WCANN: West Coast Annual survey data processing summary

fishglob, Aurore A. Maureaud, Juliano Palacios Abrantes, Zoë Kitchel, Dan Forrest, & Michelle Stuart

December, 2022

Contents

General info

This document presents the cleaning code and summary of the West Coast US Annual bottom trawl survey provided by Aimee Keller, Fisheries Research Surveys Supervisor, NOAA, NMFS, NWFSC, FRAM and John Buchanan Fisheries Biologist, Groundfish Ecology Program, Northwest Fisheries Science Center. It contains data from 2003 and up to 2018. Before 2003, a similar region is sampled in the West Coast US Triennial Slope and Shelf Survey (WCTRI).

Data cleaning in R

```
##############################################################################
#### R code to clean trawl survey West Coast US Annual Survey (WCANN)
#### Public data Ocean Adapt
#### Contacts:  Aimee Keller    smartt@dnr.sc.gov,  Fisheries Research Surveys Supervisor
#####                      NOAA, NMFS, NWFSC, FRAM
#####         John Buchanan john.buchanan@noaa.gov  Fisheries Biologist
#####                      Groundfish Ecology Program, Northwest Fisheries Science Center
#### Coding: Michelle Stuart, Dan Forrest, Zoë Kitchel November 2021
##############################################################################

#------------------------------------------------------------------------------#
#### LOAD LIBRARIES AND FUNCTIONS ####
#------------------------------------------------------------------------------#
```

```
library(rfishbase) #needs R 4.0 or more recent
library(tidyverse)
library(lubridate)
library(googledrive)
library(taxize) # for getting correct species names
library(magrittr) # for names wrangling
library(PBSmapping)


source("functions/clean_taxa.R")
source("functions/write_clean_data.R")

#Data for the West Coast US Annual Survey can be best accessed using the public
#Pinsky Lab Ocean Adapt Git Hub Repository.
#Contact malin.pinsky@rutgers.edu for questions or help accessing

#-------------------------------------------------------------------------------------------#
#### PULL IN AND EDIT RAW DATA FILES ####
#-------------------------------------------------------------------------------------------#

temp <- tempfile()
download.file(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/wcann_catch.csv.zip", temp)

wcann_catch <- read_csv(unz(temp, "wcann_catch.csv"), col_types = cols(
  catch_id = col_integer(),
  common_name = col_character(),
  cpue_kg_per_ha_der = col_double(),
  cpue_numbers_per_ha_der = col_double(),
  date_yyyymmdd = col_integer(),
  depth_m = col_double(),
  latitude_dd = col_double(),
  longitude_dd = col_double(),
  pacfin_spid = col_character(),
  partition = col_character(),
  performance = col_character(),
  program = col_character(),
  project = col_character(),
  sampling_end_hhmmss = col_character(),
  sampling_start_hhmmss = col_character(),
  scientific_name = col_character(),
  station_code = col_double(),
  subsample_count = col_integer(),
  subsample_wt_kg = col_double(),
  total_catch_numbers = col_integer(),
  total_catch_wt_kg = col_double(),
  tow_end_timestamp = col_datetime(format = ""),
  tow_start_timestamp = col_datetime(format = ""),
  trawl_id = col_double(),
  vessel = col_character(),
  vessel_id = col_integer(),
  year = col_integer(),
  year_stn_invalid = col_integer()
```

```
))

wcann_haul <- read_csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/wcann_haul.csv",
                       col_types = cols(
  area_swept_ha_der = col_double(),
  date_yyyymmdd = col_integer(),
  depth_hi_prec_m = col_double(),
  invertebrate_weight_kg = col_double(),
  latitude_hi_prec_dd = col_double(),
  longitude_hi_prec_dd = col_double(),
  mean_seafloor_dep_position_type = col_character(),
  midtow_position_type = col_character(),
  nonspecific_organics_weight_kg = col_double(),
  performance = col_character(),
  program = col_character(),
  project = col_character(),
  sample_duration_hr_der = col_double(),
  sampling_end_hhmmss = col_character(),
  sampling_start_hhmmss = col_character(),
  station_code = col_double(),
  tow_end_timestamp = col_datetime(format = ""),
  tow_start_timestamp = col_datetime(format = ""),
  trawl_id = col_double(),
  vertebrate_weight_kg = col_double(),
  vessel = col_character(),
  vessel_id = col_integer(),
  year = col_integer(),
  year_stn_invalid = col_integer()
))

# It is ok to get warning message that missing column names filled in: 'X1' [1].

#-------------------------------------------------------------------------------------------#
#### REFORMAT AND MERGE DATA FILES ####
#-------------------------------------------------------------------------------------------#


wcann <- left_join(wcann_haul, wcann_catch, by = c(
  "trawl_id", "year", "date_yyyymmdd", "station_code",
   "performance","program","project","sampling_end_hhmmss",
    "sampling_start_hhmmss","tow_end_timestamp","tow_start_timestamp",
    "vessel","vessel_id","year_stn_invalid"))
wcann <- wcann %>%
  mutate(
    # create haul_id
    haul_id = trawl_id,
    # Add "strata" (define by lat, long and depth bands) where needed # no need to use
    #lon grids on west coast (so narrow)
    stratum = paste(floor(latitude_dd)+0.5, floor(depth_m/100)*100 + 50, sep= "-"),
    # adjust for tow area # kg per km2 (hectare/100 = km2)
    area_swept = (area_swept_ha_der/100), #km^2
    wgt_cpue = total_catch_wt_kg/area_swept,
```

```
    num_cpue = total_catch_numbers/area_swept,
    #note that sample duration is already in hours
    wgt_h = total_catch_wt_kg/sample_duration_hr_der,
    #note that sample duration is already in hours
    num_h = total_catch_numbers/sample_duration_hr_der,
    date = ymd(date_yyyymmdd),
    month = month(date),
    day = day(date),
    quarter = case_when(month %in% c(1,2,3) ~ 1,
                        month %in% c(4,5,6) ~ 2,
                        month %in% c(7,8,9) ~ 3,
                        month %in% c(10,11,12) ~ 4),
    season = NA_character_,
  )


wcann <- wcann %>%
  rename(latitude = latitude_dd,
         longitude = longitude_dd,
         depth = depth_m,
         wgt = total_catch_wt_kg,
         num = total_catch_numbers,
         haul_dur = sample_duration_hr_der,
         spp = scientific_name,
         station = station_code) %>%
  # remove non-fish
  filter(!grepl("Egg", partition),
         !grepl("crushed", spp),
         #remove non satisfactory tows where target speed was not maintained
         performance == "Satisfactory"
         ) %>%
  # adjust spp names
  mutate(
    spp = ifelse(grepl("Lepidopsetta", spp), "Lepidopsetta sp.", spp),
    spp = ifelse(grepl("Bathyraja", spp), 'Bathyraja sp.', spp)
  ) %>%
  # add survey column and fill missing columns
  mutate(survey = "WCANN",
         source = "NOAA",
         timestamp = mdy("04/07/2021"),
         sbt = NA,
         sst = NA,
         country = "United States",
         continent = "n_america",
         sub_area = NA,
         stat_rec = NA,
         verbatim_name = spp,
         gear = NA) %>%
  select(survey, haul_id, source, timestamp, country, sub_area, continent, stat_rec,
         station, stratum, year,
         month, day, quarter, season, latitude, longitude, haul_dur,
         area_swept, gear, depth, sbt, sst,
         num, num_h, num_cpue, wgt, wgt_h, wgt_cpue, verbatim_name)
```

```r
#many rows with missing num_h, num_cpue, wgt_h, and wgt_cpue values
#due to missing haul_dur

#sum duplicates
wcann <- wcann %>%
  group_by(survey,
           source,timestamp,
           haul_id, country, sub_area, continent, stat_rec, station, stratum,
           year, month, day, quarter, season, latitude, longitude, haul_dur, area_swept,
           gear, depth, sbt, sst,verbatim_name) %>%
  summarise(num = sum(num, na.rm = T),
            num_h = sum(num_h, na.rm = T),
            num_cpue = sum(num_cpue, na.rm = T),
            wgt = sum(wgt, na.rm = T),
            wgt_h = sum(wgt_h, na.rm = T),
            wgt_cpue = sum(wgt_cpue, na.rm = T)) %>% ungroup()

#check for duplicates, should not be any with more than 1 obs
#check for duplicates
count_wcann <- wcann %>%
  group_by(haul_id, verbatim_name) %>%
  mutate(count = n())

#none!

#which ones are duplicated?
unique_name_match <- count_wcann %>%
  group_by(verbatim_name) %>%
  filter(count>1) %>%
  distinct(verbatim_name)

unique_name_match
#empty

#now, I will sum over these duplicated verbatim names
#Porifera
#Bathyraja sp.
#Merluccius productus
#Nudibranchia
#Strongylocentrotus
#Pagurus
#Pennatulacea
#Ceramaster
#Neptunea
#Rossellinae
#Gorgonacea
#Colus
#Munidopsis
#Sebastes sp. (aleutianus / melanostictus)
#Buccinum
#Ophiacantha
#Glyptocephalus zachirus
#Oncorhynchus tshawytscha
```

```
#Antipatharia
#Urticina
#Stomphia
#Hormathiidae
#Halipteris
#Molpadia intermedia
#Sebastes sp. (miniatus / crocotulus)
#Hexactinosida
#Suberites


#-------------------------------------------------------------------------------------------#
#### INTEGRATE CLEAN TAXA FROM TAXA ANALYSIS ####
#-------------------------------------------------------------------------------------------#

# Get WoRM's id for sourcing
wrm <- gnr_datasources() %>%
  filter(title == "World Register of Marine Species") %>%
  pull(id)

### Automatic cleaning
# Set Survey code
wcann_survey_code <- "WCANN"

wcann <- wcann %>%
  mutate(
    taxa2 = str_squish(verbatim_name),
    taxa2 = str_remove_all(taxa2," spp.| sp.| spp| sp|NO "),
    taxa2 = str_to_sentence(str_to_lower(taxa2)))

# Get clean taxa
clean_auto <- clean_taxa(unique(wcann$taxa2), input_survey = wcann_survey_code)
# takes 4.5 mins

#This cuts out the following species, one should be added

#1 Nearchaster aciculosus
#2 Cheiraster dawsoni
#3 Crangon communis
#4 Cancer gracilis
#5 Cancer anthonyi
#6 Cancer branneri
#7 Cyclopterinae (fish, but only to genus)

cyclop <- c("Cyclopterinae", NA, NA, "Cyclopterinae", "Animalia", "Chordata","Actinopteri",
            "Scorpaeniformes", "Cyclopteridae", "NA", "Family", "WCANN")

clean_auto.missing <- rbind(clean_auto, cyclop)


#-------------------------------------------------------------------------------------------#
#### INTEGRATE CLEAN TAXA in WCANN survey data ####
#-------------------------------------------------------------------------------------------#
```

```r
clean_taxa <- clean_auto.missing %>%
  select(-survey)

clean_wcann <- left_join(wcann, clean_taxa, by=c("taxa2"="query")) %>%
  filter(!is.na(taxa)) %>% # query does not indicate taxa entry that were
  #removed in the cleaning procedure
  # so all NA taxa have to be removed from the surveys because: non-existing,
  #non marine or non fish
  rename(accepted_name = taxa,
         aphia_id = worms_id) %>%
  mutate(verbatim_aphia_id = NA) %>%
  select(survey, haul_id, source, timestamp, country, sub_area, continent, stat_rec, station, stratum,
         year, month, day, quarter, season, latitude, longitude,
         haul_dur, area_swept, gear, depth, sbt, sst, num, num_h, num_cpue, wgt,
         wgt_h, wgt_cpue,
         verbatim_name, verbatim_aphia_id, accepted_name, aphia_id, SpecCode,
         kingdom, phylum, class, order, family, genus, rank)


#check for duplicates
count_clean_wcann <- clean_wcann %>%
  group_by(haul_id, accepted_name) %>%
  mutate(count = n())

#none!

#which ones are duplicated?
unique_name_match <- count_clean_wcann %>%
  group_by(verbatim_name, accepted_name) %>%
  filter(count>1) %>%
  distinct(verbatim_name, accepted_name)

unique_name_match
#not empty

#a few duplicates are maintained with different verbatim name
#and the same accepted names. Data users should decide if they want to sum over.
#currently, these are independent observations

#Sebastes or not
#verbatim name                              accepted name
#Sebastes                                  Sebastes
#Sebastes sp. (miniatus / crocotulus)      Sebastes
#Sebastes sp. (aleutianus / melanostictus) Sebastes
# ------------------------------------------------------------------------------#
#### SAVE DATABASE IN GOOGLE DRIVE ####
# ------------------------------------------------------------------------------#

# Just run this routine should be good for all
write_clean_data(data = clean_wcann, survey = "WCANN", overwrite = T)
```

