

GSL-S: Gulf of St. Lawrence South (Canada) survey data processing summary

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January, 2023

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General info

This document presents the cleaning code and summary of the Gulf of St. Lawrence South (Canada) bottom trawl survey provided by Department of Fisheries and Oceans Canada. It contains data from 1970 and up to 2019.

Data cleaning in R

```
#####
#### R code to clean trawl survey for Gulf of St. Lawrence South
#### Public data Ocean Adapt
#### Contacts: Government of Canada; Fisheries and Oceans Canada
####gddaiss-dmsaisb.XLAU@dfo-mpo.gc.ca
#### Coding: Michelle Stuart, Dan Forrest, Zoë Kitchel December 2022
#####
#NB: there are multiple events at similar locations on the same day because there
#is more than one vessel sampling, keep an eye on vessel name and haul_id

#-----#
#### 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)
library(readxl)

source("functions/clean_taxa.R")
source("functions/write_clean_data.R")
source("functions/apply_trimming_method1.R")
source("functions/apply_trimming_method2.R")
source("functions/flag_spp.R")
fishglob_data_columns <- read_excel("standard_formats/fishglob_data_columns.xlsx")

#####Types of gear:
#####Western IIA trawl width 12.497m: 1987-2019; 0.041 km^2 in 30 minutes
#(avg trawl length)
#####Yankee #36 otter trawl width 10.668m" 1970-1986; 0.035 km^2 in 30 minutes
#(avg trawl length)
#Source: Page 11; https://waves-vagues.dfo-mpo.gc.ca/Library/115732.pdf

#Southern GSL -
# Trawl Distance, 1.75 nau mi. 30 minute tow at 3.5 knots (via Daniel Ricard)

#We need to check to confirm that data we use are corrected for the gear change
#described above (Zoe, 22 Nov 2022)

#Data for the Gulf of St. Lawrence South can be accessed using the public
#Pinsky Lab OceanAdapt Git Hub Repository.
#Contact malin.pinsky@rutgers.edu for questions or help accessing

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


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

GSLsouth$haul_id <- paste(GSLsouth$year,GSLsouth$month,GSLsouth$day,
                           GSLsouth$start.hour,GSLsouth$start.minute, GSLsouth$longitude,
                           GSLsouth$latitude, sep="-")

GSLsouth <- GSLsouth %>%
  mutate(
    wgt = weight.caught,
    num = number.caught,
    sub_area = NA,
    depth = NA, #No depth data available - fill with NA

```

```

station = NA,
sst = NA,
sbt = NA,
season = NA_character_,
haul_dur = 0.5, #hours
area_swept = ifelse(gear.str == "Western IIA trawl", 0.041,
                     ifelse(
                         gear.str == "Yankee #36 otter trawl", 0.035, NA)),
#average swept area values from document above
gear = gear.str,
country = "Canada",
continent = "n_america",
stat_rec = NA,
num_h = num/haul_dur,
wgt_h = wgt/haul_dur,
num_cpue = num/area_swept,
wgt_cpue = wgt/area_swept,
verbatim_name = latin.name,
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),
)

```

GSLsouth <- GSLsouth %>%
 filter(
 # remove unidentified spp and non-species
 verbatim_name != "" | !is.na(verbatim_name),
 !grepl("EGG", verbatim_name),
 !grepl("UNIDENTIFIED", verbatim_name)) %>%
 mutate(survey = "GSL-S",
 stratum = NA) %>%
 # add survey column
 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,
 num, num_h, num_cpue, wgt, wgt_h, wgt_cpue, verbatim_name)

#check that the number of unique haul_ids * spp combinations is the same
#as the number of rows in mar
nrow(GSLsouth) == nrow(unique(GSLsouth[,c("haul_id","verbatim_name")])))

#it's not, so let's see why we have extras
which(duplicated(GSLsouth[,c("haul_id","verbatim_name")])))

#Haul_ID "1994-9-22-8-27--61.633333333333-46.416666666667," Gadus morhua
#has two separate observations
#I will delete second observation because it's only 0.48611111 kg and no count info

GSLsouth <- GSLsouth[-31057,] #be sure to only do once!

#try again

```

which(duplicated(GSLsouth[,c("haul_id","verbatim_name")])) #success!

#correcting order of columns and adding final column
GSLsouth <- GSLsouth %>%
  mutate(verbatim_aphia_id = 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)

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


# Get WoRMS id for sourcing
wrms <- gnr_datasources() %>%
  filter(title == "World Register of Marine Species") %>%
  pull(id)

### Automatic cleaning
# Set Survey code
GSLsouth_survey_code <- "GSL-S"

GSLsouth <- GSLsouth %>%
  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(GSLsouth$taxa2),
                           input_survey = GSLsouth_survey_code, save = F,
                           output=NA, fishbase=T)
#takes 1.8 minutes

#This leaves out the following species, all of which are inverts or
#only ID to genus except for Cae cae
#Caelorinchus caelorinchus      (fish)
#Coelenterata
#Nereidae
#Rhynchocoela
#Lithothamnium

cae_cae <- c("Caelorinchus caelorinchus", "398381", "1726",
            "Coelorinchus caelorrhincus", "Animalia", "Chordata",
            "Actinopteri", "Gadiformes", "Macrouridae", "Coelorinchus", "Species",
            "GSL-S")

clean_auto_missing <- rbind(clean_auto, cae_cae)

#-----#
#### INTEGRATE CLEAN TAXA in GSL-South survey data ####

```

```

#-----#
correct_taxa <- clean_auto_missing %>%
  select(-survey)

clean_GSLsouth <- left_join(GSLsouth, 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,
        source = "DFO",
        timestamp = "2021",
        num_cpua = num_cpue,
        num_cpue = num_h,
        wgt_cpua = wgt_cpue,
        wgt_cpue = wgt_h,
        survey_unit = ifelse(survey %in% c("BITS", "NS-IBTS", "SWC-IBTS"),
                             paste0(survey, "-", quarter), survey),
        survey_unit = ifelse(survey %in% c("NEUS", "SEUS", "SCS", "GMEX"),
                             paste0(survey, "-", season), survey_unit)) %>%
  select(fishglob_data_columns$`Column name fishglob`)

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

# Just run this routine should be good for all
write_clean_data(data = clean_GSLsouth, survey = "GSL-S", overwrite = T)

# -----#
##### FAGS #####
# -----#
#install required packages that are not already installed
required_packages <- c("data.table",
                      "devtools",
                      "dgridR",
                      "dplyr",
                      "fields",
                      "forcats",
                      "ggplot2",
                      "here",
                      "magrittr",
                      "maps",
                      "maptools",
                      "raster",

