MED Gear Comparison Analysis

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NOTE: References throughout this document to trade names does not imply endorsement by the National Marine Fisheries Service, NOAA.

Introduction

This document presents full statistical results and describes the R code used to conduct the analysis in Wainwright et al. *"Effect of a mammal excluder device on catches of small pelagic fishes"*. Data and scripts for the analysis are available in the R package 'GearComparisonAnalysis2018' available on GitHub.

NOTE: "R" is open source software freely available from the R Project.

Part 1: Read and Summarize data

First, read in the data.

```
#data.dir <- '.'  #Directory where the data files resides
MMEDdata <- read.csv(system.file('extdata','AllSppCounts&Lengths.csv',
                                 package = "GearComparisonAnalysis2018"))
# print(summary(MMEDdata))
```

Fix some data problems. Create consistent haul numbers, filter out "experimental" hauls, and change Chinook and coho salmon "species" names to reflect age groups. Some species are renamed to make nicer plot labels, and months and times are recoded.

```
# Haul ID is last three characters of station code:
MMEDdata$Station <- as.character(MMEDdata$Station) #remove factor levels
MMEDdata$Haul <- with(MMEDdata, substr(Station, nchar(Station)-2, nchar(Station)))
# Excluder code (Y or N) is last character of station code:
MMEDdata$Excluder <- with(MMEDdata, substr(Station, nchar(Station), nchar(Station)))
# Filter out "experimental" hauls:
MMEDdata <- MMEDdata[-grep('*X$', MMEDdata$Haul), ]
# Recode MMED types to Standard short labels
### NOTE: work around database error where some records with Excluder code "N"
###   have MMED code "Yes; Up"
MMEDdata$MMED <- as.character(MMEDdata$MMED) #remove factor levels
MMEDdata$MMED[MMEDdata$Excluder == "N"] <- "None"
MMEDdata$MMED[MMEDdata$Excluder == "Y" & grepl("Up", MMEDdata$MMED)] <- "Up"
MMEDdata$MMED[MMEDdata$Excluder == "Y" & grepl("Down", MMEDdata$MMED)] <- "Down"
# Fix a few species names, add age-classes for Chinook & coho
MMEDdata$Species <- toupper(as.character(MMEDdata$Species))    #all upper case
MMEDdata$Species[MMEDdata$Species %in% 'CALIFORNIA MARKET SQUID'] <- 'MARKET SQUID'
MMEDdata$Species[grepl('SMELT',MMEDdata$Species)] <- "SMELT SPP."
MMEDdata$SpecAge <- as.character(MMEDdata$Species)
.index <- MMEDdata$SpecAge %in% 'CHINOOK SALMON'
.newnames <- paste('CHINOOK', MMEDdata$AgeGp[.index])
```

```
MMEDdata$SpecAge[.index] <- .newnames
.index <- MMEDdata$SpecAge %in% 'COHO SALMON'
.newnames <- paste('COHO', MMEDdata$AgeGp[.index])
MMEDdata$SpecAge[.index] <- .newnames
MMEDdata$SpecAge[MMEDdata$SpecAge %in%
    c('CHINOOK subadult/adult','CHINOOK mixed age juvenile')] <- 'CHINOOK subadult'
MMEDdata$SpecAge[MMEDdata$SpecAge %in% 'COHO subadult/adult'] <- 'COHO subadult'
MMEDdata$SpecAge <- factor(as.character(MMEDdata$SpecAge))
# print(summary(MMEDdata))
```

Divide the hauls into analytic "blocks" which are combinations of Date X Location. There are 12 blocks ("A" through "L"), with the following number of hauls in each:

- May 2011: block A : 10, B : 10
- July 2011: C : 4, D : 4, E : 10
- Jun-Jul 2014: F : 4, G : 4, H : 8
- July 2015: I : 8, J : 8, K : 8, L : 8

```
# sequential along the sorted haul numbers,
blocks <- as.factor(c(rep('A',10), rep('B',10), rep('C', 4), rep('D', 4),
                      rep('E',10), rep('F', 4), rep('G', 4), rep('H', 8),
                      rep('I', 8), rep('J', 8), rep('K', 8), rep('L', 8)))
sortHauls <- sort(unique(MMEDdata$Haul))
MMEDdata$Block <- blocks[match(MMEDdata$Haul, sortHauls)]
# print(with(MMEDdata, t(tapply(as.character(Block), list(Haul,MMED), unique))))
```

Then, create a summary table of total catch by species and gear type (None=="without MED", Down=="with downward MED", Up=="with upward MED"), ...

```
cat('\n*** Total Catch By Species and Gear Type ***\n')
```

```
##
## *** Total Catch By Species and Gear Type ***
```

```
tab1 <- with(MMEDdata, tapply(Number, list(SpecAge, MMED), sum, na.rm=T))
tab1[is.na(tab1)] <- 0  #Missing values are actually zero counts
tab1 <- cbind(tab1, Total=apply(tab1, 1, sum))
print(tab1[ , c('Down', 'Up', 'None', 'Total')])
```

```
##                                  Down   Up  None  Total
## AMERICAN SHAD                       6    0     6     12
## BLACK ROCKFISH                      0    1     5      6
## BLUE SHARK                          0    0     1      1
## CABEZON                             0    1     0      1
## CHINOOK subadult                   28   36    59    123
## CHINOOK subyearling               191  713  1092   1996
## CHINOOK yearling                   90  223   364    677
## CHUM SALMON                        54    0   173    227
## COHO subadult                      41   25    61    127
## COHO yearling                      38   24   194    256
## COMB JELLIES                        0    0     0      0
## CUTTHROAT TROUT                     0    0     4      4
## EGGYOLK JELLY                      29    2    41     72
## FISH                                0    2     0      2
## FLATFISHES                          0    1     3      4
## HORMIPHORA CUCUMIS                  0    0     0      0
```

```
## HYBRID STEELHEAD AND CUTTHROAT TROUT     0    0     1      1
## JACK MACKEREL                            0    9    13     22
## LINGCOD                                  0    0     1      1
## LION'S MANE JELLY                        0    0     3      3
## MARKET SQUID                          2160  258  8285  10703
## MOON JELLY                           10259    2  1377  11638
## NORTHERN ANCHOVY                         2  200  3073   3275
## OCEAN SUNFISH                            0    1     0      1
## PACIFIC CHUB MACKEREL                    0    3     2      5
## PACIFIC HERRING                       1755   58   563   2376
## PACIFIC POMPANO                          7    0     5     12
## PACIFIC SANDDAB                          0    0     4      4
## PACIFIC SANDFISH                         0    0     1      1
## PACIFIC SARDINE                          0   45    75    120
## PACIFIC SPINY DOGFISH                    0    3     5      8
## PACIFIC STAGHORN SCULPIN                 0    1     0      1
## PACIFIC TOMCOD                           0   15    22     37
## PINK SALMON                              0    1     1      2
## REX SOLE                                 0    0     1      1
## SALPS                                    0    0     0      0
## SEA NETTLE                              21 1285  1422   2728
## SHINER PERCH                             1    0     0      1
## SMELT SPP.                             120  464  2221   2805
## SOCKEYE SALMON                           0    0    22     22
## STARRY FLOUNDER                          0    3     2      5
## STEELHEAD                                1    3     6     10
## THRESHER SHARK                           0    0     1      1
## TOPE                                     0    0     7      7
## WATER JELLY                          53291  528 71472 125291
## WESTERN RIVER LAMPREY                    6    2    16     24
## WOLF-EEL                                 6    2    29     37
## YELLOWTAIL ROCKFISH                      0    0     1      1
```

. . . and the same for number measured and subsampling rate (for size-selectivity analysis), . . .

```
cat('\n*** Total Number Measured By Species and Gear Type ***\n')
```

```
##
## *** Total Number Measured By Species and Gear Type ***
```

```
tab4 <- with(MMEDdata[!is.na(MMEDdata$Length), ],
             tapply(Number, list(SpecAge, MMED), sum, na.rm=T))
tab4[is.na(tab4)] <- 0  #Missing values are actually zero counts
tab4 <- cbind(tab4, Total=apply(tab4, 1, sum))
print(tab4[ , c('Down', 'Up', 'None', 'Total')])
```

```
##                                  Down  Up None Total
## AMERICAN SHAD                       6   0    6    12
## BLACK ROCKFISH                      0   1    5     6
## BLUE SHARK                          0   0    1     1
## CABEZON                             0   1    0     1
## CHINOOK subadult                   28  36   59   123
## CHINOOK subyearling               142 713 1035  1890
## CHINOOK yearling                   90 223  363   676
## CHUM SALMON                        54   0  173   227
## COHO subadult                      41  25   61   127
```

```
## COHO yearling                            38  24  194   256
## COMB JELLIES                              0   0    0     0
## CUTTHROAT TROUT                           0   0    4     4
## EGGYOLK JELLY                            23   2   15    40
## FISH                                      0   0    0     0
## FLATFISHES                                0   0    2     2
## HORMIPHORA CUCUMIS                        0   0    0     0
## HYBRID STEELHEAD AND CUTTHROAT TROUT      0   0    1     1
## JACK MACKEREL                             0   9   13    22
## LINGCOD                                   0   0    1     1
## LION'S MANE JELLY                         0   0    3     3
## MARKET SQUID                            347 189  582  1118
## MOON JELLY                              111   2  149   262
## NORTHERN ANCHOVY                          2 152  241   395
## OCEAN SUNFISH                             0   1    0     1
## PACIFIC CHUB MACKEREL                     0   3    2     5
## PACIFIC HERRING                          41  31   73   145
## PACIFIC POMPANO                           7   0    5    12
## PACIFIC SANDDAB                           0   0    4     4
## PACIFIC SANDFISH                          0   0    1     1
## PACIFIC SARDINE                           0  45   54    99
## PACIFIC SPINY DOGFISH                     0   3    5     8
## PACIFIC STAGHORN SCULPIN                  0   1    0     1
## PACIFIC TOMCOD                            0  15   22    37
## PINK SALMON                               0   1    1     2
## REX SOLE                                  0   0    1     1
## SALPS                                     0   0    0     0
## SEA NETTLE                               21 536  623  1180
## SHINER PERCH                              1   0    0     1
## SMELT SPP.                               44  60   99   203
## SOCKEYE SALMON                            0   0   22    22
## STARRY FLOUNDER                           0   3    2     5
## STEELHEAD                                 1   3    6    10
## THRESHER SHARK                            0   0    1     1
## TOPE                                      0   0    7     7
## WATER JELLY                             385 306  639  1330
## WESTERN RIVER LAMPREY                     6   2   16    24
## WOLF-EEL                                  6   2   29    37
## YELLOWTAIL ROCKFISH                       0   0    1     1
```

```
cat('\n*** Average Subsampling Rate By Species and Gear Type ***\n')
```

```
##
## *** Average Subsampling Rate By Species and Gear Type ***
```

```
tab5 <- round(tab4/tab1,2)
print(tab5[ , c('Down', 'Up', 'None', 'Total')])
```

```
##                                    Down   Up None Total
## AMERICAN SHAD                      1.00  NaN 1.00  1.00
## BLACK ROCKFISH                      NaN 1.00 1.00  1.00
## BLUE SHARK                          NaN  NaN 1.00  1.00
## CABEZON                             NaN 1.00  NaN  1.00
## CHINOOK subadult                   1.00 1.00 1.00  1.00
## CHINOOK subyearling                0.74 1.00 0.95  0.95
```

```
## CHINOOK yearling                     1.00 1.00 1.00  1.00
## CHUM SALMON                          1.00  NaN 1.00  1.00
## COHO subadult                        1.00 1.00 1.00  1.00
## COHO yearling                        1.00 1.00 1.00  1.00
## COMB JELLIES                          NaN  NaN  NaN   NaN
## CUTTHROAT TROUT                       NaN  NaN 1.00  1.00
## EGGYOLK JELLY                        0.79 1.00 0.37  0.56
## FISH                                  NaN 0.00  NaN  0.00
## FLATFISHES                            NaN 0.00 0.67  0.50
## HORMIPHORA CUCUMIS                    NaN  NaN  NaN   NaN
## HYBRID STEELHEAD AND CUTTHROAT TROUT  NaN  NaN 1.00  1.00
## JACK MACKEREL                         NaN 1.00 1.00  1.00
## LINGCOD                               NaN  NaN 1.00  1.00
## LION'S MANE JELLY                     NaN  NaN 1.00  1.00
## MARKET SQUID                         0.16 0.73 0.07  0.10
## MOON JELLY                           0.01 1.00 0.11  0.02
## NORTHERN ANCHOVY                     1.00 0.76 0.08  0.12
## OCEAN SUNFISH                         NaN 1.00  NaN  1.00
## PACIFIC CHUB MACKEREL                 NaN 1.00 1.00  1.00
## PACIFIC HERRING                      0.02 0.53 0.13  0.06
## PACIFIC POMPANO                      1.00  NaN 1.00  1.00
## PACIFIC SANDDAB                       NaN  NaN 1.00  1.00
## PACIFIC SANDFISH                      NaN  NaN 1.00  1.00
## PACIFIC SARDINE                       NaN 1.00 0.72  0.82
## PACIFIC SPINY DOGFISH                 NaN 1.00 1.00  1.00
## PACIFIC STAGHORN SCULPIN              NaN 1.00  NaN  1.00
## PACIFIC TOMCOD                        NaN 1.00 1.00  1.00
## PINK SALMON                           NaN 1.00 1.00  1.00
## REX SOLE                              NaN  NaN 1.00  1.00
## SALPS                                 NaN  NaN  NaN   NaN
## SEA NETTLE                           1.00 0.42 0.44  0.43
## SHINER PERCH                         1.00  NaN  NaN  1.00
## SMELT SPP.                           0.37 0.13 0.04  0.07
## SOCKEYE SALMON                        NaN  NaN 1.00  1.00
## STARRY FLOUNDER                       NaN 1.00 1.00  1.00
## STEELHEAD                            1.00 1.00 1.00  1.00
## THRESHER SHARK                        NaN  NaN 1.00  1.00
## TOPE                                  NaN  NaN 1.00  1.00
## WATER JELLY                          0.01 0.58 0.01  0.01
## WESTERN RIVER LAMPREY                1.00 1.00 1.00  1.00
## WOLF-EEL                             1.00 1.00 1.00  1.00
## YELLOWTAIL ROCKFISH                   NaN  NaN 1.00  1.00
```

... and, do the same for frequency of catch.

```
cat('\n*** Frequency of Catch By Species and Gear Type ***\n')
```

```
##
## *** Frequency of Catch By Species and Gear Type ***
```

```
.tmp.all <- with(MMEDdata, table(SpecAge, Haul))
.tmp.std <- with(MMEDdata[MMEDdata$MMED=='None', ], table(SpecAge, Haul))
.tmp.up <- with(MMEDdata[MMEDdata$MMED=='Up', ], table(SpecAge, Haul))
.tmp.dwn <- with(MMEDdata[MMEDdata$MMED=='Down', ], table(SpecAge, Haul))
tab2 <- cbind(apply(.tmp.dwn>0, 1, sum),     # Num. occurrences in STD
              apply(.tmp.up>0, 1, sum),      # . . .
```

```
              apply(.tmp.std>0, 1, sum),     # . . .
              apply(.tmp.all>0, 1, sum))    # Total Num. occurrences
colnames(tab2) <- c('Down','Up','None','Total')
print(tab2)
```

```
##                                     Down Up None Total
## AMERICAN SHAD                          2  0    3     5
## BLACK ROCKFISH                         0  1    2     3
## BLUE SHARK                             0  0    1     1
## CABEZON                                0  1    0     1
## CHINOOK subadult                      13 19   27    59
## CHINOOK subyearling                   14 18   31    63
## CHINOOK yearling                      13 16   37    66
## CHUM SALMON                           12  0   21    33
## COHO subadult                         14 11   25    50
## COHO yearling                         13 15   32    60
## COMB JELLIES                           0  2    2     4
## CUTTHROAT TROUT                        0  0    3     3
## EGGYOLK JELLY                         15  2    8    25
## FISH                                   0  1    0     1
## FLATFISHES                             0  1    4     5
## HORMIPHORA CUCUMIS                     0  0    1     1
## HYBRID STEELHEAD AND CUTTHROAT TROUT   0  0    1     1
## JACK MACKEREL                          0  3    2     5
## LINGCOD                                0  0    1     1
## LION'S MANE JELLY                      0  0    1     1
## MARKET SQUID                          16 16   36    68
## MOON JELLY                            16  2   15    33
## NORTHERN ANCHOVY                       2  8   10    20
## OCEAN SUNFISH                          0  1    0     1
## PACIFIC CHUB MACKEREL                  0  2    2     4
## PACIFIC HERRING                        4  2   10    16
## PACIFIC POMPANO                        6  0    1     7
## PACIFIC SANDDAB                        0  0    3     3
## PACIFIC SANDFISH                       0  0    1     1
## PACIFIC SARDINE                        0  3    4     7
## PACIFIC SPINY DOGFISH                  0  3    5     8
## PACIFIC STAGHORN SCULPIN               0  1    0     1
## PACIFIC TOMCOD                         0  4    5     9
## PINK SALMON                            0  1    1     2
## REX SOLE                               0  0    1     1
## SALPS                                  0  6    5    11
## SEA NETTLE                             6 17   26    49
## SHINER PERCH                           1  0    0     1
## SMELT SPP.                             7  2    9    18
## SOCKEYE SALMON                         0  0    7     7
## STARRY FLOUNDER                        0  2    2     4
## STEELHEAD                              1  3    3     7
## THRESHER SHARK                         0  0    1     1
## TOPE                                   0  0    3     3
## WATER JELLY                           16 17   29    62
## WESTERN RIVER LAMPREY                  5  2    9    16
## WOLF-EEL                               4  2   14    20
## YELLOWTAIL ROCKFISH                    0  0    1     1
```

Also, look at species by cruise to see which are "regularly caught." The final two columns give the number of cruises with nonzero catch ("Ngt0") and catch > 1 ("Ngt1") for each species.

```
cat('\n*** Total Catch By Species and Cruise ***\n')
```

```
##
## *** Total Catch By Species and Cruise ***
```

```
tab3 <- with(MMEDdata, tapply(Number, list(SpecAge, Cruise), sum, na.rm=T))
tab3[is.na(tab3)] <- 0  #Missing values are actually zero counts
ngt0 <- apply(tab3>0, 1, sum)
ngt1 <- apply(tab3>1, 1, sum)
tab3 <- cbind(tab3, Ngt0=ngt0, Ngt1=ngt1)
print(tab3)
```

```
##                                      41   43   50     53 Ngt0 Ngt1
## AMERICAN SHAD                         0    1    0     11    2    1
## BLACK ROCKFISH                        0    1    1      4    3    1
## BLUE SHARK                            0    1    0      0    1    0
## CABEZON                               0    0    1      0    1    0
## CHINOOK subadult                     21   42   11     49    4    4
## CHINOOK subyearling                   8 1451   53    484    4    4
## CHINOOK yearling                    472    9   25    171    4    4
## CHUM SALMON                          19    2    1    205    4    3
## COHO subadult                         6   31   34     56    4    4
## COHO yearling                       124   16   20     96    4    4
## COMB JELLIES                          0    0    0      0    0    0
## CUTTHROAT TROUT                       3    1    0      0    2    1
## EGGYOLK JELLY                         1    0    1     70    3    1
## FISH                                  2    0    0      0    1    1
## FLATFISHES                            1    0    0      3    2    1
## HORMIPHORA CUCUMIS                    0    0    0      0    0    0
## HYBRID STEELHEAD AND CUTTHROAT TROUT  0    0    0      1    1    0
## JACK MACKEREL                         0   22    0      0    1    1
## LINGCOD                               1    0    0      0    1    0
## LION'S MANE JELLY                     0    0    3      0    1    1
## MARKET SQUID                        126  899   65   9613    4    4
## MOON JELLY                            0    1    1  11636    3    1
## NORTHERN ANCHOVY                      0 2827  445      3    3    3
## OCEAN SUNFISH                         0    1    0      0    1    0
## PACIFIC CHUB MACKEREL                 4    0    1      0    2    1
## PACIFIC HERRING                       2    2  608   1764    4    4
## PACIFIC POMPANO                       0    0    0     12    1    1
## PACIFIC SANDDAB                       0    0    0      4    1    1
## PACIFIC SANDFISH                      0    0    0      1    1    0
## PACIFIC SARDINE                     111    8    0      1    3    2
## PACIFIC SPINY DOGFISH                 1    2    2      3    4    3
## PACIFIC STAGHORN SCULPIN              0    0    1      0    1    0
## PACIFIC TOMCOD                        0    0   37      0    1    1
## PINK SALMON                           0    2    0      0    1    1
## REX SOLE                              0    0    0      1    1    0
## SALPS                                 0    0    0      0    0    0
## SEA NETTLE                            0 1570 1111     47    3    3
## SHINER PERCH                          0    0    0      1    1    0
## SMELT SPP.                            0    0 2582    223    2    2
```

```
## SOCKEYE SALMON                    22    0    0      0    1    1
## STARRY FLOUNDER                    0    0    3      2    2    2
## STEELHEAD                          3    2    0      5    3    3
## THRESHER SHARK                     0    0    0      1    1    0
## TOPE                               0    7    0      0    1    1
## WATER JELLY                        0  377  507 124407    3    3
## WESTERN RIVER LAMPREY              0    2    2     20    3    3
## WOLF-EEL                           0    6    1     30    3    2
## YELLOWTAIL ROCKFISH                1    0    0      0    1    0
```

Examining these tables, for analysis we select the species that have total catch of at least 100 and occurred more than once in at least 3 cruises.

```
cat('\n*** Species Selected for Analysis ***\n')
```

```
##
## *** Species Selected for Analysis ***
```

```
sel.spec <- rownames(tab1)[tab1[ ,"Total"] >= 100]
sel.spec <- sel.spec[sel.spec %in% rownames(tab3[tab3[,"Ngt1"]>=3, ])]
print(sel.spec)
```

```
##  [1] "CHINOOK subadult"    "CHINOOK subyearling" "CHINOOK yearling"
##  [4] "CHUM SALMON"         "COHO subadult"       "COHO yearling"
##  [7] "MARKET SQUID"        "NORTHERN ANCHOVY"    "PACIFIC HERRING"
## [10] "SEA NETTLE"          "WATER JELLY"
```

Part2: Summary plots - CPUE by time

To estimate CPUE for each species in each haul, we need to convert the raw data that has counts by size into total counts for each species in each haul, then we need to summarize effort.

