

# NEUS: Northeast US survey data processing summary

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## General info

This document presents the cleaning code and summary of the Northeast US bottom trawl survey provided by Sean Lucey sean.lucey@noaa.gov. It contains data from 1963 and up to 2020.

## Data cleaning in R

```
#####
##### R code to clean trawl survey Northeast US (Fall and Spring)
##### Public data Ocean Adapt
##### Contacts: Sean Lucey sean.lucey@noaa.gov Fisheries Biologist,
##### Northeast Fisheries Science Center, NOAA
##### Coding: Michelle Stuart, Dan Forrest, Zoë Kitchel November 2021
#####

#NB: Note that there was a gear and vessel swap in 2008-2009 (Albatross to Bigelow)
#this code uses conversions from NEFSC to correct data post 2009 to pre 2009
#abundance and biomass
#Sampling was based on a stratified random design using area and depth zones.
#Standard tows from 1963-2008 were 30 minutes in duration. Initially, the towing
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#speed was set to approximately 3.5 knots, but in 1996, it was discovered that the
#speedlog was not working and to go
#3.5 knots by the speedlog required a speed of 3.8 knots on the Doppler. Therefore,
#speed was then changed to 3.8 knots
#for the rest of the time series. Tow direction was towards the next station unless
#wind and sea state dictated a different
#course. For tows in depths >= 183 m, a more specific depth is randomly chosen among
#four depth intervals and then
#trawling was done along that depth contour. In 2009, the tows were reduced to 20
#minutes in duration and speed was
#reduced to 3.0 knots. The direction of the tows changed to follow the depth contour.

#NB: haul_dur is raw, does not account for conversions in abundance and biomass,
#and therefore should not be used
#as the denominator for CPUE calculations without careful consideration, therefore,
#wgt_cpue, wgt_h, num_cpue, and num_h are not calculated

#Helpful documents discussing gear and vessel transition for Northeast US
#https://www.nafo.int/Portals/0/PDFs/sc/2014/scr14-024.pdf
#http://ices.dk/sites/pub/CM%20Documents/CM-2007/Q/Q2007.pdf
#https://repository.library.noaa.gov/view/noaa/3726

#-----#
##### LOAD LIBRARIES AND FUNCTIONS #####
#-----#


library(rfishbase) #needs R 4.0 or more recent
library(tidyverse)
library(lubridate)
library(googledrive)
library(taxize) # for getting correct species names
library(magrittr) # for names wrangling
library(data.table)
library(readxl)

source("functions/clean_taxa.R")
source("functions/write_clean_data.R")
source("functions/apply_trimming_method1.R")
source("functions/apply_trimming_method2.R")
source("functions/flag_spp.R")
fishglob_data_columns <- read_excel("standard_formats/fishglob_data_columns.xlsx")
#Data for the NEUS can be best accessed using the Pinsky Lab Ocean Adapt
#Public Git Hub Repository.

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


#load conversion factors to bridge Albatross (vessel before 2008)
#data with Bigelow Data (vessel after)
NEFSC_conv <- read_csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/NEFSC_conversion_factors.csv",

```

```

col_types = "_dddddd")
NEFSC_conv <- data.table::as.data.table(NEFSC_conv)
#Bigelow >2008 Vessel Conversion
#Use Bigelow conversions for Pisces as well (PC)
#Tables 56-58 from Miller et al. 2010 Biomass estimators
big_fall <- data.table::data.table(svspp =
  c('012', '022', '024', '027', '028',
    '031', '033', '034', '073', '076',
    '106', '107', '109', '121', '135',
    '136', '141', '143', '145', '149',
    '155', '164', '171', '181', '193',
    '197', '502', '512', '015', '023', '026',
    '032', '072', '074', '077', '078',
    '102', '103', '104', '105', '108',
    '131', '163', '301', '313', '401',
    '503'),
  season = c(rep('fall', 47)),
  rhoW = c(
    1.082, 3.661, 6.189, 4.45, 3.626, 1.403, 1.1, 2.12,
    1.58, 2.088, 2.086, 3.257, 12.199, 0.868, 0.665, 1.125,
    2.827, 1.347, 1.994, 1.535, 1.191, 1.354, 3.259, 0.22,
    3.912, 8.062, 1.409, 2.075, 1.21,
    2.174, 8.814, 1.95, 4.349, 1.489, 3, 2.405, 1.692,
    2.141, 2.151, 2.402, 1.901, 1.808, 2.771, 1.375, 2.479,
    3.151, 1.186))

big_spring <- data.table::data.table(svspp = c(
  '012', '022', '024', '027', '028',
  '031', '033', '034', '073', '076',
  '106', '107', '109', '121', '135',
  '136', '141', '143', '145', '149',
  '155', '164', '171', '181', '193',
  '197', '502', '512', '015', '023',
  '026', '032', '072', '074', '077',
  '078', '102', '103', '104', '105',
  '108', '131', '163', '301', '313',
  '401', '503'),
  season = c(rep('spring', 47)),
  rhoW = c(
    1.082, 3.661, 6.189, 4.45, 3.626, 1.403, 1.1, 2.12,
    1.58, 2.088, 2.086, 3.257, 12.199, 0.868, 0.665, 1.125,
    2.827, 1.347, 1.994, 1.535, 1.191, 1.354, 3.259, 0.22,
    3.912, 8.062, 1.409, 2.075, 1.166, 3.718, 2.786, 5.394,
    4.591, 0.878, 3.712, 3.483, 2.092, 3.066, 3.05, 2.244,
    3.069, 2.356, 2.986, 1.272, 3.864, 1.85, 2.861))

#read strata file
neus_strata <- read.csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/neus_strata.csv")

neus_strata <- neus_strata %>%
  select(stratum, stratum_area) %>%

```

```

    mutate(stratum = as.double(stratum)) %>%
    distinct()

#read and clean spp file
neus_spp_raw <- read_lines(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/neus_spp.csv")
neus_spp_raw <- str_replace_all(neus_spp_raw,
  'SQUID, CUTTLEFISH, AND OCTOPOD UNCL',
  'Squid/Cuttlefish/Octopod (unclear)')
neus_spp_raw <- str_replace_all(neus_spp_raw,
  'SEA STAR, BRITTLE STAR, AND BASKETSTAR UNCL',
  'Sea Star/Brittle Star/Basket Star (unclear)')
neus_spp_raw <- str_replace_all(neus_spp_raw,
  'MOON SNAIL, SHARK EYE, AND BABY-EAR UNCL',
  'Moon Snail/shark eye/baby-ear (unclear)')
neus_spp_clean <- str_replace_all(neus_spp_raw, 'SHRIMP \\(PINK,BROWN,WHITE\\)',
  'Shrimp \\(pink/brown/white\\)')
write_lines(neus_spp_clean, "neus_spp_clean.txt")
neus_spp <- read_csv("neus_spp_clean.txt", col_types = cols(.default = col_character()))
rm(neus_spp_clean, neus_spp_raw)
file.remove("neus_spp_clean.txt")

#NEUS Fall
neus_catch_raw <- read_lines(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/neus_fall_svcat.csv")
# remove comma
neus_catch_raw <- str_replace_all(
  neus_catch_raw, 'SQUID, CUTTLEFISH, AND OCTOPOD UNCL',
  'Squid/Cuttlefish/Octopod (unclear)')
neus_catch_raw <- str_replace_all(
  neus_catch_raw, 'SEA STAR, BRITTLE STAR, AND BASKETSTAR UNCL',
  'Sea Star/Brittle Star/Basket Star (unclear)')
neus_catch_raw <- str_replace_all(
  neus_catch_raw, 'MOON SNAIL, SHARK EYE, AND BABY-EAR UNCL',
  'Moon Snail/shark eye/baby-ear (unclear)')
neus_catch_raw <- str_replace_all(
  neus_catch_raw, 'MOON SNAIL, SHARK EYE, AND BABY-EAR UNCL',
  'Moon Snail/shark eye/baby-ear (unclear)')
neus_catch_clean <- str_replace_all(
  neus_catch_raw, 'SHRIMP \\(PINK,BROWN,WHITE\\)',
  'Shrimp \\(pink/brown/white\\)')
write_lines(neus_catch_clean, file = "neus_catch_clean.txt")
neus_fall_catch <- read_csv("neus_catch_clean.txt",
  col_types = cols(.default = col_character()))
file.remove("neus_catch_clean.txt")

neus_fall_haul <- read_csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/neus_fall_svsta.csv",
  col_types = cols(.default = col_character()))

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

```

```

#-----#
neus_fall <- left_join(neus_fall_catch, neus_fall_haul,
                         by = c("ID", "STATION", "CRUISE6", "STRATUM", "TOW"))
neus_fall <- left_join(neus_fall, neus_spp, by = "SVSPP")

neus_fall <- neus_fall %>%
  rename(year = EST_YEAR,
         month = EST_MONTH,
         day = EST_DAY,
         latitude = DECDEG_BEGLAT,
         longitude = DECDEG_BEGLON,
         depth = AVGDEPTH,
         stratum = STRATUM,
         haul_id = ID,
         verbatim_name = SCINAME,
         #Expanded biomass of a species caught at a given station.
         wgt = EXPCATCHWT,
         #Expanded number of individuals of a species caught at a given station.
         num = EXPCATCHNUM,
         station = STATION,
         sst = SURFTEMP,
         sbt = BOTTEMP,
         gear = SVGEAR)

neus_fall <- neus_fall %>%
  mutate(stratum = as.double(stratum),
         latitude = as.double(latitude),
         longitude = as.double(longitude),
         depth = as.double(depth),
         wgt = as.double(wgt),
         num = as.double(num),
         year = as.double(year),
         haul_dur = as.numeric(TOWDUR)/60, #convert minutes to hours
         quarter = case_when(month %in% c(1,2,3) ~ 1,
                             month %in% c(4,5,6) ~ 2,
                             month %in% c(7,8,9) ~ 3,
                             month %in% c(10,11,12) ~ 4),
         season = "Fall",
         SVSPP = as.double(SVSPP)
  )

#apply fall conversion factors
setDT(neus_fall)

dcf.spp <- NEFSC_conv[DCF_WT > 0, SVSPP]

#test for changes due to conversion with "before" and "after"
#before <- neus_fall[year < 1985 & SVSPP %in% dcf.spp,
#. (mean_wtcpue=mean(wtcpue)), by=SVSPP][order(SVSPP)]

for(i in 1:length(dcf.spp)){
  neus_fall[year < 1985 & SVSPP == dcf.spp[i], wgt := wgt * NEFSC_conv[

