AI: Aleutian Islands US survey data processing summary

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Contents

General info

This document presents the summary of the Aleutian Island bottom trawl survey provided by Stan Kotwicki and Jim Thorson It contains data from 1983-1997 (triennial) and 2000-2020 (biennial; 2008 cancelled).

Data cleaning in R

```
##############################################################################
#### R code to clean trawl survey Aleutian Islands
#### Public data Ocean Adapt
#### Contacts: Stan Kotwicki    stan.kotwicki@noaa.gov  Program Manager,
####      1 Groundfish Assessment Program, NOAA AFSC
####          Jim Thorson   james.thorson@noaa.gov  Program Leader,
####     Habitat and Ecological Processes Research, NOAA AFSC
#### Coding: Michelle Stuart, Dan Forrest, Zoë Kitchel November 2021
##############################################################################
#Alaska Fisheries Science Center - NOAA
#https://www.afsc.noaa.gov/RACE/groundfish/survey_data/
#metadata_template.php?fname=RACEweb.xml
#This NOAA center provides data for the Aleutian Islands, Eastern Bering Sea,
#and Gulf of Alaska.  (source)
#Files provided by the Alaska Fisheries Science Center

#-----------------------------------------------------------------------------#
```

```
#### 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


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

#Data for the Aleutian Islands can be accessed using the public Pinsky
#Lab OceanAdapt Git Hub Repository.
#Files obtained from data providers Mar 1, 2021  (timestamp)
#Contact malin.pinsky@rutgers.edu for questions or help accessing

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

## Special fix
#there is a comment that contains a comma in the 2014-2018 file that
#causes the delimiters to read incorrectly.  Fix that here::here:
aiURL <- "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/ai2014_2018.csv"

temp <- readLines(aiURL)
# replace the string that causes the problem
temp_fixed  <- gsub(pattern = "Stone et al., 2011", replace = "Stone et al. 2011", x = temp)
writeLines(temp_fixed, "cleaning.codes/ai2014_2018.txt") #save as text file
# read the result in as a csv
temp_csv <- read_csv(file = "cleaning.codes/ai2014_2018.txt", col_names = T)

#delete this file we temporarily made
file.remove("cleaning.codes/ai2014_2018.txt")
## End special fix

ai83_00 <- "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/ai1983_2000.csv"
ai02_12 <- "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/ai2002_2012.csv"

#make list of csv files from OceanAdapt GitHub
files <- as.list(c(ai83_00, ai02_12))

ai_data <- files %>%
  # read in all of the csv's in the files list
  map_dfr(read_csv) %>% #applies function to each element of list
  # add in the data fixed above
  rbind(temp_csv) %>%
  # remove any data rows that have headers as data rows
  filter(LATITUDE != "LATITUDE", !is.na(LATITUDE)) %>%
  mutate(stratum = as.integer(STRATUM)) %>%
```

```
  # remove any extra white space from around spp and common names
  mutate(COMMON = str_trim(COMMON),
         SCIENTIFIC = str_trim(SCIENTIFIC))

# The warning of 13 parsing failures is pointing to a row in the middle
#of the data set that contains headers instead of the numbers expected,
#this row is removed by the filter above.

aistrat <- "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/ai_strata.csv"

ai_strata <- read_csv(aistrat, col_types = cols(NPFMCArea = col_character(),
                                                SubareaDescription = col_character(),
                                                StratumCode = col_integer(),
                                                DepthIntervalm = col_character(),
                                                Areakm2 = col_integer()
))  %>%
  mutate(stratum = StratumCode)


ai <- left_join(ai_data, ai_strata, by = "stratum")

# are there any strata in the data that are not in the strata file?
stopifnot(nrow(filter(ai, is.na(Areakm2))) == 0)

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

ai <- ai %>%
  mutate(
    # Create a unique haul_id
    haul_id = paste(formatC(VESSEL, width=3, flag=0), CRUISE,
                    formatC(HAUL, width=3, flag=0), LONGITUDE, LATITUDE, sep=''),
    numcpue = ifelse(NUMCPUE < -9000,NA, NUMCPUE),
    sbt = ifelse(BOT_TEMP < -9000, NA,BOT_TEMP),
    sst = ifelse(SURF_TEMP < -9000, NA, SURF_TEMP)) %>% #get rid of any use of
                  #-9999 as a no data marker
  rename(year = YEAR,
         latitude = LATITUDE,
         longitude = LONGITUDE,
         depth = BOT_DEPTH,
         spp = SCIENTIFIC,
         station = STATION,
         num_cpue.raw = numcpue, #units = number/hectare
         wgt_cpue.raw = WTCPUE #units = kg/hectare (1 hectare = 0.01 km^2)
  ) %>%
  #convert date to month and day columns
  mutate(
    #convert date to month and day columns
    datetime = mdy_hm(DATETIME),
    month = month(datetime),
    day = day(datetime),
    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',
    #convert cpue which is currently per hectare to per km^2 by multiplying by 100
    wgt_cpue = 100*wgt_cpue.raw,
    num_cpue = 100*num_cpue.raw
  ) %>%
  # remove non-fish
  filter(
    spp != '' &
      !grepl("egg", spp)) %>%
  # adjust spp names
  mutate(
    #Manual taxa cleaning (happens later in other get.x.R scripts)
    spp = ifelse(grepl("Lepidopsetta", spp), "Lepidopsetta sp.", spp),
    spp = ifelse(grepl("Myoxocephalus", spp ) & !grepl("scorpius", spp),
                 "Myoxocephalus sp.", spp),
    spp = ifelse(grepl("Bathyraja", spp) & !grepl("panthera", spp), 'Bathyraja sp.', spp)
  ) %>%
  mutate(
    #convert cpue which is currently per hectare to per km^2 by multiplying by 100
  wgt_cpue = 100*wgt_cpue.raw,
num_cpue = 100*num_cpue.raw
) %>%
  # remove non-fish
  filter(
    spp != '' &
      !grepl("egg", spp)) %>%
  # adjust spp names
  mutate(
    #Manual taxa cleaning (happens later in other get.x.R scripts)
    spp = ifelse(grepl("Lepidopsetta", spp), "Lepidopsetta sp.", spp),
    spp = ifelse(grepl("Myoxocephalus", spp ) & !grepl("scorpius", spp),
                 "Myoxocephalus sp.", spp),
    spp = ifelse(grepl("Bathyraja", spp) & !grepl("panthera", spp), 'Bathyraja sp.', spp)
  ) %>%
  #finalize columns
  mutate(survey = "AI",
       source = "NOAA",
       timestamp = mdy("3/1/2021"),
         country = "United States",
         sub_area = NA,
         continent = "n_america",
         stat_rec = NA,
         verbatim_name = spp,
         haul_dur = NA,
         gear = NA,
         num = NA,
         num_h = NA,
         wgt = NA,
         wgt_h = NA,
         area_swept = NA
```

```
  ) %>%
  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)

#sum duplicates
ai <- ai %>%
  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_ai <- ai %>%
  group_by(haul_id, verbatim_name) %>%
  mutate(count = n())

#none!

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

unique_name_match
#check if empty

#there are some duplicates, so we will add a sum above
#1 Bathyraja sp.
#2 Malacocottus zonurus
#3 Lepidopsetta sp.
#4 Myoxocephalus sp.
#5 Aphrocallistes vastus

#-------------------------------------------------------------------------------------------#
#### 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
ai_survey_code <- "AI"

ai_taxa <- ai %>%
  select(verbatim_name) %>%
  mutate(
    taxa = str_squish(verbatim_name),
    taxa = str_remove_all(taxa," spp.| sp.| spp| sp|NO "),
    taxa = str_to_sentence(str_to_lower(taxa))
  ) %>%
  pull(taxa) %>%
  unique()

# Get clean taxa
clean_auto <- clean_taxa(ai_taxa, input_survey = ai_survey_code,
                         save = F, output=NA) # takes 9 mins

#Check those with no match from clean_taxa()
#Beringius beringii                                    no match
#Cheiraster dawsoni                                    no match
#Crangon communis                                      no match
#Pandalopsis                                           no match
#Scalpellum cornutum                                   no match
#Nearchaster variabilis                                no match
#Bathybuccinum clarki                                  no match
#Cancer branneri                                       no match
#Hippodiplosia                                         no match

#######clear, all invertebrates

#-------------------------------------------------------------------------------------------#
#### INTEGRATE CLEAN TAXA in AI survey data ####
#-------------------------------------------------------------------------------------------#

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

clean_ai <- left_join(ai, clean_taxa, by=c("verbatim_name"="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, 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,
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```
         kingdom, phylum, class, order, family, genus, rank)

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

#none!

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

unique_name_match
#check if empty


# ------------------------------------------------------------------------------------#
#### SAVE DATABASE IN GOOGLE DRIVE ####
# ------------------------------------------------------------------------------------#

# Just run this routine should be good for all if you're synced to Google Drive
write_clean_data(data = clean_ai, survey = "AI", overwrite = T)
```

