

# SP-ARSA: Gulf of Cadiz Bottom Trawl survey data processing summary

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## General info

This document presents the cleaning code and summary of the Gulf of Cadiz bottom trawl survey provided by DATRAS, ICES. It contains data from **2002** and up to **2020**.

## Data cleaning in R

```
#####  
#### R code to download and clean DATRAS data from ICES  
#### URL: https://datras.ices.dk/  
#### Coding: Aurore Maureaud + Julianio Palacios + Daniel van Denderen, December 2022  
#### Coding: + Laurene Pecuchet 2023  
#####  
rm(list=ls())  
  
date <- "3November2023"  
  
#####
```

```

#### LOAD LIBRARIES & options to decide in the code
#####
library(data.table)
library(tidyverse)
library(icesDatras)
library(worrms)
library(curl)
library(urltools)
library(here) # for easy work around on multiple computers
library(taxize) # for getting correct species names
library(googledrive)
library(readxl)
library(here)
library(ggplot2)

# load relevant functions
source("functions/write_clean_data.r")
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")
source("functions/get_length_weight_coeffs_rfishbase.R")
fishglob_data_columns <- read_excel("standard_formats/fishglob_data_columns.xlsx")

# should the last version of DATRAS be downloaded?
download_last_version <- FALSE

# should the data be loaded from the last version saved?
load_stored_datras <- FALSE

# should we save a new version of hh and hl?
save_hh_and_hl <- FALSE

# should we get the length-weight relationships from fishbase?
need_get_lw_rel <- FALSE

# check length types for conversion to TL?
check_TL_conversion <- FALSE

# apply TL conversion?
apply_TL_conversion <- FALSE

# plot length frequencies for deep sea fish with different length than TL?
plot_length_frequencies <- FALSE

# remove lengths based on issues identied for SP-NORTH and SP-ARSA?
remove_lengths_units_issue <- TRUE

#####
#### LOAD FILES
#####

```

```

if(download_last_version == TRUE){
  last.year <- 2020

  # Haul info from Datras
  hh.ns <- getDATRAS(record='HH', survey='NS-IBTS', years=c(1967:last.year),
                    quarters=c(1,3))
  hh.baltic <- getDATRAS(record='HH', survey='BITS', years=c(1991:last.year),
                       quarters=c(1,4))
  hh.evhoe <- getDATRAS(record='HH', survey='EVHOE', years=c(1997:last.year),
                      quarters=4)
  hh.cgfs <- getDATRAS(record='HH', survey='FR-CGFS', years=c(1998:last.year),
                     quarters=4)
  hh.igfs <- getDATRAS(record='HH', survey='IE-IGFS', years=c(2003:last.year),
                     quarters=4)
  hh.nigfs <- getDATRAS(record='HH', survey='NIGFS', years=c(2005:last.year),
                      quarters=c(1:4))
  hh.pt <- getDATRAS(record='HH', survey='PT-IBTS', years=c(2002:last.year),
                   quarters=c(3:4))
  hh.rock <- getDATRAS(record='HH', survey='ROCKALL', years=c(1999:2009),
                     quarters=3)
  hh.scorock <- getDATRAS(record='HH', survey='SCOROC', years=c(2011:last.year),
                        quarters=3)
  hh.swc <- getDATRAS(record='HH', survey='SWC-IBTS', years=c(1985:2010),
                    quarters=c(1:4))
  hh.scowcgfs <- getDATRAS(record='HH', survey='SCOWCGFS', years=c(2011:last.year),
                          quarters=c(1:4))
  hh.porc <- getDATRAS(record='HH', survey='SP-PORC', years=c(2001:last.year),
                     quarters=c(3,4))
  hh.spnorth <- getDATRAS(record='HH', survey='SP-NORTH', years=c(1990:last.year),
                        quarters=c(3,4))
  hh.arsa <- getDATRAS(record='HH', survey='SP-ARSA', years=c(2002:last.year),
                    quarters=c(1,4))

  # write.csv(hh.ns, file = "Publicly available/DATRAS/hh.ns.csv",
  #           row.names = F)
  # write.csv(hh.baltic, file = "Publicly available/DATRAS/hh.baltic.csv",
  #           row.names = F)
  # write.csv(hh.evhoe, file = "Publicly available/DATRAS/hh.evhoe.csv",
  #           row.names = F)
  # write.csv(hh.cgfs, file = "Publicly available/DATRAS/hh.cgfs.csv",
  #           row.names = F)
  # write.csv(hh.igfs, file = "Publicly available/DATRAS/hh.igfs.csv",
  #           row.names = F)
  # write.csv(hh.nigfs, file = "Publicly available/DATRAS/hh.nigfs.csv",
  #           row.names = F)
  # write.csv(hh.pt, file = "Publicly available/DATRAS/hh.pt.csv",
  #           row.names = F)
  # write.csv(hh.rock, file = "Publicly available/DATRAS/hh.rock.csv",
  #           row.names = F)
  # write.csv(hh.scorock, file = "Publicly available/DATRAS/hh.scorock.csv",
  #           row.names = F)
  # write.csv(hh.swc, file = "Publicly available/DATRAS/hh.swc.csv",
  #           row.names = F)

```

```

# write.csv(hh.scowcgs, file = "Publicly available/DATRAS/hh.scowcgs.csv",
#           row.names = F)
# write.csv(hh.porc, file = "Publicly available/DATRAS/hh.porc.csv",
#           row.names = F)
# write.csv(hh.spnorth, file = "Publicly available/DATRAS/hh.spnorth.csv",
#           row.names = F)
# write.csv(hh.arsa, file = "Publicly available/DATRAS/hh.arsa.csv", row.names = F)

# Length info from DATRAS
hl.ns <- getDATRAS(record='HL', survey='NS-IBTS', years=c(1967:last.year),
                  quarters=c(1,3))
hl.baltic <- getDATRAS(record='HL', survey='BITS', years=c(1991:last.year),
                    quarters=c(1,4))
hl.evhoe <- getDATRAS(record='HL', survey='EVHOE', years=c(1997:last.year),
                    quarters=4)
hl.cgfs <- getDATRAS(record='HL', survey='FR-CGFS', years=c(1998:last.year),
                    quarters=4)
hl.igfs <- getDATRAS(record='HL', survey='IE-IGFS', years=c(2003:last.year),
                    quarters=4)
hl.nigfs <- getDATRAS(record='HL', survey='NIGFS', years=c(2005:last.year),
                    quarters=c(1:4))
hl.pt <- getDATRAS(record='HL', survey='PT-IBTS', years=c(2002:last.year),
                  quarters=c(3:4))
hl.rock <- getDATRAS(record='HL', survey='ROCKALL', years=c(1999:2009),
                    quarters=3)
hl.scorock <- getDATRAS(record='HL', survey='SCOROC', years=c(2011:last.year),
                      quarters=3)
hl.swc <- getDATRAS(record='HL', survey='SWC-IBTS', years=c(1985:2010),
                   quarters=c(1:4))
hl.scowcgs <- getDATRAS(record='HL', survey='SCOWCGFS', years=c(2011:last.year),
                      quarters=c(1:4))
hl.porc <- getDATRAS(record='HL', survey='SP-PORC', years=c(2001:last.year),
                    quarters=c(3,4))
hl.spnorth <- getDATRAS(record='HL', survey='SP-NORTH', years=c(1990:last.year),
                      quarters=c(3,4))
hl.arsa <- getDATRAS(record='HL', survey='SP-ARSA', years=c(2002:last.year),
                    quarters=c(1,4))

#E:/fishglob data/
#
# write.csv(hl.ns, file = "Publicly available/DATRAS/hl.ns.csv",
#           row.names = F)
# write.csv(hl.baltic, file = "Publicly available/DATRAS/hl.baltic.csv",
#           row.names = F)
# write.csv(hl.evhoe, file = "Publicly available/DATRAS/hl.evhoe.csv",
#           row.names = F)
# write.csv(hl.cgfs, file = "Publicly available/DATRAS/hl.cgfs.csv",
#           row.names = F)
# write.csv(hl.igfs, file = "Publicly available/DATRAS/hl.igfs.csv",
#           row.names = F)
# write.csv(hl.nigfs, file = "Publicly available/DATRAS/hl.nigfs.csv",
#           row.names = F)
# write.csv(hl.pt, file = "Publicly available/DATRAS/hl.pt.csv", row.names = F)

```

```

# write.csv(hl.rock, file = "Publicly available/DATRAS/hl.rock.csv",
#           row.names = F)
# write.csv(hl.scorock, file = "Publicly available/DATRAS/hl.scorock.csv",
#           row.names = F)
# #write.csv(hl.swc, file = "E:/fishglob data/Publicly available/DATRAS/hl.swc.csv",
# #row.names = F)
# write.csv(hl.scowcgfs, file = "Publicly available/DATRAS/hl.scowcgfs.csv",
#           row.names = F)
# write.csv(hl.porc, file = "Publicly available/DATRAS/hl.porc.csv",
#           row.names = F)
# write.csv(hl.spnorth, file = "Publicly available/DATRAS/hl.spnorth.csv",
#           row.names = F)
# write.csv(hl.arsa, file = "Publicly available/DATRAS/hl.arsa.csv",
#           row.names = F)
}

if(load_stored_datras == TRUE){

hh.ns <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.ns.csv")
hh.baltic <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.baltic.csv")
hh.evhoe <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.evhoe.csv")
hh.cgfs <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.cgfs.csv")
hh.igfs <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.igfs.csv")
hh.nigfs <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.nigfs.csv")
hh.pt <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.pt.csv")
hh.rock <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.rock.csv")
hh.scorock <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.scorock.csv")
hh.swc <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.swc.csv")
hh.scowcgfs <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.scowcgfs.csv")
# hh.porc <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.porc.csv")
# hh.spnorth <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.spnorth.csv")
# hh.arsa <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.arsa.csv")

hl.ns <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.ns.csv")
hl.baltic <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.baltic.csv")
hl.evhoe <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.evhoe.csv")
hl.cgfs <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.cgfs.csv")
hl.igfs <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.igfs.csv")
hl.nigfs <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.nigfs.csv")
hl.pt <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.pt.csv") %>%
  dplyr::rename(Valid_Aphia = ValidAphiaID) %>%
  select(RecordType, Survey, Quarter, Country, Ship, Gear, SweepLngt, GearEx,
         DoorType, StNo, HaulNo, Year, SpecCodeType, SpecCode, SpecVal, Sex,
         TotalNo, CatIdentifier, NoMeas, SubFactor, SubWgt, CatCatchWgt, LngtCode,
         LngtClass, HLNoAtLngt, DevStage, LenMeasType, DateofCalculation,
         Valid_Aphia)
hl.rock <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.rock.csv")
hl.scorock <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.scorock.csv")
hl.swc <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.swc.csv") %>%
  dplyr::rename(Valid_Aphia = ValidAphiaID) %>%
  select(RecordType, Survey, Quarter, Country, Ship, Gear, SweepLngt, GearEx,
         DoorType, StNo, HaulNo, Year, SpecCodeType, SpecCode, SpecVal, Sex,

```

```

        TotalNo, CatIdentifier, NoMeas, SubFactor, SubWgt, CatCatchWgt, LngtCode,
        LngtClass, HLNoAtLngt, DevStage, LenMeasType, DateofCalculation,
        Valid_Aphia)
hl.scowcgfs <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.scowcgfs.csv")
# hl.porc <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.porc.csv")
# hl.spnorth <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.spnorth.csv")
# hl.arsa <- read.csv("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.arsa.csv")

hh <- rbind(hh.ns, hh.baltic, hh.evhoe, hh.cgfs, hh.igfs, hh.nigfs, hh.pt, hh.rock,
            hh.scorock, hh.swc, hh.scowcgfs, hh.porc, hh.spnorth, hh.arsa)

hl <- rbind(hl.ns, hl.baltic, hl.evhoe, hl.cgfs, hl.igfs, hl.nigfs, hl.pt, hl.rock,
            hl.scorock, hl.swc, hl.scowcgfs, hl.porc, hl.spnorth, hl.arsa)

rm(hl.ns, hl.baltic, hl.evhoe, hl.cgfs, hl.igfs, hl.nigfs, hl.pt, hl.rock, hl.scorock,
   hl.swc, hl.scowcgfs, hl.porc, hl.spnorth, hl.arsa,
   hh.ns, hh.baltic, hh.evhoe, hh.cgfs, hh.igfs, hh.nigfs, hh.pt, hh.rock, hh.scorock,
   hh.swc, hh.scowcgfs, hh.porc, hh.spnorth, hh.arsa)
#rm(ca.ns, ca.baltic, ca.evhoe, ca.cgfs, ca.igfs, ca.nigfs, ca.pt, ca.rock,
#   ca.scorock, ca.swc, ca.scowcgfs)
}

if(save_hh_and_hl == TRUE){
  save(hh, file = here(paste0("data/Publicly available/hh.",date,".RData")))
  save(hl, file = here(paste0("data/Publicly available/hl.",date,".RData")))
}

####----- ###
# Alternative
####----- ###

# Juliano
# hl <- fread("/Volumes/Enterprise/Data/FishGlob/Data/Raw/ices_hl.csv")
# unique(hl$Survey)
# hh <- fread("/Volumes/Enterprise/Data/FishGlob/Data/Raw/ices_hh.csv")
# unique(hh$Survey)

# Aurore
load(here("data/Publicly available/hl.3August2023.RData"))
load(here("data/Publicly available/hh.3August2023.RData"))

#####
#### CREATE A UNIQUE HAUL ID
#####
hl$HaulID <- paste(hl$Survey, hl$Year, hl$Quarter, hl$Country, hl$Ship, hl$Gear, hl$StNo,
                  hl$HaulNo)
hh$HaulID <- paste(hh$Survey, hh$Year, hh$Quarter, hh$Country, hh$Ship, hh$Gear, hh$StNo,
                  hh$HaulNo)

# Is the HaulID unique?

