Plant Community Response

2025-08-05

```r
#Load libraries
library(readxl)
```

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

```r
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.3.3
```

```r
library(dplyr)
```

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

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(viridis)
```

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

```
## Loading required package: viridisLite
```

```r
library(ggpubr)
```

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

```r
library(rstatix)
```

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

```
##
## Attaching package: 'rstatix'

## The following object is masked from 'package:stats':
##
##     filter
```

```r
library(glmmTMB)
```

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

```r
library(boot)
```

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

```r
library(tidyr)
```

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

```r
library(vegan)
```

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

## Loading required package: permute

## Warning: package 'permute' was built under R version 4.3.3

## Loading required package: lattice

##
## Attaching package: 'lattice'

## The following object is masked from 'package:boot':
##
##     melanoma
```

```r
library(tibble)
library(dplyr)
library(purrr)
```

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

```r
library(boot)
```

Load the dataset and calcualte relative biomass

To calculate relative biomass, the total biomass per species was divided by the total biomass within a mesocosm.

```r
#Import the dataset
data_mortality <- read_excel(file.path(
  "C:/Users/Joyalea/Documents/UBCO/Thesis",
  "Final_Files",
  "RQ3_PlantCommunityResponse",
  "MasterCopy_Biomass_2024.xlsx"
))

#Add treatment group column
data_mortality <- data_mortality %>%
  mutate(treatment = ifelse(mesocosm_id %in% c(1:7), "Control",
                     ifelse(mesocosm_id %in% c(8:14), "197198",
                     ifelse(mesocosm_id %in% c(15:21), "240448",
                     ifelse(mesocosm_id %in% c(22:28), "240720", NA)))),
         block = ifelse(mesocosm_id %in% c(15, 20, 22, 12, 11, 14, 24, 27,
                                          19, 21, 25, 3, 2, 7), "A",
                 ifelse(mesocosm_id %in% c(4, 17, 9, 28, 6, 1, 5, 18, 8,
                                          26, 16, 23, 13, 10), "B", NA)))
#Review the data
head(data_mortality)
```

```
## # A tibble: 6 x 7
##   date_weighed      mesocosm_id species   species_id biomass treatment block
##   <chr>                   <dbl> <chr>     <chr>        <dbl> <chr>     <chr>
## 1 September.14.2024           1 Taraxacum Ta.1          8.28 Control   B
## 2 September 14. 2024          1 Taraxacum Ta.2          7.56 Control   B
## 3 September 14. 2024          1 Taraxacum Ta.3          8.5  Control   B
## 4 September 14. 2024          3 Taraxacum Ta.4          9.18 Control   A
## 5 September 14. 2024          3 Taraxacum Ta.5          5.54 Control   A
## 6 September 14. 2024          3 Taraxacum Ta.6          8.88 Control   A
```

```r
str(data_mortality)
```

```
## tibble [336 x 7] (S3: tbl_df/tbl/data.frame)
##  $ date_weighed: chr [1:336] "September.14.2024" "September 14. 2024" "September 14. 2024" "September
##  $ mesocosm_id : num [1:336] 1 1 1 3 3 3 2 2 2 4 ...
##  $ species     : chr [1:336] "Taraxacum" "Taraxacum" "Taraxacum" "Taraxacum" ...
##  $ species_id  : chr [1:336] "Ta.1" "Ta.2" "Ta.3" "Ta.4" ...
##  $ biomass     : num [1:336] 8.28 7.56 8.5 9.18 5.54 8.88 9.55 5.52 3.9 6.7 ...
##  $ treatment   : chr [1:336] "Control" "Control" "Control" "Control" ...
##  $ block       : chr [1:336] "B" "B" "B" "A" ...
```

```r
#Summarize count of individuals
counts_df <- data_mortality %>%
  filter(species == "Bromus", is.na(biomass)) %>%
  group_by(species, treatment) %>%
  summarise(n_individuals = n(), .groups = "drop")

#Summarize relative biomass (species biomass / total meso biomass)
rel_biomass <- data_mortality %>%
  group_by(mesocosm_id) %>%
  mutate(total_biomass = sum(biomass, na.rm = TRUE)) %>%
```

```
  group_by(mesocosm_id, species, treatment) %>%
  summarise(
    species_biomass = sum(biomass, na.rm = TRUE),
    total_biomass = unique(total_biomass),
    rel_biomass = species_biomass / total_biomass,
    .groups = "drop"
  )
```

