

# Analysis of Wolffish Data, Reproduction, a supplement to:

A life history study of Atlantic wolffish resolves bias and imprecision in maturity schedules by recognizing abortive maturation | To accompany the main article in *Marine and Coastal Fisheries*.

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June 27, 2022

```
knitr::opts_chunk$set(echo = TRUE)
library(lubridate); library(tidyverse); library(knitr) # used for data
wrangling
```

## Introduction

This R markdown documents is used for auditing data and archiving analyses for a research study of Atlantic wolffish *Anarhichas lupus* reproduction. George Maynard started this code for an Atlantic halibut project, and additional analyses were added in from code developed by Yvonna Press.

We begin by calling up and wrangling the source data file for this study.

```
setwd
('C://Users/Richard.Mcbride/Documents/Enhanced_ff/Data_Poor_wolffish/DATA.ANALYSES/DataFiles_RMarkdownSummary')
datmat <- read_csv('Copy101421All_Wolffish_Data_08_30_2019.csv')

# 1. Delete some rows, specifically delete males
datmat <- datmat[datmat$SEX.y=='F',] #remove any but females

# 2. Change a few variable names or their format to match code
datmat <- datmat %>%
  mutate(CollectionDate = as.Date(TOWDATE, "%d-%b-%y")) %>%
  mutate(Length = as.numeric(TL_cm)) %>%
  mutate(Age = as.numeric(sec_consensus)) %>%
  transform(MATURITY=factor(MATURITY,levels=c("I","D","R","U","S","T","X")))
%>%
  mutate(monfac = as.factor(MONTH)) %>%
  mutate(CollectionLongitude = DECDEG_BEGLON) %>%
  mutate(CollectionLatitude = DECDEG_BEGLAT)

# 3. Derive 4 seasons, with December as the start of the winter quarter
quart <- setNames(rep(c('Winter', 'Spring', 'Summer', 'Fall'), each = 3),
c(12, 1:11))
datmat$Season <- unname(quart[as.character(datmat$MONTH)])
```

```
datmat <- datmat %>% transform(Season = factor(Season, levels=c('Winter',
'Spring', 'Summer', 'Fall')))
```

Subsequent major sections are:

- Sample sizes and the female size and age in our database
- Plotting a map of the female samples
- Female oogenesis and gonad development
- Reproductive seasonality
- Abortive maturation and size and age at maturity

## Sample sizes and the female size and age in our database

There are 255 records of females. Here is a quick confirmation of the sample sizes by date (Month, Year) and by source: the NEFSC bottom trawl survey (NEFSC.BTS), the NEFSC longline survey (NEFSC.LL), the NEFSC study fleet (NEFSC.SF), a UNH/commerical bottom trawl collaboration (UNH.trawl), and UNH/commercial lobster pot collaboartion (UNH.pot).

```
n_mon_yr <- table(datmat$MONTH, datmat$YEAR)
n_mon_yr2 <- addmargins(n_mon_yr, margin = seq_along(dim(n_mon_yr)), FUN =
sum, quiet = FALSE)

## Margins computed over dimensions
## in the following order:
## 1:
## 2:

kable(n_mon_yr2, caption = 'Number of fish by sample month and year')
```

*Number of fish by sample month and year*

	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	sum
4	12	12	1	10	2	0	7	1	5	1	51
5	0	0	2	2	7	8	3	5	23	7	57
6	0	0	0	0	0	0	0	5	28	0	33
7	0	0	0	0	0	1	0	0	38	0	39
8	0	0	0	0	0	0	0	0	28	0	28
9	0	0	0	0	0	0	0	0	11	0	11
10	0	0	5	1	0	4	6	1	1	0	18
11	5	2	2	0	1	2	2	1	0	0	15
12	0	2	0	0	0	0	0	0	0	0	2
sum	17	16	10	13	10	15	18	13	134	8	254

```
n_gear_yr <- table(datmat$GEAR, datmat$YEAR)
n_gear_yr2 <- addmargins(n_gear_yr, margin = seq_along(dim(n_gear_yr)), FUN
= sum, quiet = FALSE)
```

```
## Margins computed over dimensions
## in the following order:
## 1:
## 2:

kable(n_gear_yr2, caption = 'Number of fish by sample source and year')
```

*Number of fish by sample source and year*

	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	sum
NEFSC.BTS	17	16	10	13	10	8	12	9	5	1	101
NEFSC.LL	0	0	0	0	0	6	6	4	9	7	32
NEFSC.SF	0	0	0	0	0	1	0	0	14	0	15
UNH.pot	0	0	0	0	0	0	0	0	1	0	1
UNH.trawl	0	0	0	0	0	0	0	0	105	0	105
sum	17	16	10	13	10	15	18	13	134	8	254

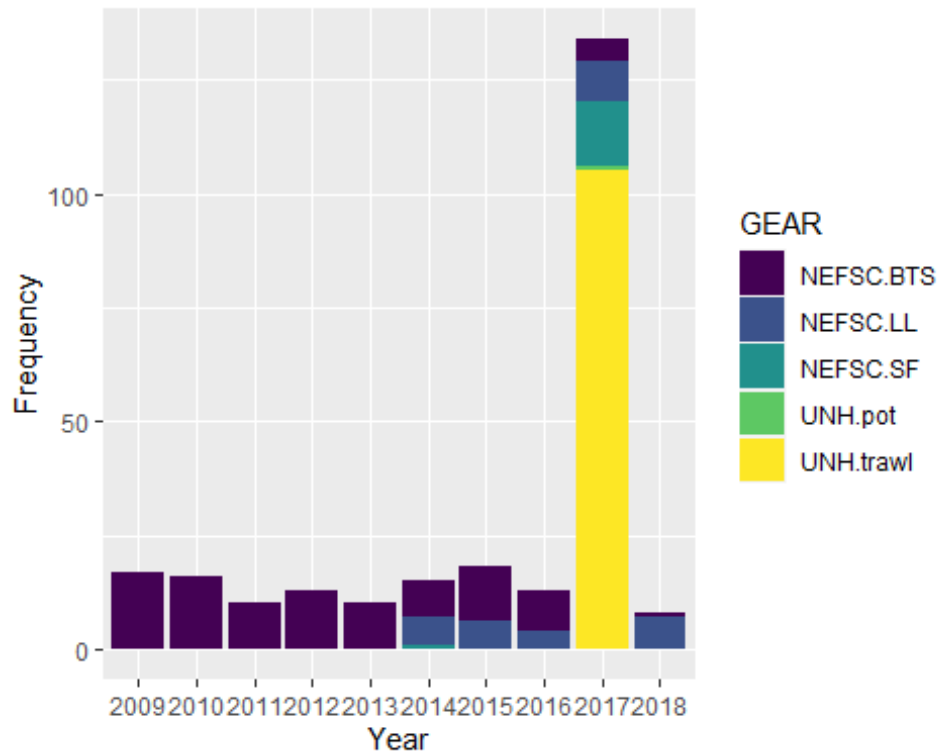
*#You can use write\_csv (objectname, "filename.csv") to save a table*

We dress these sample size summaries up as colored figures.

```
library (viridis)

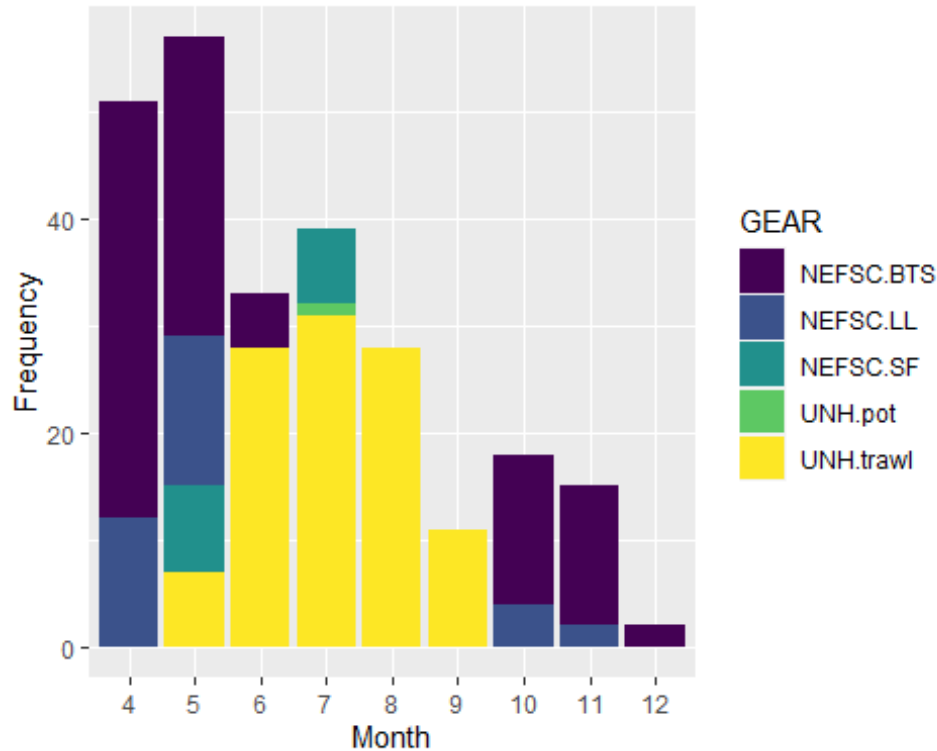
datmat.n <- datmat %>%
  drop_na(YEAR)

ggplot (datmat.n) +
  geom_bar(mapping = aes (x = factor(YEAR), fill = GEAR)) +
  #theme (Legend.position = 'top') +
  labs (x = 'Year', y = "Frequency") +
  scale_fill_viridis_d ()
```



```
ggsave("WolfFigYEARxGEAR.png")
```

```
ggplot (datmat.n) +
  geom_bar(mapping = aes (x = factor(MONTH), fill = GEAR)) +
  #theme (Legend.position = 'top') +
  labs (x = 'Month', y = "Frequency") +
  scale_fill_viridis_d ()
```



```
ggsave("WolfFigMONTHxGEAR.png")
```

