Streamlined Flathead Sole Analyses & Figures

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Contents

Flathead Sole:

Loading Data:

Flathead sole: both egg and larval data are included for this species. Flathead sole spawn from February to July, live roughly 21 years, and transform to juveniles at standard lengths between 18 to 21 mm.

These data have been trimmed. The egg data are constrained to depths between 54 and 221 meters; temporally, the egg data are constrained to above the 99th day of year and below the 283rd day of the year (temporally centered on the spawning period of flathead sole). The egg data are also joined to regional temperature indices for each year (the reg.sst dataset). The larval data are also constrained to depths between 54 and 221 m, above the 100th day of the year and below the 200th day of the year. Larvae are linked to CTD-derived, *in situ* temperature and salinity measurements. Both eggs and larvae are restricted to latitudes below 61 degrees north.

The regional temperature index data are constrained to (-180, -151) degrees W and (50.5, 67.5) degrees N and reflect the average March temperature for each year across that region. March temperatures are chosen to estimate the conditions spawning flathead sole may have experienced, roughly two months before the peak amount of eggs in the water column occurs.

Descriptive Information:

Table 1: Descriptive Metrics for Flathead Sole Egg Data

Lat Range	Lon Range	Day of Year Range	Bottom Depth Range
53-61	-178.4 to -159.6	100-282	55-220

Table 2: Descriptive Metrics for Flathead Sole Larval Data

Lat Range	Lon Range	Day of Year Range	Bottom Depth Range
53.4-60.3	-178.2 to -159.6	101-183	55-220

The following two plots show *the day of year distribution for positive Flathead sole egg catch* (left) and *the year distribution for positive Flathead sole egg catch* (right). Analogous plots for larval data are following.

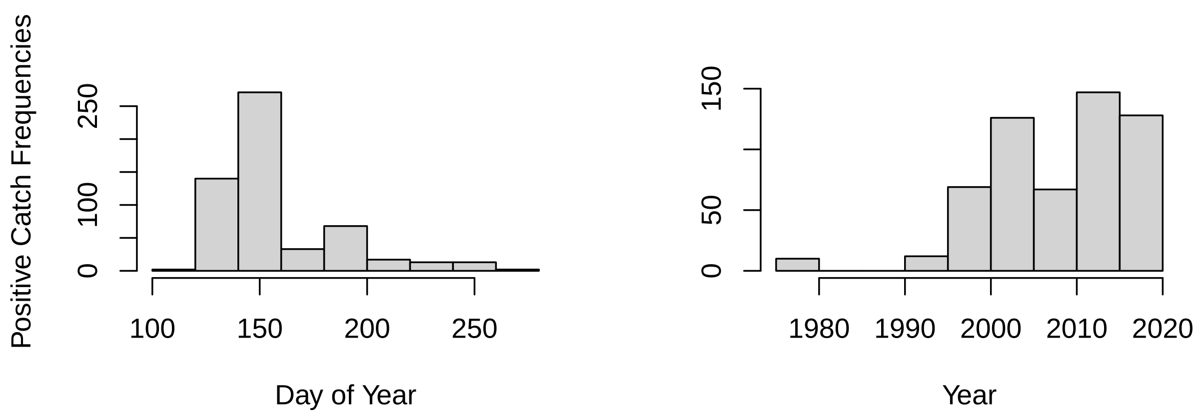


Figure 1: Flathead Sole Eggs

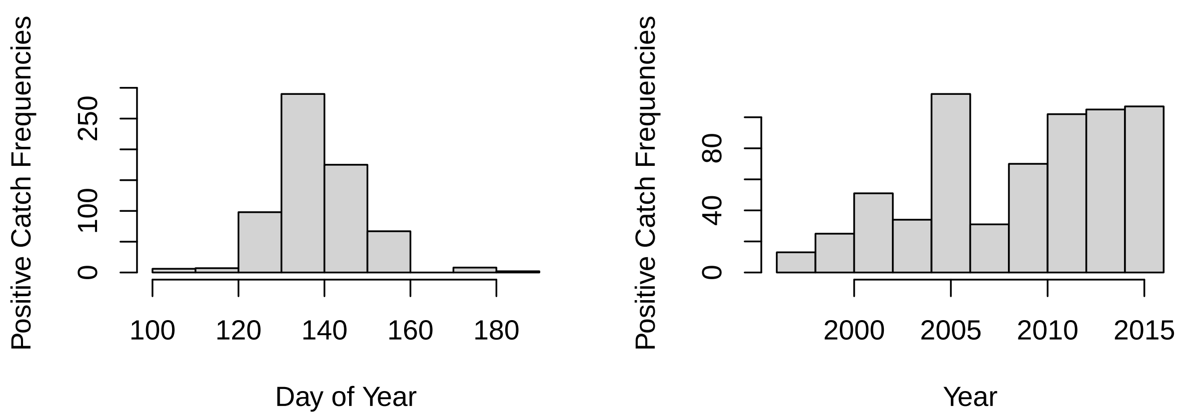


Figure 2: Flathead Sole Larvae

Now we'll move into the GAMs. The following code *is only necessary if the data were re-trimmed and new GAMs need to be run.* In this case, modify markdown document such that "{eval = TRUE}". The other model figures are marked as "eval = FALSE" if they, as of the last model run, do not produce the best model results. **Make sure to save the new models as RDS objects.**

Flathead sole eggs were best explained by the threshold phenology model, in which the temporal distribution of eggs varied differently below and above 2.29 degrees Celsius.

