Untitled

2024-11-24

```r
getwd()
```

```
## [1] "/Users/meghannadzam/Desktop/Datasets and Figs/Rank abundance curves 2024"
```

```r
library(tidyverse)
```

```
## Warning: package 'ggplot2' was built under R version 4.3.2
```

```
## Warning: package 'tidyr' was built under R version 4.3.2
```

```
## -- Attaching core tidyverse packages ----------------------- tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 4.3.3
```

```
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.6-8
```

```r
library(ggplot2)

ra_earlysumENV <- read.csv(file = "seasnail_2024_ra_earlysum_ENV.csv")
ra_earlysum <- read.csv(file = "seasnail_2024_ra_earlysum.csv")
ra_earlysumENV$site_id <- as.factor(ra_earlysumENV$site_id)
ra_earlysum2 <- ra_earlysum %>% dplyr::select(AV, DN, GA, HQ, LS, PM, SD, ST, ZL) %>%
  filter(!is.na(AV))
ra_earlysum2
```

```
##   AV DN GA HQ LS PM SD ST ZL
## 1  0  0  1  1  0  0  0  0  2
## 2  0  0  0  0 12  0  0  0  3
```

```
## 3  0  0  0  0  0  0  0  1  2
## 4  1  0  0  1  0  0  0  2 12
## 5  0  0  0  0  0  0  1  3  7
## 6  0  0  0  0  0  0  0  0  8
## 7  0  0  0  0  2  0  0  0  2
## 8  1  0  0  0  0  0  1  0  1
```

```r
ra_earlysumENV$date <- ymd(ra_earlysumENV$date)


ra_earlysumENV2 <- ra_earlysumENV %>%
  mutate(date = lubridate::floor_date(date, unit = "month")) %>%
  mutate(date = as.factor(date)) %>%
  mutate(season = "earlysummer") %>%
  mutate(season = as.factor(season))


ra_earlysumENV2
```

```
##   site_id       date infection_prevalence salinity_ppt water_temp_C      season
## 1      CI 2024-05-01                    4        29.30        25.6 earlysummer
## 2      HI 2024-04-01                   15        30.40        21.3 earlysummer
## 3      JL 2024-05-01                    3        30.00        22.2 earlysummer
## 4      MM 2024-05-01                   16        29.90        22.3 earlysummer
## 5      OH 2024-05-01                   11        29.30        21.1 earlysummer
## 6     PKS 2024-04-01                    8        28.70        22.3 earlysummer
## 7      RM 2024-05-01                    4        30.78        30.4 earlysummer
## 8      SP 2024-05-01                    3        30.10        21.8 earlysummer
```

```r
#install.packages("BiodiversityR", dependencies = TRUE)
#install.packages("XQuartz")
#install.packages("import")
#install.packages("tcltk")


library(BiodiversityR)
```

```
## Warning: package 'BiodiversityR' was built under R version 4.3.2
```

```
## Loading required package: tcltk
```

```
## Warning in check_dep_version(): ABI version mismatch:
## lme4 was built with Matrix ABI version 1
## Current Matrix ABI version is 0
## Please re-install lme4 from source or restore original 'Matrix' package
```

```
## BiodiversityR 2.16-1: Use command BiodiversityRGUI() to launch the Graphical User Interface;
## to see changes use BiodiversityRGUI(changeLog=TRUE, backward.compatibility.messages=TRUE)
```

```r
RA.date.data <- BiodiversityR::rankabuncomp(ra_earlysum2, y=ra_earlysumENV2, factor = "date", return.da
```
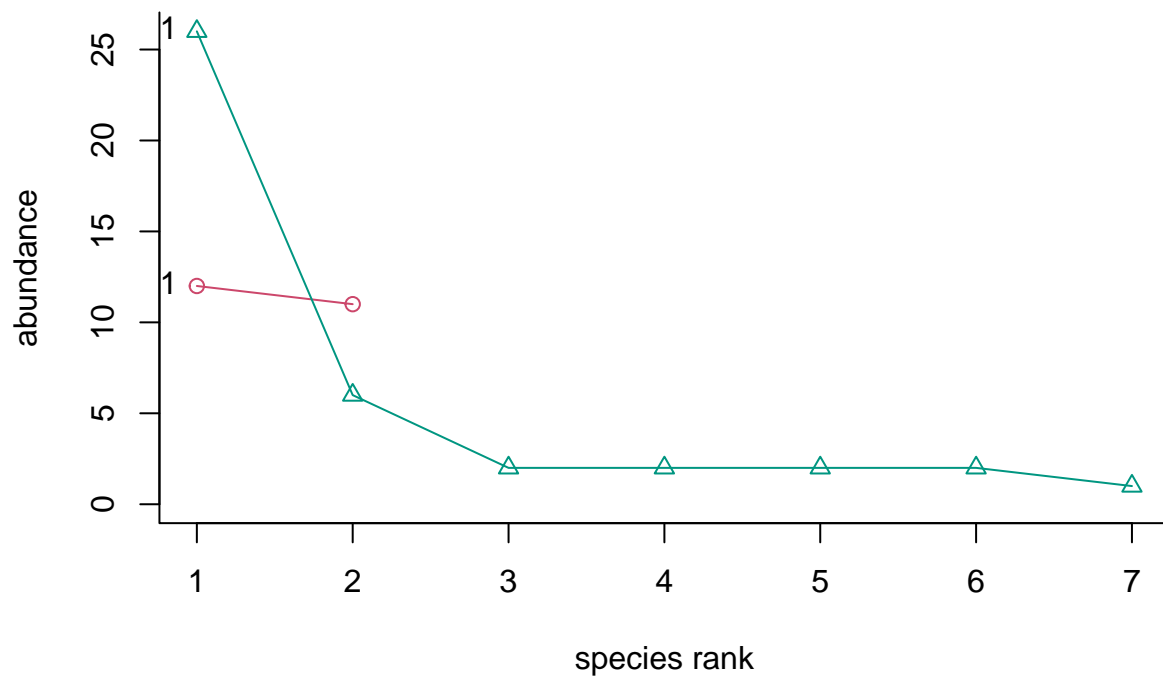
```r
#install.packages("ggrepel")
#install.packages("ggThemeAssist")
library(ggrepel)
```

```
## Warning: package 'ggrepel' was built under R version 4.3.3
```

```r
library(ggThemeAssist)

BioR.theme <- theme(
panel.background = element_blank(),
panel.border = element_blank(),
panel.grid = element_blank(),
axis.line = element_line("black"),
#text = element_text(size = 12, family="Arial"),
axis.text = element_text(size = 10, colour = "black"),
axis.title = element_text(size = 14, colour = "black"),
legend.title = element_text(size = 14),
legend.text = element_text(size = 14),
legend.key = element_blank()) +
    theme(legend.position="none")
```

```r
RA.season.data <- BiodiversityR::rankabundance(ra_earlysum2, y=ra_earlysumENV2, factor="season", level=
```

```r
RA.season.data
```

```
##    rank abundance proportion plower pupper accumfreq logabun rankfreq
## ZL    1        37       57.8   29.2   86.4      57.8     1.6     14.3
## LS    2        14       21.9  -17.6   61.4      79.7     1.1     28.6
## ST    3         6        9.4   -1.5   20.2      89.1     0.8     42.9
## AV    4         2        3.1   -1.7    8.0      92.2     0.3     57.1
## HQ    5         2        3.1   -1.6    7.9      95.3     0.3     71.4
## SD    6         2        3.1   -2.2    8.5      98.4     0.3     85.7
## GA    7         1        1.6   -2.5    5.6     100.0     0.0    100.0
```

```
plotgg1 <- ggplot(data=RA.season.data, aes(x = rank, y = abundance)) +
    scale_x_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name= NULL)) +
    scale_y_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name=NULL)) +
    geom_line(aes(color= "purple"), linewidth=1) +
    geom_point(aes(color="purple"), size=5, alpha=0.7) +
    geom_text_repel(data=subset(RA.season.data),
        aes(label=row.names(RA.season.data)),
        angle=45, nudge_x=1, nudge_y=1, show.legend=FALSE) +
    BioR.theme +
    scale_color_brewer(palette = "Set1") +
    labs(x = "Rank", y = "Abundance", title = "Rank Abundance: Early Summer 2024") +
  scale_color_manual(values = c("purple"))
```

```
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```