```

```

    "rcompendium",
    "readr",
    "remotes",
    "rrtools",
    "sf",
    "sp",
    "tidyR",
    "usethis")

not_installed <- required_packages[!(required_packages %in% installed.packages()[, "Package"])]
if(length(not_installed)) install.packages(not_installed)

#load pipe operator
library(magrittr)

##### Apply taxonomic flagging per region
#get vector of regions (here the survey column)
regions <- levels(as.factor(clean_GSLsouth$survey))

#run flag_spp function in a loop
for (r in regions) {
  flag_spp(clean_GSLsouth, r)
}

##### Apply trimming per survey_unit method 1
#apply trimming for hex size 7
dat_new_method1_hex7 <- apply_trimming_per_survey_unit_method1(clean_GSLsouth, 7)

#apply trimming for hex size 8
dat_new_method1_hex8 <- apply_trimming_per_survey_unit_method1(clean_GSLsouth, 8)

##### Apply trimming per survey_unit method 2
dat_new_method2 <- apply_trimming_per_survey_unit_method2(clean_GSLsouth)

#-----
##### ADD STANDARDIZATION FLAGS #####
#-----

surveys <- sort(unique(clean_GSLsouth$survey))
survey_units <- sort(unique(clean_GSLsouth$survey_unit))
survey_std <- clean_GSLsouth %>%
  mutate(flag_taxa = NA_character_,
        flag_trimming_hex7_0 = NA_character_,
        flag_trimming_hex7_2 = NA_character_,
        flag_trimming_hex8_0 = NA_character_,
        flag_trimming_hex8_2 = NA_character_,
        flag_trimming_2 = NA_character_)

# integrate taxonomic flags
for(i in 1:length(surveys)){
  if(!surveys[i] %in% c("FALK", "GSL-N", "MRT", "NZ-CHAT", "SCS", "SWC-IBTS")){
    xx <- data.frame(read_delim(paste0("outputs/Flags/taxonomic_flagging/",

```

```

            surveys[i], "_flagspp.txt"),
        delim = ";", escape_double = FALSE, col_names = FALSE,
        trim_ws = TRUE))
xx <- as.vector(unlist(xx[1,]))

survey_std <- survey_std %>%
  mutate(flag_taxa = ifelse(survey == surveys[i] & accepted_name %in% xx,
                            "TRUE", flag_taxa))

rm(xx)
}
}

# integrate spatio-temporal flags
for(i in 1:length(survey_units)){
  if(!survey_units[i] %in% c("DFO-SOG", "IS-TAU", "SCS-FALL", "WBLS")){
    hex_res7_0 <- read.csv(paste0("outputs/Flags/trimming_method1/hex_res7/",
                                   survey_units[i], "_hex_res_7_trimming_0_hauls_removed.csv"),
                           sep = ";")
    hex_res7_0 <- as.vector(hex_res7_0[,1])

    hex_res7_2 <- read.csv(paste0("outputs/Flags/trimming_method1/hex_res7/",
                                   survey_units[i], "_hex_res_7_trimming_02_hauls_removed.csv"),
                           sep = ";")
    hex_res7_2 <- as.vector(hex_res7_2[,1])

    hex_res8_0 <- read.csv(paste0("outputs/Flags/trimming_method1/hex_res8/",
                                   survey_units[i], "_hex_res_8_trimming_0_hauls_removed.csv"),
                           sep = ";")
    hex_res8_0 <- as.vector(hex_res8_0[,1])

    hex_res8_2 <- read.csv(paste0("outputs/Flags/trimming_method1/hex_res8/",
                                   survey_units[i], "_hex_res_8_trimming_02_hauls_removed.csv"),
                           sep = ";")
    hex_res8_2 <- as.vector(hex_res8_2[,1])

    trim_2 <- read.csv(paste0("outputs/Flags/trimming_method2/",
                               survey_units[i], "_hauls_removed.csv"))
    trim_2 <- as.vector(trim_2[,1])

    survey_std <- survey_std %>%
      mutate(flag_trimming_hex7_0 = ifelse(survey_unit == survey_units[i] & haul_id %in% hex_res7_0,
                                            "TRUE", flag_trimming_hex7_0),
             flag_trimming_hex7_2 = ifelse(survey_unit == survey_units[i] & haul_id %in% hex_res7_2,
                                            "TRUE", flag_trimming_hex7_2),
             flag_trimming_hex8_0 = ifelse(survey_unit == survey_units[i] & haul_id %in% hex_res8_0,
                                            "TRUE", flag_trimming_hex8_0),
             flag_trimming_hex8_2 = ifelse(survey_unit == survey_units[i] & haul_id %in% hex_res8_2,
                                            "TRUE", flag_trimming_hex8_2),
             flag_trimming_2 = ifelse(survey_unit == survey_units[i] & haul_id %in% trim_2,
                                       "TRUE", flag_trimming_2))
  }
}

```

```
)  
rm(hex_res7_0, hex_res7_2, hex_res8_0, hex_res8_2, trim_2)  
}  
}  
  
# Just run this routine should be good for all  
write_clean_data(data = survey_std, survey = "GSL-S_std",  
                  overwrite = T, rdata=TRUE)
```

1. Overview of the survey data table

survey	source	timestamp	haul_id	country	sub_area
GSL-S	DFO	2021	1970-9-15-12-25-64.7166666666667-47.9833333333333	Canada	NA
GSL-S	DFO	2021	1970-9-15-12-25-64.7166666666667-47.9833333333333	Canada	NA
GSL-S	DFO	2021	1970-9-15-12-25-64.7166666666667-47.9833333333333	Canada	NA
GSL-S	DFO	2021	1970-9-15-12-25-64.7166666666667-47.9833333333333	Canada	NA
GSL-S	DFO	2021	1970-9-15-12-25-64.7166666666667-47.9833333333333	Canada	NA

continent	stat_rec	station	stratum	year	month	day	quarter	season
n_america	NA	NA	NA	1970	9	15	3	NA
n_america	NA	NA	NA	1970	9	15	3	NA
n_america	NA	NA	NA	1970	9	15	3	NA
n_america	NA	NA	NA	1970	9	15	3	NA
n_america	NA	NA	NA	1970	9	15	3	NA

latitude	longitude	haul_dur	area_swept	gear	depth	sbt	sst
47.98333	-64.71667	0.5	0.035	Yankee #36 otter trawl	NA	NA	NA
47.98333	-64.71667	0.5	0.035	Yankee #36 otter trawl	NA	NA	NA
47.98333	-64.71667	0.5	0.035	Yankee #36 otter trawl	NA	NA	NA
47.98333	-64.71667	0.5	0.035	Yankee #36 otter trawl	NA	NA	NA
47.98333	-64.71667	0.5	0.035	Yankee #36 otter trawl	NA	NA	NA