```

```

    SVSPP == dcf.spp[i], DCF_WT]]
}

#after <- neus_fall[year < 1985 & SVSPP %in% dcf.spp,
#. (mean_wtcpue=mean(wtcpue)), by=SVSPP][order(SVSPP)]

#before <- neus_fall[SVVESSEL == 'DE' & SVSPP %in% vcf.spp,
#. (mean_wtcpue=mean(wtcpue)), by=SVSPP][order(SVSPP)]

vcf.spp <- NEFSC_conv[VCF_WT > 0, SVSPP]
for(i in 1:length(dcf.spp)){
  neus_fall[SVVESSEL == 'DE' & SVSPP == vcf.spp[i], wgt := wgt * NEFSC_conv[
    SVSPP == vcf.spp[i], VCF_WT]]
}

#after<- neus_fall[SVVESSEL == 'DE' & SVSPP %in% vcf.spp,
#. (mean_wtcpue=mean(wtcpue)), by=SVSPP][order(SVSPP)]

spp_fall <- big_fall[season == 'fall', svsp]

#before <- neus_fall[SVVESSEL %in% c('HB', 'PC') & SVSPP %in% spp_fall,
#. (mean_wtcpue=mean(wtcpue)), by=SVSPP][order(SVSPP)]

for(i in 1:length(big_fall$svsp)){
  neus_fall[
    SVVESSEL %in% c('HB', 'PC') & SVSPP == spp_fall[i], wgt := wgt / big_fall[i, rhoW]]
}

#after <- neus_fall[SVVESSEL %in% c('HB', 'PC') & SVSPP %in% spp_fall,
#. (mean_wtcpue=mean(wtcpue)), by=SVSPP][order(SVSPP)]

neus_fall <- as.data.frame(neus_fall)

# sum different sexes of same spp together
neus_fall <- neus_fall %>%
  group_by(year, latitude, longitude, depth, haul_id, CRUISE6, station,
           stratum, verbatim_name, gear, haul_dur) %>%
  mutate(wgt = sum(wgt)) %>%
  ungroup()

#join with strata
neus_fall <- left_join(neus_fall, neus_strata, by = "stratum")
neus_fall <- filter(neus_fall, !is.na(stratum_area))
neus_fall <- neus_fall %>%
  rename(stratumarea = stratum_area) %>%
  #convert square nautical miles to square kilometers
  mutate(stratumarea = as.double(stratumarea)* 3.429904)
neus_fall$survey <- "NEUS"

neus_fall<- neus_fall %>%
  mutate(
    source = "NOAA",

```

```

timestamp = mdy("03/01/2021"),
country = "United States",
continent = "n_america",
sub_area = NA,
stat_rec = NA,
area_swept = 0.0384, #Average tow area in km^2 for albatross
#num_h could be calculated by dividing num by haul duration,
#but use caution because of 2008-2009 conversion
num_h = NA,
#num_cpue could be calculated by dividing num by area swept,
#but use caution because of 2008-2009 conversion
num_cpue = NA,
#wgt_h could be calculated by dividing wgt by haul duration,
#but use caution because of 2008-2009 conversion
wgt_h = NA,
#wgt_cpue could be calculated by dividing wgt by area swept,
#but use caution because of 2008-2009 conversion
wgt_cpue = NA
) %%
select(survey, haul_id, source, timestamp, country, sub_area, continent, stat_rec, station,
       stratum, year, month, day, quarter, season, latitude, longitude,
       haul_dur, area_swept, gear, depth, sbt, sst,
       num, num_h, num_cpue, wgt, wgt_h, wgt_cpue, verbatim_name)

rm(neus_catch_clean, neus_catch_raw, neus_fall_catch, neus_fall_haul)

#####
#NEUS Spring

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


neus_catch_raw <- read_lines(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/neus_spring_svcat.csv")
# remove comma
neus_catch_raw <- str_replace_all(
  neus_catch_raw, 'SQUID, CUTTLEFISH, AND OCTOPOD UNCL',
                  'Squid/Cuttlefish/Octopod (unclear)')
neus_catch_raw <- str_replace_all(
  neus_catch_raw, 'SEA STAR, BRITTLE STAR, AND BASKETSTAR UNCL',
                  'Sea Star/Brittle Star/Basket Star (unclear)')
neus_catch_raw <- str_replace_all(
  neus_catch_raw, 'MOON SNAIL, SHARK EYE, AND BABY-EAR UNCL',
                  'Moon Snail/shark eye/baby-ear (unclear)')
neus_catch_raw <- str_replace_all(
  neus_catch_raw, 'MOON SNAIL, SHARK EYE, AND BABY-EAR UNCL',
                  'Moon Snail/shark eye/baby-ear (unclear)')
neus_catch_clean <- str_replace_all(neus_catch_raw, 'SHRIMP \\(PINK,BROWN,WHITE\\\\)', 
                                      'Shrimp \\(pink/brown/white\\\\)')
write_lines(neus_catch_clean, file = "neus_catch_clean.txt")
neus_spring_catch <- read_csv("neus_catch_clean.txt",

```

```

            col_types = cols(.default = col_character()))
file.remove("neus_catch_clean.txt")
rm(neus_catch_clean, neus_catch_raw)

neus_spring_haul <- read_csv(
  "https://github.com/pinskylab/OceanAdapt/raw/master/data_raw/neus_spring_svsta.csv",
  col_types = cols(.default = col_character()))
neus_spring <- left_join(neus_spring_catch, neus_spring_haul,
                           by = c("ID", "STATION", "CRUISE6", "STRATUM", "TOW"))
neus_spring <- left_join(neus_spring, neus_spp, by = "SVSPP")

rm(neus_spring_catch, neus_spring_haul)
neus_spring <- neus_spring %>%
  rename(year = EST_YEAR,
        month = EST_MONTH,
        day = EST_DAY,
        latitude = DECDEG_BEGLAT,
        longitude = DECDEG_BEGLON,
        depth = AVGDEPTH,
        stratum = STRATUM,
        haul_id = ID,
        verbatim_name = SCINAME,
        #Expanded biomass of a species caught at a given station.
        wgt = EXPCATCHWT,
        #Expanded number of individuals of a species caught at a given station.
        num = EXPCATCHNUM,
        station = STATION,
        sst = SURFTEMP,
        sbt = BOTTEMP)
neus_spring <- neus_spring %>%
  mutate(stratum = as.double(stratum),
        latitude = as.double(latitude),
        longitude = as.double(longitude),
        depth = as.double(depth),
        wgt = as.double(wgt),
        num = as.double(num),
        year = as.double(year),
        quarter = case_when(month %in% c(1,2,3) ~ 1,
                             month %in% c(4,5,6) ~ 2,
                             month %in% c(7,8,9) ~ 3,
                             month %in% c(10,11,12) ~ 4),
        season = "Spring",
        SVSPP = as.double(SVSPP),
        haul_dur = as.numeric(TOWDUR)/60, #minutes to hours,
        gear = SVEGAR
  )
}

#apply spring conversion factors
setDT(neus_spring)

dcf.spp <- NEFSC_conv[DCF_WT > 0, SVSPP]

```

```

for(i in 1:length(dcf.spp)){
  neus_spring[year < 1985 & SVSPP == dcf.spp[i],
              wgt := wgt * NEFSC_conv[SVSPP == dcf.spp[i], DCF_WT]]
}

gcf.spp <- NEFSC_conv[GCF_WT > 0, SVSPP]
for(i in 1:length(gcf.spp)){
  neus_spring[year > 1972 & year < 1982 & SVSPP == gcf.spp[i],
              wgt := wgt / NEFSC_conv[SVSPP == gcf.spp[i], GCF_WT]]
}

vcf.spp <- NEFSC_conv[VCF_WT > 0, SVSPP]
for(i in 1:length(dcf.spp)){
  neus_spring[SVVESSEL == 'DE' & SVSPP == vcf.spp[i],
              wgt := wgt* NEFSC_conv[SVSPP == vcf.spp[i], VCF_WT]]
}

spp_spring <- big_spring[season == 'spring', svspp]
#before <- neus_spring[SVVESSEL %in% c('HB', 'PC') & SVSPP %in% spp_spring,
#. (mean_wtcpue=mean(wtcpue)), by=SVSPP][order(SVSPP)]

for(i in 1:length(big_spring$svspp)){
  neus_spring[SVVESSEL %in% c('HB', 'PC') & SVSPP == spp_spring[i],
              wgt := wgt / big_spring[i, rhoW]]
}

#after <- neus_spring[SVVESSEL %in% c('HB', 'PC') & SVSPP %in% spp_spring,
#. (mean_wtcpue=mean(wtcpue)), by=SVSPP][order(SVSPP)]


neus_spring <- as.data.frame(neus_spring)

# sum different sexes of same spp together
neus_spring <- neus_spring %>%
  group_by(year, latitude, longitude, depth, haul_id, CRUISE6, station, stratum,
           verbatim_name, gear, haul_dur) %>%
  mutate(wgt = sum(wgt)) %>%
  ungroup()

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


#join with strata
neus_spring <- left_join(neus_spring, neus_strata, by = "stratum")
neus_spring <- filter(neus_spring, !is.na(stratum_area))
neus_spring <- neus_spring %>%
  rename(stratumarea = stratum_area) %>%
  #convert square nautical miles to square kilometers
  mutate(stratumarea = as.double(stratumarea)* 3.429904)
neus_spring$survey <- "NEUS"

```

```

neus_spring<- neus_spring %>%
  mutate(
    source = "NOAA",
    timestamp = mdy("03/01/2021"),
    country = "United States",
    continent = "n_america",
    sub_area = NA,
    stat_rec = NA,
    area_swept = 0.0384, #Average tow area in km^2 for albatross
    #num_h could be calculated by dividing num by haul duration,
    #but use caution because of 2008-2009 conversion
    num_h = NA,
    #num_cpue could be calculated by dividing num by area swept,
    #but use caution because of 2008-2009 conversion
    num_cpue = NA,
    #wgt_h could be calculated by dividing wgt by haul duration,
    #but use caution because of 2008-2009 conversion
    wgt_h = NA,
    #wgt_cpue could be calculated by dividing wgt by area swept,
    #but use caution because of 2008-2009 conversion
    wgt_cpue = NA
  ) %>%
  select(survey, haul_id,source, timestamp, country, sub_area, continent, stat_rec, station,
         stratum, year, month, day, quarter, season, latitude, longitude,
         haul_dur, area_swept, gear, depth, sbt, sst,
         num, num_h, num_cpue, wgt, wgt_h, wgt_cpue, verbatim_name)

rm(neus_catch_clean, neus_catch_raw, neus_spring_catch, neus_spring_haul)

#####
#bind spring and fall

neus <- rbind(neus_fall, neus_spring)

#sum abundance and wgt to fix duplicates (removes 21680 rows)
neus <- neus %>%
  group_by(survey, haul_id,source, timestamp, country, sub_area, continent, stat_rec, station,
           stratum, year, month, day, quarter, season, latitude, longitude,
           haul_dur, area_swept, gear, depth, sbt, sst, verbatim_name) %>%
  summarise(num=sum(num, na.rm = T),
            num_h=sum(num_h, na.rm = T),
            num_cpue=sum(num_cpue, na.rm = T),
            wgt=sum(wgt, na.rm = T),
            wgt_h=sum(wgt_h, na.rm = T),
            wgt_cpue=sum(wgt_cpue, na.rm = T)) %>%
  select(survey, haul_id,source, timestamp, country, sub_area, continent, stat_rec, station,
         stratum, year, month, day, quarter, season, latitude, longitude,
         haul_dur, area_swept, gear, depth, sbt, sst,
         num, num_h, num_cpue, wgt, wgt_h, wgt_cpue, verbatim_name)

#check for duplicates, should not be any with more than 1 obs
#check for duplicates
count_neus <- neus %>%