```

```

hhn <- unique(hh$HaulID)
length(hhn)==nrow(hh)

# check which one is not
pb <- c()
for (i in 1:length(hhn)){
  j <- which(hh$HaulID==hhn[i])
  if(length(j)>1){pb <- hhn[i]}
}
print(pb)
rm(hhn)

# problem with one haul in NS-IBTS
hh <- hh %>%
  filter(HaulID!=pb)
hl <- hl %>%
  filter(HaulID!=pb)

# Only keep hauls where there is the length composition.
# 69665 hauls in hh and hl
hh <- subset(hh, hh$HaulID %in% hl$HaulID)
hl <- subset(hl, hl$HaulID %in% hh$HaulID)

#####
#### MERGE HH and HL FILES
#####

haulidhl <- sort(unique(hl$HaulID))
haulidhh <- sort(unique(hh$HaulID))
identical(haulidhh, haulidhl)
rm(haulidhh, haulidhl)

# remove some columns in hl
hl$SweepLngt <- hl$SpecCodeType <- hl$SpecCode <- hl$DateofCalculation <- NULL
hl$RecordType <- hl$GearEx <- NULL

# remove some columns in hh
hh$DateofCalculation <- hh$ThClineDepth <- hh$ThermoCline <- hh$SwellHeight <- NULL
hh$SwellDir <- hh$WindSpeed <- hh$WindDir <- hh$BotCurSpeed <- NULL
hh$BotCurDir <- hh$SurCurSpeed <- hh$SurCurDir <- hh$SpeedWater <- hh$TowDir <- NULL
hh$WgtGroundRope <- hh$KiteDim <- hh$Buoyancy <- hh$Tickler <- NULL
hh$DoorWgt <- hh$DoorSurface <- hh$WarpDen <- hh$Warpdia <- hh$Warplngt <- NULL
hh$Rigging <- hh$HydroStNo <- hh$HaulLat <- hh$HaulLong <- hh$DayNight <- NULL
hh$Stratum <- hh$TimeShot <- hh$Day <- hh$RecordType <- hh$GearExp <- hh$DoorType <- NULL

#survey <- merge(hh, hl, by='HaulID', all.x=FALSE, all.y=TRUE)
survey <- right_join(hh, hl, by=c('HaulID', 'Survey', 'Quarter', 'Country', 'Ship',
                                'Gear', 'StNo', 'HaulNo', 'Year'))
nrow(survey)==nrow(hl)

survey <- survey %>%
  dplyr::rename(SBT = BotTemp,

```

```

SST = SurTemp,
Speed = GroundSpeed,
AphiaID = Valid_Aphia)

### Check if the HaulID is unique
### Not the case for the baltic sea, a lot of duplicates!!!
#ids <- unique(hh$HaulID)
# pb <- vector()
# for(i in 1:length(ids)){
#   x <- which(hh$HaulID==ids[i])
#   if(length(x)>1){pb[length(pb)+1] <- ids[i]}
# }
# print(pb) # dim 0 ok!

#####
#### REMOVE INVALID DATA
#####
survey <- survey %>%
  filter(HaulVal %in% 'V', #Remove invalid hauls
         !is.na(AphiaID), # Remove invalid species records
         SpecVal %in% c(1,10,4,5,6,7,8),
         DataType %in% c('S','R','C'))

print(length(unique(survey$HaulID)))

#####
#### RESCALE DATA INTO ABUNDANCE FOR THE HAUL DURATION AND ABUNDANCE AT LENGTH
#####
# If Data Type=='C', abundance at length already readjusted with time so get back the
# abundance for the actual duration of the haul.
# If data type=='R', abundance at length is multiplied by subfactor and adjusted to time
survey$CatCatchWgt = as.numeric(survey$CatCatchWgt)

survey <- survey %>%
  mutate(# replace -9 by NAs
         HLNAtLngt = ifelse(HLNAtLngt == (-9), NA, HLNAtLngt),
         TotalNo = ifelse(TotalNo == -9, NA, TotalNo),
         CatCatchWgt = ifelse(CatCatchWgt == -9, NA, CatCatchWgt),
         CatCatchWgt = ifelse(CatCatchWgt<0, NA, CatCatchWgt),
         # standardize by haul duration and rescale with subfactor
         HLNAtLngt = case_when(DataType=='C' ~ HLNAtLngt*SubFactor*HaulDur/60,
                                DataType %in% c('S','R') ~ HLNAtLngt*SubFactor),
         TotalNo = case_when(DataType=='C' ~ TotalNo*HaulDur/60,
                                DataType %in% c('S','R') ~ TotalNo),
         CatCatchWgt = case_when(DataType=='C' ~ CatCatchWgt*HaulDur/60,
                                DataType %in% c('S','R') ~ CatCatchWgt)) %>%
  select(-HaulVal, -DataType, -StdSpecRecCode, -SpecVal, -SubWgt, -SubFactor) %>%
  mutate(Survey = if_else(Survey=='SCOWCGFS', 'SWC-IBTS', Survey)) %>%
  mutate(Survey = if_else(Survey=='SCOROC', 'ROCKALL', Survey)) %>%
  filter(!(Survey=="NS-IBTS" & BySpecRecCode %in% c(0,2,3,4,5)), ### What is it doing here?
         # remove hauls where not all species are recorded

```

```

!(Survey=="BITS" & BySpecRecCode==0))

length(unique(survey$HaulID))

#####
#### GET THE SWEEPED AREA in km2
#####

source('cleaning_codes/source_DATRAS_wing_doorspread.R')

#####
#### GET CPUEs AND RIGHT COLUMNS NAMES
#####

# Assess size of data without length composition or negative values
xx <- subset(survey, is.na(HLNoAtLngt) | is.na(LngtClass))
no_length_hauls <- sort(unique(xx$HaulID)) # 11,113 hauls with missing length data
print(length(no_length_hauls))
rm(no_length_hauls)

# Only keep abundances/weight
survey <- survey %>%
  #filter(!(HaulID %in% no_length_hauls)) %>% # remove hauls without length data
  mutate(numcpue = TotalNo/Area.swept, # abundance/km2
         wtcue = CatCatchWgt/(Area.swept*1000), #weight in kg/km2
         numh = (TotalNo*60)/HaulDur, # abundance/hour
         wgt = CatCatchWgt*60/(HaulDur*1000), #weight in kg/h
         num = TotalNo, #raw number of individuals
         wgt = CatCatchWgt/1000, # raw weight in kg
         numlencpue = HLNoAtLngt/Area.swept, #abundance/km2 per length class
         numlenh = HLNoAtLngt*60/HaulDur, #abundance/h per length class
         Season = 'NA',
         SBT = replace(SBT, SBT== -9, NA),
         SST = replace(SST, SST== -9, NA),
         LngtClass = ifelse(LngtClass == -9, NA, LngtClass), #replace -9 values by NAs
         LngtCode = ifelse(LngtCode == -9, NA, LngtCode), #replace -9 by NAs
         LngtClass = ifelse(LngtCode %in% c('.', '0'), LngtClass*0.1, LngtClass)) %>%
  # fix unit of length class
  dplyr::rename(Length = LngtClass) %>%
  select(Survey, HaulID, StatRec, Year, Month, Quarter, Season, ShootLat, ShootLong,
         HaulDur, Area.swept, Gear, Depth, SBT, SST, AphiaID, CatIdentifier, Sex,
         numcpue, wtcue, numh, wgt, num, wgt, Length, LenMeasType, numlencpue, numlenh)
survey <- data.frame(survey)

#####
## fishglob taxa cleaning ##
#####

# Make AphiaID list per survey
aphia_datras <- survey %>%

```

```

select(Survey, AphiaID) %>%
dplyr::rename(survey = Survey,
              worms_id_datras = AphiaID) %>%
distinct()

# Clean taxa north sea
ns_data <- aphia_datras %>% filter(survey=="NS-IBTS")
clean_ns <- clean_taxa(ns_data$worms_id_datras, input_survey = "NS-IBTS",
                      save=F, fishbase=TRUE)

# Clean taxa bay of biscay
evhoe_data <- aphia_datras %>% filter(survey=="EVHOE")
clean_evhoe <- clean_taxa(evhoe_data$worms_id_datras, input_survey = "EVHOE",
                        save=F, fishbase=TRUE)

# Clean taxa english channel
cgfs_data <- aphia_datras %>% filter(survey=="FR-CGFS")
clean_cgfs <- clean_taxa(cgfs_data$worms_id_datras, input_survey = "FR-CGFS",
                        save=F, fishbase=TRUE)

# Clean taxa baltic sea
bits_data <- aphia_datras %>% filter(survey=="BITS")
clean_bits <- clean_taxa(bits_data$worms_id_datras, input_survey = "BITS",
                        save=F, fishbase=TRUE)

# Clean taxa scottish sea
swc_data <- aphia_datras %>% filter(survey %in% c("SCOWCGFS", "SWC-IBTS"))
clean_swc <- clean_taxa(swc_data$worms_id_datras, input_survey = "SWC-IBTS",
                        save=F, fishbase=TRUE)

# Clean taxa rockall
rock_data <- aphia_datras %>% filter(survey %in% c("SCOROC", "ROCKALL"))
clean_rock <- clean_taxa(rock_data$worms_id_datras, input_survey = "ROCKALL",
                        save=F, fishbase=TRUE)

# Clean taxa irish sea
ir_data <- aphia_datras %>% filter(survey=="IE-IGFS")
clean_ir <- clean_taxa(ir_data$worms_id_datras, input_survey = "IE-IGFS",
                      save=F, fishbase=TRUE)

# Clean taxa northern ireland
nigfs_data <- aphia_datras %>% filter(survey=="NIGFS")
clean_nigfs <- clean_taxa(nigfs_data$worms_id_datras, input_survey = "NIGFS",
                          save=F, fishbase=TRUE)

# Clean taxa for portugal
pt_data <- aphia_datras %>% filter(survey=="PT-IBTS")
clean_pt <- clean_taxa(pt_data$worms_id_datras, input_survey = "PT-IBTS",
                      save=F, fishbase=TRUE)

# Clean taxa for Spanish Cantabrian Sea
spnorth_data <- aphia_datras %>% filter(survey=="SP-NORTH")
clean_spnorth <- clean_taxa(spnorth_data$worms_id_datras, input_survey = "SP-NORTH",

```

```

        save=F, fishbase=TRUE)

# Clean taxa for Spanish Porcupine
porc_data <- aphia_datras %>% filter(survey=="SP-PORC")
clean_porc <- clean_taxa(porc_data$worms_id_datras, input_survey = "SP-PORC",
                        save=F, fishbase=TRUE)

# Clean taxa for Spanish Gulf of Cadiz
arsa_data <- aphia_datras %>% filter(survey=="SP-ARSA")
clean_arsa <- clean_taxa(arsa_data$worms_id_datras, input_survey = "SP-ARSA",
                        save=F, fishbase=TRUE)

clean_datras_taxa <- rbind(clean_bits, clean_cgfs, clean_evhoe, clean_ir, clean_nigfs,
                          clean_pt, clean_rock, clean_sw, clean_ns, clean_spnorth,
                          clean_porc, clean_arsa) %>%
  mutate(query = as.numeric(as.vector(query))) %>%
  distinct()

recoded_taxa <- c("Dipturus", "Liparis", "Chelon", "Mustelus", "Alosa", "Argentina",
                  "Callionymus", "Ciliata", "Gaidropsarus", "Sebastes", "Syngnatus",
                  "Pomatoschistus", "Gobius")

spp_to_recode <- c("Dipturus batis", "Dipturus flossada", "Dipturus batis-complex",
                  "Dipturus intermedia", "Liparis montagu", "Liparis liparis",
                  "Liparis liparis liparis", "Chelon aurata", "Chelon ramada",
                  "Mustelus mustelus/asterias", "Mustelus mustelus", "Mustelus asterias",
                  "Alosa alosa", "Alosa fallax", "Argentina silus", "Argentina sphyraena",
                  "Callionymus reticulatus", "Callionymus maculatus", "Ciliata mustela",
                  "Ciliata septentrionalis", "Gaidropsaurus macrophthalmus",
                  "Gaidropsaurus mediterraneus", "Gaidropsaurus vulgaris",
                  "Sebastes norvegicus", "Sebastes mentella", "Sebastes marinus",
                  "Syngnathus rostellatus", "Syngnathus acus", "Syngnathus typhle",
                  "Nerophis ophidion", "Pomatoschistus microps", "Pomatoschistus minutus",
                  "Pomatoschistus pictus", "Gobius cobitis", "Gobius niger",
                  "Leusueurigobius friesii", "Neogobius melanostomus")

alphaid <- get_wormsid(recoded_taxa)
alphaid <- tibble(taxa = recoded_taxa,
                  worms_id = alphaid[1:length(recoded_taxa)])
clean_manual_recoded <- clean_taxa(alphaid$worms_id, input_survey = "recoded",
                                  save = F, fishbase=TRUE)

clean_datras_taxa <- clean_datras_taxa %>%
  select(-survey) %>%
  mutate(SpecCode = ifelse(taxa %in% spp_to_recode, NA, SpecCode),
         rank = ifelse(taxa %in% spp_to_recode, "Genus", rank),
         #dipturus
         worms_id = ifelse(taxa %in% c("Dipturus batis", "Dipturus flossada",
                                       "Dipturus batis-complex", "Dipturus intermedia"),
                           105762, worms_id),
         taxa = ifelse(taxa %in% c("Dipturus batis", "Dipturus flossada",
                                   "Dipturus batis-complex", "Dipturus intermedia"),
                       "Dipturus", taxa),

