

ROCKALL: Rockall survey data processing summary

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General info

This document presents the cleaning code and summary of the North Sea bottom trawl survey provided by DATRAS, ICES. It contains data from **1999** 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 + Juliano 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 identieid 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.scowcgfs, file = "Publicly available/DATRAS/hh.scowcgfs.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.scowcgfs <- 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
         HLNoAtLngt = ifelse(HLNoAtLngt == (-9), NA, HLNoAtLngt),
         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
         HLNoAtLngt = case_when(DataType=='C' ~ HLNoAtLngt*SubFactor*HaulDur/60,
                                DataType %in% c('S','R') ~ HLNoAtLngt*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 SWEEP 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 montagui", "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),

```

```

# gobius
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 inverts 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$conversion_to_TL[1], xx_conce
    hist(xx_survey$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$wgth>0 & xx$wgtlenh>0,], aes(x=wgth, 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$cor_wgt[i] <- cor(x = xx$wgth, 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, wgth>0 & wgtlenh>0)

# rockall looks OK
ggplot(subset(xx, Survey=='ROCKALL'), aes(x=wgth, 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=wgth, 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=wgth, 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=wgth, 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=wgth, 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=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=='SWC-IBTS') %>%
  select(HaulID,wgtlenh,wgth) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wgtlenh', 'wgth'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wgth, 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$wgth
plot(comp$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=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=='BITS') %>%
  select(HaulID,wgtlenh,wgth) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wgtlenh', 'wgth'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wgth, 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$wgth
plot(comp$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))

# EVHOE may have an issue, no changes as not very clear
ggplot(subset(xx, Survey=='EVHOE'), aes(x=wgth, 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,wgth) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wgtlenh', 'wgth'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wgth, 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$wgth
plot(comp$factor)

# NS - IBTS issue
ggplot(subset(xx, Survey=="NS-IBTS"), aes(x=wgth, 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,wgth) %>%
  distinct() %>%
  group_by(HaulID) %>%
  summarize_at(.vars=c('wgtlenh', 'wgth'), .funs = function(x) sum(x)) %>%
  ungroup() %>%
  as.data.frame()

ggplot(comp, aes(x=wgth, 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$wgth
comp$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=wgtlenh)) + 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=wgtlenh)) + 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 & wgtlencpue > 0)
cor(x = xx$wtcpue, y = xx$wgtlencpue, method = 'pearson') # looks better

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

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

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

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

cor(x = xx$wtcpue, y = xx$wgtlencpue, 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("FALK","GSL-N","MRT","NZ-CHAT","SCS", "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
ROCKALL	DATRAS ICES	2021-07	ROCKALL 1999 3 GB-SCT 748S GOV 404 1	uk	NA
ROCKALL	DATRAS ICES	2021-07	ROCKALL 1999 3 GB-SCT 748S GOV 404 1	uk	NA
ROCKALL	DATRAS ICES	2021-07	ROCKALL 1999 3 GB-SCT 748S GOV 404 1	uk	NA
ROCKALL	DATRAS ICES	2021-07	ROCKALL 1999 3 GB-SCT 748S GOV 404 1	uk	NA
ROCKALL	DATRAS ICES	2021-07	ROCKALL 1999 3 GB-SCT 748S GOV 404 1	uk	NA

continent	stat_rec	station	stratum	year	month	day	quarter	season
europe	44D6	NA	NA	1999	8	NA	3	NA
europe	44D6	NA	NA	1999	8	NA	3	NA
europe	44D6	NA	NA	1999	8	NA	3	NA
europe	44D6	NA	NA	1999	8	NA	3	NA
europe	44D6	NA	NA	1999	8	NA	3	NA

latitude	longitude	haul_dur	area_swept	gear	depth	sbt	sst
57.9	-13.5833	0.5	0.0745362	GOV	189	NA	NA
57.9	-13.5833	0.5	0.0745362	GOV	189	NA	NA
57.9	-13.5833	0.5	0.0745362	GOV	189	NA	NA
57.9	-13.5833	0.5	0.0745362	GOV	189	NA	NA
57.9	-13.5833	0.5	0.0745362	GOV	189	NA	NA

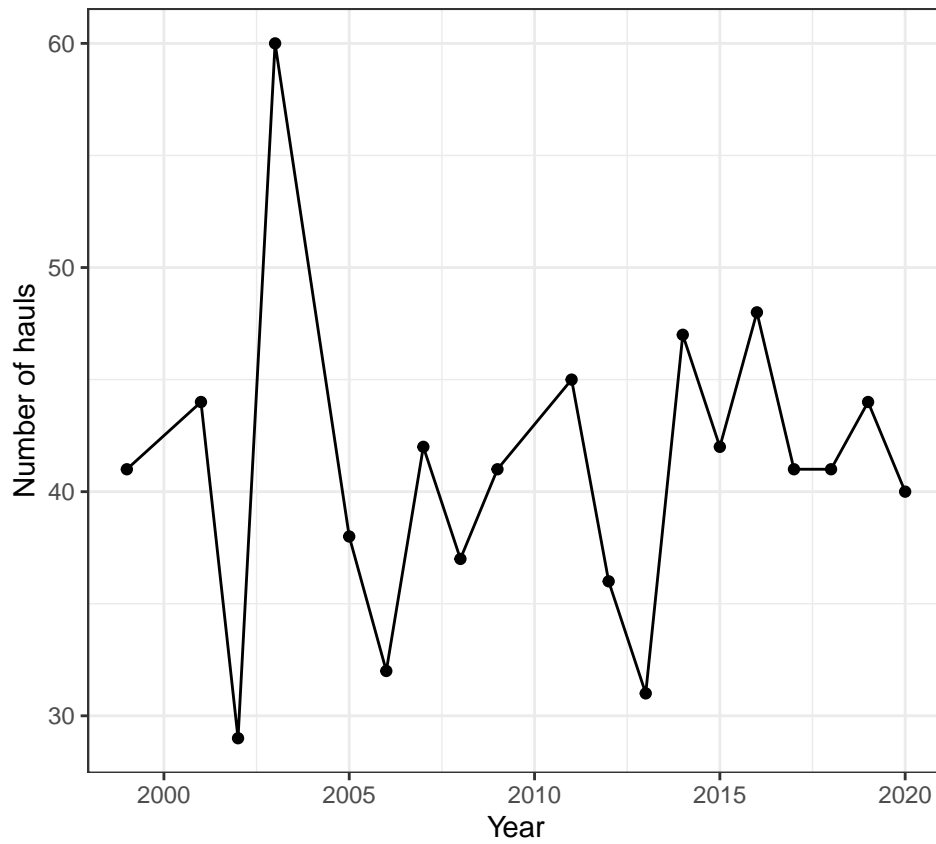
num	num_cpue	num_cpua	wgt	wgt_cpue	wgt_cpua	verbatim_name
1	2	13.4163	2.2502103	4.5004205	30.1894953	NA
35	70	469.5705	5.2893124	10.5786247	70.9630002	NA
28	56	375.6564	2.6408840	5.2817679	35.4308906	NA
1	2	13.4163	0.0328776	0.0657553	0.4410962	NA
571	1142	7660.7071	126.3947452	252.7894903	1695.7497855	NA

