

QB Final

Bryan Guevara

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```
rm(list = ls())  
getwd()
```

```
## [1] "/cloud/project/QB2025_Guevara/FINAL"
```

For the question of ‘How does fungal species diversity vary across warming and fertilization treatments?’

```
##Reading in all data files  
Fung.abund <- read.csv("/cloud/project/QB2025_Guevara/FINAL/data/MAT_fungal_abundances.csv")  
Fung.enzymes <- read.csv("/cloud/project/QB2025_Guevara/FINAL/data/MAT_enzymes.csv")  
Fung.ectocounts <- read.csv("/cloud/project/QB2025_Guevara/FINAL/data/MAT_ectocounts.csv")  
Fung.seq.enzymes <- read.csv("/cloud/project/QB2025_Guevara/FINAL/data/MAT_sequences_enzymes.csv")  
soils <- read.csv("/cloud/project/QB2025_Guevara/FINAL/data/MAT_soils.csv")  
library(ggplot2)  
library(vegan)
```

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

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

```
##To slim down the data to only columns we will need to incidence matrix
```

```
library(dplyr)
```

```
##
```

```
## 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
```

```
slim <- Fung.abund %>%
```

```
  select(Plot, Treatment, Species, Relative.Abundance)
```

```
##Changing data so that each species is a column, values are the relative.abundance, and rows are each p
```

```
library(tidyrr)
```

```
Fung.abund <- slim %>%
```

```
  pivot_wider(names_from = Species, values_from = Relative.Abundance, values_fill = 0)
```

```
## Convert nonzero values to 1 while keeping 0s as is
```

```
Fung.abund <- Fung.abund %>%
```

```
  mutate(across(-c(Plot, Treatment), ~ ifelse(. > 0, 1, 0)))
```

```

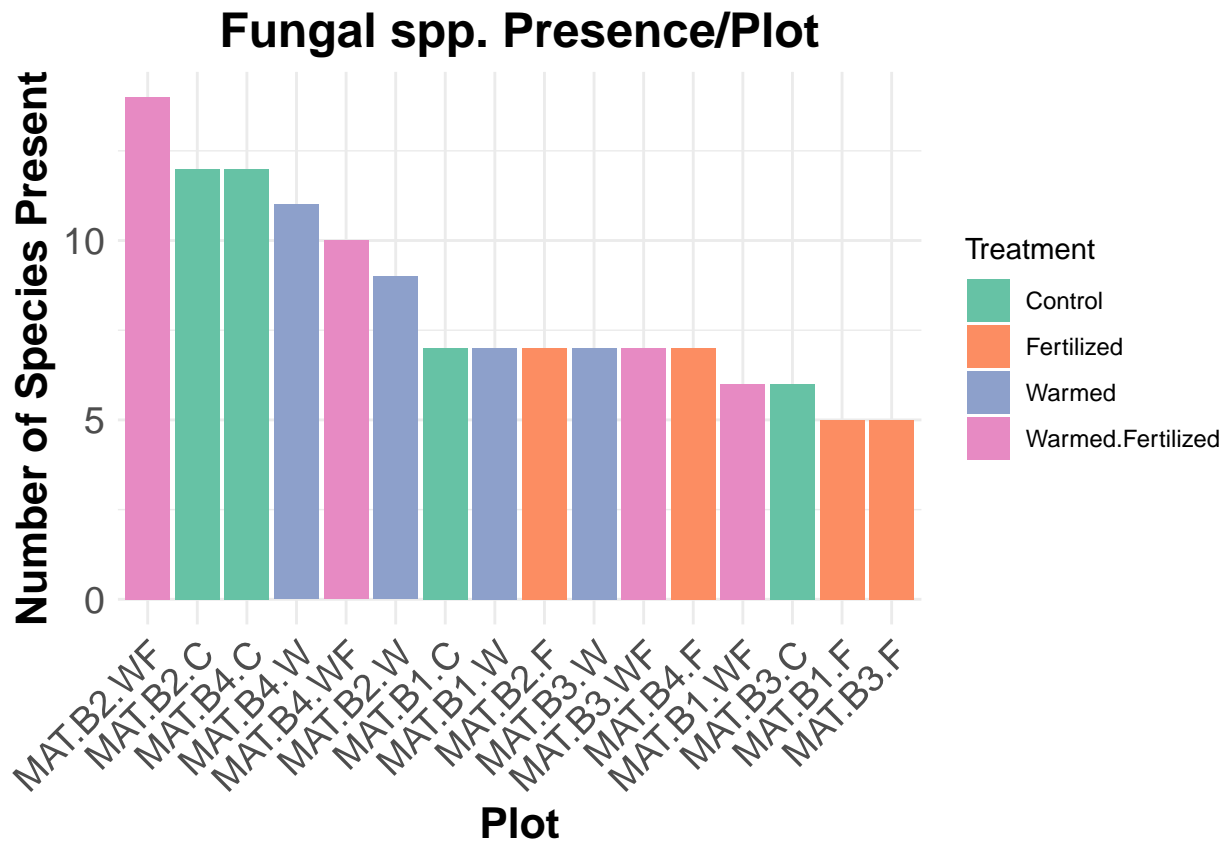
#Creating complete incidence matrix
Fung.abund.incidence <- Fung.abund %>%
  arrange(Treatment)
##Counting fungal presence
fungal_presence_counts <- Fung.abund.incidence %>%
  mutate(Presence_Count = rowSums(across(-c(Plot, Treatment))))

##ANOVA for difference in # of species
plot.incid.diff <- aov(formula = Presence_Count ~ Treatment, data = fungal_presence_counts)
summary(plot.incid.diff)

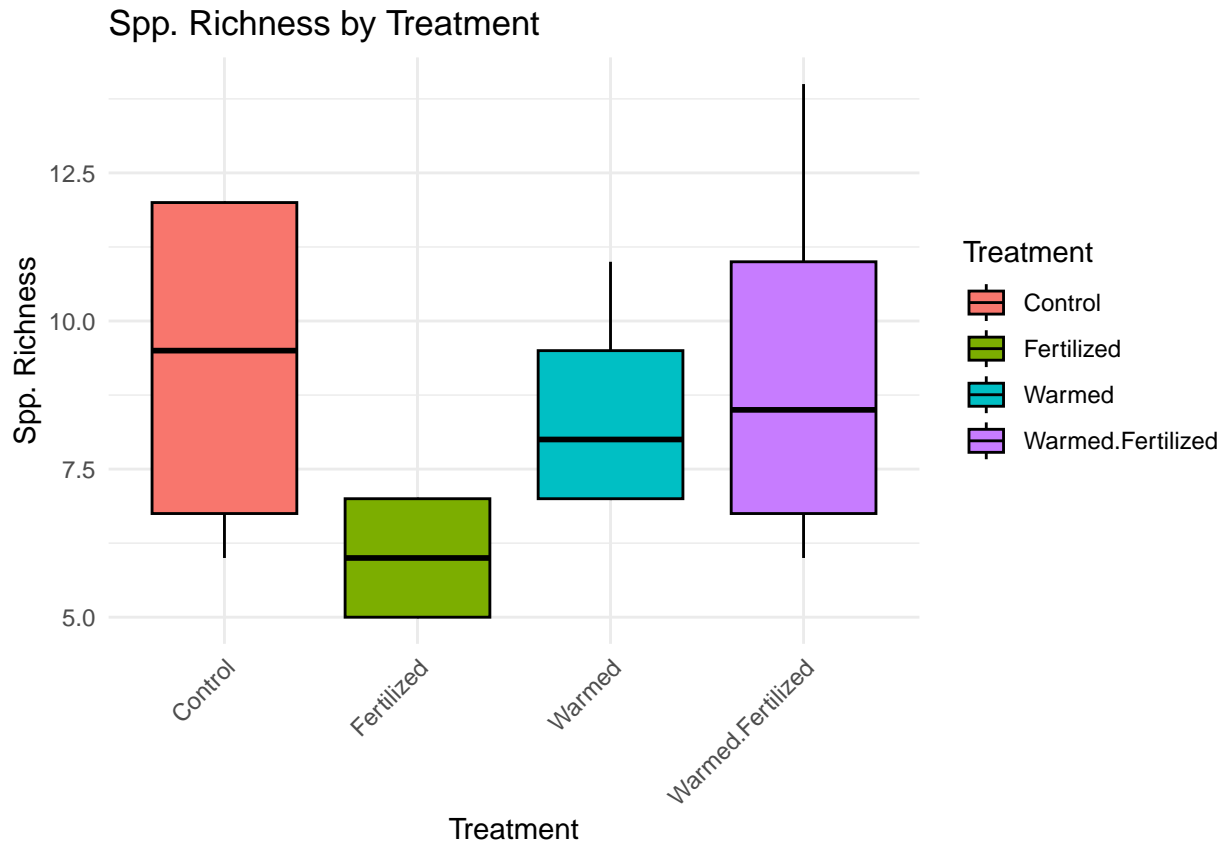
##           Df Sum Sq Mean Sq F value Pr(>F)
## Treatment   3   28.5    9.500   1.349  0.305
## Residuals  12   84.5    7.042

# Create a bar plot showing the number of species present per plot
ggplot(fungal_presence_counts, aes(x = reorder(Plot, -Presence_Count), y = Presence_Count, fill = Treatment)) +
  geom_bar(stat = "identity") +
  theme_minimal() +
  labs(title = "Fungal spp. Presence/Plot",
       x = "Plot",
       y = "Number of Species Present") +
  theme(
    plot.title = element_text(size = 18, face = "bold", hjust = 0.5), # Increase title size, bold, and
    axis.text.x = element_text(angle = 45, hjust = 1, size = 14), # Increase x-axis text size
    axis.text.y = element_text(size = 14), # Increase y-axis text size
    axis.title.x = element_text(size = 16, face = "bold"), # Increase x-axis label size
    axis.title.y = element_text(size = 16, face = "bold") # Increase y-axis label size
  ) +
  scale_fill_brewer(palette = "Set2")

```



```
ggplot(fungal_presence_counts, aes(x = Treatment, y = Presence_Count)) +
  geom_boxplot(aes(fill = Treatment), color = "black") +
  labs(title = "Spp. Richness by Treatment",
       x = "Treatment",
       y = "Spp. Richness") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



```
##Now, we will go ahead and create clustering tree
install.packages("ggdendro")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.4'
## (as 'lib' is unspecified)
```

```
library(ggdendro)
```

```
library(tibble)
```

```
# Convert tibble to a standard data frame to avoid row name issues
Fung.abund.incidence <- as.data.frame(Fung.abund.incidence)
```

```
# Set row names as Plot names and remove 'Plot' and 'Treatment' columns
rownames(Fung.abund.incidence) <- Fung.abund.incidence$Plot
fungal_matrix <- as.matrix(Fung.abund.incidence[, -c(1, 2)]) # Keep only presence/absence data
```

```
# Compute Jaccard distance matrix
jaccard_dist <- vegdist(fungal_matrix, method = "jaccard")
```

```
# Perform hierarchical clustering
jaccard_clust <- hclust(jaccard_dist, method = "average") # UPGMA clustering
```

```
# Convert clustering object to dendrogram format
dendro <- as.dendrogram(jaccard_clust)
dendro_data <- ggdendro::dendro_data(dendro)
```

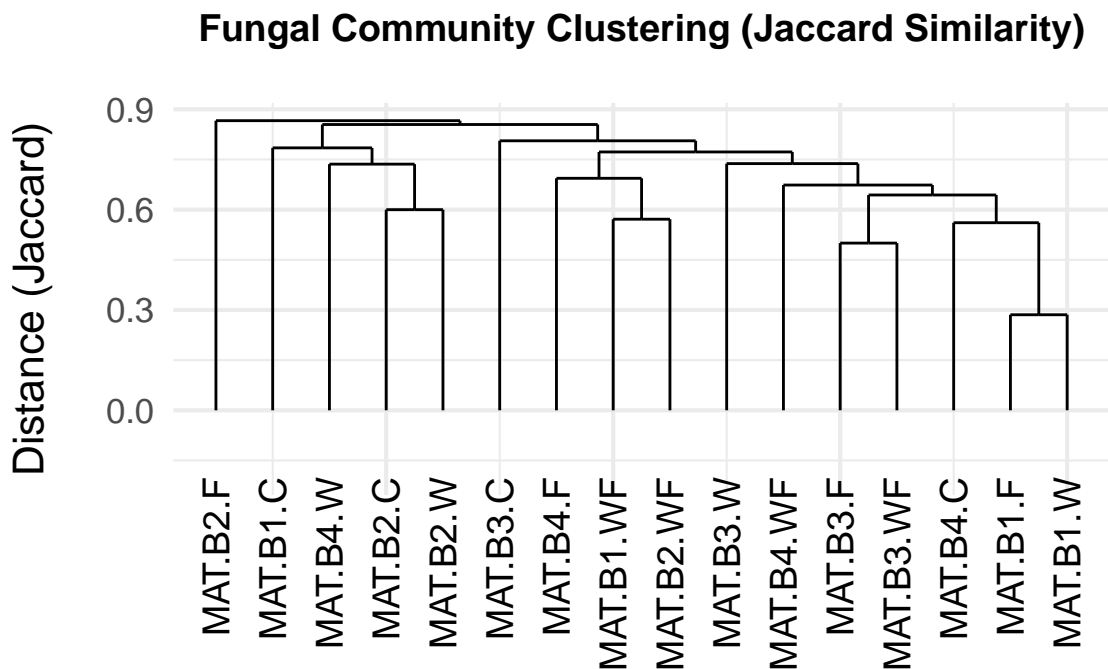
```
# Ensure correct plot labels
```

```

dendro_data$labels$label <- rownames(fungal_matrix)[jaccard_clust$order]

ggplot(dendro_data$segments) +
  geom_segment(aes(x = x, y = y, xend = xend, yend = yend)) +
  geom_text(
    data = dendro_data$labels,
    aes(x = x, y = y, label = label),
    hjust = 1, angle = 90, size = 5, nudge_y = -0.2 # Adjust branch label position
  ) +
  theme_minimal(base_size = 16) + # Increase overall text size
  labs(
    title = "Fungal Community Clustering (Jaccard Similarity)",
    x = "",
    y = "Distance (Jaccard)"
  ) +
  theme(
    plot.title = element_text(size = 14, face = "bold", hjust = 0.5, margin = margin(b = 20)), # Add space around plot title
    axis.text.x = element_blank(),
    axis.ticks.x = element_blank(),
    plot.margin = margin(1, 1, 2, 1, "cm"), # Adjust overall plot margins
    axis.title.x = element_text(margin = margin(t = 20, b = 20)), # Add space around x-axis title
    axis.title.y = element_text(margin = margin(r = 20)) # Add space around y-axis title
  ) +
  coord_cartesian(clip = "off") # Prevent text cutoff

```



```

# Count the number of Root.tip.IDs per Treatment
treatment_counts <- Fung.seq.enzymes %>%
  group_by(Treatment) %>%
  summarise(Count = n_distinct(Root.tip.ID))

##There were 165 root tips in control group, 161 root tips in fertilized group, 161 tips in warmed, and
# Count the number of Root.tip.IDs per Plot
plot_counts <- Fung.seq.enzymes %>%

```

```

group_by(Plot) %>%
  summarise(Count = n_distinct(Root.tip.ID))

# View the result
print(plot_counts)

## # A tibble: 16 x 2
##   Plot      Count
##   <chr>    <int>
## 1 MAT.B1.C      40
## 2 MAT.B1.F      40
## 3 MAT.B1.W      41
## 4 MAT.B1.WF     40
## 5 MAT.B2.C      41
## 6 MAT.B2.F      41
## 7 MAT.B2.W      40
## 8 MAT.B2.WF     40
## 9 MAT.B3.C      40
## 10 MAT.B3.F     40
## 11 MAT.B3.W      40
## 12 MAT.B3.WF     40
## 13 MAT.B4.C     44
## 14 MAT.B4.F      40
## 15 MAT.B4.W      40
## 16 MAT.B4.WF     39

# Getting actual abundances per plot
Abundances <- Fung.seq.enzymes %>%
  group_by(Plot, OTU) %>%
  summarise(Abundance = n_distinct(Root.tip.ID)) %>%
  arrange(Plot, OTU) %>%
  filter(!is.na(OTU)) # Remove rows with NA in Abundance

## `summarise()` has grouped output by 'Plot'. You can override using the
## `.groups` argument.

Abundances_transposed <- Abundances %>%
  pivot_wider(
    names_from = OTU,          # Make OTUs the column names
    values_from = Abundance,   # Fill values with Abundance
    values_fill = list(Abundance = 0) # Fill missing values with 0
  )

# Select unique Plot-Treatment pairs from Fung.seq.enzymes
treatment_data <- Fung.seq.enzymes %>%
  select(Plot, Treatment) %>%
  distinct() # Ensure only one row per Plot

# Merge the transposed Abundances matrix with the treatment data
merged_data <- Abundances_transposed %>%
  left_join(treatment_data, by = "Plot") %>%
  select(Plot, Treatment, everything()) # Ensure correct column order

# View the result
print(merged_data)