```

```

group_by(haul_id, verbatim_name) %>%
  mutate(count = n())

#none!

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

unique_name_match
#check if empty

##duplicates
#HOMARUS AMERICANUS
#SQUALUS ACANTHIAS
#MUSTELUS CANIS
#GERYON QUINQUEDENS
#OVALIPES STEPHENSONI
#MAJIDAE
#OVALIPES OCELLATUS
#MYLIOBATIS GOODEI
#CALLINECTES SAPIDUS
#PORTUNIDAE
#CANCER IRRORATUS
#LIMULUS POLYPHEMUS
#CANCER BOREALIS
#SQUATINA DUMERIL
#BATHYNECTES LONGISPINA
#PANDALUS BOREALIS
#LITHODES MAJA
#PORTUNUS SPINIMANUS
#ARENAEUS CIBRARIUS
#UNIDENTIFIED FISH
#ACANTHOCARPUS ALEXANDRI
#CHIONOECETES OPILIO
#SCYLIORHINUS RETIFER
#LOLIGO PEALEII
#CANCRIDAE

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


# Get WoRM's id for sourcing
wrn <- gnr_datasources() %>%
  filter(title == "World Register of Marine Species") %>%
  pull(id)

### Automatic cleaning
# Set Survey code
neus_survey_code <- "NEUS"

```

```

neus <- neus %>%
  mutate(
    taxa2 = str_squish(verbatim_name),
    taxa2 = str_remove_all(taxa2, " spp.| sp.| spp| sp|NO "),
    taxa2 = str_to_sentence(str_to_lower(taxa2))
  )

# Get clean taxa
clean_auto <- clean_taxa(unique(neus$taxa2), input_survey = neus_survey_code,
                           save = F, output=NA, fishbase=T)

#This leaves out the following species, of which 1 is a fish that needs to be added back
#Geryon quinquedens                               no match
#Astroscopus y-graecum                          no match      #FISH
#Portunus spinimanus                          no match
#Pandalus propinquus                         no match

ast_ygr <- c("Astroscopus y-graecum", 159252,3704, "Astroscopus y-graecum",
           "Animalia", "Chordata", "Actinopteri", "Perciformes", "Uranoscopidae",
           "Astroscopus", "Species", "NEUS")

clean_auto_missing <- rbind(clean_auto, ast_ygr)

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


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

clean_neus <- left_join(neus, correct_taxa, by=c("taxa2"="query")) %>%
  filter(!is.na(taxa)) %>% # query does not indicate taxa entry that
  #were removed in the cleaning procedure
  # so all NA taxa have to be removed from the surveys because:
  #non-existing, non marine or non fish
  rename(accepted_name = taxa) %>%
  mutate(verbatim_aphia_id = NA,
        aphia_id = worms_id,
        num_cpua = num_cpue,
        num_cpue = num_h,
        wgt_cpua = wgt_cpue,
        wgt_cpue = wgt_h,
        survey_unit = ifelse(survey %in% c("BITS", "NS-IBTS", "SWC-IBTS"),
                             paste0(survey, "-", quarter), survey),
        survey_unit = ifelse(survey %in% c("NEUS", "SEUS", "SCS", "GMEX"),
                             paste0(survey, "-", season), survey_unit)) %>%
  select(fishglob_data_columns$`Column name fishglob`)

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

```

```

#none!

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

unique_name_match
#check if empty

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

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

# -----#
#### FAGS #####
# -----#
#install required packages that are not already installed
required_packages <- c("data.table",
                      "devtools",
                      "dgridR",
                      "dplyr",
                      "fields",
                      "forcats",
                      "ggplot2",
                      "here",
                      "magrittr",
                      "maps",
                      "maptools",
                      "raster",
                      "rcompendium",
                      "readr",
                      "remotes",
                      "rrtools",
                      "sf",
                      "sp",
                      "tidyR",
                      "usethis")

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

#load pipe operator
library(magrittr)

```

```

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

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

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

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

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

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

# integrate taxonomic flags
for(i in 1:length(surveys)){
  if(!surveys[i] %in% c("FALK", "GSL-N", "MRT", "NZ-CHAT", "SCS", "SWC-IBTS")){
    xx <- data.frame(read_delim(paste0("outputs/Flags/taxonomic_flagging/",
                                         surveys[i], "_flagsp.txt"),
                                 delim=";", escape_double = FALSE, col_names = FALSE,
                                 trim_ws = TRUE))
    xx <- as.vector(unlist(xx[1,]))

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

    rm(xx)
  }
}

# integrate spatio-temporal flags
for(i in 1:length(survey_units)){

```

```

if(!survey_units[i] %in% c("DFO-SOG", "IS-TAU", "SCS-FALL", "WBLS")){

  hex_res7_0 <- read.csv(paste0("outputs/Flags/trimming_method1/hex_res7/",
                                survey_units[i], "_hex_res_7_trimming_0_hauls_removed.csv"),
                                sep = ";")
  hex_res7_0 <- as.vector(hex_res7_0[,1])

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

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

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

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

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

# Just run this routine should be good for all
write_clean_data(data = survey_std, survey = "NEUS_std",
                 overwrite = T, rdata=TRUE)

```

## 1. Overview of the survey data table

survey	source	timestamp	haul_id	country	sub_area
NEUS	NOAA	2021-03-01	196307010100010157	United States	NA
NEUS	NOAA	2021-03-01	196307010100010157	United States	NA
NEUS	NOAA	2021-03-01	196307010100010157	United States	NA
NEUS	NOAA	2021-03-01	196307010100010157	United States	NA
NEUS	NOAA	2021-03-01	196307010100010157	United States	NA

continent	stat_rec	station	stratum	year	month	day	quarter	season
n_america	NA	0157	1010	1963	12	10	4	Fall
n_america	NA	0157	1010	1963	12	10	4	Fall
n_america	NA	0157	1010	1963	12	10	4	Fall
n_america	NA	0157	1010	1963	12	10	4	Fall
n_america	NA	0157	1010	1963	12	10	4	Fall

latitude	longitude	haul_dur	area_swept	gear	depth	sbt	sst
40.73333	-72.65	0.5	0.0384	11	28	8.1	8.2
40.73333	-72.65	0.5	0.0384	11	28	8.1	8.2
40.73333	-72.65	0.5	0.0384	11	28	8.1	8.2
40.73333	-72.65	0.5	0.0384	11	28	8.1	8.2
40.73333	-72.65	0.5	0.0384	11	28	8.1	8.2

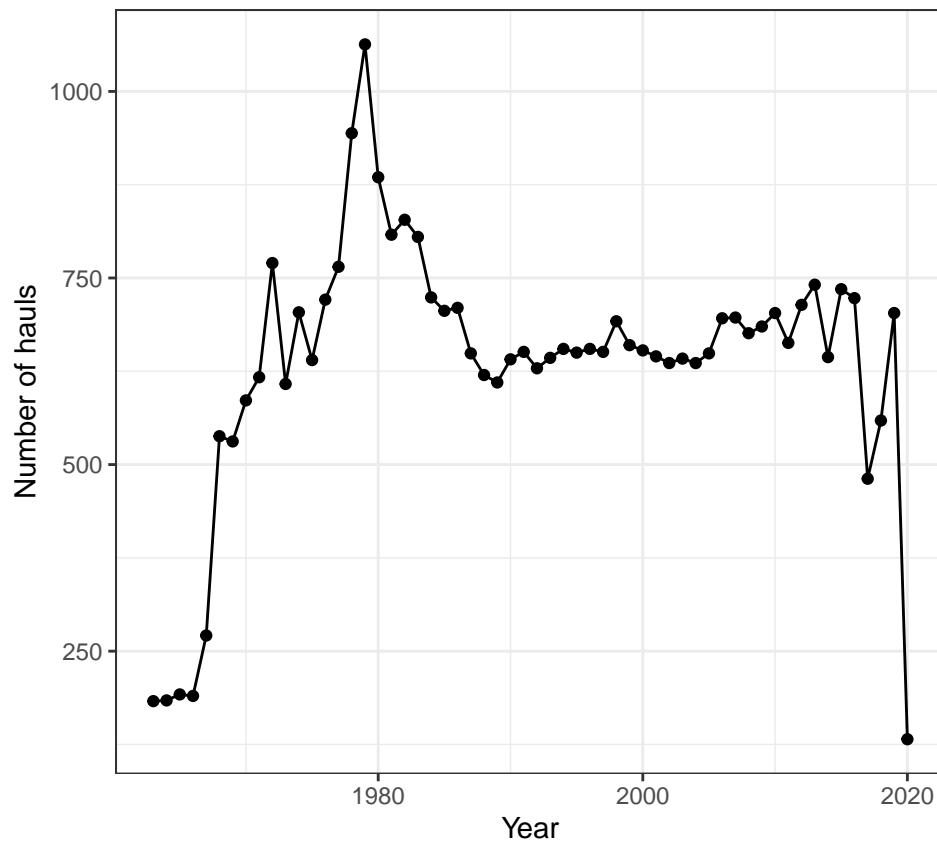
num	num_cpue	num_cpua	wgt	wgt_cpue	wgt_cpua	verbatim_name
1	0	0	0.500	0	0	ALOSA PSEUDOHARENGUS
2	0	0	0.000	0	0	BREVOORTIA TYRANNUS
1	0	0	0.000	0	0	CLUPEA HARENGUS
3	0	0	13.284	0	0	GADUS MORHUA
162	0	0	91.256	0	0	LEUCORAJA ERINACEA

verbatim_aphia_id	accepted_name	aphia_id	SpecCode	kingdom
NA	Alosa pseudoharengus	158669	1583	Animalia
NA	Brevoortia tyrannus	158691	1592	Animalia
NA	Clupea harengus	126417	24	Animalia
NA	Gadus morhua	126436	69	Animalia
NA	Leucoraja erinaceus	1577339	NA	Animalia

phylum	class	order	family	genus	rank	survey_unit
Chordata	Teleostei	Clupeiformes	Alosidae	Alosa	Species	NEUS-Fall
Chordata	Teleostei	Clupeiformes	Alosidae	Brevoortia	Species	NEUS-Fall
Chordata	Teleostei	Clupeiformes	Clupeidae	Clupea	Species	NEUS-Fall
Chordata	Teleostei	Gadiformes	Gadidae	Gadus	Species	NEUS-Fall
Chordata	Elasmobranchii	Rajiformes	Rajidae	Leucoraja	Species	NEUS-Fall