verbatim_aphia_id	accepted_name	aphia_id	SpecCode	kingdom
126758	Anarhichas lupus	126758	2501	Animalia
126715	Argentina	125885	NA	Animalia
126716	Argentina	125885	NA	Animalia
126793	Callionymus	125930	NA	Animalia
126437	Melanogrammus aeglefinus	126437	1381	Animalia

phylum	class	order	family	genus	rank	survey_unit
Chordata	Teleostei	Perciformes	Anarhichadidae	Anarhichas	Species	ROCKALL
Chordata	Teleostei	Argentiniformes	Argentinidae	Argentina	Genus	ROCKALL
Chordata	Teleostei	Argentiniformes	Argentinidae	Argentina	Genus	ROCKALL
Chordata	Teleostei	Callionymiformes	Callionymidae	Callionymus	Genus	ROCKALL
Chordata	Teleostei	Gadiformes	Gadidae	Melanogrammus	Species	ROCKALL

2. Summary of sampling intensity

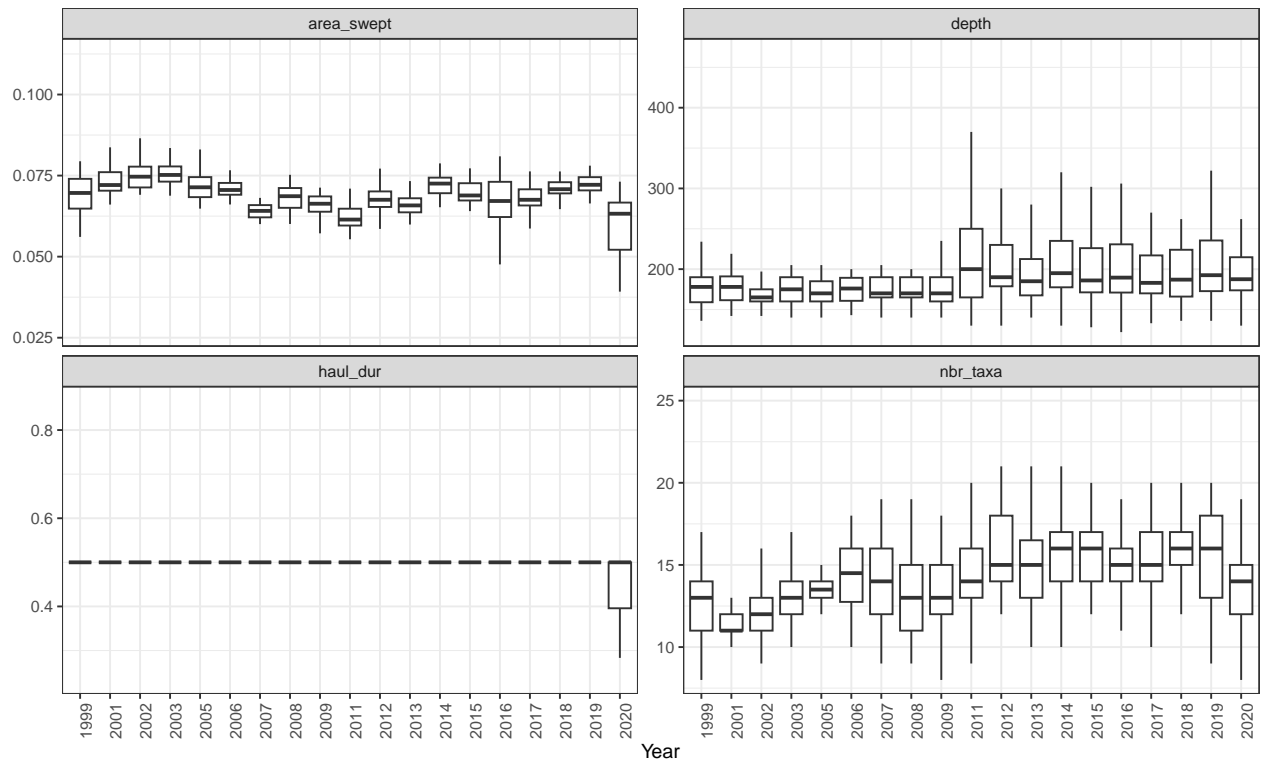
Number of hauls per year performed during the survey after data processing.



