DFO-QCS: Department of Fisheries Oceans Canada Queen Charlotte Sound survey data processing summary

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December, 2022

Contents

General info

This document presents the cleaning code and summary of the Queen Charlotte Sound (Department of Fisheries Oceans Canada) bottom trawl survey provided by Shelee Hamilton, and Maria Cornthwaite. It contains data from 2003 and up to 2019.

Data cleaning in R

```
##############################################################################
#### R code to clean trawl survey DFO Queen Charlotte Sound
#### Public data Ocean Adapt
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#### Fishery & Assessment Data Section, Science Branch, DFO Canada
####           Maria Cornthwaite    Maria.Cornthwaite@dfo-mpo.gc.ca Program Head,
#### Groundfish Data Unit, Science Branch, DFO Canada
#### Coding: Dan Forrest, Zoë Kitchel November 2021
##############################################################################

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

```
library(tidyverse)
library(lubridate)
library(googledrive)
library(taxize) # for getting correct species names
library(magrittr) # for names wrangling
library(readr)
library(dplyr)
library(PBSmapping)

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

#Data for the Queen Charlotte Sound can be best accessed using the Pinsky
#Lab Ocean Adapt Git Hub Repository.
#Contact malin.pinsky@rutgers.edu for questions or help accessing

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


#Queen Charlotte Sound

QCS_catch <- read_csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/QCS_catch.csv",
                      col_types = cols(
  Survey.Year = col_integer(),
  Trip.identifier = col_integer(),
  Set.number = col_integer(),
  ITIS.TSN = col_integer(),
  Species.code = col_character(),
  Scientific.name = col_character(),
  English.common.name = col_character(),
  French.common.name = col_character(),
  LSID = col_character(),
  Catch.weight..kg. = col_double(),
  Catch.count..pieces. = col_integer()
))

QCS_effort <- read_csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/QCS_effort.csv",
  col_types =
                          cols(
                            Survey.Year = col_integer(),
                            Trip.identifier = col_integer(),
                            Vessel.name = col_character(),
                            Trip.start.date = col_character(),
                            Trip.end.date = col_character(),
                            GMA = col_character(),
                            PFMA = col_character(),
                            Set.number = col_integer(),
                            Set.date = col_character(),
                            Start.latitude = col_double(),
```

```
                            Start.longitude = col_double(),
                            End.latitude = col_double(),
                            End.longitude = col_double(),
                            Bottom.depth..m. = col_double(),
                            Tow.duration..min. = col_integer(),
                            Distance.towed..m. = col_double(),
                            Vessel.speed..m.min. = col_double(),
                            Trawl.door.spread..m. = col_double(),
                            Trawl.mouth.opening.height..m. = col_double()
                          )) %>%
  select(Trip.identifier, Set.number,Survey.Year,Set.date, Trip.start.date,Trip.end.date,
         GMA, PFMA,Set.date, Start.latitude,Start.longitude, End.latitude, End.longitude,
         Bottom.depth..m., Tow.duration..min.,Distance.towed..m., Trawl.door.spread..m.,
         Trawl.mouth.opening.height..m. )

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


QCS <- left_join(QCS_catch, QCS_effort, by = c("Trip.identifier",
                                               "Set.number","Survey.Year"))



QCS <- QCS %>%
  # Create a unique haul_id
  mutate(
    haul_id = paste(formatC(Trip.identifier, width=3, flag=0),
                    formatC(Set.number, width=3, flag=0), sep= "-"),
    # Add "strata" (define by lat, lon and depth bands) where needed # degree bins
    # 100 m bins # no need to use lon grids on west coast (so narrow)
    stratum = paste(floor(Start.latitude), floor(Start.longitude),
                    floor(Bottom.depth..m./100)*100, sep= "-"),
# catch weight (kg.) per tow/
#                           (distance towed in m * trawl door spread m) * 1km^2/1000000m^2
    wgt_cpue = Catch.weight..kg./(Distance.towed..m.*Trawl.door.spread..m.) /1000000,
# catch weight (kg.) per tow/
#                           time of tow in minutes*60 minutes/hour
    wgt_h = Catch.weight..kg./Tow.duration..min.*60,
# catch abundance per tow/
#                           (distance towed in m * trawl door spread m) * 1km^2/1000000m^2
    num_cpue = Catch.count..pieces./(Distance.towed..m.*Trawl.door.spread..m.) /1000000,
    # catch weight (kg.) per tow/
#                           time of tow in minutes*60 minutes/hour
    num_h = Catch.count..pieces./Tow.duration..min.*60,
    area_swept = (Distance.towed..m.*Trawl.door.spread..m.)/1000000
  )

QCS <- QCS %>%
  rename(
    latitude = Start.latitude,
    longitude = Start.longitude,
```

```
    depth = Bottom.depth..m.,
    verbatim_name = Scientific.name,
    year = Survey.Year,
    num = Catch.count..pieces.,
    wgt = Catch.weight..kg.
    ) %>%
    mutate(
    date = as.Date(Set.date),
    haul_dur = Tow.duration..min./60
  ) %>%
  filter(
    verbatim_name != "" &
      !grepl("egg", verbatim_name)
  ) %>%
  # adjust verbatim_name names
  mutate(verbatim_name = ifelse(grepl("Lepidopsetta", verbatim_name),
                                "Lepidopsetta sp.", verbatim_name),
         verbatim_name = ifelse(grepl("Bathyraja", verbatim_name),
                                'Bathyraja sp.', verbatim_name),
         verbatim_name = ifelse(grepl("Squalus", verbatim_name),
                                'Squalus suckleyi', verbatim_name))


# Does the spp column contain any eggs or non-organism notes?
#As of fall 2021, nothing stuck out as needing to be removed
test <- QCS %>%
  select(verbatim_name) %>%
  filter(!is.na(verbatim_name)) %>%
  distinct() %>%
  mutate(verbatim_name = as.factor(verbatim_name)) %>%
  filter(grepl("egg", verbatim_name) & grepl("", verbatim_name))
stopifnot(nrow(test)==0)


# combine the wtcpue for each species by haul which is necessary because
#sometimes there are multiple observations for a single genus or family
#this should delete all duplicates
#i.e.
#HEXACTINELLIDA, GLASS SPONGES; WILLEMOES'S WHITE SEA PEN; CRANGONS
QCS <- QCS %>%
  group_by(haul_id,year, latitude, longitude, depth,
           verbatim_name, area_swept,date, haul_dur) %>%
  summarise(wgt_cpue = sum(wgt_cpue, na.rm = T), wgt_h = sum(wgt_h, na.rm = T),
            num_h = sum(num_h, na.rm = T), num_cpue = sum(num_cpue, na.rm = T),
            num = sum(num, na.rm = T), wgt = sum(wgt, na.rm = T)) %>%
  ungroup()

QCS <- QCS %>%
# add survey column
  mutate(survey = "DFO-QCS",
         country = "Canada",
         continent = "n_america",
         stat_rec = NA,
```

```
          verbatim_aphia_id = NA,
          aphia_id = NA,
          sub_area = NA,
          station = NA,
          stratum = NA,
          month = lubridate::month(date),
          day = lubridate::day(date),
          season = NA,
          quarter = NA,
          gear = NA,
          sbt = NA,
          sst = NA
  ) %>%
    select(survey, 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, num, num_h, num_cpue,
           wgt, wgt_h, wgt_cpue, verbatim_name, verbatim_aphia_id)

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

#none!

