PT-IBTS: Portuguese Bottom Trawl survey data processing summary

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Contents

General info

This document presents the cleaning code and summary of the Portuguese bottom trawl survey provided by DATRAS, ICES. It contains data from **2002** and up to **2018**.

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
#######################################################
rm(list=ls())

date <- "14DEC2022"

##########################################################################################
#### LOAD LIBRARIES & options to decide in the code
##########################################################################################
library(data.table)
library(tidyverse)
library(icesDatras)
```

```r
library(worrms)
library(curl)
library(urltools)
library(here) # for easy work around on multiple computers
library(taxize) # for getting correct species names
library(googledrive)

# load relevant functions
source("functions/write_clean_data.r")
source("functions/clean_taxa.R")
source("functions/get_length_weight_coeffs.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


############################################################################################
#### 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))

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

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

}

if(load_stored_datras == TRUE){

  hh.ns <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.ns.csv")
  hh.baltic <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.baltic.csv")
  hh.evhoe <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.evhoe.csv")
  hh.cgfs <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.cgfs.csv")
  hh.igfs <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.igfs.csv")
  hh.nigfs <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.nigfs.csv")
  hh.pt <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.pt.csv")
  hh.rock <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.rock.csv")
  hh.scorock <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.scorock.csv")
  hh.swc <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.swc.csv")
  hh.scowcgfs <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.scowcgfs.csv")

  hl.ns <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.ns.csv")
  hl.baltic <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.baltic.csv")
  hl.evhoe <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.evhoe.csv")
  hl.cgfs <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.cgfs.csv")
  hl.igfs <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.igfs.csv")
  hl.nigfs <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.nigfs.csv")
  hl.pt <- read.csv("E:/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("E:/fishglob data/Publicly available/DATRAS/hl.rock.csv")
  hl.scorock <- read.csv("E:/fishglob data/Publicly available/DATRAS/hl.scorock.csv")
  hl.swc <- read.csv("E:/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("E:/fishglob data/Publicly available/DATRAS/hl.scowcgfs.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)

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

  rm(hl.ns, hl.baltic, hl.evhoe, hl.cgfs, hl.igfs, hl.nigfs, hl.pt, hl.rock, hl.scorock,
     hl.swc, hl.scowcgfs,
     hh.ns, hh.baltic, hh.evhoe, hh.cgfs, hh.igfs, hh.nigfs, hh.pt, hh.rock, hh.scorock,
     hh.swc, hh.scowcgfs)
  #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 = paste0("E:/fishglob data/Publicly available/DATRAS/hh.",date,".RData"))
  save(hl, file = paste0("E:/fishglob data/Publicly available/DATRAS/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("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hl.29JUL2021.RData")
load("/Volumes/Elements/fishglob data/Publicly available/DATRAS/hh.29JUL2021.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)
```

```r
# 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]}
}

# 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.
# 70273 hauls in hh and 70273 in 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$SpecCode <- hl$Sex <- 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(1,10,4,7),
         DataType %in% c('S','R','C'))


##########################################################################################
#### 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(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)),
         # remove hauls where not all species are recorded
         !(Survey=="BITS" & BySpecRecCode==0))



##########################################################################################
#### GET THE SWEPT AREA in km2
##########################################################################################

source('cleaning.codes/source_DATRAS_wing_doorspread.R')
```

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

# Remove data without length composition or negative values
xx <- subset(survey, HLNoAtLngt<0 | is.na(LngtClass))
no_length_hauls <- sort(unique(xx$HaulID)) # 10,178 hauls without length data

# Only keep abundances/weight
survey <- survey %>%
  #filter(!(HaulID %in% no_length_hauls)) %>% # remove hauls without length data
  mutate(numcpue = TotalNo/Area.swept, # abundance/km2
         wtcpue = CatCatchWgt/(Area.swept*1000), #weight in kg/km2
         numh = (TotalNo*60)/HaulDur, # abundance/hour
         wgth = 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',
         Depth = replace(Depth, Depth<0, NA),
         SBT = replace(SBT, SBT<0, NA),
         SST = replace(SST, SST<0, NA),
         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, numcpue,
         wtcpue, numh, wgth, num, wgt, Length, 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_datras_taxa <- rbind(clean_bits, clean_cgfs, clean_evhoe, clean_ir, clean_nigfs,
                    clean_pt, clean_rock, clean_swc, clean_ns) %>%
  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(AphiaID))


##########################################################################################
#### RE-CALCULATE WEIGHTS
##########################################################################################
detach(package:worms)
detach(package:plyr)

# select only certain gears
# 1. summary of gears per survey
gears <- data.frame(survey) %>%
  group_by(Survey, Gear) %>%
  summarise(hauls = length(unique(HaulID)), years = length(unique(Year))) %>%
  select(Survey, Gear, hauls, years)

# 2. only select certain gears per survey (GOV and/or most dominant in cases without GOV)
survey <- survey %>%
  filter(!(Survey=="NS-IBTS" & Gear %in% c('ABD', 'BOT', 'DHT', 'FOT', 'GRT',
                                           'H18', 'HOB', 'HT', 'KAB', 'VIN')),
         !(Survey=="BITS" & Gear %in% c('CAM', 'CHP', 'DT', 'EGY', 'ESB', 'EXP',
                                        'FOT', 'GRT', 'H20', 'HAK', 'LBT','SON')),
         !(Survey=="PT-IBTS" & Gear=='CAR'),
         !(Survey=="Can-Mar" & Gear=='Y36'))


# 3. associate an LME to each haul and make final list of species
### Prepare list for estimating length-weight parameters
list.taxa <- survey %>%
  mutate(species = str_split(taxa, pattern = " ", simplify = TRUE)[,2]) %>%
  select(HaulID, Survey, ShootLat, ShootLong, family, genus, species) %>%
  distinct()

# get LME
library(rgdal)
shape1 <- readOGR(dsn = "length.weight/LME66",layer="LMEs66")
coords <- list.taxa %>%
  dplyr::select(ShootLat, ShootLong, Survey) %>%
  distinct()
str(coords)

coordinates(coords) <- ~ ShootLong + ShootLat
proj4string(coords) <- proj4string(shape1)
lme <- over(coords, shape1)

coords <- list.taxa %>%
  dplyr::select(ShootLat, ShootLong, Survey) %>%
  distinct()
coords <- cbind(coords, lme$LME_NUMBER)
setnames(coords, old='lme$LME_NUMBER', new='lme')

coords$lme <- as.factor(coords$lme)
#Select from each LME 50 long and lat
ind <- c()
for (i in 1:nlevels(coords$lme)){
  ind <- c(ind, sample(which(coords$lme==levels(coords$lme)[i]), 50,
                       replace = FALSE))
}
long50 <- coords$ShootLong[ind]
lat50 <- coords$ShootLat[ind]
lme50 <- rep(levels(coords$lme), each=50)
#For each haul without LME find a close LME that has an LME number already
nlme <- subset(coords, is.na(lme)) # many hauls without LME 710
nlme$ShootLat <- as.numeric(as.vector(nlme$ShootLat))
nlme$ShootLong <- as.numeric(as.vector(nlme$ShootLong))
long50 <- as.numeric(as.vector(long50))
lat50 <- as.numeric(as.vector(lat50))
```

```r
dilme <- c()
for (i in 1:length(lme50)){
  dilme <- cbind(dilme, (nlme$ShootLat-lat50[i])**2 + (nlme$ShootLong-long50[i])**2)
}
mindi <- apply(dilme, 1, which.min)
coords$lme[is.na(coords$lme)] <- lme50[mindi]
# assign the closest LME number to each haul without LME


#Check
coords$ShootLat <- as.numeric(as.vector(coords$ShootLat))
coords$ShootLong <- as.numeric(as.vector(coords$ShootLong))

# rockall not assigned to Faroe plateau but to celtic sea LME
coords$lme <- as.character(coords$lme)
coords <- coords %>%
  mutate(lme = replace(lme, Survey  =='ROCKALL', '60')) %>%
  as.data.frame()

survey <- left_join(survey, coords, by=c('ShootLat', 'ShootLong','Survey'))

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

  write.csv(data.frame(list.taxa), file="length.weight/taxa.DATRAS.FB.tofill.csv",
            row.names=FALSE)
  save.image("length.weight/DATRAS_before_lw_4AUG2021.RData")

  ### run length-weight relationships open R 32bit
  list.taxa <- read.csv("length.weight/taxa.DATRAS.FB.tofill.csv")
  get_coeffs(list.taxa, survey="DATRAS", save=TRUE)
}


# 4. re-calculate weights with length-weight relationships
#load("length.weight/DATRAS_before_lw_4AUG2021.RData")
datalw <- read.csv('length.weight/length.weight_DATRAS.csv') %>%
  rename(Survey = survey) %>%
  select(-X) %>%
  mutate(lme = as.character(lme))

survey <- survey %>%
  filter(rank!="Suborder")

# summarize abundance/weight at the haul level
survey.num <- left_join(survey, datalw, by=c("taxa","family","genus","lme",
                                             "rank","Survey")) %>%
  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,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","lme",
                                             "rank","Survey")) %>%
  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,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","lme",
                                          "rank","Survey")) %>%
  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'))

library(ggplot2)
```

