Appendix code

Map of stations

```
#Load packages


library(tidyverse)

library(rnaturalearth)

library(sf)

library(ggplot2)

theme_set(theme_bw())

library(rnaturalearthdata)

library(dplyr)

library(purrr)

library(pointdensityP)

library(ggrepel)

library(raster)

library(ncdf4)


#Create an object for the world map

world <- ne_countries(scale = "large", returnclass = "sf")


#Import the data set for the trawls-

stations2018 <- read_delim(file="Data_fishlab_2018106_stations.csv", delim=";", locale =
locale(decimal_mark = ","))


#Import the data set for the trawls 2021

stations2021 <- read_delim(file="FishStation_2021105_mindre.csv", delim=";", locale =
locale(decimal_mark = ","))


#Make the data frame

stations_data_frame2021 = data.frame(stations2021[c("Longitude", "Latitude", "SerialNo")])
```

```
stations_data_frame2018 = data.frame(stations2018[c("longitudestart", "latitudestart", "serialno")])

#Make a separate data frame for stations used in the stomach analysis
#highlight_stations2021 <- stations_data_frame2021 |>
 # slice(16, 17, 19, 20, 21, 22, 23, 29, 51,57, 64)

highlight_stations2018 <- stations_data_frame2018 |>
  slice(3, 4, 5, 7, 8, 11, 12, 16, 17, 18, 19)

highlight_stations2021 <- stations_data_frame2021[stations_data_frame2021$SerialNo %in%
c("23016", "23017", "23019", "23020", "23021", "23022", "23023", "23029", "23052", "23059",
"23066"),]

world_points<- st_centroid(world)
world_points <- cbind(world, st_coordinates(st_centroid(world$geometry)))

#Load bathymetric data
bathym <- raster("gebco_2022_n68.0_s55.0_w-30.0_e10.0.nc")

#Make data frame
bathym_df <- data.frame( rasterToPoints( bathym ) ) |>
  rename(elevation = Elevation.relative.to.sea.level)



#Plot with depth and only used stations from both cruises
trawls <- ggplot() +
  geom_sf(data = world)+
  coord_sf(xlim = c(-30.0, 10.0), ylim = c(68.0, 55.0), expand = FALSE)+
  geom_raster(data = bathym_df, aes(x=x, y=y, fill = elevation), interpolate= FALSE)+
  scale_fill_gradientn(colours = c("midnightblue", "skyblue1",
                                   "lightyellow", "orange"),
                       values = scales::rescale(c(min(bathym_df), -0.1,
```

```
                                0, max(bathym_df))))+
  geom_point(data = highlight_stations2021, alpha = 0.6, aes(x = Longitude, y = Latitude,),color =
"#893101", size = 2)+
  geom_text(data= world_points,aes(x=X, y=Y, label=name), color = "darkblue", fontface = "italic",
check_overlap = FALSE)+
  geom_point(data=highlight_stations2018, alpha = 0.6, aes(x=longitudestart,y=latitudestart),
color='magenta', size = 2)+
  geom_text_repel(data = highlight_stations2021, size = 3, max.overlaps = Inf, aes(x = Longitude, y =
Latitude, label = SerialNo))+
  geom_text_repel(data = highlight_stations2018, size = 3, max.overlaps = Inf, aes(x = longitudestart,
y = latitudestart, label = serialno))+
  labs(
    x = "Longitude",
    y = "Latitude",
    fill = "Elevation (m)")+
  annotate(geom = "text", x = -20, y = 55.5, label = "North Atlantic Ocean",
           fontface = "italic", color = "black", size = 4)+
  annotate(geom = "text", x = -4, y = 57, label = "Scotland",
           fontface = "italic", color = "darkblue", size = 4)+
  annotate(geom = "text", x = 8, y = 61, label = "Norway",
           fontface = "italic", color = "darkblue", size = 4)+
  annotate(geom = "text", x = -20, y = 62, label = "Iceland Basin",
           fontface = "italic", color = "black", size = 4)+
  annotate(geom = "text", x = 1, y = 67, label = "Norwegian Sea",
           fontface = "italic", color = "black", size = 4) +
  annotate(geom = "text", x = -11, y = 58, label = "Rockall Basin",
           fontface = "italic", color = "black", size = 4)
trawls


ggsave("map_used_stations_both_bruises.jpeg", trawls, width = 140, height = 80, units = c("mm"),
scale = 2.5)
```

Eye sizes all fish

```
library(ggplot2)

library(tidyverse)

library(dplyr)

library(purrr)

library(ggthemes)

library(cowplot)

library(glue)

library(viridis)


data <- read_delim(file="15093 - Mesopelagic stomach analysis kopi.csv", delim=";", locale =
locale(decimal_mark = ","))

colnames(data)[4] <- "fish_species"

colnames(data)[6] <- "eye_body_ratio"


unique_fish <- data |>

 distinct(fish_species, .keep_all =TRUE)

unique_fish <- data.frame(unique_fish[c("fish_species", "eye_body_ratio")])


text_italic <- element_text(face = "italic", size = 12)


fish_eyes <- ggplot(unique_fish, aes(y = (fct_reorder(fish_species, eye_body_ratio)), x =
eye_body_ratio))+

 geom_point(aes(colour = eye_body_ratio, size = 4))+

 theme_cowplot()+

 scale_color_viridis()+

 theme(axis.text.y = text_italic,

     legend.title = element_blank(),

     legend.position = "none")+

 labs(

  x = "Eye-body-ratio",

  y = "Fish species")+
```

```
  scale_x_continuous(breaks = seq(0, 0.15, 0.01))

fish_eyes


ggsave("fish_eyes.jpeg", fish_eyes, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure
```

Table all fish

```
library(tidyverse)

library(gt)

library(dplyr)

##TABLE 2018##

diet <- read_delim(file="15093 - Mesopelagic stomach analysis kopi.csv", delim=";", locale = locale(decimal_mark = "."))

colnames(diet)[3] <- "serialno"

colnames(diet)[4] <- "fish_species"

colnames(diet)[5] <- "fish_nr"

colnames(diet)[22] <- "nr_prey"

colnames(diet)[19] <- "bioluminescence"

colnames(diet)[10] <- "lengde"

colnames(diet)[11] <- "totalvekt"


diet_frame <- data.frame(diet[c("serialno", "Byttedyr", "nr_prey", "fish_species","bioluminescence", "lengde", "totalvekt", "fish_nr")])


#The previous data set lacks the names of th stations and only has the serial numbers of the trawls, load a document that has both

stations <- read_delim(file = "FishStation_2018106_kopi.csv", delim=";", locale = locale(decimal_mark = ","))

stations_frame <- data.frame(stations[c("serialno", "station")])




#Create a new data frame with the station names
```

```
new_diet <- left_join(diet_frame,stations_frame, by="serialno")

colnames(new_diet)[9] <- "fish_station"


new_diet <- data.frame(new_diet[c("fish_station", "fish_species", "lengde", "totalvekt", "Byttedyr",
"nr_prey", "bioluminescence", "fish_nr")])


unique_fishnr <- new_diet |>

  distinct(fish_nr, .keep_all =TRUE)



for_total_fish <- unique_fishnr |>

  count(fish_species)



for_total <- transform(new_diet, c(nr_prey = as.numeric(nr_prey)))

for_total[is.na(for_total)] <- 0


for_total_prey <- for_total |>

  group_by(fish_species, Byttedyr) |>

  summarise(total_prey = sum(nr_prey))



for_total_prey1 <- for_total_prey |>

  group_by(fish_species) |>

  summarise(total_prey = sum(total_prey))


for_total_prey[is.na(for_total_prey)] <- 0


for_total_prey <- for_total_prey |>

  group_by(fish_species) |>

  summarise(total_prey = sum(total_prey))
```

```
fish_frame <- transform(new_diet, c(numeric_lengde = as.numeric(lengde), numeric_totalvekt =
as.numeric(totalvekt)))


fish_frame1 <- fish_frame[-648,]


max_min_values <-  fish_frame1 |>
 group_by(fish_species) |>
 summarise(minimum_length = min(lengde),
           maximum_length = max(lengde),
           mean_length = round(mean(lengde), 0),
           minimum_totalvekt = min(totalvekt),
           maximum_totalvekt = max(totalvekt),
           mean_weight = round(mean(totalvekt), 2),
           sd_length = sd(lengde) )



fish_number <- unique_fishnr |>
 group_by(fish_station, fish_species,) |>
 summarise(total_count=n(),
           .groups = 'drop')
fish_number


prey_number <- new_diet |>
 group_by(fish_species, Byttedyr) |>
 summarise(total_count=n(),
           .groups = 'drop')


empty_stomach <- subset(prey_number,Byttedyr == "Empty")


empty_stomach <- data.frame(empty_stomach[c("fish_species", "total_count")])
```

```
colnames(empty_stomach)[2] <- "empty_stomachs"

fish_empty <- left_join(fish_number,empty_stomach, by=c( "fish_species"))
colnames(fish_empty)[3] <- "individuals_per_station"
colnames(fish_empty)[5] <- "empty_stomachs"

fish_wider <- data.frame(fish_empty[c("fish_station", "fish_species", "individuals_per_station")])

fish_wider <- pivot_wider(fish_wider, names_from = "fish_station", values_from =
"individuals_per_station")



for_table <- left_join(fish_wider,max_min_values, by= "fish_species")

for_table <- left_join(for_table, empty_stomach, by="fish_species")

for_table <- left_join(for_table, for_total_prey, by="fish_species")

for_table <- left_join(for_table, for_total_fish, by="fish_species")

for_table |>
  mutate(empty_stomachs = coalesce(empty_stomachs, 0))

for_table <- for_table |>
  relocate(n, .before = minimum_length)|>
  rename(total_fish = n)

for_table1<- for_table |>
  mutate_at(20, ~replace_na(.,0))

table_fish_2018 <- for_table1 |>
```

```
arrange(fish_species) |>
gt() |>
cols_label(fish_species = "",
           total_fish = "Total",
           minimum_length = "Min",
           maximum_length = "Max",
           mean_length = "Mean",
           minimum_totalvekt = "Min",
           maximum_totalvekt = "Max",
           mean_weight = "Mean",
           empty_stomachs = "",
           total_prey = "") |>
tab_spanner(label = md('**Fish Species**'),
            columns = 1) |>
tab_spanner(label = md('**Individuals**'),
            columns = 2:13) |>
tab_spanner(label = md('**Length (mm)**'),
            columns = 14:16) |>
tab_spanner(label = md('**Weight (g)**'),
            columns = 17:19) |>
tab_spanner(label = md('**Empty**'),
            columns = 20) |>
tab_spanner(label = md('**Total prey**'),
            columns = 21) |>
sub_missing(columns = 1:19,
            missing_text = "-")|>
cols_align(align = "center", columns = 2:20) |>
tab_options(
  data_row.padding = px(2),
  summary_row.padding = px(3),
  row_group.padding = px(4))|>
```

```
  opt_stylize(style = 6, color = 'blue')|>
  tab_style(
    style = list(
      cell_text(style = "italic")
    ),
    locations = cells_body(
      columns = 1
    ))|>
  tab_style(
    style = list(cell_fill(color = "#CF9FFF"),
      cell_text(weight = "bold")
    ),
    locations = cells_body(
      rows = c(3, 10, 12, 13)
    ))|>
  tab_style(
    style = list(cell_fill(color = "#F6C324"),
                 cell_text(weight = "bold")
    ),
    locations = cells_body(
      rows = c(1, 14)
    ))|>
  tab_header(
    title = md("**Cruise 2018106**"))
table_fish_2018
gtsave(table_fish_2021, "table_fish_2021.png", vwidth = 4000, vheight = 500)

##TABLE 2021##

library(tidyverse)
library(gt)
```

```
library(dplyr)



diet2021 <- read_delim(file="Mesopeloagic stomach analysis 2021.csv", delim=";", locale =
locale(decimal_mark = "."))

colnames(diet2021)[1] <- "fish_nr"

colnames(diet2021)[4] <- "serialno"

colnames(diet2021)[5] <- "fish_species"

colnames(diet2021)[20] <- "nr_prey"

colnames(diet2021)[17] <- "bioluminescence"

colnames(diet2021)[8] <- "lengde"

colnames(diet2021)[9] <- "totalvekt"



diet_frame <- data.frame(diet2021[c("serialno", "Byttedyr", "nr_prey",
"fish_species","bioluminescence", "lengde", "totalvekt", "fish_nr")])



#The previous data set lacks the names of th stations and only has the serial numbers of the trawls,
load a document that has both

stations <- read_delim(file = "FishStation_2021105_mindre.csv", delim=";", locale =
locale(decimal_mark = ","))

colnames(stations)[5] <- "serialno"

colnames(stations)[4] <- "station"


stations_frame <- data.frame(stations[c("serialno", "station")])


#Create a new data frame with the station names

new_diet <- left_join(diet_frame,stations_frame, by="serialno")

colnames(new_diet)[9] <- "fish_station"


new_diet <- data.frame(new_diet[c("fish_station", "fish_species", "lengde", "totalvekt", "Byttedyr",
"nr_prey", "bioluminescence", "fish_nr")])
```

```
unique_fishnr <- new_diet |>
  distinct(fish_nr, .keep_all =TRUE)

for_total_fish <- unique_fishnr |>
  count(fish_species)

for_total <- transform(new_diet, c(nr_prey = as.numeric(nr_prey)))
for_total[is.na(for_total)] <- 0

for_total_prey <- for_total |>
  group_by(fish_species, Byttedyr) |>
  summarise(total_prey = sum(nr_prey))



for_total_prey1 <- for_total_prey |>
  group_by(fish_species) |>
  summarise(total_prey = sum(total_prey))

for_total_prey[is.na(for_total_prey)] <- 0

for_total_prey <- for_total_prey |>
  group_by(fish_species) |>
  summarise(total_prey = sum(total_prey))

fish_frame <- transform(new_diet, c(lengde = as.numeric(lengde), totalvekt =
as.numeric(totalvekt)))#|>
 # na.omit(fish_frame)
fish_frame1 <- fish_frame[-267,]

max_min_values <-  fish_frame1 |>
```

```
 group_by(fish_species) |>
 summarise(minimum_length = min(lengde),
           maximum_length = max(lengde),
           mean_length = round(mean(lengde), 0),
           minimum_totalvekt = round(min(totalvekt), 2),
           maximum_totalvekt = round(max(totalvekt), 2),
           mean_weight = round(mean(totalvekt), 2),
           sd_length = sd(lengde))

fish_number <- unique_fishnr |>
 group_by(fish_station, fish_species,) |>
 summarise(total_count=n(),
           .groups = 'drop')
fish_number

prey_number <- new_diet |>
 group_by(fish_species, Byttedyr) |>
 summarise(total_count=n(),
           .groups = 'drop')

empty_stomach <- subset(prey_number,Byttedyr == "Empty")

empty_stomach <- data.frame(empty_stomach[c("fish_species", "total_count")])
colnames(empty_stomach)[2] <- "empty_stomachs"

fish_empty <- left_join(fish_number,empty_stomach, by=c( "fish_species"))
colnames(fish_empty)[3] <- "individuals_per_station"
colnames(fish_empty)[5] <- "empty_stomachs"

fish_wider <- data.frame(fish_empty[c("fish_station", "fish_species", "individuals_per_station")])
```

```
fish_wider <- pivot_wider(fish_wider, names_from = "fish_station", values_from =
"individuals_per_station")



for_table <- left_join(fish_wider,max_min_values, by= "fish_species")


for_table <- left_join(for_table, empty_stomach, by="fish_species")


for_table <- left_join(for_table, for_total_prey, by="fish_species")


for_table <- left_join(for_table, for_total_fish, by="fish_species")



for_table <- for_table |>
 relocate(n, .before = minimum_length)|>
 rename(total_fish = n)


for_table |>
 mutate(empty_stomachs = coalesce(empty_stomachs, 0))


for_table1<- for_table |>
 mutate_at(20, ~replace_na(.,0))


table_fish_2021 <- for_table1 |>
 arrange(fish_species) |>
 gt() |>
 cols_label(fish_species = "",
        total_fish = "Total",
        minimum_length = "Min",
        maximum_length = "Max",
        mean_length = "Mean",
```

```
        minimum_totalvekt = "Min",
        maximum_totalvekt = "Max",
        mean_weight = "Mean",
        empty_stomachs = "",
        total_prey = "") |>
tab_spanner(label = md('**Fish Species**'),
        columns = 1) |>
tab_spanner(label = md('**Individuals**'),
        columns = 2:13) |>
tab_spanner(label = md('**Length (mm)**'),
        columns = 14:16) |>
tab_spanner(label = md('**Weight (g)**'),
        columns = 17:19) |>
tab_spanner(label = md('**Empty**'),
        columns = 20) |>
tab_spanner(label = md('**Total prey**'),
        columns = 21) |>
sub_missing(columns = 1:19,
        missing_text = "-")|>
cols_align(align = "center", columns = 2:19) |>
tab_options(
  data_row.padding = px(2),
  summary_row.padding = px(3),
  row_group.padding = px(4))|>
opt_stylize(style = 6, color = 'blue')|>
tab_style(
  style = list(
    cell_text(style = "italic")
  ),
  locations = cells_body(
    columns = 1
```

```
  ))|>
 tab_style(
  style = list(cell_fill(color = "#CF9FFF"),
               cell_text(weight = "bold")
  ),
  locations = cells_body(
    rows = c(1)
  ))|>
 tab_header(
  title = md("**Cruise 2021105**"))
table_fish_2021


gtsave(table_fish_2021, "table_fish_2021.png", vwidth = 4000, vheight = 500)
```