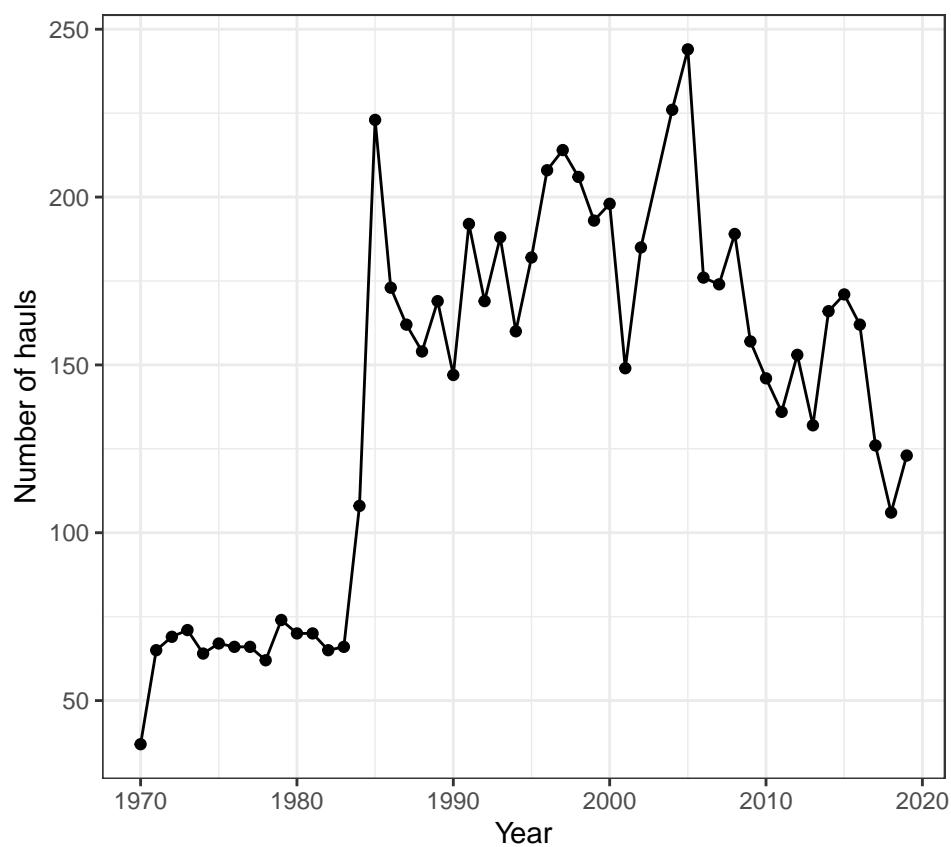
num	num_cpue	num_cpua	wgt	wgt_cpue	wgt_cpua	verbatim_name
60.328947	120.657895	1723.6842	80.840789	161.681579	2309.7368	GADUS MORHUA
316.363158	632.726316	9038.9474	60.531579	121.063158	1729.4737	HIPPOGLOSSOIDES PLATESSOIDES
4.282895	8.565789	122.3684	4.282895	8.565789	122.3684	GLYPTOCEPHALUS CYNOGLOSSUS
10.948620	21.897239	312.8177	3.515468	7.030936	100.4419	LIMANDA FERRUGINEA
59.989612	119.979224	1713.9889	15.148892	30.297784	432.8255	CLUPEA HARENGUS

verbatim_aphia_id	accepted_name	aphia_id	SpecCode	kingdom
NA	Gadus morhua	126436	69	Animalia
NA	Hippoglossoides platessoides	127137	4239	Animalia
NA	Glyptocephalus cynoglossus	127136	26	Animalia
NA	Limanda ferruginea	158879	521	Animalia
NA	Clupea harengus	126417	24	Animalia

phylum	class	order	family	genus	rank	survey_unit
Chordata	Teleostei	Gadiformes	Gadidae	Gadus	Species	GSL-S
Chordata	Teleostei	Pleuronectiformes	Pleuronectidae	Hippoglossoides	Species	GSL-S
Chordata	Teleostei	Pleuronectiformes	Pleuronectidae	Glyptocephalus	Species	GSL-S
Chordata	Teleostei	Pleuronectiformes	Pleuronectidae	Limanda	Species	GSL-S
Chordata	Teleostei	Clupeiformes	Clupeidae	Clupea	Species	GSL-S

2. Summary of sampling intensity

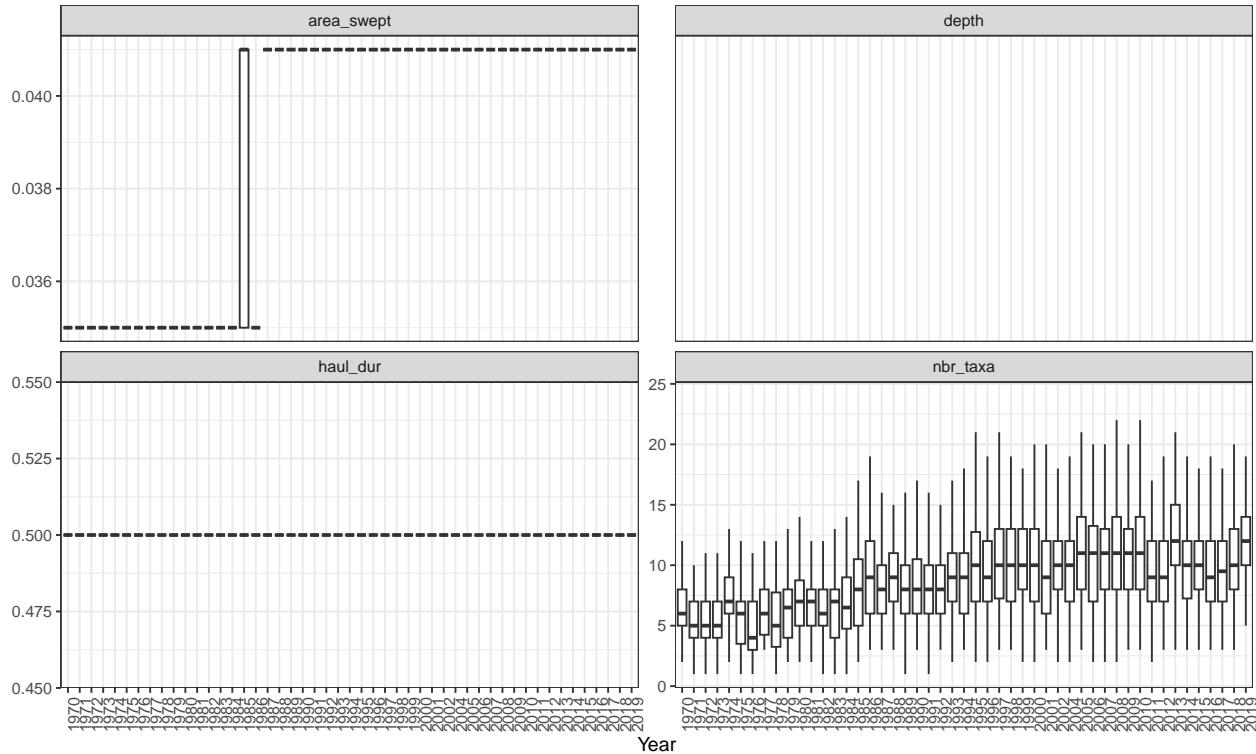
Number of hauls per year performed during the survey after data processing.



