

## 5. Worksheet: Alpha Diversity\_Bryan Guevara

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### OVERVIEW

In this exercise, we will explore aspects of local or site-specific diversity, also known as alpha ( $\alpha$ ) diversity. First we will quantify two of the fundamental components of ( $\alpha$ ) diversity: **richness** and **evenness**. From there, we will then discuss ways to integrate richness and evenness, which will include univariate metrics of diversity along with an investigation of the **species abundance distribution (SAD)**.

### Directions:

1. In the Markdown version of this document in your cloned repo, change “Student Name” on line 3 (above) to your name.
2. Complete as much of the worksheet as possible during class.
3. Use the handout as a guide; it contains a more complete description of data sets along with the proper scripting needed to carry out the exercise.
4. Answer questions in the worksheet. Space for your answer is provided in this document and indicated by the “>” character. If you need a second paragraph be sure to start the first line with “>”. You should notice that the answer is highlighted in green by RStudio (color may vary if you changed the editor theme).
5. Before you leave the classroom, **push** this file to your GitHub repo.
6. For the assignment portion of the worksheet, follow the directions at the bottom of this file.
7. When you are done, **Knit** the text and code into a PDF file.
8. After Knitting, submit the completed exercise by creating a **pull request** via GitHub. Your pull request should include this file `AlphaDiversity_Worskheet.Rmd` and the PDF output of Knitr (`AlphaDiversity_Worskheet.pdf`).

### 1) R SETUP

In the R code chunk below, please provide the code to: 1) Clear your R environment, 2) Print your current working directory, 3) Set your working directory to your **Week-2/** folder folder, and 4) Load the **vegan** R package (be sure to install first if you have not already).

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

```
## [1] "/cloud/project/QB2025_Guevara/Week2-Alpha"
```

```
setwd("/cloud/project/QB2025_Guevara/Week2-Alpha")  
install.packages("vegan")
```

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

```
library(vegan)
```

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

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

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

## 2) LOADING DATA

In the R code chunk below, do the following: 1) Load the BCI dataset, and 2) Display the structure of the dataset (if the structure is long, use the `max.level = 0` argument to show the basic information).

```
data(BCI)
str(BCI, max.level = 0)
```

```
## 'data.frame': 50 obs. of 225 variables:
```

```
## - attr(*, "original.names")= chr [1:225] "Abarema.macradenium" "Acacia.melanoceras" "Acalypha.diversa"
```

```
site1 <- BCI[1, ]
```

## 3) SPECIES RICHNESS

**Species richness (S)** refers to the number of species in a system or the number of species observed in a sample.

### Observed richness

In the R code chunk below, do the following:

1. Write a function called `S.obs` to calculate observed richness
2. Use your function to determine the number of species in `site1` of the BCI data set, and
3. Compare the output of your function to the output of the `specnumber()` function in `vegan`.

```
S.obs <- function(x = ""){
  rowSums(x > 0) * 1
}
S.obs(BCI)
```

```
## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
## 93 84 90 94 101 85 82 88 90 94 87 84 93 98 93 93 93 89 109 100
## 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
## 99 91 99 95 105 91 99 85 86 97 77 88 86 92 83 92 88 82 84 80
## 41 42 43 44 45 46 47 48 49 50
## 102 87 86 81 81 86 102 91 91 93
```

```
specnumber(BCI)
```

```
## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
## 93 84 90 94 101 85 82 88 90 94 87 84 93 98 93 93 93 89 109 100
## 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
## 99 91 99 95 105 91 99 85 86 97 77 88 86 92 83 92 88 82 84 80
## 41 42 43 44 45 46 47 48 49 50
## 102 87 86 81 81 86 102 91 91 93
```

```
help(specnumber)
```

```
# S.obs <- function( ) {
#   rowSums( ) *
# }
```

**Question 1:** Does `specnumber()` from `vegan` return the same value for observed richness in `site1` as our function `S.obs`? What is the species richness of the first four sites (i.e., rows) of the BCI matrix?

**Answer 1:**

Yes, it does appear that observed richness in `site1` from `specnumber` matches the observed richness we acquire from our function `'S.obs'`. The species richness from the first four sites are 93, 84, 90, and 94.

### Coverage: How well did you sample your site?

In the R code chunk below, do the following:

1. Write a function to calculate Good's Coverage, and
2. Use that function to calculate coverage for all sites in the BCI matrix.

```
C <- function(x = ""){1 - (rowSums(x == 1)/rowSums(x))}
C(BCI)
```

```
##           1           2           3           4           5           6           7           8
## 0.9308036 0.9287356 0.9200864 0.9468504 0.9287129 0.9174757 0.9326923 0.9443155
##           9          10          11          12          13          14          15          16
## 0.9095355 0.9275362 0.9152120 0.9071038 0.9242054 0.9132420 0.9350649 0.9267735
##          17          18          19          20          21          22          23          24
## 0.8950131 0.9193084 0.8891455 0.9114219 0.8946078 0.9066986 0.8705882 0.9030612
##          25          26          27          28          29          30          31          32
## 0.9095023 0.9115479 0.9088729 0.9198966 0.8983516 0.9221053 0.9382423 0.9411765
##          33          34          35          36          37          38          39          40
## 0.9220183 0.9239374 0.9267887 0.9186047 0.9379310 0.9306488 0.9268868 0.9386503
##          41          42          43          44          45          46          47          48
## 0.8880597 0.9299517 0.9140049 0.9168704 0.9234234 0.9348837 0.8847059 0.9228916
##          49          50
## 0.9086651 0.9143519
```

**Question 2:** Answer the following questions about coverage:

- a. What is the range of values that can be generated by Good's Coverage?
- b. What would we conclude from Good's Coverage if  $n_i$  equaled  $N$ ?
- c. What portion of taxa in `site1` was represented by singletons?
- d. Make some observations about coverage at the BCI plots.

**Answer 2a:**

The range of values that can be generated is any number between 0 and 1 as Good's Coverage is a proportion as we take the ratio of singleton species to total number of individuals in our sample and subtract this value from 1.

**Answer 2b:** If  $n_i = N$  then that would result in a 1:1 ratio and we have a Good's Coverage value of 0. This would indicate basically a complete lack of coverage.

**Answer 2c:** In site 1, approximately 6.92% of the taxa in `site1` are represented by singletons as the proportion of represented by singletons would be  $= 1 - C$  or  $1 - 0.9308$ .

**Answer 2d:** Site 23 has the greatest portion of taxa represented by singletons across all the observed sites while site 4 seems to have the lowest. Most sites have ~10% of their taxa represented by singletons.

*Answer 2b:*

*Answer 2c:*

*Answer 2d:*

### Estimated richness

In the R code chunk below, do the following:

1. Load the microbial dataset (located in the **Week-2/data** folder),
2. Transform and transpose the data as needed (see handout),
3. Create a new vector (**soilbac1**) by indexing the bacterial OTU abundances of any site in the dataset,
4. Calculate the observed richness at that particular site, and
5. Calculate coverage of that site

```
soilbac <- read.table("data/soilbac.txt", sep = "\t", header = TRUE, row.names = 1)
soilbac.t <- as.data.frame(t(soilbac))
soilbac1 <- soilbac.t[1,]
sum(soilbac1)
```

```
## [1] 2119
```

```
#observed richness of T1_1
S.obs(soilbac1)
```

```
## T1_1
```

```
## 1074
```

```
#Good's Coverage of site T1_1
C(soilbac1)
```

```
##      T1_1
```

```
## 0.6479471
```

```
dim(soilbac1)
```

```
## [1]      1 13310
```

**Question 3:** Answer the following questions about the soil bacterial dataset.

- a. How many sequences did we recover from the sample **soilbac1**, i.e.  $N$ ?
- b. What is the observed richness of **soilbac1**?
- c. How does coverage compare between the BCI sample (**site1**) and the KBS sample (**soilbac1**)?

*Answer 3a:*

There were a total of 2119 sequences recovered from our **soilbac1** sample.

