Get and summarize AFSC survey data

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Contents

AFSC Survey CPUE data: github.com/kholsman/AFSC_CPUE Repo maintained by:
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Overview

The below scripts return a list object cpue_data saved as a compressed Rdata file with the naming 'reg.srvy#.spp.cpue_data.Rdata' such as "ebs.srvy98.plk.cpue_data.Rdata". Each cpue_data list contains 8 data.frames:

```
load(paste0("data/out/",qrydate,"/cpue/ebs/ebs.srvy98.plk.cpue_data.Rdata"))

names(cpue_data)
```

The data.frames within each cpue_data object are:

1. **totalB_N**: Total biomass (kg) or abundance (# of fish) for the species in each year

2. **mnCPUE_strata_yr** : Average survey CPUE (kg per Km2) or abundance (# per Km2) for the species in each strata and year

3. **total_bin_B_N**: Total biomass (kg) or abundance (# of fish) for each bin (10 mm) for the species in each year

4. **mnCPUE_strata_bin_yr** : Average survey CPUE (kg per Km2) or abundance (# per Km2) for each size bin for the species in each strata and year

5. **CPUE_station_bin_yr**: Station specific survey CPUE (kg per Km2) or abundance (# per Km2) for each size bin for the species in each year

6. **CPUE_station_yr**: Station specific survey CPUE (kg per Km2) or abundance (# per Km2) for the species in each year

7. **propByBin**: proportion of biomass in each size bin per species per year

8. **propByStrata**: proportion of biomass in each strata per species per year
9. **propByStrataBin**: proportion of biomass in each bin and strata per species per year

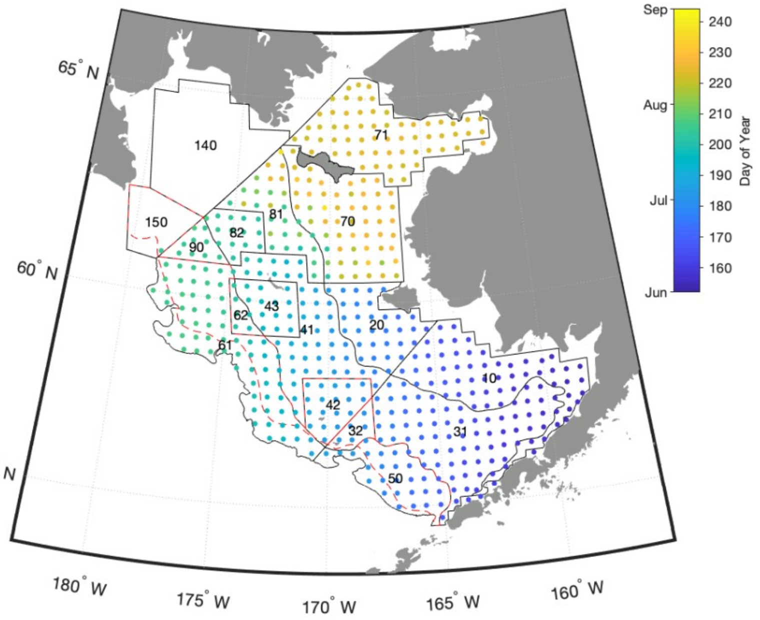


Figure 6: Regional polygons and survey-replication stations associated with the ACLIM indices.

These are calculated from the RACEBASE data tables for survey results where total CPUE was recorded for the species s (location_catch) at each haul, expanded to include stations i where CPUE=0 (location) and expanded to each size bin l using the proportional subset of frequency of fish of given length (mm), binned into 10 mm bins (l) and predicted weight ($\hat{W}$) for each size bin l at each station i:

$$B_{s,y} = CPU\bar{E}_{s,k,y} \cdot A_k$$

where A_k is the area of the strata k in Km^2 and $CPU\bar{E}_{s,k,y}$ is the strata specific average CPUE (kg per Km^2 or number per Km^2) of all stations i in strata k:

$$CPU\bar{E}_{s,k,y} = \frac{1}{n_k} \cdot \sum_{n_k} CPUE_{s,k,y,i}$$

where $ CPUE_{s,k,y,i} $ is the station specific CPUE (saves as the object `cpue_data$CPUE_station_yr`).