Generalized Additive Models: Flathead Sole Eggs

The base model formulation:

```
eg.base<-readRDS("./GAM Models/fh_egg_base.rds")
summary(eg.base)
```

```
##
## Family: Tweedie(p=1.99)
## Link function: log
##
## Formula:
## (Cper10m2 + 1) ~ factor(year) + s(lon, lat) + s(doy) + s(bottom_depth,
##     k = 5)
##
## Parametric coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -1.0027     0.1606  -6.244 4.79e-10 ***
## factor(year)1988    1.7991     0.2801   6.424 1.51e-10 ***
## factor(year)1991    1.9807     0.2750   7.203 7.21e-13 ***
## factor(year)1993    2.2811     0.3156   7.229 5.99e-13 ***
## factor(year)1994    2.4807     0.2157  11.498  < 2e-16 ***
## factor(year)1995    1.7017     0.1832   9.291  < 2e-16 ***
## factor(year)1996    1.9960     0.3170   6.295 3.46e-10 ***
## factor(year)1997    2.3863     0.2037  11.715  < 2e-16 ***
## factor(year)1998    1.4476     0.3982   3.635 0.000282 ***
## factor(year)1999    1.8234     0.2279   8.001 1.68e-15 ***
## factor(year)2000    2.4810     0.2167  11.447  < 2e-16 ***
## factor(year)2001    2.9597     0.4111   7.200 7.38e-13 ***
## factor(year)2002    3.3842     0.1963  17.243  < 2e-16 ***
## factor(year)2003    3.2020     0.2128  15.049  < 2e-16 ***
## factor(year)2004    1.8269     0.2357   7.750 1.21e-14 ***
## factor(year)2005    3.5258     0.1848  19.079  < 2e-16 ***
## factor(year)2006    2.3856     0.1763  13.532  < 2e-16 ***
## factor(year)2007    1.8878     0.1787  10.566  < 2e-16 ***
## factor(year)2008    1.6110     0.1841   8.752  < 2e-16 ***
## factor(year)2009    1.6182     0.1805   8.964  < 2e-16 ***
## factor(year)2010    1.5910     0.1763   9.025  < 2e-16 ***
## factor(year)2011    1.9551     0.1858  10.522  < 2e-16 ***
## factor(year)2012    1.2361     0.1737   7.116 1.35e-12 ***
## factor(year)2013    1.8796     0.2803   6.706 2.34e-11 ***
## factor(year)2014    2.9302     0.1682  17.419  < 2e-16 ***
## factor(year)2015    2.0992     0.1976  10.625  < 2e-16 ***
## factor(year)2016    3.7805     0.1709  22.117  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                     edf Ref.df       F p-value
## s(lon,lat)       25.800 28.359   7.326  <2e-16 ***
## s(doy)            8.793  8.987 240.588  <2e-16 ***
## s(bottom_depth)   3.554  3.870  10.638  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## R-sq.(adj) =  0.179   Deviance explained = 70.1%
## -REML = 7876.6  Scale est. = 1.1824    n = 3447
```

```
AIC(eg.base)
```

```
## [1] 15707.05
```