1. Overview of the survey data table

survey	haul_id	source	timestamp	country	sub_area	continent
WCANN	2.00303e+11	NOAA	2021-04-07	United States	NA	n_america
WCANN	2.00303e+11	NOAA	2021-04-07	United States	NA	n_america
WCANN	2.00303e+11	NOAA	2021-04-07	United States	NA	n_america
WCANN	2.00303e+11	NOAA	2021-04-07	United States	NA	n_america
WCANN	2.00303e+11	NOAA	2021-04-07	United States	NA	n_america

stat_rec	station	stratum	year	month	day	quarter	season
NA	7277	46.5-550	2003	8	31	3	NA
NA	7277	46.5-550	2003	8	31	3	NA
NA	7277	46.5-550	2003	8	31	3	NA
NA	7277	46.5-550	2003	8	31	3	NA
NA	7277	46.5-550	2003	8	31	3	NA

latitude	longitude	haul_dur	area_swept	gear	depth
46.30417	-124.725	0.294722	0.0165671	NA	527.5
46.30417	-124.725	0.294722	0.0165671	NA	527.5
46.30417	-124.725	0.294722	0.0165671	NA	527.5
46.30417	-124.725	0.294722	0.0165671	NA	527.5
46.30417	-124.725	0.294722	0.0165671	NA	527.5

