

Fishery nutrient profiles provide a practical tool
for nutrition-sensitive fisheries management

Lorenzo Longobardi

Last update: 2025-11-06

Contents

1 Content	5
2 Timor-Est nutritional maps	7
3 Nutritional contribution and economic profiling	11
4 Nutritional profiles	27

Chapter 1

Content

This book contains the code and the results for the study '*Fishery nutrient profiles provide a practical tool for nutrition-sensitive fisheries management*'.

All data and code to generate the analyses are in organised in this repository. The repository is a R package and contains both the data used for the analysis and the code used to generate the results. In order to replicate the analyses you can clone the repo and run the code.

Chapter 2

Timor-Est nutritional maps

```
bonds <- sf::st_as_sf(timor.nutrients::timor_bonds)

tot_prod <-
  timor.nutrients::map_data |>
    dplyr::rename(region = area) |>
    dplyr::rename(annual_catch_tot = annual_catch) |>
    dplyr::rename(WRA_tot = WRA) |>
    dplyr::mutate(region = ifelse(region == "Liquiça", "Liquica", region))

region_nutr <-
  timor.nutrients::map_data_adj %>%
    dplyr::rename(region = area) %>%
    dplyr::filter(!region == "National") %>%
    dplyr::mutate(region = ifelse(region == "Liquiça", "Liquica", region)) %>%
    dplyr::right_join(bonds, by = c("region")) |>
    dplyr::left_join(tot_prod, by = "region") |>
    dplyr::select(region,
                  annual_catch_tot,
                  WRA,
                  geometry)

p1 <-
  ggplot(data = region_nutr) +
    geom_sf(aes(geometry = geometry, fill = annual_catch_tot),
            color = "white", linewidth = 0.5
    ) +
    theme_void() +
    geom_sf_text(aes(label = region, geometry = geometry), size = 3, color = "grey50", fontface = "
```

```
# scale_fill_viridis_c(option = "viridis", direction = -1, begin = 0.3, end = 1, alpha = 1) +
scale_fill_distiller(palette = "YlGnBu", direction = 1) +
guides(alpha = "none") +
coord_sf(expand = FALSE) +
theme(
  legend.position = "bottom",
  legend.key.width = unit(1, "cm"),
  panel.grid = element_blank(),
  axis.ticks = element_blank(),
  axis.title = element_blank(),
  axis.text = element_blank()
) +
labs(
  fill = "Metric tons"
)

p2 <-
ggplot() +
geom_sf(
  data = region_nutr %>%
    dplyr::filter(!region == "Atauro"), mapping = aes(geometry = geometry, fill = WR)
  ) +
geom_sf(
  data = region_nutr %>%
    dplyr::filter(region == "Atauro"), mapping = aes(geometry = geometry), fill = "firebrick"
  ) +
theme_void() +
geom_sf_text(data = region_nutr %>%
  dplyr::filter(!region == "Atauro"), mapping = aes(label = region, geometry = geometry))
annotate(
  "text",
  x = 126, y = -8.2, label = "Atauro 747%", size = 3, color = "firebrick", fontface = "bold"
) +
# annotate(
#   "text", x = 125.8, y = -8.2, label = "1067.9%", size = 3, color = "firebrick", fontface = "bold"
# ) +
scale_fill_distiller(palette = "YlGnBu", direction = 1) +
guides(alpha = "none") +
coord_sf(expand = FALSE) +
theme(
  plot.margin = margin(0, 0, 0, 0, "cm"),
  legend.position = "bottom",
  legend.key.width = unit(1, "cm")
)
```

```

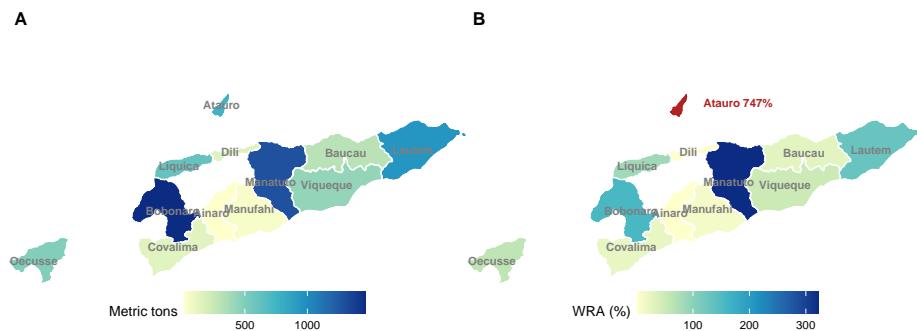
legend.key.width = unit(1, "cm"),
panel.grid = element_blank(),
axis.ticks = element_blank(),
axis.title = element_blank(),
axis.text = element_blank()
) +
labs(
  fill = "WRA (%)"
)

#title = "WRA that would meet the recommended quantity of edible fish annually, \nfrom marine cat
#title = "Timor-Leste small scale fisheries production",
#subtitle = "Annual catch in Mt per municipality, average (2020-2022)"
```

```

cowplot::plot_grid(
  p1 + theme(plot.margin = margin(0, 0, 0, 0, "cm")),
  p2 + theme(plot.margin = margin(0, 0, 0, 0, "cm")),
  ncol = 2,
  labels = "AUTO",
  rel_widths = c(1, 1),
  align = "hv"
)

```



Chapter 3

Nutritional contribution and economic profiling

```
library(ggplot2)

catch_groups_name <-
  timor.nutrients::catch_groups %>%
  dplyr::select(
    grouped_taxa = interagency_code,
    catch_name
  )

tot_catch <-
  timor.nutrients::region_stats %>%
  dplyr::mutate(year = lubridate::year(date_bin_start)) %>%
  dplyr::group_by(grouped_taxa, year) %>%
  dplyr::summarise(catch = sum(catch)) %>%
  dplyr::group_by(grouped_taxa) %>%
  dplyr::summarise(catch = mean(catch)) %>%
  dplyr::left_join(catch_groups_name) %>%
  dplyr::select(-grouped_taxa) %>%
  dplyr::select(catch_name, catch) %>%
  dplyr::mutate(catch = catch / 1000)

base_plot <-
  timor.nutrients::nutrients_table %>%
  dplyr::left_join(catch_groups_name) %>%
  dplyr::select(catch_name, grouped_taxa, Selenium_mu:Vitamin_A_mu) %>%
```

```

rename_nutrients_mu(hyphen = FALSE) %>%
tidyr::pivot_longer(-c(catch_name, grouped_taxa), names_to = "nutrient", values_to =
dplyr::filter(!nutrient == "selenium" & !catch_name %in% "Other") %>%
dplyr::left_join(RDI_tab) %>%
dplyr::mutate(
  nutrient = stringr::str_to_title(nutrient),
  nutrient = dplyr::case_when(
    nutrient == "Omega3" ~ "Omega-3",
    nutrient == "Vitamina" ~ "Vitamin-A",
    TRUE ~ nutrient
  )
) %>%
dplyr::mutate(rdi = (concentration * 100) / conv_factor) %>%
dplyr::group_by(catch_name) %>%
dplyr::mutate(tot = sum(rdi, na.rm = T)) %>%
dplyr::arrange(-tot) %>%
dplyr::left_join(tot_catch) %>%
tidyr::replace_na(list(catch = 0)) %>%
dplyr::arrange(dplyr::desc(nutrient)) %>%
dplyr::ungroup() %>%
dplyr::mutate(
  fish_group = dplyr::case_when(
    grouped_taxa %in% c("COZ", "CUX") ~ "Molluscs",
    grouped_taxa %in% c("PEZ") ~ "Shrimps",
    grouped_taxa %in% c("MZZ") ~ "Other",
    grouped_taxa %in% c("SLV", "CRA") ~ "Crustaceans",
    grouped_taxa %in% c("OCZ", "IAX") ~ "Cephalopods",
    grouped_taxa %in% c("SKH", "SRX") ~ "Sharks and rays",
    grouped_taxa %in% c("SNA", "GPX", "PWT", "GRX", "MUI", "BGX") ~ "Large demersals",
    grouped_taxa %in% c("CGX", "TUN", "BEN", "LWX", "BAR", "SFA", "CBA", "DOX", "ECN",
    grouped_taxa %in% c("YDX", "SPI", "EMP", "SUR", "TRI", "MOJ", "WRA", "BWH", "LGE",
    grouped_taxa %in% c("RAX", "SDX", "CJX", "CLP", "GZP", "FLY", "KYX", "MOO", "CLP",
    TRUE ~ NA_character_
  ),
  fish_group = ifelse(fish_group %in% c("Shrimps", "Molluscs", "Cephalopods", "Crustaceans"),
)
tot_catch_plot <-
base_plot %>%
dplyr::group_by(catch_name) %>% # Added .drop false to ensure that all factor levels
dplyr::summarise(
  catch_t = dplyr::first(catch),
  tot_t = dplyr::first(tot)
)
# base_plot %>% View()