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

# check weights
xx <- subset(survey3, wtcpue   >0 & wgtlencpue>0)
cor(x = xx$wtcpue , y = xx$wgtlencpue, method = 'pearson')

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

### cor = 0.92 and 0.90 so something does not work.

###########################################################################################
# CHECK PER SURVEY
###########################################################################################

# 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()
```

```r
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]

# 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 & 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 & 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"),
         num = numlencpue*area_swept,
         num_h = numlenh,
         num_cpue = numlencpue,
         wgt = wgtlencpue*area_swept,
         wgt_h = wgtlenh,
         wgt_cpue = wgtlencpue,
         haul_dur = haul_dur/60,
         source = "DATRAS ICES",
         timestamp = "2021-07") %>%
  # Final format
  select(fishglob_data_columns$`Column name fishglob`)



##########################################################################################
# Save database in Google drive
##########################################################################################

# Just run this routine should be good for all
write_clean_data(data = survey4, survey = "DATRAS_v3", overwrite = T)
```

1. Overview of the survey data table

survey	source	timestamp	haul_id	country	sub_area	continent	sta
PT-IBTS	DATRAS ICES	2021-07	PT-IBTS 2002 4 PT 68NA NCT 11 13	portugal	NA	europe	1
PT-IBTS	DATRAS ICES	2021-07	PT-IBTS 2002 4 PT 68NA NCT 11 13	portugal	NA	europe	1
PT-IBTS	DATRAS ICES	2021-07	PT-IBTS 2002 4 PT 68NA NCT 11 13	portugal	NA	europe	1
PT-IBTS	DATRAS ICES	2021-07	PT-IBTS 2002 4 PT 68NA NCT 11 13	portugal	NA	europe	1
PT-IBTS	DATRAS ICES	2021-07	PT-IBTS 2002 4 PT 68NA NCT 11 13	portugal	NA	europe	11

