Mortality Data

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Data Manipulation

```
# read in data
  mort.data <- read.csv("/Users/saraschaal/Documents/Northeastern/LotterhosLab/Research/Field Work/2015/
  mort.data$Treatment_Temperature <- round(mort.data$Treatment_Temperature, digits = 1)

#remove those that could not be identified to the species level
  mort.data <- mort.data[!mort.data$Species == "" & !mort.data$Species == "Hybrid",]

# calculate days dead
  mort.data$DaysDead <- 14-mort.data$Days_Survived
  mort.data$PropDaysSurv <- mort.data$Days_Survived/14

#### Combine Black and Yellowtail Data ####

# Make a new species column that combines black and yellowtail rockfish
  mort.data$Species2 <- NA

  # Find all rows where species is either black or yellowtail and add BY to new species column
    for(i in 1:nrow(mort.data)){
      if(mort.data$Species[i] == "Black" | mort.data$Species[i] == "Yellowtail"){
        mort.data$Species2[i] <- "BY"
      } else {
        mort.data$Species2[i] <- mort.data$Species[i]
      }
    }

  # Factor new species column
  mort.data$Species2 <- as.factor(mort.data$Species2)

  # Set levels to meaningful names
  levels(mort.data$Species2) <- c("Copper", "Quillback", "BY")
```

Analyses

All Species in Model

Binomial - Temperature by Species

```
###################################
#### Species in a Single Model ####
###################################

# Logistic regression for the interaction between temperature and species on survival
```

```r
log.mod.all.prop <- glm(cbind(Days_Survived, DaysDead)~Treatment_Temperature*Species,
                        family = binomial(link = 'logit'), data = mort.data)
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```r
summary(log.mod.all.prop)
```

```
##
## Call:
## glm(formula = cbind(Days_Survived, DaysDead) ~ Treatment_Temperature *
##     Species, family = binomial(link = "logit"), data = mort.data)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -6.9518   0.0000   0.5168   1.5285   3.3222
##
## Coefficients:
##                                         Estimate Std. Error z value
## (Intercept)                              27.9490     6.6715   4.189
## Treatment_Temperature                    -1.1809     0.3045  -3.879
## SpeciesCopper                           -20.5824     6.7818  -3.035
## SpeciesQuillback                        -24.0054     6.7062  -3.580
## SpeciesYellowtail                       112.0576  5971.5966   0.019
## Treatment_Temperature:SpeciesCopper       0.9103     0.3102   2.935
## Treatment_Temperature:SpeciesQuillback    1.0022     0.3067   3.268
## Treatment_Temperature:SpeciesYellowtail  -4.9894   266.5892  -0.019
##                                         Pr(>|z|)
## (Intercept)                              2.8e-05 ***
## Treatment_Temperature                   0.000105 ***
## SpeciesCopper                           0.002406 **
## SpeciesQuillback                        0.000344 ***
## SpeciesYellowtail                       0.985028
## Treatment_Temperature:SpeciesCopper     0.003337 **
## Treatment_Temperature:SpeciesQuillback  0.001084 **
## Treatment_Temperature:SpeciesYellowtail 0.985068
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 548.47  on 97  degrees of freedom
## Residual deviance: 316.21  on 90  degrees of freedom
## AIC: 416.93
##
## Number of Fisher Scoring iterations: 17
```

```r
summary(aov(log.mod.all.prop))
```

```
##  Response Days_Survived :
##                              Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment_Temperature         1  71.73  71.727 10.5009  0.001673 **
## Species                       3 229.61  76.536 11.2050 2.569e-06 ***
## Treatment_Temperature:Species  3  25.48   8.493  1.2434  0.298747
## Residuals                    90 614.75   6.831
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Response DaysDead :
##                               Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment_Temperature          1  71.73  71.727 10.5009  0.001673 **
## Species                        3 229.61  76.536 11.2050 2.569e-06 ***
## Treatment_Temperature:Species  3  25.48   8.493  1.2434  0.298747
## Residuals                     90 614.75   6.831
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
  drop1(log.mod.all.prop)
```

```
## Single term deletions
##
## Model:
## cbind(Days_Survived, DaysDead) ~ Treatment_Temperature * Species
##                               Df Deviance    AIC
## <none>                             316.21 416.93
## Treatment_Temperature:Species  3   340.86 435.58
```

