

Streamlined Alaska Plaice Analyses & Figures

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Purpose of This Document:

The purpose of this document is to streamline files and associated analyses for the creation of generalized additive models that investigate spawning behavior and larval biogeography among fishes in the Bering Sea. This is mainly an automation document, with the goal of minimizing the back-and-forth between code files should data need to be modified or analyses re-ran.

Loading Data:

Alaska plaice: both egg and larval data are included for this species. Plaice spawn during April and May, live over 30 years, and transform to juveniles at standard lengths \geq to 10.7 mm.

```
apsub<-read.csv(file='./Ichthyo Data/Cleaned_Cut_ApEggs.csv',header=TRUE,
                 check.names=TRUE)
aplarv.ctd<-read.csv(file='./Ichthyo Data/Cleaned_Cut_ApLarv_wCTD.csv',
                      header=TRUE,check.names=TRUE)
aplarv.ctd<-subset(aplarv.ctd,doy>80&doy<182)

reg.sst<-read.csv('./Environmental Data/Mar_SST_RegionalIndex_NCEP_BS.csv',
                   header=TRUE,check.names=TRUE)

str_name<-'./Environmental Data/expanded_BS_bathy.tif'
bathy<-raster(str_name)
```

These data have been trimmed. The egg data are constrained to depths < 151 meters; temporally, the egg data are constrained to above the 99th day of year and below the 182nd day of the year (temporally centered on the spawning period of plaice). The egg data are also joined to regional temperature indices for each year (the reg.sst dataset). The larval data are constrained to depths < 151 meters, between 80 and 165 day of year, and are linked to CTD-derived, *in situ* temperature and salinity measurements.

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 plaice may have experienced, roughly two months before eggs appear in the water column.

##Descriptive Information: Alaska Plaice

Table 1: Descriptive Metrics for Alaska Plaice Egg Data

Lat Range	Lon Range	Day of Year Range	Bottom Depth Range
53.4-62.6	-178.4 to -158.2	100-181	0-150

Table 2: Descriptive Metrics for Alaska Plaice Larval Data

Lat Range	Lon Range	Day of Year Range	Bottom Depth Range
53.4-60.3	-176.8 to -158.2	99-180	23-150

The following three plots show *the day of year distribution for positive plaice egg catch, the year distribution for positive plaice egg catch*.

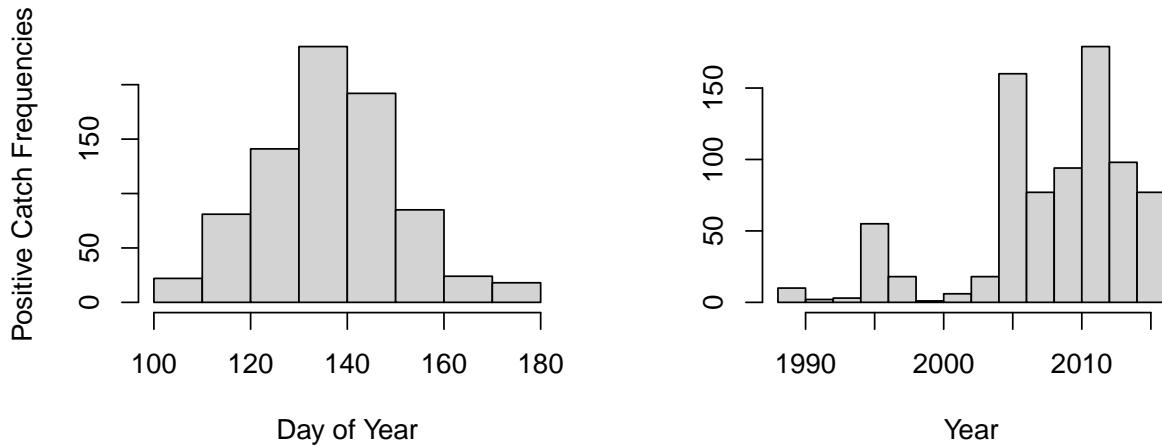
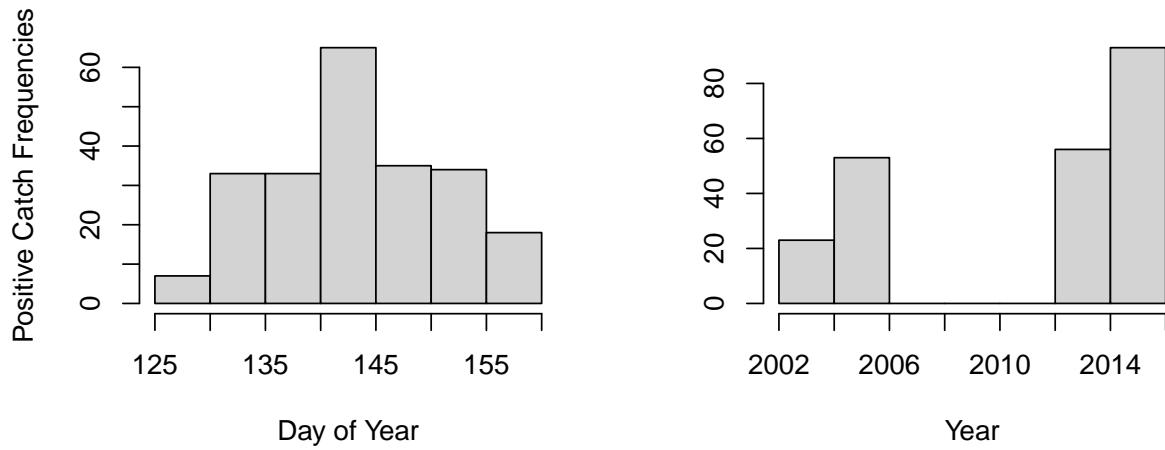