station	stratum	year	month	day	quarter	season
NA	NA	2002	10	NA	4	NA
NA	NA	2002	10	NA	4	NA
NA	NA	2002	10	NA	4	NA
NA	NA	2002	10	NA	4	NA
NA	NA	2002	10	NA	4	NA

latitude	longitude	haul_dur	area_swept	gear	depth
41.0633	-9.1899	0.5	0.0398653	NCT	145
41.0633	-9.1899	0.5	0.0398653	NCT	145
41.0633	-9.1899	0.5	0.0398653	NCT	145
41.0633	-9.1899	0.5	0.0398653	NCT	145
41.0633	-9.1899	0.5	0.0398653	NCT	145

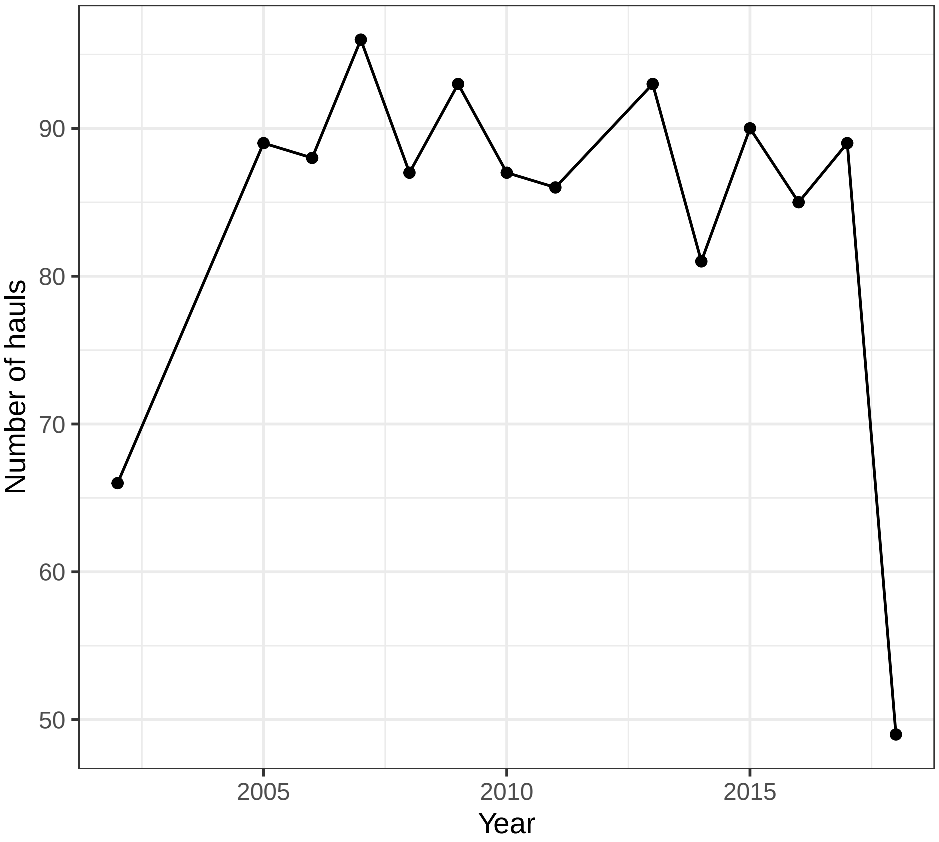
sbt	sst	num	num_h	num_cpue	wgt
NA	18.7	10.0	20	250.84454	0.0787882
NA	18.7	5.0	10	125.42227	0.1196638
NA	18.7	3.0	6	75.25336	0.2333192
NA	18.7	5834.5	11669	146355.24706	185.7344052
NA	18.7	6.0	12	150.50672	0.7176742

wgt_h	wgt_cpue	verbatim_name	verbatim_aphia_id	accepted_name
0.1575763	1.976358	NA	127419	Capros aper
0.2393275	3.001700	NA	126222	Macroramphosus
0.4666383	5.852684	NA	126421	Sardina pilchardus
371.4688104	4659.046150	NA	126439	Micromesistius poutassou
1.4353483	18.002465	NA	126445	Trisopterus luscus

aphia_id	SpecCode	kingdom	phylum	class	order	family