Generating the total catch summary is just a tabulation of numbers by size:

```
# Total number by Haul (rows) and Species
MMEDcnt <- with (MMEDdata, tapply(Number, list(Haul, SpecAge), FUN=sum, simplify=T))
MMEDcnt[is.na(MMEDcnt)] <- 0
MMEDcnt <- as.data.frame(MMEDcnt)
## print(summary(MMEDcnt)) ### DEBUG ###
```

Then, build a parallel structure of the haul data. This includes location, date, time, effort (as distance towed), and gear information.

```
MMEDhauls <- data.frame(HaulID = rownames(MMEDcnt))
MMEDhauls$Station <- with(MMEDdata, tapply(as.character(Station), list(Haul), FUN=unique))
MMEDhauls$Date <- with(MMEDdata,  tapply(as.character(Date), list(Haul), FUN=unique))
MMEDhauls$Effort <- with(MMEDdata, tapply(Distance, list(Haul), FUN=unique))
MMEDhauls$Gear <- factor(with(MMEDdata, tapply(as.character(MMED), list(Haul), FUN=unique)),
                         levels=c('None','Up','Down'))
MMEDhauls$Block <- with(MMEDdata, tapply(as.character(Block), list(Haul), FUN=unique))
```

Finally, generate CPUE plots for selected species.

For this, we create an artificial "time" scale for plotting, creating equal intervals within blocks. Then, CPUE is computed as counts for each species divided by effort.

```
MMEDhauls$PlotTime <- match(MMEDhauls$Block, LETTERS[1:13]) - 1 +
  c((1:10)/11, (1:10)/11, (1:4)/5, (1:4)/5, (1:10)/11, (1:4)/5, (1:4)/5, (1:8)/9,
```

```
    (1:8)/9, (1:8)/9, (1:4)/5, (1:4)/5, (1:8)/9)
## print(summary(MMEDhauls)) ### DEBUG ###
MMEDcpue=sweep(MMEDcnt, 1, MMEDhauls$Effort, '/')
## print(summary(MMEDcpue)) ### DEBUG ###
```

Before running the analysis, set up some plotting configurations:

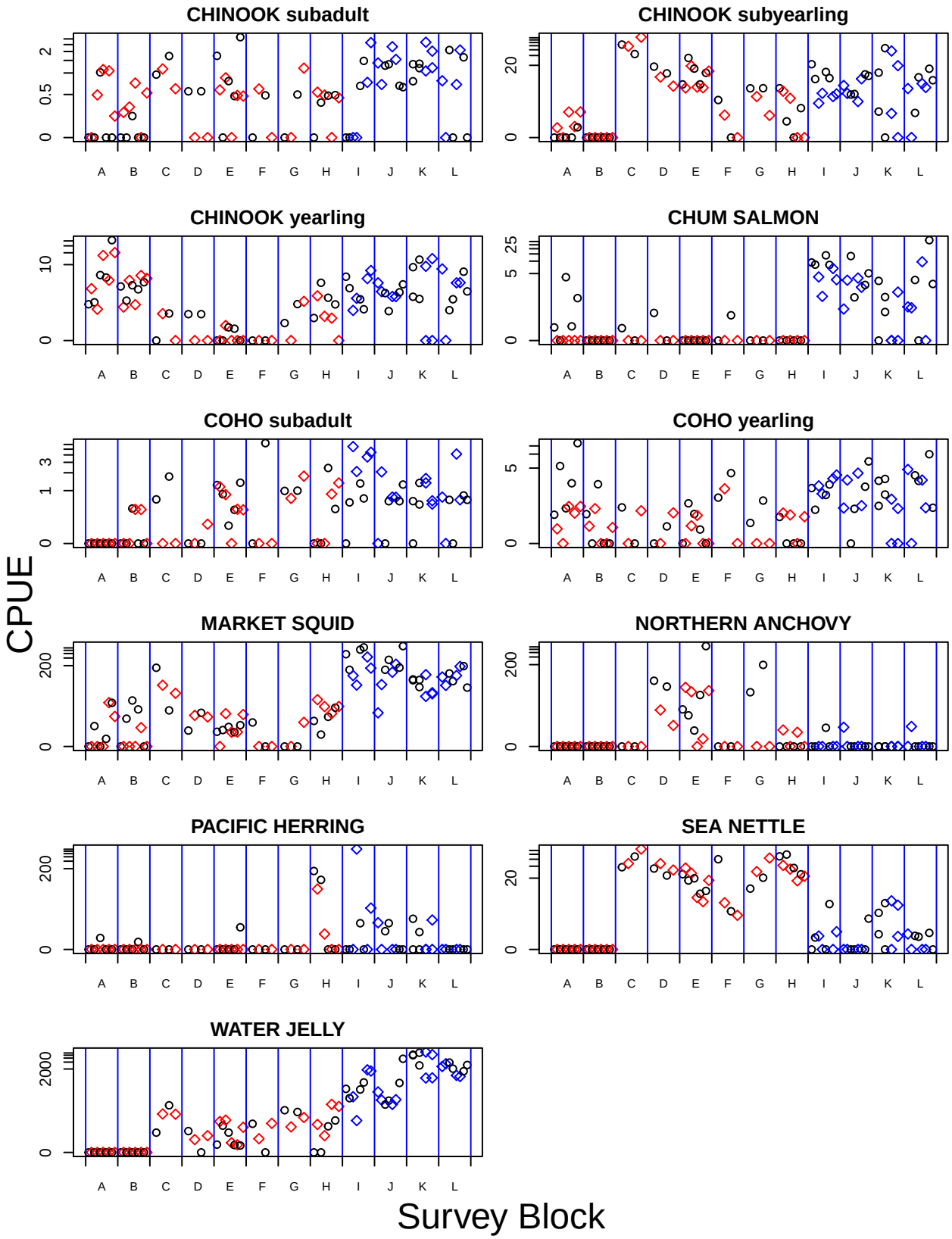
```
bw <- FALSE          #Flag for black-and-white figures
BLACK <- 'black'
BLUE <- if(bw) 'black' else 'blue'   #color code for blue
RED <-  if(bw) 'black' else 'red'    #color code for red
lndscp <- FALSE                      #flag for landscape figures
plcol <- if(lndscp) 3 else 2         #number of columns for multi-plots
```

A special plotting function is created, so it can be re-used later.

```
cpue.plot <- function(t, y, dot.col=1, log.zero=FALSE, ...) {
  minpos <- 0
  if (log.zero) {
    minpos <- min(y[y>0]) #minimum positive value
    if(any(y<=0)) {
      y[y<=0] <- minpos/2 # recode
    } # if(any...
  } # if(log.zero)
  plot(t, y, log=ifelse(log.zero,"y",""), type='p',
       axes=F, ...)
  # label blocks at midpoint:
  blocks <- seq(round(min(t)), round(max(t)))
  axis(side=1, at=blocks, labels=NA) # Ticks at day boundaries
  abline(v=blocks, col='blue')
  axis(side=1, at=blocks[-1]-0.5,
       labels=sort(unique(as.character(MMEDhauls$Block))),
       tick=FALSE, cex.axis=0.8)
  if (log.zero && any(y<minpos)) {
    tck<- axisTicks(range(y),log=FALSE) #default tick locations
    axis(side=2, at=c(minpos/2,tck), labels=c(0,tck))
  } else {
    axis(side=2)
  } # if (log.zero && ...
  box()
} # cpue.plot()
```

Generate the individual plots:

```
par(mfrow=c(ceiling(length(sel.spec)/plcol), plcol), omi=c(0.5,0.5,0,0), mar=c(3,2,2,1))
for (sp in sel.spec) {
  cpue.plot(MMEDhauls$PlotTime, MMEDcpue[[sp]], log.zero=TRUE,
            col=c(BLACK,RED,BLUE)[as.numeric(MMEDhauls$Gear)],
            pch=1+4*(MMEDhauls$Gear!='None'), xlab="", ylab="", main=sp)
} # for (sp)
mtext('Survey Block', side=1, outer=TRUE, cex=1.5)
mtext('CPUE', side=2, outer=TRUE, cex=1.5)
```


CHINOOK subadult
CHINOOK subyearling
CHINOOK yearling
CHUM SALMON
COHO subadult
COHO yearling
MARKET SQUID
NORTHERN ANCHOVY
PACIFIC HERRING
SEA NETTLE
WATER JELLY
CPUE
Survey Block
A B C D E F G H I J K L

Part 3: Overall Catch Ratio Statistics

In preliminary analyses, we considered a number of methods, including:

- *CPUE ratio estimate.* Ratio of mean CPUEs (Wilderbuer et al. 1998, North. Am. J. Fish. Manage. 18:11-18) using bootstrapped quantiles rather than a normal approximation.
- *Paired sample differences.* This method uses paired t-test statistics with a log(x+offset) transform on CPUE.
- *Nonparametric paired differences.* This method computes the median catch ratio and approximate binomial quantiles based on eq. 10.3 in Efron (1982, *"The Jacknife, the Bootstrap, and Other Resampling Plans"*) which finds the nearest observation toward the tail from the nominal quantile.
- *GLM analysis of deviance.* This method computes a GLM blocked ANODEV model of `Catch ~ Block + Gear + offset()` with either a Poisson or a negative binomial distribution, where the offset is the effort (km towed) for each sample. (Because the model uses log links, including effort as an offset is similar to using a linear model `log(CPUE) ~ Block + Gear`.)

After reviewing the methods, for the final analysis, we used only the GLM method.

3.1 The analysis

To make the coding easier, we define standard names for the gear types, and set the rounding parameters for easy-to-read results tables.

```
assign('gears', c('None', 'Up', 'Down'), 1)
options(scipen=3) # Favor non-scientific notation
```

Then, create a function to compute the GLM estimates. The *R* `glm()` method does not support negative binomial distributions, so we use the MASS library (Venables & Ripley 2002, *"Modern Applied Statistics with S, 4th ed."*). The `glm.nb()` function is used to estimate the θ parameter; if that estimation fails, it reverts to the value specified in "init.theta". Then (because `glm.nb()` fails for some species) `glm()` is used with the estimated θ to get the final statistics. This means that the distribution of the final catch ratio estimate does not inlcude error in the estimation of θ.

The GLM model is on a log scale, so exponential transformations are needed to get the catch-ratio estimate and quantiles. Predictions are returned in `$Pred` for later plotting.

NOTE that we want the ratio MED/STD, so we use the negative of the log-scale `GearStd` coefficient.

```
GLMAnoDevEst <- function (dat, qprobs=0.5, nb=TRUE, init.theta=1,
                          diag.plt=FALSE, plt.lab='') {
  rslt <- matrix(NA, ncol=length(gears)-1, nrow=1+length(qprobs),
                 dimnames=list(c("Mean",as.character(qprobs)), gears[2:length(gears)]))
  library(MASS)
  fit.data <- data.frame(Count=as.vector(dat[,1]),
                         Date=as.factor(dat$Date),
                         Station=as.factor(dat$Station),
                         Block=as.factor(dat$Block),
                         Gear=as.factor(dat$Gear),
                         Offset=as.vector(dat$Effort))
  if (nb) { # Negative Binomial fit
    cat('\n\tInitial fit to estimate theta\n')
    fit.init <- try(glm.nb(Count ~ Block + Gear + offset(log(Offset)),
                           data=fit.data, init.theta=init.theta,
                           control=list(epsilon=1e-03, maxit=500, trace=0)))
    if (inherits(fit.init, 'try-error')) {
```

```
      print(fit.init)
      warning("glm.nb failed to estimate theta; using default value")
      theta.init=init.theta  # initial estimate for herring from theta.ml
    } else {
      cat('Estimated theta: ', fit.init$theta, ', SE: ', fit.init$SE.theta, '\n')
      if(is.finite(fit.init$SE.theta)) {
        theta.init <- fit.init$theta
      } else {
        warning("glm.nb failed to estimate theta; using default value")
        theta.init <- init.theta
      }
    } # if 'try-error'
    cat('\n\tFinal fit with theta = ', theta.init, '\n')
    fit.fin <- glm(Count ~ Block + Gear + offset(log(Offset)),
                   data=fit.data, family=negative.binomial(theta.init),
                   control=list(epsilon=1e-08, maxit=500, trace=FALSE))
  } else { # Poisson fit
    fit.fin <- glm(Count ~ Block + Gear + offset(log(Offset)),
                   data=fit.data, family=poisson,
                   control=list(epsilon=1e-08, maxit=500, trace=FALSE))
  } # if (nb)
  cat("\nFIT STATISTICS:")
  # print(summary(fit.fin))
  fit.anova <- anova(fit.fin, test="Chisq")
  print(fit.anova)
  geareffects <- paste('Gear',gears[2:length(gears)], sep='')
  .lmn <- summary(fit.fin)$coefficients[geareffects, "Estimate"]
  .lsd <- summary(fit.fin)$coefficients[geareffects, "Std. Error"]
  .df <- fit.fin$df.residual
  for (g in 1:length(.lmn)) {
    if (.lsd[g] > 1000) {  # Estimate blew up, just use the mean value
      .mn <- exp(.lmn[g])
      .qnt <- rep(NA, length(qprobs))
    } else {
      .mn <- exp(.lmn[g] + .lsd[g]^2 / 2)
      .qnt <- exp(qt(qprobs, .df)*.lsd[g]+.lmn[g])
    } # if (.lsd[g])
    rslt[ , g] <- c(.mn, .qnt)
  } # for (g)
  predCatch <- predict(fit.fin, type="response", se.fit=TRUE)
  if (diag.plt) {
    rs <- resid(fit.fin, type="deviance")
    op <- par(omi=c(0,0,0.25,0), mfrow=c(1,2), mar=c(4,4,1,1))
    plot(predCatch$fit, rs, xlab="Prediction", ylab="Deviance Resids")
    qqnorm(rs, ylab="Deviance Resids")
    qqline(rs)
    mtext(paste(plt.lab, ifelse(nb, "Neg. Binomial", "Poisson"), sep=' - '),
          side=3, outer=TRUE)
    par(op)
  } # if (diat.plt)
  return(list(Smry=rslt, Pred=predCatch))
} # GLMAnoDevEst()
```

Before running the analysis, create two summary lists: one for the means and quantiles of all methods by

species, and one for storing GLM model results for plotting. The first list contains one element for each species, holding a matrix of summary results for estimates of the ratio A by each of the various estimation methods. Rows are the methods, columns are a six-number summary: Mean, Median, and quantiles (0.05, 0.25, 0.75, 0.95).

The routine then loops through the species, computing first the GLM Poisson catch ratio estimates, then the GLM negative-binomial estimates. The Poisson results are used to get a crude initial estimate of the neg-bin Θ parameter, which is used to initiate the refined estimate via `glm.nb()`. If the refined estimate fails, the initial estimate of Θ is used instead.

```
stat.sum <- list()  # structure for storing summary results
GLM.pred <- list() # structure for storing GLM predictions
for (sp in sel.spec) {
    cat('\n******************  ', sp, '  ******************\n')
  .sumtbl <- array(NA, dim=c(2, 6, length(gears)-1),
                   dimnames=list(c('GLM.Po', 'GLM.nb'),
                                 c('Mean', 'q0.05', 'q0.25', 'Median', 'q0.75', 'q0.95'),
                                 gears[2:length(gears)]))
  .qprobs <- c(0.05, 0.25, 0.50, 0.75, 0.95)
  cat("\n*** METHOD 1: GLM ANODEV, Poisson ***\n")
  .est <- GLMAnoDevEst(cbind(MMEDcnt[[sp]], MMEDhauls), .qprobs,
                       nb=FALSE, diag.plt=TRUE, plt.lab=sp)
  print(.est$Smry)
  .sumtbl['GLM.Po', , ] <- .est$Smry

  cat("\n*** METHOD 2: GLM ANODEV, negative binomial ***\n")
  init.theta <- theta.ml(y=MMEDcnt[[sp]], mu=.est$Pred$fit,
                         n=length(MMEDcnt[[sp]]), limit=100, trace=FALSE)
  cat('Initial Theta: ', init.theta, '\n')
  .est <- GLMAnoDevEst(cbind(MMEDcnt[[sp]], MMEDhauls), .qprobs,
                       nb=TRUE, init.theta=init.theta, diag.plt=TRUE, plt.lab=sp)
  print(.est$Smry)
  .sumtbl['GLM.nb', , ] <- .est$Smry

  # Add species to summary lists
  GLM.pred[[sp]] <- .est$Pred
  .sumtbl <- round(.sumtbl, 3)  # round statistical results
  stat.sum[[sp]] <- .sumtbl
} # for(sp)
```

```
##
## ******************   CHINOOK subadult   ********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev    Pr(>Chi)
```

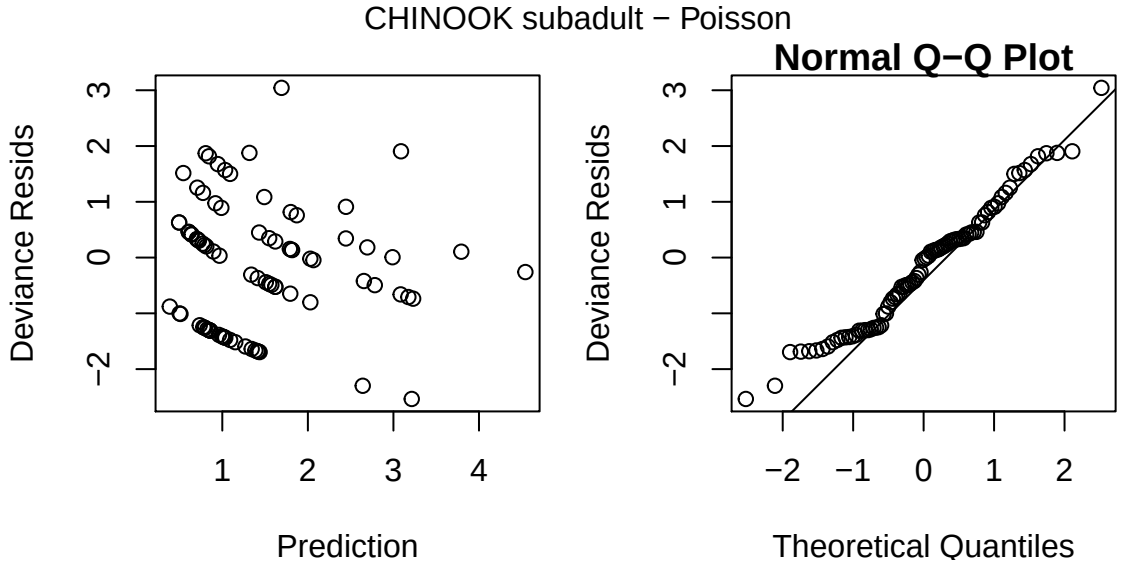


Figure 1:

```
## NULL                     85     157.50
## Block 11   47.887        74     109.61 0.000001496 ***
## Gear   2    1.179        72     108.43      0.5545
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
## Mean 1.0303668 1.4245452
## 0.05 0.6805217 0.8441632
## 0.25 0.8564966 1.1232247
## 0.5  1.0028455 1.3662921
## 0.75 1.1742010 1.6619597
## 0.95 1.4778356 2.2113664
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  11.84953
##
##  Initial fit to estimate theta
## Estimated theta:  11.4745 , SE:  15.34951
##
##  Final fit with theta =  11.4745
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(11.4745), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85    141.391
```

