DFO-WCHG: Department of Fisheries Oceans Canada Haida Gwaii survey data processing summary

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December, 2022

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General info

This document presents the cleaning code and summary of the West Coast Haida Gwaii (Department of Fisheries Oceans Canada) bottom trawl survey provided by Shelee Hamilton, and Maria Cornthwaite. It contains data from 2005 and up to 2019.

Data cleaning in R

```
################################################################################
#### R code to clean trawl survey for the DFO West Coast Haida Gwaii Survey
#### 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 ####
#--------------------------------------------------------------------------------------#
```

```r
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 West Coast Haida Gwaii Survey 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 ####
#--------------------------------------------------------------------------------------#

WCHG_catch <- read_csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/WCHG_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()
))

WCHG_effort <- read_csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/WCHG_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 ####
#---------------------------------------------------------------------------------------#

WCHG <- left_join(WCHG_catch, WCHG_effort, by = c("Trip.identifier", "Set.number",
                                                  "Survey.Year"))


WCHG <- WCHG %>%
  # 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
  )

WCHG <- WCHG %>%
  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 <- WCHG %>%
  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
#i.e.
#HEXACTINELLIDA, GLASS SPONGES; WILLEMOES'S WHITE SEA PEN; CRANGONS
WCHG <- WCHG %>%
  group_by(haul_id,year, latitude, longitude, depth, verbatim_name, area_swept,
           num, wgt, wgt_cpue, wgt_h, num_cpue, num_h, 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)) %>%
  ungroup()

WCHG <- WCHG %>%
# add survey column etc.
  mutate(survey = "DFO-WCHG",
         source = "DFO",
         timestamp = mdy("08/21/2020"),
         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
  ) %>%
  group_by(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, verbatim_name, verbatim_aphia_id) %>%
  #this step sums over matching haul_ids and species
  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)) %>%

    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)

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

#none!

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

unique_name_match
#empty

#The following are all duplicated if we don't sum over abundance and wgt (added above)
#1 SEBASTES REEDI
#2 SCYPHOZOA
#3 ACTINIARIA
#4 ZOROASTER EVERMANI
#5 CAREPROCTUS MELANURUS
#6 GLYPTOCEPHALUS ZACHIRUS
#7 PANDALUS PLATYCEROS
#8 SEBASTES DIPLOPROA
#9 XENERETMUS LEIOPS
#10 BATHYRAJA INTERRUPTA
```

```r
#11 MYCTOPHIDAE
#12 PRIMNOA
#13 ATHERESTHES STOMIAS
#14 ALLOCENTROTUS FRAGILIS
#15 CORYPHAENOIDES CINEREUS
#16 SEBASTES ALUTUS
#17 SEBASTES ALEUTIANUS/MELANOSTICTUS COMPLEX
#18 CYANEA CAPILLATA