127419	54	Animalia	Chordata	Actinopteri	Acanthuriformes	Caproidae
126222	NA	Animalia	Chordata	Actinopteri	Syngnathiformes	Centriscidae
126421	1350	Animalia	Chordata	Actinopteri	Clupeiformes	Clupeidae
126439	31	Animalia	Chordata	Actinopteri	Gadiformes	Gadidae
126445	1367	Animalia	Chordata	Actinopteri	Gadiformes	Gadidae

2. Summary of sampling intensity

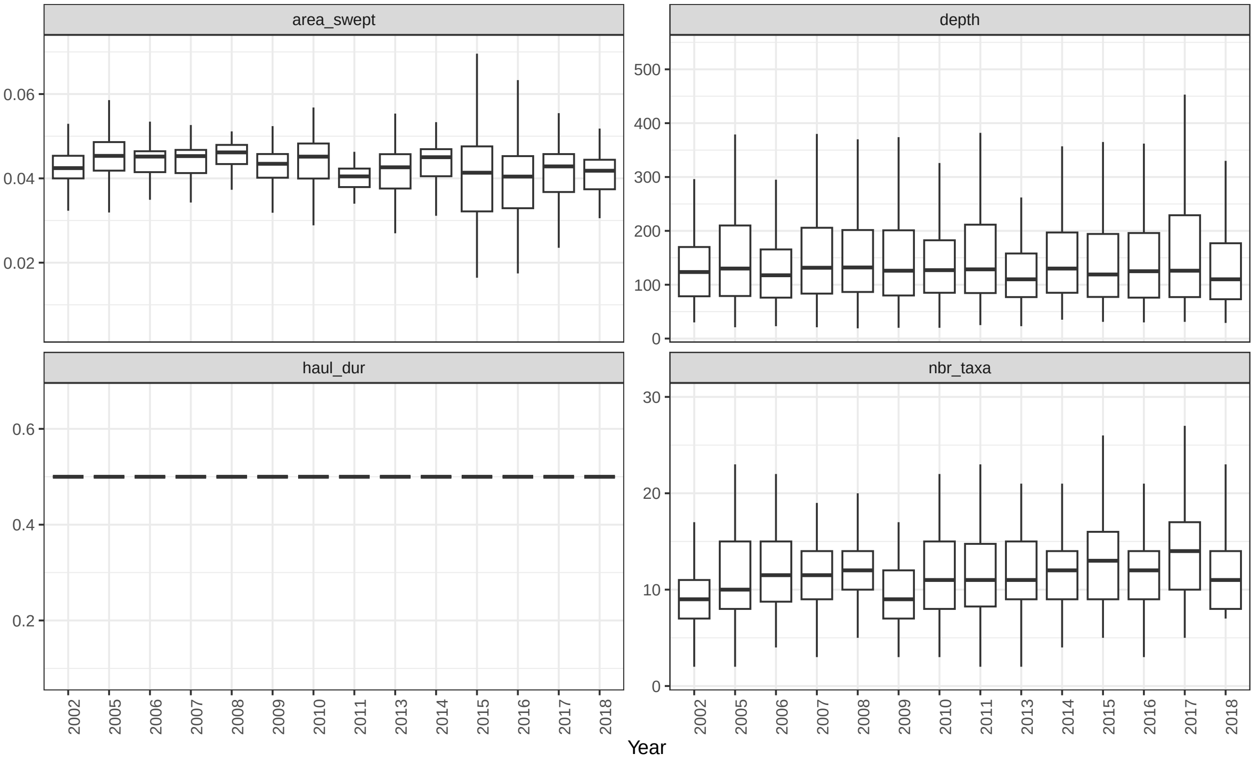
Number of hauls per year performed during the survey after data processing.



3. Summary of sampling variables from the survey

Here we show the yearly total and average of the following variables reported in the survey data:

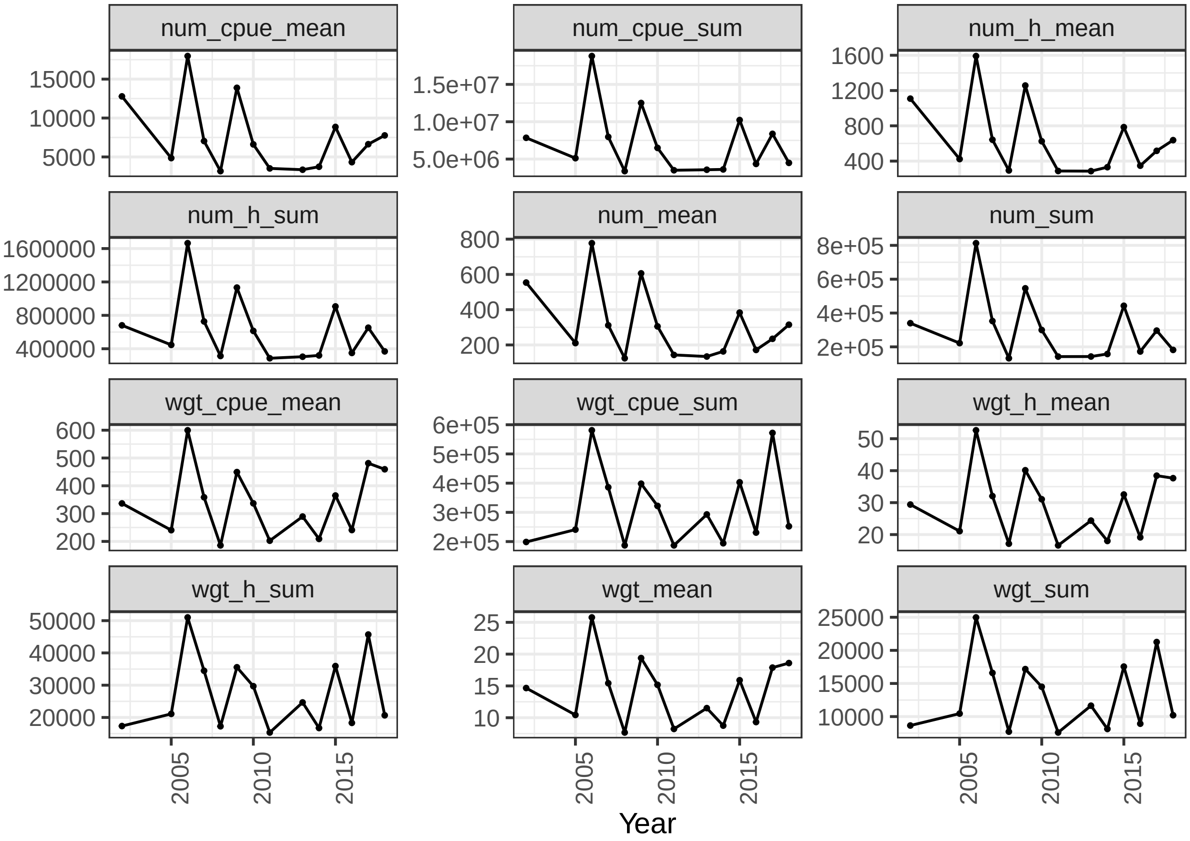
- *area_swept*, swept area by the bottom trawl gear km^2
- *depth*, sampling depth in m
- *haul_dur*, haul sampling duration $hours$
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (https://www.marinespecies.org/, October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



4. Summary of biological variables