*Answer 3b:* The observed richness of **soilbac1** seems to be 1074

*Answer 3c:* The coverage between the BCI sample and the KBS sample are very different with the KBS sample having a much smaller overall coverage

*Answer 3b:*

*Answer 3c:*

## Richness estimators

In the R code chunk below, do the following:

1. Write a function to calculate **Chao1**,
2. Write a function to calculate **Chao2**,
3. Write a function to calculate **ACE**, and
4. Use these functions to estimate richness at **site1** and **soilbac1**.

```
S.chao1 <- function(x = ""){S.obs(x) +(sum(x == 1)^2) / (2 * sum(x ==2))}
S.chao2 <- function(site = "", SbyS = ""){
  SbyS = as.data.frame(SbyS)
  x = SbyS[site, ]
  SbyS.pa <- (SbyS > 0) * 1
  Q1 = sum(colSums(SbyS.pa) ==1)
  Q2 = sum(colSums(SbyS.pa) == 2)
  S.chao2 = S.obs(x) + (Q1^2)/(2 * Q2)
  return(S.chao2)
}
```

```
#Estimated richness of site1 and soilbac1
S.chao1(soilbac1)
```

```
##      T1_1
## 2628.514
```

```
S.chao1(site1)
```

```
##      1
## 119.6944
```

```
S.chao2(1, BCI)
```

```
##      1
## 104.6053
```

```
S.chao2(1, soilbac.t)
```

```
##      T1_1
## 21055.39
```

```
S.ace <- function(x = "", thresh = 10){
  x <- x[x>0]
  S.abund <- length(which(x > thresh))
  S.rare <- length(which(x <= thresh))
  singlt <- length(which(x == 1))
  N.rare <- sum(x[which(x <= thresh)])
  C.ace <- 1 - (singlt / N.rare)
  i <- c(1:thresh)
  count <- function(i,y){length(y[y == i])}
  a.1 <- sapply(i, count, x)
  f.1 <- (i * (i -1)) * a.1
  G.ace <- (S.rare/C.ace)*(sum(f.1)/(N.rare*(N.rare-1)))
  S.ace <- S.abund + (S.rare/C.ace) + (singlt/C.ace) * max(G.ace, 0)
  return(S.ace)
}
```

```
#Estimated richness using ACE
S.ace(soilbac1)
```

```
## [1] 4465.983
```

```
S.ace(site1)
```

```
## [1] 159.3404
```

**Question 4:** What is the difference between ACE and the Chao estimators? Do the estimators give consistent results? Which one would you choose to use and why?

**Answer 4:**

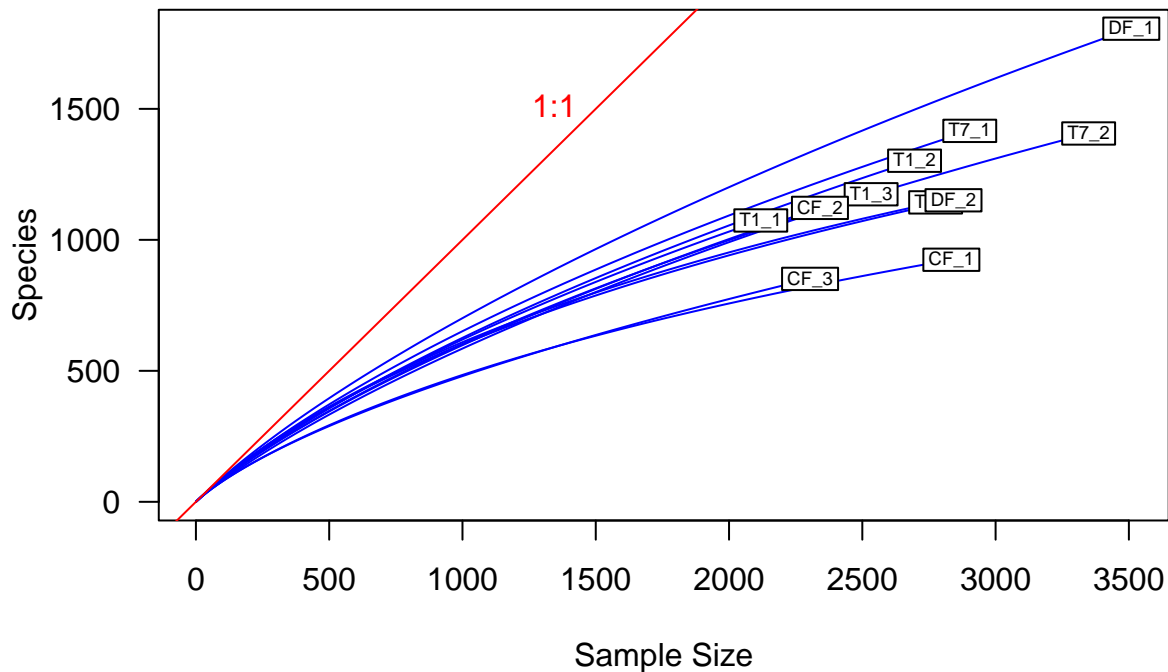
The difference between ACE and Chao estimators is that ACE uses a threshold to look at abundance of rare species and defines rare species as taxa that have 10 or fewer individuals. The estimators do not give the most consistent results as they each use different parameters in order to estimate richness (Chao1 makes inferences based on number of singletons and doubletons of species at one site; Chao2 uses the presence/absence of species across multiple sites; ACE uses a threshold to identify abundance of rare species). For our soilbac1 dataset, I would probably avoid ACE because it might underestimate richness because it assumes a sufficient enough sampling coverage and soilbac1 seems to have rather poor coverage as indicated by the Good's Coverage value meaning that there are a lot of rare species. Thus, for soilbac1, I would probably use Chao2 as it considers the presence of species across multiple sites rather than focusing on a singular site as that would be more representative of how rich a species might be in a given ecosystem. I would prefer a holistic POV rather than the richness of a single site within an ecosystem. For site1 from site1, the coverage is a lot better so I could consider using ACE in this case as there are relatively fewer rarer species in this site compared to soilbac1.

## Rarefaction

In the R code chunk below, please do the following:

1. Calculate observed richness for all samples in `soilbac`,
2. Determine the size of the smallest sample,
3. Use the `rarefy()` function to rarefy each sample to this level,
4. Plot the rarefaction results, and
5. Add the 1:1 line and label.

```
soilbac.S <- S.obs(soilbac.t)
min.N <- min(rowSums(soilbac.t))
S.rarefy <- rarefy(x = soilbac.t, sample = min.N, se = TRUE)
rarecurve(x = soilbac.t, step = 20, col = "blue", cex = 0.6, las = 1)
abline(0,1, col = 'red')
text(1500,1500, "1:1", pos = 2, col = 'red')
```



#### 4) SPECIES EVNENNESS

Here, we consider how abundance varies among species, that is, **species evenness**.

##### Visualizing evenness: the rank abundance curve (RAC)

One of the most common ways to visualize evenness is in a **rank-abundance curve** (sometime referred to as a rank-abundance distribution or Whittaker plot). An RAC can be constructed by ranking species from the most abundant to the least abundant without respect to species labels (and hence no worries about ‘ties’ in abundance).