```

```

# liparis
worms_id = ifelse(taxa %in% c("Liparis montagui","Liparis liparis",
                             "Liparis liparis liparis"),126160,worms_id),
taxa = ifelse(taxa %in% c("Liparis montagui","Liparis liparis",
                             "Liparis liparis liparis"),"Liparis",taxa),

# chelon
worms_id = ifelse(taxa %in% c("Chelon aurata","Chelon ramada"),126030,worms_id),
taxa = ifelse(taxa %in% c("Chelon aurata","Chelon ramada"),"Chelon",taxa),

# mustelus
worms_id = ifelse(taxa %in% c("Mustelus mustelus/asterias","Mustelus mustelus",
                             "Mustelus asterias"),105732,worms_id),
taxa = ifelse(taxa %in% c("Mustelus mustelus/asterias","Mustelus mustelus",
                             "Mustelus asterias"),"Mustelus",taxa),

# alosa
worms_id = ifelse(taxa %in% c("Alosa alosa","Alosa fallax"),125715,worms_id),
taxa = ifelse(taxa %in% c("Alosa alosa","Alosa fallax"),"Alosa",taxa),

# argentina
worms_id = ifelse(taxa %in% c("Argentina silus","Argentina sphyraena"),
                  125885,worms_id),
taxa = ifelse(taxa %in% c("Argentina silus","Argentina sphyraena"),
              "Argentina",taxa),

# callionymus
worms_id = ifelse(taxa %in% c("Callionymus reticulatus","Callionymus maculatus"),
                  125930,worms_id),
taxa = ifelse(taxa %in% c("Callionymus reticulatus","Callionymus maculatus"),
              "Callionymus",taxa),

# ciliata
worms_id = ifelse(taxa %in% c("Ciliata mustela","Ciliata septentrionalis"),
                  125741,worms_id),
taxa = ifelse(taxa %in% c("Ciliata mustela","Ciliata septentrionalis"),
              "Ciliata",taxa),

# gaidropsarus
worms_id = ifelse(taxa %in% c("Gaidropsaurus macrophthalmus",
                             "Gaidropsaurus mediterraneus",
                             "Gaidropsaurus vulgaris"),
                  125743,worms_id),
taxa = ifelse(taxa %in% c("Gaidropsaurus macrophthalmus",
                             "Gaidropsaurus mediterraneus",
                             "Gaidropsaurus vulgaris"),"Gaidropsarus",taxa),

# sebastes
worms_id = ifelse(taxa %in% c("Sebastes norvegicus","Sebastes mentella",
                             "Sebastes marinus"),
                  126175,worms_id),
taxa = ifelse(taxa %in% c("Sebastes norvegicus","Sebastes mentella",
                             "Sebastes marinus"),
              "Sebastes",taxa),

# syngnathus
worms_id = ifelse(taxa %in% c("Syngnathus rostellatus","Syngnathus acus",
                             "Syngnathus typhle","Nerophis ophidion"),
                  126227,worms_id),
taxa = ifelse(taxa %in% c("Syngnathus rostellatus","Syngnathus acus",
                             "Syngnathus typhle","Nerophis ophidion"),
              "Syngnathus",taxa),

```

```

# pomatosc
worms_id = ifelse(taxa %in% c("Pomatoschistus microps", "Pomatoschistus minutus",
                             "Pomatoschistus pictus"), 125999, worms_id),
taxa = ifelse(taxa %in% c("Pomatoschistus microps", "Pomatoschistus minutus",
                          "Pomatoschistus pictus"), "Pomatoschistus", taxa),

# gobioid
worms_id = ifelse(taxa %in% c("Gobius cobitis", "Gobius niger",
                              "Leusueurigobius friesii",
                              "Neogobius melanostomus"), 125988, worms_id),
taxa = ifelse(taxa %in% c("Gobius cobitis", "Gobius niger",
                          "Leusueurigobius friesii",
                          "Neogobius melanostomus"), "Gobius", taxa),

) %>%
distinct()

# add taxonomy to data
survey <- left_join(survey, clean_datras_taxa, by=c("AphiaID" = "query")) %>%
  filter(!is.na(worms_id)) # there are 622 unique invertebrate taxa in the surveys

#####
#### RE-CALCULATE WEIGHTS
#####

# 1. Check length measurement types
if(check_TL_conversion == TRUE){
  xx <- survey %>%
    filter(!is.na(LenMeasType),
           !LenMeasType %in% c(-9, 1, 12)) %>%
    group_by(Survey, taxa, LenMeasType) %>%
    summarize(n_obs = length(taxa),
              n_taxa = length(unique(taxa)))

  xx_concern <- survey %>%
    filter(taxa %in% c("Coelorinchus caelorhincus", "Malacocephalus laevis",
                      "Macrourus berglax", "Coryphaenoides rupestris",
                      "Coelorinchus labiatus", "Hymenocephalus italicus",
                      "Nezumia aequalis", "Nezumia bairdii", "Trachyrincus murrayi",
                      "Trachyrincus scabrus", "Xenodermichthys copei",
                      "Chimaeridae", "Hydrolagus mirabilis")) %>%
    group_by(Survey, taxa, LenMeasType) %>%
    summarize(n_obs = length(taxa),
              n_taxa = length(unique(taxa)))

  write.csv(xx, file = "QAQC/DATRAS/Length Types/lengthtypes.csv", row.names = F)
  write.csv(xx_concern, file = "QAQC/DATRAS/Length Types/lengthtypes_taxa_concern.csv", row.names = F)

# according to ICES manuals
family_concern <- survey %>%
  filter(family %in% c("Alepocephalidae", "Platytroctidae", "Macrouridae", "Chimaeridae")) %>%
  mutate(LenMeasType = ifelse(LenMeasType == -9, NA, LenMeasType)) %>%
  group_by(Survey, taxa, family, LenMeasType) %>%
  summarize(n_obs = length(taxa),

```

```

    n_taxa = length(unique(taxa)))

write.csv(family_concern, file = "QAQC/DATRAS/Length Types/lengthtypes_family_concern.csv", row.names = F)

taxa_not_TL <- survey %>%
  filter(family %in% c("Alepocephalidae", "Platytroctidae", "Macrouridae", "Chimaeridae")) %>%
  mutate(LenMeasType = ifelse(LenMeasType == -9, NA, LenMeasType)) %>%
  group_by(worms_id, SpecCode, taxa, family, LenMeasType) %>%
  summarize(n_obs = length(taxa))
write.csv(taxa_not_TL, file = "length_weight/Length Types/DATRAS_taxa_not_TL.csv", row.names = F)
}

# 2. apply length conversion factors when necessary
if(apply_TL_conversion == TRUE){
  conversion_to_TL <- read.csv("length_weight/DATRAS_taxa_not_TL_conversions.csv") %>%
  filter(is.na(LenMeasType)) %>%
  select(taxa, conversion_to_TL)

  survey <- left_join(survey, conversion_to_TL, by = "taxa") %>%
  mutate(Length = ifelse(!is.na(conversion_to_TL), Length*conversion_to_TL, Length))
}

# 3. Check the need for TL conversion in all surveys and for all taxa
if (plot_length_frequencies == TRUE){
  xx_concern <- read.csv("QAQC/DATRAS/Length Types/lengthtypes_taxa_concern_fishbase.csv")
  xx_conversions <- read.csv("length_weight/DATRAS_taxa_not_TL_conversions.csv") %>%
  select(taxa, conversion_to_TL) %>%
  distinct()
  xx_concern <- left_join(xx_concern, xx_conversions, by="taxa")

  for(i in 1:nrow(xx_concern)){
    xx_survey <- survey %>%
      filter(Survey == xx_concern$Survey[i],
             taxa == xx_concern$taxa[i])
    png(filename = paste0("QAQC/DATRAS/Length Types/", paste0(xx_survey$Survey[1], "-", xx_survey$taxa[1]),
                        width = 480, height = 480)
    hist(xx_survey$Length, main = paste0(xx_survey$Survey[1], "-", xx_survey$taxa[1]),
         xlab = "Length", xlim = c(0, max(max(xx_survey$Length*xx_concern$conversion_to_TL[1], xx_concern$TL_fishbase[i]))),
         hist(xx_survey$Length*xx_concern$conversion_to_TL[1], add=T, col = alpha("red", 0.2))
    abline(v = xx_concern$TL_fishbase[i], col = "red", lwd = 3, lty = "dashed")
    dev.off()
    rm(xx_survey)
  }

  rm(xx_concern, xx_conversions)
}

# 4. List of taxa for length-weight conversion coefficients

```

```

if(need_get_lw_rel == TRUE){
  list.taxa <- survey %>%
    select(taxa, family, genus, rank) %>%
    filter(!is.na(family)) %>%
    distinct()

  write.csv(data.frame(list.taxa), file=paste0("length_weight/taxa_DATRAS_FB_tofill_",date,".csv"),
    row.names=FALSE)

  # length-weight relationships using rfishbase
  get_coeffs(list.taxa, survey="DATRAS", date=date, save=TRUE)
}

# 5. Remove the list of hauls from SP-NORTH and SP-ARSA that have wrong length units
if (remove_lengths_units_issue == TRUE){
  load("QAQC/DATRAS/Spanish_hauls_species_off.RData")
  lengths.off <- unique(lengths.off$HaulID)
  survey <- survey %>%
    filter(!HaulID %in% lengths.off)
}

# 6. re-calculate weights with length-weight relationships
datalw <- read.csv('length_weight/length.weight_DATRAS_3August2023.csv') %>%
  select(-X)

# summarize abundance/weight at the haul level
survey.num <- left_join(survey, datalw, by=c("taxa","family","genus","rank")) %>%
  select(Survey,HaulID,StatRec,Year,Month,Quarter,Season,ShootLat,ShootLong,
    HaulDur,Area.swept,Gear,Depth,SBT,SST,family,genus,taxa,AphiaID,worms_id,
    SpecCode,kingdom, class, order,phylum,rank,
    CatIdentifier,Sex,numcpue,numh,num) %>%
  distinct() %>%
  group_by(Survey,HaulID,StatRec,Year,Month,Quarter,Season,ShootLat,ShootLong,
    HaulDur,Area.swept,Gear,Depth,SBT,SST,family,genus,taxa,AphiaID,
    worms_id, SpecCode,kingdom, class, order,phylum, rank) %>%
  summarize_at(.vars=c('numcpue', 'numh', 'num'), .funs = function(x) sum(x)) %>%
  ungroup()

survey.wgt <- left_join(survey, datalw, by=c("taxa","family","genus","rank")) %>%
  select(Survey,HaulID,StatRec,Year,Month,Quarter,Season,ShootLat,ShootLong,HaulDur,
    Area.swept,Gear,Depth,SBT,SST,family,genus,taxa,AphiaID,worms_id,SpecCode,
    kingdom, class, order,phylum,rank,
    CatIdentifier,Sex,wtcpue,wgth,wgt) %>%
  distinct() %>%
  group_by(Survey,HaulID,StatRec,Year,Month,Quarter,Season,ShootLat,ShootLong,
    HaulDur,Area.swept,Gear,Depth,SBT,SST,family,genus,taxa,AphiaID,worms_id,
    SpecCode,kingdom, class, order, phylum, rank) %>%
  summarize_at(.vars=c('wtcpue', 'wgth', 'wgt'), .funs = function(x) sum(x)) %>%
  ungroup()

```

```

survey1 <- full_join(survey.num, survey.wgt,
  by=c('Survey','HaulID','StatRec','Year','Month','Quarter',
        'Season','ShootLat','ShootLong','HaulDur','Area.swept',
        'Gear','Depth','SBT','SST','family','genus','taxa','AphiaID',
        'worms_id','SpecCode',
        'kingdom','phylum','class','order','rank'))

# summarize abundance/weight from length data
survey2 <- left_join(survey, datalw, by=c("taxa","family","genus","rank")) %>%
  mutate(wgtlencpue = numlencpue*a*Length^b/1000, # divide by 1000 to get kg/km2
         wgtlenh = numlenh*a*Length^b/1000) %>% # divide by 1000 to get kg/h
  group_by(Survey,HaulID,StatRec,Year,Month,Quarter,Season,ShootLat,ShootLong,HaulDur,
           Area.swept,Gear,Depth,SBT,SST,family,genus,taxa, AphiaID,worms_id,SpecCode,a, b,
           kingdom, class, order,phylum, rank) %>%
  summarize_at(.vars=c('numlencpue','numlenh','wgtlencpue','wgtlenh'),
               .funs=function(x) sum(x)) %>%
  ungroup()

# merge both and compare
nrow(survey1)==nrow(survey2)
survey3 <- full_join(survey1, survey2, by=c('Survey','HaulID','StatRec','Year','Month',
      'Quarter','Season','ShootLat','ShootLong',
      'HaulDur','Area.swept','Gear','Depth',
      'SBT','SST','family','genus','taxa',
      'AphiaID','worms_id','SpecCode',
      'kingdom','phylum','class','order','rank'))

#####
# CHECK ESTIMATES PER SURVEY AND TAXA
#####

# correlation between abundances to check calculations are right
cor(x = survey3$numh, y = survey3$numlenh, method = 'pearson', use = "complete.obs")
xx <- subset(survey3, !is.na(numcpue))
cor(x = xx$numcpue, y = xx$numlencpue, method = 'pearson', use = "complete.obs")

# correlation between weights to check calculations are right
xx <- subset(survey3, wtcpue>0 & wgtlencpue>0)
cor(x = xx$wtcpue, y = xx$wgtlencpue, method = 'pearson', use = "complete.obs")

xx <- subset(survey3, wgth>0 & wgtlenh>0)
cor(x = xx$wgth, y = xx$wgtlenh, method = 'pearson', use = "complete.obs")

# make per survey correlation table
surveys <- c(sort(unique(survey$Survey)),"all","all-SP")
corrs <- data.frame(surveys)
corrs$cor_num <- corrs$cor_wgt <- NA

for (i in 1:length(surveys)){

  # survey-specific data
  if(i==13){xx <- survey3

```

```

} else if (i==14){xx <- survey3 %>% filter(!Survey %in% c("SP-NORTH","SP-ARSA","SP-PORC"))
} else {xx <- subset(survey3, Survey == surveys[i])}

# plots
plot_weights <- ggplot(xx[xx$wgtl>0 & xx$wgtlenh>0,], aes(x=wgtl, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=1) + scale_x_log10() + scale_y_log10() +
  theme_bw() + theme(text = element_text(size = 20)) + ggtitle("Weights per hour")

plot_abundances <- ggplot(xx[xx$numlenh>0 & xx$num>0,], aes(x=numh, y=numlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=1) + scale_x_log10() + scale_y_log10() +
  theme_bw() + theme(text = element_text(size = 20)) + ggtitle("Abundances per hour")

png(paste0("QAQC/DATRAS/",surveys[i],"_per_hour.png"), width = 18*200, height = 10*200, res = 200)
gridExtra::grid.arrange(plot_weights, plot_abundances, ncol = 2)
dev.off()

# compute and save correlations
corrs$cor_wgt[i] <- cor(x = xx$wgtl, y = xx$wgtlenh, method = 'pearson', use = "complete.obs")
corrs$cor_num[i] <- cor(x = xx$numh, y = xx$numlenh, method = 'pearson', use = "complete.obs")

rm(xx, plot_weights, plot_abundances)
}

write.csv(corrs, file = "QAQC/DATRAS/correlations_weights.csv", row.names = F)

# no zeros
xx <- subset(survey3, wgtl>0 & wgtlenh>0)

# rockall looks OK
ggplot(subset(xx, Survey=='ROCKALL'), aes(x=wgtl, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

# IE-IGFS looks OK
ggplot(subset(xx, Survey=='IE-IGFS'), aes(x=wgtl, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

# NIGFS looks OK
ggplot(subset(xx, Survey=='NIGFS'), aes(x=wgtl, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

# PT-IBTS looks OK
ggplot(subset(xx, Survey=='PT-IBTS'), aes(x=wgtl, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

# FR-CGFS looks OK
ggplot(subset(xx, Survey=='FR-CGFS'), aes(x=wgtl, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",

