Praccomp Final Project

Setting Working Directory

```
knitr::opts_chunk$set(echo = TRUE)
knitr::opts_knit$set(root.dir = "C:/Users/Grace/praccomp2024/final_project")
```

Loading necessary packages

```
#Rank abundance curves for trematode diversity data
library(vegan)
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.6-8
```

```
library(BiodiversityR)
```

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

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

```
library(ggplot2)
library(ggrepel)
```

```
## Warning: package 'ggrepel' was built under R version 4.4.2
```

```
library(patchwork)
```

```
## Warning: package 'patchwork' was built under R version 4.4.2
```

```
library(tidyverse)
```

```
## — Attaching core tidyverse packages ———————————— tidyverse 2.0.0 —
## ✓ dplyr      1.1.4      ✓ readr       2.1.5
## ✓ forcats    1.0.0      ✓ stringr     1.5.1
## ✓ lubridate  1.9.3      ✓ tibble      3.2.1
## ✓ purrr      1.0.2      ✓ tidyr       1.3.1
```

```
## — Conflicts ———————————————————————— tidyverse_conflicts() —
## ✗ dplyr::filter() masks stats::filter()
## ✗ dplyr::lag()    masks stats::lag()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
e errors
```

```
#Oyster density plots
library(ggplot2)
library(MASS)
```

```
##
## Attaching package: 'MASS'
##
## The following object is masked from 'package:dplyr':
##
##     select
##
## The following object is masked from 'package:patchwork':
##
##     area
```

Trematode Diversity Analyses

Loading in the data

```
#Loading in the data
BIOR_5YR <- read.csv("BIOR_5YR.csv")
BIOR_5YR_env <- read.csv("BIOR_5YR_env.csv")

BIOR_Pre <- read.csv("BIOR_Pre.csv")
BIOR_1YR <- read.csv("BIOR_1YR.csv")
BIOR_PRE_1YR_env <- read.csv("BIOR_PRE_1YR_env.csv")
```

Changing Site Type to a Factor in the Environmental data

```
BIOR_5YR_env$site_type <-as.factor(BIOR_5YR_env$site_type)
class(BIOR_5YR_env$site_type)
```
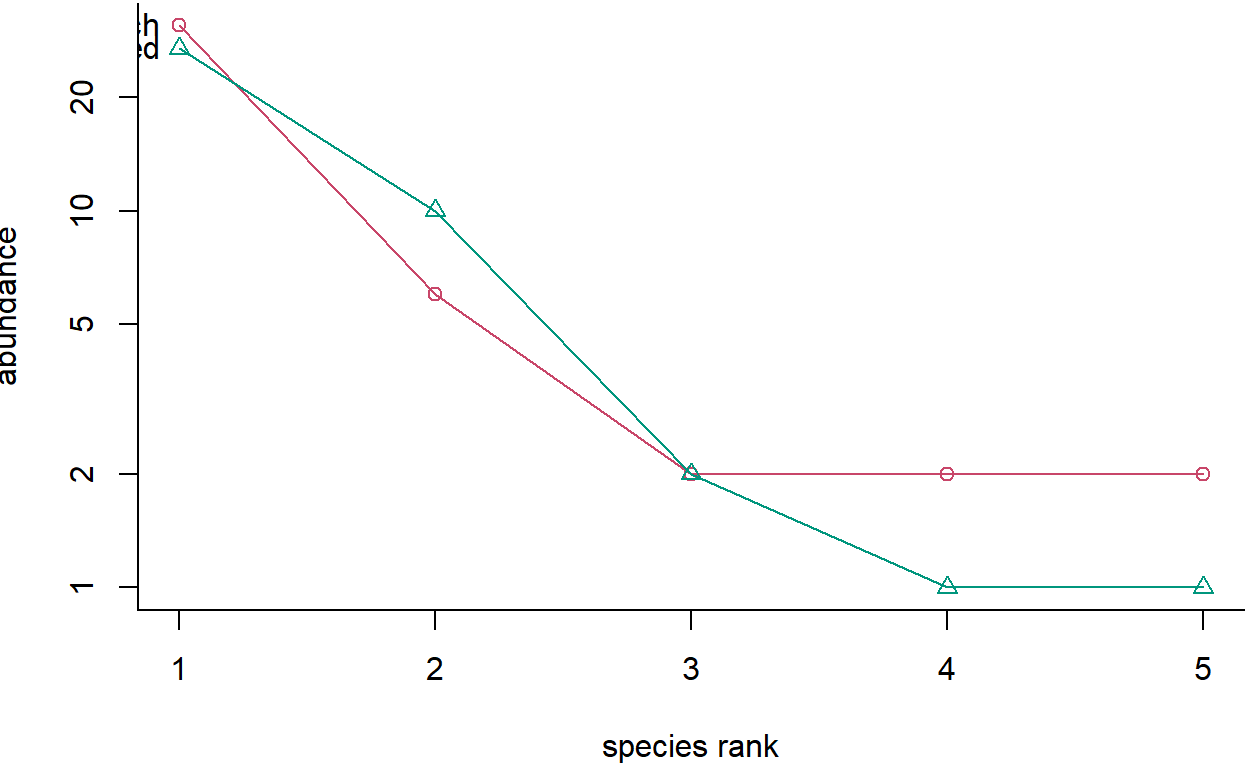
```
## [1] "factor"
```

```
BIOR_PRE_1YR_env$site_type <-as.factor(BIOR_PRE_1YR_env$site_type)
class(BIOR_PRE_1YR_env$site_type)
```

```
## [1] "factor"
```