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:

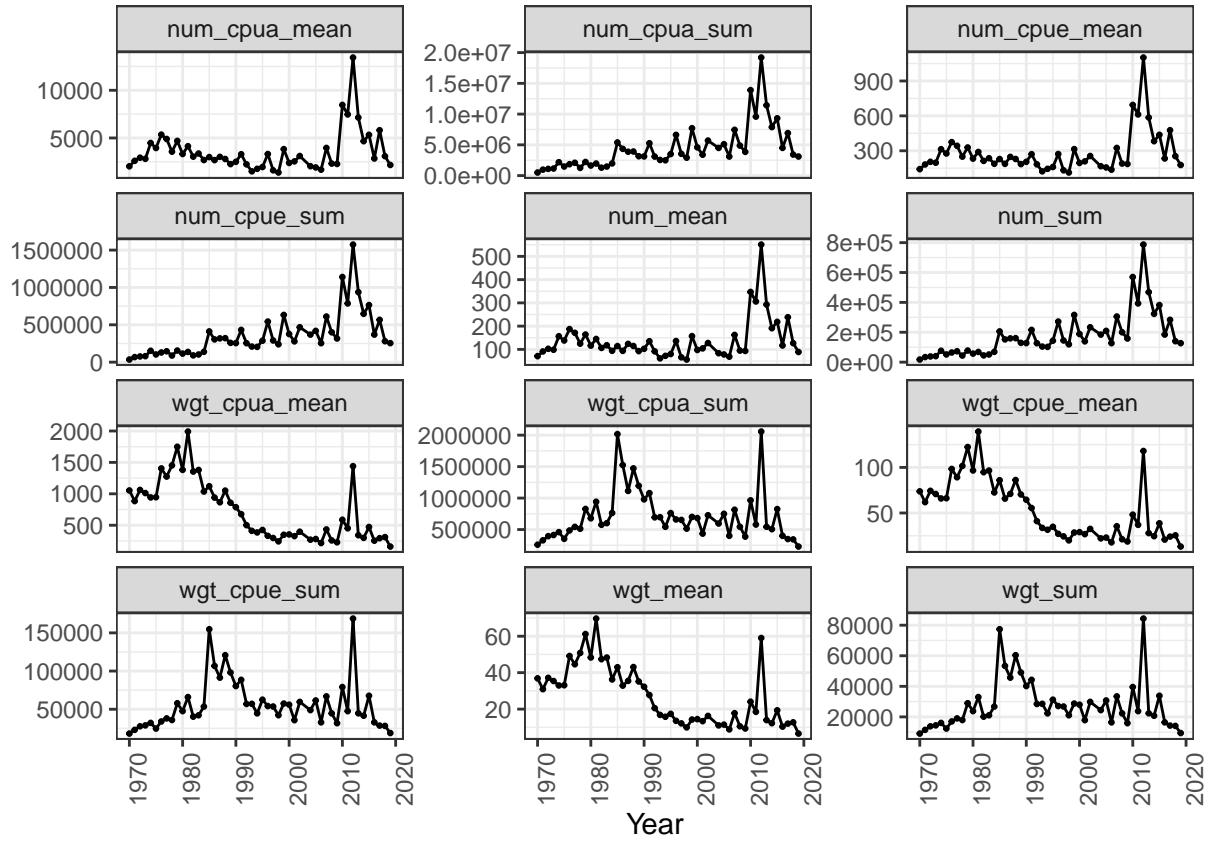
- *area_swept*, swept area by the bottom trawl gear km^2
- *depth*, sampling depth in m
- *haul_dur*, haul sampling duration *hour*
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (<https://www.marinespecies.org/>, October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



4. Summary of biological variables

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

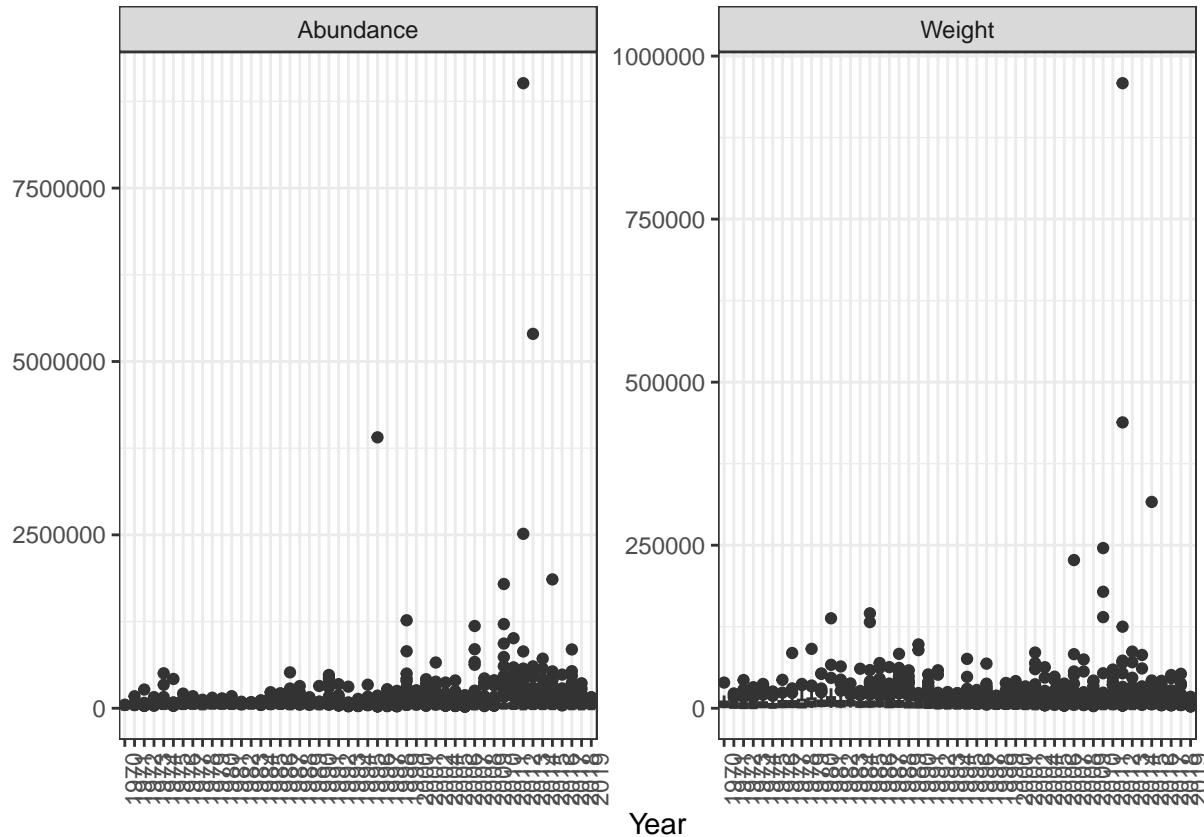
- num_cpua , number of individuals (abundance) in $\frac{individuals}{km^2}$
- num_cpue , number of individuals (abundance) in $\frac{individuals}{h}$
- num , number of individuals (abundance)
- wgt_cpua , weight in $\frac{kg}{km^2}$
- wgt_cpue , weight in $\frac{kg}{h}$
- wgt , weight in kg