Diet composition tables

```
##2018##
library(tidyverse)
library(gt)
library(dplyr)
library(naniar)


data <- read_delim(file="15093 - Mesopelagic stomach analysis kopi.csv", delim=";", locale =
locale(decimal_mark = "."))
colnames(data)[16] <- "weight"
colnames(data)[5] <- "fish_nr"



biolu_data_frame <- data.frame(data[c("Artsnavn fisk", "Byttedyr", "Bioluminescence", "nr. Prey",
"weight", "fish_nr" )])
```

```
biolu_data_frame <- biolu_data_frame[!( biolu_data_frame$Byttedyr=="Vrengt" |
biolu_data_frame$Byttedyr == "Stomach out of mouth" | biolu_data_frame$Byttedyr == "Stomach
missing" | biolu_data_frame$Byttedyr == "Empty"),]



biolu_data_frame <- biolu_data_frame|>

  mutate(Byttedyr = recode(Byttedyr,'Oikopleura (hode)' = 'Other', "Rest" = "Digested", "Thysanoessa
longicaudata (hode)" = "Thysanoessa longicaudata (head)", "Artropod" = "Other", "Copepoda" =
"Other", "Copepod (oncaeidae)" = "Other", "Empty " = "Empty", "Rest copepod" = "Other",
"Chaetognatha " = "Other", "Pleuromamma" = "Pleuromamma sp.", "Rest Copepod" = "Other",
"Reke" = "Other",  "Egg" = "Other", "Euphausiacea" = "Other", "Oncaeidae" = "Other", "Copepod" =
"Other", "Crustacea" = "Other", "Amphipoda" = "Other", "Decapoda" = "Other", "Fish egg" = "Other",
"Gastropoda"= "Other", "Krill" = "Other", "Mesopelagic fish" = "Other", "Mesopelagic teleost" =
"Other", "Ostracoda" = "Other", "Paraeuchaeta egg" = "Other", "Sagitta sp" = "Other", "Shrimp" =
"Other", "Cephalopoda" = "Other", "Chaetognatha" = "Other", "Myctophidae " = "Other"))


biolu_data_frame <- transform(biolu_data_frame, nr..Prey = as.numeric(nr..Prey))



unique_fishnr <- biolu_data_frame |>

  distinct(fish_nr, .keep_all =TRUE)


stomachs <- unique_fishnr |>

  count(Artsnavn.fisk)


biolu_data_frame[is.na(biolu_data_frame)] <- 0


prey <- biolu_data_frame |>

  group_by(fish_nr, Artsnavn.fisk)|>

  distinct(Byttedyr, .keep_all = TRUE)|>

  count(Byttedyr) |>

  rename("prey_appearance" = n) |>

  group_by(Artsnavn.fisk, Byttedyr) |>

  summarise(prey_appearance = sum(prey_appearance))
```

```
numeric_biolu <- transform(biolu_data_frame, weight = as.numeric(weight))

prey_data_species <- biolu_data_frame |>
  group_by(Artsnavn.fisk, Byttedyr) |>
  summarise(nr_prey= sum(nr..Prey), weight = sum(weight)) |>
  as.data.frame()



prey_total_species <- prey_data_species |>
  group_by(Artsnavn.fisk)|>
  summarise(total_prey = sum(nr_prey), total_weight = sum(weight))|>
  as.data.frame()

prey_total_species <- left_join(prey_data_species,prey_total_species, by="Artsnavn.fisk")

prey_total_species <- left_join(prey_total_species, stomachs, by = "Artsnavn.fisk")

prey_total_species <- left_join(prey_total_species, prey, by = c("Byttedyr", "Artsnavn.fisk"))



ratio_prey_species <- prey_total_species |>
  group_by(Artsnavn.fisk,Byttedyr, nr_prey, total_prey, n, prey_appearance)|>
  summarise(freq_prey = ((trunc((prey_appearance/n)*1000))/10), ratio_weight =
((round((weight/total_weight)*1000)/10)), ratio_prey = ((round((nr_prey/total_prey)*1000)/10)))|>
  drop_na() |>
  as.data.frame()

ratio_prey_species <- subset(ratio_prey_species,total_prey > 19 )

ratio_prey_species <- subset(ratio_prey_species,Artsnavn.fisk!='Myctophum punctatum' )
```

```
ratio_prey_species <- data.frame(ratio_prey_species[c("Artsnavn.fisk", "Byttedyr", "freq_prey",
"ratio_weight", "ratio_prey" )])


ratio_prey_species1 <- ratio_prey_species[-86,]



fish_wider1 <- pivot_wider(ratio_prey_species, names_from = "Artsnavn.fisk", values_from =
c("freq_prey", "ratio_weight", "ratio_prey"))

colnames(fish_wider1)[2] <- "n_ah"

colnames(fish_wider1)[3] <- "n_bg"

colnames(fish_wider1)[4] <- "n_lm"

colnames(fish_wider1)[5] <- "n_ns"

colnames(fish_wider1)[6] <- "n_pa"

colnames(fish_wider1)[7] <- "n_sd"

colnames(fish_wider1)[8] <- "w_ah"

colnames(fish_wider1)[9] <- "w_bg"

colnames(fish_wider1)[10] <- "w_lm"

colnames(fish_wider1)[11] <- "w_ns"

colnames(fish_wider1)[12] <- "w_pa"

colnames(fish_wider1)[13] <- "w_sd"

colnames(fish_wider1)[14] <- "r_ah"

colnames(fish_wider1)[15] <- "r_bg"

colnames(fish_wider1)[16] <- "r_lm"

colnames(fish_wider1)[17] <- "r_ns"

colnames(fish_wider1)[18] <- "r_pa"

colnames(fish_wider1)[19] <- "r_sd"



fish_wider2 <- fish_wider1 |>

  relocate(Byttedyr, n_ah, w_ah, r_ah, n_bg, w_bg, r_bg, n_lm, w_lm, r_lm, n_ns, w_ns, r_ns, n_pa,
w_pa, r_pa, n_sd, w_sd, r_sd)
```

```
table_fish_prey_other <- fish_wider2 |>
 arrange(Byttedyr) |>
 gt() |>
 sub_missing(
          missing_text = "-")|>
 cols_label(Byttedyr = "Plankton species",
          n_ah = " Occ.",
          w_ah = "Weight",
          n_bg = "Occ.",
          w_bg = "Weight",
          n_lm = "Occ.",
          w_lm = "Weight",
          n_ns = "Occ.",
          w_ns = "Weight",
          n_pa = "Occ.",
          w_pa = "Weight",
          n_sd = "Occ.",
          w_sd = "Weight",
          r_ah = "Abund.",
          r_bg = "Abund.",
          r_lm = "Abund.",
          r_ns = "Abund.",
          r_pa = "Abund.",
          r_sd = "Abund.") |>
 #tab_spanner(label = md('**Plankton species**'),
  #          columns = 1) |>
 tab_spanner(label = md('**Argyropelecus hemigymnus**'),
          columns = 2:4) |>
```

```
tab_spanner(label = md('**Benthosema glaciale**'),
            columns = 5:7) |>
tab_spanner(label = md('**Lampanyctus macdonaldi**'),
            columns = 8:10) |>
tab_spanner(label = md('**Notoscopelus kroyeri**'),
            columns = 11:13) |>
tab_spanner(label = md('**Protomyctophum arcticum**'),
            columns = 14:16) |>
tab_spanner(label = md('**Sternophyx diaphana**'),
            columns = 17:19) |>
tab_style(
  style = list(cell_fill(color = "green")),
  locations = cells_body(
    rows = c(4,7,8,9,10,11,13,17,22,26,27)
  ))|>
tab_style(
  style = list(cell_fill(color = "grey")),
  locations = cells_body(
    rows = c(1,2,5,6,18,19,20,21,23,24,25)
  ))|>
tab_style(
  style = list(cell_fill(color = "white")),
  locations = cells_body(
    rows = c(12,15,16)
  )) |>
tab_style(
  style = list(cell_fill(color = "magenta")),
  locations = cells_body(
    rows = c(3,14)
  )) |>
opt_stylize(style = 6, color = 'blue')|>
```

```
  tab_style(
    style = list(
      cell_text(style = "italic")
    ),
    locations = cells_body(
      columns = 1
    )) |>
  cols_align(align = "center", columns = 2:13)
table_fish_prey_other
gtsave(table_fish_prey_other, "table_fish_prey_other.png", vwidth = 5000, vheight = 2000)

##2021##
library(tidyverse)
library(gt)
library(dplyr)
library(naniar)


data2021 <- read_delim(file = "Mesopeloagic stomach analysis 2021.csv", delim=";", locale = locale(decimal_mark = "."))
colnames(data2021)[14] <- "weight"
colnames(data2021)[1] <- "fish_nr"

biolu_data_frame <- data.frame(data2021[c("Artsnavn fisk", "Byttedyr", "Bioluminescence", "nr. Prey", "weight", "fish_nr" )])

biolu_data_frame <- biolu_data_frame|>
  mutate(Byttedyr = recode(Byttedyr,'Oikopleura (hode)' = 'Other', "Rest" = "Digested", "Thysanoessa longicaudata (hode)" = "Thysanoessa longicaudata (head)", "Artropod" = "Other", "Copepoda" = "Other", "Copepod (oncaeidae)" = "Other", "Amphipod" = "Other", "Chaetognatha (hooks)" = "Other", "Egg" = "Other", "Euphasiacea" = "Other", "Oncaeidae" = "Other", "Copepod" = "Other", "Crustacea" = "Other"))
```

```
biolu_data_frame <- transform(biolu_data_frame, nr..Prey = as.numeric(nr..Prey))

biolu_data_frame[is.na(biolu_data_frame)] <- 0

biolu_data_frame <- biolu_data_frame[!( biolu_data_frame$Byttedyr=="Vrengt" |
biolu_data_frame$Byttedyr == "Stomach out of mouth" | biolu_data_frame$Byttedyr == "Stomach
missing"| biolu_data_frame$Byttedyr == "Empty"), ]

unique_fishnr <- biolu_data_frame |>
  distinct(fish_nr, .keep_all =TRUE)

stomachs <- unique_fishnr |>
  count(Artsnavn.fisk)

prey <- biolu_data_frame |>
  group_by(fish_nr, Artsnavn.fisk)|>
  distinct(Byttedyr, .keep_all = TRUE)|>
  count(Byttedyr) |>
  rename("prey_appearance" = n) |>
  group_by(Artsnavn.fisk, Byttedyr) |>
  summarise(prey_appearance = sum(prey_appearance))

numeric_biolu <- transform(biolu_data_frame, weight = as.numeric(weight))

prey_data_species <- biolu_data_frame |>
  group_by(Artsnavn.fisk, Byttedyr) |>
  summarise(nr_prey= sum(nr..Prey), weight = sum(weight)) |>
  as.data.frame()
```

```
prey_total_species <- prey_data_species |>
  group_by(Artsnavn.fisk)|>
  summarise(total_prey = sum(nr_prey), total_weight = sum(weight))|>
  as.data.frame()

prey_total_species <- left_join(prey_data_species,prey_total_species, by="Artsnavn.fisk")

prey_total_species <- left_join(prey_total_species, stomachs, by = "Artsnavn.fisk")

prey_total_species <- left_join(prey_total_species, prey, by = c("Byttedyr", "Artsnavn.fisk"))

ratio_prey_species <- prey_total_species |>
  group_by(Artsnavn.fisk,Byttedyr, nr_prey, total_prey, n, prey_appearance)|>
  summarise(freq_prey = ((trunc((prey_appearance/n)*1000))/10), ratio_weight =
((round((weight/total_weight)*1000)/10)), ratio_prey = ((round((nr_prey/total_prey)*1000)/10)))|>
  drop_na() |>
  as.data.frame()

ratio_prey_species <- subset(ratio_prey_species,total_prey > 19 )

ratio_prey_species <- data.frame(ratio_prey_species[c("Artsnavn.fisk", "Byttedyr", "freq_prey",
"ratio_weight", "ratio_prey" )])




fish_wider1 <- pivot_wider(ratio_prey_species, names_from = "Artsnavn.fisk", values_from =
c("freq_prey", "ratio_weight", "ratio_prey"))
colnames(fish_wider1)[2] <- "n_bg"
colnames(fish_wider1)[3] <- "w_bg"
colnames(fish_wider1)[4] <- "r_bg"
```

```
fish_wider2 <- fish_wider1 |>
  relocate(Byttedyr, n_bg, w_bg, r_bg)



fish_wider2 <-fish_wider2 |>
  replace_with_na(replace = list(n_bg = c(0.0),
                                 w_bg = c(0.0),
                                 r_bg = c(0.0)))

table_fish_prey_other <- fish_wider2 |>
  arrange(Byttedyr) |>
  gt() |>
  sub_missing(
    missing_text = "-")|>
  cols_label(Byttedyr = "Plankton species",
             n_bg = "Occ.",
             w_bg = "Weight",
             r_bg = "Abund.") |>
  #tab_spanner(label = md('**Plankton species**'),
   #           columns = 1) |>
  tab_spanner(label = md('**Benthosema glaciale**'),
              columns = 2:4) |>
  tab_style(
    style = list(cell_fill(color = "green")),
    locations = cells_body(
      rows = c(6,7,11,12,15,16)
    ))|>
  tab_style(
    style = list(cell_fill(color = "grey")),
    locations = cells_body(
```

```
    rows = c(1,2,3,5,13,14)
  ))|>
 tab_style(
  style = list(cell_fill(color = "white")),
  locations = cells_body(
   rows = c(9,10)
  )) |>
 tab_style(
  style = list(cell_fill(color = "magenta")),
  locations = cells_body(
   rows = c(4,8)
  )) |>
 opt_stylize(style = 6, color = 'blue')|>
 tab_style(
  style = list(
   cell_text(style = "italic")
  ),
  locations = cells_body(
   columns = 1
  ))
 # cols_align(align = "center", columns = 2:13)
table_fish_prey_other
gtsave(table_fish_prey_other, "table_fish_prey_other.png", vwidth = 3000, vheight = 1500)
```