```

```

        linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

# SWC-IBTS issue
ggplot(subset(xx, Survey=='SWC-IBTS'), aes(x=wgth, y=wtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

comp <- subset(xx, Survey=='SWC-IBTS') %>%
  select(HaulID,wtlenh,wgth) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wtlenh', 'wgth'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wgth, y=wtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

comp$factor <- comp$wtlenh / comp$wgth
plot(comp$factor)
resc <- comp$HaulID[comp$factor > 40]

# after check with original haul length data (HL) for some resc haulid, weight
# is clearly wrong factor 100
survey3 <- survey3 %>%
  mutate(wtcpue = if_else(HaulID %in% resc, wtcpue*100,wtcpue),
    wgth = if_else(HaulID %in% resc , wgth*100,wgth),
    wgt = if_else(HaulID %in% resc , wgt*100,wgt))

# BITS issue
ggplot(subset(xx, Survey=='BITS'), aes(x=wgth, y=wtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

comp <- subset(xx, Survey=='BITS') %>%
  select(HaulID,wtlenh,wgth) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wtlenh', 'wgth'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wgth, y=wtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

comp$factor <- comp$wtlenh / comp$wgth
plot(comp$factor)
resc <- comp$HaulID[comp$factor > 40]

# after check with original haul length data (HL) for some resc haulid, weight
# is clearly wrong factor 100

```

```

survey3 <- survey3 %>%
  mutate(wtcpue = if_else(HaulID %in% resc, wtcpue*100, wtcpue),
         wgt = if_else(HaulID %in% resc, wgt*100, wgt),
         wgt = if_else(HaulID %in% resc, wgt*100, wgt))

# EVHOE may have an issue, no changes as not very clear
ggplot(subset(xx, Survey=="EVHOE"), aes(x=wgt, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
             linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

comp <- subset(xx, Survey=="EVHOE") %>%
  select(HaulID, wgtlenh, wgt) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wgtlenh', 'wgt'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wgt, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
             linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

comp$factor <- comp$wgtlenh / comp$wgt
plot(comp$factor)

# NS - IBTS issue
ggplot(subset(xx, Survey=="NS-IBTS"), aes(x=wgt, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
             linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

comp <- subset(xx, Survey=="NS-IBTS") %>%
  select(HaulID, wgtlenh, wgt) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wgtlenh', 'wgt'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wgt, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
             linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

comp$factor <- comp$wgtlenh / comp$wgt
comp$uni <- c(1:nrow(comp))
plot(comp$factor~comp$uni, ylim=c(0,120))
points(comp$factor[comp$factor > 20]~comp$uni[comp$factor > 20], col="red")
points(comp$factor[comp$factor > 8 & comp$factor <20]~
       comp$uni[comp$factor > 8 & comp$factor <20], col="blue")

# two issues - one estimate 100 times higher based on length, the other 10 times
resc <- comp$HaulID[comp$factor > 20]
resc2 <- comp$HaulID[comp$factor > 8 & comp$factor <20]

```

```

# SP-NORTH - PROBLEMS!
ggplot(subset(xx, Survey=='SP-NORTH'), aes(x=wgth, y=wtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

# SP-ARSA - some outliers
ggplot(subset(xx, Survey=='SP-ARSA'), aes(x=wgth, y=wtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

# SP-PORC - PROBLEMS!
ggplot(subset(xx, Survey=='SP-PORC'), aes(x=wgth, y=wtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

# after check with original haul length data (HL) for some resc haulid, weight
# is clearly wrong factor 100
# and also a cluster of factor 10
survey3 <- survey3 %>%
  mutate(wtcpue = if_else(HaulID %in% resc, wtcpue*100, wtcpue),
    wgth = if_else(HaulID %in% resc, wgth*100, wgth),
    wgt = if_else(HaulID %in% resc, wgt*100, wgt))

survey3 <- survey3 %>%
  mutate(wtcpue = if_else(HaulID %in% resc2, wtcpue*10, wtcpue),
    wgth = if_else(HaulID %in% resc2, wgth*10, wgth),
    wgt = if_else(HaulID %in% resc2, wgt*10, wgt))

# check again correlations
xx <- subset(survey3, wtcpue > 0 & wgtlenh > 0)
cor(x = xx$wtcpue, y = xx$wgtlenh, method = 'pearson') # looks better

xx <- subset(survey3, wgth > 0 & wgtlenh > 0)
cor(x = xx$wgth, y = xx$wgtlenh, method = 'pearson') # looks better

# now check per haul without zeros, NAs
xx <- subset(survey3, wtcpue > 0 & wgtlenh > 0)

comp <- xx %>%
  select(HaulID, wgtlenh, wtcpue) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wgtlenh', 'wtcpue'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wtcpue, y=wgtlenh)) + geom_point() +
  geom_abline(intercept = 0, slope = 1, color="red",
    linetype="dashed", size=0.5) + scale_x_log10() + scale_y_log10()

cor(x = xx$wtcpue, y = xx$wgtlenh, method = 'pearson')
# [1] 0.9635742

```

```
#####
#### Fishglob format
#####

survey4 <- survey3 %>%
  rename(survey = Survey,
         haul_id = HaulID,
         stat_rec = StatRec,
         year = Year,
         month = Month,
         quarter = Quarter,
         season = Season,
         latitude = ShootLat,
         longitude = ShootLong,
         haul_dur = HaulDur,
         area_swept = Area.swept,
         gear = Gear,
         depth = Depth,
         sbt = SBT,
         sst = SST,
         verbatim_aphia_id = AphiaID,
         aphia_id = worms_id,
         accepted_name = taxa,
         ) %>%
  mutate(day = NA_integer_,
         verbatim_name = NA_character_,
         station = NA_character_,
         stratum = NA_character_,
         sub_area = NA_character_,
         continent = "europe",
         country = case_when(survey=="PT-IBTS" ~ "portugal",
                             survey=="EVHOE" ~ "france",
                             survey=="IE-IGFS" ~ "ireland",
                             survey %in% c("ROCKALL","SWC-IBTS","NIGFS") ~ "uk",
                             survey=="FR-CGFS" ~ "france",
                             survey %in% c("NS-IBTS","BITS") ~ "multi-countries",
                             survey %in% c("SP-NORTH","SP-ARSA") ~ "spain",
                             survey == "SP-PORC" ~ "multi-countries"),
         num = numlencpue*area_swept,
         num_cpue = numlenh,
         num_cpua = numlencpue,
         wgt = wgtlencpue*area_swept,
         wgt_cpue = wgtlenh,
         wgt_cpua = wgtlencpue,
         haul_dur = haul_dur/60,
         source = "DATRAS ICES",
         timestamp = "2021-07",
         survey_unit = ifelse(survey %in% c("BITS","NS-IBTS","SWC-IBTS","SP-ARSA"),
                              paste0(survey,"-",quarter),survey),
         survey_unit = ifelse(survey %in% c("NEUS","SEUS","SCS","GMEX"),
                              paste0(survey,"-",season),survey_unit)) %>%

  # Final format
```

```

select(fishglob_data_columns$`Column name fishglob`)

#####
# Save database
#####

# Just run this routine should be good for all
surveys <- sort(unique(survey4$survey))
for(i in 1:length(surveys)){
  xx <- survey4 %>%
    filter(survey == surveys[i])
  write_clean_data(data = xx, survey = surveys[i], overwrite = T,
                   rdata = TRUE)
}

# -----#
#### FLAGS ####
# -----#
#install required packages that are not already installed
required_packages <- c("data.table",
                       "devtools",
                       "dggridR",
                       "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(survey4$survey))

#run flag_spp function in a loop
for (r in regions) {
  flag_spp(survey4, r)
}

##### Apply trimming per survey_unit method 1
#apply trimming for hex size 7
dat_new_method1_hex7 <- apply_trimming_per_survey_unit_method1(survey4, 7)

#apply trimming for hex size 8
dat_new_method1_hex8 <- apply_trimming_per_survey_unit_method1(survey4, 8)

##### Apply trimming per survey_unit method 2
dat_new_method2 <- apply_trimming_per_survey_unit_method2(survey4)

#-----#
#### ADD STRANDARDIZATION FLAGS ####
#-----#
surveys <- sort(unique(survey4$survey))
survey_units <- sort(unique(survey4$survey_unit))
survey_std <- survey4 %>%
  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("SWC-IBTS", "SP-PORC")){
    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
for(i in 1:length(surveys)){
  xx <- survey_std %>%
    filter(survey == surveys[i])
  write_clean_data(data = xx, survey = paste0(surveys[i], "_std"), overwrite = T,
                  rdata = TRUE)
}

```

## 1. Overview of the survey data table

survey	source	timestamp	haul_id	country	sub_area
SP-ARSA	DATRAS ICES	2021-07	SP-ARSA 2002 4 ES 29CS BAK 1 38	spain	NA
SP-ARSA	DATRAS ICES	2021-07	SP-ARSA 2002 4 ES 29CS BAK 1 38	spain	NA
SP-ARSA	DATRAS ICES	2021-07	SP-ARSA 2002 4 ES 29CS BAK 1 38	spain	NA
SP-ARSA	DATRAS ICES	2021-07	SP-ARSA 2002 4 ES 29CS BAK 1 38	spain	NA
SP-ARSA	DATRAS ICES	2021-07	SP-ARSA 2002 4 ES 29CS BAK 1 38	spain	NA

continent	stat_rec	station	stratum	year	month	day	quarter	season
europe	02E3	NA	NA	2002	12	NA	4	NA
europe	02E3	NA	NA	2002	12	NA	4	NA
europe	02E3	NA	NA	2002	12	NA	4	NA
europe	02E3	NA	NA	2002	12	NA	4	NA
europe	02E3	NA	NA	2002	12	NA	4	NA

latitude	longitude	haul_dur	area_swept	gear	depth	sbt	sst
36.959	-6.765	1	0.0640948	BAK	29	NA	NA
36.959	-6.765	1	0.0640948	BAK	29	NA	NA
36.959	-6.765	1	0.0640948	BAK	29	NA	NA
36.959	-6.765	1	0.0640948	BAK	29	NA	NA
36.959	-6.765	1	0.0640948	BAK	29	NA	NA

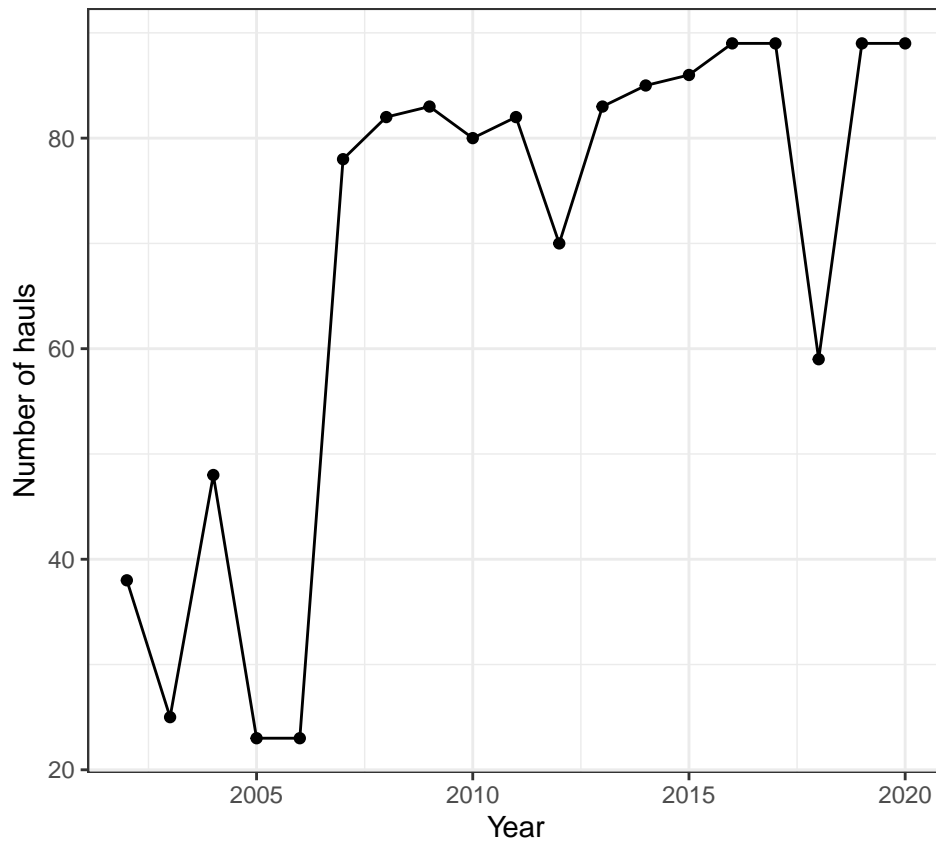
num	num_cpue	num_cpua	wgt	wgt_cpue	wgt_cpua	verbatim_name
66	66	1029.72472	1.5682761	1.5682761	24.468071	NA
16	16	249.63024	0.6787415	0.6787415	10.589650	NA
3	3	46.80567	0.5951247	0.5951247	9.285071	NA
19	19	296.43590	2.3423884	2.3423884	36.545686	NA
7	7	109.21323	0.2428370	0.2428370	3.788716	NA

verbatim_aphia_id	accepted_name	aphia_id	SpecCode	kingdom
126822	Trachurus trachurus	126822	1365	Animalia
127130	Citharus linguatula	127130	4943	Animalia
126285	Conger conger	126285	301	Animalia
126484	Merluccius merluccius	126484	30	Animalia
127154	Dicologlossa cuneata	127154	526	Animalia

phylum	class	order	family	genus	rank	survey_unit
Chordata	Teleostei	Carangiformes	Carangidae	Trachurus	Species	SP-ARSA-4
Chordata	Teleostei	Pleuronectiformes	Citharidae	Citharus	Species	SP-ARSA-4
Chordata	Teleostei	Anguilliformes	Congridae	Conger	Species	SP-ARSA-4
Chordata	Teleostei	Gadiformes	Merlucciidae	Merluccius	Species	SP-ARSA-4
Chordata	Teleostei	Pleuronectiformes	Soleidae	Dicologlossa	Species	SP-ARSA-4