```

```

base_plot <-
  dplyr::left_join(base_plot, tot_catch_plot, by = "catch_name") %>%
  dplyr::filter(catch_t > 0) %>%
  dplyr::mutate(
    VarColor = dplyr::case_when(
      fish_group == "Small pelagics" ~ "#bc4749",
      fish_group == "Small demersals" ~ "#e9c46a",
      fish_group == "Large pelagics" ~ "#2a9d8f",
      fish_group == "Large demersals" ~ "#007ea7",
      fish_group == "Sharks and rays" ~ "#264653",
      fish_group == "Marine invertebrates" ~ "#898989",
      TRUE ~ "#000000"
    ),
    ColoredVar = glue::glue("<span style='color:{VarColor}'>{catch_name}</span>"),
    fish_group = factor(fish_group, levels = c(
      "Small pelagics", "Large pelagics", "Small demersals", "Large demersals",
      "Sharks and rays", "Marine invertebrates"
    )))
  )

tons_label <- cowplot::draw_label("Mean annual\ncatch (tons)", x = 0.941, y = 0.98, size = 9)

long_plot <-
  ggplot2::ggplot() +
  ggpubr::theme_pubr() +
  ggchicklet::geom_chicklet(base_plot,
    mapping = ggplot2::aes(
      y = rdi, x = reorder(ColoredVar, tot),
      fill = nutrient,
      color = nutrient
    ),
    position = ggplot2::position_stack(reverse = FALSE),
    alpha = 0.8,
    width = 1
  ) +
  geom_text(base_plot,
    mapping = aes(y = rdi, x = reorder(ColoredVar, tot), label = round(rdi, 2) * 100),
    position = position_stack(0.5),
    color = "white",
    size = 3
  ) +
  geom_text(
    data = base_plot,
    mapping = aes(
      # Set y to a fixed position above the bars

```

```

y = 1.35, # Adjust this value if needed
x = reorder(ColoredVar, tot_t),
label = ifelse(catch_t < 1, "<1", scales::comma(round(catch_t, 0))),
alpha = sqrt(catch_t),
),
size = 3,
hjust = 0,           # Left-align the text
nudge_y = 0.05
) +
facet_grid(fish_group ~ ., scales = "free", space = "free") +
coord_flip(expand = FALSE, ylim = c(0, 1.5)) +
ggplot2::scale_fill_manual(values = timor.nutrients::palettes$nutrients_palette) +
ggplot2::scale_color_manual(values = timor.nutrients::palettes$nutrients_palette) +
ggplot2::scale_y_continuous(labels = scales::percent, n.breaks = 10) +
ggplot2::labs(x = "", y = "", fill = "Nutrient", subtitle = "Groups nutrient density",
ggplot2::theme(
  legend.position = "bottom",
  panel.grid.major.y = element_line(linetype = "dashed"),
  strip.background = ggplot2::element_blank(),
  strip.text = ggplot2::element_blank(),
  axis.text.y = ggtext::element_markdown(size = 9),
  panel.spacing = unit(0.1, "lines"),
  plot.subtitle = element_text(face = "bold")
) +
guides(
  alpha = "none",
  color = "none"
)

long_legend <- ggpubr::get_legend(long_plot)
long_plot <- long_plot +
  theme(legend.position = "none")

long_plot <- cowplot::plot_grid(long_plot) + tons_label

# groups_palette <- c("#2a9d8f", "#264653", "#007ea7", "#e9c46a", "#898989", "#bc4749").
groups_palette <- c("#bc4749", "#2a9d8f", "#e9c46a", "#007ea7", "#264653", "#898989")

groups_plot <-
  timor.nutrients::region_stats_adj %>%
  dplyr::mutate(fish_group = dplyr::case_when(
    grouped_taxa %in% c("COZ") ~ "Molluscs",
    grouped_taxa %in% c("PEZ") ~ "Shrimps",

```

```

grouped_taxa %in% c("MZZ") ~ "Other",
grouped_taxa %in% c("SLV", "CRA") ~ "Crustaceans",
grouped_taxa %in% c("OCZ", "IAX") ~ "Cephalopods",
grouped_taxa %in% c("SKH", "SRX") ~ "Sharks and rays",
grouped_taxa %in% c("SNA", "GPX", "PWT", "GRX", "MUI", "BGX") ~ "Large demersals",
grouped_taxa %in% c("CGX", "TUN", "BEN", "LWX", "BAR", "SFA", "CBA", "DOX", "ECN", "DOS") ~ "Medium demersals",
grouped_taxa %in% c("YDX", "SPI", "EMP", "SUR", "TRI", "MOJ", "WRA", "BWH", "LGE", "MOB", "MUL"),
grouped_taxa %in% c("RAX", "SDX", "CJX", "CLP", "GZP", "FLY", "KYX", "MOO", "CLP", "MUL", "DS")
TRUE ~ NA_character_
)) %>%
dplyr::select(-grouped_taxa) %>%
dplyr::group_by(fish_group) %>%
dplyr::summarise(dplyr::across(dplyr::where(is.numeric), ~ sum(.x, na.rm = T))) %>%
na.omit() %>%
tidyverse::pivot_longer(-c(fish_group, catch), names_to = "nutrient") %>%
dplyr::group_by(nutrient, fish_group) %>%
dplyr::summarise(value = sum(value)) %>%
dplyr::arrange(-value, .by_group = TRUE) %>%
dplyr::select(fish_group, nutrient, value) %>%
dplyr::ungroup() %>%
dplyr::mutate(
  nutrient = as.factor(nutrient),
  fish_group = ifelse(fish_group %in% c("Shrimps", "Molluscs", "Cephalopods", "Crustaceans"), "Shrimps", "Molluscs", "Cephalopods", "Crustaceans"),
  fish_group = factor(fish_group, levels = c(
    "Shrimps", "Molluscs", "Cephalopods", "Crustaceans",
    "Marine invertebrates", "Sharks and rays", "Large demersals",
    "Small demersals", "Large pelagics", "Small pelagics"
  )))
) %>%
dplyr::filter(!nutrient == "selenium") %>%
dplyr::mutate(
  nutrient = stringr::str_to_title(nutrient),
  nutrient = dplyr::case_when(
    nutrient == "Omega3" ~ "Omega-3",
    nutrient == "Vitamina" ~ "Vitamin-A",
    TRUE ~ nutrient
  ),
  fish_label = dplyr::case_when(
    fish_group == "Small pelagics" ~ "SP",
    fish_group == "Large pelagics" ~ "LP",
    fish_group == "Small demersals" ~ "SD",
    fish_group == "Large demersals" ~ "LD",
    fish_group == "Sharks and rays" ~ "SR",
    fish_group == "Marine invertebrates" ~ "MI"
  ),
)

```

16 CHAPTER 3. NUTRITIONAL CONTRIBUTION AND ECONOMIC PROFILING

```

fish_label = factor(fish_label, levels = rev(c(
    "SP", "LP", "SD", "LD", "SR", "MI"
)))
) %>%
ggplot(aes(fish_label, value / 1000, fill = fish_label)) +
  ggpubr::theme_pubr() +
  ggchicklet::geom_chicklet(
    alpha = 0.8,
    radius = grid::unit(5, "pt")
) +
  facet_wrap(. ~ nutrient, scales = "free", ncol = 2) +
  labs(y = "Tons (2018-2023)", x = "Functional\ngroup", fill = "Fish group", subtitle =
    theme(
      legend.position = "",
      panel.grid = element_blank(),
      strip.background = ggplot2::element_blank(), # This removes the background from the
      axis.text.y = element_text(size = 7),
      axis.ticks.y = ggplot2::element_blank(),
      panel.spacing.x = unit(0.1, "lines"),
      panel.spacing.y = unit(0, "lines"),
      plot.subtitle = element_text(face = "bold")
) +
  scale_fill_manual(
    values = groups_palette,
    breaks = c(
      "SP", "LP", "SD", "LD",
      "SR", "MI"
    )
) +
  scale_y_continuous(n.breaks = 3) +
  coord_flip(expand = F)

####

groups_palette <- c("#bc4749", "#2a9d8f", "#e9c46a", "#007ea7", "#264653", "#898989")

top_groups <-
  timor.nutrients::region_stats %>%
  dplyr::select(grouped_taxa, catch) %>%
  dplyr::mutate(
    totCatch = sum(catch, na.rm = T),
    fish_group = dplyr::case_when(
      grouped_taxa %in% c("COZ") ~ "Molluscs",
      grouped_taxa %in% c("PEZ") ~ "Shrimps",
      grouped_taxa %in% c("MZZ") ~ "Other",
      TRUE ~ "Others"
    )
  )