```

```
## # A tibble: 16 x 44
## # Groups:   Plot [16]
##   Plot      Treatment    `1`    `4`    `6`    `7`    `8`   `19`   `42`   `36`   `37`   `38`
##   <chr>     <chr>      <int> <int> <int> <int> <int> <int> <int> <int> <int>
## 1 MAT.B1~ Control        1      1     11      1      1      3     11      0      0      0
## 2 MAT.B1~ Fertiliz~      0      0      0      0      0      0      0      1      3      3
## 3 MAT.B1~ Warmed        0      0      0      0      0      0      3      2      5     12
## 4 MAT.B1~ Warmed.F~     0      0      0      0      0      0      0      7      0      0
## 5 MAT.B2~ Control        0      3      0      0      0      9      2      0      1      8
## 6 MAT.B2~ Fertiliz~      0      0      0      0      0      1      0      4      0      0
## 7 MAT.B2~ Warmed        0      5      0      1      0      1      8      0      0     14
## 8 MAT.B2~ Warmed.F~     0      0      0      0      0      1      0      2      0      1
## 9 MAT.B3~ Control        0      0      2      0      0      3      0      0      0      5
## 10 MAT.B3~ Fertiliz~      0      0      0      0      0      1      0      1      0      0
## 11 MAT.B3~ Warmed        0      0      0      0      0      0      0      1      0      0
## 12 MAT.B3~ Warmed.F~     0      0      0      0      0      0      7      2      0      0
## 13 MAT.B4~ Control        0      3      5      0      0      0      0      1      4      7
## 14 MAT.B4~ Fertiliz~      0      0      0      0      0      0      0      0      0      0
## 15 MAT.B4~ Warmed        0      2      0      0      0      3      0      0      4     17
## 16 MAT.B4~ Warmed.F~     0      8      0      0      0      8      1      1      1      0
## # i 32 more variables: `39` <int>, `40` <int>, `20` <int>, `5` <int>,
## #   `17` <int>, `18` <int>, `33` <int>, `22` <int>, `24` <int>, `26` <int>,
## #   `28` <int>, `30` <int>, `31` <int>, `2` <int>, `32` <int>, `3` <int>,
## #   `9` <int>, `29` <int>, `10` <int>, `23` <int>, `27` <int>, `44` <int>,
## #   `41` <int>, `11` <int>, `12` <int>, `25` <int>, `13` <int>, `21` <int>,
## #   `14` <int>, `34` <int>, `35` <int>, `16` <int>
```

```
long_data <- merged_data %>%
  pivot_longer(cols = -c(Plot, Treatment), names_to = "Species", values_to = "Count")

# Summarize total individuals per treatment
summary_data <- long_data %>%
  group_by(Treatment, Plot) %>%
  summarise(Total_Individuals = sum(Count, na.rm = TRUE), .groups = 'drop')

# Perform ANOVA
anova_result <- aov(Total_Individuals ~ Treatment, data = summary_data)

# Print summary of ANOVA
summary(anova_result)
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## Treatment   3   55.3   18.42   0.435  0.732
## Residuals  12  508.5   42.37
```

```
# Perform Tukey's HSD test for pairwise comparisons (optional)
TukeyHSD(anova_result)
```

```
##   Tukey multiple comparisons of means
##   95% family-wise confidence level
##
## Fit: aov(formula = Total_Individuals ~ Treatment, data = summary_data)
##
## $Treatment
##               diff             lwr             upr             p adj
```

```

## Fertilized-Control      0.50 -13.165817 14.16582 0.9995142
## Warmed-Control         4.75  -8.915817 18.41582 0.7346929
## Warmed.Fertilized-Control 2.25 -11.415817 15.91582 0.9601141
## Warmed-Fertilized      4.25  -9.415817 17.91582 0.7931627
## Warmed.Fertilized-Fertilized 1.75 -11.915817 15.41582 0.9804129
## Warmed.Fertilized-Warmed -2.50 -16.165817 11.16582 0.9466419

# Extract the first two columns (Plot and Treatment)
first_two_columns <- merged_data[, 1:2]

# Extract the remaining columns (OTUs)
otu_columns <- merged_data[, -c(1, 2)]

# Convert OTU column names to numeric and sort them
sorted_otu_columns <- otu_columns[, order(as.numeric(names(otu_columns)))]

# Combine the first two columns with the sorted OTU columns
merged_data_sorted <- cbind(first_two_columns, sorted_otu_columns)

# View the sorted dataframe
print(merged_data_sorted)

## # A tibble: 16 x 44
## # Groups:   Plot [16]
##   Plot Treatment `1` `2` `3` `4` `5` `6` `7` `8` `9` `10`
##   <chr> <chr> <int> <int> <int> <int> <int> <int> <int> <int> <int> <int>
## 1 MAT.B1~ Control 1 0 0 1 0 11 1 1 0 0
## 2 MAT.B1~ Fertiliz~ 0 0 0 0 0 0 0 0 0 0 0
## 3 MAT.B1~ Warmed 0 0 0 0 0 0 0 0 0 0 0
## 4 MAT.B1~ Warmed.F~ 0 0 0 0 1 0 0 0 0 0 0
## 5 MAT.B2~ Control 0 0 0 3 0 0 0 0 0 0 0
## 6 MAT.B2~ Fertiliz~ 0 1 0 0 0 0 0 0 0 0 0
## 7 MAT.B2~ Warmed 0 0 0 5 0 0 1 0 0 0 0
## 8 MAT.B2~ Warmed.F~ 0 0 1 0 1 0 0 0 1 0 0
## 9 MAT.B3~ Control 0 0 0 0 0 2 0 0 0 0 3
## 10 MAT.B3~ Fertiliz~ 0 0 0 0 0 0 0 0 0 0 0
## 11 MAT.B3~ Warmed 0 0 0 0 0 0 0 0 0 0 0
## 12 MAT.B3~ Warmed.F~ 0 0 0 0 0 0 0 0 0 0 0
## 13 MAT.B4~ Control 0 0 0 3 0 5 0 0 0 0 0
## 14 MAT.B4~ Fertiliz~ 0 0 0 0 0 0 0 0 0 0 0
## 15 MAT.B4~ Warmed 0 0 0 2 0 0 0 0 0 0 0
## 16 MAT.B4~ Warmed.F~ 0 0 0 8 0 0 0 0 0 2 0
## # i 32 more variables: `11` <int>, `12` <int>, `13` <int>, `14` <int>,
## # `16` <int>, `17` <int>, `18` <int>, `19` <int>, `20` <int>, `21` <int>,
## # `22` <int>, `23` <int>, `24` <int>, `25` <int>, `26` <int>, `27` <int>,
## # `28` <int>, `29` <int>, `30` <int>, `31` <int>, `32` <int>, `33` <int>,
## # `34` <int>, `35` <int>, `36` <int>, `37` <int>, `38` <int>, `39` <int>,
## # `40` <int>, `41` <int>, `42` <int>, `44` <int>

library(dplyr)
library(vegan)

# Remove non-OTU columns and ungroup to avoid issues
otu_data <- merged_data_sorted %>%
  ungroup() %>% # Remove any grouping that may have been applied

```



```

select(-Plot, -Treatment) %>%
mutate(across(everything(), as.numeric)) # Ensure all columns are numeric

# Compute Shannon Diversity Index for each plot
merged_data_sorted$Shannon_Index <- diversity(as.matrix(otu_data), index = "shannon")

# View results
print(merged_data_sorted[, c("Plot", "Treatment", "Shannon_Index")])

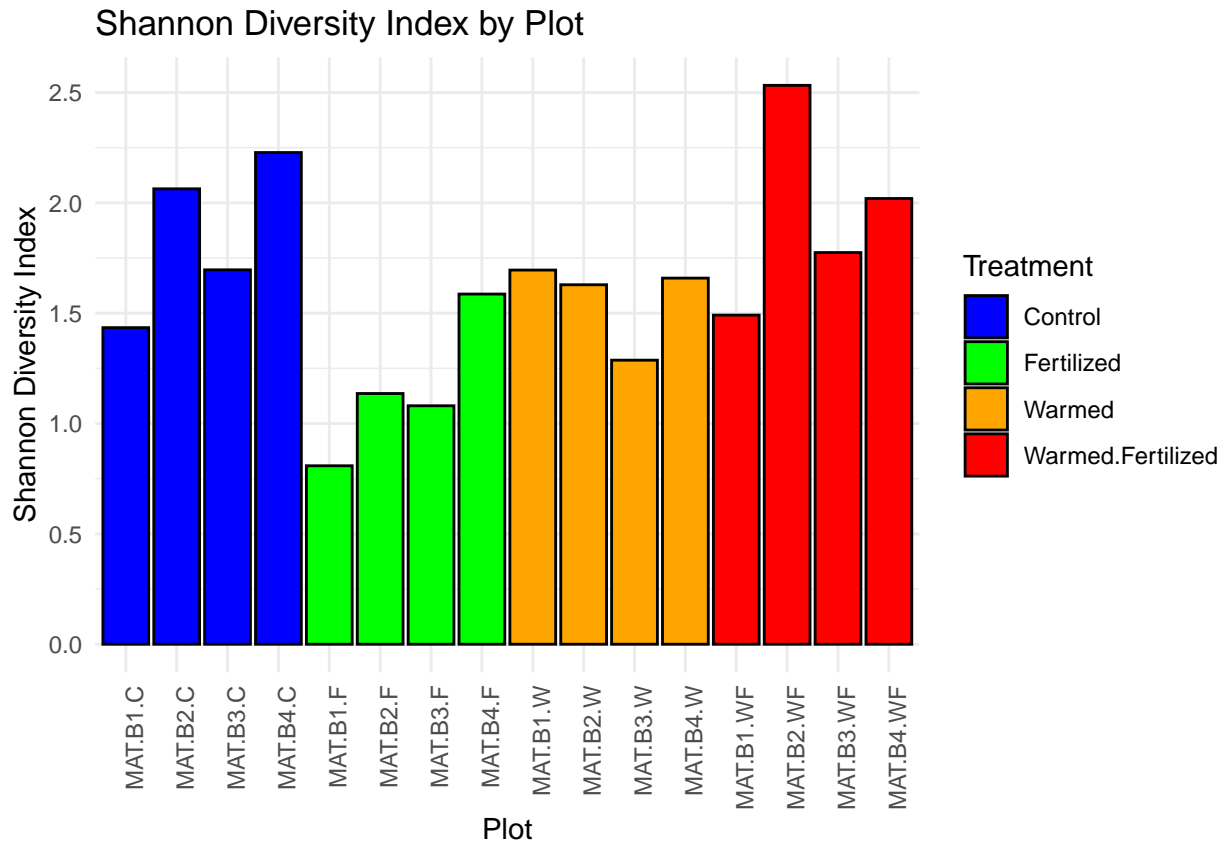
## # A tibble: 16 x 3
## # Groups:   Plot [16]
##   Plot      Treatment      Shannon_Index
##   <chr>      <chr>          <dbl>
## 1 MAT.B1.C Control          1.43
## 2 MAT.B1.F Fertilized        0.809
## 3 MAT.B1.W Warmed          1.70
## 4 MAT.B1.WF Warmed.Fertilized 1.49
## 5 MAT.B2.C Control          2.06
## 6 MAT.B2.F Fertilized        1.14
## 7 MAT.B2.W Warmed          1.63
## 8 MAT.B2.WF Warmed.Fertilized 2.53
## 9 MAT.B3.C Control          1.70
## 10 MAT.B3.F Fertilized        1.08
## 11 MAT.B3.W Warmed          1.29
## 12 MAT.B3.WF Warmed.Fertilized 1.77
## 13 MAT.B4.C Control          2.23
## 14 MAT.B4.F Fertilized        1.59
## 15 MAT.B4.W Warmed          1.66
## 16 MAT.B4.WF Warmed.Fertilized 2.02

# Ensure data is properly ordered by Treatment
merged_data_sorted <- merged_data_sorted %>%
  arrange(Treatment, Plot) # Sorting by Treatment first, then Plot

# Convert Plot to a factor to maintain order in the plot
merged_data_sorted$Plot <- factor(merged_data_sorted$Plot, levels = merged_data_sorted$Plot)

# Create the histogram (bar plot)
ggplot(merged_data_sorted, aes(x = Plot, y = Shannon_Index, fill = Treatment)) +
  geom_bar(stat = "identity", color = "black") + # Bar plot with black borders
  theme_minimal() +
  labs(x = "Plot", y = "Shannon Diversity Index", title = "Shannon Diversity Index by Plot") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) + # Rotate x-axis labels for readability
  scale_fill_manual(values = c("Control" = "blue", "Fertilized" = "green",
    "Warmed" = "orange", "Warmed.Fertilized" = "red")) # Custom colors

```



```
# Perform ANOVA
shannon_anova <- aov(Shannon_Index ~ Treatment, data = merged_data_sorted)
```

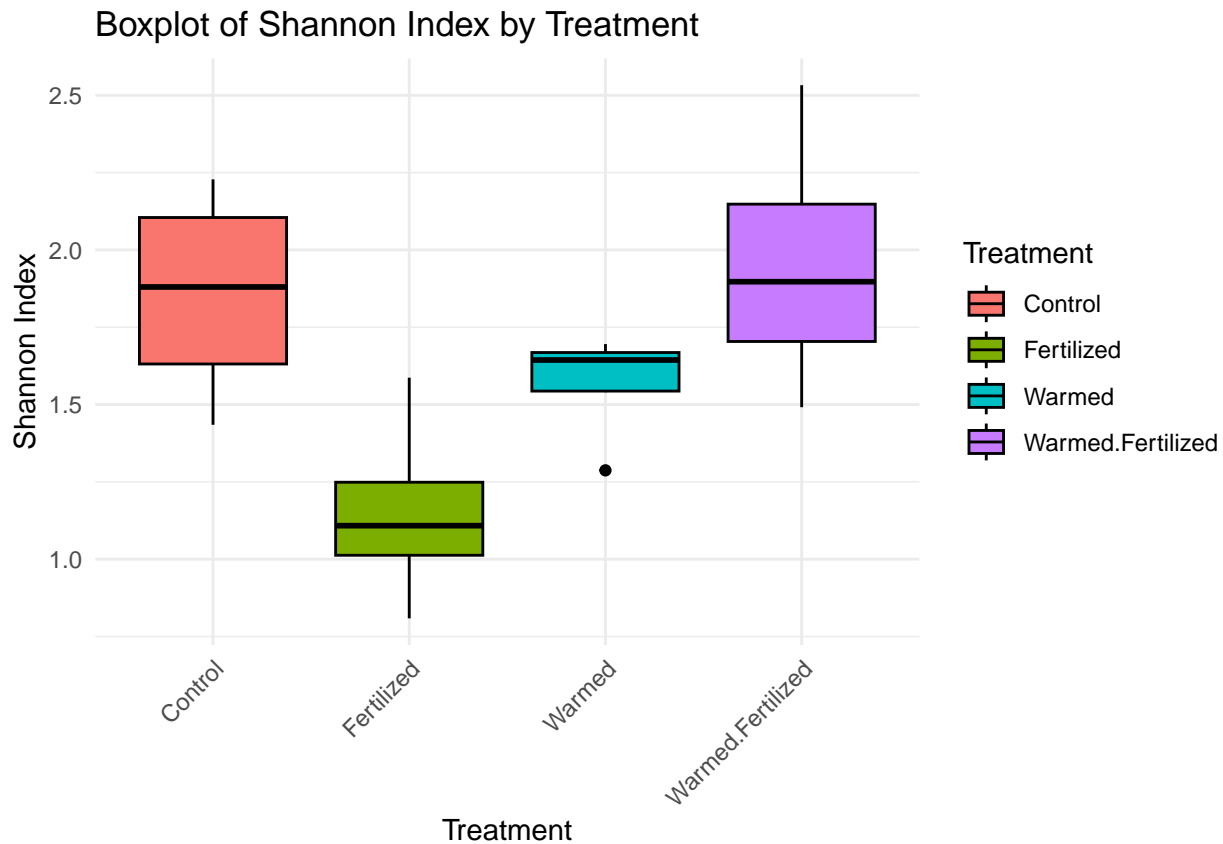
```
# View ANOVA summary
summary(shannon_anova)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Treatment      3  1.551  0.5169   4.465 0.0251 *
## Residuals     12  1.389  0.1158
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(shannon_anova)
```

```
##      Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = Shannon_Index ~ Treatment, data = merged_data_sorted)
##
## $Treatment
##              diff              lwr              upr              p adj
## Fertilized-Control      -0.70271613 -1.41699210  0.01155984  0.0543172
## Warmed-Control          -0.28807463 -1.00235060  0.42620134  0.6398631
## Warmed.Fertilized-Control  0.09887799 -0.61539798  0.81315396  0.9755299
## Warmed-Fertilized        0.41464150 -0.29963447  1.12891747  0.3542455
## Warmed.Fertilized-Fertilized 0.80159412  0.08731815  1.51587009  0.0265792
## Warmed.Fertilized-Warmed  0.38695262 -0.32732335  1.10122859  0.4102397
```

```
# Create the boxplot with the means
ggplot(merged_data_sorted, aes(x = Treatment, y = Shannon_Index)) +
  geom_boxplot(aes(fill = Treatment), color = "black") +
  labs(title = "Boxplot of Shannon Index by Treatment",
       x = "Treatment",
       y = "Shannon Index") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



Taxonomic beta-diversity

Visualization

```
package.list <- c('ape', 'seqinr', 'phylobase', 'adephylo', 'geiger', 'picante', 'stats', 'RColorBrewer')
for (package in package.list) {
  if (!require(package, character.only=TRUE, quietly=TRUE)) {
    install.packages(package)
    library(package, character.only=TRUE)
  }
}
```

```
##
## Attaching package: 'ape'
## The following object is masked from 'package:dplyr':
##
##   where
##
```