In the R code chunk below, do the following:

1. Write a function to construct a RAC,
2. Be sure your function removes species that have zero abundances,
3. Order the vector (RAC) from greatest (most abundant) to least (least abundant), and
4. Return the ranked vector

```
RAC <- function(x = ""){
  x.ab = x[x > 0]
  x.ab.ranked = x.ab[order(x.ab, decreasing = TRUE)]
  as.data.frame(lapply(x.ab.ranked, unlist))
  return(x.ab.ranked)
}

#x.ab = x[x > 0] removes species that have an abundance of zero
#x.ab.ranked orders the vectors from greatest (most abundant) to least (least abundant)
```

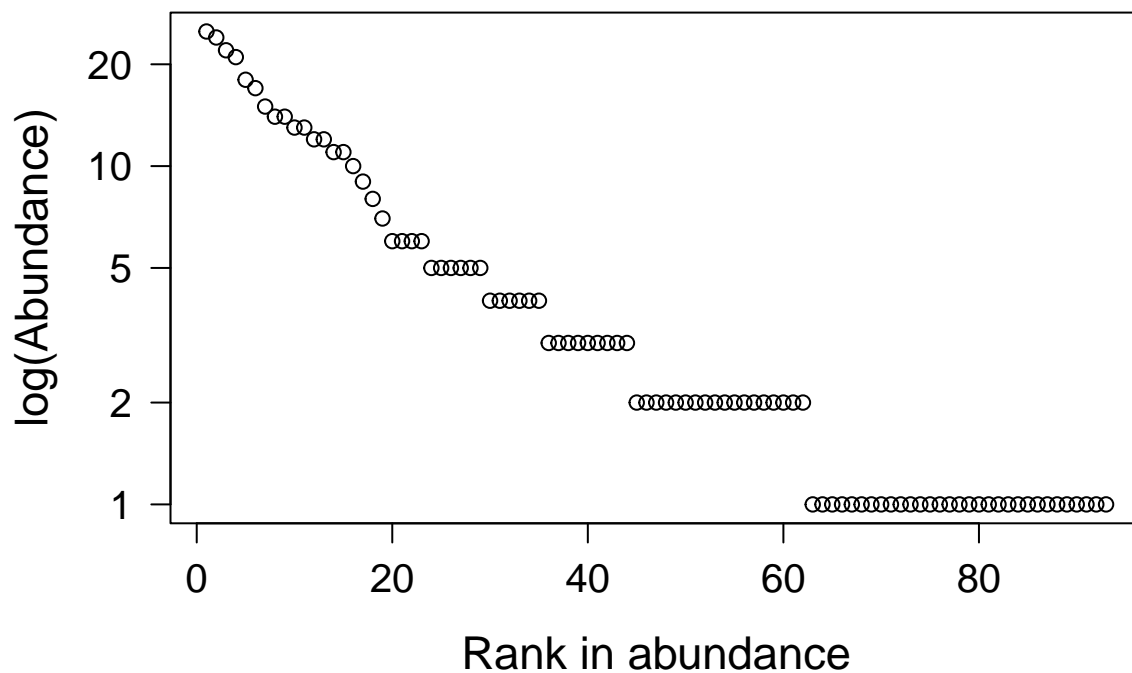
Now, let us examine the RAC for `site1` of the BCI data set.

In the R code chunk below, do the following:

1. Create a sequence of ranks and plot the RAC with natural-log-transformed abundances,

2. Label the x-axis “Rank in abundance” and the y-axis “log(abundance)”

```
plot.new()
site1 <- BCI[1, ]
rac <- RAC(x = site1)
ranks <- as.vector(seq(1, length(rac)))
opar <- par(no.readonly = TRUE)
par(mar = c(5.1, 5.1, 4.1, 2.1))
plot(ranks, log(rac), type = 'p', axes = F,
     xlab = "Rank in abundance", ylab = "log(Abundance)",
     las = 1, cex.lab = 1.4, cex.axis = 1.25)
box()
axis(side = 1, labels = T, cex.axis = 1.25)
axis(side = 2, las = 1, cex.axis = 1.25,
     labels = c(1,2,5,10,20), at = log(c(1,2,5,10,20)))
```



```
par <- opar
```

**Question 5:** What effect does visualizing species abundance data on a log-scaled axis have on how we interpret evenness in the RAC?

**Answer 5:**

From what we can see on the graph, when we log scale things, a community that might have high dominance of a few species might look less steep (like around rank 20) which can give the impression of greater evenness when there is in fact less evenness because there are some rather abundant species even though they might not be as abundant as the species ranking from 1-10. In a community with relatively strong evenness, log scaling could hide some minor variations in actual evenness, skewing how we might interpret evenness using our RAC.

Now that we have visualized unevenness, it is time to quantify it using Simpson's evenness ( $E_{1/D}$ ) and Smith and Wilson's evenness index ( $E_{var}$ ).



### Simpson's evenness ( $E_{1/D}$ )

In the R code chunk below, do the following:

1. Write the function to calculate  $E_{1/D}$ , and
2. Calculate  $E_{1/D}$  for `site1`.

```
SimpE <- function(x = ""){  
  S <- S.obs(x)  
  x = as.data.frame(x)  
  D <- diversity(x, "inv")  
  E <- (D)/S  
  return(E)  
}
```

```
site1 <- BCI[1, ]  
SimpE(site1)
```

```
##          1  
## 0.4238232
```

### Smith and Wilson's evenness index ( $E_{var}$ )

In the R code chunk below, please do the following:

1. Write the function to calculate  $E_{var}$ ,
2. Calculate  $E_{var}$  for `site1`, and
3. Compare  $E_{1/D}$  and  $E_{var}$ .

```
Evar <- function(x){  
  x <- as.vector(x[x > 0])  
  1 - (2/pi) * atan(var(log(x)))  
}
```

```
Evar(site1)
```

```
## [1] 0.5067211
```

**Question 6:** Compare estimates of evenness for `site1` of BCI using  $E_{1/D}$  and  $E_{var}$ . Do they agree? If so, why? If not, why? What can you infer from the results.

#### **Answer 6:**

The estimates for evenness for `site1` do not necessarily agree with Simpson's estimate of evenness is slightly smaller than Smith and Wilson's. They do not agree entirely because Simpson's is more sensitive to differences in the few most abundant species within the measured community. Smith and Wilson's uses the sample variance of the log-transformed abundances and then standardizes it resulting in a different value from Simpson's. From both of the results, I can infer that the evenness at `site1` really isn't all that great as the estimates are ~0.5 or lower. I would categorize them as moderately even with 1 being the most even and values of 0 being associated with low evenness.

## 5) INTEGRATING RICHNESS AND EVENNESS: DIVERSITY METRICS

So far, we have introduced two primary aspects of diversity, i.e., richness and evenness. Here, we will use popular indices to estimate diversity, which explicitly incorporate richness and evenness. We will write our own diversity functions and compare them against the functions in `vegan`.

### Shannon's diversity (a.k.a., Shannon's entropy)

In the R code chunk below, please do the following:

1. Provide the code for calculating  $H'$  (Shannon's diversity),
2. Compare this estimate with the output of `vegan`'s diversity function using `method = "shannon"`.

```
ShanH <- function(x = ""){
  H = 0
  for (n_i in x){
    if(n_i > 0){
      p = n_i / sum(x)
      H = H - p*log(p)
    }
  }
  return(H)
}

diversity(site1, index = "shannon")
```

```
## [1] 4.018412
```

### Simpson's diversity (or dominance)

In the R code chunk below, please do the following:

1. Provide the code for calculating  $D$  (Simpson's diversity),
2. Calculate both the inverse ( $1/D$ ) and  $1 - D$ ,
3. Compare this estimate with the output of `vegan`'s diversity function using `method = "simp"`.

```
SimpD <- function(x = ""){
  D = 0
  N = sum(x)
  for (n_i in x){
    D = D + (n_i^2)/(N^2)
  }
  return(D)
}

D.inv <- 1/SimpD(site1)
D.sub <- 1-SimpD(site1)

diversity(site1, "inv")
```

```
## [1] 39.41555
```

```
diversity(site1, "simp")
```

```
## [1] 0.9746293
```

### Fisher's $\alpha$

In the R code chunk below, please do the following:

1. Provide the code for calculating Fisher's  $\alpha$ ,
2. Calculate Fisher's  $\alpha$  for `site1` of BCI.

```
rac <- as.vector(site1[site1 > 0])
invD <- diversity(rac, "inv")
invD
```

```
## [1] 39.41555
```

```
Fisher <- fisher.alpha(rac)
Fisher
```

```
## [1] 35.67297
```

**Question 7:** How is Fisher's  $\alpha$  different from  $E_{H'}$  and  $E_{var}$ ? What does Fisher's  $\alpha$  take into account that  $E_{H'}$  and  $E_{var}$  do not?

**Answer 7:**

Fisher's alpha estimates diversity rather just calculating a diversity metric directly accounting for sampling error. We are not observing every single individual as we would for Smith and Wilson's Evenness Index or for Shannon's diversity.