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

Analyse changes in plant community structure (beta diversity) using relative host biomass

Relative host biomass was used as opposed to counts to account for overall growth of a species in a mesocosm, which can indirectly account for mortality

```
#Change data structure for bray analysis (convert columns to rows)
pivot_rel_biomass <- rel_biomass %>%
  select(mesocosm_id, species, rel_biomass) %>%
  pivot_wider(names_from = species, values_from = rel_biomass, values_fill = 0) %>%
  column_to_rownames("mesocosm_id")

#Create metadata
metadata <- rel_biomass %>%
  select(mesocosm_id, treatment) %>%
  distinct()

metadata <- metadata %>%
  filter(mesocosm_id %in% rownames(pivot_rel_biomass)) %>%
  arrange(match(mesocosm_id, rownames(pivot_rel_biomass)))

#Check it worked correctly
View(metadata)

#Create Bray-Curtis dissimilarity matrix
bray_dist <- vegdist(pivot_rel_biomass, method = "bray")

print(adonis2(bray_dist ~ treatment, data = metadata, permutations = 999))
```

```
## Permutation test for adonis under reduced model
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = bray_dist ~ treatment, data = metadata, permutations = 999)
##          Df SumOfSqs      R2      F Pr(>F)
## Model     3  0.08217 0.21732 2.2213  0.049 *
## Residual 24  0.29595 0.78268
## Total    27  0.37813 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```
#Significant

#Check dispersion to ensure ANOVA assumptions are met
dispersion <- betadisper(bray_dist, metadata$treatment)
```

```
## Warning in betadisper(bray_dist, metadata$treatment): some squared distances
## are negative and changed to zero
```
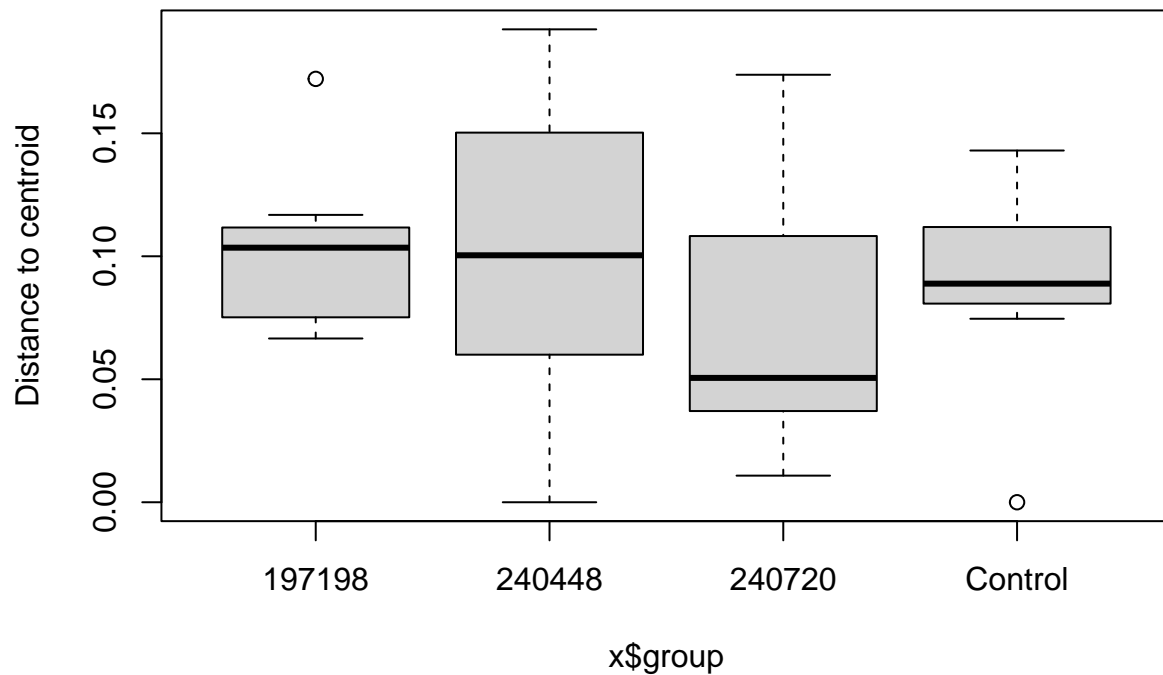
```
anova(dispersion) #Not significant
```

```
## Analysis of Variance Table
##
## Response: Distances
##            Df    Sum Sq   Mean Sq F value Pr(>F)
## Groups      3 0.003523 0.0011744  0.4049 0.7508
## Residuals  24 0.069604 0.0029002
```

```
plot(dispersion)
```
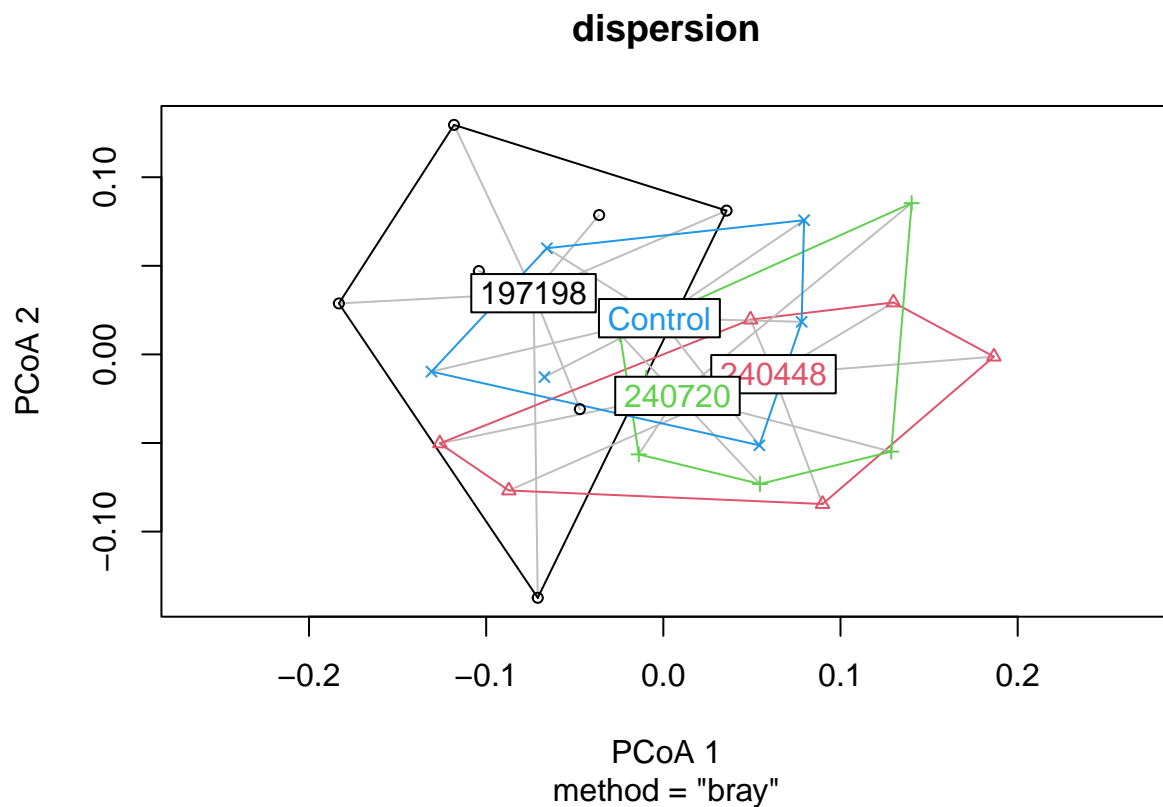