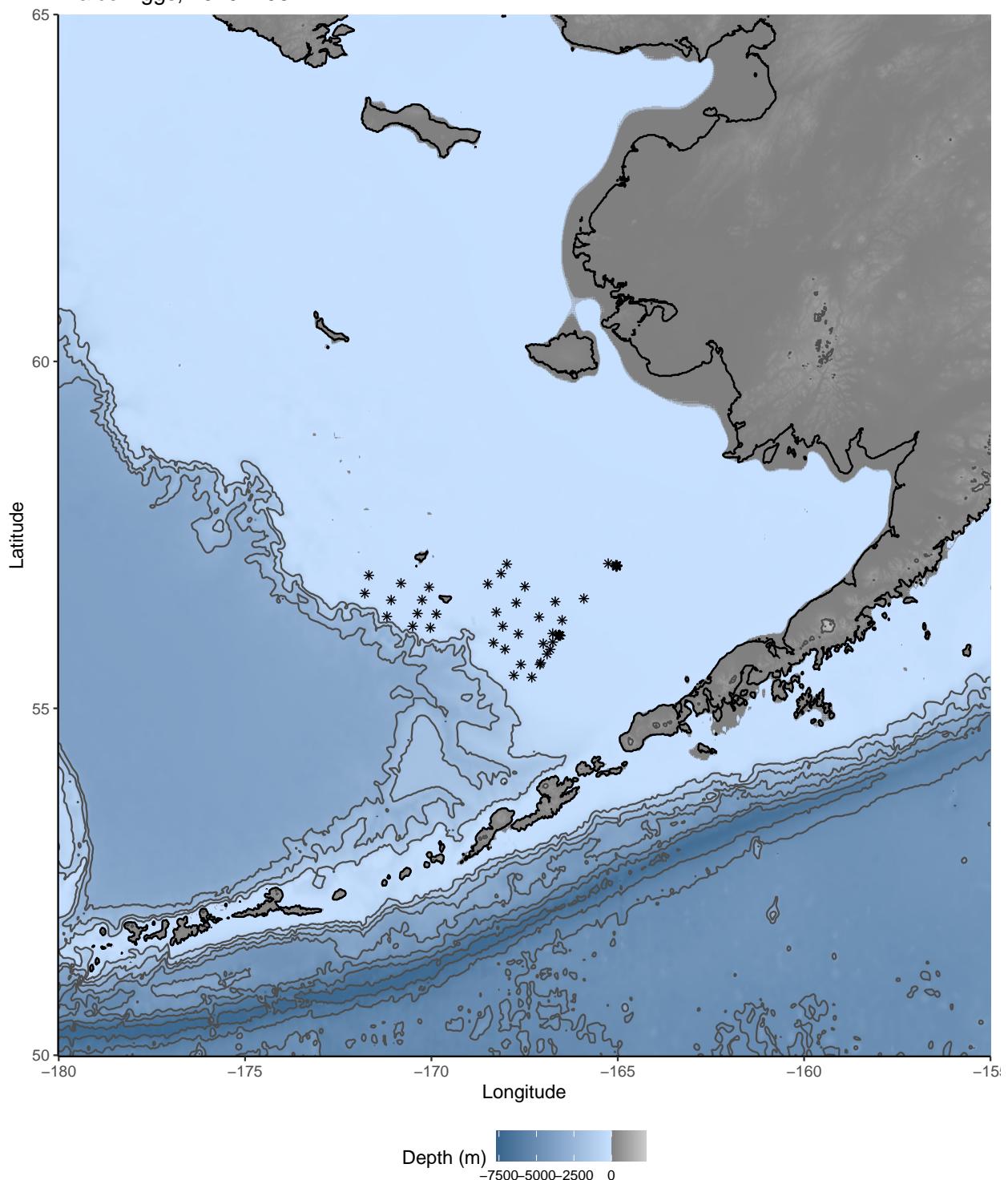
Figure 1: Alaska Plaice Eggs

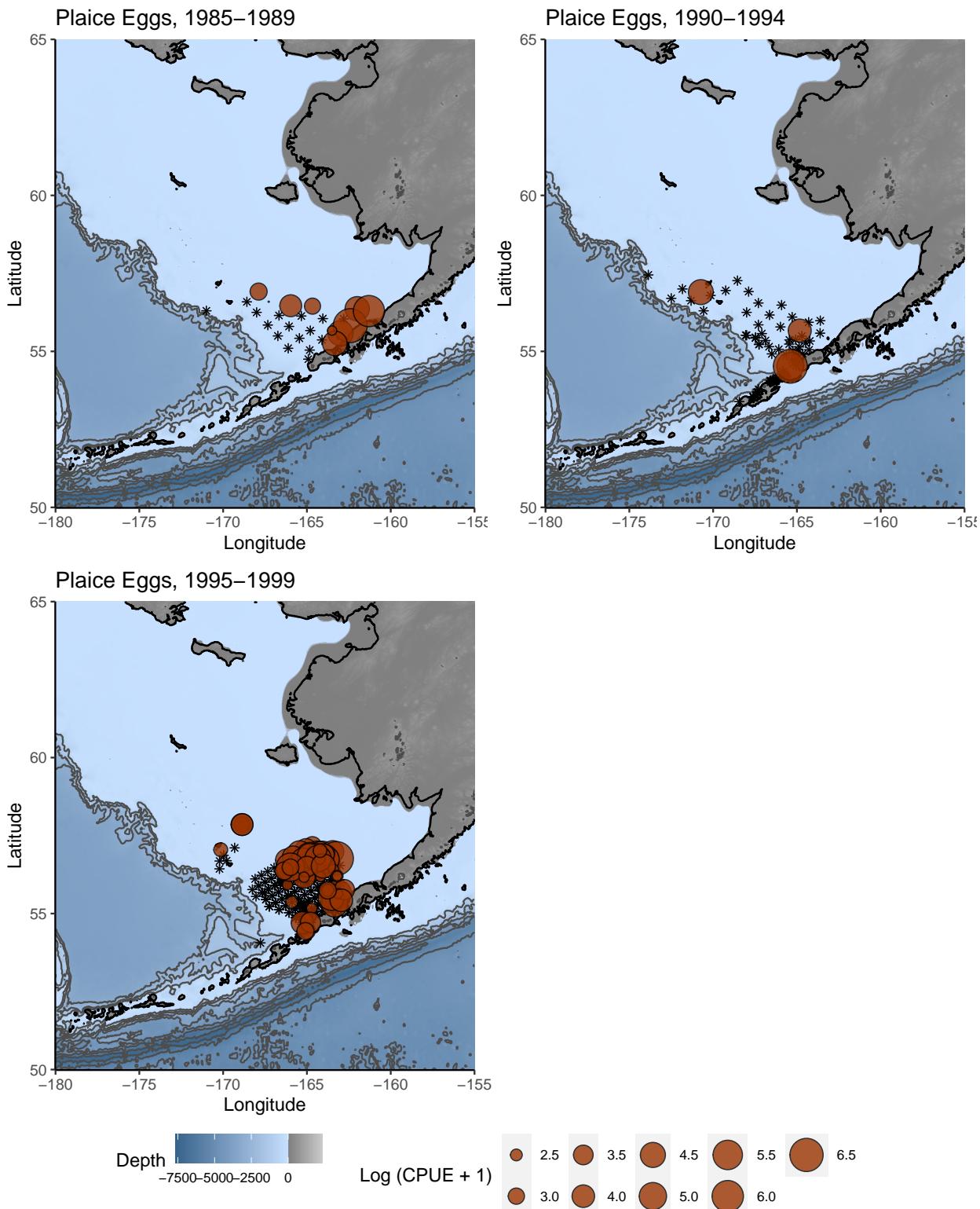
The following three plots show *the day of year distribution for positive plaice larval catch, the year distribution for positive plaice larval catch*.