```
  # Best Model
  # It is giving that weird warning because of the Yellowtail data.
  # Its because the "link" score is very large.
  # We have overfit our data
  # Drop the interaction term because it is not significant
  # I don't really understand why this is not significant?
  # The Quillback is apparently not that different from Copper slope .09 different
  # which is driving the lack of an interaction.

# Logistic regression with main effects of temp and species (only for curiosity interaction best model)
  #log.mod.all.prop2 <- glm(cbind(Days_Survived, DaysDead)~Treatment_Temperature+Species,
                           #family = binomial(link = 'logit'), data = mort.data)
  #summary(log.mod.all.prop2)
  #summary(aov(log.mod.all.prop2))

# Logistic regression with interaction of temp and species where black and yellowtail
# are combined into its species complex
  log.mod.all.prop3 <- glm(cbind(Days_Survived, DaysDead)~Treatment_Temperature*Species2,
                           family = binomial(link = 'logit'), data = mort.data)
  summary(log.mod.all.prop3)
```

```
##
## Call:
## glm(formula = cbind(Days_Survived, DaysDead) ~ Treatment_Temperature *
##     Species2, family = binomial(link = "logit"), data = mort.data)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -6.9518   0.0017   0.5338   1.5285   3.3222
##
## Coefficients:
##                                     Estimate Std. Error z value
## (Intercept)                          7.36660    1.21844   6.046
## Treatment_Temperature               -0.27062    0.05912  -4.577
```

```
## Species2Quillback                       -3.42296    1.39622  -2.452
## Species2BY                              21.60257    6.49741   3.325
## Treatment_Temperature:Species2Quillback  0.09193    0.06970   1.319
## Treatment_Temperature:Species2BY        -0.95403    0.29646  -3.218
##                                         Pr(>|z|)
## (Intercept)                             1.49e-09 ***
## Treatment_Temperature                   4.71e-06 ***
## Species2Quillback                       0.014223 *
## Species2BY                              0.000885 ***
## Treatment_Temperature:Species2Quillback 0.187178
## Treatment_Temperature:Species2BY        0.001291 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 548.47  on 97  degrees of freedom
## Residual deviance: 316.96  on 92  degrees of freedom
## AIC: 413.68
##
## Number of Fisher Scoring iterations: 7
```

```
summary(aov(log.mod.all.prop3))
```

```
##  Response Days_Survived :
##                               Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment_Temperature          1  71.73  71.727 10.7245  0.001491 **
## Species2                       2 229.61 114.803 17.1654 4.622e-07 ***
## Treatment_Temperature:Species2  2  24.92  12.462  1.8632  0.160976
## Residuals                      92 615.30   6.688
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Response DaysDead :