```

```

grouped_taxa %in% c("SLV", "CRA") ~ "Crustaceans",
grouped_taxa %in% c("OCZ", "IAX") ~ "Cephalopods",
grouped_taxa %in% c("SKH", "SRX") ~ "Sharks and rays",
grouped_taxa %in% c("SNA", "GPX", "PWT", "GRX", "MUI", "BGX") ~ "Large demersals",
grouped_taxa %in% c("CGX", "TUN", "BEN", "LWX", "BAR", "SFA", "CBA", "DOX", "ECN", "DOS") ~
grouped_taxa %in% c("YDX", "SPI", "EMP", "SUR", "TRI", "MOJ", "WRA", "BWH", "LGE", "MOB", "RAX")
grouped_taxa %in% c("RAX", "SDX", "CJX", "CLP", "GZP", "FLY", "KYX", "MOO", "CLP", "MUL", "TRUE ~ NA_character_
)
) %>%
dplyr::mutate(fish_group = ifelse(fish_group %in% c("Shrimps", "Molluscs", "Cephalopods", "Crustaceans", "Sharks and rays", "Large demersals"), "Other", fish_group)) %>%
dplyr::group_by(fish_group, grouped_taxa) %>%
dplyr::summarise(
  tot_catch = dplyr::first(tot_catch),
  catch = sum(catch, na.rm = T),
  catch_percent = catch / tot_catch * 100
) %>%
dplyr::group_by(fish_group) %>%
dplyr::slice_max(catch_percent, n = 1) %>%
dplyr::arrange(-catch_percent, .by_group = T) %>%
na.omit() %>%
dplyr::rename(interagency_code = "grouped_taxa") %>%
dplyr::left_join(timor.nutrients::catch_groups, by = "interagency_code") %>%
dplyr::select(fish_group, catch_name, interagency_code, catch_percent) %>%
dplyr::ungroup()

revenue_dat <-
  timor.nutrients::catch_data %>%
  tidyr::unnest(landing_catch) %>%
  tidyr::unnest(length_frequency) %>%
  dplyr::filter(!is.na(.data$weight), !is.na(landing_value)) %>%
  dplyr::group_by(landing_id) %>%
  dplyr::mutate(n = dplyr::n()) %>%
  dplyr::filter(n == 1) %>%
  dplyr::select(-n) %>%
  dplyr::ungroup() %>%
  dplyr::mutate(tot_obs = length(unique(landing_id))) %>%
  dplyr::group_by(catch_taxon) %>%
  dplyr::filter(catch_taxon %in% top_groups$interagency_code) %>%
  dplyr::group_by(.data$landing_id, .data$catch_taxon) %>%
  dplyr::summarise(
    landing_value = dplyr::first(landing_value),
    dplyr::across(
      c(.data$weight:.data$Vitamin_A_mu),
      ~ sum(.x)
    )
  )

```

```

        )
    )

models <-
  revenue_dat %>%
  dplyr::ungroup() %>%
  dplyr::select(catch_taxon, landing_value, weight) %>%
# dplyr::group_by(catch_taxon) %>%
# dplyr::mutate(model = broom::augment(stats::lm(formula = log(landing_value + 1) ~
# dplyr::ungroup() %>%
# dplyr::mutate(cooksd = .data$model$.cooksd) %>%
# dplyr::select(-.data$model) %>%
# dplyr::mutate(out = dplyr::case_when(.data$cooksd > (5 * mean(.data$cooksd)) ~ 1,
# dplyr::filter(out == 0) %>%
# dplyr::select(-out, -cooksd) %>%
# dplyr::select(catch_taxon, landing_value, weight) %>%
split(.\$catch_taxon) %>%
purrr::map(~ lm(log(landing_value) ~ log(weight), data = .x)) %>%
purrr::map(~ predict(.x, data.frame(weight = log(1000)))) %>%
dplyr::bind_rows(.id = "catch_taxon") %>%
dplyr::rename(price = `1`) %>%
dplyr::mutate(price = round(exp(price) * 10, 2))

revenue_dat <-
  revenue_dat %>%
  rename_nutrients_mu() %>%
  tidyr::pivot_longer(-c(landing_id:weight), names_to = "nutrient") %>%
  dplyr::filter(!nutrient == "selenium") %>%
  dplyr::left_join(RDI_tab) %>%
  dplyr::ungroup() %>%
  dplyr::mutate(
    value = value / weight * 100,
    inds = value / conv_factor * 100
  ) %>%
  dplyr::group_by(landing_id, catch_taxon) %>%
  dplyr::mutate(inds_100 = sum(inds)) %>%
  dplyr::group_by(catch_taxon) %>%
  dplyr::summarise(
    inds = dplyr::first(inds_100)
  ) %>%
  dplyr::left_join(models) %>%
  dplyr::rename(interagency_code = catch_taxon) %>%
  dplyr::left_join(timor.nutrients:::catch_groups, by = "interagency_code") %>%
  dplyr::left_join(top_groups, by = "catch_name") %>%

```

```

dplyr::select(fish_group, catch_name, price, inds, catch_percent)

revenue_plot <-
  revenue_dat %>%
  dplyr::mutate(fish_group = factor(fish_group, levels = c(
    "Small pelagics", "Large pelagics", "Small demersals", "Large demersals",
    "Sharks and rays", "Marine invertebrates"
  ))) %>%
  # dplyr::filter(!catch_name %in% c("Stingrays")) %>%
  ggplot(aes(inds, price, size = catch_percent, color = fish_group)) +
  ggpubr::theme_pubr() +
  geom_point(stroke = 2, alpha = 0.5) +
  geom_point(size = 1) +
  geom_text(aes(label = catch_name, color = fish_group), size = 3.5, vjust = -2.2, show.legend =
  scale_size(range = c(1, 15)) +
  coord_cartesian(
    ylim = c(0, 12),
    xlim = c(65, 145)
  ) +
  scale_x_continuous(labels = scales::label_percent(scale = 1), n.breaks = 5) +
  scale_y_continuous(labels = scales::label_dollar(), n.breaks = 8) +
  scale_color_manual(values = groups_palette) +
  theme(
    panel.grid = element_blank(),
    legend.position = "bottom",
    plot.subtitle = element_text(face = "bold")
  ) +
  guides(
    size = "none",
    colour = guide_legend(override.aes = list(size = 5))
  ) +
  labs(
    x = "",
    y = "Price (USD / kg)",
    subtitle = "Affordability and nutrient density",
    color = "Functional\\ngroup"
  )
)

groups_leg <- ggpubr::get_legend(revenue_plot)
revenue_plot <-
  revenue_plot +
  theme(legend.position = "none")

habitat_nutrients <-

```

```

timor.nutrients::kobo_trips %>%
  dplyr::select(habitat, weight:Vitamin_A_mu) %>%
  rename_nutrients_mu() %>%
  tidyr::pivot_longer(~c(habitat, weight), names_to = "nutrient") %>%
  dplyr::left_join(RDI_tab) %>%
  dplyr::mutate(
    value = value / weight,
    inds_kg = (value * 1000) / conv_factor
  ) %>%
  dplyr::group_by(habitat, nutrient) %>%
  dplyr::summarise(inds_kg = median(inds_kg, na.rm = T) / 10) %>%
  dplyr::mutate(inds_kg = inds_kg * 100) %>%
  dplyr::filter(!nutrient == "selenium") %>%
  dplyr::mutate(
    habitat = ifelse(habitat == "Deep", "Pelagic", habitat),
    nutrient = stringr::str_to_title(nutrient),
    nutrient = dplyr::case_when(
      nutrient == "Omega3" ~ "Omega-3",
      nutrient == "Vitamina" ~ "Vitamin-A",
      TRUE ~ nutrient
    )
  )
habitat_plot <-
  ggplot2::ggplot() +
  ggpubr::theme_pubr() +
  ggchicklet::geom_chicklet(habitat_nutrients,
    mapping = ggplot2::aes(
      y = inds_kg,
      x = reorder(habitat, inds_kg),
      fill = nutrient,
      color = nutrient
    ),
    position = ggplot2::position_stack(reverse = FALSE),
    alpha = 0.8,
    width = 0.8,
    radius = grid::unit(3, "pt")
  ) +
  ggplot2::geom_text(habitat_nutrients,
    mapping = ggplot2::aes(
      y = inds_kg,
      x = reorder(habitat, inds_kg),
      label = round(inds_kg, 0),
      group = nutrient
    ),
    position = ggplot2::position_stack(0.5, reverse = FALSE),
  )

```

```

    color = "white",
    size = 2.5
) +
ggplot2::scale_fill_manual(values = timor.nutrients::palettes$nutrients_palette) +
ggplot2::scale_color_manual(values = timor.nutrients::palettes$nutrients_palette) +
ggplot2::scale_y_continuous(labels = scales::label_percent(scale = 1)) +
ggplot2::coord_flip(expand = FALSE) +
ggplot2::theme(
  legend.position = "",
  panel.grid = ggplot2::element_blank(),
  axis.text.y = element_text(size = 7.75),
  plot.subtitle = element_text(face = "bold")
) +
ggplot2::labs(x = "", fill = "", y = "Cumulative nutrient density score", subtitle = "Habitat a
ggplot2::guides(
  alpha = "none",
  color = "none",
  fill = guide_legend(override.aes = list(size = 7)))
)

gear_nutrients <-
timor.nutrients::kobo_trips %>%
dplyr::select(gear_type, weight:Vitamin_A_mu) %>%
rename_nutrients_mu() %>%
tidy::pivot_longer(-c(gear_type, weight), names_to = "nutrient") %>%
dplyr::left_join(RDI_tab) %>%
dplyr::mutate(
  value = value / weight,
  inds_kg = (value * 1000) / conv_factor
) %>%
dplyr::group_by(gear_type, nutrient) %>%
dplyr::summarise(inds_kg = median(inds_kg, na.rm = T) / 10) %>%
dplyr::mutate(inds_kg = inds_kg * 100) %>%
dplyr::filter(!nutrient == "selenium") %>%
dplyr::mutate(
  nutrient = stringr::str_to_title(nutrient),
  nutrient = dplyr::case_when(
    nutrient == "Omega3" ~ "Omega-3",
    nutrient == "Vitamina" ~ "Vitamin-A",
    TRUE ~ nutrient
  )
) %>%
dplyr::mutate(gear_type = stringr::str_to_title(gear_type)) %>%
dplyr::ungroup()