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:

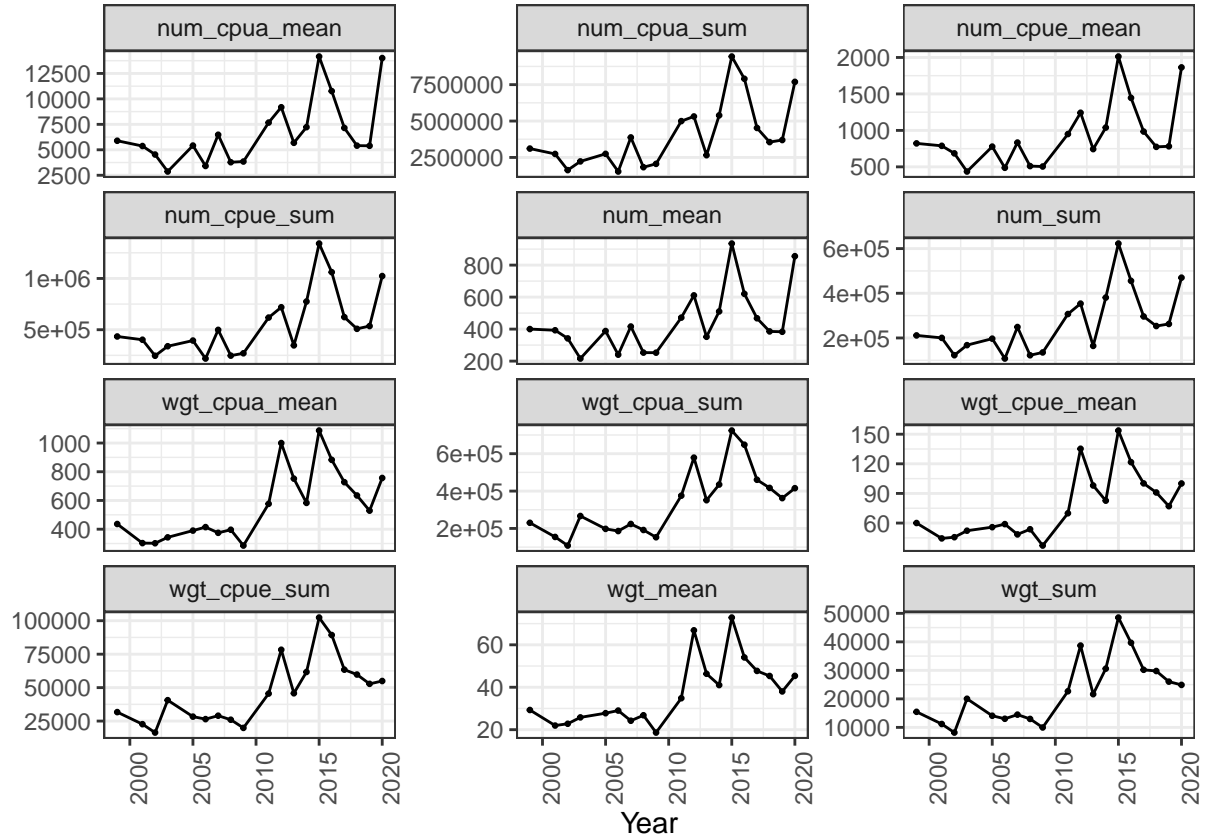
- *area_swept*, swept area by the bottom trawl gear km^2
- *depth*, sampling depth in *m*
- *haul_dur*, haul sampling duration *hours*
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (<https://www.marinespecies.org/>,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

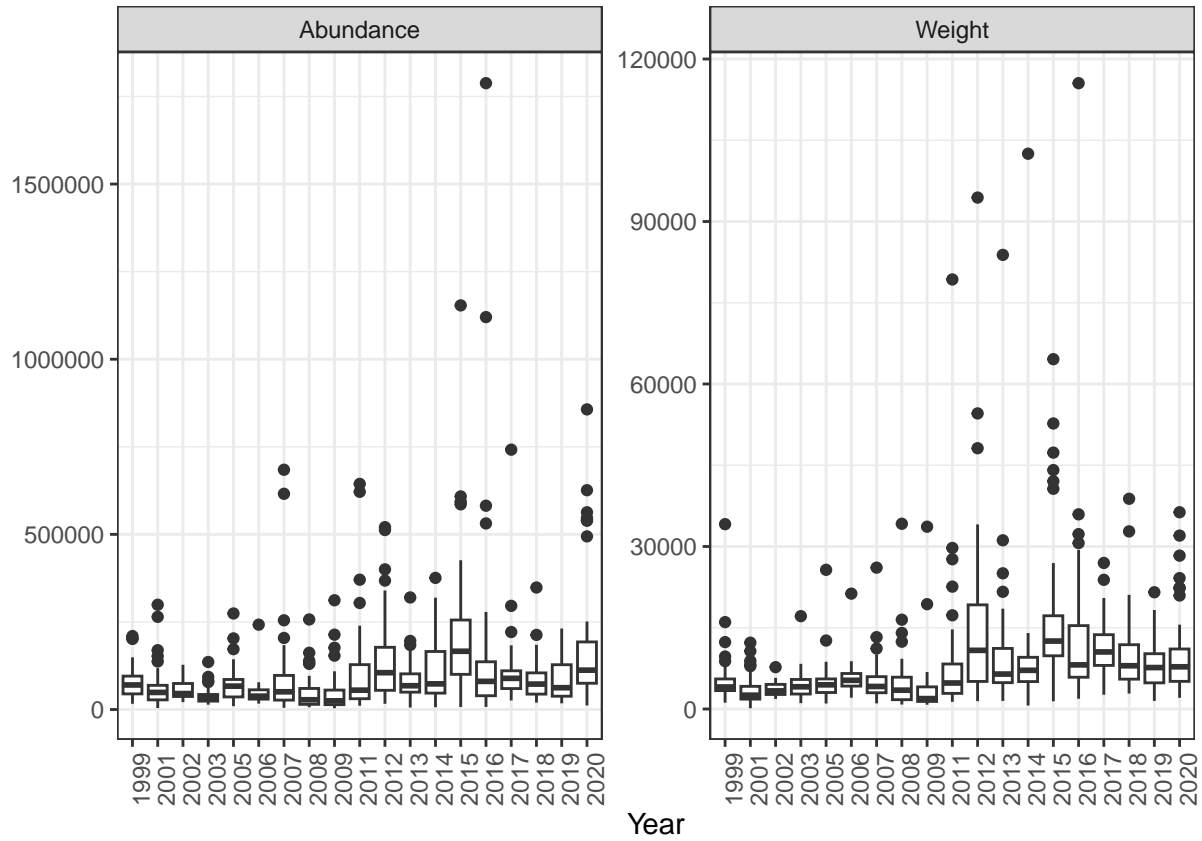
- *num_cpua*, number of individuals (abundance) in $\frac{\text{individuals}}{\text{km}^2}$
- *num_cpue*, number of individuals (abundance) in $\frac{\text{individuals}}{h}$
- *num*, number of individuals (abundance)
- *wgt_cpua*, weight in $\frac{kg}{\text{km}^2}$
- *wgt_cpue*, weight in $\frac{kg}{h}$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