```

## Attaching package: 'seqinr'
## The following objects are masked from 'package:ape':
##
##      as.alignment, consensus
## The following object is masked from 'package:dplyr':
##
##      count
## The following object is masked from 'package:permute':
##
##      getType
##
## Attaching package: 'phylobase'
## The following object is masked from 'package:ape':
##
##      edges
##
## Attaching package: 'phytools'
## The following object is masked from 'package:phylobase':
##
##      readNexus
## The following object is masked from 'package:vegan':
##
##      scores
##
## Attaching package: 'nlme'
## The following object is masked from 'package:seqinr':
##
##      gls
## The following object is masked from 'package:dplyr':
##
##      collapse
##
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##      select
##
## Attaching package: 'phangorn'
## The following objects are masked from 'package:vegan':
##
##      diversity, treedist
##
## Attaching package: 'cluster'
## The following object is masked from 'package:maps':
##

```

```

##      votes.repub
## Registered S3 method overwritten by 'dendextend':
##      method      from
##      rev.hclust  vegan
##
## -----
## Welcome to dendextend version 1.19.0
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues
## You may ask questions at stackoverflow, use the r and dendextend tags:
##      https://stackoverflow.com/questions/tagged/dendextend
##
## To suppress this message use: suppressPackageStartupMessages(library(dendextend))
## -----
##
## Attaching package: 'dendextend'
##
## The following object is masked from 'package:geiger':
##
##      is.phylo
##
## The following object is masked from 'package:phytools':
##
##      untangle
##
## The following objects are masked from 'package:phylobase':
##
##      labels<-, prune
##
## The following objects are masked from 'package:ape':
##
##      ladderize, rotate
##
## The following object is masked from 'package:ggdendro':
##
##      theme_dendro
##
## The following object is masked from 'package:permute':
##
##      shuffle
##
## The following object is masked from 'package:stats':
##
##      cutree
##
## Attaching package: 'phylogram'
##
## The following object is masked from 'package:dendextend':
##
##      prune
##
## The following object is masked from 'package:phylobase':

```

```

##
##   prune
##
## Attaching package: 'amap'
## The following object is masked from 'package:vegan':
##
##   pca
##
## Attaching package: 'scales'
## The following object is masked from 'package:phytools':
##
##   rescale
## Warning in rgl.init(initValue, onlyNULL): RGL: unable to open X11 display
## Warning: 'rgl.init' failed, will use the null device.
## See '?rgl.useNULL' for ways to avoid this warning.
##
## Attaching package: 'viridis'
## The following object is masked from 'package:scales':
##
##   viridis_pal
## The following object is masked from 'package:maps':
##
##   unemp
##
## Attaching package: 'gplots'
## The following object is masked from 'package:stats':
##
##   lowess
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("msa")

## 'getOption("repos")' replaces Bioconductor standard repositories, see
## 'help("repositories", package = "BiocManager")' for details.
## Replacement repositories:
##   CRAN: http://rspm/default/__linux__/focal/latest
## Bioconductor version 3.20 (BiocManager 1.30.25), R 4.4.2 (2024-10-31)
## Warning: package(s) not installed when version(s) same as or greater than current; use
##   `force = TRUE` to re-install: 'msa'
## Installation paths not writeable, unable to update packages
##   path: /opt/R/4.4.2/lib/R/library
##   packages:
##     class, cluster, foreign, KernSmooth, MASS, Matrix, nlme, nnet, rpart,
##     spatial, survival
## Old packages: 'cpp11', 'data.table', 'insight', 'jsonlite', 'pander',
##   'processx', 'readxl', 'segmented', 'tinytex', 'xml2', 'zoo'

```

```
library(msa)
```

```
## Loading required package: Biostrings
## Loading required package: BiocGenerics
##
## Attaching package: 'BiocGenerics'
## The following object is masked from 'package:ade4':
##
##     score
## The following objects are masked from 'package:dplyr':
##
##     combine, intersect, setdiff, union
## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##     anyDuplicated, aperm, append, as.data.frame, basename, cbind,
##     colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
##     get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
##     match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
##     Position, rank, rbind, Reduce, rownames, sapply, saveRDS, setdiff,
##     table, tapply, union, unique, unsplit, which.max, which.min
## Loading required package: S4Vectors
## Loading required package: stats4
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:gplots':
##
##     space
## The following object is masked from 'package:tidyr':
##
##     expand
## The following objects are masked from 'package:dplyr':
##
##     first, rename
## The following object is masked from 'package:utils':
##
##     findMatches
## The following objects are masked from 'package:base':
##
##     expand.grid, I, unname
## Loading required package: IRanges
##
## Attaching package: 'IRanges'
```

```

## The following object is masked from 'package:nlme':
##
## collapse
## The following objects are masked from 'package:dplyr':
##
## collapse, desc, slice
## Loading required package: XVector
## Found more than one class "Annotated" in cache; using the first, from namespace 'RNeXML'
## Also defined by 'S4Vectors'
## Found more than one class "Annotated" in cache; using the first, from namespace 'RNeXML'
## Also defined by 'S4Vectors'
## Found more than one class "Annotated" in cache; using the first, from namespace 'RNeXML'
## Also defined by 'S4Vectors'
## Found more than one class "Annotated" in cache; using the first, from namespace 'RNeXML'
## Also defined by 'S4Vectors'
## Found more than one class "Annotated" in cache; using the first, from namespace 'RNeXML'
## Also defined by 'S4Vectors'
## Found more than one class "Annotated" in cache; using the first, from namespace 'RNeXML'
## Also defined by 'S4Vectors'
## Loading required package: GenomeInfoDb
##
## Attaching package: 'Biostrings'
## The following object is masked from 'package:dendextend':
##
## nnodes
## The following object is masked from 'package:seqinr':
##
## translate
## The following object is masked from 'package:ape':
##
## complement
## The following object is masked from 'package:base':
##
## strsplit
##
## Attaching package: 'msa'
## The following object is masked from 'package:BiocManager':
##
## version
Fungi_path <- "./data/MAT_fungal_abundances.txt"
Fungi_data <- read.table(Fungi_path, header = TRUE, sep = "\t", stringsAsFactors = TRUE)
Fungi_data$Relative.Abandance <- as.numeric(Fungi_data$Relative.Abandance)

```



