# Preliminary multinomial analysis of Our Lass data

## For discussion

# 1 Data

```
library (gdata)
our.lass.neph.dat <- read.xls("../data//2015 BIM Nephrops quad rig trials/Our Lass 2 70_80
                     sheet = "All hauls",
                     stringsAsFactors = FALSE)
## Each mesh size has a unique codend number
with(our.lass.neph.dat, table(Mesh.Size, Codend.No))
## position switched
with(our.lass.neph.dat, table(Mesh.Size, Net.position))
## Show the first 2 rows
head (our.lass.neph.dat, 2)
## Make the "HAUL" variable character
our.lass.neph.dat$HAUL <- paste("H", our.lass.neph.dat$Haul.No, sep ="")
## make some factor variables used in the analyses
our.lass.neph.dat$fHAUL <- factor(our.lass.neph.dat$HAUL, levels = unique(our.lass.neph.da
our.lass.neph.dat$Mesh.Size <- factor(paste("c", our.lass.neph.dat$Mesh.Size, sep = ""))</pre>
## remove observations above 99th and below 1th length percentile
## these can be highly influential on the fits
our.lass.neph.dat <- subset (our.lass.neph.dat, Carapace.length < quantile (Carapace.length,
                   Carapace.length > quantile(Carapace.length, 0.01)
```

## Prepare the data for a multinomial fit.

```
## get count per length bin per haul by mesh size
## using the reshape package (makes it easier to process data)
library(reshape)
## variables to keep
```

```
vars2keep <- c("Mesh.Size", "Carapace.length", "fHAUL", "Count")</pre>
## melt the data frame
our.lass.neph.melt <- melt(our.lass.neph.dat[, vars2keep],</pre>
                 id = c("Mesh.Size", "Carapace.length", "fHAUL"))
## re-form the dataframe in required format
our.lass.neph.cast <- cast (our.lass.neph.melt, Carapace.length + fHAUL ~ Mesh.Size + varia
our.lass.neph.cast <- our.lass.neph.cast[order(our.lass.neph.cast$fHAUL, our.lass.neph.cast
our.lass.neph.cast[is.na(our.lass.neph.cast)] <- 0</pre>
## show the first few rows
head(our.lass.neph.cast, 2)
## Carapace.length fHAUL c100mm_Count c70mm_Count c80mm_Count c90mm_Count
## 10
                  22 H1
                                     1
                                                 1
## 23
                                                            2
                  23
                        Н1
                                                 4
                                      1
## format the subsampling ratio similarly
## unique raising factors per haul
rf.count <- with(our.lass.neph.dat, table(fHAUL, Overall.raising.factor, Mesh.Size))
apply (rf.count, 1, FUN = function (x) \{sum(x>0)\})
## H1 H2 H3 H4 H5 H6 H7 H8 H9 H10 H11 H12 H14
## 4 4 4 4 4 4 4 4 4 4 4 4 4
## convert to sub-sampling ratio as in Celtic Warrior
our.lass.neph.dat$SUBSRATIO <- 1/our.lass.neph.dat$Overall.raising.factor
vars2keep <- c("Mesh.Size", "fHAUL", "SUBSRATIO")</pre>
subs.melt <- melt(unique(our.lass.neph.dat[, vars2keep]), id = c("Mesh.Size", "fHAUL"))</pre>
subs.cast <- cast(subs.melt, fHAUL ~ Mesh.Size + variable)</pre>
## get net position of each
vars2keep <- c("Mesh.Size", "fHAUL", "Net.position")</pre>
netpos.melt <- melt(unique(our.lass.neph.dat[, vars2keep]), id = c("Mesh.Size", "fHAUL"))</pre>
netpos.cast <- cast (netpos.melt, fHAUL ~ Mesh.Size + variable)</pre>
## merge counts and subsampling ratio back together
our.lass.neph.cast0 <- merge(our.lass.neph.cast, subs.cast, by = "fHAUL", all.x = TRUE)
our.lass.neph.cast <- merge(our.lass.neph.cast0, netpos.cast, by = "fHAUL", all.x = TRUE)
## show first few lines
head(our.lass.neph.cast, 2)
## fHAUL Carapace.length c100mm_Count c70mm_Count c80mm_Count c90mm_Count
## 1 H1 22 1 1 0 1
```

```
23
## c100mm_SUBSRATIO c70mm_SUBSRATIO c80mm_SUBSRATIO c90mm_SUBSRATIO
         ## 2
          0.02904138
                        0.03969299
                                       0.03840203
                                                       0.06179486
## c100mm_Net.position c70mm_Net.position c80mm_Net.position
## 1
                     4
                                       1
                                                          3
## 2
                                                          3
## c90mm_Net.position
## 1
## 2
                     2
## Extract the matrix of counts
count.vars <- c("c100mm_Count", "c70mm_Count", "c80mm_Count", "c90mm_Count")</pre>
neph.count.mat <- as.matrix(our.lass.neph.cast[, count.vars])</pre>
## Extract the matrix of subsampling ratios
subsratio.vars <- c("c100mm_SUBSRATIO", "c70mm_SUBSRATIO", "c80mm_SUBSRATIO", "c90mm_SUBSRATIO",
subsratio.mat <- as.matrix(our.lass.neph.cast[, subsratio.vars])</pre>
## Create the offset (NEED TO CHECK THIS)
offset.mat <- log(apply(subsratio.mat, 2, FUN =
                       function(zz){zz/subsratio.mat[,1]}))
```