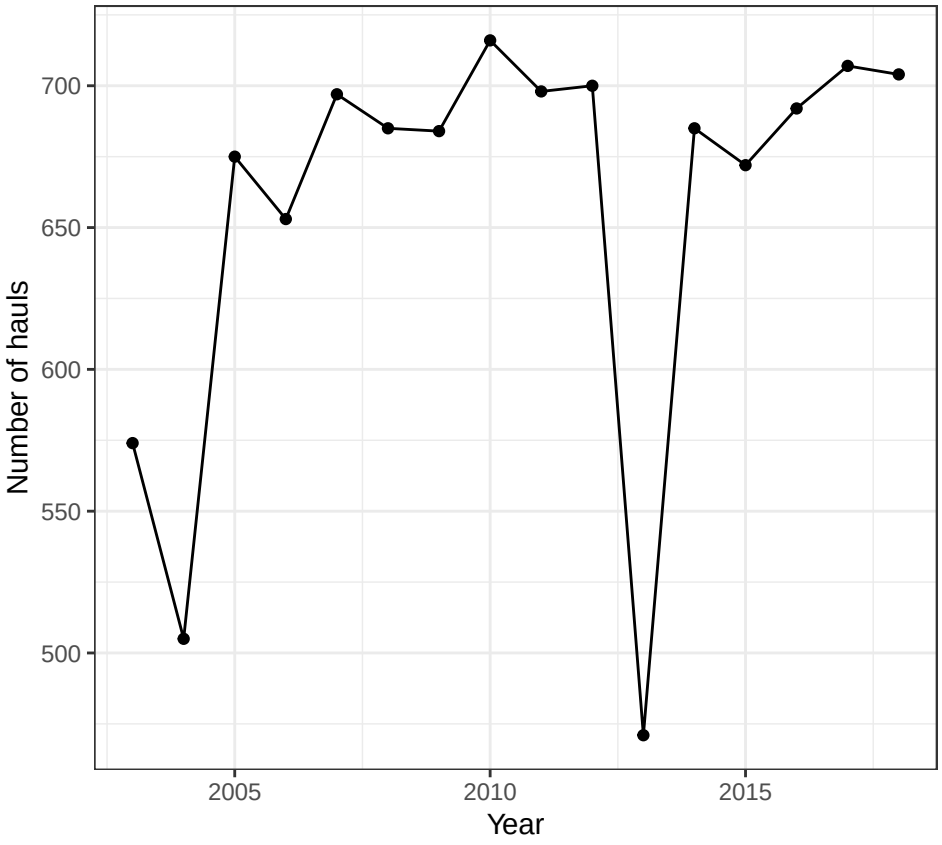
sbt	sst	num	num_h	num_cpue	wgt
NA	NA	8	27.144224	482.88335	10.800
NA	NA	20	67.860560	1207.20839	2.300
NA	NA	15	50.895420	905.40629	4.050
NA	NA	2	6.786056	120.72084	0.005
NA	NA	1	3.393028	60.36042	0.900

wgt_h	wgt_cpue	verbatim_name	verbatim_aphia_id	accepted_name
36.6447025	651.8925282	Anoplopoma fimbria	NA	Anoplopoma fimbria
7.8039644	138.8289643	Antimora microlepis	NA	Antimora microlepis
13.7417634	244.4596981	Apristurus brunneus	NA	Apristurus brunneus
0.0169651	0.3018021	Bathyagonus nigripinnis	NA	Bathyagonus nigripinnis
3.0537252	54.3243774	Bathyraja sp.	NA	Bathyraja

aphia_id	SpecCode	kingdom	phylum	class	order	family
159463	512	Animalia	Chordata	Actinopteri	Perciformes	Anoplopomatidae
272460	2006	Animalia	Chordata	Actinopteri	Gadiformes	Moridae
158512	763	Animalia	Chordata	Elasmobranchii	Carcharhiniformes	Pentanchidae
254505	4161	Animalia	Chordata	Actinopteri	Perciformes	Agonidae
105761	NA	Animalia	Chordata	Elasmobranchii	Rajiformes	Arhynchobatidae

2. Summary of sampling intensity

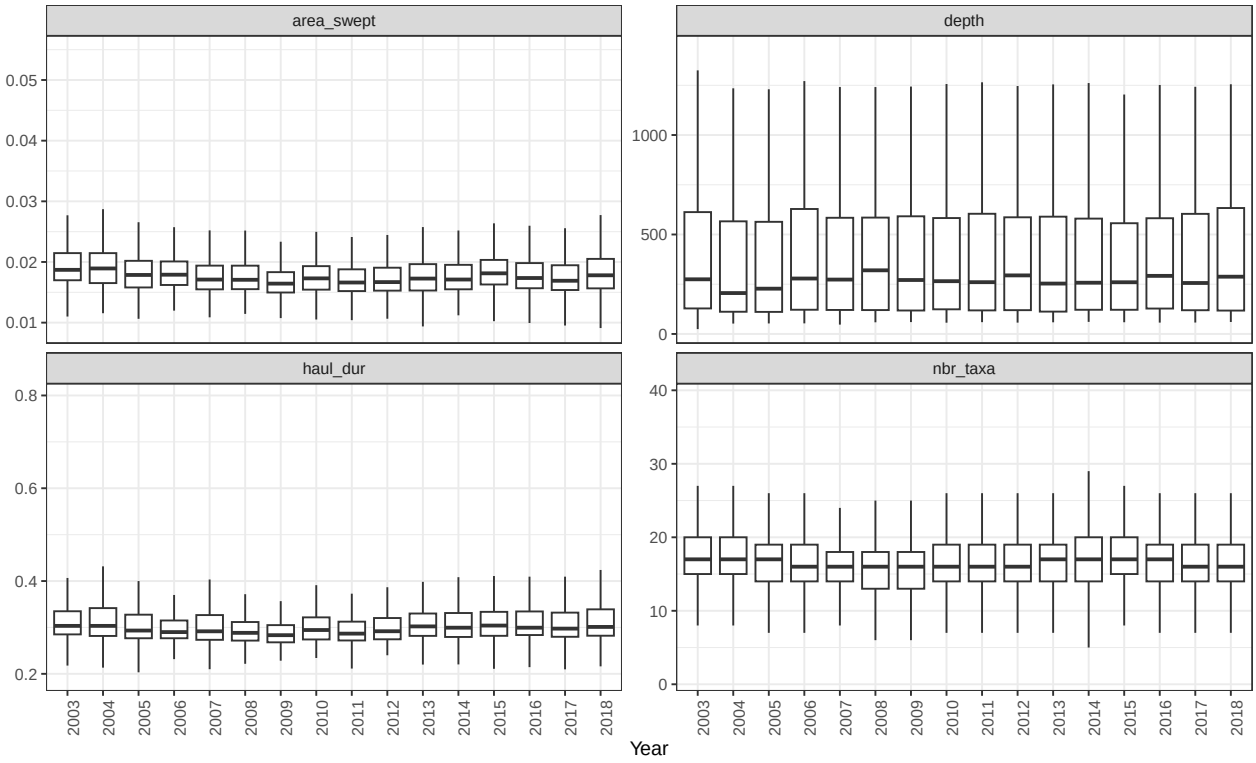
Number of hauls per year performed during the survey after data processing.