##                               Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment_Temperature          1  71.73  71.727 10.7245  0.001491 **
## Species2                       2 229.61 114.803 17.1654 4.622e-07 ***
## Treatment_Temperature:Species2  2  24.92  12.462  1.8632  0.160976
## Residuals                      92 615.30   6.688
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mx <- glm(cbind(Days_Survived, DaysDead)~Treatment_Temperature+Species2,
                        family = binomial(link = 'logit'), data = mort.data)
anova(log.mod.all.prop3, mx)
```

```
## Analysis of Deviance Table
##
## Model 1: cbind(Days_Survived, DaysDead) ~ Treatment_Temperature * Species2
## Model 2: cbind(Days_Survived, DaysDead) ~ Treatment_Temperature + Species2
##   Resid. Df Resid. Dev Df Deviance
## 1        92     316.96
## 2        94     341.64 -2  -24.682
```

```
#lrtest(mx, log.mod.all.prop3)
# AIC is highest for including the interaction (413 compared to 434) BEST MODEL
```

```
  # LRT also chooses the more complex model

# Logistic regression with main effects of temp and species where black and yellowtail
  # are combined into their species complex (curiousity but best model already determined)
  log.mod.all.prop4 <- glm(cbind(Days_Survived, DaysDead)~Treatment_Temperature + Species2,
                           family = binomial(link = 'logit'), data = mort.data)
  summary(log.mod.all.prop4)
```

```
##
## Call:
## glm(formula = cbind(Days_Survived, DaysDead) ~ Treatment_Temperature +
##     Species2, family = binomial(link = "logit"), data = mort.data)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -6.7033   0.3323   0.9080   1.4608   3.2983
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            6.76685    0.65139  10.388  < 2e-16 ***
## Treatment_Temperature -0.24122    0.03131  -7.705 1.31e-14 ***
## Species2Quillback     -1.68004    0.20341  -8.259  < 2e-16 ***
## Species2BY             1.25129    0.28457   4.397 1.10e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 548.47  on 97  degrees of freedom
## Residual deviance: 341.64  on 94  degrees of freedom
## AIC: 434.36
##
## Number of Fisher Scoring iterations: 5
```

```
  summary(aov(log.mod.all.prop4))
```

```
##  Response Days_Survived :
##                       Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment_Temperature  1  71.73  71.727  10.531  0.001627 **
## Species2               2 229.61 114.803  16.856 5.549e-07 ***
## Residuals             94 640.23   6.811
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Response DaysDead :