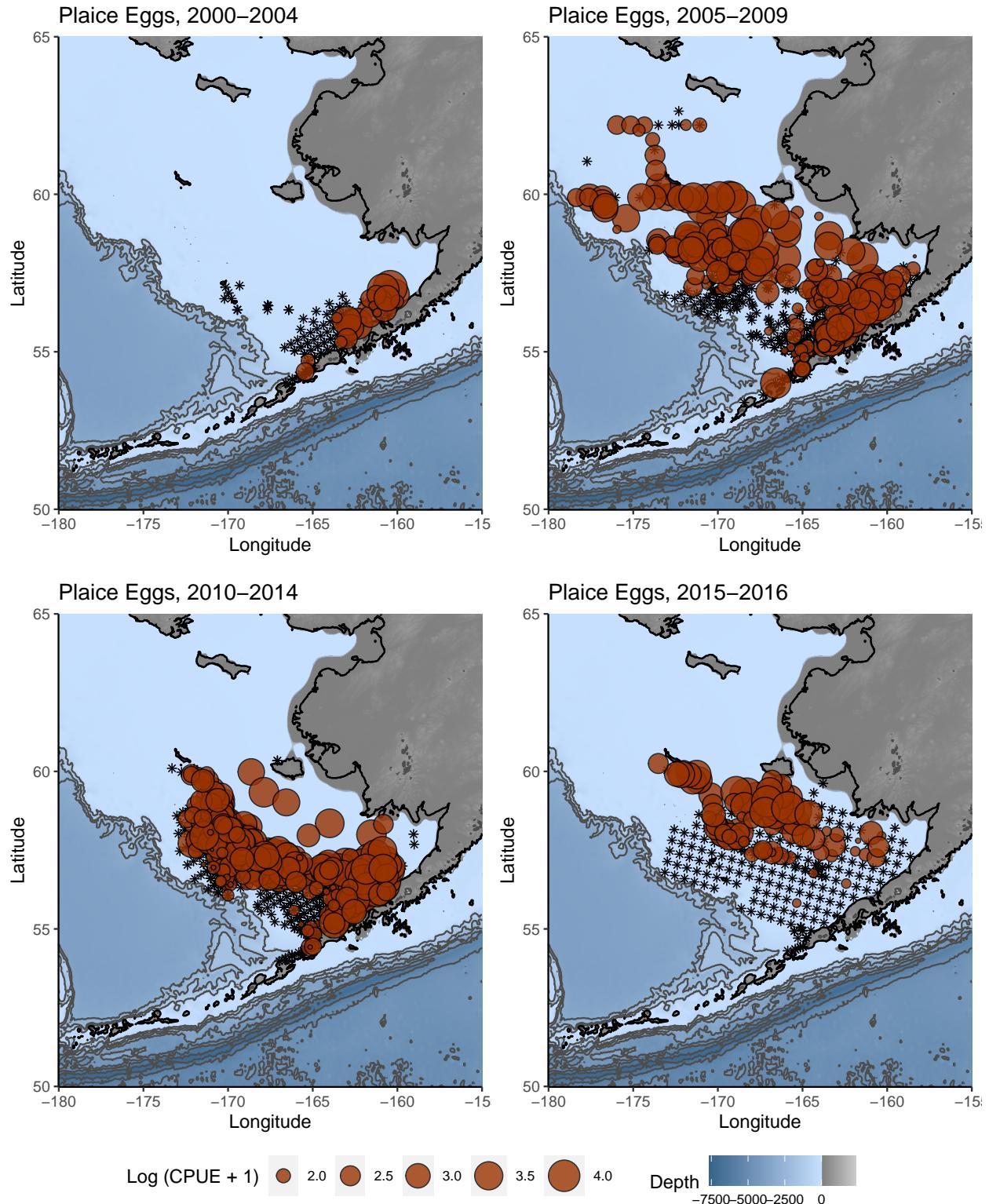


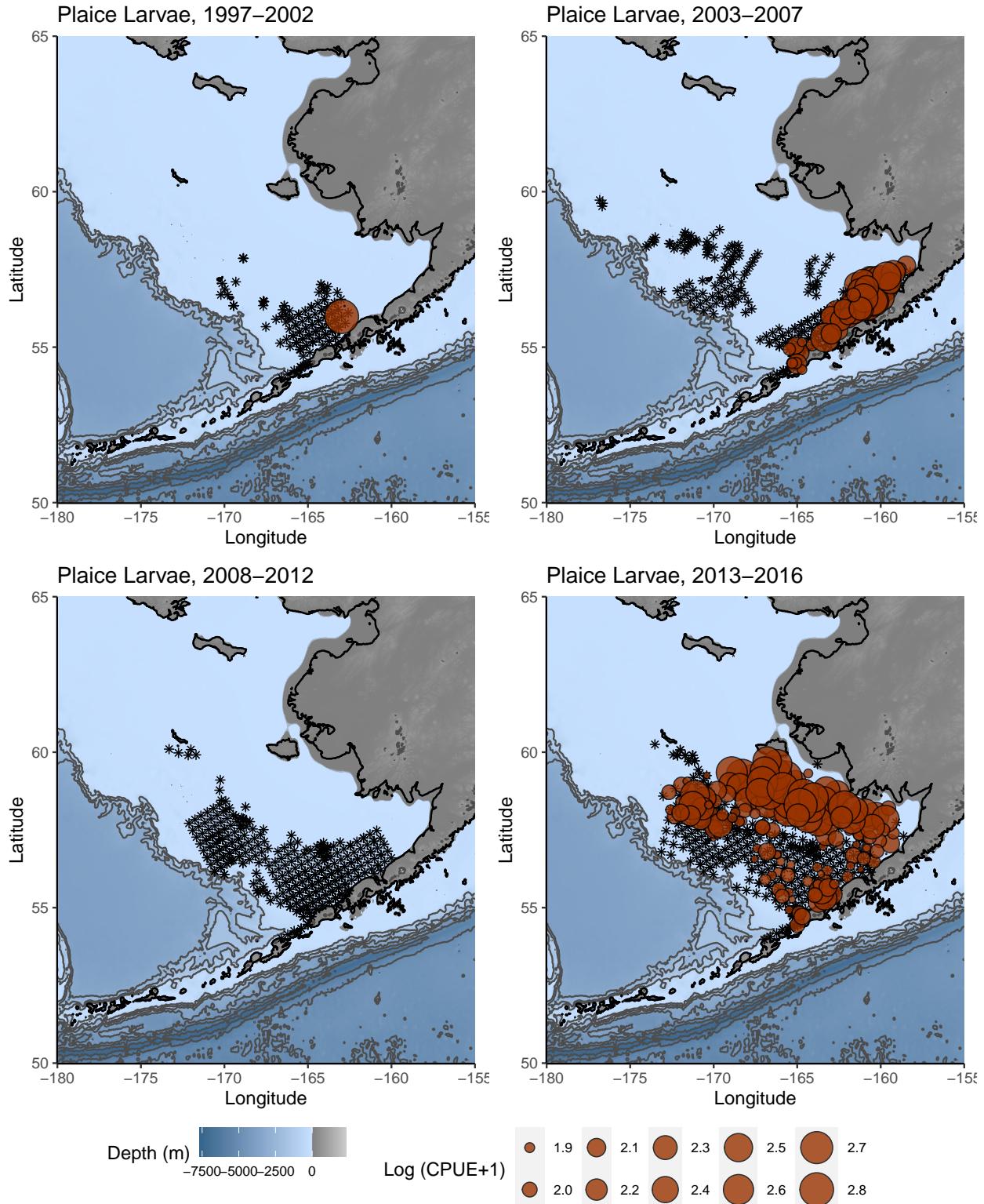
The following plots show Plaice egg and larval catch distributions (Catch per unit effort, or per 10m²) across five year increments from 1979 to 2016.

Plaice Eggs, 1979–1984









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.**

Alaska plaice eggs were best explained by the threshold geography model, in which geographic distribution of eggs varied differently below and above 2.12 degrees Celsius.