5. Extreme values

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

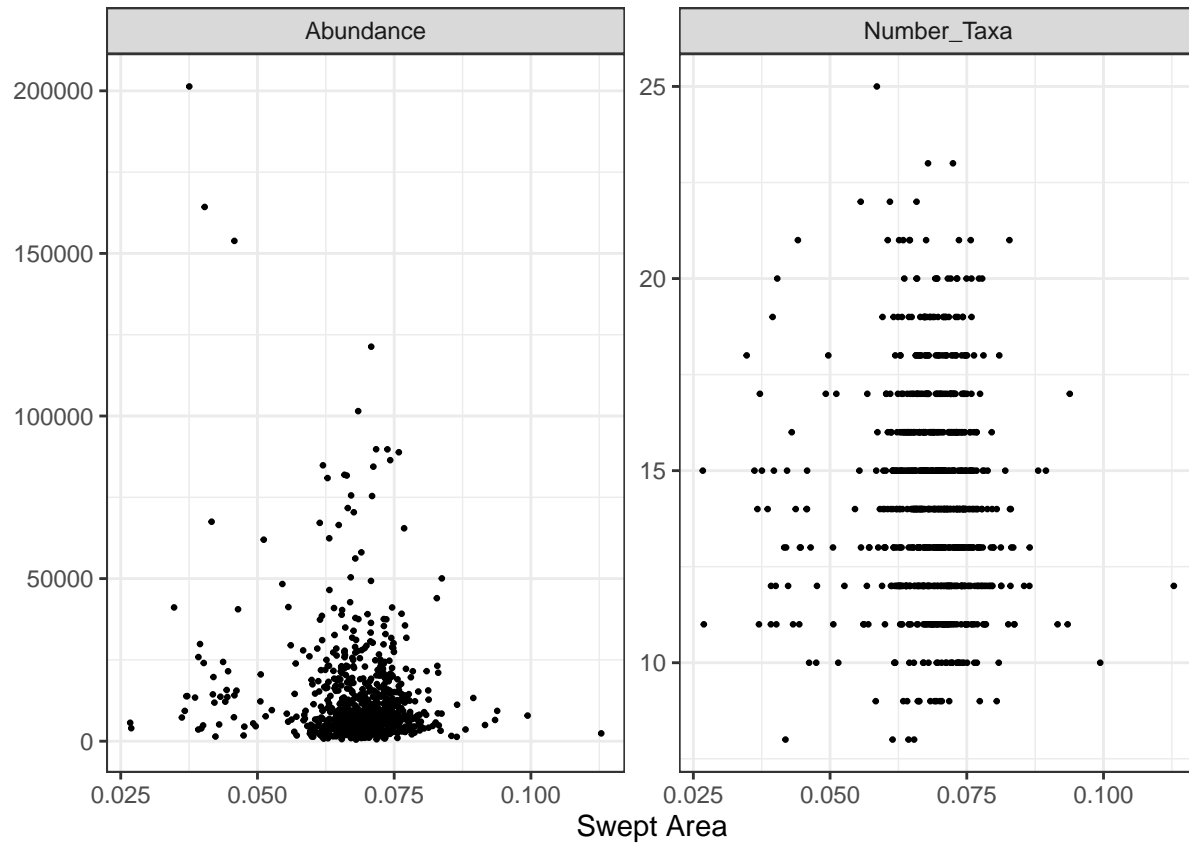
- *num_cpue*, number of individuals (abundance) in $\frac{\text{individuals}}{\text{km}^2}$
- *wgt_cpue*, weight in $\frac{\text{kg}}{\text{km}^2}$



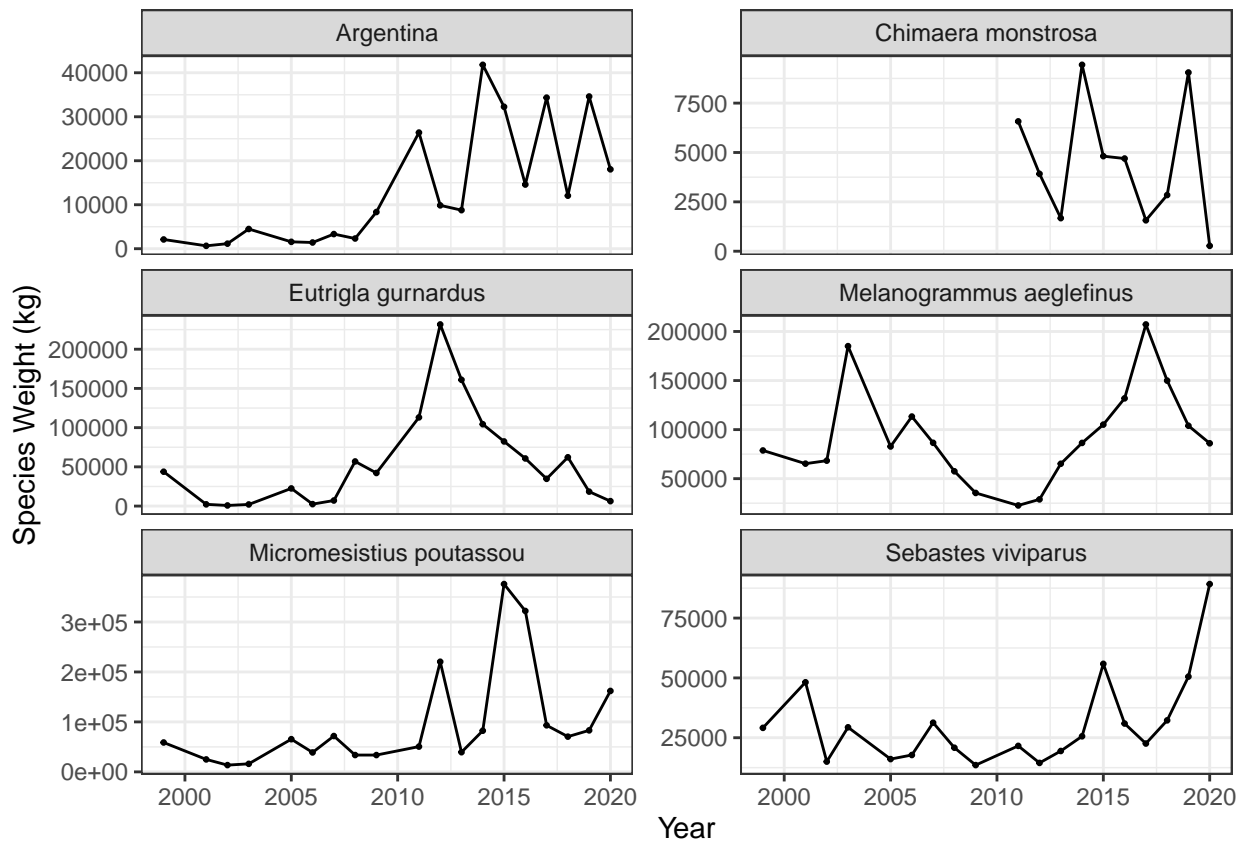
6. Summary of variables against swept area