## 2. Summary of sampling intensity

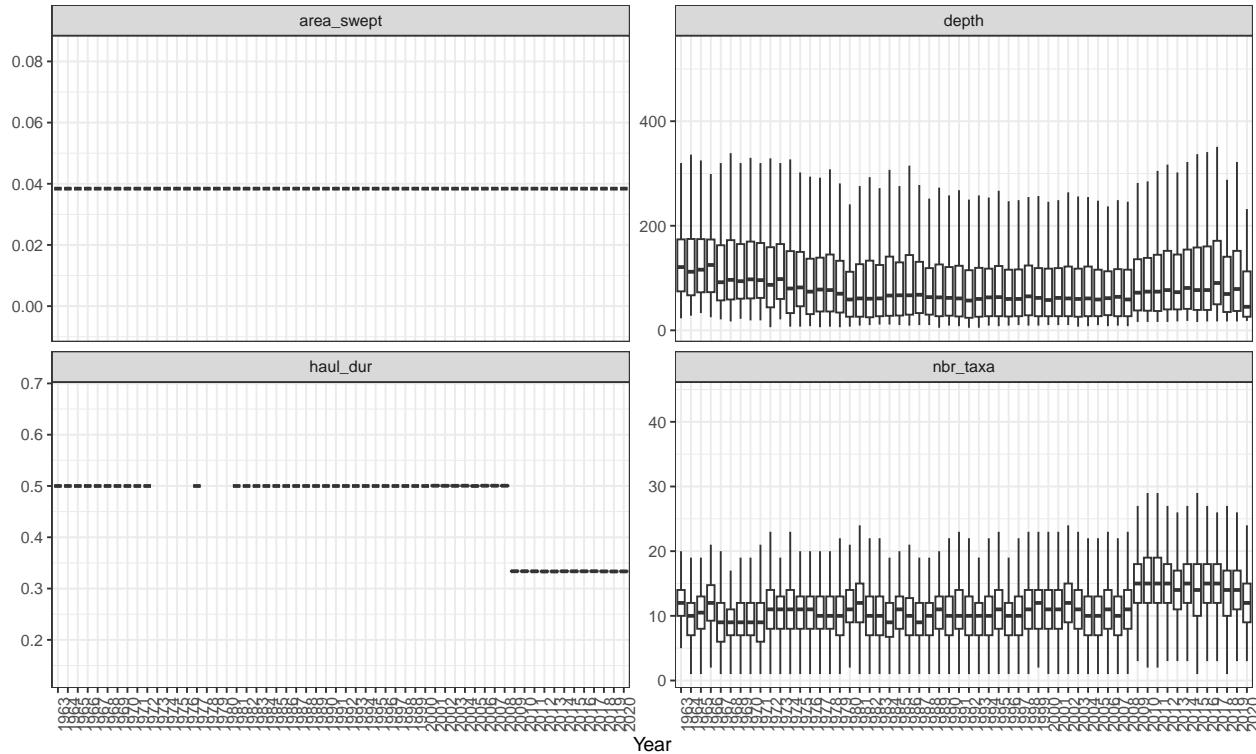
Number of hauls per year performed during the survey after data processing.



### 3. Summary of sampling variables from the survey

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

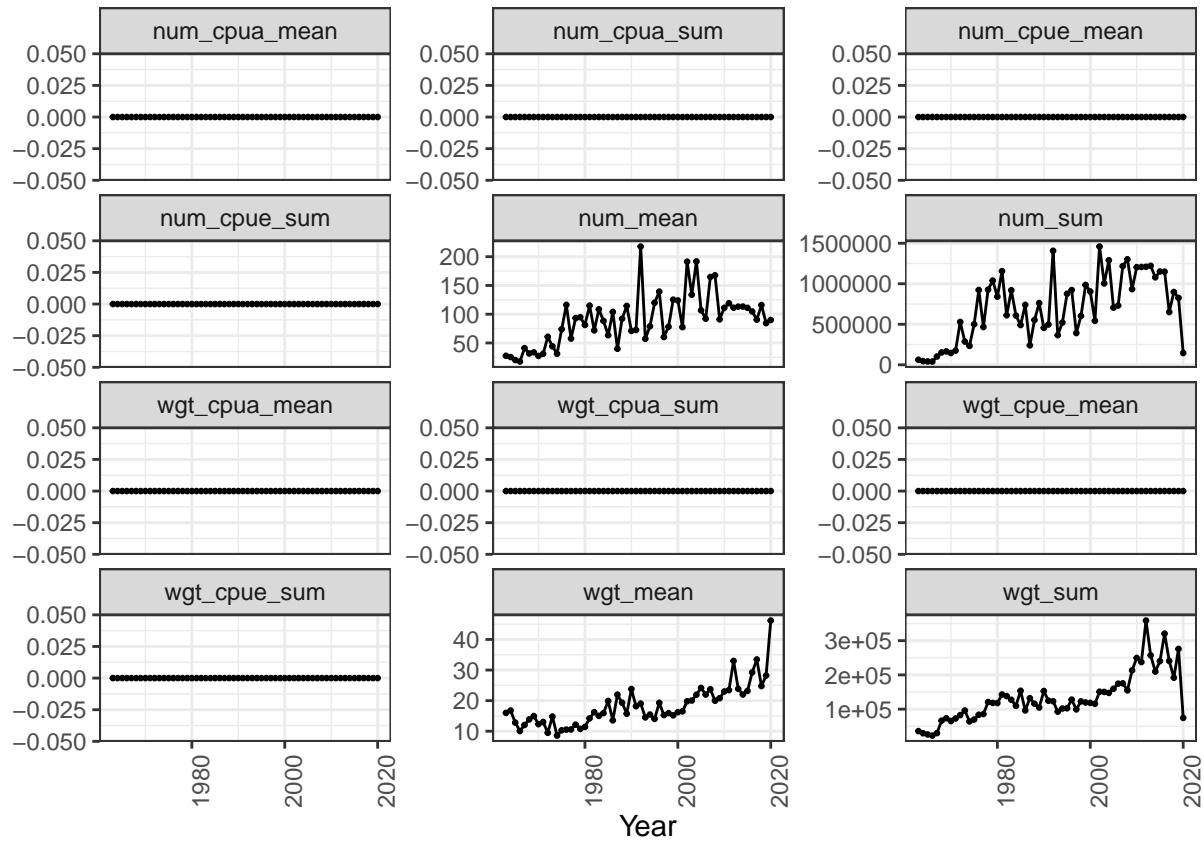
- *area\_swept*, swept area by the bottom trawl gear  $km^2$
- *depth*, sampling depth in  $m$
- *haul\_dur*, haul sampling duration *hour*
- *number of marine fish taxa*, taxa were cleaned following the last version of taxonomy from the World Register of Marine Species (<https://www.marinespecies.org/>,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



#### 4. Summary of biological variables

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

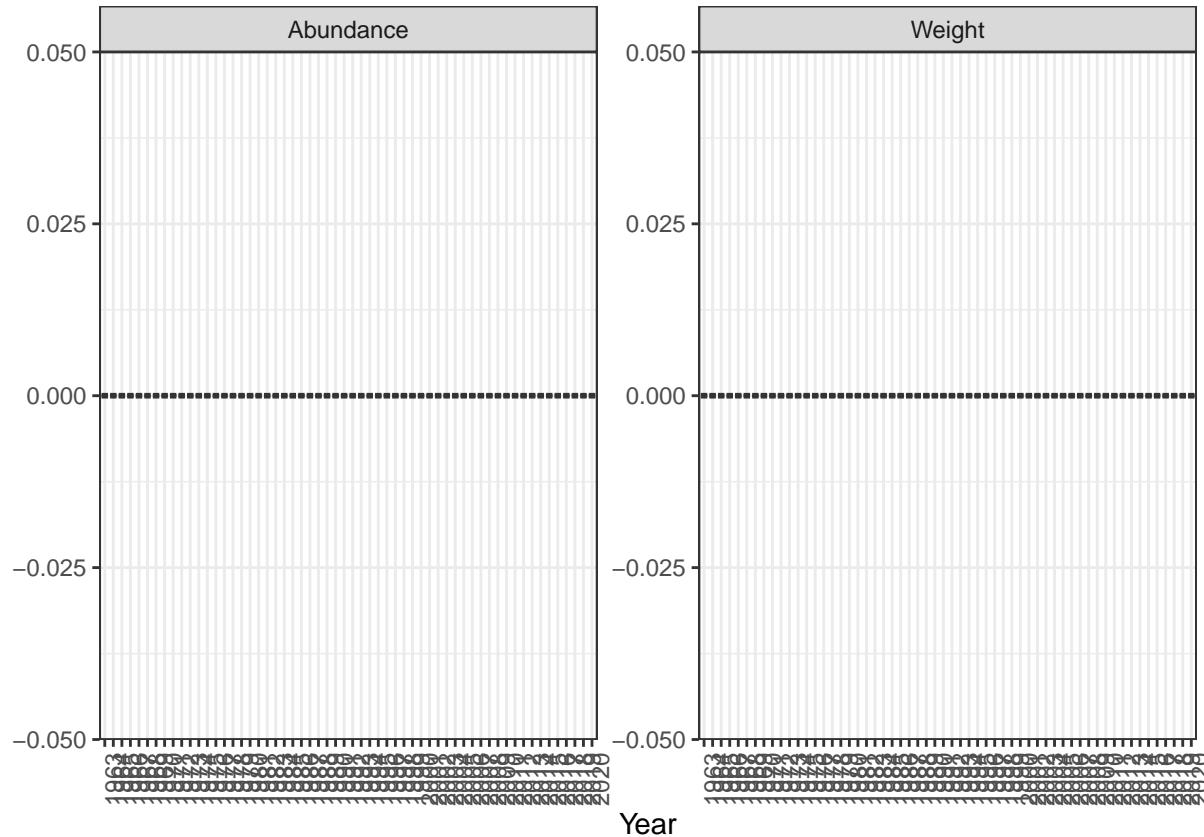
- $num\_cpua$ , number of individuals (abundance) in  $\frac{individuals}{km^2}$
- $num\_cpue$ , number of individuals (abundance) in  $\frac{individuals}{h}$
- $num$ , number of individuals (abundance)
- $wgt\_cpua$ , weight in  $\frac{kg}{km^2}$
- $wgt\_cpue$ , weight in  $\frac{kg}{h}$
- $wgt$ , weight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



