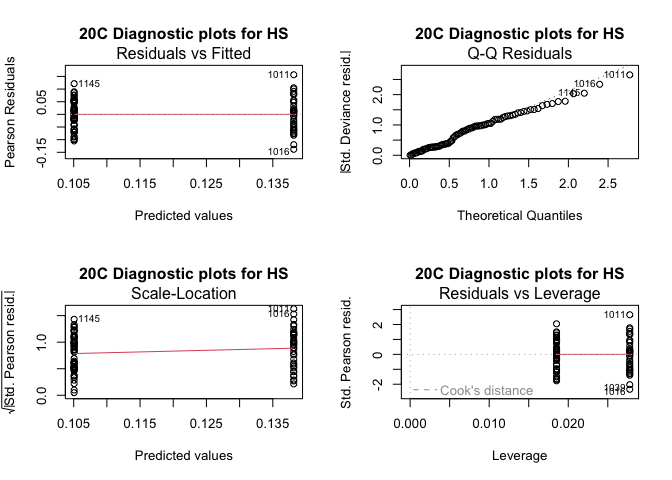


Moving on to shore crabs, I used a zero inflated model for 18C and normal GLM for the rest of the models.



A graph of a distribution

AI-generated content may be incorrect.



A graph of distribution of food

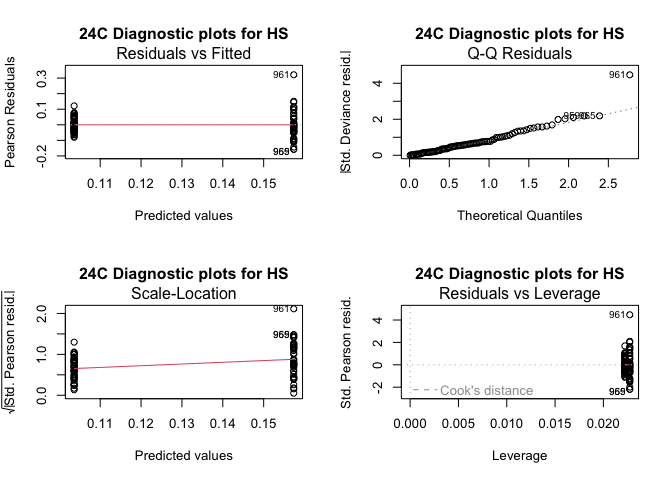
AI-generated content may be incorrect.

A group of graphs showing different results

AI-generated content may be incorrect.

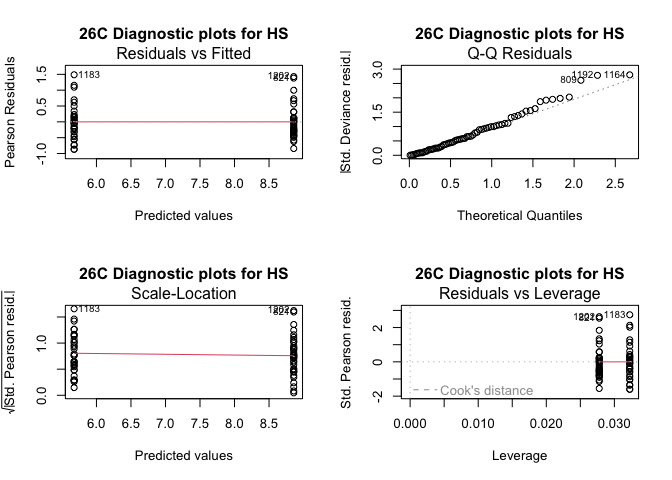
A graph of a distribution

AI-generated content may be incorrect.



A graph of a number of bars

AI-generated content may be incorrect.



### 

### **Modeling the big question: Are there differences in consumption rate across different species and temperature?**

#### **Exploratory Graphs:**

-I first graphed out what the proportion consumed across temperature looks like. Hopefully we find a model that supports what the graph suggests

-I also graphed out the proportion consumed for the whole dataset and for each species.

-When graphing the proportion consumed for the whole dataset it seems very skewed or even zero-inflated. However, what’s interesting is that the distribution for the response variable changes depending on the species Each species has their own distribution type.

-I’ll try to model the whole dataset first, but I will probably need to do model each species independently (unless there is a model that can handle multiple different distributions)

#### **Modeling the data:**

-The three explanatory variables I’m using are Period (factor), Temperature (numeric), and Species (for the whole dataset, factor)

-For each group, I began by making a full model and dredging it, then I use diagnostic plots to validate the model

-Since the Gamma family cannot work with zeros or negative numbers, for just the Gamma models, I converted all negative and zero values to .001.

-For zero-inflated gamma models, I converted them to just 0 instead of .001.

#### **All Censor Model:**

-I fit 4 types of models and dredged them to find the best ones.

-I fit a Zero-inflated Gamma (log, inverse, identity) Model and a GLM gamma model (also a gaussian model)

-I expected the Gamma or zero-inflated since the distribution seemed skewed; however, all models returned a poor fit -This was probably due to the different distributions among the species, so I moved to modeling each species separately.

#### **Rock crab censor model:**

-I tried, zero inflated Gamma (inverse, log, identity) and GLM (identity, log, inverse) and no models returned a good fit

-I also added different combinations of variables (Temperature and Period and interactions); however, all models returned poor fits

-One model fit well; however, the summary output returned NaNs mostly. Unsure of how to handle this one.