Here is a depiction of females wolffish size by gear, where size by gear is compared with a non-parametric Kruskal-Wallis test among the four major sampling sources (i.e. the lobster pot fish was not included because only a single fish was used in the final dataset). The commercial trawls operated by the UNH fishermen and the NEFSC study fleet caught larger fish in general, while the greatest size range was collected by the NEFSC Bottom Trawl Survey.

```
library(ggpubr)

datmat %>%
  group_by (GEAR) %>%
  summarize(mini = min(Length, na.rm = TRUE),
            median = median(Length, na.rm = TRUE),
            maxi = max(Length, na.rm = TRUE),
            n = n())

## # A tibble: 5 x 5
##   GEAR      mini median  maxi    n
##   <chr>    <dbl> <dbl> <dbl> <int>
## 1 NEFSC.BTS 12.5   42.2  105   102
## 2 NEFSC.LL  32.2   58.8  82.7   32
## 3 NEFSC.SF  52     66.6  88     15
## 4 UNH.pot   65     65    65     1
## 5 UNH.trawl 44     67    91   105
```

```

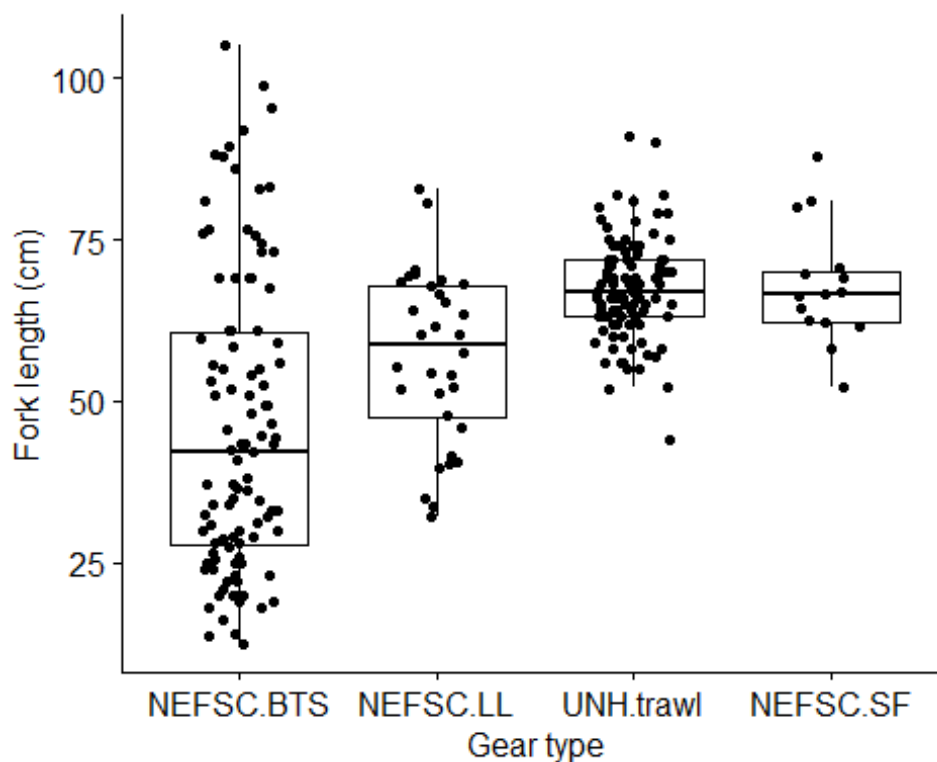
datmat.no.pot <- datmat %>%
  filter (GEAR != 'UNH.pot')

  kruskal.test(Length ~ GEAR, data = datmat.no.pot)

##
## Kruskal-Wallis rank sum test
##
## data: Length by GEAR
## Kruskal-Wallis chi-squared = 62.878, df = 3, p-value = 1.426e-13

ggboxplot (datmat.no.pot, x = "GEAR", y = "Length", add = "jitter") +
  labs (x = "Gear type", y = "Fork length (cm)") +
  theme (legend.position = 'top')

```



```
ggsave ("WolfFig2.png")
```

Note, in the Kruskal-Wallis test, the single fish (65 cm) female collected by a lobster pot has been removed.

And a quick check of ranges of female wolffish size and age by month.

```

datmat %>%
  group_by (MONTH) %>%
  summarize(mini = min(Length, na.rm = TRUE),
            maxi = max(Length, na.rm = TRUE),
            n = n())

```

```

## # A tibble: 10 x 4
##   MONTH mini maxi   n
##   <dbl> <dbl> <dbl> <int>
## 1     4  18  105   51
## 2     5 25.5  95.5   57
## 3     6 12.5   90   33
## 4     7  52   88   39
## 5     8  52   82   28
## 6     9  44   72   11
## 7    10  14  76.5   18
## 8    11  20   88   15
## 9    12  18   25    2
## 10   NA  22   22    1

datmat %>%
  filter(Age>0) %>%
  group_by (MONTH) %>%
  summarize(mini = min(Age, na.rm = TRUE),
            maxi = max(Age, na.rm = TRUE),
            n = n())

## # A tibble: 10 x 4
##   MONTH mini maxi   n
##   <dbl> <dbl> <dbl> <int>
## 1     4     2  22  46
## 2     5     2  29  47
## 3     6     2  27  30
## 4     7     7  21  30
## 5     8     6  15  28
## 6     9     6   9  11
## 7    10     1   8  15
## 8    11     2  20  13
## 9    12     1   2   2
## 10   NA     3   3   1

```

## Plotting a map of where the female reproductive samples were collected

The collection locations of female wolffish spanned the Gulf of Maine, including the Great South Channel and the northeast tip of Georges Bank. The density of collections were highest in the western Gulf of Maine, shown here by sampling source: the NEFSC bottom trawl survey (open triangles), the NEFSC longline survey (filled circles), the NEFSC study fleet (gray area, individual locations considered confidential), the UNH/commercial bottom trawl collaboration (gray diamonds), and UNH/commercial lobster pot collaboration (X).

```

library(ggspatial)
library(mapdata); library(marmap)
library(raster); library(rgdal); library(rgeos)
library(rnaturalearth); library(rnaturalearthdata)
library(sf)

```

```

namerica <- ne_countries(scale = 'medium', type = 'countries', continent =
'north america', returnclass = "sf")

LatClean <- datmat %>%
  drop_na(CollectionLatitude)

datmat.sf <- st_as_sf(LatClean, coords = c('DECDEG_BEGLON', 'DECDEG_BEGLAT'),
crs = 4326)

NEFSC.BTS.sf <- datmat.sf %>% filter (GEAR == "NEFSC.BTS")
NEFSC.LL.sf <- datmat.sf %>% filter (GEAR == "NEFSC.LL")
UNH.trawl.sf <- datmat.sf %>% filter (GEAR == "UNH.trawl")
UNH.pot.sf <- datmat.sf %>% filter (GEAR == "UNH.pot")

SFleet.sf <- datmat.sf %>% filter (GEAR == "NEFSC.SF") # These data are
confidential so they are not plotted individually
range(SFleet.sf$CollectionLatitude, na.rm=TRUE)

## [1] 42.43253 43.02887

range(SFleet.sf$CollectionLongitude, na.rm=TRUE)

## [1] -70.46497 -69.11227

b <- getNOAA.bathy (lon1 = -71.5, lon2 = -64, lat1 = 39, lat2 = 45.5, res=1)
# Turns out 1 is the finest resolution
bathyLat = as.numeric(colnames(b)); bathyLon = as.numeric(rownames(b))
bathyZ = as.numeric(b); dim(bathyZ) = dim(b)
bf = fortify.bathy(b) # explixedly spatial?

ggplot(namerica) +
  geom_sf(fill = "darkgray") +
  geom_contour(data=bf, aes(x=x, y=y, z=z), breaks=c(-100), size=c(0.3),
colour="grey") + # add 100m contour
  geom_contour(data=bf, aes(x=x, y=y, z=z), breaks=c(-250), size=c(0.6),
colour="grey") + # add 250m contour
  geom_sf(data=NEFSC.BTS.sf, x = 'CollectionLongitude', y =
'CollectionLatitude', pch = 2, size = 2.5) +
  geom_sf(data=NEFSC.LL.sf, x = 'CollectionLongitude', y =
'CollectionLatitude', pch = 19, size = 2.5) +
  geom_rect(data=SFleet.sf, mapping=aes( xmin=-70.46497, xmax=-69.11227,
ymin=42.43253, ymax=43.02887), alpha = 0.05, linetype=2) +
  geom_sf(data=UNH.trawl.sf, x = 'CollectionLongitude', y =
'CollectionLatitude', pch = 23, fill="grey80", size = 2.5) +
  geom_sf(data=UNH.pot.sf, x = 'CollectionLongitude', y =
'CollectionLatitude', pch = 4, size = 2.5) +
  coord_sf( xlim = c(-71, -65), ylim = c(41, 44) ) +
  labs(x="Longitude", y="Latitude") +
  theme_bw( ) +

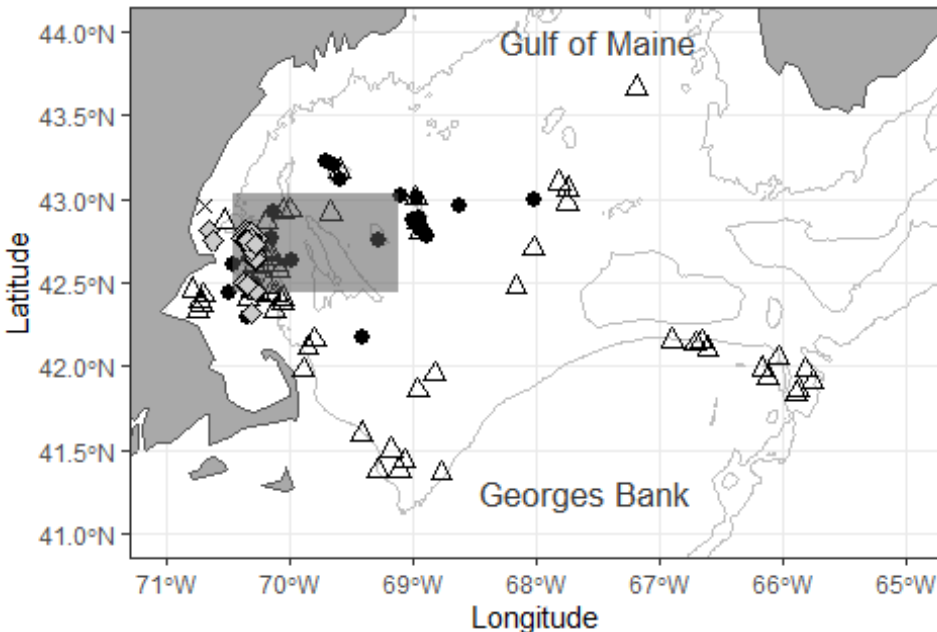
```



```

  annotate(geom = "text", x = -67.6, y = 41.25, label = "Georges Bank", color
= "grey22", size = 4.5) +
  annotate(geom = "text", x = -67.5, y = 43.95, label = "Gulf of Maine",
color = "grey22", size = 4.5)

```



```

ggsave ("WolfFig1.png")

```

## Female wolffish oogenesis, tunica thickness, and gonad development

We are specifically curious about fish size and age thresholds relative to the timing of the ordered stages of oogenesis. Here MAOS is an acronym for “most advanced oocyte stage.” We first tabulate the seasonal patterns of oogenesis (tracked by month). Then, we look at the range of MAOS by fish length and fish age. Finally, the frequency of MAOS by age is illustrated in a lattice graph.

```

datmat <- datmat %>%
  transform(MAOS = factor(MAOS,
    levels=c("PG", "C1", "C2", "C3", "C4", "V1", "V2", "V3", "V4", "H")))

n_MAOS_month <- table(datmat$MAOS, datmat$MONTH)
addmargins(n_MAOS_month, margin = seq_along(dim(n_MAOS_month)), FUN = sum,
  quiet = FALSE)

## Margins computed over dimensions
## in the following order:
## 1:
## 2:

```

```
##
##      4  5  6  7  8  9 10 11 12 sum
## PG   6  0  2  0  0  0  3  1  1 13
## C1   2  1  0  0  0  0  0  1  0  4
## C2   5  1  0  0  0  0  4  0  1 11
## C3  14  8  1  0  2  1  5 10  0 41
## C4   9 16  3  1  0  4  2  3  0 38
## V1   4 11  0  2  0  0  0  0  0 17
## V2   7 16  3  5  1  0  0  0  0 32
## V3   4  4 19 27 10  0  0  0  0 64
## V4   0  0  5  4 14  6  2  0  0 31
## H    0  0  0  0  1  0  2  0  0  3
## sum 51 57 33 39 28 11 18 15 2 254
```

*# Length range and samples size (n) of feamLes by MAOS*

```
datmat %>%
  group_by (MAOS) %>%
  summarize(mini = min(Length, na.rm = TRUE),
            maxi = max(Length, na.rm = TRUE),
            n = n())
```

```
## # A tibble: 10 x 4
##   MAOS   mini maxi   n
##   <fct> <dbl> <dbl> <int>
## 1 PG     12.5  22     13
## 2 C1     21    25.5    4
## 3 C2     23    64.1   11
## 4 C3     22    88     42
## 5 C4     33    95.5   38
## 6 V1     52    99     17
## 7 V2     52   105    32
## 8 V3     48    90     64
## 9 V4     55    82     31
## 10 H     58.5  69     3
```