Plots within the BiodiversityR package functions

```
#5YR - quick plot

rankabuncomp(BIOR_5YR, y=BIOR_5YR_env, factor='site_type',
    scale='logabun', legend=FALSE)
```
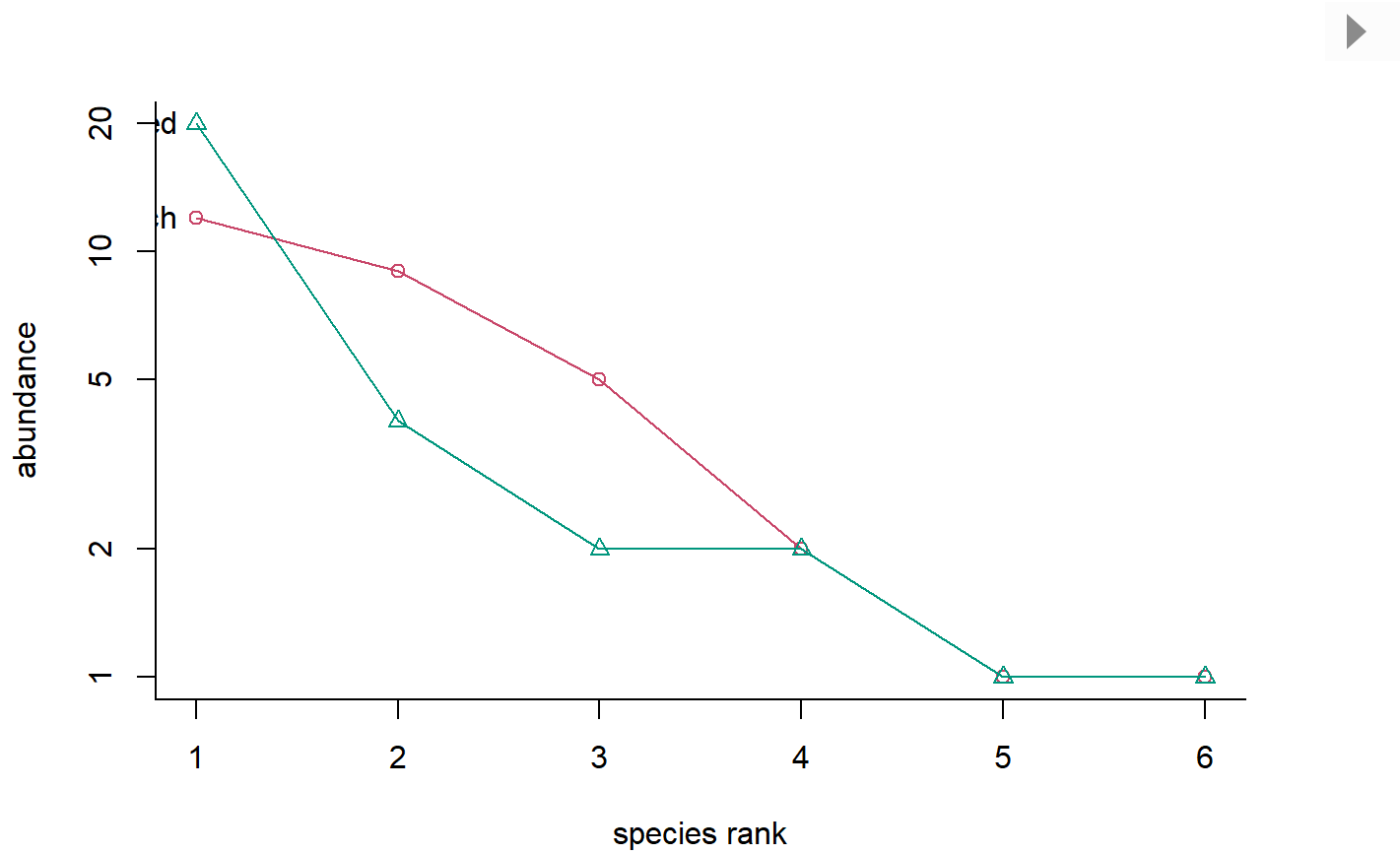

Grouping	species	labelit	r...	abunda...	proportion	plo...	pup...	accumfreq	logab...
<chr>	<chr>	<lgl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
Loose Cultch	LS	TRUE	1	31	72.1	33.7	110.4	72.1	1.5
Loose Cultch	ST	TRUE	2	6	14.0	-1.1	29.0	86.0	0.8
Loose Cultch	GA	TRUE	3	2	4.7	-7.0	16.3	90.7	0.3

Grouping	species	labelit	r...	abunda...	proportion	plo...	pup...	accumfreq	logab...
<chr>	<chr>	<lgl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
Loose Cultch	HQ	FALSE	4	2	4.7	0.4	8.9	95.3	0.3
Loose Cultch	ZL	FALSE	5	2	4.7	-7.0	16.3	100.0	0.3
Restored	LS	TRUE	1	27	65.9	56.3	75.4	65.9	1.4
Restored	ST	TRUE	2	10	24.4	11.9	36.9	90.2	1.0
Restored	HQ	TRUE	3	2	4.9	1.4	8.4	95.1	0.3
Restored	PM	FALSE	4	1	2.4	-12.2	17.1	97.6	0.0
Restored	SD	FALSE	5	1	2.4	-8.0	12.9	100.0	0.0

```
#1YR - quick plot

rankabuncomp(BIOR_1YR, y=BIOR_PRE_1YR_env, factor='site_type',
    scale='logabun', legend=FALSE)
```
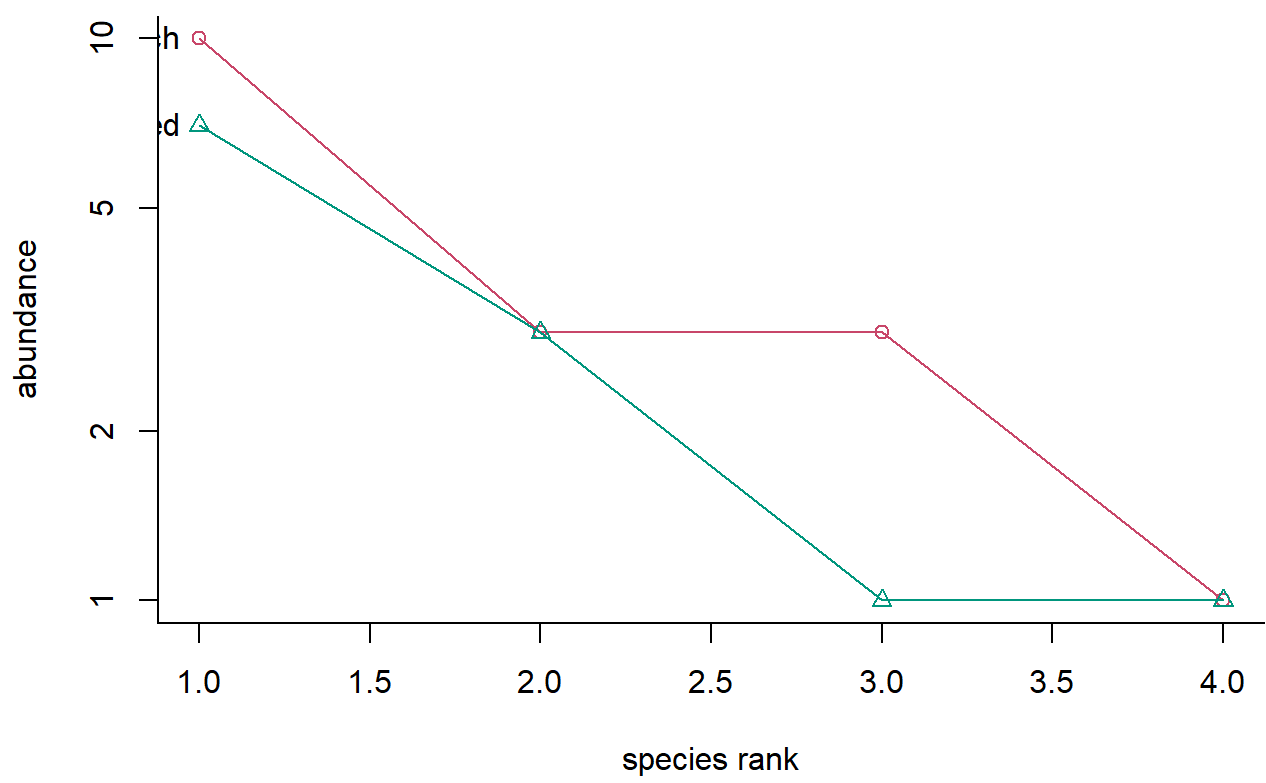