Generalized Additive Models: Alaska Plaice Eggs

The base model formulation:

```
eg.base<-gam((Cper10m2+1)~factor(year)+s(lon,lat)+s(doy)+s(bottom_depth,k=5),
               data=apsub,family=tw(link='log'),method='REML')

plot(eg.base,shade=FALSE,page=1,seWithMean=TRUE,scheme=2,scale=0)

saveRDS(eg.base,file='./GAM Models/ap_egg_base.rds')
```

The variable-coefficient geography formulation (in which geographic egg distributions vary differently in relation to regional SST indices).

The variable-coefficient phenology formulation (in which temporal (phenological) distribution of eggs vary in relation to regional SST indices).

```
vc.pheno<-gam((Cper10m2+1)~factor(year)+s(lon,lat)+s(doy)+s(bottom_depth,k=5)+
                s(doy,by=reg.SST),data=apsub,family=tw(link='log'),
                method='REML')

par(oma=c(1,1,1,0.5),mar=c(3,3,3,1.5))
plot(vc.pheno,select=2,main='Alaska Plaice VC Phenology, Eggs',seWithMean=TRUE,
      ylim=c(-25,11))
abline(h=0,col='mistyrose4',lty=2,lwd=1.3)
par(oma=c(1,1,1,0.5),mar=c(3,3,3,1.5),new=TRUE)
plot(vc.pheno,select=4,seWithMean=TRUE,shade=TRUE,shade.col=col,ylim=c(-25,11))
legend('topright',legend=c('Flexible Phenology Smooth','Deviation from Avg.Phenology'),
       col=c(NA,col),lwd=c(2,2),cex=0.8)
mtext(c("Day of Year","Anomalies in log(CPUE+1)"),side=c(1,2),line=2.5)

saveRDS(vc.pheno,file='./GAM Models/ap_egg_vc_pheno.rds')
```

The threshold phenology model formulation (in which the temporal (phenological) distribution of eggs vary differently above and below a threshold temperature):

The threshold geography model formulation (in which the geographic distribution of eggs vary differently above and below a threshold temperature: *This is the best model to explain Alaska plaice egg variation across years, as of 1/10/2021.*

```
thr.geo<-readRDS("./GAM Models/ap_egg_thr_geo.rds")
best.index.geo<-readRDS("./GAM Models/ap_egg_best_index_geo.rds")
aic.geo<-readRDS("./GAM Models/ap_egg_aic_geo_list.rds")
summary(thr.geo)
```

```
##
## Family: Tweedie(p=1.99)
## Link function: log
##
## Formula:
```

```

## (Cper10m2 + 1) ~ factor(year) + s(doy) + s(bottom_depth, k = 5) +
##   s(lon, lat, by = th)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.02544   0.18659   5.496 4.38e-08 ***
## factor(year)1988 2.61621   0.33468   7.817 8.63e-15 ***
## factor(year)1991 2.13895   0.32950   6.491 1.07e-10 ***
## factor(year)1993 0.98887   0.39266   2.518 0.011865 *
## factor(year)1994 0.96755   0.29909   3.235 0.001236 **
## factor(year)1995 1.82392   0.21488   8.488 < 2e-16 ***
## factor(year)1996 -0.28811   0.71833  -0.401 0.688403
## factor(year)1997 1.87579   0.27967   6.707 2.57e-11 ***
## factor(year)1998 1.97600   0.51276   3.854 0.000120 ***
## factor(year)1999 1.82942   0.30764   5.947 3.22e-09 ***
## factor(year)2000 -0.15258   0.31459  -0.485 0.627729
## factor(year)2002 0.68175   0.25963   2.626 0.008707 **
## factor(year)2003 -0.06705   0.27223  -0.246 0.805485
## factor(year)2005 1.30594   0.23060   5.663 1.70e-08 ***
## factor(year)2006 2.36688   0.21786  10.864 < 2e-16 ***
## factor(year)2007 0.79356   0.23138   3.430 0.000616 ***
## factor(year)2008 2.57392   0.22510  11.435 < 2e-16 ***
## factor(year)2009 1.96451   0.22090   8.893 < 2e-16 ***
## factor(year)2010 2.24061   0.22189  10.098 < 2e-16 ***
## factor(year)2011 1.81458   0.26431   6.865 8.80e-12 ***
## factor(year)2012 3.08484   0.21230  14.530 < 2e-16 ***
## factor(year)2013 2.03422   0.33288   6.111 1.18e-09 ***
## factor(year)2014 0.04052   0.20691   0.196 0.844762
## factor(year)2015 0.31682   0.31267   1.013 0.311050
## factor(year)2016 -0.50510   0.20715  -2.438 0.014843 *
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##          edf Ref.df    F p-value
## s(doy)      8.240 8.831 11.96 <2e-16 ***
## s(bottom_depth) 3.907 3.991 15.08 <2e-16 ***
## s(lon,lat):thFALSE 27.091 28.760 51.96 <2e-16 ***
## s(lon,lat):thTRUE 27.763 28.875 39.36 <2e-16 ***
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) = 0.268 Deviance explained = 75%
## -REML = 7080.7 Scale est. = 1.3654 n = 2116

```

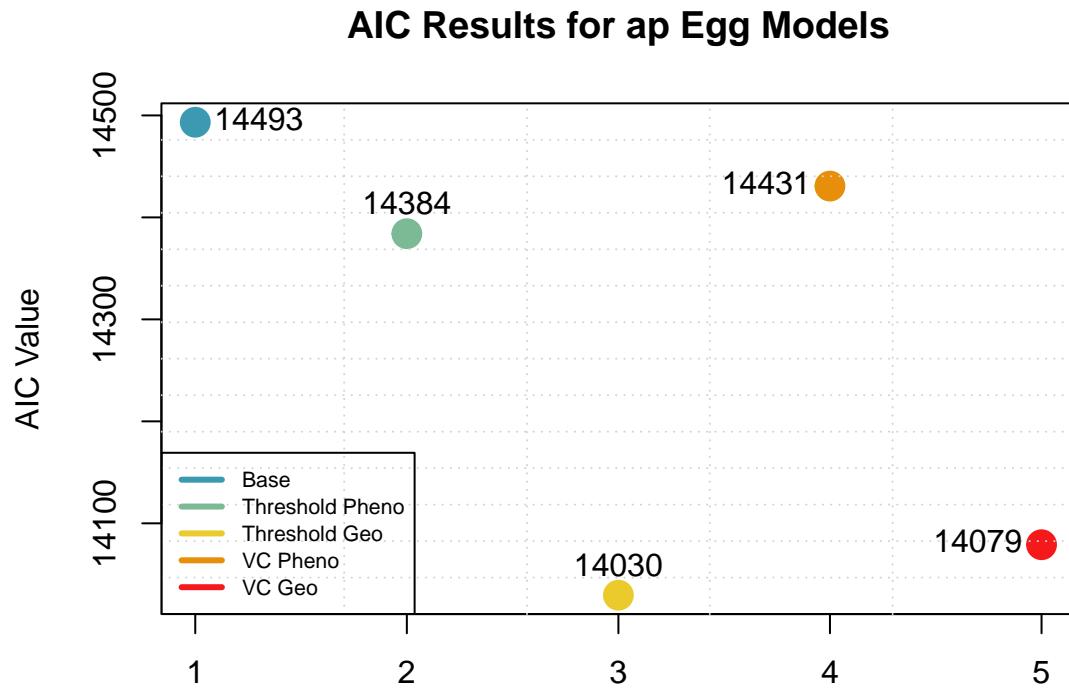
```
AIC(thr.geo)
```

```
## [1] 14029.54
```

```
print(temp.in[[best.index.geo]])
```