## 6) HILL NUMBERS

Remember that we have learned about the advantages of Hill Numbers to measure and compare diversity among samples. We also learned to explore the effects of rare species in a community by examining diversity for a series of exponents  $q$ .

```
#Simulate communities
C1 <- data.frame(t(rep(1, 500))); colnames(C1) <- paste("sp", 1:500)
C2 <- data.frame(t(c(rep(1, 250)))); colnames(C2) <- paste("sp", 1:250)
```

```
#Calculate shannon diversity
H1 <- diversity(C1, index = "shannon")
H2 <- diversity(C2, index = "shannon")
H1;H2
```

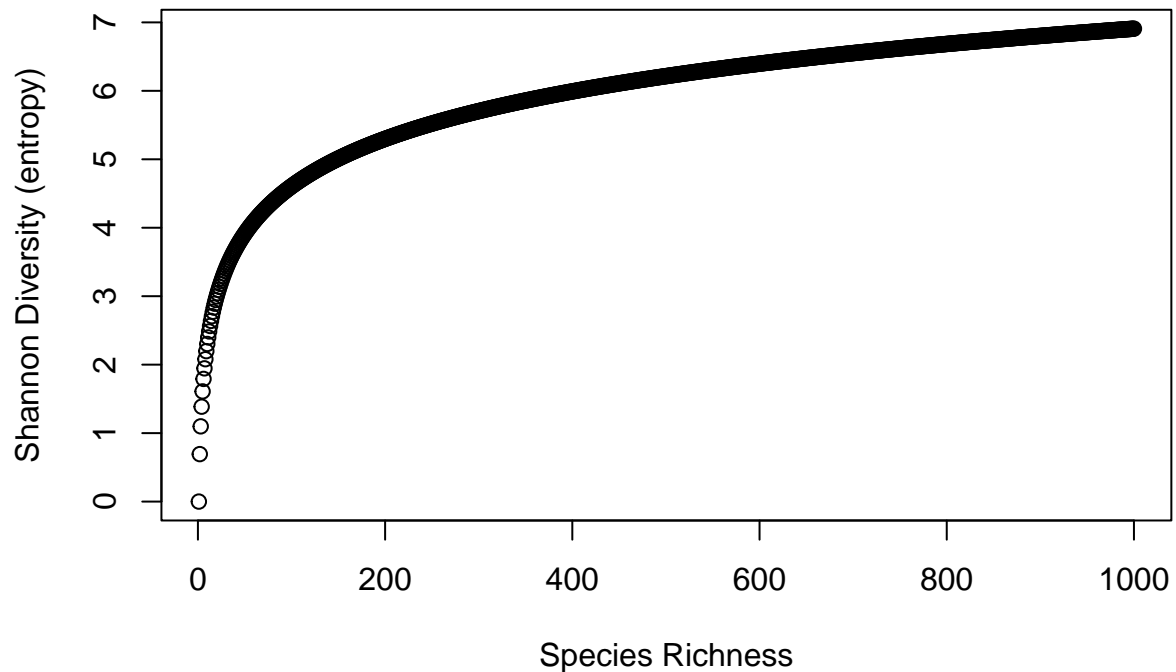
```
## [1] 6.214608
```

```
## [1] 5.521461
```

```
#Calculating Shannon's entropy for each richness level
```

```
H_all <- matrix(ncol = 2, nrow = 1000)
for(i in 1:1000){
  C <- data.frame(t(rep(1, i)))
  colnames(C) = paste("sp", 1:i)
  H_all[i,1] <- i
  H_all[i,2] <- diversity(C, index = "shannon") }
```

```
plot(H_all[,1], H_all[,2], xlab = "Species Richness", ylab = "Shannon Diversity (entropy)")
```



```
#Calculate exponential Shannon's entropy (equal to the Hill number q = 1)
```

```
H1_Hill <- exp(多样性(C1, index = "shannon"))
```

```
H2_Hill <- exp(多样性(C2, index = "shannon"))
```

```
H1_Hill; H2_Hill
```

```
## [1] 500
```

```
## [1] 250
```

```
#Calculate for each richness level to compare Shannon entropy with Hill number 1 (exponential Shannon's
```

```
H_all_Hill <- matrix(ncol = 2, nrow = 1000)
```

```
for(i in 1:1000) {
```

```
  C = data.frame(t(rep(1,i)))
```

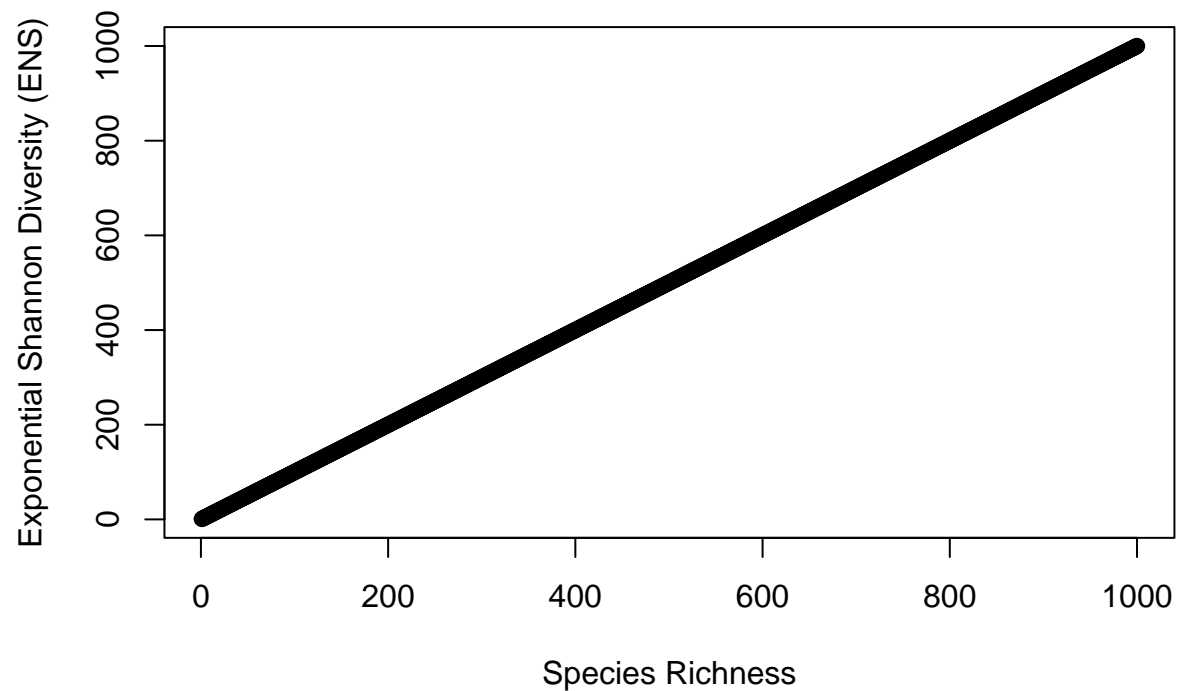
```
  colnames(C) = paste("sp", 1:i)
```

```
  H_all_Hill[i, 1] = i
```

```
  H_all_Hill[i, 2] = exp(多样性(C, index = "shannon"))}
```