3. Summary of sampling variables from the survey

Here we show the yearly total and average of the following variables reported in the survey data:

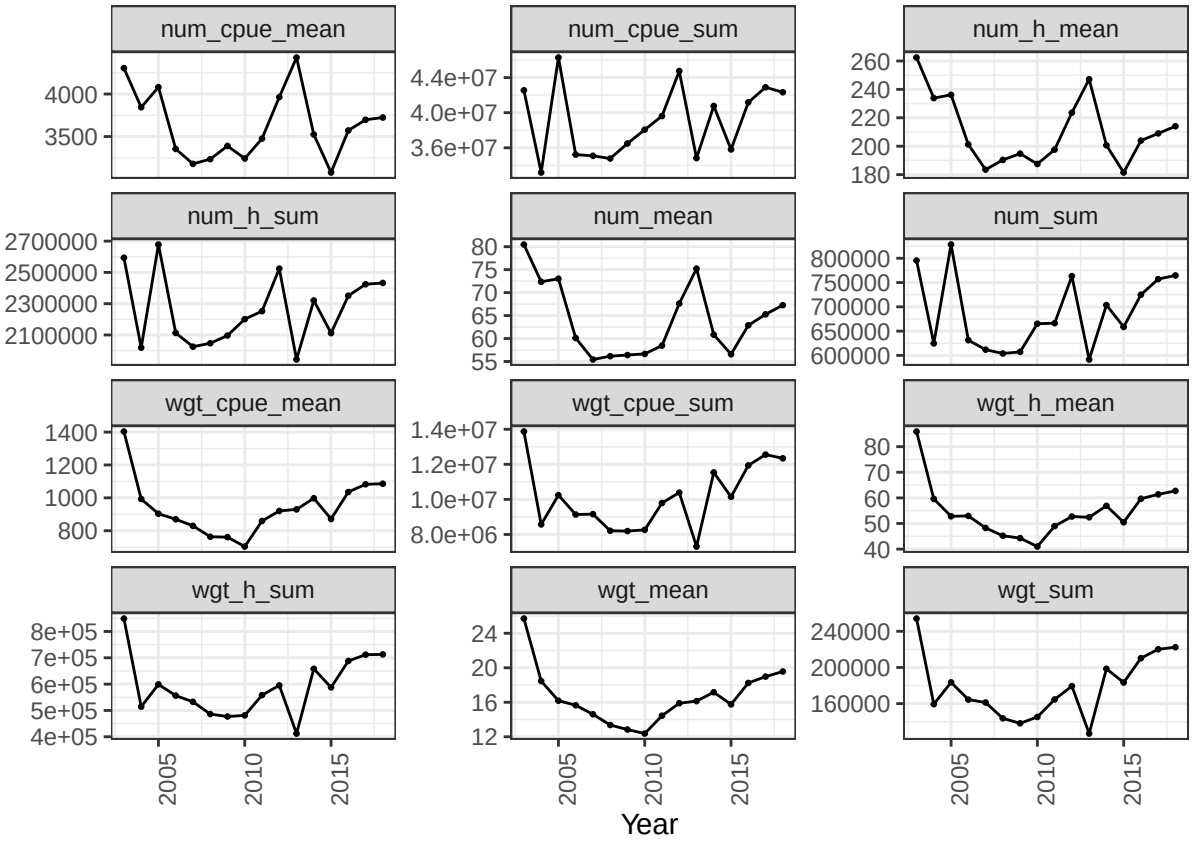
- *area_swept*, swept area by the bottom trawl gear km^2
- *depth*, sampling depth in m
- *haul_dur*, haul sampling duration *hour*
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (https://www.marinespecies.org/, October 2021)



4. Summary of biological variables

Here we display the yearly total and average across hauls of the following variables recorded in the data:

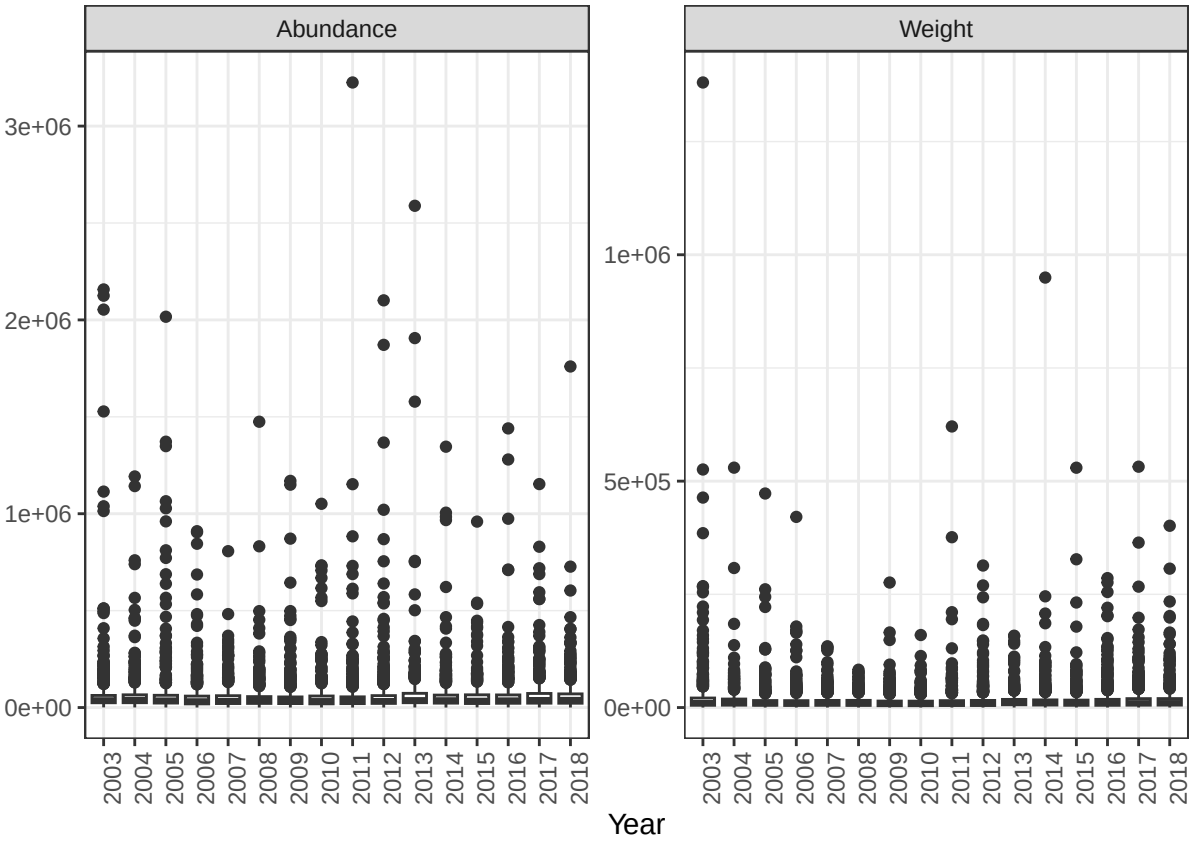
- *num_cpue*, number of individuals (abundance) in $\frac{individuals}{km^2}$
- *num_h*, number of individuals (abundance) in $\frac{individuals}{h}$
- *num*, number of individuals (abundance)
- *wgt_cpue*, weight in $\frac{kg}{km^2}$
- *wgt_h*, weight in $\frac{kg}{h}$
- *wgt*, weight in kg