#----------------------------------------------------------------------------------------#
#### 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
wchg_survey_code <- "DFO-WCHG"

WCHG <- WCHG %>%
  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(WCHG$taxa2),
                         input_survey = wchg_survey_code, save = F, output=NA)
#takes  2.5 minutes

#This leaves out the following species, which are all inverts

#Nearchaster variabilis
#Cheiraster dawsoni
#Pandalopsis
#Nearchaster aciculosus

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

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

clean_wchg <- left_join(WCHG, correct_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_wchg <- clean_wchg %>%
  group_by(haul_id, accepted_name) %>%
  mutate(count = n())

#none!

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

unique_name_match
#not empty

#one duplicate kept
#taxonomic cleaning
#verbatim_name                                accepted_name
#SEBASTES                                     Sebastes
#SEBASTES ALEUTIANUS/MELANOSTICTUS COMPLEX Sebastes
# -----------------------------------------------------------------------------------#
#### SAVE DATABASE IN GOOGLE DRIVE ####
# -----------------------------------------------------------------------------------#

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

1. Overview of the survey data table

survey	haul_id	source	timestamp	country	sub_area	continent
DFO-WCHG	62066-001	DFO	2020-08-21	Canada	NA	n_america
DFO-WCHG	62066-001	DFO	2020-08-21	Canada	NA	n_america
DFO-WCHG	62066-001	DFO	2020-08-21	Canada	NA	n_america
DFO-WCHG	62066-001	DFO	2020-08-21	Canada	NA	n_america
DFO-WCHG	62066-001	DFO	2020-08-21	Canada	NA	n_america

stat_rec	station	stratum	year	month	day	quarter	season
NA	NA	NA	2006	8	30	NA	NA
NA	NA	NA	2006	8	30	NA	NA
NA	NA	NA	2006	8	30	NA	NA
NA	NA	NA	2006	8	30	NA	NA
NA	NA	NA	2006	8	30	NA	NA

latitude	longitude	haul_dur	area_swept	gear	depth
52.98417	-132.5998	0.6166667	0.16075	NA	1067.5
52.98417	-132.5998	0.6166667	0.16075	NA	1067.5
52.98417	-132.5998	0.6166667	0.16075	NA	1067.5
52.98417	-132.5998	0.6166667	0.16075	NA	1067.5
52.98417	-132.5998	0.6166667	0.16075	NA	1067.5

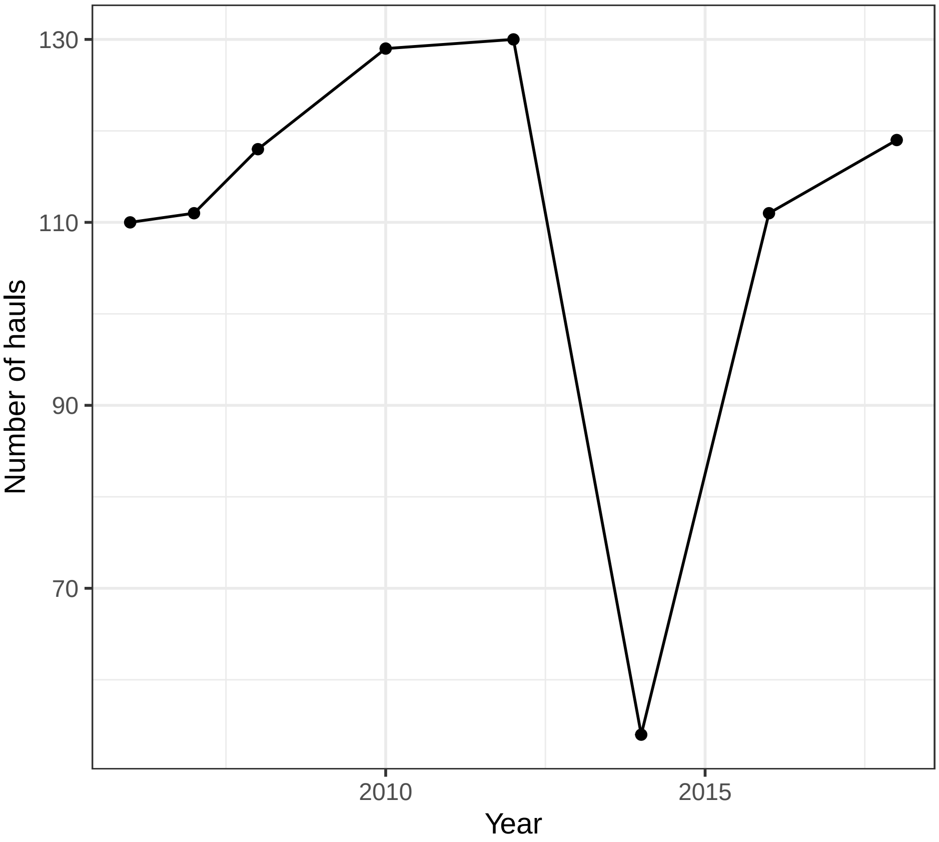
sbt	sst	num	num_h	num_cpue	wgt
NA	NA	0	0.000000	0	27.28
NA	NA	0	0.000000	0	53.58
NA	NA	0	0.000000	0	3.04
NA	NA	3	4.864865	0	0.12
NA	NA	2	3.243243	0	1.36

wgt_h	wgt_cpue	verbatim_name	verbatim_aphia_id	accepted_name
44.2378378	0	ALBATROSSIA PECTORALIS	NA	Albatrossia pectoralis
86.8864865	0	ANOPLOPOMA FIMBRIA	NA	Anoplopoma fimbria
4.9297297	0	ANTIMORA MICROLEPIS	NA	Antimora microlepis
0.1945946	0	BATHYLAGIDAE	NA	Bathylagidae
2.2054054	0	BATHYRAJA TRACHURA	NA	Bathyraja trachura

aphia_id	SpecCode	kingdom	phylum	class	order	family
236135	8435	Animalia	Chordata	Actinopteri	Gadiformes	Macrouridae
159463	512	Animalia	Chordata	Actinopteri	Perciformes	Anoplopomatidae
272460	2006	Animalia	Chordata	Actinopteri	Gadiformes	Moridae
125509	NA	Animalia	Chordata	Actinopteri	Argentiniformes	Bathylagidae
271538	2571	Animalia	Chordata	Elasmobranchii	Rajiformes	Arhynchobatidae

2. Summary of sampling intensity

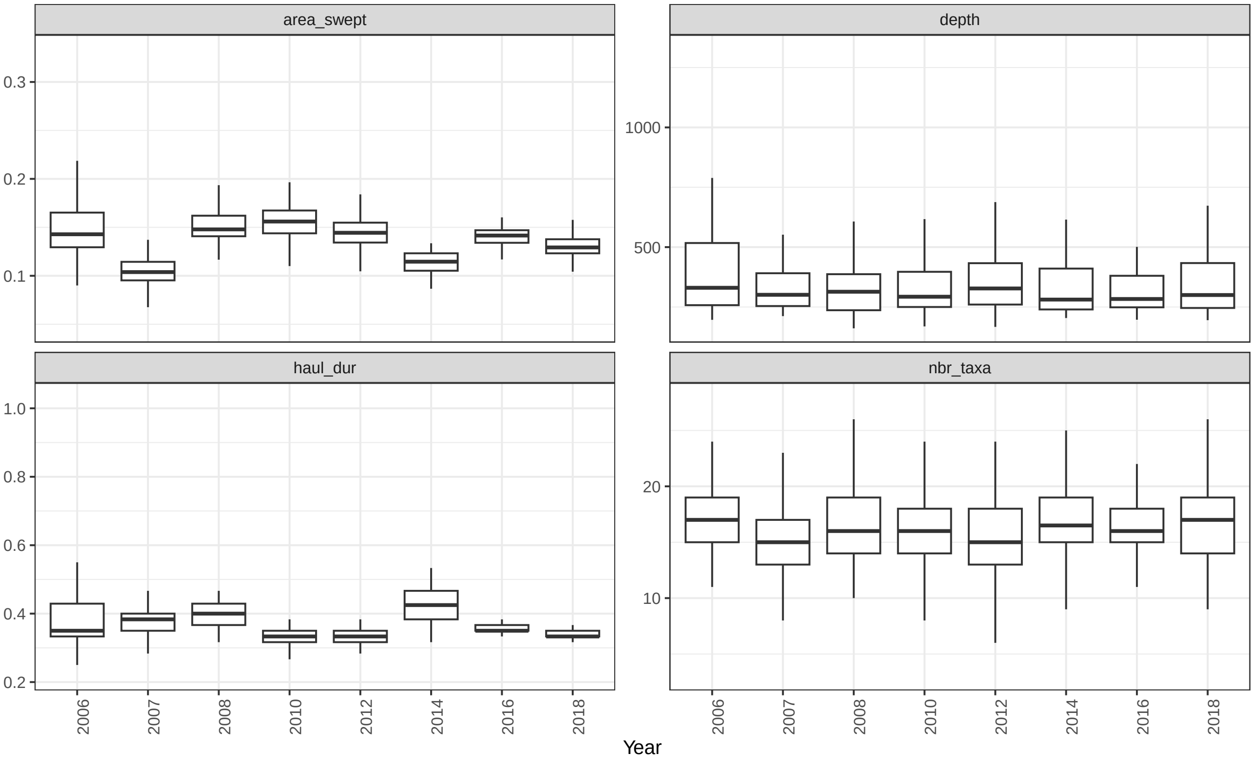
Number of hauls per year performed during the survey after data processing.