## 5. Extreme values

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

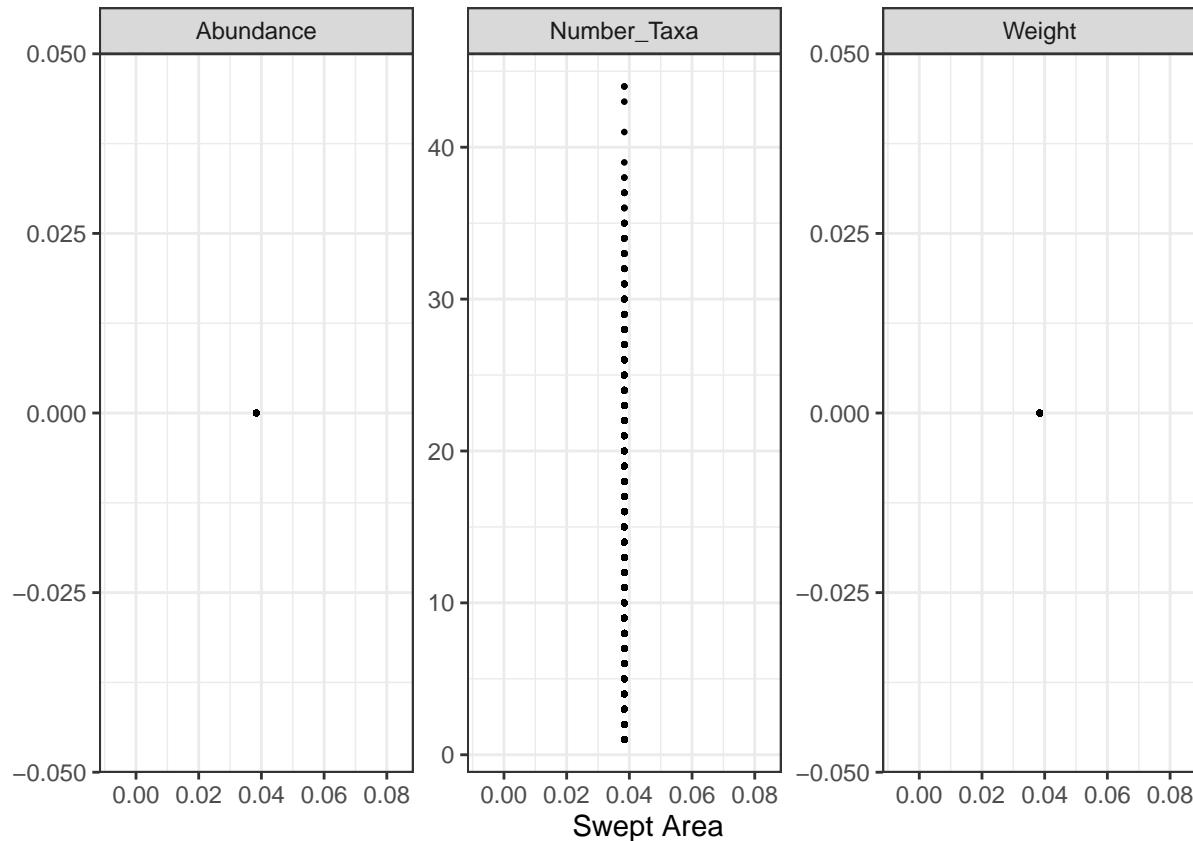
- $num\_cpue$ , number of individuals (abundance) in  $\frac{individuals}{km^2}$
- $wgt\_cpue$ , weight in  $\frac{kg}{km^2}$



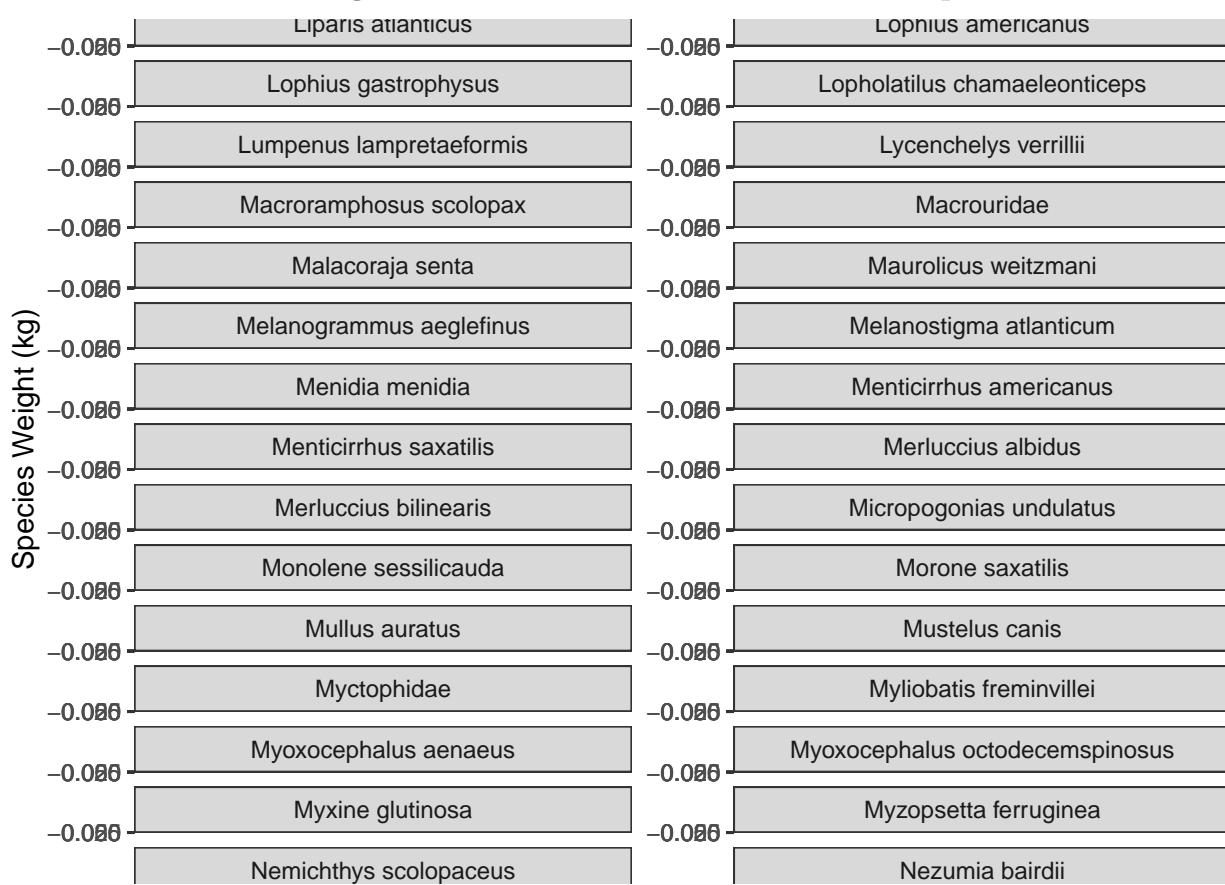
## 6. Summary of variables against swept area

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

- $nbr\_taxa$ , number of marine fish taxa after taxonomic data cleaning
- $num\_cpua$ , number of individuals (abundance) in  $\frac{individuals}{km^2}$
- $wgt\_cpua$ , weight in  $\frac{kg}{km^2}$

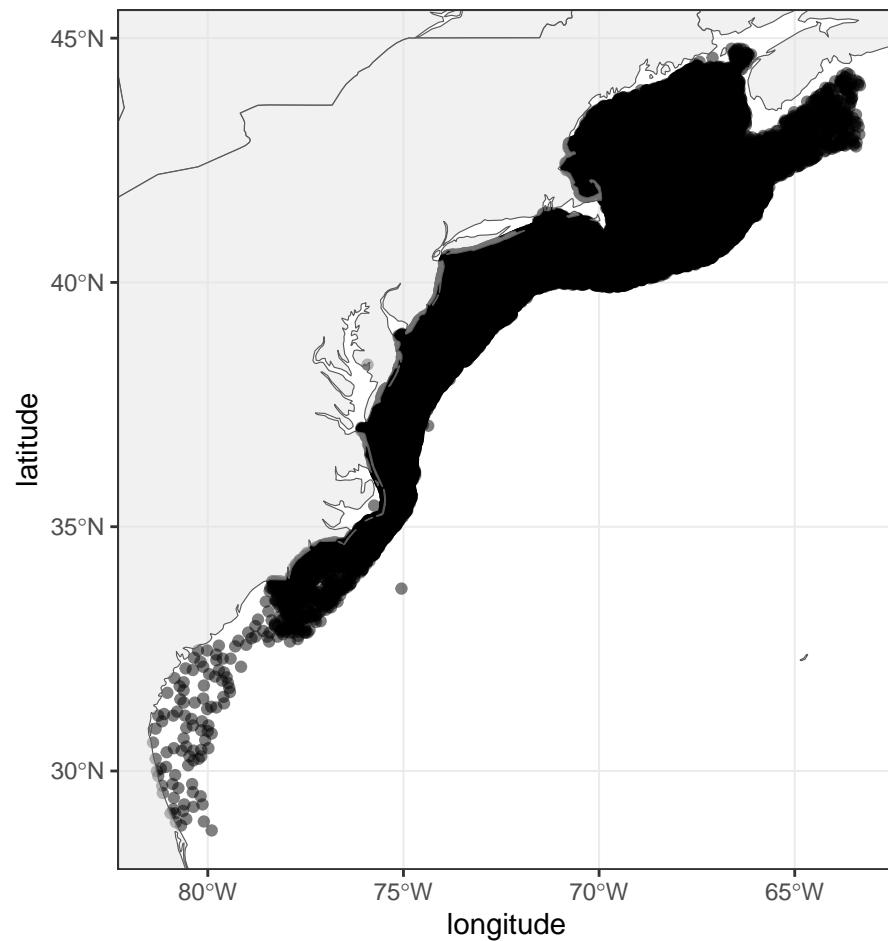


## 7. Abundance or Weight trends of the six most abundant species



## 8. Distribution mapping

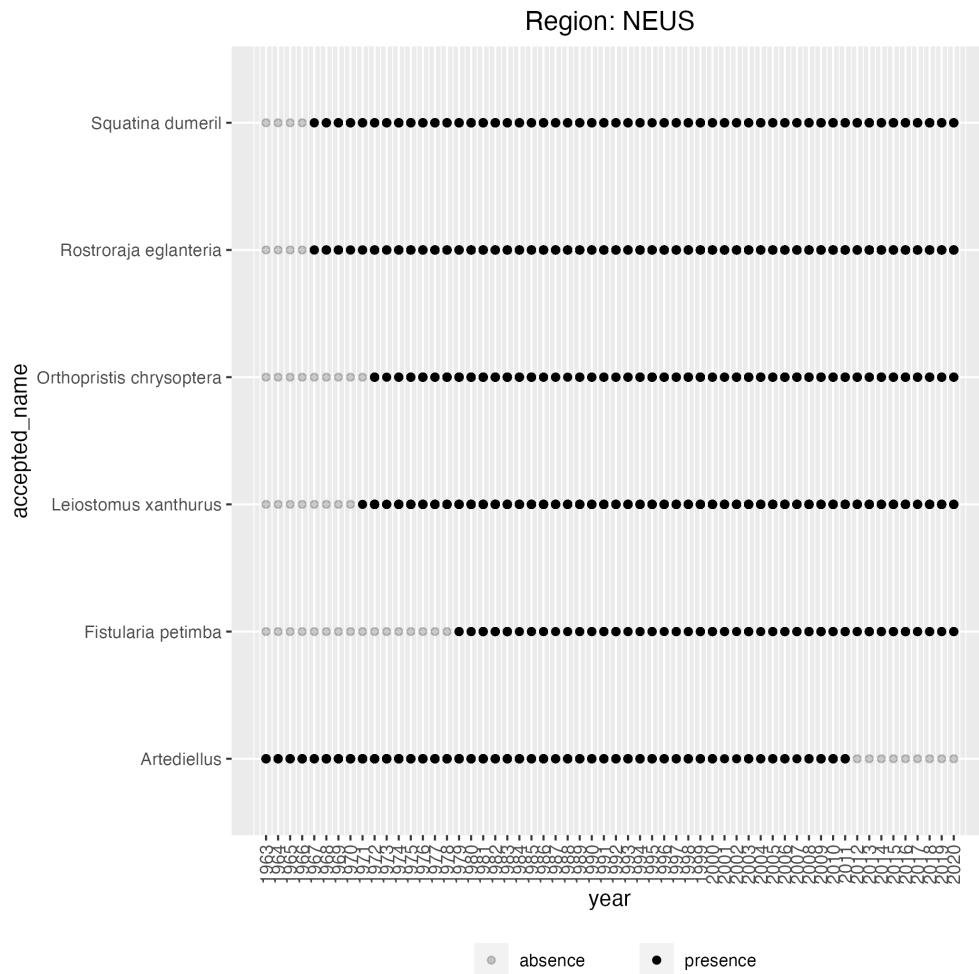
Map of the sampling distribution in space. Note that we only show one year per coordinate.