5. Extreme values

Here we show a yearly total distribution of the biomass data to visualize outliers:

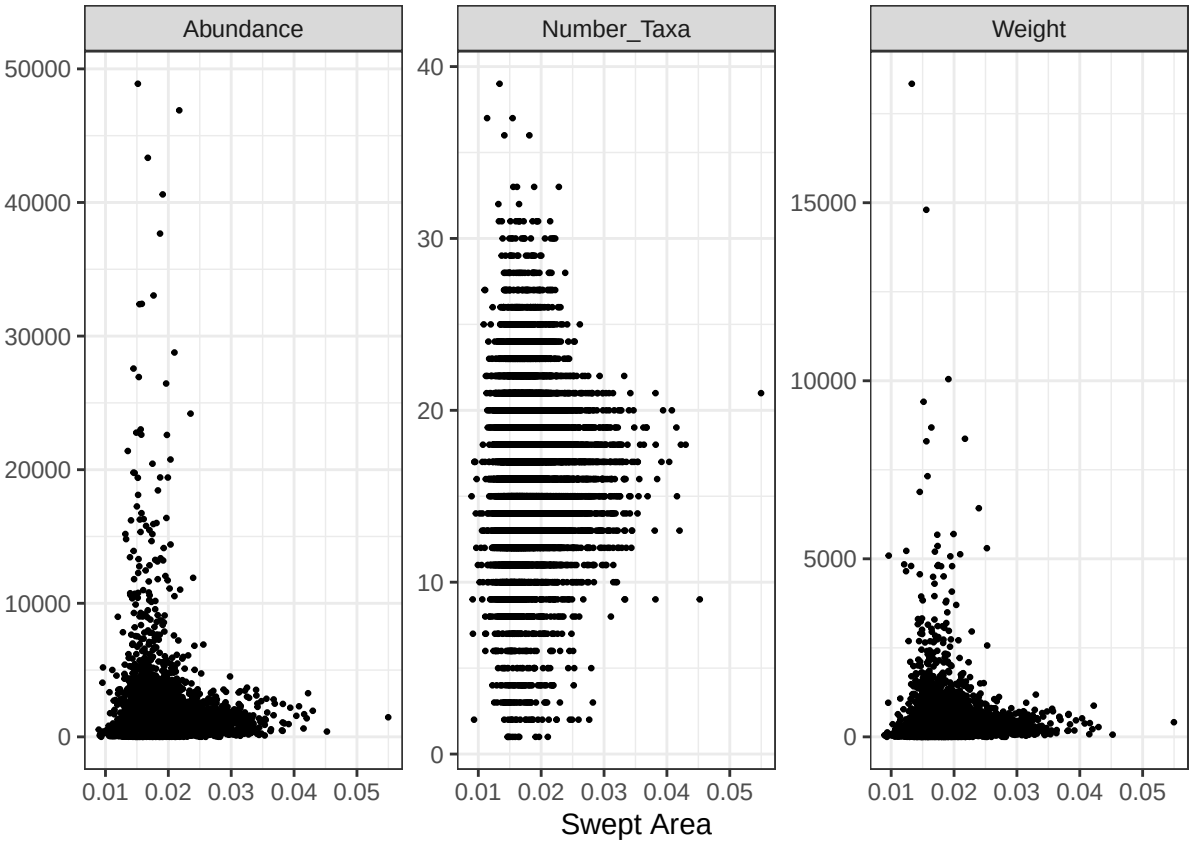
- *wgt*, total weight in *kg* per haul and year per haul and year, if available in the survey data
- *num*, total number of individuals, if available in the survey data



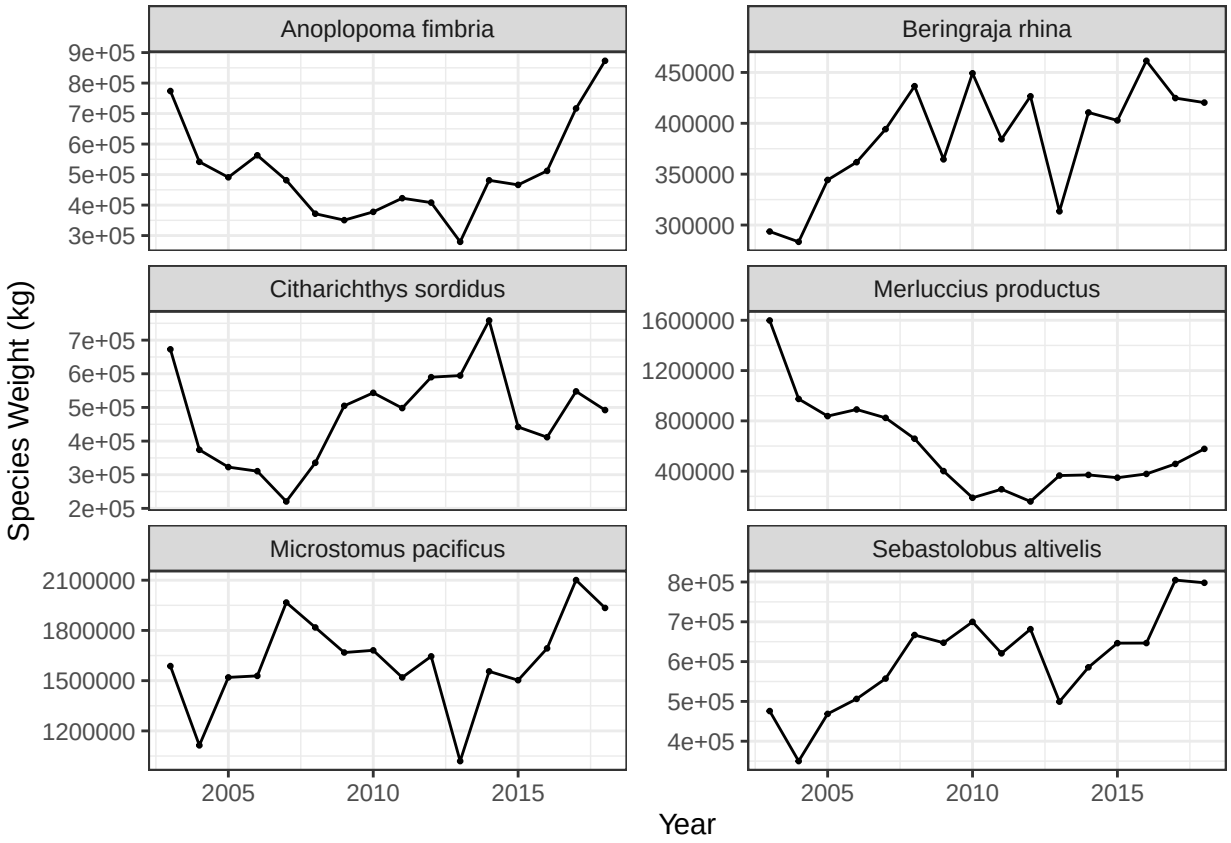
6. Summary of variables against swept area