The variable-coefficient phenology formulation (in which temporal (phenological) distribution of eggs vary in relation to regional SST indices). This was the second-best performing model for flathead sole egg variation.

```
vc.pheno<-readRDS("./GAM Models/fh_egg_vc_pheno.rds")
summary(vc.pheno)
```

```
##
## Family: Tweedie(p=1.99)
## Link function: log
##
## Formula:
## (Cper10m2 + 1) ~ factor(year) + s(lon, lat) + s(doy) + s(bottom_depth,
##     k = 5) + s(doy, by = reg.SST)
##
## Parametric coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         0.0000     0.0000     NaN      NaN
## factor(year)1988    1.7248     0.2456   7.024 2.60e-12 ***
## factor(year)1991    1.9875     0.2414   8.233 2.57e-16 ***
## factor(year)1993    2.7719     0.2896   9.572  < 2e-16 ***
## factor(year)1994    2.7808     0.1888  14.732  < 2e-16 ***
## factor(year)1995    1.8034     0.1533  11.761  < 2e-16 ***
## factor(year)1996    2.3806     0.3310   7.193 7.78e-13 ***
## factor(year)1997    2.6140     0.1855  14.093  < 2e-16 ***
## factor(year)1998    2.6578     0.4482   5.930 3.33e-09 ***
## factor(year)1999    1.7866     0.1948   9.173  < 2e-16 ***
## factor(year)2000    2.5138     0.1887  13.320  < 2e-16 ***
## factor(year)2001    3.3977     0.4053   8.383  < 2e-16 ***
## factor(year)2002    3.2767     0.1781  18.397  < 2e-16 ***
## factor(year)2003    3.0070     0.2164  13.896  < 2e-16 ***
## factor(year)2004    2.5170     0.2262  11.128  < 2e-16 ***
## factor(year)2005    3.3568     0.1933  17.367  < 2e-16 ***
## factor(year)2006    2.8134     0.1644  17.114  < 2e-16 ***
## factor(year)2007    1.8101     0.1455  12.438  < 2e-16 ***
## factor(year)2008    1.1785     0.1336   8.823  < 2e-16 ***
## factor(year)2009    1.5273     0.1462  10.444  < 2e-16 ***
## factor(year)2010    1.2986     0.1277  10.172  < 2e-16 ***
## factor(year)2011    2.4310     0.1711  14.212  < 2e-16 ***
## factor(year)2012    0.9773     0.1113   8.785  < 2e-16 ***
## factor(year)2013    1.8018     0.2397   7.516 7.20e-14 ***
## factor(year)2014    2.9196     0.1532  19.055  < 2e-16 ***
## factor(year)2015    3.4918     0.2134  16.365  < 2e-16 ***
## factor(year)2016    3.4871     0.1732  20.128  < 2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                     edf Ref.df       F p-value
## s(lon,lat)       26.068 28.457   7.632  <2e-16 ***
## s(doy)            7.668  8.336  69.094  <2e-16 ***
## s(bottom_depth)   3.602  3.895  12.200  <2e-16 ***
## s(doy):reg.SST    9.122  9.567 123.714  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Rank: 78/79
## R-sq.(adj) =  0.203   Deviance explained = 75.9%
## -REML = 7477.2  Scale est. = 0.98083   n = 3447
```

```
AIC(vc.pheno)
```

```
## [1] 14852.47
```

The threshold phenology model formulation (in which the temporal (phenological) distribution of eggs vary differently above and below a threshold temperature. *This is the best model to explain Flathead sole egg variation across years, as of 1/10/2021.*

```
aic.pheno<-NA*(temps.in)
thr.pheno<-as.list(1:(length(temps.in)))

for(i in 1:length(temps.in)){
  fhsub$th<-factor(fhsub$reg.SST<=temps.in[i])
  thr.pheno[[i]]<-gam((Cper10m2+1)~factor(year)+
                        s(lon,lat)+
                        s(bottom_depth,k=5)+
                        s(doy,by=th),
                      data=fhsub,family=tw(link='log'),method='REML')
  aic.pheno[i]<-AIC(thr.pheno[[i]])
}

best.index.phe<-order(aic.pheno)[1]
thr.pheno<-thr.pheno[[best.index.phe]]
```

```
summary(thr.pheno)
```

