# 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"
```

## Part 2: 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:

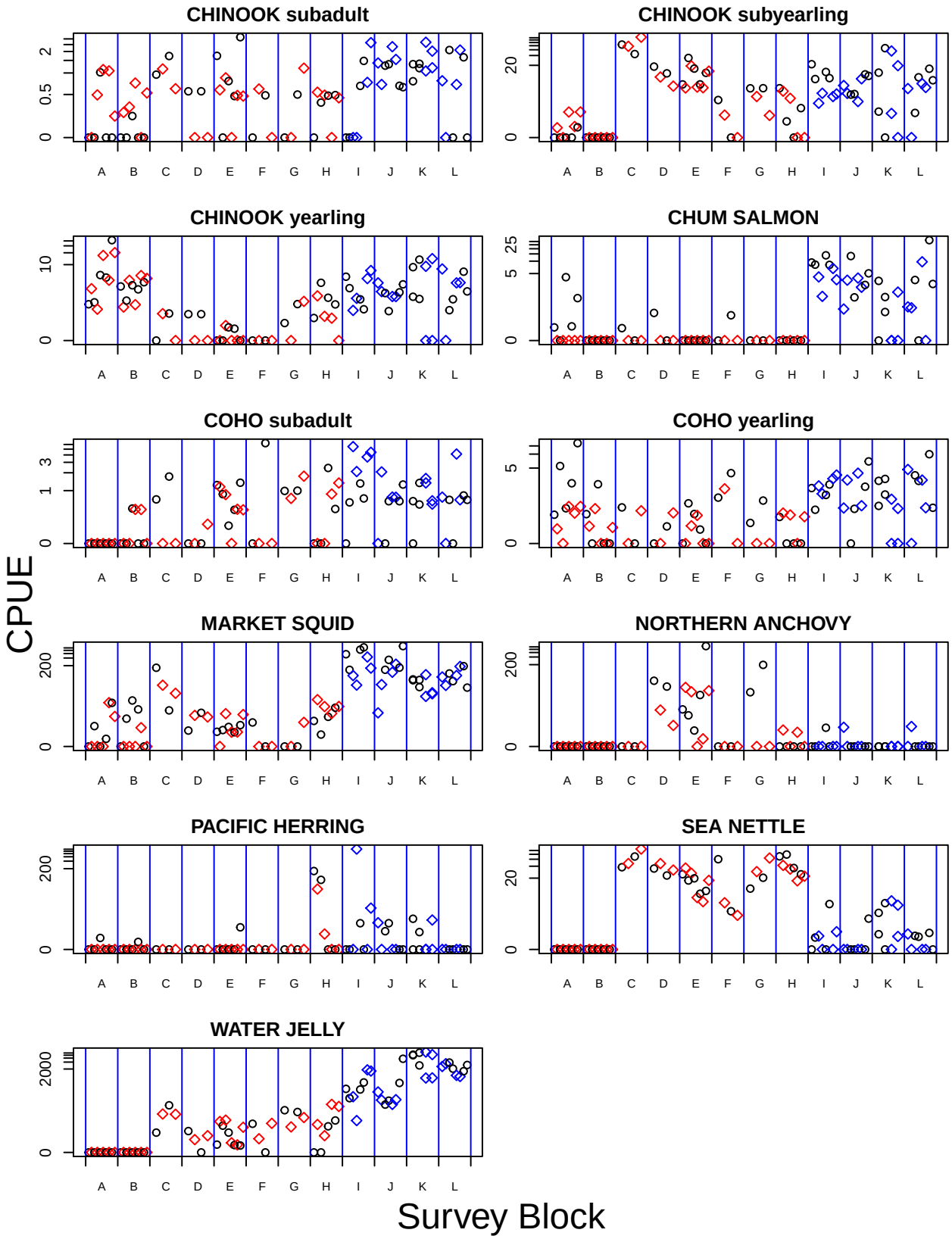
```
bw <- FALSE          #Flag for black-and-white figures
BLACK <- 'black'
BLUE <- if(bw) 'black' else 'blue'   #color code for blue
RED <-  if(bw) 'black' else 'red'    #color code for red
lndscp <- FALSE                      #flag for landscape figures
plcol <- if(lndscp) 3 else 2         #number 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 $\theta$ 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 $\theta$ to get the final statistics. This means that the distribution of the final catch ratio estimate does not inlcude error in the estimation of $\theta$.

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 $\Theta$ parameter, which is used to initiate the refined estimate via `glm.nb()`. If the refined estimate fails, the initial estimate of $\Theta$ 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)
```

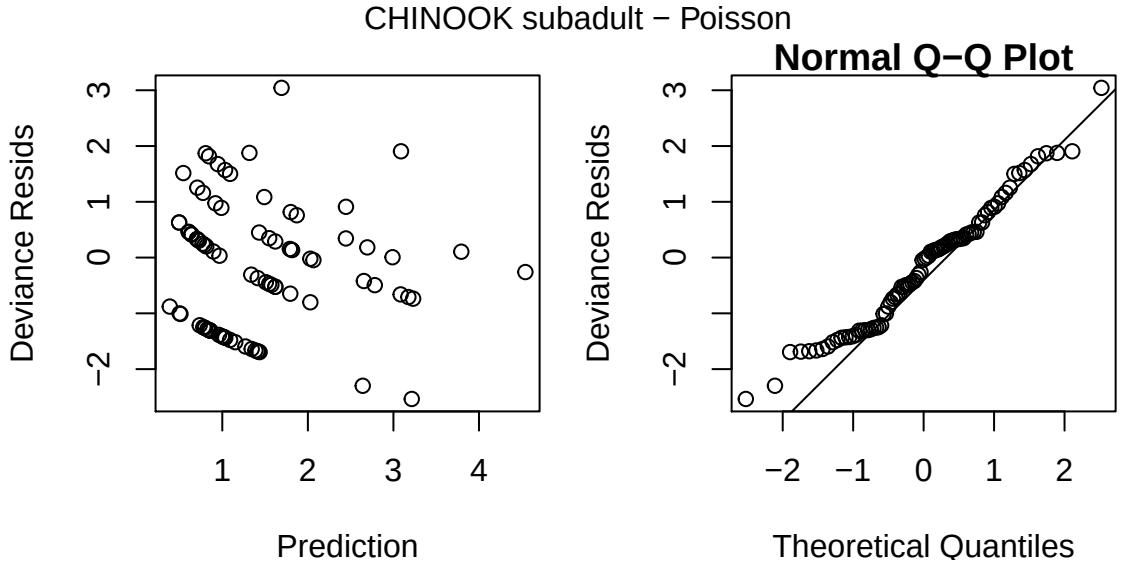



Figure 1:

```
## 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
```

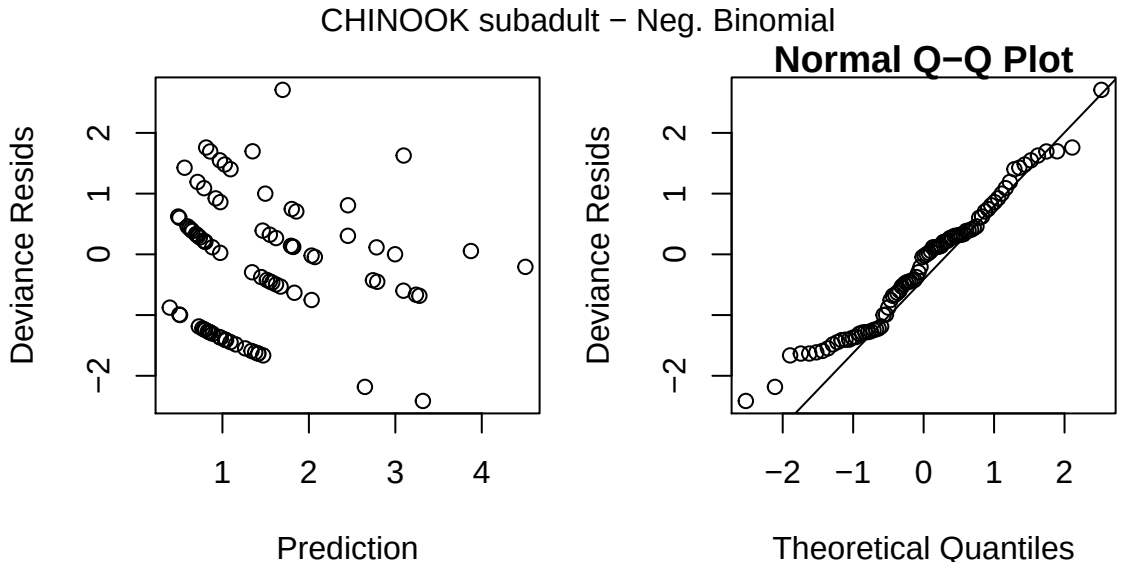



Figure 2:

```
## 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
```

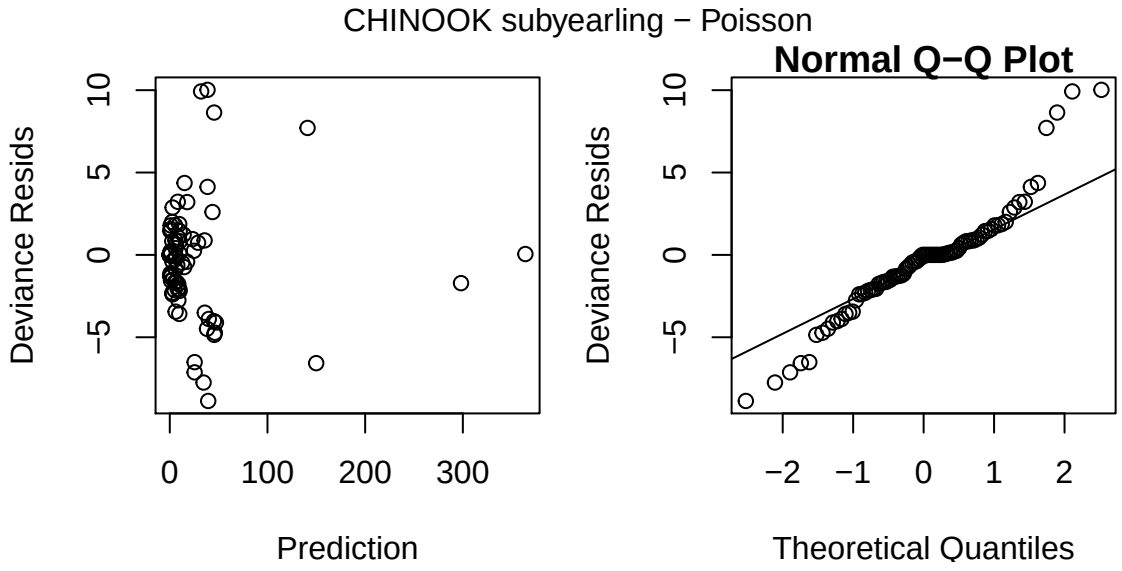



Figure 3:

```
## 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
```

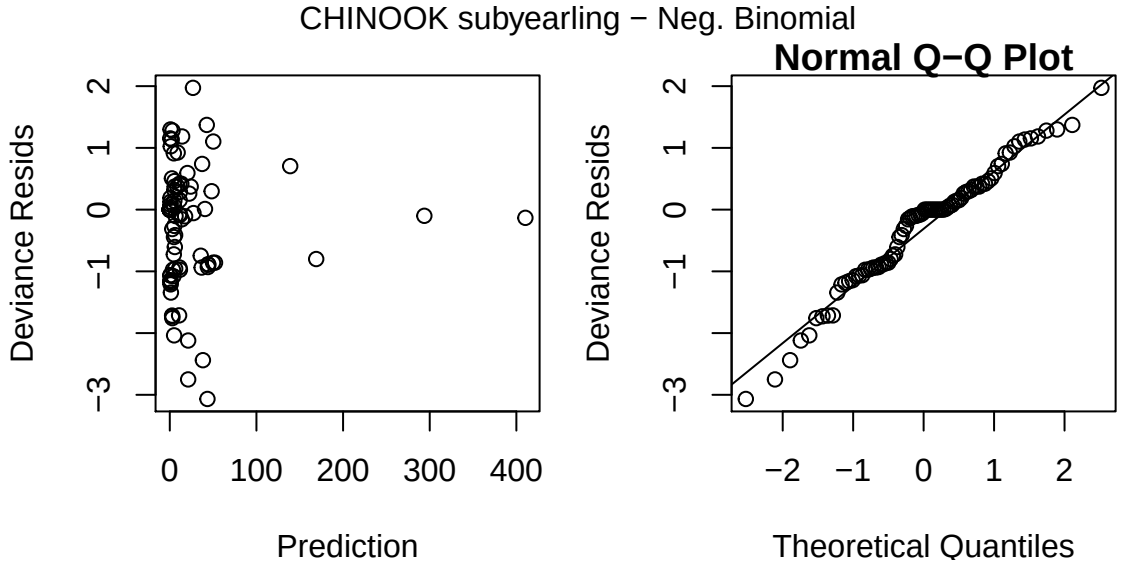



Figure 4:

```
## 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
```

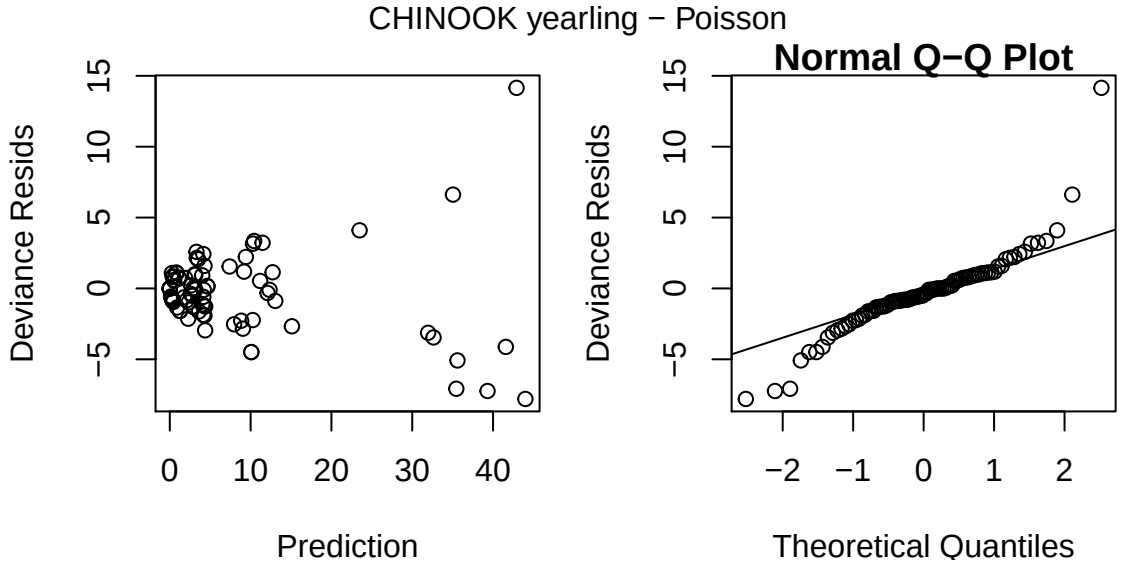



Figure 5:

```
##
## *** 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
##
```

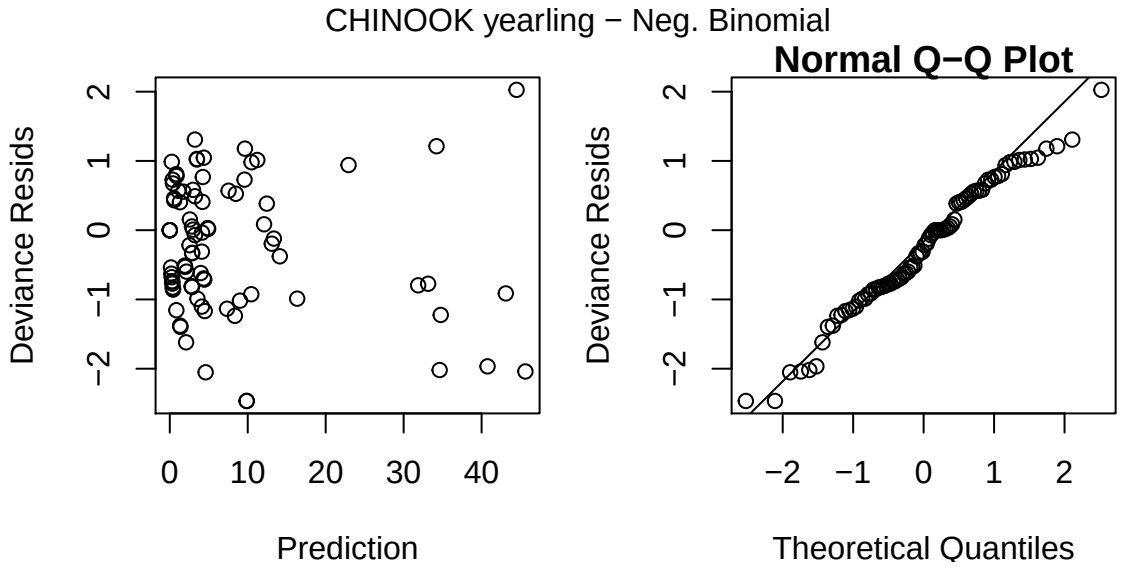



Figure 6:

```
## ********************   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
##
```

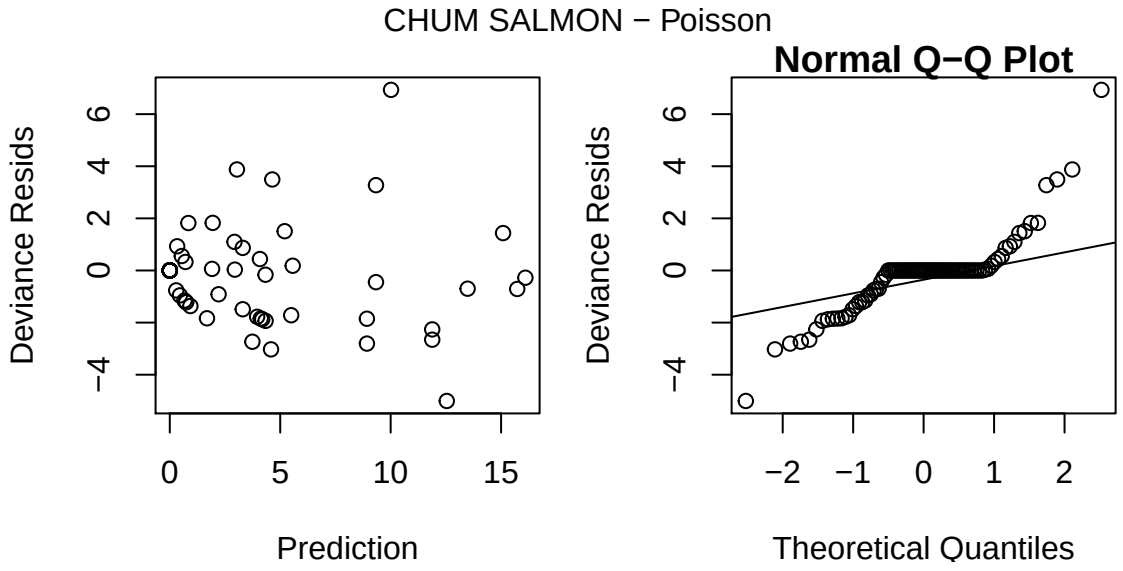



Figure 7:

```
##  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 ***
##
```

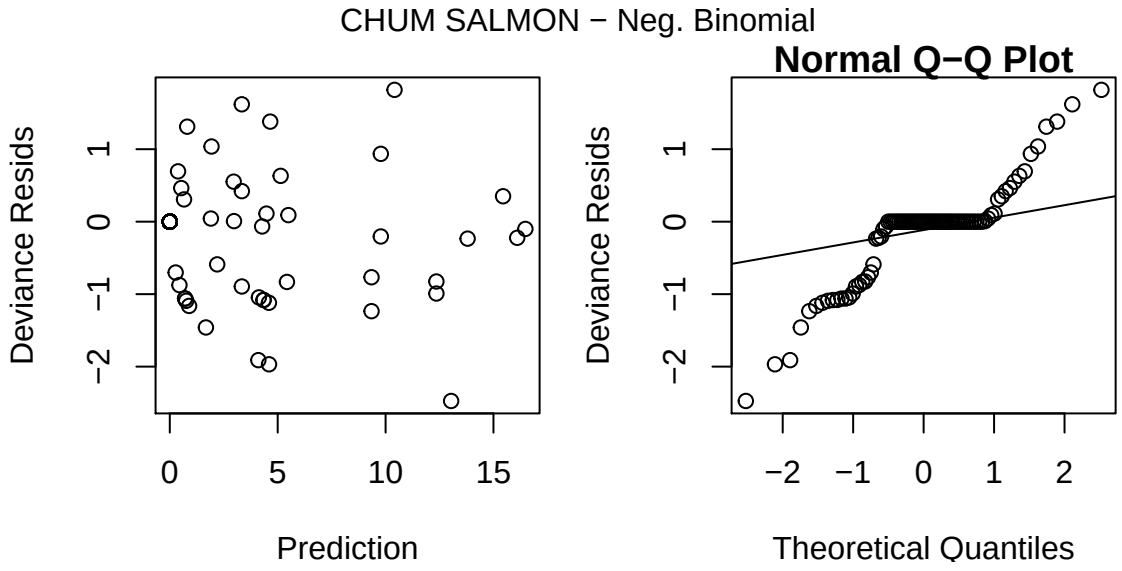



Figure 8:

```
## 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
```

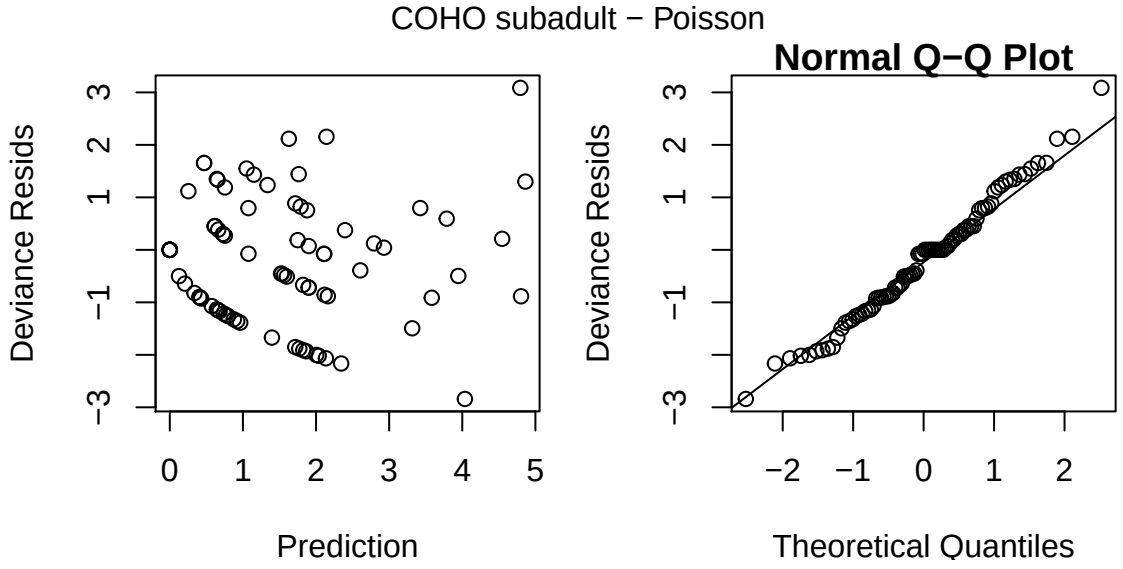



Figure 9:

```
##
## 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
##
```

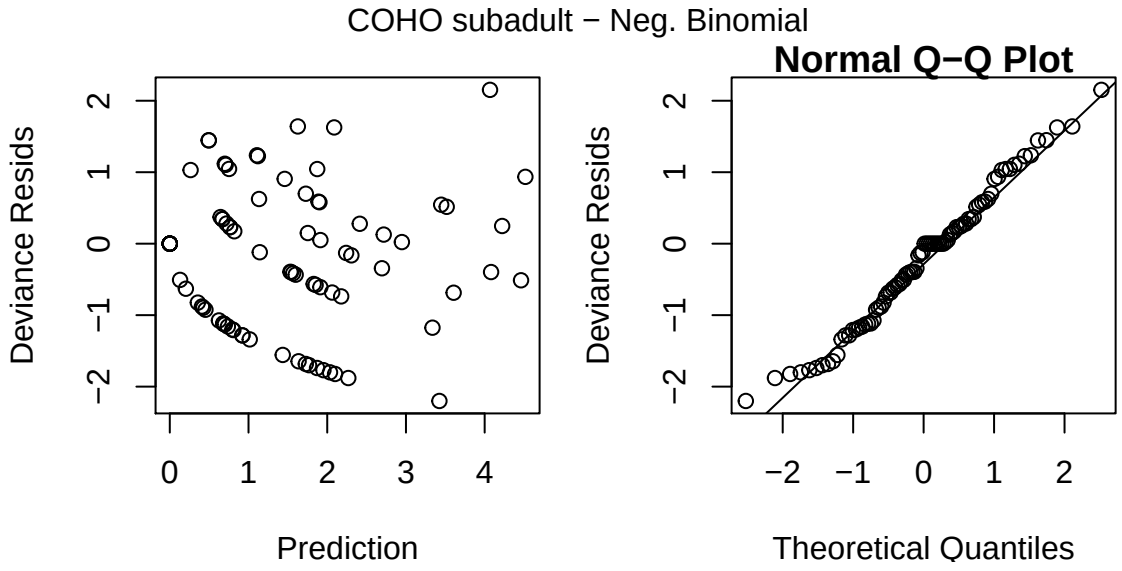



Figure 10:

```
## 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)
```

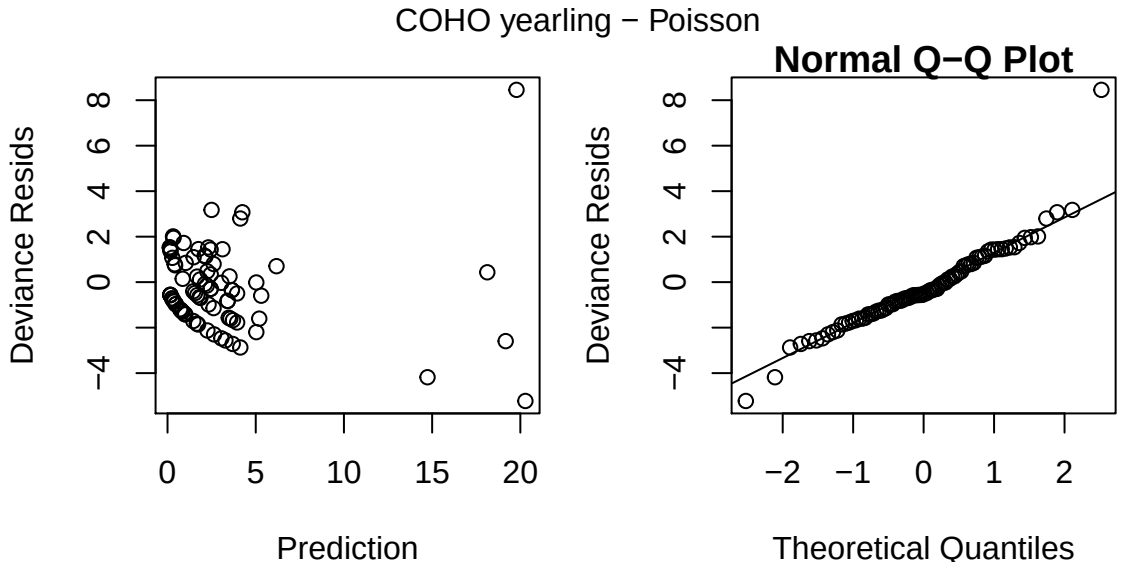



Figure 11:

```
##
##
##       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 ***
```

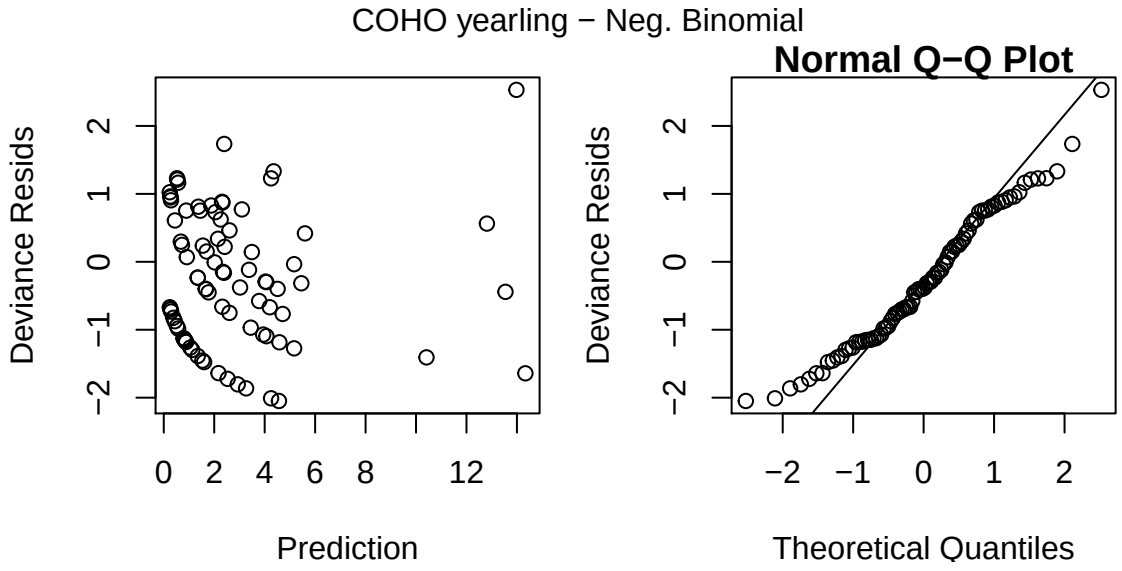



Figure 12:

```
## 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
```

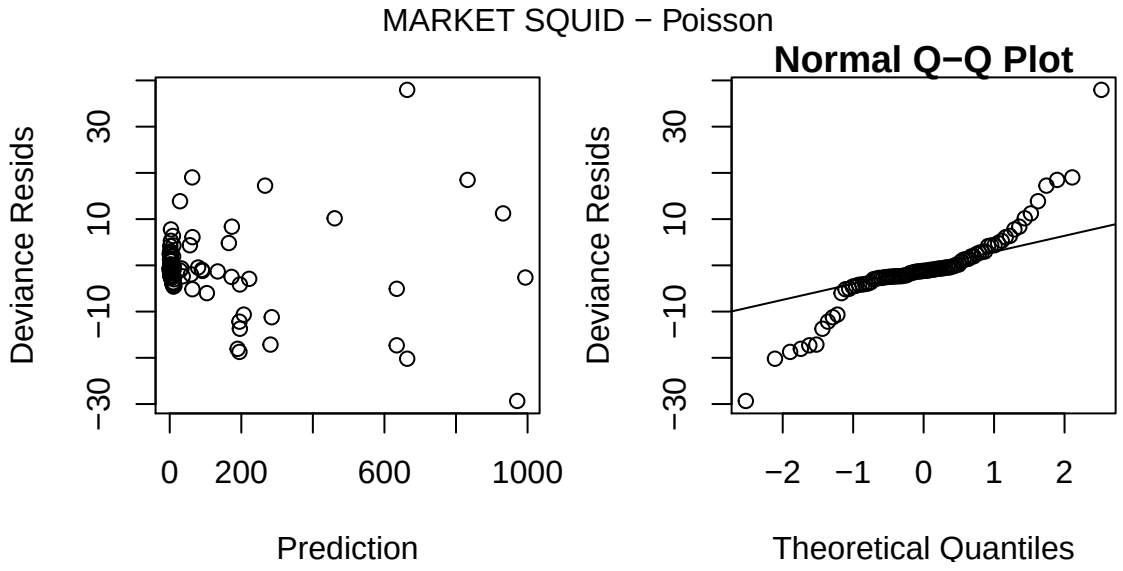



Figure 13:

```
## ---
## 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
```

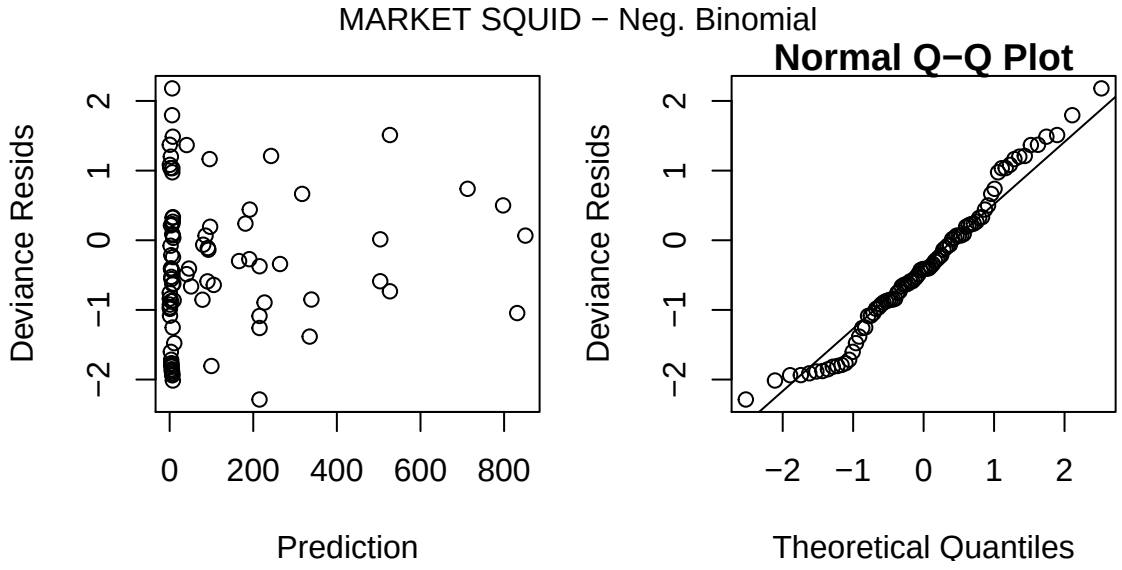



Figure 14:

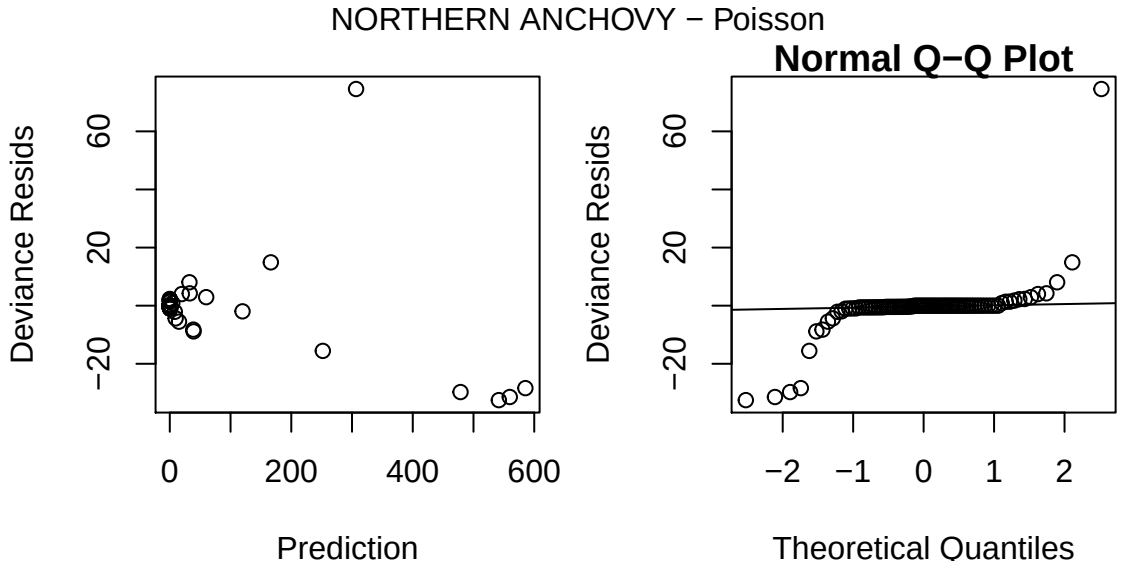



Figure 15:

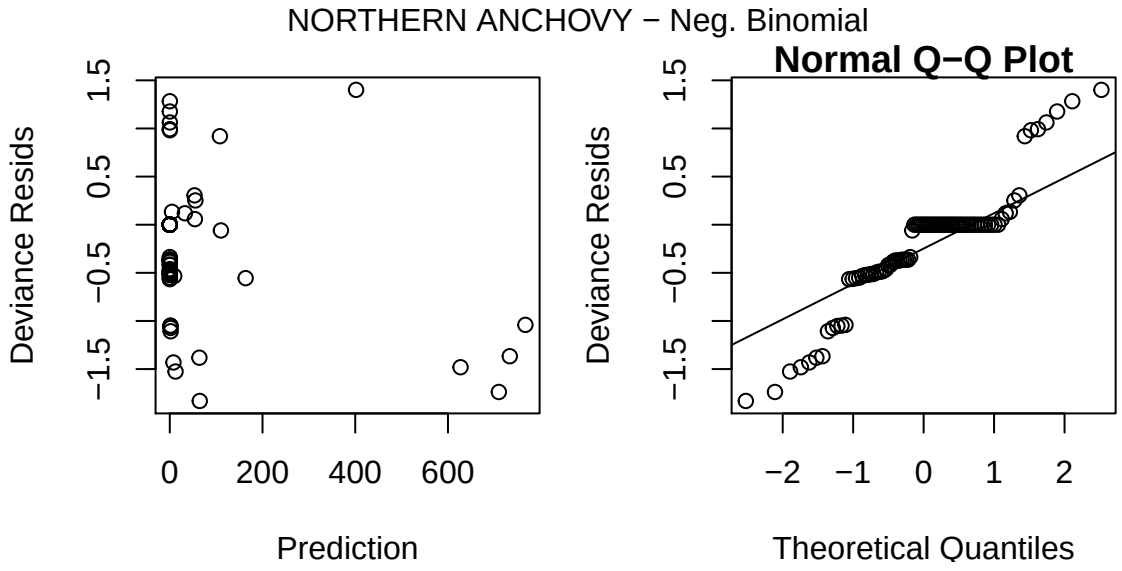



Figure 16:

```
## 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)
```

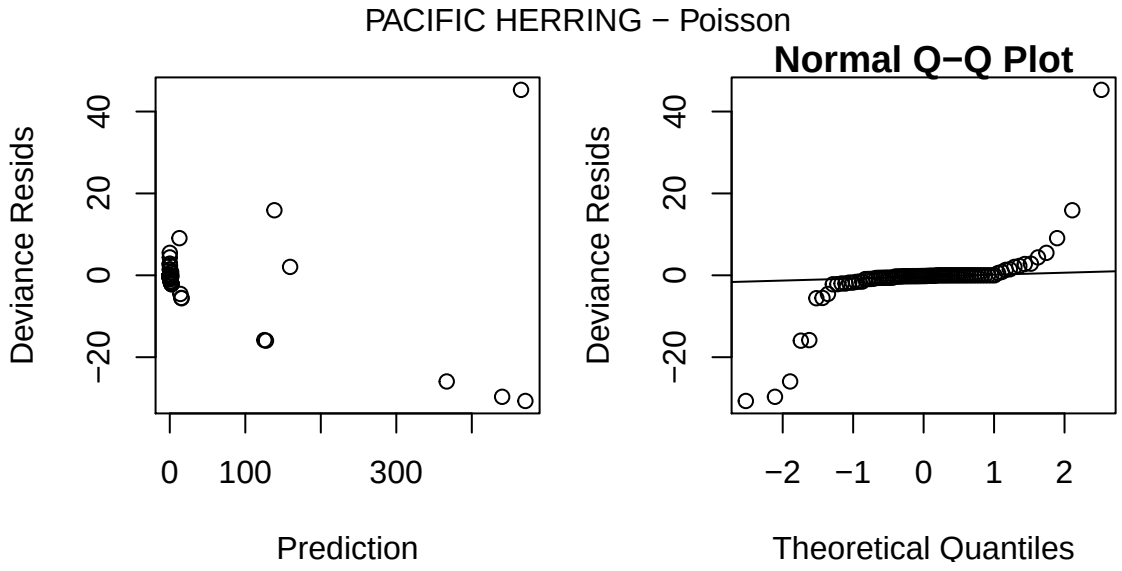



Figure 17:

```
##
##
##       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 ***
```

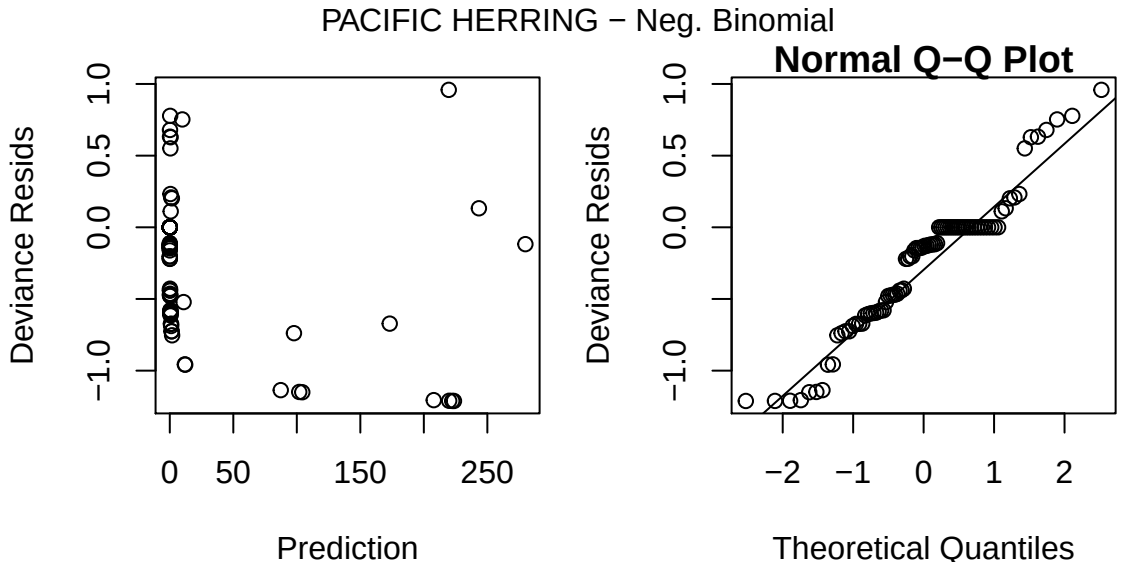



Figure 18:

```
## 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
```

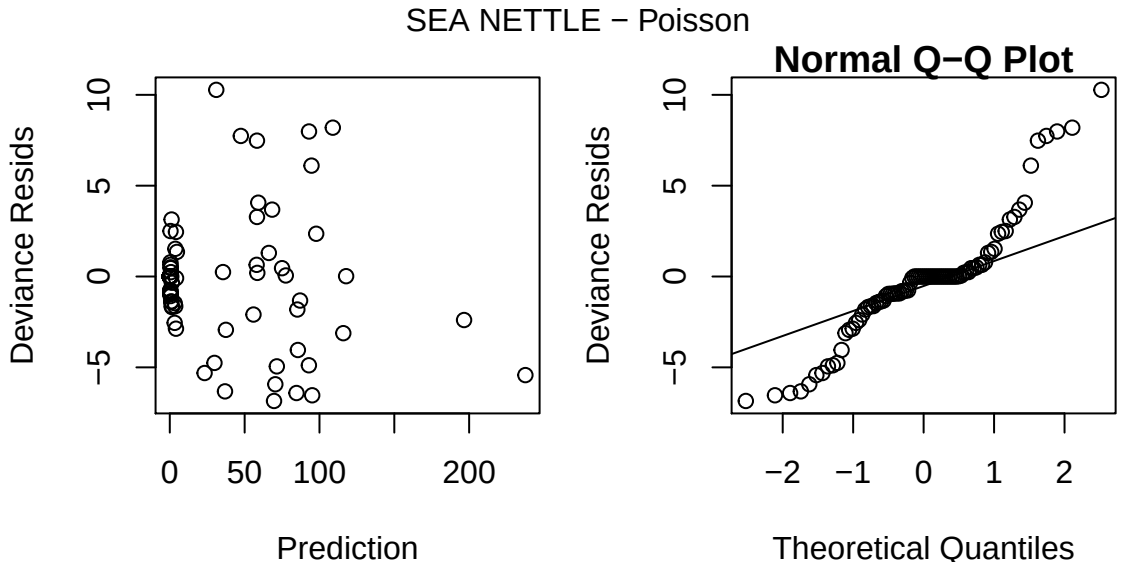



Figure 19:

```
## ---
## 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
```

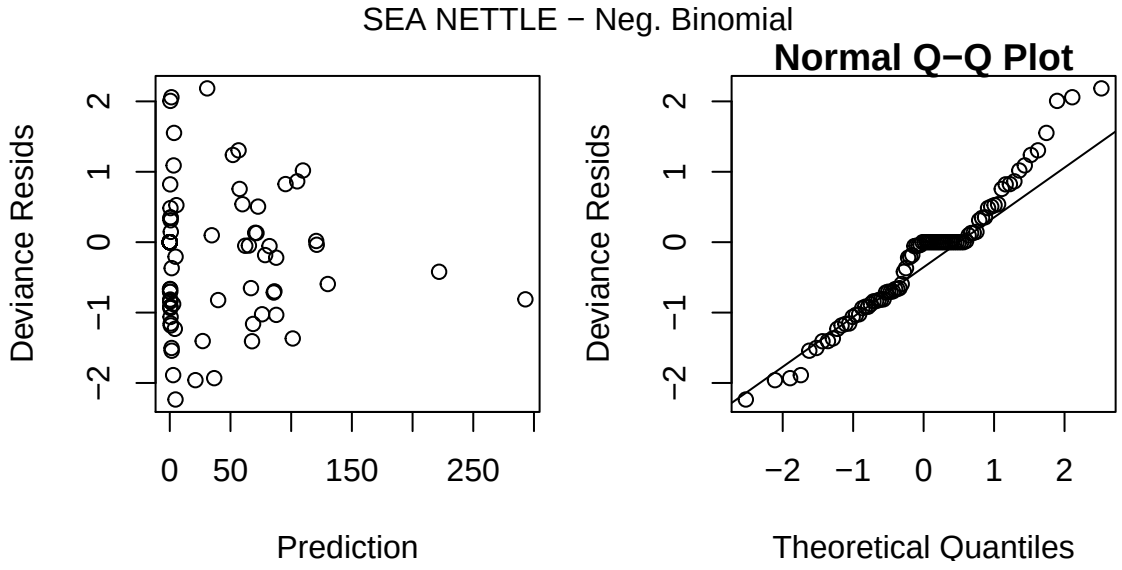



Figure 20:

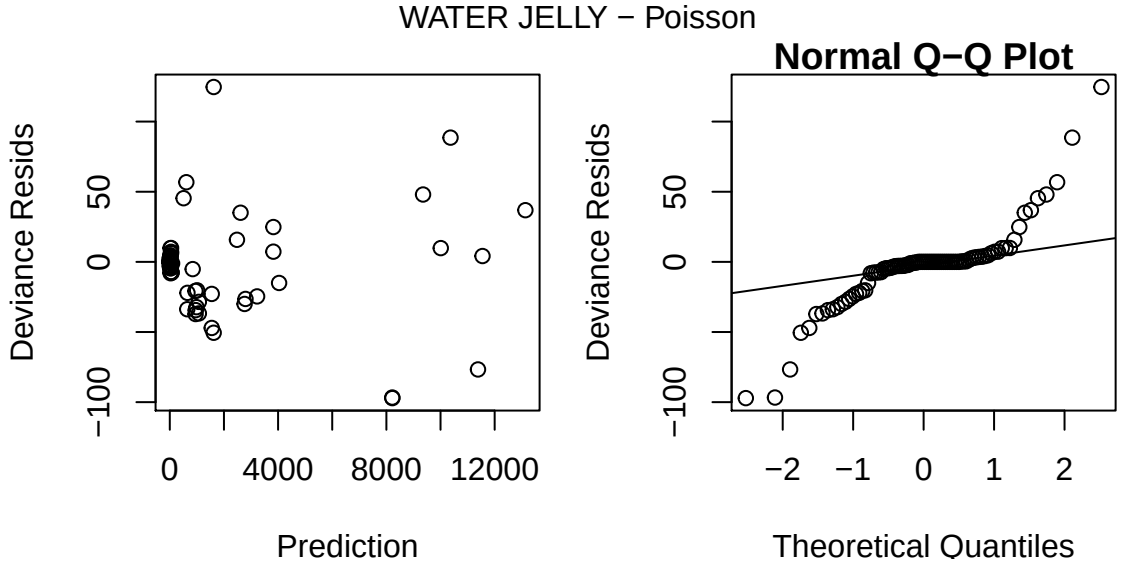



Figure 21:

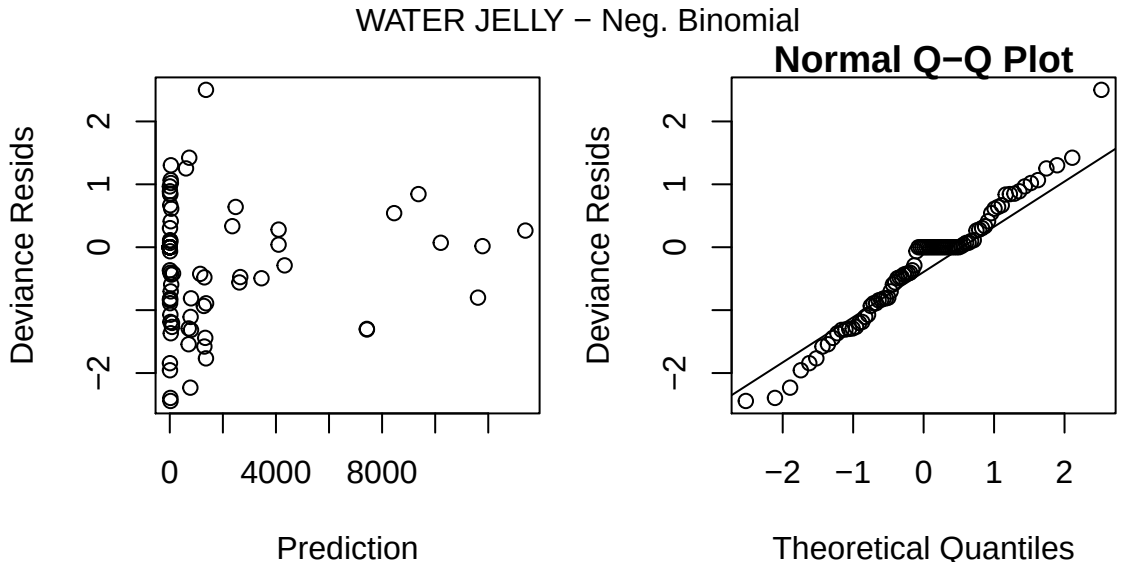



Figure 22:

```
## 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
##
```

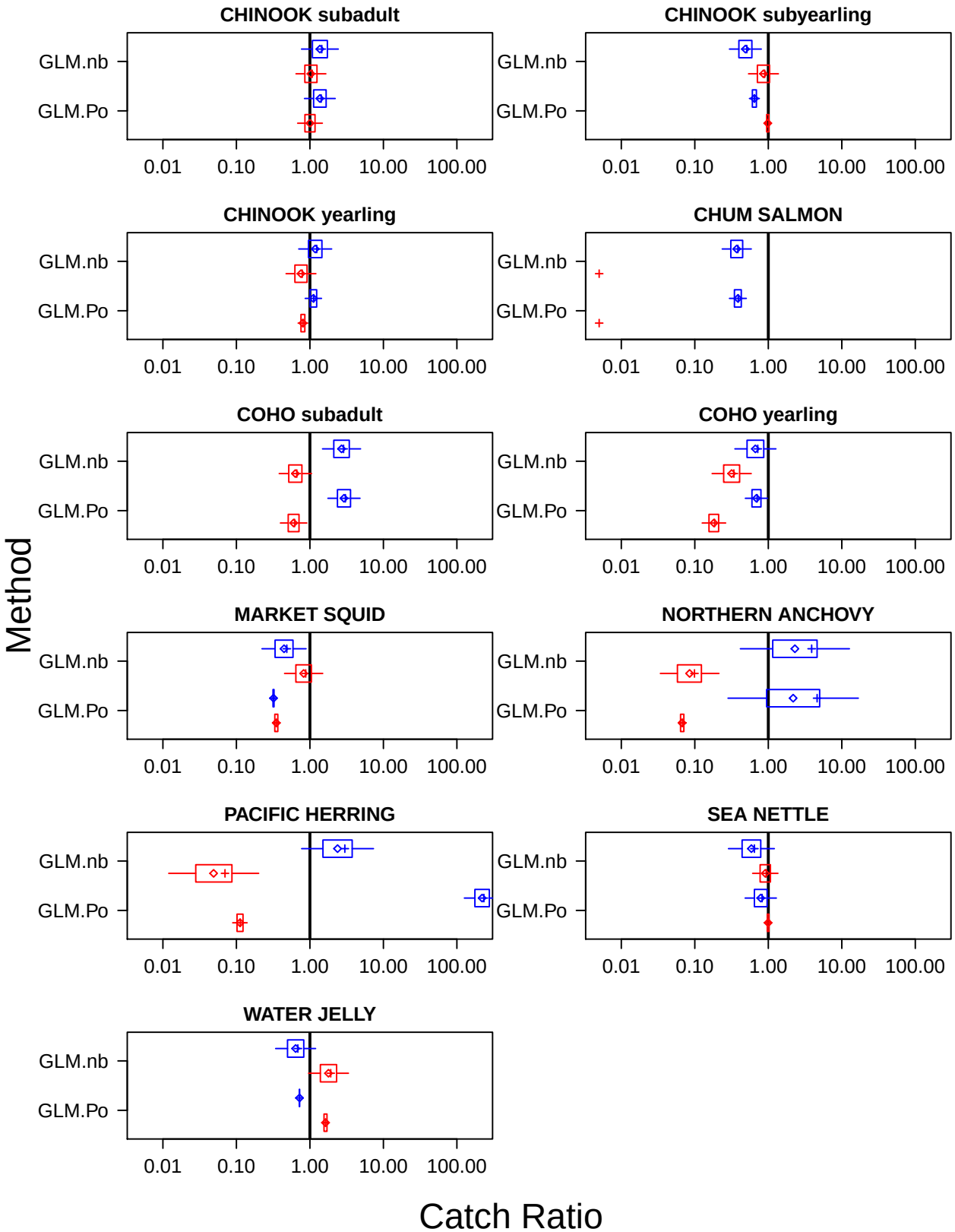
```
##
## $`CHUM SALMON`
## , , Up
##
##        Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po    0    NA    NA     NA    NA    NA
## GLM.nb    0    NA    NA     NA    NA    NA
##
## , , Down
##
##         Mean q0.05 q0.25 Median q0.75 q0.95
## GLM.Po 0.391 0.296 0.346  0.386 0.429 0.502
## GLM.nb 0.386 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
```

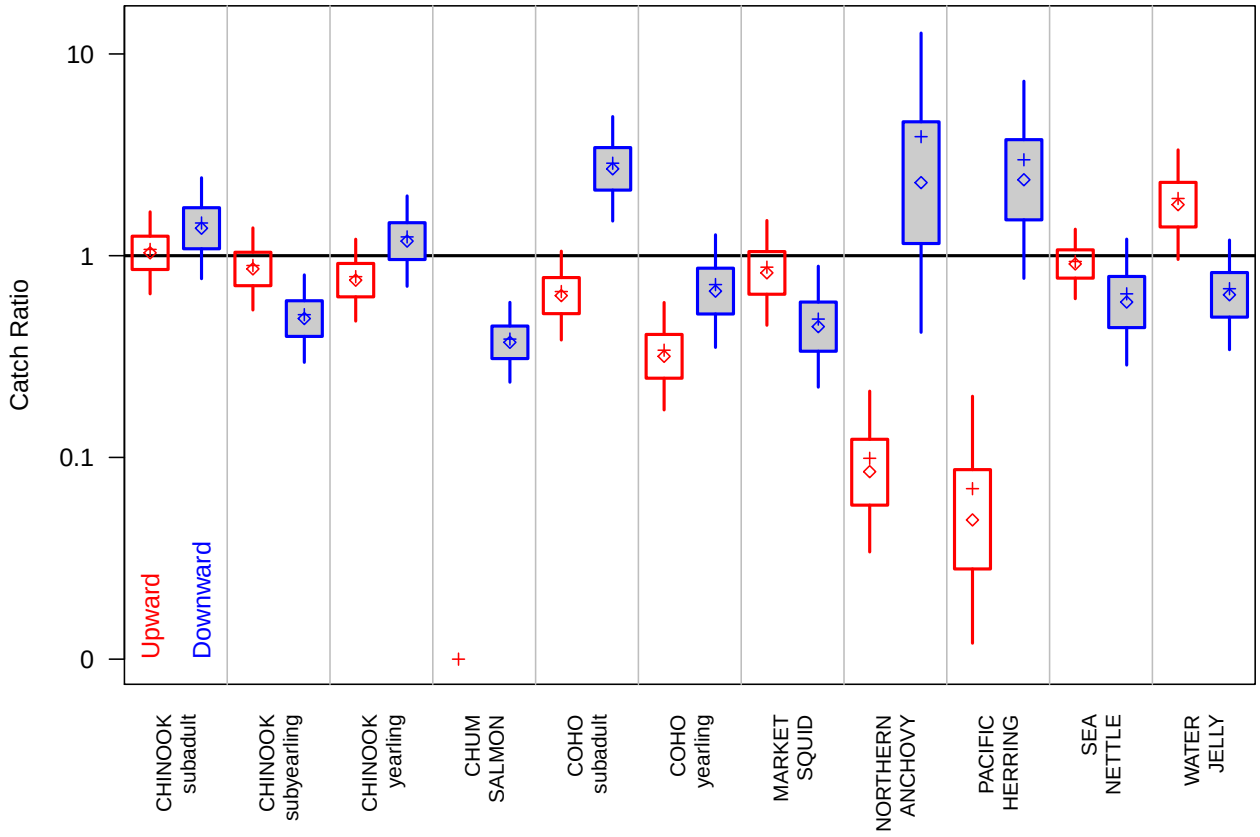
Next, generate summary figures of catch ratio estimates. In the plots, the estimated mean is marked with "+" and the median with a diamond; boxes span the quartiles, and whiskers extend to the 5% and 95% quantiles.

```
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)
```

```r
# Subsampling ratio by Haul & Species:
ssr <- meas / cnt
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
## ties

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## glm!

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```

```
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## ties

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## 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
```

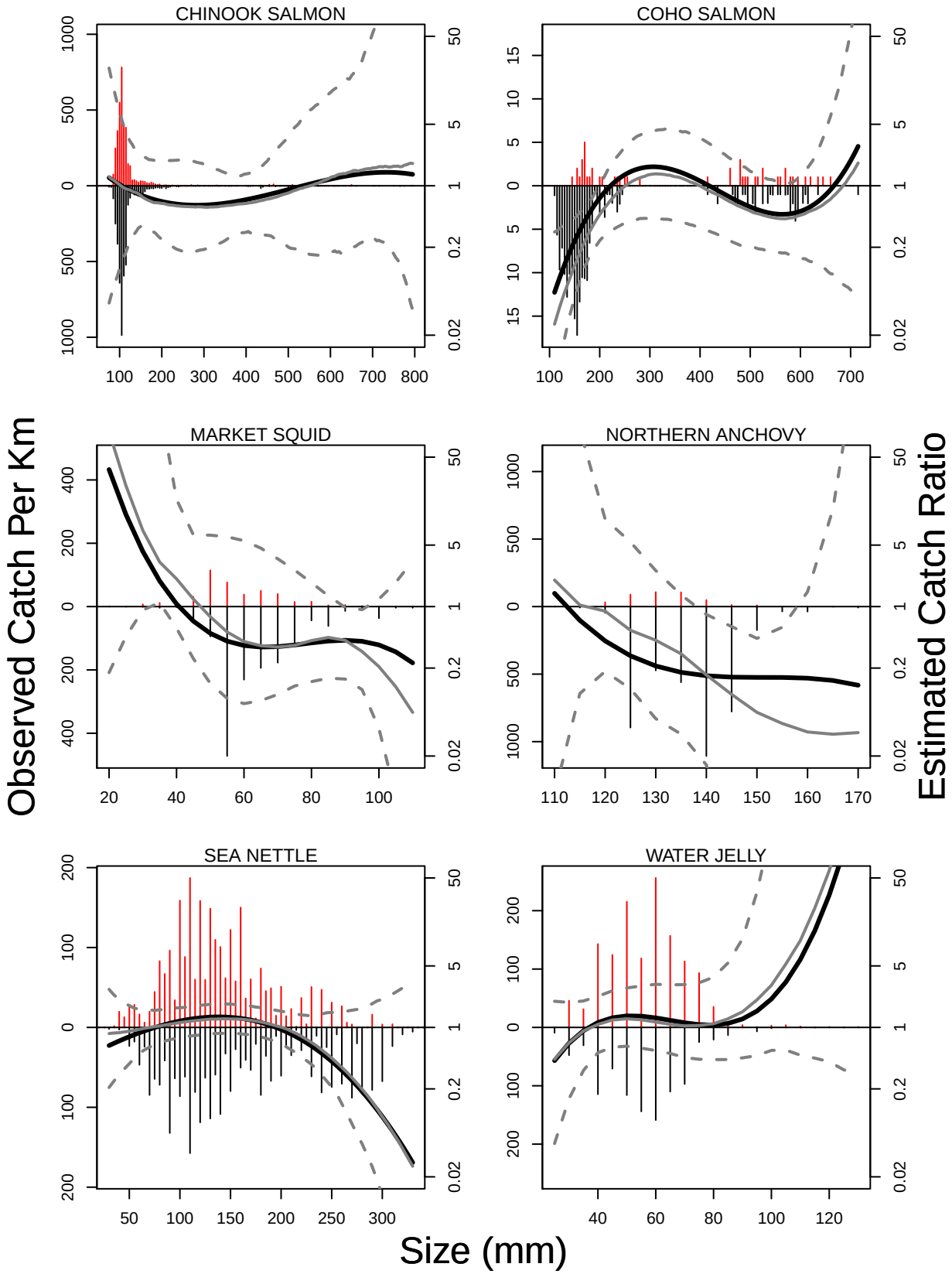
CHINOOK SALMON
COHO SALMON
MARKET SQUID
NORTHERN ANCHOVY
SEA NETTLE
WATER JELLY
Observed Catch Per Km
Estimated Catch Ratio
Size (mm)