## 2. Summary of sampling intensity

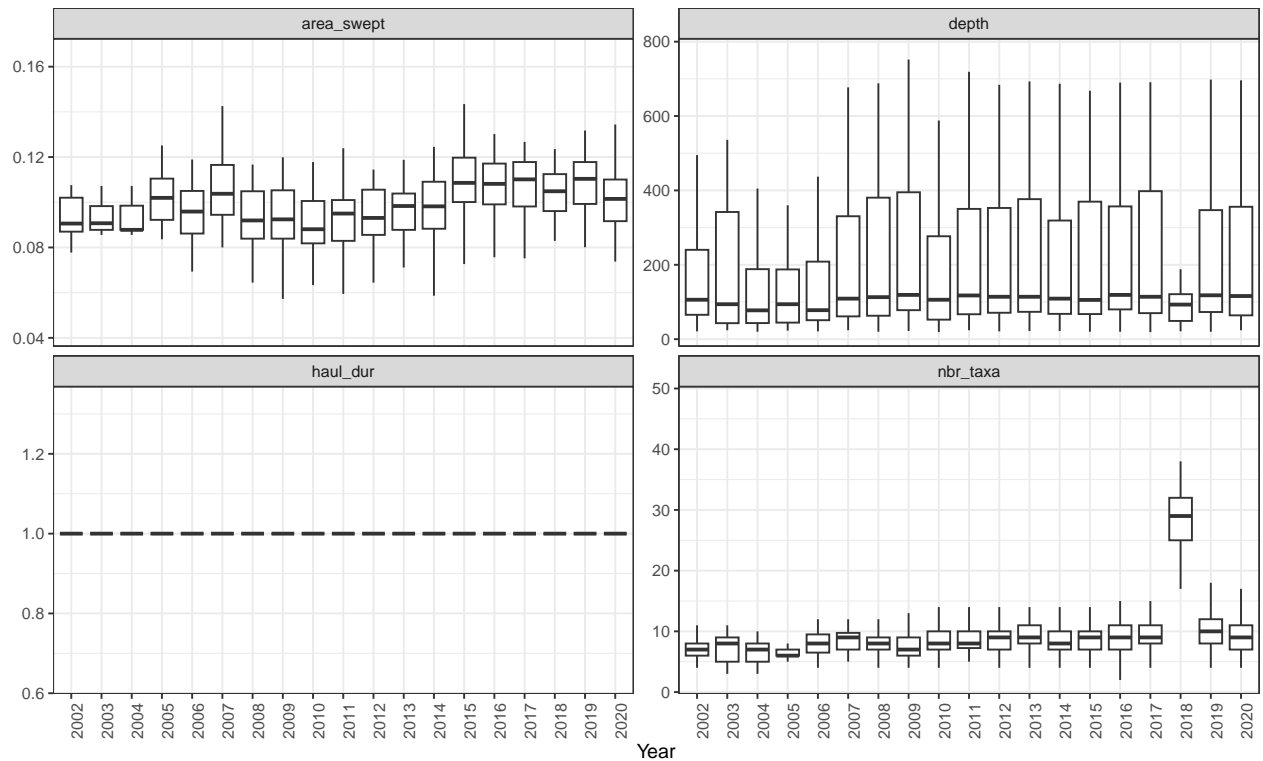
Number of hauls per year performed during the survey after data processing.



### 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:

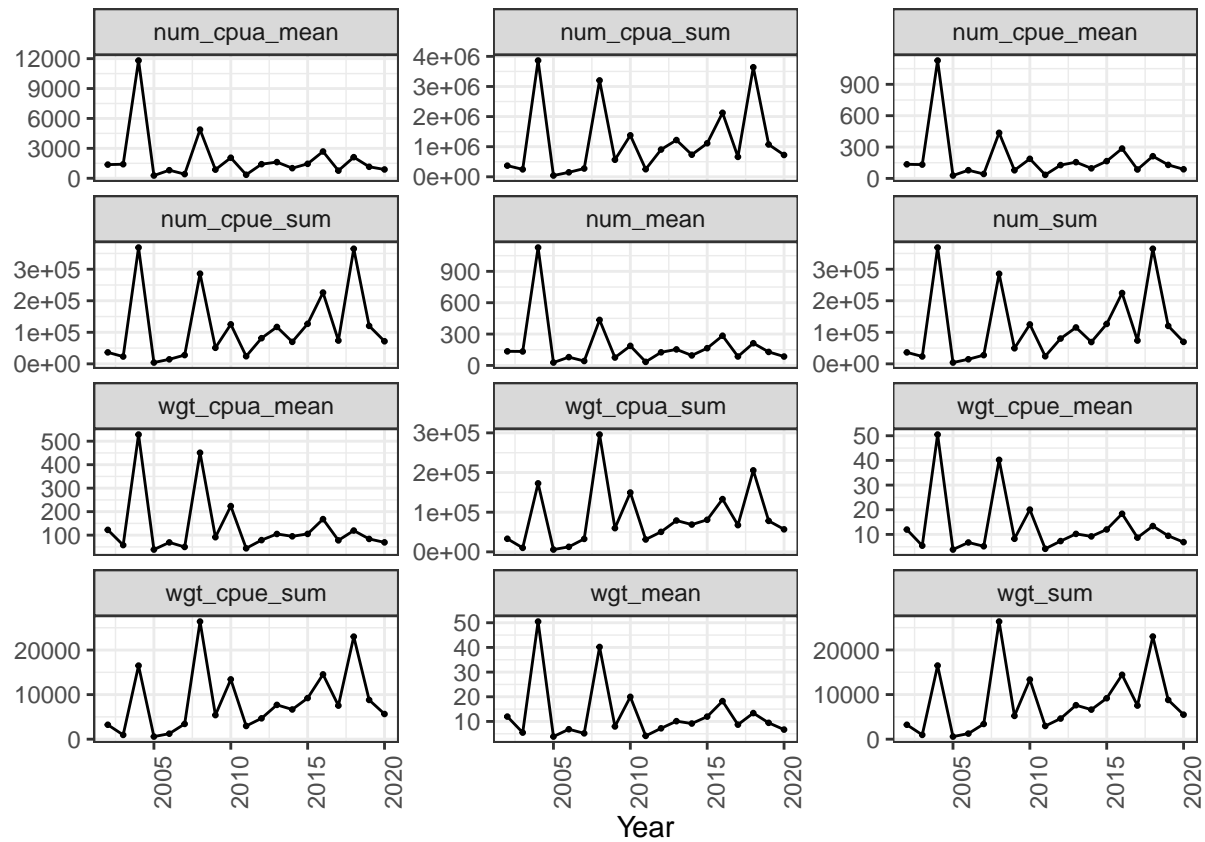
- *area\_swept*, swept area by the bottom trawl gear  $km^2$
- *depth*, sampling depth in *m*
- *haul\_dur*, haul sampling duration *hours*
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (<https://www.marinespecies.org/>,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

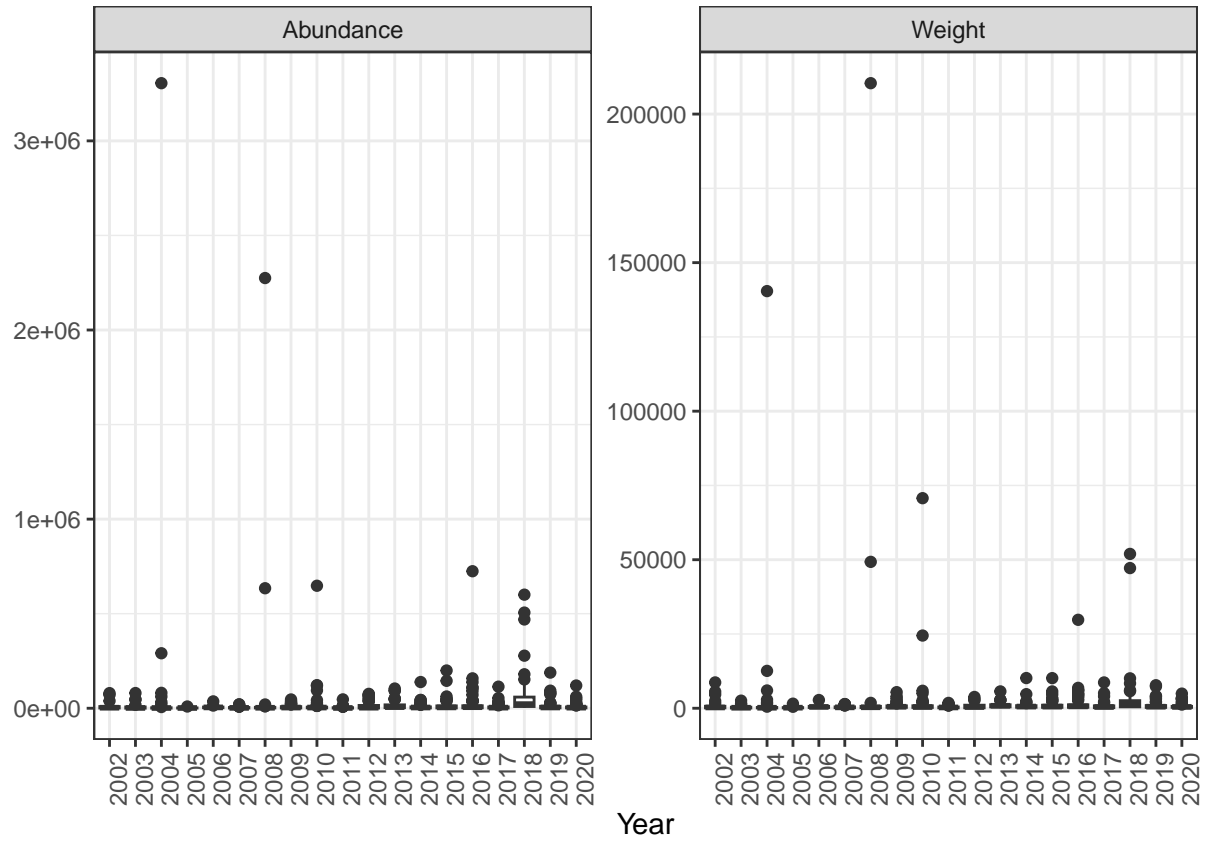
- *num\_cpua*, number of individuals (abundance) in  $\frac{\text{individuals}}{\text{km}^2}$
- *num\_cpue*, number of individuals (abundance) in  $\frac{\text{individuals}}{h}$
- *num*, number of individuals (abundance)
- *wgt\_cpua*, weight in  $\frac{kg}{\text{km}^2}$
- *wgt\_cpue*, weight in  $\frac{kg}{h}$
- *wgt*, weight in *kg*



## 5. Extreme values

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

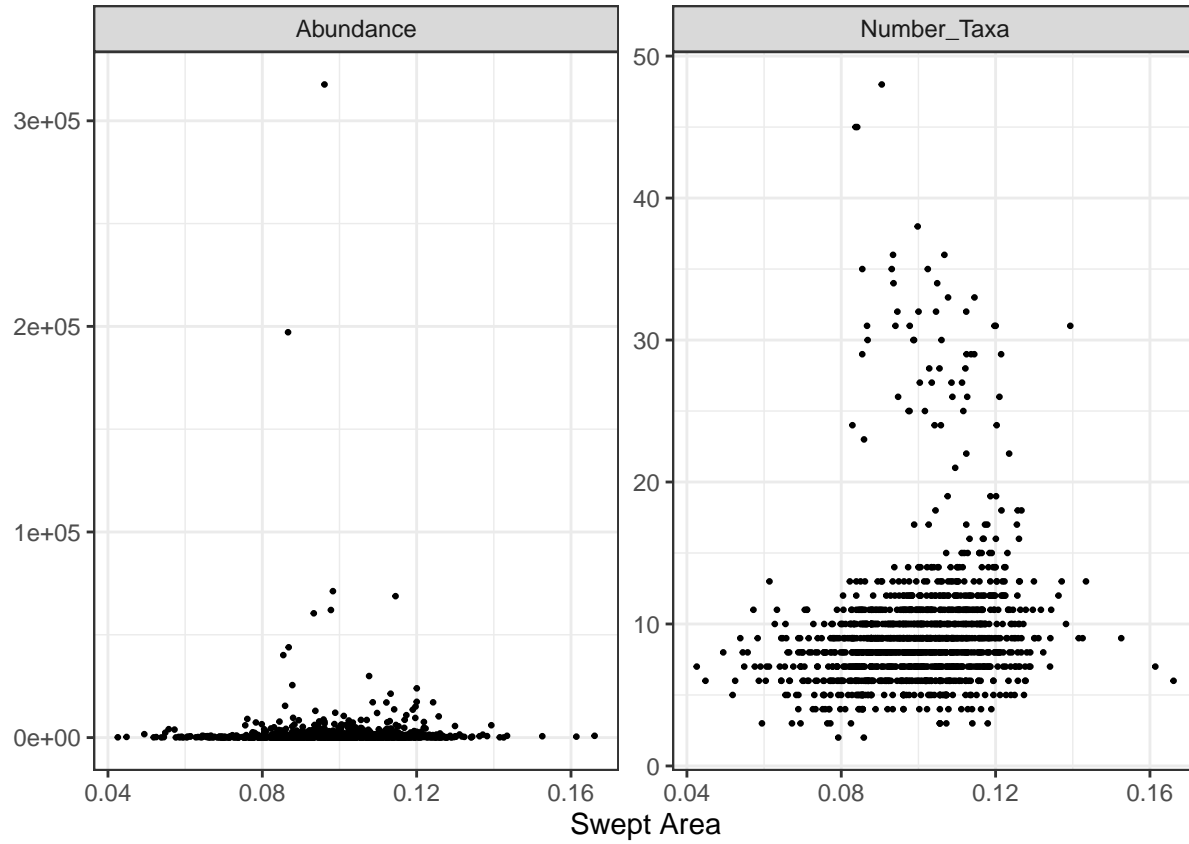
- *num\_cpue*, number of individuals (abundance) in  $\frac{\text{individuals}}{\text{km}^2}$
- *wgt\_cpue*, weight in  $\frac{\text{kg}}{\text{km}^2}$