```
plotgg1
```

```
## Warning: ggrepel: Repulsion works correctly only for rotation angles multiple
## of 90 degrees
```

Rank Abundance: Early Summer 2024
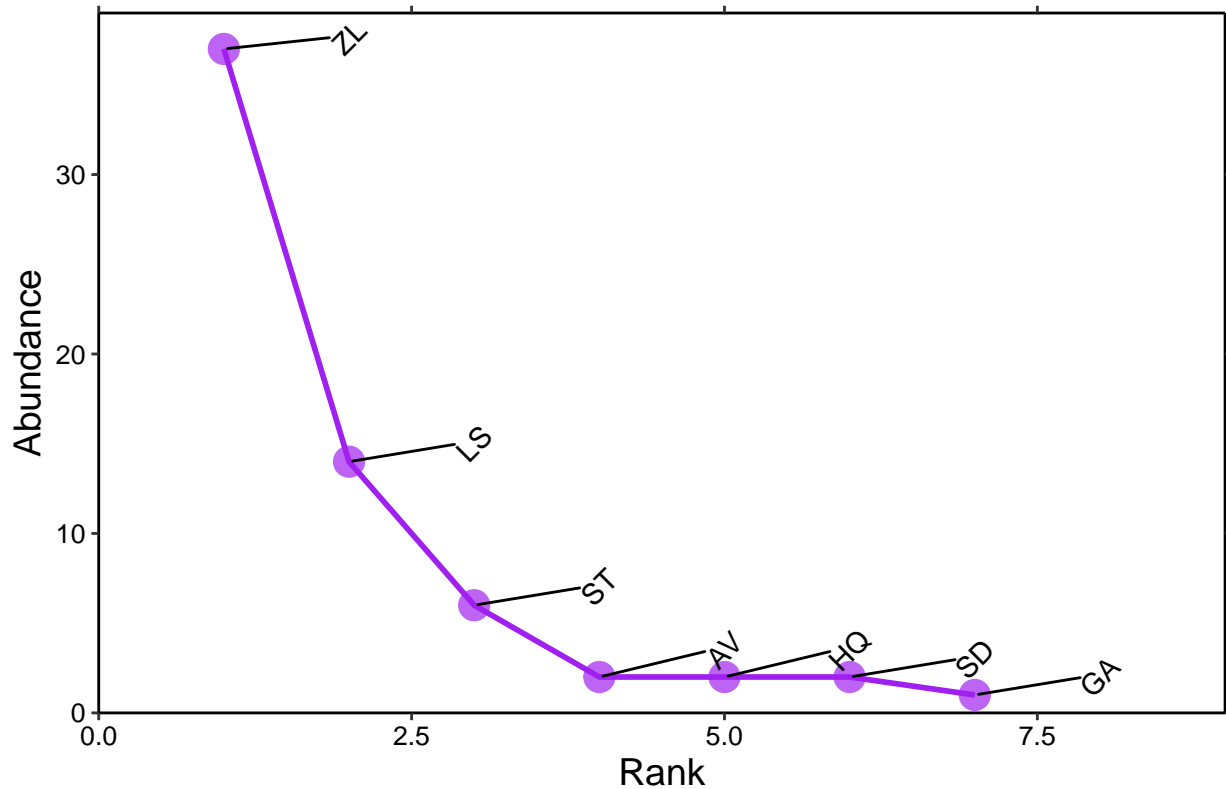