5. Extreme values

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

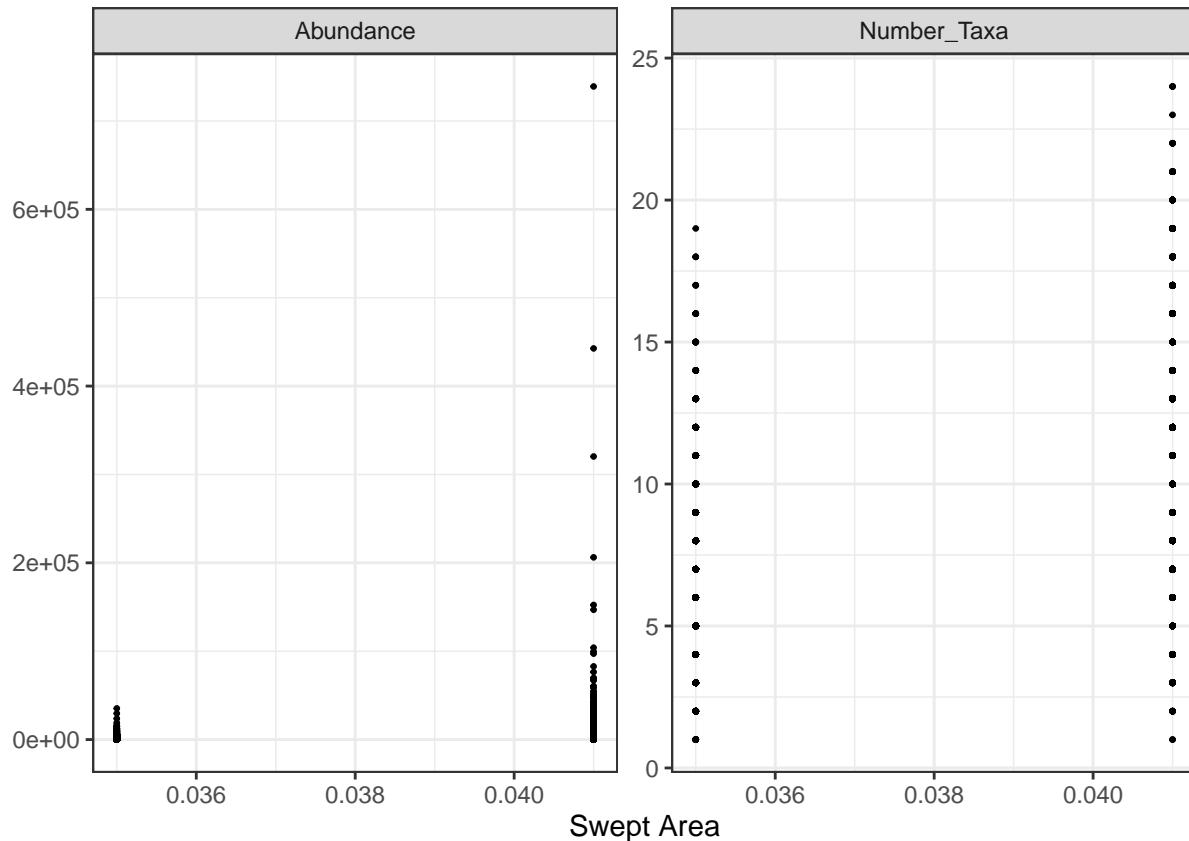
- num_cpue , number of individuals (abundance) in $\frac{individuals}{km^2}$
- wgt_cpue , weight in $\frac{kg}{km^2}$



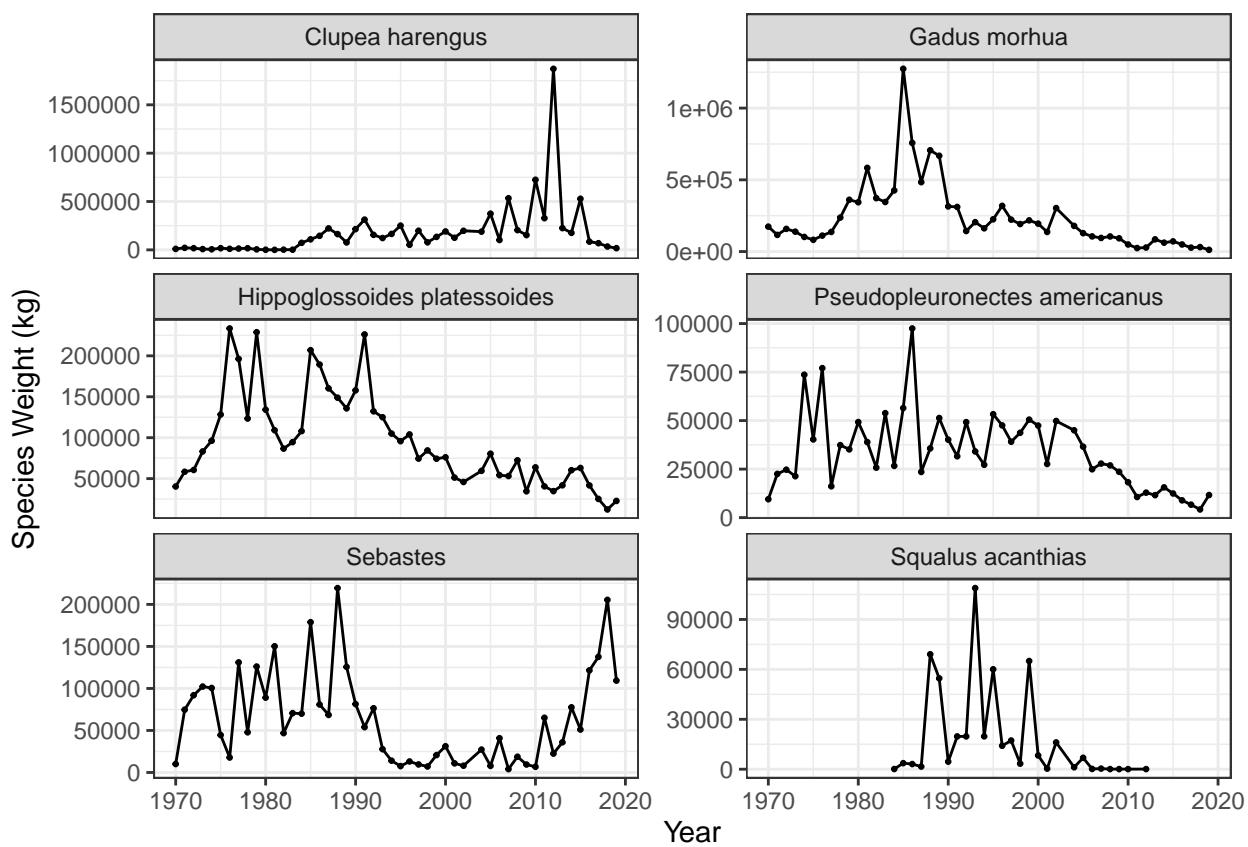
6. Summary of variables against swept area

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_cpua , number of individuals (abundance) in $\frac{individuals}{km^2}$
- wgt_cpua , weight in $\frac{kg}{km^2}$