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

unique_name_match
#empty


#-------------------------------------------------------------------------------------------#
#### 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
qcs_survey_code <- "DFO-QCS"

QCS <- QCS %>%
  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(QCS$taxa2), input_survey = qcs_survey_code,
                         save = F, output=NA)

#This leaves out the following species, which are all inverts
#Cancer branneri
#Cheiraster dawsoni
#Nearchaster variabilis
#Trochacea
#Nearchaster aciculosus
#Crangonyctidae

#-------------------------------------------------------------------------------------------#
#### INTEGRATE CLEAN TAXA in DFO-QCS survey data ####
#-------------------------------------------------------------------------------------------#

correct_taxa <- clean_auto %>%
  select(-survey)

clean_qcs <- left_join(QCS, correct_taxa, by=c("taxa2"="query")) %>%
  filter(!is.na(taxa)) %>% # query does not indicate taxa entry that were removed in the cleaning proce
  # 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,
         source = "DFO",
         timestamp = my("08/2020")) %>%
  select(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, 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_qcs <- clean_qcs %>%
  group_by(haul_id, verbatim_name, accepted_name) %>%
  mutate(count = n())

#none!

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

unique_name_match
#empty
```

```r
# ------------------------------------------------------------------------------#
#### SAVE DATABASE IN GOOGLE DRIVE ####
# ------------------------------------------------------------------------------#

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

1. Overview of the survey data table

survey	source	timestamp	haul_id	country	sub_area	continent
DFO-QCS	DFO	2020-08-01	49750-001	Canada	NA	n_america
DFO-QCS	DFO	2020-08-01	49750-001	Canada	NA	n_america
DFO-QCS	DFO	2020-08-01	49750-001	Canada	NA	n_america
DFO-QCS	DFO	2020-08-01	49750-001	Canada	NA	n_america
DFO-QCS	DFO	2020-08-01	49750-001	Canada	NA	n_america

stat_rec	station	stratum	year	month	day	quarter	season
NA	NA	NA	2003	7	4	NA	NA
NA	NA	NA	2003	7	4	NA	NA
NA	NA	NA	2003	7	4	NA	NA
NA	NA	NA	2003	7	4	NA	NA
NA	NA	NA	2003	7	4	NA	NA

latitude	longitude	haul_dur	area_swept	gear	depth
50.9865	-128.1804	0.4	0.13268	NA	79
50.9865	-128.1804	0.4	0.13268	NA	79
50.9865	-128.1804	0.4	0.13268	NA	79
50.9865	-128.1804	0.4	0.13268	NA	79
50.9865	-128.1804	0.4	0.13268	NA	79

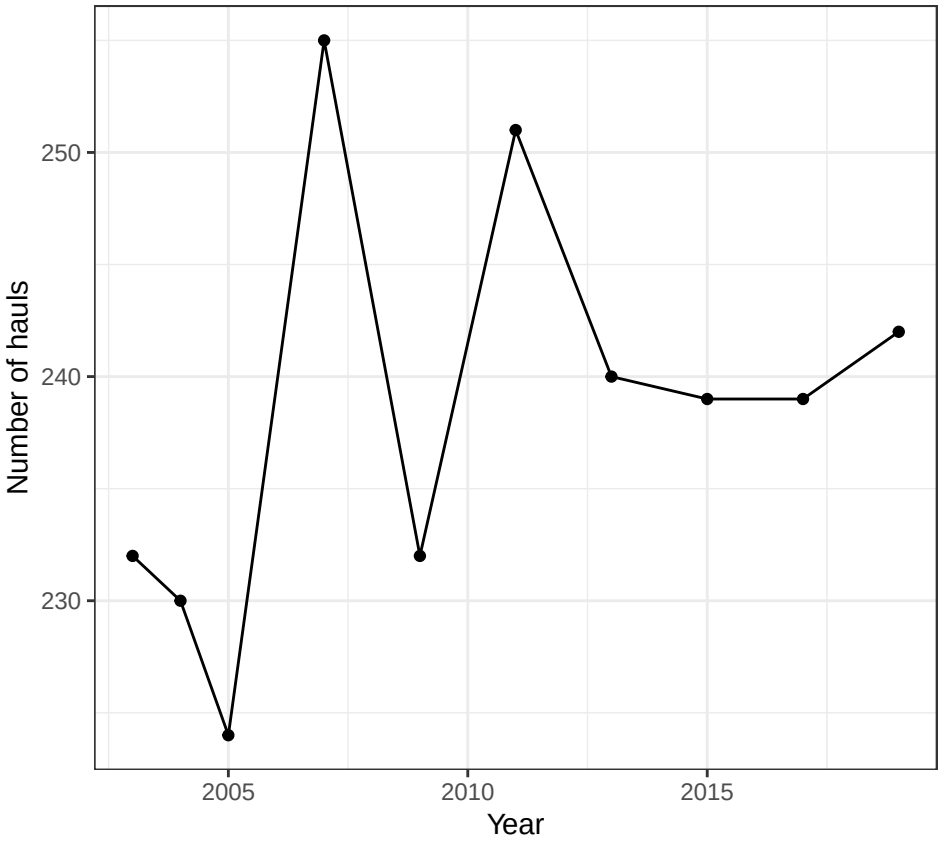
sbt	sst	num	num_h	num_cpue	wgt
NA	NA	0	0	0	12.74
NA	NA	0	0	0	30.10
NA	NA	0	0	0	3.30
NA	NA	0	0	0	7.80
NA	NA	0	0	0	4.40

wgt_h	wgt_cpue	verbatim_name	verbatim_aphia_id	accepted_name
31.85	0	ATHERESTHES STOMIAS	NA	Atheresthes stomias
75.25	0	CITHARICHTHYS SORDIDUS	NA	Citharichthys sordidus
8.25	0	EOPSETTA JORDANI	NA	Eopsetta jordani
19.50	0	GADUS MACROCEPHALUS	NA	Gadus macrocephalus
11.00	0	GLYPTOCEPHALUS ZACHIRUS	NA	Glyptocephalus zachirus

aphia_id	SpecCode	kingdom	phylum	class	order	family
279792	517	Animalia	Chordata	Actinopteri	Pleuronectiformes	Pleuronectidae
275694	4215	Animalia	Chordata	Actinopteri	Pleuronectiformes	Paralichthyidae
280690	4237	Animalia	Chordata	Actinopteri	Pleuronectiformes	Pleuronectidae
254538	308	Animalia	Chordata	Actinopteri	Gadiformes	Gadidae
274287	4238	Animalia	Chordata	Actinopteri	Pleuronectiformes	Pleuronectidae