Grouping	species	labelit	r...	abunda...	proportion	plo...	pup...	accumfreq	logab...
<chr>	<chr>	<lgl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
Loose Cultch	LS	TRUE	1	12	40.0	NaN	NaN	40.0	1.1

Grouping <chr>	species <chr>	labelit <lgl>	r... <dbl>	abunda... <dbl>	proportion <dbl>	plo... <dbl>	pup... <dbl>	accumfreq <dbl>	logab... <dbl>
Loose Cultch	ZL	TRUE	2	9	30.0	NaN	NaN	70.0	1.0
Loose Cultch	ST	TRUE	3	5	16.7	NaN	NaN	86.7	0.7
Loose Cultch	SD	FALSE	4	2	6.7	NaN	NaN	93.3	0.3
Loose Cultch	GA	FALSE	5	1	3.3	NaN	NaN	96.7	0.0
Loose Cultch	HQ	FALSE	6	1	3.3	NaN	NaN	100.0	0.0
Restored	LS	TRUE	1	20	66.7	22.9	110.5	66.7	1.3
Restored	ZL	TRUE	2	4	13.3	-15.4	42.1	80.0	0.6
Restored	SD	TRUE	3	2	6.7	-12.9	26.2	86.7	0.3
Restored	ST	FALSE	4	2	6.7	-24.3	37.6	93.3	0.3

#Pre - quick plot

```
rankabuncomp(BIOR_Pre, y=BIOR_PRE_1YR_env, factor='site_type',
    scale='logabun', legend=FALSE)
```

Grouping	species	labelit	r...	abunda...	proportion	plo...	pup...	accumfreq	logab...
<chr>	<chr>	<lgl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
Loose Cultch	LS	TRUE	1	10	58.8	-9.5	127.2	58.8	1.0
Loose Cultch	ST	TRUE	2	3	17.6	-46.5	81.8	76.5	0.5
Loose Cultch	ZL	TRUE	3	3	17.6	-9.3	44.6	94.1	0.5
Loose Cultch	HQ	FALSE	4	1	5.9	-23.9	35.6	100.0	0.0
Restored	LS	TRUE	1	7	58.3	-17.9	134.6	58.3	0.8
Restored	HQ	TRUE	2	3	25.0	-31.0	81.0	83.3	0.5
Restored	DN	TRUE	3	1	8.3	-32.1	48.8	91.7	0.0
Restored	ZL	FALSE	4	1	8.3	-27.9	44.6	100.0	0.0

8 rows | 1-10 of 11 columns

Defining a theme to use in the ggplot curves

```
#This is an online theme that is provided along with rank-abundance curve code, I included it here to help enhance the visual produced by the rank abundance curve plots.
BioR.theme <- theme(
        panel.background = element_blank(),
        panel.border = element_blank(),
        panel.grid = element_blank(),
        axis.line = element_line("gray25"),
        text = element_text(size = 12),
        axis.text = element_text(size = 10, colour = "gray25"),
        axis.title = element_text(size = 14, colour = "gray25"),
        legend.title = element_text(size = 14),
        legend.text = element_text(size = 14),
        legend.key = element_blank())
```
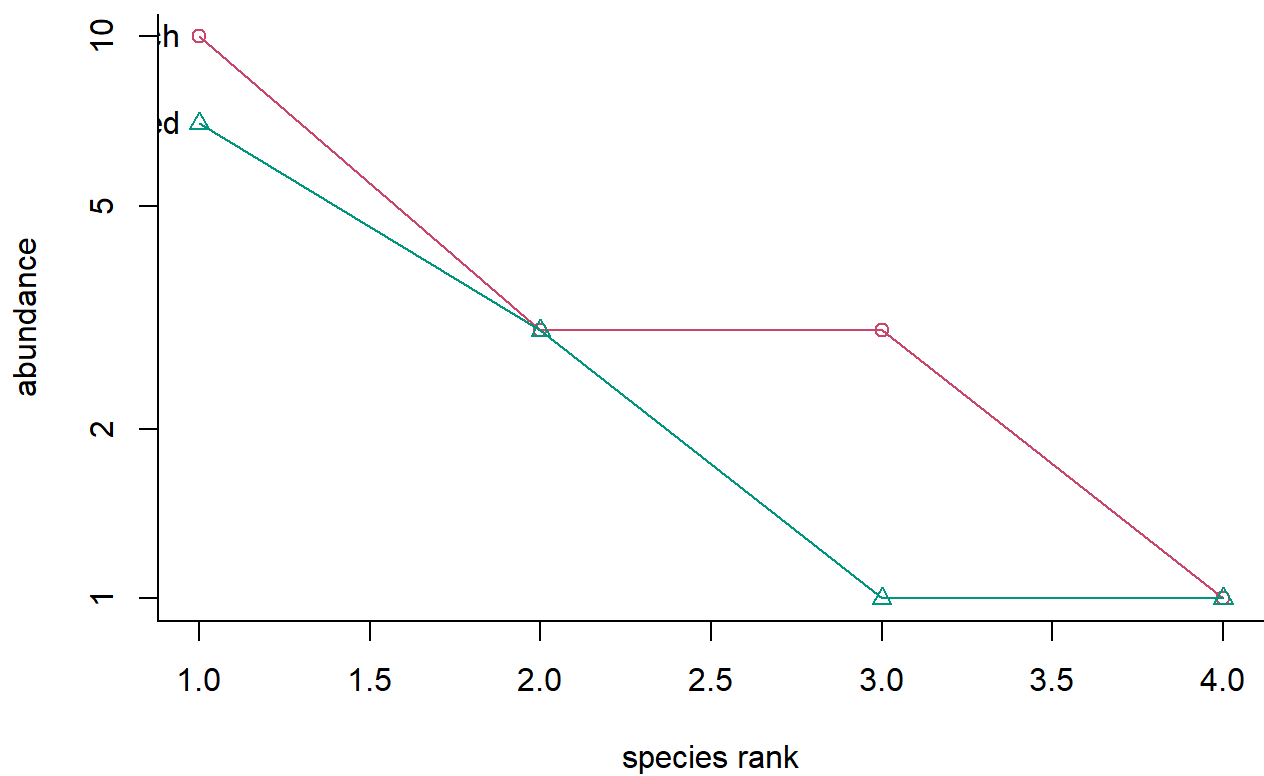
Making Rank-Abundance Curves using ggplot

```
#fancier plots

#PRE

fancy_Pre <- rankabuncomp(BIOR_Pre, y=BIOR_PRE_1YR_env, factor='site_type', scale='logabun',  return.data=TRUE, legend=FALSE)
```

fancy_Pre

| Grouping <chr>	species <chr>	labelit <lgl>	r… <dbl>	abunda… <dbl>	proportion <dbl>	plo… <dbl>	pup… <dbl>	accumfreq <dbl>	logab… <dbl>
Loose Cultch	LS	TRUE	1	10	58.8	-9.5	127.2	58.8	1.0
Loose Cultch	ST	TRUE	2	3	17.6	-46.5	81.8	76.5	0.5
Loose Cultch	ZL	TRUE	3	3	17.6	-9.3	44.6	94.1	0.5
Loose Cultch	HQ	FALSE	4	1	5.9	-23.9	35.6	100.0	0.0
Restored	LS	TRUE	1	7	58.3	-17.9	134.6	58.3	0.8
Restored	HQ	TRUE	2	3	25.0	-31.0	81.0	83.3	0.5
Restored	DN	TRUE	3	1	8.3	-32.1	48.8	91.7	0.0
Restored	ZL	FALSE	4	1	8.3	-27.9	44.6	100.0	0.0