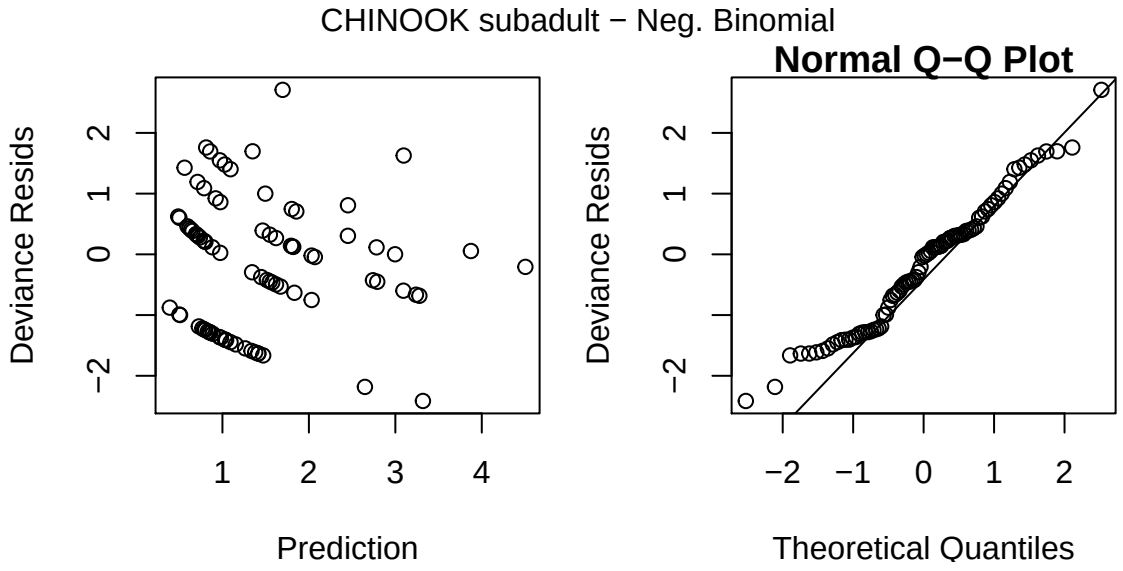


Figure 2:

```
## Block 11   42.336        74     99.055 0.0003957 ***
## Gear   2    1.051        72     98.004 0.6575545
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
## Mean 1.0744294 1.4517892
## 0.05 0.6471796 0.7688163
## 0.25 0.8540238 1.0819175
## 0.5  1.0329542 1.3676013
## 0.75 1.2493731 1.7287207
## 0.95 1.6486834 2.4327441
##
## ******************   CHINOOK subyearling   ********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev   Pr(>Chi)
## NULL                     85     5379.7
## Block 11   4427.6        74      952.1  < 2.2e-16 ***
## Gear   2     22.5        72      929.5 0.00001275 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
```

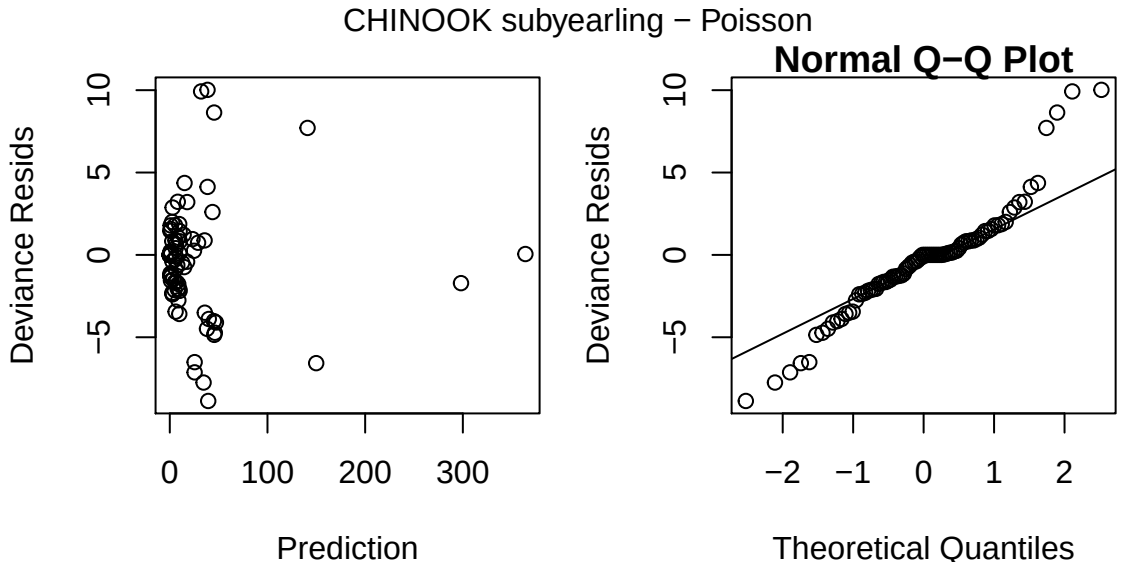


Figure 3:

```
## Mean 0.9848031 0.6494879
## 0.05 0.9025556 0.5537613
## 0.25 0.9497254 0.6071303
## 0.5  0.9834959 0.6466797
## 0.75 1.0184673 0.6888055
## 0.95 1.0716949 0.7551895
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  1.310679
##
##  Initial fit to estimate theta
## Estimated theta:  1.340598 , SE:  0.2734801
##
##  Final fit with theta =  1.340598
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(1.3406), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                     85     357.53
## Block 11  267.174        74      90.36  < 2e-16 ***
## Gear   2    4.698        72      85.66  0.06016 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##             Up      Down
## Mean 0.8942809 0.5101777
```

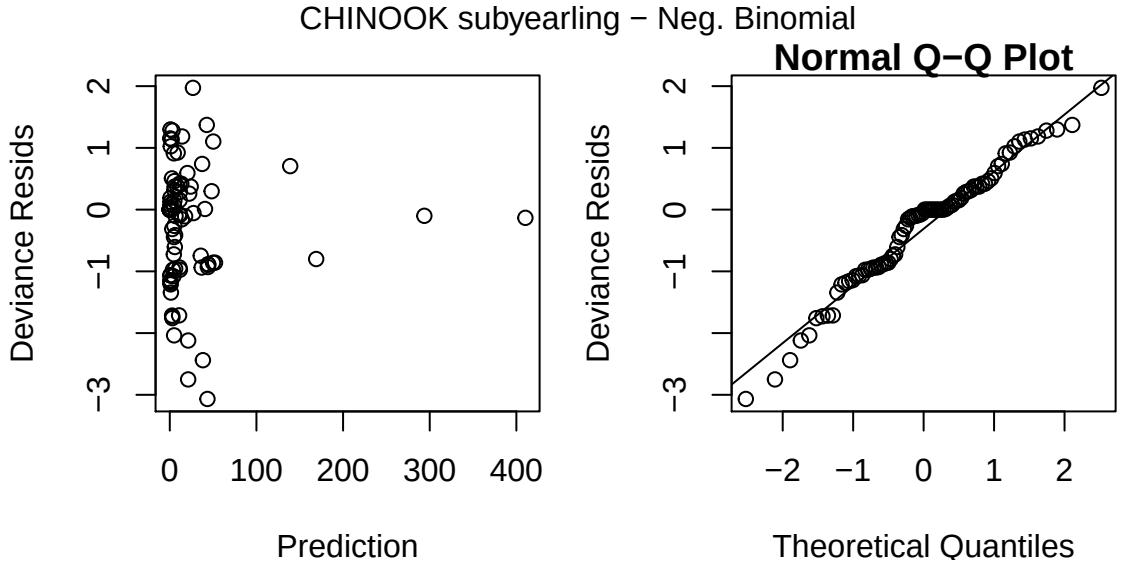


Figure 4:

```
## 0.05 0.5381177 0.2964244
## 0.25 0.7104730 0.3983538
## 0.5  0.8596332 0.4878714
## 0.75 1.0401087 0.5975053
## 0.95 1.3732482 0.8029653
##
## ******************   CHINOOK yearling   *********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                     85    1456.63
## Block 11   766.09        74     690.54  < 2e-16 ***
## Gear   2     6.53        72     684.01  0.03822 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##             Up      Down
## Mean 0.8063947 1.1275647
## 0.05 0.6918107 0.8631587
## 0.25 0.7558489 1.0043845
## 0.5  0.8031664 1.1143906
## 0.75 0.8534461 1.2364452
## 0.95 0.9324461 1.4387464
```

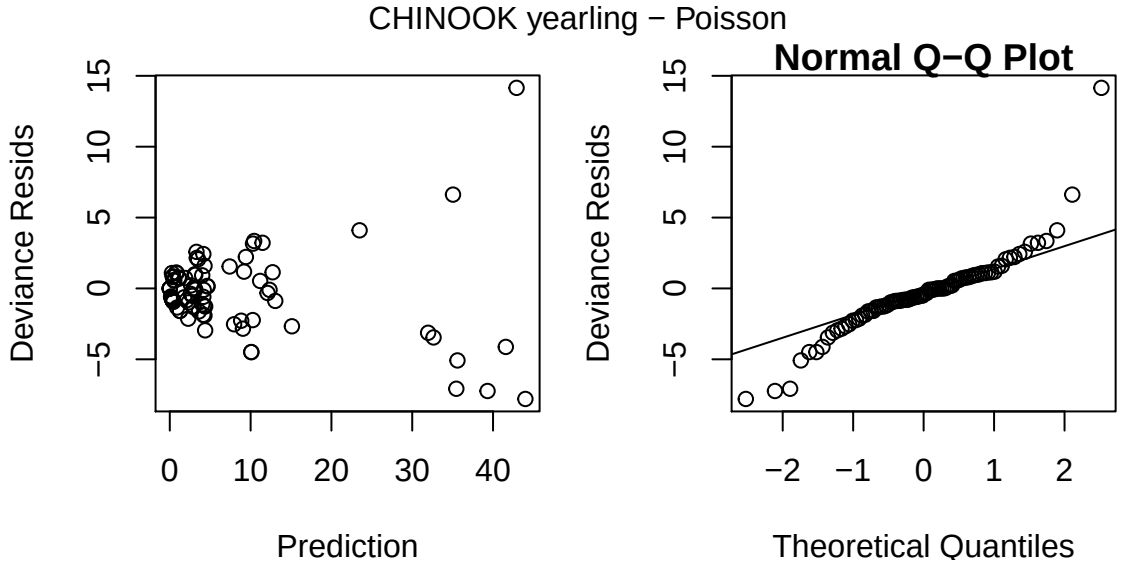


Figure 5:

```
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  1.5042
##
##  Initial fit to estimate theta
## Estimated theta:  1.503116 , SE:  0.3096866
##
##  Final fit with theta =  1.503116
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(1.5031), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                     85    219.731
## Block 11  138.594        74     81.138   <2e-16 ***
## Gear   2    1.083        72     80.055   0.5341
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##             Up      Down
## Mean 0.7867095 1.2389568
## 0.05 0.4741009 0.7050806
## 0.25 0.6254745 0.9574429
## 0.5  0.7563934 1.1809969
## 0.75 0.9147153 1.4567488
## 0.95 1.2067706 1.9781479
##
```

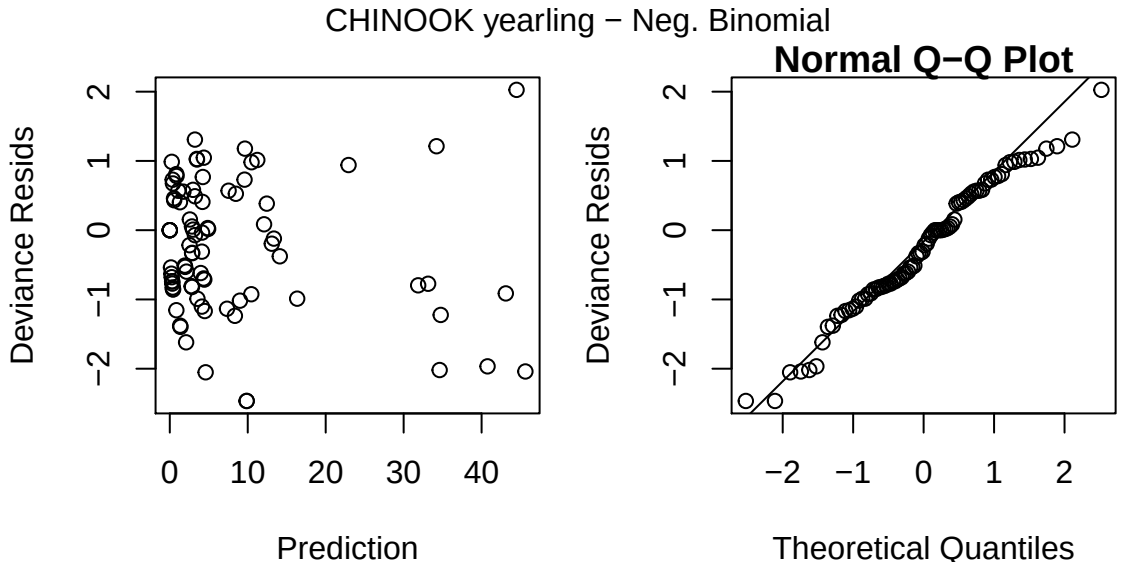


Figure 6:

```
## ********************   CHUM SALMON   ********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
## Warning: glm.fit: fitted rates numerically 0 occurred
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85     882.42
## Block 11   613.58        74     268.84 < 2.2e-16 ***
## Gear   2    71.07        72     197.77 3.696e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##                Up      Down
## Mean 8.724456e-09 0.3905847
## 0.05           NA 0.2961159
## 0.25           NA 0.3463782
## 0.5            NA 0.3857016
## 0.75           NA 0.4294894
## 0.95           NA 0.5023904
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  1.259582
##
```

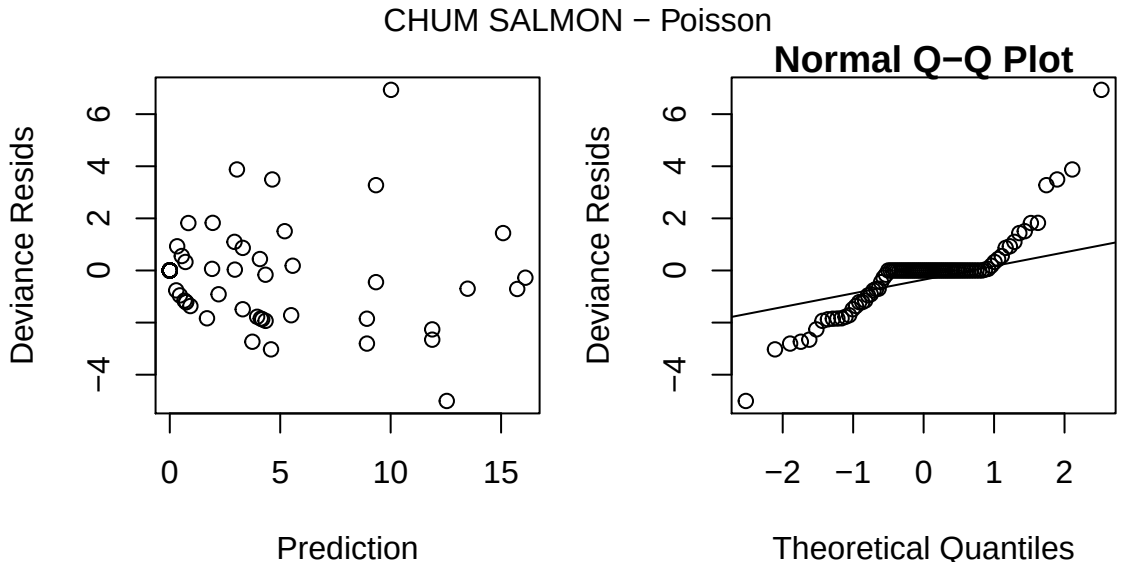


Figure 7:

```
##  Initial fit to estimate theta
## Estimated theta:  1.259586 , SE:  0.3875694
##
##  Final fit with theta =  1.259586
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(1.2596), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85    292.744
## Block 11  221.763        74     70.981 < 2.2e-16 ***
## Gear   2   25.384        72     45.597 1.216e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##                Up      Down
## Mean 2.679148e-09 0.3863633
## 0.05           NA 0.2359931
## 0.25           NA 0.3092175
## 0.5            NA 0.3721880
## 0.75           NA 0.4479821
## 0.95           NA 0.5869828
##
## ******************   COHO subadult   ********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
```

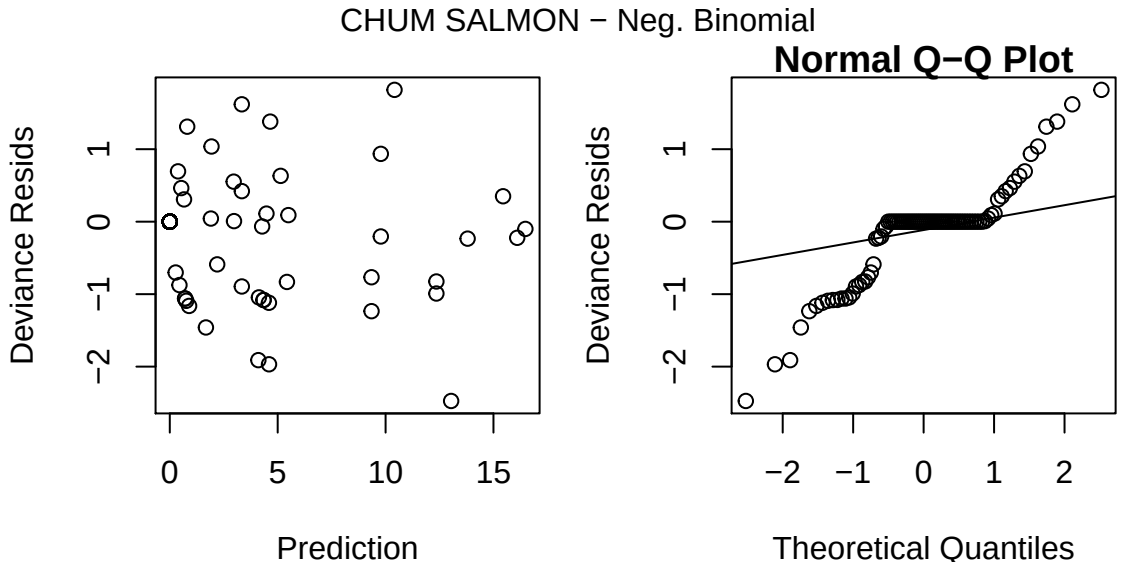


Figure 8:

```
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev   Pr(>Chi)
## NULL                     85     251.80
## Block 11  118.686        74     133.11  < 2.2e-16 ***
## Gear   2   18.565        72     114.55 0.00009303 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up     Down
## Mean 0.6194021 3.043432
## 0.05 0.3968357 1.758135
## 0.25 0.5073904 2.369548
## 0.5  0.6005476 2.907803
## 0.75 0.7108086 3.568325
## 0.95 0.9088332 4.809254
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  3.830574
##
##  Initial fit to estimate theta
## Estimated theta:  3.686582 , SE:  2.051033
##
##  Final fit with theta =  3.686582
##
## FIT STATISTICS:Analysis of Deviance Table
```