#### **Green crab censor model:**

-Dredged a full model and ran diagnostic plots on the best model.

-I found a good fit for the model that suggests a significantly small increase (.1% for every 1C) for proportion consumption in green crabs.

-Period was left out since it was not in a model ranked high enough in the AIC

#### **Shore crab censor model:**

-Dredged a full model and ran diagnostic plots on the best model.

-I ran an AIC on the best models and different families; however, the fits were not the best.

-When I tried a different model that the AIC did not determine the best - the fit was great

-Further, when looking at the estimates for the temperature slope, I found that this model has a slight significant slope increase (.7% for every temperature unit increase) for proportion consumed.

-I’m likely to believe the best fitting model even though AIC didn’t rank it the highest as it the diagnostic plots show evidence towards it being a good fitting model

-Also, all model summaries indicate this positive consumption increase as temperature increases.

### **I then went back to model each species for the inclusive model**

#### **All Inclusive Model**

- I tried 4 types of models and dredged to find no good models!

-The models I tried were, normal and Gamma GLMs along with normal and Gamma zero-inflated; however, none seemed to fit.

**Rock crab inclusive model**

-I fitted GLM models first and an okay fit; however, there were some concerns over the qqplot, and scale-location plot indicate a wrong fit

-I then moved to zero-inflated models and found a model that fit well!

-The model summary suggests a decrease in decrease consumption as temperature increases AND it also suggests as temperature increases the amount of “0”s or those who aren’t eating are also increasing as temperature increases

**Green crabs (inclusive model)**

-I fitted and dredged GLM models to the data

-I found a great model fit that included temperature and period (no interaction)

-There was no change in consumption across multiple temperatures; however, there was a slight increase in period 2 consumption compared to period 1 (significant)

**Shore crabs (inclusive model)**

-I fitted and dredged GLM models to the data

-I found two models that were great fits (3 outliers that seemed possible to throw out)

-Both models suggested a slight increase in consumption however one includes period and an interaction (between period and temperature).

-I’m leaning on throwing out the model that includes period since there is no significant change and therefore it’s not important to include

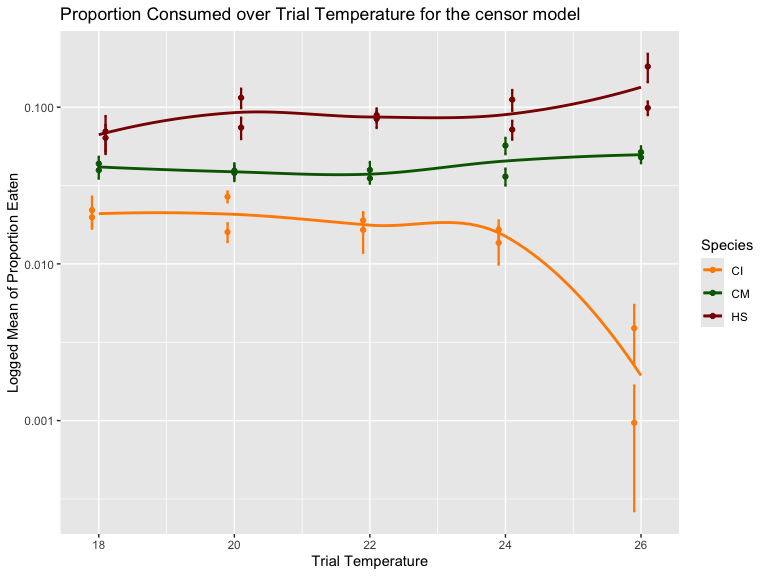
**Result Summary:**

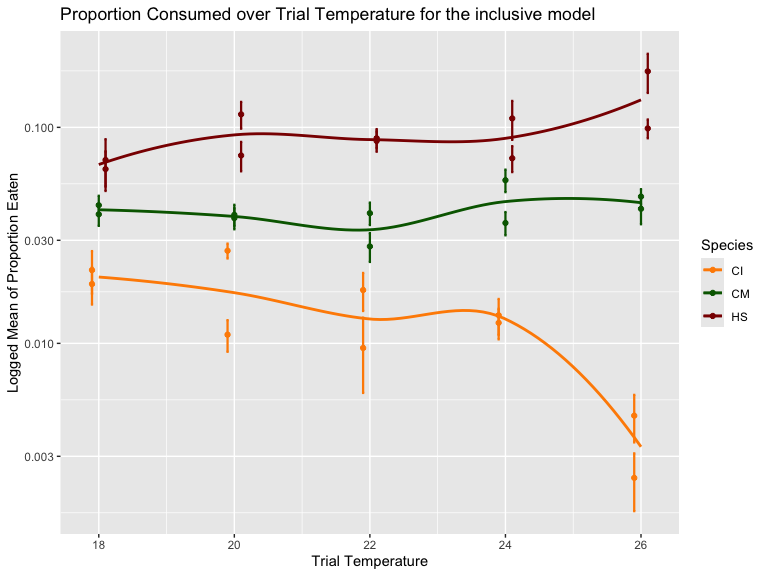
Censor Model:When fitting the censor model all together I couldn’t find a good fitting model; however, when I fit green and shore crabs from the censor data, the models fit well. I ran into trouble when fitting rock crabs as the model fit well (zero-inflated model), but it returned NaN values for its summary output. Both the shore crab and green crab has positive trends between temperature and consumption.