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:

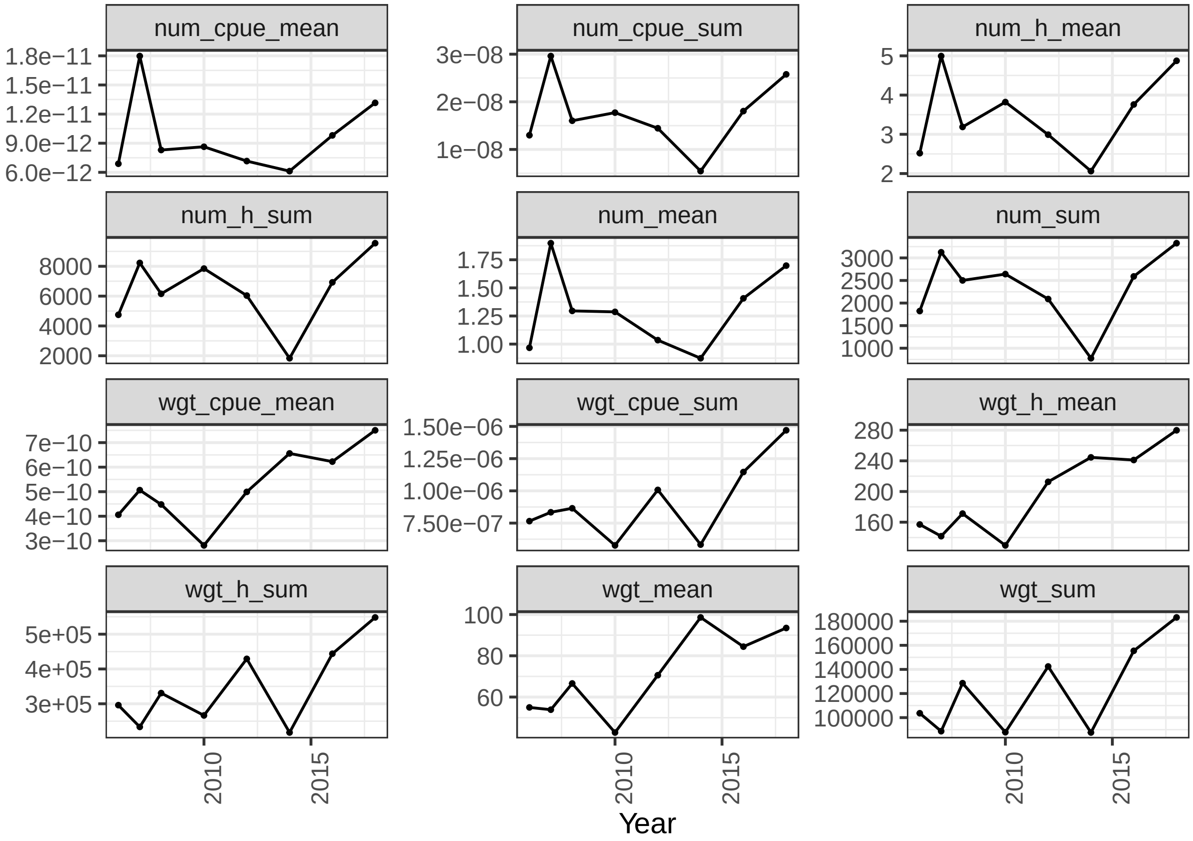
- *area_swept*, swept area by the bottom trawl gear km^2
- *depth*, sampling depth in m
- *haul_dur*, haul sampling duration *hour*
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (https://www.marinespecies.org/, October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



4. Summary of biological variables

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