2. Summary of sampling intensity

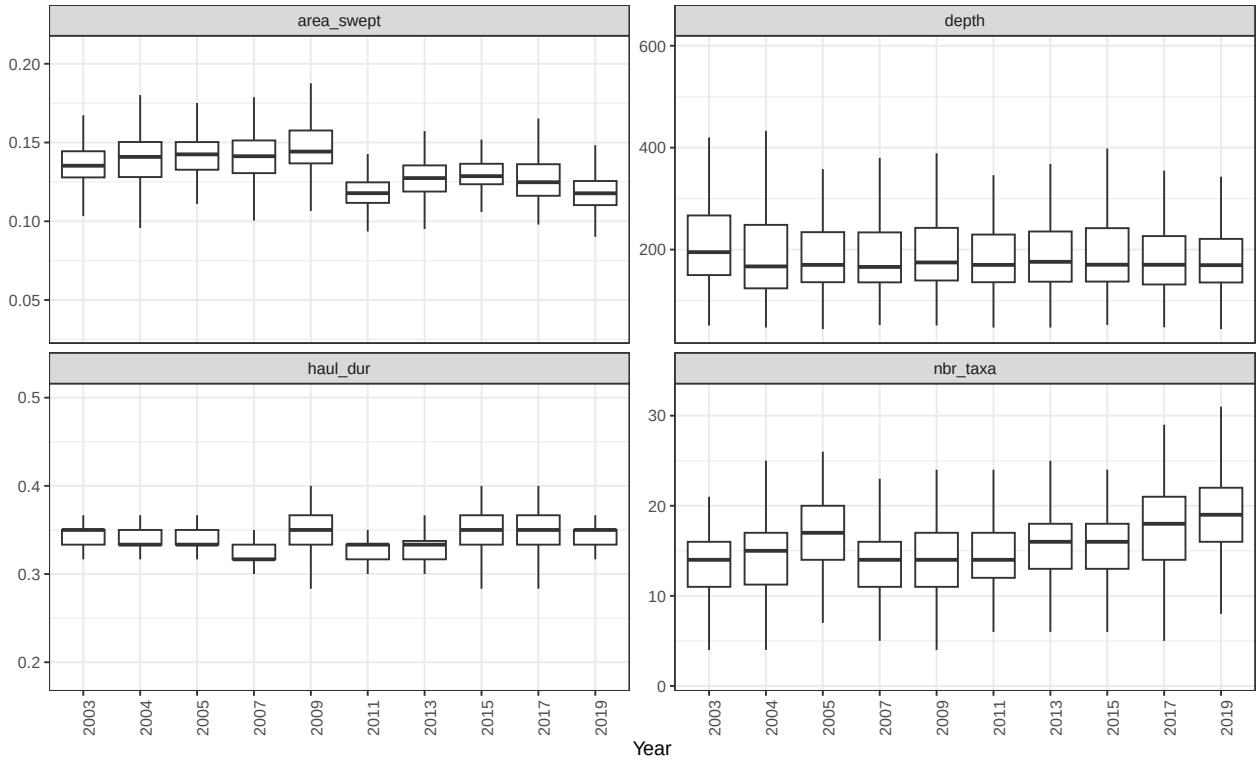
Number of hauls per year performed during the survey after data processing.



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:

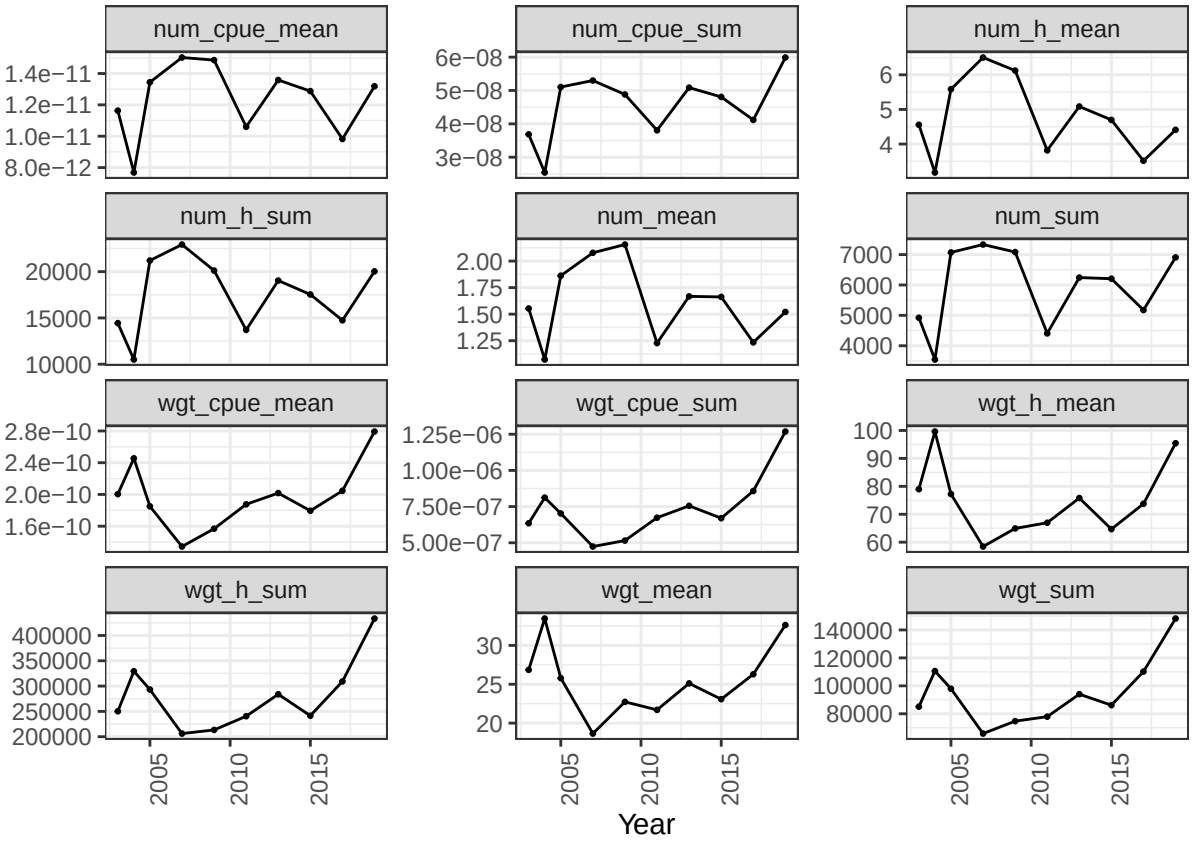
- *area_swept*, swept area by the bottom trawl gear km^2
- *depth*, sampling depth in m
- *haul_dur*, haul sampling duration *hour*
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (https://www.marinespecies.org/, October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