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

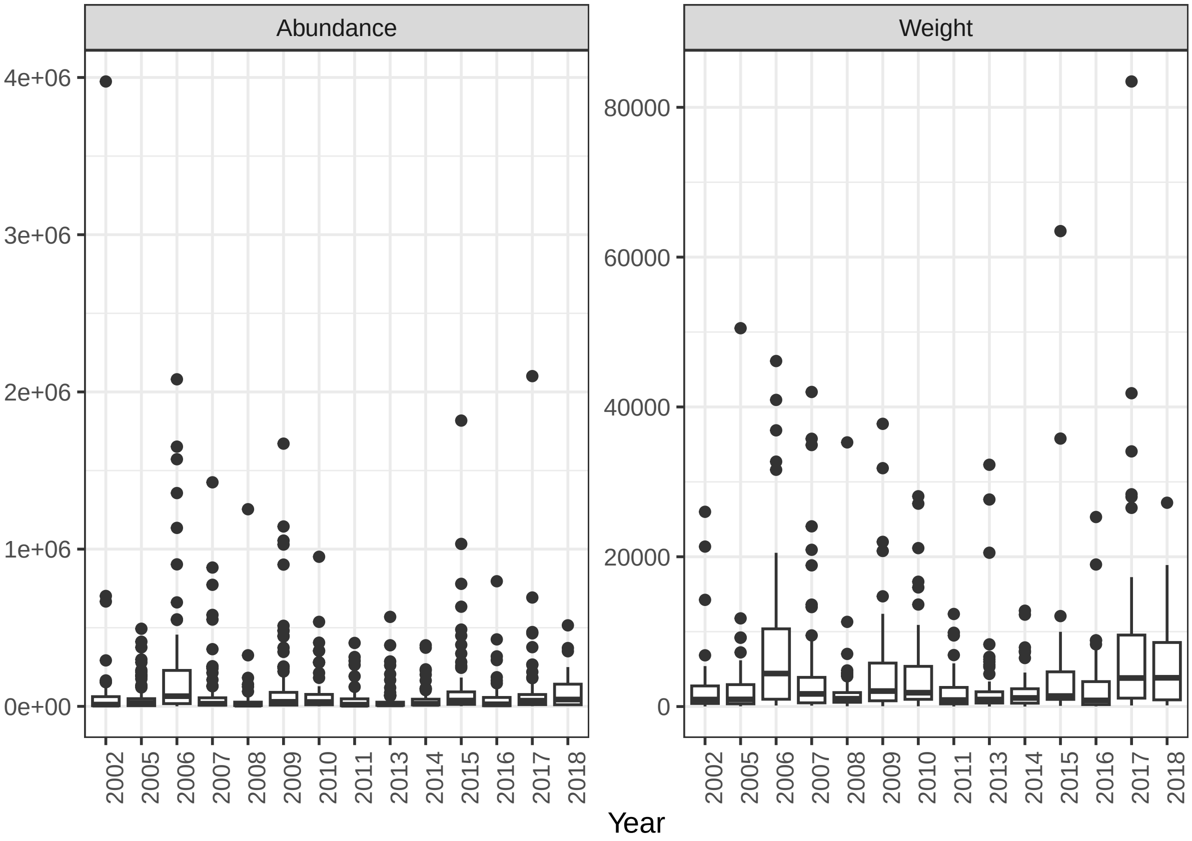
- *num_cpue*, number of individuals (abundance) in $\frac{individuals}{km^2}$
- *num_h*, number of individuals (abundance) in $\frac{individuals}{h}$
- *num*, number of individuals (abundance)
- *wgt_cpue*, weight in $\frac{kg}{km^2}$
- *wgt_h*, weight in $\frac{kg}{h}$
- *wgt*, weight in kg



5. Extreme values

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

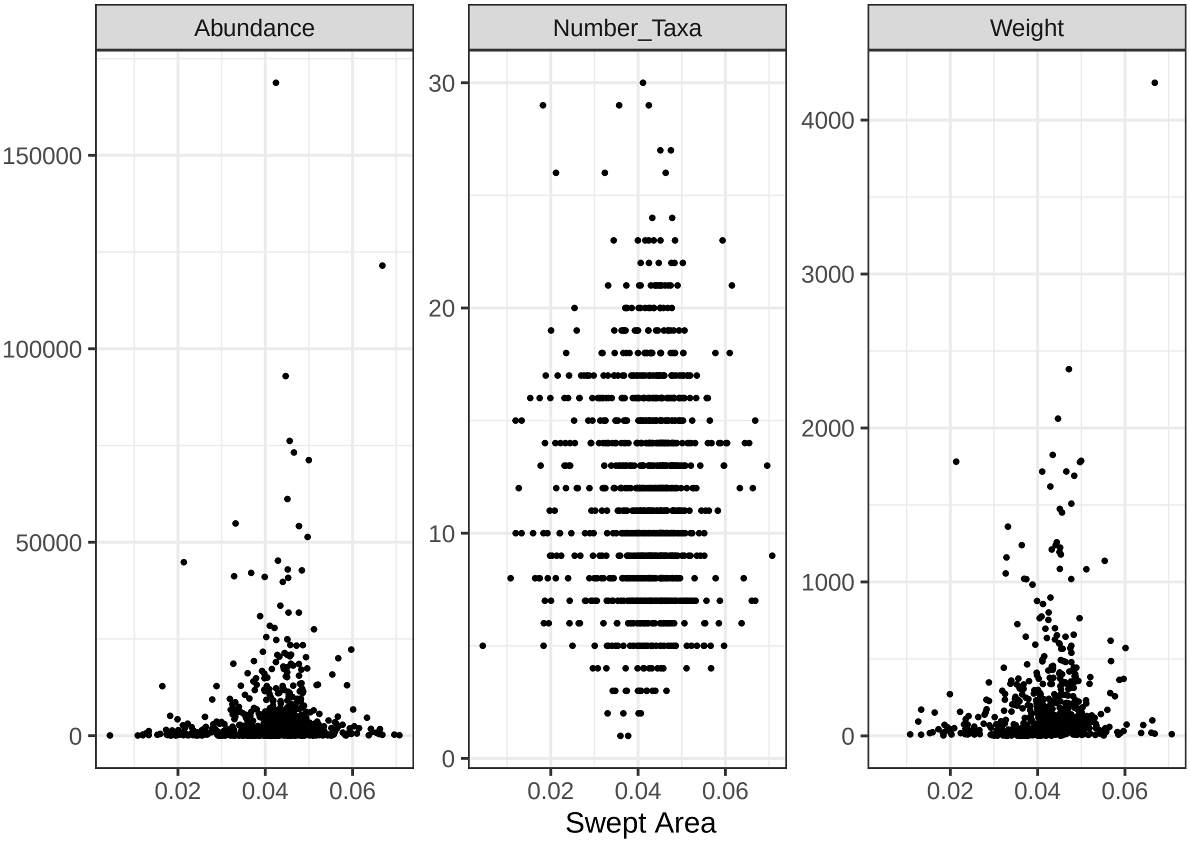
- *wgt*, total weight in *kg* per haul and year per haul and year, if available in the survey data
- *num*, total number of individuals, if available in the survey data



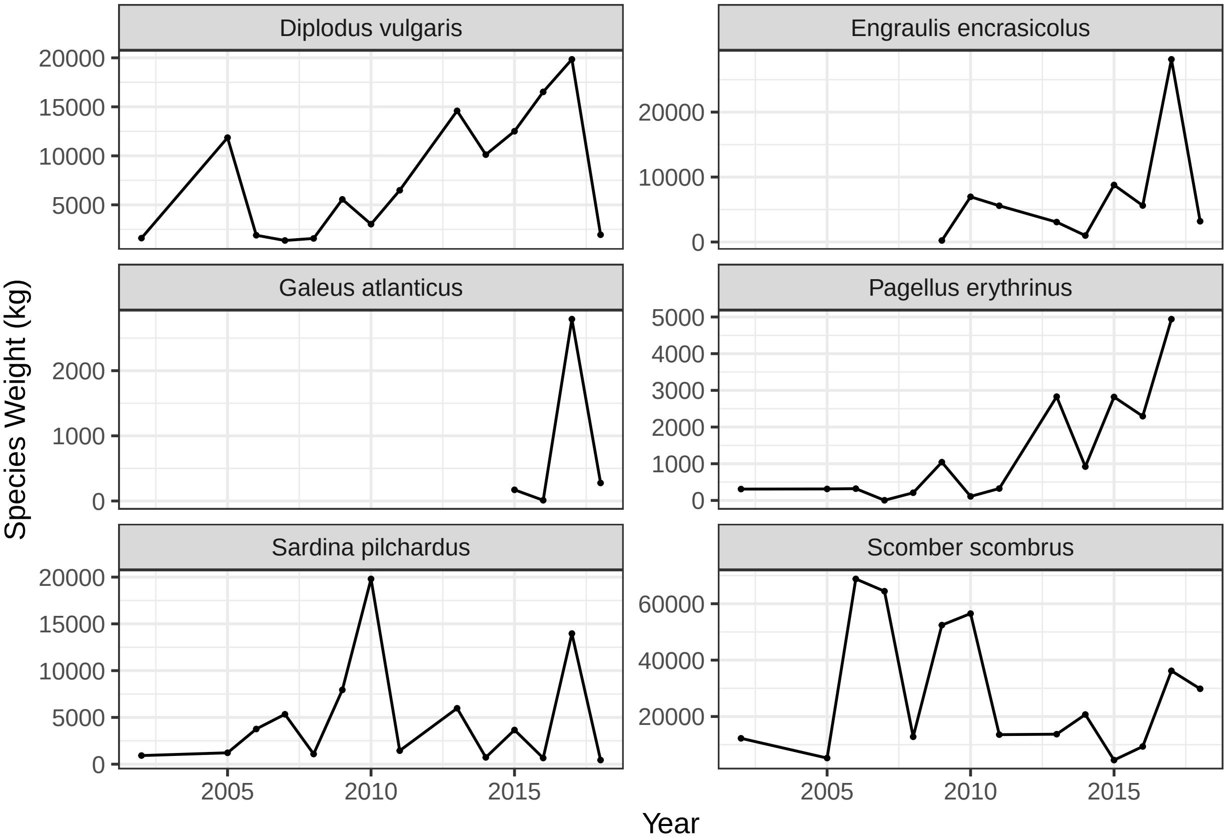
6. Summary of variables against swept area

Here we show the total abundance and number of taxa relationships with the area swept:

- *nbr_taxa*, number of marine fish taxa after taxonomic data cleaning
- *num*, number of individuals, if available in the survey data
- *wgt*, weight in *kg*, if available in the survey data