Large prey groups

```
#PACKAGES

library(tidyverse)
library(sf)
library(ggplot2)
library(viridis)
```

```
library(glue)

library(cowplot)


#PALETTE

custom_final28 = c("#771155", "#A55E18",  "#EA6CC0","#D2D21E", "#114477",
"#D2781E","#1E78D2", "#1ED278" , "#117777", "#AA4455", "#3FE4E4", "#AAAA44",
"#117744","#44AA77", "#77AADD", "#88CCAA", "#771122", "#44AAAA",
"#D21E2C","#DD7788","#777711", "#77CCCC", "#CC99BB", "#DDDD77","#774411", "#AA7744",
"#4477AA", "#DDAA77", "#AA4488")




data2018 <- read_delim(file="15093 - Mesopelagic stomach analysis kopi.csv", delim=";", locale =
locale(decimal_mark = "."))

colnames(data2018)[5] <- "fish_nr"

colnames(data2018)[4] <- "fish_species"



data2018 <- data2018|>

  mutate(fish_species = recode(fish_species,'Benthosema glaciale' = 'Benthosema glaciale 2018'))


biolu_data_frame2018 <- data.frame(data2018[c("fish_species", "Byttedyr", "nr. Prey", "Group" )])
|>

  drop_na()


data2021 <- read_delim(file="Mesopeloagic stomach analysis 2021.csv", delim=";", locale =
locale(decimal_mark = "."))

colnames(data2021)[1] <- "fish_nr"

colnames(data2021)[5] <- "fish_species"


data2021 <- data2021|>

  mutate(fish_species = recode(fish_species,'Benthosema glaciale' = 'Benthosema glaciale 2021'))
```

```
biolu_data_frame2021 <- data.frame(data2021[c("fish_species", "Byttedyr", "nr. Prey", "Group" )])
|>
  drop_na()



biolu_data_frame <- rbind(biolu_data_frame2018, biolu_data_frame2021) |>
  drop_na()



biolu_data_frame <- transform(biolu_data_frame, nr..Prey = as.numeric(nr..Prey))
biolu_data_frame[is.na(biolu_data_frame)] <- 0


biolu_data_frame <- biolu_data_frame[!( biolu_data_frame$Byttedyr== "Rest" |
biolu_data_frame$Group== "Crus" | biolu_data_frame$Group== "Crust" |
biolu_data_frame$Group== "Deca"),]


prey_data <- biolu_data_frame |>
  group_by(fish_species, Group) |>
  summarise(nr_prey= sum(nr..Prey)) |>
  as.data.frame()



prey_total <- prey_data |>
  group_by(fish_species)|>
  summarise(total_prey = sum(nr_prey))|>
  as.data.frame()



prey_total <- left_join(prey_data,prey_total, by="fish_species")


ratio_prey <- prey_total |>
  group_by(fish_species, nr_prey, total_prey, Group)|>
```

```
  summarise(ratio_prey = nr_prey/total_prey)|>
  as.data.frame()

prey_over20 <- subset(ratio_prey, fish_species %in% c("Benthosema glaciale 2018","Benthosema glaciale 2021", "Lampanyctus macdonaldi", "Notoscopelus kroyeri", "Protomyctophum arcticum", "Argyropelecus hemigyrus", "Sternophyx diaphana"))

prey_groups <- ggplot(prey_over20, aes(fill= Group, x = Group, y = ratio_prey)) +
  geom_bar(position="stack", stat="identity", color = "black") +
  theme_cowplot()+
  #coord_flip()+
  facet_wrap(~fish_species, scales = "free", ncol = 2)+
  scale_y_continuous(labels=scales::percent)+
  labs(
    x = "Prey group",
    y = "Prey percentage in diet",
    fill = "Prey group")+
  geom_text(color = "red",aes(x=Group, y = 1.05, label = glue("n={nr_prey}")))+
  scale_fill_manual(values = custom_final28)+
  scale_x_discrete(guide = guide_axis(n.dodge = 2))+
  theme(strip.text = element_text(size=10, face="italic"))+
  theme(legend.position = "none")
prey_groups
ggsave("prey_groups.jpeg", prey_groups, width = 120, height = 140, units = c("mm"), scale = 2.5)
##!> save the figure
```