4. Summary of biological variables

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

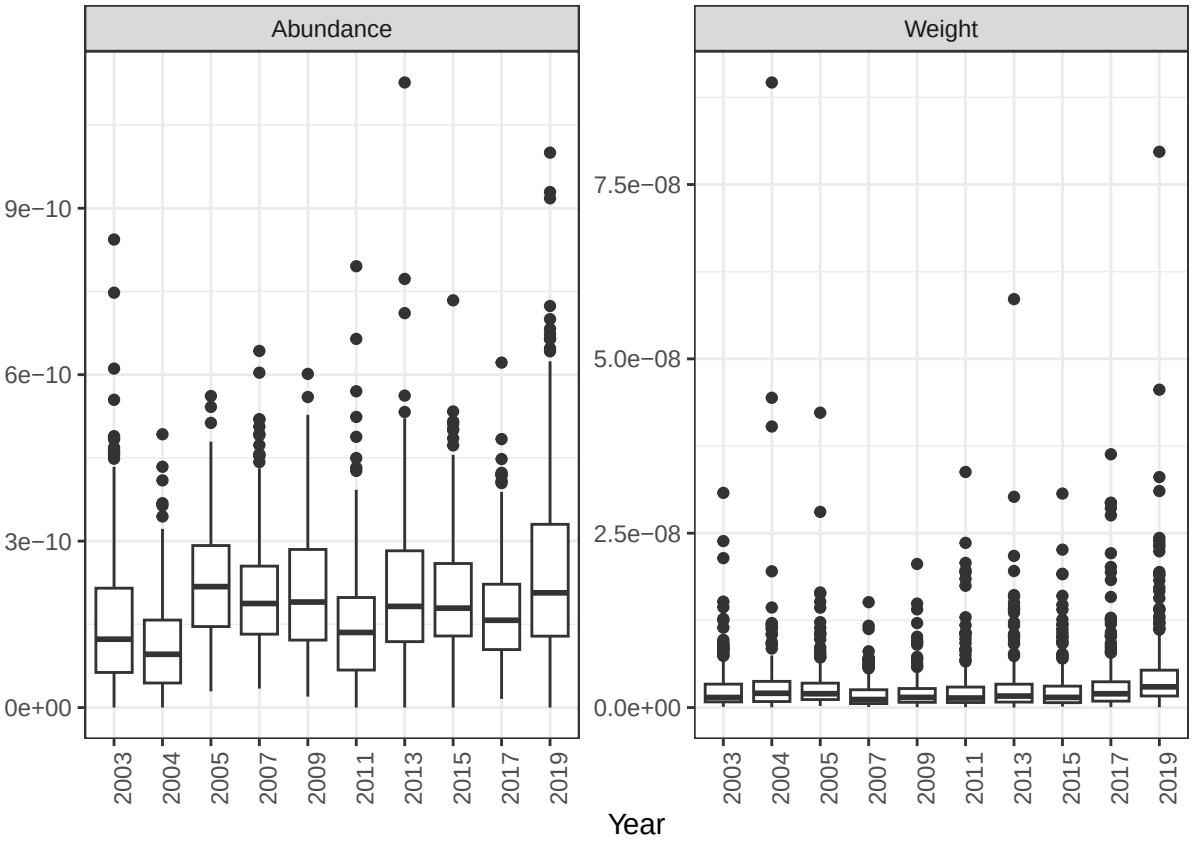
- *num_cpue*, number of individuals (abundance) in $\frac{individuals}{km^2}$
- *num_h*, number of individuals (abundance) in $\frac{individuals}{h}$
- *num*, number of individuals (abundance)
- *wgt_cpue*, weight in $\frac{kg}{km^2}$
- *wgt_h*, weight in $\frac{kg}{h}$
- *wgt*, weight in kg



5. Extreme values

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

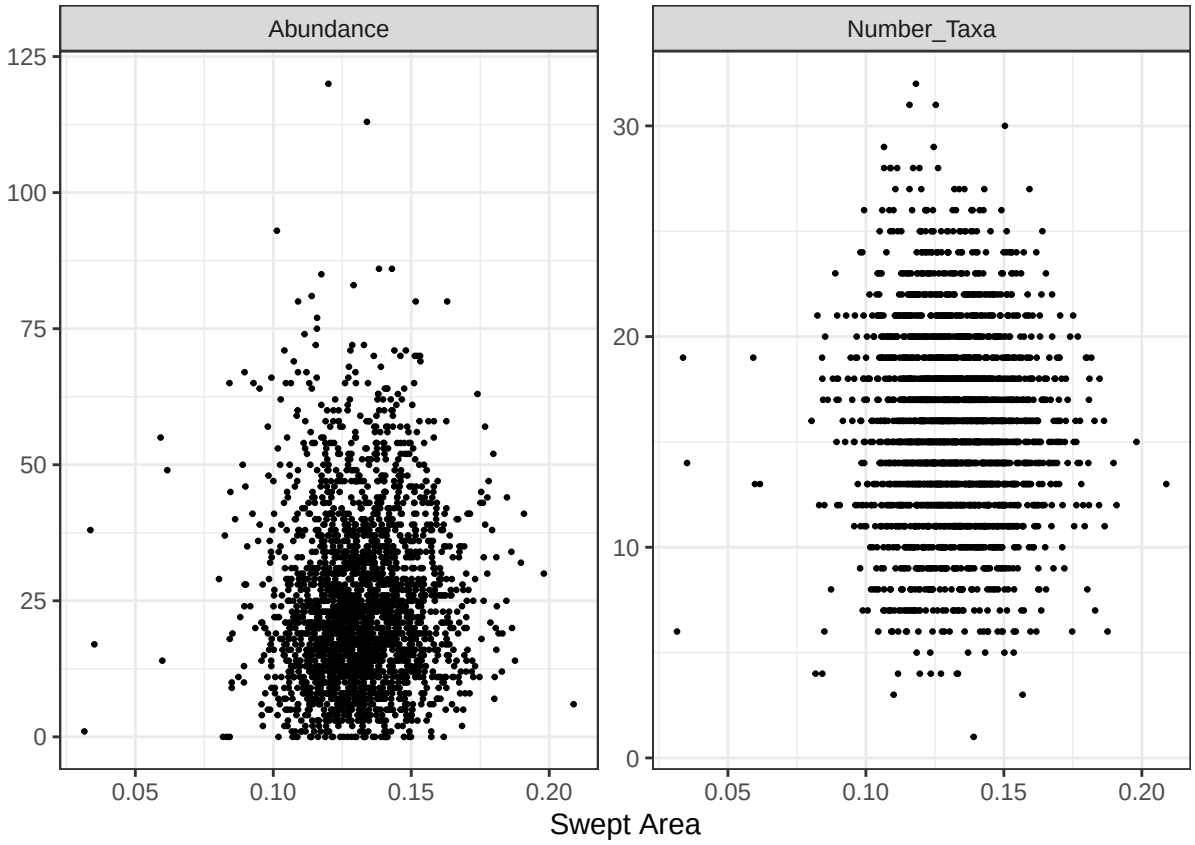
- *wgt*, total weight in *kg* per haul and year per haul and year, if available in the survey data
- *num*, total number of individuals, if available in the survey data



