```
setwd("C:/Users/bruger/OneDrive - UiT Office 365/Desktop/Master thesis")
library(tidyverse)
library(readxl)
library(dplyr)
library(ggplot2)
library(janitor)
library(lubridate)
library(tibble)
library(ggOceanMaps)
{.ggOceanMapsenv <- new.env();
  .ggOceanMapsenv$datapath <- 'YourCustomPath'}
library(ggspatial)
library(viridisLite)
library(viridis)
library(cowplot)
library(sf)
library(vegan)
library(RColorBrewer)
library(forcats)
library(gridExtra)
library(knitr)
library(kableExtra)
library(ggrepel)
library(patchwork)
library(reshape2)
library(ggpubr)
library(sfheaders)
library(ggthemes)
library(pals)
library(grid)
# STATION DATA
#####
TUNU_Diversity_station_data12des23 <- read_excel("Station_data_NEGreenland_Malou_May2024.xlsx")

TUNU_Diversity_station_data12des23$Station_ID <-

paste(TUNU_Diversity_station_data12des23$Year,TUNU_Diversity_station_data12des23$Station_number,
sep = "_")

CTD_data <- data.frame(Station_ID=TUNU_Diversity_station_data12des23$Station_ID,
                       Location=TUNU_Diversity_station_data12des23$Major_locality,
                       Location_category =
TUNU_Diversity_station_data12des23$Location_category,
                       Temp=TUNU_Diversity_station_data12des23$Trawl_temp,
                       Depth=TUNU_Diversity_station_data12des23$Trawl_depth,
                       Longitude=TUNU_Diversity_station_data12des23$Lon,
                       Latitude=TUNU_Diversity_station_data12des23$Lat,
                       Trawling_min=TUNU_Diversity_station_data12des23$Trawl_time_rounded,
                       Year = TUNU_Diversity_station_data12des23$Year)

CTD_data <- CTD_data %>% mutate(Decade = case_when(Year %in%
c("2002","2003","2005","2007","2010") ~ "Early",
                                                   Year
%in%c("2013","2015","2017","2022")~"Late"))

CTD_data$Latitude <- as.numeric(CTD_data$Latitude)
CTD_data$Longitude <- as.numeric(CTD_data$Longitude)
CTD_data$Temp <- as.numeric(CTD_data$Temp)
CTD_data$Location_category <- as.factor(CTD_data$Location_category)
CTD_data$Year <- as.factor(CTD_data$Year)

#####
# TWO EXCEL FILES TOGETHER
#####
# We already have CTD_data as one file, which is above

# Fish data abundance
Fish_abundance <- read_excel("Inverted_data_number.xlsx")

# Added and combing year and station
Fish_abundance$Station_ID <-
  paste(Fish_abundance$Year,Fish_abundance$Station, sep = "_")

# Omitting stuff not needed
```

```
Fish_abundance <- Fish_abundance[, -which(names(Fish_abundance) == "Extra stuff")]

# Merging the two data sets into one
CTD_Fish_Abundance <- merge(CTD_data, Fish_abundance, by =c("Station_ID","Year"))

# Another merge event with other data = weight
Fish_weight <- read_excel("Inverted_fish_weight.xlsx")

# Added and combing year and station
Fish_weight$Station_ID <-
  paste(Fish_weight$Year,Fish_weight$Station, sep = "_")

# Omitting stuff not needed
Fish_weight <- Fish_weight[, -which(names(Fish_weight) == "Extra stuff")]

# Merging the two data sets into one
CTD_Fish_Weight <- merge(CTD_data, Fish_weight, by =c("Station_ID","Year"))

# Pivot longer format of above such as CTD_fish_abundance, and CTD_fish_weight
CTD_Fish_Abundance[, 5:72] <- apply(CTD_Fish_Abundance[, 5:72], 2, as.numeric)

Abundance <- CTD_Fish_Abundance %>%
  pivot_longer(cols = -c(Station_ID, Location, Location_category, Temp, Depth, Longitude,
Latitude,Year, Station,Trawling_min, Decade),
               names_to = "Species",
               values_to = "Count",
               values_drop_na = TRUE)

CTD_Fish_Weight[, 5:71] <- apply(CTD_Fish_Weight[, 5:71], 2, as.numeric)

Weight <- CTD_Fish_Weight %>%
  pivot_longer(cols = -c(Station_ID, Location, Location_category, Temp, Depth, Longitude,
Latitude,Year, Station,Trawling_min, Decade),
               names_to = "Species",
               values_to = "Count",
               values_drop_na = TRUE)

#####
#for list of species without amount of species
# ABUNDANCE
#####
Abundance_no_amount_species <- CTD_Fish_Abundance[, !(names(CTD_Fish_Abundance) %in%
                                                        c( "Amount of species"
                                                        ))]

Abundance_no_amount_species[, 5:71] <- apply(Abundance_no_amount_species[, 5:71], 2,
as.numeric)

Pivot_abundance_no_amount_of_species <- Abundance_no_amount_species %>%
  pivot_longer(cols = -c(Station_ID, Location, Location_category, Temp, Depth, Longitude,
Latitude,Year, Station,Trawling_min, Decade),
               names_to = "Species",
               values_to = "Count",
               values_drop_na = TRUE)

Pivot_abundance_no_amount_of_species <- Pivot_abundance_no_amount_of_species %>%
  mutate(Decade = case_when(Year %in% c("2002","2003","2005","2007","2010") ~ "Early",
                            Year %in%c("2013","2015","2017","2022")~"Late"))
#####
#WEIGHT
#####
Weight_no_amount_species <- CTD_Fish_Weight[, !(names(CTD_Fish_Weight) %in%
                                                  c( "Amount of species"
                                                  ))]

Weight_no_amount_species[, 5:71] <- apply(Weight_no_amount_species[, 5:71], 2, as.numeric)

Pivot_weight_no_amount_of_species <- Weight_no_amount_species %>%
  pivot_longer(cols = -c(Station_ID, Location, Location_category, Temp, Depth, Longitude,
Latitude,Year, Station,Trawling_min, Decade),
               names_to = "Species",
               values_to = "Weight",
               values_drop_na = TRUE)

Pivot_weight_no_amount_of_species <- Pivot_weight_no_amount_of_species %>%
```

```
  mutate(Decade = case_when(Year %in% c("2002","2003","2005","2007","2010") ~ "Early",
                            Year %in%c("2013","2015","2017","2022")~"Late"))

# Correcting weight data
Pivot_weight_no_amount_of_species <- Pivot_weight_no_amount_of_species %>%
  mutate(Weight = if_else(Weight > 1000, Weight / 1e3, Weight))

#####
# Pivot all data coding
#####
Pivot_all_data <- merge(Pivot_abundance_no_amount_of_species,
Pivot_weight_no_amount_of_species,
                        by = c("Station_ID",
                               "Year",
                               "Location",
                               "Location_category",
                               "Temp",
                               "Depth",
                               "Longitude",
                               "Latitude",
                               "Trawling_min",
                               "Station",
                               "Species",
                               "Decade"
                        ))

names(Pivot_all_data)[names(Pivot_all_data)=="Count.y"] <- "Weight"
names(Pivot_all_data)[names(Pivot_all_data)=="Count.x"] <- "Count"

Pivot_all_data <- Pivot_all_data %>% mutate(Decade = case_when(Year %in%
c("2002","2003","2005","2007","2010") ~ "Early",
                                                               Year
%in%c("2013","2015","2017","2022")~"Late"))

Pivot_all_data <- Pivot_all_data %>% mutate(Order = case_when
                                            (Species %in% c("Somniosus microcephalus") ~
"Squaliformes",
                                              Species %in%c("Amblyraja hyperborea",
                                                            "Amblyraja radiata")
                                              ~"Rajiformes",
                                              Species %in% c("Mallotus villosus") ~
"Osmeriformes",
                                              Species %in% c("Argyropelecus hemigymnus") ~
"Stomiiformes",
                                              Species %in% c("Benthosema glaciale") ~
"Myctophiformes",
                                              Species %in% c("Arctogadus glacialis",
                                                             "Boreogadus saida",
                                                             "Gadus morhua",
                                                             "Gaidropsarus argentatus")
                                              ~ "Gadiformes",
                                              Species %in% c("Gasterosteus aculeatus") ~
"Gasterosteiformes",
                                              Species %in% c("Sebastes mentella",
                                                             "Artediellus atlanticus",
                                                             "Artediellus uncinatus",
                                                             "Gymnocanthus tricuspis",
                                                             "Icelus bicornis",
                                                             "Myoxocephalus quadricornis",
                                                             "Myoxocephalus scorpius",
                                                             "Triglops nybelini",
                                                             "Triglops pingelii",
                                                             "Cottunculus microps",
                                                             "Cottunculus subspinosus",
                                                             "Leptagonus decagonus",
                                                             "Eumicrotremus spinosus",
                                                             "Careproctus micropus",
                                                             "Careproctus reinhardti",
                                                             "Liparis bathyarcticus",
                                                             "Liparis fabricii",
                                                             "Liparis tunicatus",
                                                             "Paraliparis bathybius",
                                                             "Rhodichthys regina")
                                              ~ "Scorpaeniformes",
                                              Species %in% c("Gymnelus retrodorsalis",
```

```
                                                             "Lycenchelys kolthoffi",
                                                             "Lycenchelys muraena",
                                                             "Lycodes eudipleurostictus",
                                                             "Lycodes frigidus",
                                                             "Lycodes paamiuti",
                                                             "Lycodes pallidus",
                                                             "Lycodes reticulatus",
                                                             "Lycodes rossi",
                                                             "Lycodes seminudus",
                                                             "Lycodes squamiventer",
                                                             "Lycodonus flagellicauda",
                                                             "Leptoclinus maculatus",
                                                             "Anarhichas denticulatus")
                                              ~ "Perciformes",
                                              Species %in% c("Hippoglossoides platessoides",
                                                             "Reinhardtius hippoglossoides")
                                              ~ "Pleuronectiformes"
                                            ))

Pivot_all_data <- Pivot_all_data %>% mutate(Family = case_when
                                            (Species %in% c("Somniosus microcephalus") ~
"Somniosidae",
                                              Species %in% c("Amblyraja hyperborea",
                                                             "Amblyraja radiata"
                                              )~"Rajidae",
                                              Species %in% c("Mallotus villosus") ~
"Osmeridae",
                                              Species %in% c("Argyropelecus hemigymnus") ~
"Sternoptychidae",
                                              Species %in% c("Benthosema glaciale") ~
"Myctophidae",
                                              Species %in% c("Arctogadus glacialis",
                                                             "Boreogadus saida",
                                                             "Gadus morhua"
                                              )~ "Gadidae",
                                              Species %in% c("Gaidropsarus argentatus") ~
"Lotidae",
                                              Species %in% c("Gasterosteus aculeatus") ~
"Gasterosteidae",
                                              Species %in% c("Sebastes mentella")~
"Sebastidae",
                                              Species %in% c("Artediellus atlanticus",
                                                             "Artediellus uncinatus",
                                                             "Gymnocanthus tricuspis",
                                                             "Icelus bicornis",
                                                             "Myoxocephalus quadricornis",
                                                             "Myoxocephalus scorpius",
                                                             "Triglops nybelini",
                                                             "Triglops pingelii"
                                              )~ "Cottidae",
                                              Species %in% c("Cottunculus microps",
                                                             "Cottunculus subspinosus"
                                              )~ "Psychrolutidae",
                                              Species %in% c("Leptagonus decagonus") ~
"Agonidae",
                                              Species %in% c("Eumicrotremus spinosus") ~
"Cyclopteridae",
                                              Species %in% c("Careproctus micropus",
                                                             "Careproctus reinhardti",
                                                             "Liparis bathyarcticus",
                                                             "Liparis fabricii",
                                                             "Liparis tunicatus",
                                                             "Paraliparis bathybius",
                                                             "Rhodichthys regina"
                                              )~ "Lipiridae",
                                              Species %in% c("Gymnelus retrodorsalis",
                                                             "Lycenchelys kolthoffi",
                                                             "Lycenchelys muraena",
                                                             "Lycodes eudipleurostictus",
                                                             "Lycodes frigidus",
                                                             "Lycodes paamiuti",
                                                             "Lycodes pallidus",
                                                             "Lycodes reticulatus",
                                                             "Lycodes rossi",
                                                             "Lycodes seminudus",
```

```
                                                             "Lycodes squamiventer",
                                                             "Lycodonus flagellicauda"
                                              )~ "Zoarchidae",
                                              Species %in% c("Leptoclinus maculatus") ~
"Stichaeidae",
                                              Species %in% c("Anarhichas denticulatus") ~
"Anarhichadidae",
                                              Species %in% c("Hippoglossoides platessoides",
                                                             "Reinhardtius hippoglossoides"
                                              )~ "Pleuronectidae"
                                            ))


Pivot_all_data <- Pivot_all_data %>% mutate( Zoogeography = case_when
                                          (Species %in% c("Amblyraja hyperborea",
                                                          "Artediellus uncinatus",
                                                          "Boreogadus saida",
                                                          "Careproctus micropus",
                                                          "Careproctus reinhardti",
                                                          "Cottunculus subspinosus",
                                                          "Eumicrotremus spinosus",
                                                          "Gymnelus retrodorsalis",
                                                          "Gymnocanthus tricuspis",
                                                          "Icelus bicornis",
                                                          "Liparis bathyarcticus",
                                                          "Liparis fabricii",
                                                          "Liparis tunicatus",
                                                          "Lycenchelys kolthoffi",
                                                          "Lycenchelys muraena",