To obtain population level estimates of the biomass or abundance of fish by size bin l, we used a length weight regression to esimate the weight of each size fish j measured ($\hat{W}$) to calculate the proportion by weight or frequency at each station where

$$\hat{W} = \alpha_s + L_j^{\beta_s}$$

where α_s and β_s are fit (updated each year) to all available length and weight data from surveys from all years across the EBS, GOA, and AI (rather than each basin separately) and

$$p^{w}_{l,i} = \frac{N_{l,i}\cdot\hat{\bar{W}}_{l,i}}{\sum N_{l,i}\cdot\hat{\bar{W}}_{l,i}}$$

and

$$p^{N}_{l,i} = \frac{N_{l,i}}{\sum N_{l,i}}$$

This was then multiplied by the CPUE at each station ($CPUE_{s,k,y,i}$) to obtain a station estimate of CPUE by size bin l

$$CPUE_{s,k,y,l,i} = p^{N}_{l,i}\cdot CPUE_{s,k,y,i}$$

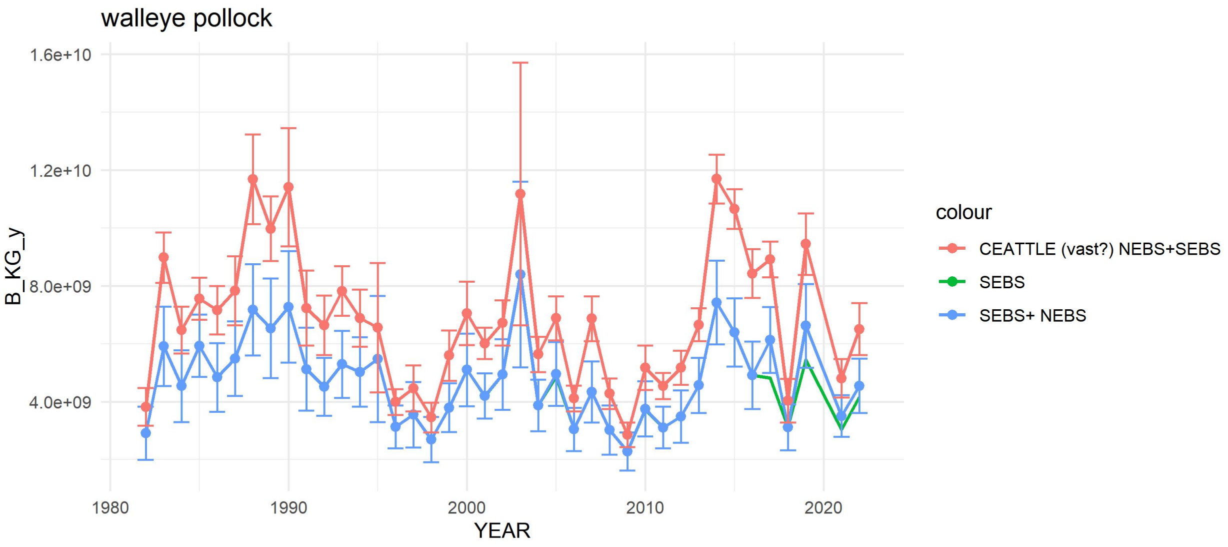
Finally, the average strata CPUE ($CPU\bar{E}_{s,k,y,l}$) and whole of EBS biomass by size bin ($B_{s,y,l}$) was calculated as:

$$CPU\bar{E}_{s,k,y,l} = \frac{1}{n_k}\cdot\sum_{n_k} CPUE_{s,k,y,l,i}$$

and

$$B_{s,y,l} = \frac{CPU\bar{E}_{s,k,y,l}\cdot A_k}{\sum_{n_k} CPU\bar{E}_{s,k,y,l}\cdot A_k}\cdot B_{s,y}$$