Inclusive Model: When fitting the inclusive model all together, I found that the normal GLM model worked kind of well; however, the fit could possible better by fitting specific species rather than all together. I found great fitting models that support the exploratory graphs at the beginning as well (increase slope for shore crabs, 0 for green crabs, and negative slope for rock crabs). Slope referring to consumption across temperature.

**How to read this section:** This section contains distributions, followed by the best fitting model diagnostic plots and its summary output for each species in each model (censor vs inclusive). The order is as follows:

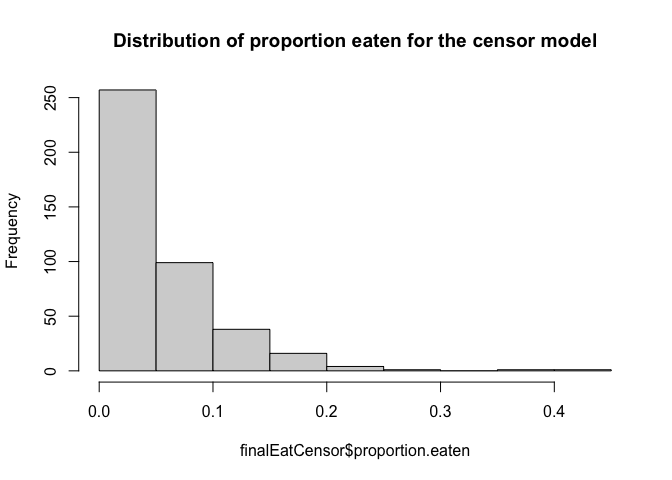
* Exploratory graphs including general summary of the data and distributions plots between all species and total dataset for both censor and inclusive models
* All censor model (note – for this model I put multiple diagnostic plots as there was no one great fit model)
  + Censor model rock crabs
  + Censor model green crabs
  + Censor model shore crabs
* All-inclusive model
  + Inclusive model shore crabs
  + Inclusive model green crabs
  + Inclusive model rock crabs



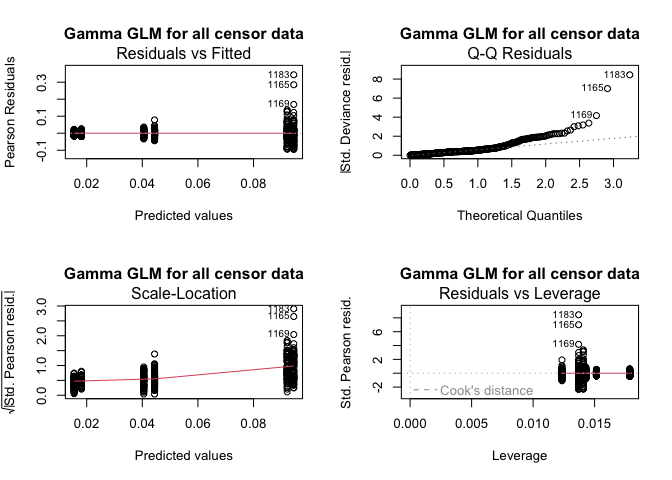
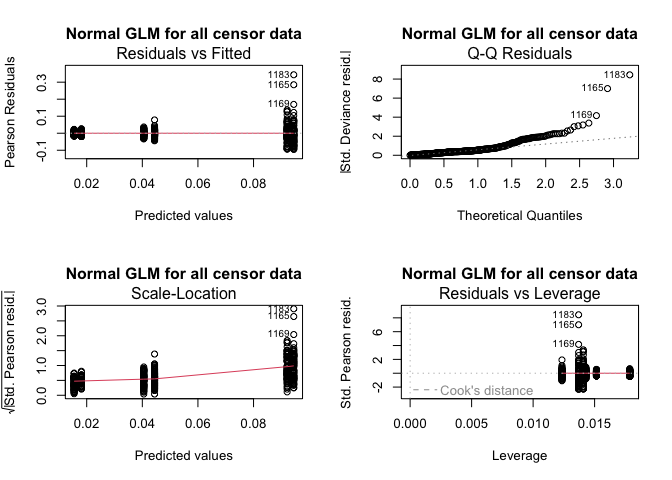


Little to no difference between censor and inclusive model. Start with censor model since it’s safer

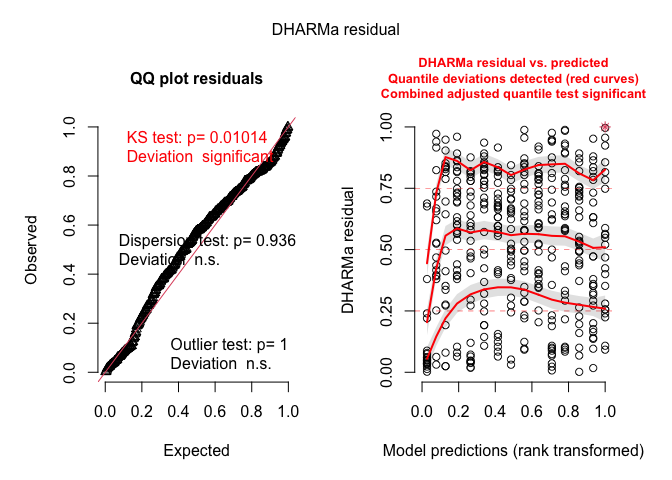
I’ll begin with graphing proportions of the total dataset and then graphing distributions of each species.