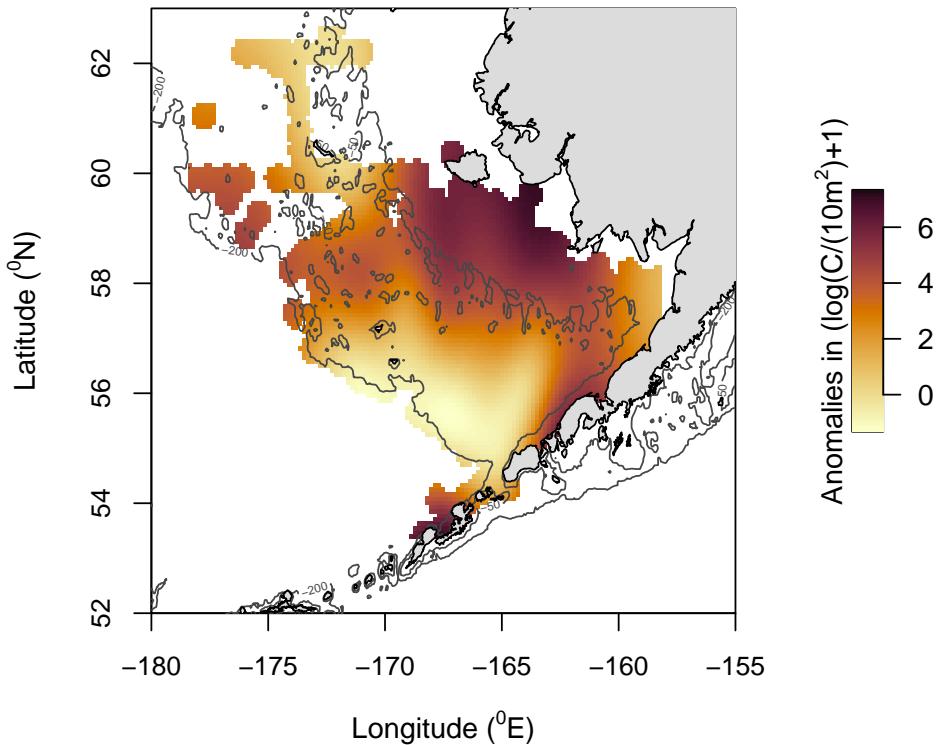
```
## [1] 2.121005
```

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

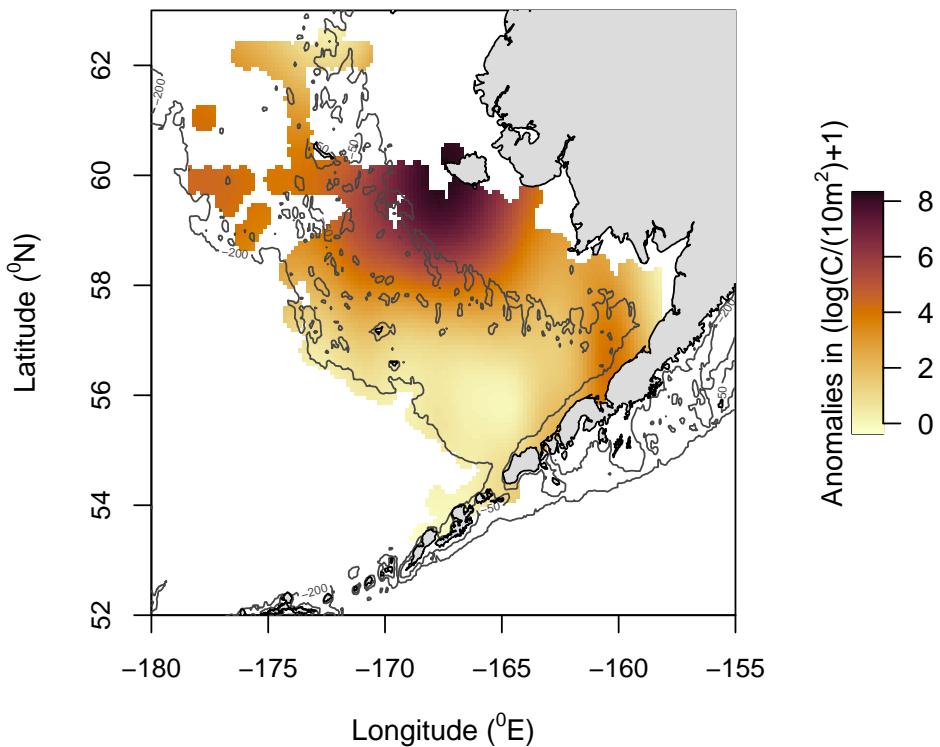


This is the below threshold (2.12 deg C) and above threshold predicted geographical distribution of Alaska plaice eggs (based on the threshold geography model).