##                       Df Sum Sq Mean Sq F value    Pr(>F)
## Treatment_Temperature  1  71.73  71.727  10.531  0.001627 **
## Species2               2 229.61 114.803  16.856 5.549e-07 ***
## Residuals             94 640.23   6.811
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Black and Yellowtail ##
 # Logistic Regression Model #
  log.mod.blkyt.prop <- glm(cbind(mort.data$Days_Survived[mort.data$Species=="Black"
```

```
                                                        | mort.data$Species=="Yellowtail"],
                                    mort.data$DaysDead[mort.data$Species=="Black"
                                                        | mort.data$Species=="Yellowtail"])
                                ~Treatment_Temperature,
                               family = binomial(link = 'logit'), data = mort.data[mort.data$Species=="Bla
                                                    | mort.data$Species=="Yellowtail",])
  summary(log.mod.blkyt.prop)
```

```
##
## Call:
## glm(formula = cbind(mort.data$Days_Survived[mort.data$Species ==
##     "Black" | mort.data$Species == "Yellowtail"], mort.data$DaysDead[mort.data$Species ==
##     "Black" | mort.data$Species == "Yellowtail"]) ~ Treatment_Temperature,
##     family = binomial(link = "logit"), data = mort.data[mort.data$Species ==
##         "Black" | mort.data$Species == "Yellowtail", ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.7110   0.0152   0.2251   0.5258   2.6067
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)              28.9692     6.3839   4.538 5.68e-06 ***
## Treatment_Temperature  -1.2246     0.2906  -4.214 2.50e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 89.031  on 37  degrees of freedom
## Residual deviance: 43.608  on 36  degrees of freedom
## AIC: 58.764
##
## Number of Fisher Scoring iterations: 8
```

```
### Copper Rockfish ###

  # Logistic Regression Model
  log.mod.copper.prop <- glm(cbind(mort.data$Days_Survived[mort.data$Species=="Copper"],
                                    mort.data$DaysDead[mort.data$Species=="Copper"])
                              ~Treatment_Temperature,
                             family = binomial(link = 'logit'),
                              data = mort.data[mort.data$Species == "Copper",])
  summary(log.mod.copper.prop)
```

```
##
## Call:
## glm(formula = cbind(mort.data$Days_Survived[mort.data$Species ==
##     "Copper"], mort.data$DaysDead[mort.data$Species == "Copper"]) ~
##     Treatment_Temperature, family = binomial(link = "logit"),
##     data = mort.data[mort.data$Species == "Copper", ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
```

```
## -6.9518   0.5338   0.8438   1.7393   2.4698
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            7.36660    1.21840   6.046 1.48e-09 ***