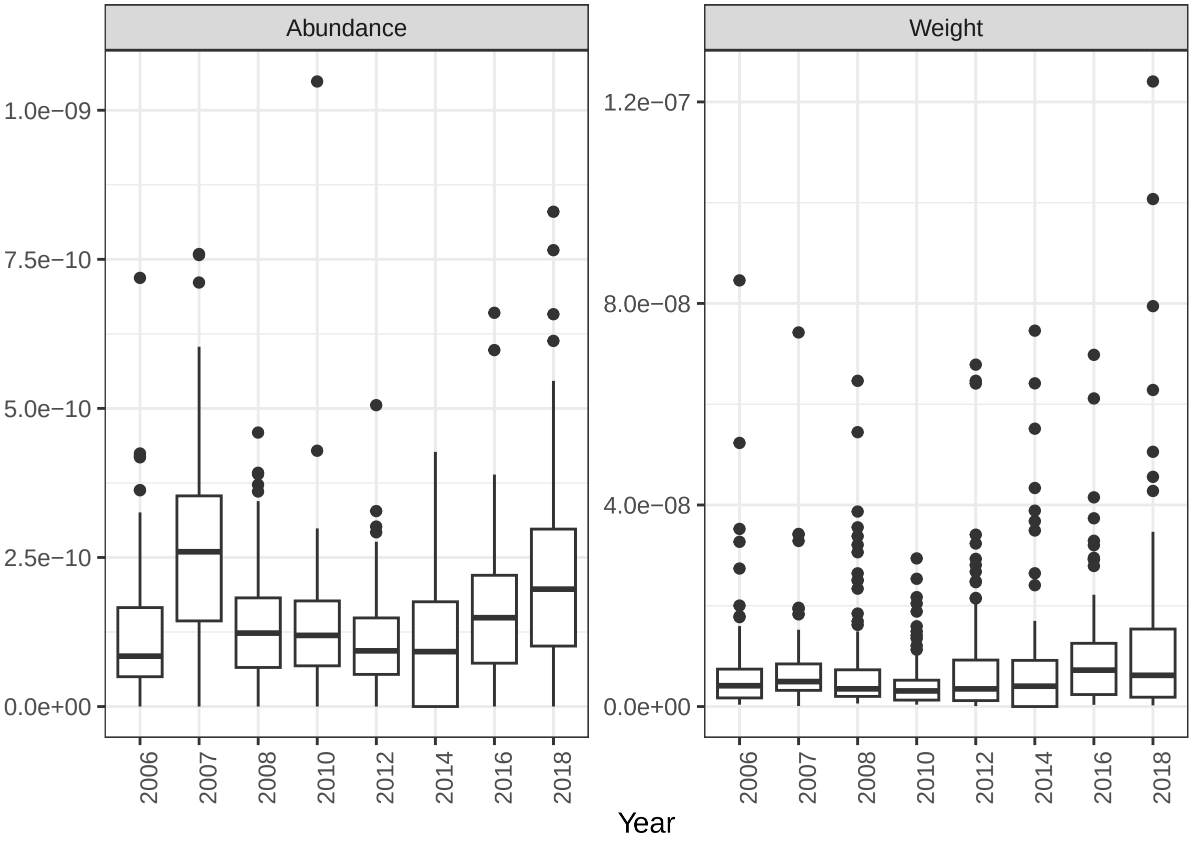
- *num_cpue*, number of individuals (abundance) in $\frac{individuals}{km^2}$
- *num_h*, number of individuals (abundance) in $\frac{individuals}{h}$
- *num*, number of individuals (abundance)
- *wgt_cpue*, weight in $\frac{kg}{km^2}$
- *wgt_h*, weight in $\frac{kg}{h}$
- *wgt*, weight in kg



5. Extreme values

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

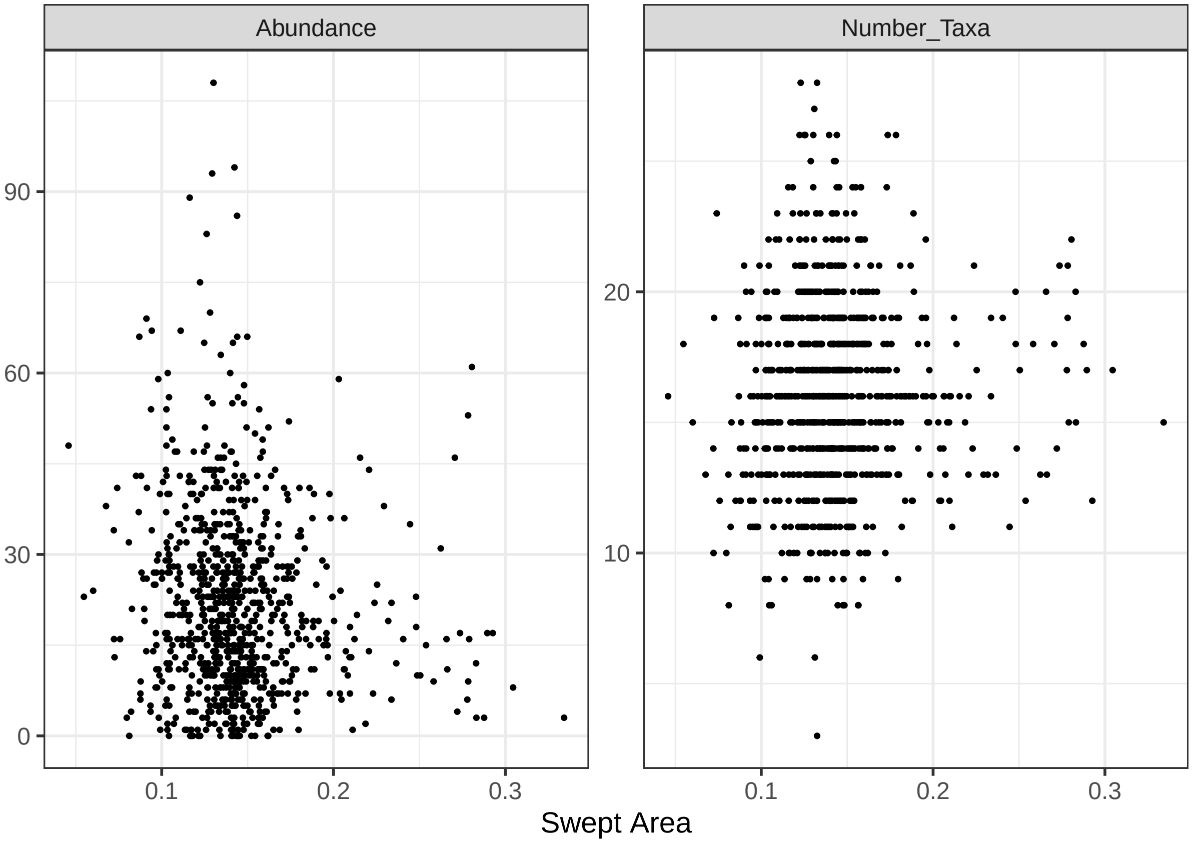