```
# Slim down the data to only columns needed
```

```
library(dplyr)
```

```
Fungi_data %>% dplyr::select(Plot, Treatment, Species, Relative.Abandance)
```

##	Plot	Treatment	Species	Relative.Abandance
## 1	MAT.B1.C	Control	Alternaria_alternata	0.03448276
## 2	MAT.B1.C	Control	Articulospora_tetracladia	0.00000000
## 3	MAT.B1.C	Control	Cadophora_finlandica	0.00000000
## 4	MAT.B1.C	Control	Cenococcum_geophilum	0.03448276
## 5	MAT.B1.C	Control	Chalara_sp._1	0.00000000
## 6	MAT.B1.C	Control	Cortinarius_sp._1	0.37931034
## 7	MAT.B1.C	Control	Cortinarius_croceus_1	0.03448276
## 8	MAT.B1.C	Control	Cortinarius_glandicolor	0.03448276
## 9	MAT.B1.C	Control	Cortinarius_casimiri	0.00000000
## 10	MAT.B1.C	Control	Cortinarius_croceus_2	0.00000000
## 11	MAT.B1.C	Control	Cortinarius_herpeticus	0.00000000
## 12	MAT.B1.C	Control	Cortinarius_tabularis	0.00000000
## 13	MAT.B1.C	Control	Cortinarius_delibutus	0.00000000
## 14	MAT.B1.C	Control	Cortinarius_sp._2	0.00000000
## 15	MAT.B1.C	Control	Cortinarius_paragaudis	0.00000000
## 16	MAT.B1.C	Control	Cortinarius_sp._3	0.00000000
## 17	MAT.B1.C	Control	Helotiales_sp._1	0.00000000
## 18	MAT.B1.C	Control	Laccaria_laccata	0.00000000
## 19	MAT.B1.C	Control	Lactarius_vietus_1	0.10344828
## 20	MAT.B1.C	Control	Lactarius_glyciosmus	0.00000000
## 21	MAT.B1.C	Control	Lactarius_vietus_2	0.00000000
## 22	MAT.B1.C	Control	Leccinum_holopus	0.00000000
## 23	MAT.B1.C	Control	Leccinum_scabrum	0.00000000
## 24	MAT.B1.C	Control	Leccinum_variicolor_1	0.00000000
## 25	MAT.B1.C	Control	Leccinum_variicolor_2	0.00000000
## 26	MAT.B1.C	Control	Leccinum_variicolor_3	0.00000000
## 27	MAT.B1.C	Control	Leptodontidium_elatius	0.00000000
## 28	MAT.B1.C	Control	Meliniomyces_variabilis	0.00000000
## 29	MAT.B1.C	Control	Meliniomyces_bicolor	0.00000000
## 30	MAT.B1.C	Control	Phialocephala_fortinii	0.00000000
## 31	MAT.B1.C	Control	Pseudotomentella_sp._1	0.00000000
## 32	MAT.B1.C	Control	Rhizoscyphus_ericae	0.00000000
## 33	MAT.B1.C	Control	Thelephora_terrestris	0.00000000
## 34	MAT.B1.C	Control	Tomentella_sublilacina	0.00000000
## 35	MAT.B1.C	Control	Tomentella_sp._1	0.00000000
## 36	MAT.B1.C	Control	Tomentellopsis_submollis	0.00000000
## 37	MAT.B1.C	Control	Russula_chamiteae	0.00000000
## 38	MAT.B1.C	Control	Russula_decolorans	0.00000000
## 39	MAT.B1.C	Control	Russula_nitida/sphagnicola	0.00000000
## 40	MAT.B1.C	Control	Russula_sp._1	0.00000000
## 41	MAT.B1.C	Control	Russula_sp._2	0.00000000
## 42	MAT.B1.C	Control	Russula_sp._3	0.37931034
## 43	MAT.B1.C	Control	Russula_sp._4	0.00000000
## 44	MAT.B1.C	Control	Russula_vinosa	0.00000000
## 45	MAT.B1.F	Fertilized	Alternaria_alternata	0.00000000
## 46	MAT.B1.F	Fertilized	Articulospora_tetracladia	0.00000000
## 47	MAT.B1.F	Fertilized	Cadophora_finlandica	0.00000000
## 48	MAT.B1.F	Fertilized	Cenococcum_geophilum	0.00000000
## 49	MAT.B1.F	Fertilized	Chalara_sp._1	0.00000000

## 50	MAT.B1.F	Fertilized	Cortinarius_sp._1	0.00000000
## 51	MAT.B1.F	Fertilized	Cortinarius_croceus_1	0.00000000
## 52	MAT.B1.F	Fertilized	Cortinarius_glandicolor	0.00000000
## 53	MAT.B1.F	Fertilized	Cortinarius_casimiri	0.00000000
## 54	MAT.B1.F	Fertilized	Cortinarius_croceus_2	0.00000000
## 55	MAT.B1.F	Fertilized	Cortinarius_herpeticus	0.00000000
## 56	MAT.B1.F	Fertilized	Cortinarius_tabularis	0.00000000
## 57	MAT.B1.F	Fertilized	Cortinarius_delibutus	0.00000000
## 58	MAT.B1.F	Fertilized	Cortinarius_sp._2	0.00000000
## 59	MAT.B1.F	Fertilized	Cortinarius_paragaudis	0.00000000
## 60	MAT.B1.F	Fertilized	Cortinarius_sp._3	0.00000000
## 61	MAT.B1.F	Fertilized	Helotiales_sp._1	0.00000000
## 62	MAT.B1.F	Fertilized	Laccaria_laccata	0.00000000
## 63	MAT.B1.F	Fertilized	Lactarius_vietus_1	0.00000000
## 64	MAT.B1.F	Fertilized	Lactarius_glyciosmus	0.00000000
## 65	MAT.B1.F	Fertilized	Lactarius_vietus_2	0.00000000
## 66	MAT.B1.F	Fertilized	Leccinum_holopus	0.00000000
## 67	MAT.B1.F	Fertilized	Leccinum_scabrum	0.00000000
## 68	MAT.B1.F	Fertilized	Leccinum_variicolor_1	0.00000000
## 69	MAT.B1.F	Fertilized	Leccinum_variicolor_2	0.00000000
## 70	MAT.B1.F	Fertilized	Leccinum_variicolor_3	0.00000000
## 71	MAT.B1.F	Fertilized	Leptodontidium_elatius	0.00000000
## 72	MAT.B1.F	Fertilized	Meliniomyces_variabilis	0.00000000
## 73	MAT.B1.F	Fertilized	Meliniomyces_bicolor	0.00000000
## 74	MAT.B1.F	Fertilized	Phialocephala_fortinii	0.00000000
## 75	MAT.B1.F	Fertilized	Pseudotomentella_sp._1	0.00000000
## 76	MAT.B1.F	Fertilized	Rhizoscyphus_ericae	0.00000000
## 77	MAT.B1.F	Fertilized	Thelephora_terrestris	0.00000000
## 78	MAT.B1.F	Fertilized	Tomentella_sublilacina	0.00000000
## 79	MAT.B1.F	Fertilized	Tomentella_sp._1	0.00000000
## 80	MAT.B1.F	Fertilized	Tomentellopsis_submollis	0.02777778
## 81	MAT.B1.F	Fertilized	Russula_chamiteae	0.08333333
## 82	MAT.B1.F	Fertilized	Russula_decolorans	0.08333333
## 83	MAT.B1.F	Fertilized	Russula_nitida/sphagnicola	0.77777778
## 84	MAT.B1.F	Fertilized	Russula_sp._1	0.02777778
## 85	MAT.B1.F	Fertilized	Russula_sp._2	0.00000000
## 86	MAT.B1.F	Fertilized	Russula_sp._3	0.00000000
## 87	MAT.B1.F	Fertilized	Russula_sp._4	0.00000000
## 88	MAT.B1.F	Fertilized	Russula_vinosa	0.00000000
## 89	MAT.B1.W	Warmed	Alternaria_alternata	0.00000000
## 90	MAT.B1.W	Warmed	Articulospora_tetracladia	0.00000000
## 91	MAT.B1.W	Warmed	Cadophora_finlandica	0.00000000
## 92	MAT.B1.W	Warmed	Cenococcum_geophilum	0.00000000
## 93	MAT.B1.W	Warmed	Chalara_sp._1	0.00000000
## 94	MAT.B1.W	Warmed	Cortinarius_sp._1	0.00000000
## 95	MAT.B1.W	Warmed	Cortinarius_croceus_1	0.00000000
## 96	MAT.B1.W	Warmed	Cortinarius_glandicolor	0.00000000
## 97	MAT.B1.W	Warmed	Cortinarius_casimiri	0.00000000
## 98	MAT.B1.W	Warmed	Cortinarius_croceus_2	0.00000000
## 99	MAT.B1.W	Warmed	Cortinarius_herpeticus	0.00000000
## 100	MAT.B1.W	Warmed	Cortinarius_tabularis	0.00000000
## 101	MAT.B1.W	Warmed	Cortinarius_delibutus	0.00000000
## 102	MAT.B1.W	Warmed	Cortinarius_sp._2	0.00000000
## 103	MAT.B1.W	Warmed	Cortinarius_paragaudis	0.00000000

## 104	MAT.B1.W	Warmed	Cortinarius_sp._3	0.00000000
## 105	MAT.B1.W	Warmed	Helotiales_sp._1	0.00000000
## 106	MAT.B1.W	Warmed	Laccaria_laccata	0.00000000
## 107	MAT.B1.W	Warmed	Lactarius_vietus_1	0.00000000
## 108	MAT.B1.W	Warmed	Lactarius_glyciosmus	0.03225807
## 109	MAT.B1.W	Warmed	Lactarius_vietus_2	0.00000000
## 110	MAT.B1.W	Warmed	Leccinum_holopus	0.00000000
## 111	MAT.B1.W	Warmed	Leccinum_scabrum	0.00000000
## 112	MAT.B1.W	Warmed	Leccinum_variicolor_1	0.00000000
## 113	MAT.B1.W	Warmed	Leccinum_variicolor_2	0.00000000
## 114	MAT.B1.W	Warmed	Leccinum_variicolor_3	0.00000000
## 115	MAT.B1.W	Warmed	Leptodontidium_elatius	0.00000000
## 116	MAT.B1.W	Warmed	Meliniomyces_variabilis	0.00000000
## 117	MAT.B1.W	Warmed	Meliniomyces_bicolor	0.00000000
## 118	MAT.B1.W	Warmed	Phialocephala_fortinii	0.00000000
## 119	MAT.B1.W	Warmed	Pseudotomentella_sp._1	0.00000000
## 120	MAT.B1.W	Warmed	Rhizoscyphus_ericae	0.00000000
## 121	MAT.B1.W	Warmed	Thelephora_terrestris	0.00000000
## 122	MAT.B1.W	Warmed	Tomentella_sublilacina	0.00000000
## 123	MAT.B1.W	Warmed	Tomentella_sp._1	0.00000000
## 124	MAT.B1.W	Warmed	Tomentellopsis_submollis	0.06451613
## 125	MAT.B1.W	Warmed	Russula_chamiteae	0.16129032
## 126	MAT.B1.W	Warmed	Russula_decolorans	0.38709677
## 127	MAT.B1.W	Warmed	Russula_nitida/sphagnicola	0.16129032
## 128	MAT.B1.W	Warmed	Russula_sp._1	0.09677419
## 129	MAT.B1.W	Warmed	Russula_sp._2	0.00000000
## 130	MAT.B1.W	Warmed	Russula_sp._3	0.09677419
## 131	MAT.B1.W	Warmed	Russula_sp._4	0.00000000
## 132	MAT.B1.W	Warmed	Russula_vinosa	0.00000000
## 133	MAT.B1.WF	Warmed.Fertilized	Alternaria_alternata	0.00000000
## 134	MAT.B1.WF	Warmed.Fertilized	Articulospora_tetracladia	0.00000000
## 135	MAT.B1.WF	Warmed.Fertilized	Cadophora_finlandica	0.00000000
## 136	MAT.B1.WF	Warmed.Fertilized	Cenococcum_geophilum	0.00000000
## 137	MAT.B1.WF	Warmed.Fertilized	Chalara_sp._1	0.02857143
## 138	MAT.B1.WF	Warmed.Fertilized	Cortinarius_sp._1	0.00000000
## 139	MAT.B1.WF	Warmed.Fertilized	Cortinarius_croceus_1	0.00000000
## 140	MAT.B1.WF	Warmed.Fertilized	Cortinarius_glandicolor	0.00000000
## 141	MAT.B1.WF	Warmed.Fertilized	Cortinarius_casimiri	0.00000000
## 142	MAT.B1.WF	Warmed.Fertilized	Cortinarius_croceus_2	0.00000000
## 143	MAT.B1.WF	Warmed.Fertilized	Cortinarius_herpeticus	0.00000000
## 144	MAT.B1.WF	Warmed.Fertilized	Cortinarius_tabularis	0.00000000
## 145	MAT.B1.WF	Warmed.Fertilized	Cortinarius_delibutus	0.00000000
## 146	MAT.B1.WF	Warmed.Fertilized	Cortinarius_sp._2	0.00000000
## 147	MAT.B1.WF	Warmed.Fertilized	Cortinarius_paragaudis	0.00000000
## 148	MAT.B1.WF	Warmed.Fertilized	Cortinarius_sp._3	0.00000000
## 149	MAT.B1.WF	Warmed.Fertilized	Helotiales_sp._1	0.02857143
## 150	MAT.B1.WF	Warmed.Fertilized	Laccaria_laccata	0.40000000
## 151	MAT.B1.WF	Warmed.Fertilized	Lactarius_vietus_1	0.00000000
## 152	MAT.B1.WF	Warmed.Fertilized	Lactarius_glyciosmus	0.00000000
## 153	MAT.B1.WF	Warmed.Fertilized	Lactarius_vietus_2	0.00000000
## 154	MAT.B1.WF	Warmed.Fertilized	Leccinum_holopus	0.00000000
## 155	MAT.B1.WF	Warmed.Fertilized	Leccinum_scabrum	0.00000000
## 156	MAT.B1.WF	Warmed.Fertilized	Leccinum_variicolor_1	0.00000000
## 157	MAT.B1.WF	Warmed.Fertilized	Leccinum_variicolor_2	0.00000000

## 158	MAT.B1.WF	Warmed.Fertilized	Leccinum_variicolor_3	0.00000000
## 159	MAT.B1.WF	Warmed.Fertilized	Leptodontidium_elatius	0.00000000
## 160	MAT.B1.WF	Warmed.Fertilized	Meliniomyces_variabilis	0.00000000
## 161	MAT.B1.WF	Warmed.Fertilized	Meliniomyces_bicolor	0.00000000
## 162	MAT.B1.WF	Warmed.Fertilized	Phialocephala_fortinii	0.00000000
## 163	MAT.B1.WF	Warmed.Fertilized	Pseudotomentella_sp._1	0.00000000
## 164	MAT.B1.WF	Warmed.Fertilized	Rhizoscyphus_ericae	0.00000000
## 165	MAT.B1.WF	Warmed.Fertilized	Thelephora_terrestris	0.14285714
## 166	MAT.B1.WF	Warmed.Fertilized	Tomentella_sublilacina	0.00000000
## 167	MAT.B1.WF	Warmed.Fertilized	Tomentella_sp._1	0.00000000
## 168	MAT.B1.WF	Warmed.Fertilized	Tomentellopsis_submollis	0.20000000
## 169	MAT.B1.WF	Warmed.Fertilized	Russula_chamiteae	0.00000000
## 170	MAT.B1.WF	Warmed.Fertilized	Russula_decolorans	0.00000000
## 171	MAT.B1.WF	Warmed.Fertilized	Russula_nitida/sphagnicola	0.20000000
## 172	MAT.B1.WF	Warmed.Fertilized	Russula_sp._1	0.00000000
## 173	MAT.B1.WF	Warmed.Fertilized	Russula_sp._2	0.00000000
## 174	MAT.B1.WF	Warmed.Fertilized	Russula_sp._3	0.00000000
## 175	MAT.B1.WF	Warmed.Fertilized	Russula_sp._4	0.00000000
## 176	MAT.B1.WF	Warmed.Fertilized	Russula_vinosa	0.00000000
## 177	MAT.B2.C	Control	Alternaria_alternata	0.00000000
## 178	MAT.B2.C	Control	Articulospora_tetracladia	0.00000000
## 179	MAT.B2.C	Control	Cadophora_finlandica	0.00000000
## 180	MAT.B2.C	Control	Cenococcum_geophilum	0.09677419
## 181	MAT.B2.C	Control	Chalara_sp._1	0.00000000
## 182	MAT.B2.C	Control	Cortinarius_sp._1	0.00000000
## 183	MAT.B2.C	Control	Cortinarius_croceus_1	0.00000000
## 184	MAT.B2.C	Control	Cortinarius_glandicolor	0.00000000
## 185	MAT.B2.C	Control	Cortinarius_casimiri	0.00000000
## 186	MAT.B2.C	Control	Cortinarius_croceus_2	0.00000000
## 187	MAT.B2.C	Control	Cortinarius_herpeticus	0.00000000
## 188	MAT.B2.C	Control	Cortinarius_tabularis	0.00000000
## 189	MAT.B2.C	Control	Cortinarius_delibutus	0.00000000
## 190	MAT.B2.C	Control	Cortinarius_sp._2	0.00000000
## 191	MAT.B2.C	Control	Cortinarius_paragaudis	0.00000000
## 192	MAT.B2.C	Control	Cortinarius_sp._3	0.00000000
## 193	MAT.B2.C	Control	Helotiales_sp._1	0.00000000
## 194	MAT.B2.C	Control	Laccaria_laccata	0.00000000
## 195	MAT.B2.C	Control	Lactarius_vietus_1	0.29032258
## 196	MAT.B2.C	Control	Lactarius_glyciosmus	0.06451613
## 197	MAT.B2.C	Control	Lactarius_vietus_2	0.00000000
## 198	MAT.B2.C	Control	Leccinum_holopus	0.03225807
## 199	MAT.B2.C	Control	Leccinum_scabrum	0.00000000
## 200	MAT.B2.C	Control	Leccinum_variicolor_1	0.03225807
## 201	MAT.B2.C	Control	Leccinum_variicolor_2	0.00000000
## 202	MAT.B2.C	Control	Leccinum_variicolor_3	0.03225807
## 203	MAT.B2.C	Control	Leptodontidium_elatius	0.00000000
## 204	MAT.B2.C	Control	Meliniomyces_variabilis	0.03225807
## 205	MAT.B2.C	Control	Meliniomyces_bicolor	0.00000000
## 206	MAT.B2.C	Control	Phialocephala_fortinii	0.03225807
## 207	MAT.B2.C	Control	Pseudotomentella_sp._1	0.03225807
## 208	MAT.B2.C	Control	Rhizoscyphus_ericae	0.00000000
## 209	MAT.B2.C	Control	Thelephora_terrestris	0.00000000
## 210	MAT.B2.C	Control	Tomentella_sublilacina	0.00000000
## 211	MAT.B2.C	Control	Tomentella_sp._1	0.00000000

## 212	MAT.B2.C	Control	Tomentellopsis_submollis	0.00000000
## 213	MAT.B2.C	Control	Russula_chamiteae	0.03225807
## 214	MAT.B2.C	Control	Russula_decolorans	0.25806452
## 215	MAT.B2.C	Control	Russula_nitida/sphagnicola	0.00000000
## 216	MAT.B2.C	Control	Russula_sp._1	0.00000000
## 217	MAT.B2.C	Control	Russula_sp._2	0.00000000
## 218	MAT.B2.C	Control	Russula_sp._3	0.06451613
## 219	MAT.B2.C	Control	Russula_sp._4	0.00000000
## 220	MAT.B2.C	Control	Russula_vinosa	0.00000000
## 221	MAT.B2.F	Fertilized	Alternaria_alternata	0.00000000
## 222	MAT.B2.F	Fertilized	Articulospora_tetracladia	0.03571429
## 223	MAT.B2.F	Fertilized	Cadophora_finlandica	0.00000000
## 224	MAT.B2.F	Fertilized	Cenococcum_geophilum	0.00000000
## 225	MAT.B2.F	Fertilized	Chalara_sp._1	0.00000000
## 226	MAT.B2.F	Fertilized	Cortinarius_sp._1	0.00000000
## 227	MAT.B2.F	Fertilized	Cortinarius_croceus_1	0.00000000
## 228	MAT.B2.F	Fertilized	Cortinarius_glandicolor	0.00000000
## 229	MAT.B2.F	Fertilized	Cortinarius_casimiri	0.00000000
## 230	MAT.B2.F	Fertilized	Cortinarius_croceus_2	0.00000000
## 231	MAT.B2.F	Fertilized	Cortinarius_herpeticus	0.00000000
## 232	MAT.B2.F	Fertilized	Cortinarius_tabularis	0.00000000
## 233	MAT.B2.F	Fertilized	Cortinarius_delibutus	0.00000000
## 234	MAT.B2.F	Fertilized	