```r
ra_latesumENV <- read.csv(file = "seasnail_2024_ra_latesum_ENV.csv")
ra_latesum <- read.csv(file = "seasnail_2024_ra_latesum.csv")
ra_latesumENV$site_id <- as.factor(ra_latesumENV$site_id)
ra_latesum2 <- ra_latesum %>% dplyr::select(AV, DN, GA, HQ, LS, PM, SD, ST, ZL) %>%
  filter(!is.na(AV))
ra_latesumENV2 <- ra_latesumENV %>% dplyr::select(site_id, date, salinity_ppt, water_temp_C) %>%
  filter(!is.na(date))
ra_latesum2
```

```
##   AV DN GA HQ LS PM SD ST ZL
## 1  0  0  0  1  0  0  2  0  2
## 2  0  0  0  0  2  0  0  2 13
## 3  0  0  0  0  0  0  0  0  1
## 4  0  1  0  1  2  0  1  0  6
## 5  0  0  0  0  1  0  2  1 19
## 6  0  3  0  0  0  0  0  4 13
## 7  0  0  0  0  1  0  0  0  1
## 8  0  0  0  0  0  0  0  1  6
## 9  0  0  0  0  3  0  0  0  1
```

```r
ra_latesumENV2
```

```
##   site_id     date salinity_ppt water_temp_C
## 1      HI 20240614         31.5         28.3
## 2     IMS 20240711         32.5         33.4
```

```
## 3       JL 20240702         33.3         29.6
## 4       MM 20240616         33.2         33.3
## 5       MP 20240703         31.0         28.5
## 6       OH 20240616         32.5         28.0
## 7      PKS 20240617         34.0         30.9
## 8       RM 20240705         33.0         31.2
## 9       SP 20240702         32.0         31.4
```

```r
ra_latesumENV2$date <- ymd(ra_latesumENV2$date)

ra_latesumENV3 <- ra_latesumENV2 %>%
  mutate(date = lubridate::floor_date(date, unit = "month")) %>%
  mutate(date = as.factor(date)) %>%
  mutate(season = "latesummer") %>%
  mutate(season = as.factor(season))

ra_latesumENV3
```

```
##   site_id       date salinity_ppt water_temp_C     season
## 1      HI 2024-06-01         31.5         28.3 latesummer
## 2     IMS 2024-07-01         32.5         33.4 latesummer
## 3      JL 2024-07-01         33.3         29.6 latesummer
## 4      MM 2024-06-01         33.2         33.3 latesummer
## 5      MP 2024-07-01         31.0         28.5 latesummer
## 6      OH 2024-06-01         32.5         28.0 latesummer
## 7     PKS 2024-06-01         34.0         30.9 latesummer
## 8      RM 2024-07-01         33.0         31.2 latesummer
## 9      SP 2024-07-01         32.0         31.4 latesummer
```

```r
BioR.theme <- theme(
panel.background = element_blank(),
panel.border = element_blank(),
panel.grid = element_blank(),
axis.line = element_line("black"),
#text = element_text(size = 12, family="Arial"),
axis.text = element_text(size = 10, colour = "black"),
axis.title = element_text(size = 14, colour = "black"),
legend.title = element_text(size = 14),
legend.text = element_text(size = 14),
legend.key = element_blank()) +
    theme(legend.position="none")
```

```r
RA.season.data2 <- BiodiversityR::rankabundance(ra_latesum2, y=ra_latesumENV3, factor="season", level="]

RA.season.data2
```

```
##    rank abundance proportion plower pupper accumfreq logabun rankfreq
## ZL    1        62       68.9   56.3   81.5      68.9     1.8     16.7
## LS    2         9       10.0   -0.4   20.4      78.9     1.0     33.3
## ST    3         8        8.9    1.3   16.4      87.8     0.9     50.0
## SD    4         5        5.6   -1.1   12.2      93.3     0.7     66.7
## DN    5         4        4.4   -2.5   11.4      97.8     0.6     83.3
## HQ    6         2        2.2   -1.6    6.1     100.0     0.3    100.0
```

```
plotgg2 <- ggplot(data=RA.season.data2, aes(x = rank, y = abundance)) +
    scale_x_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name= NULL)) +
    scale_y_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name=NULL)) +
    geom_line(aes(color= "darkorange"), size=1) +
    geom_point(aes(color="darkorange"), size=5, alpha=0.7) +
    geom_text_repel(data=subset(RA.season.data2),
        aes(label=row.names(RA.season.data2)),
        angle=45, nudge_x=1, nudge_y=1, show.legend=FALSE) +
    BioR.theme +
    scale_color_brewer(palette = "Set1") +
    labs(x = "Rank", y = "Abundance", title = "Rank Abundance: Late Summer 2024") +
  scale_color_manual(values = c("darkorange"))
```

