Source: Ichthyoplankton Information System, Alaska Fisheries Science Center

ENVIRONMENTAL RELATIONSHIPS OF FISHES

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Analytical Workflows

December 2, 2021

BRIEF REMINDER OF RESEARCH OBJECTIVES

How flexible is spawning geography and phenology?

Do water mass characteristics better explain larval biogeography?

INITIAL AND MID-TERM GOALS

- Create a repository with all analytical workflow processes

- Create a separate folder with data cleaning practices

- Create a style guide with a workflow map and figure conventions

- Add comments and introductions to all code files

- Create a streamlined figure creation workflow

ACCOMPLISHED GOALS: CLEAN REPOSITORY

```
##Bering Sea Yellowfin Sole:
#the following code loads and cleans the yellowfin sole egg and larval data from ecoFOCI cruises.
#at the end of this script are finalized datasets to load in the future.
###CTD Loading: ##########################################################
allctd<-read.csv(file="All_CTD_Data_8302021.csv")
names(allctd)
allctd<-allctd[c('Latitude','Longitude','Date','Time','Pressure','Depth',
                 'Temperature','Conductivity','Salinity','Sigma.T',
                 'Flag','Cruise','Station','Haul','Grid','FOCI_HAUL_ID',
                 'FOCI_file')]

allctd$Year<-NA
allctd$Year<-str_sub(allctd$Date,start=-4) #to get easy year reference

allctd<-allctd[allctd$Temperature<14,] #these 2 lines remove anomalous temp/sal values
allctd<-allctd[allctd$Salinity>29&allctd$Salinity<36,] #this loads a compilation of all CTD data from ecoFOCI trawls
  #ultimately, these data will be matched with larval data for larval biogeography GAMs.

###loading data, subsetting and cleaning properly
yfeggraw<-read.csv(file='YFSole_Egg_Catch.csv',header=TRUE,check.names=TRUE)
yflarvraw<-read.csv(file='YFSole_Larvae_Catch.csv',header=TRUE,check.names=TRUE)
```

```
####Generalized Additive Analyses: Yellowfin Sole
#the following code creates generalized additive models for eggs and larvae of yellowfin sole.
#these analyses form the basis of my MS thesis.
#egg data uses an averaged sea surface temperature for the month of March in the Southeastern Bering Sea
#May index was chosen because it is two months before the peak of yellowfin sole CPUE, and thus May
#conditions are likely more relevant to spawning behavior than temperatures in later months.
#load egg and larval data:

yfsub<-read.csv(file='./Ichthyo Data/Cleaned_Cut_YfEggs.csv',header=TRUE,check.names=TRUE)

yflarv.ctd<-read.csv(file='./Ichthyo Data/Cleaned_Cut_YfLarv_wCTD.csv',header=TRUE,check.names=TRUE)


###EGGS: Spawning Behavior
##Load in local and regional temperature index for May (2 mos before peak in egg CPUE in July)
```
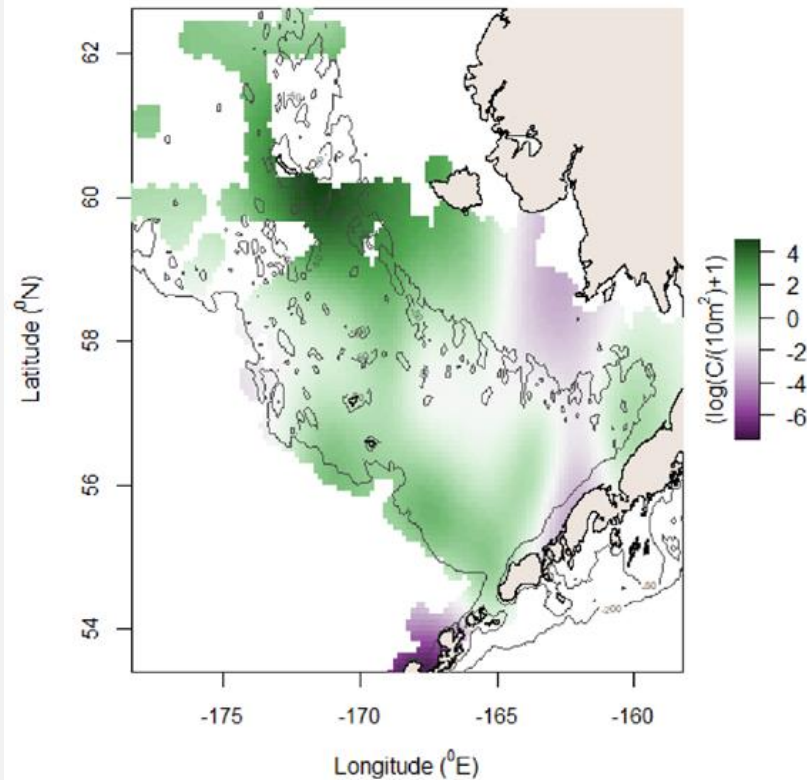
ACCOMPLISHED GOAL:
COMMENTED CODE & CODE FOR CLEANING