#### Plot the data

```
library(ggplot2)
## Get the proportions
count.mesh <- as.matrix(our.lass.neph.cast[, count.vars])</pre>
prop.mesh <- prop.table(count.mesh, margin = 1)</pre>
m <- dim(prop.mesh)[1]</pre>
## make a dataframe of the proportions for ggplot
netpos.vars <- c("c100mm_Net.position", "c70mm_Net.position", "c80mm_Net.position", "c90mm_</pre>
prop.mesh.df <- data.frame(</pre>
                  Mesh.Size = factor(rep(count.vars, each = m)),
                   Carapace.length = rep (our.lass.neph.cast$Carapace.length, times = 4),
                   fHAUL = rep(our.lass.neph.cast$fHAUL, times = 4),
                  Net.position = unlist(our.lass.neph.cast[, netpos.vars]),
                   proportion = c(prop.mesh),
                   count = c(count.mesh))
ggplot(prop.mesh.df, aes(x = Carapace.length, y = proportion)) +
  geom_point(colour = "#F8766D", alpha = 0.2, aes(size = log(count))) +
 facet_wrap(~ Mesh.Size) + ylab("Proportion of Nephrops per cod-end")
```

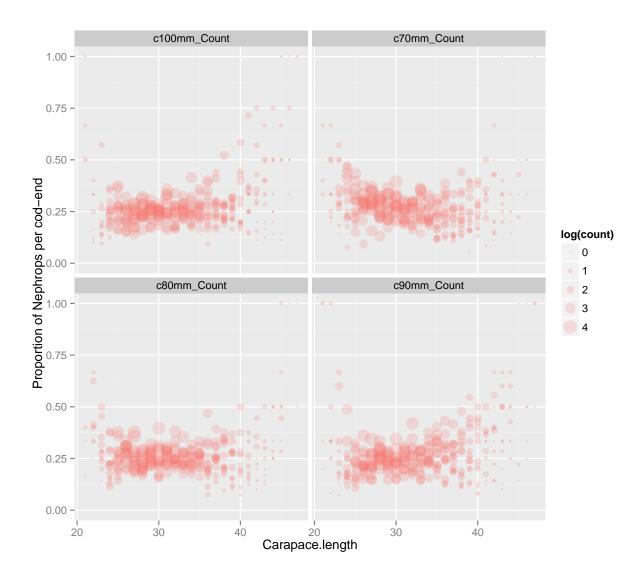


Figure 1: Proportion of Nephrops catch retained per haul. Each point represents the proportion of the Nephrops catch (in number) per haul and length class retained in a given cod-end (70mm, 80mm, 90mm, or 100mm). The size of the point is proportional to the log of the count.