## Treatment_Temperature -0.27062    0.05912  -4.578 4.70e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 188.45  on 38  degrees of freedom
## Residual deviance: 157.01  on 37  degrees of freedom
## AIC: 195.19
##
## Number of Fisher Scoring iterations: 5
```

```
### Quillback Rockfish ###
  ##### fix this ####
  log.mod.quill.prop <- glm(cbind(mort.data$Days_Survived[mort.data$Species=="Quillback"],
                                  mort.data$DaysDead[mort.data$Species=="Quillback"])
                            ~Treatment_Temperature, family = binomial(link = 'logit'),
                            data = mort.data[mort.data$Species=="Quillback",])
  summary(log.mod.quill.prop)
```

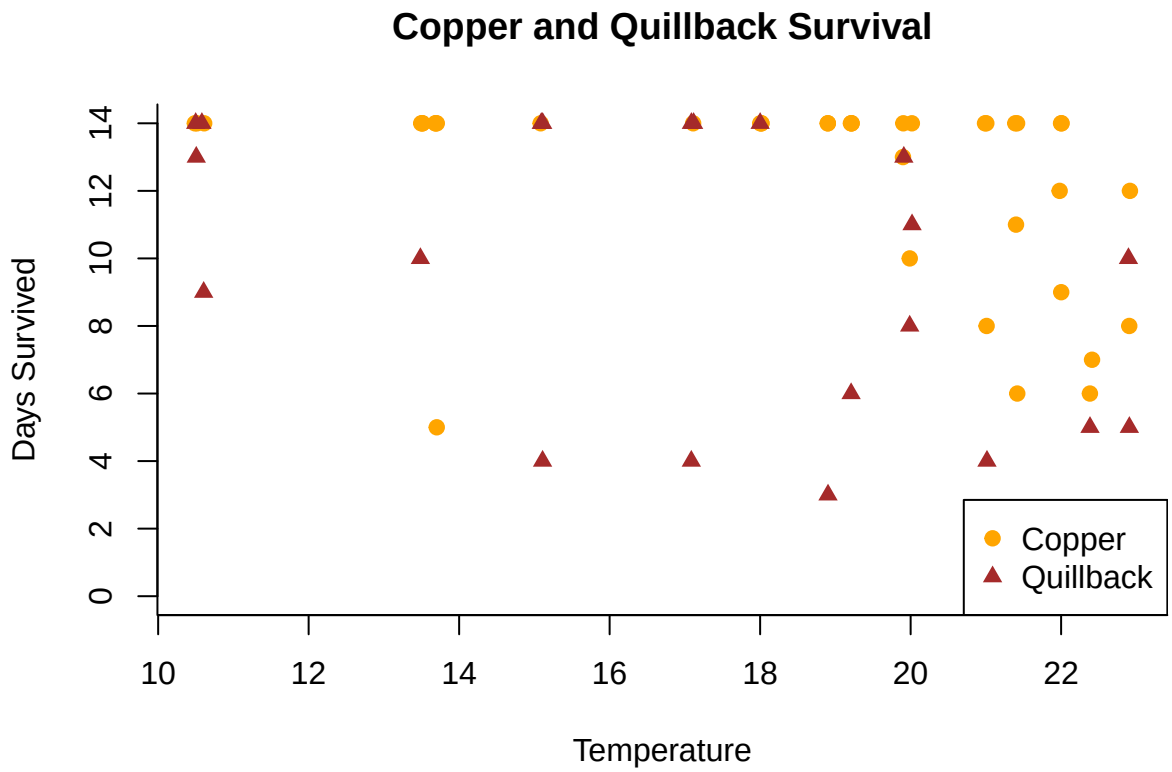
```
##
## Call:
## glm(formula = cbind(mort.data$Days_Survived[mort.data$Species ==
##     "Quillback"], mort.data$DaysDead[mort.data$Species == "Quillback"]) ~
##     Treatment_Temperature, family = binomial(link = "logit"),
##     data = mort.data[mort.data$Species == "Quillback", ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.9040  -1.4912   0.5151   2.6612   3.3222
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            3.94364    0.68178   5.784 7.28e-09 ***
## Treatment_Temperature -0.17868    0.03692  -4.840 1.30e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 143.55  on 20  degrees of freedom
## Residual deviance: 116.34  on 19  degrees of freedom
## AIC: 159.72
##
## Number of Fisher Scoring iterations: 5
```

```
##### fix this ####
```

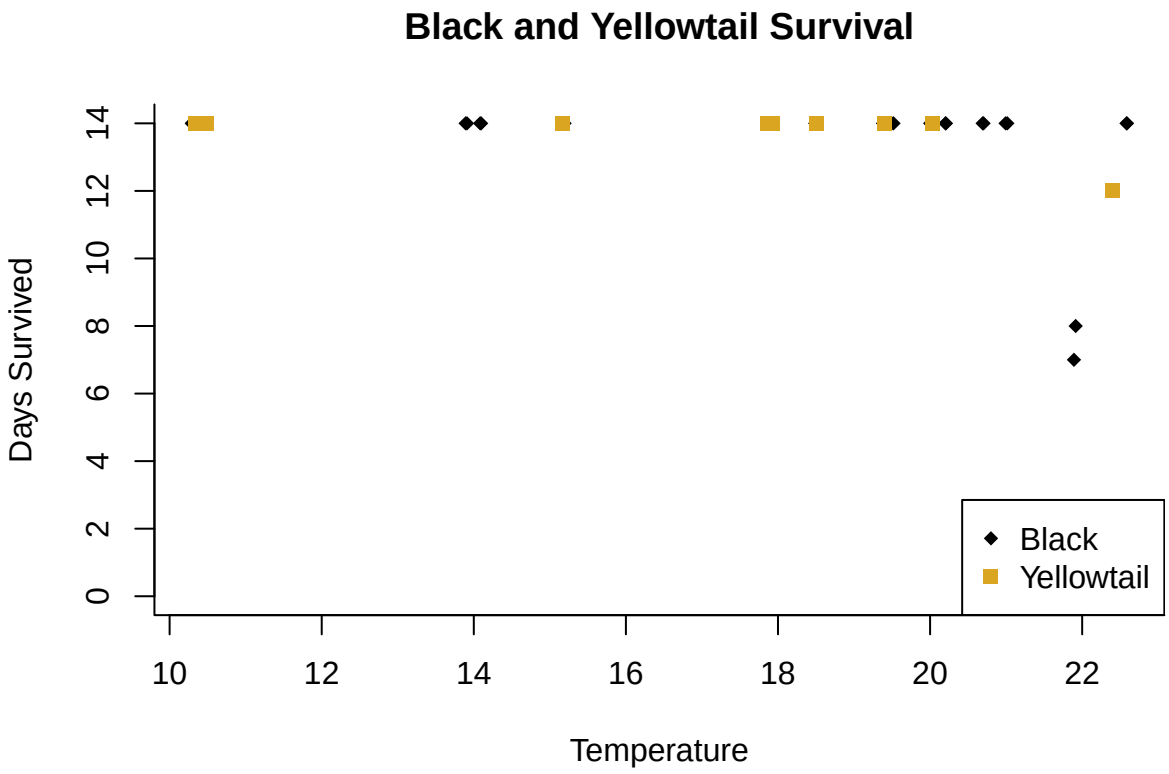
Plotting

Days Survived against Temperature

```
# copper
  plot(mort.data$Days_Survived[mort.data$Species == "Copper"] ~
       jitter(mort.data$Treatment_Temperature[mort.data$Species == "Copper"],1),
       col = "orange",
       pch = 19, bty = "l", ylim = c(0,14), xlab = "Temperature", ylab = "Days Survived",
       main = "Copper and Quillback Survival")
  points(mort.data$Days_Survived[mort.data$Species == "Quillback"] ~
         jitter(mort.data$Treatment_Temperature[mort.data$Species == "Quillback"], 1),
         col = "brown", pch = 17)
  legend("bottomright", legend = c("Copper", "Quillback"), pch = c(19,17), col = c("orange", "brown"))
```




```
# black
  plot(mort.data$Days_Survived[mort.data$Species == "Black"] ~
       jitter(mort.data$Treatment_Temperature[mort.data$Species == "Black"], 1),
       col = "black", pch = 18, bty = "l", ylim = c(0,14), xlab = "Temperature",
       ylab = "Days Survived", main = "Black and Yellowtail Survival")
  points(mort.data$Days_Survived[mort.data$Species == "Yellowtail"] ~
         jitter(mort.data$Treatment_Temperature[mort.data$Species == "Yellowtail"], 1),
         col = "goldenrod", pch = 15)