1. Overview of the survey data table

survey	source	timestamp	haul_id	country	sub_area	continent
AI	NOAA	2021-03-01	001198304005-166.3183354.11833	United States	NA	n_america
AI	NOAA	2021-03-01	001198304005-166.3183354.11833	United States	NA	n_america
AI	NOAA	2021-03-01	001198304005-166.3183354.11833	United States	NA	n_america
AI	NOAA	2021-03-01	001198304005-166.3183354.11833	United States	NA	n_america
AI	NOAA	2021-03-01	001198304005-166.3183354.11833	United States	NA	n_america

stat_rec	station	stratum	year	month	day	quarter	season
NA	316-72	721	1983	8	18	3	NA
NA	316-72	721	1983	8	18	3	NA
NA	316-72	721	1983	8	18	3	NA
NA	316-72	721	1983	8	18	3	NA
NA	316-72	721	1983	8	18	3	NA

latitude	longitude	haul_dur	area_swept	gear	depth
54.11833	-166.3183	NA	NA	NA	99
54.11833	-166.3183	NA	NA	NA	99
54.11833	-166.3183	NA	NA	NA	99
54.11833	-166.3183	NA	NA	NA	99
54.11833	-166.3183	NA	NA	NA	99

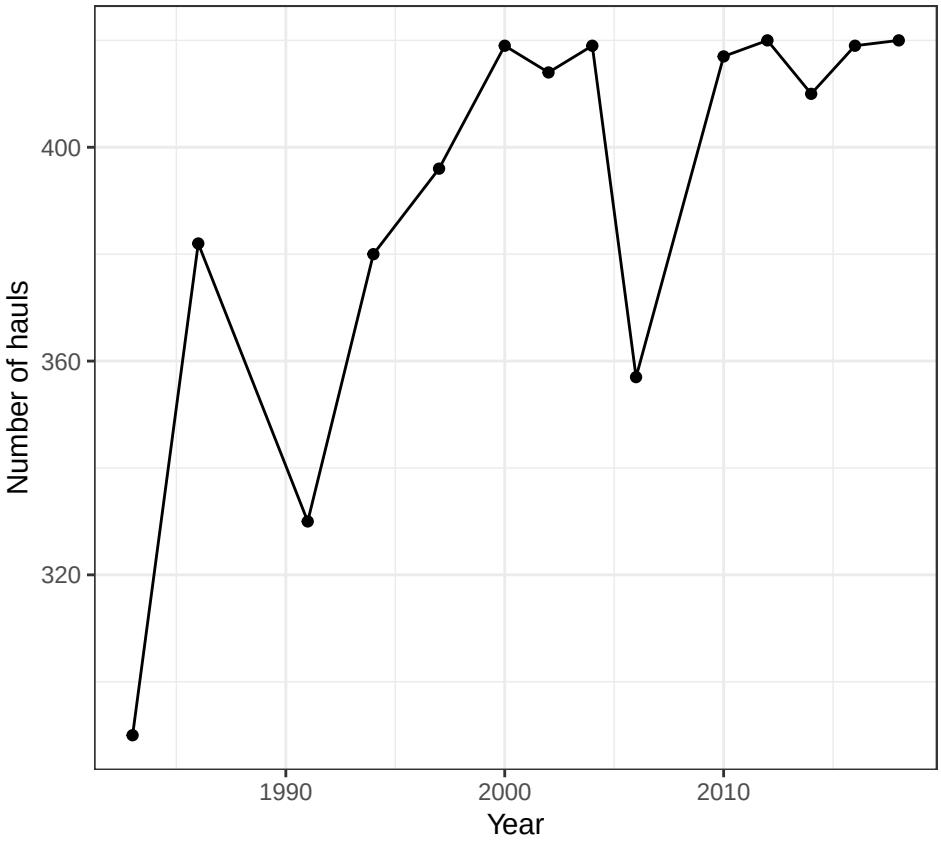
sbt	sst	num	num_h	num_cpue	wgt
4.7	8.5	0	0	952.96	0
4.7	8.5	0	0	762.37	0
4.7	8.5	0	0	89577.97	0
4.7	8.5	0	0	163336.86	0
4.7	8.5	0	0	8195.43	0