Figure 23:

```
## glm!

## 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
```

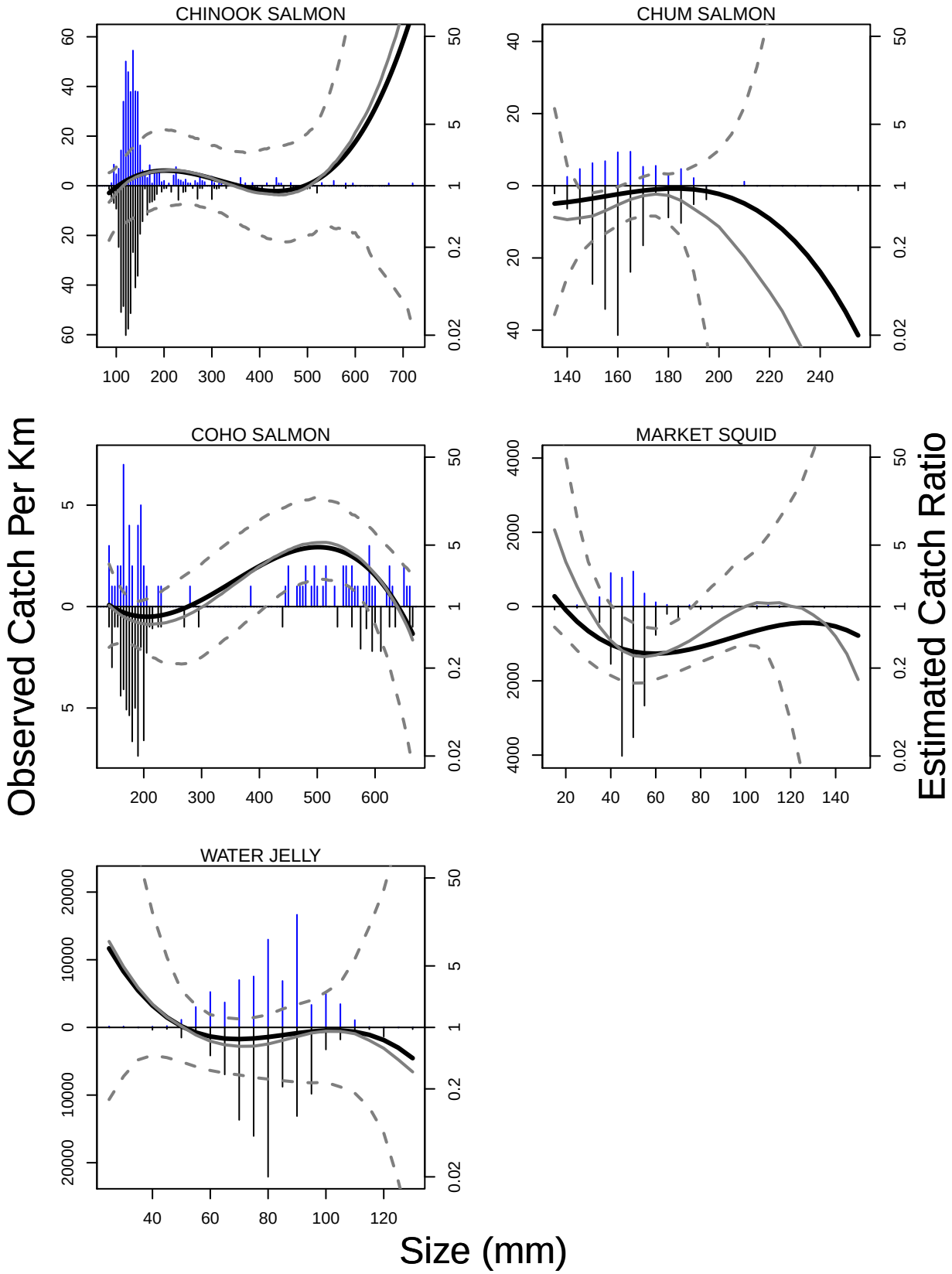
CHINOOK SALMON
CHUM SALMON
COHO SALMON
MARKET SQUID
WATER JELLY
Observed Catch Per Km
Estimated Catch Ratio
Size (mm)

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.
##  Min.   :0.3902   Min.   :0.00000000   Min.   :0.0001529
##  1st Qu.:0.4444   1st Qu.:0.00000013   1st Qu.:0.0616491
##  Median :0.5391   Median :0.01323901   Median :0.2390987
##  Mean   :0.5218   Mean   :0.06716751   Mean   :0.2176188
##  3rd Qu.:0.6022   3rd Qu.:0.14559488   3rd Qu.:0.3443235
##  Max.   :0.6221   Max.   :0.24163374   Max.   :0.4366905
##      q.25.            q.50.            q.75.            q.95.
##  Min.   :0.1042   Min.   :0.3563   Min.   :0.5619   Min.   :0.7385
##  1st Qu.:0.2580   1st Qu.:0.4315   1st Qu.:0.6245   1st Qu.:0.7958
##  Median :0.4289   Median :0.5451   Median :0.6662   Median :0.8310
##  Mean   :0.3824   Mean   :0.5252   Mean   :0.6582   Mean   :0.8284
##  3rd Qu.:0.4964   3rd Qu.:0.6161   3rd Qu.:0.6917   3rd Qu.:0.8510
##  Max.   :0.5500   Max.   :0.6368   Max.   :0.7377   Max.   :0.9627
##      q.100.
##  Min.   :0.8635
##  1st Qu.:0.9342
##  Median :0.9868
##  Mean   :0.9654
##  3rd Qu.:0.9999
##  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.   :0.3961   Min.   :0.0000032   Min.   :0.006155   Min.   :0.07508
##  1st Qu.:0.4783   1st Qu.:0.0395857   1st Qu.:0.200755   1st Qu.:0.34968
##  Median :0.5860   Median :0.0592154   Median :0.314754   Median :0.47896
##  Mean   :0.5969   Mean   :0.1047656   Mean   :0.341188   Mean   :0.49390
##  3rd Qu.:0.6768   3rd Qu.:0.1543375   3rd Qu.:0.458398   3rd Qu.:0.61253
##  Max.   :0.9413   Max.   :0.3645572   Max.   :0.770243   Max.   :0.94389
```

```
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.3554   Min.   :0.5529   Min.   :0.7011   Min.   :0.8534
##  1st Qu.:0.4804   1st Qu.:0.6164   1st Qu.:0.7430   1st Qu.:0.8996
##  Median :0.6023   Median :0.7159   Median :0.8340   Median :0.9508
##  Mean   :0.6064   Mean   :0.7075   Mean   :0.8232   Mean   :0.9410
##  3rd Qu.:0.6874   3rd Qu.:0.7616   3rd Qu.:0.8818   3rd Qu.:0.9837
##  Max.   :0.9740   Max.   :0.9862   Max.   :0.9948   Max.   :1.0000
##
## ********** 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.   :0.1532   Min.   :0.00000000   Min.   :0.0000   Min.   :0.000322
##  1st Qu.:0.3924   1st Qu.:0.00007122   1st Qu.:0.0950   1st Qu.:0.242251
##  Median :0.6281   Median :0.05662546   Median :0.1781   Median :0.353357
##  Mean   :0.5458   Mean   :0.07445468   Mean   :0.2175   Mean   :0.393210
##  3rd Qu.:0.6844   3rd Qu.:0.11301016   3rd Qu.:0.3475   3rd Qu.:0.589240
##  Max.   :0.8474   Max.   :0.28676700   Max.   :0.5202   Max.   :0.825744
##      q.50.             q.75.             q.95.            q.100.
##  Min.   :0.01021   Min.   :0.1503   Min.   :0.4741   Min.   :0.8566
##  1st Qu.:0.38874   1st Qu.:0.5320   1st Qu.:0.8228   1st Qu.:0.9596
##  Median :0.70756   Median :0.7956   Median :0.8818   Median :0.9743
##  Mean   :0.57214   Mean   :0.6787   Mean   :0.8356   Mean   :0.9681
##  3rd Qu.:0.73920   3rd Qu.:0.8333   3rd Qu.:0.9191   3rd Qu.:0.9999
##  Max.   :0.94100   Max.   :0.9877   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.
##  Min.   :0.4172   Min.   :0.00000000   Min.   :0.000051
##  1st Qu.:0.5937   1st Qu.:0.00000069   1st Qu.:0.073082
##  Median :0.7661   Median :0.01096009   Median :0.280418
##  Mean   :0.7183   Mean   :0.02776678   Mean   :0.303741
##  3rd Qu.:0.8772   3rd Qu.:0.04494582   3rd Qu.:0.551359
##  Max.   :0.9043   Max.   :0.11618760   Max.   :0.696894
##      q.25.             q.50.            q.75.            q.95.
##  Min.   :0.04638   Min.   :0.3330   Min.   :0.6918   Min.   :0.8453
##  1st Qu.:0.42662   1st Qu.:0.6504   1st Qu.:0.7858   1st Qu.:0.9495
##  Median :0.69782   Median :0.8567   Median :0.9202   Median :0.9925
##  Mean   :0.59171   Mean   :0.7724   Mean   :0.8889   Mean   :0.9645
##  3rd Qu.:0.84126   3rd Qu.:0.9552   3rd Qu.:0.9949   3rd Qu.:1.0000
##  Max.   :0.86736   Max.   :0.9658   Max.   :1.0000   Max.   :1.0000
##      q.100.
##  Min.   :0.9999
##  1st Qu.:1.0000
##  Median :1.0000
##  Mean   :1.0000
##  3rd Qu.:1.0000
##  Max.   :1.0000
```

