

Streamlined Yellowfin Analyses & Figures

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Yellowfin sole (YFS):

Loading Data:

Yellowfin sole: larval data only are included for this species. Yellowfin sole spawn in April and May, live roughly 17 to 19 years, and transform to juveniles at standard lengths between 15 and 17 mm.

These data have been trimmed. The larval data are constrained to depths less than 176 meters and day of year greater than 220. Larvae are linked to CTD-derived, *in situ* temperature and salinity measurements.

Descriptive Information:

Table 1: Descriptive Metrics for Yellowfin Sole Larval Data

Lat Range	Lon Range	Day of Year Range	Bottom Depth Range
54-65	-177.6 to -158.1	230-283	16-165

The following two plots show *the day of year distribution for positive yellowfin sole larval catch* (left) and *the year distribution for positive yellowfin sole larval catch* (right).

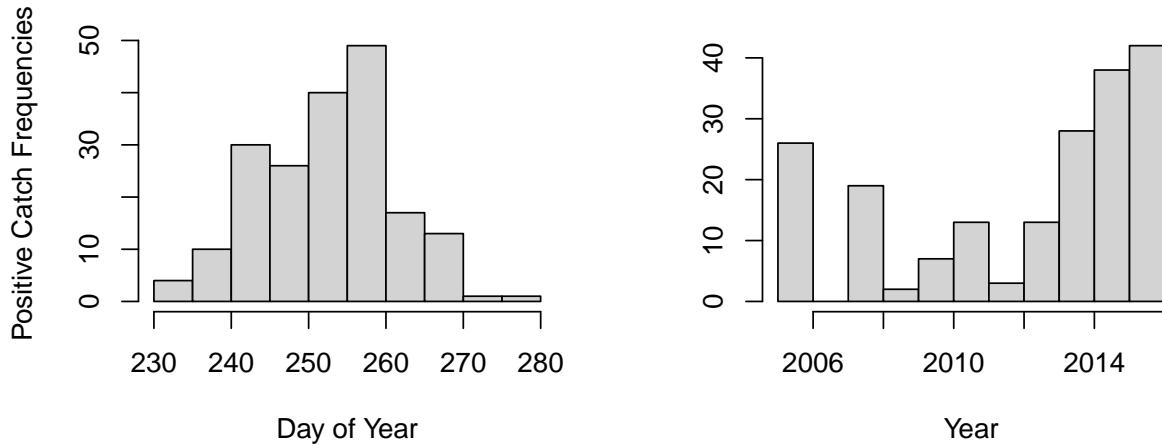


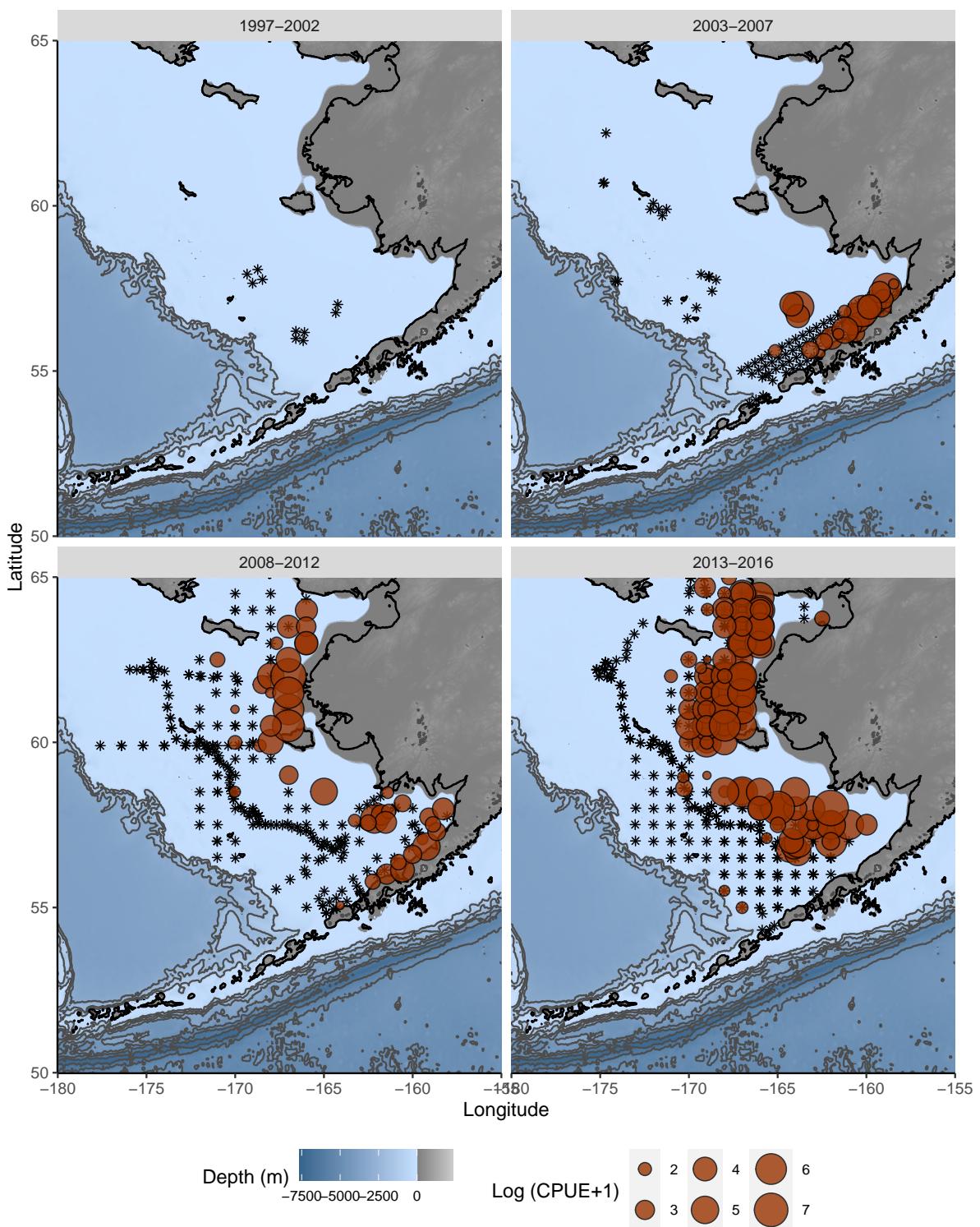
Figure 1: Yellowfin Sole Larvae

The following plots show yellowfin sole larval catch distributions (Catch per unit effort, or per 10m²) across five year increments from 1997 to 2016

```
yfylarv<-yfylarv.ctd%>%mutate(yearbin=case_when(year<=2002~'1997-2002',
                                                 year<=2007&year>2002~'2003-2007',
                                                 year<=2012&year>2007~'2008-2012',
                                                 year<=2017&year>2012~'2013-2016'))
```

```
yfylpos<-yfylarv[yfylarv$Cper10m2>0,]
yfylpos$logcpue<-log(yfylpos$Cper10m2+1)
yfylz<-yfylarv[yfylarv$Cper10m2==0,]
```

Yellowfin Sole Larvae



Larval Generalized Additive Models:

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.**