8 rows | 1-10 of 11 columns

```
fancy_Pre_plot <- ggplot(data=fancy_Pre, aes(x = rank, y = log(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(colour=Grouping), size=1) +
    geom_point(aes(colour=Grouping, shape=Grouping), size=5, alpha=0.7) +
    geom_text_repel(data=subset(fancy_Pre, labelit == TRUE),
        aes(colour=Grouping, label=species),
        angle=45, nudge_x=1, nudge_y=1, show.legend=FALSE) +
  BioR.theme +
    labs(x = "Rank", y = "Abundance", title= "Pre-restoration (2017-2018)", colour = "Site Typ
e", shape = "Site Type") +
  scale_color_manual(values=c("#666666","#669933"))
```

```
## 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.
```

```
fancy_Pre_plot
```

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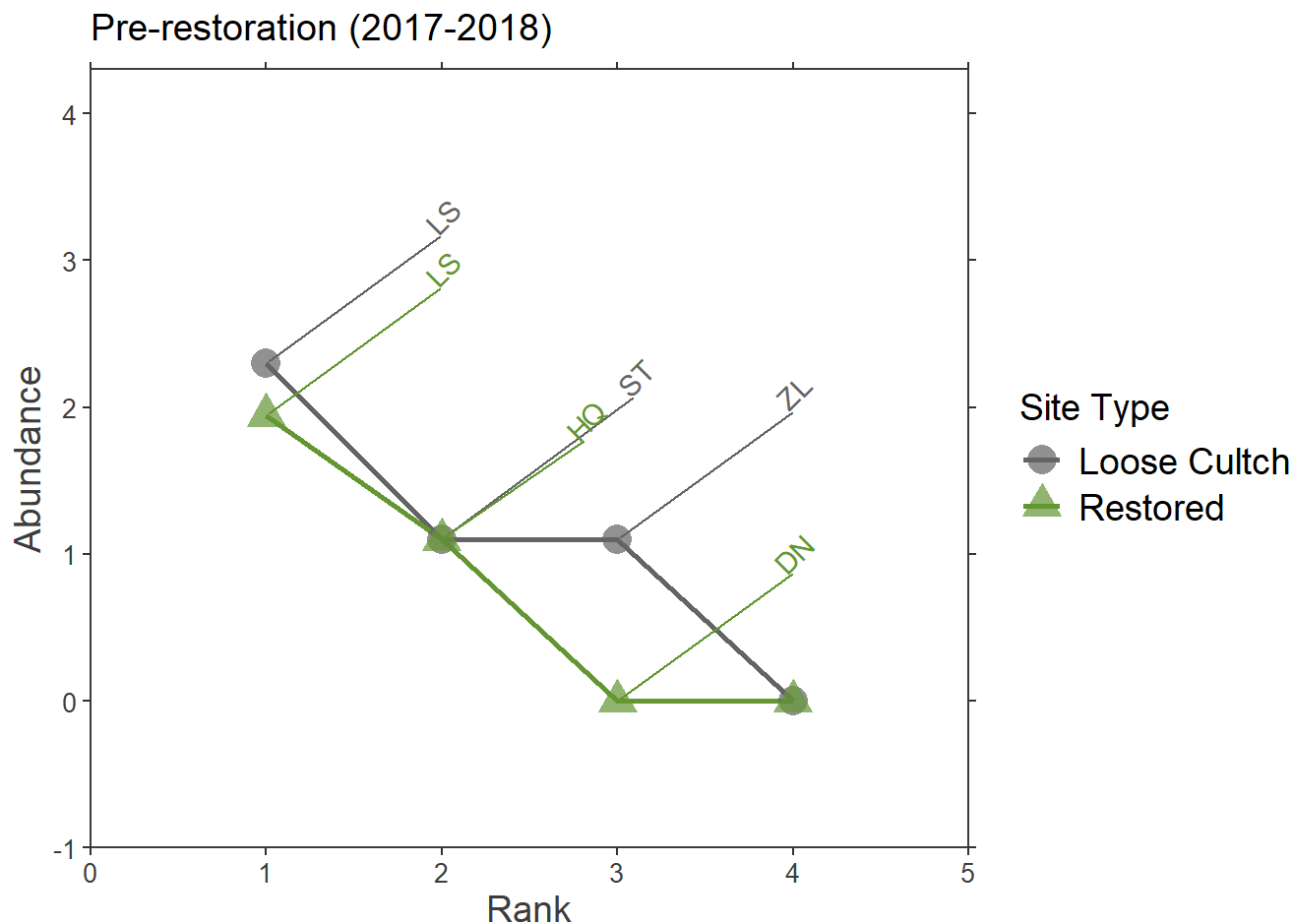
```
#1 YR

fancy_1YR <- rankabuncomp(BIOR_1YR, y=BIOR_PRE_1YR_env, factor='site_type', scale='logabun',retu
rn.data=TRUE, legend=FALSE)