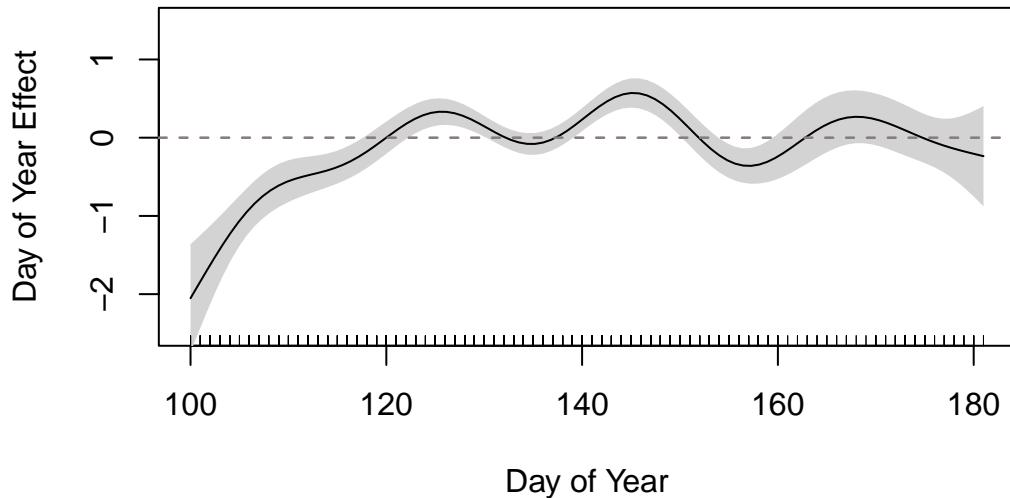
Below



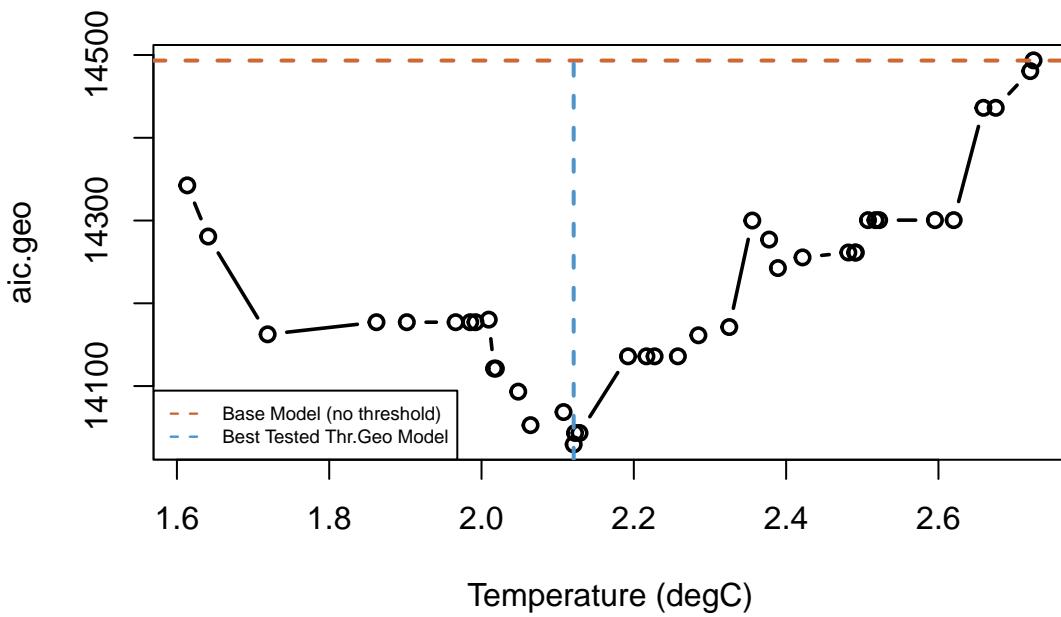
Above



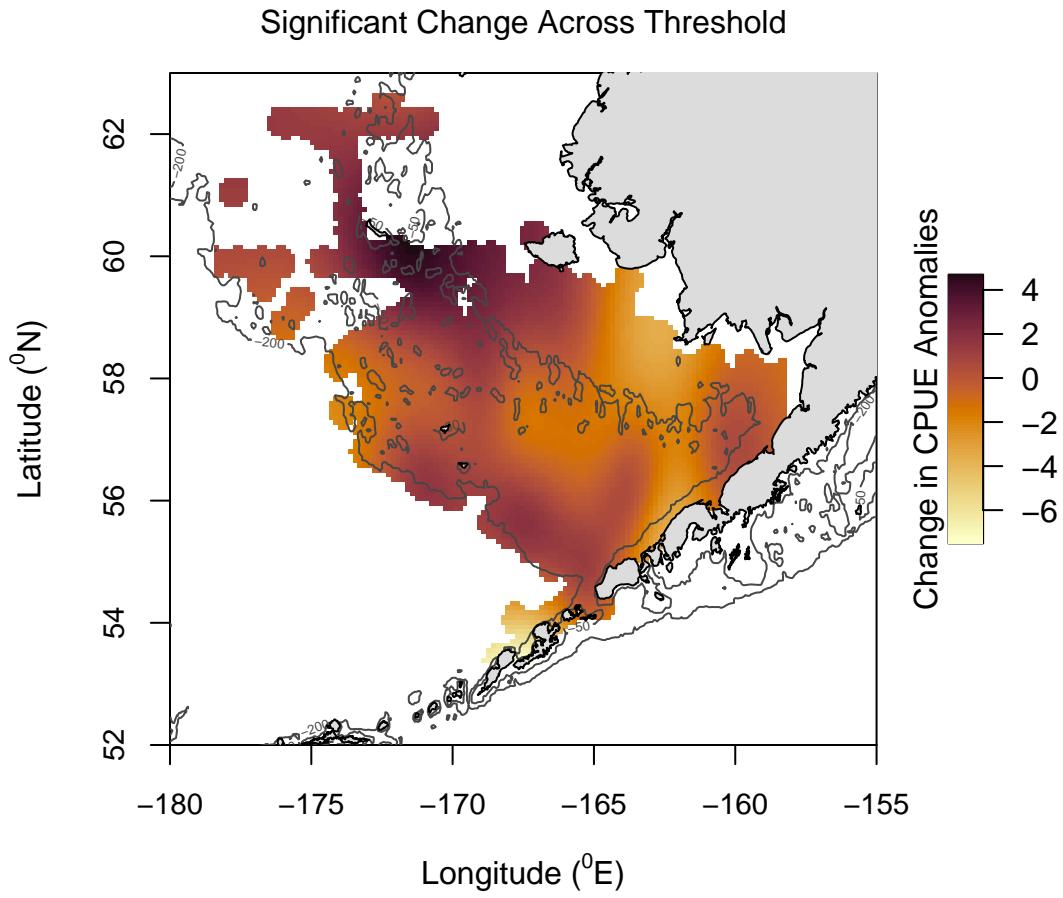
Plaice Egg Phenology (thr.geo model)



Temperature Threshold Flex Geography



With the threshold geography model, we can predict places where there is a significant *difference* in predictions when comparing the above threshold spatial prediction to the below threshold spatial prediction. This plot is calculated by subtracting the spatial distribution *below* the threshold from the prediction *above* the threshold.



Reduction in MSE (%):

```
## [1] 14.94038
```

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:

```
lv.base<-gam((Cper10m2+1)~factor(year)+s(doy,k=7)+s(lon,lat)+  
  s(bottom_depth,k=5),  
  data=aplarv.ctd,family=tw(link='log'),method='REML')  
  
saveRDS(lv.base,file='./GAM Models/ap_larval_base.rds')
```

Then we add in additive salinity:

```

lv.add.sal<-gam((Cper10m2+1)~factor(year)+s(doy,k=7)+s(lon,lat)+  

                  s(bottom_depth,k=5)+  

                  s(salinity),data=aplarv.ctd,family=tw(link='log'),  

                  method='REML')

saveRDS(lv.add.sal,file="./GAM Models/ap_larval_addsal.rds")

```

Then additive temperature:

```

lv.add.temp<-gam((Cper10m2+1)~factor(year)+s(doy,k=7)+s(lon,lat)+  

                  s(bottom_depth,k=5)+  

                  s(temperature),data=aplarv.ctd,family=tw(link='log'),  

                  method='REML')

saveRDS(lv.add.temp,file="./GAM Models/ap_larval_addtemp.rds")

```

Then additive temperature and salinity, in individual additive terms:

```

lv.temp.sal<-gam((Cper10m2+1)~factor(year)+s(doy,k=7)+s(lon,lat)+  

                  s(bottom_depth,k=5)+  

                  s(temperature)+s(salinity),data=aplarv.ctd,  

                  family=tw(link='log'),method='REML')

saveRDS(lv.temp.sal,file="./GAM Models/ap_larval_addtempsal.rds")

```

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

```

lv.2d<-gam((Cper10m2+1)~factor(year)+s(lon,lat)+s(doy,k=7)+s(bottom_depth,k=5)+  

              te(salinity,temperature),data=aplarv.ctd,family=tw(link='log'),  

              method='REML')

saveRDS(lv.2d,file="./GAM Models/ap_larval_2d.rds")

```

```

##  

## Family: Tweedie(p=1.99)  

## Link function: log  

##  

## Formula:  

## (Cper10m2 + 1) ~ factor(year) + s(lon, lat) + s(doy, k = 7) +  

##   s(bottom_depth, k = 5) + te(salinity, temperature)  

##  

## Parametric coefficients:  

##                               Estimate Std. Error t value Pr(>|t|)  

## (Intercept)          0.614210  0.234478  2.619 0.008911 **  

## factor(year)1998    0.686424  0.363255  1.890 0.059032 .  

## factor(year)1999    1.021116  0.294075  3.472 0.000533 ***  

## factor(year)2000   -0.099012  0.310653 -0.319 0.749989  

## factor(year)2002   -0.056671  0.276383 -0.205 0.837570  

## factor(year)2003    0.437833  0.288013  1.520 0.128713  

## factor(year)2005    1.264438  0.271872  4.651 3.65e-06 ***  

## factor(year)2006    0.506688  0.252880  2.004 0.045317 *  

## factor(year)2007    0.493034  0.284493  1.733 0.083333 .