Cortinarius_sp._2	0.00000000
## 235	MAT.B2.F	Fertilized	Cortinarius_paragaudis	0.00000000
## 236	MAT.B2.F	Fertilized	Cortinarius_sp._3	0.00000000
## 237	MAT.B2.F	Fertilized	Helotiales_sp._1	0.00000000
## 238	MAT.B2.F	Fertilized	Laccaria_laccata	0.00000000
## 239	MAT.B2.F	Fertilized	Lactarius_vietus_1	0.03571429
## 240	MAT.B2.F	Fertilized	Lactarius_glyciosmus	0.00000000
## 241	MAT.B2.F	Fertilized	Lactarius_vietus_2	0.00000000
## 242	MAT.B2.F	Fertilized	Leccinum_holopus	0.00000000
## 243	MAT.B2.F	Fertilized	Leccinum_scabrum	0.00000000
## 244	MAT.B2.F	Fertilized	Leccinum_variicolor_1	0.00000000
## 245	MAT.B2.F	Fertilized	Leccinum_variicolor_2	0.00000000
## 246	MAT.B2.F	Fertilized	Leccinum_variicolor_3	0.00000000
## 247	MAT.B2.F	Fertilized	Leptodontidium_elatius	0.00000000
## 248	MAT.B2.F	Fertilized	Meliniomyces_variabilis	0.03571429
## 249	MAT.B2.F	Fertilized	Meliniomyces_bicolor	0.00000000
## 250	MAT.B2.F	Fertilized	Phialocephala_fortinii	0.00000000
## 251	MAT.B2.F	Fertilized	Pseudotomentella_sp._1	0.03571429
## 252	MAT.B2.F	Fertilized	Rhizoscyphus_ericae	0.03571429
## 253	MAT.B2.F	Fertilized	Thelephora_terrestris	0.67857143
## 254	MAT.B2.F	Fertilized	Tomentella_sublilacina	0.00000000
## 255	MAT.B2.F	Fertilized	Tomentella_sp._1	0.00000000
## 256	MAT.B2.F	Fertilized	Tomentellopsis_submollis	0.14285714
## 257	MAT.B2.F	Fertilized	Russula_chamiteae	0.00000000
## 258	MAT.B2.F	Fertilized	Russula_decolorans	0.00000000
## 259	MAT.B2.F	Fertilized	Russula_nitida/sphagnicola	0.00000000
## 260	MAT.B2.F	Fertilized	Russula_sp._1	0.00000000
## 261	MAT.B2.F	Fertilized	Russula_sp._2	0.00000000
## 262	MAT.B2.F	Fertilized	Russula_sp._3	0.00000000
## 263	MAT.B2.F	Fertilized	Russula_sp._4	0.00000000
## 264	MAT.B2.F	Fertilized	Russula_vinosa	0.00000000
## 265	MAT.B2.W	Warmed	Alternaria_alternata	0.00000000

## 266	MAT.B2.W	Warmed	Articulospora_tetracladia	0.00000000
## 267	MAT.B2.W	Warmed	Cadophora_finlandica	0.00000000
## 268	MAT.B2.W	Warmed	Cenococcum_geophilum	0.15151515
## 269	MAT.B2.W	Warmed	Chalara_sp._1	0.00000000
## 270	MAT.B2.W	Warmed	Cortinarius_sp._1	0.00000000
## 271	MAT.B2.W	Warmed	Cortinarius_croceus_1	0.03030303
## 272	MAT.B2.W	Warmed	Cortinarius_glandicolor	0.00000000
## 273	MAT.B2.W	Warmed	Cortinarius_casimiri	0.00000000
## 274	MAT.B2.W	Warmed	Cortinarius_croceus_2	0.00000000
## 275	MAT.B2.W	Warmed	Cortinarius_herpeticus	0.00000000
## 276	MAT.B2.W	Warmed	Cortinarius_tabularis	0.00000000
## 277	MAT.B2.W	Warmed	Cortinarius_delibutus	0.00000000
## 278	MAT.B2.W	Warmed	Cortinarius_sp._2	0.00000000
## 279	MAT.B2.W	Warmed	Cortinarius_paragaudis	0.00000000
## 280	MAT.B2.W	Warmed	Cortinarius_sp._3	0.00000000
## 281	MAT.B2.W	Warmed	Helotiales_sp._1	0.00000000
## 282	MAT.B2.W	Warmed	Laccaria_laccata	0.00000000
## 283	MAT.B2.W	Warmed	Lactarius_vietus_1	0.03030303
## 284	MAT.B2.W	Warmed	Lactarius_glyciosmus	0.03030303
## 285	MAT.B2.W	Warmed	Lactarius_vietus_2	0.00000000
## 286	MAT.B2.W	Warmed	Leccinum_holopus	0.00000000
## 287	MAT.B2.W	Warmed	Leccinum_scabrum	0.00000000
## 288	MAT.B2.W	Warmed	Leccinum_variicolor_1	0.00000000
## 289	MAT.B2.W	Warmed	Leccinum_variicolor_2	0.00000000
## 290	MAT.B2.W	Warmed	Leccinum_variicolor_3	0.00000000
## 291	MAT.B2.W	Warmed	Leptodontidium_elatius	0.00000000
## 292	MAT.B2.W	Warmed	Meliniomyces_variabilis	0.03030303
## 293	MAT.B2.W	Warmed	Meliniomyces_bicolor	0.00000000
## 294	MAT.B2.W	Warmed	Phialocephala_fortinii	0.00000000
## 295	MAT.B2.W	Warmed	Pseudotomentella_sp._1	0.00000000
## 296	MAT.B2.W	Warmed	Rhizoscyphus_ericae	0.03030303
## 297	MAT.B2.W	Warmed	Thelephora_terrestris	0.00000000
## 298	MAT.B2.W	Warmed	Tomentella_sublilacina	0.00000000
## 299	MAT.B2.W	Warmed	Tomentella_sp._1	0.00000000
## 300	MAT.B2.W	Warmed	Tomentellopsis_submollis	0.00000000
## 301	MAT.B2.W	Warmed	Russula_chamiteae	0.00000000
## 302	MAT.B2.W	Warmed	Russula_decolorans	0.42424242
## 303	MAT.B2.W	Warmed	Russula_nitida/sphagnicola	0.03030303
## 304	MAT.B2.W	Warmed	Russula_sp._1	0.00000000
## 305	MAT.B2.W	Warmed	Russula_sp._2	0.00000000
## 306	MAT.B2.W	Warmed	Russula_sp._3	0.24242424
## 307	MAT.B2.W	Warmed	Russula_sp._4	0.00000000
## 308	MAT.B2.W	Warmed	Russula_vinosa	0.00000000
## 309	MAT.B2.WF	Warmed.Fertilized	Alternaria_alternata	0.00000000
## 310	MAT.B2.WF	Warmed.Fertilized	Articulospora_tetracladia	0.00000000
## 311	MAT.B2.WF	Warmed.Fertilized	Cadophora_finlandica	0.04761905
## 312	MAT.B2.WF	Warmed.Fertilized	Cenococcum_geophilum	0.00000000
## 313	MAT.B2.WF	Warmed.Fertilized	Chalara_sp._1	0.04761905
## 314	MAT.B2.WF	Warmed.Fertilized	Cortinarius_sp._1	0.00000000
## 315	MAT.B2.WF	Warmed.Fertilized	Cortinarius_croceus_1	0.00000000
## 316	MAT.B2.WF	Warmed.Fertilized	Cortinarius_glandicolor	0.00000000
## 317	MAT.B2.WF	Warmed.Fertilized	Cortinarius_casimiri	0.04761905
## 318	MAT.B2.WF	Warmed.Fertilized	Cortinarius_croceus_2	0.00000000
## 319	MAT.B2.WF	Warmed.Fertilized	Cortinarius_herpeticus	0.00000000

## 320	MAT.B2.WF	Warmed.Fertilized	Cortinarius_tabularis	0.00000000
## 321	MAT.B2.WF	Warmed.Fertilized	Cortinarius_delibutus	0.00000000
## 322	MAT.B2.WF	Warmed.Fertilized	Cortinarius_sp._2	0.00000000
## 323	MAT.B2.WF	Warmed.Fertilized	Cortinarius_paragaudis	0.00000000
## 324	MAT.B2.WF	Warmed.Fertilized	Cortinarius_sp._3	0.00000000
## 325	MAT.B2.WF	Warmed.Fertilized	Helotiales_sp._1	0.04761905
## 326	MAT.B2.WF	Warmed.Fertilized	Laccaria_laccata	0.04761905
## 327	MAT.B2.WF	Warmed.Fertilized	Lactarius_vietus_1	0.04761905
## 328	MAT.B2.WF	Warmed.Fertilized	Lactarius_glyciosmus	0.14285714
## 329	MAT.B2.WF	Warmed.Fertilized	Lactarius_vietus_2	0.00000000
## 330	MAT.B2.WF	Warmed.Fertilized	Leccinum_holopus	0.00000000
## 331	MAT.B2.WF	Warmed.Fertilized	Leccinum_scabrum	0.00000000
## 332	MAT.B2.WF	Warmed.Fertilized	Leccinum_variicolor_1	0.00000000
## 333	MAT.B2.WF	Warmed.Fertilized	Leccinum_variicolor_2	0.00000000
## 334	MAT.B2.WF	Warmed.Fertilized	Leccinum_variicolor_3	0.00000000
## 335	MAT.B2.WF	Warmed.Fertilized	Leptodontidium_elatius	0.00000000
## 336	MAT.B2.WF	Warmed.Fertilized	Meliniomyces_variabilis	0.00000000
## 337	MAT.B2.WF	Warmed.Fertilized	Meliniomyces_bicolor	0.04761905
## 338	MAT.B2.WF	Warmed.Fertilized	Phialocephala_fortinii	0.00000000
## 339	MAT.B2.WF	Warmed.Fertilized	Pseudotomentella_sp._1	0.14285714
## 340	MAT.B2.WF	Warmed.Fertilized	Rhizoscyphus_ericae	0.04761905
## 341	MAT.B2.WF	Warmed.Fertilized	Thelephora_terrestris	0.09523809
## 342	MAT.B2.WF	Warmed.Fertilized	Tomentella_sublilacina	0.00000000
## 343	MAT.B2.WF	Warmed.Fertilized	Tomentella_sp._1	0.00000000
## 344	MAT.B2.WF	Warmed.Fertilized	Tomentellopsis_submollis	0.09523809
## 345	MAT.B2.WF	Warmed.Fertilized	Russula_chamiteae	0.00000000
## 346	MAT.B2.WF	Warmed.Fertilized	Russula_decolorans	0.04761905
## 347	MAT.B2.WF	Warmed.Fertilized	Russula_nitida/sphagnicola	0.09523809
## 348	MAT.B2.WF	Warmed.Fertilized	Russula_sp._1	0.00000000
## 349	MAT.B2.WF	Warmed.Fertilized	Russula_sp._2	0.00000000
## 350	MAT.B2.WF	Warmed.Fertilized	Russula_sp._3	0.00000000
## 351	MAT.B2.WF	Warmed.Fertilized	Russula_sp._4	0.00000000
## 352	MAT.B2.WF	Warmed.Fertilized	Russula_vinosa	0.00000000
## 353	MAT.B3.C	Control	Alternaria_alternata	0.00000000
## 354	MAT.B3.C	Control	Articulospora_tetracladia	0.00000000
## 355	MAT.B3.C	Control	Cadophora_finlandica	0.00000000
## 356	MAT.B3.C	Control	Cenococcum_geophilum	0.00000000
## 357	MAT.B3.C	Control	Chalara_sp._1	0.00000000
## 358	MAT.B3.C	Control	Cortinarius_sp._1	0.11764706
## 359	MAT.B3.C	Control	Cortinarius_croceus_1	0.00000000
## 360	MAT.B3.C	Control	Cortinarius_glandicolor	0.00000000
## 361	MAT.B3.C	Control	Cortinarius_casimiri	0.00000000
## 362	MAT.B3.C	Control	Cortinarius_croceus_2	0.17647059
## 363	MAT.B3.C	Control	Cortinarius_herpeticus	0.00000000
## 364	MAT.B3.C	Control	Cortinarius_tabularis	0.00000000
## 365	MAT.B3.C	Control	Cortinarius_delibutus	0.00000000
## 366	MAT.B3.C	Control	Cortinarius_sp._2	0.00000000
## 367	MAT.B3.C	Control	Cortinarius_paragaudis	0.00000000
## 368	MAT.B3.C	Control	Cortinarius_sp._3	0.00000000
## 369	MAT.B3.C	Control	Helotiales_sp._1	0.00000000
## 370	MAT.B3.C	Control	Laccaria_laccata	0.00000000
## 371	MAT.B3.C	Control	Lactarius_vietus_1	0.17647059
## 372	MAT.B3.C	Control	Lactarius_glyciosmus	0.00000000
## 373	MAT.B3.C	Control	Lactarius_vietus_2	0.00000000

## 374	MAT.B3.C	Control	Leccinum_holopus	0.00000000
## 375	MAT.B3.C	Control	Leccinum_scabrum	0.00000000
## 376	MAT.B3.C	Control	Leccinum_variicolor_1	0.00000000
## 377	MAT.B3.C	Control	Leccinum_variicolor_2	0.00000000
## 378	MAT.B3.C	Control	Leccinum_variicolor_3	0.00000000
## 379	MAT.B3.C	Control	Leptodontidium_elatius	0.00000000
## 380	MAT.B3.C	Control	Meliniomyces_variabilis	0.00000000
## 381	MAT.B3.C	Control	Meliniomyces_bicolor	0.00000000
## 382	MAT.B3.C	Control	Phialocephala_fortinii	0.00000000
## 383	MAT.B3.C	Control	Pseudotomentella_sp._1	0.00000000
## 384	MAT.B3.C	Control	Rhizoscyphus_ericae	0.00000000
## 385	MAT.B3.C	Control	Thelephora_terrestris	0.00000000
## 386	MAT.B3.C	Control	Tomentella_sublilacina	0.00000000
## 387	MAT.B3.C	Control	Tomentella_sp._1	0.00000000
## 388	MAT.B3.C	Control	Tomentellopsis_submollis	0.00000000
## 389	MAT.B3.C	Control	Russula_chamiteae	0.00000000
## 390	MAT.B3.C	Control	Russula_decolorans	0.29411765
## 391	MAT.B3.C	Control	Russula_nitida/sphagnicola	0.05882353
## 392	MAT.B3.C	Control	Russula_sp._1	0.17647059
## 393	MAT.B3.C	Control	Russula_sp._2	0.00000000
## 394	MAT.B3.C	Control	Russula_sp._3	0.00000000
## 395	MAT.B3.C	Control	Russula_sp._4	0.00000000
## 396	MAT.B3.C	Control	Russula_vinosa	0.00000000
## 397	MAT.B3.F	Fertilized	Alternaria_alternata	0.00000000
## 398	MAT.B3.F	Fertilized	Articulospora_tetracladia	0.00000000
## 399	MAT.B3.F	Fertilized	Cadophora_finlandica	0.00000000
## 400	MAT.B3.F	Fertilized	Cenococcum_geophilum	0.00000000
## 401	MAT.B3.F	Fertilized	Chalara_sp._1	0.00000000
## 402	MAT.B3.F	Fertilized	Cortinarius_sp._1	0.00000000
## 403	MAT.B3.F	Fertilized	Cortinarius_croceus_1	0.00000000
## 404	MAT.B3.F	Fertilized	Cortinarius_glandicolor	0.00000000
## 405	MAT.B3.F	Fertilized	Cortinarius_casimiri	0.00000000
## 406	MAT.B3.F	Fertilized	Cortinarius_croceus_2	0.00000000
## 407	MAT.B3.F	Fertilized	Cortinarius_herpeticus	0.00000000
## 408	MAT.B3.F	Fertilized	Cortinarius_tabularis	0.00000000
## 409	MAT.B3.F	Fertilized	Cortinarius_delibutus	0.00000000
## 410	MAT.B3.F	Fertilized	Cortinarius_sp._2	0.00000000
## 411	MAT.B3.F	Fertilized	Cortinarius_paragaudis	0.00000000
## 412	MAT.B3.F	Fertilized	Cortinarius_sp._3	0.00000000
## 413	MAT.B3.F	Fertilized	Helotiales_sp._1	0.00000000
## 414	MAT.B3.F	Fertilized	Laccaria_laccata	0.06666667
## 415	MAT.B3.F	Fertilized	Lactarius_vietus_1	0.06666667
## 416	MAT.B3.F	Fertilized	Lactarius_glyciosmus	0.13333333
## 417	MAT.B3.F	Fertilized	Lactarius_vietus_2	0.00000000
## 418	MAT.B3.F	Fertilized	Leccinum_holopus	0.00000000
## 419	MAT.B3.F	Fertilized	Leccinum_scabrum	0.00000000
## 420	MAT.B3.F	Fertilized	Leccinum_variicolor_1	0.00000000
## 421	MAT.B3.F	Fertilized	Leccinum_variicolor_2	0.00000000
## 422	MAT.B3.F	Fertilized	Leccinum_variicolor_3	0.00000000
## 423	MAT.B3.F	Fertilized	Leptodontidium_elatius	0.00000000
## 424	MAT.B3.F	Fertilized	Meliniomyces_variabilis	0.00000000
## 425	MAT.B3.F	Fertilized	Meliniomyces_bicolor	0.00000000
## 426	MAT.B3.F	Fertilized	Phialocephala_fortinii	0.00000000
## 427	MAT.B3.F	Fertilized	Pseudotomentella_sp._1	0.00000000

## 428	MAT.B3.F	Fertilized	Rhizoscyphus_ericae	0.00000000
## 429	MAT.B3.F	Fertilized	Thelephora_terrestris	0.00000000
## 430	MAT.B3.F	Fertilized	Tomentella_sublilacina	0.00000000
## 431	MAT.B3.F	Fertilized	Tomentella_sp._1	0.00000000
## 432	MAT.B3.F	Fertilized	Tomentellopsis_submollis	0.06666667
## 433	MAT.B3.F	Fertilized	Russula_chamiteae	0.00000000
## 434	MAT.B3.F	Fertilized	Russula_decolorans	0.00000000
## 435	MAT.B3.F	Fertilized	Russula_nitida/sphagnicola	0.66666667
## 436	MAT.B3.F	Fertilized	Russula_sp._1	0.00000000
## 437	MAT.B3.F	Fertilized	Russula_sp._2	0.00000000
## 438	MAT.B3.F	Fertilized	Russula_sp._3	0.00000000
## 439	MAT.B3.F	Fertilized	Russula_sp._4	0.00000000
## 440	MAT.B3.F	Fertilized	Russula_vinosa	0.00000000
## 441	MAT.B3.W	Warmed	Alternaria_alternata	0.00000000
## 442	MAT.B3.W	Warmed	Articulospora_tetracladia	0.00000000
## 443	MAT.B3.W	Warmed	Cadophora_finlandica	0.00000000
## 444	MAT.B3.W	Warmed	Cenococcum_geophilum	0.00000000
## 445	MAT.B3.W	Warmed	Chalara_sp._1	0.00000000
## 446	MAT.B3.W	Warmed	Cortinarius_sp._1	0.00000000
## 447	MAT.B3.W	Warmed	Cortinarius_croceus_1	0.00000000
## 448	MAT.B3.W	Warmed	Cortinarius_glandicolor	0.00000000
## 449	MAT.B3.W	Warmed	Cortinarius_casimiri	0.00000000
## 450	MAT.B3.W	Warmed	Cortinarius_croceus_2	0.00000000
## 451	MAT.B3.W	Warmed	Cortinarius_herpeticus	0.00000000
## 452	MAT.B3.W	Warmed	Cortinarius_tabularis	0.00000000
## 453	MAT.B3.W	Warmed	Cortinarius_delibutus	0.00000000
## 454	MAT.B3.W	Warmed	Cortinarius_sp._2	0.00000000
## 455	MAT.B3.W	Warmed	Cortinarius_paragaudis	0.00000000
## 456	MAT.B3.W	Warmed	Cortinarius_sp._3	0.00000000
## 457	MAT.B3.W	Warmed	Helotiales_sp._1	0.00000000
## 458	MAT.B3.W	Warmed	Laccaria_laccata	0.00000000
## 459	MAT.B3.W	Warmed	Lactarius_vietus_1	0.00000000
## 460	MAT.B3.W	Warmed	Lactarius_glyciosmus	0.11111111
## 461	MAT.B3.W	Warmed	Lactarius_vietus_2	0.00000000
## 462	MAT.B3.W	Warmed	Leccinum_holopus	0.00000000
## 463	MAT.B3.W	Warmed	Leccinum_scabrum	0.03703704
## 464	MAT.B3.W	Warmed	Leccinum_variicolor_1	0.00000000
## 465	MAT.B3.W	Warmed	Leccinum_variicolor_2	0.00000000
## 466	MAT.B3.W	Warmed	Leccinum_variicolor_3	0.00000000
## 467	MAT.B3.W	Warmed	Leptodontidium_elatius	0.07407407
## 468	MAT.B3.W	Warmed	Meliniomyces_variabilis	0.00000000
## 469	MAT.B3.W	Warmed	Meliniomyces_bicolor	