```
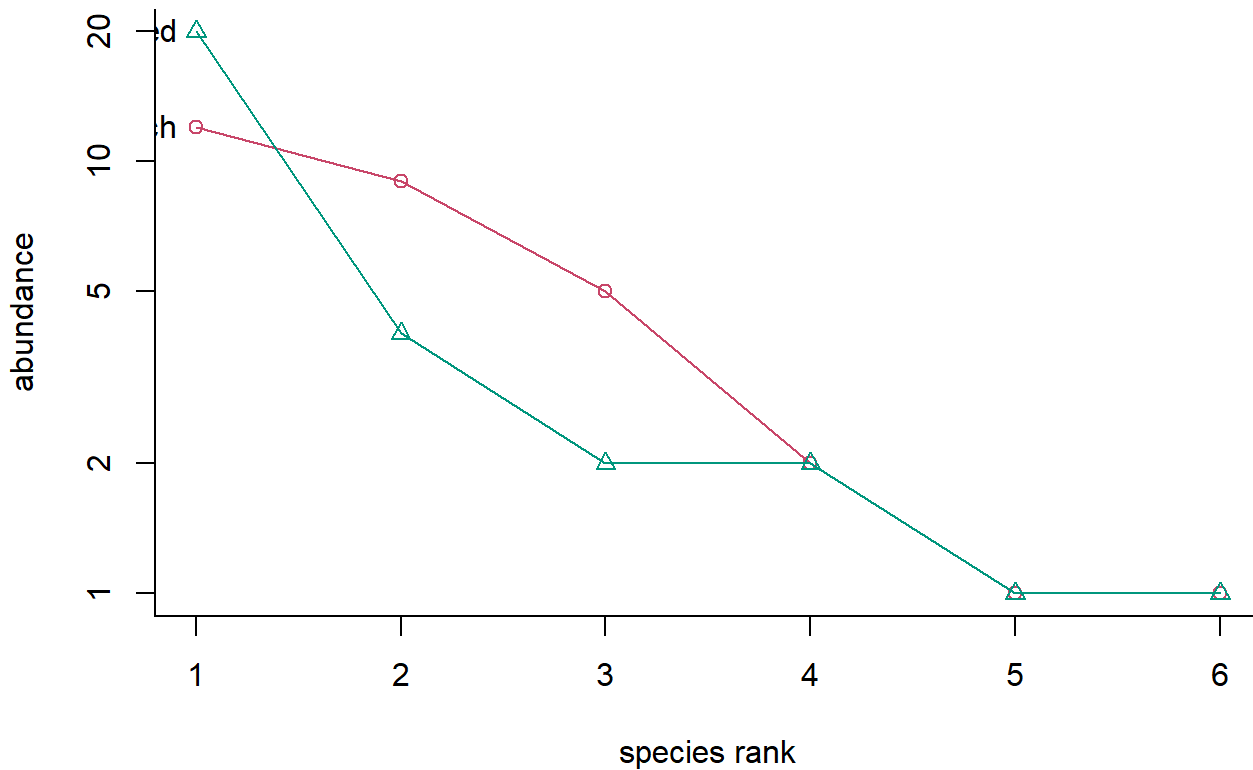


```
fancy_1YR_plot <- ggplot(data=fancy_1YR, aes(x = rank, y = log(abundance))) +
    scale_x_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name=NULL)) +
    scale_y_continuous(expand=c(0, 1), sec.axis = dup_axis(labels=NULL, name=NULL)) +
    geom_line(aes(colour=Grouping), size=1) +
    geom_point(aes(colour=Grouping, shape=Grouping), size=5, alpha=0.7) +
    geom_text_repel(data=subset(fancy_1YR, labelit == TRUE),
        aes(colour=Grouping, label=species),
        angle=45, nudge_x=1, nudge_y=1, show.legend=FALSE) +
  BioR.theme +
    labs(x = "Rank", y = "Abundance", title= "One year Post-restoration (2018-2019)", colour =
"Site Type", shape = "Site Type") +
  scale_color_manual(values=c("#666666","#669933"))



fancy_1YR_plot
```
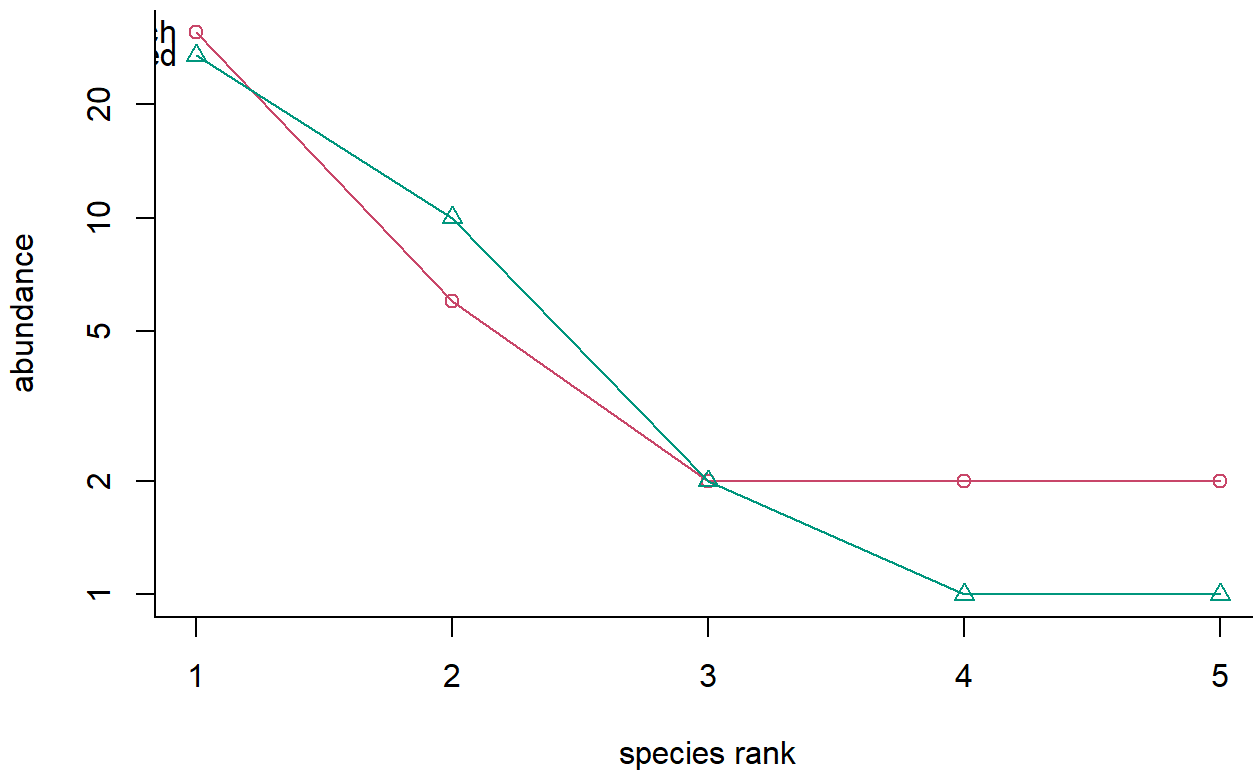
One year Post-restoration (2018-2019)
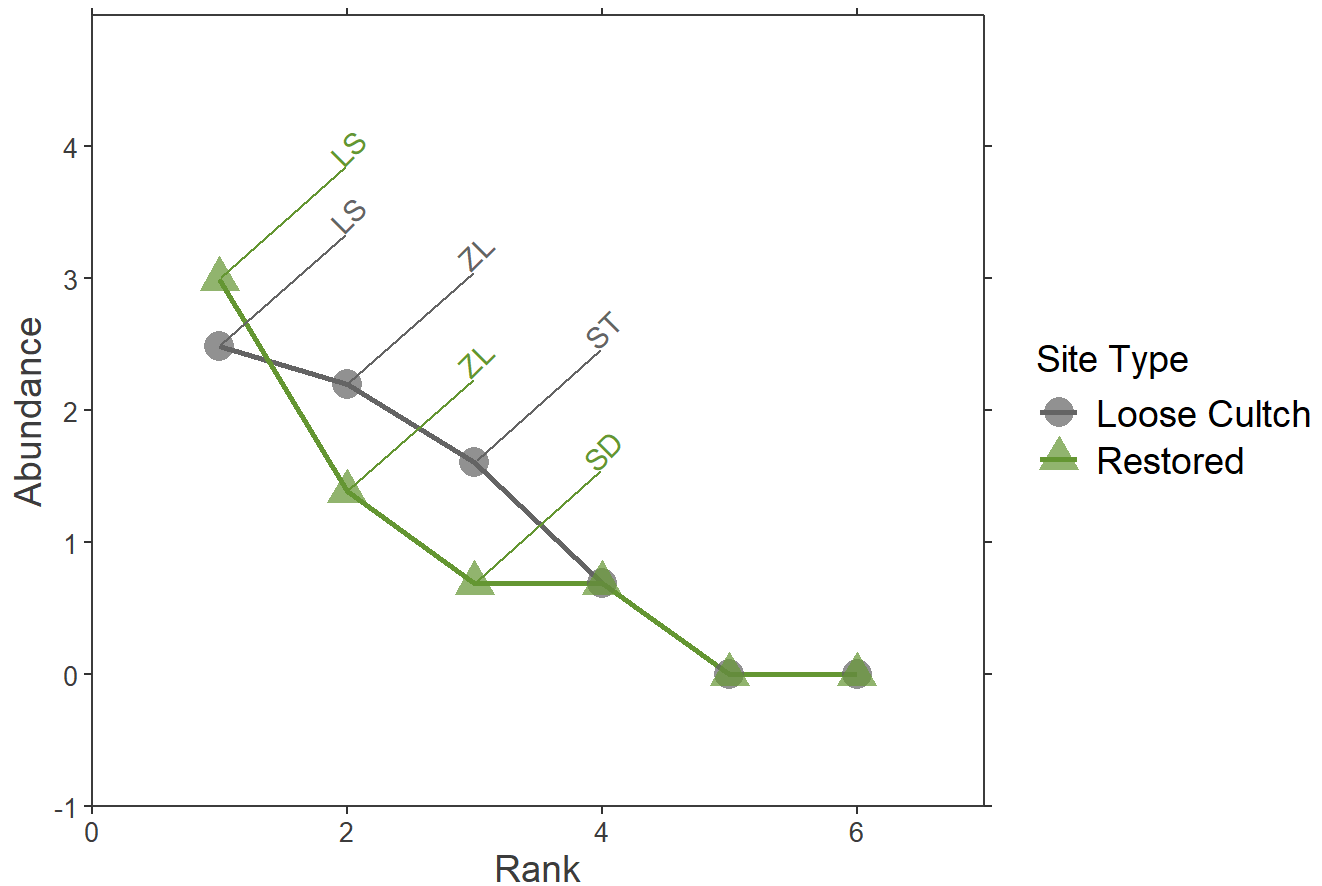