                                                          "Lycodes eudipleurostictus",
                                                          "Lycodes frigidus",
                                                          "Lycodes pallidus",
                                                          "Lycodes paamiuti",
                                                          "Lycodes reticulatus",
                                                          "Lycodes rossi",
                                                          "Lycodes seminudus",
                                                          "Lycodes squamiventer",
                                                          "Lycodonus flagellicauda",
                                                          "Myoxocephalus quadricornis",
                                                          "Paraliparis bathybius",
                                                          "Rhodichthys regina",
                                                          "Triglops nybelini"
                                                                   ) ~ "Arctic",
                                           Species %in% c("Amblyraja radiata",
                                                          "Anarhichas denticulatus",
                                                          "Arctogadus glacialis",
                                                          "Artediellus atlanticus",
                                                          "Benthosema glaciale",
                                                          "Cottunculus microps",
                                                          "Gaidropsarus argentatus",
                                                          "Hippoglossoides platessoides",
                                                          "Leptagonus decagonus",
                                                          "Leptoclinus maculatus",
                                                          "Mallotus villosus",
                                                          "Myoxocephalus scorpius",
                                                          "Reinhardtius hippoglossoides",
                                                          "Triglops pingelii"
                                                                   ) ~ "Arctic-Boreal",
                                           Species %in% c("Gadus morhua",
                                                          "Sebastes mentella"
                                                                   ) ~ "Boreal",
                                           Species %in% c("Argyropelecus hemigymnus"
                                                                   ) ~ "Widely distributed"
                                            ))

Pivot_all_data <- Pivot_all_data %>%  mutate(Comparison_station = case_when(
                                                Station_ID %in% c("2010_7","2013_2") ~ "Ella Ø
East",
                                                Station_ID %in% c("2010_13","2013_3") ~
"Moskusoksefjord",
                                                Station_ID %in%
c("2002_1291","2003_897","2013_5","2022_17") ~ "Godthåb gulf",
                                                Station_ID %in% c("2003_895","2013_6") ~
"Tyrolerfjord",
                                                Station_ID %in%
```

```
c("2003_892","2013_8","2022_15") ~ "Bredefjord",
                                                Station_ID %in% c("2003_893","2022_16") ~
"Ardencaple fjord",
                                                Station_ID %in%
c("2003_889","2017_1300","2022_9") ~ "Bessel fjord A",
                                                Station_ID %in%
c("2003_890","2017_1284","2022_7") ~ "Bessel fjord B",
                                                Station_ID %in% c("2003_891","2017_1306") ~
"Store belt",
                                                Station_ID %in%
c("2002_1287","2003_887","2017_1316","2022_3") ~ "Dove bugt",
                                                Station_ID %in% c("2002_1272","2017_1365") ~
"Belgica bank",
                                                Station_ID %in% c("2003_883","2013_11") ~
"Offshore Haystack",
                                                Station_ID %in% c("2005_640","2010_1","2013_1")
~ "Davy sund A",
                                                Station_ID %in% c("2005_642","2022_18") ~ "Davy
sund B",
                                                Station_ID %in% c("2003_901","2010_15") ~
"Offshore Bontekoe Ø",
                                                Station_ID %in% c("2007_171","2005_643") ~
"Scoresbysund fjord",
                                                Station_ID %in% c("2003_894", "2013_10") ~
"Offshore Hochstetter"
                                              ))

# Adding columns for oceanic stratification category
Pivot_all_data <- Pivot_all_data %>%
  mutate(Oceanic_stratification = case_when(
    between(Depth, 0, 200)  ~ "Epipelagic",
    between(Depth, 201, 1000)  ~ "Mesopelagic",
    between(Depth, 1001, 2000)  ~ "Bathypelagic",
    TRUE ~ NA_character_
  ))

# Filtering the species that I do not need, because they're from other gear
Pivot_all_data <- Pivot_all_data[!((Pivot_all_data$Station_ID == "2010_7" &
Pivot_all_data$Species == "Icelus bicornis")|
                                     (Pivot_all_data$Station_ID =="2010_7" &
Pivot_all_data$Species == "Myoxocephalus scorpius")|
                                     (Pivot_all_data$Station_ID =="2010_9" &
Pivot_all_data$Species == "Gymnocanthus tricuspis")|
                                     (Pivot_all_data$Station_ID =="2010_9" &
Pivot_all_data$Species == "Myoxocephalus scorpius")|
                                     (Pivot_all_data$Station_ID =="2010_9" &
Pivot_all_data$Species == "Myoxocephalus quadricornis")|
                                     (Pivot_all_data$Station_ID =="2010_14" &
Pivot_all_data$Species == "Gasterosteus aculeatus")|
                                     (Pivot_all_data$Station_ID =="2010_14" &
Pivot_all_data$Species == "Gymnocanthus tricuspis")|
                                     (Pivot_all_data$Station_ID =="2010_14" &
Pivot_all_data$Species == "Myoxocephalus quadricornis")|
                                     (Pivot_all_data$Station_ID =="2015_1312" &
Pivot_all_data$Species == "Gaidropsarus argentatus")|
                                     (Pivot_all_data$Station_ID =="2015_1321" &
Pivot_all_data$Species == "Gymnelus retrodorsalis")|
                                     (Pivot_all_data$Station_ID =="2015_1329" &
Pivot_all_data$Species == "Gymnelus retrodorsalis")|
                                     (Pivot_all_data$Station_ID =="2015_1339" &
Pivot_all_data$Species == "Gymnelus retrodorsalis")|
                                     (Pivot_all_data$Station_ID =="2015_1339" &
Pivot_all_data$Species == "Lycodes eudipleurostictus")|
                                     (Pivot_all_data$Station_ID =="2015_1345" &
Pivot_all_data$Species == "Lycenchelys muraena")|
                                     (Pivot_all_data$Station_ID =="2015_1345" &
Pivot_all_data$Species == "Cottunculus microps")|
                                     (Pivot_all_data$Station_ID =="2015_1345" &
Pivot_all_data$Species == "Lycodes eudipleurostictus")|
                                     (Pivot_all_data$Station_ID =="2015_1355" &
Pivot_all_data$Species == "Lycodonus flagellicauda")
),]

# Species richness SPECIES
SR_SPECIES <- Pivot_all_data %>% group_by(Station_ID) %>%
```

```r
summarise(SR_Species=length(unique(Species)))
CTD_data <- merge(CTD_data, SR_SPECIES, by =c("Station_ID"))

#Species richness FAMILY
SR_FAMILY <- Pivot_all_data %>% group_by(Station_ID) %>%
summarise(SR_Family=length(unique(Family)))
CTD_data <- merge(CTD_data, SR_FAMILY, by =c("Station_ID"))

#Species richness ORDER
SR_ORDER <- Pivot_all_data %>% group_by(Station_ID) %>%
summarise(SR_Order=length(unique(Order)))
CTD_data <- merge(CTD_data, SR_ORDER, by =c("Station_ID"))

# Cumulated weight SPECIES

# Calculate the sum of weights for each species within each station
Species_weights <- Pivot_all_data %>%
  group_by(Station_ID, Species) %>%
  summarise(CW_Species = sum(Weight, na.rm = TRUE))

# Summarize the total weight for each station
Sta_wei_SPECIES <- Species_weights %>%
  group_by(Station_ID) %>%
  summarise(Total_weight = sum(CW_Species, na.rm = TRUE))

# Merge the summarized data back into CTD_data
CTD_data <- merge(CTD_data, Sta_wei_SPECIES, by = "Station_ID")

# Cumulated abundance
Species_total_count <- Pivot_all_data %>%
  group_by(Station_ID, Species) %>%
  summarise(TL_Species = sum(Count, na.rm = TRUE))

# Summarize the total abundace for each station
Sta_abun_species <- Species_total_count %>%
  group_by(Station_ID) %>%
  summarise(Total_species_count = sum(TL_Species, na.rm = TRUE))

# Merge the summarized data back into CTD_data
CTD_data <- merge(CTD_data, Sta_abun_species, by = "Station_ID")

# SPECIES DIVERSITY
Shannon_diversity <- with(Pivot_all_data, tapply(Count, Station_ID, FUN = function(x)
diversity(x, index = "shannon")))

Simpson_diversity <- with(Pivot_all_data, tapply(Count, Station_ID, FUN = function(x)
diversity(x, index = "simpson")))

Diversity_table <- data.frame(Station_ID = names(Shannon_diversity),
                              Shannon_diversity = Shannon_diversity,
                              Simpson_diversity = Simpson_diversity)

# Create a nice-looking table
Diversity_visual_table <- Diversity_table %>%
  kable("html") %>%
  kable_styling()

Diversity_visual_table

# Export the table to a file (e.g., CSV)
#write.csv(Diversity_table, "Diversity_table.csv", row.names = FALSE)

# "Putting diversity values to main dataset

CTD_data <- mutate(CTD_data, Diversity_table)

# Overlapping stations
CTD_data <- CTD_data %>%
  mutate(Comparison_station = case_when(
    Station_ID %in% c("2010_7","2013_2") ~ "Ella Ø East",
    Station_ID %in% c("2010_13","2013_3") ~ "Moskusoksefjord",
    Station_ID %in% c("2002_1291","2003_897","2013_5","2022_17") ~ "Godthåb gulf",
    Station_ID %in% c("2003_895","2013_6") ~ "Tyrolerfjord",
    Station_ID %in% c("2003_892","2013_8","2022_15") ~ "Bredefjord",
    Station_ID %in% c("2003_893","2022_16") ~ "Ardencaple fjord",
```

```
    Station_ID %in% c("2003_889","2017_1300","2022_9") ~ "Bessel fjord A",
    Station_ID %in% c("2003_890","2017_1284","2022_7") ~ "Bessel fjord B",
    Station_ID %in% c("2003_891","2017_1306") ~ "Store belt",
    Station_ID %in% c("2002_1287","2003_887","2017_1316","2022_3") ~ "Dove bugt",
    Station_ID %in% c("2002_1272","2017_1365") ~ "Belgica bank",
    Station_ID %in% c("2003_883","2013_11") ~ "Offshore Haystack",
    Station_ID %in% c("2005_640","2010_1","2013_1") ~ "Davy sund A",
    Station_ID %in% c("2005_642","2022_18") ~ "Davy sund B",
    Station_ID %in% c("2003_901","2010_15") ~ "Offshore Bontekoe Ø",
    Station_ID %in% c("2003_894", "2013_10") ~ "Offshore Hochstetter"
    ))

#EARLY time period
EARLY_CTD <- subset (CTD_data, Decade =="Early")
EARLY_pivot <- subset (Pivot_all_data, Decade == "Early")

# LATE time period
LATE_CTD <- subset (CTD_data, Decade =="Late")
LATE_pivot <- subset (Pivot_all_data, Decade =="Late")

# Data set for comparing time series
Time_series_data_PIVOT <- subset(Pivot_all_data, Latitude >= 72.000)
Time_series_data_CTD <- subset(CTD_data, Latitude >= 72.000)
Time_series_data_CTD_EARLY <- subset (Time_series_data_CTD, Decade =="Early")
Time_series_data_CTD_LATE <- subset (Time_series_data_CTD, Decade =="Late")
Time_series_data_PIVOT_EARLY <- subset (Time_series_data_PIVOT, Decade =="Early")
Time_series_data_PIVOT_LATE <- subset (Time_series_data_PIVOT, Decade =="Late")

#####
# MAPS
#####
# Defining the map locations

basemap(limits = c(-65,-15,59,85))

basemap(limits = c(-40,-15,70,85))

#Maps with bathymetry information
basemap(limits = c(-45, -15, 70, 85), bathymetry = TRUE)

# Scalebar and north arrow in map
basemap(limits = c(-45, -15, 70, 85), rotate = TRUE) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true")

#Fishing regions on map
data(fdir_areas)

basemap(fdir_main_areas) +
  ggspatial::annotation_spatial(fdir_main_areas, fill = NA)
#####
# firkant til map af grønland
basemap(limits = c(-30, -5, 70, 80))

# The two maps next to each other
# Does not really align
grid.arrange(Study_area_map, Map_all_stations,nrow = 1)

# But this do!
Study_area_map|Map_all_stations

# Another way
facet_grid()

plot_annotation(tag_levels = "A")

#####
# Greenland whole
.ggOceanMapsenv <- new.env()
.ggOceanMapsenv$datapath <- "C:/Users/bruger/OneDrive - UiT Office 365/Desktop/Master thesis"

Greenland <- basemap(limits = c(-50,-10,59,85), bathymetry = TRUE, glaciers = TRUE, shapefiles
= "Arctic", grid.col = "NA")

Study_area_map <- Greenland +
```

```
  geom_sf() +
  geom_spatial_rect(aes(xmin = -30, xmax = -5, ymin = 70, ymax = 80),color =
"red",fill="transparent")  +
  ggspatial::annotation_scale(location = "br") +
  labs(
    title = "Study area",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)") +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 32),
    axis.title = element_text(size = 16)
  ) +
  guides(fill = guide_none())

Study_area_map
# Picture save for poster
ggsave("Greenland_and_area.png", Study_area_map, width = 12, height = 9, dpi = 600)

# Map with all stations 2002-2022
Map_all_stations <-
  basemap(limits = c(-30, -5, 70, 80), data = CTD_data, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(CTD_data),
    aes(x = Longitude, y = Latitude, color = (CTD_data$Year), size= 4)
  ) +scale_size(guide = "none") +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "All stations 2002-2022",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)",
    color = "Stations for each year"
  ) +
scale_color_brewer(palette = "YlOrRd", name = "Year") +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 32),
    axis.title = element_text(size = 16)
  ) +
  guides(
    color = guide_legend(override.aes = list(fill = "white", size = 5))
  )

Map_all_stations

ggsave("Stations map.png", Map_all_stations, width = 12, height = 9, dpi = 600)

MAP1 <- Study_area_map|Map_all_stations
MAP1
ggsave("Study_area.png", MAP1, width = 12, height = 8, dpi = 600)

# Cut off line for temporal comparisons
Cut_off_line <- geom_spatial_rect(aes(xmin = -40, xmax = -0, ymin = 71.97, ymax = 72.03),color
= "red",fill="red")

#####
#####
# Kort med navne på
#####
# EARLY STATION ID
EARLY_stations <-
basemap(limits = c(-30, -5, 70, 80), data = EARLY_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(EARLY_CTD),
    aes(x = Longitude, y = Latitude, color = as.factor(EARLY_CTD$Year))
  ) +
```

```
  geom_text(
    data = transform_coord(EARLY_CTD),
    aes(x = Longitude, y = Latitude, label = EARLY_CTD$Station_ID),
    vjust = 0, hjust = 0,
    color = "black",
    size = 2
  ) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Early time period stations",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)",
    color = "Stations for each year"
  ) +
  scale_color_brewer(palette = "YlOrRd",
                     name = "Year",
                     labels = as.character(unique(EARLY_CTD$Year))) +
  theme(
    legend.box.background = element_blank(),
    legend.background = element_rect(fill= "white"),
    legend.key = element_rect(color = "white",fill = "white"),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white",size=5)),
    color = guide_legend(override.aes = list(fill = "white", size=5))
  )+
  Cut_off_line

EARLY_stations

# LATE STATION ID
LATE_stations <-
basemap(limits = c(-30, -5, 70, 80), data = LATE_CTD, bathymetry = TRUE) +
geom_point(
  data = transform_coord(LATE_CTD),
  aes(x = Longitude, y = Latitude, color = as.factor(LATE_CTD$Year))
) +
  geom_text_repel(
    data = transform_coord(LATE_CTD),
    aes(x = Longitude, y = Latitude, label = LATE_CTD$Station_ID),
    vjust = 0, hjust = 0,
    color = "black",
    size = 2
  ) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Late time period stations",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)",
    color = "Stations for each year"
  ) +
  scale_color_brewer(palette = "YlOrRd",
                     name = "Year",
                     labels = as.character(unique(LATE_CTD$Year))) +
  theme(
    legend.box.background = element_blank(),
    legend.background = element_rect(fill= "white"),
    legend.key = element_rect(color = "white",fill = "white"),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white",size=5)),
    color = guide_legend(override.aes = list(fill = "white", size=5))
  )+
```

```
  Cut_off_line

LATE_stations

Station_ID <- EARLY_stations|LATE_stations
Station_ID

ggsave("Station_ID maps.png", Station_ID, width = 18, height = 9, dpi=600)

# MORE MAPS
#####
# Time period and geographical map
#####
Station_category <-
  basemap(limits = c(-30, -5, 70, 80), data = CTD_data, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(CTD_data),
    aes(x = Longitude, y = Latitude, color = as.factor(CTD_data$Decade), shape =
(CTD_data$Location_category),size = 3, alpha = 0.999)
  ) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Station categorization",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)",
    shape = "Geographical \ncategorization"
  ) +
  scale_color_viridis(discrete=T,name = "Decade\ncategorization", na.translate=FALSE) +
  scale_shape_manual(values = c("Fjord" = 20, "Shelf" = 15, "Slope" = 17),na.translate=FALSE) +