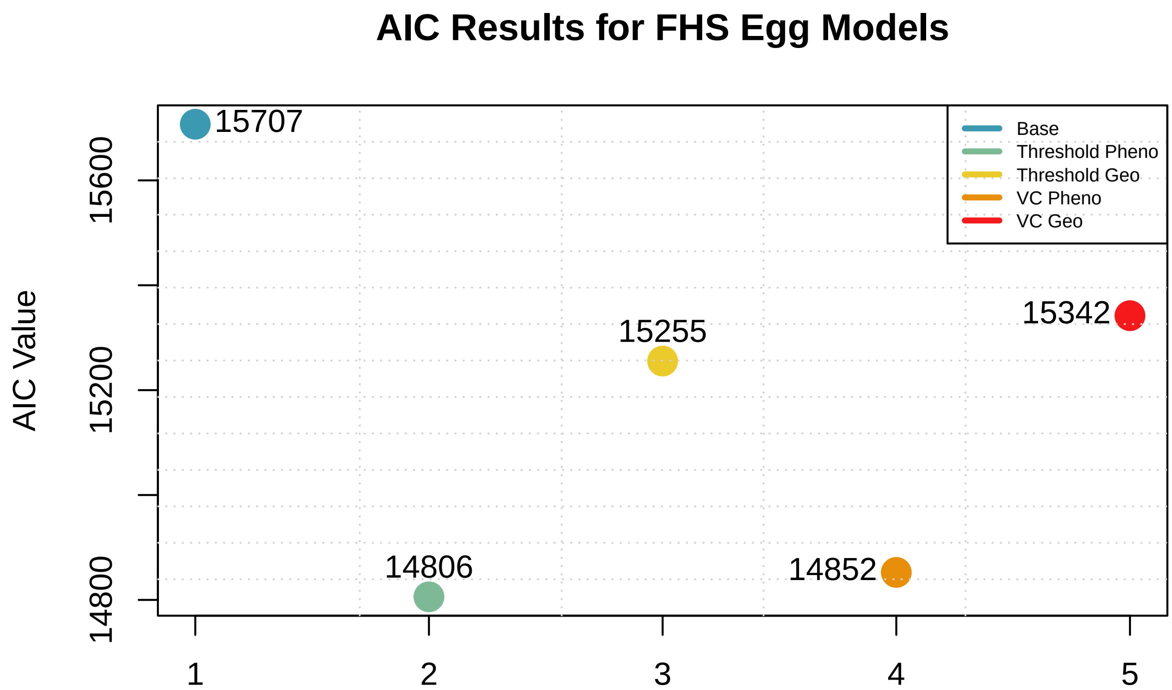
```
##
## Family: Tweedie(p=1.99)
## Link function: log
##
## Formula:
## (Cper10m2 + 1) ~ factor(year) + s(lon, lat) + s(bottom_depth,
##     k = 5) + s(doy, by = th)
##
## Parametric coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         -0.9655     0.1569  -6.152 8.52e-10 ***
```

```
## factor(year)1988   1.5372     0.2614   5.880 4.50e-09 ***
## factor(year)1991   1.5886     0.2579   6.159 8.18e-10 ***
## factor(year)1993   1.9031     0.2918   6.523 7.93e-11 ***
## factor(year)1994   1.9054     0.2048   9.303  < 2e-16 ***
## factor(year)1995   1.7115     0.1758   9.735  < 2e-16 ***
## factor(year)1996   1.6320     0.3090   5.281 1.37e-07 ***
## factor(year)1997   2.5309     0.1953  12.960  < 2e-16 ***
## factor(year)1998   1.3295     0.4858   2.737  0.00624 **
## factor(year)1999   1.8165     0.2155   8.429  < 2e-16 ***
## factor(year)2000   1.7940     0.2117   8.473  < 2e-16 ***
## factor(year)2001   2.9755     0.3983   7.470 1.02e-13 ***
## factor(year)2002   2.7133     0.1905  14.241  < 2e-16 ***
## factor(year)2003   2.4997     0.2050  12.193  < 2e-16 ***
## factor(year)2004   2.1995     0.2270   9.689  < 2e-16 ***
## factor(year)2005   2.9392     0.1808  16.252  < 2e-16 ***
## factor(year)2006   2.5640     0.1699  