*# Age range and samples size (n) of feamLes by MAOS*

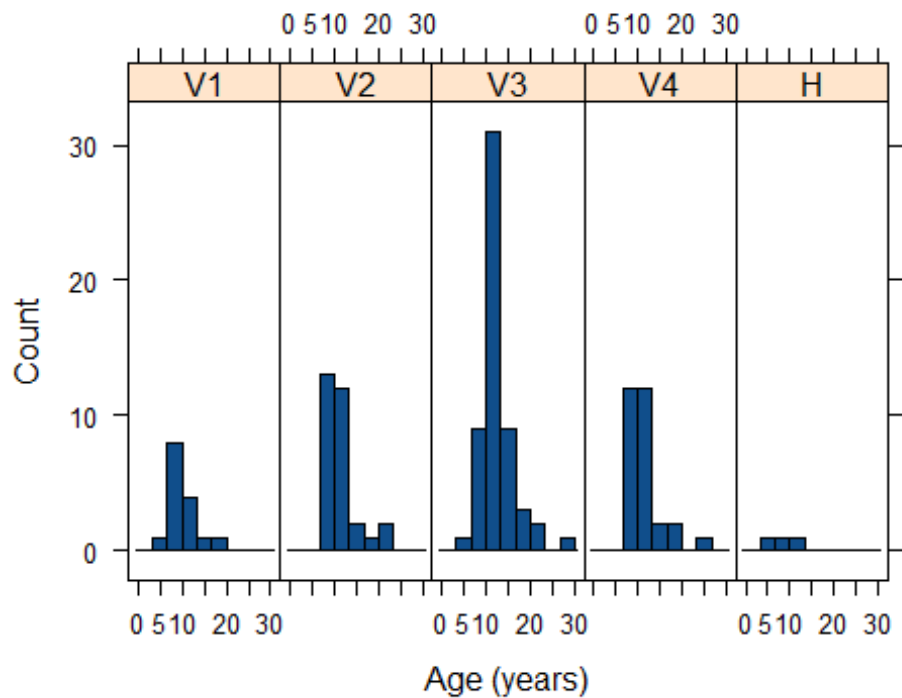
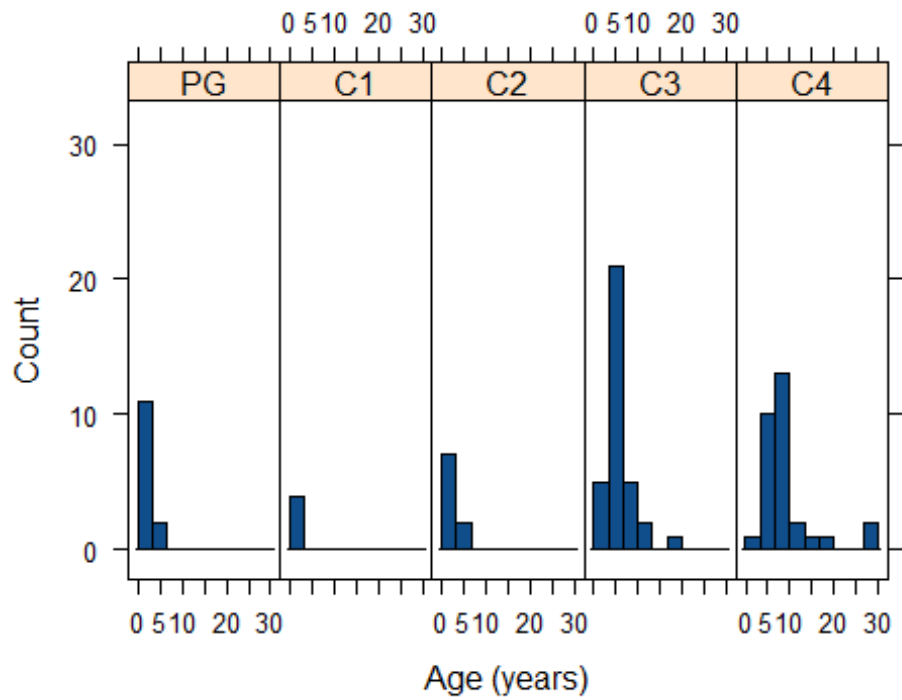
```
datmat %>%
  filter(Age>0) %>%
  group_by (MAOS) %>%
  summarize(mini = min(Age, na.rm = TRUE),
            maxi = max(Age, na.rm = TRUE),
            n = n())
```

```
## # A tibble: 10 x 4
##   MAOS   mini maxi   n
##   <fct> <dbl> <dbl> <int>
## 1 PG     1     5    13
## 2 C1     2     3     4
## 3 C2     2     4     9
## 4 C3     3    20    34
## 5 C4     3    29    30
```

```
## 6 V1      6   19   15
## 7 V2      7   22   30
## 8 V3      6   27   56
## 9 V4      7   25   29
## 10 H      6   13    3

library (lattice)

histogram(~Age|MAOS, data=datmat, # breaks=seq(0,12,5),
          type="count", layout=c(5,1), col="dodgerblue4",
          xlab="Age (years)")
```



We collected few fish in spawning condition, which would be evident by individual females with mature oocytes (i.e., neither nucleus migration nor breakdown were observed). We did, however, collect three females with fresh post-ovulatory follicles (i.e., POF1, table

below) in October and November, verifying these two months as part of the spawning season.

```
datpof <- datmat %>%
  dplyr::select(monfac, POF_STAGE)

datpof[is.na(datpof)] <- 0 #changes any NA's to zero, and one of the months
is a NA so we get a benign error

## Warning in `[<-.factor`(`*tmp*`, thisvar, value = 0): invalid factor
level, NA
## generated

head(datpof)

##   monfac POF_STAGE
## 1     4         0
## 2     4         0
## 3     4         3
## 4     4         0
## 5     4         0
## 6     4         0

nrow(datpof) # this is the total sample size but it includes immature fish,
which inflates the fish with no POFs (see next section where that is
adjusted)

## [1] 255

tabpof <- as.data.frame(table(datpof))
head (tabpof)

##   monfac POF_STAGE Freq
## 1     4         0    38
## 2     5         0    29
## 3     6         0    14
## 4     7         0    24
## 5     8         0    21
## 6     9         0    10

# switch from long to wide format
spread(tabpof, POF_STAGE, Freq ) %>%
  rename (POF0 = '0', POF1 = '1', POF2 = '2', POF3 = '3')

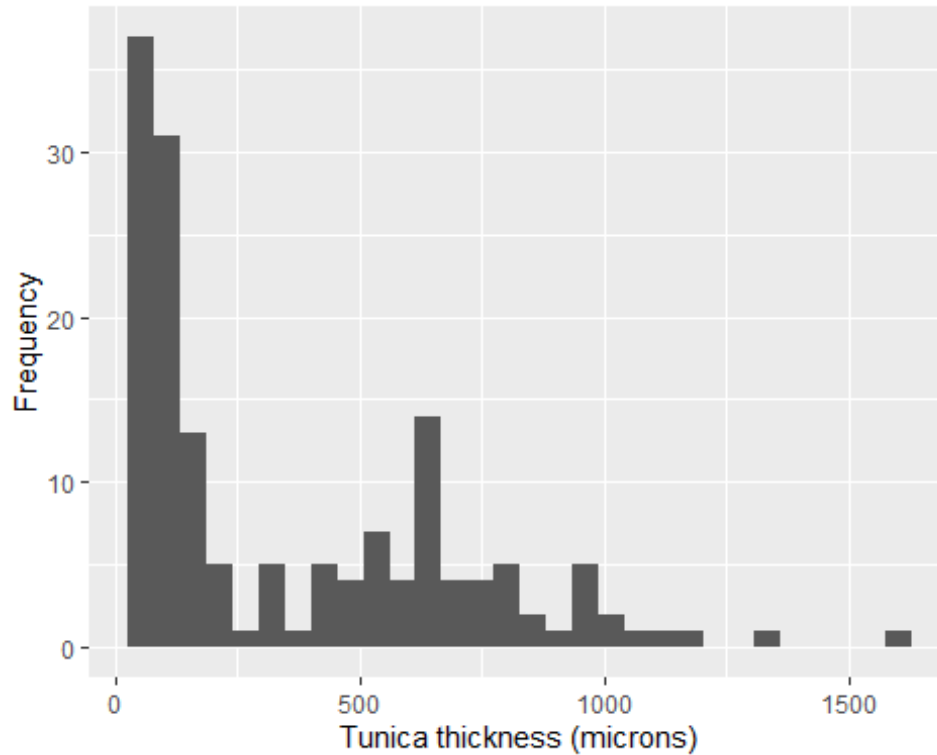
##   monfac POF0 POF1 POF2 POF3
## 1     4    38     0     0    13
## 2     5    29     0     3    25
## 3     6    14     0     0    19
## 4     7    24     0     0    15
## 5     8    21     0     3     4
## 6     9    10     0     0     1
## 7    10    16     2     0     0
```

```
## 8    11   13    1    1    0
## 9    12    2    0    0    0
```

We did not see a post-spawning period of spent fish, those with older post-ovulatory follicles (i.e., POF2), which we attribute these gaps in coverage as a result of low sampling effort in the winter season (December-February). We did see many females with the oldest post-ovulatory follicles (POF3) from April to September, but these POFs were typically mixed in with yolked oocytes. The interpretation is that POF degeneration takes up to a year.

Another important histological criterion we are using for assigning maturity class to individual fish is the thickness of the gonad wall. We assume a bimodal distribution of the gonad wall (often referred to as the tunica) thickness is a result of immature fish that have a relatively thin gonad wall, whereas fish that have spawned in the past, including skippers (by definition), have a thick gonad wall as a result of the expansion, collapse, and reworking on the gonad from the process of spawning. While we expect a bimodal distribution, the specific measurements of what constitutes thin versus thick varies by species. We can determine that here because we actually measured the tunica thickness on the histology slides of a subset of females.

```
ggplot(data = datmat) +
  geom_histogram(mapping = aes (x = TUNICA_MEASUREMENT)) +
  labs (x = 'Tunica thickness (microns)', y = 'Frequency')
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## Warning: Removed 100 rows containing non-finite values (stat_bin).
```



```
ggsave("WolfFig5.png")

## Saving 5 x 4 in image
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## Warning: Removed 100 rows containing non-finite values (stat_bin).

datmat %>%
  group_by (TUNICA_THICKNESS) %>%
  summarize(mini = min (TUNICA_MEASUREMENT, na.rm = TRUE),
            mean = mean (TUNICA_MEASUREMENT, na.rm = TRUE),
            sd = sd (TUNICA_MEASUREMENT, na.rm = TRUE),
            maxi = max (TUNICA_MEASUREMENT, na.rm = TRUE),
            n = n())

## # A tibble: 3 x 6
##   TUNICA_THICKNESS  mini  mean   sd  maxi    n
##   <chr>             <dbl> <dbl> <dbl> <dbl> <int>
## 1 K                 258 691.  246.  1576   68
## 2 T                  28  94.1  48.9   343   84
## 3 <NA>             170 230.   58.1   306  103

kruskal.test(TUNICA_MEASUREMENT ~ TUNICA_THICKNESS, data = datmat)

##
##   Kruskal-Wallis rank sum test
##
```

```
## data: TUNICA_MEASUREMENT by TUNICA_THICKNESS
## Kruskal-Wallis chi-squared = 110.8, df = 1, p-value < 2.2e-16
```

This histogram of tunica thickness indicates an anitmode, and therefore a multiparous or skip spawner threshold, at about 250 microns. Our notation for thin (T) versus thick (K), which is assigned qualitatively by a reader in the laboratory, indicates that the mean gonad wall measurement for a thin tunica is about 1/7th (94 microns) of a thick tunica (691 microns), which was statistically different in thickness (Kruskal-Wallis,  $P < 0.001$ ).