- *wgt*, total weight in *kg* per haul and year per haul and year, if available in the survey data
- *num*, total number of individuals, if available in the survey data



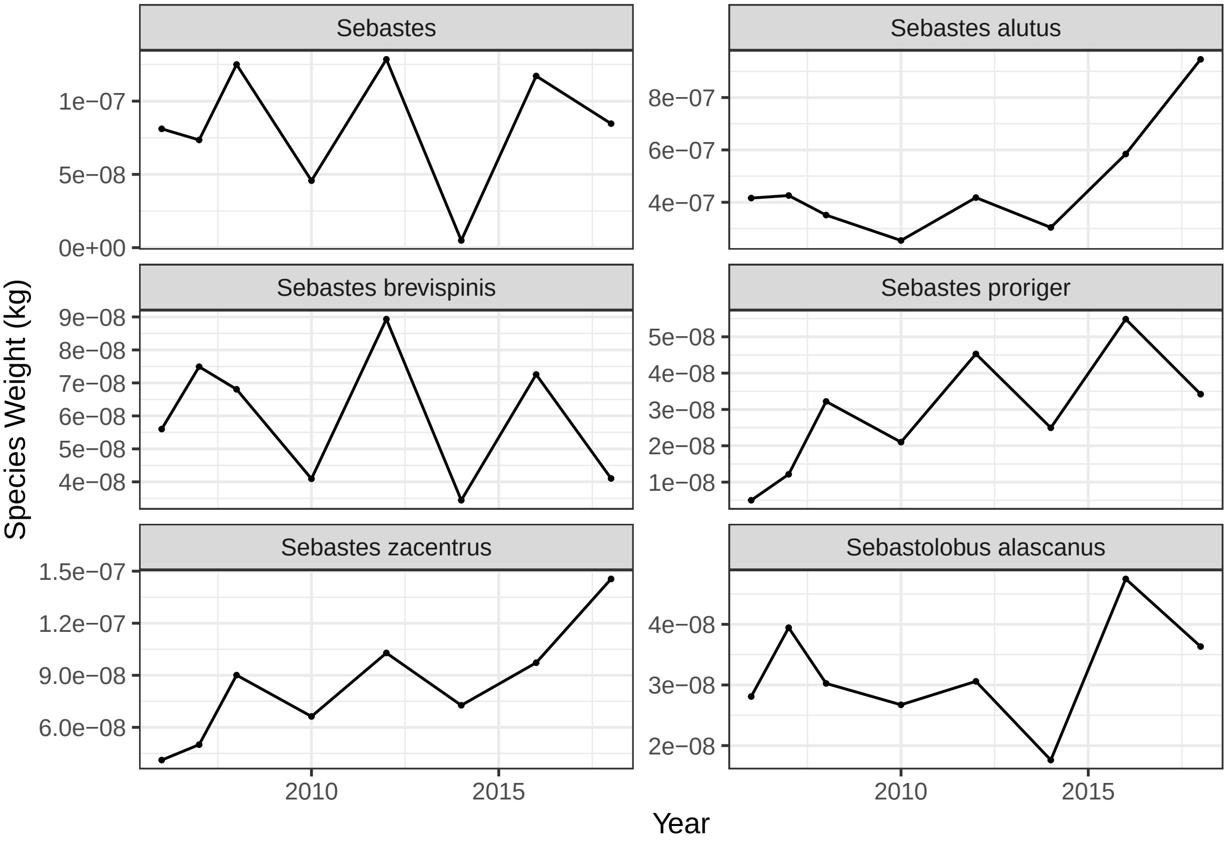
6. Summary of variables against swept area

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

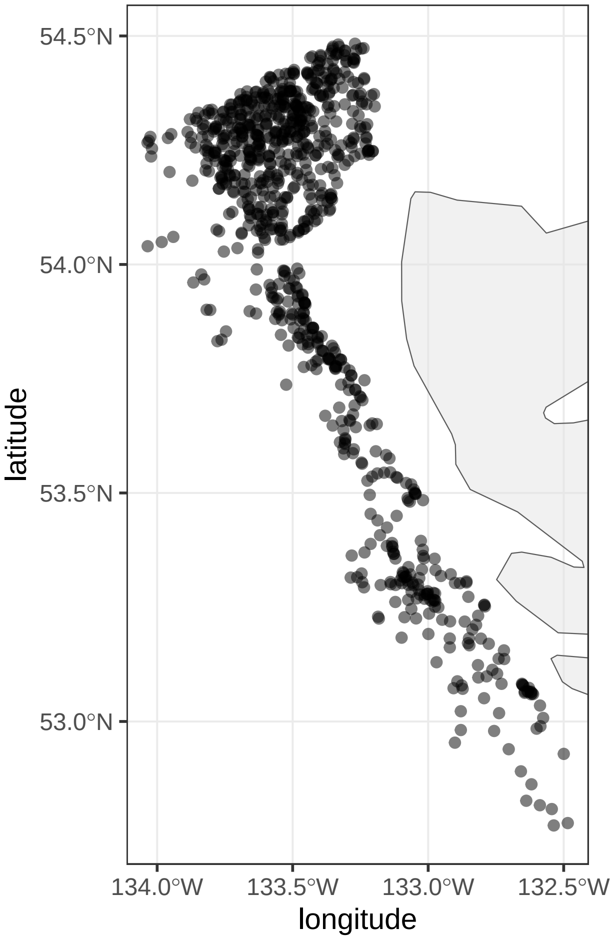


7. Abundance or Weight trends of the six most abundant species



8. Distribution mapping

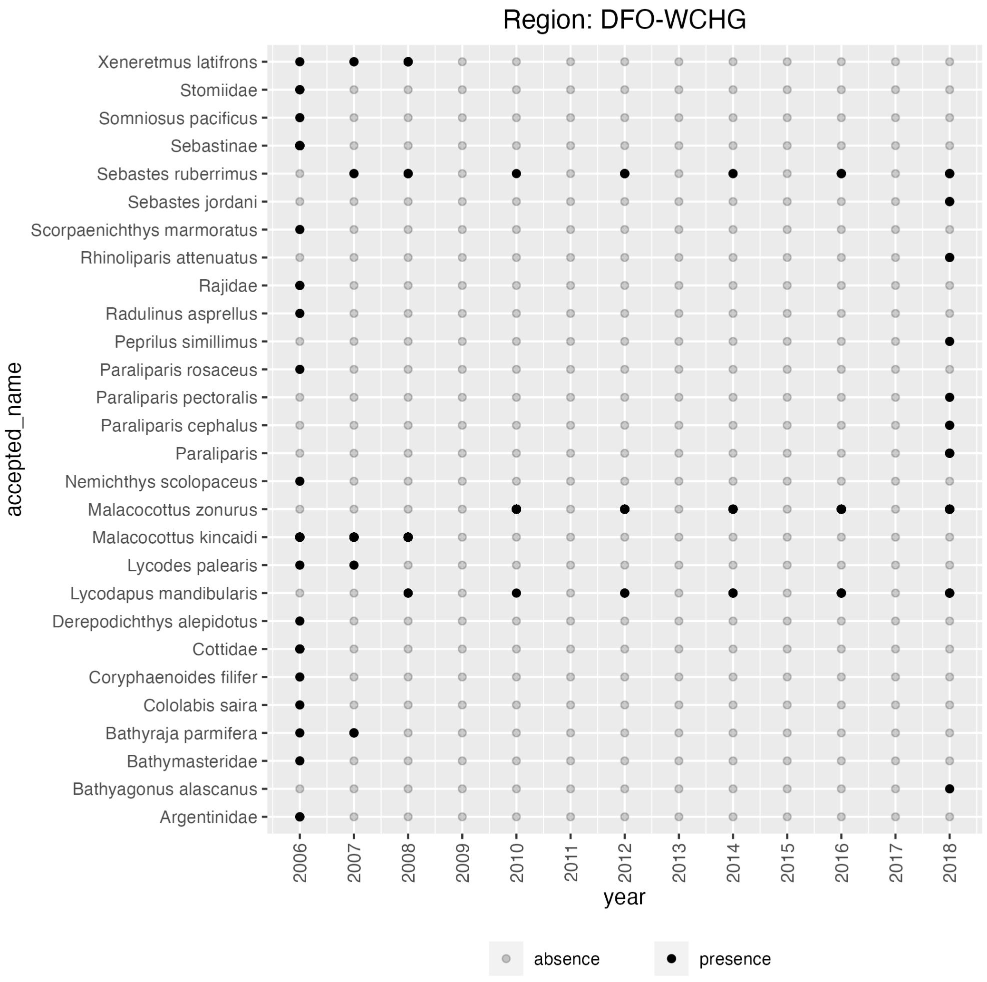