Yellowfin sole larvae were best explained by the bivariate salinity-temperature model, in which the spatial and temporal distribution of larvae were modelled in association with a smooth containing *in situ* salinity-temperature data.

We begin with the base larval model:

```
lv.base<-readRDS("./GAM Models/yf_larvae_base.rds")
summary(lv.base)

##
## Family: Tweedie(p=1.99)
## Link function: log
##
## Formula:
## (Cper10m2 + 1) ~ factor(year) + s(doy, k = 7) + s(lon, lat) +
##     s(bottom_depth, k = 5)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.32006   0.34956   3.776 0.000172 ***
## factor(year)2004 0.03783   0.56902   0.066 0.947008
## factor(year)2005 1.40341   0.45749   3.068 0.002236 **
## factor(year)2006 0.12531   0.39628   0.316 0.751924
## factor(year)2007 -0.33983   0.68459   -0.496 0.619757
## factor(year)2008 -0.58526   0.41186   -1.421 0.155733
## factor(year)2009 -0.13714   0.40097   -0.342 0.732432
## factor(year)2010 -0.59252   0.38387   -1.544 0.123121
## factor(year)2011  0.40026   0.40688   0.984 0.325568
## factor(year)2012 -0.66649   0.38594   -1.727 0.084597 .
## factor(year)2013 -0.48109   0.41556   -1.158 0.247364
## factor(year)2014  0.21059   0.35591   0.592 0.554243
## factor(year)2015  0.99657   0.36310   2.745 0.006204 **
## factor(year)2016  1.24189   0.39755   3.124 0.001854 **
## ---
## 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)       5.155  5.726  5.677 1.1e-05 ***
## s(lon,lat)  25.534 28.270 20.555 < 2e-16 ***
## s(bottom_depth) 3.860  3.981 14.733 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.0647  Deviance explained = 75.8%
## -REML = 2062.7  Scale est. = 1.1087    n = 793
```

```
AIC(lv.base)
```

```
## [1] 4075.912
```