Prey taxa

```
library(tidyverse)
library(gt)
library(dplyr)
library(naniar)
library(cowplot)
```

```
data2018 <- read_delim(file="15093 - Mesopelagic stomach analysis kopi.csv", delim=";", locale = locale(decimal_mark = "."))

colnames(data2018)[5] <- "fish_nr"

colnames(data2018)[4] <- "fish_species"



data2018 <- data2018|>

  mutate(fish_species = recode(fish_species,'Benthosema glaciale' = 'Benthosema glaciale 2018'))


biolu_data_frame2018 <- data.frame(data2018[c("fish_species", "Byttedyr", "Bioluminescence", "nr. Prey", "fish_nr" )])


data2021 <- read_delim(file="Mesopeloagic stomach analysis 2021.csv", delim=";", locale = locale(decimal_mark = "."))

colnames(data2021)[1] <- "fish_nr"

colnames(data2021)[5] <- "fish_species"


data2021 <- data2021|>

  mutate(fish_species = recode(fish_species,'Benthosema glaciale' = 'Benthosema glaciale 2021'))


biolu_data_frame2021 <- data.frame(data2021[c("fish_species", "Byttedyr", "Bioluminescence", "nr. Prey", "fish_nr" )])



biolu_data_frame <- rbind(biolu_data_frame2018, biolu_data_frame2021)



biolu_data_frame <- data.frame(biolu_data_frame[c("fish_species", "Byttedyr", "Bioluminescence", "fish_nr" )])


biolu_data_frame <- biolu_data_frame|>
```

```
  mutate(Byttedyr = recode(Byttedyr,'Oikopleura (hode)' = 'Oikopleura (head)', "Thysanoessa longicaudata (hode)" = "Thysanoessa longicaudata (head)", "Artropod" = "Crustacea", "Copepoda" = "Copepod", "Copepod (oncaeidae)" = "Oncaeidae", "Empty " = "Empty", "Rest copepod" = "Digested copepod", "Chaetognatha " = "Chaetognatha", "Myctophidae " = "Myctophidae", "Pleuromamma" = "Pleuromamma sp.", "Rest Copepod" = "Copepod", "Reke" = "Shrimp", "Sagitta sp." = "Chaetognatha", "Euphausiacea" = "Krill", "Paraeuchaeta norvegica" = "Paraeuchaeta sp.", "Pleuromamma robusta" = "Pleuromamma sp."))



biolu_data_frame <- biolu_data_frame[!( biolu_data_frame$Byttedyr=="Vrengt" | biolu_data_frame$Byttedyr == "Stomach out of mouth" | biolu_data_frame$Byttedyr == "Stomach missing" | biolu_data_frame$Byttedyr == "Empty" | biolu_data_frame$Byttedyr == "Rest" |biolu_data_frame$Byttedyr ==  "Calanus sp." |  biolu_data_frame$Byttedyr ==  "Metridia sp." | biolu_data_frame$Byttedyr=="Oncaeidae" | biolu_data_frame$Byttedyr == "Copepod" | biolu_data_frame$Byttedyr == "Stomach missing" | biolu_data_frame$Byttedyr == "Crustacea" | biolu_data_frame$Byttedyr == "Mesopelagic fish" | biolu_data_frame$Byttedyr ==  "Mesopelagic teleost" | biolu_data_frame$Byttedyr ==  "Amphipoda" | biolu_data_frame$Byttedyr == "Amphipod"),]



unique_fishnr <- biolu_data_frame |>

  distinct(fish_nr, .keep_all =TRUE)


stomachs <- unique_fishnr |>

  count(fish_species)



prey <- biolu_data_frame |>

  group_by(fish_nr, fish_species)|>

  distinct(Byttedyr, .keep_all = TRUE)|>

  count(Byttedyr) |>

  rename("prey_appearance" = n) |>

  group_by(fish_species, Byttedyr) |>

  summarise(prey_appearance = sum(prey_appearance))
```

```
prey_over20  <- subset(prey, fish_species %in% c("Benthosema glaciale 2018", "Benthosema glaciale 2021", "Lampanyctus macdonaldi", "Notoscopelus kroyeri", "Protomyctophum arcticum", "Argyropelecus hemigyrus", "Sternophyx diaphana"))


prey_over201 <- prey_over20[-c(15,25, 37,39, 50,53, 57,66, 69, 70,74,89),]



number_species <- prey_over201 |>
 group_by(fish_species) |>
 summarise(distinct_byttedyr = n_distinct(Byttedyr))


df <- left_join(prey_over201, number_species, by = "fish_species")


species_number <- ggplot(number_species, aes(fill = distinct_byttedyr, x = (fct_reorder(fish_species, -distinct_byttedyr)), y = distinct_byttedyr)) +
 geom_bar(position="stack", stat="identity", color = "black") +
 theme_cowplot()+
 scale_y_continuous(breaks = seq(0, 15, 1))+
 #facet_wrap(~fish_species, scales = "free")+
 #scale_y_continuous(labels=scales::percent)+
 labs(
  x = "Fish species",
  y = "Number of prey taxa",
  fill = "Number of prey taxa")+
 scale_x_discrete(guide = guide_axis(n.dodge = 2))+
 theme(legend.position = "none")
 #geom_text(color = "red",aes(x=Group, y = 1.05, label = glue("n={nr_prey}")))+
# scale_fill_manual(values = custom_final28)
species_number


ggsave("number_of_species.jpeg", species_number, width = 140, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure
```

Diet composition bioluminescence

```
##2018##

#PACKAGES


library(tidyverse)

library(sf)

library(ggplot2)

library(viridis)

library(glue)

library(cowplot)


data2018 <- read_delim(file="15093 - Mesopelagic stomach analysis kopi.csv", delim=";", locale =
locale(decimal_mark = ","))


biolu_data_frame <- data.frame(data2018[c("Artsnavn fisk", "Byttedyr", "Bioluminescence", "nr.
Prey" )]) |>

  mutate_at(('Bioluminescence'), ~replace_na(.,"Other"))



#biolu_data_frame = rbind(biolu_data_frame2018,biolu_data_frame2021)


biolu_data_frame<-biolu_data_frame[!(biolu_data_frame$Byttedyr=="Tom" |
biolu_data_frame$Byttedyr=="Vrengt" | biolu_data_frame$Byttedyr =="Empty" |
biolu_data_frame$Byttedyr == "Stomach out of mouth" | biolu_data_frame$Byttedyr == "Stomach
missing"),]


biolu_data_frame <- transform(biolu_data_frame, nr..Prey = as.numeric(nr..Prey))

biolu_data_frame[is.na(biolu_data_frame)] <- 0


biolu_data_frame <- within(biolu_data_frame, Bioluminescence[Bioluminescence == 'Not confirmed'
& Byttedyr == 'Paraeuchaeta norvegica'] <- 'Potential')
```

```
prey_data <- biolu_data_frame |>
  group_by(Artsnavn.fisk, Bioluminescence) |>
  summarise(nr_prey= sum(nr..Prey)) |>
  as.data.frame()



prey_total <- prey_data |>
  group_by(Artsnavn.fisk)|>
  summarise(total_prey = sum(nr_prey))|>
  as.data.frame()

prey_total <- left_join(prey_data,prey_total, by="Artsnavn.fisk")

ratio_prey <- prey_total |>
  group_by(Artsnavn.fisk,Bioluminescence, nr_prey, total_prey)|>
  summarise(ratio_prey = nr_prey/total_prey)|>
  as.data.frame()



prey_over20  <- subset(ratio_prey, Artsnavn.fisk %in% c("Benthosema glaciale", "Lampanyctus
macdonaldi", "Notoscopelus kroyeri", "Protomyctophum arcticum", "Argyropelecus hemigyrus",
"Sternophyx diaphana"))


prey_over20 <- prey_over20 |>
  mutate(colors = case_when(
  Bioluminescence == "Not confirmed" ~"grey20",
  Bioluminescence == "Confirmed" ~ "limegreen",
  Bioluminescence == "Potential" ~ "white",
  Bioluminescence == "Other" ~ "grey",
)) |>
  mutate(bioluminescence = case_when(
    Bioluminescence == "Not confirmed" ~"Non-bioluminescent",
```

```
   Bioluminescence == "Confirmed" ~ "Bioluminescent",
   Bioluminescence == "Potential" ~ "Potentially bioluminescent",
   Bioluminescence == "Other" ~ "Inconclusive",
  ))



prey_other2018 <- ggplot(prey_over20, aes(fill = colors, (x = fct_relevel(bioluminescence,
"Inconclusive", after = 3)), y = ratio_prey)) +
  geom_bar(position="stack", stat="identity", color = "black") +
  theme_cowplot()+
  scale_fill_identity(
  #                  labels = unique(prey_over20$bioluminescence),
                   breaks = unique(prey_over20$colors))+
  facet_wrap(~Artsnavn.fisk)+
  scale_y_continuous(labels=scales::percent)+
  labs(
    x = "Bioluminescence",
    y = "Prey percentage in diet",
    fill = "Bioluminescence")+
  geom_text(color = "red",aes(x=bioluminescence, y = 1.05, label = glue("n = {nr_prey}", position =
position_jitter(width=prey_over20$jit,height=prey_over20$jit))))+
  theme(strip.text = element_text(face = "italic")) +
  scale_x_discrete(guide = guide_axis(n.dodge = 2))
prey_other2018
ggsave("prey_other2018.jpeg", prey_other2018, width = 120, height = 80, units = c("mm"), scale =
2.5) ##!> save the figure


##2021#
data2021 <- read_delim(file = "Mesopeloagic stomach analysis 2021.csv", delim=";", locale =
locale(decimal_mark = ","))
```

```
biolu_data_frame <- data.frame(data2021[c("Artsnavn fisk", "Byttedyr", "Bioluminescence", "nr. Prey" )]) |>
  mutate_at(('Bioluminescence'), ~replace_na(.,"Other"))

biolu_data_frame<-biolu_data_frame[!(biolu_data_frame$Byttedyr=="Tom" | biolu_data_frame$Byttedyr=="Vrengt" | biolu_data_frame$Byttedyr =="Empty" | biolu_data_frame$Byttedyr == "Stomach out of mouth" | biolu_data_frame$Byttedyr == "Stomach missing"),]

biolu_data_frame <- transform(biolu_data_frame, nr..Prey = as.numeric(nr..Prey))

biolu_data_frame[is.na(biolu_data_frame)] <- 0

biolu_data_frame <- within(biolu_data_frame, Bioluminescence[Bioluminescence == 'Not confirmed' & Byttedyr == 'Paraeuchaeta norvegica'] <- 'Potential')

prey_data <- biolu_data_frame |>
  group_by(Artsnavn.fisk, Bioluminescence) |>
  summarise(nr_prey= sum(nr..Prey)) |>
  as.data.frame()


prey_total <- prey_data |>
  group_by(Artsnavn.fisk)|>
  summarise(total_prey = sum(nr_prey))|>
  as.data.frame()

prey_total <- left_join(prey_data,prey_total, by="Artsnavn.fisk")

ratio_prey <- prey_total |>
  group_by(Artsnavn.fisk,Bioluminescence, nr_prey, total_prey)|>
  summarise(ratio_prey = nr_prey/total_prey)|>
  as.data.frame()
```

```
ratio_prey <- ratio_prey |>
  mutate(colors = case_when(
    Bioluminescence == "Not confirmed" ~"grey20",
    Bioluminescence == "Confirmed" ~ "limegreen",
    Bioluminescence == "Potential" ~ "white",
    Bioluminescence == "Other" ~ "grey",
  )) |>
  mutate(bioluminescence = case_when(
    Bioluminescence == "Not confirmed" ~"Non-bioluminescent",
    Bioluminescence == "Confirmed" ~ "Bioluminescent",
    Bioluminescence == "Potential" ~ "Potentially bioluminescent",
    Bioluminescence == "Other" ~ "Inconclusive",
  ))


prey_other2021<- ggplot(ratio_prey, aes(fill = colors, (x = fct_relevel(bioluminescence,
"Inconclusive", after = 3)), y = ratio_prey)) +
  geom_bar(position="stack", stat="identity", color = "black") +
  theme_cowplot()+
  scale_fill_identity(
    #                 labels = unique(prey_over20$bioluminescence),
    breaks = unique(ratio_prey$colors))+
  facet_wrap(~Artsnavn.fisk)+
  scale_y_continuous(labels=scales::percent)+
  labs(
    x = "Bioluminescence",
    y = "Prey percentage in diet",
    fill = "Bioluminescence")+
  geom_text(color = "red",aes(x=bioluminescence, y = 1.05, label = glue("n = {nr_prey}", position =
position_jitter(width=prey_over20$jit,height=prey_over20$jit))))+
  theme(strip.text = element_text(face = "italic")) +
  scale_x_discrete(guide = guide_axis(n.dodge = 2))
```

prey_other2021

ggsave("prey_other2021.jpeg", prey_other2021, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure

Plankton distribution across stations

##2018##

library(ggplot2)

library(tidyverse)

library(dplyr)

library(purrr)

library(ggthemes)

library(cowplot)

library(glue)

library(viridis)

library(pals)

custom_final28 = c("#771155", "#A55E18", "#EA6CC0","#D2D21E", "#114477", "#FFFFFF", "#D2781E","#1E78D2", "#1ED278" , "#117777", "#AA4455", "#3FE4E4", "#AAAA44", "#117744","#44AA77", "#77AADD", "#88CCAA", "#771122", "#44AAAA", "#D21E2C","#DD7788","#777711", "#77CCCC", "#CC99BB", "#DDDD77","#774411", "#AA7744", "#4477AA", "#DDAA77", "#AA4488")

#Load the background data for the the stations

background <- read_delim(file="2018106 - all stations - opparbeiding av MOCNESS.csv")

colnames(background)[3] <- "plankton_station"

colnames(background)[17] <- "Byttedyr"

colnames(background)[18] <- "density"

#Make data frame with needed variables

background_data_frame <- data.frame(background[c("plankton_station", "Byttedyr", "density")])

```
#Make numeric

numeric_background <- transform(background_data_frame, density = as.numeric(density))


numeric_background <- numeric_background[numeric_background$plankton_station %in% c("275",
"276", "278", "280", "281", "282"),]



sum_background <- numeric_background |>

  group_by(plankton_station, Byttedyr) |>

  summarise( density= sum(density)) |>

  group_by(plankton_station)|>

  mutate(total_per_station = sum(density))|>

  group_by(plankton_station, Byttedyr, total_per_station, density)|>

  summarise(ratio_plankton = density/total_per_station)


high_abundance <- sum_background |>

  mutate(Byttedyr = replace(Byttedyr, ratio_plankton < 0.01, "Other"))|>

  group_by(plankton_station, Byttedyr, total_per_station)|>

  summarise(density= sum(density)) |>

  group_by(plankton_station, Byttedyr, total_per_station, density)|>

  summarise(ratio_plankton = density/total_per_station)


ration_plankton <- left_join(high_abundance, sum_background, by = c("plankton_station",
"Byttedyr", "total_per_station", "density"))


high_abundance <- transform(high_abundance, density = as.numeric(density))


high_abundance <- high_abundance |>

  mutate(plankton_station = recode(plankton_station, '275' = 'Station 275', '276' = 'Station 276', '278'
=  'Station 278', '280' = 'Station 280', '281' = 'Station 281', '282' = 'Station 282'))


high_abundance <- high_abundance |>
```

```
  arrange(density)


high_abundance[,-c(1,2,3)] <- round(high_abundance[,-c(1,2,3)], 2)


text_italic <- element_text(face = "italic", size = 12)



plankton_distribution <- ggplot(high_abundance, aes(fill = (fct_reorder(Byttedyr, -density)),
x=(fct_reorder(plankton_station,-total_per_station)), y = density)) +
  geom_bar(position="stack", stat="identity", color = "black")+
  theme_cowplot()+
  coord_flip()+
  scale_fill_manual(values = custom_final28)+
  labs(x = "Station",
       y = "Individuals per cubic meter",
       fill = "Species")+
  theme( legend.position = "bottom")+
  geom_text(aes(label = glue("{ratio_plankton*100}%")), size = 3, color = "black", position =
position_stack(vjust = 0.5), angle = 270)
plankton_distribution


ggsave("plankton_2018.jpeg", plankton_distribution, width = 120, height = 80, units = c("mm"), scale
= 2.5) ##!> save the figure


##2021##
library(ggplot2)
library(tidyverse)
library(dplyr)
library(purrr)
library(ggthemes)
library(cowplot)
library(glue)
```

```
library(viridis)

library(pals)


text_italic <- element_text(face = "italic", size = 12)


custom_final28 = c("#771155", "#A55E18",  "#EA6CC0","#D2D21E", "#114477",
"#D2781E","#1E78D2", "#1ED278", "#FFFFFF", "#117777", "#AA4455", "#3FE4E4", "#AAAA44",
"#117744","#44AA77", "#77AADD", "#88CCAA", "#771122", "#44AAAA",
"#D21E2C","#DD7788","#777711", "#77CCCC", "#CC99BB", "#DDDD77","#774411", "#AA7744",
"#4477AA", "#DDAA77", "#AA4488")



#Load the background data for the the stations

background <- read_delim(file="2021105_allstations opparbeiding av Multinet Mammoth.csv",
delim=";", locale =locale(decimal_mark = "."))

colnames(background)[1] <- "plankton_station"

colnames(background)[4] <- "Byttedyr"

colnames(background)[5] <- "density"


#Make data frame with needed variables

background_data_frame <- data.frame(background[c("plankton_station", "Byttedyr", "density")])


background_data_frame[is.na(background_data_frame)] <- 0


#Make numeric

numeric_background <- transform(background_data_frame, density = as.numeric(density))


numeric_background <- numeric_background[numeric_background$plankton_station %in% c("171",
"175", "178", "179"),]


sum_background <- numeric_background |>

  group_by(plankton_station, Byttedyr) |>

  summarise( density= sum(density)) |>
```

```
  group_by(plankton_station)|>
  mutate(total_per_station = sum(density))|>
  group_by(plankton_station, Byttedyr, total_per_station, density)|>
  summarise(ratio_plankton = density/total_per_station)

high_abundance <- sum_background |>
  mutate(Byttedyr = replace(Byttedyr, ratio_plankton < 0.01, "Other"))|>
  group_by(plankton_station, Byttedyr, total_per_station)|>
  summarise(density= sum(density)) |>
  group_by(plankton_station, Byttedyr, total_per_station, density)|>
  summarise(ratio_plankton = density/total_per_station)

high_abundance <- transform(high_abundance,density = as.numeric(density))

high_abundance <- high_abundance |>
  mutate(plankton_station = recode(plankton_station, '171' = 'Station 171', '175' = 'Station 175', '178' =  'Station 178', '179' = 'Station 179'))


high_abundance <- high_abundance |>
  arrange(density)

high_abundance[,-c(1,2,3)] <- round(high_abundance[,-c(1,2,3)], 2)



plankton_distribution <- ggplot(high_abundance, aes(fill = (fct_reorder(Byttedyr, -density)), x=(fct_reorder(plankton_station,-total_per_station)), y = density)) +
  geom_bar(position="stack", stat="identity", color = "black")+
  theme_cowplot()+
  coord_flip()+
  scale_fill_manual(values = custom_final28)+
```

```
 labs(x = "Station",
      y = "Number of individuals",
      fill = "Species"
 )+
 theme(legend.position = "bottom")+
 geom_text(aes(label = glue("{ratio_plankton*100}%")), size = 3, color = "black", position = position_stack(vjust = 0.5), angle = 270)
# scale_fill_viridis(discrete = TRUE, option = "magma", direction = -1)
plankton_distribution


pdf(file = "C:/Users/ingri/OneDrive - University of Bergen/Master/Data/plankton_2021.pdf",
   width = 13,
   height = 8)
```

Plankton depth distribution

```
library(ggplot2)
library(tidyverse)
library(dplyr)
library(purrr)
library(ggthemes)
library(cowplot)
library(glue)

##2018##

background <- read_delim(file="2018106 - all stations - opparbeiding av MOCNESS.csv")
colnames(background)[18] <- "density"
background <- background[background$plankton_station %in% c("275", "276", "278", "280", "281", "282"),]

background <- subset(background, Byttedyr %in% c("Aetidius aratus", "Calanus finmarchicus", "Euaugaptilus magnus", "Gaetanus brevispinus", "Gaetanus tenuispinus", "Metridia lucens", "Paraeuchaeta norvegica", "Oithona", "Oncaea", "Heterorhabdus norvegicus", "Hymenodora sp.", "Pleuromamma sp.", "Pseudocalanus glaciale", "Pseudocalanus sp.", "Paraeuchaeta sp.",
```

```
"Pseudochirella pustulifera", "Sagitta sp", "Scottocalanus securifrons", "Sergestes sp", "Themisto abyssorum", "Thysanoessa tenera", "Themisto compressa", "Thysanoessa sp.", "Calanus finmarchicus/helgolandicus", "Calanus hyperboreus", "Pleuromamma robusta", "Thysanoessa longicaudata", "Aetideus armatus" ))

background <- background |>
  mutate(Byttedyr = recode(Byttedyr, 'Pleuromamma robusta' = 'Pleuromamma sp.', 'Oithona' = 'Oithona spp.', 'Paraeuchaeta norvegica' =  'Paraeuchaeta sp.', 'Heterorhabdus' = 'Heterorhabus sp.', 'Thysanoessa longicaudata' = 'Thysanoessa sp.', 'Calanus finmarchicus/helgolandicus' = 'Calanus finmarchicus', "Oncaea" = "Oncaea spp.", "Scottocalanus securifrons" = "Scottocalanus sp.", "Heterorhabdus norvegicus"= "Heterorhabdus sp."))

background <- data.frame(background[c("plankton_station", "Byttedyr", "Lower_depth", "density")])

df_2018 <- transform(background, density = as.numeric(density))

df_size2018 <- df_2018 |>
  group_by(Byttedyr, Lower_depth)|>
  summarise(total_density = sum(density))

text_italic <- element_text(face = "italic", size = 12)

plankton_depth2018 <- ggplot(df_size2018, aes(y = Lower_depth, x = Byttedyr))+
  geom_point(aes(size = total_density, color = Byttedyr), alpha = 0.5) +
  scale_size(range = c(4, 12))+
  #facet_wrap(~plankton_station)+
  theme_cowplot()+
  scale_y_reverse(limits=c(1100, 0), breaks = seq(1000, 0, by = -100))+
  scale_color_viridis_d()+
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))+
  theme(axis.text.x = text_italic,
        axis.text.y = text_italic,
        legend.title = element_blank(),
        legend.position = "none")+
```

```
  labs(
    y = "Lower depth of trawl net",
    x = "Plankton species")
plankton_depth2018

ggsave("plankton_depth2018.jpeg", plankton_depth2018, width = 100, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure

##2021##

background1 <- read_delim(file="2021105 - st163-168 opparbeiding av Multinet Mammoth.csv")
colnames(background1)[18] <- "density"
colnames(background1)[17] <- "Byttedyr"
colnames(background1)[14] <- "bottom_depth"
colnames(background1)[3] <- "plankton_station"

df1 <- data.frame(background1[c("Byttedyr", "bottom_depth", "density", "plankton_station")])

background2 <- read_delim(file="2021105 - st171-175 opparbeiding av Multinet Mammoth.csv")
colnames(background2)[18] <- "density"
colnames(background2)[17] <- "Byttedyr"
colnames(background2)[14] <- "bottom_depth"
colnames(background2)[3] <- "plankton_station"

df2 <- data.frame(background2[c("Byttedyr", "bottom_depth", "density", "plankton_station")])

background3 <- read_delim(file="2021105 - st176-177 opparbeiding av Multinet Mammoth.csv")
colnames(background3)[18] <- "density"
colnames(background3)[17] <- "Byttedyr"
```

```
colnames(background3)[14] <- "bottom_depth"

colnames(background3)[3] <- "plankton_station"


df3 <- data.frame(background3[c("Byttedyr", "bottom_depth", "density", "plankton_station")])


background4 <- read_delim(file="2021105 - st178-179 opparbeiding av Multinet Mammoth.csv")

colnames(background4)[18] <- "density"

colnames(background4)[17] <- "Byttedyr"

colnames(background4)[14] <- "bottom_depth"

colnames(background4)[3] <- "plankton_station"


df4 <- data.frame(background4[c("Byttedyr", "bottom_depth", "density", "plankton_station")])


df <- rbind(df1,df2,df3,df4)


df <- df[df$plankton_station %in% c("171", "175", "178", "179"),]


df <- subset(df, Byttedyr %in% c( "Calanus finmarchicus", "Paraeuchaeta norvegica", "Pleuromamma sp.", "Paraeuchaeta sp.",  "Calanus finmarchicus/helgolandicus", "Calanus hyperboreus", "Pleuromamma robusta", "Metridia longa" ))


df <- df|>

  mutate(Byttedyr = recode(Byttedyr, 'Pleuromamma robusta' = 'Pleuromamma sp.', 'Paraeuchaeta norvegica' =  'Paraeuchaeta sp.', 'Calanus finmarchicus/helgolandicus' = 'Calanus finmarchicus'))


df <- within(df, bottom_depth[bottom_depth == 4001] <- 401)


text_italic <- element_text(face = "italic", size = 12)



numeric_df <- transform(df, density = as.numeric(density))
```

```
df_size <- numeric_df |>
  group_by(Byttedyr, bottom_depth)|>
  summarise(total_density = sum(density))


plankton_depth2021 <- ggplot(df_size, aes(y = bottom_depth, x = Byttedyr))+
  geom_point(aes(size = total_density, color = Byttedyr), alpha = 0.5) +
  scale_size(range = c(4, 12))+
  theme_cowplot()+
  #facet_wrap(~plankton_station)+
  scale_y_reverse(limits=c(1100, 0), breaks = seq(1000, 0, by = -100))+
  scale_color_viridis_d()+
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))+
  theme(axis.text.x = text_italic,
        axis.text.y = text_italic,
        legend.title = element_blank(),
        legend.position = "none")+
  labs(
    y = "Lower depth of trawl net",
    x = "Plankton species")
plankton_depth2021


ggsave("plankton_depth2021.jpeg", plankton_depth2021, width = 100, height = 80, units = c("mm"),
scale = 2.5) ##!> save the figure
```