  scale_alpha(guide = "none") +
  scale_size(guide = "none") +
  theme(
    legend.box.background = element_blank(),
    legend.background = element_blank(),
    legend.key = element_rect(color = "transparent",fill = "transparent"),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "transparent",size=5)),
    color = guide_legend(override.aes = list(fill = "transparent", size=5))
  )+
  Cut_off_line

Station_category

ggsave("Station category.png", Station_category, width = 12, height = 9, dpi = 600)
#####
#####
# DISTANCE TO COAST
#####
Distance_to_coast <- dist2land(CTD_data, verbose = FALSE)
colnames(Distance_to_coast)[colnames(Distance_to_coast) == "ldist"] <- "Coast_distance"

# Define distance ranges
Distance_ranges <- c(0,50, 100, 150, 200, 250, 300, 350,400)
Distance_labels <- c("0-50", "51-100", "101-150", "151-200","201-250","251-300","301-350","351-
400")

# Create a new column with categorical labels for distance ranges
Distance_to_coast <- Distance_to_coast %>%
  mutate(
    Distance_Group = cut(
      Coast_distance,
      breaks = Distance_ranges,
      labels = Distance_labels,
      include.lowest = TRUE
    )
  )

# Plot with grouped distance to coast
```

```
Distance_to_coast_map <-
  basemap(limits = c(-30, -5, 70, 80), data = Distance_to_coast, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(Distance_to_coast),
    aes(x = Longitude,
        y = Latitude,
        color = as.factor(Distance_to_coast$Distance_Group),
        alpha = 0.999,
        shape = Distance_to_coast$Decade),
        size = 4
  ) +
  scale_colour_viridis_d(
    option = "plasma",
    name = "Distance \nto coast (km)",
    labels = Distance_labels,
    breaks = Distance_labels,
    guide = "legend"
  ) +
  scale_size(guide = "none") +
  scale_alpha(guide = "none")+
  scale_shape_manual(values = c("Early" = 17, "Late" = 15),
                     name = "Decade \ncategorization") +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Distance to coast",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
      ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "transparent",size=5)),
    color = guide_legend(override.aes = list(fill = "transparent", size=5)),
  ) +
  Cut_off_line

Distance_to_coast_map
ggsave("Distance to coast.png", Distance_to_coast_map, width = 12, height = 9, dpi = 600)

#####
#####
# SPECIES RICHNESS
#####
# Graph amount of species number
SR_Species_graph <- ggplot(data = CTD_data, (aes(x = Station_ID, y = SR_Species, fill =
as.character(Year)))) +
  geom_bar(stat = "identity") +
  scale_fill_brewer(palette = "Paired") +
  scale_y_continuous(expand = c(0,0))+
  labs(
    title = "Number of species per station 2002-2022",
    x = "Station",
    y = "Number",
    fill = "Year") +
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 14),
    legend.text = element_text(color = "black", size = 12),
    axis.text.x = element_text(angle = 90, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 12)
  )

SR_Species_graph
#ggsave("Species number per station.png", SR_Species_graph, width = 16, height = 9, dpi = 600)
```

```
#####
#####
# BOXPLOTS
#####
# Boxplot of early and late decade
CTD_data$Year <- as.character(CTD_data$Year)

# SPECIES
#####
Boxplot_species_richness_year <-
  ggplot(data = CTD_data, aes(x = Year, y = SR_Species, fill = as.character(Year))) +
  geom_boxplot() +
  scale_fill_brewer(palette = "Paired") +
  labs(title = "Species richness over year",
       x = "Year",
       y = "Species richness",
       fill = "Year") +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 40),
    axis.title = element_text(size = 28),
  ) +
  scale_y_continuous(breaks = seq(0, max(CTD_data$SR_Species), by = 4))

Boxplot_species_richness_year

ggsave("Boxplot_species_richness_year.png", Boxplot_species_richness_year, width = 16, height =
9, dpi = 600)

# Boxplot by decade ALL
Boxplot_SR_Species_decade_ALL <-
  ggplot(data = CTD_data, aes(x = Decade, y = SR_Species, fill = Decade)) +
  geom_boxplot() +
  labs(title = "Species richness by decade (all)",
       x = "Decade",
       y = "Species richness") +
  scale_fill_manual(values = c("skyblue", "forestgreen")) +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 30),
    axis.title = element_text(size = 28)
  )  +
  scale_y_continuous(breaks = c(4, 8, 12, 16, 20), limits = c(0,20))

Boxplot_SR_Species_decade_ALL

# Boxplot by decade TIME SERIES
Boxplot_SR_Species_decade_NOT <-
  ggplot(data = Time_series_data_CTD, aes(x = Decade, y = SR_Species, fill = Decade)) +
  geom_boxplot() +
  labs(title = "Species richness by decade (cut)",
       x = "Decade",
       y = "Species richness") +
  scale_fill_manual(values = c("skyblue", "forestgreen")) +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 30),
    axis.title = element_text(size = 28)
  )  +
  scale_y_continuous(breaks = c(4, 8, 12, 16, 20), limits = c(0,20))

Boxplot_SR_Species_decade_NOT

Boxplot_richness_decade_species <- Boxplot_SR_Species_decade_ALL +
Boxplot_SR_Species_decade_NOT
Boxplot_richness_decade_species
```

```
ggsave("Boxplot_richness_decade_species.png", Boxplot_richness_decade_species, width = 15,
height = 9, dpi = 600)

# SPECIES RICHNESS ON MAP
#####
# 17 colours
#####
Map_colours_17 <- c("2"="aquamarine","3"="magenta","4"="darkslategrey","5"="deeppink",
                     "6"="deeppink3","7"="brown1","8"="darkorange3","9"="antiquewhite3",
                     "10"="yellow", "11"="black","12"="pink2","13"="cyan",
                     "14"="cyan3","15"="darkolivegreen","16"="red","17"="blue1")
#####
# EARLY map Species richness
#####
SR_Species_map_EARLY <-
  basemap(limits = c(-30, -5, 70, 80), data = EARLY_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(EARLY_CTD),
    aes(x = Longitude, y = Latitude,
        size = EARLY_CTD$SR_Species,
        color = EARLY_CTD$SR_Species),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8),
             breaks = c(0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18),
             name = "Species \nrichness") +
  scale_color_viridis_c(name = "Species \nrichness",
                        option = "rocket",
                        n = 18,
                        direction = 1) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Species richness early time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "transparent")),
    color = guide_legend(override.aes = list(fill = "transparent"))
  ) +
  Cut_off_line

SR_Species_map_EARLY

# LATE map Species richness
SR_Species_map_LATE <-
  basemap(limits = c(-30, -5, 70, 80), data = LATE_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(LATE_CTD),
    aes(x = Longitude, y = Latitude,
        size = LATE_CTD$SR_Species,
        color = LATE_CTD$SR_Species),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8),
             breaks = c(0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18),
             name = "Species \nrichness") +
  scale_color_viridis_c(name = "Species \nrichness",
                        option = "rocket",
                        n = 18,
                        direction = 1) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
```

```
    title = "Species richness late time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "transparent")),
    color = guide_legend(override.aes = list(fill = "transparent"))
  ) +
  Cut_off_line

SR_Species_map_LATE

Species_richness_map <- SR_Species_map_EARLY|SR_Species_map_LATE
Species_richness_map

ggsave("Species richness BOTH.png", Species_richness_map, width = 18, height = 9, dpi = 600)

#####
# FAMILY
#####
Boxplot_family_richness_year <-
  ggplot(data = CTD_data, aes(x = Year, y = SR_Family, fill = as.character(Year))) +
  geom_boxplot() +
  scale_fill_brewer(palette = "Paired") +
  labs(title = "Family richness over year",
       x = "Year",
       y = "Family richness",
       fill = "Year") +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 40),
    axis.title = element_text(size = 28),
  ) +
  scale_y_continuous(breaks = seq(0, max(CTD_data$SR_Family), by = 4))

Boxplot_family_richness_year

ggsave("Boxplot_family_richness_year.png", Boxplot_family_richness_year, width = 16, height =
9, dpi = 600)

# Boxplot by decade ALL
Boxplot_SR_Family_decade_ALL <-
  ggplot(data = CTD_data, aes(x = Decade, y = SR_Family, fill = Decade)) +
  geom_boxplot() +
  labs(title = "Family richness by decade (all)",
       x = "Decade",
       y = "Family richness") +
  scale_fill_manual(values = c("skyblue", "forestgreen")) +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 30),
    axis.title = element_text(size = 28)
  )  +
  scale_y_continuous(breaks = seq(0, max(CTD_data$SR_Family), by = 4))

Boxplot_SR_Family_decade_ALL

# Boxplot by decade TIME SERIES

Boxplot_SR_Family_decade_NOT <-
```

```
  ggplot(data = Time_series_data_CTD, aes(x = Decade, y = SR_Family, fill = Decade)) +
  geom_boxplot() +
  labs(title = "Family richness by decade (cut)",
       x = "Decade",
       y = "Family richness") +
  scale_fill_manual(values = c("skyblue", "forestgreen")) +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 30),
    axis.title = element_text(size = 28)
  )  +
  scale_y_continuous(breaks = seq(0, max(Time_series_data_CTD$SR_Family), by = 4))

Boxplot_SR_Family_decade_NOT

Boxplot_richness_decade_family <- Boxplot_SR_Family_decade_ALL|Boxplot_SR_Family_decade_NOT
Boxplot_richness_decade_family

ggsave("Boxplot_richness_decade_family.png", Boxplot_richness_decade_family, width = 15, height
= 9, dpi = 600)

# COMBINED THE TWO CODES INTO ONE
SR_Family_map_EARLY <-
  basemap(limits = c(-30, -5, 70, 80), data = EARLY_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(EARLY_CTD),
    aes(x = Longitude, y = Latitude,
        size = EARLY_CTD$SR_Family,
        color = EARLY_CTD$SR_Family),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8),
             breaks = c(0,1,2,3,4,5,6,7,8,9,10),
             name = "Family \nrichness") +
  scale_color_viridis_c(name = "Family \nrichness",
                        option = "plasma",
                        n = 10,
                        direction = 1) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Family richness early time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white"))
  ) +
  Cut_off_line

SR_Family_map_EARLY

# LATE map Species richness
SR_Family_map_LATE <-
  basemap(limits = c(-30, -5, 70, 80), data = LATE_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(LATE_CTD),
    aes(x = Longitude, y = Latitude,
        size = LATE_CTD$SR_Family,
        color = LATE_CTD$SR_Family),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
```

```
  scale_size(range = c(3, 8),
             breaks = c(0,1,2,3,4,5,6,7,8,9,10),
             name = "Family \nrichness") +
  scale_color_viridis_c(name = "Family \nrichness",
                        option = "plasma",
                        n = 10,
                        direction = 1) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Family richness late time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white"))
  ) +
  Cut_off_line

SR_Family_map_LATE

Family_richness_map <- SR_Family_map_EARLY|SR_Family_map_LATE
Family_richness_map

ggsave("Family richness BOTH.png", Family_richness_map, width = 18, height = 9, dpi = 600)

#####
# ORDER
#####
# ORDER RICHNESS ON MAP
Boxplot_order_richness_year <-
  ggplot(data = CTD_data, aes(x = Year, y = SR_Order, fill = as.character(Year))) +
  geom_boxplot() +
  scale_fill_brewer(palette = "Paired") +
  labs(title = "Order richness over year",
       x = "Year",
       y = "Order richness",
       fill = "Year") +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 40),
    axis.title = element_text(size = 28),
  ) +
  scale_y_continuous(breaks = seq(0, max(CTD_data$SR_Order), by = 4))

Boxplot_order_richness_year

ggsave("Boxplot_order_richness_year.png", Boxplot_order_richness_year, width = 16, height = 9,
dpi = 600)

# Boxplot by decade ALL
Boxplot_SR_Order_decade_ALL <-
  ggplot(data = CTD_data, aes(x = Decade, y = SR_Order, fill = Decade)) +
  geom_boxplot() +
  labs(title = "Order richness by decade (all)",
       x = "Decade",
       y = "Order richness") +
  scale_fill_manual(values = c("skyblue", "forestgreen")) +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(size = 18, color = "black"),
```

```
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 30),
    axis.title = element_text(size = 28)
  )  +
  scale_y_continuous(breaks = seq(0, max(CTD_data$SR_Order), by = 4))

Boxplot_SR_Order_decade_ALL

# Boxplot by decade TIME SERIES

Boxplot_SR_Order_decade_NOT <-
  ggplot(data = Time_series_data_CTD, aes(x = Decade, y = SR_Order, fill = Decade)) +
  geom_boxplot() +
  labs(title = "Order richness by decade (cut)",
       x = "Decade",
       y = "Order richness") +
  scale_fill_manual(values = c("skyblue", "forestgreen")) +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 30),
    axis.title = element_text(size = 28)
  )  +
  scale_y_continuous(breaks = seq(0, max(Time_series_data_CTD$SR_Order), by = 4))

Boxplot_SR_Order_decade_NOT

Boxplot_richness_decade_order <- Boxplot_SR_Order_decade_ALL|Boxplot_SR_Order_decade_NOT
Boxplot_richness_decade_order

ggsave("Boxplot_richness_decade_order.png", Boxplot_richness_decade_order, width = 15, height =
9, dpi = 600)

# ORDER RICHNESS ON MAP
SR_Order_map_EARLY <-
  basemap(limits = c(-30, -5, 70, 80), data = EARLY_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(EARLY_CTD),
    aes(x = Longitude, y = Latitude,
        size = EARLY_CTD$SR_Order,
        color = EARLY_CTD$SR_Order),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8),
             breaks = c(0,1,2,3,4,5,6),
             name = "Order \nrichness") +
  scale_color_viridis_c(name = "Order \nrichness",
                        option = "magma",
                        n = 6,
                        direction = 1) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Order richness early time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white"))
  ) +
  Cut_off_line

SR_Order_map_EARLY
```

```
# LATE map Species richness
SR_Order_map_LATE <-
  basemap(limits = c(-30, -5, 70, 80), data = LATE_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(LATE_CTD),
    aes(x = Longitude, y = Latitude,
        size = LATE_CTD$SR_Order,
        color = LATE_CTD$SR_Order),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8),
             breaks = c(0,1,2,3,4,5,6),
             name = "Order \nrichness") +
  scale_color_viridis_c(name = "Order \nrichness",
                        option = "magma",
                        n = 6,
                        direction = 1) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Order richness late time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white"))
  ) +
  Cut_off_line

SR_Order_map_LATE

Order_richness_map <- SR_Order_map_EARLY|SR_Order_map_LATE
Order_richness_map

ggsave("Order richness BOTH.png", Order_richness_map, width = 18, height = 9, dpi = 600)


#####
# TRAWLING VS. SPECIES RICHNESS/TOTAL WEIGHT/TOTAL FISH COUNT
#####

#SPECIES RICHESS
# Calculate R-squared values for each factor LOCATION CATEGORY
lm_models <- by(CTD_data, CTD_data$Location_category, function(subset) {
  lm_fit <- lm(SR_Species ~ Trawling_min, data = subset)
  rsq <- summary(lm_fit)$r.squared
  return(data.frame(Location_category = unique(subset$Location_category), R_squared = rsq[1]))
})

# Merge the R-squared values with the original dataset
CTD_data <- merge(CTD_data, do.call(rbind, lm_models), by = "Location_category")

# Plot
Trawl_SR <-
ggplot(data = subset(CTD_data, !is.na(Trawling_min)), aes(x = Trawling_min, y = SR_Species,
color = Location_category)) +
  geom_point(size = 5) +
  labs(x = "Trawling time (min)", y = "Species richness", title = "Trawling time vs. species
richness") +
  geom_smooth(method = "lm", aes(group = Location_category, color = Location_category, size =
0.5)) +
  scale_color_viridis_d(name = "Geographical\ncategory", option = "D") +
  theme_classic() +
  theme(
```

```
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 16),
    legend.text = element_text(color = "black", size = 16),
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 16),
    axis.title = element_text(size = 16)
  ) +
  scale_x_continuous(breaks = c(0, 5, 10, 15, 20, 25, 30, 35, 40, 45)) +
  scale_y_continuous(breaks = c(0, 4, 8, 12, 16, 20)) +
  scale_size(guide = "none") +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white"))
  ) +
  geom_text(data = subset(CTD_data, !duplicated(Location_category)),
            aes(label = paste("R² =", round(R_squared, 3))),
            hjust = -0.1, vjust =2, size = 5)

Trawl_SR

ggsave("Trawl_vs_species_richness.png", Trawl_SR, width = 16, height = 9, dpi = 600)

# TOTAL CATCH  WEIGHT
# Calculate R-squared values for each factor LOCATION CATEGORY
lm_models1 <- by(CTD_data, CTD_data$Location_category, function(subset) {
  lm_fit1 <- lm(Total_weight ~ Trawling_min, data = subset)
  rsq1 <- summary(lm_fit1)$r.squared
  return(data.frame(Location_category = unique(subset$Location_category), R_squared1 =
rsq1[1]))
})


# Merge the R-squared values with the original dataset
CTD_data <- merge(CTD_data, do.call(rbind, lm_models1), by = "Location_category")

# Plot
Trawl_TL_Catch <-
  ggplot(data = subset(CTD_data, !is.na(Trawling_min)), aes(x = Trawling_min, y = Total_weight,
color = Location_category)) +
  geom_point(size = 5) +
  labs(x = "Trawling time (min)", y = "Catch weight (kg)", title = "Trawling time vs. total