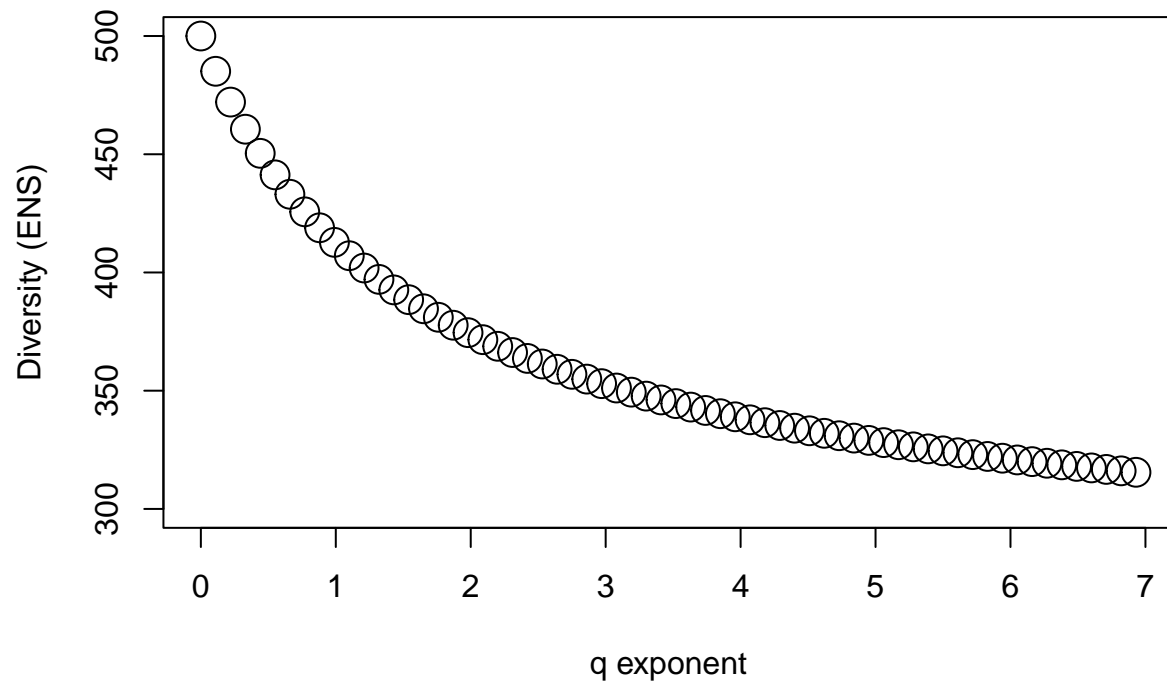
```
plot(H_all_Hill[,1], H_all_Hill[,2], xlab = "Species Richness",
```

```
      ylab = "Exponential Shannon Diversity (ENS)")
```



```
#Function profile to calculate diversity from thje equation above along a continuum of q values
profile <- function(C) {
  cbind(seq(0,7, by = 0.11),
    unlist(lapply(seq(0,7, by = 0.11), function(q) sum(apply(C, 1, function(x)
      (x/sum(x))^q))^(1/(1-q))))))}

set.seed(42)
C3 <- data.frame(t(sample(1:1000, 500))); colnames(C3) = paste("sp", 1:500)
C3_profile <- profile(C3)
plot(C3_profile[,1], C3_profile[,2], ylim=c(300,500), cex = 2,
  xlab = "q exponent", ylab = "Diversity (ENS)")
```



*#For question 8 on site1*

```
H3 <- diversity(site1, index = "shannon")
H3
```

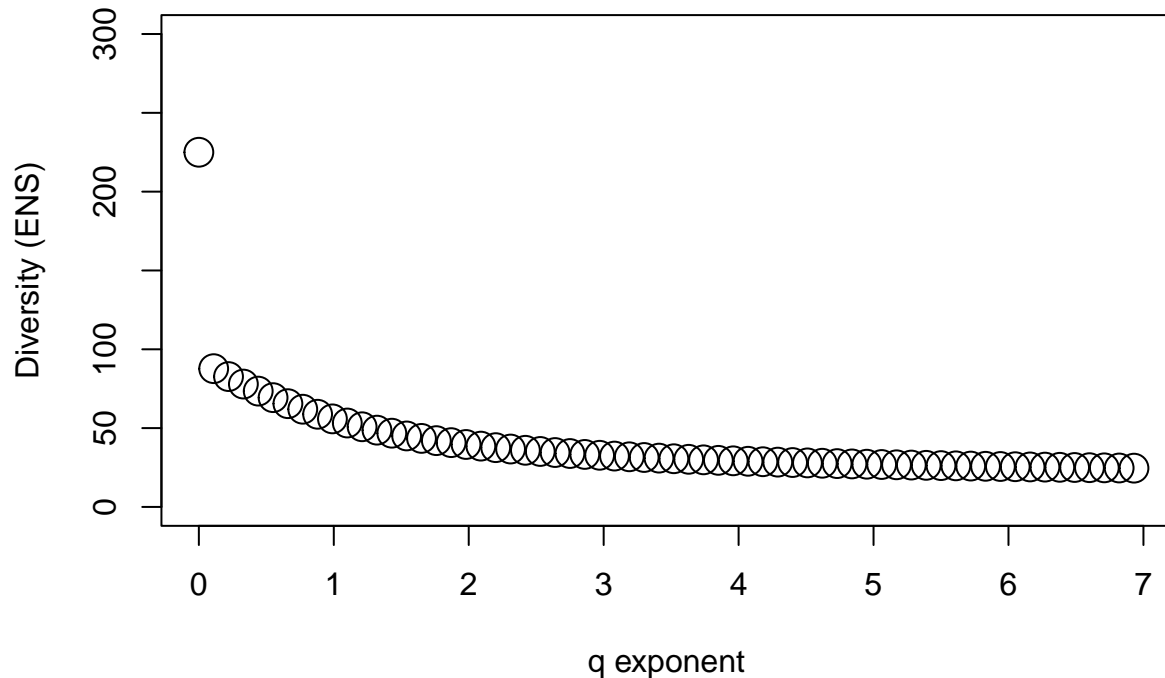
```
## [1] 4.018412
```

```
H3_Hill <- exp(diversity(site1, index = "shannon"))
H3_Hill
```

```
## [1] 55.6127
```

```
profile_H3 <- function(site1) {
  cbind(seq(0,7, by = 0.11),
        unlist(lapply(seq(0,7, by = 0.11), function(q) sum(apply(site1, 1, function(x)
          (x/sum(x))^q))^(1/(1-q))))))}
```

```
site1_profile <- profile_H3(site1)
plot(site1_profile[,1], site1_profile[,2], ylim=c(0,300), cex = 2,
     xlab = "q exponent", ylab = "Diversity (ENS)")
```



**Question 8:** Using `site1` of BCI and `vegan` package, a) calculate Hill numbers for  $q$  exponent 0, 1 and 2 (richness, exponential Shannon's entropy, and inverse Simpson's diversity). b) Interpret the effect of rare species in your community based on the response of diversity to increasing exponent  $q$ .

**Answer 8a:** It seems that when  $q = 0$  (diversity is species richness), our value is 225. When  $q = 1$  (diversity is exponential Shannon diversity), our value is roughly 55.86. When  $q = 2$  (where diversity is reciprocal of Simpson's diversity), our value is roughly 39.61 **Answer 8b:** There are many rare species in our community based on our species richness ( $q = 0$ ) but once we start considering abundance using our Shannon's and Simpson's diversity metrics, their impact on diversity becomes relatively small.

**Question 8:** Using `site1` of BCI and `vegan` package, a) calculate Hill numbers for  $q$  exponent 0, 1 and 2 (richness, exponential Shannon's entropy, and inverse Simpson's diversity). b) Interpret the effect of rare species in your community based on the response of diversity to increasing exponent  $q$ .

**Answer 8a:**

**Answer 8b:**

## ##7) MOVING BEYOND UNIVARIATE METRICS OF $\alpha$ DIVERSITY

The diversity metrics that we just learned about attempt to integrate richness and evenness into a single, univariate metric. Although useful, information is invariably lost in this process. If we go back to the rank-abundance curve, we can retrieve additional information – and in some cases – make inferences about the processes influencing the structure of an ecological system.