wgt_h	wgt_cpue	verbatim_name	verbatim_aphia_id	accepted_name
0	1037.41	Anoplopoma fimbria	NA	Anoplopoma fimbria
0	216.13	Atheresthes stomias	NA	Atheresthes stomias
0	19883.69	Clupea pallasii	NA	Clupea pallasii
0	136332.96	Gadus chalcogrammus	NA	Gadus chalcogrammus
0	14264.39	Gadus macrocephalus	NA	Gadus macrocephalus

aphia_id	SpecCode	kingdom	phylum	class	order	family
159463	512	Animalia	Chordata	Actinopteri	Perciformes	Anoplopomatidae
279792	517	Animalia	Chordata	Actinopteri	Pleuronectiformes	Pleuronectidae
151159	1520	Animalia	Chordata	Actinopteri	Clupeiformes	Clupeidae
300735	318	Animalia	Chordata	Actinopteri	Gadiformes	Gadidae
254538	308	Animalia	Chordata	Actinopteri	Gadiformes	Gadidae

2. Summary of sampling intensity

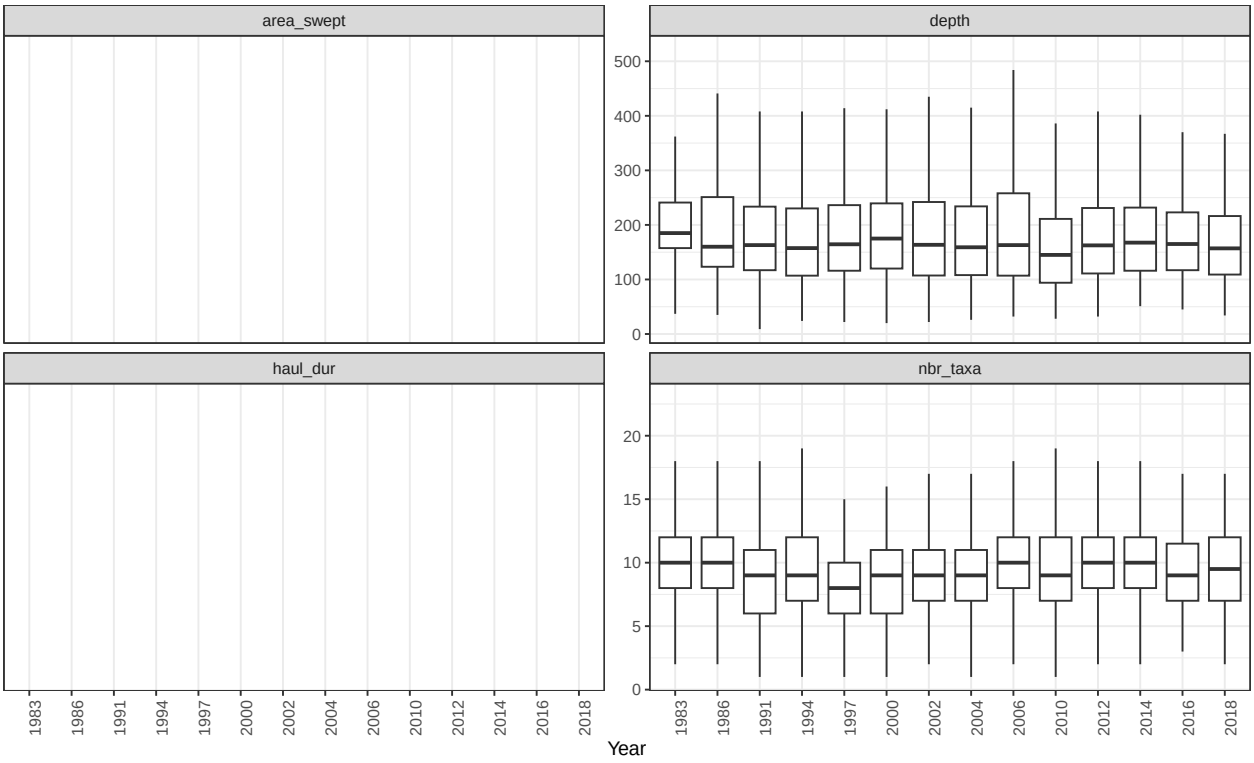
Number of hauls per year performed during the survey after data processing.