0.07407407
## 470	MAT.B3.W	Warmed	Phialocephala_fortinii	0.00000000
## 471	MAT.B3.W	Warmed	Pseudotomentella_sp._1	0.00000000
## 472	MAT.B3.W	Warmed	Rhizoscyphus_ericae	0.00000000
## 473	MAT.B3.W	Warmed	Thelephora_terrestris	0.00000000
## 474	MAT.B3.W	Warmed	Tomentella_sublilacina	0.00000000
## 475	MAT.B3.W	Warmed	Tomentella_sp._1	0.00000000
## 476	MAT.B3.W	Warmed	Tomentellopsis_submollis	0.03703704
## 477	MAT.B3.W	Warmed	Russula_chamiteae	0.00000000
## 478	MAT.B3.W	Warmed	Russula_decolorans	0.00000000
## 479	MAT.B3.W	Warmed	Russula_nitida/sphagnicola	0.62962963
## 480	MAT.B3.W	Warmed	Russula_sp._1	0.00000000
## 481	MAT.B3.W	Warmed	Russula_sp._2	0.00000000

## 482	MAT.B3.W	Warmed	Russula_sp._3	0.00000000
## 483	MAT.B3.W	Warmed	Russula_sp._4	0.00000000
## 484	MAT.B3.W	Warmed	Russula_vinosa	0.03703704
## 485	MAT.B3.WF	Warmed.Fertilized	Alternaria_alternata	0.00000000
## 486	MAT.B3.WF	Warmed.Fertilized	Articulospora_tetracladia	0.00000000
## 487	MAT.B3.WF	Warmed.Fertilized	Cadophora_finlandica	0.00000000
## 488	MAT.B3.WF	Warmed.Fertilized	Cenococcum_geophilum	0.00000000
## 489	MAT.B3.WF	Warmed.Fertilized	Chalara_sp._1	0.00000000
## 490	MAT.B3.WF	Warmed.Fertilized	Cortinarius_sp._1	0.00000000
## 491	MAT.B3.WF	Warmed.Fertilized	Cortinarius_croceus_1	0.00000000
## 492	MAT.B3.WF	Warmed.Fertilized	Cortinarius_glandicolor	0.00000000
## 493	MAT.B3.WF	Warmed.Fertilized	Cortinarius_casimiri	0.00000000
## 494	MAT.B3.WF	Warmed.Fertilized	Cortinarius_croceus_2	0.00000000
## 495	MAT.B3.WF	Warmed.Fertilized	Cortinarius_herpeticus	0.00000000
## 496	MAT.B3.WF	Warmed.Fertilized	Cortinarius_tabularis	0.00000000
## 497	MAT.B3.WF	Warmed.Fertilized	Cortinarius_delibutus	0.00000000
## 498	MAT.B3.WF	Warmed.Fertilized	Cortinarius_sp._2	0.00000000
## 499	MAT.B3.WF	Warmed.Fertilized	Cortinarius_paragaudis	0.00000000
## 500	MAT.B3.WF	Warmed.Fertilized	Cortinarius_sp._3	0.00000000
## 501	MAT.B3.WF	Warmed.Fertilized	Helotiales_sp._1	0.00000000
## 502	MAT.B3.WF	Warmed.Fertilized	Laccaria_laccata	0.14285714
## 503	MAT.B3.WF	Warmed.Fertilized	Lactarius_vietus_1	0.00000000
## 504	MAT.B3.WF	Warmed.Fertilized	Lactarius_glyciosmus	0.25000000
## 505	MAT.B3.WF	Warmed.Fertilized	Lactarius_vietus_2	0.00000000
## 506	MAT.B3.WF	Warmed.Fertilized	Leccinum_holopus	0.00000000
## 507	MAT.B3.WF	Warmed.Fertilized	Leccinum_scabrum	0.00000000
## 508	MAT.B3.WF	Warmed.Fertilized	Leccinum_variicolor_1	0.00000000
## 509	MAT.B3.WF	Warmed.Fertilized	Leccinum_variicolor_2	0.00000000
## 510	MAT.B3.WF	Warmed.Fertilized	Leccinum_variicolor_3	0.00000000
## 511	MAT.B3.WF	Warmed.Fertilized	Leptodontidium_elatius	0.00000000
## 512	MAT.B3.WF	Warmed.Fertilized	Meliniomyces_variabilis	0.00000000
## 513	MAT.B3.WF	Warmed.Fertilized	Meliniomyces_bicolor	0.00000000
## 514	MAT.B3.WF	Warmed.Fertilized	Phialocephala_fortinii	0.00000000
## 515	MAT.B3.WF	Warmed.Fertilized	Pseudotomentella_sp._1	0.00000000
## 516	MAT.B3.WF	Warmed.Fertilized	Rhizoscyphus_ericae	0.00000000
## 517	MAT.B3.WF	Warmed.Fertilized	Thelephora_terrestris	0.00000000
## 518	MAT.B3.WF	Warmed.Fertilized	Tomentella_sublilacina	0.00000000
## 519	MAT.B3.WF	Warmed.Fertilized	Tomentella_sp._1	0.00000000
## 520	MAT.B3.WF	Warmed.Fertilized	Tomentellopsis_submollis	0.07142857
## 521	MAT.B3.WF	Warmed.Fertilized	Russula_chamiteae	0.00000000
## 522	MAT.B3.WF	Warmed.Fertilized	Russula_decolorans	0.00000000
## 523	MAT.B3.WF	Warmed.Fertilized	Russula_nitida/sphagnicola	0.17857143
## 524	MAT.B3.WF	Warmed.Fertilized	Russula_sp._1	0.03571429
## 525	MAT.B3.WF	Warmed.Fertilized	Russula_sp._2	0.07142857
## 526	MAT.B3.WF	Warmed.Fertilized	Russula_sp._3	0.25000000
## 527	MAT.B3.WF	Warmed.Fertilized	Russula_sp._4	0.00000000
## 528	MAT.B3.WF	Warmed.Fertilized	Russula_vinosa	0.00000000
## 529	MAT.B4.C	Control	Alternaria_alternata	0.00000000
## 530	MAT.B4.C	Control	Articulospora_tetracladia	0.00000000
## 531	MAT.B4.C	Control	Cadophora_finlandica	0.00000000
## 532	MAT.B4.C	Control	Cenococcum_geophilum	0.10000000
## 533	MAT.B4.C	Control	Chalara_sp._1	0.00000000
## 534	MAT.B4.C	Control	Cortinarius_sp._1	0.16666667
## 535	MAT.B4.C	Control	Cortinarius_croceus_1	0.00000000

## 536	MAT.B4.C	Control	Cortinarius_glandicolor	0.00000000
## 537	MAT.B4.C	Control	Cortinarius_casimiri	0.00000000
## 538	MAT.B4.C	Control	Cortinarius_croceus_2	0.00000000
## 539	MAT.B4.C	Control	Cortinarius_herpeticus	0.10000000
## 540	MAT.B4.C	Control	Cortinarius_tabularis	0.03333333
## 541	MAT.B4.C	Control	Cortinarius_delibutus	0.00000000
## 542	MAT.B4.C	Control	Cortinarius_sp._2	0.00000000
## 543	MAT.B4.C	Control	Cortinarius_paragaudis	0.00000000
## 544	MAT.B4.C	Control	Cortinarius_sp._3	0.00000000
## 545	MAT.B4.C	Control	Helotiales_sp._1	0.00000000
## 546	MAT.B4.C	Control	Laccaria_laccata	0.03333333
## 547	MAT.B4.C	Control	Lactarius_vietus_1	0.00000000
## 548	MAT.B4.C	Control	Lactarius_glyciosmus	0.03333333
## 549	MAT.B4.C	Control	Lactarius_vietus_2	0.00000000
## 550	MAT.B4.C	Control	Leccinum_holopus	0.00000000
## 551	MAT.B4.C	Control	Leccinum_scabrum	0.00000000
## 552	MAT.B4.C	Control	Leccinum_variicolor_1	0.00000000
## 553	MAT.B4.C	Control	Leccinum_variicolor_2	0.03333333
## 554	MAT.B4.C	Control	Leccinum_variicolor_3	0.00000000
## 555	MAT.B4.C	Control	Leptodontidium_elatius	0.00000000
## 556	MAT.B4.C	Control	Meliniomyces_variabilis	0.00000000
## 557	MAT.B4.C	Control	Meliniomyces_bicolor	0.00000000
## 558	MAT.B4.C	Control	Phialocephala_fortinii	0.00000000
## 559	MAT.B4.C	Control	Pseudotomentella_sp._1	0.00000000
## 560	MAT.B4.C	Control	Rhizoscyphus_ericae	0.00000000
## 561	MAT.B4.C	Control	Thelephora_terrestris	0.00000000
## 562	MAT.B4.C	Control	Tomentella_sublilacina	0.00000000
## 563	MAT.B4.C	Control	Tomentella_sp._1	0.00000000
## 564	MAT.B4.C	Control	Tomentellopsis_submollis	0.03333333
## 565	MAT.B4.C	Control	Russula_chamiteae	0.13333333
## 566	MAT.B4.C	Control	Russula_decolorans	0.23333333
## 567	MAT.B4.C	Control	Russula_nitida/sphagnicola	0.03333333
## 568	MAT.B4.C	Control	Russula_sp._1	0.06666667
## 569	MAT.B4.C	Control	Russula_sp._2	0.00000000
## 570	MAT.B4.C	Control	Russula_sp._3	0.00000000
## 571	MAT.B4.C	Control	Russula_sp._4	0.00000000
## 572	MAT.B4.C	Control	Russula_vinosa	0.00000000
## 573	MAT.B4.F	Fertilized	Alternaria_alternata	0.00000000
## 574	MAT.B4.F	Fertilized	Articulospora_tetracladia	0.00000000
## 575	MAT.B4.F	Fertilized	Cadophora_finlandica	0.00000000
## 576	MAT.B4.F	Fertilized	Cenococcum_geophilum	0.00000000
## 577	MAT.B4.F	Fertilized	Chalara_sp._1	0.00000000
## 578	MAT.B4.F	Fertilized	Cortinarius_sp._1	0.00000000
## 579	MAT.B4.F	Fertilized	Cortinarius_croceus_1	0.00000000
## 580	MAT.B4.F	Fertilized	Cortinarius_glandicolor	0.00000000
## 581	MAT.B4.F	Fertilized	Cortinarius_casimiri	0.00000000
## 582	MAT.B4.F	Fertilized	Cortinarius_croceus_2	0.00000000
## 583	MAT.B4.F	Fertilized	Cortinarius_herpeticus	0.00000000
## 584	MAT.B4.F	Fertilized	Cortinarius_tabularis	0.00000000
## 585	MAT.B4.F	Fertilized	Cortinarius_delibutus	0.10000000
## 586	MAT.B4.F	Fertilized	Cortinarius_sp._2	0.00000000
## 587	MAT.B4.F	Fertilized	Cortinarius_paragaudis	0.00000000
## 588	MAT.B4.F	Fertilized	Cortinarius_sp._3	0.00000000
## 589	MAT.B4.F	Fertilized	Helotiales_sp._1	0.00000000

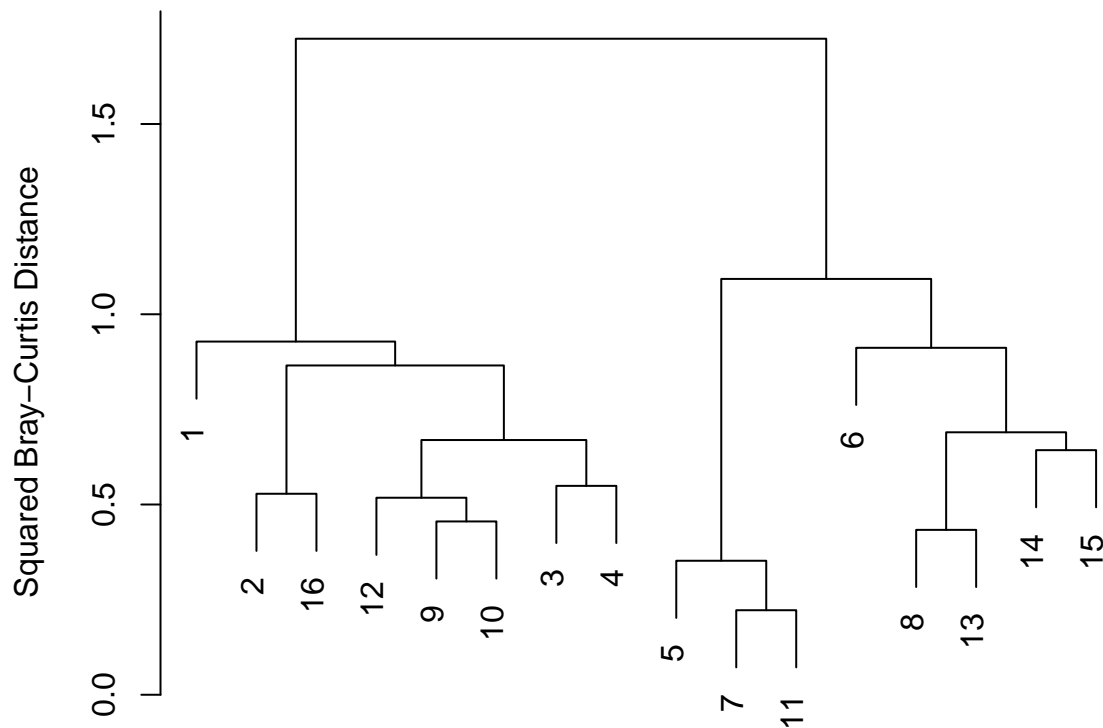
## 590	MAT.B4.F	Fertilized	Laccaria_laccata	0.26666667
## 591	MAT.B4.F	Fertilized	Lactarius_vietus_1	0.00000000
## 592	MAT.B4.F	Fertilized	Lactarius_glyciosmus	0.06666667
## 593	MAT.B4.F	Fertilized	Lactarius_vietus_2	0.03333333
## 594	MAT.B4.F	Fertilized	Leccinum_holopus	0.00000000
## 595	MAT.B4.F	Fertilized	Leccinum_scabrum	0.00000000
## 596	MAT.B4.F	Fertilized	Leccinum_variicolor_1	0.00000000
## 597	MAT.B4.F	Fertilized	Leccinum_variicolor_2	0.00000000
## 598	MAT.B4.F	Fertilized	Leccinum_variicolor_3	0.00000000
## 599	MAT.B4.F	Fertilized	Leptodontidium_elatius	0.00000000
## 600	MAT.B4.F	Fertilized	Meliniomyces_variabilis	0.00000000
## 601	MAT.B4.F	Fertilized	Meliniomyces_bicolor	0.00000000
## 602	MAT.B4.F	Fertilized	Phialocephala_fortinii	0.00000000
## 603	MAT.B4.F	Fertilized	Pseudotomentella_sp._1	0.00000000
## 604	MAT.B4.F	Fertilized	Rhizoscyphus_ericae	0.03333333
## 605	MAT.B4.F	Fertilized	Thelephora_terrestris	0.10000000
## 606	MAT.B4.F	Fertilized	Tomentella_sublilacina	0.00000000
## 607	MAT.B4.F	Fertilized	Tomentella_sp._1	0.00000000
## 608	MAT.B4.F	Fertilized	Tomentellopsis_submollis	0.00000000
## 609	MAT.B4.F	Fertilized	Russula_chamiteae	0.00000000
## 610	MAT.B4.F	Fertilized	Russula_decolorans	0.00000000
## 611	MAT.B4.F	Fertilized	Russula_nitida/sphagnicola	0.40000000
## 612	MAT.B4.F	Fertilized	Russula_sp._1	0.00000000
## 613	MAT.B4.F	Fertilized	Russula_sp._2	0.00000000
## 614	MAT.B4.F	Fertilized	Russula_sp._3	0.00000000
## 615	MAT.B4.F	Fertilized	Russula_sp._4	0.00000000
## 616	MAT.B4.F	Fertilized	Russula_vinosa	0.00000000
## 617	MAT.B4.W	Warmed	Alternaria_alternata	0.00000000
## 618	MAT.B4.W	Warmed	Articulospora_tetracladia	0.00000000
## 619	MAT.B4.W	Warmed	Cadophora_finlandica	0.00000000
## 620	MAT.B4.W	Warmed	Cenococcum_geophilum	0.03389830
## 621	MAT.B4.W	Warmed	Chalara_sp._1	0.00000000
## 622	MAT.B4.W	Warmed	Cortinarius_sp._1	0.00000000
## 623	MAT.B4.W	Warmed	Cortinarius_croceus_1	0.00000000
## 624	MAT.B4.W	Warmed	Cortinarius_glandicolor	0.00000000
## 625	MAT.B4.W	Warmed	Cortinarius_casimiri	0.00000000
## 626	MAT.B4.W	Warmed	Cortinarius_croceus_2	0.01694915
## 627	MAT.B4.W	Warmed	Cortinarius_herpeticus	0.00000000
## 628	MAT.B4.W	Warmed	Cortinarius_tabularis	0.00000000
## 629	MAT.B4.W	Warmed	Cortinarius_delibutus	0.00000000
## 630	MAT.B4.W	Warmed	Cortinarius_sp._2	0.08474576
## 631	MAT.B4.W	Warmed	Cortinarius_paragaudis	0.01694915
## 632	MAT.B4.W	Warmed	Cortinarius_sp._3	0.00000000
## 633	MAT.B4.W	Warmed	Helotiales_sp._1	0.00000000
## 634	MAT.B4.W	Warmed	Laccaria_laccata	0.00000000
## 635	MAT.B4.W	Warmed	Lactarius_vietus_1	0.10169491
## 636	MAT.B4.W	Warmed	Lactarius_glyciosmus	0.01694915
## 637	MAT.B4.W	Warmed	Lactarius_vietus_2	0.00000000
## 638	MAT.B4.W	Warmed	Leccinum_holopus	0.00000000
## 639	MAT.B4.W	Warmed	Leccinum_scabrum	0.00000000
## 640	MAT.B4.W	Warmed	Leccinum_variicolor_1	0.00000000
## 641	MAT.B4.W	Warmed	Leccinum_variicolor_2	0.00000000
## 642	MAT.B4.W	Warmed	Leccinum_variicolor_3	0.00000000
## 643	MAT.B4.W	Warmed	Leptodontidium_elatius	0.00000000

## 644	MAT.B4.W	Warmed	Meliniomyces_variabilis	0.00000000
## 645	MAT.B4.W	Warmed	Meliniomyces_bicolor	0.00000000
## 646	MAT.B4.W	Warmed	Phialocephala_fortinii	0.00000000
## 647	MAT.B4.W	Warmed	Pseudotomentella_sp._1	0.00000000
## 648	MAT.B4.W	Warmed	Rhizoscyphus_ericae	0.00000000
## 649	MAT.B4.W	Warmed	Thelephora_terrestris	0.00000000
## 650	MAT.B4.W	Warmed	Tomentella_sublilacina	0.08474576
## 651	MAT.B4.W	Warmed	Tomentella_sp._1	0.05084746
## 652	MAT.B4.W	Warmed	Tomentellopsis_submollis	0.00000000
## 653	MAT.B4.W	Warmed	Russula_chamiteae	0.08474576
## 654	MAT.B4.W	Warmed	Russula_decolorans	0.49152542
## 655	MAT.B4.W	Warmed	Russula_nitida/sphagnicola	0.00000000
## 656	MAT.B4.W	Warmed	Russula_sp._1	0.00000000
## 657	MAT.B4.W	Warmed	Russula_sp._2	0.00000000
## 658	MAT.B4.W	Warmed	Russula_sp._3	0.00000000
## 659	MAT.B4.W	Warmed	Russula_sp._4	0.01694915
## 660	MAT.B4.W	Warmed	Russula_vinosa	0.00000000
## 661	MAT.B4.WF	Warmed.Fertilized	Alternaria_alternata	0.00000000
## 662	MAT.B4.WF	Warmed.Fertilized	Articulospora_tetracladia	0.00000000
## 663	MAT.B4.WF	Warmed.Fertilized	Cadophora_finlandica	0.00000000
## 664	MAT.B4.WF	Warmed.Fertilized	Cenococcum_geophilum	0.25000000
## 665	MAT.B4.WF	Warmed.Fertilized	Chalara_sp._1	0.00000000
## 666	MAT.B4.WF	Warmed.Fertilized	Cortinarius_sp._1	0.00000000
## 667	MAT.B4.WF	Warmed.Fertilized	Cortinarius_croceus_1	0.00000000
## 668	MAT.B4.WF	Warmed.Fertilized	Cortinarius_glandicolor	0.00000000
## 669	MAT.B4.WF	Warmed.Fertilized	Cortinarius_casimiri	0.06250000
## 670	MAT.B4.WF	Warmed.Fertilized	Cortinarius_croceus_2	0.00000000
## 671	MAT.B4.WF	Warmed.Fertilized	Cortinarius_herpeticus	0.00000000
## 672	MAT.B4.WF	Warmed.Fertilized	Cortinarius_tabularis	0.00000000
## 673	MAT.B4.WF	Warmed.Fertilized	Cortinarius_delibutus	0.00000000
## 674	MAT.B4.WF	Warmed.Fertilized	Cortinarius_sp._2	0.00000000
## 675	MAT.B4.WF	Warmed.Fertilized	Cortinarius_paragaudis	0.00000000
## 676	MAT.B4.WF	Warmed.Fertilized	Cortinarius_sp._3	0.09375000
## 677	MAT.B4.WF	Warmed.Fertilized	Helotiales_sp._1	0.00000000
## 678	MAT.B4.WF	Warmed.Fertilized	Laccaria_laccata	0.00000000
## 679	MAT.B4.WF	Warmed.Fertilized	Lactarius_vietus_1	0.25000000
## 680	MAT.B4.WF	Warmed.Fertilized	Lactarius_glyciosmus	0.06250000
## 681	MAT.B4.WF	Warmed.Fertilized	Lactarius_vietus_2	0.00000000
## 682	MAT.B4.WF	Warmed.Fertilized	Leccinum_holopus	0.00000000
## 683	MAT.B4.WF	Warmed.Fertilized	Leccinum_scabrum	0.00000000
## 684	MAT.B4.WF	Warmed.Fertilized	Leccinum_variicolor_1	0.00000000
## 685	MAT.B4.WF	Warmed.Fertilized	Leccinum_variicolor_2	0.00000000
## 686	MAT.B4.WF	Warmed.Fertilized	Leccinum_variicolor_3	0.00000000
## 687	MAT.B4.WF	Warmed.Fertilized	Leptodontidium_elatius	0.00000000
## 688	MAT.B4.WF	Warmed.Fertilized	Meliniomyces_variabilis	0.00000000
## 689	MAT.B4.WF	Warmed.Fertilized	Meliniomyces_bicolor	0.06250000
## 690	MAT.B4.WF	Warmed.Fertilized	Phialocephala_fortinii	0.00000000
## 691	MAT.B4.WF	Warmed.Fertilized	Pseudotomentella_sp._1	0.00000000
## 692	MAT.B4.WF	Warmed.Fertilized	Rhizoscyphus_ericae	0.00000000
## 693	MAT.B4.WF	Warmed.Fertilized	Thelephora_terrestris	0.00000000
## 694	MAT.B4.WF	Warmed.Fertilized	Tomentella_sublilacina	0.00000000
## 695	MAT.B4.WF	Warmed.Fertilized	Tomentella_sp._1	0.00000000
## 696	MAT.B4.WF	Warmed.Fertilized	Tomentellopsis_submollis	0.03125000
## 697	MAT.B4.WF	Warmed.Fertilized	Russula_chamiteae	0.03125000