Comparison of Bering Sea survey values



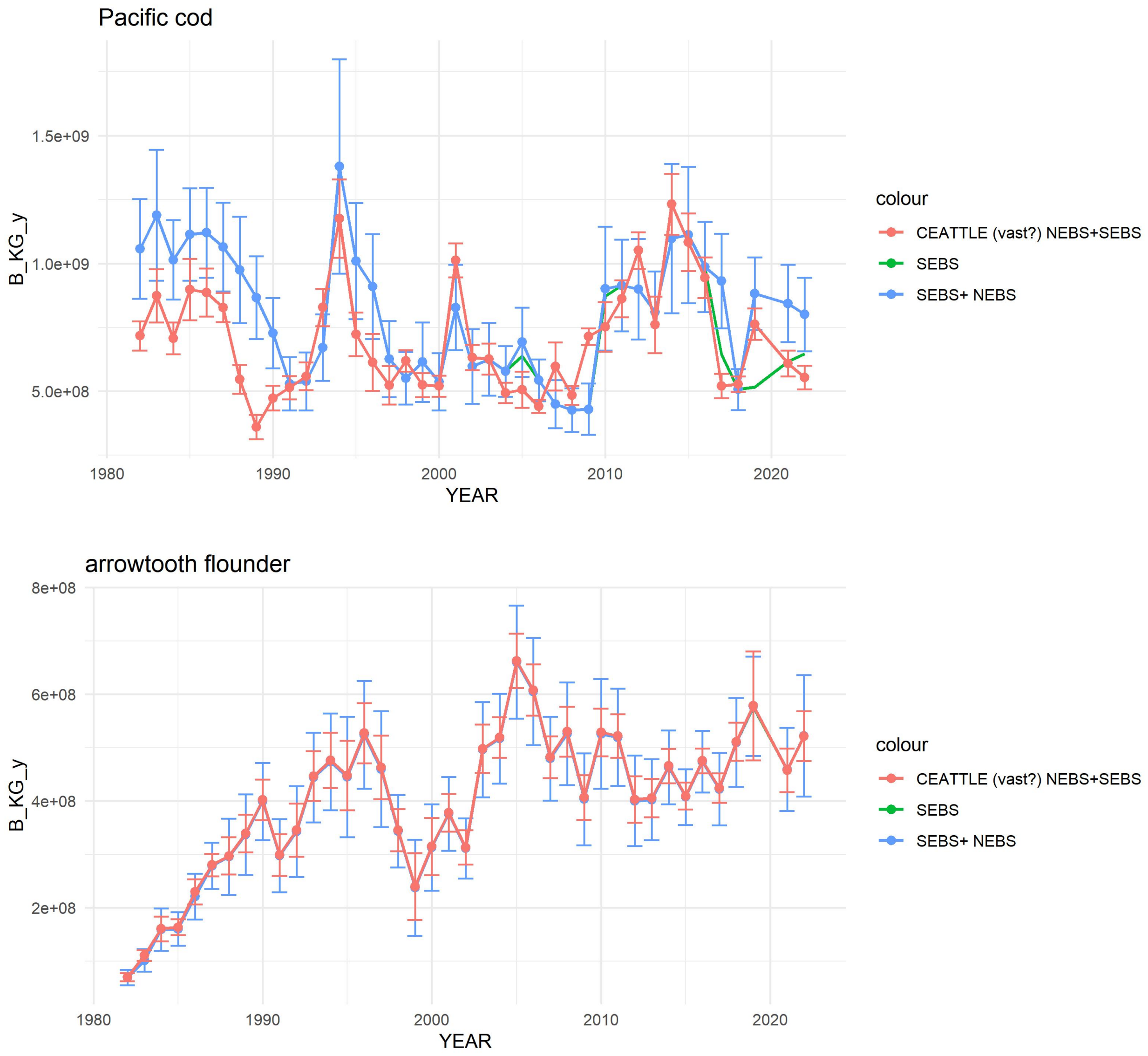


Figure 1: “arrowtooth”