Selectivity plots

```
library(ggplot2)
library(tidyverse)
library(dplyr)
library(purrr)
library(ggthemes)
library(cowplot)
```

```
library(glue)


cbPalette <- c("#999933", "#882255", "#88ccee")


#Load stomach analysis file and change names to make the easier to work with

diet <- read_delim(file="15093 - Mesopelagic stomach analysis kopi (version 1).csv", delim=";", locale = locale(decimal_mark = ","))

colnames(diet)[3] <- "serialno"

colnames(diet)[4] <- "fish_species"

colnames(diet)[22] <- "nr_prey"

colnames(diet)[19] <- "bioluminescence"

colnames(diet)[21] <- "dig_rate"


digestion_under4 <- subset(diet,dig_rate < 4)



#Create data frame with the needed variables

diet_frame <- data.frame(diet[c("serialno", "Byttedyr", "nr_prey", "fish_species","bioluminescence", "dig_rate")])



#The previous data set lacks the names of th stations and only has the serial numbers of the trawls, load a document that has both

stations <- read_delim(file = "FishStation_2018106_kopi.csv", delim=";", locale = locale(decimal_mark = ","))

stations_frame <- data.frame(stations[c("serialno", "station")])



#Create a new data frame with the station names

new_diet <- left_join(diet_frame,stations_frame, by="serialno")

colnames(new_diet)[7] <- "fish_station"
```

```
new_diet <- data.frame(new_diet[c("fish_station", "fish_species", "Byttedyr", "nr_prey", "bioluminescence", "dig_rate")])


write.csv(new_diet, "C:/Users/ingri/OneDrive - University of Bergen/Master/Stomach_analysis_stations1.csv", row.names=FALSE)




#Change NA to 0

new_diet[is.na(new_diet)] <- 0




#Make the number of prey numeric because it was read in as character

transform(new_diet, nr_prey = as.numeric(nr_prey))


new_diet<-new_diet[!(new_diet$Byttedyr=="Tom" | new_diet$Byttedyr=="Vrengt" | new_diet$Byttedyr =="Empty" | new_diet$Byttedyr == "Stomach out of mouth" | new_diet$Byttedyr == "Stomach missing" | new_diet$Byttedyr == "Rest"),]


new_diet <- new_diet|>

  mutate(Byttedyr = recode(Byttedyr,'Paraeuchaeta norvegica' = 'Paraeuchaeta sp.', "Themisto abyssorum" = "Themisto spp.", 'Themisto compressa' = 'Themisto spp.', "Themisto sp." = "Themisto spp."))


new_diet <- within(new_diet, bioluminescence[bioluminescence == 'Not confirmed' & Byttedyr == 'Paraeuchaeta sp.'] <- 'Potential')




#Create a total of prey of each species for each species of fish from one station instead of one observation for each fish

sum_diet <- new_diet |>

  group_by(fish_station, fish_species, Byttedyr, bioluminescence) |>

  dplyr::summarise(nr_prey= sum(nr_prey)) |>

  as.data.frame()
```

```
sum_diet

sum_diet <- sum_diet[apply(sum_diet!=0, 1, all),]

sum_diet <- sum_diet[apply(sum_diet!='Other', 1, all),]



#Create a data frame with total number of prey for each fish species on each station
prey_total <- sum_diet |>
  group_by(fish_station, fish_species)|>
  summarise(total_prey = sum(nr_prey))|>
  as.data.frame()
prey_total

for_over_20 <- prey_total |>
  group_by(fish_species)|>
  summarise(total_prey = sum(total_prey))



#Combine the two data frames
ratio_diet <- left_join(sum_diet,prey_total, by=c("fish_station", "fish_species"))

#Add the ratio of each of the prey species for each fish species on each station
final_diet <- ratio_diet |>
  group_by(fish_station, fish_species,Byttedyr, bioluminescence, nr_prey, total_prey, )|>
  summarise(ratio_prey = nr_prey/total_prey)|>
  as.data.frame()



#Load data set with matched plankton- and fish stations
```

```
combined_stations <- read_delim(file = "fish_plankton_stations.csv")



diet_combined <- left_join(final_diet, combined_stations, by=c("fish_station"))


diet_combined <- data.frame(diet_combined[c("plankton_station", "fish_station", "fish_species",
"Byttedyr", "nr_prey", "total_prey", "ratio_prey", "bioluminescence")])



#Load the background data for the the stations

background1 <- read_delim(file="2018106 - st280-282  opparbeiding av MOCNESS.csv")

colnames(background1)[3] <- "plankton_station"

colnames(background1)[17] <- "Byttedyr"

colnames(background1)[18] <- "density"


background2 <- read_delim(file="2018106 - st275-2788 opparbeiding av MOCNESS.csv")

colnames(background2)[3] <- "plankton_station"

colnames(background2)[17] <- "Byttedyr"

colnames(background2)[18] <- "density"


background = rbind(background2,background1)



#Make data frame with needed variables

background_data_frame <- data.frame(background[c("plankton_station", "Byttedyr", "density")])


#Make numeric

numeric_background <- transform(background_data_frame, density = as.numeric(density))


numeric_background <- numeric_background[numeric_background$plankton_station %in% c("275",
"276", "278", "280", "281", "282"),]
```

```
#Some species in the water column are identified to a lower taxonomic level than in the diet, change the names so they can me matched

numeric_background <- numeric_background |>

  mutate(Byttedyr = recode(Byttedyr, 'Pleuromamma robusta' = 'Pleuromamma sp.', 'Paraeuchaeta barbata' = 'Paraeuchaeta sp.', 'Paraeuchaeta glacialis' =  'Paraeuchaeta.sp', 'Heterorhabdus' = 'Heterorhabus sp.', 'Heterorhabdus norvegicus' = 'Heterorhabdus sp.', 'Calanus hyperboreus' = 'Calanus sp.', 'Calanus glacialis' = 'Calanus sp.', 'Hymenodora' = 'Hymenodora sp.', 'Oithona' = 'Oithona sp.', 'Oncaea' = 'Oncaea sp.', 'Oncaea conifera'= 'Oncaea sp.', 'Pseudocalanus' = 'Pseodocalanus sp.', 'Themisto' = 'Themisto spp.', 'Paraeuchaeta norvegica' = 'Paraeuchaeta sp.', "Calanus finmarchicus/helgolandicus" = "Calanus finmarchicus", "Themisto abyssorum" = "Themisto spp.", 'Themisto compressa' = 'Themisto spp.'))



sum_background <- numeric_background |>

  group_by(plankton_station, Byttedyr) |>

  summarise( density= sum(density)) |>

  as.data.frame()



#Keep only plankton species in background that is also present in diet

shared_plankton <- left_join(diet_combined, sum_background, by=c("plankton_station", "Byttedyr"))

shared_plankton[is.na(shared_plankton)] <- 0


#Create a data frame with total number of prey for each fish species on each station

background_total <- shared_plankton |>

  group_by(plankton_station)|>

  summarise(total_density = sum(density))|>

  as.data.frame()

background_total


#Combine the two data frames

ratio_background <- left_join(shared_plankton,background_total, by=c("plankton_station"))
```

```
final_background <- ratio_background |>
  group_by(plankton_station, fish_species, Byttedyr, ratio_prey, bioluminescence)|>
  reframe(ratio_plankton = density/total_density)|>
  as.data.frame()
final_background <- final_background[apply(final_background!=0, 1, all),]

final_background1 <- ratio_background |>
  group_by(plankton_station, fish_species, Byttedyr, ratio_prey, bioluminescence, nr_prey)|>
  reframe(ratio_plankton = density/total_density)|>
  as.data.frame()
final_background1 <- final_background1[apply(final_background1!=0, 1, all),]

ratio_prey_over_2percent <- subset(final_background,ratio_prey > 0.02)



prey_over_20 <- left_join(ratio_prey_over_2percent, for_over_20, by = c("fish_species"))

prey_over20 <- left_join(final_background, for_over_20, by = c("fish_species"))
prey_over20 <- subset(prey_over20,total_prey > 19 )

for_glue <- sum_diet |>
  group_by(fish_species, Byttedyr)|>
  summarise(sum_prey_by_species = sum(nr_prey))

for_glue1 <- left_join(prey_over20, for_glue, by = c("fish_species", "Byttedyr"))



text_italic <- element_text(face = "italic", size = 12)

##!> code by TOM
selectivity_df <- for_glue1 |>
```

```
 as_tibble() |>
 mutate(selectivity = ((ratio_prey-ratio_plankton)/(ratio_prey + ratio_plankton)))|>
 group_by(fish_species, Byttedyr, bioluminescence, total_prey, sum_prey_by_species)|>
 summarise(selectivity_mean = mean(selectivity), standard_deviation = sd(selectivity), n = n())



plot_selectivity_by_prey_species <- function(species_in) {

 ##!> subset the dataframe to plot
 df <- selectivity_df |>
  # filter(fish_species %in% c("Benthosema glaciale")) |>
  filter(fish_species %in% species_in) |>
  mutate(colors = case_when(
   bioluminescence == "Not confirmed" ~"grey20",
   bioluminescence == "Confirmed" ~ "green",
   bioluminescence == "Potential" ~ "white",
  ))|>
  mutate(bioluminescence = case_when(
   bioluminescence == "Not confirmed" ~"Non-bioluminescent",
   bioluminescence == "Confirmed" ~ "Bioluminescent",
   bioluminescence == "Potential" ~ "Potentially bioluminescent",
  ))

 ##!> plot the subset
 ggplot(df, aes(fill = colors, x = reorder(Byttedyr, -selectivity_mean), y= selectivity_mean)) +
  geom_bar(position="stack", stat="identity",  color = "black")+
  facet_wrap(~fish_species)+
  scale_fill_identity(guide = "legend",
                      labels = unique(df$bioluminescence),
                      breaks = unique(df$colors)
  )+
```

```
  # scale_fill_manual(values= c("limegreen", "grey20", "white"),
  #                   labels = c("Bioluminescent", "Non-bioluminescent", "Potential"))+
  labs(
    y = "Prey selectivity",
    x = "Prey species",
    fill = "Bioluminescence"
  )+
  scale_x_discrete(guide = guide_axis(n.dodge = 2))+
  theme(strip.text = element_text(size=10, face="italic")) +
  geom_errorbar(color ="magenta",
                aes(ymin = selectivity_mean-standard_deviation,
                    ymax = selectivity_mean+standard_deviation),
                width = 0.2) +
  theme_cowplot()+
  theme(axis.text.x = text_italic,
        legend.title = element_blank(),
        legend.position = "bottom")+
  theme(strip.text = element_text(face = "italic"))+
  geom_hline(yintercept = 0)+
  geom_text(color ="blue", aes(x=Byttedyr, y = 1.2, label = glue("n = {sum_prey_by_species}")))+
  scale_y_continuous(breaks = seq(-1,1,0.25), limits =c(-1,1.3))
}


p_bg1 <- plot_selectivity_by_prey_species("Benthosema glaciale") ##!> produce the figure
p_bg1 ##!> to view the figure
#ggsave("selectivity_prey_bg.jpeg", p_bg1, width = 120, height = 80, units = c("mm"), scale = 2.5)
##!> save the figure


p_pa1 <- plot_selectivity_by_prey_species("Protomyctophum arcticum")
p_pa1