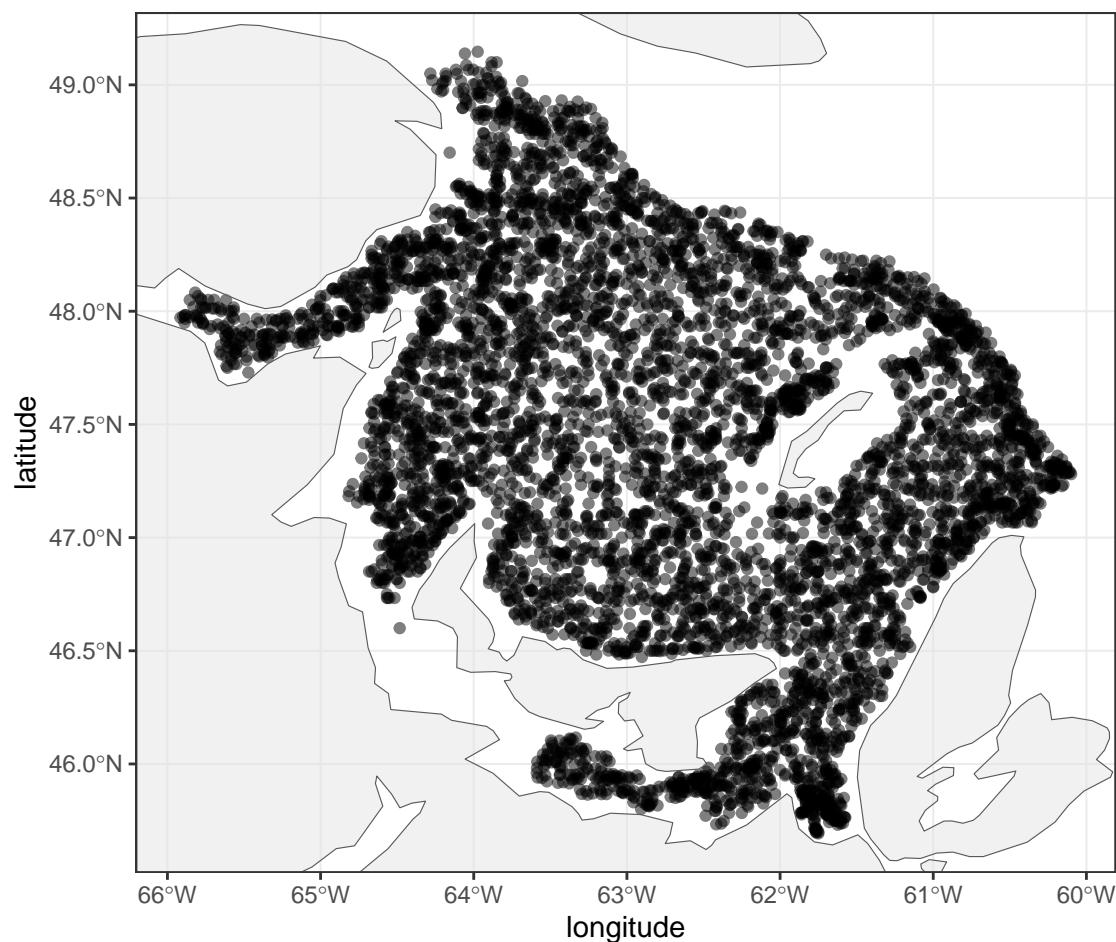


7. Abundance or Weight trends of the six most abundant species



8. Distribution mapping

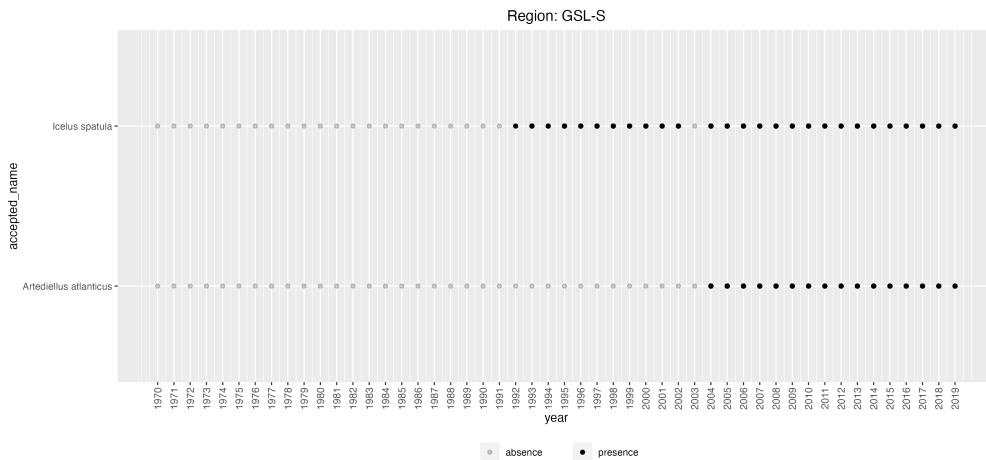
Map of the sampling distribution in space. Note that we only show one year per coordinate.



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 taxa



Statistics related to the taxonomic flagging outputs

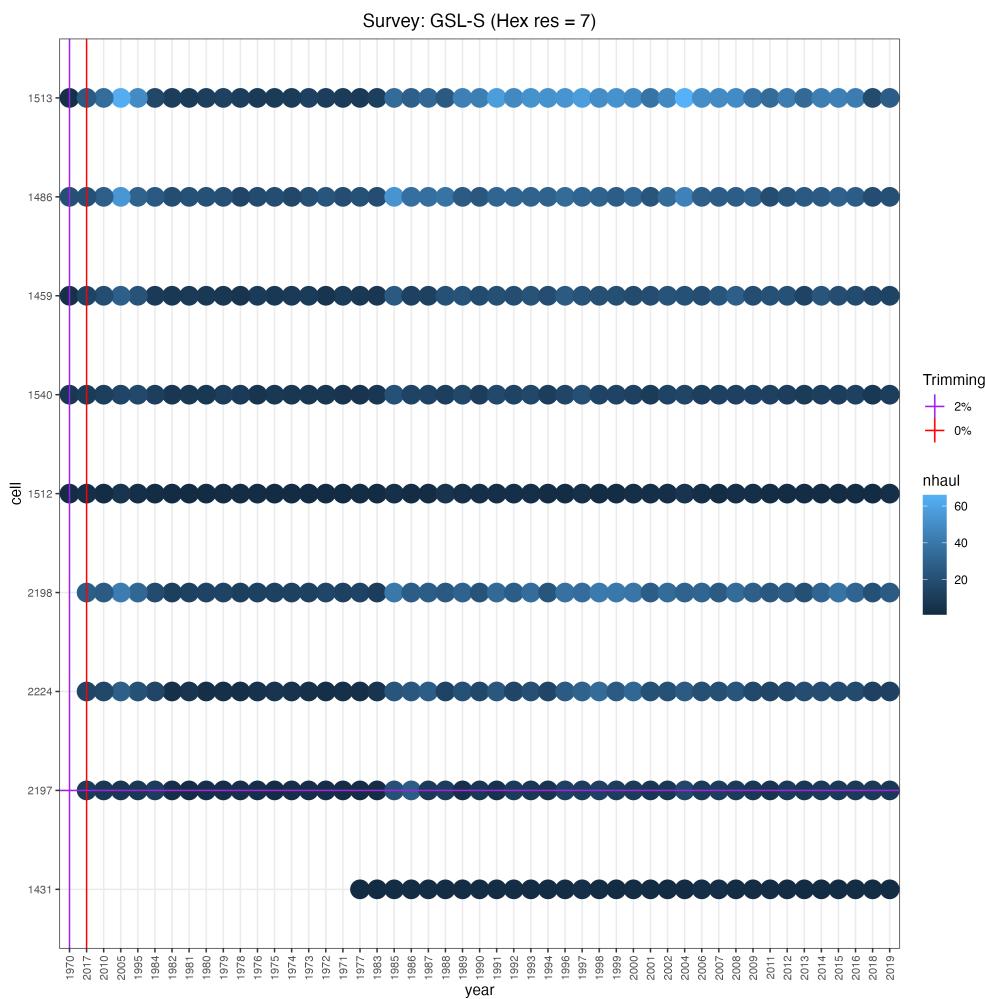
Total number of species	134.0
Percentage of species flagged	1.5