## 9. Taxonomic flagging

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

## Visualization of flagged taxa



## Statistics related to the taxonomic flagging outputs

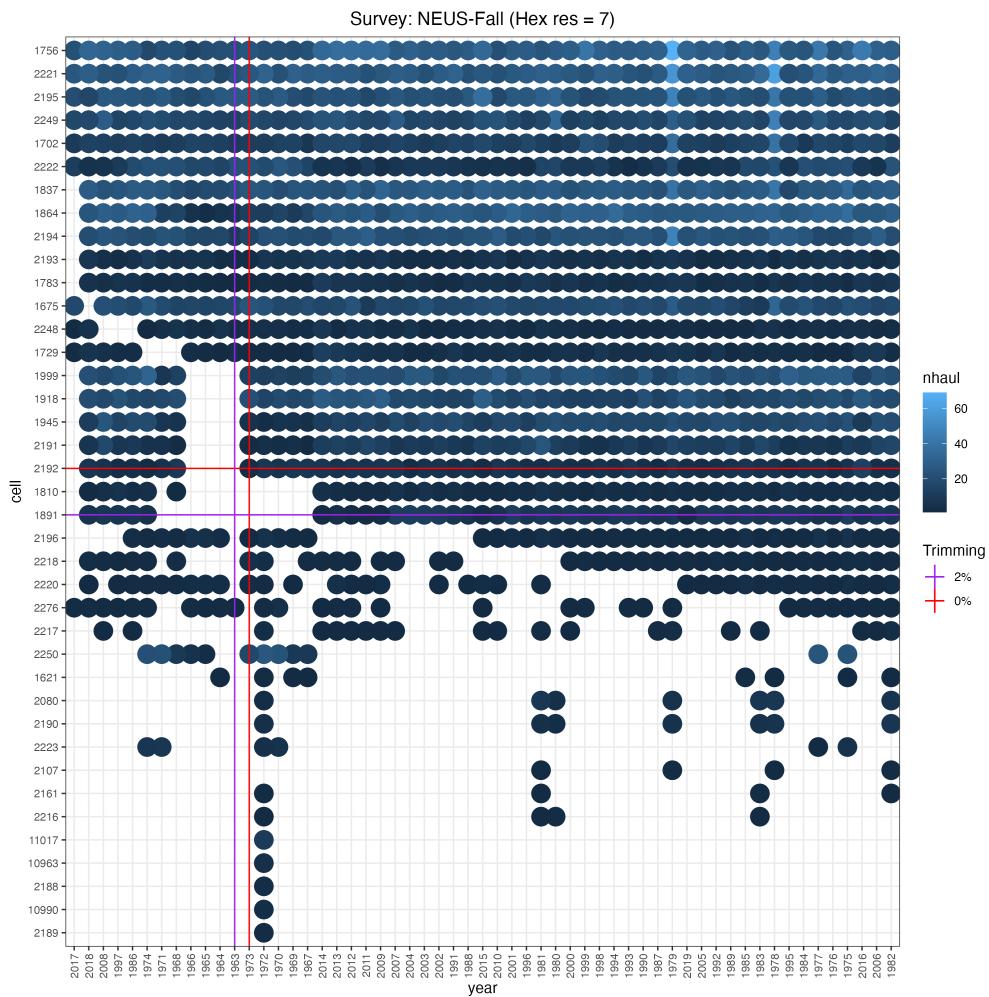
Total number of species	560.0
Percentage of species flagged	1.1

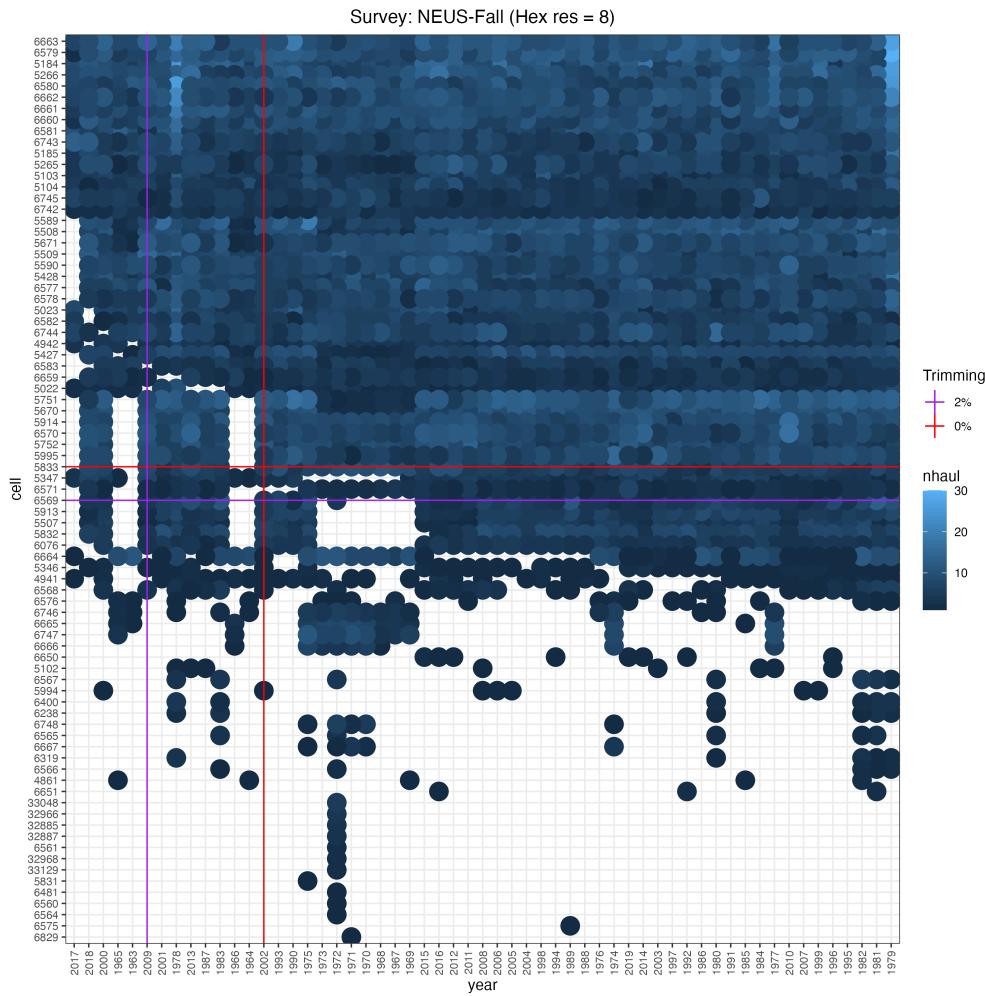
## 10. Spatio-temporal standardization: NEUS-Fall

### a. Standardization method 1

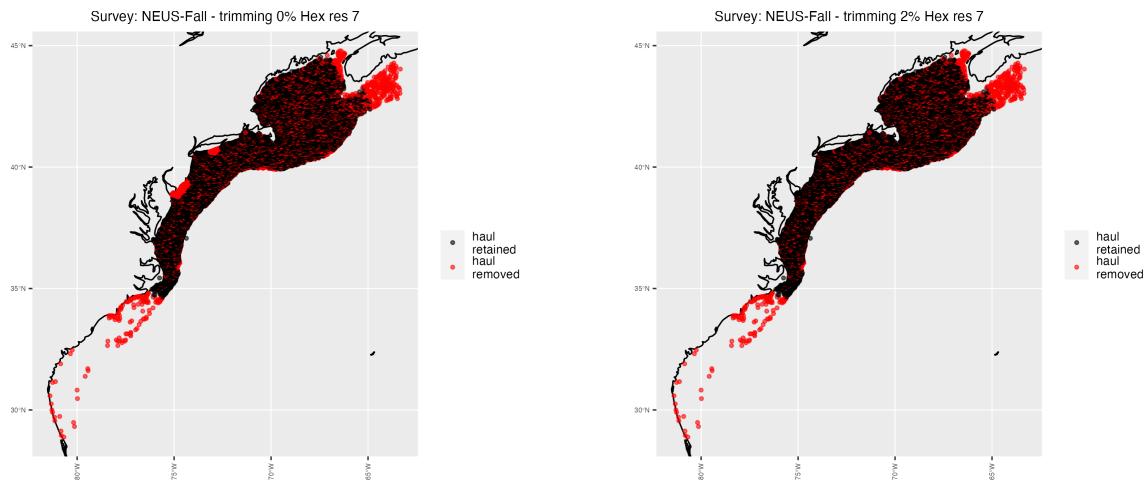
This standardization method was adapted from [https://github.com/zookitchel/trawl\\_spatial\\_turnover/blob/master/data\\_prep\\_code/species/explore\\_NorthSea\\_trimming.Rmd](https://github.com/zookitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd)  
It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

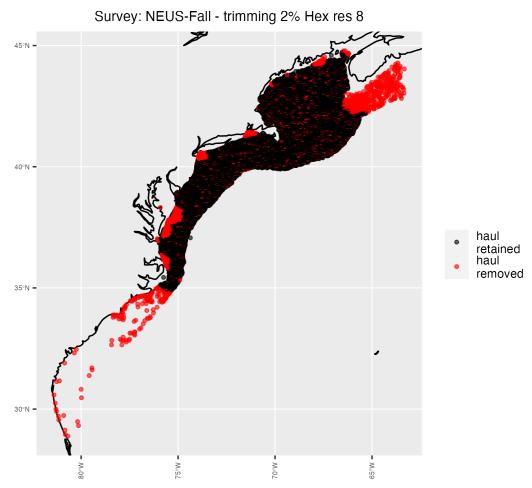
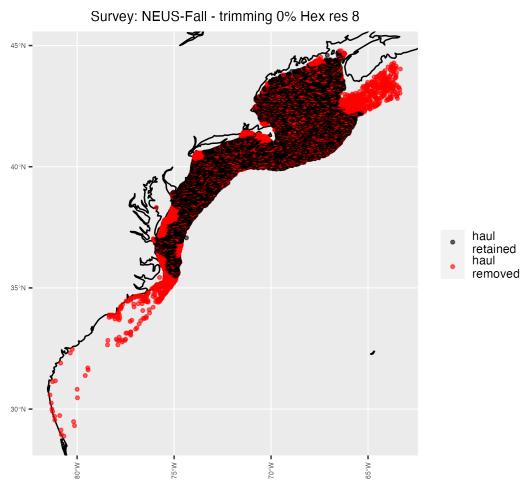
Plot of number of cells x years with overlaid flagging options