  legend("bottomright", legend = c("Black", "Yellowtail"), pch = c(18,15), col = c("black", "goldenrod"
```



Proportion of Days Survived Against Temperature with Bar Graph of Predictions at 3 Temperatures (4 panels)

```
# set the plotting window - 4 panels
  par(mfrow = c(2,2))
  par(oma = c(4, 4, 1, 1))
  par(mar = c(2, 2, 1, 1))

###### Panel 1 ######
## Copper Rockfish ##
######################
  plot(PropDaysSurv[mort.data$Species=="Copper"]~Treatment_Temperature[mort.data$Species=="Copper"],
       data = mort.data, pch = 19, col = "orange",
       xlab = "", ylab = "", bty = "l", xaxt = "n", ylim = c(0,1), xlim = c(10,23))

 # Create Prediction for Fitting Data and Standard Error
  cop.prop.daysurv.pred <- predict(log.mod.copper.prop,
                                   data.frame(Treatment_Temperature = 10:23),
                                   se.fit = TRUE)
  points(y=exp(cop.prop.daysurv.pred$fit)/(1+exp(cop.prop.daysurv.pred$fit)), x = 10:23,
         type = "l")
  points(y = exp(cop.prop.daysurv.pred$fit+1.96*cop.prop.daysurv.pred$se.fit)/
           (1+exp(cop.prop.daysurv.pred$fit+1.96*cop.prop.daysurv.pred$se.fit)),
           x = 10:23, type = "l", col = "lightgrey")
  points(y = exp(cop.prop.daysurv.pred$fit-1.96*cop.prop.daysurv.pred$se.fit)/
             (1+exp(cop.prop.daysurv.pred$fit-1.96*cop.prop.daysurv.pred$se.fit)),
           x = 10:23, type = "l", col = "lightgrey")
```

```
  text(14, 0.07, label = "slope = -0.27 +/- 0.06")
 # text(14, 0.03, label = "p < 0.001***")
  legend(19.5, 0.15, legend = "Copper", pch = 19, col = "orange", cex = 0.8)

########### Panel 2 ###########
## Black/Yellowtail Rockfish ##
################################
  plot(mort.data$PropDaysSurv[mort.data$Species=="Black"]~Treatment_Temperature[mort.data$Species=="Bla
       data = mort.data, pch = 18, col = "black",
       xlab = "", ylab = "", bty = "l", yaxt = "n", xlim = c(10,23), ylim = c(0,1))
  points(mort.data$PropDaysSurv[mort.data$Species=="Yellowtail"]~
         Treatment_Temperature[mort.data$Species=="Yellowtail"],
         data = mort.data, pch = 22, bg = "goldenrod", col = "black")

 # Create Prediction for Fitting Data and Standard Error
  blkyt.prop.daysurv.pred <- predict(log.mod.blkyt.prop,
                                     data.frame(Treatment_Temperature = 10:23),
                                     se.fit = TRUE)
  points(y=exp(blkyt.prop.daysurv.pred$fit)/(1+exp(blkyt.prop.daysurv.pred$fit)),
         x = 10:23, type = "l")
  points(y = exp(blkyt.prop.daysurv.pred$fit+1.96*blkyt.prop.daysurv.pred$se.fit)/
           (1+exp(blkyt.prop.daysurv.pred$fit+1.96*blkyt.prop.daysurv.pred$se.fit)),
           x = 10:23, type = "l", col = "darkgrey")
  points(y = exp(blkyt.prop.daysurv.pred$fit-1.96*blkyt.prop.daysurv.pred$se.fit)/