Code

```
# ## Step 0: Set up the R workspace
#
# The first step is to set up the switches for what files to update and create in the file `R/setup.R`.
#
# ## Step 1: Update SQL queries
# This step must be run on a computer that has access to RACEBASE. The code below will generate the bas

# **IMPORTANT:**
#
#   * **This step  must be connected to the RACEBASE SQL database**
```

```
#
#   * **To change R studio from the default 64 bit to 32 bit go to Tools>Global options and select the
#
#   * **The code will connect to the SQL database using your password and username. Remember to update
#
# <!-- ![Header of `setup.R` where `username_path` can be adjusted. This file also is where species, re
#


 # get everything set up:
 #-----------------------------------------
  # rm(list=ls())
  # this uses the password saved in R/password.R
  suppressMessages(source("R/make.R"))

 # update the SQL queries
 #----------------------------------------------

 source(file.path(code.path,"R/sub_scripts/runRACE_qrys.R"))

 # combine sebs and nebs into one region: ebs
 if(dir.exists(file.path(data.path,"ebs")))
   system(paste("rm -r",file.path(data.path,"ebs")))
  dir.create(file.path(data.path,"ebs"))

 # combine files and rename survey area to all of EBS
 for(sp in names(splist)){
  if(dir.exists(file.path(data.path,"ebs",sp)))
   system(paste("rm -r",file.path(data.path,"ebs",sp)))
   dir.create(file.path(data.path,"ebs",sp))
  #"length.Rdata"
  load(file.path(data.path,"nebs",sp,"length.Rdata"))
  length_nebs <- length;rm(length)
  load(file.path(data.path,"sebs",sp,"length.Rdata"))
  length_sebs <- length;rm(length)
  length<- rbind(length_nebs%>%
   mutate(SURVEY_DEFINITION_ID_aka =SURVEY_DEFINITION_ID,SURVEY_DEFINITION_ID =98),
  length_sebs%>%
   mutate(SURVEY_DEFINITION_ID_aka =SURVEY_DEFINITION_ID,SURVEY_DEFINITION_ID =98))

  save(length,file = file.path(data.path,"ebs",sp,"length.Rdata"))
  rm(length)

  #"location.Rdata"
  load(file.path(data.path,"nebs",sp,"location.Rdata"))
  location_nebs <- location;rm(location)
  load(file.path(data.path,"sebs",sp,"location.Rdata"))
  location_sebs <- location;rm(location)
  location<- rbind(location_nebs, location_sebs)

  save(location,file = file.path(data.path,"ebs",sp,"location.Rdata"))
```

```
    #"location_catch.Rdata"
    load(file.path(data.path,"nebs",sp,"location_catch.Rdata"))
    location_catch_nebs <- location_catch;rm(location_catch)
    load(file.path(data.path,"sebs",sp,"location_catch.Rdata"))
    location_catch_sebs <- location_catch;rm(location_catch)
    location_catch <- rbind(location_catch_nebs%>%
      mutate(SURVEY_DEFINITION_ID_aka =SURVEY_DEFINITION_ID,SURVEY_DEFINITION_ID =98),
     location_catch_sebs%>%
      mutate(SURVEY_DEFINITION_ID_aka =SURVEY_DEFINITION_ID,SURVEY_DEFINITION_ID =98))

    save(location_catch,file = file.path(data.path,"ebs",sp,"location_catch.Rdata"))

  }


#```


## Step 2: Update the LWA regressions

# The default code for RACEBASE uses set LW relationships, however we prefer to update the LW regressio
#
# #```{r updateLWglms, echo=TRUE, eval=FALSE}

  # update the LW regressions
  #----------------------------------------------

  if(update_LWdata){
     source(file.path(code.path,"R/sub_scripts/updateLW.R"))