```
#5 YR

fancy_5YR_nolog <- rankabuncomp(BIOR_5YR, y=BIOR_5YR_env, factor='site_type', scale='logabun', return.data=TRUE, legend=FALSE)
```

```
fancy_5YR_plot2 <- ggplot(data=fancy_5YR_nolog, aes(x = rank, y = log(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(colour=Grouping), size=1) +
    geom_point(aes(colour=Grouping, shape=Grouping), size=5, alpha=0.7) +
    geom_text_repel(data=subset(fancy_5YR_nolog, labelit == TRUE),
        aes(colour=Grouping, label=species),
        angle=45, nudge_x=1, nudge_y=1, show.legend=FALSE) +
    BioR.theme +
    labs(x = "Rank", y = "Abundance", title = "Five years Post-restoration (2023-2024)", colour
= "Site Type", shape = "Site Type") + scale_color_manual(values=c("#666666","#669933"))



fancy_5YR_plot2
```
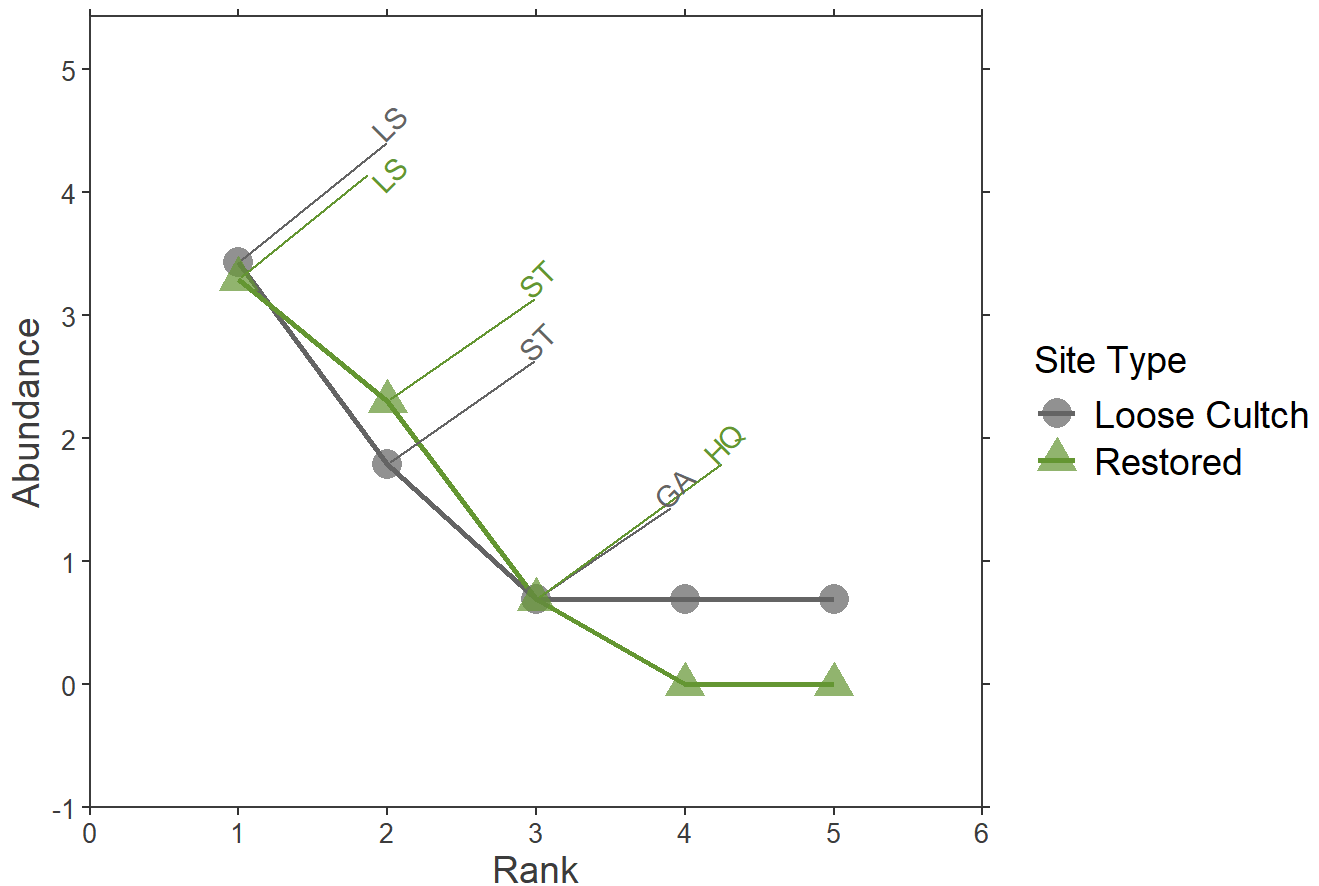
```
## Warning: ggrepel: Repulsion works correctly only for rotation angles multiple
## of 90 degrees
```