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

```
lv.temp.sal<-readRDS("./GAM Models/yf_larvae_addtempsal.rds")
summary(lv.temp.sal)
```

```
##
## Family: Tweedie(p=1.99)
## Link function: log
##
## Formula:
## (Cper10m2 + 1) ~ factor(year) + s(doy, k = 7) + s(lon, lat) +
##   s(bottom_depth, k = 5) + s(temperature) + s(salinity)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.33850  0.34591  3.870 0.000119 ***
## factor(year)2004 0.24633  0.55262  0.446 0.655910
## factor(year)2005 1.72332  0.45281  3.806 0.000153 ***
## factor(year)2006 0.29538  0.38666  0.764 0.445148
## factor(year)2007 -0.26337  0.66562 -0.396 0.692466
## factor(year)2008 -0.63699  0.39961 -1.594 0.111363
## factor(year)2009  0.02592  0.39936  0.065 0.948264
## factor(year)2010 -0.62100  0.37323 -1.664 0.096567 .
## factor(year)2011  0.53565  0.40121  1.335 0.182263
## factor(year)2012 -0.70387  0.38952 -1.807 0.071167 .
## factor(year)2013 -0.82812  0.41170 -2.011 0.044643 *
## factor(year)2014 -0.18586  0.37773 -0.492 0.622832
## factor(year)2015  0.99144  0.35918  2.760 0.005920 **
## factor(year)2016  1.14979  0.41246  2.788 0.005446 **
##
## ---
## 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)        4.686  5.396  3.402 0.00242 **
## s(lon,lat)    24.711 27.892 14.385 < 2e-16 ***
## s(bottom_depth) 3.853  3.978 13.640 < 2e-16 ***
## s(temperature) 7.223  8.254 10.012 < 2e-16 ***
## s(salinity)    5.733  6.972  7.240 < 2e-16 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.123  Deviance explained = 78.4%
## -REML =     2029  Scale est. = 1.0112     n = 793
```

```
AIC(lv.temp.sal)
```

```
## [1] 3994.397
```

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

```
lv.2d<-readRDS("./GAM Models/yf_larvae_2d.rds")
summary(lv.2d)
```