dispersion

```
boxplot(dispersion)
```

```r
#Pairwise comparisons
pairwiseAdonis::pairwise.adonis(
  x = as.matrix(bray_dist),
  factors = metadata$treatment,
  sim.function = "vegdist",
  sim.method = "bray",
  p.adjust.m = "BH"
)
```

```
##                   pairs Df  SumsOfSqs    F.Model         R2 p.value p.adjusted sig
## 1 Control vs 197198   1 0.04071127 1.3760489 0.10287409   0.236     0.4332
## 2 Control vs 240448   1 0.03694359 0.9737752 0.07505719   0.361     0.4332
## 3 Control vs 240720   1 0.02668014 0.8157614 0.06365298   0.504     0.5040
## 4  197198 vs 240448   1 0.08615613 2.5548590 0.17553306   0.094     0.2820
## 5  197198 vs 240720   1 0.10911738 3.8300576 0.24194843   0.011     0.0660
## 6  240448 vs 240720   1 0.04228909 1.1478299 0.08730185   0.326     0.4332
```

```r
#SIMPER analysis to see which species are driving the difference
simper_results <- simper(pivot_rel_biomass, group = metadata$treatment,
                         permutations = 999)

#View SIMPER results for each treatment pair
summary(simper_results) #Driven by Gaillardia
```

```
##
```