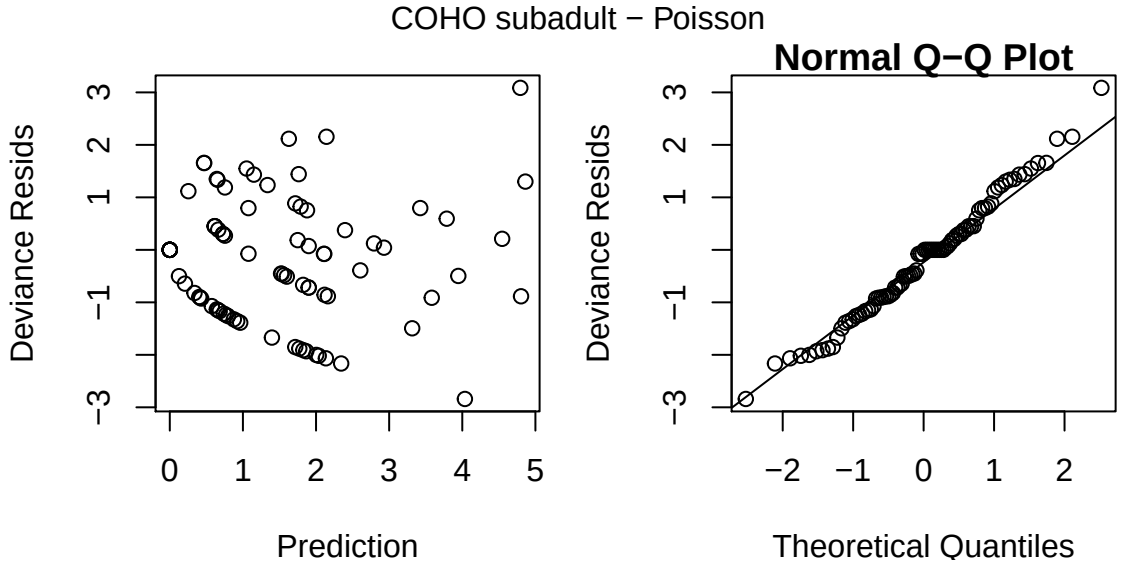


Figure 9:

```
##
## Model: Negative Binomial(3.6866), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85    180.195
## Block 11   87.323        74     92.872 5.602e-14 ***
## Gear   2   10.248        72     82.624  0.005957 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##             Up     Down
## Mean 0.6639356 2.872783
## 0.05 0.3817730 1.484663
## 0.25 0.5157354 2.114405
## 0.5  0.6338960 2.694712
## 0.75 0.7791285 3.434287
## 0.95 1.0525212 4.890992
##
## ******************   COHO yearling   ********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
```

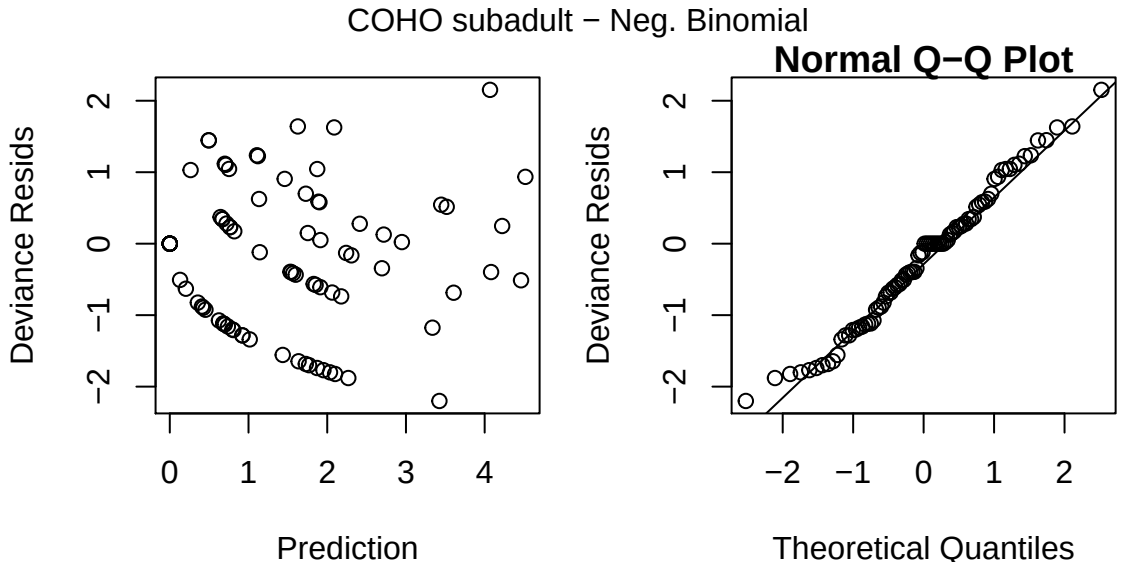


Figure 10:

```
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85     588.09
## Block 11  220.599        74     367.49 < 2.2e-16 ***
## Gear   2   86.535        72     280.96 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
## Mean 0.1860394 0.7047559
## 0.05 0.1255099 0.4868875
## 0.25 0.1562238 0.5985192
## 0.5  0.1815321 0.6895519
## 0.75 0.2109403 0.7944304
## 0.95 0.2625601 0.9765742
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  1.554399
##
##  Initial fit to estimate theta
## Estimated theta:  1.504939 , SE:  0.3966753
##
##  Final fit with theta =  1.504939
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(1.5049), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
```

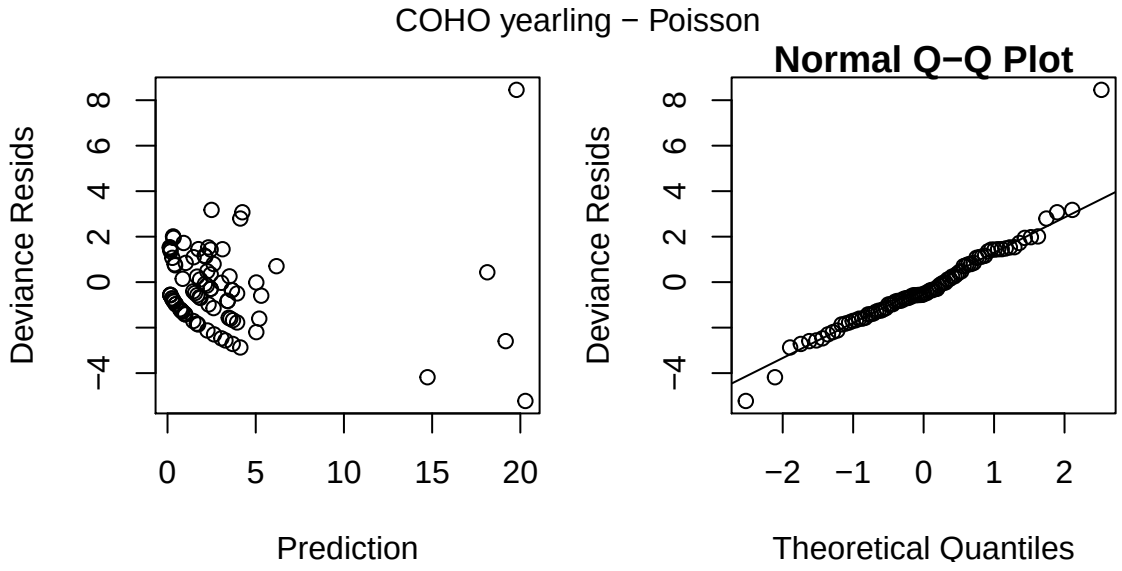


Figure 11:

```
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85    171.099
## Block 11   72.115        74     98.983 3.228e-09 ***
## Gear   2   11.723        72     87.260  0.006241 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
## Mean 0.3397104 0.7189217
## 0.05 0.1718611 0.3510543
## 0.25 0.2473126 0.5139029
## 0.5  0.3174407 0.6674197
## 0.75 0.4074544 0.8667963
## 0.95 0.5863376 1.2688893
##
## ******************   MARKET SQUID   ********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85      41497
## Block 11    31995        74       9502 < 2.2e-16 ***
```

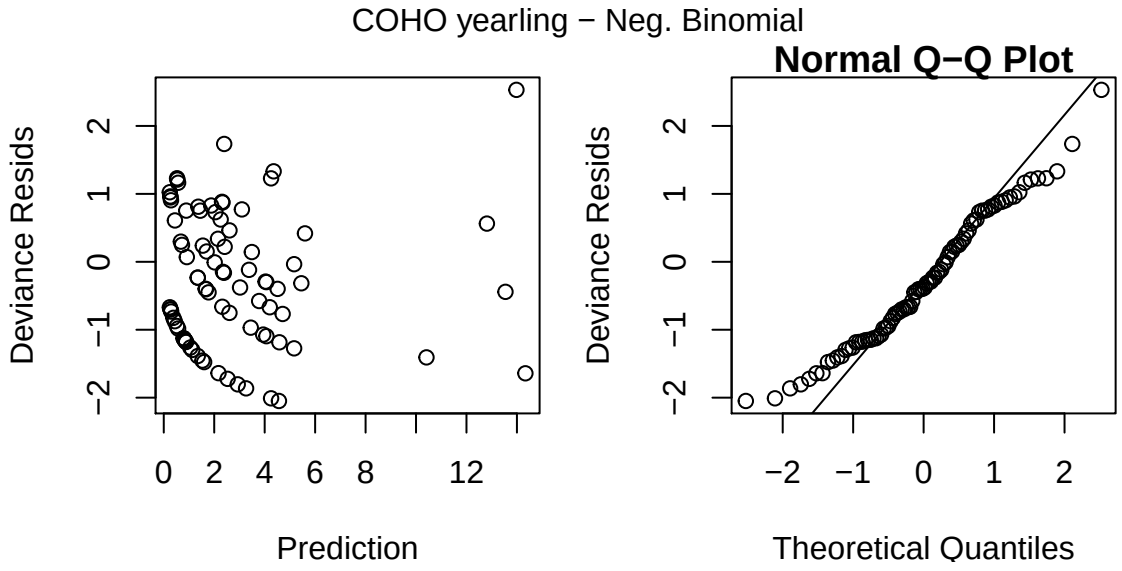


Figure 12:

```
## Gear   2     2833        72       6670 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
## Mean 0.3499610 0.3202018
## 0.05 0.3099832 0.3073303
## 0.25 0.3326078 0.3148456
## 0.5  0.3490732 0.3201062
## 0.75 0.3663537 0.3254546
## 0.95 0.3930925 0.3334131
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  0.7905173
##
##  Initial fit to estimate theta
## Estimated theta:  0.9008459 , SE:  0.1607128
##
##  Final fit with theta =  0.9008459
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(0.9008), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                     85     433.55
## Block 11   329.48        74     104.08   <2e-16 ***
## Gear   2     4.46        72      99.61   0.1631
```

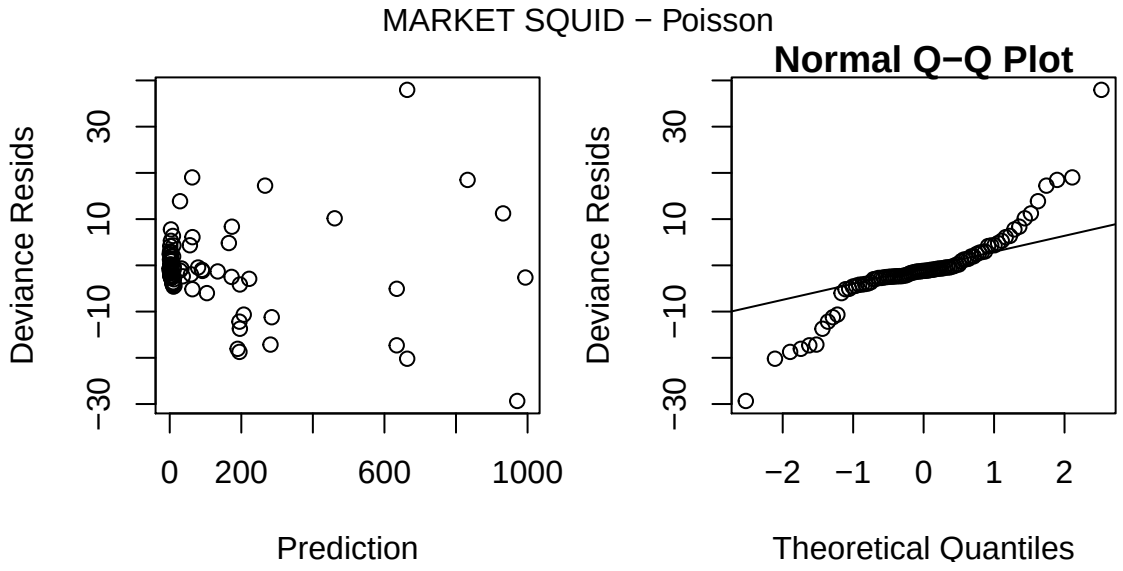


Figure 13:

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
## Mean 0.8765406 0.4845325
## 0.05 0.4519912 0.2228432
## 0.25 0.6444103 0.3356991
## 0.5  0.8218839 0.4446347
## 0.75 1.0482347 0.5889203
## 0.95 1.4944830 0.8871711
```

```
## ********************   NORTHERN ANCHOVY   **********************
```

```
## *** METHOD 1: GLM ANODEV, Poisson ***
```

```
## FIT STATISTICS:Analysis of Deviance Table
```

```
## Model: poisson, link: log
```

```
## Response: Count
```

```
## Terms added sequentially (first to last)
```

```
##
```

```
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85      22390
## Block 11   9361.5        74      13029 < 2.2e-16 ***
## Gear   2   2929.5        72      10100 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##              Up       Down
## Mean 0.06762749  4.6141497
## 0.05 0.05972477  0.2828815
```

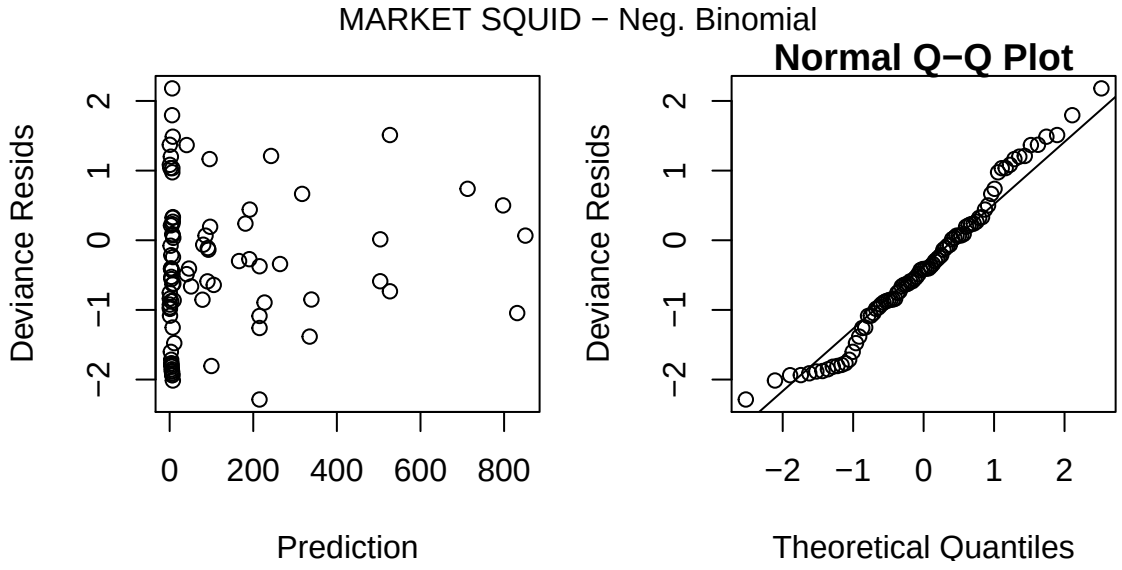


Figure 14:

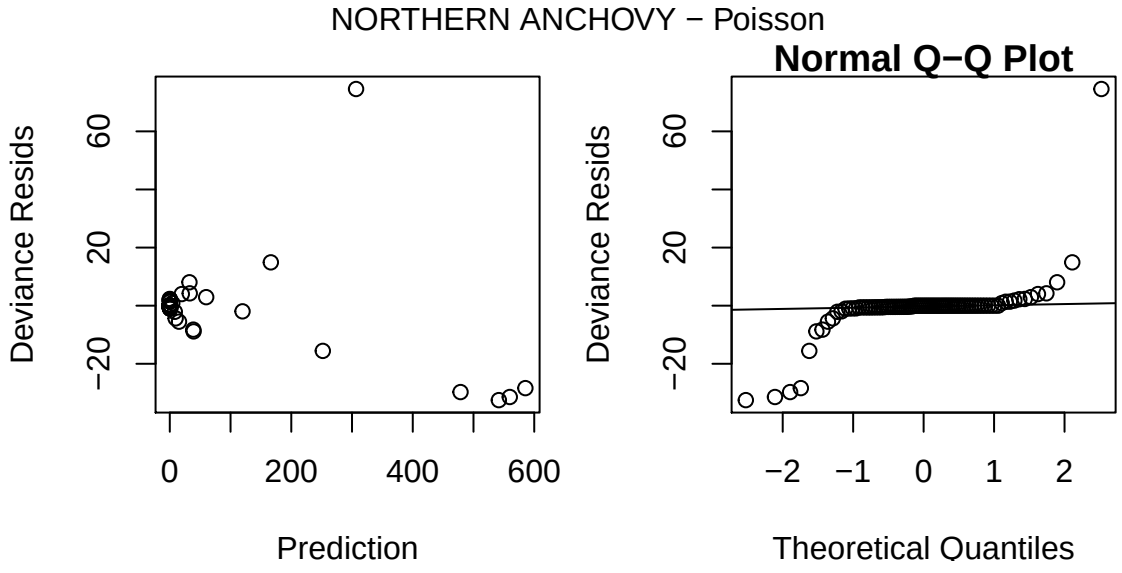


Figure 15:

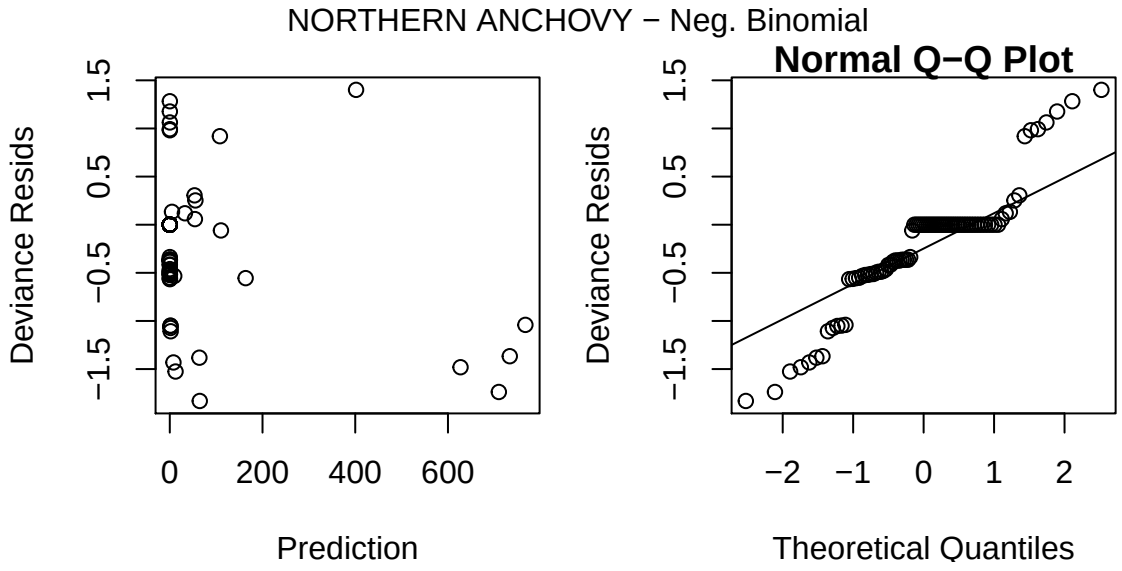


Figure 16:

```
## 0.25 0.06419196  0.9494745
## 0.5  0.06744764  2.1785820
## 0.75 0.07086843  4.9987855
## 0.95 0.07616913 16.7781196
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  0.3260892
##
##  Initial fit to estimate theta
## Estimated theta:  0.314627 , SE:  0.09187918
##
##  Final fit with theta =  0.314627
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(0.3146), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85    253.813
## Block 11  210.880        74     42.933 < 2.2e-16 ***
## Gear   2    6.113        72     36.821  0.002488 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##              Up       Down
## Mean 0.09891328  3.8901959
## 0.05 0.03385024  0.4174618
## 0.25 0.05841659  1.1492074
```

```
## 0.5  0.08493225  2.3016355
## 0.75 0.12348353  4.6097213
## 0.95 0.21310000 12.6898443
##
## ******************   PACIFIC HERRING   ********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85    19043.0
## Block 11  10470.5        74     8572.5 < 2.2e-16 ***
## Gear   2   2986.8        72     5585.7 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##              Up     Down
## Mean 0.11263741 233.0833
## 0.05 0.08864923 126.3052
## 0.25 0.10160500 175.7400
## 0.5  0.11156983 220.4245
## 0.75 0.12251196 276.4707
## 0.95 0.14041665 384.6789
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  0.09446641
##
##  Initial fit to estimate theta
## [1] "Error in while ((it <- it + 1) < limit && abs(del) > eps) { : \n  missing value where TRUE/FALSE
## attr(,"class")
## [1] "try-error"
## attr(,"condition")
## <simpleError in while ((it <- it + 1) < limit && abs(del) > eps) {    t0 <- abs(t0)    del <- score(

## Warning in GLMAnoDevEst(cbind(MMEDcnt[[sp]], MMEDhauls), .qprobs, nb =
## TRUE, : glm.nb failed to estimate theta; using default value