catch weight") +
  geom_smooth(method = "lm", aes(group = Location_category, color = Location_category, size =
0.5)) +
  scale_color_viridis_d(name = "Geographical\ncategory", option = "D") +
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 20),
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 34),
    axis.title = element_text(size = 24)
  ) +
  scale_x_continuous(breaks = c(0, 5, 10, 15, 20, 25, 30, 35, 40, 45)) +
  scale_y_continuous(breaks = c(0,50,100,150,200,250,300)) +
  scale_size(guide = "none") +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white"))
  ) +
  geom_text(data = subset(CTD_data, !duplicated(Location_category)),
            aes(label = paste("R² =", round(R_squared1, 3))),
            hjust = -0.1, vjust =2, size = 5)

Trawl_TL_Catch

ggsave("Trawl_vs_total_weight.png", Trawl_TL_Catch, width = 16, height = 9, dpi = 600)

Trawl_TL_Catch2 <-
  ggplot(data = subset(CTD_data, !is.na(Trawling_min)), aes(x = Trawling_min, y = Total_weight,
```

```
color = Location_category)) +
  geom_point(size = 5) +
  labs(x = "Trawling time (min)", y = "Catch weight (kg)", title = "Trawling time vs. total
catch weight") +
  geom_smooth(method = "lm", aes(group = Location_category, color = Location_category, size =
0.5)) +
  scale_color_viridis_d(option = "D") +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 16),
    axis.title = element_text(size = 16)
  ) +
  scale_x_continuous(breaks = c(0, 5, 10, 15, 20, 25, 30, 35, 40, 45)) +
  scale_y_continuous(breaks = c(0,50,100,150,200,250,300)) +
  scale_size(guide = "none") +
  geom_text(data = subset(CTD_data, !duplicated(Location_category)),
            aes(label = paste("R² =", round(R_squared1, 3))),
            hjust = -0.1, vjust = 2, size = 5)



#TOTAL ABUNDANCE
# Calculate R-squared values for each factor LOCATION CATEGORY
lm_models2 <- by(CTD_data, CTD_data$Location_category, function(subset) {
  lm_fit2 <- lm(Total_species_count ~ Trawling_min, data = subset)
  rsq2 <- summary(lm_fit2)$r.squared
  return(data.frame(Location_category = unique(subset$Location_category), R_squared2 =
rsq2[1]))
})

# Merge the R-squared values with the original dataset
CTD_data <- merge(CTD_data, do.call(rbind, lm_models2), by = "Location_category")

# Plot
Trawl_TL_Count <-
  ggplot(data = subset(CTD_data, !is.na(Trawling_min)), aes(x = Trawling_min, y =
Total_species_count, color = Location_category)) +
  geom_point(size = 5) +
  labs(x = "Trawling time (min)", y = "Fish count (n)", title = "Trawling time vs. total fish
count") +
  geom_smooth(method = "lm", aes(group = Location_category, color = Location_category, size =
0.5)) +
  scale_color_viridis_d(name = "Geographical\ncategory", option = "D") +
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 20),
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 34),
    axis.title = element_text(size = 24)
  ) +
  scale_x_continuous(breaks = c(0, 5, 10, 15, 20, 25, 30, 35, 40, 45)) +
  scale_size(guide = "none") +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white"))
  ) +
  geom_text(data = subset(CTD_data, !duplicated(Location_category)),
            aes(label = paste("R² =", round(R_squared2, 3))),
            hjust = -0.1, vjust =2, size = 5)

Trawl_TL_Count
ggsave("Trawl_vs_total_count.png", Trawl_TL_Count, width = 16, height = 9, dpi = 600)

Trawl_TL_Count2 <-
  ggplot(data = subset(CTD_data, !is.na(Trawling_min)), aes(x = Trawling_min, y =
Total_species_count, color = Location_category)) +
  geom_point(size = 5) +
  labs(x = "Trawling time (min)", y = "Fish count (n)", title = "Trawling time vs. total fish
```

```
count") +
  geom_smooth(method = "lm", aes(group = Location_category, color = Location_category, size =
0.5)) +
  scale_color_viridis_d(option = "D") +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 16),
    axis.title = element_text(size = 16)
  ) +
  scale_x_continuous(breaks = c(0, 5, 10, 15, 20, 25, 30, 35, 40, 45)) +
  scale_size(guide = "none") +
  geom_text(data = subset(CTD_data, !duplicated(Location_category)),
            aes(label = paste("R² =", round(R_squared2, 3))),
            hjust = -0.1, vjust = 2, size = 5)


Figure_3 <- Trawl_TL_Count2|Trawl_TL_Catch2|Trawl_SR
ggsave("Graphs3.png", Figure_3, width = 16, height = 8, dpi = 600)

#####
# DEPTH CATEGORIZATION
#####
# Calculate R-squared values for each factor LOCATION CATEGORY
lm_models3 <- by(CTD_data, CTD_data$Location_category, function(subset) {
  lm_fit3 <- lm(Depth ~ Trawling_min, data = subset)
  rsq3 <- summary(lm_fit3)$r.squared
  return(data.frame(Location_category = unique(subset$Location_category), R_squared3 =
rsq3[1]))
})

# Merge the R-squared values with the original dataset
CTD_data <- merge(CTD_data, do.call(rbind, lm_models3), by = "Location_category")

Trawl_depth_graph <-
  ggplot(data = subset(CTD_data, !is.na(Trawling_min)), aes(x = Trawling_min, y = Depth, color
= Location_category)) +
  geom_point(size = 5) +
  labs(x = "Trawling minutes", y = "Depth", title = "Trawling time vs. depth") +
  geom_smooth(method = "lm", aes(group = Location_category, color = Location_category, size =
0.5)) +
  scale_color_viridis_d(name = "Geographical\ncategory", option = "D") +
  scale_size(guide = "none") +
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 20),
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 34),
    axis.title = element_text(size = 24)
  )  +
  scale_x_continuous(expand = expansion(add = c(0, 0))) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white"))
  ) +
  geom_text(data = subset(CTD_data, !duplicated(Location_category)),
            aes(label = paste("R² =", round(R_squared3, 3))),
            hjust = -0.4, vjust =-10, size = 5)

Trawl_depth_graph

ggsave("Trawl_vs_depth.png", Trawl_depth_graph, width = 16, height = 9, dpi = 600)

# Check for duplicate column names
duplicated_cols <- duplicated(names(CTD_data))
if (any(duplicated_cols)) {
  print(names(CTD_data)[duplicated_cols])
  # Remove duplicate columns
  CTD_data <- CTD_data[, !duplicated_cols, drop = FALSE]
```

```
}

# Now, create the plot
Trawl_depth_BOXPLOT <-
ggplot(data = CTD_data, aes(x = Location_category, y = Depth, fill = Location_category)) +
  geom_boxplot() +
  scale_fill_viridis_d(option = "D") +
  labs(title = "Depth at different geographical categorizations",
       x = "Location category",
       y = "Depth") +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 18, color = "black"),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 40),
    axis.title = element_text(size = 28)
  ) +
  scale_y_continuous(breaks = c(0,200,400,600,800,1000,1200,1400))

Trawl_depth_BOXPLOT

ggsave("Trawl_vs_depth_boxplot.png", Trawl_depth_BOXPLOT, width = 16, height = 9, dpi = 600)
#####
# Adding columns for oceanic stratification category
Depth_map_EARLY <-
  basemap(limits = c(-30, -5, 70, 80), data = EARLY_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(EARLY_CTD),
    aes(x = Longitude,
        y = Latitude,
        color = (EARLY_CTD$Depth),
        size = (EARLY_CTD$Depth),
        shape = (EARLY_CTD$Location_category))
  ) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Depth categorizations \nearly time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  scale_size(range = c(3, 8),
             breaks = c(0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300),
             name = "Depth \ncategorization") +
  scale_colour_viridis_c(option = "inferno",
                         n=14,
                         name ="Depth \ncategorization",
                         direction = 1) +
  scale_shape_manual(values = c("Fjord" = 20, "Shelf" = 15, "Slope" = 17),
                     name = "Geograhical \ncategorization") +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 12, color = "black"),
    axis.text.y = element_text(size = 12, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 26),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white",size=5), order = 3),
    color = guide_legend(override.aes = list(fill = "white"), order = 2),
    size = guide_legend(order = 2)
  ) +
  Cut_off_line

Depth_map_EARLY
#####
# LATE
#####
Depth_map_LATE <-
  basemap(limits = c(-30, -5, 70, 80), data = LATE_CTD, bathymetry = TRUE) +
  geom_point(
```

```
    data = transform_coord(LATE_CTD),
    aes(x = Longitude,
        y = Latitude,
        color = (LATE_CTD$Depth),
        size = (LATE_CTD$Depth),
        shape = (LATE_CTD$Location_category))
  ) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Depth categorizations \nlate time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  scale_size(range = c(3, 8),
             breaks = c(0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300),
             name = "Depth \ncategorization") +
  scale_colour_viridis_c(option = "inferno",
                         n=14,
                         name ="Depth \ncategorization",
                         direction = 1) +
  scale_shape_manual(values = c("Fjord" = 20, "Shelf" = 15, "Slope" = 17),
                     name = "Geograhical \ncategorization") +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5, size = 12, color = "black"),
    axis.text.y = element_text(size = 12, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 26),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white",size=5), order = 3),
    color = guide_legend(override.aes = list(fill = "white"), order = 2),
    size =guide_legend(order = 2)
  ) +
  Cut_off_line

Depth_map_LATE

# Depth map BOTH

Depth_map_BOTH <- Depth_map_EARLY|Depth_map_LATE
Depth_map_BOTH

ggsave("Depth map BOTH.png", Depth_map_BOTH, width = 18, height = 9, dpi = 600)

#####
# SPECIES DIVERSITY
#####
# Shannon map
Shannon_index_map_EARLY <-
  basemap(limits = c(-30, -5, 70, 80), data = EARLY_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(EARLY_CTD),
    aes(x = Longitude,
        y = Latitude,
        size = EARLY_CTD$Shannon_diversity,
        color = EARLY_CTD$Shannon_diversity),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8), name = "Shannon diversity \nindex") +
  scale_color_gradient(low = "yellow", high = "red", name = "Shannon diversity \nindex") +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Species diversity using the Shannon index\nin early time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
```

```
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 20),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white")),
  ) +
  Cut_off_line

Shannon_index_map_EARLY

Shannon_index_map_LATE <-
  basemap(limits = c(-30, -5, 70, 80), data = LATE_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(LATE_CTD),
    aes(x = Longitude,
        y = Latitude,
        size = LATE_CTD$Shannon_diversity,
        color = LATE_CTD$Shannon_diversity),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8), name = "Shannon diversity \nindex") +
  scale_color_gradient(low = "yellow", high = "red", name = "Shannon diversity \nindex") +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Species diversity using the Shannon index\nin late time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 20),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white")),
  ) +
  Cut_off_line

Shannon_index_map_LATE

Shannon_index_maps <- Shannon_index_map_EARLY|Shannon_index_map_LATE
Shannon_index_maps

ggsave("Shannon index maps BOTH.png", Shannon_index_maps, width = 18, height = 9, dpi = 600)

#Simpson map
Simpson_index_map_EARLY <-
  basemap(limits = c(-30, -5, 70, 80), data = EARLY_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(EARLY_CTD),
    aes(x = Longitude,
        y = Latitude,
        size = EARLY_CTD$Simpson_diversity,
        color = EARLY_CTD$Simpson_diversity),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8), name = "Simpson diversity \nindex") +
  scale_color_gradient(low = "yellow", high = "red", name = "Simpson diversity \nindex") +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Species diversity using the Simpson index\nin early time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
```

```
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 20),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white")),
  ) +
  Cut_off_line

Simpson_index_map_EARLY

Simpson_index_map_LATE <-
  basemap(limits = c(-30, -5, 70, 80), data = LATE_CTD, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(LATE_CTD),
    aes(x = Longitude,
        y = Latitude,
        size = LATE_CTD$Simpson_diversity,
        color = LATE_CTD$Simpson_diversity),
    position = position_jitter(h = 0.15, w = 0.15)
  ) +
  scale_size(range = c(3, 8), name = "Simpson diversity \nindex") +
  scale_color_gradient(low = "yellow", high = "red", name = "Simpson diversity \nindex") +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
    title = "Species diversity using the Simpson index\nin late time period",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 20),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "white")),
    color = guide_legend(override.aes = list(fill = "white")),
  ) +
  Cut_off_line

Simpson_index_map_LATE

Simpson_index_maps <- Simpson_index_map_EARLY|Simpson_index_map_LATE
Simpson_index_maps

ggsave("Simpson index maps BOTH.png", Simpson_index_maps, width = 18, height = 9, dpi = 600)

#####
# REVISITED STATIONS
#####
Revisited_stations <-
  basemap(limits = c(-30, -5, 70, 80), data = CTD_data, bathymetry = TRUE) +
  geom_point(
    data = transform_coord(CTD_data),
    aes(x = Longitude,
        y = Latitude,
        color = CTD_data$Comparison_station,
        shape = (CTD_data$Decade),
        size = 3,
        alpha = 0.9)
  ) +
  ggspatial::annotation_scale(location = "br") +
  ggspatial::annotation_north_arrow(location = "tr", which_north = "true") +
  labs(
```

```
    title = "Revisited locations",
    x = "Longitude (decimal degrees)",
    y = "Latitude (decimal degrees)"
  ) +
  scale_color_viridis(discrete=T,
                      option = "C",
                      name = "Revisited \narea name",
                      na.translate=FALSE
                      ) +
  scale_shape_manual(values = c("Early" = 17, "Late" = 15),
                     name = "Decade \ncategorization") +
  scale_size(guide = "none") +
  scale_alpha(guide = "none") +
  theme(
    legend.box.background = element_blank(),
    legend.background = element_rect(fill= "transparent"),
    legend.key = element_rect(color = "transparent",fill = "transparent"),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 16)
  ) +
  guides(
    shape = guide_legend(override.aes = list(fill = "transparent",size=5)),
    color = guide_legend(override.aes = list(fill = "transparent", size=5))
  )+
  Cut_off_line

Revisited_stations

ggsave("Revisited stations.png", Revisited_stations, width = 12, height = 9, dpi = 600)

Figure_2 <- Station_category|Revisited_stations
ggsave("Station category + Revisited stations.png", Figure_2, width = 16, height = 12, dpi =
600)

#####
#STACKED BAR PLOTS
#####
# Stacked bar plot Order with location category
Pivot_all_data %>% filter(Location_category != "NA") %>%
  ggplot(aes(fill = Order, y= Count, x= Location_category)) +
  geom_bar(position="fill", stat="identity") +
labs(x = "Location type", y = "Percentage of order", title = "Order category on location type")
+
  scale_fill_viridis_d(option="magma")+
   theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5,size = 18, color = "black"),
    axis.text.y = element_text(size=18,color = "black"),
    plot.title = element_text(hjust = 0.5, size = 26),
    axis.title = element_text(size = 22)) +
scale_y_continuous(expand = c(0,0))

# Stacked bar plot Family with location category
Pivot_all_data %>% filter(Location_category != "NA") %>%
  ggplot(aes(fill = Family, y= Count, x= Location_category)) +
  geom_bar(position="fill", stat="identity") +
  labs(x = "Location type", y = "Percentage of family", title = "Family category on location
type") +
  scale_fill_viridis_d(option="magma")+
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5,size = 18, color = "black"),
    axis.text.y = element_text(size=18,color = "black"),
    plot.title = element_text(hjust = 0.5, size = 26),
```

```
    axis.title = element_text(size = 22)) +
  scale_y_continuous(expand = c(0,0))

# Stacked bar plot with order and oceanic stratification
Pivot_all_data %>% filter(Oceanic_stratification != "NA") %>%
  ggplot(aes(fill = Order, y= Count, x= Oceanic_stratification)) +
  geom_bar(position="fill", stat="identity") +
  labs(x = "Location type", y = "Percentage of order", title = "Order category on
stratification type") +
  scale_fill_viridis_d(option="magma")+
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5,size = 18, color = "black"),
    axis.text.y = element_text(size=18,color = "black"),
    plot.title = element_text(hjust = 0.5, size = 26),
    axis.title = element_text(size = 22)) +
  scale_y_continuous(expand = c(0,0))

# Stacked bar plot Family with location category
Pivot_all_data %>% filter(Oceanic_stratification != "NA") %>%
  ggplot(aes(fill = Family, y= Count, x= Oceanic_stratification)) +
  geom_bar(position="fill", stat="identity") +
  labs(x = "Location type", y = "Percentage of family", title = "Family category on
stratification type") +
  scale_fill_viridis_d(option="magma")+
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18),
    axis.text.x = element_text(angle = 0, hjust = 0.5,size = 18, color = "black"),
    axis.text.y = element_text(size=18,color = "black"),