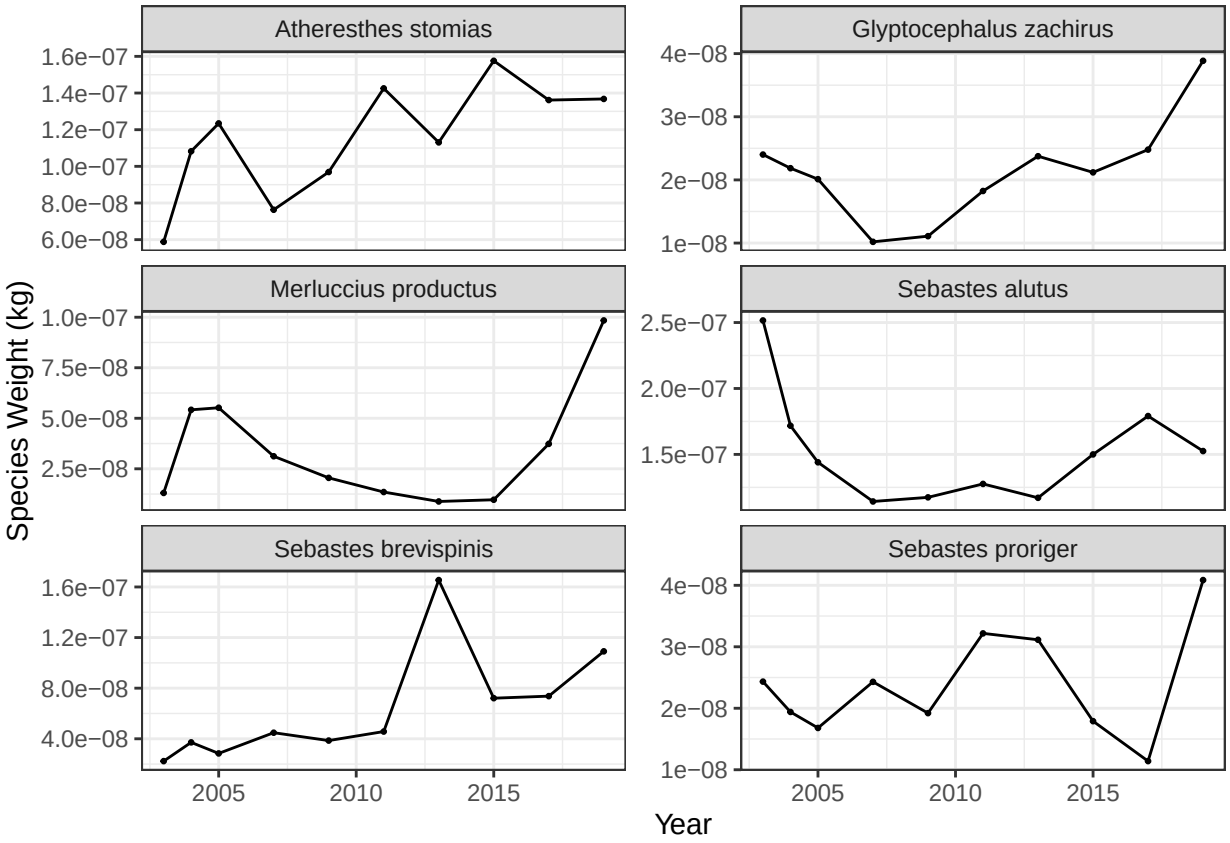
6. Summary of variables against swept area