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 $\frac{\text{kg}}{\text{km}^2}$

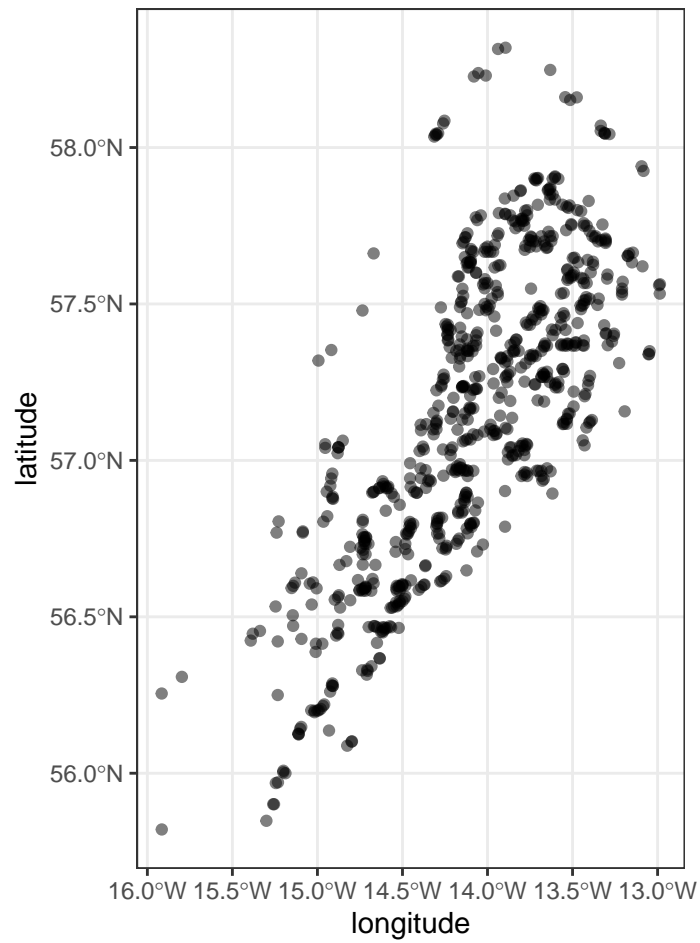


7. Abundance or Weight trends of the six most abundant species



8. Distribution mapping

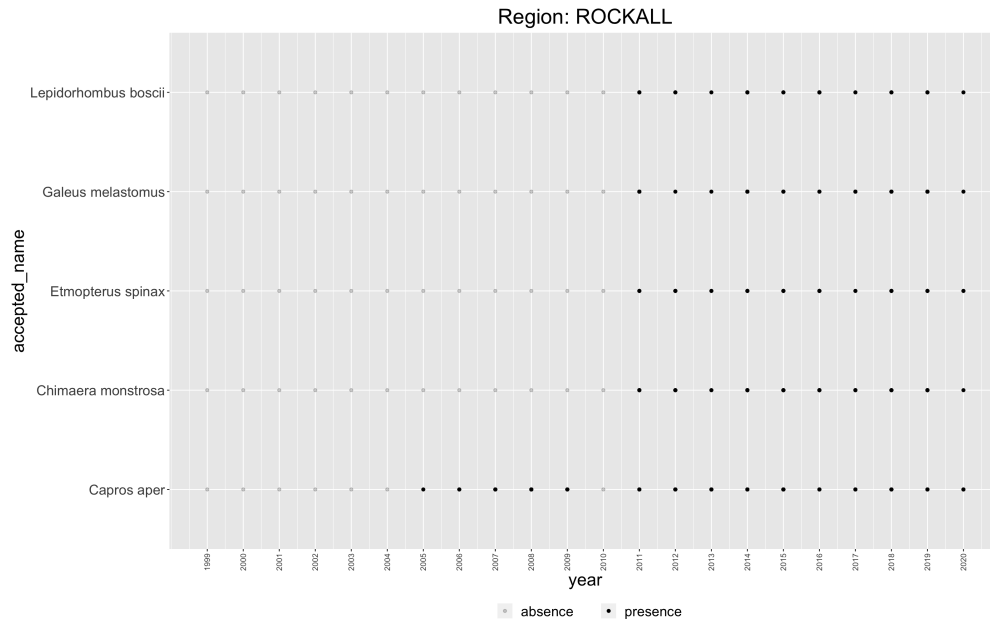
Map of the sampling distribution in space. Note that we only show one year per coordinate.