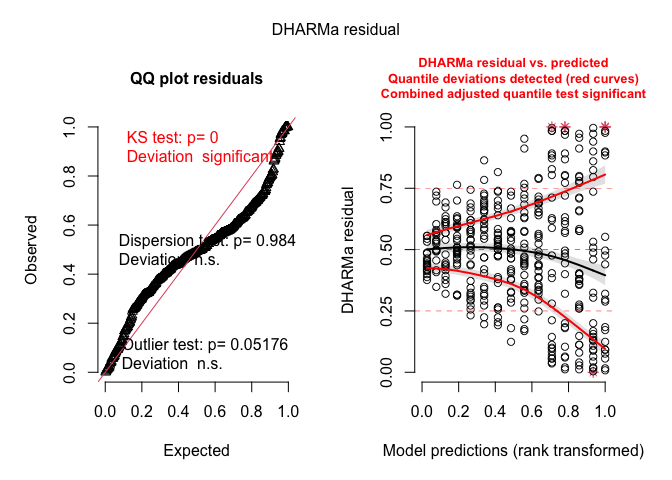
I’ll first model all the data in the censor model (all species). I’m trying zero-inflated models and normal GLMs with Gamma and Gaussian families.



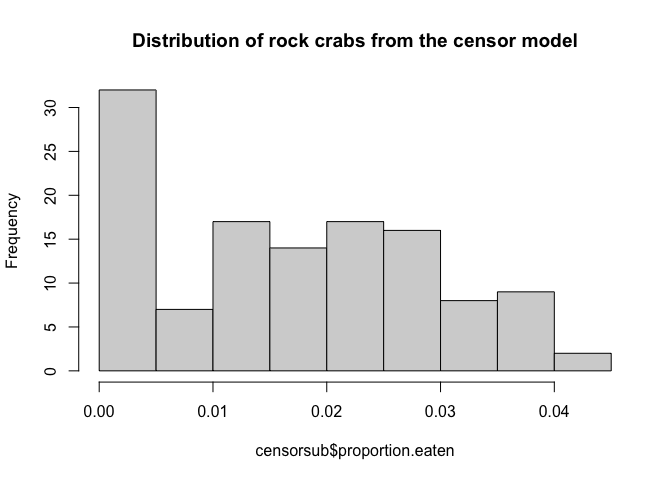
## Zero-inflated Gamma for all censor data

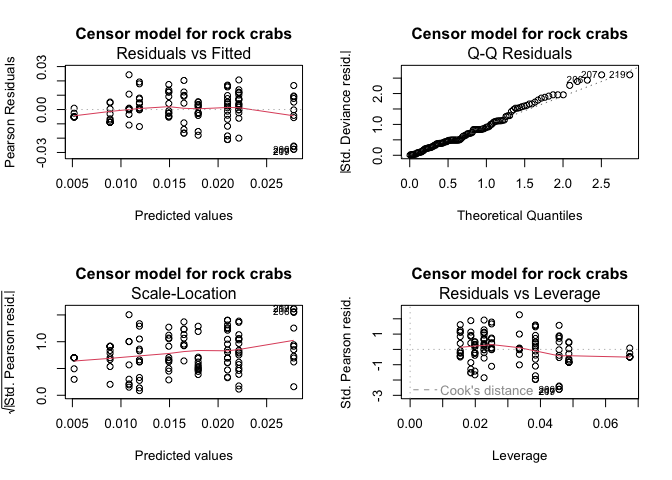


## Zero-inflated normal for all censor data



I tried, zero inflated Gamma (inverse, log, identity) and GLM (identity, log, inverse) and no models returned a good fit Let’s try modeling each species separately since they all have different distributions. We’ll begin with rock crabs. I’ll use zero inflated models since the distribution seems to be zero inflated.



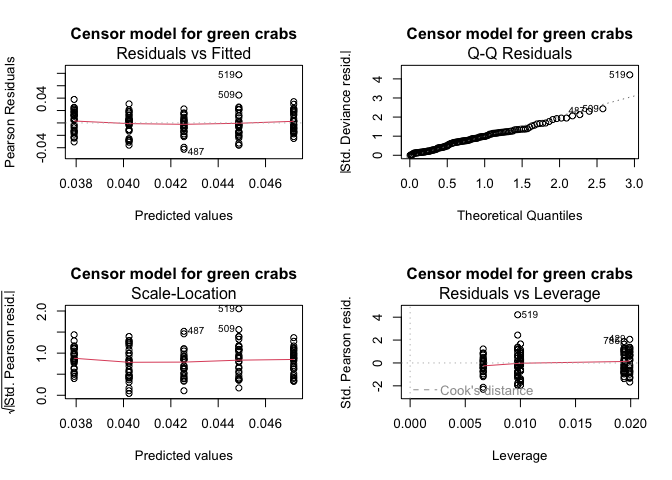
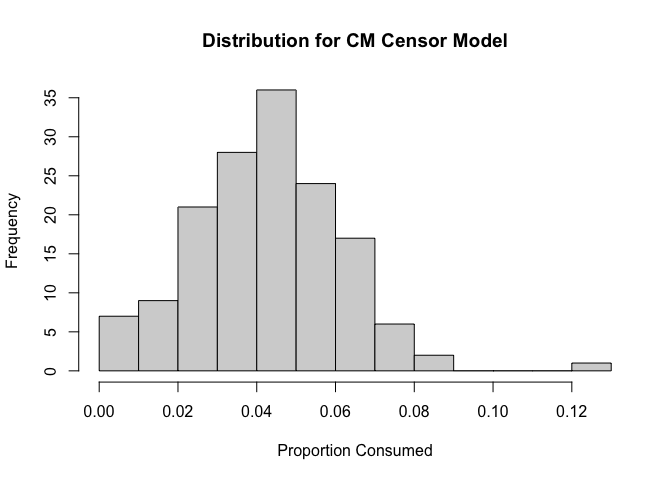