Here we show the total abundance and number of taxa relationships with the area swept:

- *nbr_taxa*, number of marine fish taxa after taxonomic data cleaning
- *num*, number of individuals, if available in the survey data
- *wgt*, weight in *kg*, if available in the survey data

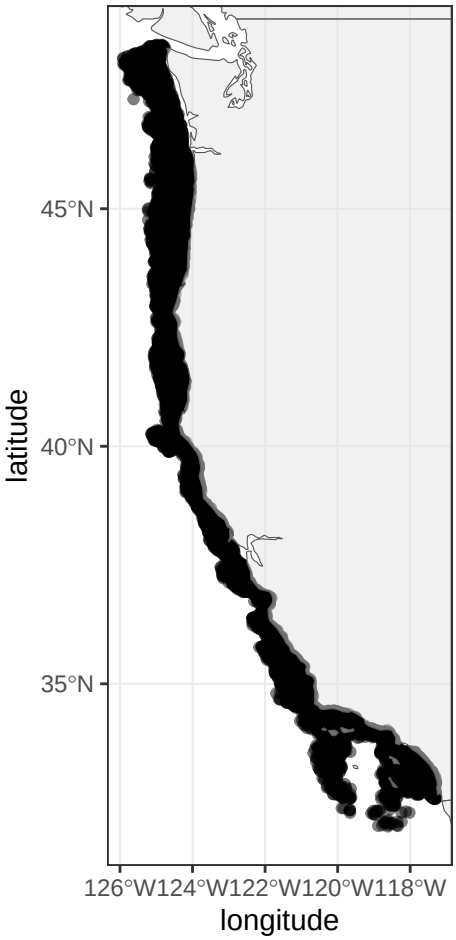


7. Abundance or Weight trends of the six most abundant species



8. Distribution mapping

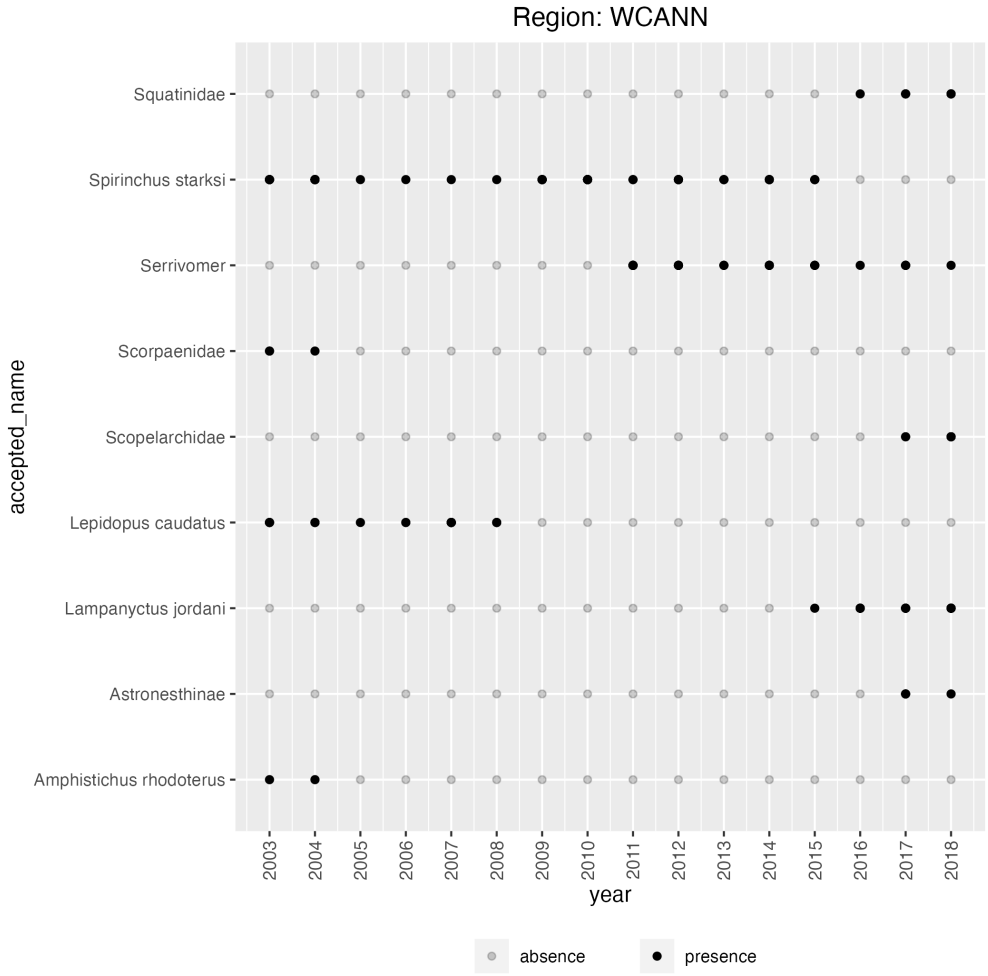
Map of the sampling distribution in space. Note that we only show one year per coordinate.