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	79.0
Percentage of species flagged	6.3

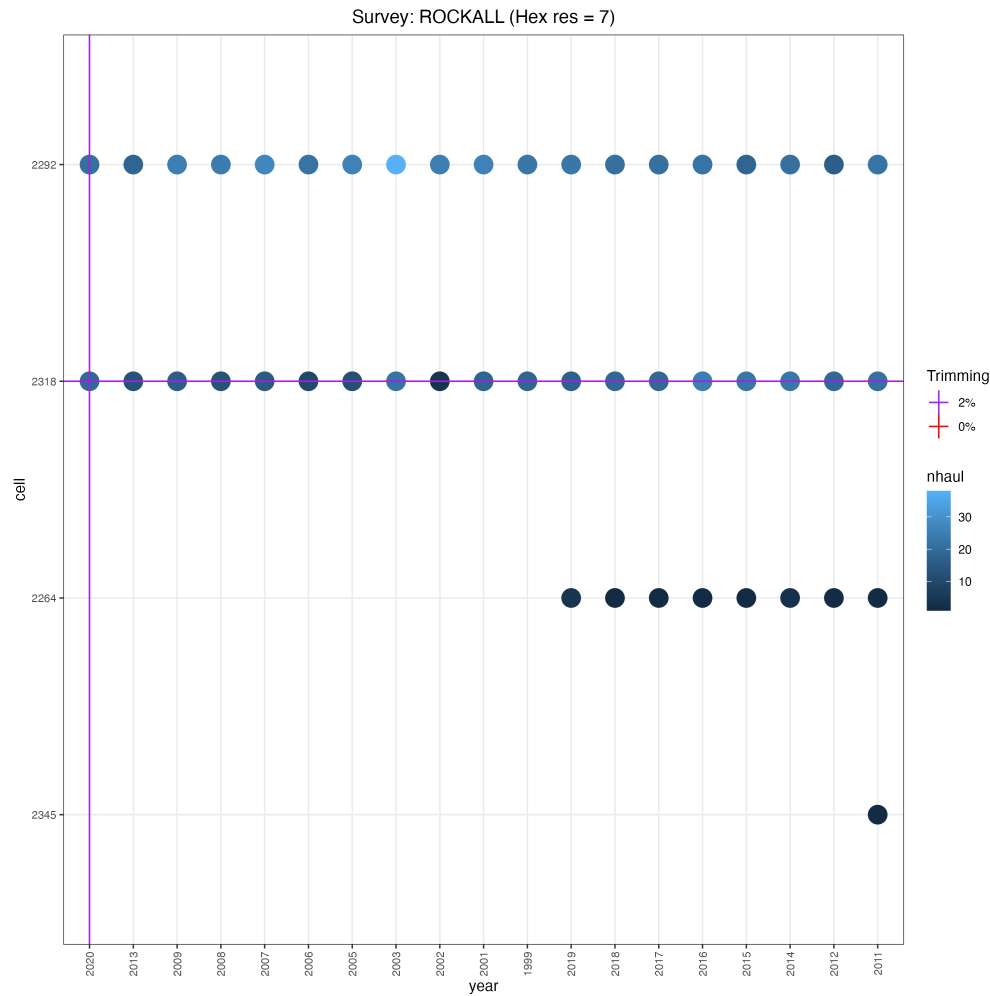
10. Spatio-temporal standardization

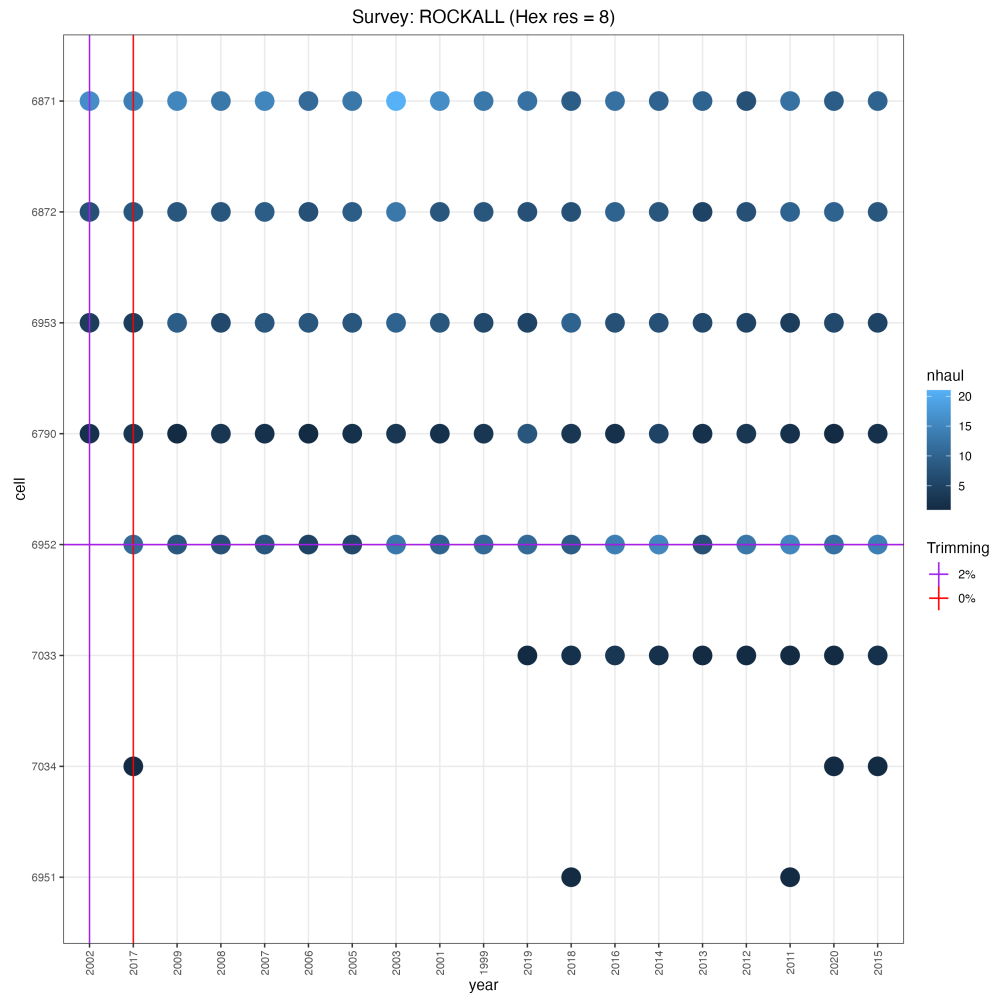
a. Standardization method 1

This standardization method was adapted from https://github.com/zoekitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd

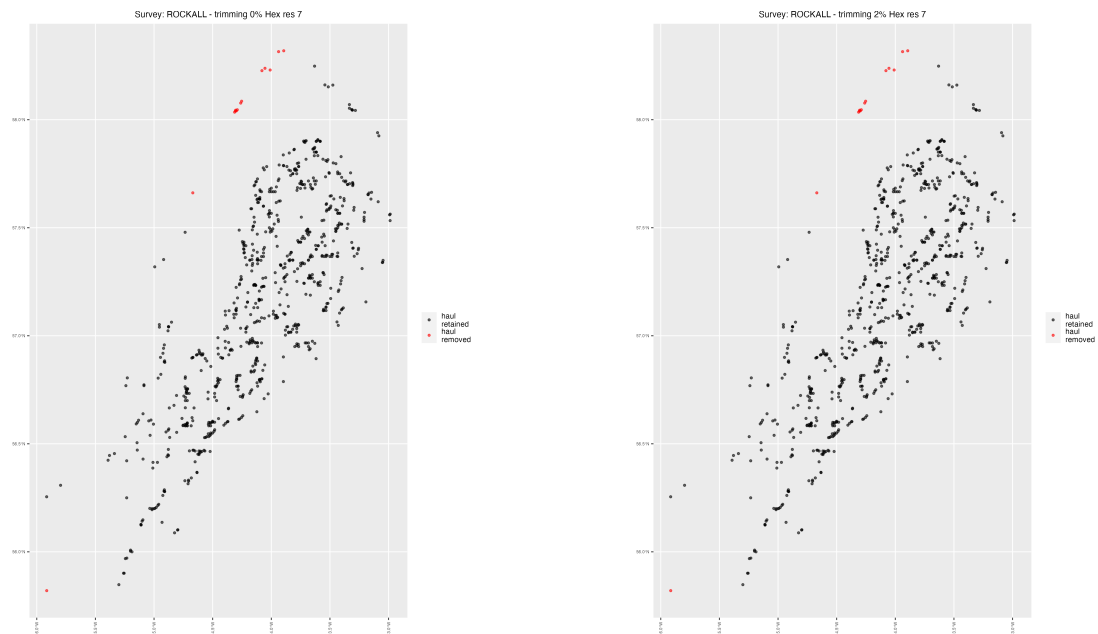
It was run for hex resolution 7 and 8.

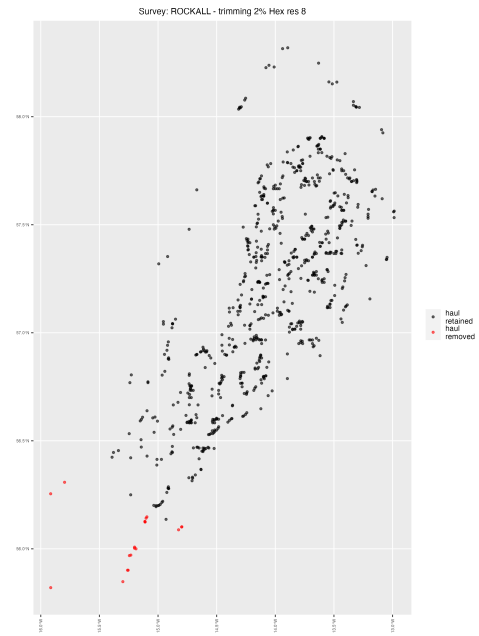
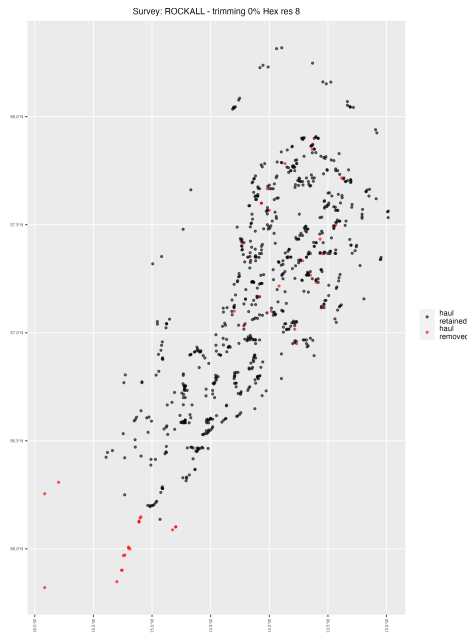
Plot of number of cells x years with overlaid flagging options



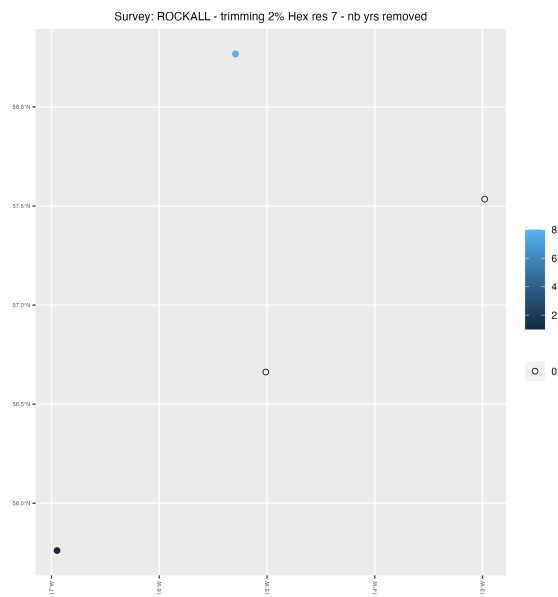
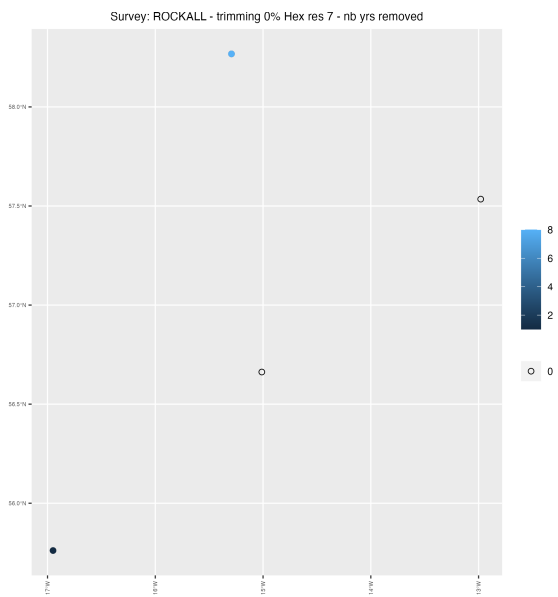