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:

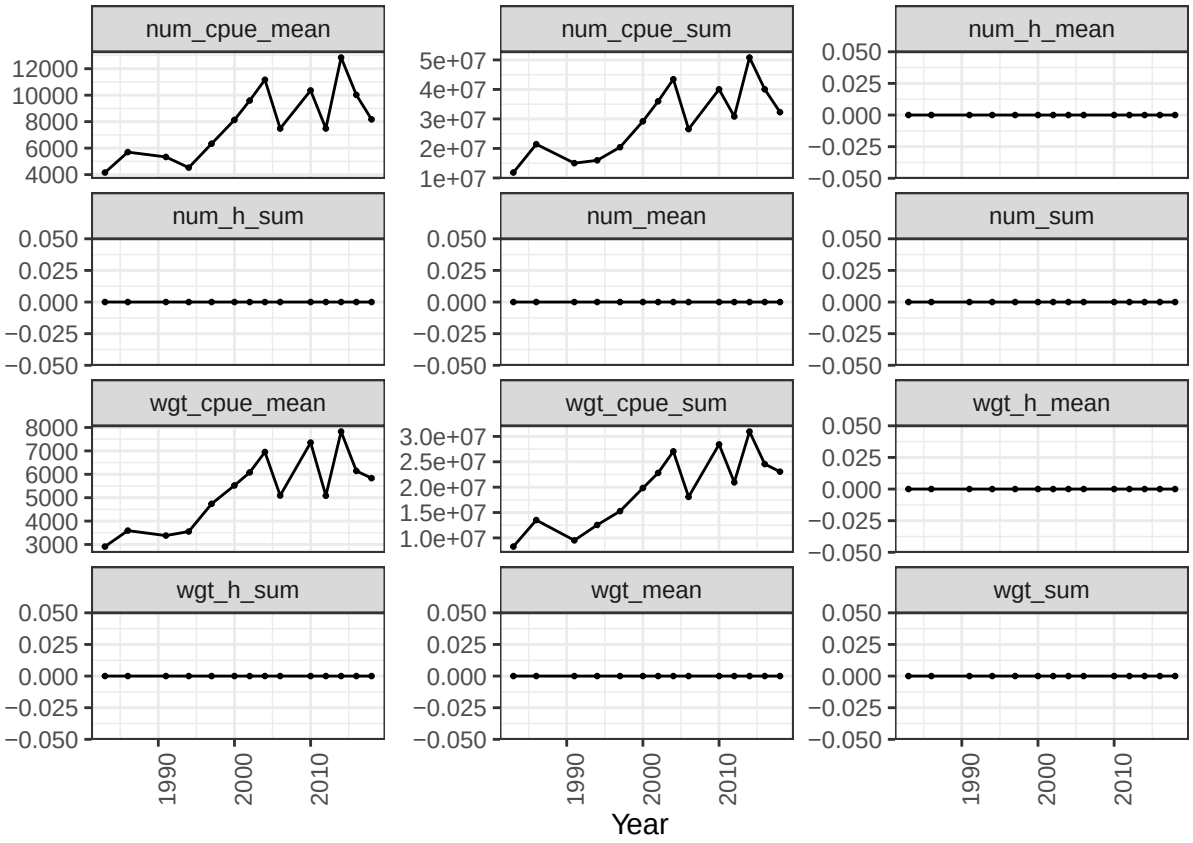
- *area_swept*, swept area by the bottom trawl gear km^2
- *depth*, sampling depth in m
- *haul_dur*, haul sampling duration *hour*
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (https://www.marinespecies.org/, October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



4. Summary of biological variables

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

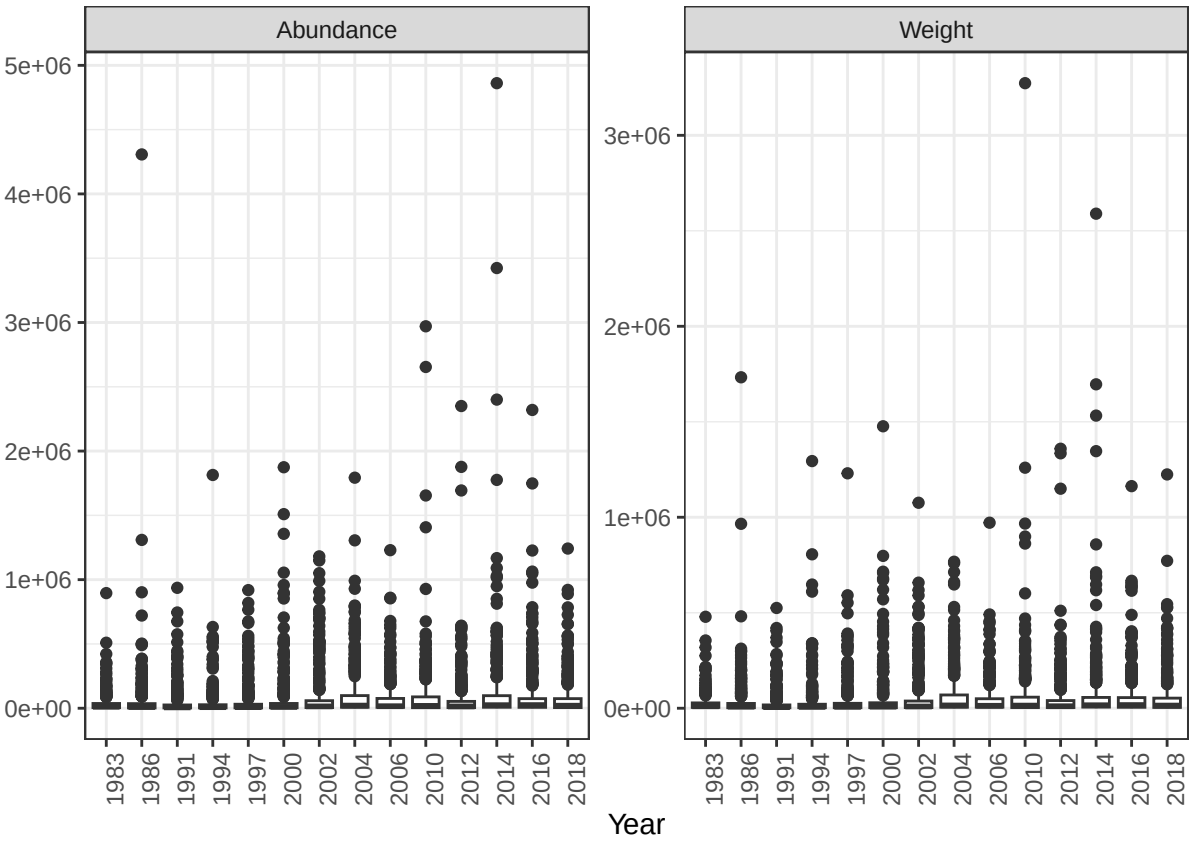
- *num_cpue*, number of individuals (abundance) in $\frac{individuals}{km^2}$
- *num_h*, number of individuals (abundance) in $\frac{individuals}{h}$
- *num*, number of individuals (abundance)
- *wgt_cpue*, weight in $\frac{kg}{km^2}$
- *wgt_h*, weight in $\frac{kg}{h}$
- *wgt*, weight in kg



