Figure1B

2025-08-06

Intro

Non-Metric Multidimensional Scaling (NMDS) performed on the Bray-Curtis compositional dissimilarity matrices of Operational Protein Units (OPUs), to reproduce the analyses and the Figure 1A from the original publication Seasonal dynamics of the coastal microbiome and its association with environmental factors.

1. Set the environment

```
library(tidyverse)
## -- Attaching core tidyverse packages ------ tidyverse 2.0.0 --
## v dplyr
               1.1.4
                         v readr
                                      2.1.5
## v forcats
               1.0.0
                                      1.5.1
                         v stringr
## v ggplot2
               3.5.1
                         v tibble
                                      3.2.1
## v lubridate 1.9.3
                                      1.3.1
                         v tidyr
## v purrr
               1.0.2
                                          ------tidyverse_conflicts() --
## -- Conflicts -----
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                     masks stats::lag()
## i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become error
library(vegan)
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.6-8
library(ggpubr)
library(corrgram)
## Attaching package: 'corrgram'
## The following object is masked from 'package:lattice':
##
##
       panel.fill
library(lubridate)
library(grid)
2. Load data
```

```
ABUND <- readr::read_tsv("../data/opus_workable.tsv", show_col_types = FALSE)
METADATA <- readr::read_tsv("../data/metadata_workable.tsv", show_col_types = FALSE)</pre>
```

3. Format abundance table

Because the OPU abundance table is in long format (to speed up import), we need to convert it back to wide format.

```
ABUND <- ABUND %>%
tidyr::pivot_wider(names_from = opu_id, values_from = abundance) %>%
tibble::column_to_rownames("Date") %>%
as.matrix()
```

3. Run NMDS

NMDS is performed on Bray–Curtis dissimilarities computed from Hellinger-transformed OPU abundance profiles.

```
ABUND_norm <- vegan::decostand(ABUND, method = "hellinger")
set.seed(123)
ABUND norm nmds <- vegan::metaMDS(ABUND norm, k = 2, try = 50, trymax = 50, threshold = 0.9)
## Run 0 stress 0.1759656
## Run 1 stress 0.1725844
## ... New best solution
## ... Procrustes: rmse 0.06349945 max resid 0.2089412
## Run 2 stress 0.1687237
## ... New best solution
## ... Procrustes: rmse 0.1273724 max resid 0.5343585
## Run 3 stress 0.1682768
## ... New best solution
## ... Procrustes: rmse 0.01184472 max resid 0.0462124
## Run 4 stress 0.1725844
## Run 5 stress 0.1750414
## Run 6 stress 0.1682768
## ... New best solution
## ... Procrustes: rmse 5.858705e-06 max resid 1.428457e-05
## ... Similar to previous best
## Run 7 stress 0.1682768
## ... Procrustes: rmse 4.732532e-05 max resid 0.0001709377
## ... Similar to previous best
## Run 8 stress 0.1682768
## ... Procrustes: rmse 1.560506e-05 max resid 4.755194e-05
## ... Similar to previous best
## Run 9 stress 0.1753588
## Run 10 stress 0.1688158
## Run 11 stress 0.1750414
## Run 12 stress 0.1682769
## ... Procrustes: rmse 2.740805e-05 max resid 7.00654e-05
## ... Similar to previous best
## Run 13 stress 0.1734958
## Run 14 stress 0.1725844
## Run 15 stress 0.1688158
## Run 16 stress 0.1685561
## ... Procrustes: rmse 0.02410741 max resid 0.07368704
## Run 17 stress 0.1725844
## Run 18 stress 0.1685561
## ... Procrustes: rmse 0.02410765 max resid 0.07367428
## Run 19 stress 0.1750414
```

```
## Run 20 stress 0.1759655
## Run 21 stress 0.1773317
## Run 22 stress 0.1734958
## Run 23 stress 0.1753587
## Run 24 stress 0.1688158
## Run 25 stress 0.1759655
## Run 26 stress 0.1759655
## Run 27 stress 0.1753587
## Run 28 stress 0.1725844
## Run 29 stress 0.178165
## Run 30 stress 0.2098772
## Run 31 stress 0.1767414
## Run 32 stress 0.173496
## Run 33 stress 0.1682768
## ... Procrustes: rmse 4.19164e-06 max resid 1.576108e-05
## ... Similar to previous best
## Run 34 stress 0.1734958
## Run 35 stress 0.178165
## Run 36 stress 0.1734958
## Run 37 stress 0.1750414
## Run 38 stress 0.1682768
## ... Procrustes: rmse 6.700011e-06 max resid 2.522765e-05
## ... Similar to previous best
## Run 39 stress 0.1682768
## ... Procrustes: rmse 3.524255e-05 max resid 0.0001320547
## ... Similar to previous best
## Run 40 stress 0.1753587
## Run 41 stress 0.1682768
## ... Procrustes: rmse 1.399582e-05 max resid 3.780497e-05
## ... Similar to previous best
## Run 42 stress 0.1688158
## Run 43 stress 0.1725844
## Run 44 stress 0.1759655
## Run 45 stress 0.192892
## Run 46 stress 0.1682768
## ... Procrustes: rmse 3.165445e-05 max resid 0.000110926
## ... Similar to previous best
## Run 47 stress 0.178165
## Run 48 stress 0.178165
## Run 49 stress 0.178165
## Run 50 stress 0.1682768
## ... Procrustes: rmse 8.605362e-06 max resid 2.957725e-05
## ... Similar to previous best
## *** Best solution repeated 10 times
```