##
##  Final fit with theta =  0.09446641
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(0.0945), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
```

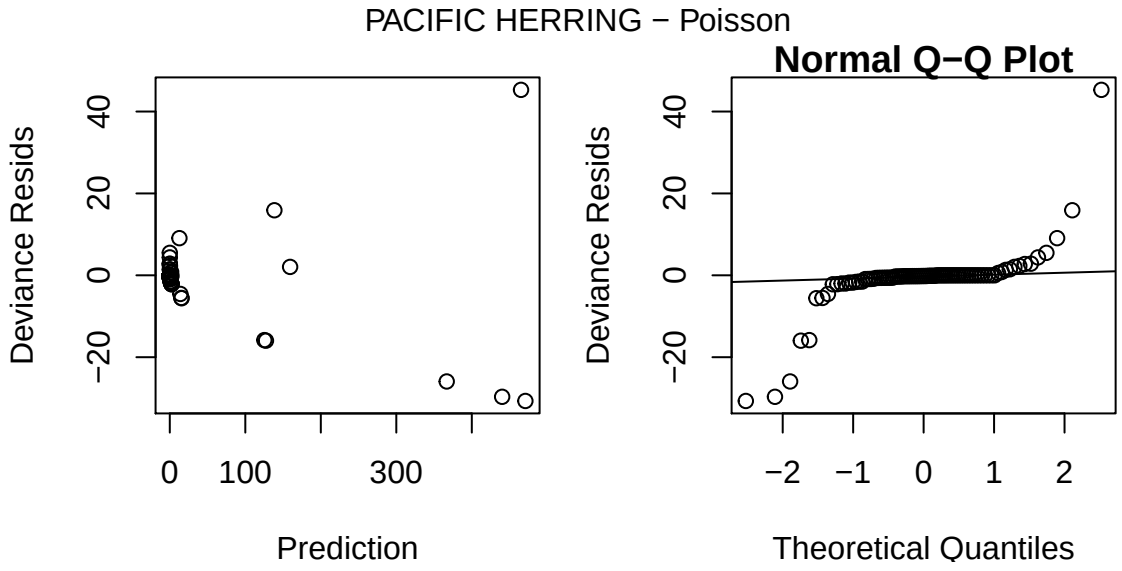


Figure 17:

```
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85     98.474
## Block 11   70.323        74     28.151 < 2.2e-16 ***
## Gear   2    3.531        72     24.620 0.0006172 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##              Up      Down
## Mean 0.07043164 2.9876844
## 0.05 0.01206889 0.7724318
## 0.25 0.02781045 1.5053250
## 0.5  0.04930240 2.3789116
## 0.75 0.08740338 3.7594672
## 0.95 0.20140445 7.3264980
##
## ******************   SEA NETTLE   ********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                     85     5737.1
## Block 11   4848.0        74      889.0   <2e-16 ***
```

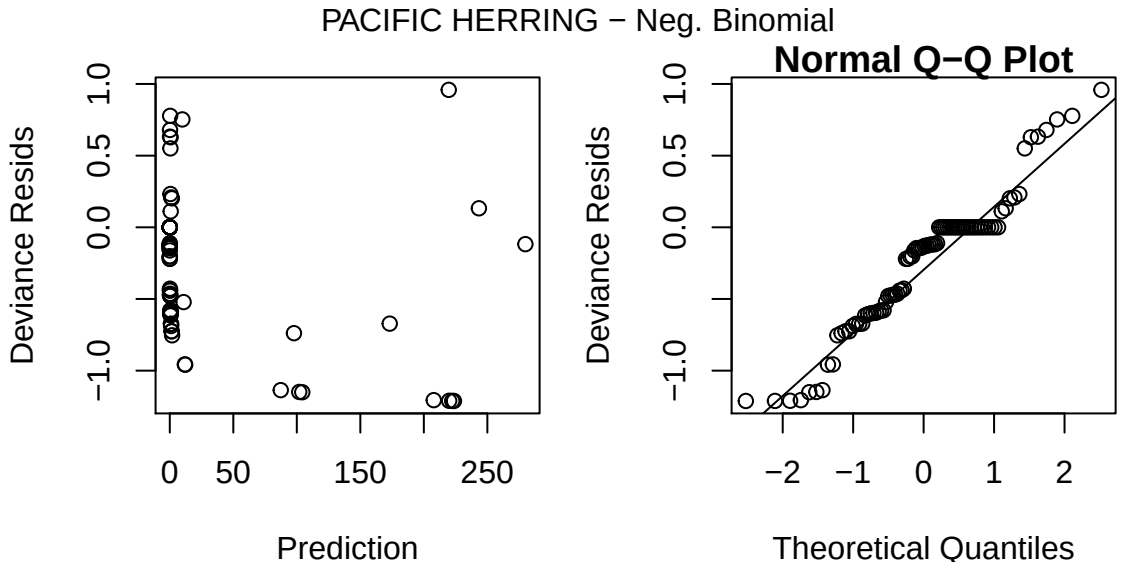


Figure 18:

```
## Gear   2      0.7        72      888.4   0.7119
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
## Mean 0.9945518 0.8239794
## 0.05 0.9317755 0.4837972
## 0.25 0.9680875 0.6467325
## 0.5  0.9938081 0.7892015
## 0.75 1.0202120 0.9630551
## 0.95 1.0599704 1.2873971
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  2.154861
##
##  Initial fit to estimate theta
## Estimated theta:  2.16212 , SE:  0.5290027
##
##  Final fit with theta =  2.16212
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(2.1621), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                     85     632.74
## Block 11   559.76        74      72.98   <2e-16 ***
## Gear   2     1.65        72      71.33   0.4406
```

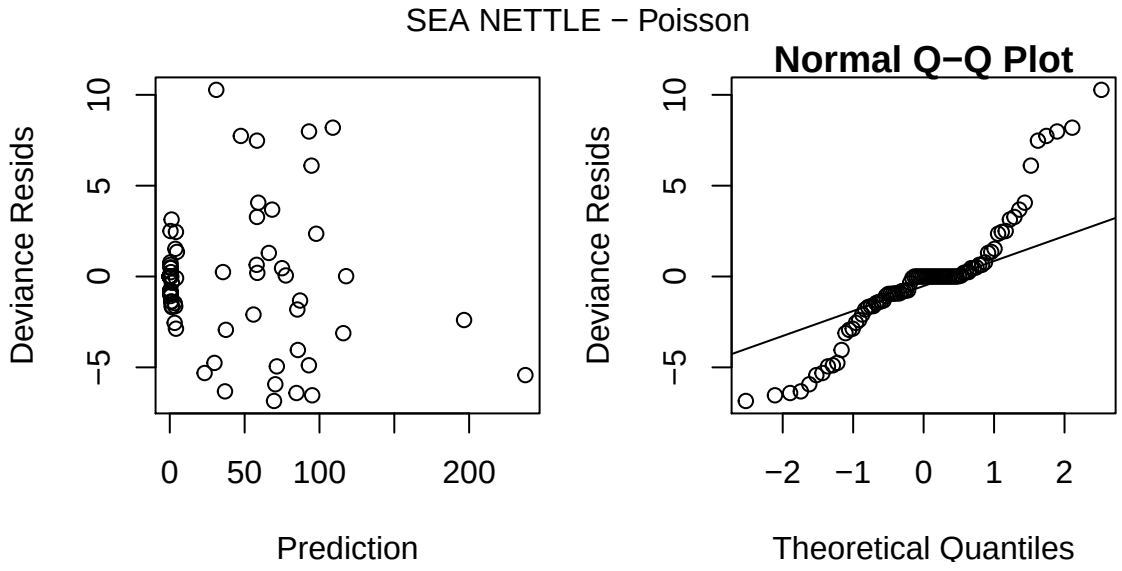


Figure 19:

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##             Up      Down
## Mean 0.9357340 0.6465416
## 0.05 0.6115211 0.2874541
## 0.25 0.7738936 0.4400243
## 0.5  0.9095491 0.5892529
## 0.75 1.0689838 0.7890904
## 0.95 1.3528226 1.2079109
##
## ********************   WATER JELLY   **********************
##
## *** METHOD 1: GLM ANODEV, Poisson ***
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                     85     547720
## Block 11   468382        74      79338 < 2.2e-16 ***
## Gear   2     3313        72      76025 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##            Up      Down
## Mean 1.634405 0.7221444
## 0.05 1.454432 0.7152668
```

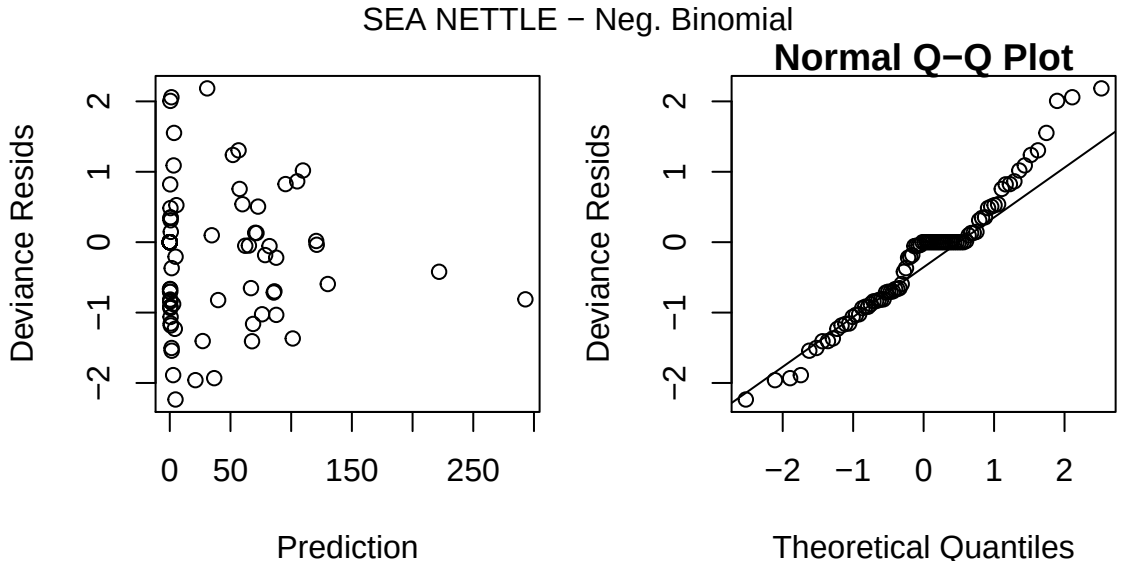


Figure 20:

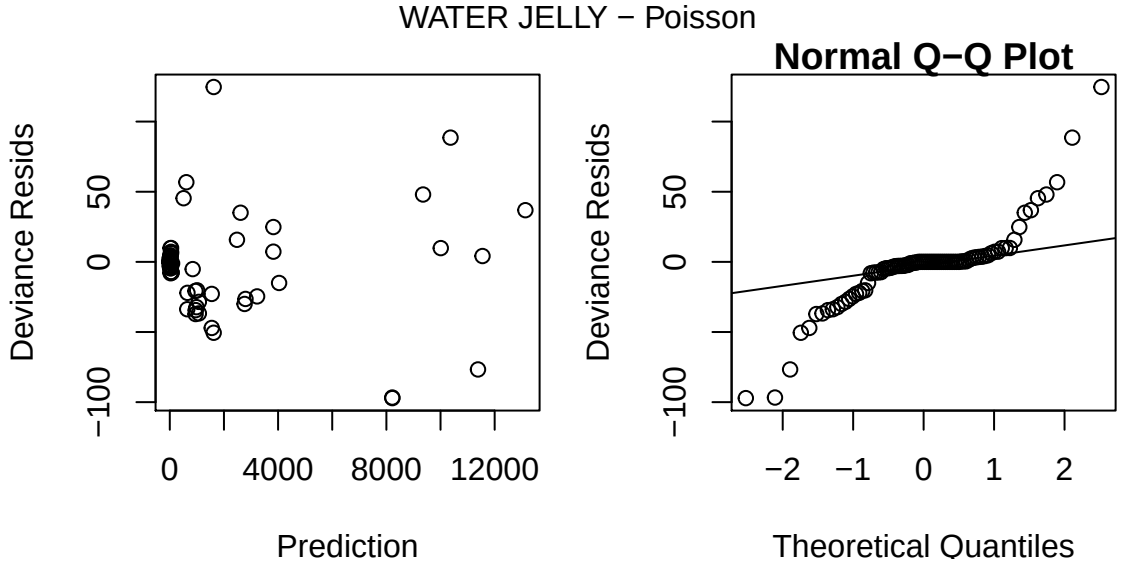


Figure 21:

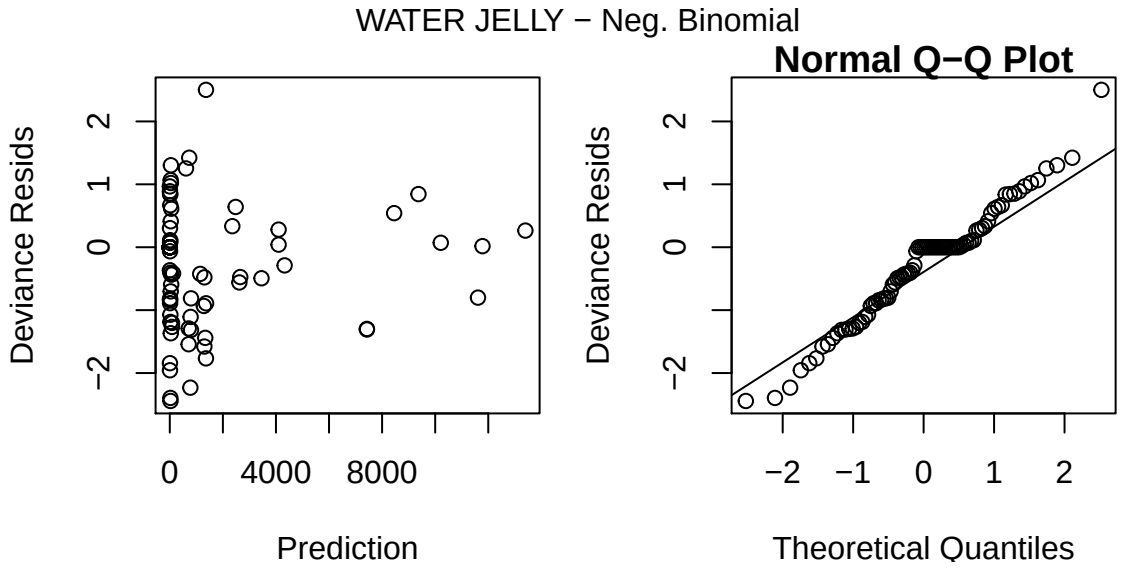


Figure 22:

```
## 0.25 1.556469 0.7193314
## 0.5  1.630563 0.7221325
## 0.75 1.708185 0.7249445
## 0.95 1.828025 0.7290641
##
## *** METHOD 2: GLM ANODEV, negative binomial ***
## Initial Theta:  0.85263
##
##  Initial fit to estimate theta
## Estimated theta:  0.8668664 , SE:  0.1430373
##
##  Final fit with theta =  0.8668664
##
## FIT STATISTICS:Analysis of Deviance Table
##
## Model: Negative Binomial(0.8669), link: log
##
## Response: Count
##
## Terms added sequentially (first to last)
##
##
##       Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                     85     653.02
## Block 11   572.25        74      80.77   <2e-16 ***
## Gear   2     2.98        72      77.79    0.217
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##             Up      Down
## Mean 1.9209114 0.6862222
## 0.05 0.9583039 0.3424639
## 0.25 1.3884082 0.4960827
```

```
## 0.5  1.7904148 0.6396456
## 0.75 2.3088203 0.8247545
## 0.95 3.3450611 1.1947141
```

3.2 Summary of results

Method abbreviations for the summary are:

- GLM.Po - GLM blocked AnoDev with Poisson
- GLM.nb - GLM blocked AnoDev with negative binomial

```
print(stat.sum)
```

```
## $`CHINOOK subadult`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 1.030 0.681 0.856  1.003 1.174 1.478
## GLM.nb 1.074 0.647 0.854  1.033 1.249 1.649
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 1.425 0.844 1.123  1.366 1.662 2.211
## GLM.nb 1.452 0.769 1.082  1.368 1.729 2.433
##
##
## $`CHINOOK subyearling`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.985 0.903  0.95  0.983 1.018 1.072
## GLM.nb 0.894 0.538  0.71  0.860 1.040 1.373
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.649 0.554 0.607  0.647 0.689 0.755
## GLM.nb 0.510 0.296 0.398  0.488 0.598 0.803
##
##
## $`CHINOOK yearling`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.806 0.692 0.756  0.803 0.853 0.932
## GLM.nb 0.787 0.474 0.625  0.756 0.915 1.207
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 1.128 0.863 1.004  1.114 1.236 1.439
## GLM.nb 1.239 0.705 0.957  1.181 1.457 1.978
##
```

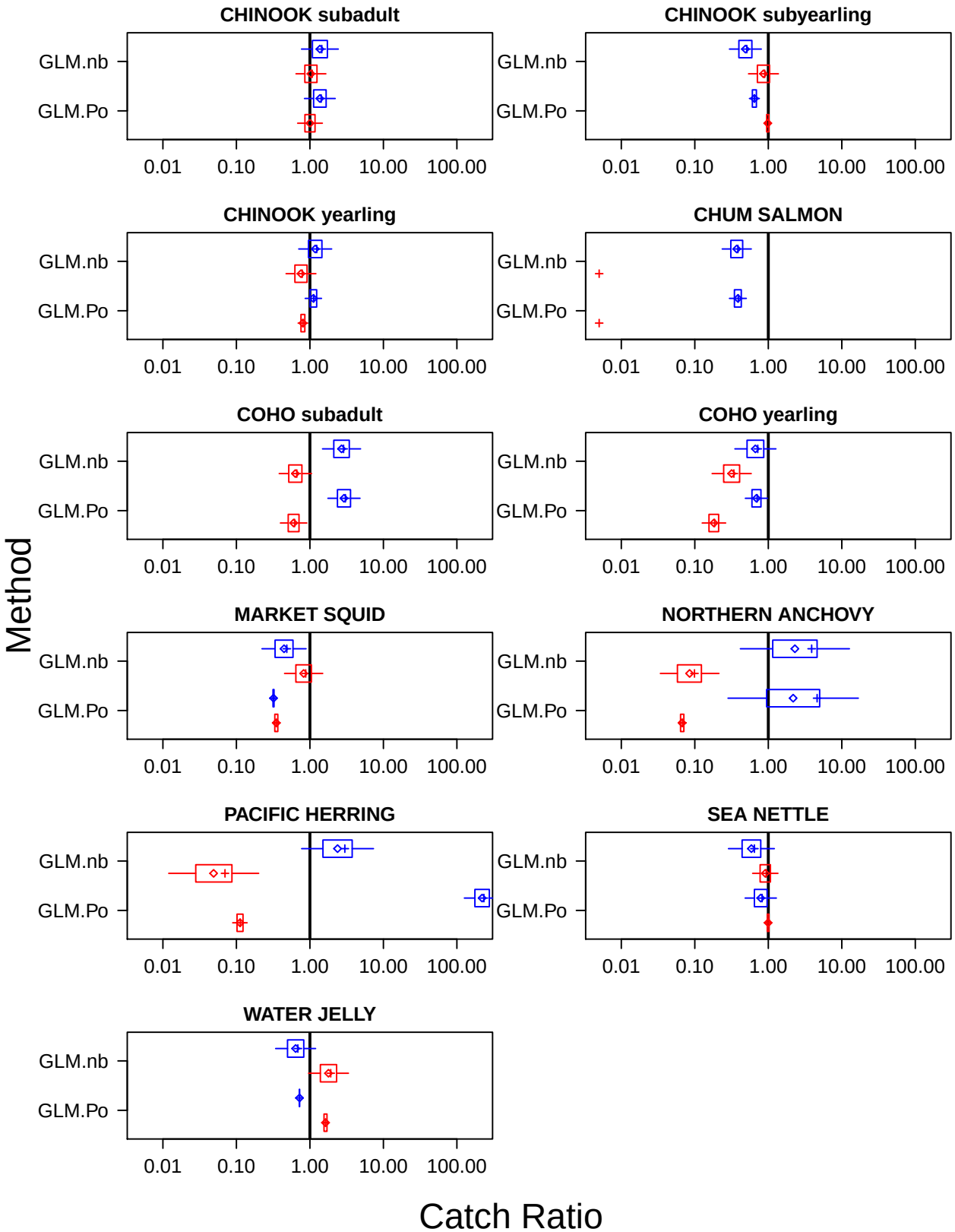
```
##
## $`CHUM SALMON`
## , , Up
##
##        Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po    0    NA    NA     NA    NA    NA
## GLM.nb    0    NA    NA     NA    NA    NA
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.391 0.296 0.346  0.386 0.429 0.502
## GLM.nb 0.386 0.236 0.309  0.372 0.448 0.587
##
##
## $`COHO subadult`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.619 0.397 0.507  0.601 0.711 0.909
## GLM.nb 0.664 0.382 0.516  0.634 0.779 1.053
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 3.043 1.758 2.370  2.908 3.568 4.809
## GLM.nb 2.873 1.485 2.114  2.695 3.434 4.891
##
##
## $`COHO yearling`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.186 0.126 0.156  0.182 0.211 0.263
## GLM.nb 0.340 0.172 0.247  0.317 0.407 0.586
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.705 0.487 0.599  0.690 0.794 0.977
## GLM.nb 0.719 0.351 0.514  0.667 0.867 1.269
##
##
## $`MARKET SQUID`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.350 0.310 0.333  0.349 0.366 0.393
## GLM.nb 0.877 0.452 0.644  0.822 1.048 1.494
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.320 0.307 0.315  0.320 0.325 0.333
```

```
## GLM.nb 0.485 0.223 0.336  0.445 0.589 0.887
##
##
## $`NORTHERN ANCHOVY`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.068 0.060 0.064  0.067 0.071 0.076
## GLM.nb 0.099 0.034 0.058  0.085 0.123 0.213
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75  q0.95
## GLM.Po 4.614 0.283 0.949  2.179 4.999 16.778
## GLM.nb 3.890 0.417 1.149  2.302 4.610 12.690
##
##
## $`PACIFIC HERRING`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.113 0.089 0.102  0.112 0.123 0.140
## GLM.nb 0.070 0.012 0.028  0.049 0.087 0.201
##
## , , Down
##
##           Mean   q0.05   q0.25  Median   q0.75   q0.95
## GLM.Po 233.083 126.305 175.740 220.424 276.471 384.679
## GLM.nb   2.988   0.772   1.505   2.379   3.759   7.326
##
##
## $`SEA NETTLE`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.995 0.932 0.968  0.994 1.020 1.060
## GLM.nb 0.936 0.612 0.774  0.910 1.069 1.353
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.824 0.484 0.647  0.789 0.963 1.287
## GLM.nb 0.647 0.287 0.440  0.589 0.789 1.208
##
##
## $`WATER JELLY`
## , , Up
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 1.634 1.454 1.556  1.631 1.708 1.828
## GLM.nb 1.921 0.958 1.388  1.790 2.309 3.345
##
## , , Down
##
```

```
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.722 0.715 0.719  0.722 0.725 0.729
## GLM.nb 0.686 0.342 0.496  0.640 0.825 1.195
```