             (1+exp(blkyt.prop.daysurv.pred$fit-1.96*blkyt.prop.daysurv.pred$se.fit)),
           x = 10:23, type = "l", col = "darkgrey")
  text(14, 0.07, label = "slope = -1.22 +/- 0.29")
#  text(14, 0.03, label = "p < 0.001***")
  legend(19.5, 0.2, legend = c("Black", "Yellowtail"), pch = c(18, 22),
         pt.bg = c("black", "goldenrod"), col = c("black", "black"),
         cex = 0.8)

####### Panel 3 ########
## Quillback Rockfish ##
########################

  plot(mort.data$PropDaysSurv[mort.data$Species=="Quillback"]~Treatment_Temperature,
       data = mort.data[mort.data$Species=="Quillback",], pch = 17, col = "brown",
       xlab = "Temperature", ylab = "Proportion of Days Survived", bty = "l", ylim = c(0,1), xlim = c(10

  # Create Prediction for Fitting Data and Standard Error
  quill.prop.daysurv.pred <- predict(log.mod.quill.prop,
                                     data.frame(Treatment_Temperature = 10:23),
                                     se.fit = TRUE)
  points(y=exp(quill.prop.daysurv.pred$fit)/(1+exp(quill.prop.daysurv.pred$fit)), x = 10:23, type = "l"
  points(y = exp(quill.prop.daysurv.pred$fit+1.96*quill.prop.daysurv.pred$se.fit)/
           (1+exp(quill.prop.daysurv.pred$fit+1.96*quill.prop.daysurv.pred$se.fit)),
           x = 10:23, type = "l", col = "lightgrey")
  points(y = exp(quill.prop.daysurv.pred$fit-1.96*quill.prop.daysurv.pred$se.fit)/
             (1+exp(quill.prop.daysurv.pred$fit-1.96*quill.prop.daysurv.pred$se.fit)),
           x = 10:23, type = "l", col = "lightgrey")
  text(14, 0.07, label = "slope = -0.18 +/- 0.04")
#  text(14, 0.03, label = "p < 0.001***")
```

```
  legend(19.5, 0.15, legend = "Quillback", pch = 17, col = "brown", cex = 0.8)

  mtext("Temperature", side = 1, outer = TRUE, cex = 1, line = 2.2)
  mtext("Proportion of Days Survived", side = 2, outer = TRUE, cex = 1, line = 2.2)

### Panel 4 ###
## Bar Graph ##
###############

# Copper rockfish
  cp.fit <- as.data.frame(exp(cop.prop.daysurv.pred$fit)/(1+exp(cop.prop.daysurv.pred$fit)))
  cp.up.CI <- as.data.frame(exp(cop.prop.daysurv.pred$fit+1.96*cop.prop.daysurv.pred$se.fit)/
              (1+exp(cop.prop.daysurv.pred$fit+1.96*cop.prop.daysurv.pred$se.fit)))
  cp.low.CI <- as.data.frame(exp(cop.prop.daysurv.pred$fit-1.96*cop.prop.daysurv.pred$se.fit)/
               (1+exp(cop.prop.daysurv.pred$fit-1.96*cop.prop.daysurv.pred$se.fit)))
  cp.logistic.data <- cbind(cp.fit, cp.up.CI, cp.low.CI)
  colnames(cp.logistic.data) <- c("cp.log.fit", "cp.up.CI", "cp.low.CI")

# Quillback rockfish
  qb.fit <- as.data.frame(exp(quill.prop.daysurv.pred$fit)/(1+exp(quill.prop.daysurv.pred$fit)))
  qb.up.CI <- as.data.frame(exp(quill.prop.daysurv.pred$fit+1.96*quill.prop.daysurv.pred$se.fit)/