    plot.title = element_text(hjust = 0.5, size = 26),
    axis.title = element_text(size = 22)) +
  scale_y_continuous(expand = c(0,0))

#####
# Colour codes
#####
c(
  "Ardencaple fjord"="#f0f921",
  "Belgica back"="#f9dc24",
  "Bessel fjord A"="#fec029",
  "Bessel fjord B"="#fca636",
  "Bessel fjord D"="#f68f44",
  "Bredefjord"="#ed7953",
  "Davy sund A"="#e16462",
  "Davy sund B"="#d35171",
  "Dove bugt"="#c33d80",
  "Ella Ø East"="#b12a90",
  "Godthåb gulf"="#9c179e",
  "Moskusoksefjord"="#8405a7",
  "Offshore Bontekoe Ø"="#6a00a8",
  "Offshore Haystack"="#5002a2",
  "Scoresbysund fjord"="#330597",
  "Tyrolerfjord"="#0d0887"
)
#####
#####
#Pie charts
#####
# ORDER RICHNESS PIE
#####
Order_colour <-
  c(
"Gadiformes" = "#440154",
"Myctophiformes" = "#46327e",
"Osmeriformes" = "#365c8d",
"Perciformes" = "#277f8e",
"Pleuronectiformes" = "#1fa187",
```

```
"Rajiformes" = "#4ac16d",
"Scorpaeniformes" = "#a0da39",
"Stomiiformes" = "#fde725"
            )

# Pie chart of Order count early
Order_pie_EARLY <-
ggplot(data = Time_series_data_PIVOT_EARLY, aes(x = "", y = Count, fill = Order)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance of each order \nin early time period",
    fill = "Order"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Order_colour) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )

Order_pie_EARLY

# Pie chart of Order count late
Order_pie_LATE <-
ggplot(data = Time_series_data_PIVOT_LATE,
       aes(x = "",
           y = Count,
           fill = Order)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance of each order \nin late time period",
    fill = "Order"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Order_colour) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )

Order_pie_LATE

Order_richness_pie <- Order_pie_EARLY|Order_pie_LATE
Order_richness_pie

ggsave("Order pie BOTH.png", Order_richness_pie, width = 16, height = 8, dpi = 600)

#
ORDER_info <- Time_series_data_PIVOT %>% group_by(Order) %>%
summarise(OR=length(unique(Species)))
ORDER_info$Order <- as.factor(ORDER_info$Order)

Order_Species_richness <-
ggplot(ORDER_info, aes(x = Order, y = OR, fill = Order)) +
  geom_bar(stat = "identity") +
  scale_fill_viridis_d(option = "viridis") +
  scale_y_continuous(breaks = seq(0, max(ORDER_info$OR),
                      by = 2),
                     limits = c(0, max(ORDER_info$OR)),
                     expand = c(0,0)) +
  labs(x = NULL, y = "Species richness", title = "Species richness\nwithin each order") +
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 20),
```

```
    axis.text.x = element_blank(),
    axis.ticks.x = element_blank(),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 34),
    axis.title = element_text(size = 24))

Order_Species_richness
ggsave("Order SR graph.png", Order_Species_richness, width = 16, height = 9, dpi = 600)

#####
# FAMILY RICHNESS PIE
#####
Family_colour <-
  c( "Agonidae" = "#fcfdbf",
     "Anarhichadidae" = "#fddea0",
     "Cottidae" = "#febf84",
     "Cyclopteridae" = "#fe9f6d",
     "Gadidae" = "#fa7f5e",
     "Lipiridae" = "#f1605d",
     "Lotidae" = "#de4968",
     "Myctophidae" = "#c43c75",
     "Osmeridae" = "#a8327d",
     "Pleuronectidae" = "#8c2981",
     "Psychrolutidae" = "#721f81",
     "Rajidae" = "#57157e",
     "Sebastidae" = "#3b0f70",
     "Sternoptychidae" = "#20114b",
     "Stichaeidae" = "#0b0924",
     "Zoarchidae" = "#000004"
  )

# Pie chart of Family count early
Family_pie_EARLY <-
  ggplot(data = Time_series_data_PIVOT_EARLY,
         aes(x = "",
             y = Count,
             fill = Family)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance of each family \nin early time period",
    fill = "Family"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Family_colour,
                    breaks = names(Family_colour)) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )

Family_pie_EARLY

# Pie chart of Family count late
Family_pie_LATE <-
  ggplot(data = Time_series_data_PIVOT_LATE,
         aes(x = "",
             y = Count,
             fill = Family )) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance of each family \nin late time period",
    fill = "Family"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Family_colour) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
```

```
    legend.title = element_text(color = "black", size =20)
  )

Family_pie_LATE

Family_richness_pie <- Family_pie_EARLY|Family_pie_LATE
Family_richness_pie

ggsave("Family pie BOTH.png", Family_richness_pie, width = 16, height = 8, dpi = 600)

Family_Species_richness <-
  ggplot(FAMILY_info, aes(x = Family, y = FR, fill = Family)) +
  geom_bar(stat = "identity") +
  scale_fill_viridis_d(option = "viridis") +
  scale_y_continuous(breaks = seq(0, max(FAMILY_info$FR),
                                  by = 2),
                     limits = c(0, max(FAMILY_info$FR)),
                     expand = c(0,0)) +
  labs(x = NULL, y = "Family richness", title = "Family richness\nwithin each order") +
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 20),
    axis.text.x = element_blank(),
    axis.ticks.x = element_blank(),
    axis.text.y = element_text(size = 18, color = "black"),
    plot.title = element_text(hjust = 0.5, size = 34),
    axis.title = element_text(size = 24))

Family_Species_richness
ggsave("Order SR graph.png", Order_Species_richness, width = 16, height = 9, dpi = 600)

# REVISTED FAMILY ABUNDANCE PIE CHART

Time_series_data_PIVOT %>% filter(Comparison_station == "Ardencaple fjord", Year == 2003)

# ARDENCAPLE FJORD
#####
ARD_1 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Ardencaple fjord",
Year == 2003),
       aes(x = "",
           y = Count,
           fill = Family )) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each family in 2003",
    fill = "Family"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Family_colour) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )

ARD_2 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Ardencaple fjord",
Year == 2022),
         aes(x = "",
             y = Count,
             fill = Family )) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each family in 2022",
    fill = "Family"
  ) +
  scale_fill_viridis(discrete = TRUE) +
```

```
  scale_fill_manual(values = Family_colour) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )


ARD_PIES <- (ARD_1|ARD_2) +
plot_annotation(
  title = "Ardencaple fjord",
  theme = theme(
    plot.title = element_text(hjust = 0.5, size = 34)
  )
)
ggsave("Ardencaple fjord.png", ARD_PIES, width = 16, height = 8, dpi = 600)

# BELGICA BANK
BEL_1 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Belgica back", Year ==
2002),
         aes(x = "",
             y = Count,
             fill = Family )) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each family in 2002",
    fill = "Family"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Family_colour) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )

BEL_2 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Belgica back", Year ==
2017),
         aes(x = "",
             y = Count,
             fill = Family )) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each family in 2017",
    fill = "Family"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Family_colour) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )

BEL_PIES <- (BEL_1|BEL_2) +
  plot_annotation(
    title = "Belgica bank",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Belgica bank.png", BEL_PIES, width = 16, height = 8, dpi = 600)

#####
# SPECIES PIE
```

```
# Species colours
#####
species <- c(
  "Amblyraja hyperborea", "Artediellus uncinatus", "Boreogadus saida",
  "Careproctus micropus", "Careproctus reinhardti", "Cottunculus subspinosus",
  "Eumicrotremus spinosus", "Gymnelus retrodorsalis", "Gymnocanthus tricuspis",
  "Icelus bicornis", "Liparis bathyarcticus", "Liparis fabricii", "Liparis tunicatus",
  "Lycenchelys kolthoffi", "Lycenchelys muraena", "Lycodes eudipleurostictus",
  "Lycodes frigidus", "Lycodes pallidus", "Lycodes paamiuti", "Lycodes reticulatus",
  "Lycodes rossi", "Lycodes seminudus", "Lycodes squamiventer", "Lycodonus flagellicauda",
  "Myoxocephalus quadricornis", "Paraliparis bathybius", "Rhodichthys regina",
  "Triglops nybelini", "Amblyraja radiata", "Anarhichas denticulatus",
  "Arctogadus glacialis", "Artediellus atlanticus", "Benthosema glaciale",
  "Cottunculus microps", "Gaidropsarus argentatus", "Hippoglossoides platessoides",
  "Leptagonus decagonus", "Leptoclinus maculatus", "Mallotus villosus",
  "Myoxocephalus scorpius", "Reinhardtius hippoglossoides", "Triglops pingelii",
  "Gadus morhua", "Sebastes mentella", "Argyropelecus hemigymnus"
)

species_sorted <- sort(species)

# Generate a turbo color palette with enough colors for all species
species_colors <- turbo(length(species_sorted))

# Create a named vector associating each species with a unique color
names(species_colors) <- species

#####

# REVISITED SPECIES ABUNDANCE PIE CHART
# EARLY and LATE decade
#####
Species_pie_EARLY <-
  ggplot(data = Time_series_data_PIVOT_EARLY,
         aes(x = "",
             y = Count,
             fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance of each species \nin early time period",
    fill = "Species"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = species_colors,
                    breaks = names(species_colors)) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )

Species_pie_EARLY

# Pie chart of Species count late
Species_pie_LATE <-
  ggplot(data = Time_series_data_PIVOT_LATE,
         aes(x = "",
             y = Count,
             fill = Species )) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance of each species \nin late time period",
    fill = "Species"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
```

```
    legend.title = element_text(color = "black", size =20)
  )

Species_pie_LATE

Species_richness_pie <- Species_pie_EARLY|Species_pie_LATE
Species_richness_pie

ggsave("Species pie BOTH.png", Species_richness_pie, width = 16, height = 8, dpi = 600)

#####
# ARDENCAPLE FJORD species
#####
ARD_3 <-
ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Ardencaple fjord", Year
== 2003),
       aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )


ARD_4 <-
ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Ardencaple fjord", Year
== 2022),
       aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2022",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

ARD_SP_PIES <- (ARD_3|ARD_4) +
  plot_annotation(
    title = "Ardencaple fjord",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Ardencaple fjord SPECIES.png", ARD_SP_PIES, width = 16, height = 8, dpi = 600)
#####
# BELGICA BANK species
#####
BEL_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Belgica bank", Year ==
2002),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2002",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
```

```
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BEL_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Belgica bank", Year ==
2017),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2017",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BEL_SP_PIES <- (BEL_3|BEL_4) +
  plot_annotation(
    title = "Belgica bank",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Belgica bank SPECIES.png", BEL_SP_PIES, width = 16, height = 8, dpi = 600)
######
# BESSEL FJORD A species
#####
BES_a_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bessel fjord A", Year
== 2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BES_a_5 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bessel fjord A", Year
== 2017),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2017",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )
```

```
BES_a_6 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bessel fjord A", Year
== 2022),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2022",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BES_a_SP_PIES <- (BES_a_4|BES_a_5|BES_a_6) +
  plot_annotation(
    title = "Bessel fjord A",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Bessel fjord a SPECIES.png", BES_a_SP_PIES, width = 20, height = 8, dpi = 600)

#####
# BESSEL FJORD B species
#####
BES_b_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bessel fjord B", Year
== 2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BES_b_5 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bessel fjord B", Year
== 2017),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2017",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BES_b_6 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bessel fjord B", Year
== 2022),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
```

```
  labs(
    title = "Relative abundance \nof each species in 2022",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BES_b_SP_PIES <- (BES_b_4|BES_b_5|BES_b_6) +
  plot_annotation(
    title = "Bessel fjord B",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Bessel fjord b SPECIES.png", BES_b_SP_PIES, width = 20, height = 8, dpi = 600)
#####
# Store belt species
#####
BES_d_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Store belt", Year ==
2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BES_d_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Store belt", Year ==
2017),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2017",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BES_d_SP_PIES <- (BES_d_3|BES_d_4) +
  plot_annotation(
    title = "Store belt",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )

ggsave("Store belt SPECIES.png", BES_d_SP_PIES, width = 16, height = 8, dpi = 600)
#####
# BREDE FJORD
#####
BRE_4 <-
```

```
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bredefjord", Year ==
2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BRE_5 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bredefjord", Year ==
2013),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2013",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BRE_6 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Bredefjord", Year ==
2022),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2022",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

BRE_SP_PIES <- (BRE_4|BRE_5|BRE_6) +
  plot_annotation(
    title = "Bredefjord",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Bredefjord SPECIES.png", BRE_SP_PIES, width = 20, height = 8, dpi = 600)
#####
# DAVY SUND A species
#####
DS_a_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Davy sund A", Year ==
2005),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2005",
```

```
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

DS_a_5 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Davy sund A", Year ==
2010),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2010",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

DS_a_6 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Davy sund A", Year ==
2013),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2013",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

DS_a_SP_PIES <- (DS_a_4|DS_a_5|DS_a_6) +
  plot_annotation(
    title = "Davy sund A",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Davy sund A SPECIES.png", DS_a_SP_PIES, width = 22, height = 12, dpi = 600)
#####
# Davy sund B species
######
DS_b_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Davy sund B", Year ==
2005),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2005",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
```

```
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

DS_b_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Davy sund B", Year ==
2022),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2022",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

DS_b_SP_PIES <- (DS_b_3|DS_b_4) +
  plot_annotation(
    title = "Davy sund B",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Davy sund B SPECIES.png", DS_b_SP_PIES, width = 16, height = 10, dpi = 600)
#####
# Dove bugt species
#####
Dove_5 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Dove bugt", Year ==
2002),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2002",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

Dove_6 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Dove bugt", Year ==
2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

Dove_7 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Dove bugt", Year ==
2017),
```

```
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2017",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

Dove_8 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Dove bugt", Year ==
2022),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2022",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

Dove_SP_PIES <- (Dove_5|Dove_6)/(Dove_7|Dove_8) +
  plot_annotation(
    title = "Dove bugt",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Dove bugt SPECIES.png", Dove_SP_PIES, width = 16, height = 12, dpi = 600)
#####
# Ella Ø East
#####
Ella_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Ella Ø East", Year ==
2010),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2010",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

Ella_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Ella Ø East", Year ==
2013),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2013",
    fill = "Species"
  ) +
```

```
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