## Species abundance models

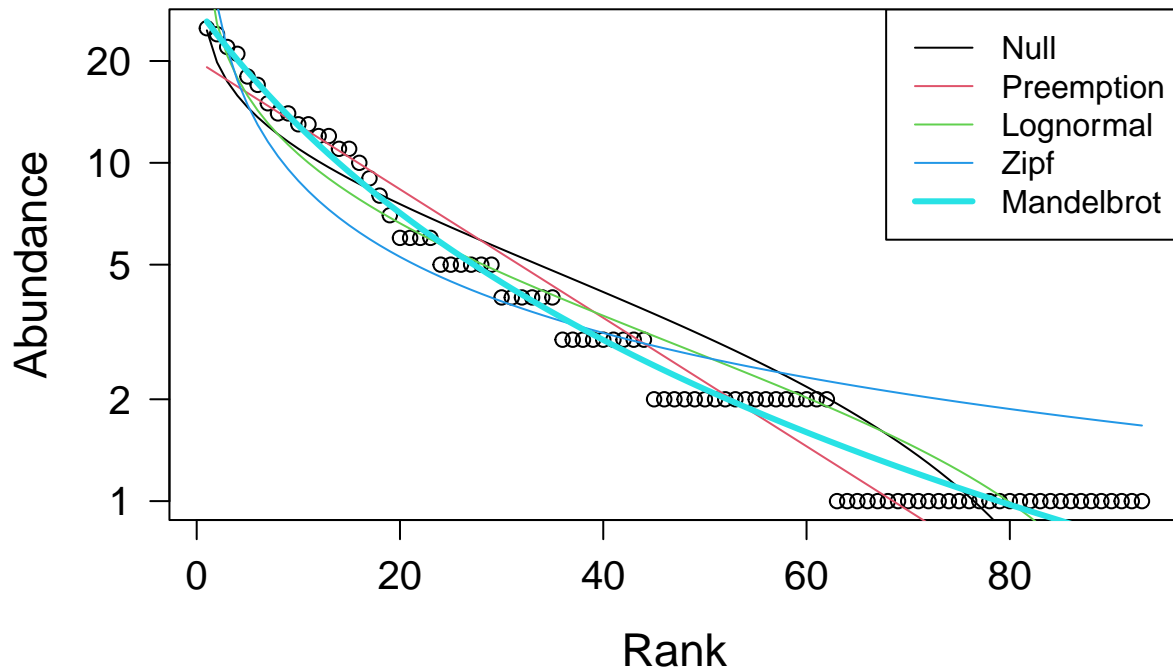
The RAC is a simple data structure that is both a vector of abundances. It is also a row in the site-by-species matrix (minus the zeros, i.e., absences).

Predicting the form of the RAC is the first test that any biodiversity theory must pass and there are no less than 20 models that have attempted to explain the uneven form of the RAC across ecological systems.

In the R code chunk below, please do the following:

1. Use the `radfit()` function in the `vegan` package to fit the predictions of various species abundance models to the RAC of `site1` in BCI,
2. Display the results of the `radfit()` function, and
3. Plot the results of the `radfit()` function using the code provided in the handout.

```
RACresults <- radfit(site1)
plot.new()
plot(RACresults, las = 1, cex.lab = 1.4, cex.axis = 1.25)
```



**Question 9:** Answer the following questions about the rank abundance curves: a) Based on the output of `radfit()` and plotting above, discuss which model best fits our rank-abundance curve for `site1`? b) Can we make any inferences about the forces, processes, and/or mechanisms influencing the structure of our system, e.g., an ecological community?

**Answer 9a:**

It seems that the Mandelbrot model best fits our RAC **Answer 9b:** Because the RAC best fits the Mandelbrot model, we can infer that there is some sort of niche partitioning or structuring going on as the Mandelbrot model suggests some sort of self-organizing structure amongst species.

**Question 10:** Answer the following questions about the preemption model: a. What does the preemption model assume about the relationship between total abundance ( $N$ ) and total resources that can be preempted? b. Why does the niche preemption model look like a straight line in the RAD plot?

**Answer 10a:**

The preemption model from above assumes that total abundance is linked to the resources available within the ecosystem, with species acquiring resources in a hierarchical or sequential manner as they are the species that have arrived first thus “preempting” the resources as the rest of species in lowers ranks have less abundance because there are less resources due to these early species. **Answer 10b:** It looks like a straight line because it assumes that each subsequential species acquires a fixed proportion of the remaining resources that the first arrivers did not acquire, leading to a linear decline in species abundances.



**Question 11:** Why is it important to account for the number of parameters a model uses when judging how well it explains a given set of data?

**Answer 11:** The more parameters a model uses, the better it will fit a given data set so that we can better determine the best fitting model when we perform a `radfit()` like we did here.

## SYNTHESIS

1. As stated by Magurran (2004) the  $D = \sum p_i^2$  derivation of Simpson's Diversity only applies to communities of infinite size. For anything but an infinitely large community, Simpson's Diversity index is calculated as  $D = \sum \frac{n_i(n_i-1)}{N(N-1)}$ . Assuming a finite community, calculate Simpson's D, 1 - D, and Simpson's inverse (i.e. 1/D) for **site 1** of the BCI site-by-species matrix.

```
SimpD(site1)
```

```
## [1] 0.0253707
```

```
#Simpson's inverse for site1
```

```
D.inv
```

```
## [1] 39.41555
```

```
#Simpson's 1-D
```

```
D.sub
```

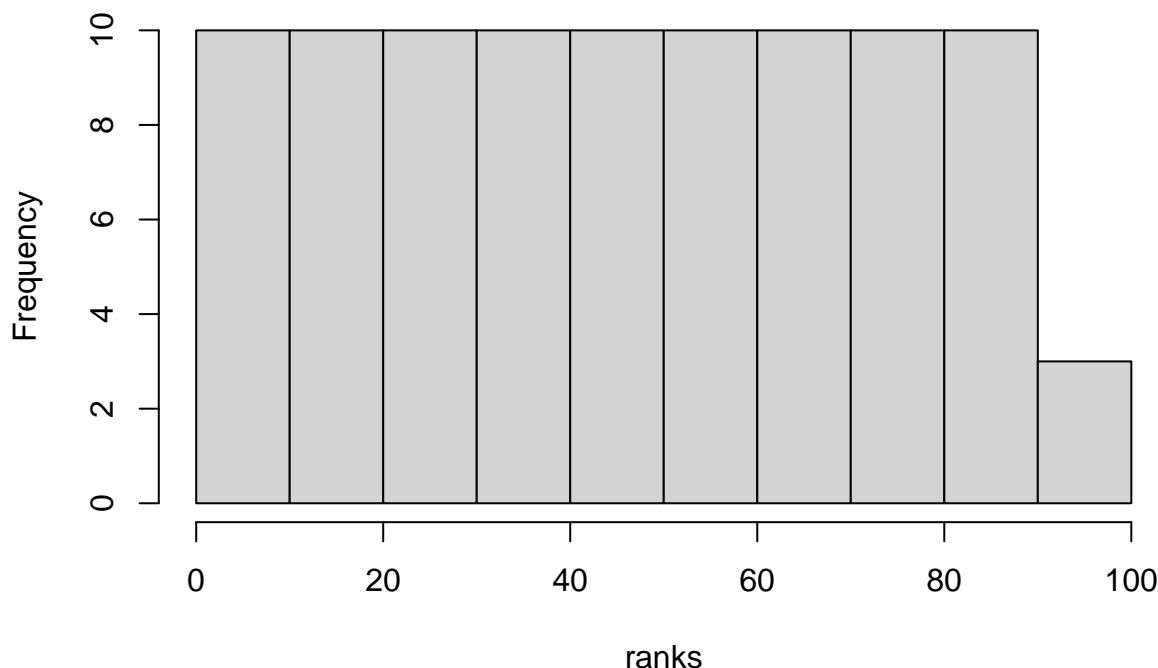
```
## [1] 0.9746293
```

2. Along with the rank-abundance curve (RAC), another way to visualize the distribution of abundance among species is with a histogram (a.k.a., frequency distribution) that shows the frequency of different abundance classes. For example, in a given sample, there may be 10 species represented by a single individual, 8 species with two individuals, 4 species with three individuals, and so on. In fact, the rank-abundance curve and the frequency distribution are the two most common ways to visualize the species-abundance distribution (SAD) and to test species abundance models and biodiversity theories. To address this homework question, use the R function **hist()** to plot the frequency distribution for **site 1** of the BCI site-by-species matrix, and describe the general pattern you see.

```
plot.new()
```

```
hist(ranks)
```

## Histogram of ranks



answer to Synthesis #2 >When I perform the histogram, the general pattern that I am seeing is one in which the majority of the species have a relatively high and equal frequency of abundance at site 1. This would lead to faulty and misleading interpretation of the diversity and evenness of the species that we see within site 1.