15.089  < 2e-16 ***
## factor(year)2007   1.4266     0.1724   8.274  < 2e-16 ***
## factor(year)2008   1.1653     0.1765   6.601 4.71e-11 ***
## factor(year)2009   1.1551     0.1744   6.624 4.05e-11 ***
## factor(year)2010   1.1925     0.1708   6.982 3.50e-12 ***
## factor(year)2011   2.2509     0.1793  12.555  < 2e-16 ***
## factor(year)2012   1.0735     0.1691   6.349 2.46e-10 ***
## factor(year)2013   1.5798     0.2625   6.018 1.95e-09 ***
## factor(year)2014   2.4708     0.1633  15.126  < 2e-16 ***
## factor(year)2015   2.5614     0.1898  13.497  < 2e-16 ***
## factor(year)2016   3.2820     0.1656  19.818  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                     edf Ref.df       F p-value
## s(lon,lat)       26.279 28.528   7.816  <2e-16 ***
## s(bottom_depth)   3.572  3.881  13.288  <2e-16 ***
## s(doy):thFALSE    8.818  8.990 409.768  <2e-16 ***
## s(doy):thTRUE     8.300  8.854  54.858  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =    0.2   Deviance explained = 76.2%
## -REML = 7453.3  Scale est. = 0.97022   n = 3447
```

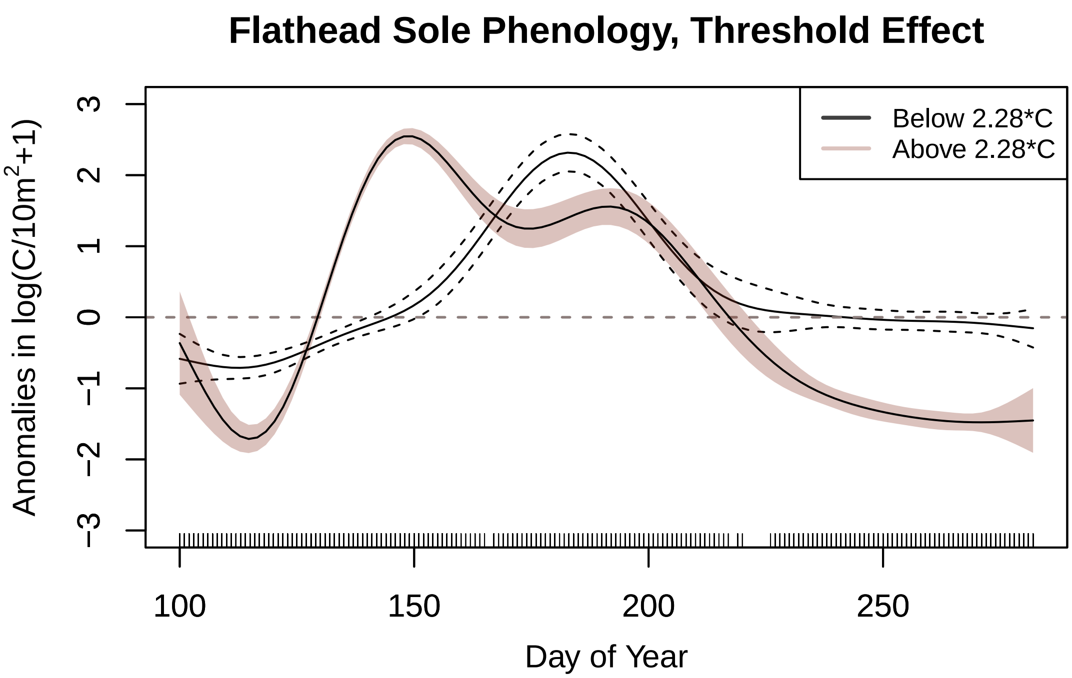
```
AIC(thr.pheno)
```

```
## [1] 14805.92
```

To confirm that the threshold phenology model is indeed the best model, we can compare AIC values across all five tested models.