5. Extreme values

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

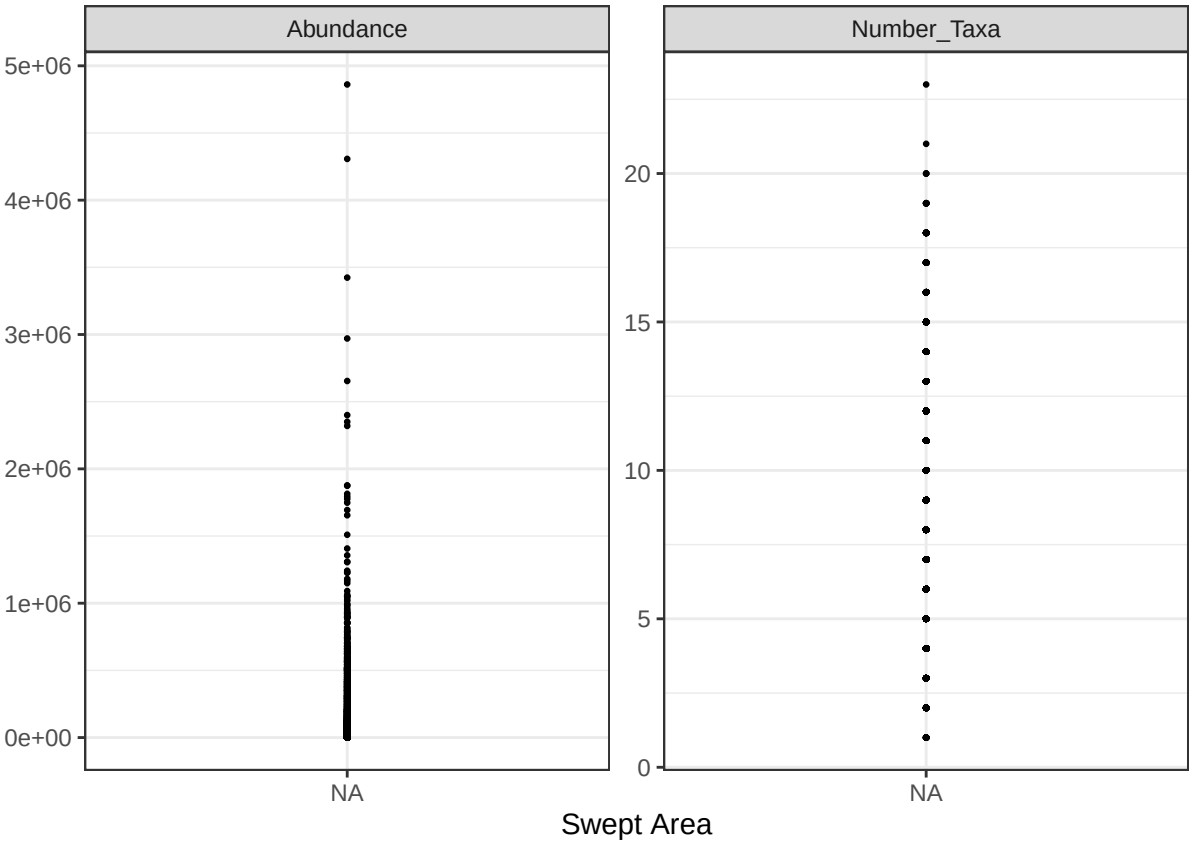
- *num_cpue*, number of individuals (abundance) in $\frac{individuals}{km^2}$
- *wgt_cpue*, weight in $\frac{kg}{km^2}$