#ggsave("selectivity_prey_pa.jpeg", p_pa1, width = 120, height = 80, units = c("mm"), scale = 2.5)
##!> save the figure
```

```
p_nk1 <- plot_selectivity_by_prey_species("Notoscopelus kroyeri")

p_nk1

#ggsave("selectivity_prey_nk.jpeg", p_nk1, width = 120, height = 80, units = c("mm"), scale = 2.5)
##!> save the figure


p_lm1 <- plot_selectivity_by_prey_species("Lampanyctus macdonaldi")

p_lm1

#ggsave("selectivity_prey_lm.jpeg", p_lm1, width = 120, height = 80, units = c("mm"), scale = 2.5)
##!> save the figure


p_ah1 <- plot_selectivity_by_prey_species("Argyropelecus hemigyrus")

p_ah1

#ggsave("selectivity_prey_ah.jpeg", p_ah1, width = 120, height = 80, units = c("mm"), scale = 2.5)
##!> save the figure


p_sd1 <- plot_selectivity_by_prey_species("Sternophyx diaphana")

p_sd1

#ggsave("selectivity_prey_sd.jpeg", p_sd1, width = 120, height = 80, units = c("mm"), scale = 2.5)
##!> save the figure




for_glue2 <- final_background1 |>

  group_by(plankton_station, fish_species, bioluminescence) |>

  summarise(sum_confirmed = sum(nr_prey[bioluminescence == "Confirmed"]),
sum_notconfirmed = sum(nr_prey[bioluminescence == "Not confirmed"]), sum_potential =
sum(nr_prey[bioluminescence == "Potential"])) |>

  filter(!bioluminescence =='Other') |>

  mutate(sum_confirmed = ifelse(bioluminescence ==
'Confirmed',sum_confirmed,sum_notconfirmed)) |>

  mutate(sum_confirmed = ifelse(bioluminescence == 'Potential',sum_potential,sum_confirmed)) |>

  select(-c(sum_notconfirmed, sum_potential)) |>

  rename(sum_bioluminescence = sum_confirmed)
```

```
total_bioluminescence <- for_glue2 |>
  group_by(plankton_station, fish_species) |>
  summarise(total_bioluminescence = sum(sum_bioluminescence))


for_glue3 <- left_join( for_glue2, total_bioluminescence, by= c("fish_species", "plankton_station"))|>
  group_by(plankton_station, fish_species, bioluminescence, sum_bioluminescence,
total_bioluminescence)|>
  summarise(ratio_bioluminescence = (sum_bioluminescence/total_bioluminescence))

for_total_biolu <- for_glue3 |>
  group_by(fish_species, bioluminescence)|>
  summarise(complete_total_bioluminescence = sum(sum_bioluminescence))


shared_plankton <- left_join(diet_combined, sum_background, by=c("plankton_station", "Byttedyr"))
shared_plankton[is.na(shared_plankton)] <- 0

bioluminescence_background <- shared_plankton |>
  group_by(plankton_station, bioluminescence) |>
  summarise(background_sum_confirmed = sum(density[bioluminescence == "Confirmed"]),
background_sum_notconfirmed = sum(density[bioluminescence == "Not confirmed"]),
background_sum_potential = sum(density[bioluminescence == "Potential"])) |>
  filter(!bioluminescence =='Other') |>
  mutate(background_sum_confirmed = ifelse(bioluminescence ==
'Confirmed',background_sum_confirmed,background_sum_notconfirmed)) |>
  mutate(background_sum_confirmed = ifelse(bioluminescence ==
'Potential',background_sum_potential,background_sum_confirmed)) |>
  select(-c(background_sum_notconfirmed, background_sum_potential)) |>
  rename(background_sum_bioluminescence = background_sum_confirmed)

total_background_bioluminescence <- bioluminescence_background |>
  group_by(plankton_station) |>
```

```
  summarise(background_total_bioluminescence = sum(background_sum_bioluminescence))


ratio_background_bioluminescence <- left_join(bioluminescence_background,
total_background_bioluminescence, by= c("plankton_station"))


ratio_background_bioluminescence <- ratio_background_bioluminescence |>
  group_by(plankton_station, bioluminescence, background_sum_bioluminescence,
background_total_bioluminescence)|>
  summarise(background_ratio_bioluminescence =
(background_sum_bioluminescence/background_total_bioluminescence))



for_glue4 <- left_join(for_glue3, ratio_background_bioluminescence, by= c("bioluminescence",
"plankton_station"))



for_glue5 <- left_join(for_glue4, for_total_biolu, by = c("bioluminescence", "fish_species"))



plot_selectivity_by_prey_type <- function(species_in) {


  ##!> subset dataframe
  df <- for_glue5 |>
    as_tibble() |>
    mutate(selectivity = ((ratio_bioluminescence-
background_ratio_bioluminescence)/(ratio_bioluminescence +
background_ratio_bioluminescence)))|>
    group_by(fish_species, bioluminescence, complete_total_bioluminescence)|>
    summarise(selectivity_mean = mean(selectivity), standard_deviation = sd(selectivity), n = n()) |>
    filter(fish_species %in% species_in)|>
    mutate(colors = case_when(
      bioluminescence == "Not confirmed" ~"grey20",
      bioluminescence == "Confirmed" ~ "green",
```

```
    bioluminescence == "Potential" ~ "white",
  )) |>
  mutate(bioluminescence = case_when(
    bioluminescence == "Not confirmed" ~"Non-bioluminescent",
    bioluminescence == "Confirmed" ~ "Bioluminescent",
    bioluminescence == "Potential" ~ "Potentially bioluminescent",
  ))


##!> plot subset dataframe
ggplot(df, aes(fill = colors, x = bioluminescence, y= selectivity_mean)) +
  geom_bar(position="stack", stat="identity",  color = "black")+
  facet_wrap(~fish_species)+
  scale_fill_identity()+
  # scale_fill_manual(values= c("limegreen", "grey20", "white"),
  #                   labels = c("Bioluminescent", "Non-bioluminescent", "Potential"))+
  labs(
    y = "Prey selectivity",
    x = "Bioluminescence",
    fill = "Bioluminescence"
  )+
  theme(strip.text = element_text(size=10, face="italic")) +
  geom_errorbar(color = "magenta",
                aes(ymin = selectivity_mean-standard_deviation,
                    ymax = selectivity_mean+standard_deviation),
                width = 0.2) +
  theme_cowplot()+
  theme(strip.text = element_text(face = "italic"))+
  geom_hline(yintercept = 0)+
  geom_hline(yintercept = 0)+
  geom_text(color ="blue", aes(x=bioluminescence, y = 1.3, label = glue("n =
{complete_total_bioluminescence}")))+
```

```
   scale_y_continuous(breaks = seq(-1,1,0.25), limits =c(-1,1.3))


}


t_bg1 <- plot_selectivity_by_prey_type("Benthosema glaciale")

t_bg1 ##!> to view the figure

ggsave("selectivity_type_grouped_bg.jpeg", t_bg1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure


t_pa1 <- plot_selectivity_by_prey_type("Protomyctophum arcticum")

t_pa1 ##!> to view the figure

ggsave("selectivity_type_grouped_pa.jpeg", t_pa1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure


t_nk1 <- plot_selectivity_by_prey_type("Notoscopelus kroyeri")

t_nk1 ##!> to view the figure

ggsave("selectivity_type_grouped_nk.jpeg", t_nk1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure


t_lm1 <- plot_selectivity_by_prey_type("Lampanyctus macdonaldi")

t_lm1 ##!> to view the figure

ggsave("selectivity_type_grouped_lm.jpeg", t_lm1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure


t_ah1 <- plot_selectivity_by_prey_type("Argyropelecus hemigyrus")

t_ah1 ##!> to view the figure

ggsave("selectivity_type_grouped_ah.jpeg", t_ah1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure


t_sd1 <- plot_selectivity_by_prey_type("Sternophyx diaphana")

t_sd1 ##!> to view the figure

ggsave("selectivity_type_grouped_sd.jpeg", t_sd1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure
```

```
#Combine the plots

my_plots7 <- plot_grid(t_sd1, t_ah1, NULL, NULL) #, t_nk1, t_lm1)

combined_plot1 <- plot_grid(my_plots7, ncol = 1, rel_heights = c(1, .1))

combined_plot1

ggsave("selectivity_combined_grouped2.jpeg", combined_plot1, width = 140, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure

my_plots8 <- plot_grid( t_pa1, t_bg1, t_nk1, t_lm1)

combined_plot2 <- plot_grid(my_plots8, ncol = 1, rel_heights = c(1, .1))

combined_plot2

ggsave("selectivity_combined_grouped4.jpeg", combined_plot2, width = 140, height = 80, units = c("mm"), scale = 2.5) ##!> save the figure


##SPECIES GROUPED##

library(ggplot2)

library(tidyverse)

library(dplyr)

library(purrr)

library(ggthemes)

library(cowplot)

library(glue)


cbPalette <- c("#999933", "#882255", "#88ccee")


#Load stomach analysis file and change names to make the easier to work with

diet <- read_delim(file="15093 - Mesopelagic stomach analysis kopi.csv", delim=";", locale = locale(decimal_mark = ","))

colnames(diet)[3] <- "serialno"

colnames(diet)[4] <- "fish_species"

colnames(diet)[22] <- "nr_prey"

colnames(diet)[19] <- "bioluminescence"

colnames(diet)[21] <- "dig_rate"
```

```
digestion_under4 <- subset(diet,dig_rate < 4)



#Create data frame with the needed variables

diet_frame <- data.frame(diet[c("serialno", "Byttedyr", "nr_prey", "fish_species","bioluminescence",
"dig_rate")])



#The previous data set lacks the names of th stations and only has the serial numbers of the trawls,
load a document that has both

stations <- read_delim(file = "FishStation_2018106_kopi.csv", delim=";", locale =
locale(decimal_mark = ","))

stations_frame <- data.frame(stations[c("serialno", "station")])



#Create a new data frame with the station names

new_diet <- left_join(diet_frame,stations_frame, by="serialno")

colnames(new_diet)[7] <- "fish_station"



new_diet <- data.frame(new_diet[c("fish_station", "fish_species", "Byttedyr", "nr_prey",
"bioluminescence", "dig_rate")])



write.csv(new_diet, "C:/Users/ingri/OneDrive - University of
Bergen/Master/Stomach_analysis_stations1.csv", row.names=FALSE)



#Change NA to 0

new_diet[is.na(new_diet)] <- 0



#Make the number of prey numeric because it was read in as character

transform(new_diet, nr_prey = as.numeric(nr_prey))
```

```
new_diet<-new_diet[!(new_diet$Byttedyr=="Tom" | new_diet$Byttedyr=="Vrengt" |
new_diet$Byttedyr =="Empty" | new_diet$Byttedyr == "Stomach out of mouth" |
new_diet$Byttedyr == "Stomach missing" | new_diet$Byttedyr == "Rest"),]


new_diet <- new_diet|>

  mutate(Byttedyr = recode(Byttedyr,'Paraeuchaeta norvegica' = 'Paraeuchaeta sp.'))


new_diet <- within(new_diet, bioluminescence[bioluminescence == 'Not confirmed' & Byttedyr ==
'Paraeuchaeta sp.'] <- 'Potential')



#Create a data frame with unique species in diet

unique_diet <- new_diet |>

  distinct(Byttedyr, .keep_all =TRUE)


unique_diet <- data.frame(unique_diet[c("Byttedyr", "bioluminescence")])