ACCOMPLISHED* GOAL:
CLEAN FIGURES, MODEL OUTPUT TABLE

Species	Life Stage	Best Model	ΔMSE	ΔAIC	Deviance Explained
Alaska Plaice	Egg	$(\text{Log}(\text{Catch per 10m}^2)+1) = factor(\text{year}) + s(\text{doy}) + s(\text{bottom depth, k=5}) + g(\text{longitude, latitude, by = threshold regional SST}) + e_{\text{doy,year,(lon,lat)}}$	0.149	463.75	75%
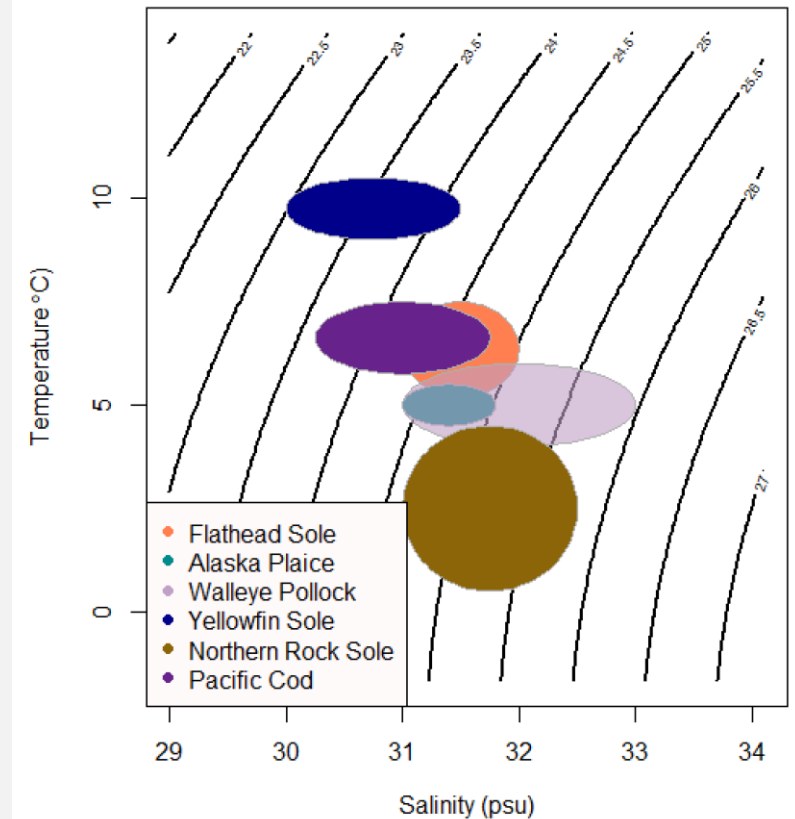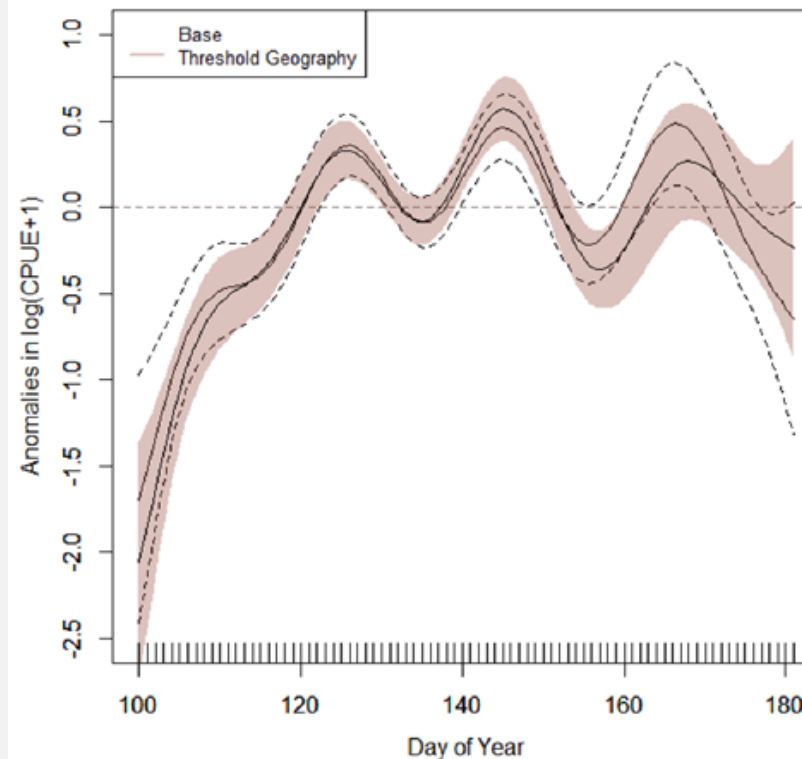
GOALS IN PROGRESS

Generate a streamlined figure process (that saves figures too)

Write a style guide for figures and code