```

```

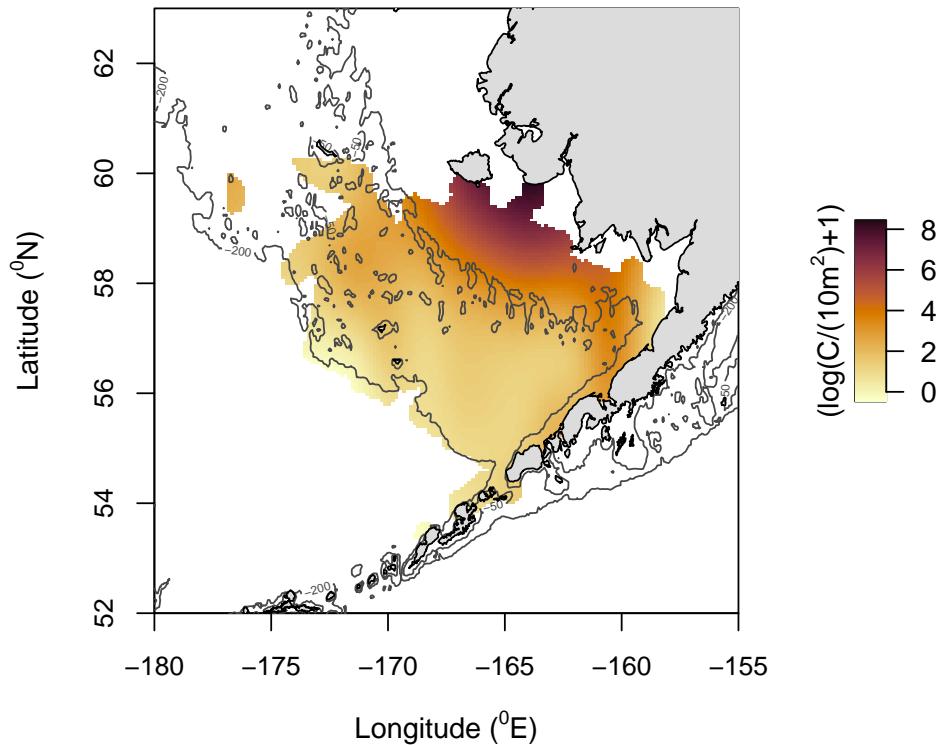
## factor(year)2008 0.697257  0.382321  1.824 0.068425 .
## factor(year)2009 -0.063489  0.260341 -0.244 0.807372
## factor(year)2010  0.236880  0.255236  0.928 0.353540
## factor(year)2011 -0.315271  0.319531 -0.987 0.323992
## factor(year)2012 -0.129643  0.255120 -0.508 0.611425
## factor(year)2013  0.391386  0.314177  1.246 0.213086
## factor(year)2014 -0.008963  0.260672 -0.034 0.972577
## factor(year)2015 -0.291407  0.296308 -0.983 0.325569
## factor(year)2016  0.742205  0.284329  2.610 0.009150 **
## ---
## 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)    26.996 28.714 21.970 < 2e-16 ***
## s(doy)        1.000  1.000 28.337 3.61e-07 ***
## s(bottom_depth) 3.808  3.971  7.495 5.13e-05 ***
## te(salinity,temperature) 15.723 18.351 14.055 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.0321  Deviance explained = 81.2%
## -REML =     2657  Scale est. = 0.73566  n = 1341

```

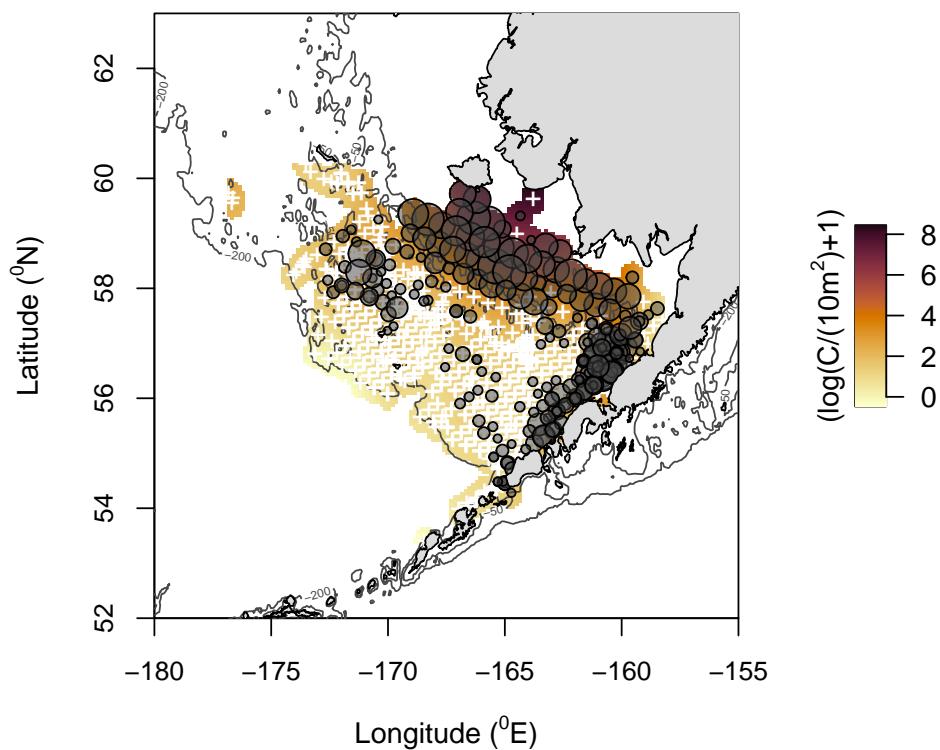
To confirm that this is indeed the best model, we can compare AIC values across all five tested models.

The following plot is the predicted Alaska Plaice larval biogeography based on the best performing model, the bivariate salinity-temperature GAM, next to the same plot with log(CPUE+1) observations shown.