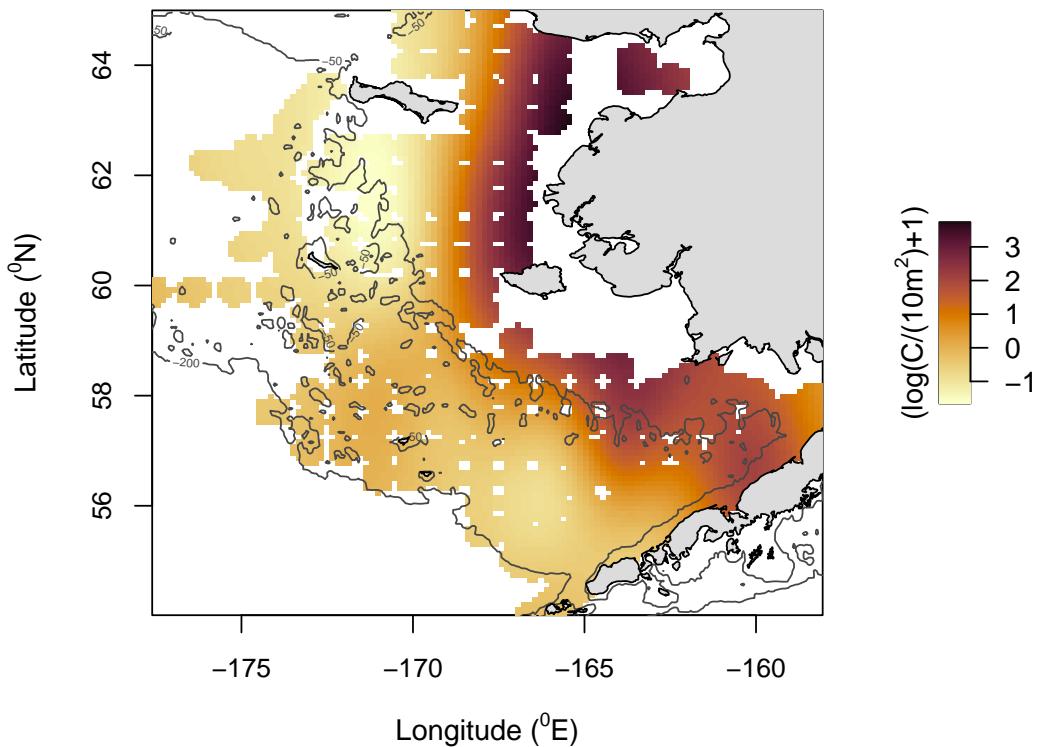
```
##
## Family: Tweedie(p=1.99)
## Link function: log
##
## Formula:
## (Cper10m2 + 1) ~ factor(year) + s(lon, lat) + s(doy, k = 7) +
##   s(bottom_depth) + te(salinity, temperature)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.13224   0.34547  3.277  0.00110 **
## factor(year)2004 -0.22113   0.55059 -0.402  0.68808
## factor(year)2005  1.71310   0.44752  3.828  0.00014 ***
## factor(year)2006  0.35749   0.38368  0.932  0.35178
## factor(year)2007  0.14144   0.66813  0.212  0.83241
## factor(year)2008 -0.46947   0.39660 -1.184  0.23691
## factor(year)2009  0.27772   0.39750  0.699  0.48498
## factor(year)2010 -0.29576   0.37965 -0.779  0.43622
## factor(year)2011  0.72599   0.40006  1.815  0.06998 .
## factor(year)2012 -0.47420   0.38707 -1.225  0.22093
## factor(year)2013 -0.73774   0.41931 -1.759  0.07893 .
## factor(year)2014  0.08987   0.37915  0.237  0.81270
## factor(year)2015  1.13930   0.36053  3.160  0.00164 **
## factor(year)2016  1.21381   0.41248  2.943  0.00336 **
##
## ---
## 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)    24.719 27.868 14.037 < 2e-16 ***
## s(doy)        5.056  5.657  3.094 0.00361 **
## s(bottom_depth) 6.602  7.721  9.808 < 2e-16 ***
## te(salinity,temperature) 15.742 18.117  6.559 < 2e-16 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.166  Deviance explained = 79.1%
## -REML = 2017.7  Scale est. = 0.99012  n = 793
```