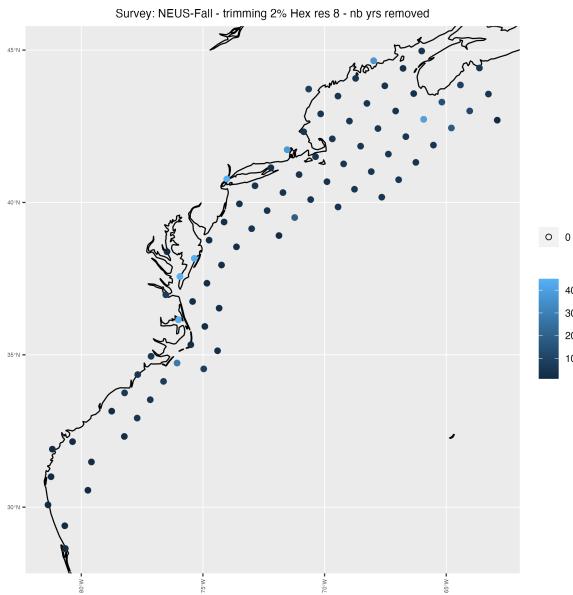
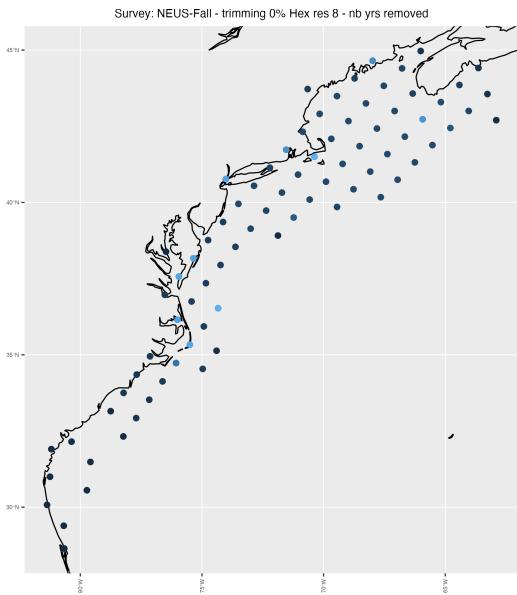
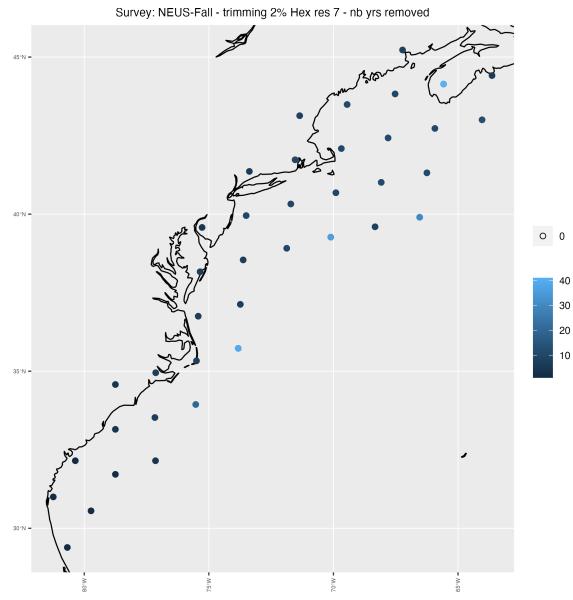
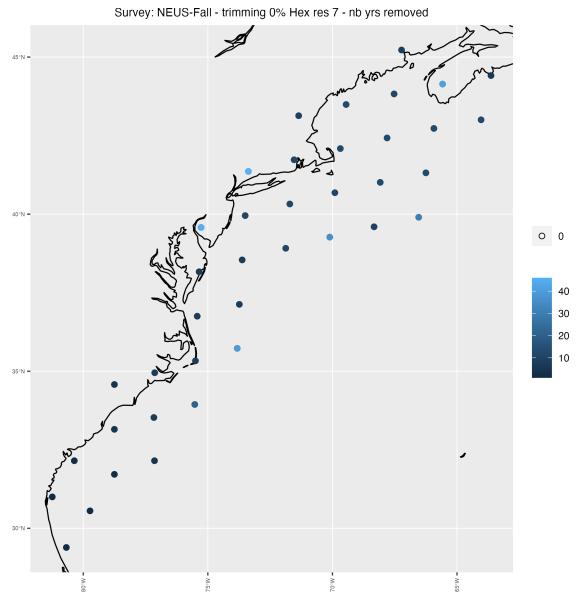


Map of hauls retained and removed per flagging method and threshold





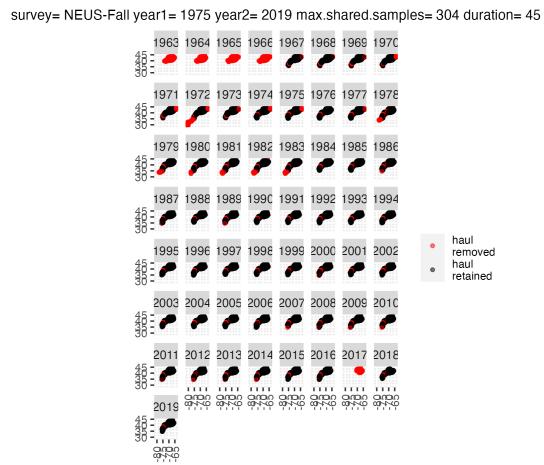
Map of numbers of years removed per grid cell and flagging method/threshold



## b. Standardization method 2

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

Map of hauls retained and removed



## c. Standardization summary

Statistics of hauls removed for each standardization method

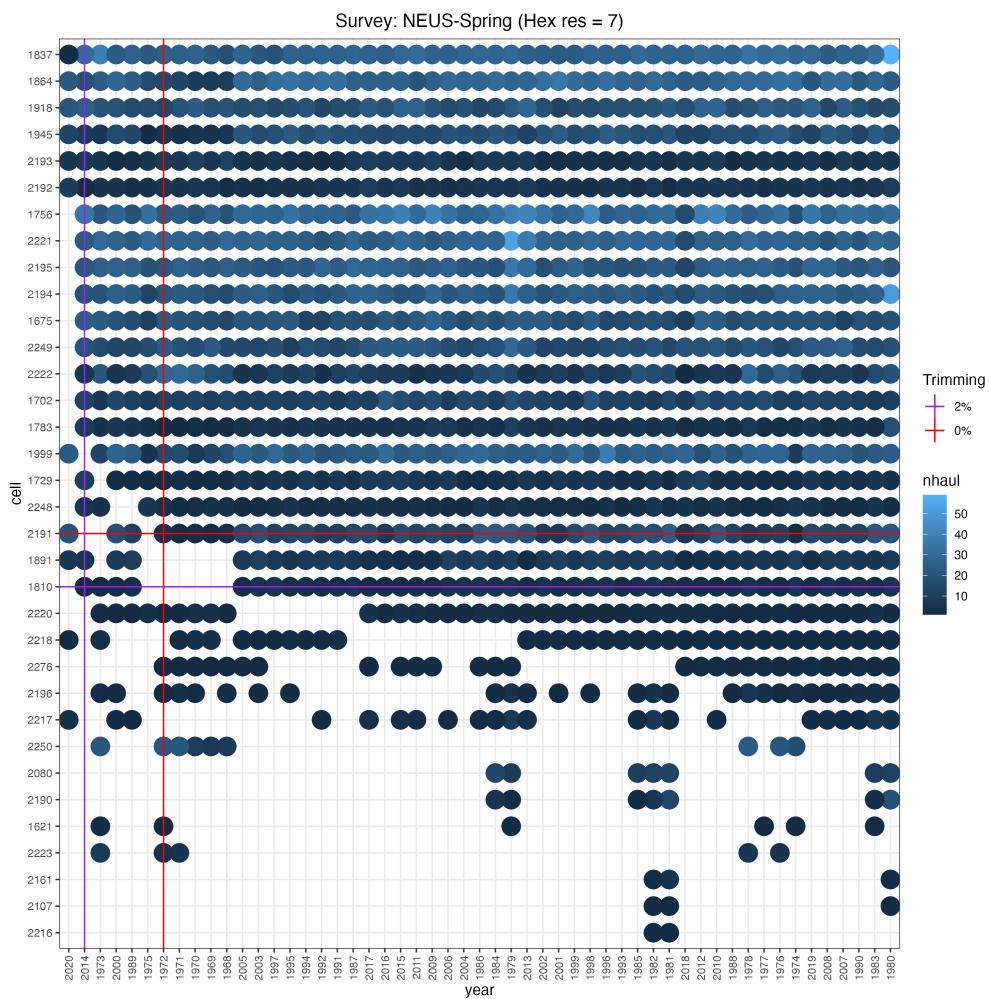
summary	grid cell 7, 0% threshold	grid cell 7, 2% threshold	grid cell 8, 0% threshold	grid cell 8, 2% threshold	method 2 (biotime)
number of hauls removed	3996.0	3394.0	5526.0	2778.0	11971.0
percentage of hauls removed	22.2	18.8	30.6	15.4	9.3

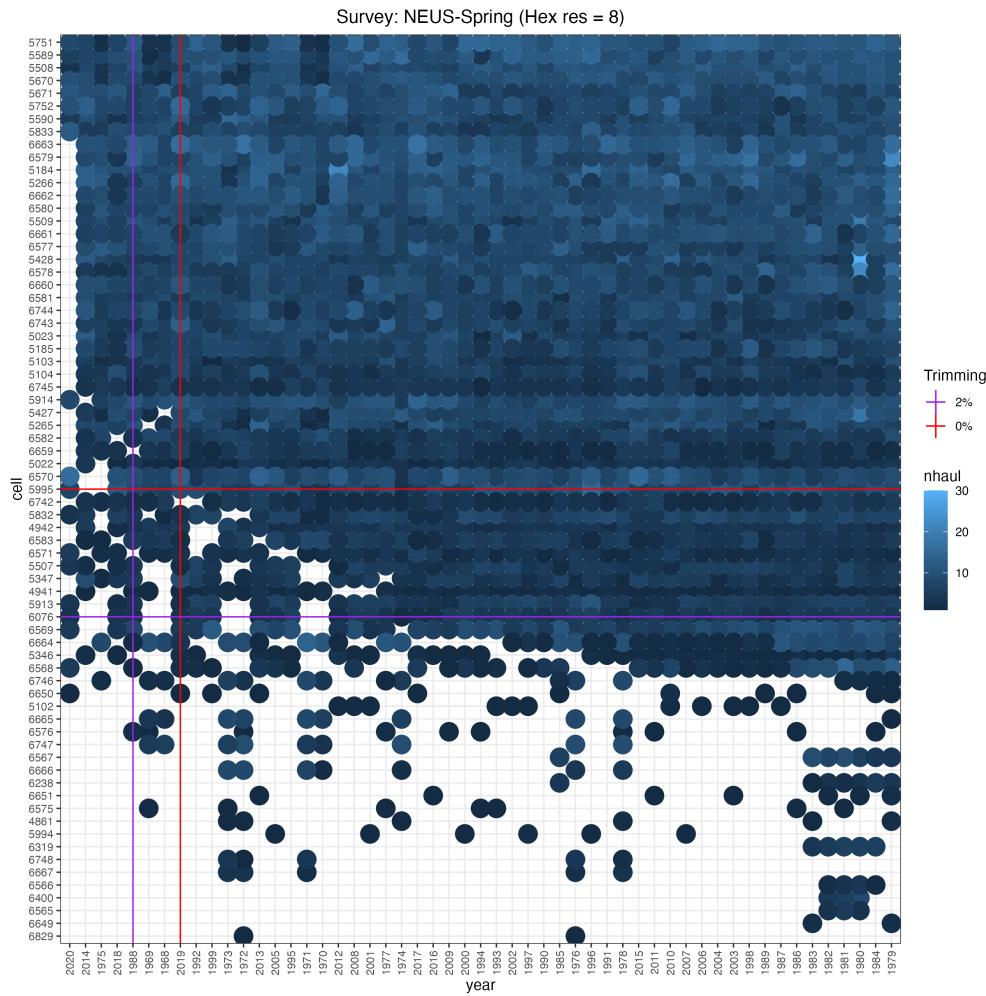
## 11. Spatio-temporal standardization: NEUS-Spring