The classification of MAOS and tunica thickness can be used to define classes of maturity, as follows:

```
datmat$HISTO_CLASS <- NA # Assign a maturity class based on histology traits

sel <- ((datmat$MAOS=="PG" | datmat$MAOS=="C1" | datmat$MAOS=="C2")
      & datmat$POF_PRESENCE=="N" & datmat$TUNICA_THICKNESS=="T")
  datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'I') ##Immature

sel <-
((datmat$MAOS=="C2" | datmat$MAOS=="C3" | datmat$MAOS=="C4" | datmat$MAOS=="V1")
  & ( datmat$Season == "Summer" | datmat$Season == "Fall")
  & datmat$POF_PRESENCE=="N" & datmat$TUNICA_THICKNESS == "T")
  datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'IMA') #IMMATURE MATURING -
  CONSIDER TIME OF YEAR--Summer and Fall

sel <- ((datmat$MAOS=="C3" | datmat$MAOS=="C4" | datmat$MAOS=="V1")
      & ( datmat$Season == "Winter" | datmat$Season == "Spring")
      & datmat$POF_PRESENCE=="N" & datmat$TUNICA_THICKNESS == "T")
  datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'FTM') #FIRST TIME MATURE -
  CONSIDER TIME OF YEAR--Winter and Spring

sel <-
((datmat$MAOS=="C1" | datmat$MAOS=="C2" | datmat$MAOS=="C3" | datmat$MAOS=="C4")
  # & datmat$TUNICA_MEASUREMENT >250 &
  (datmat$POF_STAGE==2 | datmat$POF_STAGE==3))
  & datmat$TUNICA_THICKNESS=="K" &
  (datmat$POF_STAGE==2 | datmat$POF_STAGE==3))
  datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'RGT') #RESTING/REGENERATING

sel <- ((datmat$MAOS=="H"))
  datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'SA') #RIPE (spawning
  active)

sel <- ((datmat$MAOS=="C1" | datmat$MAOS=="C2" | datmat$MAOS=="C3") &
  datmat$POF_STAGE==1)
  datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'RGS') #SPENT

sel <- ((datmat$MAOS=="C4" | datmat$MAOS=="V1")
      & (datmat$TUNICA_THICKNESS=="K" | datmat$POF_PRESENCE!="N"))
```



```

datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'ED') #Repeat Spawner

#sel <- ((datmat$MAOS=="V1")
#       & (datmat$TUNICA_THICKNESS=="K"|datmat$POF_PRESENCE!="N"))
# datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'ED') #Repeat Spawner

sel <- (datmat$MAOS=="V2"|datmat$MAOS=="V3"|datmat$MAOS=="V4")
datmat$HISTO_CLASS[sel]<- with (datmat[sel,], 'LD') ##Developing

sel <- ((datmat$MAOS=="C1"| datmat$MAOS=="C2"|datmat$MAOS=="C3" )
       & datmat$POF_PRESENCE=="N" & datmat$TUNICA_THICKNESS=="K"
       & datmat$ATRESIA_PRESENCE=="L")
datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'X') ##SKIP SPAWNER
(resorbing)

sel <- ((datmat$MAOS=="C1"| datmat$MAOS=="C2"|datmat$MAOS=="C3" )
       & datmat$POF_PRESENCE=="N" & datmat$TUNICA_THICKNESS=="K"
       & datmat$ATRESIA_PRESENCE=="N")
datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'XT') #SKIP SPAWNER
(resting)

sel<- ((datmat$MAOS=="C1"| datmat$MAOS=="C2"|datmat$MAOS=="C3" |
datmat$MAOS=="C4")
       & datmat$POF_PRESENCE=="N"
       & datmat$TUNICA_MEASUREMENT<=250
       & datmat$ATRESIA_PRESENCE=="L")
datmat$HISTO_CLASS[sel] <- with (datmat[sel,], 'ABM') ##ABORTIVE MATURATION

datmat <- datmat %>%
  transform(HISTO_CLASS = factor(HISTO_CLASS,
  levels=c("I", "IMA", "FTM", "ABM", "ED", "LD", "SA", "RGS", "RGT", "X",
  "XT", "NA"))) %>%
  transform(MATURITY = factor (MATURITY,
  levels=c("I", "D", "R", "U", "S", "T", "X")))

datmat$MAT01 <-NA # Assign a binary maturity class
tel <- (datmat$HISTO_CLASS=="I" | datmat$HISTO_CLASS=="IMA" |
datmat$HISTO_CLASS=="ABM")
datmat$MAT01[tel]<- with (datmat[tel,], 0) ##Immature as a binary
variable
tel <- (datmat$HISTO_CLASS=="FTM" | datmat$HISTO_CLASS=="ED"
|datmat$HISTO_CLASS=="LD"| datmat$HISTO_CLASS=="SA" |
       datmat$HISTO_CLASS=="RGS" | datmat$HISTO_CLASS=="RGT" |
datmat$HISTO_CLASS=="X" | datmat$HISTO_CLASS=="XT")
datmat$MAT01[tel]<- with (datmat[tel,], 1) # Mature as a binary variable

```

Three immature classes were observed in the samples collected were: immature (I), immature, first-time maturing (IMA), and abortive (im)mature (ABM). Seven defined mature classes were possible: first-time maturing (FTM, also referred to as primiparous),

early developing of a repeat spawner (ED, also referred to as multiparous), late developing (LD), actively spawning (SA, either ripe or ripe & running), spent (RGS), resting (RGT), and two possible types of skipping – 1) resorption of the vitellogenic oocytes (X) or 2) by resting through then entire spawning season (XT).

Here we list the tables of maturity classes by month, then fish length (10cm bins), and fish age.

```
library(psych)

##
## Attaching package: 'psych'

## The following objects are masked from 'package:ggplot2':
##
##   %+%, alpha

# This code can be used for quality assurance and quality control, seen here
# for a particular fish #

QAQMatclass <- datmat %>%
  #filter (MATURITY != ' ' & HISTO_CLASS != ' ') %>%
  filter (ORGANISM_ID == 137702) %>%
  dplyr::select (CRUISE_ID, ORGANISM_ID, MATURITY, HISTO_CLASS, SEX.x,
SEX.y, TL_cm, FISH_MASS_kg, GONAD_MASS_kg, HISTO_ID)
#nrow(QAQMatclass)
#QAQMatclass

n_HistoClass_MATURITY <- table(datmat$HISTO_CLASS, datmat$MATURITY)
n_HistoClass_MATURITY2 <- addmargins(n_HistoClass_MATURITY, margin =
seq_along(dim(n_HistoClass_MATURITY)), FUN = sum, quiet = FALSE)

## Margins computed over dimensions
## in the following order:
## 1:
## 2:

kable(n_HistoClass_MATURITY2, caption = 'Number of fish by histology-
assigned maturity class assigned to an at-sea maturity')
```

*Number of fish by histology-assigned maturity class assigned to an at-sea maturity*

	I	D	R	U	S	T	X	sum
I	23	0	0	0	0	0	1	24
IMA	7	1	0	0	0	4	1	13
FTM	11	7	0	0	0	13	0	31
ABM	0	3	0	0	0	6	0	9
ED	0	11	0	0	2	11	0	24
LD	0	23	3	0	2	8	0	36

	I	D	R	U	S	T	X	sum
SA	0	1	1	0	0	0	0	2
RGS	0	1	1	0	0	1	0	3
RGT	0	1	0	0	1	0	0	2
X	0	0	0	0	0	0	0	0
XT	0	0	0	0	0	0	0	0
NA	0	0	0	0	0	0	0	0
sum	41	48	5	0	5	43	2	144

```
n_HistoClass_month <- table(datmat$HISTO_CLASS, datmat$MONTH)
n_HistoClass_month2 <- addmargins(n_HistoClass_month, margin =
seq_along(dim(n_HistoClass_month)), FUN = sum, quiet = FALSE)

## Margins computed over dimensions
## in the following order:
## 1:
## 2:

kable(n_HistoClass_month2, caption = 'Number of fish by histology-assigned
maturity class and sampling month')
```

*Number of fish by histology-assigned maturity class and sampling month*

	4	5	6	7	8	9	10	11	12	sum
I	13	2	2	0	0	0	3	2	2	24
IMA	0	0	3	0	0	1	4	8	0	16
FTM	18	13	0	0	0	0	0	0	0	31
ABM	0	0	0	1	2	3	5	3	0	14
ED	7	19	1	2	0	0	0	0	0	29
LD	11	20	27	36	25	6	2	0	0	127
SA	0	0	0	0	1	0	2	0	0	3
RGS	0	0	0	0	0	0	2	1	0	3
RGT	1	0	0	0	0	0	0	1	0	2
X	0	0	0	0	0	1	0	0	0	1
XT	0	0	0	0	0	0	0	0	0	0
NA	0	0	0	0	0	0	0	0	0	0
sum	50	54	33	39	28	11	18	15	2	250

```
n_HistoClass_Length <- table(datmat$HISTO_CLASS, floor(datmat$Length/10))
n_HistoClass_Length2 <- addmargins(n_HistoClass_Length, margin =
seq_along(dim(n_HistoClass_Length)), FUN = sum, quiet = FALSE)

## Margins computed over dimensions
## in the following order:
```



	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	9	0	1	2	2	2	2	2	2	su
A	0	0	1	1	2	2	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
B																										2
M																										
E	0	0	0	0	0	0	3	5	2	1	1	2	2	1	0	1	1	1	1	0	0	0	0	1	1	2
D																										2
LD	0	0	0	0	0	1	1	9	1	1	1	1	1	7	4	2	2	4	3	1	1	1	1	0		1
							3		2	1	9	4	1													1
																										5
SA	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3
RG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
S																										
RG	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
T																										
X	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
XT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A																										
su	3	1	1	1	1	1	2	1	1	1	2	1	1	8	4	3	3	6	3	1	1	2	1	2		2
m		4	0	4	0	1	4	8	8	3	1	6	4													1
																										8