9. Taxonomic flagging

This species flagging method was adapted from https://github.com/pinskylab/OceanAdapt/blob/master/R/add-spp-to-taxonomy.Rmd#L33

Visualization of flagged taxa



Statistics related to the taxonomic flagging outputs

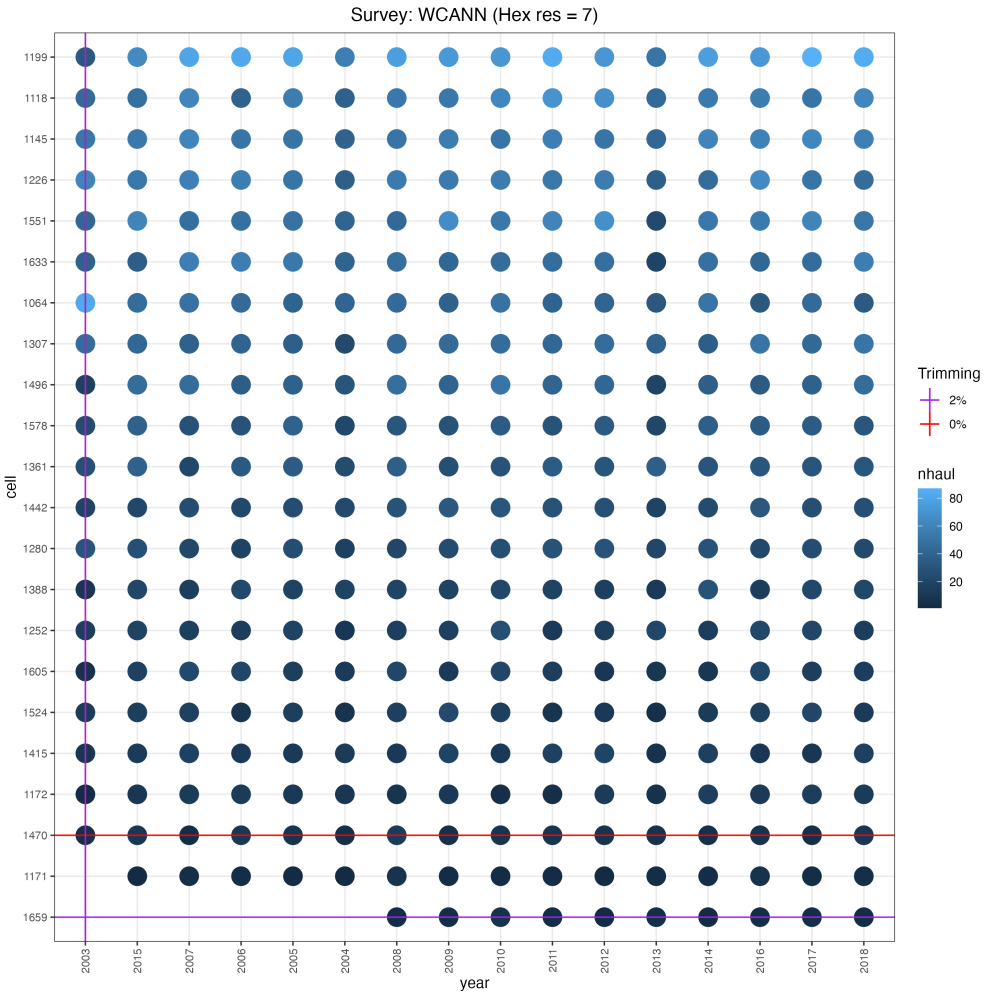
Total number of species	455
Percentage of species flagged	2

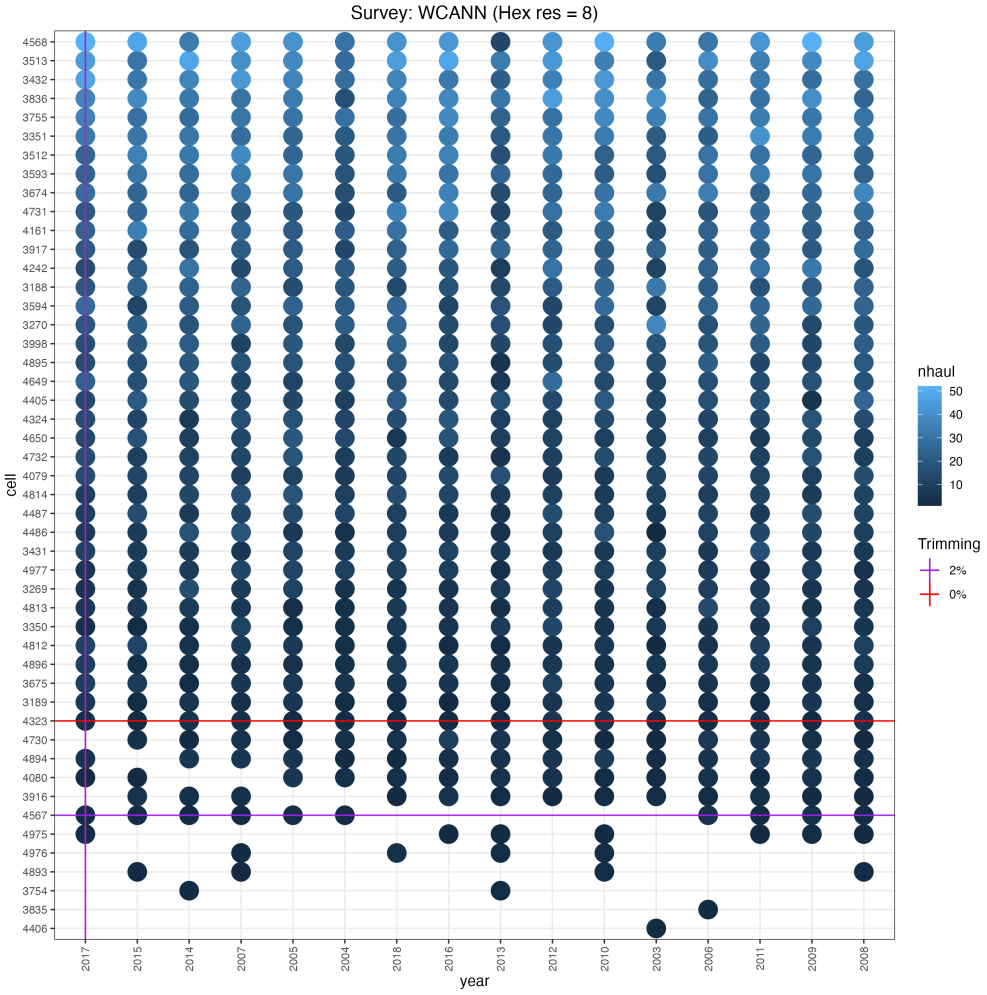
10. Spatio-temporal standardization

a. Standardization method 1

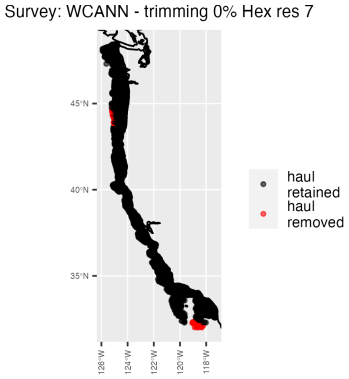
This standardization method was adapted from https://github.com/zoekitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd
It was run for hex resolution 7 and 8.