```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use 'linewidth' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

```
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```
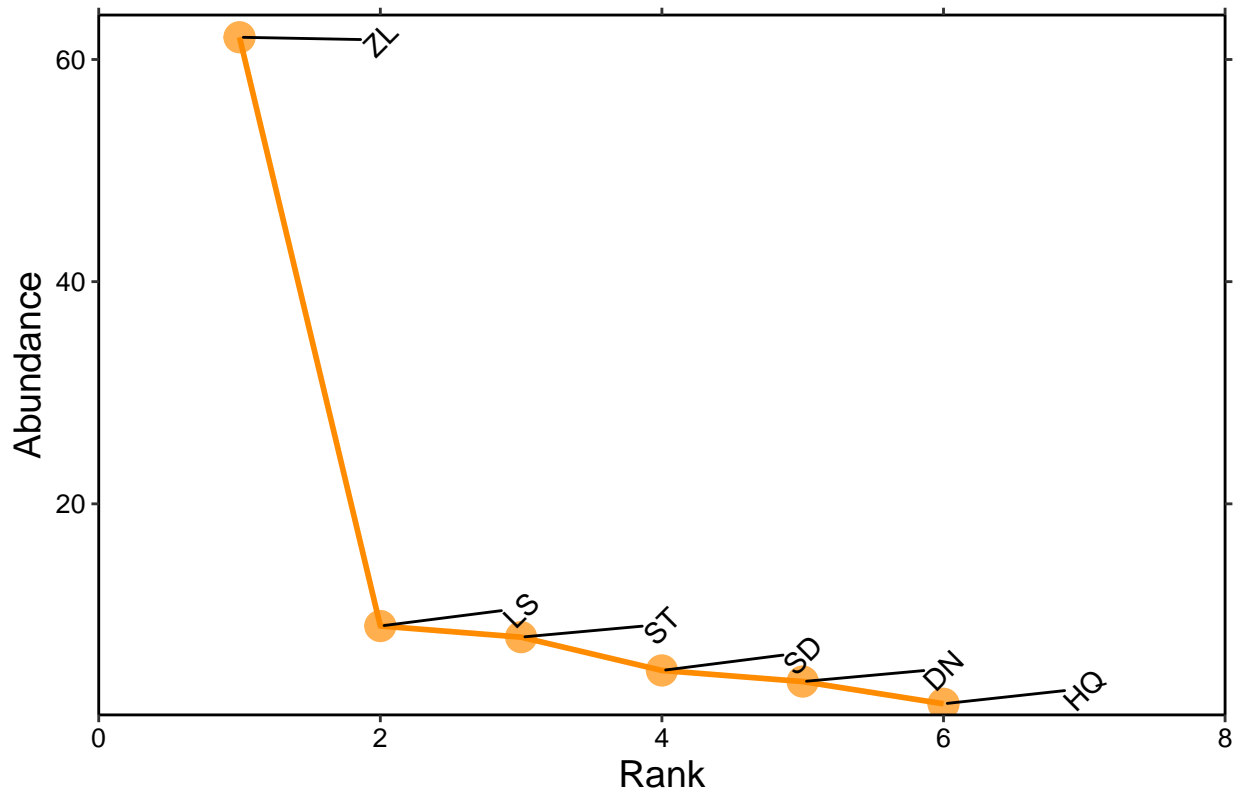
```
plotgg2
```

```
## Warning: ggrepel: Repulsion works correctly only for rotation angles multiple
## of 90 degrees
```

Rank Abundance: Late Summer 2024


```r
ra_fallENV <- read.csv(file = "seasnail_2024_ra_fall_ENV.csv")
ra_fall <- read.csv(file = "seasnail_2024_ra_fall_2.csv")
ra_fallENV$site_id <- as.factor(ra_fallENV$site_id)
ra_fall2 <- ra_fall %>% dplyr::select(AV, DN, GA, HQ, LS, PM, SD, ST, ZL) %>%
  filter(!is.na(AV))
ra_fallENV2 <- ra_fallENV %>% dplyr::select(site_id, date, salinity_ppt, water_temp_C) %>%
  filter(!is.na(date))
ra_fall2
```

```
##    AV DN GA HQ LS PM SD ST ZL
## 1   0  0  0  0  6  0  0  0  2
## 2   0  0  0  0  0  0  0  0  1
## 3   0  0  0  0  6  0  0  4  9
## 4   1  0  0  0  3  0  0  0  1
## 5   0  0  0  0  4  0  1  0  2
## 6   0  0  0  0  8  0  0  0  5
## 7   0  0  0  0  8  0  0  0  1
## 8   0  0  0  0  6  0  0  0  1
## 9   0  0  0  0 11  0  0  0  1
## 10  0  0  0  0  1  0  0  0  3
```

```r
ra_latesumENV2
```

```
##   site_id       date salinity_ppt water_temp_C
## 1      HI 2024-06-14         31.5         28.3
```

```
## 2      IMS 2024-07-11          32.5          33.4
## 3       JL 2024-07-02          33.3          29.6
## 4       MM 2024-06-16          33.2          33.3
## 5       MP 2024-07-03          31.0          28.5
## 6       OH 2024-06-16          32.5          28.0
## 7      PKS 2024-06-17          34.0          30.9
## 8       RM 2024-07-05          33.0          31.2
## 9       SP 2024-07-02          32.0          31.4
```

```
ra_fallENV2$date <- ymd(ra_fallENV2$date)


ra_fallENV3 <- ra_fallENV2 %>%
  mutate(date = lubridate::floor_date(date, unit = "month")) %>%
  mutate(date = as.factor(date)) %>%
  mutate(season = "latesummer") %>%
  mutate(season = as.factor(season))

ra_fallENV3
```

```
##     site_id       date salinity_ppt water_temp_C      season
## 1        CI 2024-08-01         31.5         27.3 latesummer
## 2        HI 2024-08-01         33.9         33.3 latesummer
## 3       IMS 2024-08-01         28.8         27.2 latesummer
## 4        JL 2024-09-01         28.8         29.0 latesummer
## 5        MM 2024-09-01         27.4         30.4 latesummer
## 6        MP 2024-08-01         28.2         29.0 latesummer
## 7        OH 2024-09-01         26.8         29.5 latesummer
## 8       PKS 2024-08-01         27.9         27.3 latesummer
## 9        RM 2024-09-01         24.9         28.7 latesummer
## 10       SP 2024-10-01         26.8         22.9 latesummer
```

```
BioR.theme <- theme(
panel.background = element_blank(),
panel.border = element_blank(),
panel.grid = element_blank(),
axis.line = element_line("black"),
#text = element_text(size = 12, family="Arial"),
axis.text = element_text(size = 10, colour = "black"),
axis.title = element_text(size = 14, colour = "black"),
legend.title = element_text(size = 14),
legend.text = element_text(size = 14),
legend.key = element_blank()) +
    theme(legend.position="none")
```

```
RA.season.data3 <- BiodiversityR::rankabundance(ra_fall2, y=ra_fallENV3, factor="season", level="latesu

RA.season.data3
```

```
##    rank abundance proportion plower pupper accumfreq logabun rankfreq
## LS    1        53       62.4   40.9   83.9      62.4     1.7       20
## ZL    2        26       30.6   16.0   45.1      92.9     1.4       40
## ST    3         4        4.7   -4.6   14.0      97.6     0.6       60
## AV    4         1        1.2   -1.6    4.0      98.8     0.0       80
## SD    5         1        1.2   -1.6    3.9     100.0     0.0      100
```

9