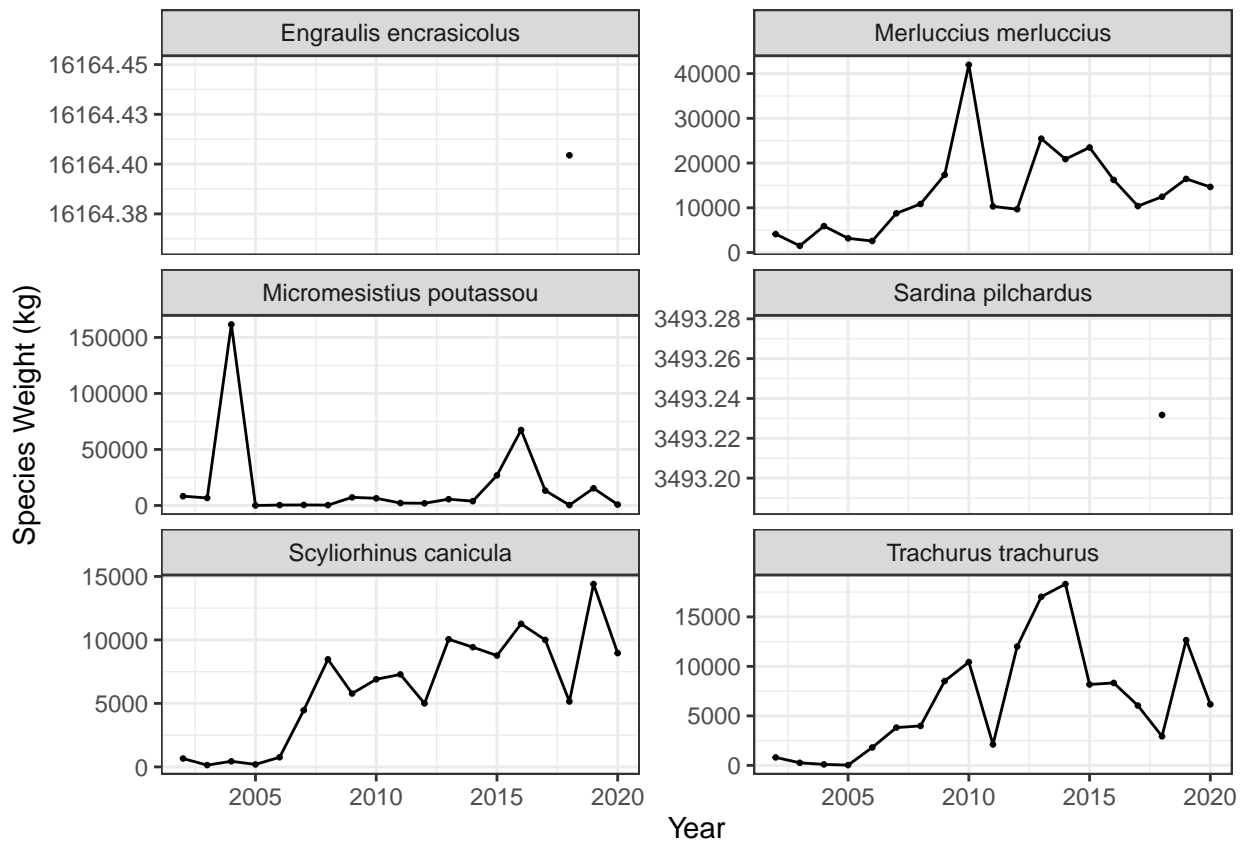
## 6. Summary of variables against swept area

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  $\frac{\text{individuals}}{\text{km}^2}$
- *wgt\_cpua*, weight in  $\frac{\text{kg}}{\text{km}^2}$

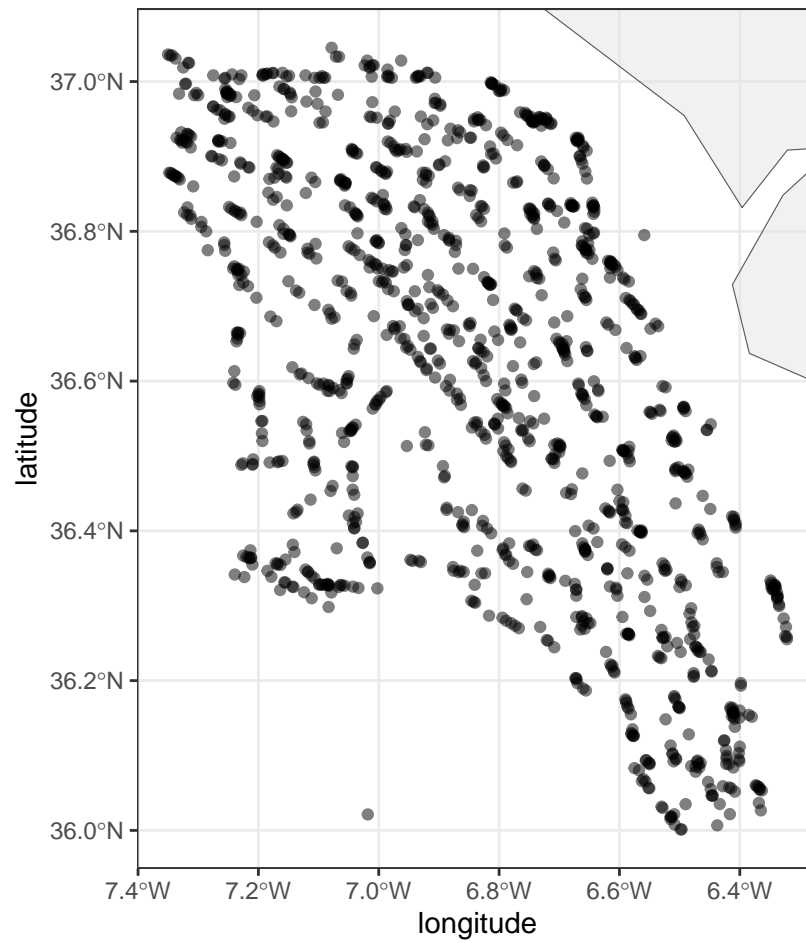


## 7. Abundance or Weight trends of the six most abundant species



## 8. Distribution mapping

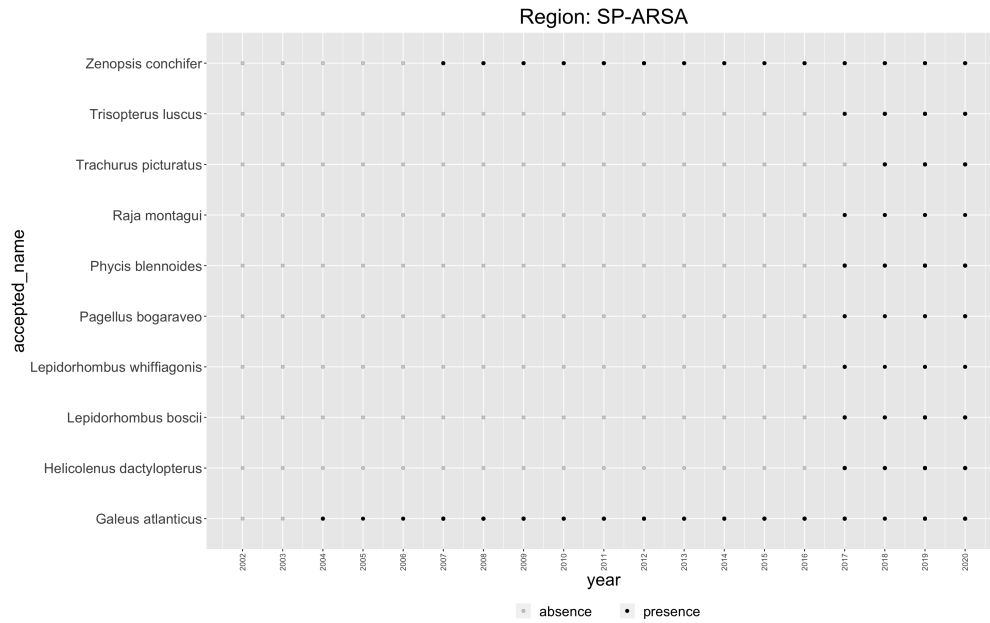
Map of the sampling distribution in space. Note that we only show one year per coordinate.



## 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

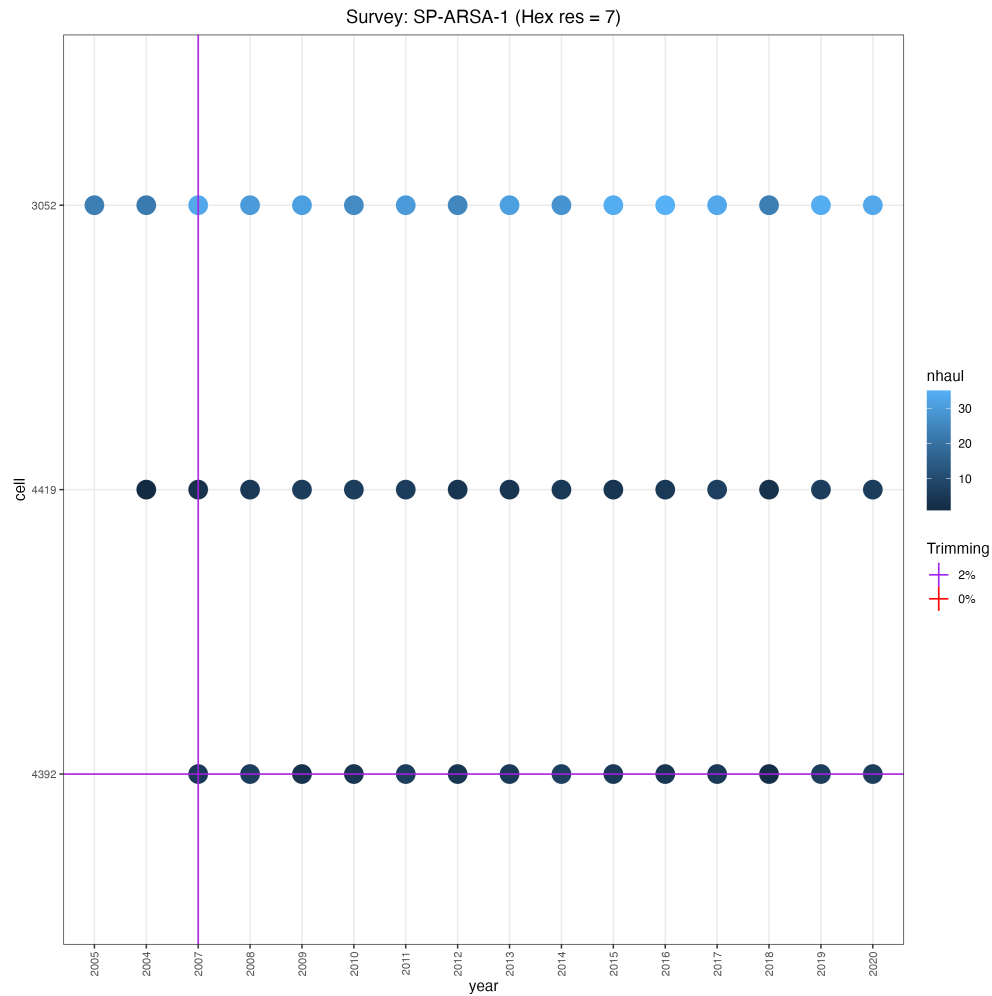
Total number of species	159.0
Percentage of species flagged	6.3

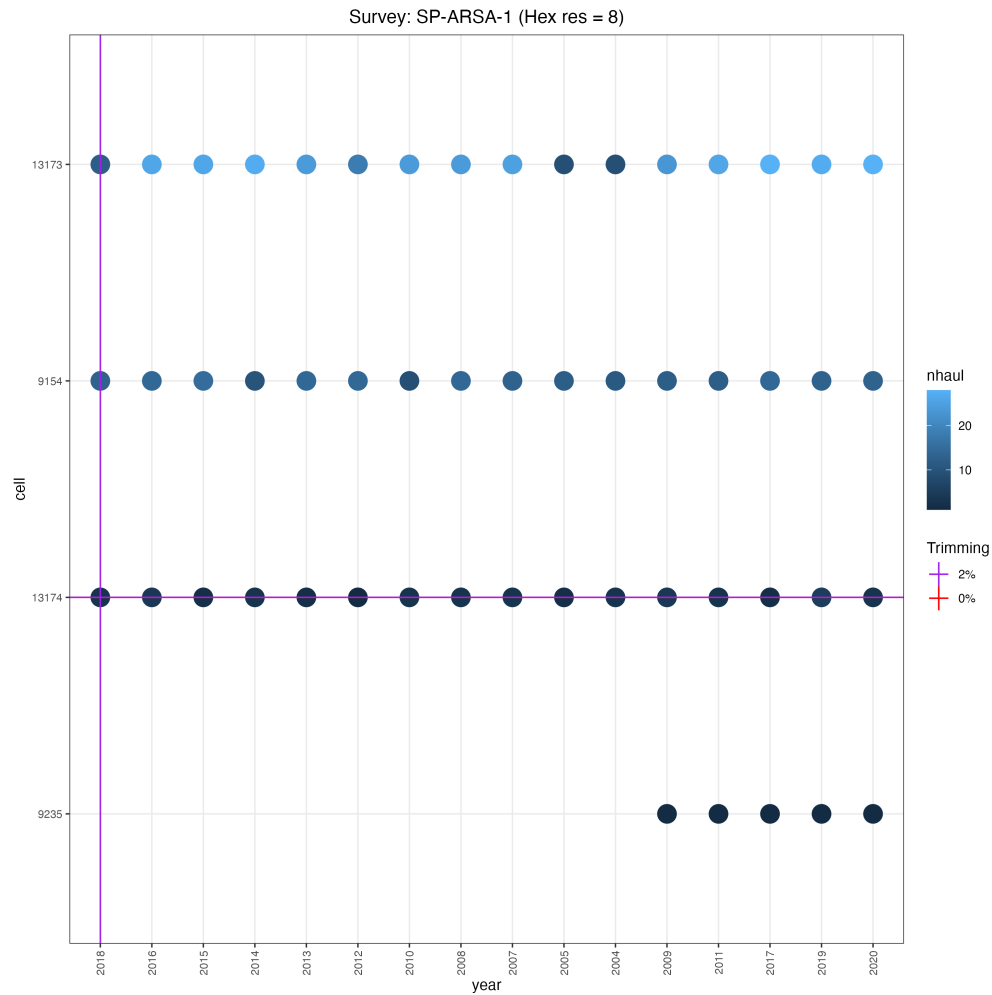
## 10. Spatio-temporal standardization: SP-ARSA-1