```

```

gear_nutrients <-
  ggplot2::ggplot() +
  ggpubr::theme_pubr() +
  ggchicklet::geom_chicklet(gear_nutrients,
    mapping = ggplot2::aes(
      y = inds_kg,
      x = reorder(gear_type, inds_kg),
      fill = nutrient,
      color = nutrient
    ),
    position = ggplot2::position_stack(reverse = FALSE),
    alpha = 0.8,
    width = 0.8,
    radius = grid::unit(3, "pt")
  ) +
  ggplot2::geom_text(gear_nutrients,
    mapping = ggplot2::aes(
      y = inds_kg,
      x = reorder(gear_type, inds_kg),
      label = round(inds_kg, 0),
      group = nutrient
    ),
    position = ggplot2::position_stack(0.5, reverse = FALSE),
    color = "white",
    size = 2.5
  ) +
  ggplot2::scale_fill_manual(values = timor.nutrients::palettes$nutrients_palette) +
  ggplot2::scale_color_manual(values = timor.nutrients::palettes$nutrients_palette) +
  ggplot2::scale_y_continuous(labels = scales::label_percent(scale = 1)) +
  ggplot2::coord_flip(expand = FALSE) +
  ggplot2::theme(
    legend.position = "",
    panel.grid = ggplot2::element_blank(),
    axis.text.y = element_text(size = 7.75),
    plot.subtitle = element_text(face = "bold")
  ) +
  ggplot2::labs(x = "", fill = "", y = "Cumulative nutrient density score", subtitle =
  ggplot2::guides(
    alpha = "none",
    color = "none",
    fill = guide_legend	override.aes = list(size = 7))
  )

second_row_plot <- cowplot::plot_grid(

```

```

groups_plot, #+ theme(plot.margin = unit(c(0, 0, 0, +2.2), "cm")),
revenue_plot,
ncol = 1,
align = "hv",
labels = c("B", "C"),
rel_heights = c(1.2, 1)
)

p1 <-
cowplot::plot_grid(
  long_plot,
  second_row_plot,
  ncol = 2,
  align = "hv",
  rel_widths = c(1.75, 1),
  labels = "AUTO"
)

bottom_row_plot <- cowplot::plot_grid(
  habitat_plot + labs(y = ""),
  gear_nutrients + labs(y = ""),
  ncol = 2,
  align = "hv",
  labels = c("", ""),
  rel_heights = c(1, 1)
)

p2 <- cowplot::plot_grid(
  p1 + theme(plot.margin = unit(c(0, 0, 0, 0), "cm")),
  bottom_row_plot + theme(plot.margin = unit(c(-0.5, 0, 0, 0), "cm")),
  nrow = 2,
  labels = c("A", "D"),
  rel_heights = c(1, 0.25),
  align = "v" # align vertically
)

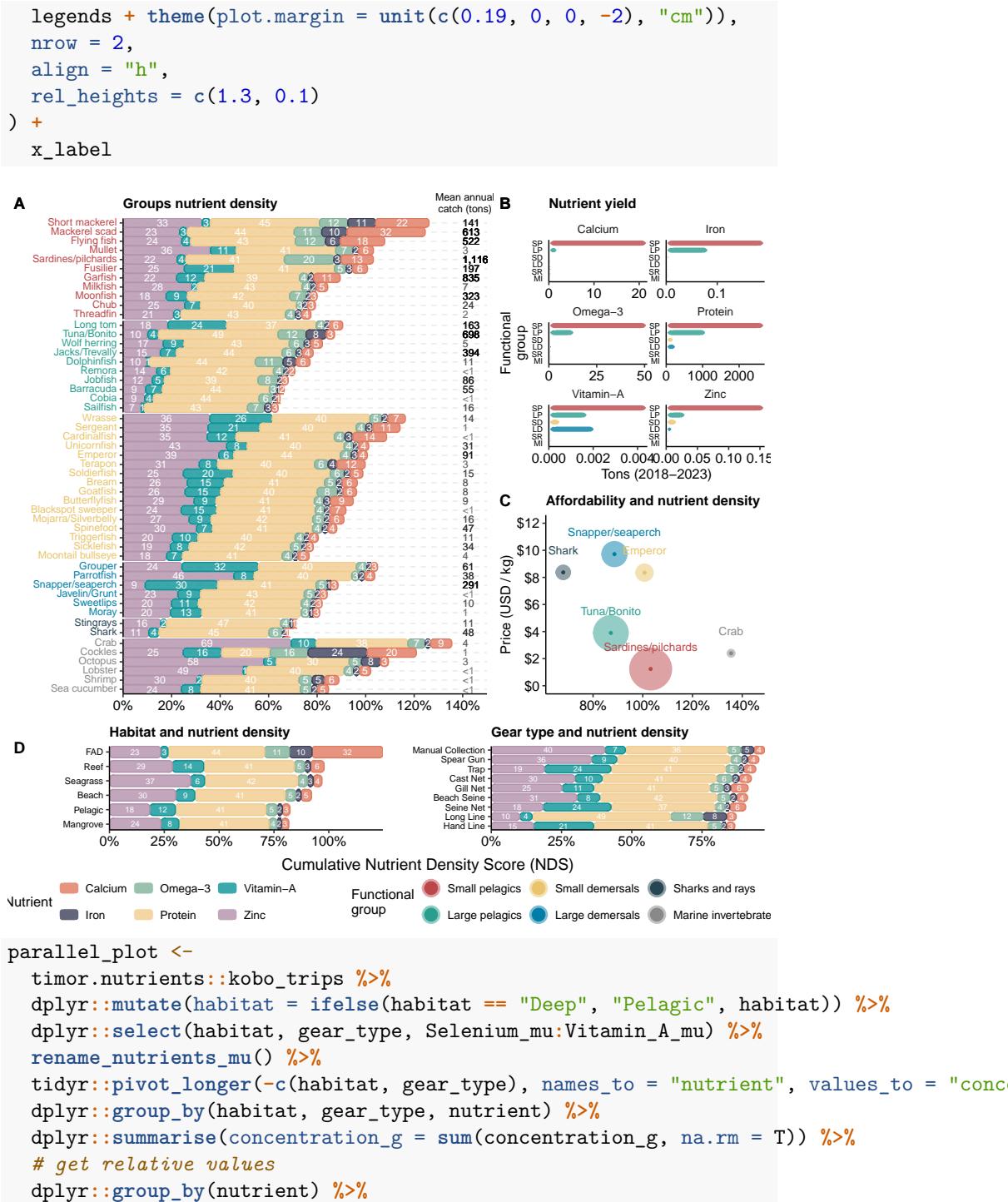
legends <-
cowplot::plot_grid(
  long_legend, groups_leg
)

x_label <- cowplot::draw_label("Cumulative Nutrient Density Score (NDS)", x = 0.55, y = 0.0825)

cowplot::plot_grid(
  p2,