*#You can use write\_csv (objectname, "filename.csv") to save a table*

## Reproductive seasonality of female wolffish

We examine reproductive seasonality in three ways: first using a simple ratio of the gonad weight ratioed to the ovary-free body weight, often called the gonadosomatic index (GSI); second by plotting the seasonality of post-ovulatory follicle stages, and third by plotting the monthly proportions of maturity classes.

```
datmat <- datmat %>%
  mutate(GSI2 = (as.numeric(GONAD_MASS_kg)/(FISH_MASS_kg-
as.numeric(GONAD_MASS_kg)))*100)

## Warning in mask$eval_all_mutate(quo): NAs introduced by coercion
## Warning in mask$eval_all_mutate(quo): NAs introduced by coercion

# A quick check of GSI by histo class
datmat %>%
  filter(GSI2>0 & GSI2 < 30) %>% # del outliers; Templeman 1982 for max GSI=28
  group_by (HISTO_CLASS) %>%
  summarize(mini = min (GSI2, na.rm = TRUE),
            mean = mean (GSI2, na.rm = TRUE),
```

```

sd = sd      (GSI2, na.rm = TRUE),
maxi = max   (GSI2, na.rm = TRUE),
n = n())

## # A tibble: 11 x 6
##   HISTO_CLASS  mini   mean    sd   maxi    n
##   <fct>        <dbl> <dbl>  <dbl> <dbl> <int>
## 1 I            0.0910 1.76   2.23   8.33   20
## 2 IMA          0.147  0.477  0.247  0.877  15
## 3 FTM          0.251  0.438  0.212  1.12   26
## 4 ABM          0.124  0.308  0.111  0.589  14
## 5 ED           0.386  0.909  0.376  2.15   25
## 6 LD           0.106  2.93   2.68   18.2   120
## 7 SA           2.78   11.2   7.43   16.9   3
## 8 RGS          1.37   1.56   0.257  1.85   3
## 9 RGT          0.587  0.596  0.0129 0.605  2
## 10 X           0.416  0.416  NA      0.416  1
## 11 <NA>        0.322  0.701  0.332  1.19   5

# Set up GSI data for depicting reproductive seasonality
GSI.Matonly <- datmat %>%
  filter(MAT01 == 1) %>%
  filter(GSI2>0 & GSI2 < 30) %>% # get rid of some outliers
  drop_na(monfac) # delete one fish without month
recorded

# Calculate sample size for next plot
totalgsi <- GSI.Matonly %>%
  group_by(monfac) %>%
  summarize(totalgsi = sum(MAT01))
totalgsi

## # A tibble: 8 x 2
##   monfac totalgsi
##   <fct>    <dbl>
## 1 4          30
## 2 5          47
## 3 6          28
## 4 7          36
## 5 8          25
## 6 9           7
## 7 10         5
## 8 11         2

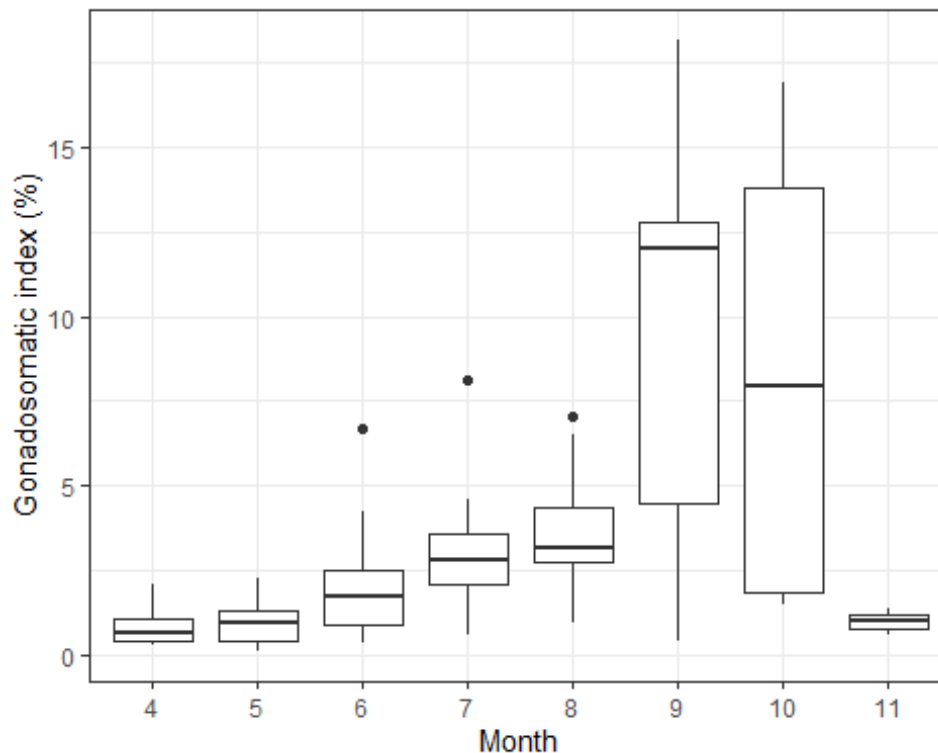
nrow(GSI.Matonly)

## [1] 180

# Plot GSI of mature fish only, by month
ggplot (data=GSI.Matonly, mapping = aes(x = monfac, y = GSI2)) +
  geom_boxplot() +

```

```
labs (x = "Month", y = 'Gonadosomatic index (%)') +
theme_bw ()
```



```
ggsave("WolfFig8.png")
```

```
## Saving 5 x 4 in image
```

In this plot of mature females only, the index increases from spring to winter, peaking in September. The sudden drop in October, which persists into November, indicates spawning occurred. The oocyte diameter distributions presented in the main paper indicate that wolffish exhibit group-synchronous oocyte development with respect to vitellogenesis. Wolffish also appear to be total spawners, meaning they ovulate all their advanced oocytes in a single wave.

This seasonality and evidence for for October-November spawning is depicted in this proportional plot of post-ovulatory follicles stages.

```
datpof2 <- datmat %>%
  filter(MAT01 == 1) %>%
  dplyr::select (monfac, POF_STAGE)
datpof2[is.na(datpof2)] <- 0 #changes any NA's to zero
# head(datpof2)
nrow(datpof2) # this is the sample size for mature females only
## [1] 196
```

```

tabpof2 <- as.data.frame(table(datpof2))

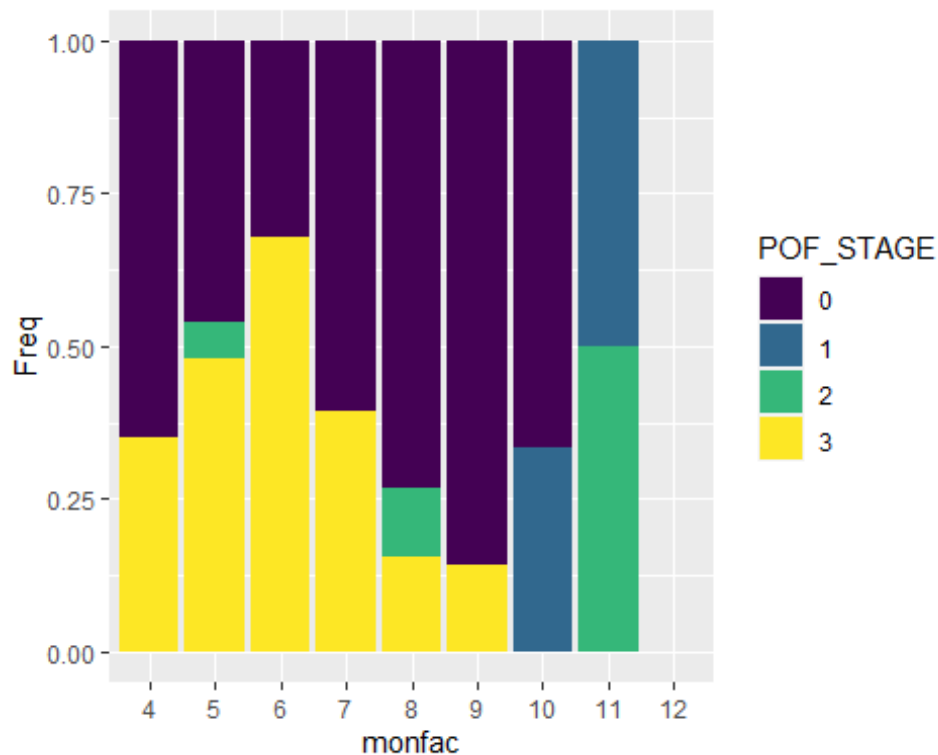
# switch from long to wide format
spread(tabpof2, POF_STAGE, Freq ) %>%
  rename (POF0 = '0', POF1 = '1', POF2 = '2', POF3 = '3')

##   monfac POF0 POF1 POF2 POF3
## 1     4    24     0     0    13
## 2     5    24     0     3    25
## 3     6     9     0     0    19
## 4     7    23     0     0    15
## 5     8    19     0     3     4
## 6     9     6     0     0     1
## 7    10     4     2     0     0
## 8    11     0     1     1     0
## 9    12     0     0     0     0

ggplot(tabpof2, aes(fill=POF_STAGE, y=Freq, x=monfac)) +
  geom_bar(position="fill", stat="identity") +
  scale_fill_viridis_d()

## Warning: Removed 4 rows containing missing values (geom_bar).

```



```

MATmat <- datmat %>%
  filter(MAT01 == 1) %>%
  drop_na(monfac)

```



```

# Calculate sample size for next plot
totals <- MATmat %>%
  group_by(monfac) %>%
  summarize(total = sum(MAT01))

totals

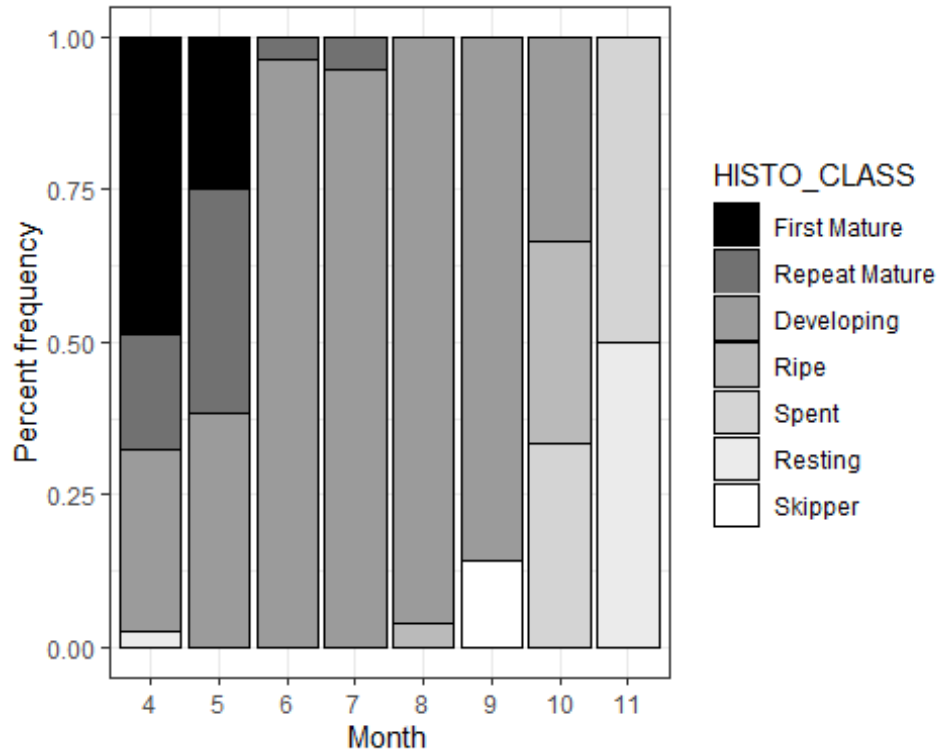
## # A tibble: 8 x 2
##   monfac total
##   <fct> <dbl>
## 1 4      37
## 2 5      52
## 3 6      28
## 4 7      38
## 5 8      26
## 6 9       7
## 7 10     6
## 8 11     2

nrow(MATmat)

## [1] 196

# Plt stacked maturity classes by month
ggplot (data=MATmat) +
  geom_bar (mapping = aes (x=monfac, fill=HISTO_CLASS), position = "fill",
color="black") +
  scale_fill_grey (start=0, end = 1.0, name="HISTO_CLASS",
  labels = c("First Mature", "Repeat Mature", "Developing", "Ripe",
"Spent", "Resting", "Skipper")) +
  # labels = c("FTM", "ED", "LD", "SA", "RGS", "RGT", "X")) +
  labs (x = "Month", y = 'Percent frequency') +
  theme_bw()