### a. Standardization method 1

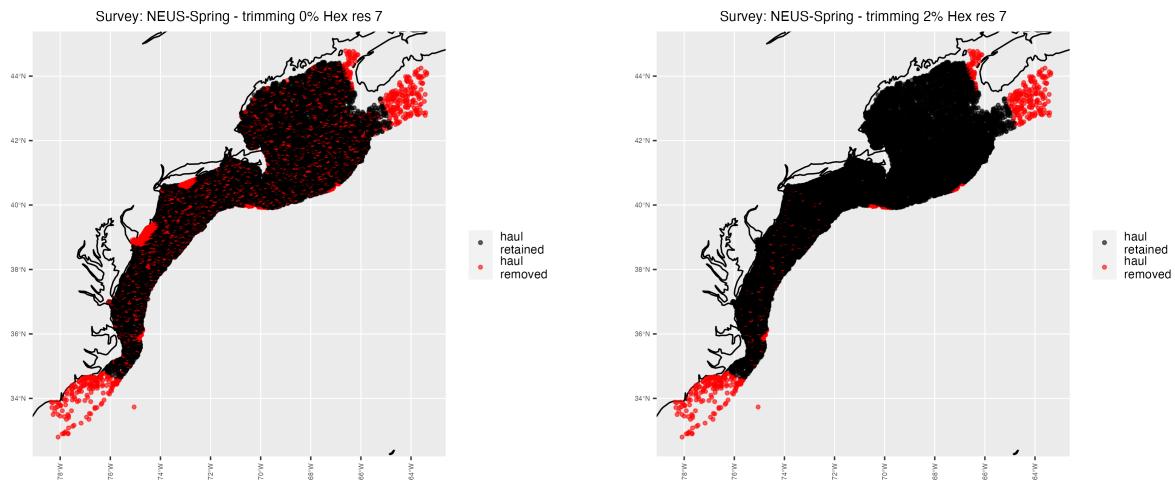
This standardization method was adapted from [https://github.com/zookitchel/trawl\\_spatial\\_turnover/blob/master/data\\_prep\\_code/species/explore\\_NorthSea\\_trimming.Rmd](https://github.com/zookitchel/trawl_spatial_turnover/blob/master/data_prep_code/species/explore_NorthSea_trimming.Rmd)  
It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

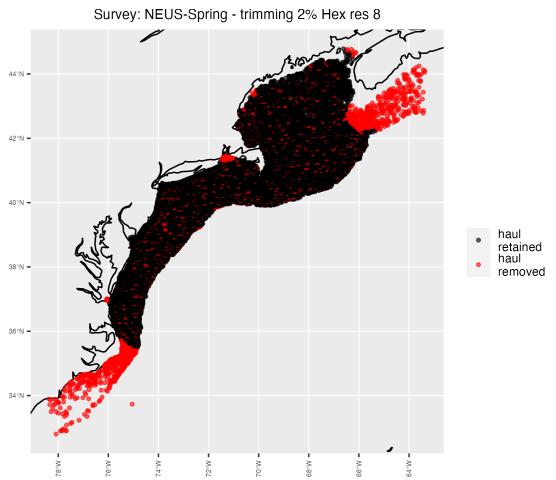
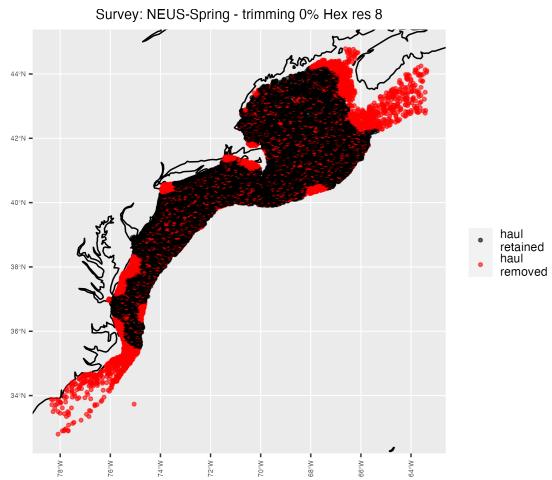
Plot of number of cells x years with overlaid flagging options



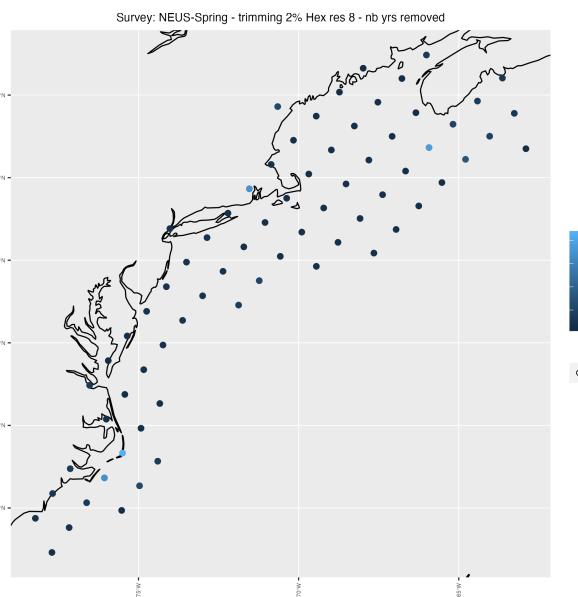
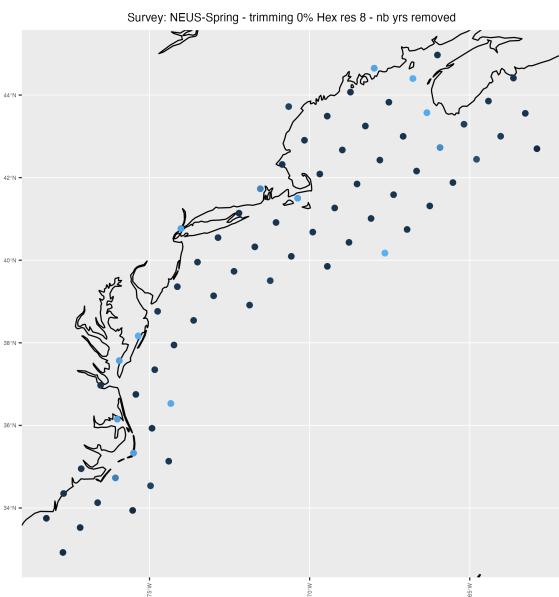
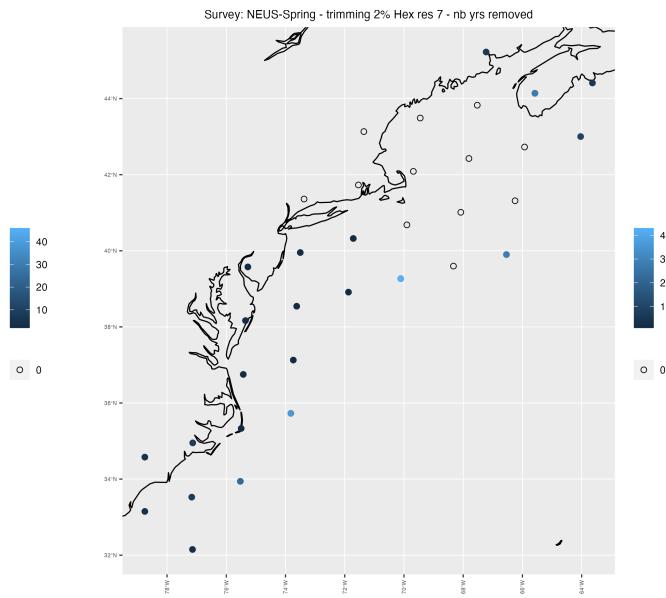
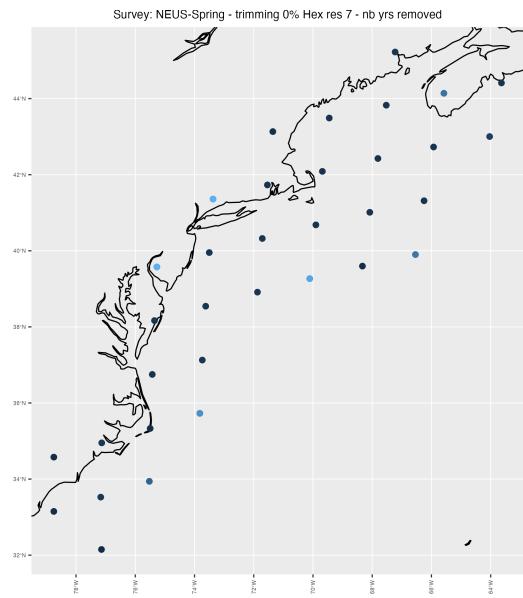


Map of hauls retained and removed per flagging method and threshold





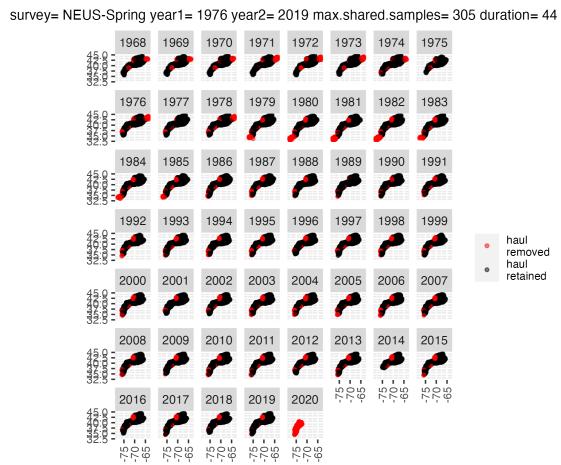
Map of numbers of years removed per grid cell and flagging method/threshold



## b. Standardization method 2

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

Map of hauls retained and removed



## c. Standardization summary

Statistics of hauls removed for each standardization method

summary	grid cell 7, 0% threshold	grid cell 7, 2% threshold	grid cell 8, 0% threshold	grid cell 8, 2% threshold	method 2 (biotime)
number of hauls removed	2543.0	719.0	4539	2058.0	12146.0
percentage of hauls removed	14.6	4.1	26	11.8	8.2