## Summary output for the best GLM Censor model for rock crabs

##   
## Call:  
## glm(formula = proportion.eaten ~ Temperature \* Period, data = censorsub,   
## na.action = "na.fail")  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.0786634 0.0114810 6.852 3.53e-10 \*\*\*  
## Temperature -0.0028263 0.0005314 -5.318 5.04e-07 \*\*\*  
## Period2 -0.0304902 0.0152284 -2.002 0.0476 \*   
## Temperature:Period2 0.0013151 0.0007017 1.874 0.0634 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.0001191032)  
##   
## Null deviance: 0.018927 on 121 degrees of freedom  
## Residual deviance: 0.014054 on 118 degrees of freedom  
## AIC: -750.18  
##   
## Number of Fisher Scoring iterations: 2

Rock crabs didn’t have a great model. The normal GLM model was an okay fit, but potentially alarming due to the scale-location plot.

Next is green crabs. I dredged the full model then compared all the top models within 2 delta units of the top across a normal GLM.

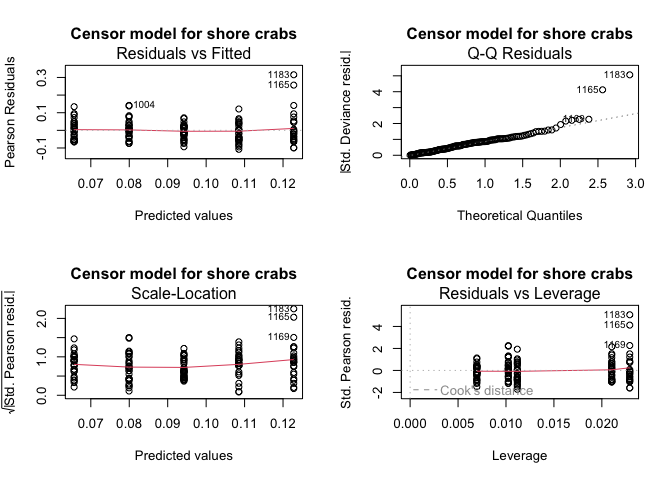
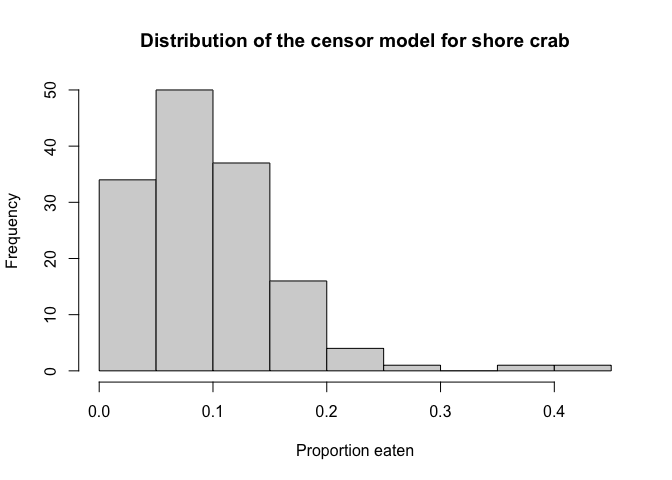


## Summary output for the best GLM Censor model for green crabs

##   
## Call:  
## glm(formula = proportion.eaten ~ Temperature, data = censorsub,   
## na.action = "na.fail")  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.017039 0.011756 1.449 0.1493   
## Temperature 0.001160 0.000529 2.192 0.0299 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.0003435967)  
##   
## Null deviance: 0.052847 on 150 degrees of freedom  
## Residual deviance: 0.051196 on 149 degrees of freedom  
## AIC: -771.88  
##   
## Number of Fisher Scoring iterations: 2

Green crabs had 3 great models, interaction (between period and temperature), additive, and just temperature model all seem like great fits. Models 1 and 2 both say temperature has a significant slight increase while model 3 does not (interaction model). Model 3 also suggests period and its interaction are not different. I am more likely to believe there is a slight increase based on the exploratory graphs and since period is not significant I’ll choose model 1 to go with.

Moving on to the shore crabs. I’ll first try a Gamma since it seems slightly skewed then a normal GLM.



##   
## Call: glm(formula = proportion.eaten ~ Temperature, family = Gamma(link = "inverse"),   
## data = censorsub, na.action = "na.fail")  
##   
## Coefficients:  
## (Intercept) Temperature   
## 29.0951 -0.8191   
##   
## Degrees of Freedom: 143 Total (i.e. Null); 142 Residual  
## Null Deviance: 108   
## Residual Deviance: 101.8 AIC: -409.6