4. Merge tables to plot

```
ABUND_norm_nmds_ext <- ABUND_norm_nmds$points %>%
as.data.frame() %>%
tibble::rownames_to_column("Date") %>%
dplyr::mutate(Date = as.Date(Date)) %>%
dplyr::left_join(METADATA, by = "Date")

# Factor order for seasons
```

```
ABUND_norm_nmds_ext$Season <- factor(ABUND_norm_nmds_ext$Season,

levels = c("Summer", "Autumn", "Winter", "Spring"))
```

5. Add centroid coordinates

The centroid coordinates for each season are calculated to draw segments connecting the centroids.

```
ctd_coords <- ABUND_norm_nmds_ext %>%
  dplyr::mutate(Year = lubridate::year(Date)) %>%
  dplyr::group_by(Season) %>%
  dplyr::summarize(mean_nmds1 = mean(MDS1), mean_nmds2 = mean(MDS2), .groups = "drop") %>%
  dplyr::arrange(Season)
ctd_coords$segment_x
                        <- NA
ctd_coords$segment_y
ctd_coords$segment_xend <- NA
ctd_coords$segment_yend <- NA
for (i in 1:(nrow(ctd_coords) - 1)) {
  ctd_coords$segment_x[i] <- ctd_coords$mean_nmds1[i]</pre>
  ctd_coords$segment_y[i] <- ctd_coords$mean_nmds2[i]</pre>
  ctd_coords$segment_xend[i] <- ctd_coords$mean_nmds1[i + 1]</pre>
  ctd_coords$segment_yend[i] <- ctd_coords$mean_nmds2[i + 1]</pre>
i_last <- nrow(ctd_coords)</pre>
ctd_coords$segment_x[i_last]
                              <- ctd_coords$mean_nmds1[i_last]</pre>
ctd_coords$segment_y[i_last] <- ctd_coords$mean_nmds2[i_last]</pre>
ctd_coords$segment_xend[i_last] <- ABUND_norm_nmds_ext %>%
  dplyr::filter(Season == "Summer") %>% dplyr::summarize(mean_nmds1 = mean(MDS1)) %>% dplyr::pull(mean_
ctd_coords$segment_yend[i_last] <- ABUND_norm_nmds_ext %>%
  dplyr::filter(Season == "Summer") %>% dplyr::summarize(mean_nmds2 = mean(MDS2)) %>% dplyr::pull(mean_
```