```

24 CHAPTER 3. NUTRITIONAL CONTRIBUTION AND ECONOMIC PROFILING



```

dplyr::mutate(
  nutrient_sum = sum(concentration_g),
  concentration_g = concentration_g / nutrient_sum * 100
) %>%
dplyr::ungroup() %>%
dplyr::mutate(dplyr::across(habitat:nutrient, ~ as.factor(.x))) %>%
dplyr::mutate(
  nutrient = as.factor(nutrient)
) %>%
dplyr::mutate(
  nutrient = stringr::str_to_title(nutrient),
  nutrient = dplyr::case_when(
    nutrient == "Omega3" ~ "Omega-3",
    nutrient == "Vitamina" ~ "Vitamin-A",
    TRUE ~ nutrient
  )
) %>%
dplyr::rename(
  "Nutrient" = nutrient,
  "Habitat" = habitat,
  "Gear type" = gear_type
) %>%
ggforce::gather_set_data(c(3, 1, 2))

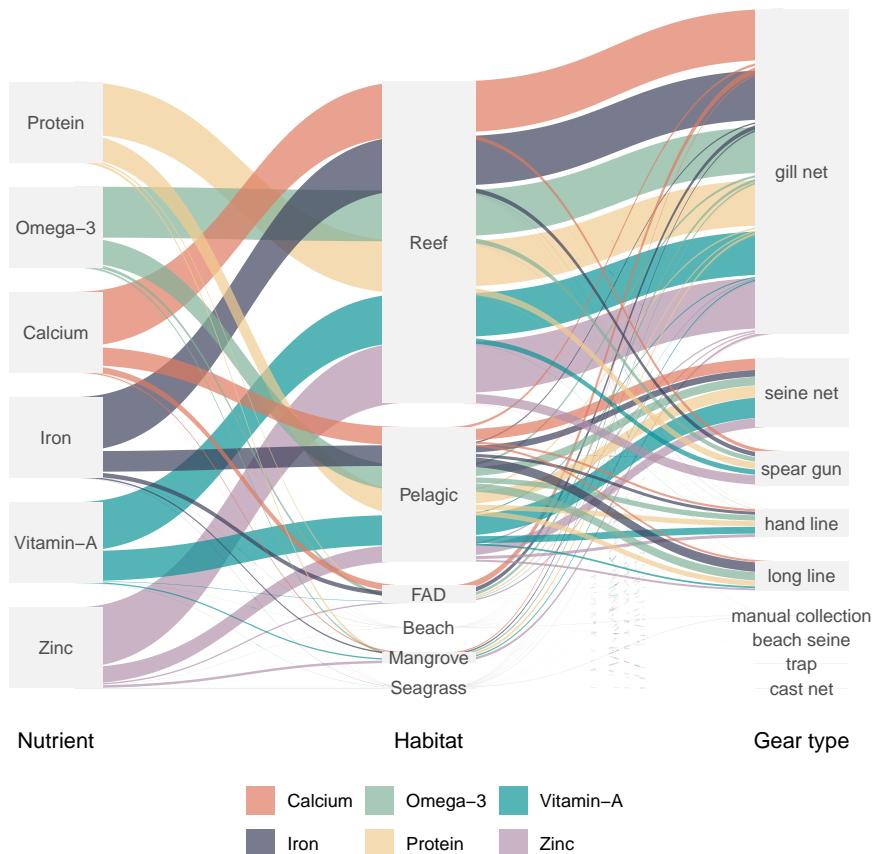
parallel_plot$x <- factor(parallel_plot$x,
                           levels = c("3", "1", "2"),
                           labels = c("Nutrient", "Habitat", "Gear type")
)

parallel_plot$y <- factor(parallel_plot$y, levels = c(
  "Protein", "Omega-3", "Calcium", "Iron", "Vitamin-A", "Zinc", "Selenium",
  "Reef", "Pelagic", "FAD", "Beach", "Traditional FAD", "Mangrove", "Seagrass",
  "gill net", "seine net", "spear gun", "hand line", "long line", "manual collection",
  "beach seine", "trap", "cast net"
))
parallel_plot %>%
  dplyr::filter(!Nutrient == "Selenium") %>%
  na.omit() %>%
  ggplot(aes(x, id = id, split = y, value = concentration_g)) +
  ggforce::geom_parallel_sets(aes(fill = Nutrient), alpha = 0.7, axis.width = 0.1) +
  ggforce::geom_parallel_sets_axes(axis.width = 0.25, fill = "grey95") +
  ggforce::geom_parallel_sets_labels(colour = "grey30", angle = 0, size = 3.5) +
  scale_x_discrete(name = NULL, expand = c(0, 0.2)) +
  scale_y_continuous(breaks = NULL, expand = c(0.05, 0)) +

```

26 CHAPTER 3. NUTRITIONAL CONTRIBUTION AND ECONOMIC PROFILING

```
theme_minimal(12) +
scale_fill_manual(values = timor.nutrients::palettes$nutrients_palette) +
# scale_fill_manual(values = c("#508AA8", "grey95", "#BD9391")) +
theme(
  axis.line = element_blank(),
  axis.ticks = element_blank(),
  legend.position = "bottom",
  panel.grid.major = element_blank(),
  axis.text = element_text(size = 12, color = "black")
) +
labs(fill = "")
```



Chapter 4

Nutritional profiles

```
library(ggplot2)
data <- get_model_data()
data$data_raw$timor_GN_raw$clusters <- paste0("FNP-", data$data_raw$timor_GN_raw$clusters)
data$data_raw$timor_AG_raw$clusters <- paste0("FNP-", data$data_raw$timor_AG_raw$clusters)

plot_profiles <- function(x) {
  means_dat <-
  x %>%
  dplyr::rename_with(~ stringr::str_to_title(.x), .cols = c(.data$zinc:.data$vitaminA)) %>%
  dplyr::rename(
    "Vitamin-A" = .data$Vitamina,
    "Omega-3" = .data$Omega3
  ) %>%
  tidyr::pivot_longer(c(Zinc:"Vitamin-A")) %>%
  dplyr::group_by(clusters, name) %>%
  dplyr::summarise(
    mean = mean(value, na.rm = TRUE),
    sd = sd(value, na.rm = TRUE),
    n = dplyr::n(),
    se = sd / sqrt(n),
    ci_lower = mean - qt(0.99, df = n - 1) * se,
    ci_upper = mean + qt(0.99, df = n - 1) * se
  )

  all_dat <-
  x %>%
  dplyr::rename_with(~ stringr::str_to_title(.x), .cols = c(.data$zinc:.data$vitaminA)) %>%
  dplyr::rename(
```

```

    "Vitamin-A" = .data$Vitamina,
    "Omega-3" = .data$Omega3
) %>%
tidyverse::pivot_longer(c(Zinc:"Vitamin-A"))

ggplot() +
  ggpubr::theme_pubr() +
  geom_jitter(data = all_dat, mapping = aes(x = value, y = name, color = clusters),
  geom_point(data = means_dat, mapping = aes(x = mean, y = name, color = clusters),
  labs(
    x = "",
    y = "",
    color = "Profiles"
  ) +
  ggplot2::theme(
    legend.position = "",
    plot.margin = unit(c(0, 0, 0, 0), "cm"),
    panel.grid = ggplot2::element_blank()
  ) +
  coord_cartesian(xlim = c(0, 5)) +
  scale_fill_manual(values = timor.nutrients::palettes$clusters_palette) +
  scale_color_manual(values = timor.nutrients::palettes$clusters_palette)
}

plots1 <- plot_profiles(data$data_raw$timor_AG_raw) #purrr::map(data$data_raw$timor_AG_raw, ~

means_dat <-
data$data_raw$timor_GN_raw %>%
dplyr::rename_with(~ stringr::str_to_title(.x), .cols = c(.data$zinc:.data$vitaminA))
dplyr::rename(
  "Vitamin-A" = .data$Vitamina,
  "Omega-3" = .data$Omega3
) %>%
tidyverse::pivot_longer(c(Zinc:"Vitamin-A")) %>%
dplyr::group_by(clusters, name) %>%
dplyr::summarise(
  mean = mean(value, na.rm = TRUE),
  sd = sd(value, na.rm = TRUE),
  n = dplyr::n(),
  se = sd / sqrt(n),
  ci_lower = mean - qt(0.99, df = n - 1) * se,
  ci_upper = mean + qt(0.99, df = n - 1) * se
)

```

```

all_dat <-
  data$data_raw$timor_GN_raw %>%
  dplyr::rename_with(~ stringr::str_to_title(.x), .cols = c(.data$zinc:.data$vitaminA)) %>%
  dplyr::rename(
    "Vitamin-A" = .data$Vitamina,
    "Omega-3" = .data$Omega3
  ) %>%
  tidyr::pivot_longer(c(Zinc:"Vitamin-A"))

plots2 <-
  ggplot() +
  ggpubr::theme_pubr() +
  geom_jitter(data = all_dat, mapping = aes(x = value, y = name, color = clusters), alpha = 0.01,
  geom_point(data = means_dat, mapping = aes(x = mean, y = name, color = clusters), size = 5, pos
  labs(
    x = "",
    y = "",
    color = "Profiles"
  ) +
  ggplot2::theme(
    legend.position = "",
    plot.margin = unit(c(0, 0, 0, 0), "cm"),
    panel.grid = ggplot2::element_blank()
  ) +
  coord_cartesian(xlim = c(0, 5)) +
  scale_fill_manual(values = timor.nutrients::palettes$clusters_palette) +
  scale_color_manual(values = timor.nutrients::palettes$clusters_palette) +
  annotate(
    'text',
    x = 3.5,
    y = 2.5,
    label = 'On average, FNP-3 provides enough calcium for 2.2 people per 1kg of catch,\nwhile F
    size = 2.75
  ) +
  #annotate(
  #  'rect',
  #  xmin = 0,
  #  ymin = 0.5,
  #  ymax = 1.5,
  #  xmax = 4.5,
  #  alpha = 0.5,
  #  color = rgb(0, 0, 0, alpha = 0.85),
  #  linewidth = 0.3,
  #  fill = "transparent",
  #  linetype = 2