Ella_SP_PIES <- (Ella_3|Ella_4) +
  plot_annotation(
    title = "Ella Ø East",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Ella Ø East SPECIES.png", Ella_SP_PIES, width = 16, height = 12, dpi = 600)
#####
# Godthåb gulf
#####
GG_5 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Godthåb gulf", Year ==
2002),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2002",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

GG_6 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Godthåb gulf", Year ==
2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

GG_7 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Godthåb gulf", Year ==
2013),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2013",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
```

```
  )

GG_8 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Godthåb gulf", Year ==
2022),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2022",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

GG_SP_PIES <- (GG_5|GG_6)/(GG_7|GG_8) +
  plot_annotation(
    title = "Godthåb gulf",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Godthåb gulf SPECIES.png", GG_SP_PIES, width = 16, height = 12, dpi = 600)
#####
# MOSKUSOKSEFJORD
#####
Mos_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Moskusoksefjord", Year
== 2010),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2010",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

Mos_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Moskusoksefjord", Year
== 2013),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2013",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

Mos_SP_PIES <- (Mos_3|Mos_4) +
  plot_annotation(
    title = "Moskusoksefjord",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
```

```
    )
  )
ggsave("Moskusoksefjord.png", Mos_SP_PIES, width = 16, height = 12, dpi = 600)
#####
# OFFSHORE BONTEKOE Ø
#####
OB_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Offshore Bontekoe Ø",
Year == 2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

OB_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Offshore Bontekoe Ø",
Year == 2010),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2010",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

OB_SP_PIES <- (OB_3|OB_4) +
  plot_annotation(
    title = "Offshore Bontekoe Ø",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Offshore Bontekoe Ø.png", OB_SP_PIES, width = 16, height = 12, dpi = 600)
#####
# Offshore Haystack
#####
OH_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Offshore Haystack",
Year == 2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

OH_4 <-
```

```
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Offshore Haystack",
Year == 2013),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2013",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

OH_SP_PIES <- (OH_3|OH_4) +
  plot_annotation(
    title = "Offshore Haystack",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Offshore Haystack.png", OH_SP_PIES, width = 16, height = 12, dpi = 600)
#####
# Offshore Hochstetter
#####
HOC_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Offshore Hochstetter",
Year == 2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

HOC_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Offshore Hochstetter",
Year == 2013),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2013",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

HOC_SP_PIES <- (HOC_3|HOC_4) +
  plot_annotation(
    title = "Offshore Hochstetter",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Offshore Hochstetter.png", HOC_SP_PIES, width = 16, height = 12, dpi = 600)
```

```
#####
# TYROLERFJORD
#####
TYR_3 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Tyrolerfjord", Year ==
2003),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2003",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

TYR_4 <-
  ggplot(data = Time_series_data_PIVOT %>% filter(Comparison_station == "Tyrolerfjord", Year ==
2013),
         aes(x = "", y = Count, fill = Species)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance \nof each species in 2013",
    fill = "Species"
  ) +
  scale_fill_manual(values = species_colors) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    legend.title = element_text(color = "black", size = 20)
  )

TYR_SP_PIES <- (TYR_3|TYR_4) +
  plot_annotation(
    title = "Tyrolerfjord",
    theme = theme(
      plot.title = element_text(hjust = 0.5, size = 34)
    )
  )
ggsave("Tyrolerfjord.png", TYR_SP_PIES, width = 16, height = 12, dpi = 600)

#####
# DECADE Zoogeography
#####
# Zoogeography colours
#####
Zoogeography_colours <-
  c("Arctic" = "#00204D",
    "Arctic-Boreal" = "#4A6FE3",
    "Boreal" = "#A5F723",
   "Widely distributed" = "#FFD500")

# Create a grid layout for the legend box
legend_labels <- names(Zoogeography_colours)
legend_colors <- unname(Zoogeography_colours)

# Define a function to create the legend box
create_legend <- function(labels, colors) {
  grid.newpage()  # Create a new page for the grid layout

  # Set up layout with 2 columns
  pushViewport(viewport(layout = grid.layout(length(labels) + 2, 2)))  # Added 2 for title and
spacing

  # Title
  grid.text("Zoogeography category",
```

```
           x = unit(0.5, "npc"), y = unit(2, "lines"),  # Adjusted y for better visibility
           gp = gpar(fontsize = 74, fontface = "bold"),
           just = "center", vp = viewport(layout.pos.row = 1, layout.pos.col = 1:2))

  # Add color boxes and labels side by side
  for (i in seq_along(labels)) {
    # Increase width and height to make the squares larger
    grid.rect(x = unit(0.5, "npc"),
              y = unit(length(labels) - i + 1.5, "native") / (length(labels) + 2),
              width = unit(0.7, "npc"),  # Adjusted width for better visibility
              height = unit(0.7, "npc"),  # Adjusted height for better visibility
              gp = gpar(fill = colors[i], col = NA),
              vp = viewport(layout.pos.row = i + 2, layout.pos.col = 1))

    # Text label next to the color square
    grid.text(labels[i],
              x = unit(0.3, "npc"),  # Place text further to the right for side-by-side effect
              y = unit(length(labels) - i + 1.5, "native") / (length(labels) + 2),
              gp = gpar(fontsize = 50),  # Adjusted font size for better visibility
              vp = viewport(layout.pos.row = i + 2, layout.pos.col = 2))
  }

  popViewport()
}

# Call the function to create the legend
create_legend(legend_labels, legend_colors)
#####
# ZOO PIE
#####
Zoo_pie_EARLY <-
  ggplot(data = Time_series_data_PIVOT_EARLY,
         aes(x = "",
             y = Count,
             fill = Zoogeography)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance of zoogeography \nin early time period",
    fill = "Zoogeography \ncategory"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Zoogeography_colours,
                    breaks = names(Zoogeography_colours)) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
  )

Zoo_pie_EARLY

# Pie chart of Species count late
Zoo_pie_LATE <-
  ggplot(data = Time_series_data_PIVOT_LATE,
         aes(x = "",
             y = Count,
             fill = Zoogeography )) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar(theta = "y") +
  labs(
    title = "Relative abundance of zoogeography \nin late time period",
    fill = "Zoogeography \ncategory"
  ) +
  scale_fill_viridis(discrete = TRUE) +
  scale_fill_manual(values = Zoogeography_colours,
                    breaks = names(Zoogeography_colours)) +
  theme_void() +
  theme(
    plot.title = element_text(hjust = 0.5, size = 24),
    legend.position = "right",
    legend.text = element_text(color = "black", size = 18),
    legend.title = element_text(color = "black", size =20)
```

```
  )

Zoo_pie_LATE

Zoo_richness_pie <- Zoo_pie_EARLY|Zoo_pie_LATE
Zoo_richness_pie

ggsave("Zoogeography pie BOTH.png", Zoo_richness_pie, width = 16, height = 8, dpi = 600)

#####
# NMDS
#####
# Making data into wide format, but species, family, and order to themselves
# they cannot be in the same data set
# WIDE DATA making ALL
#####
# Species
wide_data_species_COUNT <- dcast(Pivot_all_data, Station_ID + Temp + Location_category +
                           Depth + Latitude + Longitude + Decade + Oceanic_stratification
                           + Trawling_min  ~ Species,
                         value.var="Count", fun.aggregate=sum, fill=0)

# Family
wide_data_family_COUNT <- dcast(Pivot_all_data, Station_ID + Temp + Location_category +
                           Depth + Latitude + Longitude + Decade + Oceanic_stratification
                           + Trawling_min  ~ Family,
                         value.var="Count", fun.aggregate=sum, fill=0)

# Order
wide_data_order_COUNT <- dcast(Pivot_all_data, Station_ID + Temp + Location_category +
                           Depth + Latitude + Longitude + Decade + Oceanic_stratification
                           + Trawling_min  ~ Order,
                         value.var="Count", fun.aggregate=sum, fill=0)
# Species
wide_data_species_WEIGHT <- dcast(Pivot_all_data, Station_ID + Temp + Location_category +
                                   Depth + Latitude + Longitude + Decade +
Oceanic_stratification
                                  + Trawling_min  ~ Species,
                                 value.var="Weight", fun.aggregate=sum, fill=0)

# Family
wide_data_family_WEIGHT <- dcast(Pivot_all_data, Station_ID + Temp + Location_category +
                                  Depth + Latitude + Longitude + Decade +
Oceanic_stratification
                                 + Trawling_min  ~ Family,
                                value.var="Weight", fun.aggregate=sum, fill=0)

# Order
wide_data_order_WEIGHT <- dcast(Pivot_all_data, Station_ID + Temp + Location_category +
                                 Depth + Latitude + Longitude + Decade + Oceanic_stratification
                                + Trawling_min  ~ Order,
                               value.var="Weight", fun.aggregate=sum, fill=0)

#####
#####
# Bray-Curtis dissimilar matrix COUNT ALL
# To use for statistical calculations and look at values to see obvious differences
# COUNT ALL
#####
# SPECIES
For_NMDS_species_COUNT <- vegdist(wide_data_species_COUNT[,10:53], method = "bray", na.rm =
TRUE)
NMDS_data_format_s_COUNT <- metaMDS(comm = wide_data_species_COUNT[,10:53], k=2, distance =
"bray",trymax = 100, autotransform = T)

# FAMILY
For_NMDS_family_COUNT <- vegdist(wide_data_family_COUNT[,10:25], method = "bray", na.rm = TRUE)
NMDS_data_format_f_COUNT <- metaMDS(comm = wide_data_family_COUNT[,10:25], k=2, distance =
"bray",trymax = 100, autotransform = T)

# ORDER
For_NMDS_order_COUNT <- vegdist(wide_data_order_COUNT[,10:17], method = "bray", na.rm = TRUE)
NMDS_data_format_o_COUNT <- metaMDS(comm = wide_data_order_COUNT[,10:17], k=2, distance =
"bray",trymax = 100, autotransform = T)
```

```
# Making predictor variables usable for NMDS
Predictor_variables_s_COUNT <- wide_data_species_COUNT[,1:9]
Predictor_variables_f_COUNT <- wide_data_species_COUNT[,1:9]
Predictor_variables_o_COUNT <- wide_data_species_COUNT[,1:9]

#####
# COUNT Analyzing with station_ID ALL
#####
# Analyzing SPECIES with station_ID

# Extract species and sites
plot_nmds_s_COUNT = as.data.frame(scores(NMDS_data_format_s_COUNT)$sites)
plot_nmds_s1_COUNT = as.data.frame(scores(NMDS_data_format_s_COUNT)$species)
plot_nmds_s1_COUNT$species <- rownames(plot_nmds_s1_COUNT)

# Combing plot values and predictor values together into one function
plot_species_COUNT <- cbind(Predictor_variables_s_COUNT, plot_nmds_s_COUNT)

# Analyzing FAMILY with station_ID

# Extract species and sites
plot_nmds_f_COUNT = as.data.frame(scores(NMDS_data_format_f_COUNT)$sites)
plot_nmds_f1_COUNT = as.data.frame(scores(NMDS_data_format_f_COUNT)$species)
plot_nmds_f1_COUNT$family <- rownames(plot_nmds_f1_COUNT)

# Combing plot values and predictor values together into one function
plot_family_COUNT <- cbind(Predictor_variables_f_COUNT, plot_nmds_f_COUNT)

# Analyzing ORDER with station_ID

# Extract species and sites
plot_nmds_o_COUNT = as.data.frame(scores(NMDS_data_format_o_COUNT)$sites)
plot_nmds_o1_COUNT = as.data.frame(scores(NMDS_data_format_o_COUNT)$species)
plot_nmds_o1_COUNT$order <- rownames(plot_nmds_o1_COUNT)

# Combing plot values and predictor values together into one function
plot_order_COUNT <- cbind(Predictor_variables_o_COUNT, plot_nmds_o_COUNT)

plot_nmds_s1_COUNT <- plot_nmds_s1_COUNT %>%
  mutate(Zoogeography_category = case_when(
    species %in% c("Amblyraja hyperborea",
                   "Artediellus uncinatus",
                   "Boreogadus saida",
                   "Careproctus micropus",
                   "Careproctus reinhardti",
                   "Cottunculus subspinosus",
                   "Eumicrotremus spinosus",
                   "Gymnelus retrodorsalis",
                   "Gymnocanthus tricuspis",
                   "Icelus bicornis",
                   "Liparis bathyarcticus",
                   "Liparis fabricii",
                   "Liparis tunicatus",
                   "Lycenchelys kolthoffi",
                   "Lycenchelys muraena",
                   "Lycodes eudipleurostictus",
                   "Lycodes frigidus",
                   "Lycodes pallidus",
                   "Lycodes paamiuti",
                   "Lycodes reticulatus",
                   "Lycodes rossi",
                   "Lycodes seminudus",
                   "Lycodes squamiventer",
                   "Lycodonus flagellicauda",
                   "Myoxocephalus quadricornis",
                   "Paraliparis bathybius",
                   "Rhodichthys regina",
                   "Triglops nybelini") ~ "Arctic",

    species %in% c("Amblyraja radiata",
                   "Anarhichas denticulatus",
                   "Arctogadus glacialis",
                   "Artediellus atlanticus",
                   "Benthosema glaciale",
                   "Cottunculus microps",
```

```
                  "Gaidropsarus argentatus",
                  "Hippoglossoides platessoides",
                  "Leptagonus decagonus",
                  "Leptoclinus maculatus",
                  "Mallotus villosus",
                  "Myoxocephalus scorpius",
                  "Reinhardtius hippoglossoides",
                  "Triglops pingelii") ~ "Arctic-Boreal",

    species %in% c("Gadus morhua",
                  "Sebastes mentella") ~ "Boreal",

    species %in% c("Argyropelecus hemigymnus") ~ "Widely distributed",

    TRUE ~ "Unknown"  # Catch any species that don't match the above categories
  ))

#####
#####
# Plot NMDS COUNT ALL ----
#SPECIES COUNT NMDS ALL
#####
NMDS_theme <-
  theme(legend.title = element_text(color = "black", size = 20),
        legend.text = element_text(color = "black", size = 18),
        axis.title = element_text(size = 16),
        axis.text = element_text(color = "black", size = 16),
        panel.background = element_blank(),
        panel.border = element_rect(colour = "black", fill = NA, size = 1.2)
  )
#####
# Zoogeography colours
#####
  # Zoogeography colors vector (modify species names as needed)
  Zoogeography_colours_NMDS <- c(
    "Amblyraja hyperborea" = "#00204D",
    "Artediellus uncinatus" = "#00204D",
    "Boreogadus saida" = "#00204D",
    "Careproctus micropus" = "#00204D",
    "Careproctus reinhardti" = "#00204D",
    "Cottunculus subspinosus" = "#00204D",
    "Eumicrotremus spinosus" = "#00204D",
    "Gymnelus retrodorsalis" = "#00204D",
    "Gymnocanthus tricuspis" = "#00204D",
    "Icelus bicornis" = "#00204D",
    "Liparis bathyarcticus" = "#00204D",
    "Liparis fabricii" = "#00204D",
    "Liparis tunicatus" = "#00204D",
    "Lycenchelys kolthoffi" = "#00204D",
    "Lycenchelys muraena" = "#00204D",
    "Lycodes eudipleurostictus" = "#00204D",
    "Lycodes frigidus" = "#00204D",
    "Lycodes pallidus" = "#00204D",
    "Lycodes paamiuti" = "#00204D",
    "Lycodes reticulatus" = "#00204D",
    "Lycodes rossi" = "#00204D",
    "Lycodes seminudus" = "#00204D",
    "Lycodes squamiventer" = "#00204D",
    "Lycodonus flagellicauda" = "#00204D",
    "Myoxocephalus quadricornis" = "#00204D",
    "Paraliparis bathybius" = "#00204D",
    "Rhodichthys regina" = "#00204D",
    "Triglops nybelini" = "#00204D",
    "Amblyraja radiata" = "#4A6FE3",
    "Anarhichas denticulatus" = "#4A6FE3",
    "Arctogadus glacialis" = "#4A6FE3",
    "Artediellus atlanticus" = "#4A6FE3",
    "Benthosema glaciale" = "#4A6FE3",
    "Cottunculus microps" = "#4A6FE3",
    "Gaidropsarus argentatus" = "#4A6FE3",
    "Hippoglossoides platessoides" = "#4A6FE3",
    "Leptagonus decagonus" = "#4A6FE3",
    "Leptoclinus maculatus" = "#4A6FE3",
    "Mallotus villosus" = "#4A6FE3",
    "Myoxocephalus scorpius" = "#4A6FE3",
```

```r
    "Reinhardtius hippoglossoides" = "#4A6FE3",
    "Triglops pingelii" = "#4A6FE3",
    "Gadus morhua" = "#A5F723",
    "Sebastes mentella" = "#A5F723",
    "Argyropelecus hemigymnus" = "#FFD500"
  )

# Location category
NMDS_LOC_C_ALL <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Location_category),
size = 4) +
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -1.2, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  stat_ellipse(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour =
Location_category), size = 1) +
  scale_color_viridis(discrete = TRUE, na.translate = FALSE, name = "Location category") +