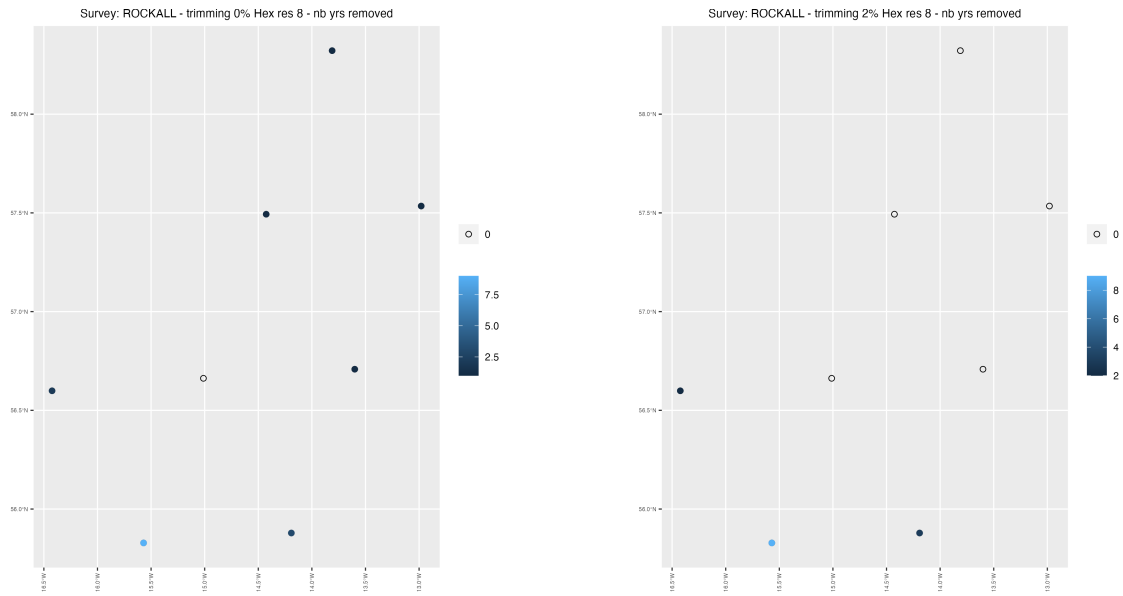
Map of hauls retained and removed per flagging method and threshold





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

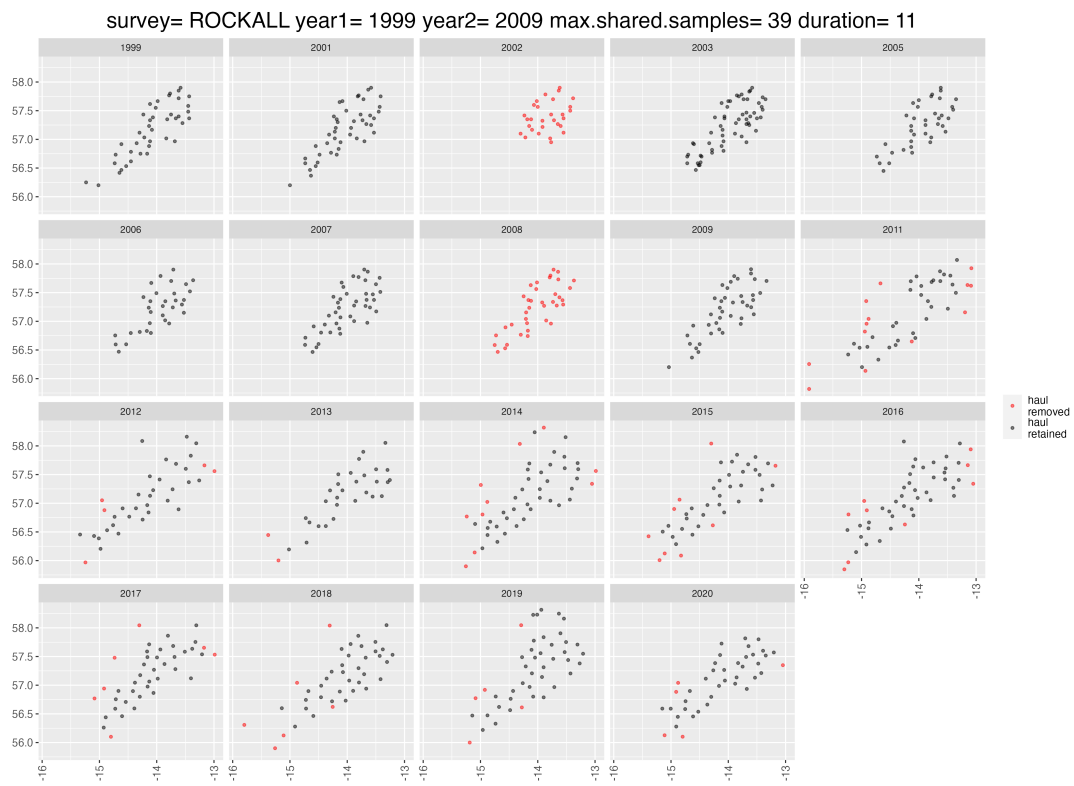




b. Standardization method 2

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	14.0	14.0	48.0	19.0	2039.0
percentage of hauls removed	1.8	1.8	6.2	2.4	18.3