```

```

#) +
annotate(
  'curve',
  x = 3.4, # Play around with the coordinates until you're satisfied
  y = 1.8,
  yend = 1.3,
  xend = 2.45,
  col = 'black',
  curvature = -0.05,
  linewidth = 0.3,
  arrow = arrow(length = unit(0.25, 'cm')))
)

plots <-
list(
  plots2 + ggplot2::labs(subtitle = "Gill nets"),
  plots1 + ggplot2::labs(subtitle = "Other gears")
)

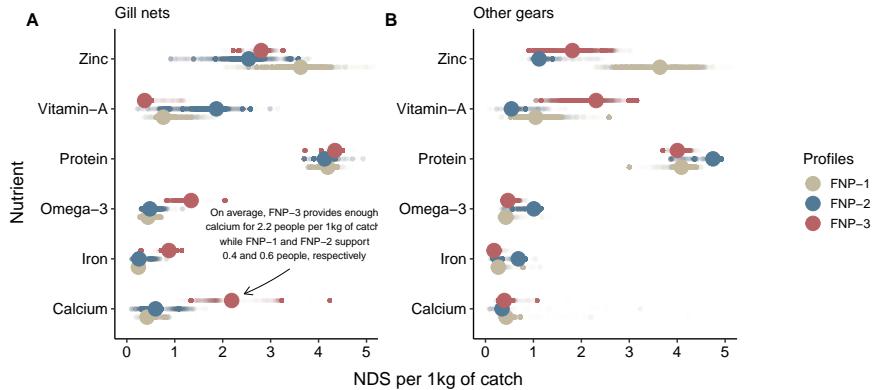
legend_plot <- cowplot::get_legend(plots[[1]] +
  ggplot2::theme(
    legend.position = "right",
    legend.key.size = ggplot2::unit(0.55, "cm"),
    legend.title = ggplot2::element_text(size = 12)
))
combined_plots <- cowplot::plot_grid(plotlist = plots, ncol = 2, labels = "AUTO")

x_label <- cowplot::draw_label("NDS per 1kg of catch", x = 0.5, y = 0.05)
y_label <- cowplot::draw_label("Nutrient", x = 0.04, y = 0.5, angle = 90)

final_plot <-
cowplot::plot_grid(
  combined_plots,
  legend_plot,
  ncol = 2,
  rel_widths = c(1, 0.15),
  scale = 0.9
) +
x_label +
y_label

final_plot

```



```

kmean_plots <- data$kmeans_plots

plots <-
  list(
    kmean_plots$timor_GN + ggplot2::labs(subtitle = "Gill nets"),
    kmean_plots$timor_AG + ggplot2::labs(subtitle = "Other gears")
  )

plots <- lapply(plots, function(x) {
  x +
    ggpubr::theme_pubr() +
    ggplot2::theme(
      legend.position = "none",
      plot.margin = unit(c(0, 0, 0, 0), "cm"),
      panel.grid = ggplot2::element_blank()
    ) +
    ggplot2::labs(
      fill = "Profiles",
      color = "Profiles"
    ) +
    ggplot2::scale_color_manual(
      values = timor.nutrients::palettes$clusters_palette,
      labels = function(x) paste0("FNP-", x)
    ) +
    ggplot2::scale_fill_manual(
      values = timor.nutrients::palettes$clusters_palette,
      labels = function(x) paste0("FNP-", x)
    )
})

legend_plot <- cowplot::get_legend(plots[[1]]) +
  ggplot2::theme(

```

```

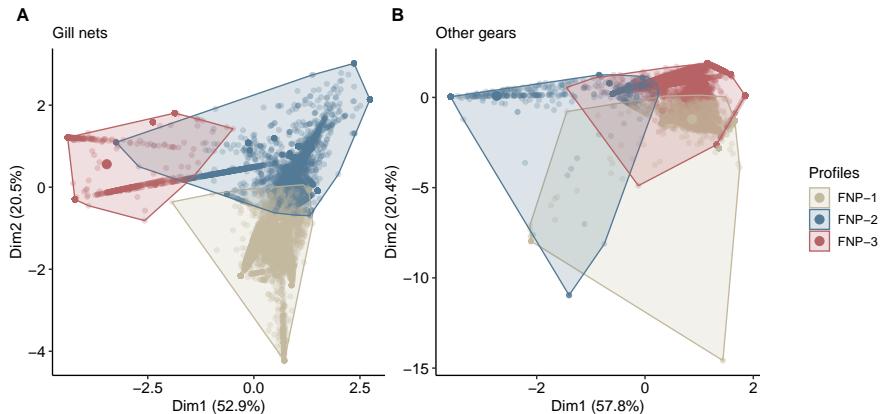
    legend.position = "right",
    legend.key.size = ggplot2::unit(0.6, "cm"),
    legend.title = ggplot2::element_text(size = 12)
  ))
combined_plots <- cowplot::plot_grid(plotlist = plots, ncol = 2, labels = "AUTO")

# x_label <- cowplot::draw_label("False positive rate\n(1 - Specificity)", x = 0.5, y =
# y_label <- cowplot::draw_label("True positive rate\n(Sensitivity)", x = 0.02, y = 0.5)

final_plot <-
  cowplot::plot_grid(
    combined_plots,
    legend_plot,
    ncol = 2,
    rel_widths = c(1, 0.1),
    scale = 0.9
  )

final_plot

```



```

timor.nutrients::perm_results %>%
  dplyr::bind_rows(.id = "subset") %>%
  dplyr::mutate(dplyr::across(c(SumOfSqs, R2, statistic), ~ round(.x, 2)),
    p.value = ifelse(p.value <= 0.001, "< 0.001", p.value),
    subset = stringr::str_remove(subset, "_perm"),
    subset = stringr::str_replace(subset, "timor", "mainland"))
) %>%
  reactable::reactable(
    theme = reactablefmtr::fivethirtyeight(centered = TRUE),
    groupBy = "subset",

```

```
    defaultExpanded = TRUE,  
    pagination = FALSE,  
    compact = FALSE,  
    borderless = FALSE,  
    striped = FALSE,  
    defaultColDef = reactable::colDef(  
        align = "center"  
)  
,  
    columns = list(  
        subset = reactable::colDef(  
            minWidth = 120  
)  
)
```

SUBSET	TERM	DF	SUMOFS
▼ mainland_GN (3)			
	clusters	2	12464.9
	Residual	10168	5914.5
	Total	10170	18379.4
▼ mainland_AG (3)			
	clusters	2	9487.8
	Residual	5479	3303.1
	Total	5481	12790.9

```
models_auc <-  
  timor.nutrients::model_outputs %>%  
  purrr::map(purrr::pluck(8)) %>%  
  dplyr::bind_rows(.id = "subset") %>%  
  dplyr::select(-estimator) %>%  
  tidyr::pivot_wider(names_from = subset, values_from = estimate)
```

```

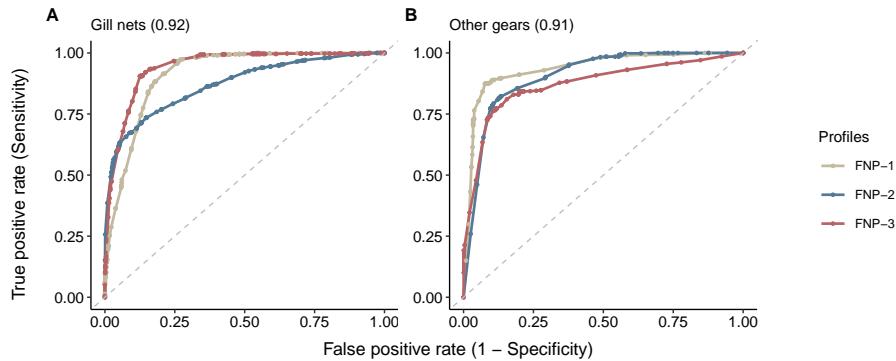
plots <- 
  list(
    timor.nutrients::model_outputs$model_timor_GN$roc_curves + ggplot2::labs(subtitle = "ROC Curves for Model Timor GN"),
    timor.nutrients::model_outputs$model_timor_AG$roc_curves + ggplot2::labs(subtitle = "ROC Curves for Model Timor AG")
  )
plots <- lapply(plots, function(x) {
  x +
    ggpubr::theme_pubr() +
    ggplot2::theme(
      panel.grid = ggplot2::element_blank(),
      legend.position = "none",
      plot.margin = unit(c(0, 0, 0, -0.1), "cm")
    ) +
    ggplot2::coord_cartesian(expand = T) +
    ggplot2::labs(x = "", y = "", color = "Profiles") +
    ggplot2::scale_color_manual(
      values = timor.nutrients::palettes$clusters_palette,
      labels = function(x) paste0("FNP-", x)
    ) +
    ggplot2::scale_fill_manual(
      values = timor.nutrients::palettes$clusters_palette,
      labels = function(x) paste0("FNP-", x)
    )
  })
legend_plot <- cowplot::get_legend(plots[[1]]) +
  ggplot2::theme(
    legend.position = "right",
    legend.key.size = ggplot2::unit(0.8, "cm"),
    legend.title = ggplot2::element_text(size = 12)
  )
combined_plots <- cowplot::plot_grid(plotlist = plots, ncol = 2, labels = "AUTO", vjust = 0)

x_label <- cowplot::draw_label("False positive rate (1 - Specificity)", x = 0.5, y = 0.5)
y_label <- cowplot::draw_label("True positive rate (Sensitivity)", x = 0.02, y = 0.5, a = 90)

final_plot <-
  cowplot::plot_grid(
    combined_plots,
    legend_plot,
    ncol = 2,
    rel_widths = c(1, 0.15),
    scale = 0.9
  ) +
  x_label +
  y_label