```



```
ggsave("WolfFig9.png")
## Saving 5 x 4 in image
```

## Abortive maturation

Before we estimate size and age at female maturity, we call attention to the indications of abortive maturation evident in the assignment of maturity classes based on the histology (See Class ABM in the tables above). During spring, females mature as either primiparous (FTM; first-time spawner) or multiparous (ED; repeat spawner) individuals but some of these primiparous are aborting that advanced cohort, based on evidence of extensive atresia later in the summer or fall.

```
ABM1 <- datmat %>%
  drop_na(MAT01) %>%
  filter(!HISTO_CLASS %in% c("I", "IMA")) %>% # Select ABM and the mature
  classes
  filter(Season == "Spring" | Season == 'Fall')

L_ABM <- ABM1 %>%
  drop_na(Length)

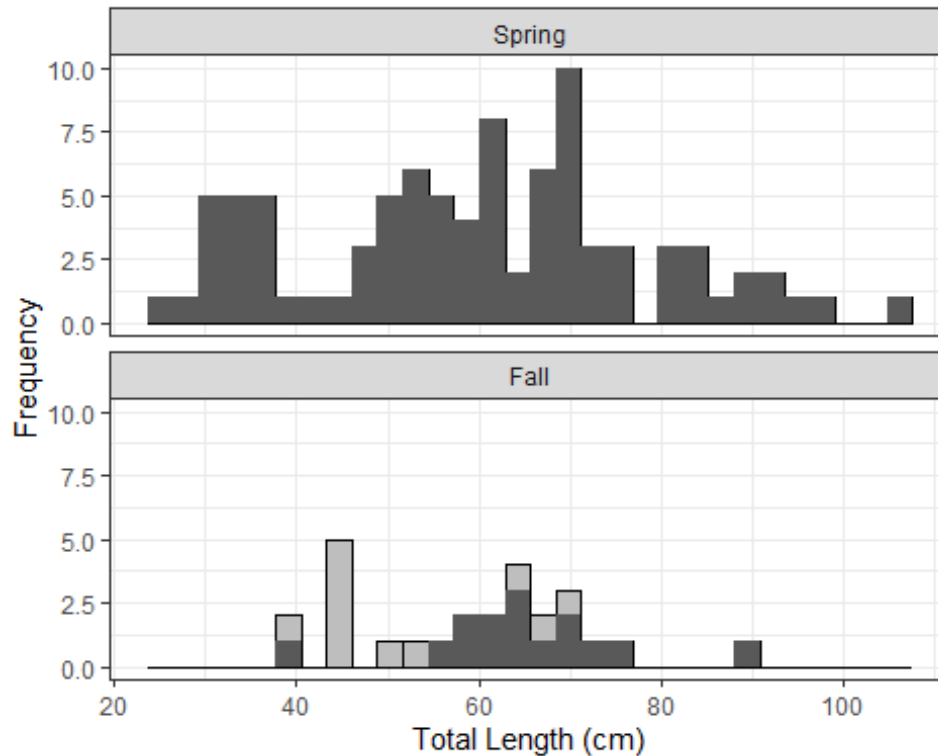
ggplot(L_ABM, aes(x=Length)) +
  geom_histogram(fill = "gray", color="black") +
  geom_histogram(data = subset(L_ABM, MAT01 == 1)) +
```

```

xlab("Total Length (cm)") + ylab("Frequency") +
facet_wrap(~ Season, nrow=2) +
theme_bw()

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

```



```

ggsave("WolfFig10a.png")

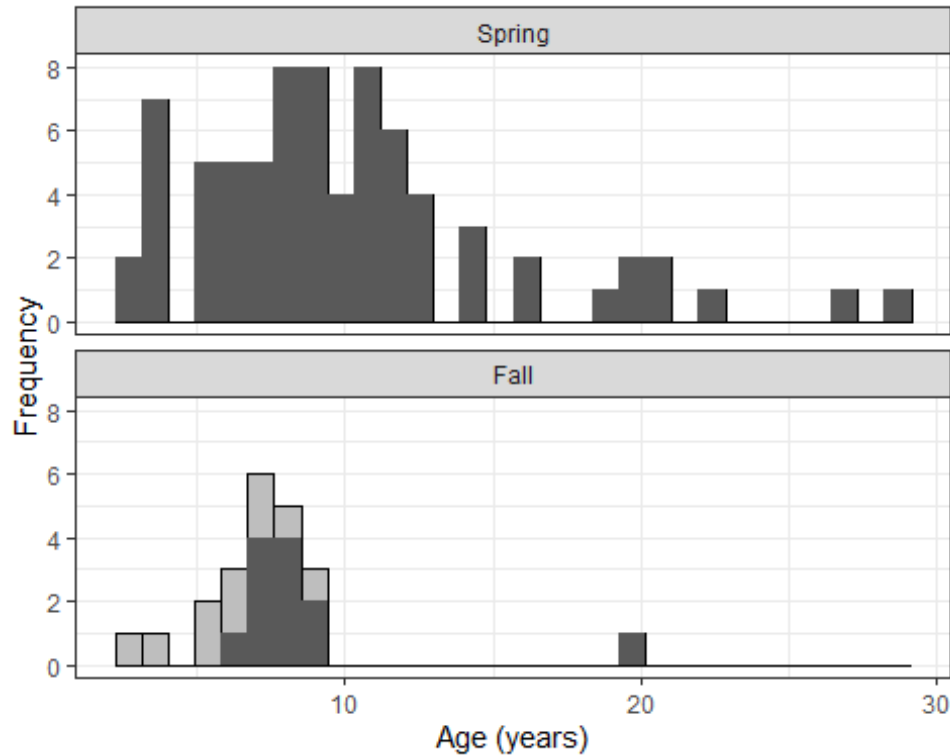
## Saving 5 x 4 in image
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

A_ABM <- ABM1 %>%
  drop_na(Age)

ggplot(A_ABM, aes(x=Age)) +
  geom_histogram(fill = "gray", color="black") +
  geom_histogram(data = subset(A_ABM, MAT01 == 1)) +
  xlab("Age (years)") + ylab("Frequency") +
  facet_wrap(~ Season, nrow=2) +
  theme_bw()

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

```



```
ggsave("WolfFig10b.png")
```

```
## Saving 5 x 4 in image
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Females demonstrating abortive maturation, the lighter shade of gray in the plots, are smaller and younger on average than other mature females. This is not surprising, in that it is consistent with expected energetic constraints (i.e., smaller and younger fish start vitellogenesis but don't have sufficient resources to carry the vitellogenic cohort to ovulation). We see that here:

```
L_ABM$ABMx <-NA
```

```
L_ABM <- L_ABM %>%
```

```
  filter (Season=='Fall') %>%
```

```
  mutate (ABMx = if_else (HISTO_CLASS == 'ABM', "AbortNotMat", "OtherMat"))
```

```
L_ABM %>%
```

```
  group_by (ABMx) %>%
```

```
  summarize(mini = min (Length, na.rm = TRUE),
```

```
            mean = mean (Length, na.rm = TRUE),
```

```
            sd = sd (Length, na.rm = TRUE),
```

```
            maxi = max (Length, na.rm = TRUE),
```

```
            n = n())
```

```

## # A tibble: 2 x 6
##   ABMx      mini mean   sd maxi   n
##   <chr>    <dbl> <dbl> <dbl> <dbl> <int>
## 1 AbortNotMat 39.7  50.9 10.3   69   11
## 2 OtherMat    40.4  64.6 10.6   88   15

A_ABM$ABMx <-NA

A_ABM <- A_ABM %>%
  filter (Season=='Fall') %>%
  mutate (ABMx = if_else (HISTO_CLASS == 'ABM', "AbortNotMat", "OtherMat"))

A_ABM %>%
  group_by (ABMx) %>%
  summarize(mini = min (Age, na.rm = TRUE),
            mean = mean (Age, na.rm = TRUE),
            sd = sd (Age, na.rm = TRUE),
            maxi = max (Age, na.rm = TRUE),
            n = n())

## # A tibble: 2 x 6
##   ABMx      mini mean   sd maxi   n
##   <chr>    <dbl> <dbl> <dbl> <dbl> <int>
## 1 AbortNotMat 3 6 1.83 9 10
## 2 OtherMat    6 8.67 3.68 20 12

kruskal.test(Length ~ ABMx, data = L_ABM)

##
## Kruskal-Wallis rank sum test
##
## data: Length by ABMx
## Kruskal-Wallis chi-squared = 6.6113, df = 1, p-value = 0.01013

kruskal.test(Age ~ ABMx, data = A_ABM)

##
## Kruskal-Wallis rank sum test
##
## data: Age by ABMx
## Kruskal-Wallis chi-squared = 5.846, df = 1, p-value = 0.01561

```

## Size and age at female maturity

We will examine size and age at maturity of the females twice, once with a canned program (sizeMat), which does bootstrapping and has some very nice diagnostics, and a second way to plot a final figure for the publication using some organically written code.

```

library(MASS)
library(car)
library (sizeMat)