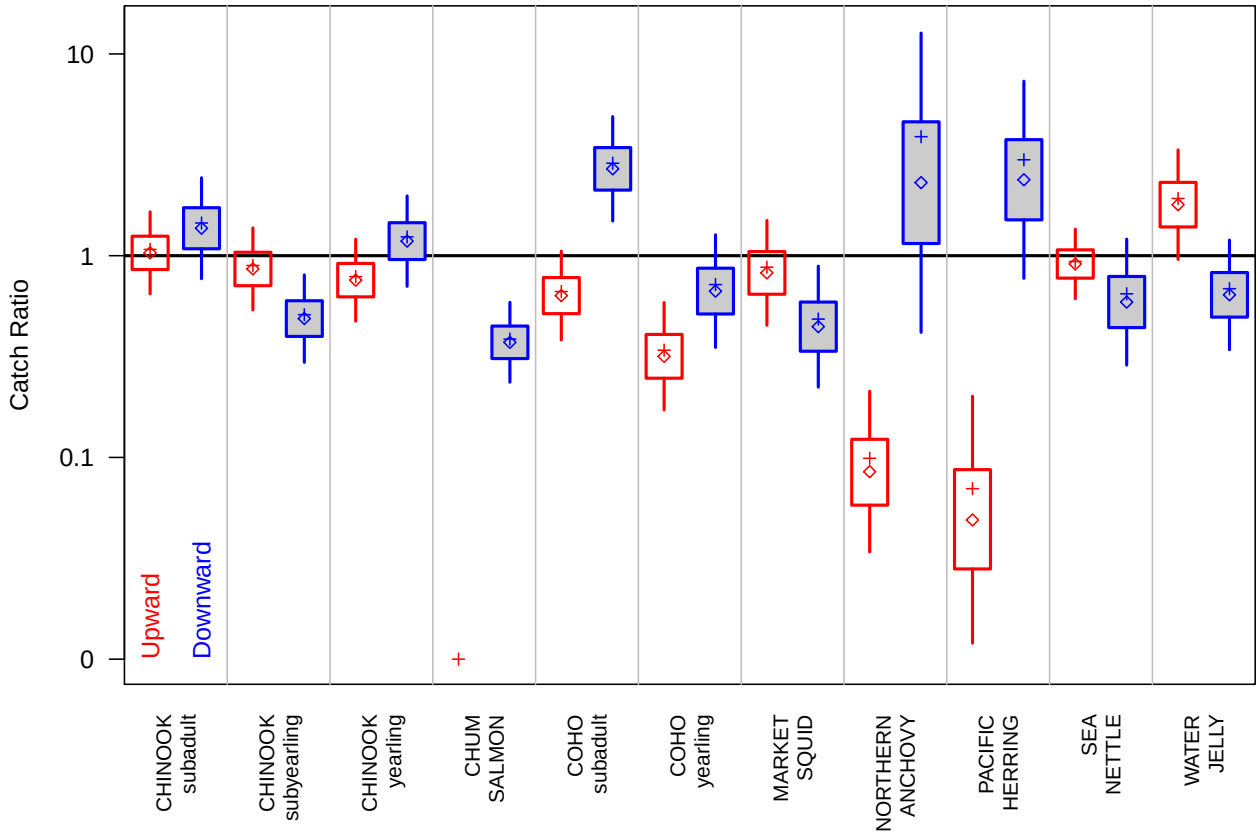
Next, generate summary figures of catch ratio estimates. In the plots, the estimated mean is marked with "+" and the median with a diamond; boxes span the quartiles, and whiskers extend to the 5% and 95% quantiles.

```
par(mfrow=c(ceiling(length(stat.sum)/plcol), plcol), omi=c(0.5,0.5,0,0), mar=c(3,4,2,1))
for (sp in names(stat.sum)) {
  .sumtbl <- stat.sum[[sp]]
  .sumtbl[.sumtbl==Inf] <- 99 # recode infinite values as +99
  .minx <- 5e-3
  .sumtbl[.sumtbl<.minx] <- .minx # recode zeros as small pos. value (for log scale plots)
  .nstats <- dim(.sumtbl)[1]
  .ngears <- dim(.sumtbl)[3]
  .ny <- .ngears*.nstats # number of elements along y axis.
  .gclr <- rep(c('red','blue','green3')[1:.ngears], .nstats) # gear color codes
  .xmax <- ceiling(max(.sumtbl[ , 'q0.75', ], na.rm=TRUE)) # make sure the quartiles are covered
  .xmax <- max(.xmax, 2) #make sure upper bound is above 1
  .xmax <- min(.xmax, 10) #truncate high values so plot is readable
  .xlim <- c(.minx, 1/.minx)
  plot(t(.sumtbl[ ,'Mean', ]), log='x', 1:.ny, col=.gclr, pch=3, cex=0.75, axes=F,
       xlim=.xlim, ylim=c(0.5, .ny+0.5),
       main=sp, xlab='', ylab='')
  box()
  abline(v=1, lwd=2, col='black')
  axis(side=1, cex.axis=1.2)
  axis(side=2, at=seq(1,.ny,.ngears)+1/.ngears, labels=dimnames(.sumtbl)[[1]], las=2, cex.axis=1.2)
  points(t(.sumtbl[ ,'Median', ]), 1:.ny, col=.gclr, pch=5, cex=0.75)
  rect(t(.sumtbl[ ,'q0.25', ]), (1:.ny)-0.35, t(.sumtbl[ ,'q0.75', ]), (1:.ny)+0.35, border=.gclr)
  segments(t(.sumtbl[ ,'q0.05', ]), 1:.ny, t(.sumtbl[ ,'q0.25', ]), 1:.ny, col=.gclr, lwd=1)
  segments(t(.sumtbl[ ,'q0.75', ]), 1:.ny, t(.sumtbl[ ,'q0.95', ]), 1:.ny, col=.gclr, lwd=1)
} # for (sp)
mtext('Catch Ratio', outer=T, side=1, line=1, cex=1.5)
mtext('Method', outer=T, side=2, line=1, cex=1.5)
```



And a single panel summary of just the GLM.nb results for both excluder types.

```r
par(mfrow=c(1,1), omi=c(0.5,0.5,0,0), mar=c(4,4,1,1))
.sumtbl <- simplify2array(stat.sum)[ "GLM.nb", , , ] # array: probs x gear x species
.sumtbl[.sumtbl==Inf] <- 99 # recode infinite values as +99
.miny <- 1e-2
.sumtbl[.sumtbl<.minx] <- .miny # recode zeros as small pos. value (for log scale plots)
.ngears <- dim(.sumtbl)[2]
.nspecs <- dim(.sumtbl)[3]
.nx <- .ngears*.nspecs      # number of elements along y axis.
.gbox <- rep(c('red','blue','green3')[1:.ngears], .nspecs) # box colors
.gpnt <- rep(c('red','blue','grey80')[1:.ngears], .nspecs) # point colors
.gfill <- rep(c(NA,'grey80','green3')[1:.ngears], .nspecs) # fill colors
.maxy <- ceiling(max(.sumtbl[ 'q0.95', , ], na.rm=TRUE))
.ylim <- c(.miny, .maxy)
plot(1:.nx, .sumtbl['Mean', , ], type='n', log='y', xaxs='i', axes=F,
     ylim=.ylim, xlim=c(0.5, .nx+0.5),
     xlab='', ylab='Catch Ratio')
box()
abline(h=1, lwd=2, col='black')
# label "fake zero" as zero:
axis(side=2, at=c(.miny,0.10,1,10,100), labels=c('0','0.1','1','10','100'), las=2)
.labs <- dimnames(.sumtbl)[[3]]
.labs <- sub(' ', '\n', .labs)
axis(side=1, at=seq(1, .nx, .ngears) + 1/.ngears, tick=FALSE, labels=.labs,
     las=2, cex.axis=0.8)
abline(v=seq(.ngears+1, .nx, .ngears) - 1/.ngears, col="grey")
rect((1:.nx)-0.35, .sumtbl['q0.25', , ], (1:.nx)+0.35, .sumtbl['q0.75', , ],
     border=.gbox, col=.gfill, lwd=2)
segments(1:.nx, .sumtbl['q0.05', , ], 1:.nx, .sumtbl['q0.25', , ], col=.gbox, lwd=2)
segments(1:.nx, .sumtbl['q0.75', , ], 1:.nx, .sumtbl['q0.95', , ], col=.gbox, lwd=2)
points(1:.nx, .sumtbl['Median', , ], col=.gpnt, pch=5, cex=0.75)
points(1:.nx, .sumtbl['Mean', , ], col=.gpnt, pch=3, cex=0.75)
text(1, .miny, "Upward", col="red", adj=c(0,0.5), srt=90)
text(2, .miny, "Downward", col="blue", adj=c(0,0.5), srt=90)
```



Part 4: Size-selectivity analysis

4.1: Size-frequency Data

We analyze size-frequencies for the same set of species selected above, but do not subdivide salmon species by age group. For an unbiased analysis, we first compute the size subsampling ratio (individuals measured / number caught) for each species in each haul, and compute adjusted counts by size We then bin sizes into 5 mm intervals, and eliminate a couple size outliers for anchovy and water jelly (appear to be erroneous data that are overly influential in the analysis).

```
# Restrict to species selected above, but no age groups for salmon
len.spec <- c("CHINOOK SALMON", "CHUM SALMON", "COHO SALMON",
              "MARKET SQUID", "NORTHERN ANCHOVY", "PACIFIC HERRING",
              "SEA NETTLE", "WATER JELLY")
lenData <- MMEDdata[ , c("Cruise","MMED","Species","Length",
                         "Number","Distance","Haul")]
lenData <- lenData[lenData$Species %in% len.spec, ]
# Add subsample ratio:
# Total number by Haul (rows) and Species (cols)
cnt <- with (lenData, tapply(Number, list(Haul, Species), FUN=sum, simplify=T))
cnt[is.na(cnt)] <- 0
cnt <- as.data.frame(cnt)
# Total measured by Haul & species
meas <- with(lenData, tapply(!is.na(Length), list(Haul, Species), FUN=sum, simplify=T))
meas[is.na(meas)] <- 0
meas <- as.data.frame(meas)
# Subsampling ratio by Haul & Species:
ssr <- meas / cnt
```

```r
cat('\nSubsampling Ratios:\n')
```

```
##
## Subsampling Ratios:
```

```r
print(summary(ssr))
```

```
##  CHINOOK SALMON    CHUM SALMON      COHO SALMON      MARKET SQUID
##  Min.   :0.1328   Min.   :0.6923   Min.   :0.6618   Min.   :0.008602
##  1st Qu.:0.7674   1st Qu.:0.8000   1st Qu.:1.0000   1st Qu.:0.114096
##  Median :0.9045   Median :1.0000   Median :1.0000   Median :0.660256
##  Mean   :0.8346   Mean   :0.9054   Mean   :0.9851   Mean   :0.542583
##  3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.000000
##  Max.   :1.0000   Max.   :1.0000   Max.   :1.0000   Max.   :1.000000
##  NA's   :2        NA's   :53       NA's   :11       NA's   :18
##  NORTHERN ANCHOVY  PACIFIC HERRING     SEA NETTLE       WATER JELLY
##  Min.   :0.00253   Min.   :0.01261   Min.   :0.06829   Min.   :0.000679
##  1st Qu.:0.33095   1st Qu.:0.46711   1st Qu.:0.21333   1st Qu.:0.010392
##  Median :0.92857   Median :1.00000   Median :0.41463   Median :0.140222
##  Mean   :0.67990   Mean   :0.75391   Mean   :0.53817   Mean   :0.287572
##  3rd Qu.:1.00000   3rd Qu.:1.00000   3rd Qu.:1.00000   3rd Qu.:0.528846
##  Max.   :1.00000   Max.   :1.00000   Max.   :1.00000   Max.   :1.000000
##  NA's   :66        NA's   :70        NA's   :37        NA's   :24
```

```r
# Adjusted Numbers (expanded by ssr)
lenData <- lenData[!is.na(lenData$Length), ] #remove non-measured counts
lenData$AdjNum <- lenData$Number / unlist(apply(lenData[c("Haul","Species")], 1,
                  function(x){ssr[x["Haul"], x["Species"]]}))
# Length bin size (mm)
binsize <- 5
lenData$LenBin <- binsize * round(lenData$Length/binsize)
# Remove size outliers for anchovy & water jelly (likely data errors)
lenData <- lenData[!((lenData$Species == "NORTHERN ANCHOVY") &
                       (lenData$Length < 100)), ]
lenData <- lenData[!((lenData$Species =="WATER JELLY") &
                       (lenData$Length > 150)), ]
cat('\nSummary of Length Data:\n')
```

```
##
## Summary of Length Data:
```

```r
print(summary(lenData))
```

```
##      Cruise          MMED             Species             Length
##  Min.   :41.00   Length:4385        Length:4385        Min.   : 15.0
##  1st Qu.:43.00   Class :character   Class :character   1st Qu.: 73.0
##  Median :50.00   Mode  :character   Mode  :character   Median :115.0
##  Mean   :47.99                                         Mean   :137.1
##  3rd Qu.:53.00                                         3rd Qu.:158.0
##  Max.   :53.00                                         Max.   :794.0
##      Number          Distance         Haul               AdjNum
##  Min.   : 1.000   Min.   :1.129   Length:4385        Min.   :   1.000
##  1st Qu.: 1.000   1st Qu.:1.506   Class :character   1st Qu.:   1.179
##  Median : 1.000   Median :1.860   Mode  :character   Median :   3.154
##  Mean   : 1.702   Mean   :2.396                      Mean   :  51.898
##  3rd Qu.: 2.000   3rd Qu.:3.513                      3rd Qu.:  12.056
```

```
##  Max.   :33.000   Max.   :4.906                      Max.   :5890.571
##      LenBin
##  Min.   : 15.0
##  1st Qu.: 75.0
##  Median :115.0
##  Mean   :137.1
##  3rd Qu.:160.0
##  Max.   :795.0
```

4.2: Analysis Methods

Next, run the Size-Frequency (SF) analysis for each species. Because the length data is sparse for most species, we analyze only the bulk data across all haul samples, ignoring the data blocks. First tabulate the distributions across all samples by species and gear type. Then, apply both a Wilcox-Mann-Whitney test and a Kolmogorov-Smirnov test for gear differences. **NOTE** the several warnings that p-values are approximate for the K-S test. We'll ignore the warnings, assuming they're close enough as we're concerned with the patterns of size-selectivity, and only note the highly significant results.

Then, conduct full gear Size-Selectivity Analysis, fitting a smooth curve (3rd-order polynomial) to the size-specific catch ratio data using a binomial GLM with logit link function, similar to models in Krag et al. (2014 PLOS One), Herrmann et al. (2017 Fish. Res.), & Kotwicki et al. (2017 Fish. Res.). The model is first fit to the full data set, then the error distribution is approximated via a double bootstrap (Millar 1993 Fish. Bull.) resampling both among hauls and among fish within hauls. We define a function for this analysis, so it can be applied to combinations of gear and species.

```
boot_GLM3P <- function(sdat, nrep=10, binsz=5, L.pr=NULL) {
  fit.model <- function(sdat) {
    NumTotL <- with(sdat, tapply(AdjNum, list(LenBin, MMED), sum,
                                 na.rm=TRUE, default=0))
    EffTotL <- with(sdat, tapply(Distance, list(LenBin, MMED),sum,
                                 na.rm=TRUE, default=0))
    cpue <- NumTotL/EffTotL
    cpue[is.na(cpue)] <- 0
    STD <- match("None", colnames(cpue))
    TST <- match("Up", colnames(cpue))
    if (is.na(TST)) TST <- match("Down", colnames(cpue))
    std <- cpue[ , STD]
    tst <- cpue[ , TST]
    p.L12 <- std / (std + tst)
    # Binomial weights based on number measured in both gears:
    Nmeas <- with(sdat, tapply(Number, list(LenBin, MMED), sum,
                               na.rm=TRUE, default=0))
    wts <- Nmeas[ , STD] + Nmeas[ , TST]
    L <- as.numeric(names(p.L12))
    old.opt <- options(warn = -1) # suppress warnings about non-integer values
    fit.glm <- glm(p.L12 ~ L + I(L^2) + I(L^3), family=binomial, weights=wts)
    options(old.opt)
    return(fit.glm)
  } # fit.model()

  # Fit the model to the original (full) dataset:
  fit.full <- fit.model(sdat)
  # Predictions of full model, with rough SE's
  if (is.null(L.pr)) L.pr <- seq(min(sdat$LenBin), max(sdat$LenBin), 5)
```

```
  pred.full <- predict(fit.full, newdata=data.frame(L=L.pr, wts=1.0),
                       type="response")
  names(pred.full) <- L.pr
  # Bootstrap predictions:
  bs <- matrix(NA, nrow=length(L.pr), ncol=nrep, dimnames=list(L.pr, NULL))
  rep <- 0
  while (rep < nrep) {
    hauls <- unique(sdat$Haul)
    hauls.samp <- sample(hauls, length(hauls), replace=TRUE)
    .data <- data.frame()
    for (h in hauls.samp) {
      .hdata <- sdat[sdat$Haul == h, ]
      ssr <- with(.hdata, sum(Number)/sum(AdjNum)) # subsample rate
      L.ex <- with(.hdata, rep(LenBin, Number))  #expand Number to indiv. lengths
      if(length(L.ex) > 1) {
        L.smp <- sample(L.ex, length(L.ex), replace=TRUE)  #resample lengths
      } else {
        L.smp <- L.ex  # sample() doesn't work for length 1 vector
      }
      new.freq <- as.data.frame(table(L.smp))
      .ndata <- data.frame(MMED=unique(.hdata$MMED),
                           Haul=unique(.hdata$Haul),
                           Distance=mean(.hdata$Distance),
                           LenBin=as.numeric(levels(new.freq$L.smp)),
                           Number=new.freq$Freq,
                           AdjNum=new.freq$Freq/ssr)
      .data <- rbind(.data, .ndata)
    } # for (h)
    names(.data) <- names(sdat)
    fit.rep <- fit.model(.data)
    rep <- rep+1
    bs[ , rep] <- predict(fit.rep, newdata=data.frame(L=L.pr, wts=1.0),
                          type="response")
  } # for (rep)
  rownames(bs) <- L.pr
  bs.mn <- apply(bs, 1, mean, na.rm=FALSE)
  bs.q <- t(apply(bs, 1, quantile, probs=c(0,0.05,0.25,0.50,0.75,0.95,1),
                  na.rm=FALSE))
  return(list(glm=fit.full, pred=pred.full, boot=bs,
              boot.sum=data.frame(mean=bs.mn, q=bs.q)))
} # boot_GLM3P()
```