```
plotgg3 <- ggplot(data=RA.season.data3, aes(x = rank, y = abundance)) +
    scale_x_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name= NULL)) +
    scale_y_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name=NULL)) +
    geom_line(aes(color= "darkgreen"), size=1) +
    geom_point(aes(color="darkgreen"), size=5, alpha=0.7) +
    geom_text_repel(data=subset(RA.season.data3),
        aes(label=row.names(RA.season.data3)),
        angle=0, nudge_x=1, nudge_y=1, show.legend=FALSE) +
    BioR.theme +
    scale_color_brewer(palette = "Set1") +
    labs(x = "Rank", y = "Abundance", title = "Rank Abundance: Fall 2024") +
  scale_color_manual(values = c("darkgreen"))
```

```
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```
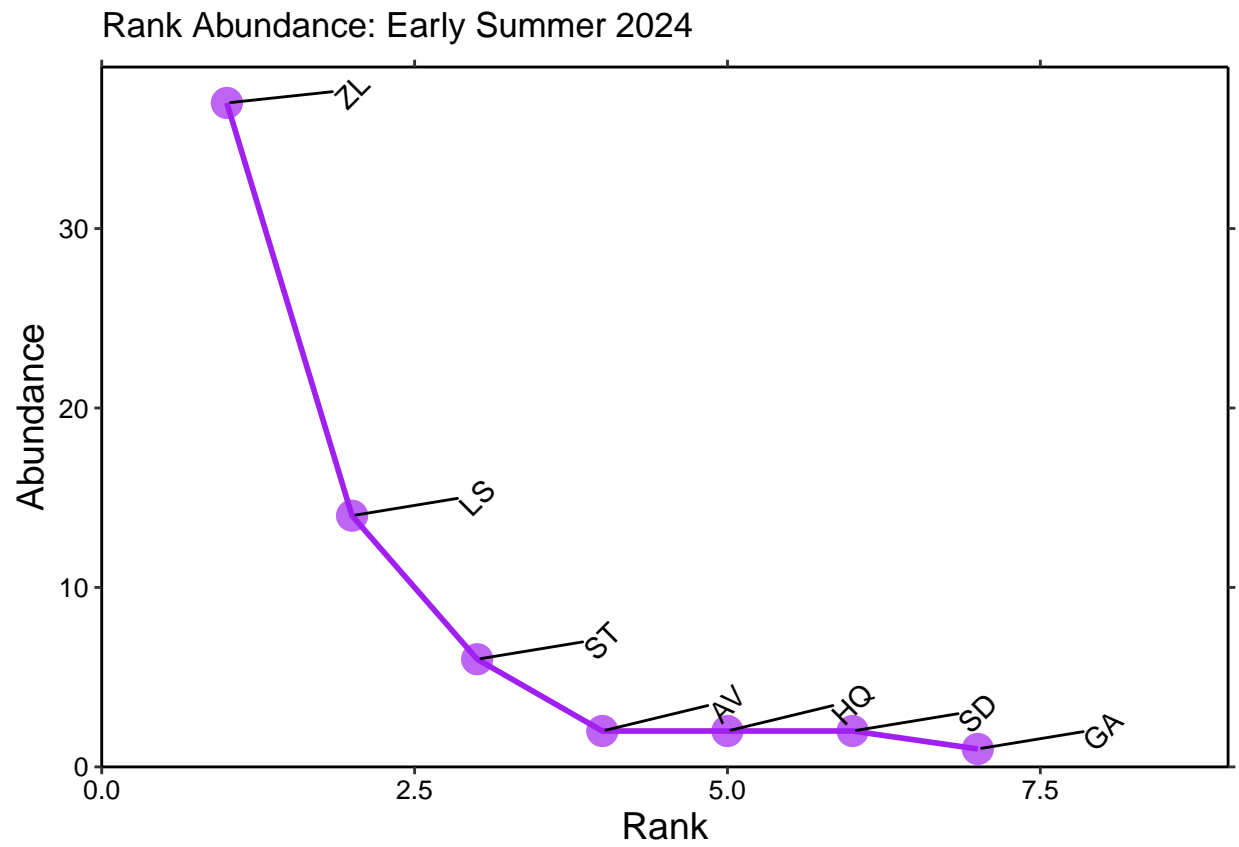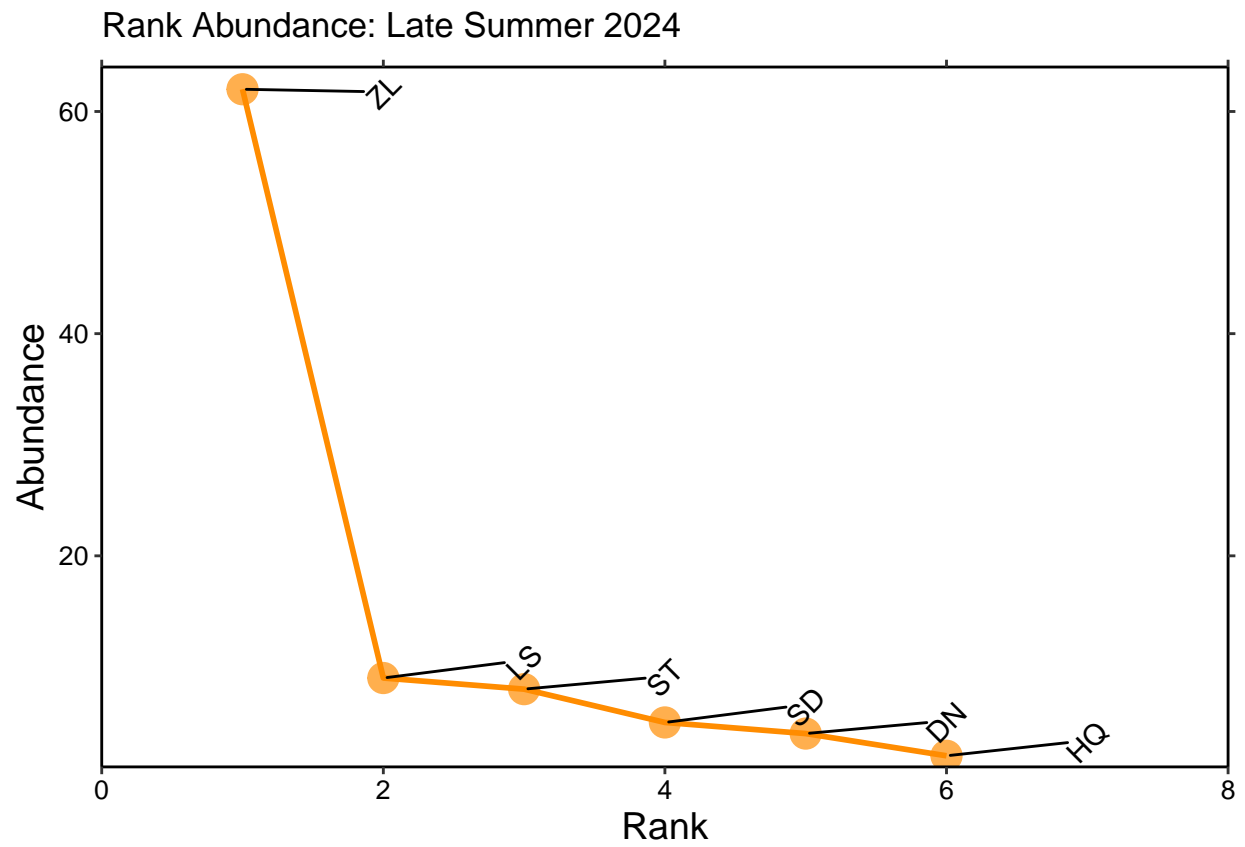
plotgg3
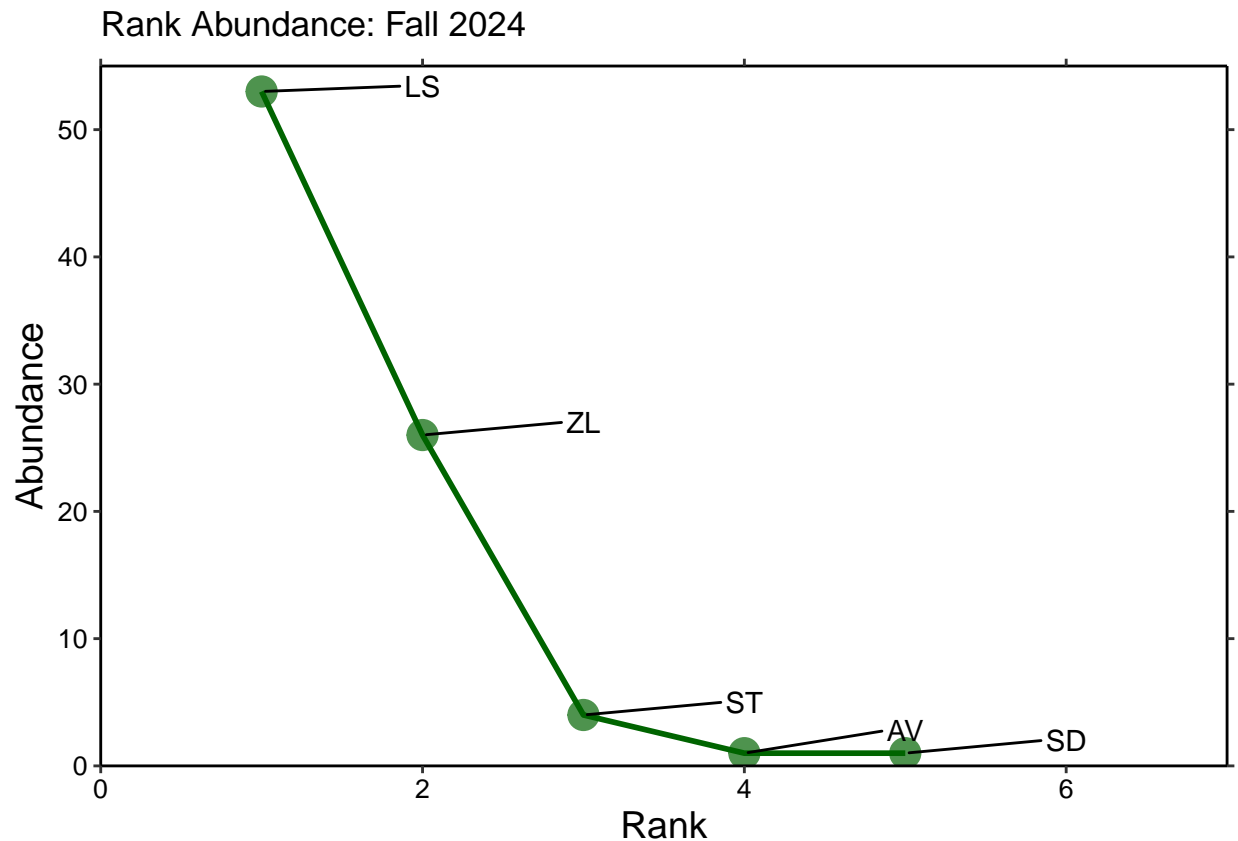
plotgg1

```
## Warning: ggrepel: Repulsion works correctly only for rotation angles multiple
## of 90 degrees
```
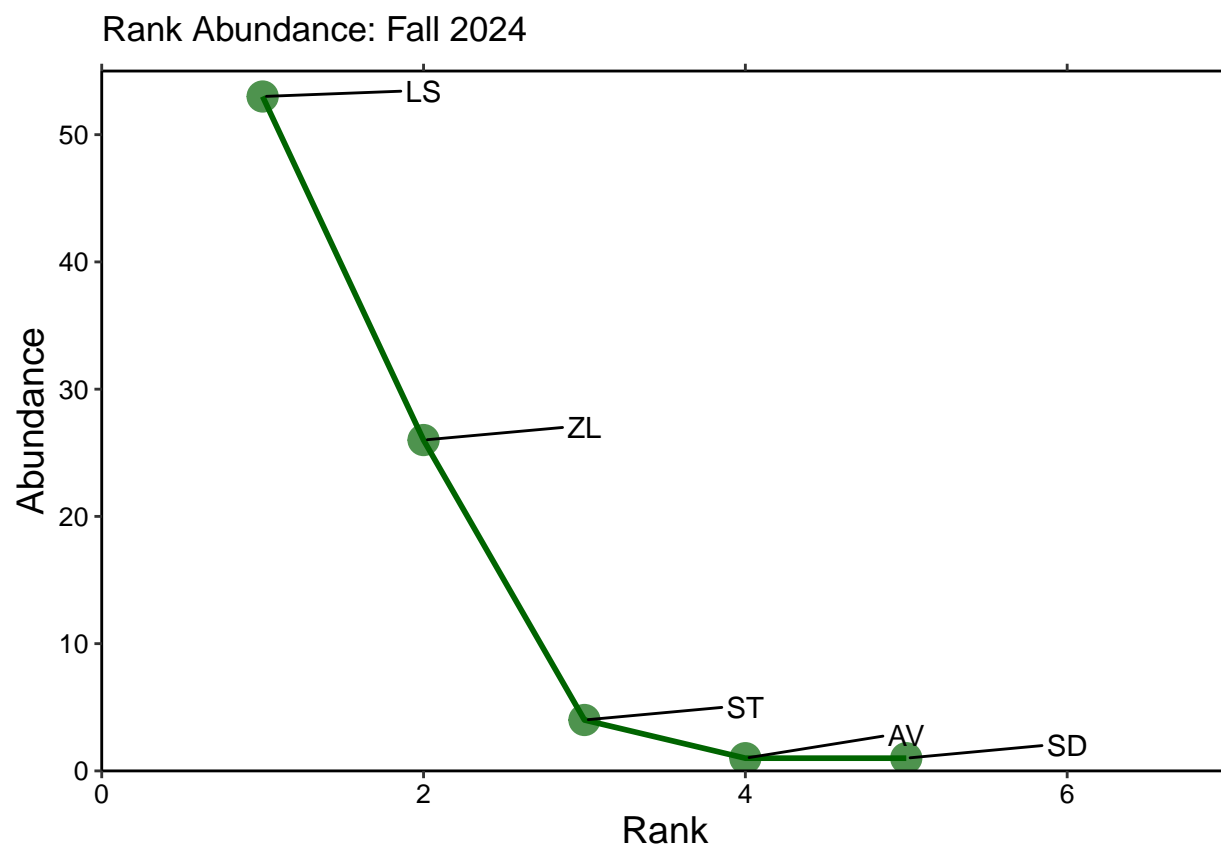
Rank Abundance: Early Summer 2024

```
plotgg2
```

```
## Warning: ggrepel: Repulsion works correctly only for rotation angles multiple
## of 90 degrees
```