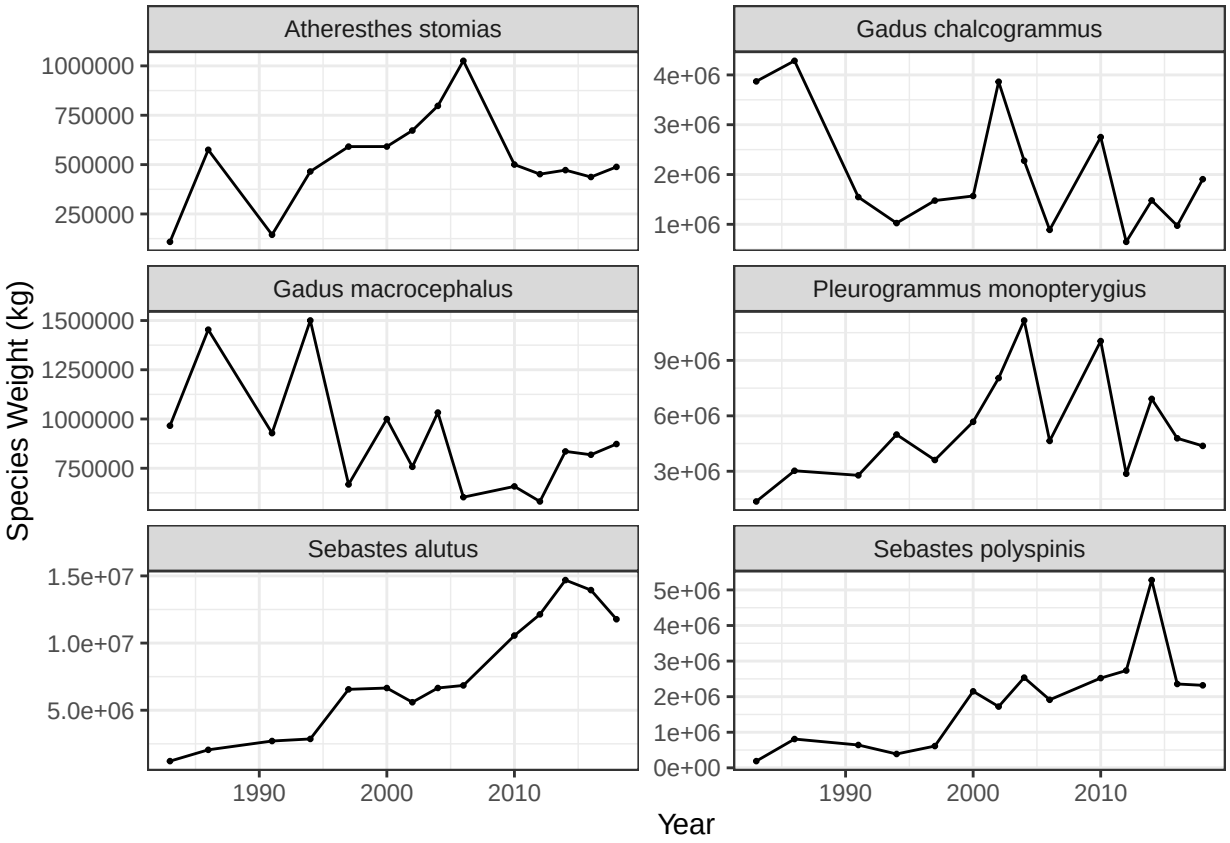
6. Summary of variables against swept area

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_cpue*, number of individuals (abundance) in $\frac{individuals}{km^2}$
- *wgt_cpue*, weight in $\frac{kg}{km^2}$