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```
## Contrast: Control_197198
##
##            average      sd   ratio     ava     avb cumsum     p
## Bromus     0.05041 0.03449 1.46160 0.27900 0.34830  0.339 0.676
## Festuca    0.04484 0.03113 1.44030 0.40620 0.37130  0.641 0.746
## Taraxacum  0.02884 0.02317 1.24460 0.21890 0.21620  0.835 0.343
## Gaillardia 0.02449 0.01694 1.44540 0.09590 0.06420  1.000 0.268
##
## Contrast: Control_240448
##
##            average      sd   ratio     ava     avb cumsum     p
## Bromus     0.05604 0.03942 1.42160 0.27900 0.21420  0.371 0.418
## Festuca    0.05360 0.03768 1.42230 0.40620 0.42720  0.726 0.300
## Taraxacum  0.02352 0.01962 1.19900 0.21890 0.23890  0.881 0.770
## Gaillardia 0.01795 0.01270 1.41320 0.09590 0.11970  1.000 0.849
##
## Contrast: Control_240720
##
##            average      sd   ratio     ava     avb cumsum     p
## Bromus     0.04455 0.03169 1.40590 0.27900 0.22370  0.337 0.900
## Festuca    0.04126 0.03053 1.35140 0.40620 0.42100  0.649 0.905
## Taraxacum  0.02458 0.01613 1.52450 0.21890 0.22740  0.835 0.705
## Gaillardia 0.02178 0.01725 1.26250 0.09590 0.12800  1.000 0.519
##
## Contrast: 197198_240448
##
##            average      sd   ratio     ava     avb cumsum     p
## Bromus     0.07606 0.04678 1.62600 0.34830 0.21420  0.391 0.004 **
## Festuca    0.05862 0.03895 1.50480 0.37130 0.42720  0.692 0.118
## Taraxacum  0.03107 0.02262 1.37350 0.21620 0.23890  0.852 0.215
## Gaillardia 0.02891 0.01733 1.66800 0.06420 0.11970  1.000 0.031 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Contrast: 197198_240720
##
##            average      sd   ratio     ava     avb cumsum     p
## Bromus     0.06337 0.04392 1.44300 0.34830 0.22370  0.369 0.116
## Festuca    0.04417 0.03521 1.25470 0.37130 0.42100  0.626 0.758
## Gaillardia 0.03331 0.02116 1.57420 0.06420 0.12800  0.820 0.001 ***
## Taraxacum  0.03086 0.02089 1.47750 0.21620 0.22740  1.000 0.210
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Contrast: 240448_240720
##
##            average      sd   ratio     ava     avb cumsum     p
## Festuca    0.05460 0.03311 1.64890 0.42720 0.42100  0.401 0.227
## Bromus     0.04724 0.03066 1.54080 0.21420 0.22370  0.747 0.828
## Taraxacum  0.02244 0.01897 1.18290 0.23890 0.22740  0.912 0.846
## Gaillardia 0.01197 0.01086 1.10190 0.11970 0.12800  1.000 0.995
## Permutation: free
## Number of permutations: 999
```

Visualise relative biomass by treatment using a stacked barplot

```r
#Calculate mean +/- SD of relative biomass per species per treatment
rel_biomass <- rel_biomass %>%
  group_by(treatment, species) %>%
  summarise(mean_rel_biomass = mean(rel_biomass, na.rm = TRUE),
            sd_rel_biomass = sd(rel_biomass, na.rm = TRUE),
            .groups = "drop")