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

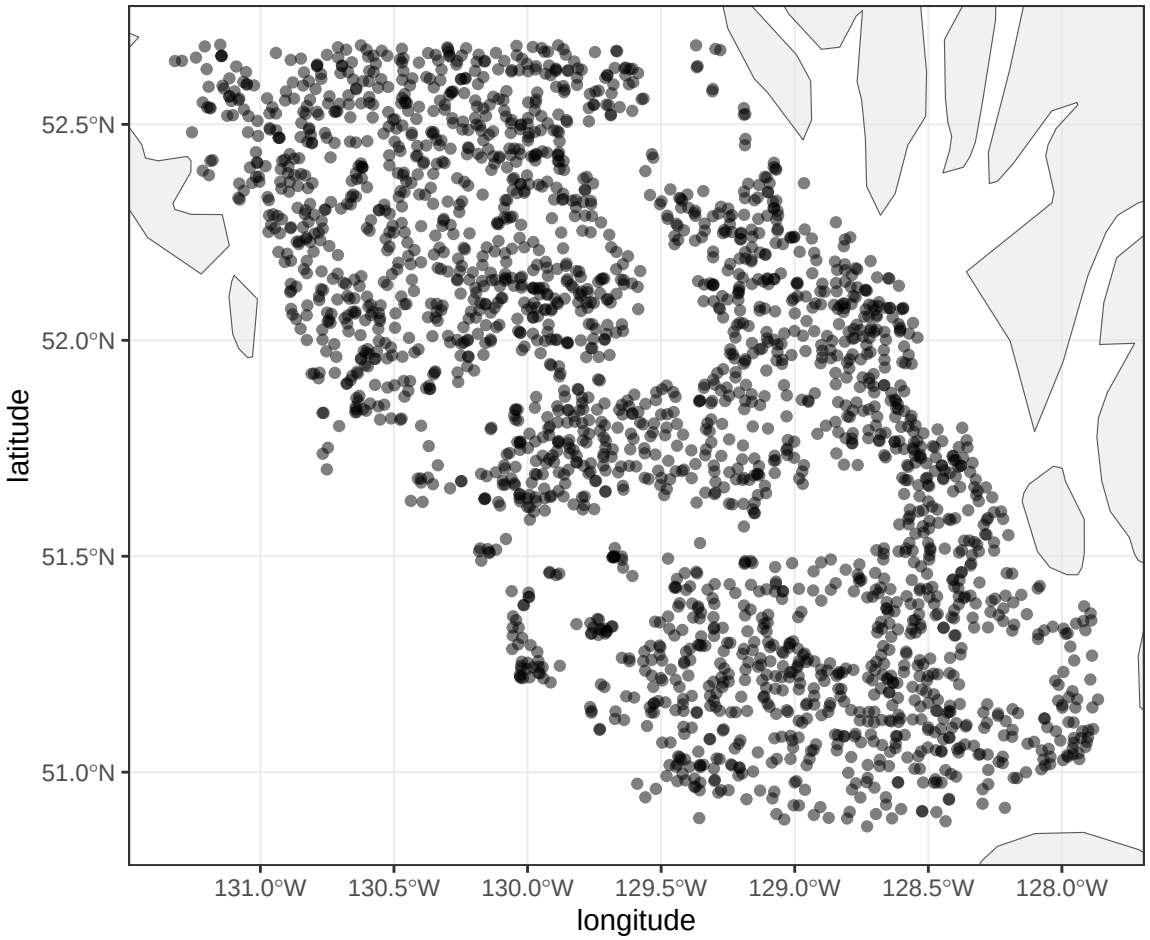


7. Abundance or Weight trends of the six most abundant species



8. Distribution mapping

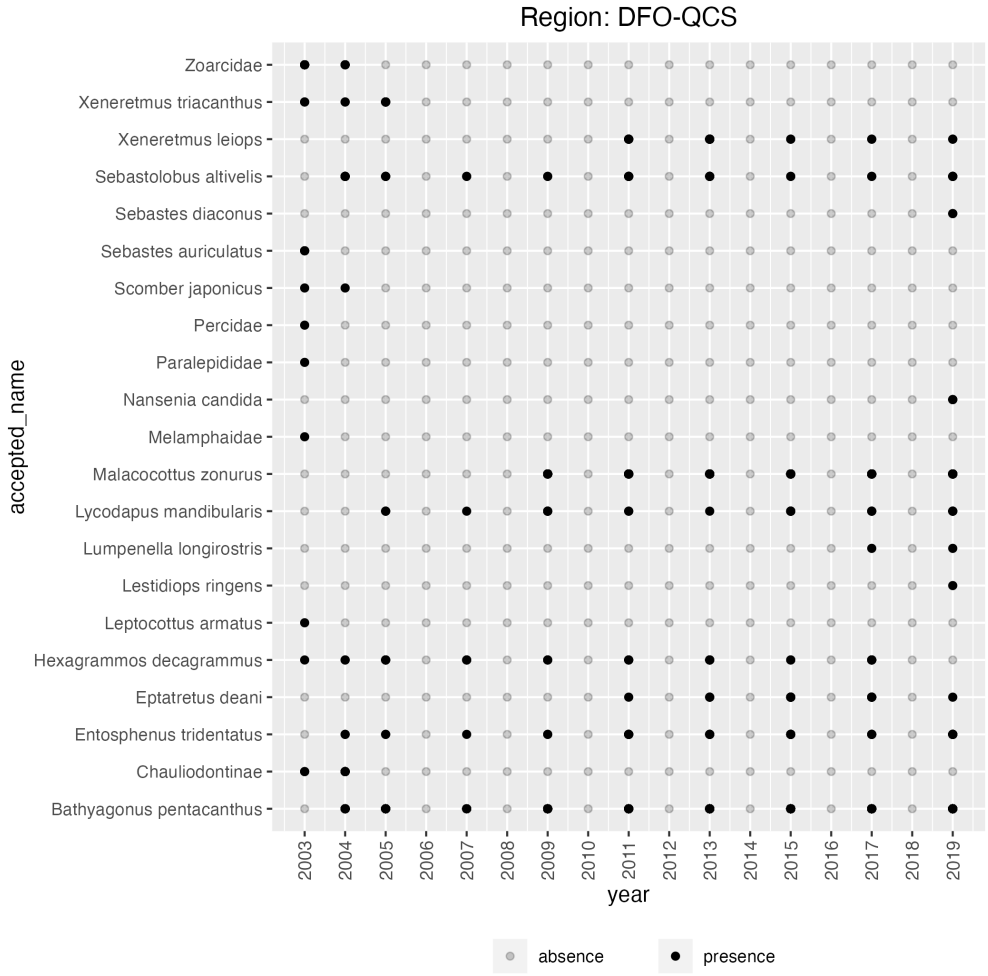
Map of the sampling distribution in space. Note that we only show one year per coordinate.



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

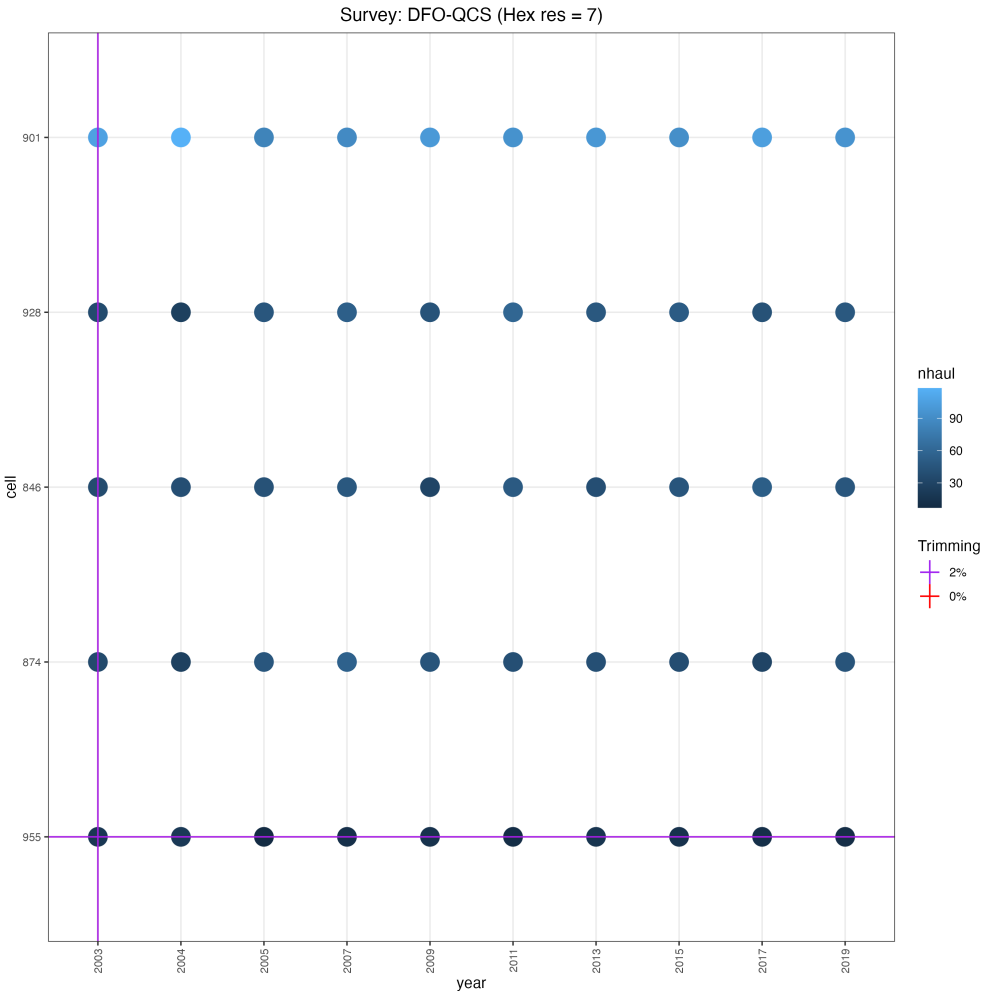
Total number of species	196.0
Percentage of species flagged	10.7