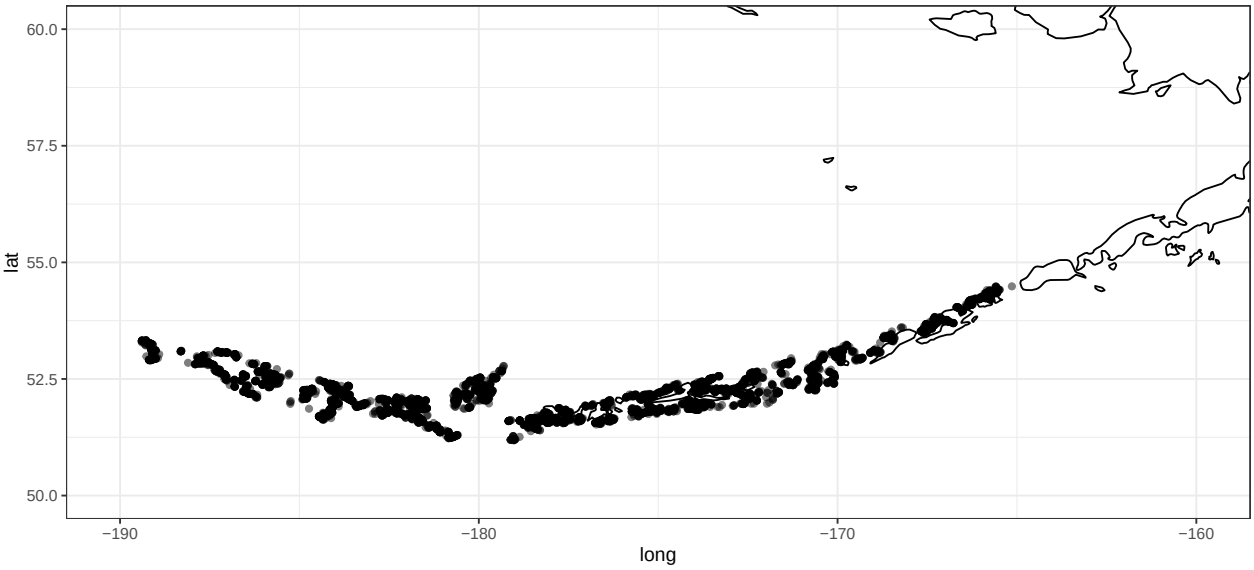


7. Abundance or Weight trends of the six most abundant species



8. Distribution mapping

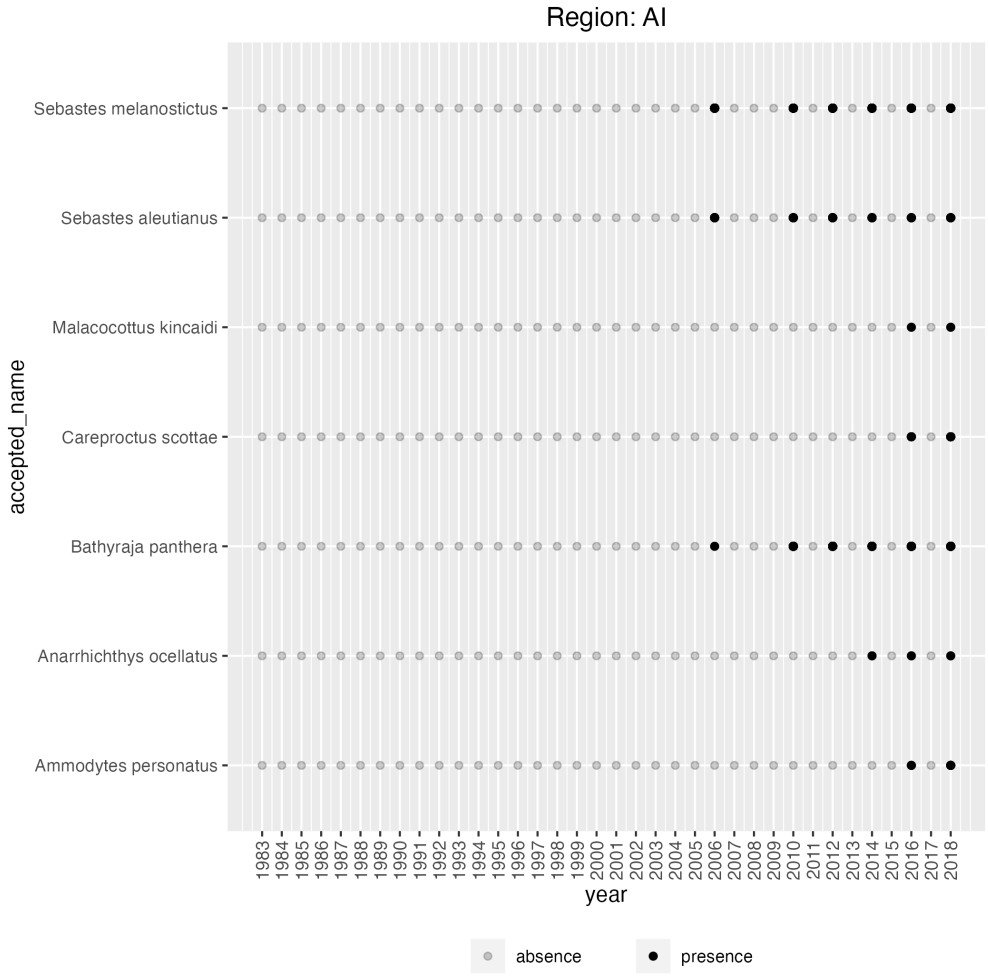
Map of the sampling distribution in space. Note that we only show one year per coordinate.



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 species



Statistics of flagged species

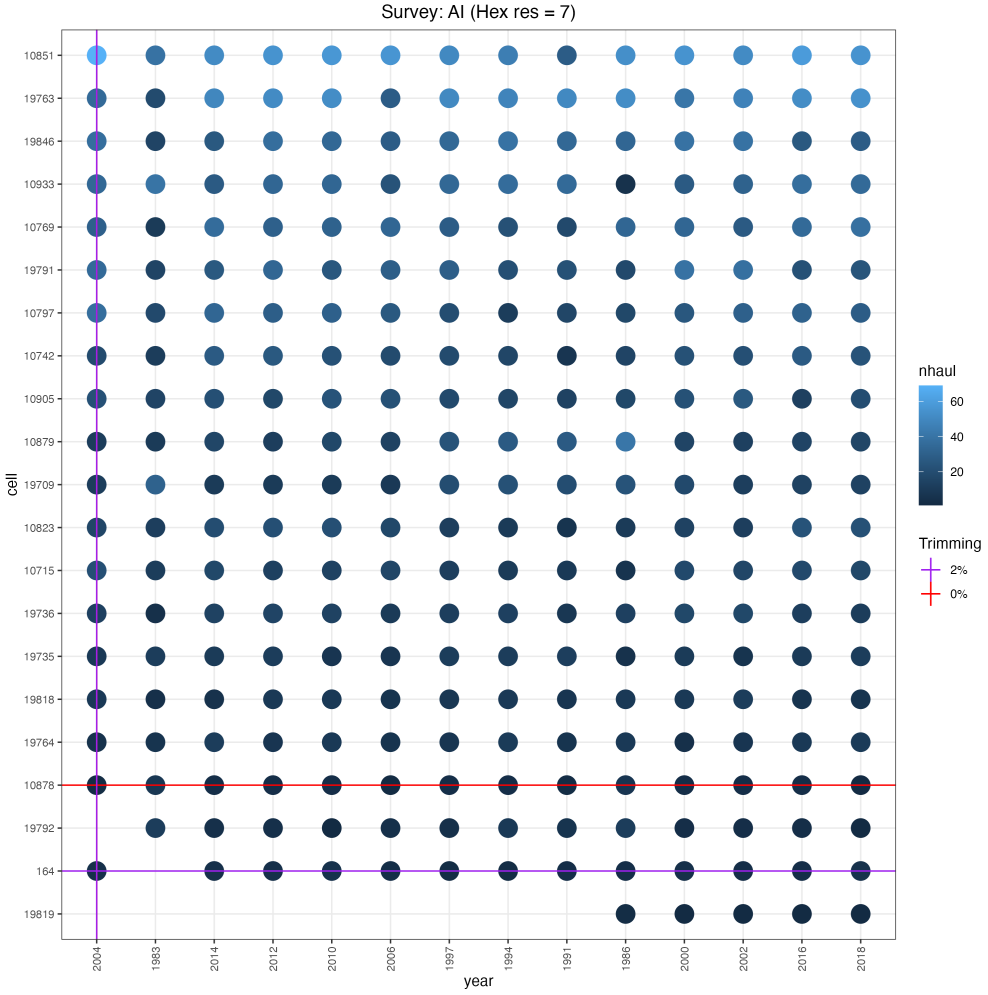
Total number of species	247.0
Percentage of species flagged	2.8