```
## 698 MAT.B4.WF Warmed.Fertilized Russula_decolorans 0.00000000
## 699 MAT.B4.WF Warmed.Fertilized Russula_nitida/sphagnicola 0.12500000
## 700 MAT.B4.WF Warmed.Fertilized Russula_sp._1 0.00000000
## 701 MAT.B4.WF Warmed.Fertilized Russula_sp._2 0.00000000
## 702 MAT.B4.WF Warmed.Fertilized Russula_sp._3 0.03125000
## 703 MAT.B4.WF Warmed.Fertilized Russula_sp._4 0.00000000
## 704 MAT.B4.WF Warmed.Fertilized Russula_vinosa 0.00000000

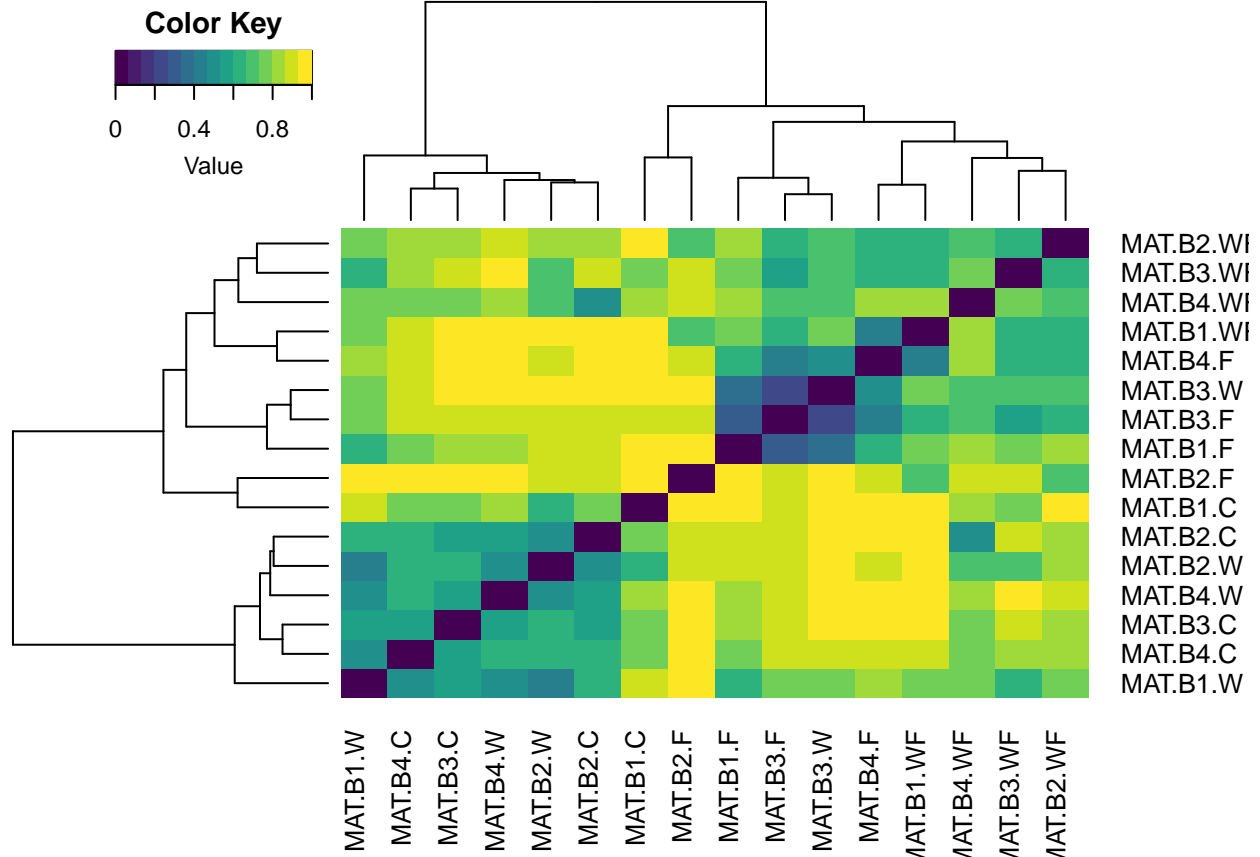
# Change data so that each species is a column, values are the relative.abundance, and rows are each pl
ExpandFungi_data <- slim %>%
  pivot_wider(names_from = Species, values_from = Relative.Abundance, values_fill = list(Relative.Abund
# Sort the expanded data
Sorted_ExpandFungi_data <- ExpandFungi_data %>%
  arrange(Treatment)
# Calculate Bray-Curtis distance
ExpandFun_data.db <- vegdist(Sorted_ExpandFungi_data[, -c(1,2)], method = "bray", upper = TRUE, diag = TRUE)
# Create a new variable and classify it as a matrix
heatmap_matrix <- as.matrix(ExpandFun_data.db)
# Assign row and column names using the "Plot" column from Sorted_ExpandFungi_data
rownames(heatmap_matrix) <- Sorted_ExpandFungi_data$Plot
colnames(heatmap_matrix) <- Sorted_ExpandFungi_data$Plot
#Ward's Clustering with heat map
fun.ward <- hclust(ExpandFun_data.db, method = "ward.D2")
par(mar = c(1, 5, 2, 2) + 0.1)
plot(fun.ward, main = "Fungal Diversity: Ward's Clustering",
      ylab = "Squared Bray-Curtis Distance")
```

Fungal Diversity: Ward's Clustering



```
gplots::heatmap.2(heatmap_matrix,
  distfun = function(x) vegdist(x, method = "bray"),
  hclustfun = function(x) hclust(x, method = "ward.D2"),
```

```
col = "viridis", trace = "none", density.info = "none")
```



```
### PERMANOVA
```

```
# Check and handle missing values
Fungi_data <- na.omit(Fungi_data)
# Ensure correct data types
Fungi_data$Treatment <- as.factor(Fungi_data$Treatment)
Fungi_data$Relative.Abandance <- as.numeric(Fungi_data$Relative.Abandance)
# Verify no negative values
if (any(Fungi_data$Relative.Abandance < 0)) {
  stop("Abundance data contains negative values.")
}
# Replace zero values
Fungi_data$Relative.Abandance[Fungi_data$Relative.Abandance == 0] <- 0.0001
# Run adonis2
adonis2_result <- adonis2(Fungi_data$Relative.Abandance ~ Fungi_data$Treatment, method = "bray", permutations = 999)
print(adonis2_result)
```

```
## Permutation test for adonis under reduced model
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = Fungi_data$Relative.Abandance ~ Fungi_data$Treatment, permutations = 999, method = "bray")
##          Df SumOfSqs      R2      F Pr(>F)
## Model      3    0.661 0.00603 1.4166 0.219
## Residual 700   108.829 0.99397
```

```
## Total      703  109.490 1.00000
```

Phylogenetic diversity

Tree

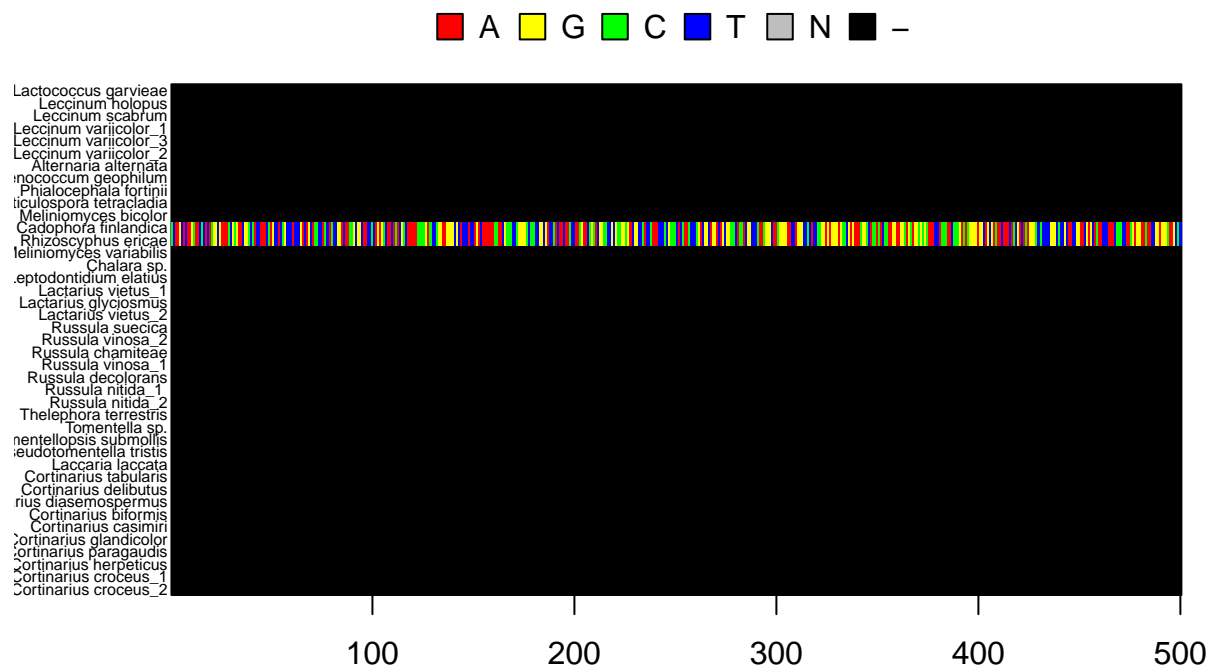
```
funseqs <- readDNAStringSet("./data/Fungal_seq.txt", format = 'fasta')
funseqs

## DNAStringSet object of length 41:
##      width seq                                     names
## [1]   556 GTAGGTGAACCTGCGGAGGGATC...CCGCTGAACTTAAGCATATCAT Alternaria alternata
## [2]  1073 CATTACAGAGTTTCATGCCCTCAC...GAGGACCGCGCTTCGGCTAGGA Articulospora tet...
## [3]  3380 CTAAGTATAAGCAATCTATACGG...AACTTCTAAGGTTGACCTCGGA Cadophora finlandica
## [4]   996 GGTTTCCGTAGAACAAAGTCTTGC...CCGGAAGACCTACTCGCAAGGT Cenococcum geophilum
## [5]   467 CGGAAGGATCATTACAGAGTTCA...GTGGCCGCTGGCCAGCAACCCC Chalara sp.
## ...   ...
## [37]   672 TGCGGAGGACATTATCGTACAAC...CCCGCTGAACTTAAGCATATAA Russula decolorans
## [38]   700 AAGTCGTAACAAGGTTTCCGTAG...TGAGACTACCCGCTGAACTTAA Russula nitida_2
## [39]   662 AAGGATCATTATCATACAAGTGA...TGAGACTACCCGCTGAACTTAA Russula suecica
## [40]   721 TTCTTGGTCAATTTTAGGGAAGT...CAAATCGGGTGAGACTACCCGC Russula vinosa_2
## [41]   506 GTTGTCTACTTTATTTCAGTTT...GAATACATAGCTTACGCGAAGG Lactococcus garvieae

funread.aln <- msaMuscle(funseqs)
funread.aln

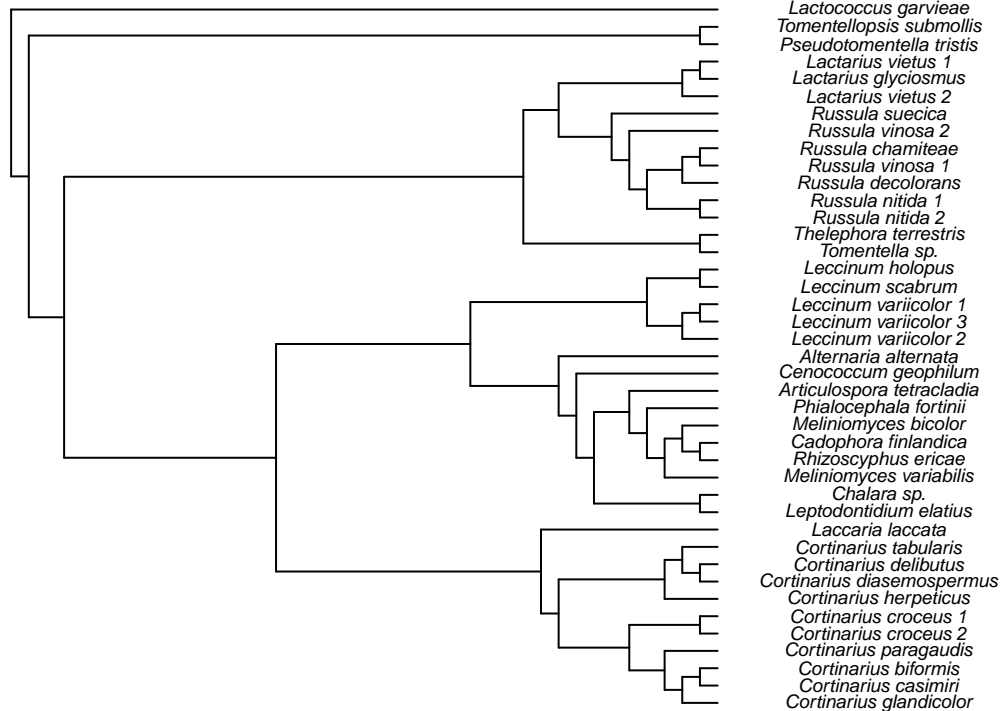
## MUSCLE 3.8.31
##
## Call:
##   msaMuscle(funseqs)
##
## MsaDNAMultipleAlignment with 41 rows and 5567 columns
##      aln                                     names
## [1] -----...----- Lactococcus garvieae
## [2] -----...----- Leccinum holopus
## [3] -----...----- Leccinum scabrum
## [4] -----...----- Leccinum variicol...
## [5] -----...----- Leccinum variicol...
## [6] -----...----- Leccinum variicol...
## [7] -----...----- Alternaria alternata
## [8] -----...----- Cenococcum geophilum
## [9] -----...----- Phialocephala for...
## ...   ...
## [34] -----...----- Cortinarius diase...
## [35] -----...ATTTGGGTATAGGGGCGAAAGACTA Cortinarius biformis
## [36] -----...----- Cortinarius casimiri
## [37] -----...----- Cortinarius gland...
## [38] -----...----- Cortinarius parag...
## [39] -----...----- Cortinarius herpe...
## [40] -----...----- Cortinarius croce...
## [41] -----...----- Cortinarius croce...
## Con -----...----- Consensus

funp.DNABin <- as.DNABin(funread.aln)
funwindow <- funp.DNABin[, 0:500]
image.DNABin(funwindow, cex.lab = 0.50)
```

```
seq.dist.fun <- dist.dna(funp.DNAbin, model = "F84", pairwise.deletion = FALSE)
fun.tree <- bionj(seq.dist.fun)
fun.outgroup <- match("Lactococcus garvieae", fun.tree$tip.label)
fun.rooted <- root(fun.tree, fun.outgroup, resolve.root = TRUE)
par(mar = c(1, 0, 2, 1))
plot.phylo(fun.rooted, type = "phylogram", direction = "right",
  show.tip.label = TRUE, use.edge.length = FALSE, adj = 0.5,
  cex = 0.6, label.offset = 2, main = "Fungal Phylogeny")
```

Fungal Phylogeny



Mapping enzy-

matic activity onto phylogeny

```
library(ape)
library(phylobase)
library(tidyr)
library(dplyr)
library(tibble)
fun.enz <- read.table("./data/MAT_sequences_enzymes.txt", sep = "\t", header = TRUE)
fun.enz_avg <- fun.enz %>%
  group_by(Species, Treatment) %>%
  summarize(
    LAP = mean(LAP, na.rm = TRUE),
    NAG = mean(NAG, na.rm = TRUE),
    PHOS = mean(PHOS, na.rm = TRUE),
    ABTS = mean(ABTS, na.rm = TRUE),
    TMB = mean(TMB, na.rm = TRUE)
  )
```

`summarise()` has grouped output by 'Species'. You can override using the
`.groups` argument.