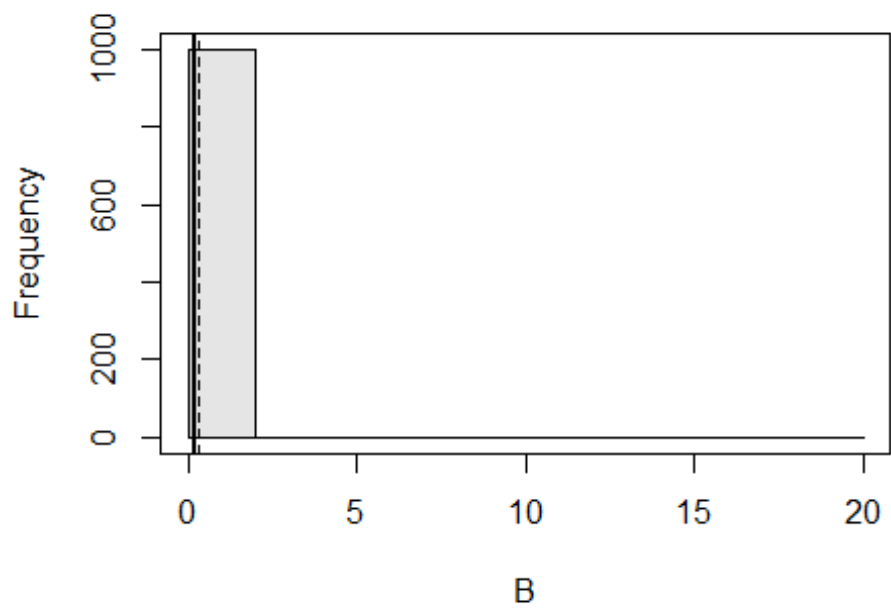
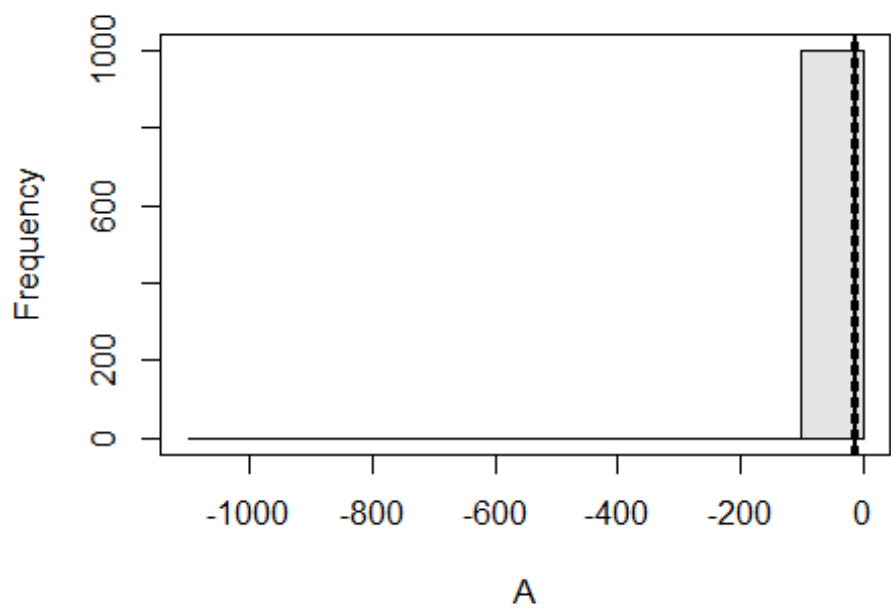
```

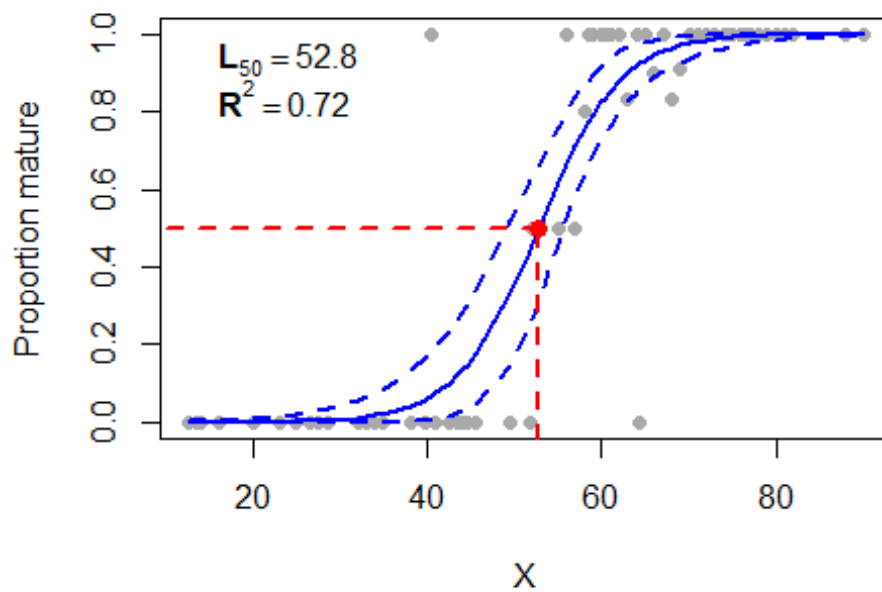
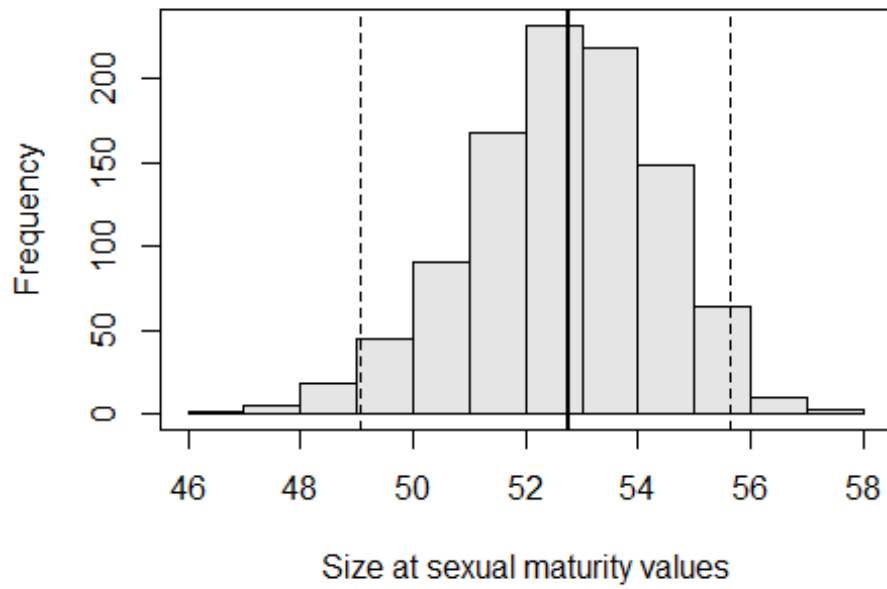
```
# set NA free matrices for both length, age, and maturity status

datmat_L <- datmat %>%
  drop_na(Length) %>% # Select fish with lengths measured
  drop_na(MAT01) %>% # Select fish with maturity (0, 1) assigned
  filter(Season == "Summer" | Season == 'Fall') # Select the period post-
abortive maturation

# quick check with sizeMat, use bootstrap intervals

L_ogive_fq <- gonad_mature(datmat_L, varNames = c("Length", "MAT01"), inmName
= 0, matName = 1, method="fq", niter = 1000)
plot(L_ogive_fq)
```



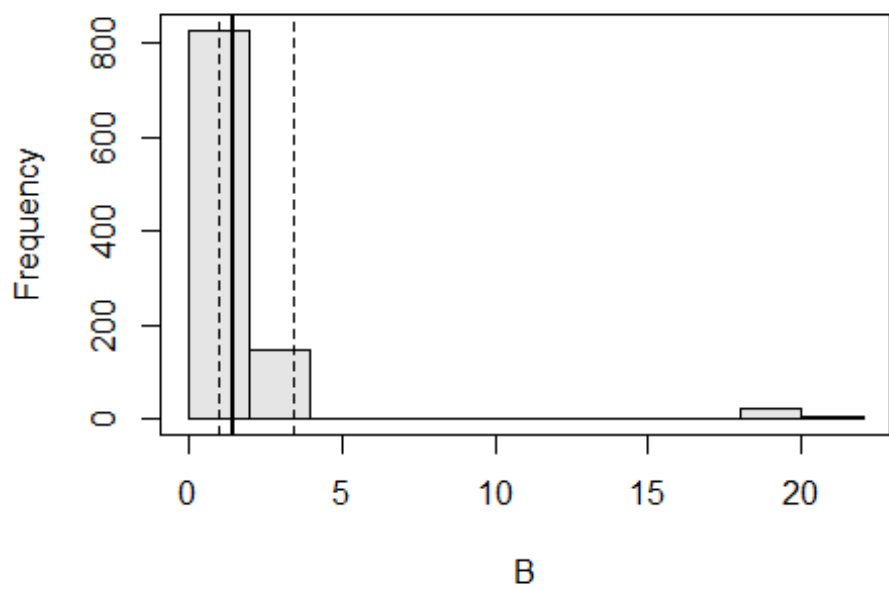
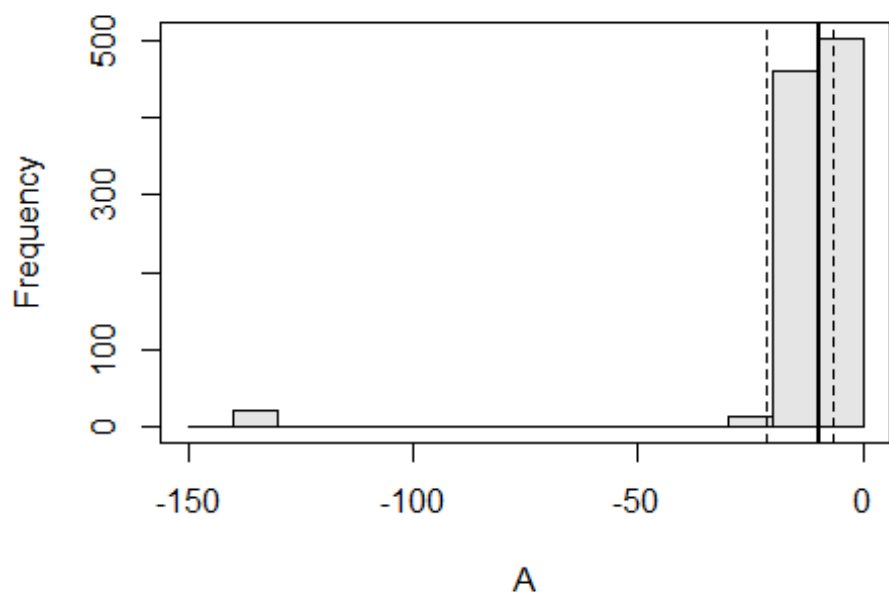


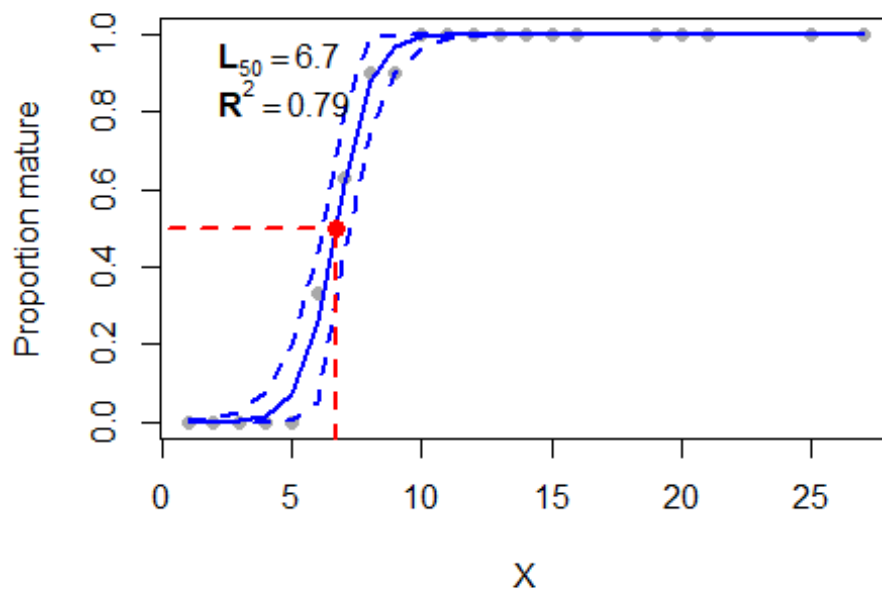
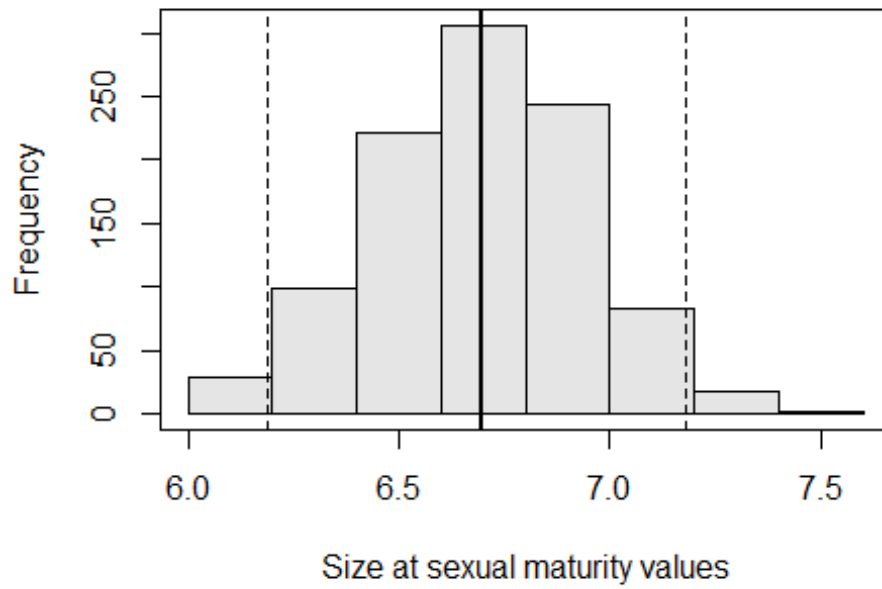
```
## Size at gonad maturity = 52.8
## Confidence intervals = 49.1 - 55.6
## Rsquare = 0.72
```



