

Get and summarize AFSC survey data

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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("data/out/2023_01_03/cpue/ebs/ebs.srvy98.plk.cpue_data.Rdata")
names(cpue_data)
```

```
## [1] "totalB_N_SEBS_NBS"      "totalB_N_SEBS"          "mnCPUE_strata_yr"
## [4] "total_bin_B_N_SEBS"     "total_bin_B_N_SEBS_NBS" "mnCPUE_strata_bin_yr"
## [7] "CPUE_station_bin_yr"    "CPUE_station_yr"
```

The data.frames are

1. **totalB_N_SEBS_NBS**: Total biomass (kg) or abundance (# of fish) for the species in each year for NEBS + SEBS survey results

2. **totalB_N_SEBS**: Total biomass (kg) or abundance (# of fish) for the species in each year for only SEBS survey results
3. **mnCPUE_strata_yr** : Average survey CPUE (kg per Km2) or abundance (# per Km2) for the species in each strata and year
4. **total_bin_B_N_SEBS**: Total biomass (kg) or abundance (# of fish) for each bin (10 mm) for the species in each year for NEBS + SEBS survey results
5. **total_bin_B_N_SEBS_NBS** : Total biomass (kg) or abundance (# of fish) for each bin (10 mm) for the species in each year for only the SEBS survey results
6. **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
7. **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
8. **CPUE_station_yr**: Station specific survey CPUE (kg per Km2) or abundance (# per Km2) for the species in each year

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 :

$$B_{s,y} = CPUE_{s,k,y} \cdot A_k$$

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

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

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 estimate the weight of each size fish j measured (\hat{W}) to calculate the proportion by weight or frequency at each station where

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

and

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

and

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

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

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

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

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

and

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

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`. The code below then loads these settings as well as base data, functions, and packages.

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

Step 1: Update SQL queries (level1)

This step must be run on a computer that has access to RACEBASE. The code below will generate the base files for steps 2 and 3 below, and will save them in the folder `data/in/2023_01_03` under subfolders for each region in `srvys$reg` and each species in `splist` (see `R/setup.R` to change these settings).

IMPORTANT:

- This step must be run in 32 bit R (RODBC doesn't run in 64 bit R) and 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 32 bit version of R.
- The code will connect to the SQL database using your password and username. Remember to update the `username_path` in the first line of the `R/setup.R` file and corresponding username and password under `username_password.R`. A template is available under `R/`.

```
# update the SQL queries
#-----
source(file.path(code.path, "R/sub_scripts/runRACE_qrys.R"))
```

Step 2: Update the LWA regressions

The default code for RACEBASE uses set LW relationships, however we prefer to update the LW regressions using glms. Depending on how many observations exist the LW relationships can be region specific or use data across all regions. The default below is all regions combined. This code generates two outputs in `data/out/2023_01_03`, `LWGlms_srvy_all_regs.Rdata` and `LW_SmryTable.Rdata`. It also updates the `species_lkup$LW_a` and `species_lkup$LW_b` parms used in Step 3.

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

if(update_LWdata==1){
  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, region, and species.

```

nreg <- length(srvys$reg)
nspp <- length(species_lkup$sp)

for (r in 1:nreg){
  for(s in 1:nspp){
    flnm <- paste0(srvys[r,]$reg, ".srvy",
                  srvys[r,]$num, ".",
                  species_lkup[s,]$sp)
    cat("now getting data for: ", flnm, "\n")
    cpue_data <- suppressMessages(
      get_CPUE_DATA(
        datapath = data.path,
        out_dir  = file.path(data.out),
        flnm     = flnm,
        species  = species_lkup[s,]$SPECIES_CODE,
        survey   = srvys[r,]$num,
        includeNBS = TRUE,
        saveit   = T,
        bins     = sp_bins[[ species_lkup[s,]$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 data/out/2023_01_03/..

Step 4: calc propB for use in biomass weighting age or diet data

TBA

AFSC_CPUE			
Name	Date Modified	Size	Kind
data	Today at 1:14 PM	--	Folder
in	Today at 1:14 PM	--	Folder
newest	Today at 2:24 PM	--	Folder
out	Today at 2:26 PM	--	Folder
cpue	Today at 2:28 PM	--	Folder
ai	Today at 2:28 PM	--	Folder
ebs	Today at 2:28 PM	--	Folder
goa	Today at 2:28 PM	--	Folder
goa.srvy47.atf.cpue.Rdata	Today at 2:53 PM	4.5 MB	R Data File
goa.srvy47.halibut.cpue.Rdata	Today at 2:53 PM	2.4 MB	R Data File
goa.srvy47.pcod.cpue.Rdata	Today at 2:52 PM	2 MB	R Data File
goa.srvy47.plk.cpue.Rdata	Today at 2:52 PM	2.1 MB	R Data File
goa.srvy47.sablefish.cpue.Rdata	Today at 2:53 PM	1.3 MB	R Data File
Out_SMRY_QRYS	Today at 3:00 PM	--	Folder
figs	Apr 21, 2021 at 7:26 PM	--	Folder

Step

5: Get annual biomass by age and CEATTLE bins:

Appendix 1: R/setup.Rprimary setup script

```

#*
#* setup.R
#*
#* Base script for setting up the queries and code
#* Kirstin.holsman@noaa.gov
#*
#*

# Set up SQL stuff:
#-----
username_path <- "not_shared" # copy the template from the data/in folder to not_shared
qrydate      <- format(Sys.time(), "%Y_%m_%d")

# Set switches for this code
#-----
fromPC      <- FALSE # Set to true if on the PC
update.qrys <- 0
update.srv_biomass <- 0 # do you want to update the survey biomass data; 1=yes, 0= no
update.LWdatat <- 0 # set to 1 to update LW regressions
update.species_lookup <- 0 # update the species_lookup table? (needed if species or regions below change)
all.dat      <- 1 # run query for full data?
update_srvyArea <- FALSE # re-query survey area?

# KEY : Specify the size bins & species and order for the query (get_CPUE_srvy.R)
#-----
subreg      <- "GOA" # can be "BS", "GOA", or "AI"

splist <- c(
  plk      = "walleye pollock",
  pcod     = "Pacific cod",
  atf      = "arrowtooth flounder",
  sablefish = "sablefish",
  halibut  = "Pacific halibut")

sp_bins <- list()
for(s in 1:length(splist))
  sp_bins[[ names(splist)[s]]] <- c(0,400,800,2000) # juvenile adult designations:

sp_bins <- list()
for(s in 1:length(splist))
  sp_bins[[ names(splist)[s]]] <- c(seq(0,1500,10),1e6) # 1 cm bins

srvs <- data.frame(reg=c("ebs","goa","ai"),num=c(98,47,52) )
# surveys%>%filter(REGION=="GOA",SURVEY_NAME=="Gulf of Alaska Bottom Trawl Survey")%>%select(SURVEY_DEFINITION_ID)
# survey = 143 Northern Bering Sea survey
# survey = 98 Eastern Bering Sea Crab/Groundfish Bottom Trawl Survey
# survey = 52 Aleutian Islands Bottom Trawl Survey
# survey = 47 Gulf of Alaska Bottom Trawl Survey

# General setup
#-----

```