  theme_classic() +
  NMDS_theme

NMDS_LOC_C_ALL
ggsave("NMDS Location category ALL.png", NMDS_LOC_C_ALL, width = 10.35, height = 5.76, dpi =
600)

NMDS_LOC_C_ALL_2 <-
ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Location_category),
size = 4) +
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species], alpha = 0.5) +
  annotate(geom = "label", x = -1.2, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  stat_ellipse(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour =
Location_category), size = 1) +
  scale_color_viridis(discrete = TRUE, na.translate = FALSE, name = "Location category") +
  theme_classic() +
  guides(color = "none") +  # This line removes the color legend
  NMDS_theme

# Depth
NMDS_Depth_C_ALL <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Depth), size = 3) +
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.7, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  scale_color_viridis(name = "Depth") +
  theme_classic() +
  NMDS_theme
ggsave("NMDS Depth ALL.png", NMDS_Depth_C_ALL, width = 10.35, height = 5.76, dpi = 600)

NMDS_Depth_ALL_2 <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Depth), size = 3) +
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.7, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  scale_color_viridis(name = "Depth") +
  theme_classic() +
  theme(legend.position = "none") +
  NMDS_theme


# Latitude
```

```
NMDS_LAT_C_ALL <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Latitude), size = 3)
+
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.7, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  scale_color_viridis(name = "Latitude") +
  theme_classic() +
  NMDS_theme

NMDS_LAT_C_ALL
ggsave("NMDS Latitude ALL.png", NMDS_LAT_C_ALL, width = 10.35, height = 5.76, dpi = 600)

NMDS_LAT_ALL_2 <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Latitude), size = 3)
+
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.7, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  scale_color_viridis(name = "Latitude") +
  theme_classic() +
  theme(legend.position = "none") +
  NMDS_theme


# Decade
NMDS_Decade_C_ALL <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Decade), size = 3) +
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.6, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  stat_ellipse(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Decade), size = 1)
+
  scale_color_viridis(discrete = TRUE, na.translate = FALSE, name = "Decade category") +
  theme_classic() +
  NMDS_theme

NMDS_Decade_C_ALL
ggsave("NMDS Decade category ALL.png", NMDS_Decade_C_ALL, width = 10.35, height = 5.76, dpi =
600)

# Oceanic stratification
NMDS_Oce_str_ALL <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour =
Oceanic_stratification), size = 3) +
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.9, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  stat_ellipse(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour =
Oceanic_stratification), size = 1) +
  scale_color_viridis(discrete = TRUE, na.translate = FALSE, name = "Oceanic
stratification\ncategory") +
  theme_classic() +
  NMDS_theme

NMDS_Oce_str_ALL
ggsave("NMDS Oceanic stratification category ALL.png", NMDS_Oce_str_ALL, width = 10.35, height
= 5.76, dpi = 600)
```

```
# Temp
NMDS_temp_ALL <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Temp), size = 3) +
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.65, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  scale_color_viridis(name = "Temperature") +
  theme_classic() +
  NMDS_theme

NMDS_temp_ALL
ggsave("NMDS temp ALL.png", NMDS_temp_ALL, width = 10.35, height = 5.76, dpi = 600)

NMDS_TEMP_ALL_2 <-
  ggplot() +
  geom_point(data = plot_species_COUNT, aes(x = NMDS1, y = NMDS2, colour = Temp), size = 3) +
  geom_text_repel(data = plot_nmds_s1_COUNT,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.65, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT$stress, digits = 2))) +
  scale_color_viridis(name = "Temperature") +
  theme_classic() +
  theme(legend.position = "none") +  # Hiding the legend
  NMDS_theme


#####
# FAMILY COUNT NMDS ALL
#####
# Location category
NMDS_f_loc_ALL <-
ggplot()+
  geom_point(data= plot_family_COUNT, aes(x=NMDS1, y=NMDS2,colour=Location_category),size=4)+
  geom_text_repel(data= plot_nmds_f1_COUNT, aes (x=NMDS1, y=NMDS2, label=family), alpha=0.5) +
  stat_ellipse(data= plot_family_COUNT, aes(x=NMDS1, y=NMDS2, colour=Location_category),
size=1)+
  annotate(geom = "label", x = -0.6, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT$stress, digits=2))) +
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Location \ncategory") +
  theme_classic() +
  NMDS_theme

NMDS_f_loc_ALL
ggsave("NMDS Location category family ALL.png", NMDS_f_loc_ALL, width = 10.35, height = 5.76,
dpi = 600)

# Depth
NMDS_f_Depth_ALL <-
ggplot()+
  geom_point(data= plot_family_COUNT, aes(x=NMDS1, y=NMDS2,colour=Depth),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT, aes (x=NMDS1, y=NMDS2, label=family), alpha=0.5)+
  annotate(geom = "label", x = -0.7, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT$stress, digits=2))) +
  scale_color_viridis(name="Depth") +
  theme_classic() +
  NMDS_theme

NMDS_f_Depth_ALL
ggsave("NMDS Family Depth ALL.png", NMDS_f_Depth_ALL, width = 10.35, height = 5.76, dpi = 600)

# Latitude
NMDS_f_lat_ALL <-
ggplot()+
  geom_point(data= plot_family_COUNT, aes(x=NMDS1, y=NMDS2,colour=Latitude),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT, aes (x=NMDS1, y=NMDS2, label=family), alpha=0.5)+
  annotate(geom = "label", x = -0.65, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT$stress, digits=2))) +
  scale_color_viridis(name ="Latitude") +
  theme_classic() +
```

```
  NMDS_theme

NMDS_f_lat_ALL
ggsave("NMDS family Latitude ALL.png", NMDS_f_lat_ALL, width = 10.35, height = 5.76, dpi = 600)

# Decade
NMDS_f_Decade_ALL <-
ggplot()+
  geom_point(data= plot_family_COUNT, aes(x=NMDS1, y=NMDS2,colour=Decade),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT, aes (x=NMDS1, y=NMDS2, label=family), alpha=0.5)+
  annotate(geom = "label", x = -0.8, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT$stress, digits=2))) +
  stat_ellipse(data= plot_family_COUNT, aes(x=NMDS1, y=NMDS2, colour=Decade), size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Decade category") +
  theme_classic() +
  NMDS_theme

NMDS_f_Decade_ALL
ggsave("NMDS family Decade category ALL.png", NMDS_f_Decade_ALL, width = 10.35, height = 5.76,
dpi = 600)

# Oceanic stratification
NMDS_Family_Oce_str_ALL <-
ggplot()+
  geom_point(data= plot_family_COUNT, aes(x=NMDS1,
y=NMDS2,colour=Oceanic_stratification),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT, aes (x=NMDS1, y=NMDS2, label=family), alpha=0.5)+
  annotate(geom = "label", x = -0.55, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT$stress, digits=2))) +
  stat_ellipse(data= plot_family_COUNT, aes(x=NMDS1, y=NMDS2, colour=Oceanic_stratification),
size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Oceanic stratification
\ncategory") +
  theme_classic() +
  NMDS_theme

NMDS_Family_Oce_str_ALL
ggsave("NMDS Family Oceanic stratification ALL.png", NMDS_Family_Oce_str_ALL, width = 10.35,
height = 5.76, dpi = 600)

# Temp
NMDS_Family_Temp_ALL <-
ggplot()+
  geom_point(data= plot_family_COUNT, aes(x=NMDS1, y=NMDS2,colour=Temp),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT, aes (x=NMDS1, y=NMDS2, label=family), alpha=0.5)+
  annotate(geom = "label", x = -0.65, y = 2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT$stress, digits=2))) +
  scale_color_viridis(name="Temperature") +
  theme_classic() +
  NMDS_theme

NMDS_Family_Temp_ALL
ggsave("NMDS Family Temperature ALL.png", NMDS_Family_Temp_ALL, width = 10.35, height = 5.76,
dpi = 600)

# NMDS side by side
NMDS_LOCATION <- NMDS_LOC_C_ALL_2|NMDS_f_loc_ALL
ggsave("NMDS LOATION.png", NMDS_LOCATION, width = 10.35, height = 5.76, dpi = 600)

NMDS_DEPTH <- NMDS_Depth_ALL_2|NMDS_f_Depth_ALL
ggsave("NMDS DEPTH.png", NMDS_DEPTH, width = 10.35, height = 5.76, dpi = 600)

NMDS_TEMP <- NMDS_TEMP_ALL_2|NMDS_Family_Temp_ALL
ggsave("NMDS TEMP.png", NMDS_TEMP, width = 10.35, height = 5.76, dpi = 600)

NMDS_LAT <- NMDS_LAT_ALL_2|NMDS_f_lat_ALL
ggsave("NMDS LATITUDE.png", NMDS_LAT, width = 10.35, height = 5.76, dpi = 600)


#####
#####
# ORDER COUNT NMDS ALL
#####
# Location category
NMDS_Order_LOC_ALL <-
```

```
ggplot()+
  geom_point(data= plot_order_COUNT, aes(x=NMDS1, y=NMDS2,colour=Location_category),size=4)+
  geom_text_repel(data= plot_nmds_o1_COUNT, aes (x=NMDS1, y=NMDS2, label=order), alpha=0.5) +
  annotate(geom = "label", x = -0.6, y = 0.8, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT$stress, digits=2))) +
  stat_ellipse(data= plot_order_COUNT, aes(x=NMDS1, y=NMDS2, colour=Location_category),
size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Location category") +
  theme_classic() +
  NMDS_theme

NMDS_Order_LOC_ALL
ggsave("NMDS Order Location category ALL.png", NMDS_Order_LOC_ALL, width = 10.35, height =
5.76, dpi = 600)

# Depth
NMDS_Order_Depth_ALL <-
ggplot()+
  geom_point(data= plot_order_COUNT, aes(x=NMDS1, y=NMDS2,colour=Depth),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT, aes (x=NMDS1, y=NMDS2, label=order), alpha=0.5)+
  annotate(geom = "label", x = -0.51, y = 1, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT$stress, digits=2))) +
  scale_color_viridis(name="Depth") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Depth_ALL
ggsave("NMDS Order Depth ALL.png", NMDS_Order_Depth_ALL, width = 10.35, height = 5.76, dpi =
600)

# Latitude
NMDS_Order_Lat_ALL <-
ggplot()+
  geom_point(data= plot_order_COUNT, aes(x=NMDS1, y=NMDS2,colour=Latitude),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT, aes (x=NMDS1, y=NMDS2, label=order), alpha=0.5)+
  annotate(geom = "label", x = -0.52, y = 0.8, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT$stress, digits=2))) +
  scale_color_viridis(name ="Latitude") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Lat_ALL
ggsave("NMDS Order latitude ALL.png", NMDS_Order_Lat_ALL, width = 10.35, height = 5.76, dpi =
600)

# Decade
NMDS_Order_Decade_ALL <-
ggplot()+
  geom_point(data= plot_order_COUNT, aes(x=NMDS1, y=NMDS2,colour=Decade),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT, aes (x=NMDS1, y=NMDS2, label=order), alpha=0.5)+
  annotate(geom = "label", x = -0.6, y = 0.8, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT$stress, digits=2))) +
  stat_ellipse(data= plot_order_COUNT, aes(x=NMDS1, y=NMDS2, colour=Decade), size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Decade category") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Decade_ALL
ggsave("NMDS Order Decade ALL.png", NMDS_Order_Decade_ALL, width = 10.35, height = 5.76, dpi =
600)

# Oceanic stratification
NMDS_Order_Oce_str_ALL <-
ggplot()+
  geom_point(data= plot_order_COUNT, aes(x=NMDS1,
y=NMDS2,colour=Oceanic_stratification),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT, aes (x=NMDS1, y=NMDS2, label=order), alpha=0.5)+
  stat_ellipse(data= plot_order_COUNT, aes(x=NMDS1, y=NMDS2, colour=Oceanic_stratification),
size=1)+
  annotate(geom = "label", x = -0.48, y = 1.2, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT$stress, digits=2))) +
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Oceanic stratification
\ncategory") +
  theme_classic() +
  NMDS_theme
```

```
NMDS_Order_Oce_str_ALL
ggsave("NMDS Order Oceanic stratification ALL.png", NMDS_Order_Oce_str_ALL, width = 10.35,
height = 5.76, dpi = 600)

# Temp
NMDS_Order_Temp_ALL <-
ggplot()+
  geom_point(data= plot_order_COUNT, aes(x=NMDS1, y=NMDS2,colour=Temp),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT, aes (x=NMDS1, y=NMDS2, label=order), alpha=0.5)+
  annotate(geom = "label", x = -0.5, y = 0.8, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT$stress, digits=2))) +
  scale_color_viridis(name="Temperature") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Temp_ALL
ggsave("NMDS Order Temperature ALL.png", NMDS_Order_Temp_ALL, width = 10.35, height = 5.76, dpi
= 600)


#####
# NMDS time series
#####
# Making data into wide format, but species, family, and order to themselves
# they cannot be in the same data set
# WIDE DATA making TIME
#####
# Species
wide_data_species_COUNT_time <- dcast(Time_series_data_PIVOT, Station_ID + Temp +
Location_category +
                                   Depth + Latitude + Longitude + Decade +
Oceanic_stratification
                                 + Trawling_min ~ Species,
                                 value.var="Count", fun.aggregate=sum, fill=0)

# Family
wide_data_family_COUNT_time <- dcast(Time_series_data_PIVOT, Station_ID + Temp +
Location_category +
                                  Depth + Latitude + Longitude + Decade +
Oceanic_stratification
                                + Trawling_min ~ Family,
                                value.var="Count", fun.aggregate=sum, fill=0)

# Order
wide_data_order_COUNT_time <- dcast(Time_series_data_PIVOT, Station_ID + Temp +
Location_category +
                                 Depth + Latitude + Longitude + Decade + Oceanic_stratification
                               + Trawling_min ~ Order,
                               value.var="Count", fun.aggregate=sum, fill=0)
# Species
wide_data_species_WEIGHT_time <- dcast(Time_series_data_PIVOT, Station_ID + Temp +
Location_category +
                                    Depth + Latitude + Longitude + Decade +
Oceanic_stratification
                                  + Trawling_min ~ Species,
                                  value.var="Weight", fun.aggregate=sum, fill=0)

# Family
wide_data_family_WEIGHT_time <- dcast(Time_series_data_PIVOT, Station_ID + Temp +
Location_category +
                                   Depth + Latitude + Longitude + Decade +
Oceanic_stratification
                                 + Trawling_min ~ Family,
                                 value.var="Weight", fun.aggregate=sum, fill=0)

# Order
wide_data_order_WEIGHT_time <- dcast(Time_series_data_PIVOT, Station_ID + Temp +
Location_category +
                                  Depth + Latitude + Longitude + Decade +
Oceanic_stratification
                                + Trawling_min ~ Order,
                                value.var="Weight", fun.aggregate=sum, fill=0)

#####
```

```
#####
# Bray-Curtis dissimilar matrix COUNT
# To use for statistical calculations and look at values to see obvious differences
# COUNT TIME
#####
# SPECIES
For_NMDS_species_COUNT_time <- vegdist(wide_data_species_COUNT_time[,10:53], method = "bray",
na.rm = TRUE)
NMDS_data_format_s_COUNT_time <- metaMDS(comm = wide_data_species_COUNT_time[,10:53], k=2,
distance = "bray",trymax = 100, autotransform = T)

# FAMILY
For_NMDS_family_COUNT_time <- vegdist(wide_data_family_COUNT_time[,10:25], method = "bray",
na.rm = TRUE)
NMDS_data_format_f_COUNT_time <- metaMDS(comm = wide_data_family_COUNT_time[,10:25], k=2,
distance = "bray",trymax = 100, autotransform = T)

# ORDER
For_NMDS_order_COUNT_time <- vegdist(wide_data_order_COUNT_time[,10:17], method = "bray", na.rm
= TRUE)
NMDS_data_format_o_COUNT_time <- metaMDS(comm = wide_data_order_COUNT_time[,10:17], k=2,
distance = "bray",trymax = 100, autotransform = T)

# Making predictor variables usable for NMDS
Predictor_variables_s_COUNT_time <- wide_data_species_COUNT_time[,1:9]
Predictor_variables_f_COUNT_time <- wide_data_species_COUNT_time[,1:9]
Predictor_variables_o_COUNT_time <- wide_data_species_COUNT_time[,1:9]

#####
# COUNT Analyzing with station_ID TIME
#####
# Analyzing SPECIES with station_ID

# Extract species and sites
plot_nmds_s_COUNT_time = as.data.frame(scores(NMDS_data_format_s_COUNT_time)$sites)
plot_nmds_s1_COUNT_time = as.data.frame(scores(NMDS_data_format_s_COUNT_time)$species)
plot_nmds_s1_COUNT_time$species <- rownames(plot_nmds_s1_COUNT_time)

# Combing plot values and predictor values together into one function
plot_species_COUNT_time <- cbind(Predictor_variables_s_COUNT_time, plot_nmds_s_COUNT_time)


# Analyzing FAMILY with station_ID

# Extract species and sites
plot_nmds_f_COUNT_time = as.data.frame(scores(NMDS_data_format_f_COUNT_time)$sites)
plot_nmds_f1_COUNT_time = as.data.frame(scores(NMDS_data_format_f_COUNT_time)$species)
plot_nmds_f1_COUNT_time$family <- rownames(plot_nmds_f1_COUNT)

# Combing plot values and predictor values together into one function
plot_family_COUNT_time <- cbind(Predictor_variables_f_COUNT_time, plot_nmds_f_COUNT_time)

# Analyzing ORDER with station_ID

# Extract species and sites
plot_nmds_o_COUNT_time = as.data.frame(scores(NMDS_data_format_o_COUNT_time)$sites)
plot_nmds_o1_COUNT_time = as.data.frame(scores(NMDS_data_format_o_COUNT_time)$species)
plot_nmds_o1_COUNT_time$order <- rownames(plot_nmds_o1_COUNT_time)

# Combing plot values and predictor values together into one function
plot_order_COUNT_time <- cbind(Predictor_variables_o_COUNT_time, plot_nmds_o_COUNT_time)


#####
# Plot NMDS COUNT TIME ----
#SPECIES COUNT NMDS TIME
#####
# Location category
NMDS_LOC_C_time <-
ggplot()+
  geom_point(data= plot_species_COUNT_time, aes(x=NMDS1,
y=NMDS2,colour=Location_category),size=4)+
  geom_text_repel(data= plot_nmds_s1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=species),
alpha=0.5) +
  annotate(geom = "label", x = -1.2, y = 1.5, size = 3,
```

```r
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT_time$stress, digits=2)))
+