```

```
final_plot
```



```
models_metrics <-
  timor.nutrients::model_outputs %>%
  purrr::map(purrr::pluck(4)) %>%
  purrr::imap(~ summary(.x)) %>%
  dplyr::bind_rows(.id = "subset") %>%
  dplyr::select(-estimator) %>%
  tidyverse::pivot_wider(names_from = subset, values_from = .estimate) %>%
  dplyr::rename(metric = .metric) %>%
  na.omit()

dplyr::bind_rows(models_auc, models_metrics) %>%
  dplyr::rename(
    "Other gears" = model_timor_AG,
    "Gill nets" = model_timor_GN
  ) %>%
  dplyr::mutate(dplyr::across(.cols = dplyr::where(is.numeric), ~ round(.x, 2))) %>%
  reactable::reactable(
    theme = reactablefmtr::fivethirtyeight(centered = TRUE),
    defaultExpanded = TRUE,
    pagination = FALSE,
    compact = FALSE,
    borderless = FALSE,
    striped = FALSE,
    defaultColDef = reactable::colDef(
      align = "center"
    ),
    columns = list(
      metric = reactable::colDef(
        minWidth = 120
      )
    )
  )
```

```
)  
)
```

METRIC	OTHER GEARS	GILL NETS
roc_auc	0.91	0.92
accuracy	0.8	0.76
kap	0.7	0.62
sens	0.81	0.77
spec	0.9	0.88
ppv	0.8	0.74
npv	0.9	0.87
mcc	0.7	0.62
j_index	0.71	0.65
bal_accuracy	0.86	0.82
detection_prevalence	0.33	0.33
precision	0.8	0.74
recall	0.81	0.77
f_meas	0.8	0.75

```
importance_ag <-
  model_outputs$model_timor_AG$fit %>%
  workflows::extract_fit_parsnip() %>%
  vip::vi() %>%
  dplyr::mutate(
    category = dplyr::case_when(
      stringr::str_detect(Variable, "gear_type") ~ "gear_type",
      stringr::str_detect(Variable, "habitat_gear") ~ "habitat_gear",
      stringr::str_detect(Variable, "habitat") ~ "habitat",
      stringr::str_detect(Variable, "quarter") ~ "quarter",
      stringr::str_detect(Variable, "vessel_type") ~ "vessel_type",
      TRUE ~ "other"
    )
  )
```

```

    )
) %>%
dplyr::group_by(category) %>%
dplyr::summarize(Aggregated_Importance = sum(Importance)) %>%
dplyr::arrange(dplyr::desc(Aggregated_Importance))

importance_gn <-
model_outputs$model_timor_GN$fit %>%
workflows::extract_fit_parsnip() %>%
vip::vi() %>%
dplyr::mutate(
  category = dplyr::case_when(
    stringr::str_detect(Variable, "mesh_size") ~ "mesh_size",
    stringr::str_detect(Variable, "habitat_mesh") ~ "habitat_mesh",
    stringr::str_detect(Variable, "habitat") ~ "habitat",
    stringr::str_detect(Variable, "quarter") ~ "quarter",
    stringr::str_detect(Variable, "vessel_type") ~ "vessel_type",
    TRUE ~ "other"
  )
) %>%
dplyr::group_by(category) %>%
dplyr::summarize(Aggregated_Importance = sum(Importance)) %>%
dplyr::arrange(dplyr::desc(Aggregated_Importance))

importance_plot <-
dplyr::bind_rows(
  importance_ag %>% dplyr::mutate(model = "Other gears"),
  importance_gn %>% dplyr::mutate(model = "Gill nets")
) %>%
dplyr::mutate(category = dplyr::case_when(category == "habitat_gear" ~ "habitat x gear type",
                                             category == "habitat_mesh" ~ "habitat x mesh size",
                                             TRUE ~ category),
  category = stringr::str_replace(category, "_", " "),
  category = stringr::str_to_title(category)
) %>%
ggplot(aes(x = reorder(category, Aggregated_Importance), y = Aggregated_Importance)) +
ggpubr::theme_pubr(border = TRUE) +
facet_wrap(~model, scales = "free") +
geom_col(width = 0.2, fill = "#1c8097", alpha = 0.75) +
coord_flip() +
labs(
  x = "Predictor",
  y = "Aggregated Feature Importance\n(XGBoost Gain)"
) +
theme(
  plot.title = element_text(hjust = 0.5, vjust = 1, size = 14, color = "#1c8097"),
  plot.subtitle = element_text(hjust = 0.5, vjust = 0, size = 12, color = "#1c8097"),
  plot.caption = element_text(hjust = 0.5, vjust = 0, size = 10, color = "#1c8097"),
  axis.title.x = element_text(vjust = 0, size = 12, color = "#1c8097"),
  axis.title.y = element_text(hjust = 0, size = 12, color = "#1c8097"),
  axis.text.x = element_text(size = 10, color = "#1c8097"),
  axis.text.y = element_text(size = 10, color = "#1c8097"),
  legend.title = element_text(size = 12, color = "#1c8097"),
  legend.text = element_text(size = 10, color = "#1c8097"),
  panel.grid.major = grid::gpar(linew = 1, color = "#1c8097"),
  panel.grid.minor = grid::gpar(linew = 1, color = "#1c8097"),
  panel.border = grid::gpar(linew = 1, color = "#1c8097"),
  panel.background = element_rect(fill = "#1c8097", color = "#1c8097"),
  text = element_text(size = 10, color = "#1c8097")
)

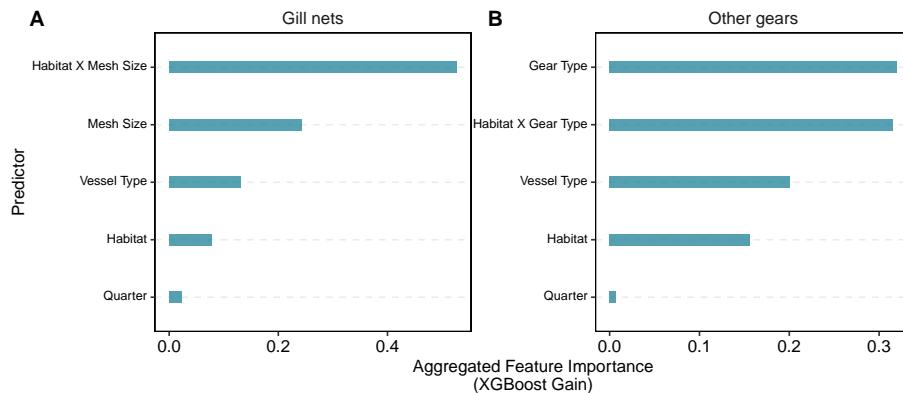
```

```

panel.grid.major.y = element_line(linetype = "dashed"),
strip.background = ggplot2::element_blank(),
strip.text = element_text(size = 12),
axis.text.y = ggtext::element_markdown(size = 9),
panel.spacing = unit(0.1, "lines"),
)

cowplot::ggdraw(importance_plot) +
cowplot::draw_plot_label(
  label = c("A", "B"),
  x = c(0.02, 0.52), # Adjust the x position of labels
  y = c(0.98, 0.98), # Adjust the y position of labels
  size = 15
)

```



```

sha_Mgn <- shapviz::shapviz(timor.nutrients::shap_results$model_timor_GN)

annotation_data <- data.frame(
  profile = "FNP-3",
  x = 0.175,
  y = 120,
  label = 'FNP-3 profile likelihood increases\nwith <40mm mesh in pelagic and\nmangrove'
)

p2 <-
  sha_Mgn %>%
  purrr::map(get_shaps, model_type = "gn") %>%
  dplyr::bind_rows(.id = "profile") %>%
  dplyr::mutate(profile = stringr::str_replace(profile, ".pred_", "FNP-")) %>%
  dplyr::group_by(profile, habitat_fact, mesh_fact) %>%
  dplyr::summarise(mesh_shap = median(mesh_shap, na.rm = TRUE)) %>%
  dplyr::ungroup() %>%