#Plot: stacked bar of mean relative biomass per treatment
rel_biomass_plot<-ggplot(rel_biomass, aes(x = treatment, y = mean_rel_biomass, fill = species)) +
  geom_col(position = "stack", width = 0.8, alpha = 0.95) +
  labs(title = "Mean Relative Biomass Composition by Treatment",
       y = "Relative Biomass",
       x = "Treatment") +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1),
                     limits = c(0, 1), expand = c(0, 0)) +
  scale_fill_brewer(palette = "Paired", name = "Species") +
  theme_minimal() +
  theme(
    panel.grid = element_blank(),
    axis.line = element_line(color = "black"),
    axis.ticks = element_line(color = "black")
  )
print(rel_biomass_plot)
```
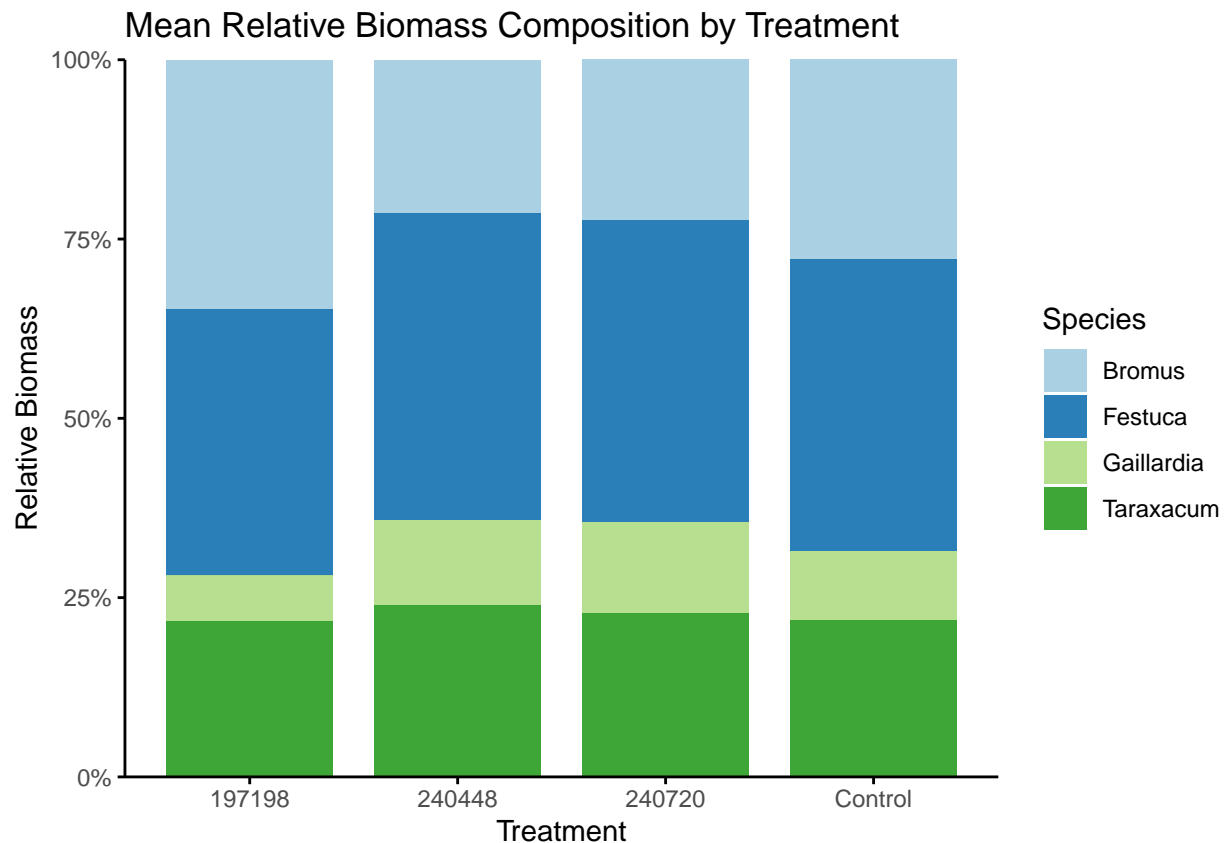
Evaluate alpha diversity metrics

```r
#Evaluate community richness (# of species present in a mesocosm)
richness <- specnumber(pivot_rel_biomass) #All species present in all mesocosms

#Shannon diversity
shannon_div <- diversity(pivot_rel_biomass, index = "shannon")

#Pielou's Evenness
evenness <- shannon_div / log(richness)