     # reload with updated data:
     source(file.path(code.path,"R/load_data.R"))
  }
  species_lkup

#```


## Step 3: Get CPUE data from the surveys

#This code is the core script for generating the CPUE_NUMKM2 and CPUE_BIOMKM2 values by size bin, regio

#```{r updateCPUE, echo=TRUE, eval=FALSE}

  STRATA_AREA%>%filter(REGION=="BS")%>%
    group_by(YEAR)%>%summarise(mnAREA  = mean(AREA, na.rm=T),
                               sumAREA = sum(AREA, na.rm=T),
                               cnt = length(unique(STRATUM)))

   STRATA_AREA%>%filter(REGION=="GOA")%>%
    group_by(YEAR)%>%summarise(mnAREA  = mean(AREA, na.rm=T),
                               sumAREA = sum(AREA, na.rm=T),
                               cnt = length(unique(STRATUM)))
```

```
 STRATA_AREA%>%filter(REGION=="BS",YEAR==2022)%>%select(STRATUM)

 # overwrite the NEBS frame from setup for the next set of code (ebs = sebs+nebs now forward)
srvys <- data.frame(reg=c("ebs","goa","ai","slope"),RGN = c("BS","GOA","AI","SLOPE"), num=c(98,47,52,7
# srvys <- data.frame(reg=c("ebs","goa","ai"),RGN = c("BS","GOA","AI"), num=c(98,47,52)  )
nreg <- length(srvys$reg)
nspp <- length(species_lkup$sp)

for (r in 1:nreg){
  for(s in 1:nspp){

    if(srvys[r,]$reg =="ebs"){
      # first SEBS only:
      # -------------------------------
      STRATA_AREAUSE <- STRATA_AREA%>%filter(REGION==srvys$RGN[r])
      maxyr <- max(STRATA_AREAUSE$YEAR)
      STRATA_AREAUSE <- STRATA_AREAUSE%>%
        filter(YEAR==2022)%>%
        group_by(REGION,STRATUM)%>%
        summarize(AREA = mean(AREA, na.rm=T))%>%ungroup()

       flnm <- paste0("s",srvys[r,]$reg,".srvy",
                   srvys[r,]$num,".",
                   species_lkup[s,]$sp)
      cat("now getting data for: ",flnm,"\n")
      cpue_data <- suppressMessages(
        get_CPUE_DATA(
        datapath   = data.path,
        out_dir    = file.path(data.out),
        STRATA_AREAIN = STRATA_AREAUSE,
        flnm       = flnm,
        species    = species_lkup[s,]$SPECIES_CODE,
        survey     = srvys[r,]$num,
        includeNBS = FALSE,
        NEBSStrataIN = NEBS_strata ,
        saveit     = T,
        bins       = sp_bins[[ species_lkup[s,]$sp ]]))

      rm(cpue_data)

      # Now NESB + SEBS
      # -------------------------------
      flnm <- paste0(srvys[r,]$reg,".srvy",
                   srvys[r,]$num,".",
                   species_lkup[s,]$sp)
      cat("now getting data for: ",flnm,"\n")
      cpue_data <- suppressMessages(
        get_CPUE_DATA(
        datapath   = data.path,
        out_dir    = file.path(data.out),
        STRATA_AREAIN = STRATA_AREAUSE,
        flnm       = flnm,
        species    = species_lkup[s,]$SPECIES_CODE,
        survey      = srvys[r,]$num,
        includeNBS   = TRUE,
        NEBSStrataIN = NEBS_strata ,
        saveit      = T,
        bins        = sp_bins[[ species_lkup[s,]$sp ]]))

    }
    if(srvys[r,]$reg =="goa"){
      STRATA_AREAUSE <- STRATA_AREA%>%filter(REGION==srvys$RGN[r])
      maxyr <- max(STRATA_AREAUSE$YEAR)
      STRATA_AREAUSE <- STRATA_AREAUSE%>%
        filter(YEAR==1993)%>%
        group_by(REGION,STRATUM)%>%
        summarize(AREA = mean(AREA, na.rm=T))%>%ungroup()