              (1+exp(quill.prop.daysurv.pred$fit+1.96*quill.prop.daysurv.pred$se.fit)))
  qb.low.CI <- as.data.frame(exp(quill.prop.daysurv.pred$fit-1.96*quill.prop.daysurv.pred$se.fit)/
               (1+exp(quill.prop.daysurv.pred$fit-1.96*quill.prop.daysurv.pred$se.fit)))
  qb.logistic.data <- cbind(qb.fit, qb.up.CI, qb.low.CI)
  colnames(qb.logistic.data) <- c("qb.log.fit", "qb.up.CI", "qb.low.CI")

# Black & Yellowtail rockfish
  blkyt.fit <- as.data.frame(exp(blkyt.prop.daysurv.pred$fit)/(1+exp(blkyt.prop.daysurv.pred$fit)))
  blkyt.up.CI <- as.data.frame(exp(blkyt.prop.daysurv.pred$fit+1.96*blkyt.prop.daysurv.pred$se.fit)/
              (1+exp(blkyt.prop.daysurv.pred$fit+1.96*blkyt.prop.daysurv.pred$se.fit)))
  blkyt.low.CI <- as.data.frame(exp(blkyt.prop.daysurv.pred$fit-1.96*blkyt.prop.daysurv.pred$se.fit)/
               (1+exp(blkyt.prop.daysurv.pred$fit-1.96*blkyt.prop.daysurv.pred$se.fit)))
  blkyt.logistic.data <- cbind(blkyt.fit, blkyt.up.CI, blkyt.low.CI)
  colnames(blkyt.logistic.data) <- c("blkyt.log.fit", "blkyt.up.CI", "blkyt.low.CI")
  logistic.CI.data <- cbind(cp.logistic.data,qb.logistic.data, blkyt.logistic.data)
  rownames(logistic.CI.data) <- c(10:23)

# Create Data Frame for Bar Graph
  cpfit <- cbind(logistic.CI.data$cp.log.fit[c(5,10,13)])
  qbfit <- cbind(logistic.CI.data$qb.log.fit[c(5,10,13)])
  blkytfit <- cbind(logistic.CI.data$blkyt.log.fit[c(5,10,13)])
  log.fits <- t(cbind(blkytfit, cpfit, qbfit))

# Create Data Frame for upper CI
  cpup <- cbind(logistic.CI.data$cp.up.CI[c(5,10,13)])
  qbup <- cbind(logistic.CI.data$qb.up.CI[c(5,10,13)])
  blkytup <- cbind(logistic.CI.data$blkyt.up.CI[c(5,10,13)])
  up.CI <- t(cbind(blkytup, cpup, qbup))

# Create Data Frame for lower CI
  cplow <- cbind(logistic.CI.data$cp.low.CI[c(5,10,13)])
  qblow <- cbind(logistic.CI.data$qb.low.CI[c(5,10,13)])
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```r
  blkytlow <- cbind(logistic.CI.data$blkyt.low.CI[c(5,10,13)])
  low.CI <- t(cbind(blkytlow, cplow, qblow))

# Create barplot of
  par(lwd = 2)
  bp <- barplot(log.fits, beside = T, names = c("14°C", "19°C", "22°C"),
                col = c("black","orange", "brown"), border = c("goldenrod", NA, NA),
                ylim = c(0,1.12), ylab = "Proportion of Days Survived")
  par(lwd = 1)
  legend("topright", legend = c("Black & Yellowtail", "Copper", "Quillback"),
         fill = c("black", "orange", "brown"), border = c("goldenrod", NA, NA),
         cex = 0.55)
  arrows(x0 = bp, x1 = bp, y0 = low.CI, y1 = up.CI, angle = 90, len = 0.1, code = 3, xpd = NA,
         col = "darkgrey")
```

```
## Warning in arrows(x0 = bp, x1 = bp, y0 = low.CI, y1 = up.CI, angle = 90, :
## zero-length arrow is of indeterminate angle and so skipped
```