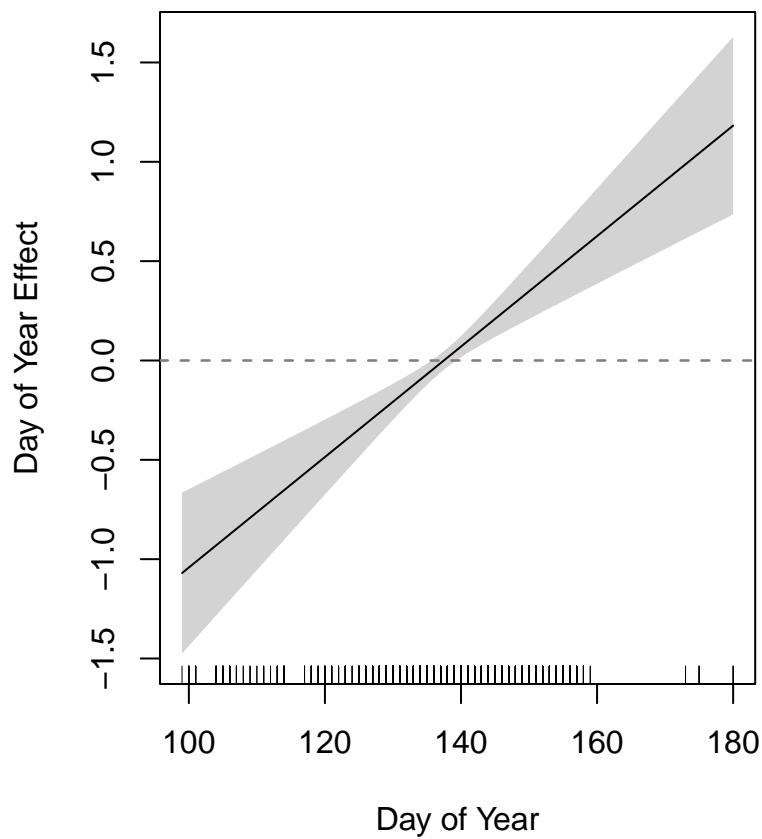
Predicted Larval Biogeography, 2D Model



Predicted Larval Biogeography, 2D Model

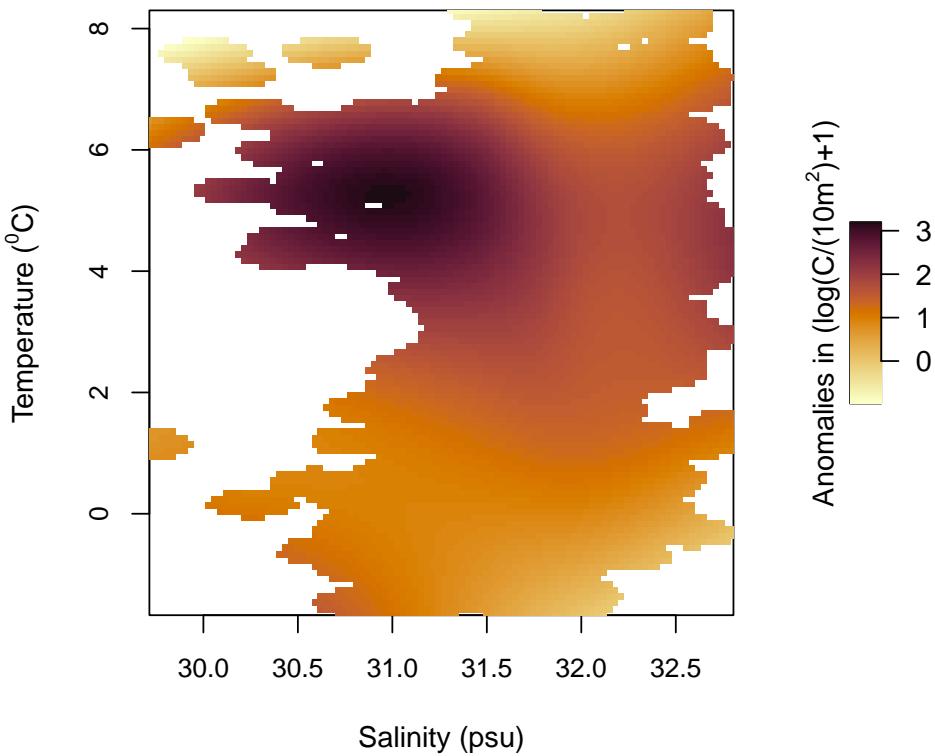


Larval Phenology (2D model)

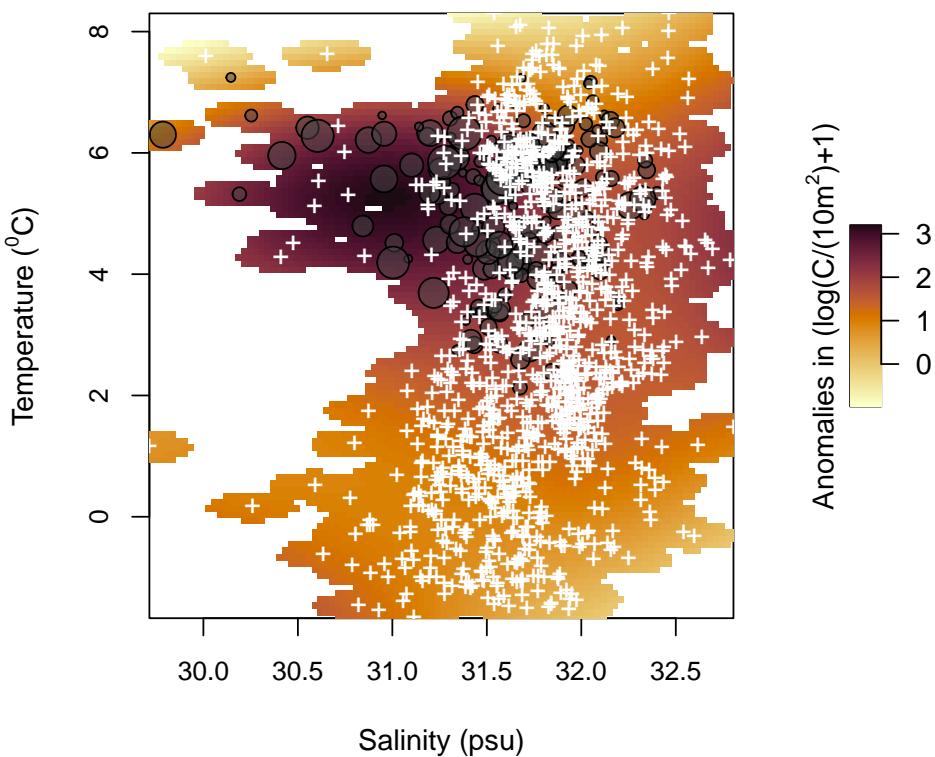


With this bivariate model, we can also calculate the predicted anomalous larval catch (more or less than expected) on a salinity-temperature plot. This figure shows that prediction, with observed larval catch ($\log(n=1)$) overlaid.

Larval Biogeography By Temperature and Salinity



Larval Biogeography By Temperature and Salinity



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, Alaska plaice

	Best Divided By Base	Best Divided By Second Best
Eggs	0.9680024	0.9964871
Larvae	0.9709863	0.9961160

Appendices:

The following plots investigate the phenological peaks in egg distribution to evaluate any spatial differences in egg distribution among these three peaks.