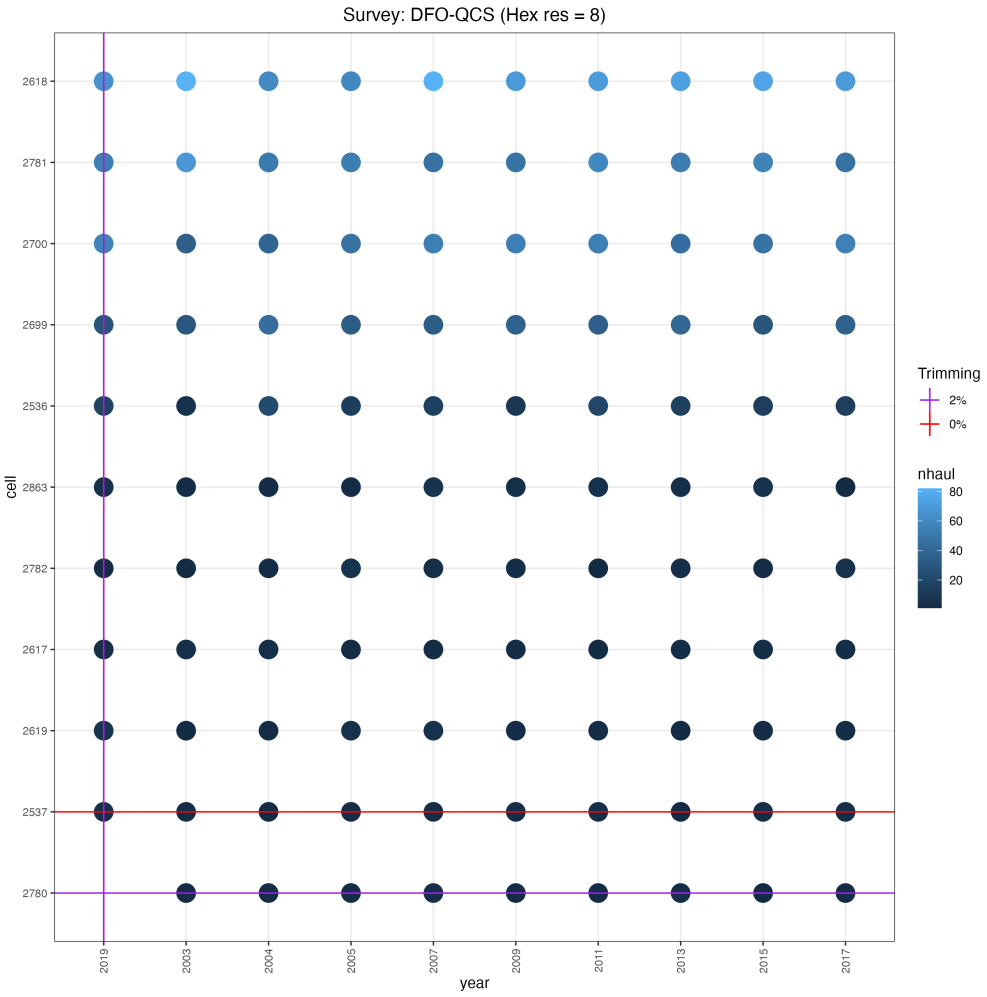
10. Spatio-temporal standardization

a. Standardization method 1

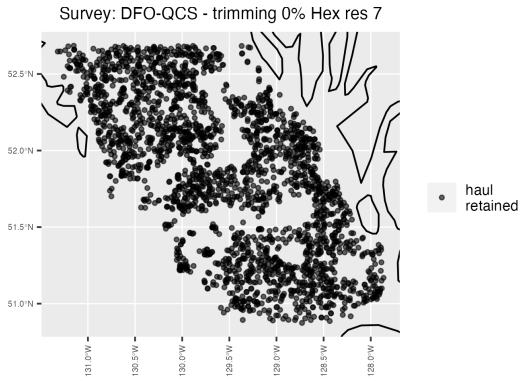
This standardization method was adapted from https://github.com/zoekitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd
It was run for hex resolution 7 and 8.

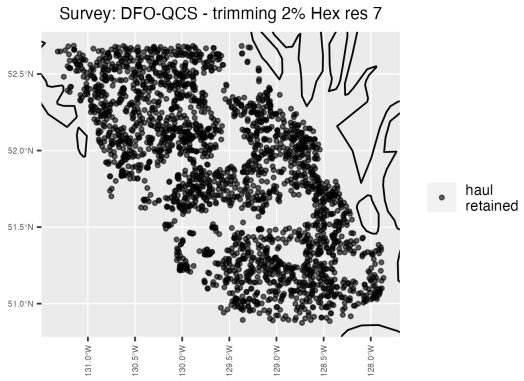
Plot of number of cells x years with overlaid flagging options

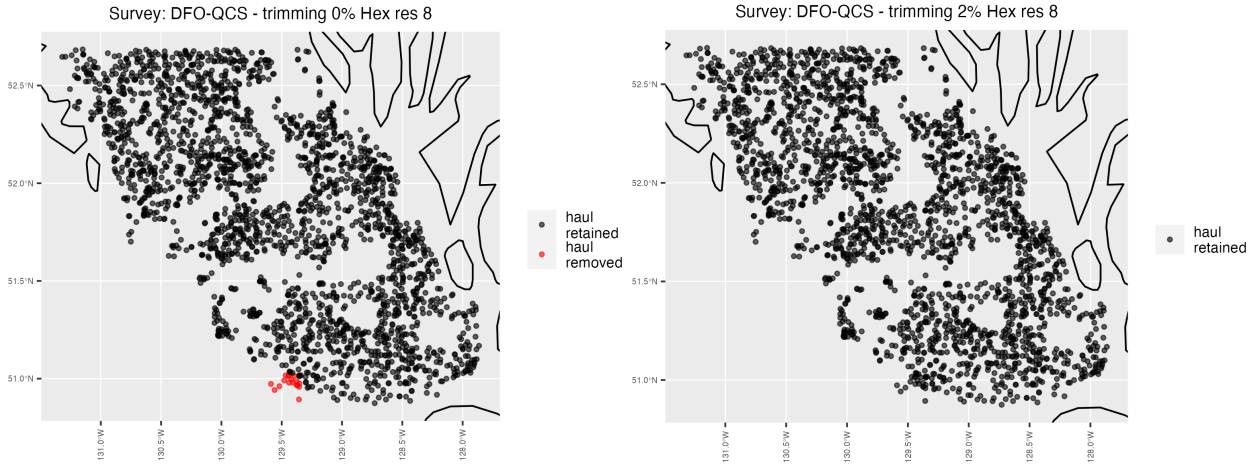

Survey: DFO-QCS (Hex res = 7)
cell
901
928
846
874
955
year
2003
2004
2005
2007
2009
2011
2013
2015
2017
2019
nhaul
90
60
30
Trimming
2%
0%