```

```

dplyr::filter(mesh_shap > 0) %>%
dplyr::mutate(habitat_fact = dplyr::case_when(habitat_fact == "Deep" ~ "Pelagic", TRUE ~ habitat_fact))
ggplot2::ggplot(ggplot2::aes(mesh_shap, mesh_fact, color = habitat_fact)) +
  facet_grid(. ~ factor(profile, levels = c("FNP-1", "FNP-2", "FNP-3")), scales = "free") +
  ggplot2::geom_point(ggplot2::aes(alpha = sqrt(mesh_shap), size = mesh_shap)) +
  ggpubr::theme_pubr(border = TRUE) +
  ggplot2::scale_color_manual(values = c("#f28f3b", "#c27ba0", "#ffd5c2", "#588b8b", "#c8553d", "#ffccbc"))
  ggplot2::coord_cartesian(expand = TRUE) +
  ggplot2::scale_y_reverse(n.breaks = 10) +
  ggplot2::labs(color = "Habitat") +
  ggplot2::theme(
    panel.grid = ggplot2::element_blank(),
    strip.background = ggplot2::element_blank(),
    strip.text.x = ggplot2::element_text(face = "bold")
  ) +
  ggplot2::guides(
    color = ggplot2::guide_legend(override.aes = list(size = 3)),
    alpha = "none",
    size = "none"
  ) +
  ggplot2::geom_text(
    data = annotation_data,
    aes(x = x, y = y, label = label),
    size = 3,
    fontface = "plain",
    inherit.aes = FALSE
  ) +
  ggplot2::geom_rect(
    data = annotation_data,
    aes(xmin = 0.27, xmax = 0.36, ymin = 19, ymax = 57),
    fill = "white",
    alpha = 0.2,
    color = "black",
    inherit.aes = FALSE,
    linetype = "dashed"
  ) +
  ggplot2::geom_curve(
    data = annotation_data,
    aes(x = 0.32, y = 60, xend = 0.29, yend = 90),
    curvature = -0.1,
    color = 'black',
    linewidth = 0.4,
    arrow = arrow(length = unit(0.4, 'cm')),
    inherit.aes = FALSE
  )
)

```

```

ggplot2::labs(x = "", y = "")

leg <- cowplot::get_legend(p2 +
  ggplot2::theme(
    plot.margin = unit(c(2, 0, 0, 0.9), "cm"),
    # legend.title = ggplot2::element_text(size = 11),
    legend.position = "right",
    legend.direction = "vertical",
    legend.justification = "right",
    legend.box.just = "right",
    legend.background = element_rect(fill = "transparent",
    legend.box.background = element_rect(fill = "transparent"
  )))

base_plot <-
  cowplot::plot_grid(
    p2 + theme(
      legend.position = "none",
      plot.margin = unit(c(-0.2, 0.5, 0, 0.9), "cm")
    ),
    ncol = 1,
    labels = c("A", "B"),
    hjust = -3.5,
    vjust = 1.2,
    align = "v"
  )

grid <-
  cowplot::plot_grid(
    base_plot,
    nrow = 1
  )

pp1 <-
  cowplot::ggdraw() +
  cowplot::draw_plot(grid) +
  cowplot::draw_label("Mesh size (mm)", x = 0.03, y = 0.7, angle = 90, hjust = 1, size = 10)

sha_Mag <- shapviz::shapviz(timor.nutrients::shap_results$model_timor_AG)

process_shap <-
  sha_Mag %>%
  purrr::map(get_shaps, model_type = "ag") %>%
  dplyr::bind_rows(.id = "profile") %>%

```

```

tidyR::separate(habitat_gear_fact, into = c("habitat", "gear_fact"), sep = "_") %>%
dplyr::mutate(
  gear_fact = stringr::str_to_title(gear_fact),
  profile = stringr::str_replace(profile, ".pred_", "FNP-"),
  habitat_gear_fact = paste0(habitat, " x ", gear_fact),
  habitat_gear_fact = stringr::str_replace(habitat_gear_fact, "Deep", "Pelagic")
)

to_group <-
process_shap %>%
dplyr::mutate(
  zero_dist = 0 - abs(gear_fact_shap)
) %>%
dplyr::group_by(gear_fact) %>%
dplyr::summarise(zero_dist = mean(zero_dist)) %>%
dplyr::slice_max(order_by = zero_dist, n = 15) %>%
magrittr::extract2("gear_fact")

annotation_data <- data.frame(
  profile = "FNP-2",
  x = 0.171,
  y = 5.3,
  label = 'Long lines in pelagic, FADs\nand mangroves areas boost chances\nof obtaining FNP-2 prof'
)

p2 <-
process_shap %>%
dplyr::mutate(gear_fact_shap = ifelse(gear_fact_shap %in% to_group, "Others", gear_fact_shap))
dplyr::group_by(profile, gear_fact, habitat_fact) %>%
dplyr::summarise(gear_fact_shap = median(gear_fact_shap, na.rm = TRUE)) %>%
dplyr::ungroup() %>%
dplyr::filter(gear_fact_shap > 0) %>%
dplyr::mutate(habitat_fact = dplyr::case_when(habitat_fact == "Deep" ~ "Pelagic", TRUE ~ habitat_fact))
ggplot2::ggplot(ggplot2::aes(gear_fact_shap, gear_fact, color = habitat_fact)) +
  facet_grid(. ~ profile, scales = "free") +
  ggplot2::geom_point(ggplot2::aes(alpha = sqrt(gear_fact_shap), size = gear_fact_shap)) +
  ggpubr::theme_pubr(border = TRUE) +
  ggplot2::scale_color_manual(values = c("#f28f3b", "#c27ba0", "#ffd5c2", "#588b8b", "#c8553d", "#ff9933")) +
  ggplot2::coord_cartesian(expand = TRUE) +
  ggplot2::scale_x_continuous(n.breaks = 4) +
  ggplot2::labs(color = "Habitat") +
  ggplot2::theme(
    panel.grid = ggplot2::element_blank(),
    strip.background = ggplot2::element_blank(),
    strip.text.x = ggplot2::element_text(face = "bold")
)

```

```

) +
ggplot2::geom_text(
  data = annotation_data,
  aes(x = x, y = y, label = label),
  size = 3,
  fontface = "plain",
  inherit.aes = FALSE
) +
ggplot2::geom_curve(
  data = annotation_data,
  aes(x = 0.174, y = 3, xend = 0.172, yend = 4.2),
  curvature = -0.2,
  color = 'black',
  linewidth = 0.4,
  arrow = arrow(length = unit(0.4, 'cm')),
  inherit.aes = FALSE
) +
ggplot2::geom_rect(
  data = annotation_data,
  aes(xmin = 0.1745, xmax = 0.178, ymin = 2.5, ymax = 3.5),
  fill = "white",
  alpha = 0.2,
  color = "black",
  inherit.aes = FALSE,
  linetype = "dashed"
) +
ggplot2::guides(
  color = ggplot2::guide_legend	override.aes = list(size = 3)),
  alpha = "none",
  size = "none"
) +
ggplot2::labs(x = "", y = "")

leg <- cowplot::get_legend(p2 +
  ggplot2::theme(
    plot.margin = unit(c(2, 0, 0, 0.9), "cm"),
    # legend.title = ggplot2::element_text(size = 11),
    legend.position = "right",
    legend.direction = "vertical",
    legend.justification = "right",
    legend.box.just = "right",
    legend.background = element_rect(fill = "transparent",
    legend.box.background = element_rect(fill = "transparent"
  )))

```

```

base_plot <-
  cowplot::plot_grid(
    p2 + theme(
      legend.position = "none",
      plot.margin = unit(c(-0.2, 0.5, 0, 0.9), "cm")
    ),
    ncol = 1,
    labels = c("B", "D"),
    hjust = -3.5,
    vjust = 1.2,
    align = "v"
  )

grid <-
  cowplot::plot_grid(
    base_plot,
    nrow = 1
  )

pp2 <-
  cowplot::ggdraw(ylim = c(-.05, NA)) +
  cowplot::draw_plot(grid) +
  cowplot::draw_label("Gear type", x = 0.03, y = 0.7, angle = 90, hjust = 1, size = 12) +
  cowplot::draw_label("Impact on model output (SHAP value)", x = 0.5, y = 0, size = 12)

# Extract the shared legend with larger text and key sizes
shared_legend <- cowplot::get_legend(
  p2 +
  ggplot2::theme(
    legend.position = "right",                      # Position the legend on the right
    legend.direction = "vertical",                  # Vertical orientation
    legend.justification = "center",
    legend.box.just = "center",
    legend.text = ggplot2::element_text(size = 12),  # Increase text size
    legend.title = ggplot2::element_text(size = 14), # Increase title size
    legend.key.size = unit(1.5, "lines"),           # Increase legend key size
    legend.background = ggplot2::element_rect(fill = "transparent", colour = NA),
    legend.box.background = ggplot2::element_rect(fill = "transparent", colour = NA)
  )
)

# Remove legends from individual plots
pp1_no_legend <-
  pp1 +
  ggplot2::theme(legend.position = "none")

```

```

pp2_no_legend <-
  pp2 +
  ggplot2::theme(legend.position = "none")

# Combine the two plots vertically without legends
plots_combined <- cowplot::plot_grid(
  pp1_no_legend,
  pp2_no_legend,
  align = "v",           # Align the plots vertically
  ncol = 1,              # Stack in one column
  rel_heights = c(1, 1)  # Adjust heights if necessary
)

# Add the shared legend to the right
final_plot <- cowplot::plot_grid(
  plots_combined,
  shared_legend,
  ncol = 2,              # Add legend to the right of the plots
  rel_widths = c(3, 0.5)  # Adjust widths for the plots and legend
)

# Display the final plot
print(final_plot)

```