# 2 Model

The model we focus on is the multinomial, which is a generalization of the binomial to cases with more than two categories (here 4 categories: 70, 80, 90 and 100mm). Under the assumption that each net fishes the same, we would expect 25% of the catch to be retained in each net. We can test that hypothesis.

```
library(nnet)
## First fit is constant proportions
## not accounting for length
mnom0 <- multinom(neph.count.mat ~ 1)</pre>
## # weights: 8 (3 variable)
## initial value 23374.309223
## final value 23367.514160
## converged
## include carapace length
## first scale it to range between zero and one
max.length <- max(our.lass.neph.cast$Carapace.length)</pre>
our.lass.neph.cast$prop.Carapace.length <- our.lass.neph.cast$Carapace.length/max.length
## Extend to third order polynomial (based on AIC and BIC)
our.lass.neph.cast$prop.Carapace.length2 <- our.lass.neph.cast$prop.Carapace.length^2
our.lass.neph.cast$prop.Carapace.length3 <- our.lass.neph.cast$prop.Carapace.length^3
##
mnom.length <- multinom(neph.count.mat ~</pre>
                        prop.Carapace.length + prop.Carapace.length2 + prop.Carapace.lengtl
## # weights: 20 (12 variable)
## initial value 23374.309223
## iter 10 value 23336.622678
## iter 20 value 23336.444786
## final value 23336.392881
## converged
AIC (mnom0, mnom.length)
##
              df
                      AIC
               3 46741.03
## mnom0
## mnom.length 12 46696.79
```

```
## try a VGAM fit for comparison
library (VGAM)
df.vec <- seq(1,10)
aic.vec <- rep(NA, 10)
for(i in 1:10){
  mnom.length.vgam <- vgam(neph.count.mat ~ s(prop.Carapace.length, df = df.vec[i]), famil</pre>
  aic.vec[i] <- AIC(mnom.length.vgam)</pre>
df.best <- df.vec[which.min(aic.vec)]</pre>
mnom.length.vgam <- vgam(neph.count.mat ~ s(prop.Carapace.length, df = df.best), family = 1
pred.prop.length <- seq(min(our.lass.neph.cast$prop.Carapace.length),</pre>
                         max(our.lass.neph.cast$prop.Carapace.length), length = 100)
pred.length <- seq(min(our.lass.neph.cast$Carapace.length),</pre>
                         max(our.lass.neph.cast$Carapace.length), length = 100)
pred.vgam <- predict (mnom.length.vgam, newdata = data.frame (prop.Carapace.length = pred.pre
m <- length(pred.length)</pre>
pred.vgam.df <- data.frame(</pre>
                   Mesh.Size = factor(rep(count.vars, each = m)),
                   Carapace.length = rep(pred.length, times = 4),
                   proportion = c(pred.vgam))
```

# Get predictions for the fitted model (note this is long-winded here but will be better coded for more than the preliminary example).

```
X <- cbind(1, pred.prop.length, pred.prop.length^2, pred.prop.length^3)</pre>
## number of times to resample predictions to get CIs
nresamp <- 100
pred.array <- array(NA, dim = c(nlength, 4, nresamp))</pre>
## package to draw from multivariate normal
library (mvtnorm)
for(i in 1:nresamp){
  ## print(i)
 beta <- matrix(rmvnorm(1, mean = beta.mu, sigma = Sigma),
                 nrow = 3, byrow = TRUE)
 p70mmPort <- exp(X %*% matrix(beta[1,]))/(1 + rowSums(exp(X %*% t(beta))))
  p100mmStarboard <- exp(X %*% matrix(beta[2,]))/(1 + rowSums(exp(X %*% t(beta))))
  p70mmStarboard <- exp(X %*% matrix(beta[3,]))/(1 + rowSums(exp(X %*% t(beta))))
  p100mmPort <- 1 - p70mmPort - p100mmStarboard - p70mmStarboard
  pred.p <- cbind(p100mmPort, p70mmPort, p100mmStarboard, p70mmStarboard)</pre>
  pred.array[ , , i] <- pred.p</pre>
  rm (pred.p)
## mean across samples
pred.mu <- apply(pred.array, c(1, 2), mean)</pre>
## upper across samples
pred.upper <- apply (pred.array, c(1, 2), quantile, p = 0.975)
## lower across samples
pred.lower <- apply (pred.array, c(1, 2), quantile, p = 0.025)
## bring all together in a data frame for ggplot
m <- dim(pred.mu)[1]</pre>
pred.ci.df <- data.frame(</pre>
                Mesh.Size = factor(rep(count.vars, each = m)),
                Carapace.length = rep(pred.length, times = 4),
                proportion = c(pred.mu),
                 lower = c(pred.lower),
                upper = c(pred.upper))
```