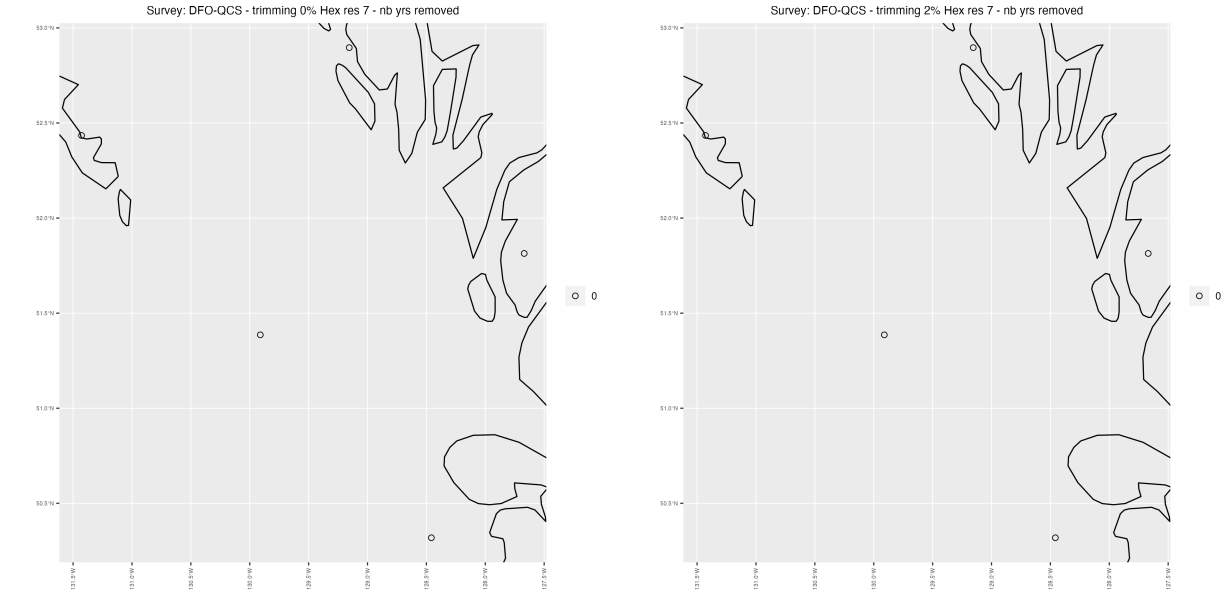
Map of hauls retained and removed per flagging method and threshold

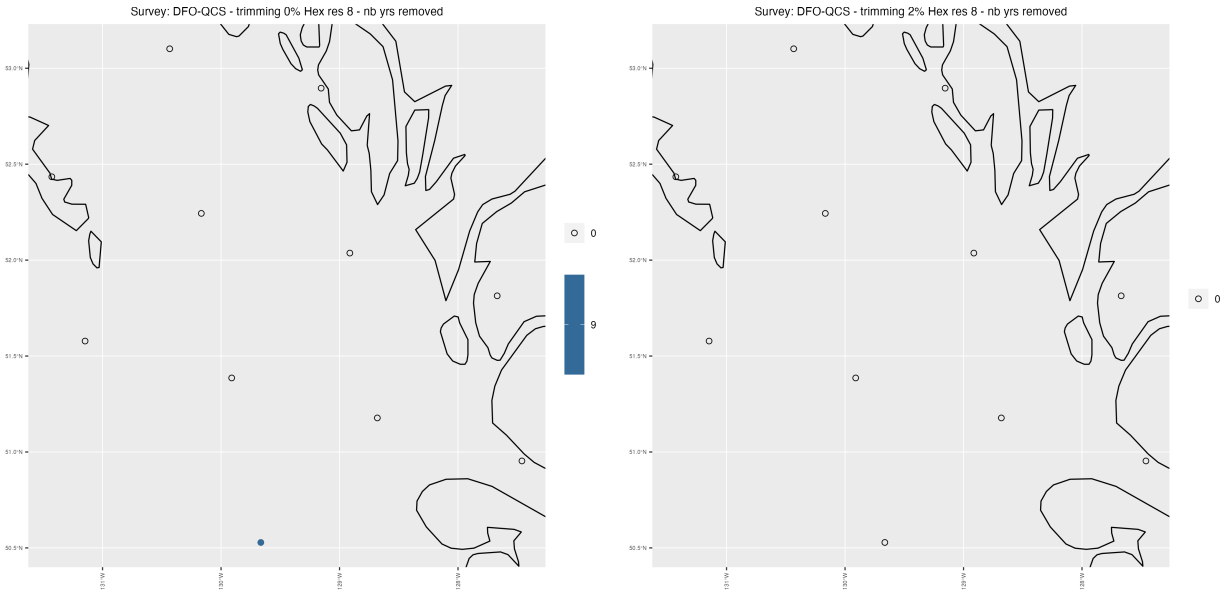






Map of numbers of years removed per grid cell and flagging method/threshold

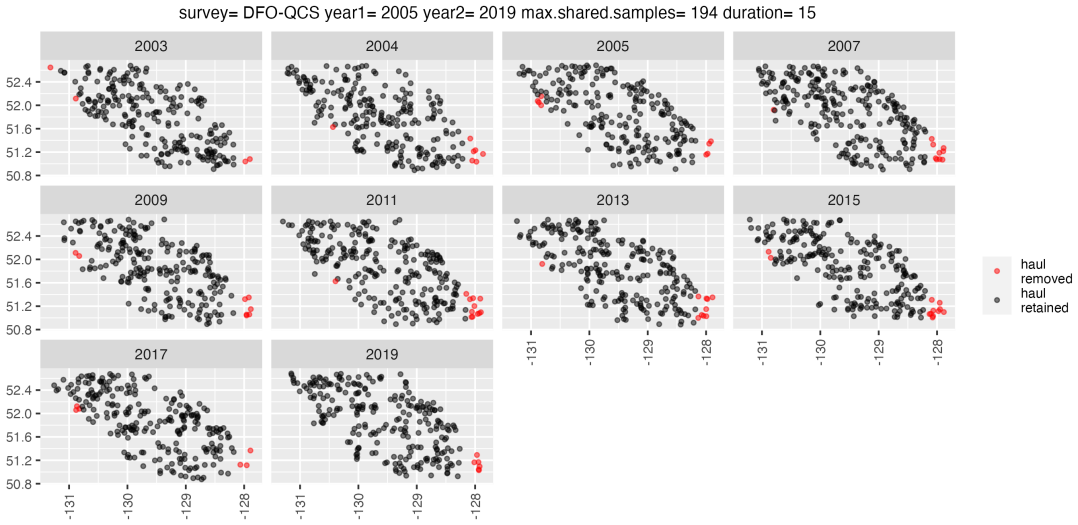




b. Standardization method 2

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	0	0	18.0	0	1345.0
percentage of hauls removed	0	0	0.8	0	3.6