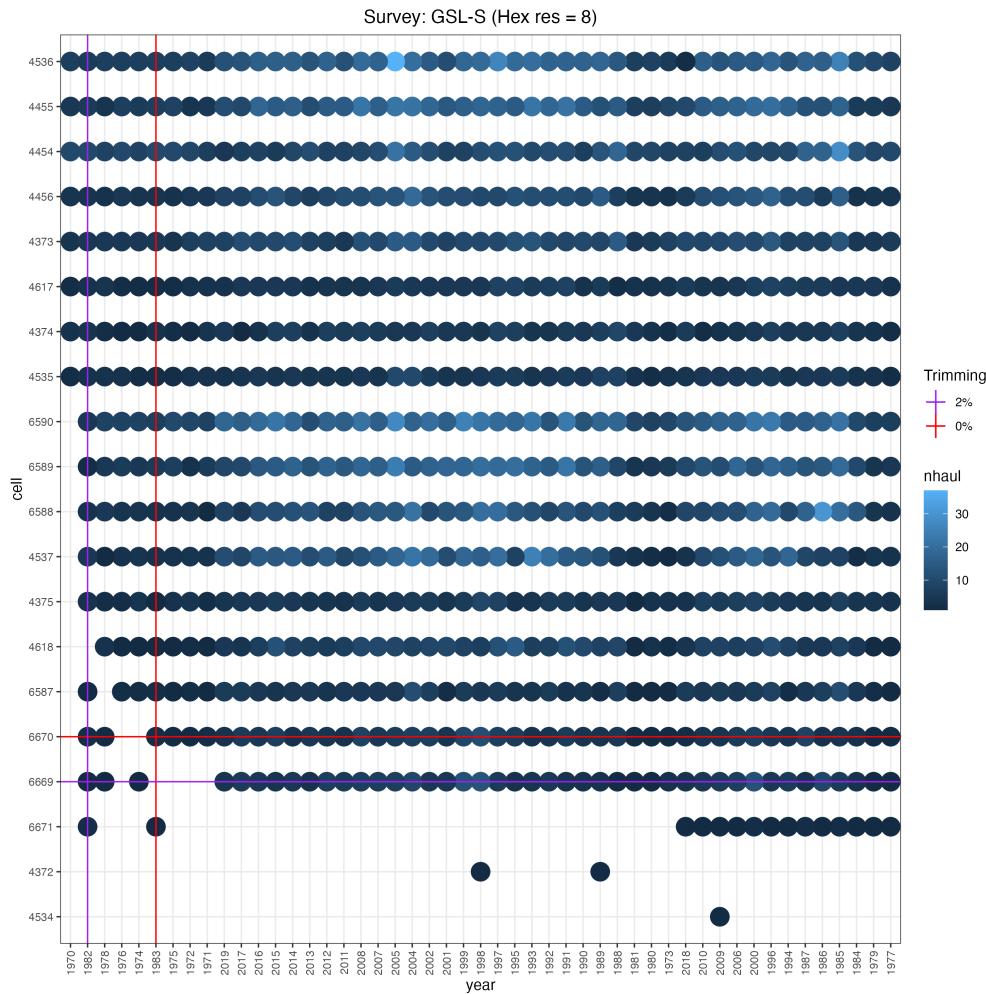
10. Spatio-temporal standardization

a. Standardization method 1

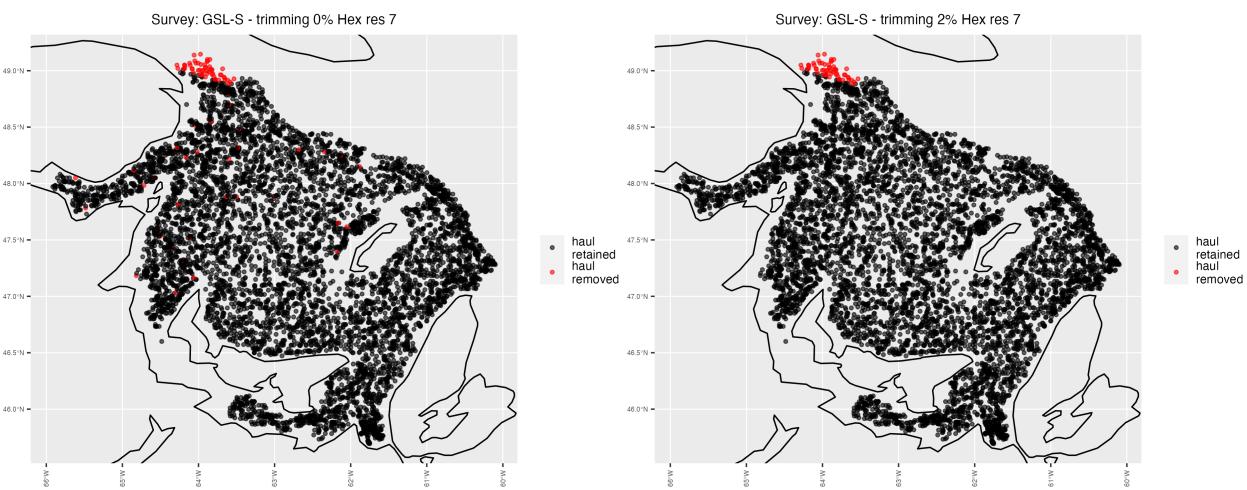
This standardization method was adapted from https://github.com/zoekitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd
It was run for hex resolution 7 and 8.