#### Finally overlay the fit on the sample proportions

# 2.1 Including net position as a covariate

```
## create factor variables
our.lass.neph.cast$f100mm_Net.position <- paste("pos", our.lass.neph.cast$c100mm_Net.posit.
our.lass.neph.cast$f90mm_Net.position <- paste("pos", our.lass.neph.cast$c90mm_Net.position
our.lass.neph.cast$f80mm_Net.position <- paste("pos", our.lass.neph.cast$c80mm_Net.position")
our.lass.neph.cast$f70mm_Net.position <- paste("pos", our.lass.neph.cast$c70mm_Net.position
mnom.length.netpos <- multinom(neph.count.mat ~</pre>
                               prop.Carapace.length +
                               prop.Carapace.length2 +
                               prop.Carapace.length3 +
                               f100mm_Net.position +
                               f70mm_Net.position +
                               f80mm_Net.position +
                               f90mm Net.position,
                               data = our.lass.neph.cast)
## # weights: 68 (48 variable)
## initial value 23374.309223
## iter 10 value 23326.650060
## iter 20 value 23319.754756
## iter 30 value 23318.476676
## final value 23318.304129
## converged
AIC (mnom.length, mnom.length.netpos)
##
                      df
                              AIC
                      12 46696.79
## mnom.length
## mnom.length.netpos 24 46684.61
```

## Plot the net position predictions

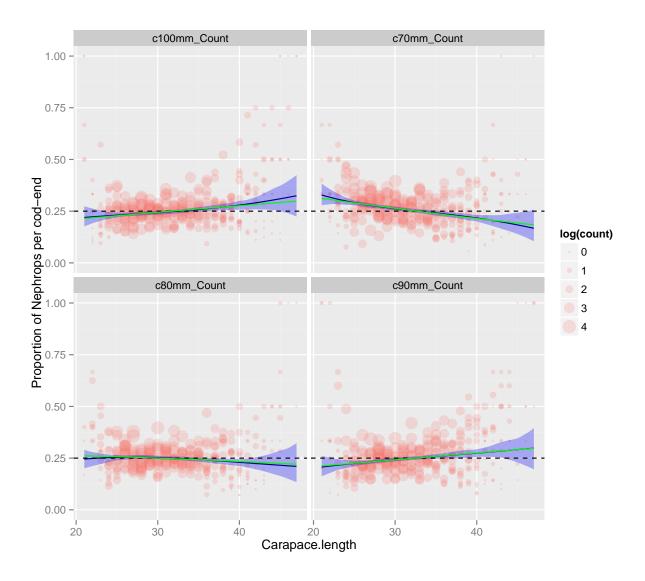


Figure 2: Proportion of Nephrops catch retained per haul with fitted multinomial model and associated re-sampled intervals. Null hypothesis of equal retention is displayed as the dashed line at 0.25.

```
pos.vec <- paste("pos", 1:4, sep = "")</pre>
## removing fifth row for now
netpos.unique <- as.data.frame(apply(unique(netpos.cast[,2:5])[-5, ], 2, FUN = function(x)
names (netpos.unique) <- names (netpos.cast[, 2:5])</pre>
names (netpos.unique) <- gsub("c", "f", names (netpos.unique))</pre>
m <- length (pred.prop.length)</pre>
pred.df <- netpos.unique[rep(1:4, each = m), ]</pre>
pred.df$prop.Carapace.length <- rep(pred.prop.length, times = 4)</pre>
pred.df$prop.Carapace.length2 <- pred.df$prop.Carapace.length^2</pre>
pred.df$prop.Carapace.length3 <- pred.df$prop.Carapace.length^3</pre>
pred.df$Carapace.length <- rep(pred.length, times = 4)</pre>
pred.netpos <- predict(mnom.length.netpos, newdata = pred.df, type = "prob")</pre>
m <- dim(pred.df)[1]</pre>
pred.netpos.df <- data.frame(</pre>
                     Mesh.Size = factor(rep(count.vars, each = m)),
                     Carapace.length = rep(pred.df$Carapace.length, times = 4),
                     Net.position = unlist(pred.df[, 1:4]),
                     proportion = c(pred.netpos))
ggplot (prop.mesh.df2, aes(x = Carapace.length, y = proportion, colour = Net.position)) +
  geom point(alpha = 0.2, aes(size = log(count))) +
facet_wrap(~ Mesh.Size) + ylab("Proportion of Nephrops per cod-end") +
  ##scale colour manual(values=rainbow(4)) +
geom_line(data = pred.netpos.df, aes(x = Carapace.length, y = proportion))
```