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

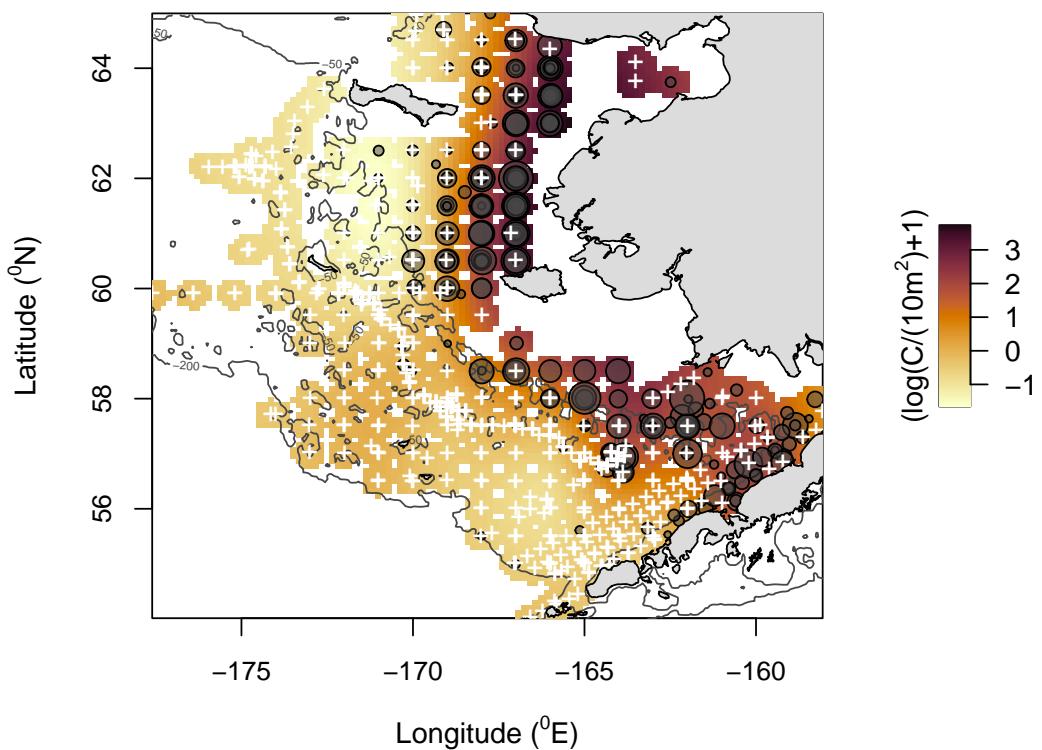
```
## [1] 3978.235
```

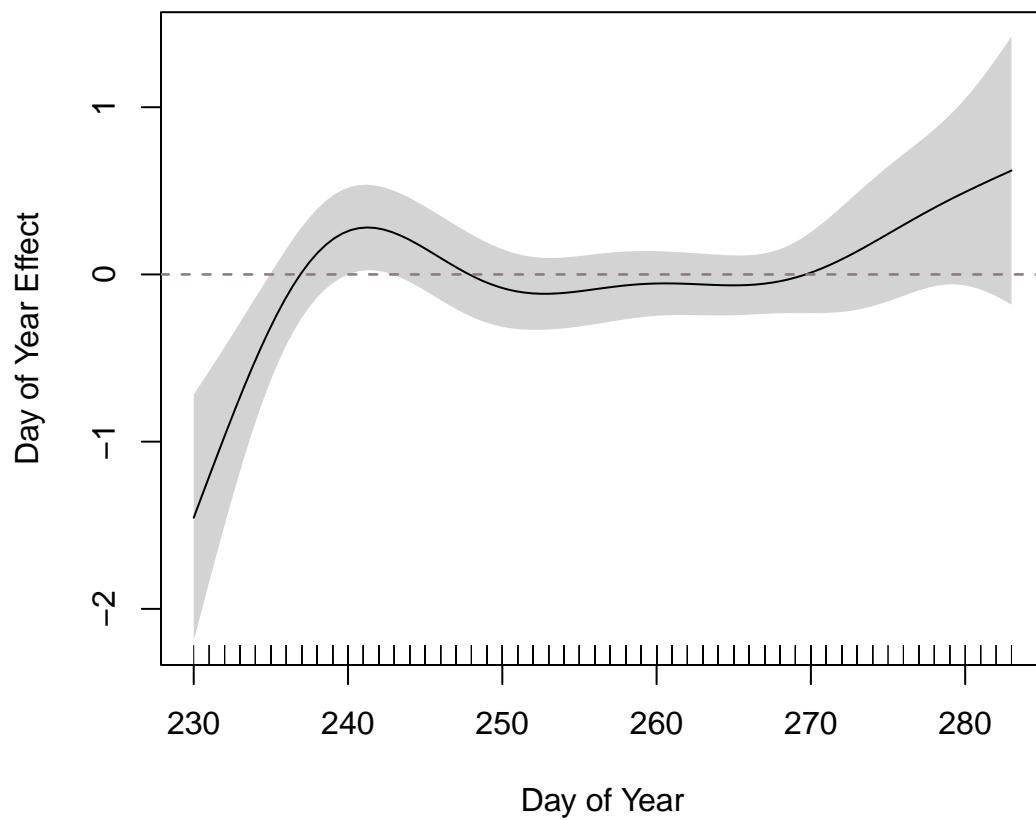
The following plot is the predicted yellowfin sole larval biogeography based on the best performing model, the bivariate salinity-temperature GAM. Observations (log transformed, n+1) are shown as well.