7. Plot: MDS1 vs MDS2

```
x title <- "MDS1"; y title <- "MDS2"
x_max <- max(ABUND_norm_nmds_ext$MDS1) + max(ABUND_norm_nmds_ext$MDS1)/10
x_min <- min(ABUND_norm_nmds_ext$MDS1) - abs(min(ABUND_norm_nmds_ext$MDS1)/10)</pre>
y_max <- max(ABUND_norm_nmds_ext$MDS2) + max(ABUND_norm_nmds_ext$MDS2)/10
y min <- min(ABUND norm nmds ext$MDS2) - abs(min(ABUND norm nmds ext$MDS2)/10)
text size <- 13
season_colors <- c("#c93f1b", "#98482b", "#154360", "#3c7810")
nmds_plot_margin \leftarrow c(0.2, 1, 0.2, 0.2)
nmds_plot_mds1_vs_mds2 <- ggplot(ABUND_norm_nmds_ext, aes(MDS1, MDS2, color = Season), alpha = 0.8) +
  geom_point(alpha = 0.95, size = 3) +
  scale_color_manual(values = season_colors) +
  geom_vline(xintercept = 0, color = "gray40", linetype = "dotted") +
  geom_hline(yintercept = 0, color = "gray40", linetype = "dotted") +
  xlab(x_title) + ylab(y_title) +
  theme bw() +
  theme(
   axis.title = element_text(size = text_size + 4),
```

```
axis.text = element_text(size = text_size),
 legend.text = element_text(size = text_size),
 legend.title = element_text(size = text_size),
 plot.margin = grid::unit(nmds_plot_margin, "lines")
) +
guides(shape = guide legend(override.aes = list(size = 3)),
       color = guide_legend(override.aes = list(shape = 19, size = 3))) +
x\lim(c(x \min, x \max)) + y\lim(c(y \min, y \max)) +
annotate("text", label = paste("Stress:", round(ABUND_norm_nmds$stress, 3)),
         x = -1.4, y = 0.85, size = 3) +
geom_segment(data = ctd_coords,
             aes(x = segment_x, y = segment_y, xend = segment_xend, yend = segment_yend),
             arrow = arrow(length = grid::unit(0.1, "inches")),
             color = "gray10", alpha = 0.7, linewidth = 1) +
geom_text(data = ctd_coords, aes(x = mean_nmds1, y = mean_nmds2),
          label = c("Summer", "Autumn", "Winter", "Spring"),
          vjust = c(-0.5, 0, 1.4, 0), hjust = c(0.5, 1.2, 0, -0.3),
          fontface = "bold", size = 2, show.legend = FALSE) +
geom_text(aes(label = Date), vjust = 2, size = 1.5, check_overlap = TRUE, show.legend = FALSE)
```

8. Create box plot for MDS1

```
ABUND norm nmds ext$Season rev <- factor(ABUND norm nmds ext$Season,
                                            levels = c("Spring", "Winter", "Autumn", "Summer"))
x_title_boxplot_mds1 <- x_title</pre>
y_title_boxplot_mds1 <- "Season"</pre>
boxplot_margin_pc1 <- c(0.2, 7.5, 0.2, 4.85)
boxplot_mds1_vs_season <- ggplot(ABUND_norm_nmds_ext, aes(x = MDS1, y = Season_rev, fill = Season_rev))
  geom_boxplot() +
  scale fill manual(values = rev(season colors), name = "Season") +
  xlab(x_title_boxplot_mds1) + ylab(y_title_boxplot_mds1) +
  theme bw() +
  theme(
    axis.title.x = element_text(size = text_size + 4, margin = grid::unit(c(4,0,0,0), "mm")),
   axis.title.y = element_text(size = text_size + 1, margin = grid::unit(c(0,2,0,0), "mm")),
   axis.text.x = element text(size = text size),
   axis.text.y = element_text(size = text_size - 3),
   legend.text = element_text(size = text_size),
   legend.title = element_text(size = text_size),
   plot.margin = grid::unit(boxplot_margin_pc1, "lines")
  ) +
  xlim(c(x_min, x_max)) +
  geom\_segment(aes(x = 0.7, y = 1.5, xend = 0.7, yend = 3.5),
               color = "gray10", alpha = 0.7, linewidth = 0.1) +
  annotate("text", x = 0.75, y = 2.5, label = "***", size = 2, angle = 90)
```