Five years Post-restoration (2023-2024)

Combining the RA curves to one figure

```
fancy_Pre_plot + fancy_1YR_plot + fancy_5YR_plot2
```

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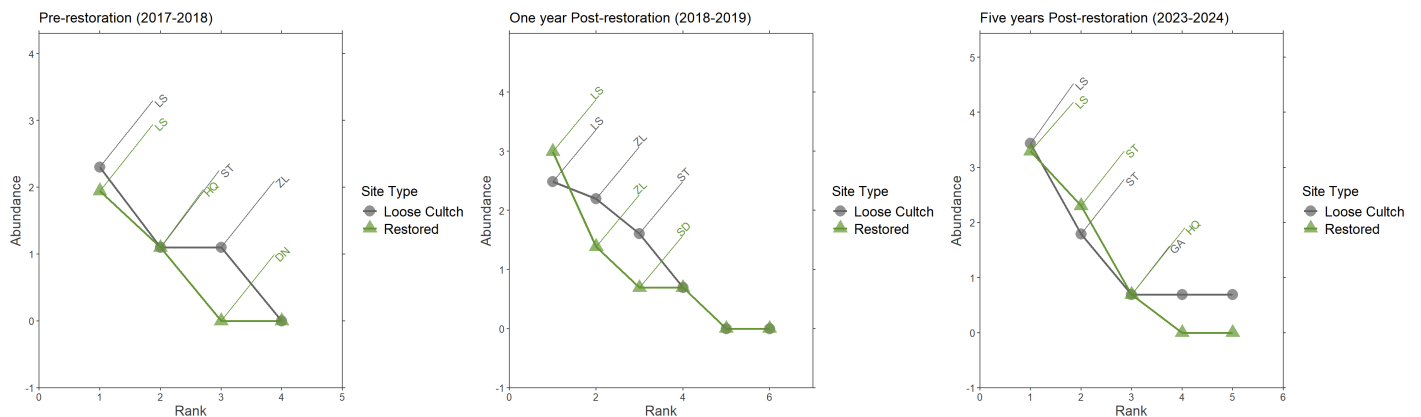

Oyster density data analyses

Loading the data

```
Newoysdens1 <- read.csv("Newoysdens1.csv")
```

#Plotting the oyster density data

```
stackedoys1<-ggplot(Newoysdens1, aes(x=as.factor(Method), y=Oysdens, fill=Shoreline)) +
  geom_boxplot()+
  xlab("Restoration Method")+ ylab("Oyster Densities (Oysters/m2)") + labs(fill="Shoreline and A
ge")

stackedoys1 + scale_fill_manual(values=c("#BDD7EE","#3B4F23","#317ABD","#82AD4D")) + theme(pane
l.background = element_rect(fill = 'lightyellow3'))+
  theme(axis.text=element_text(size=14),
        axis.title=element_text(size=15,face="bold"),
        legend.text = element_text(size=12),
        legend.title = element_text(size=13))
```
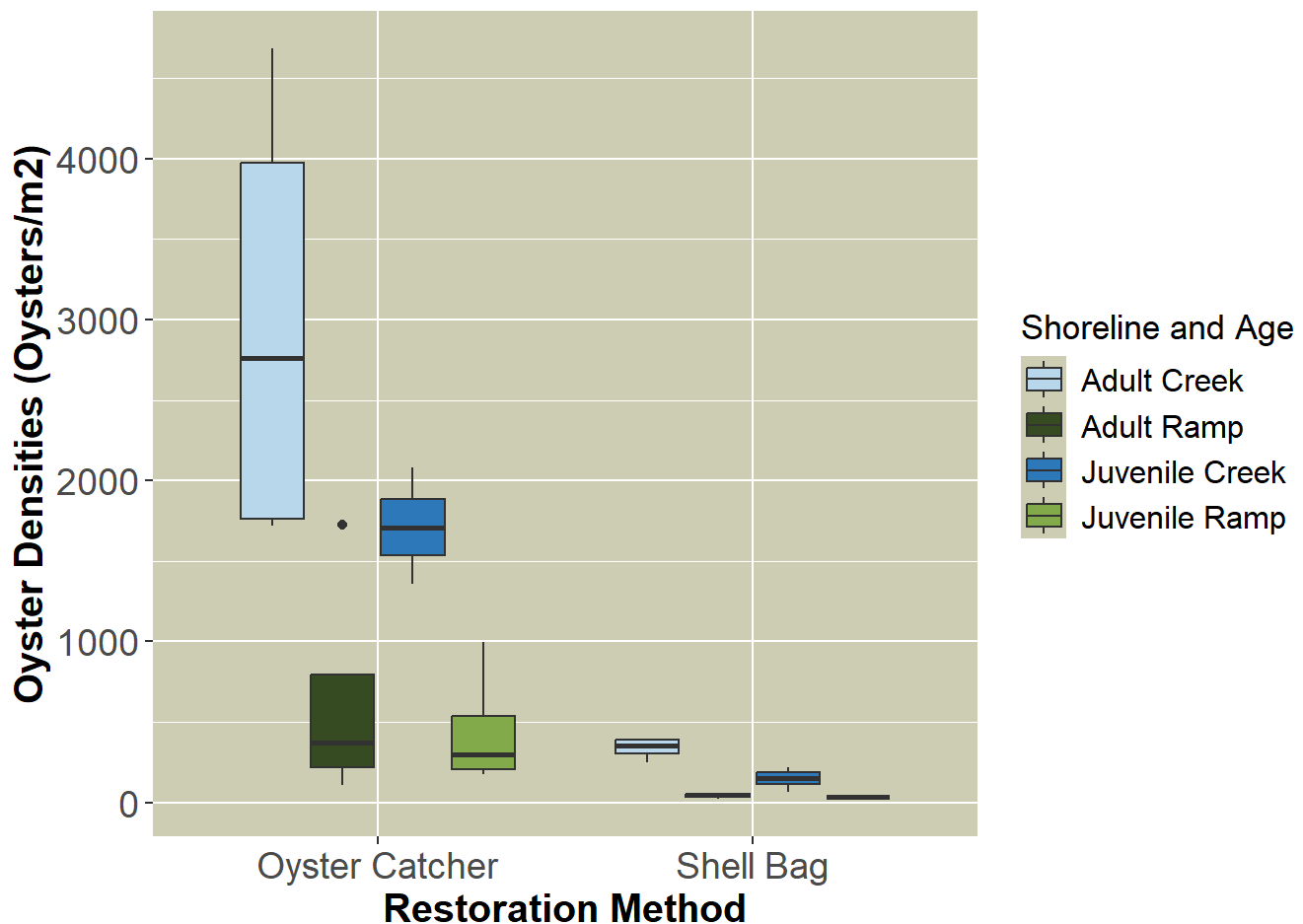