This is the below threshold (2.29 deg C) and above threshold temporal distribution of flathead eggs (based on the threshold phenology model).



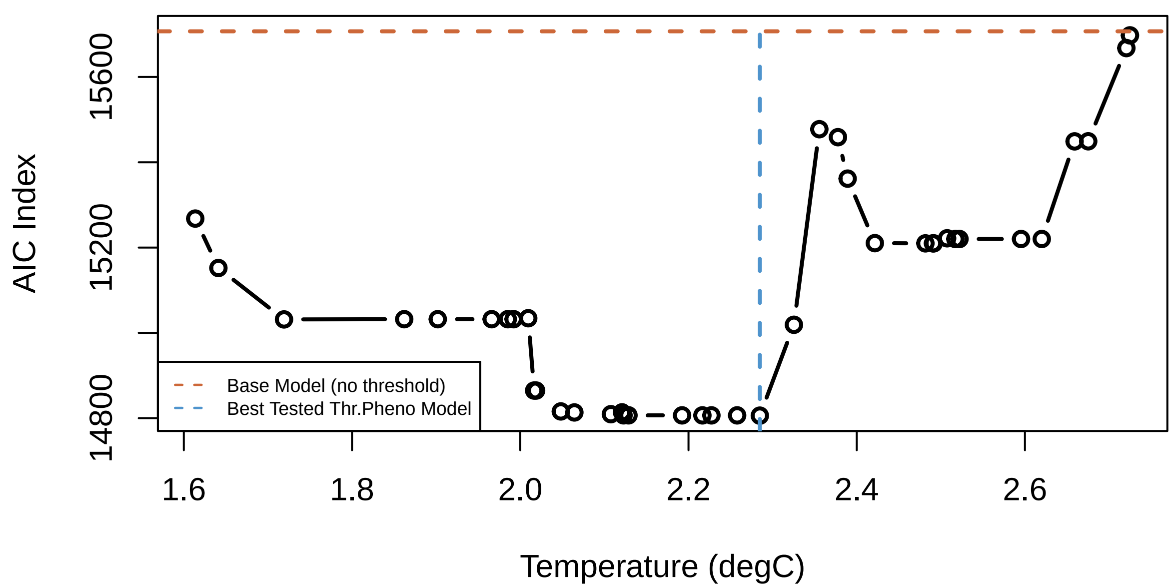
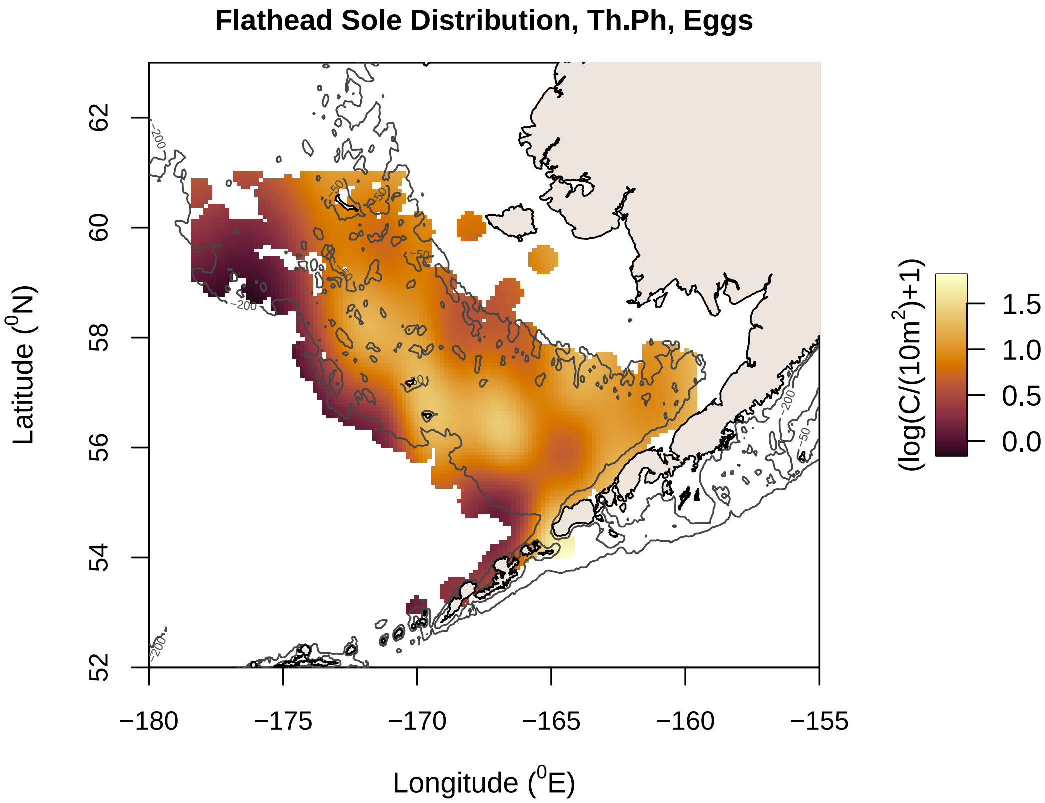
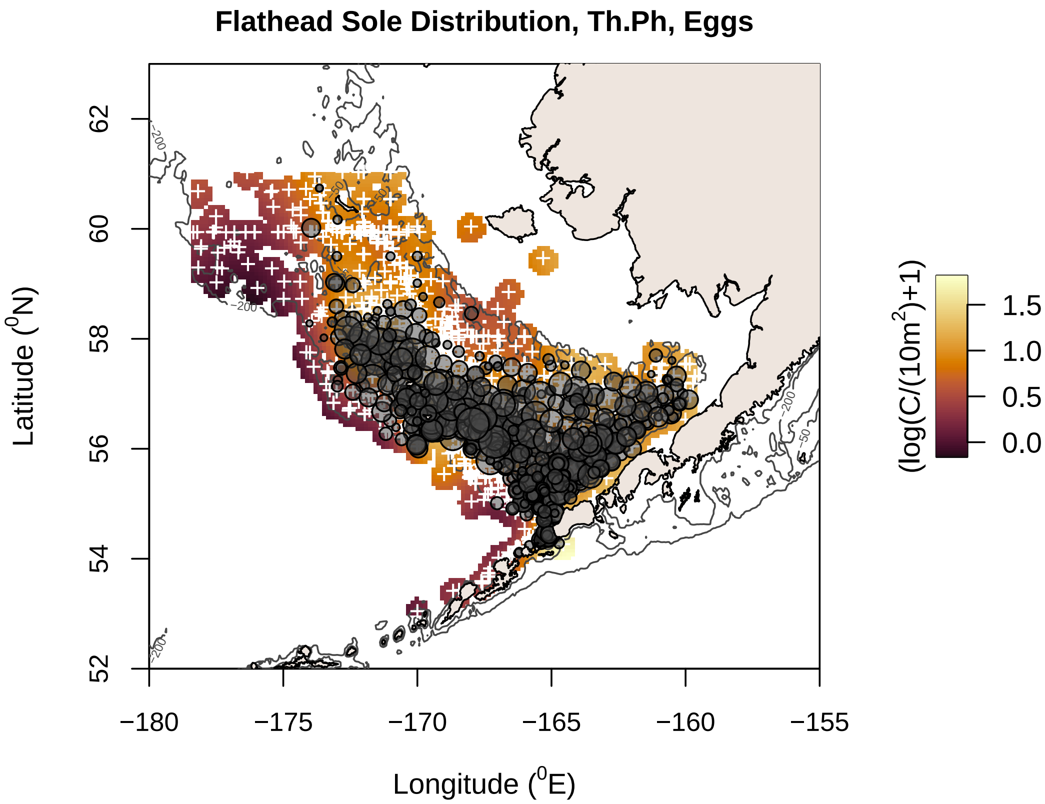