Predicted Larval Biogeography, 2D Model



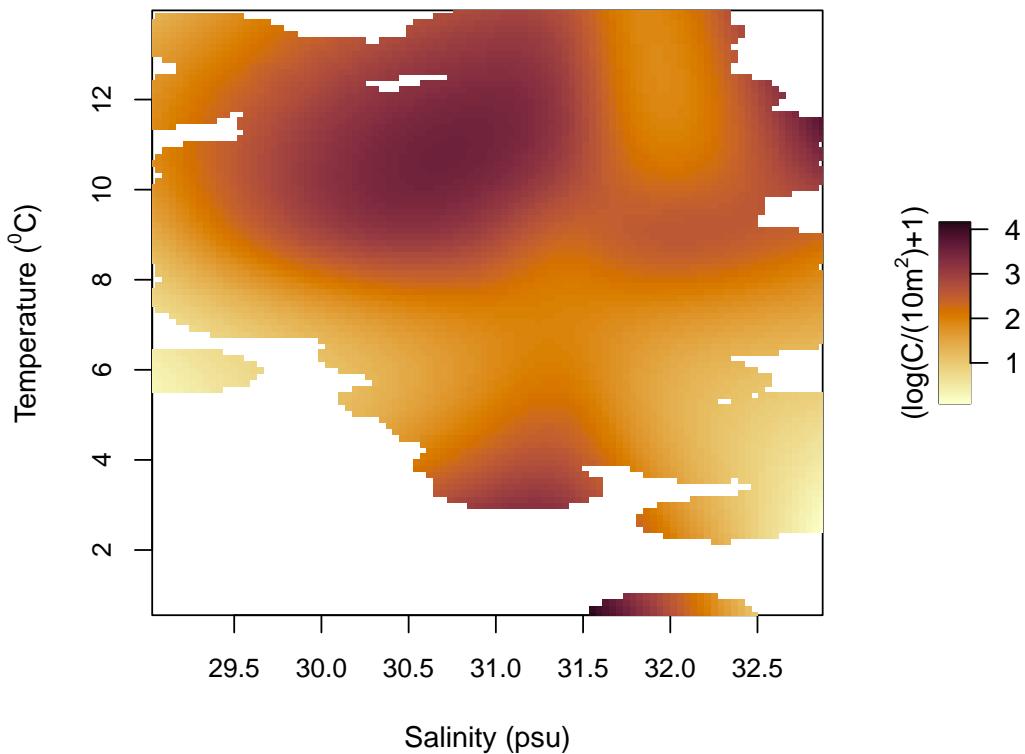
Predicted Larval Biogeography, 2D Model



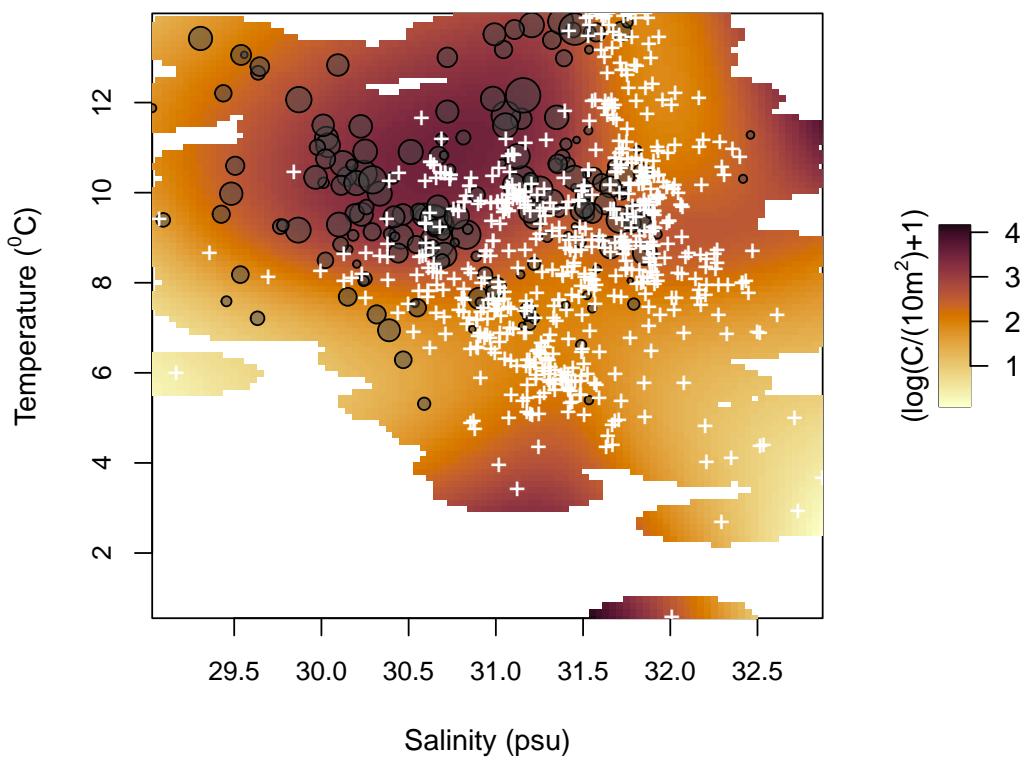


With this bivariate model, we can also calculate the predicted anomalous larval catch (more or less than expected) on a salinity-temperature plot. This figure shows that prediction, with observed larval catch ($\log(n=1)$) overlaid.

Larval Biogeography By Temperature and Salinity



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 2: Model Power through AIC Comparisons, Yellowfin Sole

	Best Divided By Base	Best Divided By Second Best
Larvae	0.9760357	0.995954

Reduction in MSE (%):

```
## [1] 10.6984
```