Map of the sampling distribution in space. Note that we only show one year per coordinate.



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

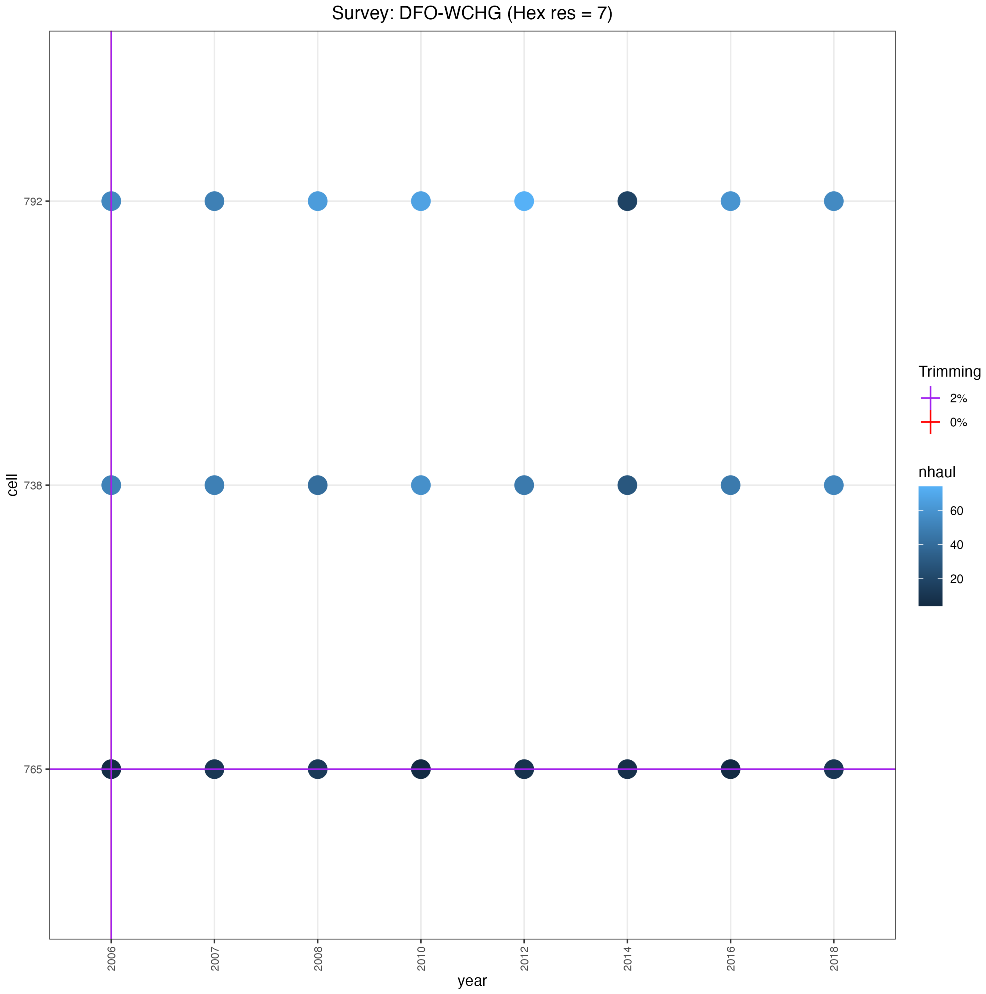
Total number of species	176.0
Percentage of species flagged	15.9

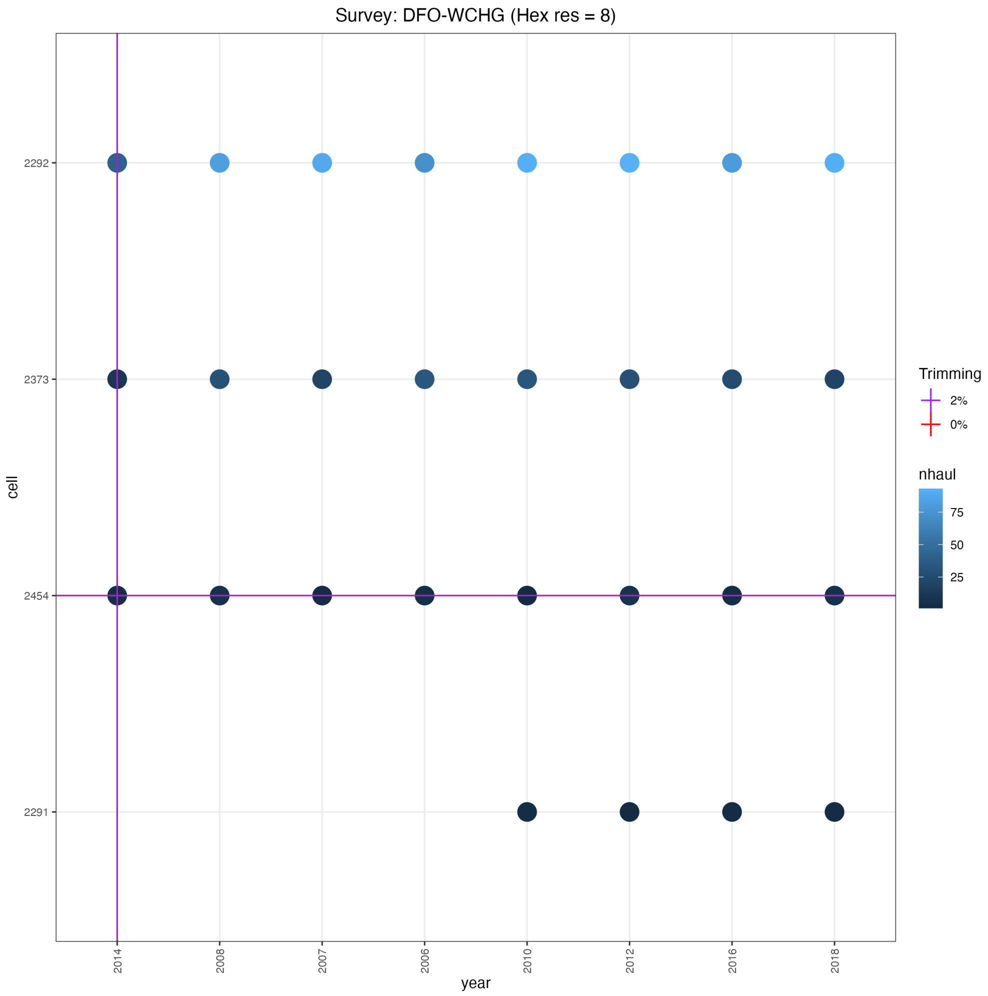
10. Spatio-temporal standardization

a. Standardization method 1

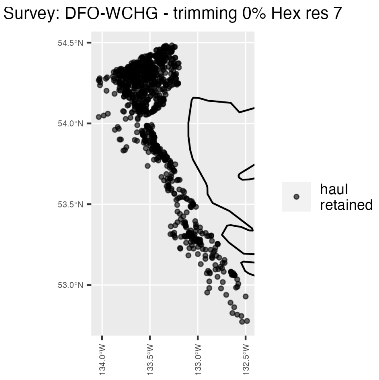
This standardization method was adapted from https://github.com/zoekitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd
It was run for hex resolution 7 and 8.

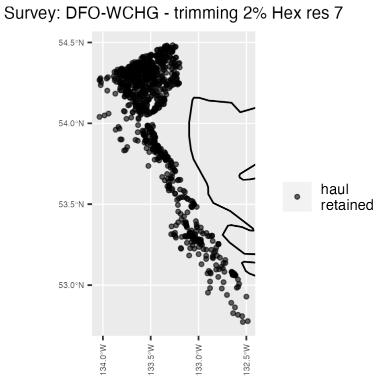
Plot of number of cells x years with overlaid flagging options

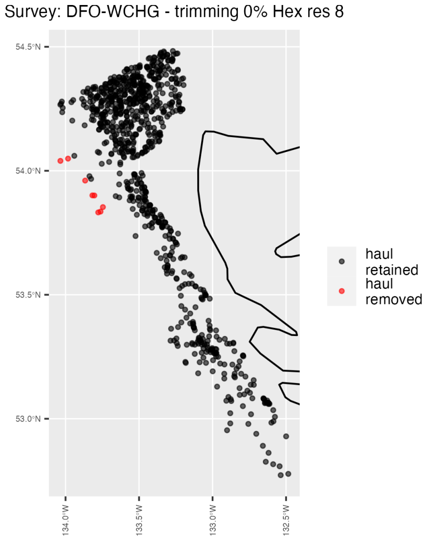

Survey: DFO-WCHG (Hex res = 7)
cell
792
738
765
year
2006
2007
2008
2010
2012
2014
2016
2018
Trimming
2%
0%
nhaul
60
40
20

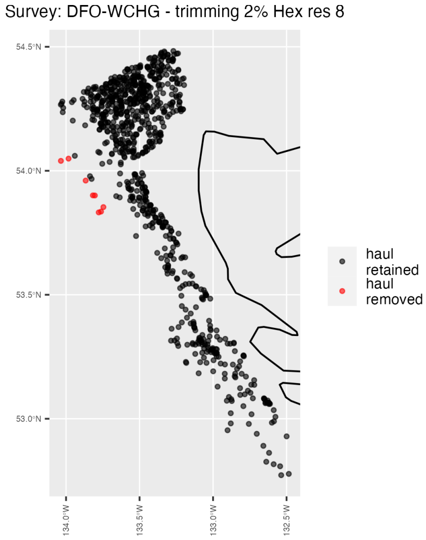


Map of hauls retained and removed per flagging method and threshold

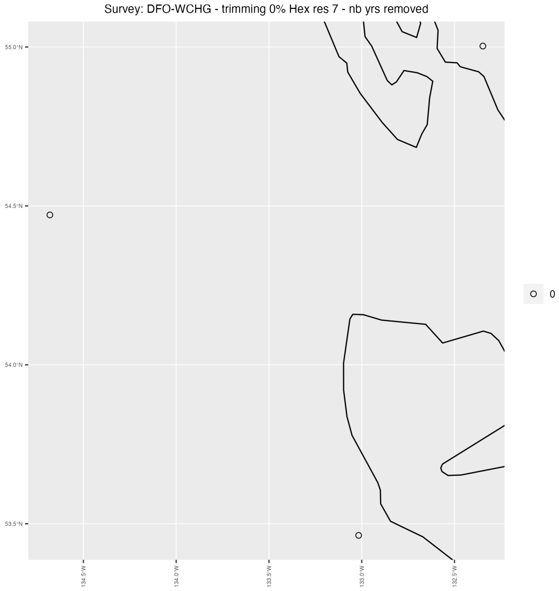