```
##
## ***************** 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.   :0.4438   Min.   :0.0001812   Min.   :0.2295   Min.   :0.4044
##  1st Qu.:0.4652   1st Qu.:0.0879409   1st Qu.:0.3520   1st Qu.:0.4241
##  Median :0.5228   Median :0.2446409   Median :0.3738   Median :0.4560
##  Mean   :0.5840   Mean   :0.1877368   Mean   :0.3641   Mean   :0.5448
##  3rd Qu.:0.6907   3rd Qu.:0.2703587   3rd Qu.:0.3900   3rd Qu.:0.6499
##  Max.   :0.8840   Max.   :0.3241655   Max.   :0.4263   Max.   :0.9125
##      q.50.            q.75.            q.95.            q.100.
##  Min.   :0.4443   Min.   :0.4806   Min.   :0.5365   Min.   :0.6427
##  1st Qu.:0.4643   1st Qu.:0.5048   1st Qu.:0.5611   1st Qu.:0.6778
##  Median :0.5191   Median :0.5734   Median :0.6603   Median :0.8729
##  Mean   :0.5998   Mean   :0.6482   Mean   :0.7157   Mean   :0.8407
##  3rd Qu.:0.7156   3rd Qu.:0.7696   3rd Qu.:0.8506   3rd Qu.:0.9928
##  Max.   :0.9743   Max.   :0.9932   Max.   :0.9994   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.
##  Min.   :0.07644   Min.   :0.00000   Min.   :0.000000
##  1st Qu.:0.23379   1st Qu.:0.00000   1st Qu.:0.001802
##  Median :0.44572   Median :0.03658   Median :0.224365
##  Mean   :0.37369   Mean   :0.06175   Mean   :0.162569
##  3rd Qu.:0.47749   3rd Qu.:0.11636   3rd Qu.:0.260059
##  Max.   :0.67676   Max.   :0.18025   Max.   :0.342250
##      q.25.               q.50.              q.75.             q.95.
##  Min.   :0.0000046   Min.   :0.001102   Min.   :0.01853   Min.   :0.6206
##  1st Qu.:0.0649222   1st Qu.:0.182144   1st Qu.:0.33289   1st Qu.:0.6502
##  Median :0.3672193   Median :0.447266   Median :0.52927   Median :0.6884
##  Mean   :0.2663983   Mean   :0.353706   Mean   :0.45013   Mean   :0.7032
##  3rd Qu.:0.3849117   3rd Qu.:0.480274   3rd Qu.:0.57478   3rd Qu.:0.7077
##  Max.   :0.5520815   Max.   :0.697481   Max.   :0.82569   Max.   :0.9543
##      q.100.
##  Min.   :0.7631
##  1st Qu.:0.7784
##  Median :0.9306
##  Mean   :0.8994
##  3rd Qu.:0.9998
##  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.
##  Min.   :0.1232   Min.   :0.00000000   Min.   :0.00000
##  1st Qu.:0.3557   1st Qu.:0.00001409   1st Qu.:0.04716
##  Median :0.4353   Median :0.04307969   Median :0.21158
##  Mean   :0.4074   Mean   :0.06034946   Mean   :0.18122
##  3rd Qu.:0.5134   3rd Qu.:0.09348079   3rd Qu.:0.26970
##  Max.   :0.6063   Max.   :0.27082138   Max.   :0.41556
##      q.25.               q.50.              q.75.             q.95.
##  Min.   :0.0000701   Min.   :0.004112   Min.   :0.06027   Min.   :0.6186
##  1st Qu.:0.1983125   1st Qu.:0.340148   1st Qu.:0.47950   1st Qu.:0.6698
##  Median :0.3432419   Median :0.432840   Median :0.52269   Median :0.7553
##  Mean   :0.2931052   Mean   :0.385038   Mean   :0.48908   Mean   :0.7549
##  3rd Qu.:0.4209261   3rd Qu.:0.515784   3rd Qu.:0.61276   3rd Qu.:0.8020
##  Max.   :0.5186597   Max.   :0.606557   Max.   :0.68849   Max.   :0.9765
##      q.100.
##  Min.   :0.8104
##  1st Qu.:0.8211
##  Median :0.9721
##  Mean   :0.9306
##  3rd Qu.:1.0000
##  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.   :0.5535   Min.   :0.000000   Min.   :0.000000   Min.   :0.4540
##  1st Qu.:0.6444   1st Qu.:0.000000   1st Qu.:0.001665   1st Qu.:0.4980
##  Median :0.6978   Median :0.004384   Median :0.282614   Median :0.5234
##  Mean   :0.6794   Mean   :0.108969   Mean   :0.245462   Mean   :0.5648
##  3rd Qu.:0.7187   3rd Qu.:0.218413   3rd Qu.:0.424109   3rd Qu.:0.6049
##  Max.   :0.7687   Max.   :0.430386   Max.   :0.546367   Max.   :0.8578
##      q.50.            q.75.            q.95.           q.100.
##  Min.   :0.5543   Min.   :0.6035   Min.   :0.688   Min.   :0.7865
##  1st Qu.:0.6462   1st Qu.:0.7060   1st Qu.:0.790   1st Qu.:0.9630
##  Median :0.7083   Median :0.8928   Median :0.981   Median :1.0000
##  Mean   :0.7791   Mean   :0.8538   Mean   :0.902   Mean   :0.9640
##  3rd Qu.:0.9637   3rd Qu.:1.0000   3rd Qu.:1.000   3rd Qu.:1.0000
##  Max.   :0.9996   Max.   :1.0000   Max.   :1.000   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.   :0.1703   Min.   :0.002003   Min.   :0.05464   Min.   :0.1067
##  1st Qu.:0.2209   1st Qu.:0.009981   1st Qu.:0.07820   1st Qu.:0.1433
##  Median :0.3908   Median :0.042147   Median :0.15457   Median :0.2698
##  Mean   :0.3926   Mean   :0.069699   Mean   :0.19752   Mean   :0.2996
##  3rd Qu.:0.5601   3rd Qu.:0.067002   3rd Qu.:0.29512   3rd Qu.:0.4547
##  Max.   :0.6791   Max.   :0.331104   Max.   :0.46525   Max.   :0.5561
##      q.50.            q.75.             q.95.            q.100.
##  Min.   :0.1571   Min.   :0.2210   Min.   :0.3256   Min.   :0.5498
##  1st Qu.:0.2068   1st Qu.:0.2865   1st Qu.:0.4235   1st Qu.:0.6821
##  Median :0.3698   Median :0.4909   Median :0.6969   Median :0.9256
##  Mean   :0.3830   Mean   :0.4760   Mean   :0.6260   Mean   :0.8481
##  3rd Qu.:0.5558   3rd Qu.:0.6457   3rd Qu.:0.7883   3rd Qu.:0.9862
##  Max.   :0.7061   Max.   :0.8555   Max.   :0.9845   Max.   :1.0000
##
## ***************** 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.   :0.1979   Min.   :0.000000   Min.   :0.00037   Min.   :0.02925
##  1st Qu.:0.4936   1st Qu.:0.000000   1st Qu.:0.03269   1st Qu.:0.30470
##  Median :0.5952   Median :0.002488   Median :0.22954   Median :0.41600
##  Mean   :0.5833   Mean   :0.127351   Mean   :0.26872   Mean   :0.44954
##  3rd Qu.:0.6960   3rd Qu.:0.270746   3rd Qu.:0.49721   3rd Qu.:0.63374
##  Max.   :0.7767   Max.   :0.483968   Max.   :0.63985   Max.   :0.73470
##      q.50.            q.75.             q.95.             q.100.
##  Min.   :0.1182   Min.   :0.3064   Min.   :0.6313   Min.   :0.9266
##  1st Qu.:0.4978   1st Qu.:0.6392   1st Qu.:0.7817   1st Qu.:0.9520
##  Median :0.6147   Median :0.7504   Median :0.8523   Median :0.9834
##  Mean   :0.5977   Mean   :0.7342   Mean   :0.8505   Mean   :0.9744
##  3rd Qu.:0.7461   3rd Qu.:0.8266   3rd Qu.:0.8990   3rd Qu.:1.0000
##  Max.   :0.8711   Max.   :0.9966   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.   :0.2147   Min.   :0.00000000   Min.   :0.0001474
##  1st Qu.:0.5001   1st Qu.:0.00001532   1st Qu.:0.0317395
##  Median :0.5486   Median :0.02125233   Median :0.2555259
##  Mean   :0.5097   Mean   :0.07386762   Mean   :0.2187846
##  3rd Qu.:0.5926   3rd Qu.:0.15971778   3rd Qu.:0.3757919
##  Max.   :0.6209   Max.   :0.20495237   Max.   :0.4450655
##      q.25.             q.50.             q.75.            q.95.
```

```
##  Min.   :0.01037   Min.   :0.09531   Min.   :0.3203   Min.   :0.6748
##  1st Qu.:0.31371   1st Qu.:0.50002   1st Qu.:0.5975   1st Qu.:0.7583
##  Median :0.39863   Median :0.55449   Median :0.6700   Median :0.7979
##  Mean   :0.36862   Mean   :0.51600   Mean   :0.6427   Mean   :0.8070
##  3rd Qu.:0.48796   3rd Qu.:0.61073   3rd Qu.:0.6864   3rd Qu.:0.8427
##  Max.   :0.54865   Max.   :0.76207   Max.   :0.9350   Max.   :0.9961
##      q.100.
##  Min.   :0.8321
##  1st Qu.:0.9104
##  Median :0.9352
##  Mean   :0.9343
##  3rd Qu.:0.9841
##  Max.   :1.0000
```