3. We asked you to find a biodiversity dataset with your partner. This data could be one of your own or it could be something that you obtained from the literature. Load that dataset. How many sites are there? How many species are there in the entire site-by-species matrix? Any other interesting observations based on what you learned this week?

```
Synthdata <- read.csv("MAT_fungal_abundances.csv")
Synthdata_reform <- Synthdata[,c(1,5)]
Synthdata_reform
```

##	Plot	Species
## 1	MAT.B1.C	Alternaria_alternata
## 2	MAT.B1.C	Articulospora_tetracladia
## 3	MAT.B1.C	Cadophora_finlandica
## 4	MAT.B1.C	Cenococcum_geophilum
## 5	MAT.B1.C	Chalara_sp._1
## 6	MAT.B1.C	Cortinarius_sp._1
## 7	MAT.B1.C	Cortinarius_croceus_1
## 8	MAT.B1.C	Cortinarius_glandicolor
## 9	MAT.B1.C	Cortinarius_casimiri
## 10	MAT.B1.C	Cortinarius_croceus_2
## 11	MAT.B1.C	Cortinarius_herpeticus
## 12	MAT.B1.C	Cortinarius_tabularis
## 13	MAT.B1.C	Cortinarius_delibutus
## 14	MAT.B1.C	Cortinarius_sp._2
## 15	MAT.B1.C	Cortinarius_paragaudis
## 16	MAT.B1.C	Cortinarius_sp._3
## 17	MAT.B1.C	Helotiales_sp._1

## 18	MAT.B1.C	Laccaria_laccata
## 19	MAT.B1.C	Lactarius_vietus_1
## 20	MAT.B1.C	Lactarius_glyciosmus
## 21	MAT.B1.C	Lactarius_vietus_2
## 22	MAT.B1.C	Leccinum_holopus
## 23	MAT.B1.C	Leccinum_scabrum
## 24	MAT.B1.C	Leccinum_variicolor_1
## 25	MAT.B1.C	Leccinum_variicolor_2
## 26	MAT.B1.C	Leccinum_variicolor_3
## 27	MAT.B1.C	Leptodontidium_elatius
## 28	MAT.B1.C	Meliniomyces_variabilis
## 29	MAT.B1.C	Meliniomyces_bicolor
## 30	MAT.B1.C	Phialocephala_fortinii
## 31	MAT.B1.C	Pseudotomentella_sp._1
## 32	MAT.B1.C	Rhizoscyphus_ericae
## 33	MAT.B1.C	Thelephora_terrestris
## 34	MAT.B1.C	Tomentella_sublilacina
## 35	MAT.B1.C	Tomentella_sp._1
## 36	MAT.B1.C	Tomentellopsis_submollis
## 37	MAT.B1.C	Russula_chamiteae
## 38	MAT.B1.C	Russula_decolorans
## 39	MAT.B1.C	Russula_nitida/sphagnicola
## 40	MAT.B1.C	Russula_sp._1
## 41	MAT.B1.C	Russula_sp._2
## 42	MAT.B1.C	Russula_sp._3
## 43	MAT.B1.C	Russula_sp._4
## 44	MAT.B1.C	Russula_vinosa
## 45	MAT.B1.F	Alternaria_alternata
## 46	MAT.B1.F	Articulospora_tetracladia
## 47	MAT.B1.F	Cadophora_finlandica
## 48	MAT.B1.F	Cenococcum_geophilum
## 49	MAT.B1.F	Chalara_sp._1
## 50	MAT.B1.F	Cortinarius_sp._1
## 51	MAT.B1.F	Cortinarius_croceus_1
## 52	MAT.B1.F	Cortinarius_glandicolor
## 53	MAT.B1.F	Cortinarius_casimiri
## 54	MAT.B1.F	Cortinarius_croceus_2
## 55	MAT.B1.F	Cortinarius_herpeticus
## 56	MAT.B1.F	Cortinarius_tabularis
## 57	MAT.B1.F	Cortinarius_delibutus
## 58	MAT.B1.F	Cortinarius_sp._2
## 59	MAT.B1.F	Cortinarius_paragaudis
## 60	MAT.B1.F	Cortinarius_sp._3
## 61	MAT.B1.F	Helotiales_sp._1
## 62	MAT.B1.F	Laccaria_laccata
## 63	MAT.B1.F	Lactarius_vietus_1
## 64	MAT.B1.F	Lactarius_glyciosmus
## 65	MAT.B1.F	Lactarius_vietus_2
## 66	MAT.B1.F	Leccinum_holopus
## 67	MAT.B1.F	Leccinum_scabrum
## 68	MAT.B1.F	Leccinum_variicolor_1
## 69	MAT.B1.F	Leccinum_variicolor_2
## 70	MAT.B1.F	Leccinum_variicolor_3
## 71	MAT.B1.F	Leptodontidium_elatius

## 72	MAT.B1.F	Meliniomyces_variabilis
## 73	MAT.B1.F	Meliniomyces_bicolor
## 74	MAT.B1.F	Phialocephala_fortinii
## 75	MAT.B1.F	Pseudotomentella_sp._1
## 76	MAT.B1.F	Rhizoscyphus_ericae
## 77	MAT.B1.F	Thelephora_terrestris
## 78	MAT.B1.F	Tomentella_sublilacina
## 79	MAT.B1.F	Tomentella_sp._1
## 80	MAT.B1.F	Tomentellopsis_submollis
## 81	MAT.B1.F	Russula_chamiteae
## 82	MAT.B1.F	Russula_decolorans
## 83	MAT.B1.F	Russula_nitida/sphagnicola
## 84	MAT.B1.F	Russula_sp._1
## 85	MAT.B1.F	Russula_sp._2
## 86	MAT.B1.F	Russula_sp._3
## 87	MAT.B1.F	Russula_sp._4
## 88	MAT.B1.F	Russula_vinosa
## 89	MAT.B1.W	Alternaria_alternata
## 90	MAT.B1.W	Articulospora_tetracladia
## 91	MAT.B1.W	Cadophora_finlandica
## 92	MAT.B1.W	Cenococcum_geophilum
## 93	MAT.B1.W	Chalara_sp._1
## 94	MAT.B1.W	Cortinarius_sp._1
## 95	MAT.B1.W	Cortinarius_croceus_1
## 96	MAT.B1.W	Cortinarius_glandicolor
## 97	MAT.B1.W	Cortinarius_casimiri
## 98	MAT.B1.W	Cortinarius_croceus_2
## 99	MAT.B1.W	Cortinarius_herpeticus
## 100	MAT.B1.W	Cortinarius_tabularis
## 101	MAT.B1.W	Cortinarius_delibutus
## 102	MAT.B1.W	Cortinarius_sp._2
## 103	MAT.B1.W	Cortinarius_paragaudis
## 104	MAT.B1.W	Cortinarius_sp._3
## 105	MAT.B1.W	Helotiales_sp._1
## 106	MAT.B1.W	Laccaria_laccata
## 107	MAT.B1.W	Lactarius_vietus_1
## 108	MAT.B1.W	Lactarius_glyciosmus
## 109	MAT.B1.W	Lactarius_vietus_2
## 110	MAT.B1.W	Leccinum_holopus
## 111	MAT.B1.W	Leccinum_scabrum
## 112	MAT.B1.W	Leccinum_variicolor_1
## 113	MAT.B1.W	Leccinum_variicolor_2
## 114	MAT.B1.W	Leccinum_variicolor_3
## 115	MAT.B1.W	Leptodontidium_elatius
## 116	MAT.B1.W	Meliniomyces_variabilis
## 117	MAT.B1.W	Meliniomyces_bicolor
## 118	MAT.B1.W	Phialocephala_fortinii
## 119	MAT.B1.W	Pseudotomentella_sp._1
## 120	MAT.B1.W	Rhizoscyphus_ericae
## 121	MAT.B1.W	Thelephora_terrestris
## 122	MAT.B1.W	Tomentella_sublilacina
## 123	MAT.B1.W	Tomentella_sp._1
## 124	MAT.B1.W	Tomentellopsis_submollis
## 125	MAT.B1.W	Russula_chamiteae