4.3 Results

Because the two MED orientations were used in different years and locations, we can't compare either MED to all the samples from the standard net, so we run this analysis into two groups: the upward MED tests in years 2011 & 2014, and the downward MED tests in 2015.

```
# Set number of bootstrap replicates:
## nbsr <- 50   ### TESTING ###
nbsr <- 1000 ### PRODUCTION ###

for (excl in c("Up","Down")) {
```

```
cat('\n***************** Excluder: ', excl, ' ******************\n')
lD <- if(excl %in% "Up") {
  lenData[lenData$Cruise %in% c(41,43,50), ]
} else {
  lenData[lenData$Cruise %in% 53, ]
}
lD$Species <- factor(as.character(lD$Species))
.tab <- with(lD, tapply(AdjNum, list(Species), sum, na.rm=T))
cat('Total Adjusted Catch:\n')
print(.tab)
lf.sel.spec <- names(.tab)[.tab >= 100]
lenFreq <- with(lD, tapply(AdjNum, list(LenBin, MMED, Species), sum, na.rm=TRUE))
lenFreq[is.na(lenFreq)] <- 0
.mfrow <- if(lndscp) c(3,3) else c(3,2)
par(mfrow=.mfrow, omi=c(0.5,0.5,0,0.5), mar=c(3,3,2,3))
for (sp in lf.sel.spec) {
  cat('\n*****************', sp, '******************\n')
  if (sp %in% dimnames(lenFreq)[[3]]) {
    .dat <- lenFreq[ , , sp]
    .maxN <- max(.dat,na.rm=T)
    .len <- lD[lD$Species %in% sp,
               c("MMED", "Haul", "Distance", "LenBin", "Number", "AdjNum")]
    .maxL <- max(.len$LenBin, na.rm=T)
    .minL <- min(.len$LenBin, na.rm=T)
    .len.std <- .len[.len$MMED=='None', ]
    .len.mmed <- .len[.len$MMED==excl, ]
    .x <- rep(.len.std$LenBin, .len.std$Number)
    .y <- rep(.len.mmed$LenBin, .len.mmed$Number)
    # Run analysis only if > 40 measurements in each gear:
    if ((length(.x) > 40) & (length(.y) > 40)) {
      # Wilcox & KS test for overall difference in size-frequencies
      print(wilcox.test(.x, .y, alt="two.sided"))
      print(ks.test(.x, .y))
      # GLM fit of Catch Ratio to size:
      mod.fit <- boot_GLM3P(sdat=.len, nrep=nbsr, binsz=binsize)
      cat("\tSummary of GLM fit: \n")
      print(summary(mod.fit$glm))
      print(anova(mod.fit$glm, test="Chisq"))
      cat("\n\tSummary of bootstrap fits: \n")
      print(summary(mod.fit$boot.sum))
      p.pred <- mod.fit$pred
      L.pred <- as.numeric(names(p.pred))
      # Convert probability to Catch Ratio:
      CR.obs <- 1/mod.fit$glm$model$p.L12 - 1
      CR.pred <- 1/p.pred - 1
      CR.boot <- 1/mod.fit$boot.sum - 1
      CR.boot[CR.boot > 1000] <- 1000 #recode infinite values
      CR.boot[CR.boot < 1/1000] <- 1/1000 #recode zero values
      plot(as.numeric(rownames(.dat)), -.dat[, 'None'], type='h', col=BLACK, lwd=1,
           xlim=c(.minL,.maxL), ylim=c(-.maxN,.maxN), axes=F,
           xlab='', ylab='')
      box()
      axis(side=1, lwd=0, lwd.ticks=1)
```

```
        axis(side=2, at=pretty(c(-max(.dat,na.rm=T),max(.dat,na.rm=T))),
             labels=abs(pretty(c(-max(.dat,na.rm=T),max(.dat,na.rm=T)))))
        points(as.numeric(rownames(.dat)), .dat[, excl], type='h',
               col={if(excl %in% "Up") RED else BLUE}, lwd=1)
        mtext(sp, side=3, cex=0.75, line=0)
        abline(h=0, lwd=1)
        # add Catch Ratio plot on right axis
        par(new=TRUE)
        plot(L.pred, CR.pred, log="y", type='l', lwd=3, axes=FALSE, bty="n",
             ylim=c(1/50, 50), xlab="", ylab="")
        axis(side=4, at=c(0.02, 0.2, 1, 5, 50),
             labels=c("0.02", "0.2", "1", "5", "50"))
        lines(L.pred, CR.boot[ , "q.50."], lty=1, col='gray50', lwd=2) # bs median
        lines(L.pred, CR.boot[ , "q.5."], lty=2, col='gray50', lwd=2) # bs lower 5%
        lines(L.pred, CR.boot[ , "q.95."], lty=2, col='gray50', lwd=2) # bs upper 5%
      } else {
        cat('\n Insufficient data \n')
      } # if (length...)
    } else {
      cat('\n\tNO LENGTH DATA FOR ', sp, '\n')
    } # if (sp %in% ...)
  } # for(sp)
  mtext('Size (mm)', side=1, outer=TRUE, at=c(0.5,0.5), cex=1.5)
  mtext('Observed Catch Per Km', side=2, outer=TRUE, at=c(0.5,0.5), cex=1.5)
  mtext('Estimated Catch Ratio', side=4, outer=TRUE, at=c(0.5,0.5), cex=1.5)
} # for (excl)
```

```
## Warning in ks.test(.x, .y): p-value will be approximate in the presence of
## ties
```

```
## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!
```

```
## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!
```

```
## Warning in ks.test(.x, .y): cannot compute exact p-value with ties
```

```
## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!
```

```
## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!
```

```
## Warning in ks.test(.x, .y): p-value will be approximate in the presence of
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```

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## Warning in ks.test(.x, .y): p-value will be approximate in the presence of
## ties
```

```
## Warning in eval(family$initialize): non-integer #successes in a binomial
```

```
## glm!

## Warning in eval(family$initialize): non-integer #successes in a binomial
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## Warning in ks.test(.x, .y): p-value will be approximate in the presence of
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## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in ks.test(.x, .y): p-value will be approximate in the presence of
## ties

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in ks.test(.x, .y): p-value will be approximate in the presence of
## ties

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in ks.test(.x, .y): cannot compute exact p-value with ties

## Warning in ks.test(.x, .y): non-integer #successes in a binomial glm!

## Warning in ks.test(.x, .y): non-integer #successes in a binomial glm!

## Warning in ks.test(.x, .y): cannot compute exact p-value with ties

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in ks.test(.x, .y): p-value will be approximate in the presence of
## ties

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!

## Warning in ks.test(.x, .y): p-value will be approximate in the presence of
## ties

## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!
```

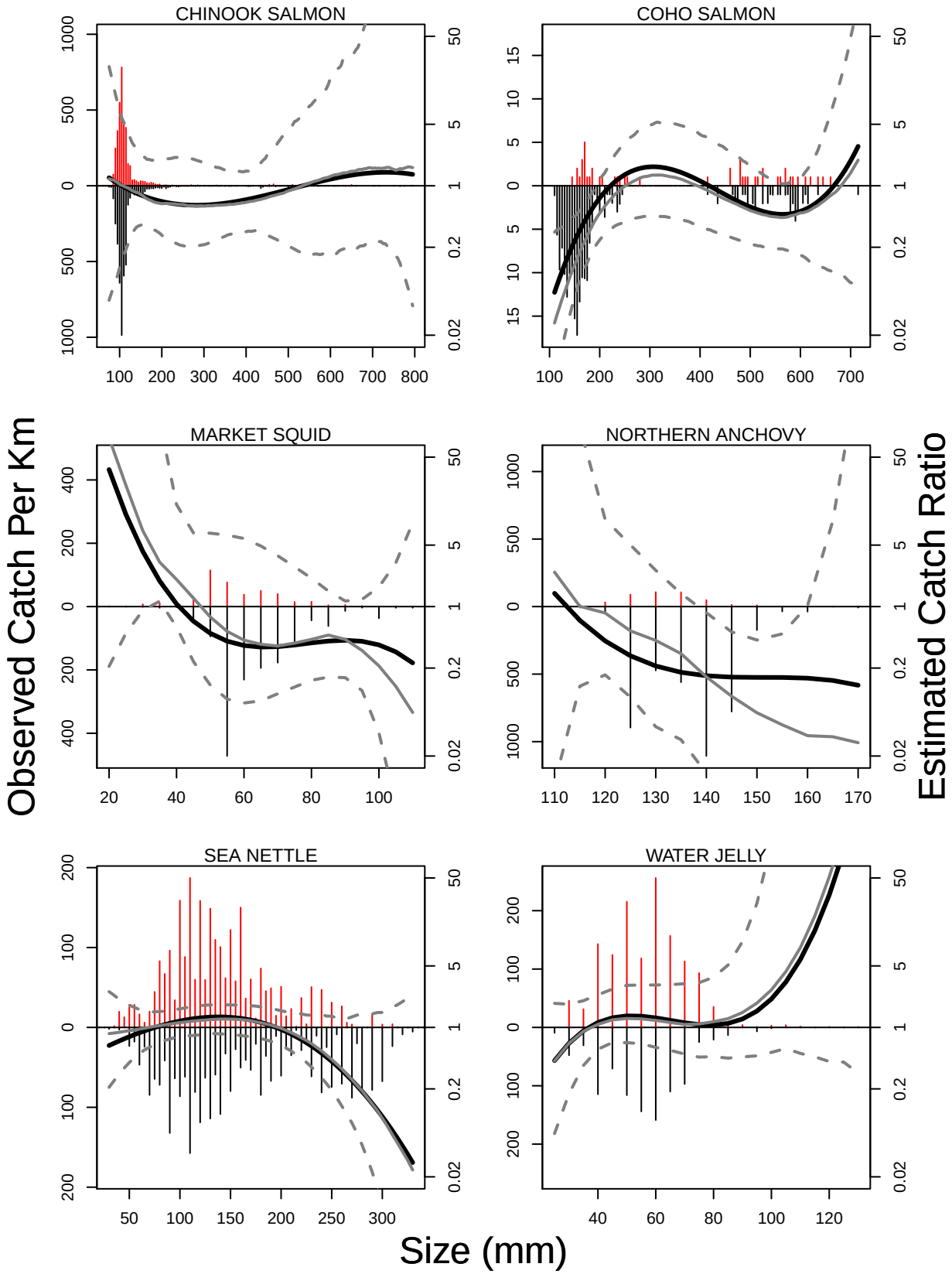
CHINOOK SALMON
COHO SALMON
MARKET SQUID
NORTHERN ANCHOVY
SEA NETTLE
WATER JELLY
Observed Catch Per Km
Estimated Catch Ratio
Size (mm)

Figure 23:

```
## Warning in eval(family$initialize): non-integer #successes in a binomial
## glm!
##
## ********** Excluder:  Up  **********
## Total Adjusted Catch:
##   CHINOOK SALMON      CHUM SALMON      COHO SALMON     MARKET SQUID
##       7806.36006         24.34091        271.59921       1930.73203
## NORTHERN ANCHOVY  PACIFIC HERRING       SEA NETTLE      WATER JELLY
##       4545.80019        788.94286       5328.01283       2321.85789
##
## ********** CHINOOK SALMON **********
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 557520, p-value = 0.3175
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.028936, p-value = 0.7764
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.4824  -1.0048   0.0389   1.0590   3.2229
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -9.376e-01  3.682e-01  -2.546   0.0109 *
## L            1.175e-02  4.754e-03   2.471   0.0135 *
## I(L^2)      -2.881e-05  1.573e-05  -1.832   0.0670 .
## I(L^3)       1.893e-08  1.423e-08   1.330   0.1835
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 132.65  on 87  degrees of freedom
## Residual deviance: 120.58  on 84  degrees of freedom
## AIC: 275.2
##
## Number of Fisher Scoring iterations: 4
##
```

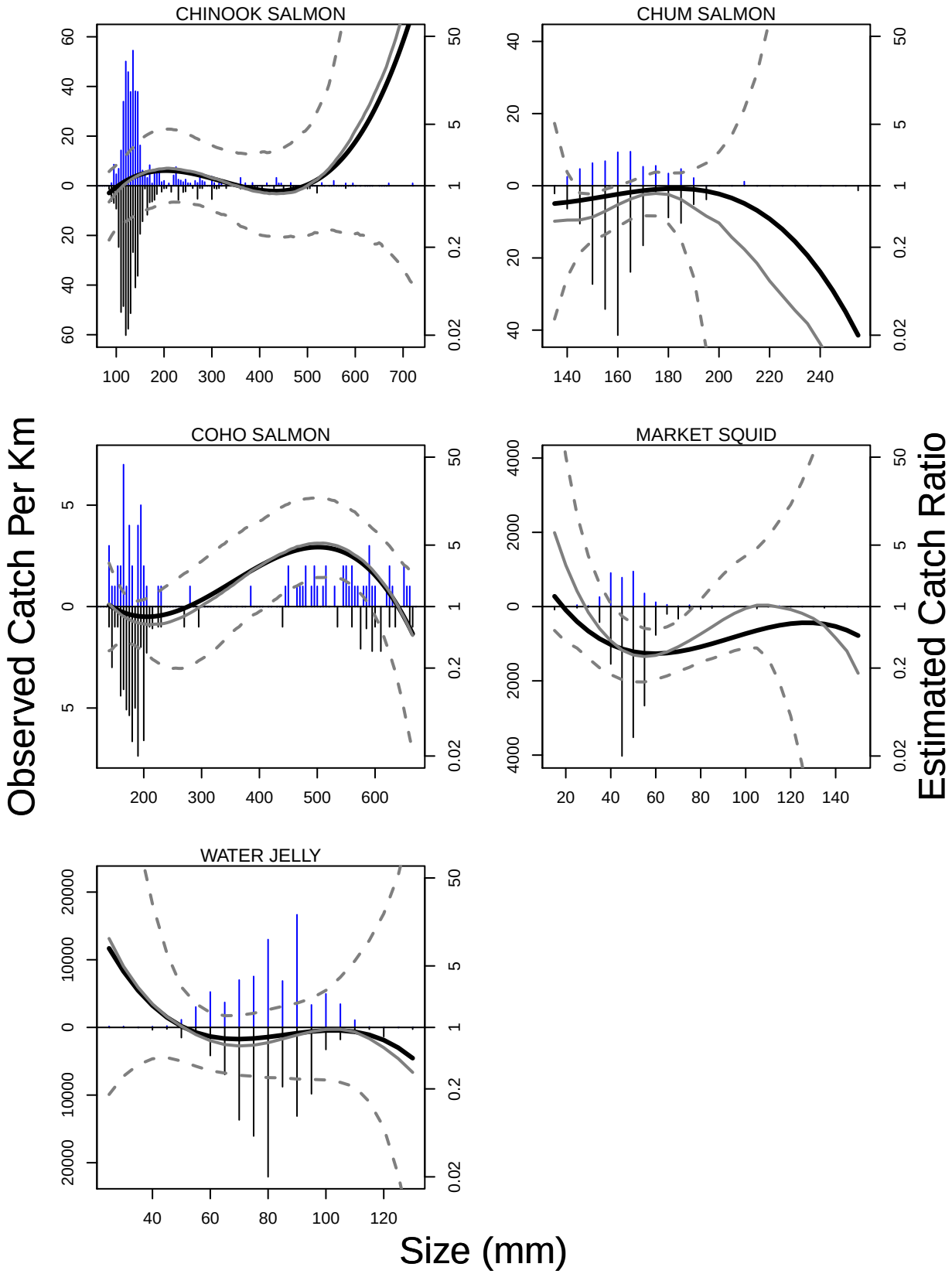
CHINOOK SALMON
CHUM SALMON
COHO SALMON
MARKET SQUID
WATER JELLY
Observed Catch Per Km
Estimated Catch Ratio
Size (mm)

Figure 24:

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      87     132.65
## L       1   1.8014        86     130.85   0.1795
## I(L^2)  1   8.5266        85     122.32   0.0035 **
## I(L^3)  1   1.7446        84     120.58   0.1866
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.              q.5.               q.25.
##  Min.   :0.3934   Min.   :0.00000   Min.   :0.0000753   Min.   :0.1196
##  1st Qu.:0.4412   1st Qu.:0.00000   1st Qu.:0.0438000   1st Qu.:0.2456
##  Median :0.5291   Median :0.01454   Median :0.2182649   Median :0.4172
##  Mean   :0.5167   Mean   :0.05429   Mean   :0.2035302   Mean   :0.3756
##  3rd Qu.:0.5941   3rd Qu.:0.09490   3rd Qu.:0.3370246   3rd Qu.:0.4924
##  Max.   :0.6155   Max.   :0.20724   Max.   :0.4112790   Max.   :0.5377
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.3786   Min.   :0.5583   Min.   :0.7325   Min.   :0.8186
##  1st Qu.:0.4281   1st Qu.:0.6313   1st Qu.:0.7898   1st Qu.:0.9282
##  Median :0.5381   Median :0.6581   Median :0.8231   Median :0.9721
##  Mean   :0.5206   Mean   :0.6544   Mean   :0.8227   Mean   :0.9589
##  3rd Qu.:0.6136   3rd Qu.:0.6899   3rd Qu.:0.8483   3rd Qu.:0.9987
##  Max.   :0.6295   Max.   :0.7293   Max.   :0.9586   Max.   :1.0000
##
## ***************** COHO SALMON *****************
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 2478.5, p-value = 0.000001831
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.37991, p-value = 0.00002893
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
```

```
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3673  -0.9730   0.1931   1.2725   2.2525
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  9.004e+00  2.250e+00   4.001 0.000063 ***
## L           -7.567e-02  2.202e-02  -3.437 0.000588 ***
## I(L^2)       1.904e-04  6.037e-05   3.154 0.001610 **
## I(L^3)      -1.457e-07  5.075e-08  -2.872 0.004084 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 106.243  on 63  degrees of freedom
## Residual deviance:  87.423  on 60  degrees of freedom
## AIC: 143.29
##
## Number of Fisher Scoring iterations: 4
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      63    106.243
## L       1   4.8453        62    101.398  0.02772 *
## I(L^2)  1   5.1492        61     96.249  0.02326 *
## I(L^3)  1   8.8261        60     87.423  0.00297 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.               q.5.              q.25.
##  Min.   :0.3854   Min.   :0.0002299   Min.   :0.008153   Min.   :0.06874
##  1st Qu.:0.4684   1st Qu.:0.0481034   1st Qu.:0.181501   1st Qu.:0.33857
##  Median :0.5765   Median :0.0860872   Median :0.287034   Median :0.46960
##  Mean   :0.5887   Mean   :0.1431427   Mean   :0.325847   Mean   :0.48068
##  3rd Qu.:0.6683   3rd Qu.:0.2050709   3rd Qu.:0.455102   3rd Qu.:0.59969
##  Max.   :0.9414   Max.   :0.4960444   Max.   :0.770876   Max.   :0.93796
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.3382   Min.   :0.5485   Min.   :0.6862   Min.   :0.8389
##  1st Qu.:0.4832   1st Qu.:0.6094   1st Qu.:0.7338   1st Qu.:0.9003
##  Median :0.5936   Median :0.7083   Median :0.8199   Median :0.9219
##  Mean   :0.6028   Mean   :0.7021   Mean   :0.8147   Mean   :0.9310
##  3rd Qu.:0.6808   3rd Qu.:0.7533   3rd Qu.:0.8868   3rd Qu.:0.9758
##  Max.   :0.9732   Max.   :0.9863   Max.   :0.9949   Max.   :0.9999
##
```

```
## ***************** MARKET SQUID *****************
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 23156, p-value = 4.907e-08
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.23432, p-value = 0.00006958
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.9502  -0.9026   0.2298   1.1338   2.3714
##
## Coefficients:
##                 Estimate   Std. Error z value Pr(>|z|)
## (Intercept) -10.81427430   3.97277650  -2.722  0.00649 **
## L             0.47533570   0.19060262   2.494  0.01264 *
## I(L^2)       -0.00623093   0.00292930  -2.127  0.03341 *
## I(L^3)        0.00002659   0.00001440   1.846  0.06482 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 57.182  on 17  degrees of freedom
## Residual deviance: 35.140  on 14  degrees of freedom
## AIC: 91.578
##
## Number of Fisher Scoring iterations: 5
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      17     57.182
## L       1  10.0445        16     47.138 0.001528 **
```