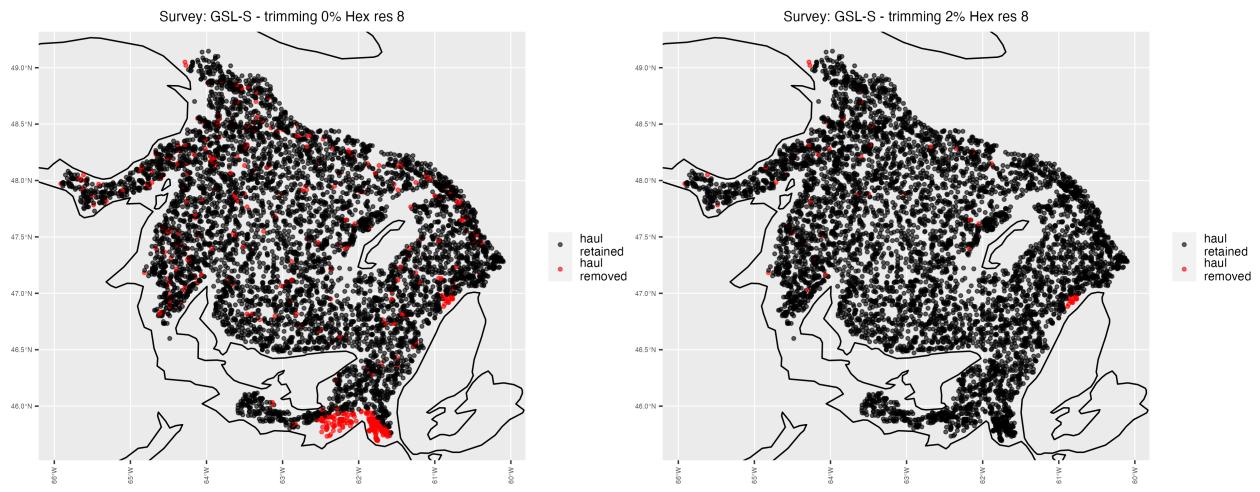
Plot of number of cells x years with overlaid flagging options



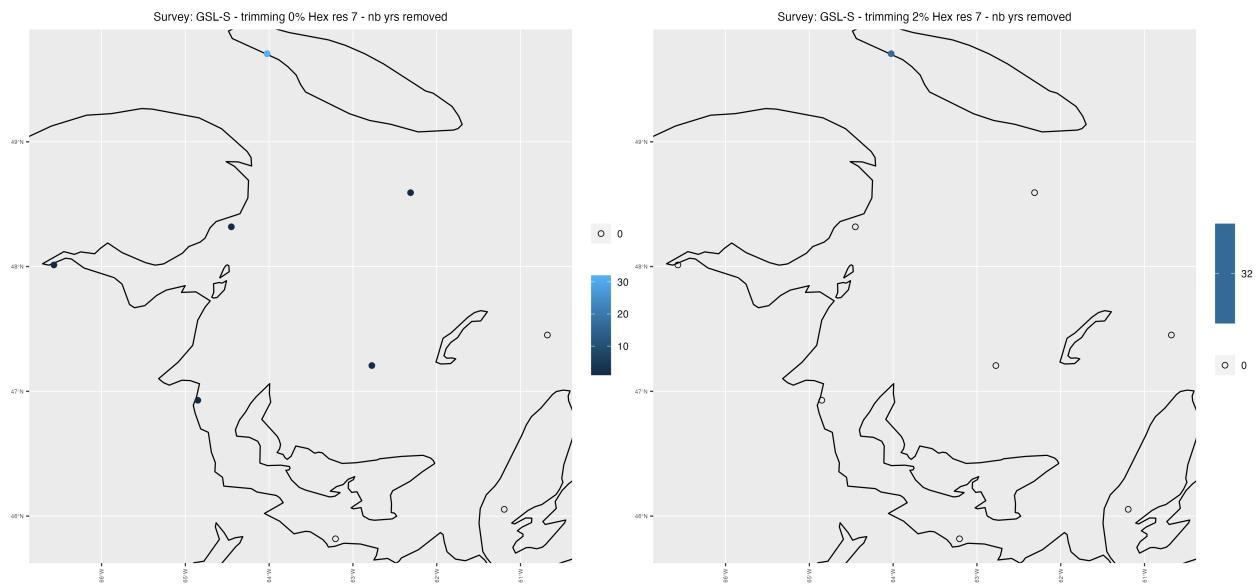


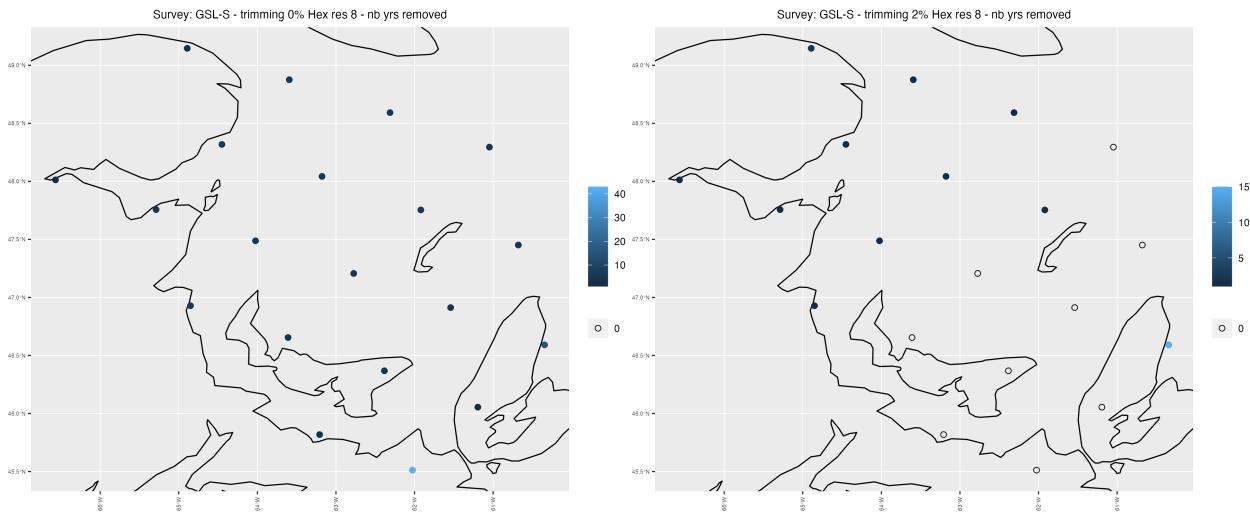
Map of hauls retained and removed per flagging method and threshold





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

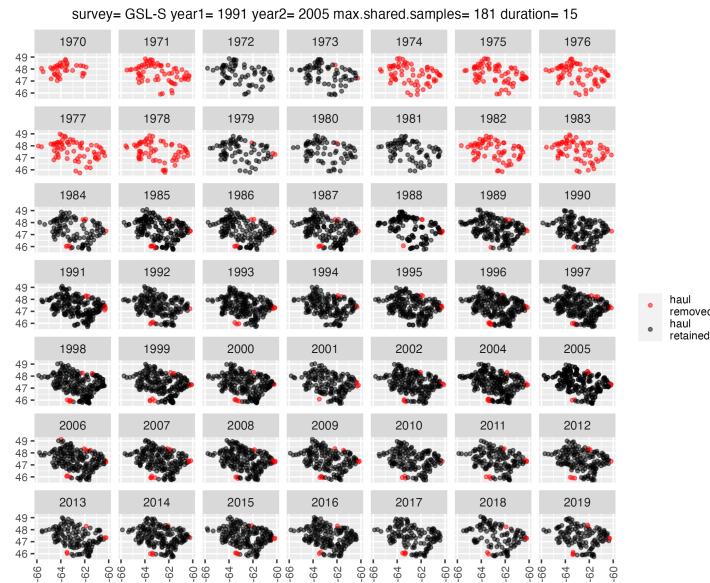




b. Standardization method 2

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	94.0	57.0	519.0	59.0	5973.0
percentage of hauls removed	1.4	0.8	7.5	0.9	9.4