Figure 3: Thr. Pheno AIC scores across varying threshold temperatures, Flathead Sole.

With the threshold phenology model, we can model the spatial distribution of flathead sole eggs through predictions based on this model. Observed, log-transformed (n+1) egg catches are displayed as well.


Flathead Sole Distribution, Th.Ph, Eggs
Latitude (⁰N)
Longitude (⁰E)
(log(C/(10m²)+1)
62
60
58
56
54
52
−180
−175
−170
−165
−160
−155
1.5
1.0
0.5
0.0


Flathead Sole Distribution, Th.Ph, Eggs
Latitude (⁰N)
Longitude (⁰E)
(log(C/(10m²)+1)
62
60
58
56
54
52
−180
−175
−170
−165
−160
−155
1.5
1.0
0.5
0.0

Larval Generalized Additive Models:

The following code *is only necessary if the data were re-trimmed and new GAMs need to be run.* In this case, modify markdown document such that "{eval = TRUE}". The other model figures are marked as "eval = FALSE" if they, as of the last model run, do not produce the best model results. These models are produced using conductivity-temperature-depth derived temperature and salinity measurements.

We begin with the base larval model:

Then additive temperature and salinity, in individual additive terms. This is the second-best performing model.

And finally, the best performing model: the bivariate salinity-temperature additive term:

```r
lv.2d<-readRDS("./GAM Models/fh_larv_2d.rds")
summary(lv.2d)
```

```
##
## Family: Tweedie(p=1.99)
## Link function: log
##
## Formula:
## (Cper10m2 + 1) ~ factor(year) + s(lon, lat) + s(doy, k = 7) +
##     s(bottom_depth) + s(salinity, temperature)
##
## Parametric coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.35086    0.34796   6.756 2.23e-11 ***
## factor(year)1998 -0.06278    0.91972  -0.068  0.94559
## factor(year)1999  0.02095    0.60686   0.035  0.97247
## factor(year)2000  1.33299    0.49144   2.712  0.00678 **
## factor(year)2002  2.66686    0.43644   6.111 1.35e-09 ***
## factor(year)2003  1.15266    0.45750   2.519  0.01189 *
## factor(year)2005  1.35807    0.42557   3.191  0.00145 **
## factor(year)2006  1.81173    0.38205   4.742 2.38e-06 ***
## factor(year)2007  0.21601    0.42804   0.505  0.61390
## factor(year)2008  0.34178    0.55110   0.620  0.53527
## factor(year)2009 -1.67759    0.38795  -4.324 1.66e-05 ***
## factor(year)2010 -0.08302    0.36819  -0.225  0.82164
## factor(year)2011  0.01925    0.50175   0.038  0.96940
## factor(year)2012  1.01807    0.39671   2.566  0.01040 *
## factor(year)2013 -0.40018    0.45712  -0.875  0.38151
## factor(year)2014  0.19594    0.39504   0.496  0.61998
## factor(year)2015 -0.52105    0.45027  -1.157  0.24744
## factor(year)2016  0.89360    0.44094   2.027  0.04293 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                             edf Ref.df      F p-value
## s(lon,lat)               24.817 27.902  9.750  <2e-16 ***
## s(doy)                    4.503  5.193 23.192  <2e-16 ***
## s(bottom_depth)           7.225  8.171 18.246  <2e-16 ***
## s(salinity,temperature)  25.076 28.028  8.983  <2e-16 ***
## ---
```

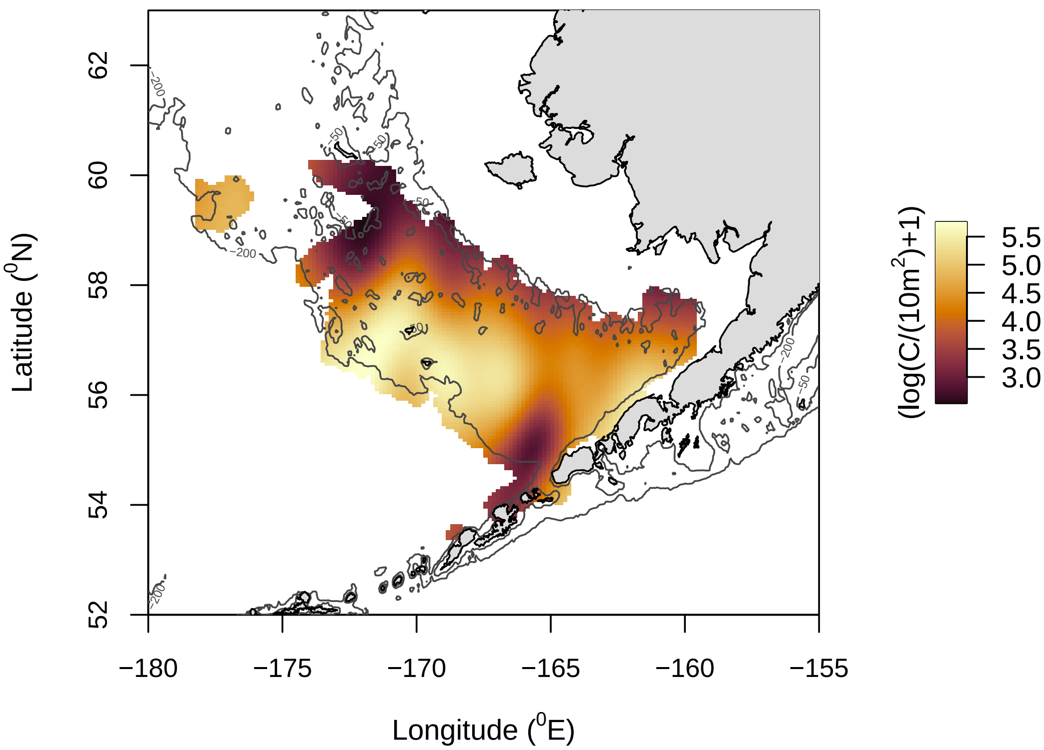
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.159   Deviance explained = 61.8%
## -REML = 5041.6  Scale est. = 1.6702    n = 1244
```