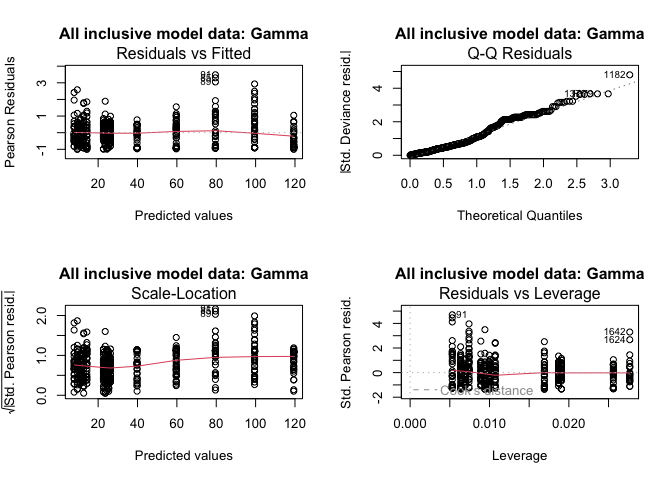
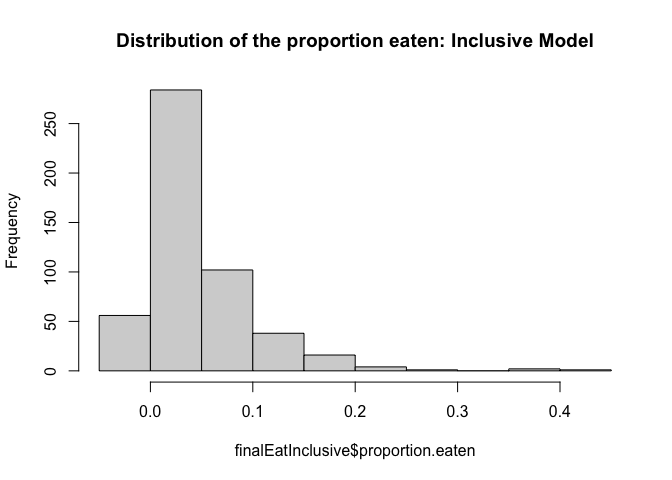
## Summary output for the best GLM Censor model for shore crabs

##   
## Call:  
## glm(formula = proportion.eaten ~ Temperature, data = censorsub,   
## na.action = "na.fail")  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.062881 0.042539 -1.478 0.141571   
## Temperature 0.007141 0.001930 3.700 0.000307 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.003968901)  
##   
## Null deviance: 0.61793 on 143 degrees of freedom  
## Residual deviance: 0.56358 on 142 degrees of freedom  
## AIC: -383.57  
##   
## Number of Fisher Scoring iterations: 2

The normal GLM fit the best; however, it ranked lower on the AIC. There were other higher ranking models according to the AIC but the diagnostic plots proved problematic. Models okay, let’s compare these to the inclusive model and see how they fit over that data.

### **THIS IS NOW SWITCHING TO THE INCLUSIVE MODEL GRAPHS**

I’ll begin with modeling all the data as a whole same way I started with my censor data. I’ll try GLMs and then zero inflated models.



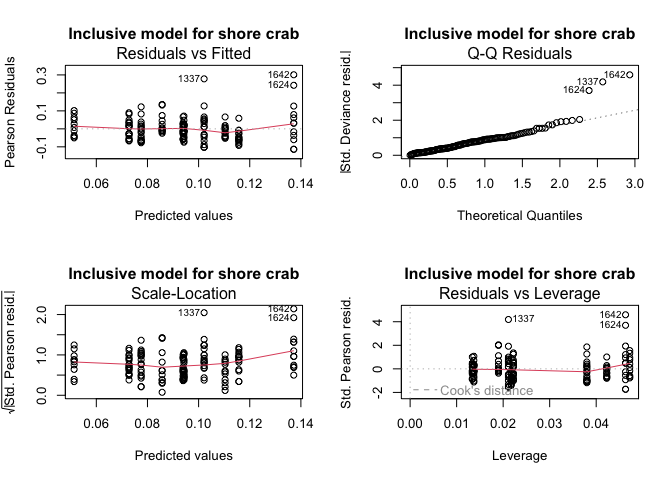
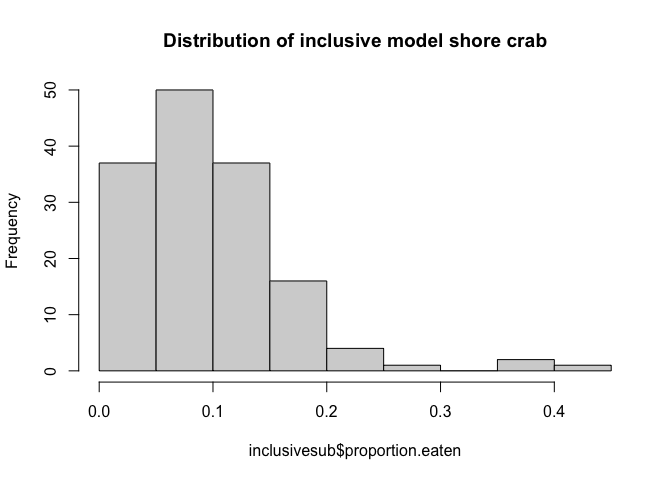
## Summary output for the best GLM Gamma Inclusive model

##   
## Call:  
## glm(formula = proportion.eaten ~ Temperature \* Species.x, family = Gamma(link = "inverse"),   
## data = finalEatInclusivenozero)  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -139.309 28.755 -4.845 1.70e-06 \*\*\*  
## Temperature 9.949 1.410 7.056 5.77e-12 \*\*\*  
## Species.xCM 173.597 30.969 5.606 3.44e-08 \*\*\*  
## Species.xHS 168.145 29.303 5.738 1.66e-08 \*\*\*  
## Temperature:Species.xCM -10.395 1.499 -6.934 1.27e-11 \*\*\*  
## Temperature:Species.xHS -10.758 1.431 -7.519 2.60e-13 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for Gamma family taken to be 0.5517156)  
##   
## Null deviance: 780.13 on 503 degrees of freedom  
## Residual deviance: 447.35 on 498 degrees of freedom  
## AIC: -2430  
##   
## Number of Fisher Scoring iterations: 6

## All inclusive model data: Zero-Inflation

The fits aren’t good. The normal GLMs have an almost good fit, but by modeling each species separately the fits can be better.