#Combine into data frame
diversity_df <- data.frame(
  mesocosm_id = rownames(pivot_rel_biomass),
  shannon = shannon_div,
  richness = richness,
  evenness = evenness
) %>%
  # Ensure mesocosm_id is character for joining
  mutate(mesocosm_id = as.factor(mesocosm_id)) %>%
  # Add treatment or other metadata
  left_join(metadata %>% mutate(mesocosm_id = as.factor(mesocosm_id)),
            by = "mesocosm_id")

#Test for treatment effects on evenness
kruskal_result <- kruskal.test(evenness ~ treatment, data = diversity_df)
kruskal_result
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  evenness by treatment
## Kruskal-Wallis chi-squared = 3.3125, df = 3, p-value = 0.3459
```

```r
#Test for treatment effects on shannon diversity
#Test for treatment effects on evenness
kruskal_result_shannon <- kruskal.test(shannon_div ~ treatment, data = diversity_df)
kruskal_result_shannon
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  shannon_div by treatment
## Kruskal-Wallis chi-squared = 3.3125, df = 3, p-value = 0.3459
```

Analysis of host mortality

Number of Individuals by Species and Treatment

Percent Survival by Species and Treatment
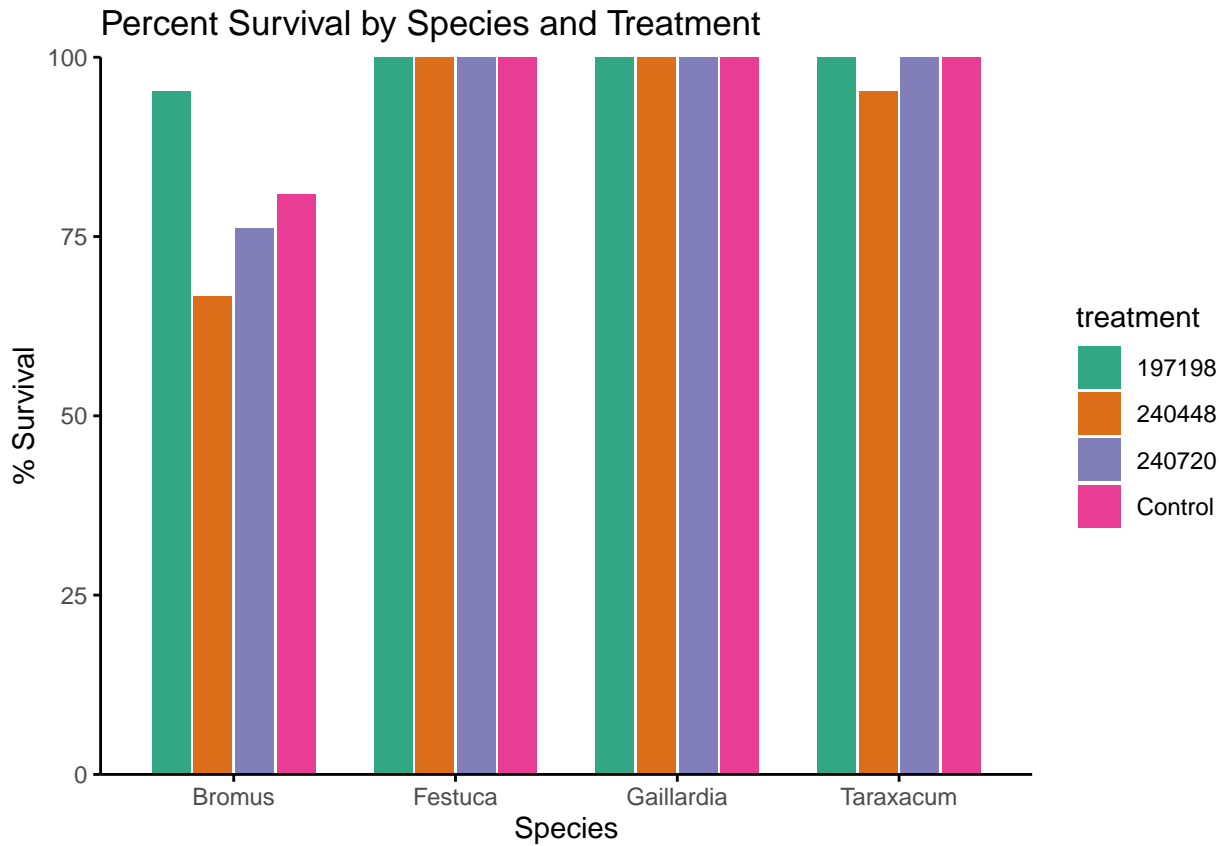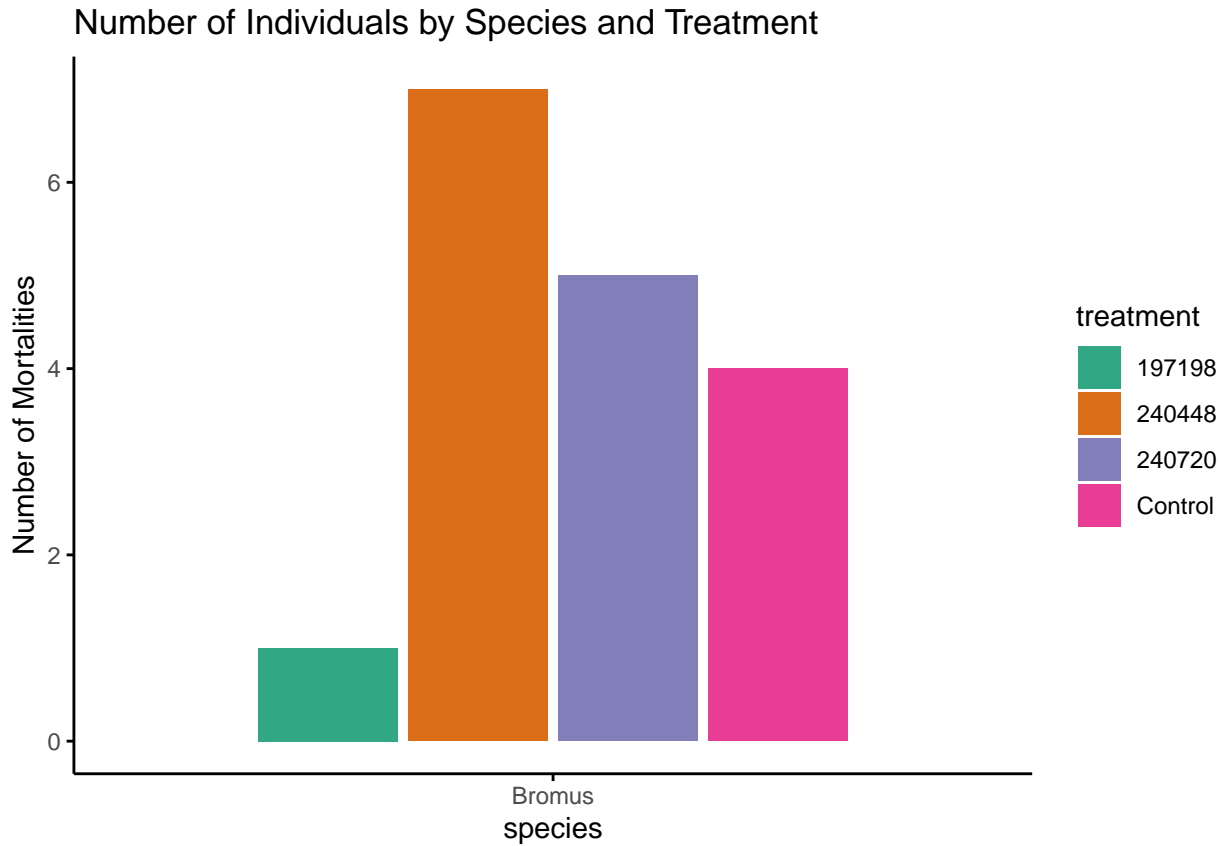
```
## # A tibble: 4 x 5
##   species treatment n_total n_survived percent_survival
##   <chr>   <chr>       <int>      <int>            <dbl>
## 1 Bromus  197198         21         20             95.2
## 2 Bromus  240448         21         14             66.7
## 3 Bromus  240720         21         16             76.2
## 4 Bromus  Control        21         17             81.0


##
##  Fisher's Exact Test for Count Data
##
## data:  fisher_matrix
## p-value = 0.127
## alternative hypothesis: two.sided
```