```
AIC(lv.2d)
```

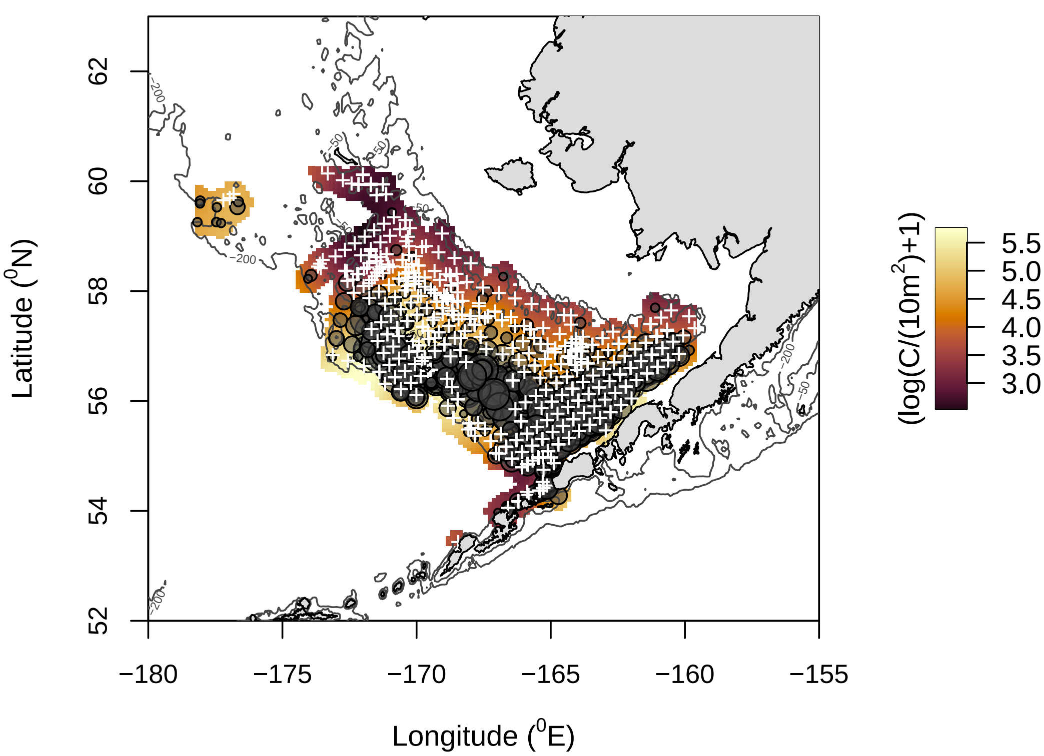
```
## [1] 10019.28
```

The following plot is the predicted Flathead sole larval biogeography based on the best performing model, the bivariate salinity-temperature GAM. Observations (log transformed, n+1) are shown as well.

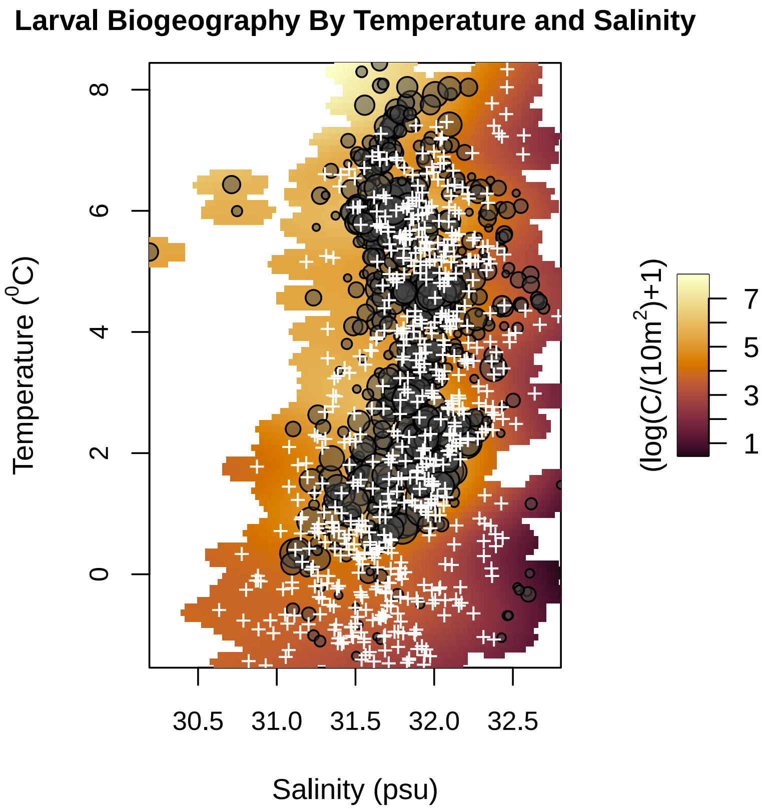
Predicted FHS Larval Biogeography, 2D Model



Predicted FHS Larval Biogeography, 2D Model



With this bivariate model, we can also calculate the predicted anomalous larval catch (more or less than expected) on a salinity-temperature plot. This figure shows that prediction, with observed larval catch (log(n=1)) overlaid.


Larval Biogeography By Temperature and Salinity
Temperature (⁰C)
8
6
4
2
0
30.5
31.0
31.5
32.0
32.5
Salinity (psu)
(log(C/(10m²)+1)
7
5
3
1

To again share the improvements of the best performing models from the base models, we can look at the AIC division produces.

Table 3: Model Power through AIC Comparisons, Flathead Sole

	Best Divided By Base	Best Divided By Second Best
Eggs	0.9712500	0.9943591
Larvae	0.9811238	0.9941747