Rank Abundance: Late Summer 2024


```
plotgg3
```
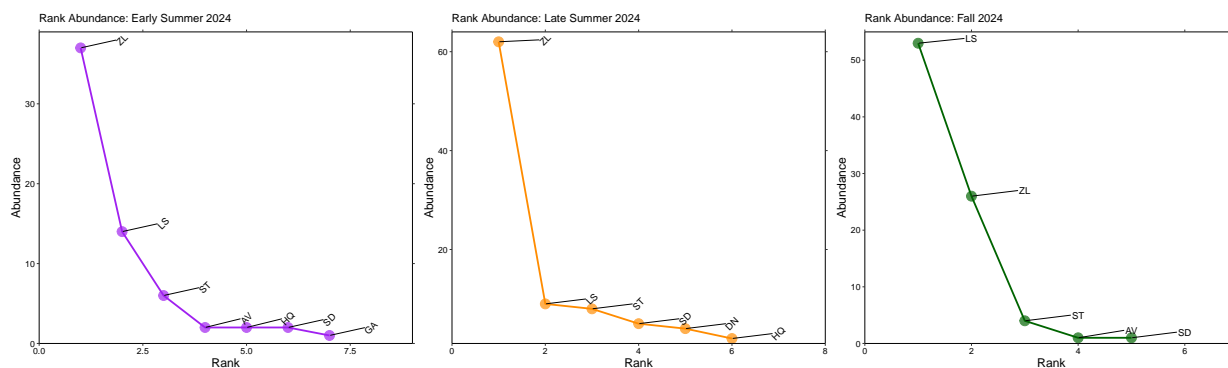
Rank Abundance: Fall 2024


```
#install.packages("patchwork")
```

```
library(patchwork)
```

```
## Warning: package 'patchwork' was built under R version 4.3.3
```

```
plotgg1 + plotgg2 + plotgg3
```

```
## Warning: ggrepel: Repulsion works correctly only for rotation angles multiple of 90 degrees
## ggrepel: Repulsion works correctly only for rotation angles multiple of 90 degrees
```