  stat_ellipse(data= plot_species_COUNT_time, aes(x=NMDS1, y=NMDS2, colour=Location_category),
size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Location category") +
  theme_classic() +
  NMDS_theme

NMDS_LOC_C_time
ggsave("NMDS Location category TIME.png", NMDS_LOC_C_time, width = 10.35, height = 5.76, dpi =
600)

# Depth
NMDS_Depth_C_time <-
ggplot()+
  geom_point(data= plot_species_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Depth),size=3)+
  geom_text_repel(data= plot_nmds_s1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=species),
alpha=0.5)+
  annotate(geom = "label", x = -0.95, y = 1.55, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT_time$stress, digits=2)))
+
  scale_color_viridis(name="Depth") +
  theme_classic() +
  NMDS_theme

NMDS_Depth_C_time
ggsave("NMDS Depth TIME.png", NMDS_Depth_C_time, width = 10.35, height = 5.76, dpi = 600)

# Latitude
NMDS_LAT_C_time <-
ggplot()+
  geom_point(data= plot_species_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Latitude),size=3)+
  geom_text_repel(data= plot_nmds_s1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=species),
alpha=0.5)+
  annotate(geom = "label", x = -0.95, y = 1.6, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT_time$stress, digits=2)))
+
  scale_color_viridis(name ="Latitude") +
  theme_classic() +
  NMDS_theme

NMDS_LAT_C_time
ggsave("NMDS Latitude TIME.png", NMDS_LAT_C_time, width = 10.35, height = 5.76, dpi = 600)

# Decade
NMDS_Decade_TIME <-
  ggplot() +
  geom_point(data = plot_species_COUNT_time, aes(x = NMDS1, y = NMDS2, colour = Decade), size =
3) +
  geom_text_repel(data = plot_nmds_s1_COUNT_time,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT_time$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.9, y = 1.65, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT_time$stress, digits =
2))) +
  stat_ellipse(data = plot_species_COUNT_time, aes(x = NMDS1, y = NMDS2, colour = Decade), size
= 1) +
  scale_color_viridis(discrete = TRUE, na.translate = FALSE, name = "Decade \ncategory") +
  theme_classic() +
  NMDS_theme
ggsave("NMDS Decade TIME.png", NMDS_Decade_TIME, width = 10.35, height = 5.76, dpi = 600)

NMDS_Decade_TIME_2 <-
  ggplot() +
  geom_point(data = plot_species_COUNT_time, aes(x = NMDS1, y = NMDS2, colour = Decade), size =
3) +
  geom_text_repel(data = plot_nmds_s1_COUNT_time,
                  aes(x = NMDS1, y = NMDS2, label = species),
                  color = Zoogeography_colours_NMDS[plot_nmds_s1_COUNT_time$species],
                  alpha = 0.5) +
  annotate(geom = "label", x = -0.9, y = 1.65, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT_time$stress, digits =
2))) +
  stat_ellipse(data = plot_species_COUNT_time, aes(x = NMDS1, y = NMDS2, colour = Decade), size
```

```
= 1) +
  scale_color_viridis(discrete = TRUE, na.translate = FALSE, name = "Decade category") +
  theme_classic() +
  theme(legend.position = "none") +  # Legend hidden
  NMDS_theme


# Oceanic stratification
NMDS_Oce_str_TIME <-
ggplot()+
  geom_point(data= plot_species_COUNT_time, aes(x=NMDS1,
y=NMDS2,colour=Oceanic_stratification),size=3)+
  geom_text_repel(data= plot_nmds_s1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=species),
alpha=0.5)+
  annotate(geom = "label", x = -0.85, y = 1.7, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT_time$stress, digits=2)))
+
  stat_ellipse(data= plot_species_COUNT_time, aes(x=NMDS1, y=NMDS2,
colour=Oceanic_stratification), size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Oceanic
stratification\ncategory") +
  theme_classic() +
  NMDS_theme

NMDS_Oce_str_TIME
ggsave("NMDS Oceanic stratification TIME.png", NMDS_Oce_str_TIME, width = 10.35, height = 5.76,
dpi = 600)

# Temp
NMDS_temp_TIME <-
ggplot()+
  geom_point(data= plot_species_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Temp),size=3)+
  geom_text_repel(data= plot_nmds_s1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=species),
alpha=0.5)+
  annotate(geom = "label", x = -0.9, y = 1.6, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_s_COUNT_time$stress, digits=2)))
+
  scale_color_viridis(name="Temperature") +
  theme_classic() +
  NMDS_theme

NMDS_temp_TIME
ggsave("NMDS Temperature TIME.png", NMDS_temp_TIME, width = 10.35, height = 5.76, dpi = 600)

#####
# FAMILY COUNT NMDS TIME
#####
# Location category
NMDS_f_loc_TIME <-
ggplot()+
  geom_point(data= plot_family_COUNT_time, aes(x=NMDS1,
y=NMDS2,colour=Location_category),size=4)+
  geom_text_repel(data= plot_nmds_f1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=family),
alpha=0.5) +
  annotate(geom = "label", x = -0.62, y = 1.4, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT_time$stress, digits=2)))
+
  stat_ellipse(data= plot_family_COUNT_time, aes(x=NMDS1, y=NMDS2, colour=Location_category),
size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Location category") +
  theme_classic() +
  NMDS_theme

NMDS_f_loc_TIME
ggsave("NMDS Family Location category TIME.png", NMDS_f_loc_TIME, width = 10.35, height = 5.76,
dpi = 600)

# Depth
NMDS_f_Depth_TIME <-
ggplot()+
  geom_point(data= plot_family_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Depth),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=family),
alpha=0.5)+
  annotate(geom = "label", x = -0.6, y = 1.3, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT_time$stress, digits=2)))
```

```
+
  scale_color_viridis(name="Depth") +
  theme_classic() +
  NMDS_theme

NMDS_f_Depth_TIME
ggsave("NMDS Family Depth TIME.png", NMDS_f_Depth_TIME, width = 10.35, height = 5.76, dpi =
600)

# Latitude
NMDS_f_lat_TIME <-
ggplot()+
  geom_point(data= plot_family_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Latitude),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=family),
alpha=0.5)+
  annotate(geom = "label", x = -0.6, y = 1.3, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT_time$stress, digits=2)))
+
  scale_color_viridis(name ="Latitude") +
  theme_classic() +
  NMDS_theme

NMDS_f_lat_TIME
ggsave("NMDS Family Latitude TIME.png", NMDS_f_lat_TIME, width = 10.35, height = 5.76, dpi =
600)

# Decade
NMDS_f_Decade_TIME <-
ggplot()+
  geom_point(data= plot_family_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Decade),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=family),
alpha=0.5)+
  annotate(geom = "label", x = -0.8, y = 1.3, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT_time$stress, digits=2)))
+
  stat_ellipse(data= plot_family_COUNT_time, aes(x=NMDS1, y=NMDS2, colour=Decade), size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Decade \ncategory") +
  theme_classic() +
  NMDS_theme

NMDS_f_Decade_TIME
ggsave("NMDS Family Decade TIME.png", NMDS_f_Decade_TIME, width = 10.35, height = 5.76, dpi =
600)

# Oceanic stratification
NMDS_Family_Oce_str_TIME <-
ggplot()+
  geom_point(data= plot_family_COUNT_time, aes(x=NMDS1,
y=NMDS2,colour=Oceanic_stratification),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=family),
alpha=0.5)+
  annotate(geom = "label", x = -0.6, y = 1.65, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT_time$stress, digits=2)))
+
  stat_ellipse(data= plot_family_COUNT_time, aes(x=NMDS1, y=NMDS2,
colour=Oceanic_stratification), size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Oceanic stratification
\ncategory") +
  theme_classic() +
  NMDS_theme

NMDS_Family_Oce_str_TIME
ggsave("NMDS Family Oceanic stratification TIME.png", NMDS_Family_Oce_str_TIME, width = 10.35,
height = 5.76, dpi = 600)

# Temp
NMDS_Family_Temp_TIME <-
ggplot()+
  geom_point(data= plot_family_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Temp),size=3)+
  geom_text_repel(data= plot_nmds_f1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=family),
alpha=0.5)+
  annotate(geom = "label", x = -0.6, y = 1.25, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_f_COUNT_time$stress, digits=2)))
+
  scale_color_viridis(name="Temperature") +
```

```
  theme_classic() +
  NMDS_theme

NMDS_Family_Temp_TIME
ggsave("NMDS Family Temperature TIME.png", NMDS_Family_Temp_TIME, width = 10.35, height = 5.76,
dpi = 600)

#####
# NMDS Zoogeography






#####
# ORDER COUNT NMDS TIME
#####
# Location category
NMDS_Order_LOC_TIME <-
ggplot()+
  geom_point(data= plot_order_COUNT_time, aes(x=NMDS1,
y=NMDS2,colour=Location_category),size=4)+
  geom_text_repel(data= plot_nmds_o1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=order),
alpha=0.5) +
  annotate(geom = "label", x = -0.85, y = 0.8, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT_time$stress, digits=2)))
+
  stat_ellipse(data= plot_order_COUNT_time, aes(x=NMDS1, y=NMDS2, colour=Location_category),
size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Location category") +
  theme_classic() +
  NMDS_theme

NMDS_Order_LOC_TIME
ggsave("NMDS Order Location category TIME.png", NMDS_Order_LOC_TIME, width = 10.35, height =
5.76, dpi = 600)

# Depth
NMDS_Order_Depth_TIME <-
ggplot()+
  geom_point(data= plot_order_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Depth),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=order),
alpha=0.5)+
  annotate(geom = "label", x = -0.95, y = 0.75, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT_time$stress, digits=2)))
+
  scale_color_viridis(name="Depth") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Depth_TIME
ggsave("NMDS Order Depth TIME.png", NMDS_Order_Depth_TIME, width = 10.35, height = 5.76, dpi =
600)

# Latitude
NMDS_Order_Lat_TIME <-
ggplot()+
  geom_point(data= plot_order_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Latitude),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=order),
alpha=0.5)+
  annotate(geom = "label", x = -0.95, y = 0.75, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT_time$stress, digits=2)))
+
  scale_color_viridis(name ="Latitude") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Lat_TIME
ggsave("NMDS Order Latitude TIME.png", NMDS_Order_Lat_TIME, width = 10.35, height = 5.76, dpi =
600)

# Decade
NMDS_Order_Decade_TIME <-
ggplot()+
  geom_point(data= plot_order_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Decade),size=3)+
```

```
  geom_text_repel(data= plot_nmds_o1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=order),
alpha=0.5)+
  annotate(geom = "label", x = -0.9, y = 0.77, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT_time$stress, digits=2)))
+
  stat_ellipse(data= plot_order_COUNT_time, aes(x=NMDS1, y=NMDS2, colour=Decade), size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Decade category") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Decade_TIME
ggsave("NMDS Order Decade TIME.png", NMDS_Order_Decade_TIME, width = 10.35, height = 5.76, dpi
= 600)

# Oceanic stratification
NMDS_Order_Oce_str_TIME <-
ggplot()+
  geom_point(data= plot_order_COUNT_time, aes(x=NMDS1,
y=NMDS2,colour=Oceanic_stratification),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=order),
alpha=0.5)+
  annotate(geom = "label", x = -0.95, y = 1.3, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT_time$stress, digits=2)))
+
  stat_ellipse(data= plot_order_COUNT_time, aes(x=NMDS1, y=NMDS2,
colour=Oceanic_stratification), size=1)+
  scale_color_viridis(discrete=TRUE, na.translate=FALSE, name="Oceanic stratification
\ncategory") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Oce_str_TIME
ggsave("NMDS Order Oceanic stratification TIME.png", NMDS_Order_Oce_str_TIME, width = 10.35,
height = 5.76, dpi = 600)

# Temp
NMDS_Order_Temp_TIME <-
ggplot()+
  geom_point(data= plot_order_COUNT_time, aes(x=NMDS1, y=NMDS2,colour=Temp),size=3)+
  geom_text_repel(data= plot_nmds_o1_COUNT_time, aes (x=NMDS1, y=NMDS2, label=order),
alpha=0.5)+
  annotate(geom = "label", x = -0.9, y = 0.78, size = 3,
           label = paste("2D Stress: ", round(NMDS_data_format_o_COUNT_time$stress, digits=2)))
+
  scale_color_viridis(name="Temperature") +
  theme_classic() +
  NMDS_theme

NMDS_Order_Temp_TIME
ggsave("NMDS Order Temperature TIME.png", NMDS_Order_Temp_TIME, width = 10.35, height = 5.76,
dpi = 600)


#####

# NMDS side by side
NMDS_DECADE <- NMDS_Decade_TIME_2|NMDS_f_Decade_TIME
ggsave("NMDS DECADE minus below 72.png", NMDS_DECADE, width = 10.35, height = 5.76, dpi = 600)

#####

##### Linear model using NMDS outputs
#####
# All data COUNT
# Adding distance to coast to dataframe
#NMDS 1
plot_species_COUNT <- left_join(plot_species_COUNT, Distance_to_coast[,c(1,19)])

# Linear model
Model1 <- lm(NMDS1 ~ Depth + Temp + Latitude + Trawling_min + Coast_distance,
             data = plot_species_COUNT)
summary(Model1)
AIC(Model1)

Model1.2 <- lm(NMDS1 ~ Depth + Temp + Latitude + Coast_distance,
```

```
             data = plot_species_COUNT)
summary(Model1.2)
AIC(Model1.2)

Model1.3 <- lm(NMDS1 ~ Depth + Temp + Coast_distance,
               data = plot_species_COUNT)
summary(Model1.3)
AIC(Model1.3)

Model1.4 <- lm(NMDS1 ~ Depth + Coast_distance,
               data = plot_species_COUNT)
summary(Model1.4)
AIC(Model1.4)

Model1.5 <- lm(NMDS1 ~ Depth,
               data = plot_species_COUNT)
summary(Model1.5)
AIC(Model1.5)

cor(plot_species_COUNT$Depth,plot_species_COUNT$Coast_distance)
plot(plot_species_COUNT$Depth,plot_species_COUNT$Coast_distance)

# USE Model 1.4 since it is the best fit !!!! It has the lowest AIC value

Last_1 <- ggplot(plot_species_COUNT, aes(x = Coast_distance, y = Depth, color = Decade)) +
  geom_point() +
  labs(x = "Distance to Coast (km)", y = "Depth (m)", title = "NMDS1 & NMDS2") +
  scale_color_viridis_d(option = "D") +
  scale_y_reverse() +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 12)
  )


# NMDS 2
Model2 <- lm(NMDS2 ~ Depth + Temp + Latitude + Trawling_min + Coast_distance,
             data = plot_species_COUNT)
summary(Model2)
AIC(Model2)

Model2.2 <- lm(NMDS2 ~ Depth + Temp + Coast_distance +Trawling_min,
               data = plot_species_COUNT)
summary(Model2.2)
AIC(Model2.2)

Model2.3 <- lm(NMDS2 ~ Temp + Coast_distance + Depth,
               data = plot_species_COUNT)
summary(Model2.3)
AIC(Model2.3)

Model2.4 <- lm(NMDS2 ~ Temp + Coast_distance,
               data = plot_species_COUNT)
summary(Model2.4)
AIC(Model2.4)

Model2.5 <- lm(NMDS2 ~ Coast_distance,
               data = plot_species_COUNT)
summary(Model2.5)
AIC(Model2.5)

# USE Model 2.3 since it is the best fit !!!! It has the lowest AIC value
# Temp and coast_distance are the most significant values
# Explains the best variability

Last_2 <-
  ggplot(plot_species_COUNT, aes(x = Coast_distance, y = Temp, color = Decade)) +
  geom_point() +
  labs(x = "Distance to Coast (km)", y = "Temperature (°C)", title = "NMDS2") +
  scale_color_viridis_d(name = "Decade\ncategory", option = "D") +
  theme_classic() +
  theme(
```

```
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 14),
    legend.text = element_text(color = "black", size = 12),
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 12))

Last_3 <- ggplot(plot_species_COUNT, aes(x = Temp, y = Depth, color = Decade)) +
  geom_point() +
  labs(x = "Temperature (°C)", y = "Depth (m)", title = "NMDS2") +
  scale_color_viridis_d(option = "D") +
  scale_y_reverse() +
  theme_classic() +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 0, hjust = 0.5),
    plot.title = element_text(hjust = 0.5, size = 24),
    axis.title = element_text(size = 12)
  )

Last_all <- (Last_1+Last_3+Last_2) +
plot_annotation(title = "Best linear model fits from AIC calculations",
                theme = theme(plot.title = element_text(size = 24, hjust = 0.5)))

ggsave("AIC plots.png", Last_all, width = 18, height = 8, dpi = 600)

#####
# GADIFORMES
Gadidae_PIVOT <- subset (Pivot_all_data, Order == "Gadiformes")

Gadiformes_species <-
Gadidae_PIVOT %>% filter(Location_category != "NA") %>%
  ggplot(aes(fill = Species, y= Count, x= Location_category)) +
  geom_bar(position="fill", stat="identity") +
  labs(x = "Location type", y = "Percentage of species", title = "Relative abundance within the
order Gadiformes \nin the three location types") +
  scale_fill_viridis_d(option="magma")+
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    axis.text.x = element_text(angle = 0, hjust = 0.5,size = 18, color = "black"),
    axis.text.y = element_text(size=18,color = "black"),
    plot.title = element_text(hjust = 0.5, size = 26),
    axis.title = element_text(size = 22)) +
  scale_y_continuous(expand = c(0,0))

Gadiformes_species

ggsave("Gadiformes species.png", Gadiformes_species, width = 12, height = 6, dpi = 600)

Scorp_PIVOT <- subset (Pivot_all_data, Order == "Scorpaeniformes")

Scorp_species <-
  Scorp_PIVOT %>% filter(Location_category != "NA") %>%
  ggplot(aes(fill = Species, y= Count, x= Location_category)) +
  geom_bar(position="fill", stat="identity") +
  labs(x = "Location type", y = "Percentage of species", title = "Relative abundance within the
order Scorpaeniformes \nin the three location types") +
  scale_fill_viridis_d(option="viridis")+
  theme_classic() +
  theme(
    legend.background = element_blank(),
    legend.key = element_blank(),
    legend.title = element_text(color = "black", size = 20),
    legend.text = element_text(color = "black", size = 18, face = "italic"),
    axis.text.x = element_text(angle = 0, hjust = 0.5,size = 18, color = "black"),
    axis.text.y = element_text(size=18,color = "black"),
    plot.title = element_text(hjust = 0.5, size = 26),
    axis.title = element_text(size = 22)) +
  scale_y_continuous(expand = c(0,0))
```

```
Scorp_species

ggsave("Scorpaeniformes species.png", Scorp_species, width = 12, height = 6, dpi = 600)
```