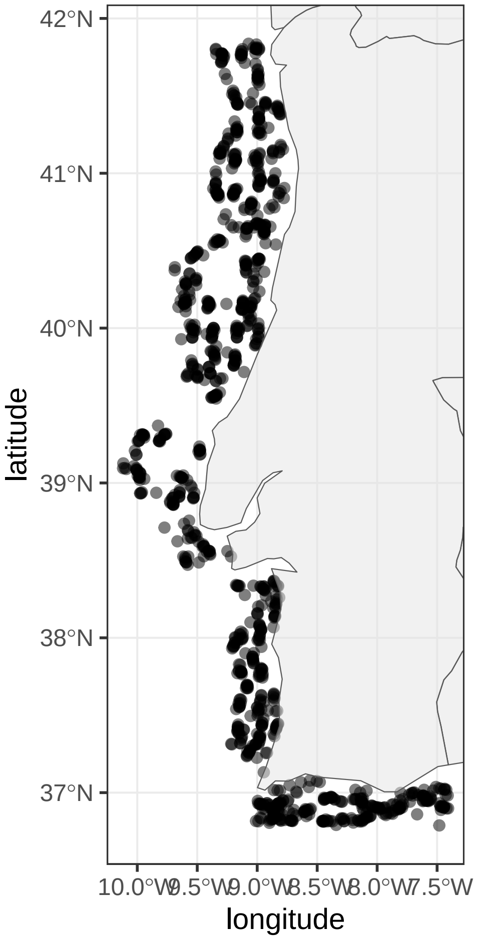


7. Abundance or Weight trends of the six most abundant species



8. Distribution mapping

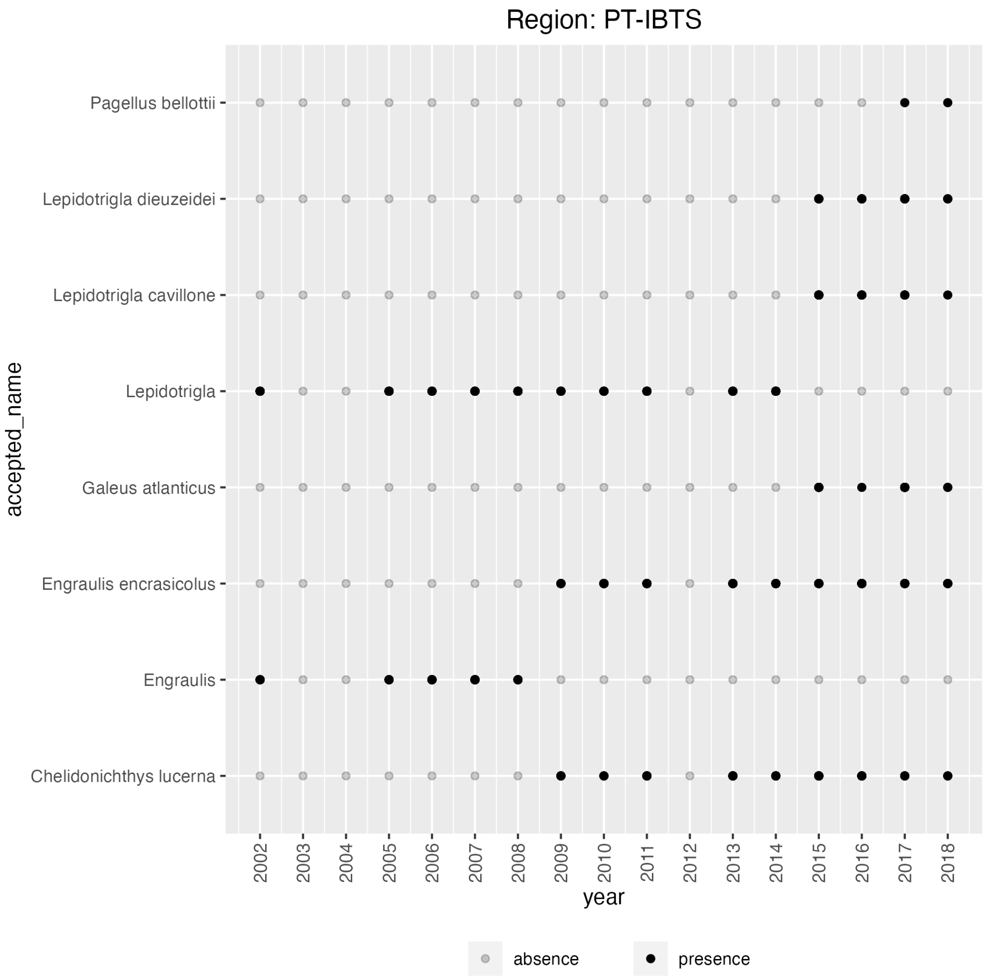
Map of the sampling distribution in space. Note that we only show one year per coordinate.



9. Taxonomic flagging

This species flagging method was adapted from https://github.com/pinskylab/OceanAdapt/blob/master/R/add-spp-to-taxonomy.Rmd#L33

Visualization of flagged taxa



Statistics related to the taxonomic flagging outputs

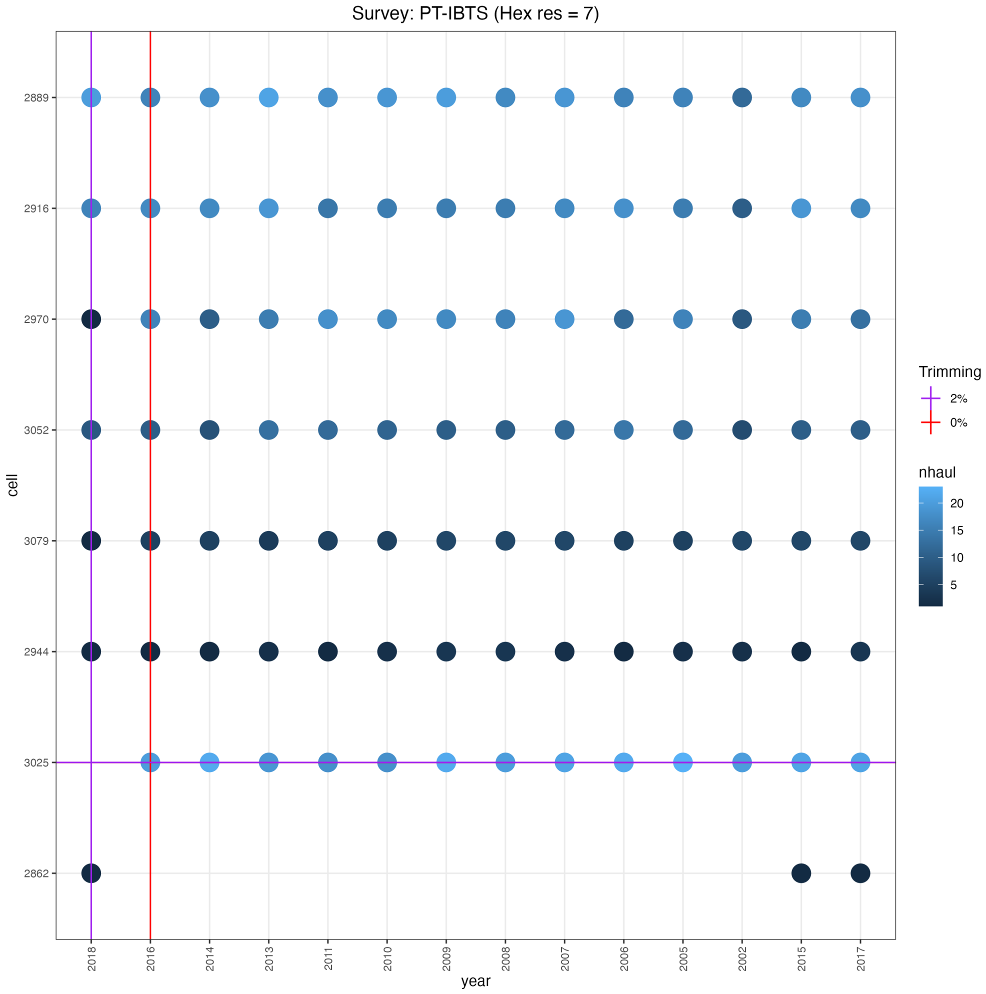
Total number of species	191.0
Percentage of species flagged	4.2

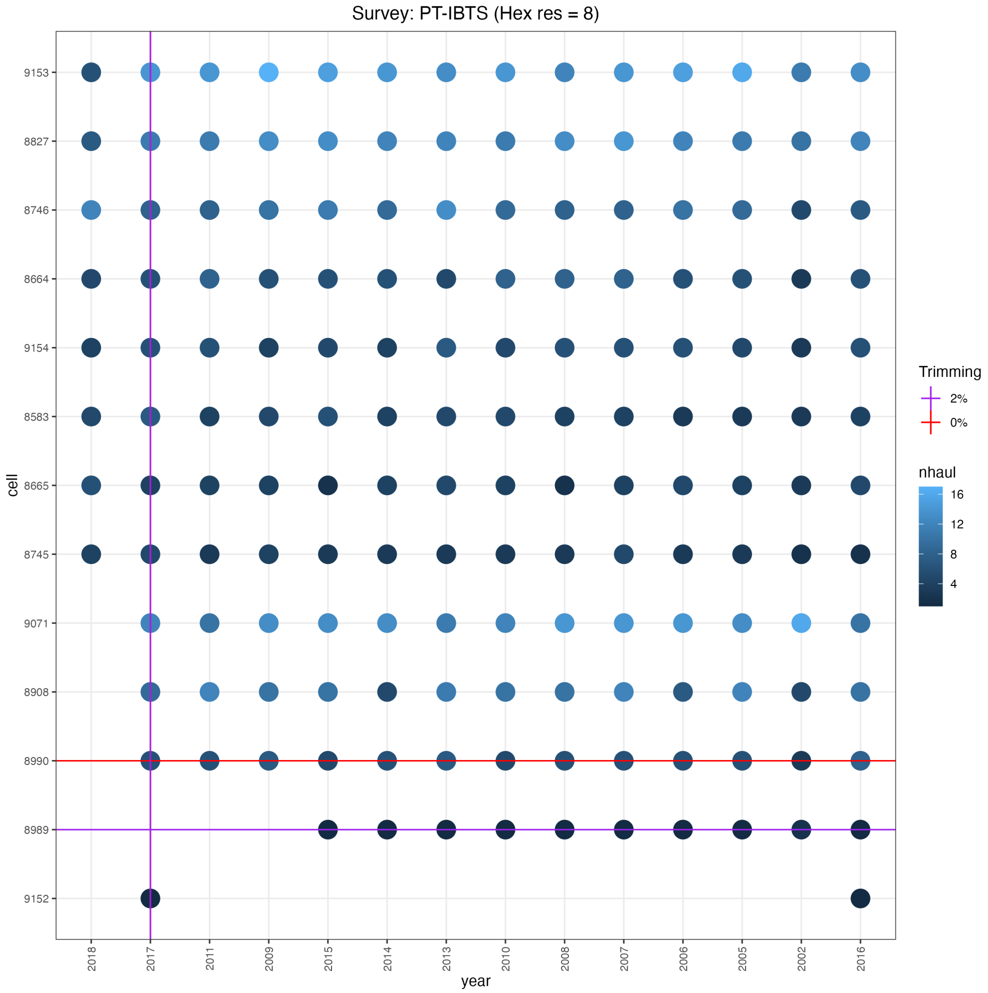
10. Spatio-temporal standardization

a. Standardization method 1

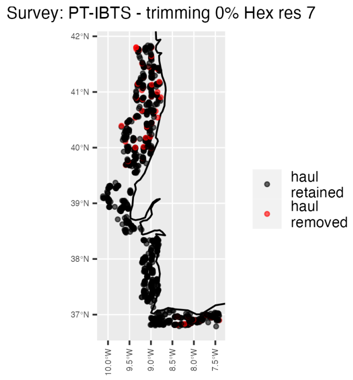
This standardization method was adapted from https://github.com/zoekitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd
It was run for hex resolution 7 and 8.

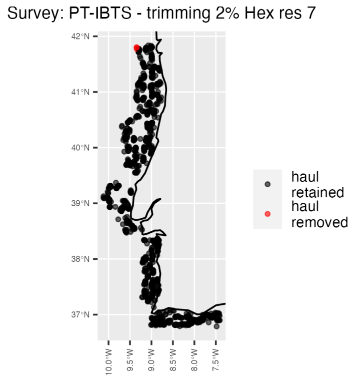