Survey: DFO-WCHG - trimming 0% Hex res 7

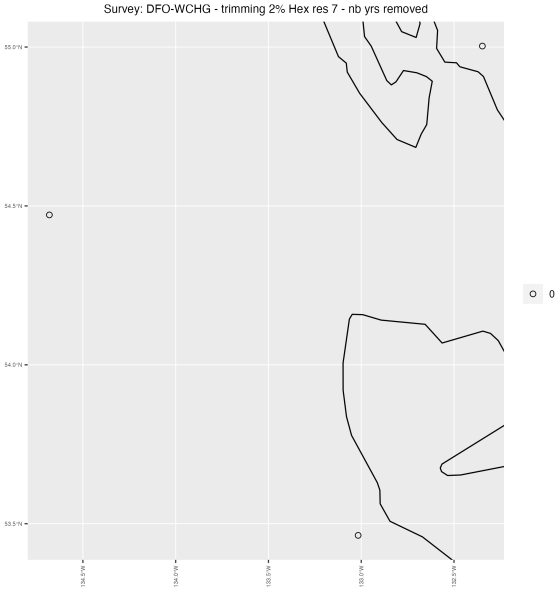

Survey: DFO-WCHG - trimming 2% Hex res 7

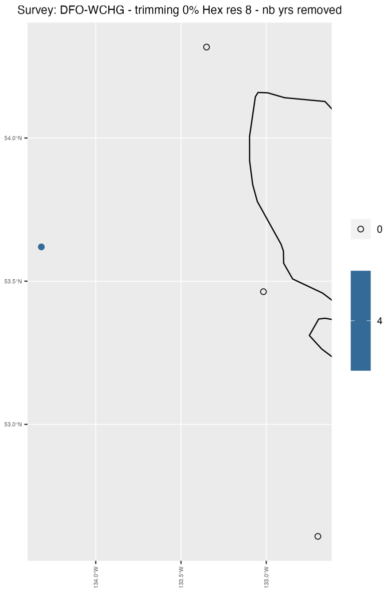


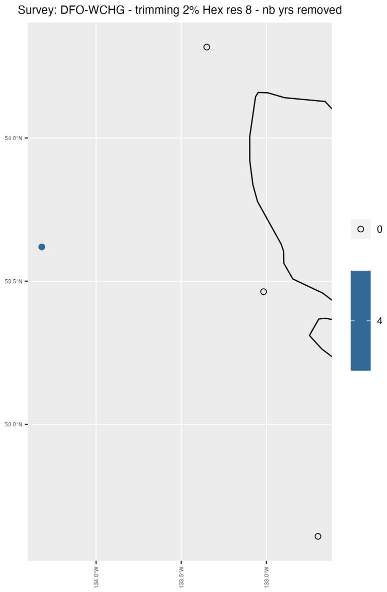


Map of numbers of years removed per grid cell and flagging method/threshold





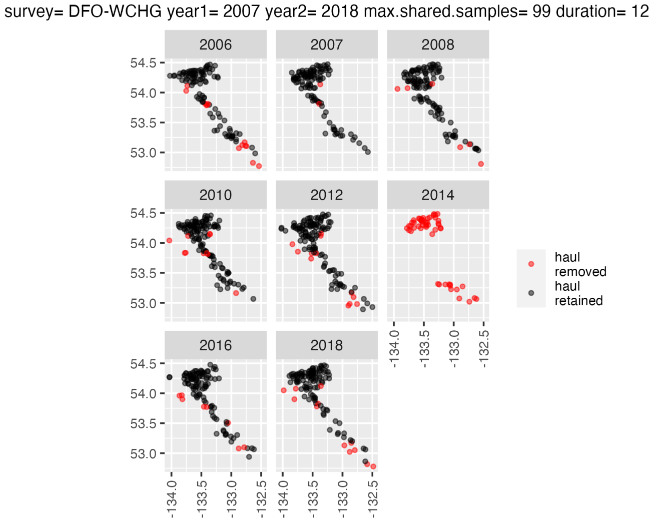




b. Standardization method 2

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	8.0	8.0	1937.0
percentage of hauls removed	0	0	0.9	0.9	13.6