I’ll now move to modeling shore crabs which have a normal distribution, so I’ll try normal GLMs.

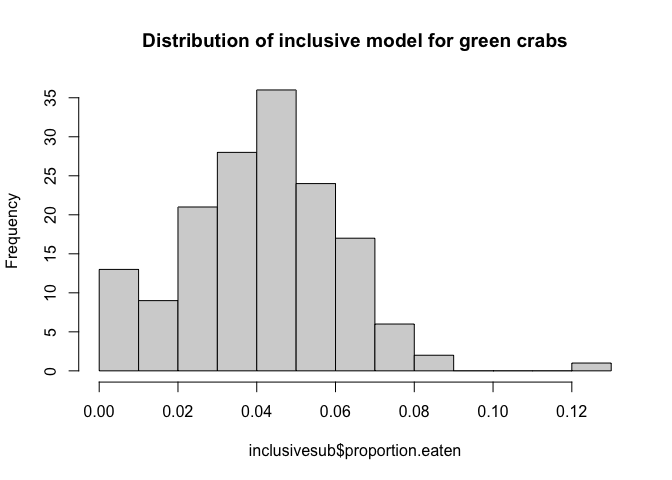


## Summary output for the best GLM Inclusive model for shore crabs

##   
## Call:  
## glm(formula = proportion.eaten ~ Temperature \* Period, data = inclusivesub,   
## na.action = "na.fail")  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) -0.287497 0.148151 -1.941 0.0543 .  
## Temperature 0.017367 0.006688 2.597 0.0104 \*  
## Period 0.145580 0.090690 1.605 0.1106   
## Temperature:Period -0.006632 0.004102 -1.617 0.1081   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.004501282)  
##   
## Null deviance: 0.71409 on 147 degrees of freedom  
## Residual deviance: 0.64818 on 144 degrees of freedom  
## AIC: -373.75  
##   
## Number of Fisher Scoring iterations: 2

Shore crabs had two good models; however, one included period and an interaction with temperature, but the other one did not. Both had great fits, but I’ll go with the model including the period interaction since it can tell us that period has no effect on the model.

Next up is green crabs. Again, their distribution is normal, so I’ll try using normal GLMs.

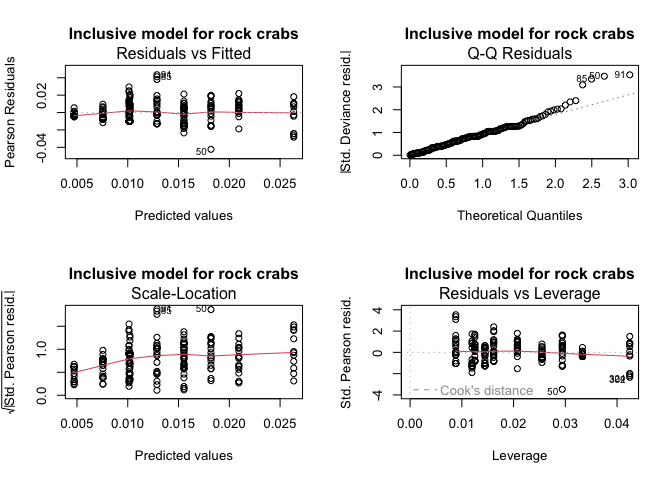
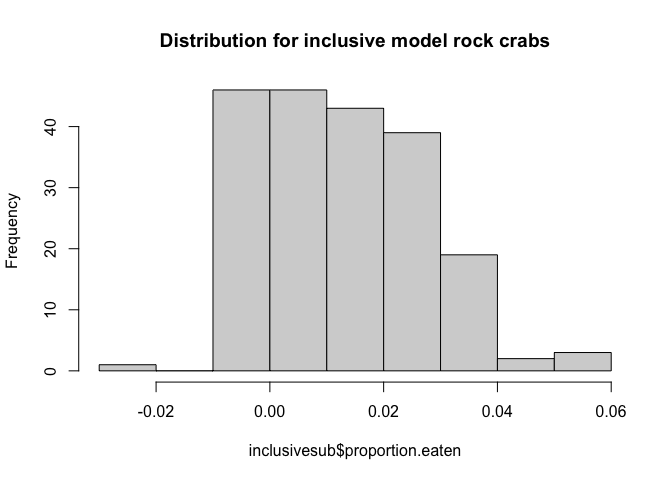


## Summary output for the best GLM Inclusive model for green crabs

##   
## Call:  
## glm(formula = proportion.eaten ~ Temperature + Period, data = inclusivesub,   
## na.action = "na.fail")  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.0117084 0.0135222 0.866 0.3879   
## Temperature 0.0008163 0.0005546 1.472 0.1431   
## Period 0.0074136 0.0031611 2.345 0.0203 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.0003904229)  
##   
## Null deviance: 0.062968 on 156 degrees of freedom  
## Residual deviance: 0.060125 on 154 degrees of freedom  
## AIC: -781.66  
##   
## Number of Fisher Scoring iterations: 2

Green crabs had a good fitting model. The temperature had no effect on proportion consumption for green crabs and there was a slight difference in period between the two.