unique_diet <- unique_diet |>

  arrange(Byttedyr)


bioluminescent <- subset(unique_diet,bioluminescence == "Confirmed" )

write.csv(bioluminescent, "C:/Users/ingri/OneDrive - University of
Bergen/Master/bioluminescent.csv", row.names=FALSE)


non_bioluminescent <- subset(unique_diet, bioluminescence == "Not confirmed")

write.csv(non_bioluminescent , "C:/Users/ingri/OneDrive - University of
Bergen/Master/non_bioluminescent .csv", row.names=FALSE)


potentially_bioluminescent <- subset(unique_diet, bioluminescence == "Potential")

write.csv(potentially_bioluminescent, "C:/Users/ingri/OneDrive - University of
Bergen/Master/potentially_bioluminescent.csv", row.names=FALSE)
```

```
inconlusive <- subset(unique_diet, bioluminescence == "Other")

write.csv(inconlusive, "C:/Users/ingri/OneDrive - University of Bergen/Master/inconlusive.csv",
row.names=FALSE)



#Create a total of prey of each species for each species of fish from one station instead of one
observation for each fish

sum_diet <- new_diet |>

 group_by(fish_station, fish_species, Byttedyr, bioluminescence) |>

 dplyr::summarise(nr_prey= sum(nr_prey)) |>

 as.data.frame()

sum_diet


sum_diet <- sum_diet[apply(sum_diet!=0, 1, all),]


sum_diet <- sum_diet[apply(sum_diet!='Other', 1, all),]



#Create a data frame with total number of prey for each fish species on each station

prey_total <- sum_diet |>

 group_by(fish_station, fish_species)|>

 summarise(total_prey = sum(nr_prey))|>

 as.data.frame()

prey_total


for_over_20 <- prey_total |>

 group_by(fish_species)|>

 summarise(total_prey = sum(total_prey))



#Combine the two data frames

ratio_diet <- left_join(sum_diet,prey_total, by=c("fish_station", "fish_species"))
```

```
#Add the ratio of each of the prey species for each fish species on each station
final_diet <- ratio_diet |>
  group_by(fish_station, fish_species,Byttedyr, bioluminescence, nr_prey, total_prey, )|>
  summarise(ratio_prey = nr_prey/total_prey)|>
  as.data.frame()



#Load data set with matched plankton- and fish stations
combined_stations <- read_delim(file = "fish_plankton_stations.csv")



diet_combined <- left_join(final_diet, combined_stations, by=c("fish_station"))


diet_combined <- data.frame(diet_combined[c("plankton_station", "fish_station", "fish_species",
"Byttedyr", "nr_prey", "total_prey", "ratio_prey", "bioluminescence")])



#Load the background data for the the stations
background1 <- read_delim(file="2018106 - st280-282  opparbeiding av MOCNESS.csv")
colnames(background1)[3] <- "plankton_station"
colnames(background1)[17] <- "Byttedyr"
colnames(background1)[18] <- "density"

background2 <- read_delim(file="2018106 - st275-2788 opparbeiding av MOCNESS.csv")
colnames(background2)[3] <- "plankton_station"
colnames(background2)[17] <- "Byttedyr"
colnames(background2)[18] <- "density"

background = rbind(background2,background1)
```

```
write.csv(background, "C:/Users/ingri/OneDrive - University of Bergen/Master/Data/2018106 - all stations - opparbeiding av MOCNESS.csv", row.names=FALSE)



#Make data frame with needed variables

background_data_frame <- data.frame(background[c("plankton_station", "Byttedyr", "density")])


#Make numeric

numeric_background <- transform(background_data_frame, density = as.numeric(density))


numeric_background <- numeric_background[numeric_background$plankton_station %in% c("275", "276", "278", "280", "281", "282"),]


#Some species in the water column are identified to a lower taxonomic level than in the diet, change the names so they can me matched

numeric_background <- numeric_background |>

  mutate(Byttedyr = recode(Byttedyr, 'Pleuromamma robusta' = 'Pleuromamma sp.', 'Paraeuchaeta barbata' = 'Paraeuchaeta sp.', 'Paraeuchaeta glacialis' =  'Paraeuchaeta.sp', 'Heterorhabdus' = 'Heterorhabus sp.', 'Heterorhabdus norvegicus' = 'Heterorhabdus sp.', 'Calanus hyperboreus' = 'Calanus sp.', 'Calanus glacialis' = 'Calanus sp.', 'Hymenodora' = 'Hymenodora sp.', 'Oithona' = 'Oithona sp.', 'Oncaea' = 'Oncaea sp.', 'Oncaea conifera'= 'Oncaea sp.', 'Pseudocalanus' = 'Pseodocalanus sp.', 'Themisto' = 'Themisto sp.', 'Paraeuchaeta norvegica' = 'Paraeuchaeta sp.', "Calanus finmarchicus/helgolandicus" = "Calanus finmarchicus", "Scottocalanus securifrons" = "Scottocalanus sp.", "Sergestes" = "Sergestes sp.", "Pseodocalanus"= "Pseudocalanus sp.", "Thysanoessa longicaudata" = "Thysanoessa sp."))



sum_background <- numeric_background |>

  group_by(plankton_station, Byttedyr) |>

  summarise( density= sum(density)) |>

  as.data.frame()



#Keep only plankton species in background that is also present in diet
```

```
shared_plankton <- left_join(diet_combined, sum_background, by=c("plankton_station", "Byttedyr"))
shared_plankton[is.na(shared_plankton)] <- 0


#Create a data frame with total number of prey for each fish species on each station
background_total <- shared_plankton |>
  group_by(plankton_station)|>
  summarise(total_density = sum(density))|>
  as.data.frame()
background_total

#Combine the two data frames
ratio_background <- left_join(shared_plankton,background_total, by=c("plankton_station"))


final_background <- ratio_background |>
  group_by(fish_station, fish_species, Byttedyr, ratio_prey, bioluminescence)|>
  reframe(ratio_plankton = density/total_density)|>
  as.data.frame()
final_background <- final_background[apply(final_background!=0, 1, all),]

final_background1 <- ratio_background |>
  group_by(fish_station, fish_species, Byttedyr, ratio_prey, bioluminescence, nr_prey)|>
  reframe(ratio_plankton = density/total_density)|>
  as.data.frame()
final_background1 <- final_background1[apply(final_background1!=0, 1, all),]

ratio_prey_over_2percent <- subset(final_background,ratio_prey > 0.02)


prey_over_20 <- left_join(ratio_prey_over_2percent, for_over_20, by = c("fish_species"))
```

```
prey_over20 <- left_join(final_background, for_over_20, by = c("fish_species"))

prey_over20 <- subset(prey_over20,total_prey > 19 )


for_glue <- sum_diet |>

  group_by(fish_species, Byttedyr)|>

  summarise(sum_prey_by_species = sum(nr_prey))


for_glue1 <- left_join(prey_over20, for_glue, by = c("fish_species", "Byttedyr"))


for_glue2 <- final_background1 |>

  group_by(fish_species, bioluminescence) |>

  summarise(sum_confirmed = sum(nr_prey[bioluminescence == "Confirmed"]),
sum_notconfirmed = sum(nr_prey[bioluminescence == "Not confirmed"]), sum_potential =
sum(nr_prey[bioluminescence == "Potential"])) |>

  filter(!bioluminescence =='Other') |>

  mutate(sum_confirmed = ifelse(bioluminescence ==
'Confirmed',sum_confirmed,sum_notconfirmed)) |>

  mutate(sum_confirmed = ifelse(bioluminescence == 'Potential',sum_potential,sum_confirmed)) |>

  select(-c(sum_notconfirmed, sum_potential)) |>

  rename(sum_bioluminescence = sum_confirmed)

for_glue3 <- left_join(prey_over20, for_glue2, by= c("fish_species", "bioluminescence"))

plot_selectivity_by_prey_type <- function(species_in) {


  ##!> subset dataframe

  df <- for_glue3 |>

     as_tibble() |>

     mutate(selectivity = ((ratio_prey-ratio_plankton)/(ratio_prey + ratio_plankton)))|>

     group_by(fish_species, bioluminescence, sum_bioluminescence)|>

     summarise(selectivity_mean = mean(selectivity), standard_deviation = sd(selectivity), n = n()) |>

     filter(fish_species %in% species_in)|>

    mutate(colors = case_when(
```

```
  bioluminescence == "Not confirmed" ~"grey20",
  bioluminescence == "Confirmed" ~ "green",
  bioluminescence == "Potential" ~ "white",
)) |>
mutate(bioluminescence = case_when(
  bioluminescence == "Not confirmed" ~"Non-bioluminescent",
  bioluminescence == "Confirmed" ~ "Bioluminescent",
  bioluminescence == "Potential" ~ "Potentially bioluminescent",
))

##!> plot subset dataframe
 ggplot(df, aes(fill = colors, x = bioluminescence, y= selectivity_mean)) +
  geom_bar(position="stack", stat="identity",  color = "black")+
  facet_wrap(~fish_species)+
  scale_fill_identity()+
  # scale_fill_manual(values= c("limegreen", "grey20", "white"),
  #                   labels = c("Bioluminescent", "Non-bioluminescent", "Potential"))+
  labs(
    y = "Prey selectivity",
    x = "Bioluminescence",
    fill = "Bioluminescence"
  )+
  theme(strip.text = element_text(size=10, face="italic")) +
  geom_errorbar(color = "magenta",
    aes(ymin = selectivity_mean-standard_deviation,
        ymax = selectivity_mean+standard_deviation),
    width = 0.2) +
  theme_cowplot()+
  theme(strip.text = element_text(face = "italic"))+
  geom_hline(yintercept = 0)+
  geom_hline(yintercept = 0)+
```

```
    geom_text(color ="blue", aes(x=bioluminescence, y = 1.3, label = glue("n =
{sum_bioluminescence}")))+

     scale_y_continuous(breaks = seq(-1,1,0.25), limits =c(-1,1.3))


 }


 t_bg1 <- plot_selectivity_by_prey_type("Benthosema glaciale")

 t_bg1 ##!> to view the figure

 ggsave("selectivity_type_bg.jpeg", t_bg1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!>
save the figure


 t_pa1 <- plot_selectivity_by_prey_type("Protomyctophum arcticum")

 t_pa1 ##!> to view the figure

 ggsave("selectivity_type_pa.jpeg", t_pa1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!>
save the figure


 t_nk1 <- plot_selectivity_by_prey_type("Notoscopelus kroyeri")

 t_nk1 ##!> to view the figure

 ggsave("selectivity_type_nk.jpeg", t_nk1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!>
save the figure


 t_lm1 <- plot_selectivity_by_prey_type("Lampanyctus macdonaldi")

 t_lm1 ##!> to view the figure

 ggsave("selectivity_type_lm.jpeg", t_lm1, width = 120, height = 80, units = c("mm"), scale = 2.5)
##!> save the figure


 t_ah1 <- plot_selectivity_by_prey_type("Argyropelecus hemigyrus")

 t_ah1 ##!> to view the figure

 ggsave("selectivity_type_ah.jpeg", t_ah1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!>
save the figure


 t_sd1 <- plot_selectivity_by_prey_type("Sternophyx diaphana")

 t_sd1 ##!> to view the figure
```

```
  ggsave("selectivity_type_sd.jpeg", t_sd1, width = 120, height = 80, units = c("mm"), scale = 2.5) ##!>
```
save the figure