### a. Standardization method 1

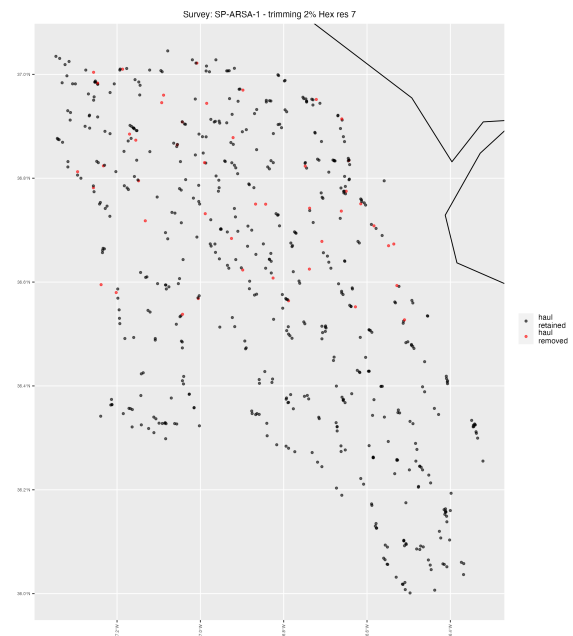
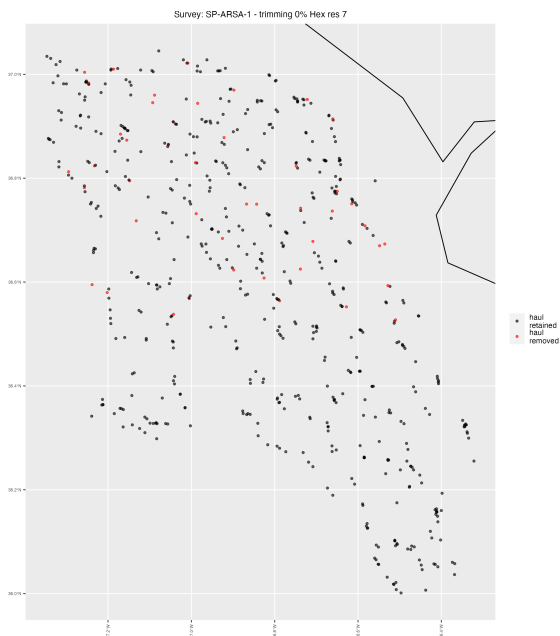
This standardization method was adapted from [https://github.com/zoekitchel/trawl\\_spatial\\_turnover/blob/master/data\\_prep\\_code/species/explore\\_NorthSea\\_trimming.Rmd](https://github.com/zoekitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd)  
It was run for hex resolution 7 and 8.

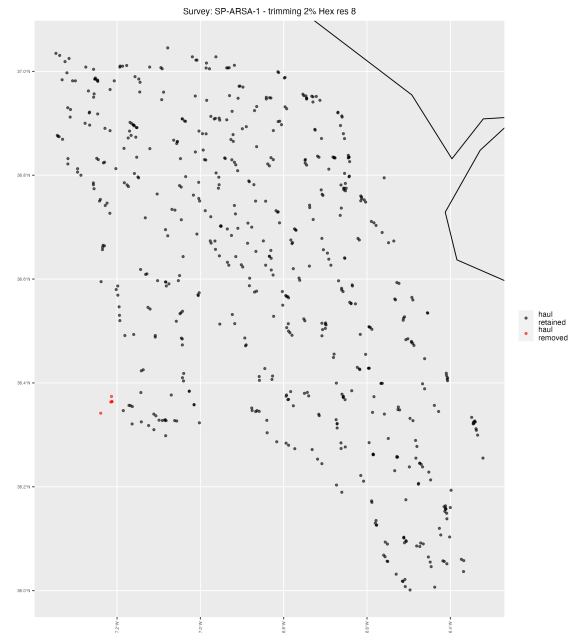
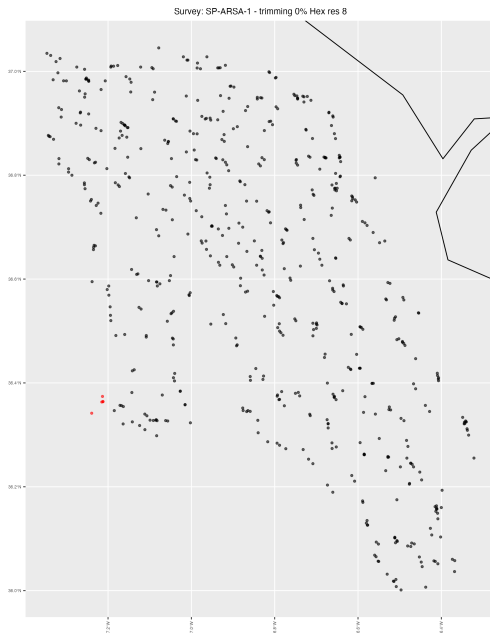
Plot of number of cells x years with overlaid flagging options



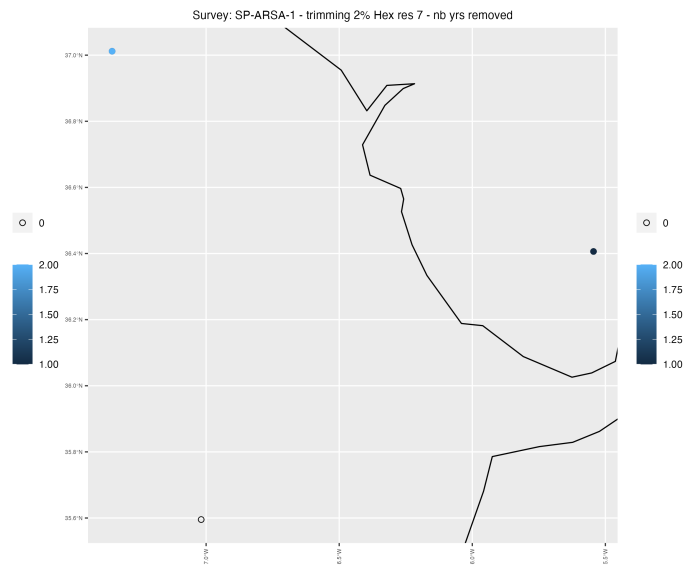
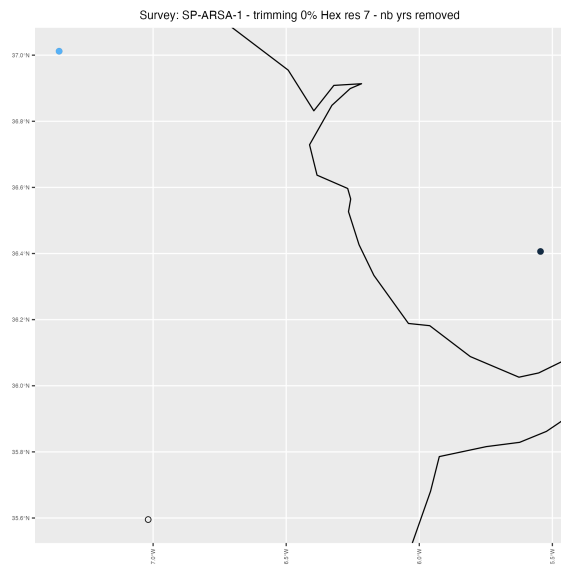


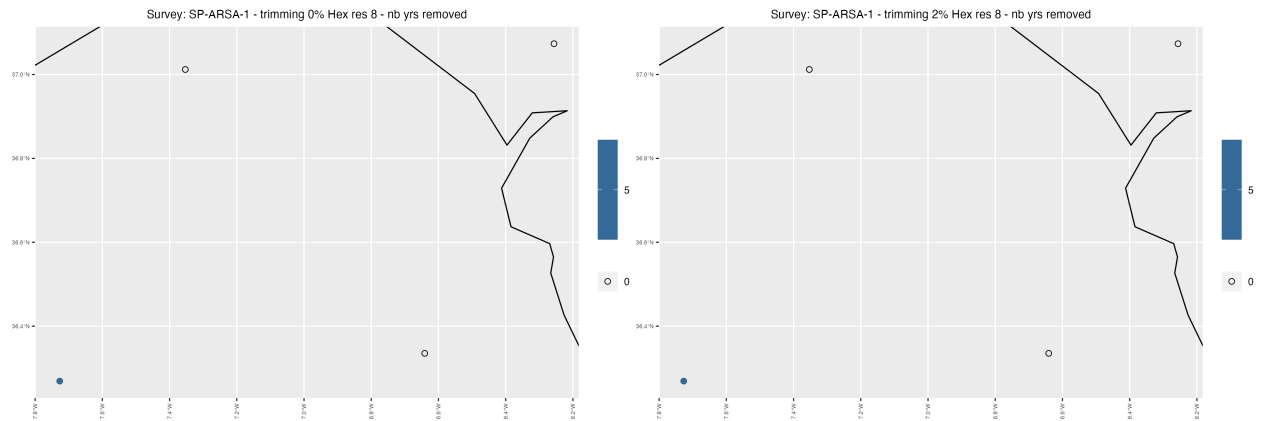
Map of hauls retained and removed per flagging method and threshold





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



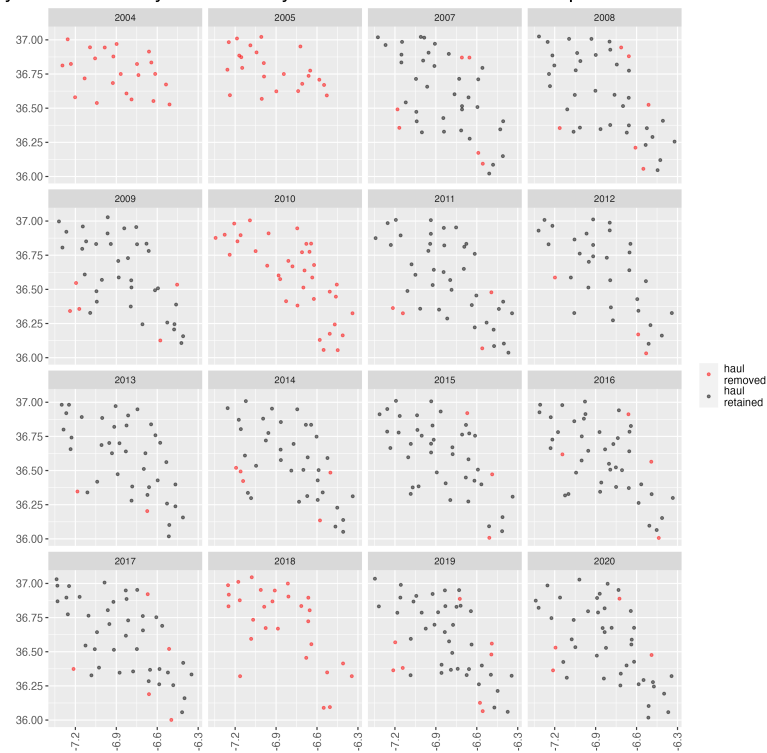


## b. Standardization method 2

This standardization method was adapted from BioTIME code from [https://github.com/Wubing-Xu/Range\\_size\\_winners\\_losers](https://github.com/Wubing-Xu/Range_size_winners_losers)

Map of hauls retained and removed

survey= SP-ARSA-1 year1= 2007 year2= 2020 max.shared.samples= 29 duration= 14



## c. Standardization summary

Statistics of hauls removed for each standardization method

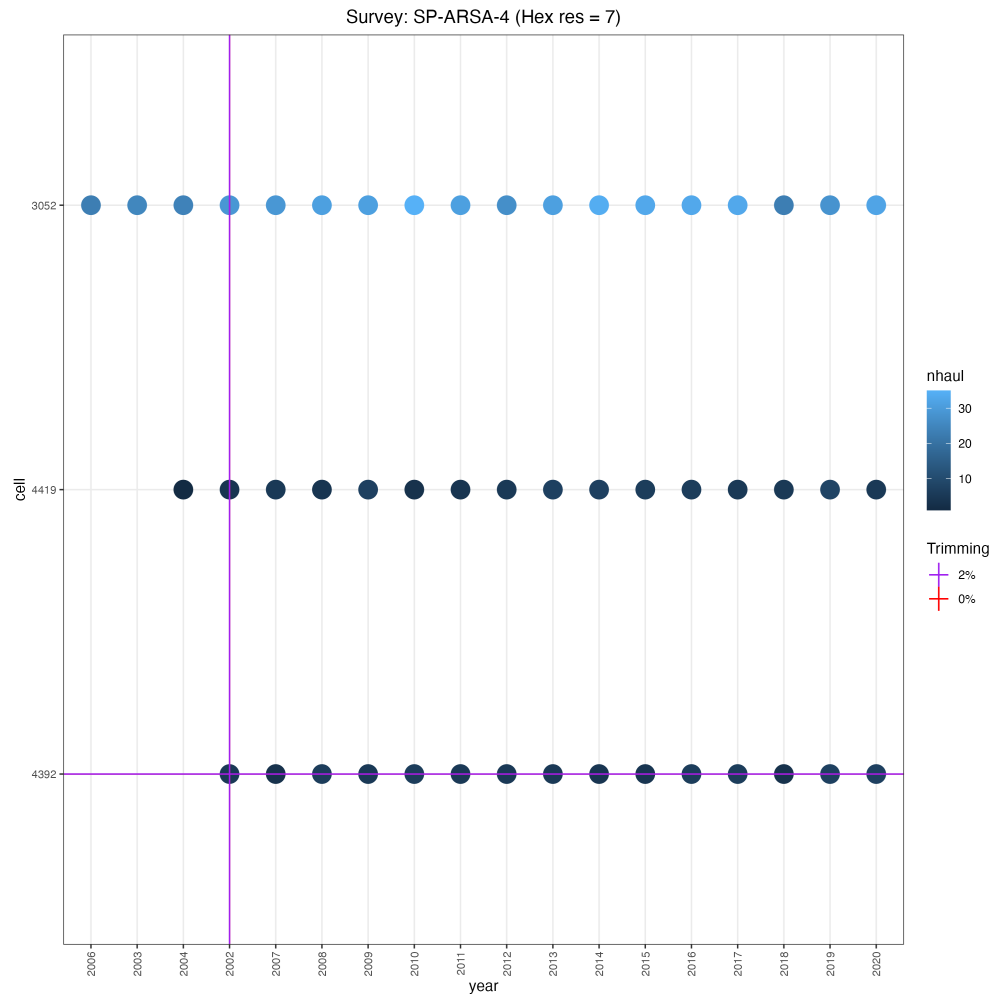
summary	grid cell 7, 0% threshold	grid cell 7, 2% threshold	grid cell 8, 0% threshold	grid cell 8, 2% threshold	method 2 (biotime)
number of hauls removed	46.0	46.0	5.0	5.0	1799.0
percentage of hauls removed	7.5	7.5	0.8	0.8	31.7