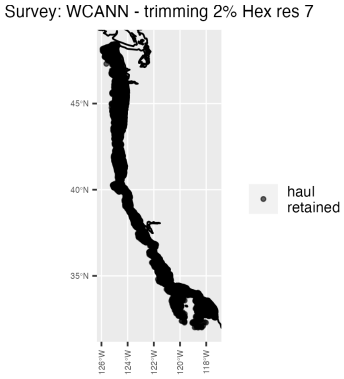
Plot of number of cells x years with overlaid flagging options

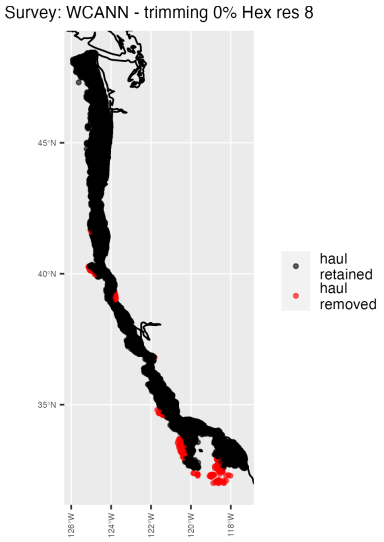

Survey: WCANN (Hex res = 7)
cell
1199
1118
1145
1226
1551
1633
1064
1307
1496
1578
1361
1442
1280
1388
1252
1605
1524
1415
1172
1470
1171
1659
year
2003
2015
2007
2006
2005
2004
2008
2009
2010
2011
2012
2013
2014
2016
2017
2018
Trimming
2%
0%
nhaul
80
60
40
20

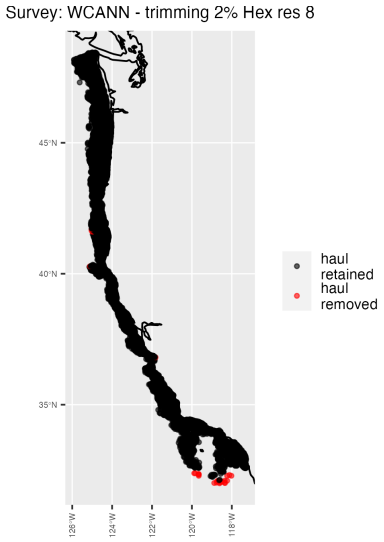


Map of hauls retained and removed per flagging method and threshold

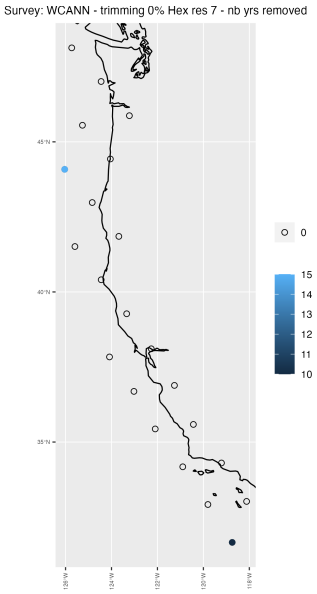


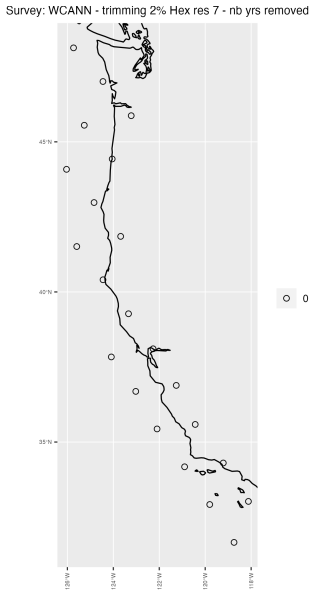


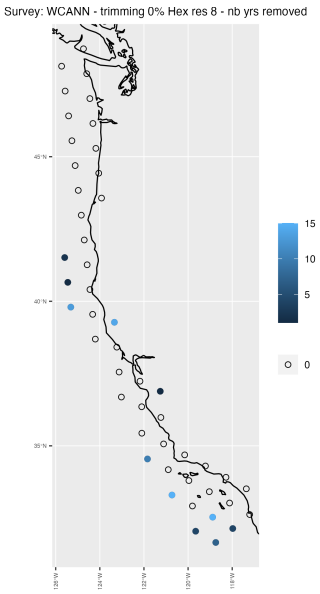


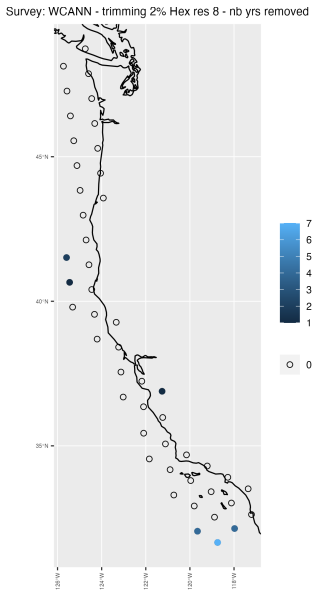


Map of numbers of years removed per grid cell and flagging method/threshold





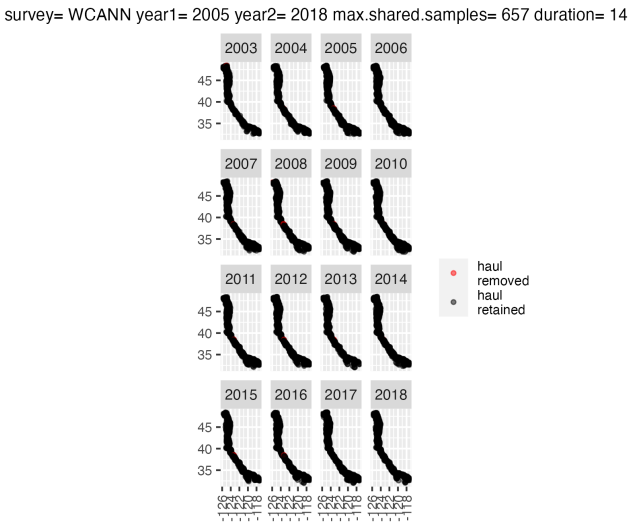




b. Standardization method 2

This standardization method was adapted from BioTIME code from https://github.com/Wubing-Xu/Range_size_winners_losers

Map of hauls retained and removed



c. Standardization summary

Statistics of hauls removed for each standardization method

summary	grid cell 7, 0% threshold	grid cell 7, 2% threshold	grid cell 8, 0% threshold	grid cell 8, 2% threshold	method 2 (biotime)
number of hauls removed	70.0	0	236.0	28.0	526.0
percentage of hauls removed	0.7	0	2.2	0.3	0.3