Plot of number of cells x years with overlaid flagging options

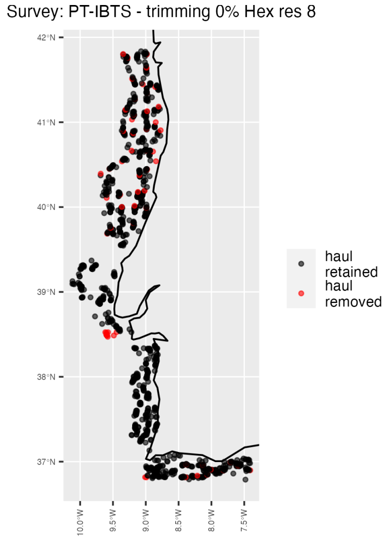

Survey: PT-IBTS (Hex res = 7)
cell
2889
2916
2970
3052
3079
2944
3025
2862
year
2018
2016
2014
2013
2011
2010
2009
2008
2007
2006
2005
2002
2015
2017
Trimming
2%
0%
nhaul
20
15
10
5

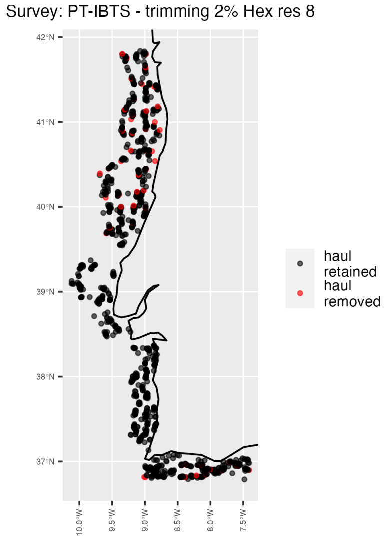


Map of hauls retained and removed per flagging method and threshold

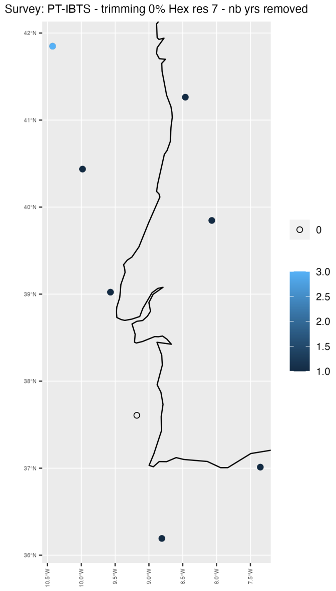


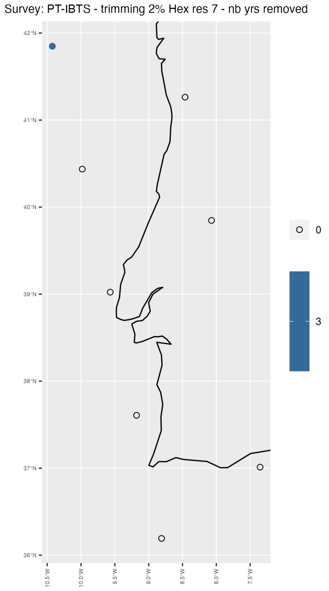


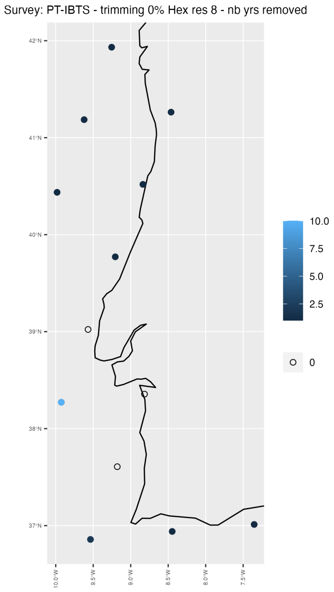

Survey: PT-IBTS - trimming 0% Hex res 8

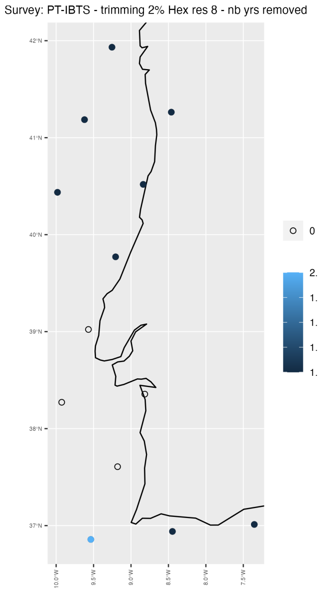

Survey: PT-IBTS - trimming 2% Hex res 8

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


Survey: PT-IBTS - trimming 0% Hex res 7 - nb yrs removed


Survey: PT-IBTS - trimming 2% Hex res 7 - nb yrs removed

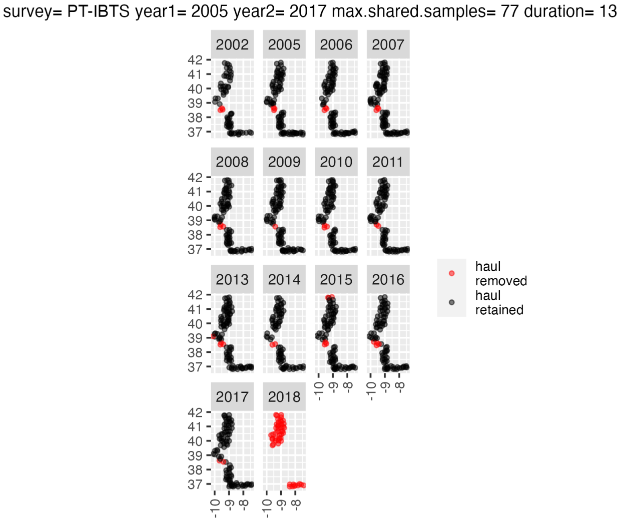




b. Standardization method 2

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	51.0	3.0	62.0	51.0	1082.0
percentage of hauls removed	4.3	0.3	5.3	4.3	7.8