```
species_list <- unique(fun.enz$Species)
treatment_list <- unique(fun.enz$Treatment)
complete_data <- expand.grid(Species = species_list, Treatment = treatment_list)
fun.enz_complete <- complete_data %>%
  left_join(fun.enz_avg, by = c("Species", "Treatment"))
fun.enz_wide <- fun.enz_complete %>%
  pivot_wider(names_from = Treatment, values_from = c(LAP, NAG, PHOS, ABTS, TMB))
fun.enz_wide <- fun.enz_wide %>%
  mutate(Species = make.unique(as.character(Species))) %>%
```

```

column_to_rownames(var = "Species")
fun.rooted <- root(fun.tree, fun.outgroup, resolve.root = TRUE)
fun.rooted.noout <- drop.tip(fun.rooted, "Lactococcus garvieae")
fun.rooted.noout$edge.length[fun.rooted.noout$edge.length <= 0] <- 1e-6
mypalette <- colorRampPalette(c("#edf8fb", "#b3cde3", "#8c96c6", "#88419d"))
enzymes <- c("LAP", "NAG", "PHOS", "ABTS", "TMB")
for (enzyme in enzymes) {
  enzyme_data <- fun.enz_wide %>%
    dplyr::select(starts_with(enzyme))

  enzyme_data[is.na(enzyme_data)] <- -1

  custom_palette <- c("black", mypalette(25))

  phylo_combined <- phylo4d(fun.rooted.noout, enzyme_data)

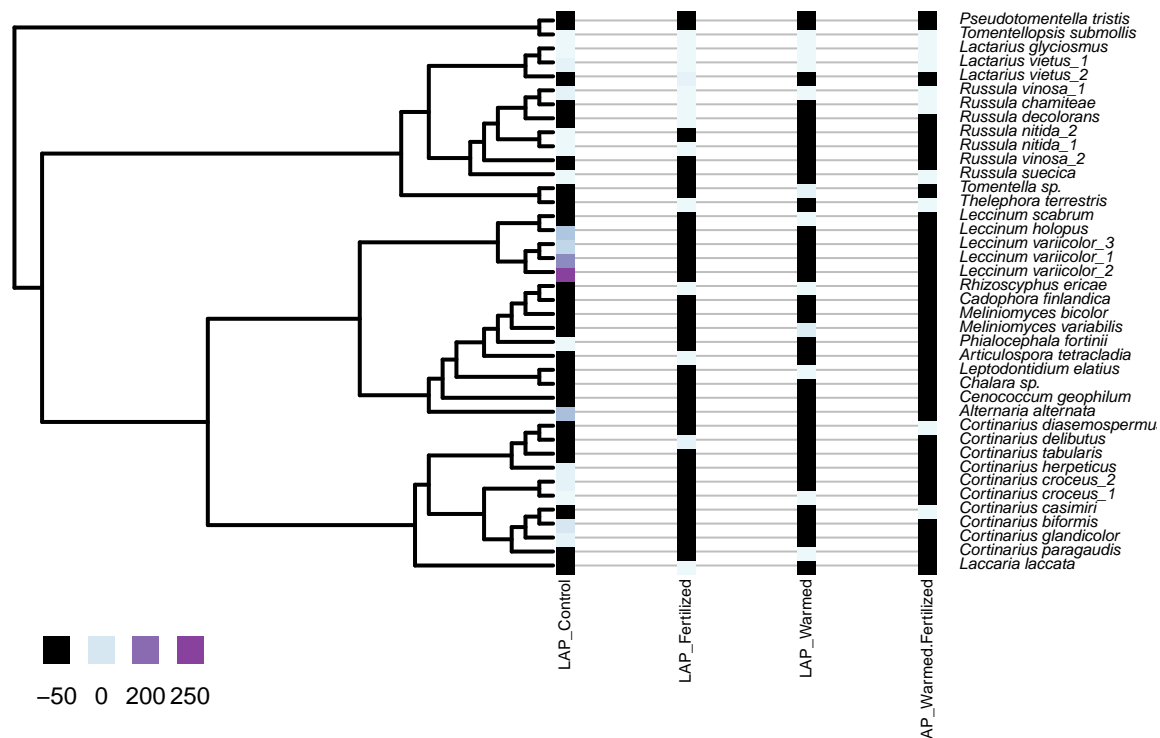
  par(mar = c(1, 1, 1, 1) + 0.1, las = 2)
  table.phylo4d(phylo_combined, treetype = "phylo", symbol = "colors", show.node = TRUE, cex.label = 0.5,
    use.edge.length = FALSE, edge.color = "black", edge.width = 2, box = FALSE, col = custom_palette,
    pch = 15, cex.symbol = 1.25, ratio.tree = 0.5, cex.legend = 1.5, center = FALSE)
  dev.copy(png, filename = paste0(enzyme, "_phylogenetic_tree.png"))
  dev.off()
}

```

```

## Warning in formatData(phy = x, dt = tip.data, type = "tip", ...): The following
## names are not found in the tree: Russula nitida_1, Lactarius thyinos

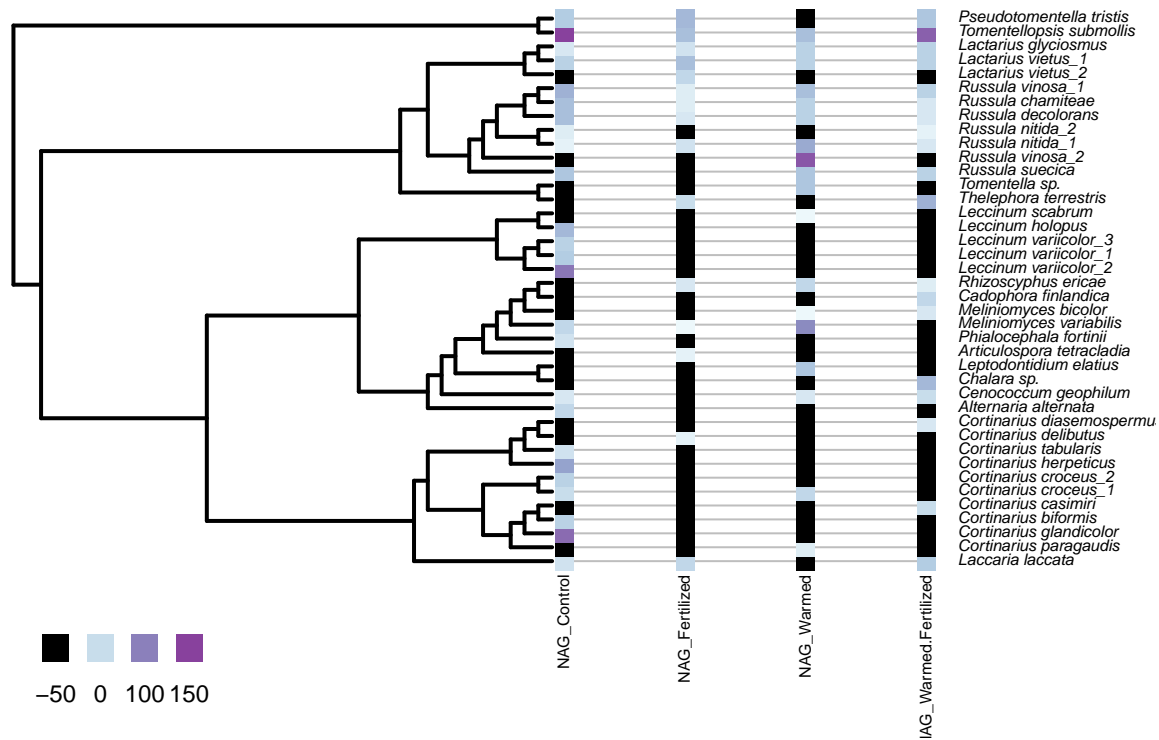
```



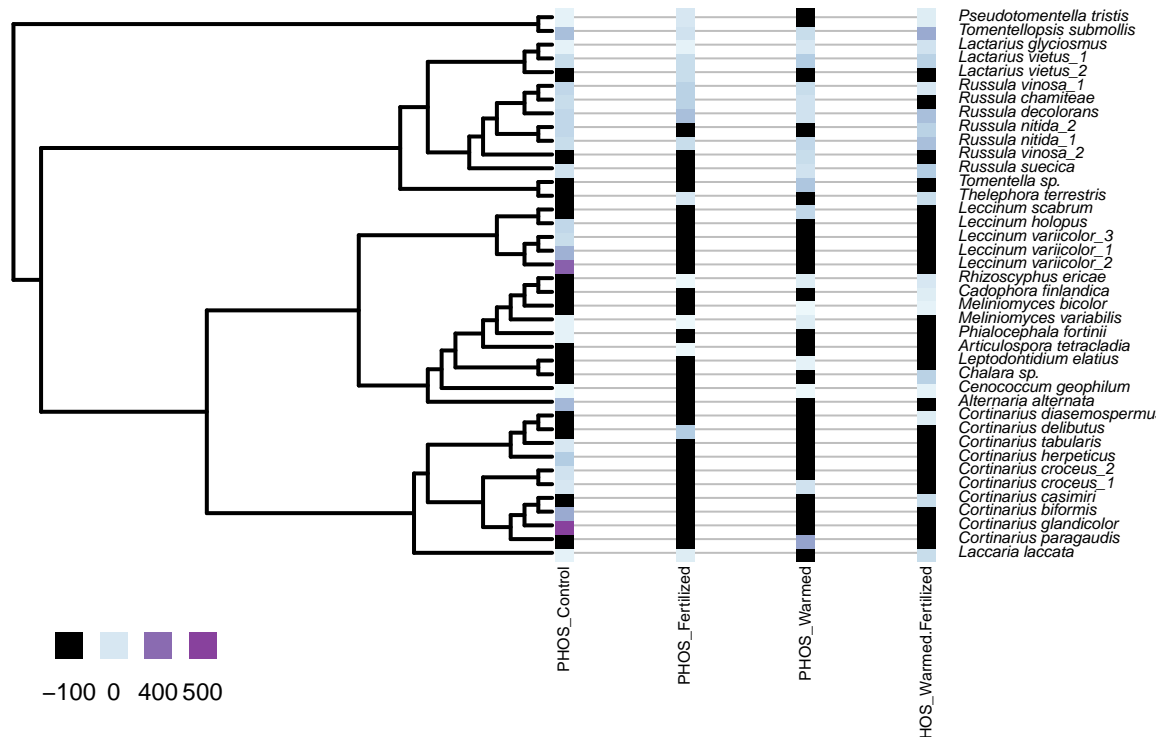
```

## Warning in formatData(phy = x, dt = tip.data, type = "tip", ...): The following
## names are not found in the tree: Russula nitida_1, Lactarius thyinos

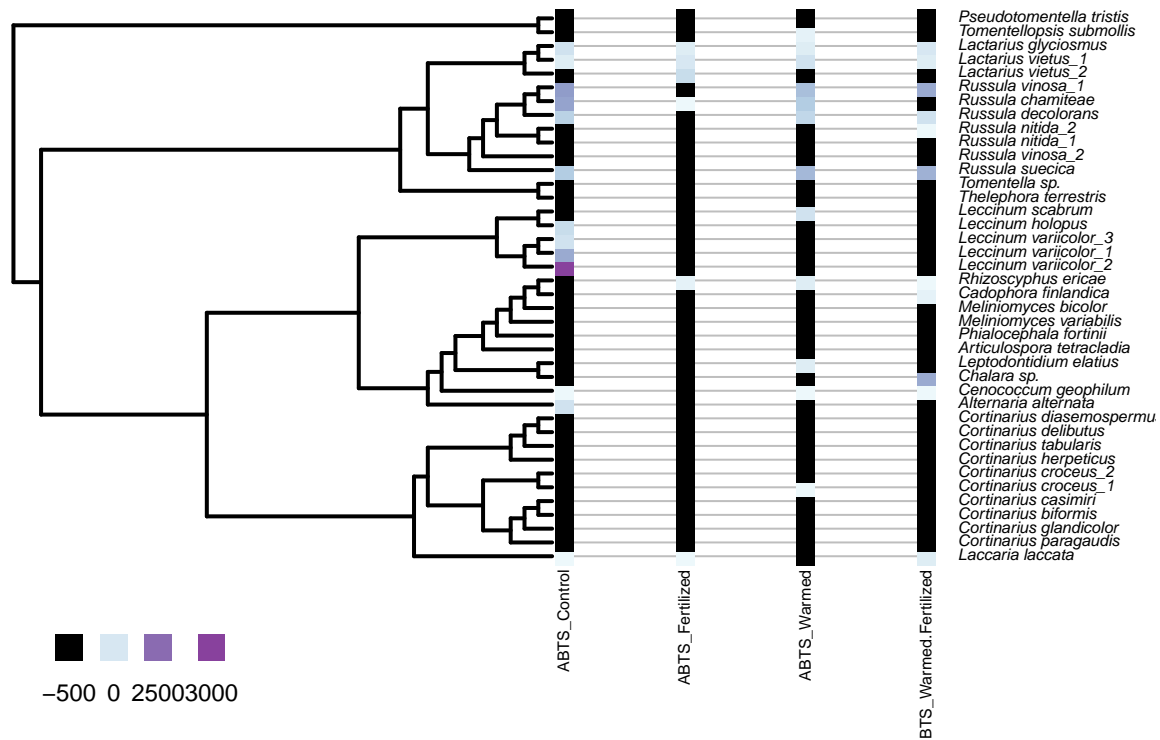
```



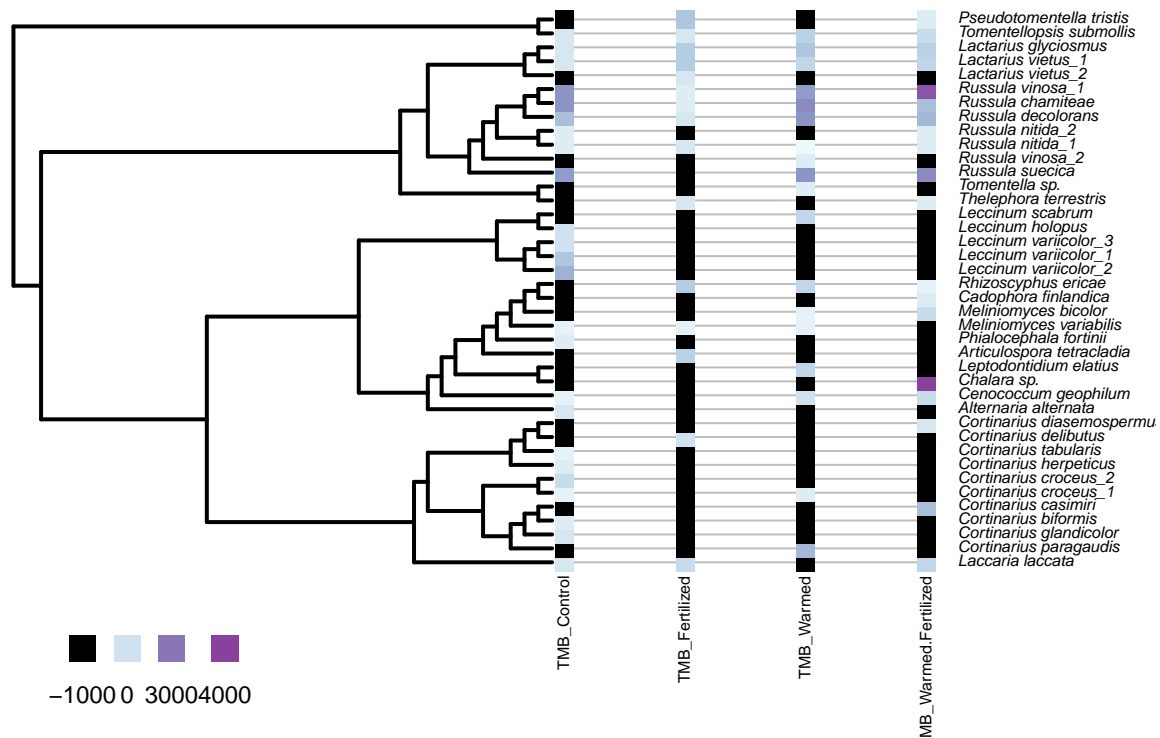
Warning in formatData(phy = x, dt = tip.data, type = "tip", ...): The following
names are not found in the tree: *Russula nitida_1*, *Lactarius thynos*



Warning in formatData(phy = x, dt = tip.data, type = "tip", ...): The following
names are not found in the tree: *Russula nitida_1*, *Lactarius thynos*



```
## Warning in formatData(phy = x, dt = tip.data, type = "tip", ...): The following
## names are not found in the tree: Russula nitida_1, Lactarius thynios
```



PERMANOVA

```
fun.enz_avg <- fun.enz_avg %>%
  mutate(Species = make.unique(as.character(Species)))
enz_data <- fun.enz_avg %>%
```

###

```

dplyr::select(-Species) %>%
pivot_wider(names_from = Treatment, values_from = c(LAP, NAG, PHOS, ABTS, TMB)) %>%
column_to_rownames(var = "Species")

## Adding missing grouping variables: `Species`

enz_data <- enz_data %>%
  mutate(across(everything(), ~ ifelse(is.na(.), mean(., na.rm = TRUE), .)))
treatment_factor <- fun.enz_avg %>%
  dplyr::select(Species, Treatment) %>%
  distinct() %>%
  column_to_rownames(var = "Species")
permanova_result <- adonis2(enx_data ~ Treatment, data = treatment_factor, permutations = 999)
print(permanova_result)

## Permutation test for adonis under reduced model
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = enz_data ~ Treatment, data = treatment_factor, permutations = 999)
##           Df SumOfSqs      R2      F Pr(>F)
## Model       3  0.46126 0.3737 15.315  0.001 ***
## Residual   77  0.77307 0.6263
## Total      80  1.23433 1.0000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```