PKS rank curve

```
knitr::opts_chunk$set(echo = TRUE)
knitr::opts_knit$set(root.dir = "/Users/meghannadzam/Desktop/Datasets and Figs/Rank abundance curves 20
```

```
ra_PKSENV <- read.csv(file = "seasnail_2024_ra_PKS_ENV.csv")
ra_PKS <- read.csv(file = "seasnail_2024_ra_PKS.csv")
ra_PKSENV$site_id <- as.factor(ra_PKSENV$site_id)
ra_PKS2 <- ra_PKS %>% dplyr::select(AV, DN, GA, HQ, LS, PM, SD, ST, ZL) %>%
  filter(!is.na(AV))
ra_PKS2
```

```
##   AV DN GA HQ LS PM SD ST ZL
## 1  0  0  0  0  0  0  0  0  8
## 2  0  0  0  0  1  0  0  0  1
## 3  0  0  0  0  6  0  0  0  1
```

```
ra_PKSENV$date <- ymd(ra_PKSENV$date)

ra_PKSENV2 <- ra_PKSENV %>%
  mutate(date = lubridate::floor_date(date, unit = "month")) %>%
  mutate(date = as.factor(date))%>%
  filter(!is.na(date))
ra_PKSENV3 <- ra_PKSENV2 %>% dplyr::select(site_id, date, salinity_ppt, water_temp_C) %>%
  filter(!is.na(date))

ra_PKSENV3
```

```
##   site_id       date salinity_ppt water_temp_C
## 1     PKS 2024-04-01         28.7         22.3
## 2     PKS 2024-06-01         34.0         30.9
## 3     PKS 2024-08-01         27.9         27.3
```

```
BioR.theme <- theme(
panel.background = element_blank(),
panel.border = element_blank(),
panel.grid = element_blank(),
axis.line = element_line("black"),
#text = element_text(size = 12, family="Arial"),
axis.text = element_text(size = 10, colour = "black"),
axis.title = element_text(size = 14, colour = "black"),
legend.title = element_text(size = 14),
legend.text = element_text(size = 14),
legend.key = element_blank()) +
    theme(legend.position="none")
```

```
RA.siteid.data2 <- BiodiversityR::rankabundance(ra_PKS2, y=ra_PKSENV3, factor="site_id", level="PKS")

RA.siteid.data2
```

```
##    rank abundance proportion plower pupper accumfreq logabun rankfreq
## ZL    1        10       58.8  -81.9  199.5      58.8     1.0       50
## LS    2         7       41.2  -99.5  181.9     100.0     0.8      100
```

```
plotgg4 <- ggplot(data=RA.siteid.data2, aes(x = rank, y = abundance)) +
    scale_x_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name= NULL)) +
    scale_y_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name=NULL)) +
    geom_line(aes(color= "darkturquoise"), size=1) +
    geom_point(aes(color="darkturquoise"), size=5, alpha=0.7) +
    geom_text_repel(data=subset(RA.siteid.data2),
        aes(label=row.names(RA.siteid.data2)),
        angle=0, nudge_x=1, nudge_y=1, show.legend=FALSE) +
    BioR.theme +
    scale_color_brewer(palette = "Set1") +
    labs(x = "Rank", y = "Abundance", title = "Rank Abundance: Pine Knoll Shores 2024") +
  scale_color_manual(values = c("darkturquoise"))
```
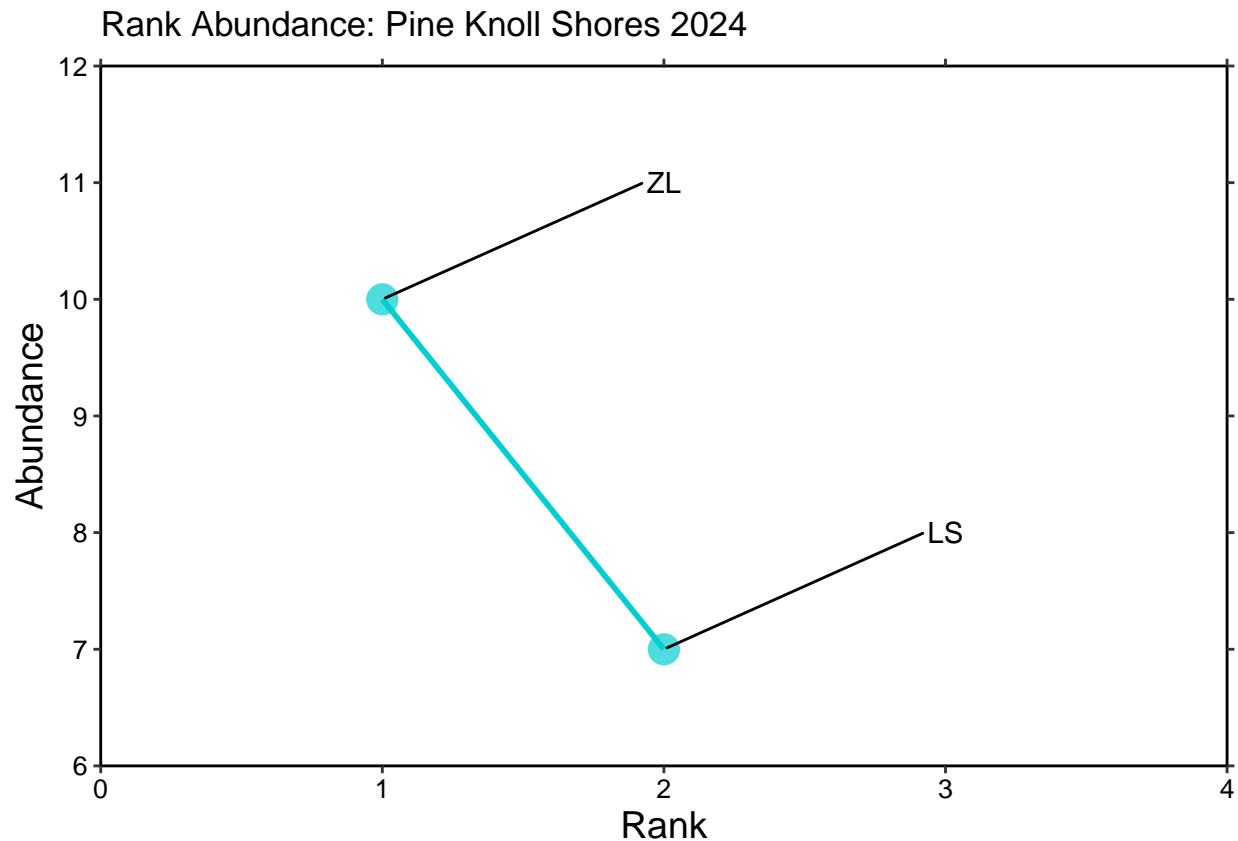
```
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```

```
plotgg4
```


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```
ggplot2::ggsave("Datasets and Figs/plotgg4.png", create.dir = TRUE)
```

```
## Saving 6.5 x 4.5 in image
```