Next is rock crabs. Their distribution is a bit odd? I’ll try normal and Gamma first then zero-inflated if I have to.

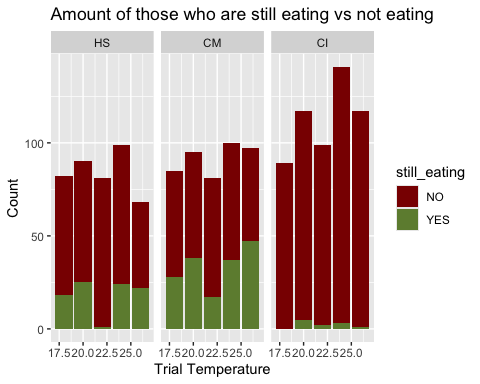
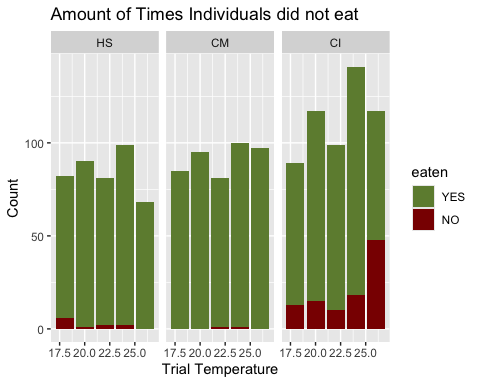


## Inclusive model for rock crabs summary output.

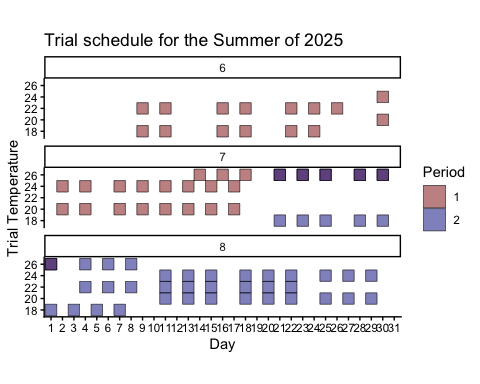
##   
## Call:  
## glm(formula = proportion.eaten ~ Temperature \* Period, data = inclusivesub,   
## na.action = "na.fail")  
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 0.1078706 0.0243033 4.439 1.51e-05 \*\*\*  
## Temperature -0.0040764 0.0010804 -3.773 0.000214 \*\*\*  
## Period -0.0328642 0.0146443 -2.244 0.025946 \*   
## Temperature:Period 0.0013730 0.0006521 2.106 0.036514 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for gaussian family taken to be 0.0001527323)  
##   
## Null deviance: 0.036007 on 198 degrees of freedom  
## Residual deviance: 0.029783 on 195 degrees of freedom  
## AIC: -1177.9  
##   
## Number of Fisher Scoring iterations: 2

The normal GLM looks the best!

**EXTRAS**

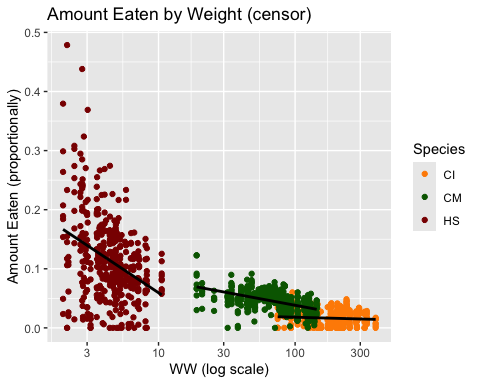


### Schedule

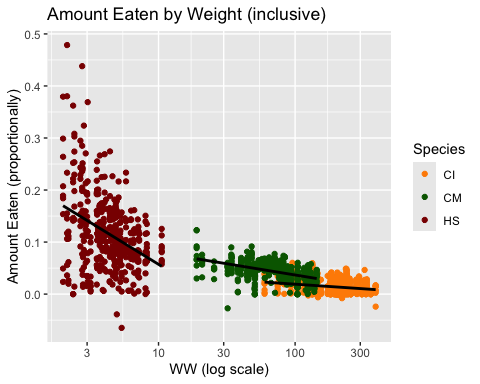


### Size effect on Consumption

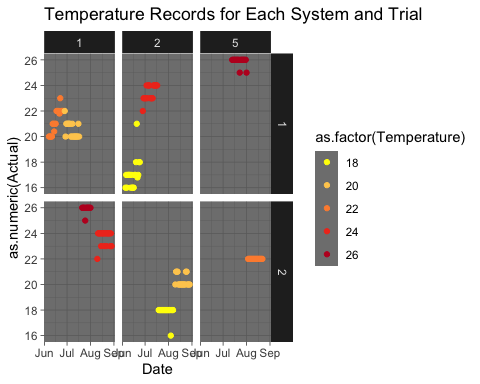
## `geom\_smooth()` using formula = 'y ~ x'



## `geom\_smooth()` using formula = 'y ~ x'



### Graphing the Husbandry Logs



### Graphing Crab mass before and after the experiment