```
## I(L^2)  1   8.2683        15     38.869 0.004034 **
## I(L^3)  1   3.7298        14     35.140 0.053450 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.               q.5.             q.25.
##  Min.   :0.1580   Min.   :0.000000   Min.   :0.00000   Min.   :0.0003288
##  1st Qu.:0.3921   1st Qu.:0.000245   1st Qu.:0.08284   1st Qu.:0.2295661
##  Median :0.6117   Median :0.028827   Median :0.14399   Median :0.3013745
##  Mean   :0.5373   Mean   :0.057190   Mean   :0.18944   Mean   :0.3720510
##  3rd Qu.:0.6721   3rd Qu.:0.084406   3rd Qu.:0.29174   3rd Qu.:0.5775720
##  Max.   :0.8371   Max.   :0.208333   Max.   :0.46349   Max.   :0.8156187
##      q.50.             q.75.            q.95.            q.100.
##  Min.   :0.01195   Min.   :0.1848   Min.   :0.4649   Min.   :0.8525
##  1st Qu.:0.38712   1st Qu.:0.5279   1st Qu.:0.8176   1st Qu.:0.9659
##  Median :0.70216   Median :0.7909   Median :0.8864   Median :0.9736
##  Mean   :0.56856   Mean   :0.6814   Mean   :0.8334   Mean   :0.9700
##  3rd Qu.:0.73289   3rd Qu.:0.8380   3rd Qu.:0.9201   3rd Qu.:0.9998
##  Max.   :0.94112   Max.   :0.9872   Max.   :0.9994   Max.   :1.0000
##
## ***************** NORTHERN ANCHOVY ******************
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 24497, p-value = 3.043e-09
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.32536, p-value = 6.01e-09
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.58746  -1.04605  -0.00453   1.13477   1.85831
##
## Coefficients:
##                  Estimate    Std. Error z value Pr(>|z|)
## (Intercept) -106.87895097  145.70040268  -0.734    0.463
## L              2.15694582    3.19635961   0.675    0.500
## I(L^2)        -0.01426172    0.02328293  -0.613    0.540
## I(L^3)         0.00003143    0.00005632   0.558    0.577
##
## (Dispersion parameter for binomial family taken to be 1)
```

```
##
##     Null deviance: 26.876  on 11  degrees of freedom
## Residual deviance: 18.727  on  8  degrees of freedom
## AIC: 54.403
##
## Number of Fisher Scoring iterations: 4
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      11     26.876
## L       1   6.1933        10     20.683  0.01282 *
## I(L^2)  1   1.6251         9     19.058  0.20238
## I(L^3)  1   0.3305         8     18.727  0.56537
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.                q.5.              q.25.
##  Min.   :0.4058   Min.   :0.0000000   Min.   :0.000028   Min.   :0.05113
##  1st Qu.:0.6008   1st Qu.:0.0000001   1st Qu.:0.092484   1st Qu.:0.42175
##  Median :0.7934   Median :0.0324816   Median :0.279141   Median :0.77341
##  Mean   :0.7265   Mean   :0.0407347   Mean   :0.317851   Mean   :0.60818
##  3rd Qu.:0.8841   3rd Qu.:0.0691386   3rd Qu.:0.539925   3rd Qu.:0.84873
##  Max.   :0.9117   Max.   :0.1044731   Max.   :0.705958   Max.   :0.88293
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.2888   Min.   :0.6826   Min.   :0.8567   Min.   :1
##  1st Qu.:0.6539   1st Qu.:0.7948   1st Qu.:0.9587   1st Qu.:1
##  Median :0.8629   Median :0.9295   Median :0.9902   Median :1
##  Mean   :0.7728   Mean   :0.8904   Mean   :0.9666   Mean   :1
##  3rd Qu.:0.9567   3rd Qu.:0.9948   3rd Qu.:1.0000   3rd Qu.:1
##  Max.   :0.9724   Max.   :1.0000   Max.   :1.0000   Max.   :1
##
## ********** PACIFIC HERRING **********
##
##  Insufficient data
##
## ********** SEA NETTLE **********
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 161020, p-value = 0.9677
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
```

```
##
## data:  .x and .y
## D = 0.064328, p-value = 0.1919
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3007  -0.8560   0.1096   0.9071   2.5380
##
## Coefficients:
##                  Estimate    Std. Error z value Pr(>|z|)
## (Intercept)  0.8708333569  0.8311327335   1.048    0.295
## L           -0.0140396513  0.0180557455  -0.778    0.437
## I(L^2)       0.0000232098  0.0001210210   0.192    0.848
## I(L^3)       0.0000001328  0.0000002502   0.531    0.596
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 113.782  on 55  degrees of freedom
## Residual deviance:  69.779  on 52  degrees of freedom
## AIC: 232.81
##
## Number of Fisher Scoring iterations: 4
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                      55    113.782
## L       1  15.2083        54     98.573 9.628e-05 ***
## I(L^2)  1  28.5074        53     70.066 9.334e-08 ***
## I(L^3)  1   0.2869        52     69.779    0.5922
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.                 q.5.            q.25.
##  Min.   :0.4466   Min.   :0.00009821   Min.   :0.2816   Min.   :0.4048
##  1st Qu.:0.4692   1st Qu.:0.08633950   1st Qu.:0.3586   1st Qu.:0.4263
##  Median :0.5208   Median :0.22947680   Median :0.3850   Median :0.4538
##  Mean   :0.5887   Mean   :0.18142280   Mean   :0.3813   Mean   :0.5487
##  3rd Qu.:0.7009   3rd Qu.:0.26332753   3rd Qu.:0.4080   3rd Qu.:0.6616
```

```
##  Max.   :0.8944   Max.   :0.29427590   Max.   :0.4427   Max.   :0.9224
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.4456   Min.   :0.4848   Min.   :0.5399   Min.   :0.6495
##  1st Qu.:0.4693   1st Qu.:0.5093   1st Qu.:0.5636   1st Qu.:0.6995
##  Median :0.5194   Median :0.5829   Median :0.6652   Median :0.8166
##  Mean   :0.6033   Mean   :0.6523   Mean   :0.7193   Mean   :0.8318
##  3rd Qu.:0.7231   3rd Qu.:0.7791   3rd Qu.:0.8637   3rd Qu.:0.9769
##  Max.   :0.9766   Max.   :0.9937   Max.   :0.9995   Max.   :1.0000
##
## ********** WATER JELLY **********
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 30119, p-value = 0.0192
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.099297, p-value = 0.1566
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.15870  -0.60214   0.04482   0.72553   1.81500
##
## Coefficients:
##               Estimate  Std. Error z value Pr(>|z|)
## (Intercept)  5.73520424  2.98626868   1.921   0.0548 .
## L           -0.29910317  0.15325488  -1.952   0.0510 .
## I(L^2)       0.00479145  0.00251495   1.905   0.0568 .
## I(L^3)      -0.00002448  0.00001324  -1.849   0.0644 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 29.520  on 19  degrees of freedom
## Residual deviance: 23.455  on 16  degrees of freedom
## AIC: 82.13
##
## Number of Fisher Scoring iterations: 5
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
```

```
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      19     29.520
## L       1   0.9636        18     28.556  0.32627
## I(L^2)  1   0.0609        17     28.495  0.80513
## I(L^3)  1   5.0398        16     23.455  0.02477 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.              q.5.              q.25.
##  Min.   :0.0843   Min.   :0.00000   Min.   :0.000000   Min.   :0.0000198
##  1st Qu.:0.2448   1st Qu.:0.00000   1st Qu.:0.003028   1st Qu.:0.0860607
##  Median :0.4369   Median :0.04005   Median :0.224277   Median :0.3505161
##  Mean   :0.3729   Mean   :0.05378   Mean   :0.163054   Mean   :0.2670565
##  3rd Qu.:0.4642   3rd Qu.:0.09941   3rd Qu.:0.249009   3rd Qu.:0.3689303
##  Max.   :0.6809   Max.   :0.15506   Max.   :0.352928   Max.   :0.5628794
##      q.50.              q.75.             q.95.            q.100.
##  Min.   :0.001415   Min.   :0.01977   Min.   :0.5980   Min.   :0.7273
##  1st Qu.:0.209401   1st Qu.:0.35123   1st Qu.:0.6406   1st Qu.:0.8366
##  Median :0.443781   Median :0.52233   Median :0.6801   Median :0.9337
##  Mean   :0.356115   Mean   :0.44815   Mean   :0.6888   Mean   :0.9077
##  3rd Qu.:0.475020   3rd Qu.:0.56342   3rd Qu.:0.7051   3rd Qu.:0.9999
##  Max.   :0.706089   Max.   :0.82215   Max.   :0.9415   Max.   :1.0000
##
## ***************** Excluder:  Down  *****************
## Total Adjusted Catch:
##   CHINOOK SALMON      CHUM SALMON      COHO SALMON     MARKET SQUID
##        1002.0864         255.3848         155.4833       17572.2192
## NORTHERN ANCHOVY  PACIFIC HERRING       SEA NETTLE      WATER JELLY
##           3.0000        2400.1818          47.0000      183119.7267
##
## ***************** CHINOOK SALMON *****************
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 34425, p-value = 0.000005302
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.17929, p-value = 0.0001577
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
```

```
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.27913  -1.05892   0.02342   0.95216   1.90680
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.645e+00  1.030e+00   1.597   0.1102
## L           -2.376e-02  1.329e-02  -1.787   0.0739 .
## I(L^2)       8.571e-05  4.855e-05   1.766   0.0775 .
## I(L^3)      -8.979e-08  5.197e-08  -1.728   0.0840 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 79.036  on 74  degrees of freedom
## Residual deviance: 74.352  on 71  degrees of freedom
## AIC: 175.45
##
## Number of Fisher Scoring iterations: 5
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      74     79.036
## L       1   0.5877        73     78.449  0.44333
## I(L^2)  1   0.0303        72     78.418  0.86174
## I(L^3)  1   4.0662        71     74.352  0.04375 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.              q.5.             q.25.
##  Min.   :0.1137   Min.   :0.00000   Min.   :0.00000   Min.   :0.0000496
##  1st Qu.:0.3509   1st Qu.:0.00000   1st Qu.:0.02879   1st Qu.:0.1964383
##  Median :0.4295   Median :0.01713   Median :0.20650   Median :0.3300689
##  Mean   :0.4009   Mean   :0.04579   Mean   :0.17861   Mean   :0.2866721
##  3rd Qu.:0.5074   3rd Qu.:0.07319   3rd Qu.:0.27843   3rd Qu.:0.4121642
##  Max.   :0.6056   Max.   :0.19220   Max.   :0.40821   Max.   :0.5294551
##      q.50.             q.75.            q.95.            q.100.
##  Min.   :0.00395   Min.   :0.0503   Min.   :0.6053   Min.   :0.7908
##  1st Qu.:0.33047   1st Qu.:0.4766   1st Qu.:0.6688   1st Qu.:0.8369
##  Median :0.42611   Median :0.5201   Median :0.7691   Median :0.9654
```

```
##  Mean   :0.37941   Mean   :0.4828   Mean   :0.7422   Mean   :0.9209
##  3rd Qu.:0.51048   3rd Qu.:0.6084   3rd Qu.:0.7908   3rd Qu.:1.0000
##  Max.   :0.60440   Max.   :0.6838   Max.   :0.9284   Max.   :1.0000
##
## ********** CHUM SALMON **********
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 3579, p-value = 0.1798
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.14104, p-value = 0.4074
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3788  -0.6636   0.1496   0.5312   1.9372
##
## Coefficients:
##                  Estimate    Std. Error z value Pr(>|z|)
## (Intercept) -15.301418766  67.256511774  -0.228    0.820
## L             0.324906462   1.156819324   0.281    0.779
## I(L^2)       -0.002174849   0.006600616  -0.329    0.742
## I(L^3)        0.000004691   0.000012502   0.375    0.707
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 14.167  on 14  degrees of freedom
## Residual deviance: 12.646  on 11  degrees of freedom
## AIC: 55.107
##
## Number of Fisher Scoring iterations: 6
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
```

```
## NULL                       14     14.166
## L       1  0.03756        13     14.129   0.8463
## I(L^2)  1  1.29445        12     12.835   0.2552
## I(L^3)  1  0.18892        11     12.646   0.6638
##
##  Summary of bootstrap fits:
##       mean             q.0.              q.5.              q.25.
##  Min.   :0.5495   Min.   :0.00000   Min.   :0.000000   Min.   :0.4308
##  1st Qu.:0.6457   1st Qu.:0.00000   1st Qu.:0.002317   1st Qu.:0.4945
##  Median :0.7052   Median :0.01162   Median :0.292037   Median :0.5199
##  Mean   :0.6778   Mean   :0.11755   Mean   :0.251715   Mean   :0.5689
##  3rd Qu.:0.7151   3rd Qu.:0.21143   3rd Qu.:0.417583   3rd Qu.:0.6082
##  Max.   :0.7662   Max.   :0.41454   Max.   :0.554902   Max.   :0.8774
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.5499   Min.   :0.6051   Min.   :0.6868   Min.   :0.8499
##  1st Qu.:0.6400   1st Qu.:0.7066   1st Qu.:0.8044   1st Qu.:0.9311
##  Median :0.7166   Median :0.8895   Median :0.9863   Median :1.0000
##  Mean   :0.7721   Mean   :0.8531   Mean   :0.9037   Mean   :0.9655
##  3rd Qu.:0.9465   3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.0000
##  Max.   :0.9982   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
##
## ********** COHO SALMON **********
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 2252.5, p-value = 0.01996
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.31455, p-value = 0.001098
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8298  -0.7191  -0.3292   0.5503   2.4104
##
## Coefficients:
##                  Estimate    Std. Error z value Pr(>|z|)
## (Intercept) -3.5712824495  3.4261844962  -1.042   0.2972
## L            0.0432693656  0.0322471088   1.342   0.1797
## I(L^2)      -0.0001484696  0.0000864551  -1.717   0.0859 .
## I(L^3)       0.0000001400  0.0000000711   1.969   0.0490 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 69.991  on 56  degrees of freedom
## Residual deviance: 55.305  on 53  degrees of freedom
## AIC: 104.59
##
## Number of Fisher Scoring iterations: 4
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      56     69.991
## L       1   7.0902        55     62.901  0.00775 **
## I(L^2)  1   3.6468        54     59.254  0.05618 .
## I(L^3)  1   3.9485        53     55.305  0.04691 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.               q.5.             q.25.
##  Min.   :0.1691   Min.   :0.006330   Min.   :0.05510   Min.   :0.1112
##  1st Qu.:0.2212   1st Qu.:0.008683   1st Qu.:0.07558   1st Qu.:0.1429
##  Median :0.3855   Median :0.041698   Median :0.14638   Median :0.2606
##  Mean   :0.3900   Mean   :0.076715   Mean   :0.19264   Mean   :0.2951
##  3rd Qu.:0.5527   3rd Qu.:0.097809   3rd Qu.:0.28581   3rd Qu.:0.4420
##  Max.   :0.6654   Max.   :0.323010   Max.   :0.46416   Max.   :0.5552
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.1595   Min.   :0.2130   Min.   :0.3167   Min.   :0.5079
##  1st Qu.:0.2071   1st Qu.:0.2748   1st Qu.:0.4174   1st Qu.:0.7609
##  Median :0.3670   Median :0.4989   Median :0.6793   Median :0.9190
##  Mean   :0.3800   Mean   :0.4757   Mean   :0.6188   Mean   :0.8478
##  3rd Qu.:0.5520   3rd Qu.:0.6526   3rd Qu.:0.7893   3rd Qu.:0.9758
##  Max.   :0.6806   Max.   :0.8359   Max.   :0.9777   Max.   :0.9998
##
## ***************** MARKET SQUID ******************
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 77344, p-value = 0.003271
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
```

```
## D = 0.12, p-value = 0.009663
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.71791  -0.94032   0.00664   0.87627   1.82742
##
## Coefficients:
##                 Estimate   Std. Error z value Pr(>|z|)
## (Intercept) -1.730989505  1.529021884  -1.132   0.2576
## L            0.118148391  0.067601893   1.748   0.0805 .
## I(L^2)      -0.001458737  0.000946183  -1.542   0.1231
## I(L^3)       0.000005212  0.000004133   1.261   0.2074
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 38.511  on 24  degrees of freedom
## Residual deviance: 33.295  on 21  degrees of freedom
## AIC: 97.49
##
## Number of Fisher Scoring iterations: 4
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      24     38.511
## L       1  0.45022        23     38.061  0.50223
## I(L^2)  1  3.13409        22     34.927  0.07667 .
## I(L^3)  1  1.63221        21     33.295  0.20140
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Summary of bootstrap fits:
##       mean             q.0.              q.5.               q.25.
##  Min.   :0.2063   Min.   :0.00000   Min.   :0.0002774   Min.   :0.03008
##  1st Qu.:0.5043   1st Qu.:0.00000   1st Qu.:0.0324803   1st Qu.:0.31165
##  Median :0.6015   Median :0.00336   Median :0.2094750   Median :0.42239
##  Mean   :0.5880   Mean   :0.11489   Mean   :0.2675123   Mean   :0.45524
##  3rd Qu.:0.6971   3rd Qu.:0.23866   3rd Qu.:0.4927264   3rd Qu.:0.64031
```

```
##  Max.   :0.7762   Max.   :0.45413   Max.   :0.6483986   Max.   :0.73924
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.1263   Min.   :0.3312   Min.   :0.6514   Min.   :0.9234
##  1st Qu.:0.5176   1st Qu.:0.6460   1st Qu.:0.7908   1st Qu.:0.9344
##  Median :0.6267   Median :0.7483   Median :0.8504   Median :0.9610
##  Mean   :0.6068   Mean   :0.7368   Mean   :0.8526   Mean   :0.9630
##  3rd Qu.:0.7454   3rd Qu.:0.8223   3rd Qu.:0.8962   3rd Qu.:0.9947
##  Max.   :0.8513   Max.   :0.9979   Max.   :1.0000   Max.   :1.0000
##
## ********** PACIFIC HERRING **********
##
##  Insufficient data
##
## ********** WATER JELLY **********
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  .x and .y
## W = 79448, p-value = 0.8924
## alternative hypothesis: true location shift is not equal to 0
##
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  .x and .y
## D = 0.025505, p-value = 0.9995
## alternative hypothesis: two-sided
##
##  Summary of GLM fit:
##
## Call:
## glm(formula = p.L12 ~ L + I(L^2) + I(L^3), family = binomial,
##     weights = wts)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.5114  -0.5073   0.2832   0.9065   2.5335
##
## Coefficients:
##                 Estimate   Std. Error z value Pr(>|z|)
## (Intercept) -7.018755017  3.943695235  -1.780   0.0751 .
## L            0.272045342  0.159724393   1.703   0.0885 .
## I(L^2)      -0.003280210  0.002107257  -1.557   0.1196
## I(L^3)       0.000012696  0.000009052   1.403   0.1607
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 44.978  on 19  degrees of freedom
## Residual deviance: 40.236  on 16  degrees of freedom
## AIC: 110.61
##
## Number of Fisher Scoring iterations: 3
```

```
##
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: p.L12
##
## Terms added sequentially (first to last)
##
##
##        Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                      19     44.978
## L       1  0.22654        18     44.751   0.6341
## I(L^2)  1  2.39043        17     42.361   0.1221
## I(L^3)  1  2.12431        16     40.236   0.1450
##
##  Summary of bootstrap fits:
##       mean             q.0.                q.5.
##  Min.   :0.2142   Min.   :0.0000000   Min.   :0.0000541
##  1st Qu.:0.4971   1st Qu.:0.0001554   1st Qu.:0.0405347
##  Median :0.5431   Median :0.0373356   Median :0.2345563
##  Mean   :0.5062   Mean   :0.1080724   Mean   :0.2115019
##  3rd Qu.:0.5930   3rd Qu.:0.2291246   3rd Qu.:0.3614782
##  Max.   :0.6254   Max.   :0.2953500   Max.   :0.4242308
##      q.25.             q.50.             q.75.            q.95.
##  Min.   :0.01017   Min.   :0.08892   Min.   :0.3148   Min.   :0.6877
##  1st Qu.:0.33944   1st Qu.:0.49707   1st Qu.:0.6011   1st Qu.:0.7593
##  Median :0.39869   Median :0.54857   Median :0.6552   Median :0.7888
##  Mean   :0.37196   Mean   :0.51063   Mean   :0.6367   Mean   :0.8024
##  3rd Qu.:0.48714   3rd Qu.:0.60762   3rd Qu.:0.6797   3rd Qu.:0.8213
##  Max.   :0.54969   Max.   :0.76425   Max.   :0.9400   Max.   :0.9961
##      q.100.
##  Min.   :0.8376
##  1st Qu.:0.8947
##  Median :0.9267
##  Mean   :0.9297
##  3rd Qu.:0.9880
##  Max.   :1.0000
```