Checking the distribution of the data and log-transforming for GLMs

```
hist(Newoysdens1$Counts)
```
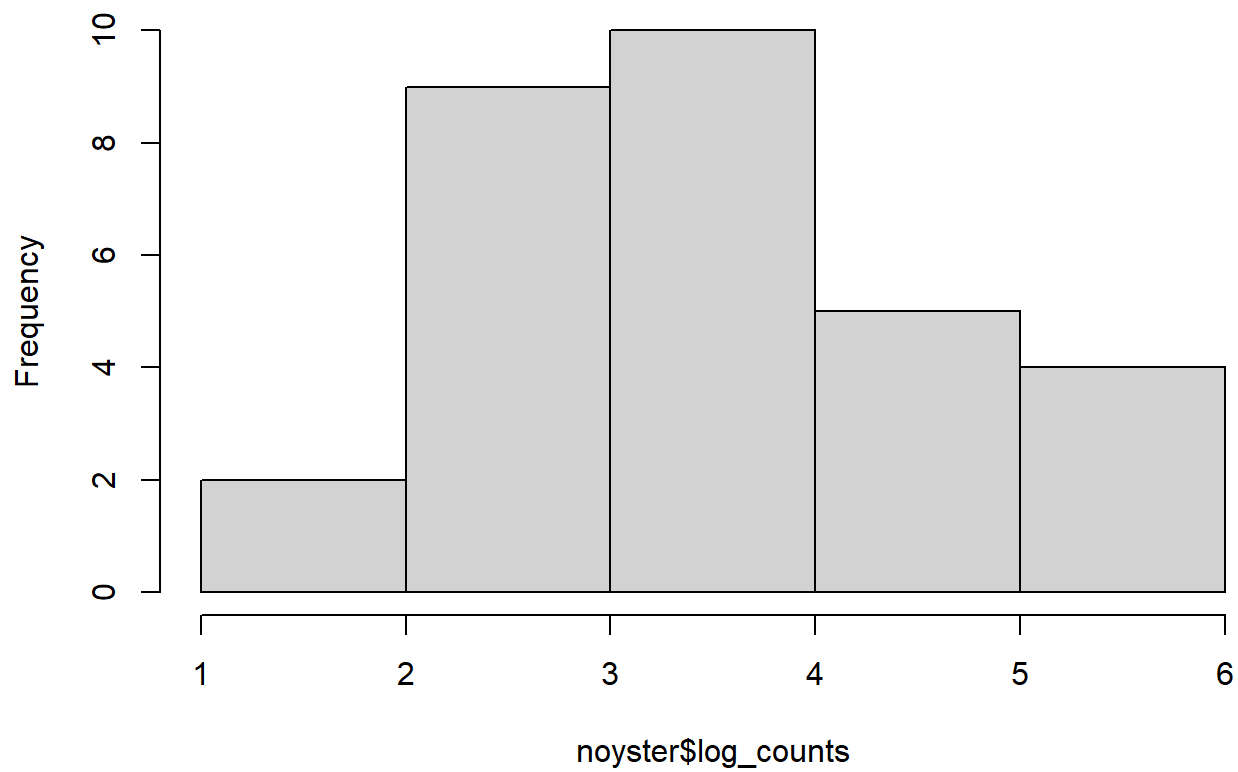
Histogram of Newoysdens1$Counts
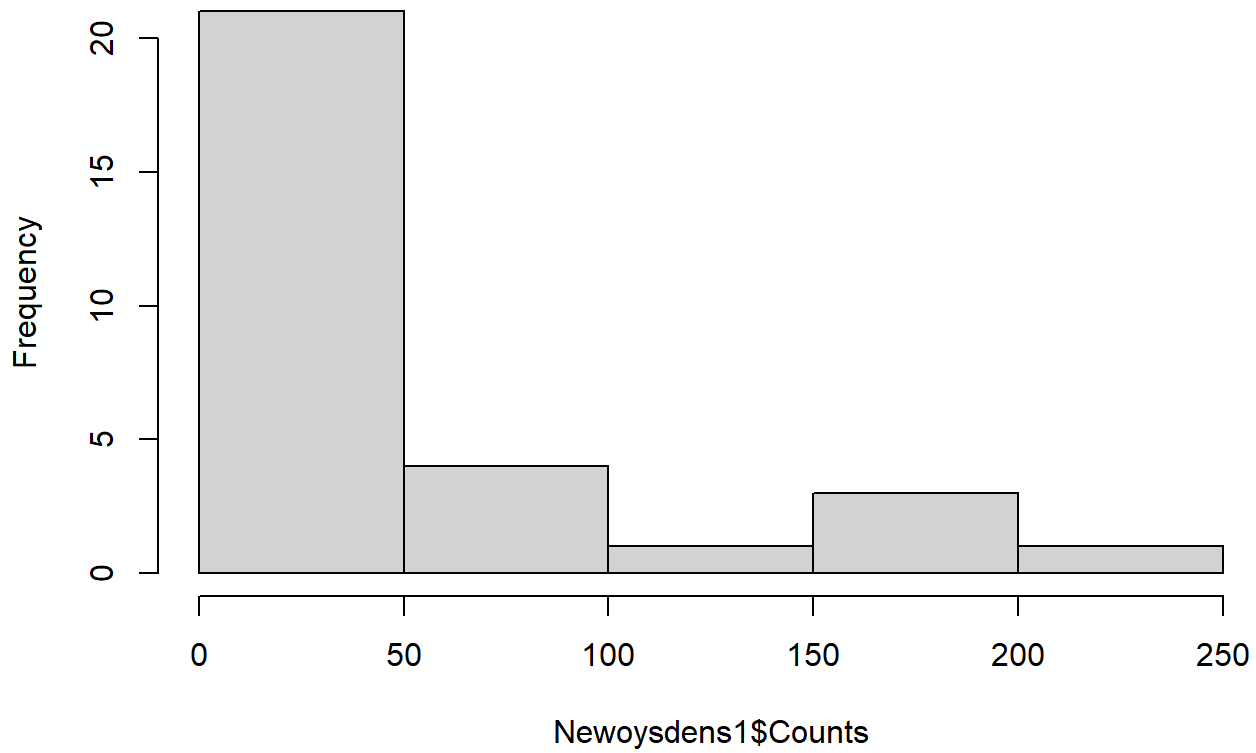

```
log_counts<-log(Newoysdens1$Counts)

noyster<-cbind(Newoysdens1,log_counts)
hist(noyster$log_counts)
```

Histogram of noyster$log_counts

noyster$log_counts

#Preliminary Analysis with Generalized Linear Models (GLMs)

```
# I ran multiple models and this one appeared to have the best AIC score.
GLM_combo<-glm(Counts~Shoreline+Method, data = noyster, family = poisson)
summary(GLM_combo)
```

```
## 
## Call:
## glm(formula = Counts ~ Shoreline + Method, family = poisson,
##     data = noyster)
## 
## Coefficients:
##                        Estimate Std. Error z value  Pr(>|z|)
## (Intercept)            4.207648   0.050836  82.769 < 2.2e-16 ***
## ShorelineAdult Ramp   -1.888350   0.095248 -19.826 < 2.2e-16 ***
## ShorelineJuvenile Creek -0.749543 0.055738 -13.448 < 2.2e-16 ***
## ShorelineJuvenile Ramp -2.176032  0.108445 -20.066 < 2.2e-16 ***
## MethodShell Bag        1.004848   0.054427  18.462 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for poisson family taken to be 1)
## 
##     Null deviance: 1732.028  on 29  degrees of freedom
## Residual deviance:  260.246  on 25  degrees of freedom
## AIC: 429.186
## 
## Number of Fisher Scoring iterations: 5
```

#Future Analyses

```
#Linear mixed effects model with time, season, and water quality as fixed effects
#In addition to oyster densities, I want to look at how these effects may impact the reef footpr
int, marsh edge location, and marsh stem density/heights.
```