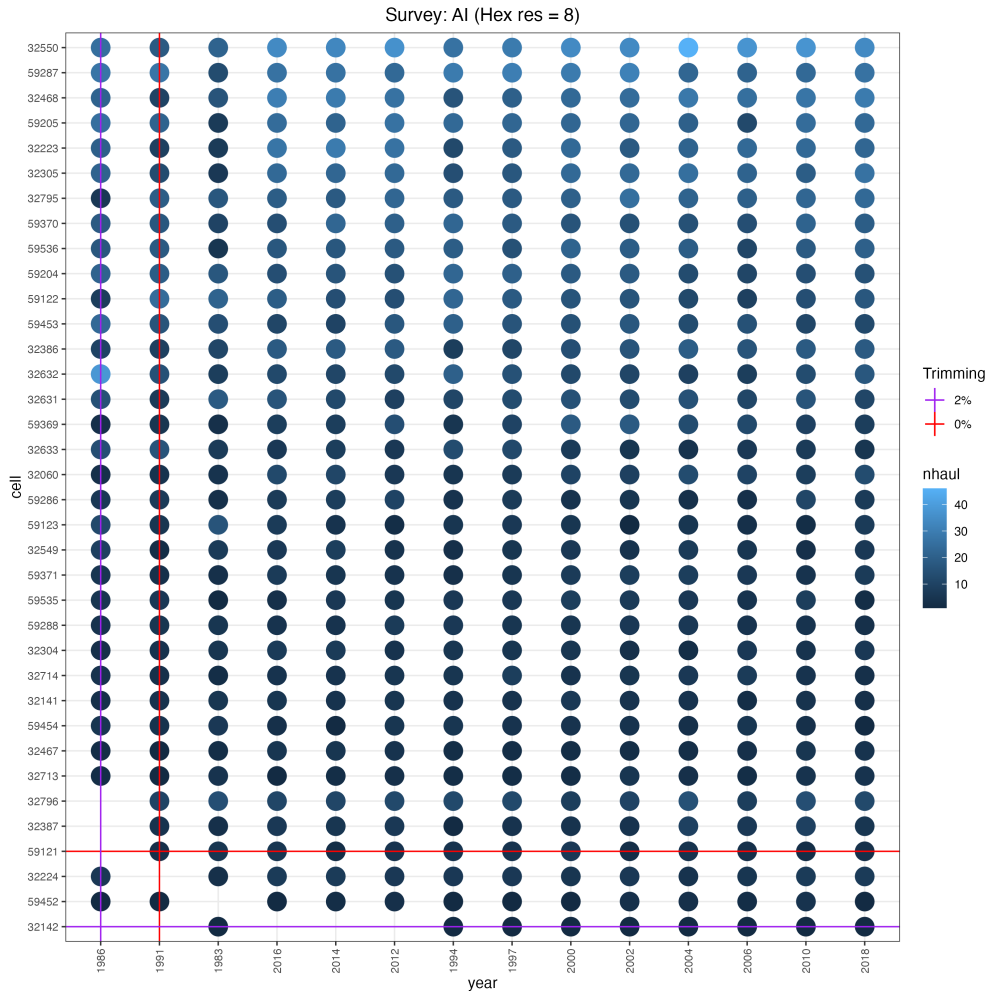
10. Spatio-temporal standardization

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.

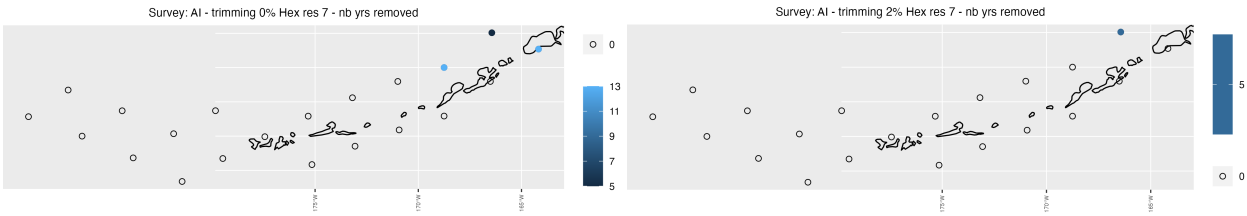
Plot of number of cells x years with overlaid flagging options

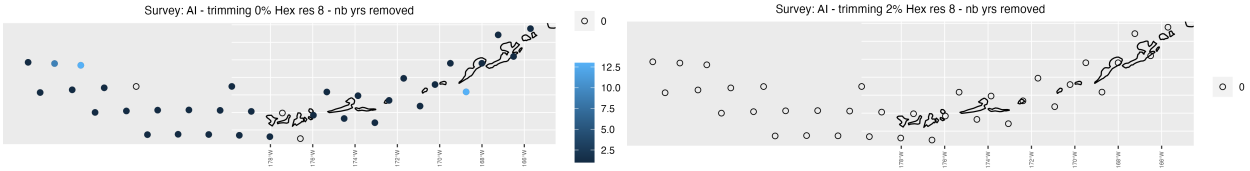




Map of hauls retained and removed per flagging method and threshold

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

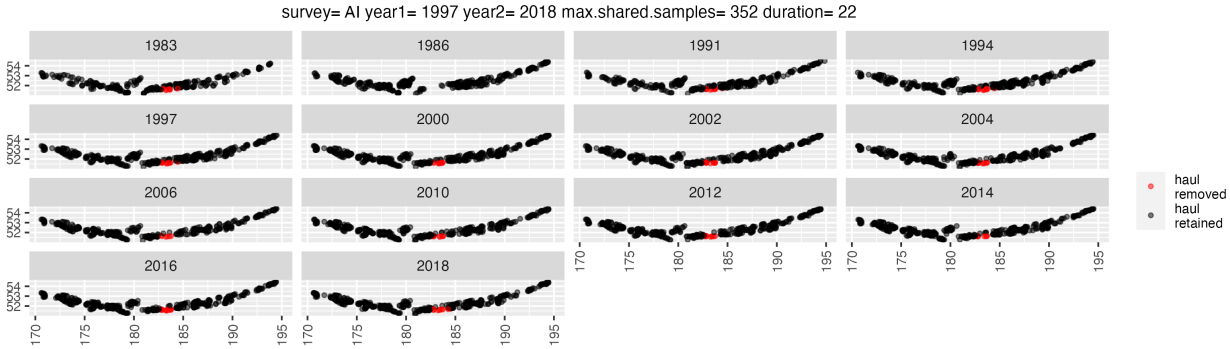




b. Standardization method 2

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	115.0	6.0	483.0	0	1193.0
percentage of hauls removed	2.1	0.1	8.8	0	2.3