9. Create boxplot for MDS2

```
x_title_boxplot_mds2 <- "Season"
y_title_boxplot_mds2 <- y_title
boxplot_margin_pc2 <- c(0.2, 0.2, 0.2)</pre>
```

```
boxplot_mds2_vs_season <- ggplot(ABUND_norm_nmds_ext, aes(x = Season_rev, y = MDS2, fill = Season_rev))
geom_boxplot() +
scale_fill_manual(values = rev(season_colors), name = "Season") +
xlab(x_title_boxplot_mds2) + ylab(y_title_boxplot_mds2) +
theme_bw() +
theme(
    axis.title.x = element_text(size = text_size + 4, margin = grid::unit(c(4,0,0,0), "mm")),
    axis.title.y = element_text(size = text_size + 4, margin = grid::unit(c(0,2,0,0), "mm")),
    axis.text = element_text(size = text_size),
    legend.text = element_text(size = text_size),
    legend.title = element_text(size = text_size),
    plot.margin = grid::unit(boxplot_margin_pc2, "lines")
) +
ylim(c(y_min, y_max))</pre>
```

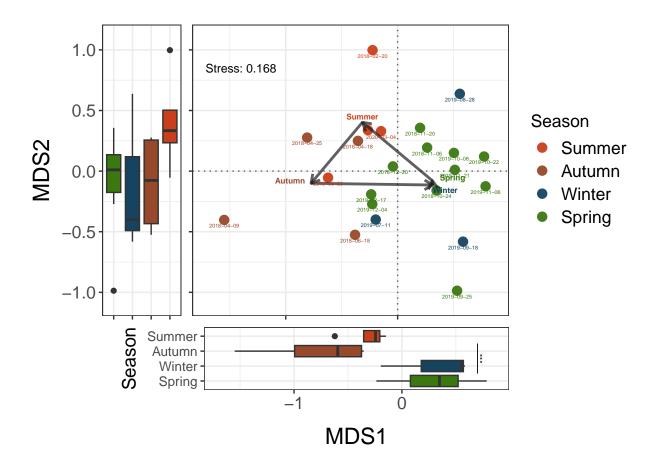
10. Merge plots

```
nmds_plot_and_mds1_boxplot <- ggpubr::ggarrange(
  boxplot_mds2_vs_season + ggpubr::rremove("legend") + ggpubr::rremove("x.title") + ggpubr::rremove("x.
  nmds_plot_mds1_vs_mds2 + ggpubr::rremove("x.title") + ggpubr::rremove("x.text") + ggpubr::rremove("y.
  ncol = 2, nrow = 1, widths = c(0.25, 0.75)
)

nmds_plot_and_mds1_and_mds2_boxplot <- ggpubr::ggarrange(
  nmds_plot_and_mds1_boxplot,
  boxplot_mds1_vs_season + ggpubr::rremove("legend"),
  nrow = 2, ncol = 1, heights = c(0.70, 0.3)
)</pre>
```

11. Visualize plot

```
nmds_plot_and_mds1_and_mds2_boxplot
```



12. Perform ANOVA Welch test: MDS1

data: MDS2 and Semester2

```
ABUND_norm_nmds_ext$Semester <- ifelse(ABUND_norm_nmds_ext$Season %in% c("Winter", "Spring"),
                                          "Winter-Spring", "Autumn-Summer")
anova_welch_mds1 <- oneway.test(MDS1 ~ Semester, data = ABUND_norm_nmds_ext, var.equal = FALSE)
anova_welch_mds1
   One-way analysis of means (not assuming equal variances)
##
## data: MDS1 and Semester
## F = 20.42, num df = 1.00, denom df = 11.95, p-value = 0.0007106
13. Perform ANOVA Welch test: MDS2
ABUND_norm_nmds_ext$Semester2 <- ifelse(ABUND_norm_nmds_ext$Season %in% c("Summer", "Spring"),
                                           "Summer-Spring", "Autumn-Winter")
anova_welch_mds2 <- oneway.test(MDS2 ~ Semester2, data = ABUND_norm_nmds_ext, var.equal = FALSE)</pre>
anova_welch_mds2
##
   One-way analysis of means (not assuming equal variances)
##
##
```

F = 0.53877, num df = 1.000, denom df = 10.491, p-value = 0.479