```
datmat_A <- datmat %>%
  drop_na(Age) %>%
  drop_na(MAT01) %>%
  filter(Season == "Summer" | Season == 'Fall') # Select seasons where
  abortive maturation can be recognized

A_ogive_fq <- gonad_mature(datmat_A, varNames = c("Age", "MAT01"), inmName =
0, matName = 1, method="fq", niter = 1000)
plot(A_ogive_fq)
```





```
## Size at gonad maturity = 6.7
## Confidence intervals = 6.2 - 7.2
## Rsquare = 0.79
```

Here, I want to completely control the format of the image for the publication, so I have redone the plotting and bootstrapping.

*#NB: you need to run the previous check to get the boot strap parameters to roll over to this chunk*

```
par (mfcol=c(2,1))
par(mai = c(0.5, 1.5, 0, 0))
par (las=1)

# Length first, use all data (all months)
maxL <- 120
plotL1 <- 25
plotL2 <- 100
predL <- function(cf,x) exp(cf[1]+cf[2]*x)/(1+exp(cf[1]+cf[2]*x))
lens <- seq(1,maxL,1)

#The Logit model
#fitting and bootstrapping
logitETt <- glm (MAT01 ~ Length, data =datmat_L, family=binomial);
summary (logitETt)

##
## Call:
## glm(formula = MAT01 ~ Length, family = binomial, data = datmat_L)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.63340  -0.02164   0.22705   0.37913   2.29648
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -11.03579     2.31112  -4.775 1.80e-06 ***
## Length       0.20973     0.03936   5.328 9.91e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 164.113  on 143  degrees of freedom
## Residual deviance:  66.488  on 142  degrees of freedom
## AIC: 70.488
##
## Number of Fisher Scoring iterations: 6

BLETt <- matrix (NaN, maxL, 2); bcE <- bootCase(logitETt, B=1000)
for (i in 1:maxL){BLETt[i,] <- as.numeric(quantile(apply(bcE,1,predL,x=i),
c(0.025, 0.975)))}

#   insert plotting for Length here
```

```

pETt <- predict(logitETt,data.frame(Length=lens),type="response")
plot (lens, pETt, type = 'l', col = 1, xlab = '', ylab = '', xlim = c(0,
maxL), ylim = c(0,1), main = "")
  lines (lens, BLETt[,1], type = 'l', col = 4, lty=2, xlab = '', ylab = '',
xlim = c(0, maxL), ylim = c(0,1), main = "")
  lines (lens, BLETt[,2], type = 'l', col = 4, lty=2, xlab = '', ylab =
'', xlim = c(0, maxL), ylim = c(0,1), main = "")

rug ((datmat_L$Length[datmat_L$MAT01==0]))
rug ((datmat_L$Length[datmat_L$MAT01==1]), side=3)
# arrows(67,.85,67,1, col="red")

min (datmat_L$Length)
## [1] 12.5

max (datmat_L$Length)
## [1] 90

MatL.N <- length (datmat_L$Length)
MatL.025 <- signif(quantile(L_ogive_fq$L50_boot, probs = 0.025, na.rm =
TRUE), 3)
MatL.50 <- signif(quantile(L_ogive_fq$L50_boot, probs = 0.5, na.rm =
TRUE), 3)
MatL.975 <- signif(quantile(L_ogive_fq$L50_boot, probs = 0.975, na.rm =
TRUE), 3)

text (20, 0.95, "Maturity at Length (cm)")
text(20, 0.80, bquote(italic(n)==.(MatL.N)))
text (85, 0.3, bquote(italic(L)[50]==.(MatL.50)~cm))
text (85, 0.15, bquote(. (MatL.025)~" - " ~.(MatL.975)~ "cm 95% c.l.))
mtext ("Proportional mature", 2, at = -0.1, line = 3, las = 3)

# Age next, use all data (all months)

par (las=1)
predL <- function(cf,x) exp(cf[1]+cf[2]*x)/(1+exp(cf[1]+cf[2]*x))
lens <- seq(1,20,1)

#The Logit model
#fitting and bootstrapping
logitETt <- glm (MAT01 ~ Age, data =datmat_A, family=binomial); summary
(logitETt)

##
## Call:
## glm(formula = MAT01 ~ Age, family = binomial, data = datmat_A)
##
## Deviance Residuals:

```

```

##      Min      1Q      Median      3Q      Max
## -2.59886 -0.03631  0.03070  0.19642  1.60938
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -9.6096     2.6114  -3.680 0.000233 ***
## Age           1.4391     0.3695   3.895 9.84e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 147.567  on 126  degrees of freedom
## Residual deviance:  47.857  on 125  degrees of freedom
## AIC: 51.857
##
## Number of Fisher Scoring iterations: 8

      BLEtT <- matrix (NaN, 20, 2); bcE <- bootCase(logitETt, B=1000)

      for (i in 1:20){BLEtT[i,] <-
as.numeric(quantile(apply(bcE,1,predL,x=i), c(0.025, 0.975)))}

      #   insert plotting for length here
      pETt <- predict(logitETt,data.frame(Age=lens),type="response")
      plot (lens, pETt, type = 'l', col = 1, xlab = '', ylab = '', xlim =
c(0, 20), ylim = c(0,1), main = "")
      lines (lens, BLEtT[,1], type = 'l', col = 4, lty=2, xlab = '', ylab =
'', xlim = c(0, 20), ylim = c(0,1), main = "")
      lines (lens, BLEtT[,2], type = 'l', col = 4, lty=2, xlab = '', ylab =
'', xlim = c(0, 20), ylim = c(0,1), main = "")

      rug (jitter(datmat_A$Age[datmat_A$MAT01==0]))
      rug (jitter(datmat_A$Age[datmat_A$MAT01==1]), side=3)
      # arrows(67,.85,67,1, col="red")

      min (datmat_A$Age)
## [1] 1

      max (datmat_A$Age)
## [1] 27

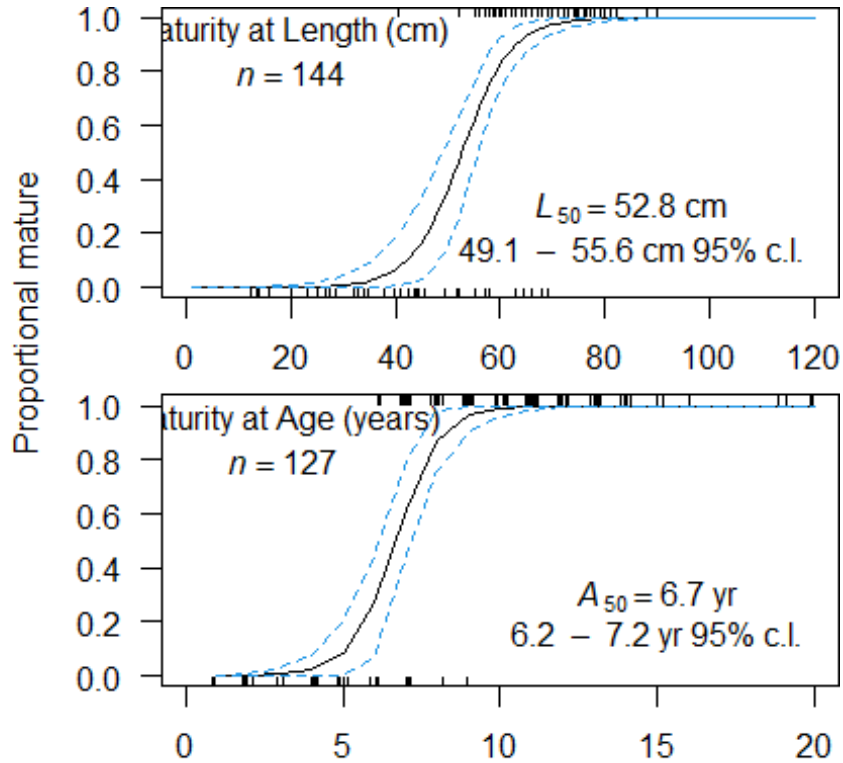
      MatA.N <- length (datmat_A$Age)
      MatA.025 <- signif(quantile(A_ogive_fq$L50_boot, probs = 0.025, na.rm =
TRUE), 2)
      MatA.50 <- signif(quantile(A_ogive_fq$L50_boot, probs = 0.5, na.rm =
TRUE), 2)
      MatA.975 <- signif(quantile(A_ogive_fq$L50_boot, probs = 0.975, na.rm =
TRUE), 2)

```

```

text (3.1, 0.95, "Maturity at Age (years)")
text(3.1, 0.80, bquote(italic(n)==.(MatA.N)))
text (15, 0.3, bquote(italic(A)[50]==.(MatA.50)~yr))
text (15, 0.15, bquote(. (MatA.025)~" - "~.(MatA.975)~ "yr 95% c.l.))

```



*#need to save figure manually*

## Skip spawning

Here we want to check for skippers. We pull the larger complete data set of females lengths and maturity and examine those fish with a thick gonad wall in the months of July-September, which precede the presumed spawning period (October).

```

skip.check <- datmat_L %>%
  filter(MAT01==1) %>%
  filter (MONTH == 7 | MONTH == 8 | MONTH == 9) %>%
  dplyr::select(CollectionDate, TUNICA_MEASUREMENT, Length, MAOS, GSI2,
Age, HISTO_CLASS, MAT01)

nrow(skip.check) # number of mature females in the period July-Sept
## [1] 71

skip.check %>% filter(TUNICA_MEASUREMENT > 250)

```

##	CollectionDate	TUNICA_MEASUREMENT	Length	MAOS	GSI2	Age
HISTO_CLASS						
## 1	<NA>	558	64	V2	0.8016128	7
LD						
## 2	<NA>	585	69	V2	1.3137010	11
LD						
## 3	2017-07-10	521	66	V2	0.5783254	8
LD						
## 4	2017-07-10	617	77	V4	3.9520686	19
LD						
## 5	2017-07-10	666	67	V3	1.8569302	8
LD						
## 6	2017-07-10	548	69	V3	2.7628527	12
LD						
## 7	2017-08-07	617	69	V3	2.9542140	13
LD						
## 8	2017-07-04	986	65	V3	NA	10
LD						
## 9	2017-07-04	617	56	V3	2.0881671	7
LD						
## 10	2017-07-04	617	75	V3	8.1081081	15
LD						
## 11	2017-07-04	959	69	V2	NA	11
LD						
## 12	2017-07-12	1069	66	V3	3.4482759	NA
LD						
## 13	2017-07-12	685	75	V3	4.5751634	13
LD						
## 14	2017-07-12	1165	71	V3	2.7900147	20
LD						
## 15	2017-07-12	891	66	V3	2.3890785	NA
LD						
## 16	2017-09-02	452	65	V4	18.1818182	7
LD						
## 17	2017-09-02	466	58	V4	13.4751773	8
LD						
## 18	2017-09-24	658	67	C3	0.4155125	9
X						
##	MAT01					
## 1	1					
## 2	1					
## 3	1					
## 4	1					
## 5	1					
## 6	1					
## 7	1					
## 8	1					
## 9	1					
## 10	1					
## 11	1					



## 12	1
## 13	1
## 14	1
## 15	1
## 16	1
## 17	1
## 18	1

Selection of a thick gonad wall indicates past maturity. One of these 18 fish, a 9 year old, 67 cm) does not have a cohort of vitellogenic oocytes, so it is not about to spawn in the next spawning event. It also does not have any fresh postovulatory follicles (POFs) which would have indicated that it just finished spawning recently (as POFs are understood to persist for over a year in wolffish). This indicates a skipping rate among repeat spawners at  $1/18 = 5.56\%$ , and among all 35 mature females collected in these months at  $2.86\%$ .

**End**