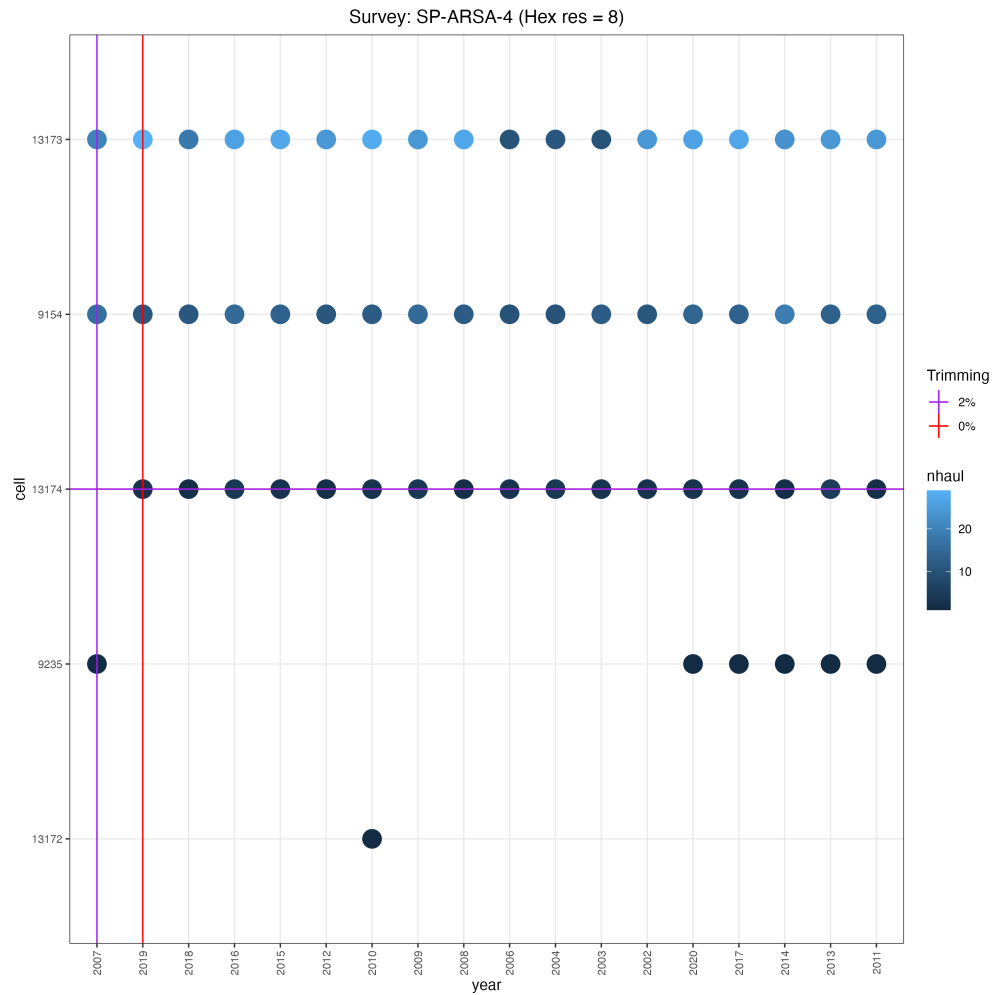
## 11. Spatio-temporal standardization SP-ARSA 4

### a. Standardization method 1

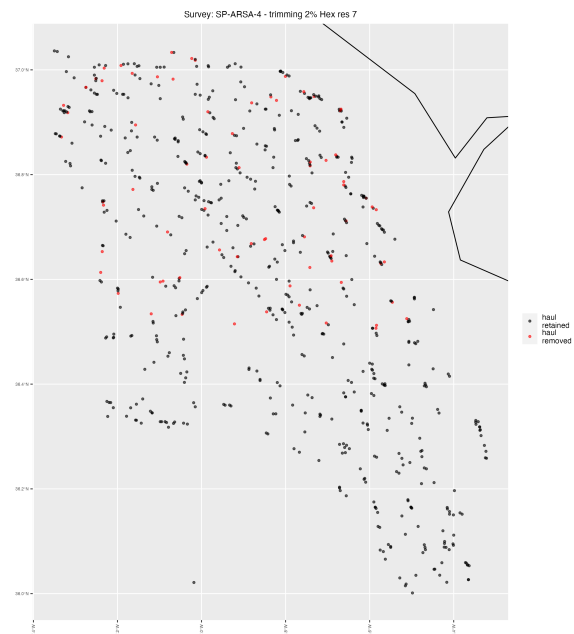
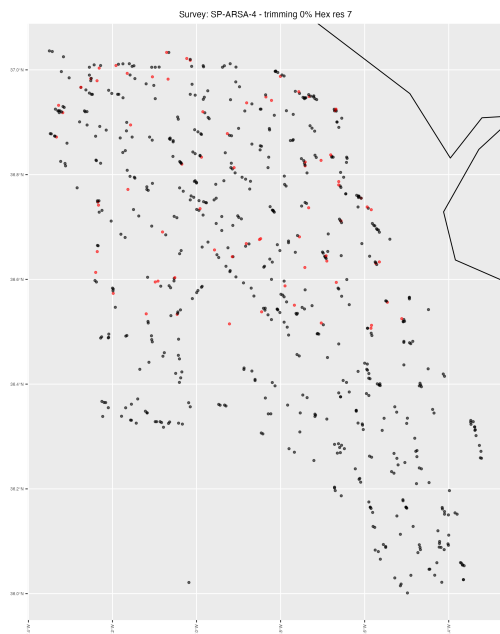
This standardization method was adapted from [https://github.com/zoekitchel/trawl\\_spatial\\_turnover/blob/master/data\\_prep\\_code/species/explore\\_NorthSea\\_trimming.Rmd](https://github.com/zoekitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd)  
It was run for hex resolution 7 and 8.

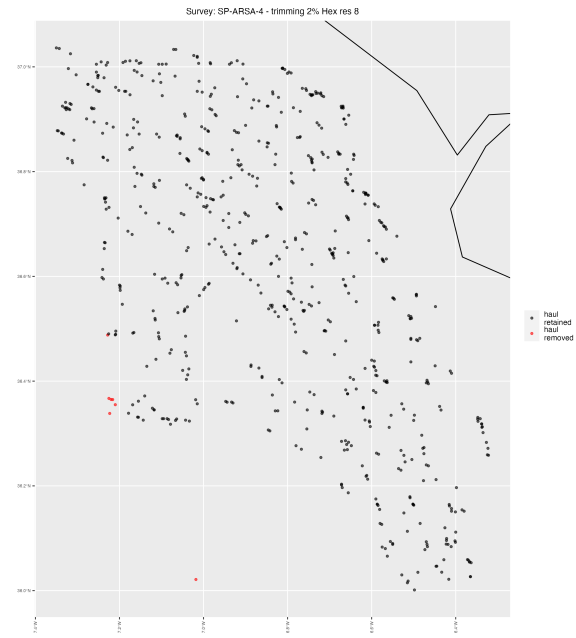
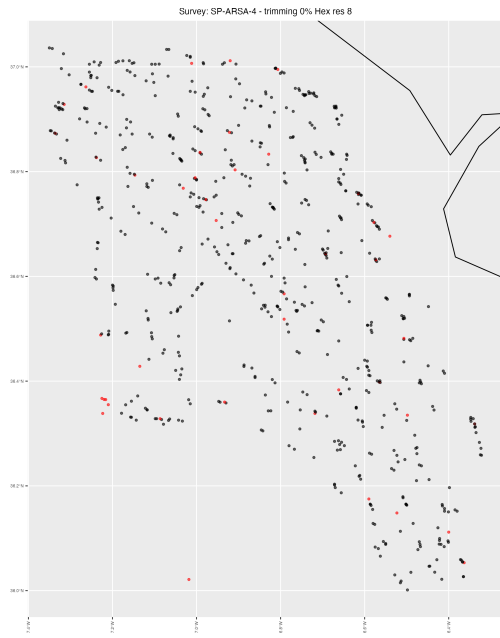
Plot of number of cells x years with overlaid flagging options



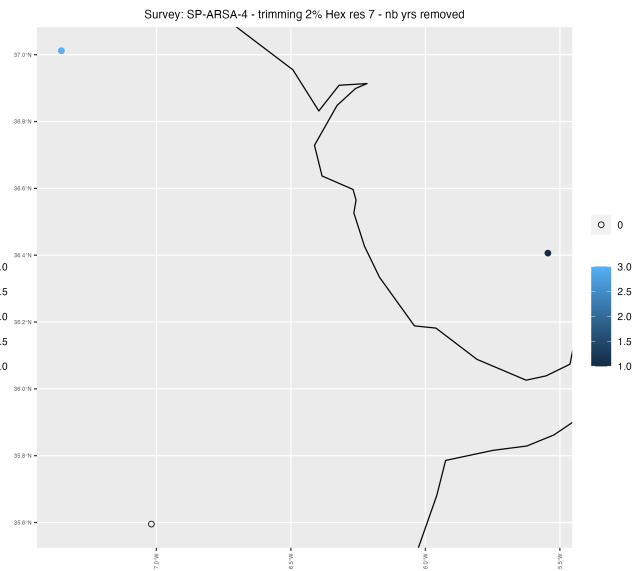
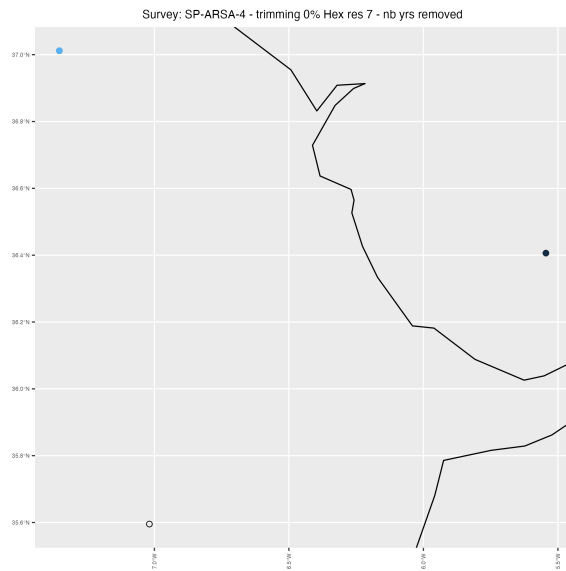


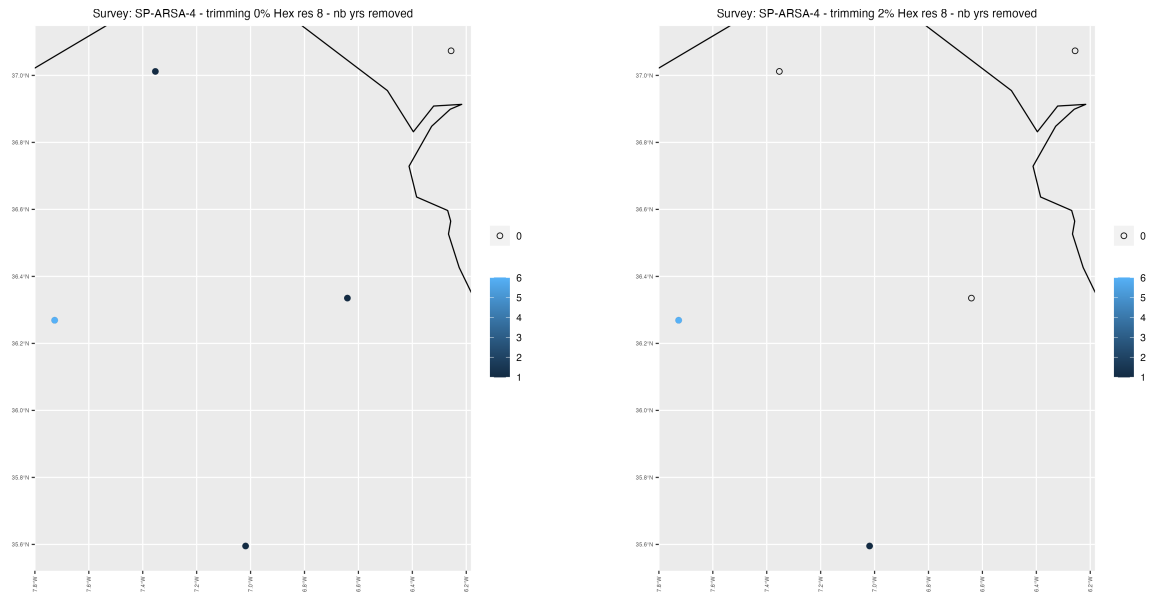
Map of hauls retained and removed per flagging method and threshold





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](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	73.0	73.0	43.0	7	2628.0
percentage of hauls removed	10.6	10.6	6.2	1	38.7