      flnm <- paste0(srvys[r,]$reg,".srvy",
                     srvys[r,]$num,".",
                     species_lkup[s,]$sp)
      cat("now getting data for: ",flnm,"\n")
      cpue_data <- suppressMessages(
        get_CPUE_DATA(
        datapath    = data.path,
        out_dir     = file.path(data.out),
        STRATA_AREAIN = STRATA_AREAUSE,
        flnm        = flnm,
        species     = species_lkup[s,]$SPECIES_CODE,
        survey      = srvys[r,]$num,
        includeNBS = FALSE,
        NEBSStrataIN = NEBS_strata ,
        saveit      = T,
        bins        = sp_bins[[ species_lkup[s,]$sp ]]))

    }
    if(!srvys[r,]$reg%in%c("ebs","goa")){
      flnm <- paste0(srvys[r,]$reg,".srvy",
                     srvys[r,]$num,".",
                     species_lkup[s,]$sp)
      cat("now getting data for: ",flnm,"\n")
      cpue_data <- suppressMessages(
        get_CPUE_DATA(
        datapath    = data.path,
        out_dir     = file.path(data.out),
        STRATA_AREAIN = NULL,
        flnm        = flnm,
        species     = species_lkup[s,]$SPECIES_CODE,
        survey      = srvys[r,]$num,
        includeNBS = FALSE,
        NEBSStrataIN = NEBS_strata ,
        saveit      = T,
        bins        = sp_bins[[ species_lkup[s,]$sp ]]))

    }
```

```
      # # check the data :
      if(1==10){
        tt <- cpue_data%>%
              group_by(YEAR,REGION,STATIONID,SN)%>%
              filter(BIN ==400)%>%
              summarize(cnt =length(STATIONID))
         max(tt$cnt)  #Should be 1
        #this looks to be a duplicate sampling...
        #mis-entry or code error ?
         cpue_data%>%filter(YEAR==1988,STATIONID=="J-13")
      }
       rm(cpue_data)

    }
  }
#
# ```
#
# *The cpue files are now saved in the directory `r file.path(data.out,"../")`*
#
# ```{r viewcpue_data, echo=TRUE, eval=FALSE}
  # this uses the password saved in R/password.R
  #  suppressMessages(source("R/make.R"))
load(file.path(data.out,"cpue/ebs/ebs.srvy98.pcod.cpue_data.Rdata"))

names(cpue_data)

library(dplyr)

checkit <-function(x){
   if(round(max(x ),1)!=1) {
     warning("ERROR! propB > 1 ")
     print(x)}

}

  #double check the results
  cnt_ByStrataBin <- cpue_data$propByStrataBin%>%
    select("REGION","YEAR","STRATUM",BIN,BIN_mm,
           SPECIES_CODE,CN,SN,sp,num,
           "propB_ykl","propN_ykl")%>%
    group_by(YEAR,REGION,SN,CN)%>%
    summarise(sum_propB_ykl=sum(propB_ykl,na.rm=T),
              sum_propN_ykl=sum(propN_ykl,na.rm=T))

  cnt_ByStrata <- cpue_data$propByStrata%>%
    select("REGION","YEAR","STRATUM",
           SPECIES_CODE,CN,SN,sp,num,
           "propB_yk","propN_yk")%>%
    group_by(YEAR,REGION,SN,CN)%>%
    summarise(sum_propB_yk=sum(propB_yk,na.rm=T),
              sum_propN_yk=sum(propN_yk,na.rm=T))
```

```
  cnt_ByBin <- cpue_data$propByBin%>%
    select("REGION","YEAR",BIN,BIN_mm,num,
           SPECIES_CODE,CN,SN,sp,
           "propB_yl","propN_yl")%>%
    group_by(YEAR,REGION,SN,CN)%>%
    summarise(sum_propB_yl=sum(propB_yl ,na.rm=T),
              sum_propN_yl=sum(propN_yl ,na.rm=T))

  checkit(cnt_ByStrataBin$sum_propB_ykl)
  checkit(cnt_ByStrata$sum_propB_yk)
  checkit(cnt_ByBin$sum_propB_yl)

#
```

Appendix 1: `R/setup.R`primary setup script