## 126	MAT.B1.W	Russula_decolorans
## 127	MAT.B1.W	Russula_nitida/sphagnicola
## 128	MAT.B1.W	Russula_sp._1
## 129	MAT.B1.W	Russula_sp._2
## 130	MAT.B1.W	Russula_sp._3
## 131	MAT.B1.W	Russula_sp._4
## 132	MAT.B1.W	Russula_vinosa
## 133	MAT.B1.WF	Alternaria_alternata
## 134	MAT.B1.WF	Articulospora_tetracladia
## 135	MAT.B1.WF	Cadophora_finlandica
## 136	MAT.B1.WF	Cenococcum_geophilum
## 137	MAT.B1.WF	Chalara_sp._1
## 138	MAT.B1.WF	Cortinarius_sp._1
## 139	MAT.B1.WF	Cortinarius_croceus_1
## 140	MAT.B1.WF	Cortinarius_glandicolor
## 141	MAT.B1.WF	Cortinarius_casimiri
## 142	MAT.B1.WF	Cortinarius_croceus_2
## 143	MAT.B1.WF	Cortinarius_herpeticus
## 144	MAT.B1.WF	Cortinarius_tabularis
## 145	MAT.B1.WF	Cortinarius_delibutus
## 146	MAT.B1.WF	Cortinarius_sp._2
## 147	MAT.B1.WF	Cortinarius_paragaudis
## 148	MAT.B1.WF	Cortinarius_sp._3
## 149	MAT.B1.WF	Helotiales_sp._1
## 150	MAT.B1.WF	Laccaria_laccata
## 151	MAT.B1.WF	Lactarius_vietus_1
## 152	MAT.B1.WF	Lactarius_glyciosmus
## 153	MAT.B1.WF	Lactarius_vietus_2
## 154	MAT.B1.WF	Leccinum_holopus
## 155	MAT.B1.WF	Leccinum_scabrum
## 156	MAT.B1.WF	Leccinum_variicolor_1
## 157	MAT.B1.WF	Leccinum_variicolor_2
## 158	MAT.B1.WF	Leccinum_variicolor_3
## 159	MAT.B1.WF	Leptodontidium_elatius
## 160	MAT.B1.WF	Meliniomyces_variabilis
## 161	MAT.B1.WF	Meliniomyces_bicolor
## 162	MAT.B1.WF	Phialocephala_fortinii
## 163	MAT.B1.WF	Pseudotomentella_sp._1
## 164	MAT.B1.WF	Rhizoscyphus_ericae
## 165	MAT.B1.WF	Thelephora_terrestris
## 166	MAT.B1.WF	Tomentella_sublilacina
## 167	MAT.B1.WF	Tomentella_sp._1
## 168	MAT.B1.WF	Tomentellopsis_submollis
## 169	MAT.B1.WF	Russula_chamiteae
## 170	MAT.B1.WF	Russula_decolorans
## 171	MAT.B1.WF	Russula_nitida/sphagnicola
## 172	MAT.B1.WF	Russula_sp._1
## 173	MAT.B1.WF	Russula_sp._2
## 174	MAT.B1.WF	Russula_sp._3
## 175	MAT.B1.WF	Russula_sp._4
## 176	MAT.B1.WF	Russula_vinosa
## 177	MAT.B2.C	Alternaria_alternata
## 178	MAT.B2.C	Articulospora_tetracladia
## 179	MAT.B2.C	Cadophora_finlandica

## 180	MAT.B2.C	Cenococcum_geophilum
## 181	MAT.B2.C	Chalara_sp._1
## 182	MAT.B2.C	Cortinarius_sp._1
## 183	MAT.B2.C	Cortinarius_croceus_1
## 184	MAT.B2.C	Cortinarius_glandicolor
## 185	MAT.B2.C	Cortinarius_casimiri
## 186	MAT.B2.C	Cortinarius_croceus_2
## 187	MAT.B2.C	Cortinarius_herpeticus
## 188	MAT.B2.C	Cortinarius_tabularis
## 189	MAT.B2.C	Cortinarius_delibutus
## 190	MAT.B2.C	Cortinarius_sp._2
## 191	MAT.B2.C	Cortinarius_paragaudis
## 192	MAT.B2.C	Cortinarius_sp._3
## 193	MAT.B2.C	Helotiales_sp._1
## 194	MAT.B2.C	Laccaria_laccata
## 195	MAT.B2.C	Lactarius_vietus_1
## 196	MAT.B2.C	Lactarius_glyciosmus
## 197	MAT.B2.C	Lactarius_vietus_2
## 198	MAT.B2.C	Leccinum_holopus
## 199	MAT.B2.C	Leccinum_scabrum
## 200	MAT.B2.C	Leccinum_variicolor_1
## 201	MAT.B2.C	Leccinum_variicolor_2
## 202	MAT.B2.C	Leccinum_variicolor_3
## 203	MAT.B2.C	Leptodontidium_elatius
## 204	MAT.B2.C	Meliniomyces_variabilis
## 205	MAT.B2.C	Meliniomyces_bicolor
## 206	MAT.B2.C	Phialocephala_fortinii
## 207	MAT.B2.C	Pseudotomentella_sp._1
## 208	MAT.B2.C	Rhizoscyphus_ericae
## 209	MAT.B2.C	Thelephora_terrestris
## 210	MAT.B2.C	Tomentella_sublilacina
## 211	MAT.B2.C	Tomentella_sp._1
## 212	MAT.B2.C	Tomentellopsis_submollis
## 213	MAT.B2.C	Russula_chamiteae
## 214	MAT.B2.C	Russula_decolorans
## 215	MAT.B2.C	Russula_nitida/sphagnicola
## 216	MAT.B2.C	Russula_sp._1
## 217	MAT.B2.C	Russula_sp._2
## 218	MAT.B2.C	Russula_sp._3
## 219	MAT.B2.C	Russula_sp._4
## 220	MAT.B2.C	Russula_vinosa
## 221	MAT.B2.F	Alternaria_alternata
## 222	MAT.B2.F	Articulospora_tetracladia
## 223	MAT.B2.F	Cadophora_finlandica
## 224	MAT.B2.F	Cenococcum_geophilum
## 225	MAT.B2.F	Chalara_sp._1
## 226	MAT.B2.F	Cortinarius_sp._1
## 227	MAT.B2.F	Cortinarius_croceus_1
## 228	MAT.B2.F	Cortinarius_glandicolor
## 229	MAT.B2.F	Cortinarius_casimiri
## 230	MAT.B2.F	Cortinarius_croceus_2
## 231	MAT.B2.F	Cortinarius_herpeticus
## 232	MAT.B2.F	Cortinarius_tabularis
## 233	MAT.B2.F	Cortinarius_delibutus

##	234	MAT.B2.F	Cortinarius_sp._2
##	235	MAT.B2.F	Cortinarius_paragaudis
##	236	MAT.B2.F	Cortinarius_sp._3
##	237	MAT.B2.F	Helotiales_sp._1
##	238	MAT.B2.F	Laccaria_laccata
##	239	MAT.B2.F	Lactarius_vietus_1
##	240	MAT.B2.F	Lactarius_glyciosmus
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##	242	MAT.B2.F	Leccinum_holopus
##	243	MAT.B2.F	Leccinum_scabrum
##	244	MAT.B2.F	Leccinum_variicolor_1
##	245	MAT.B2.F	Leccinum_variicolor_2
##	246	MAT.B2.F	Leccinum_variicolor_3
##	247	MAT.B2.F	Leptodontidium_elatius
##	248	MAT.B2.F	Meliniumyces_variabilis
##	249	MAT.B2.F	Meliniumyces_bicolor
##	250	MAT.B2.F	Phialocephala_fortinii
##	251	MAT.B2.F	Pseudotomentella_sp._1
##	252	MAT.B2.F	Rhizoscyphus_ericae
##	253	MAT.B2.F	Thelephora_terrestris
##	254	MAT.B2.F	Tomentella_sublilacina
##	255	MAT.B2.F	Tomentella_sp._1
##	256	MAT.B2.F	Tomentellopsis_submollis
##	257	MAT.B2.F	Russula_chamiteae
##	258	MAT.B2.F	Russula_decolorans
##	259	MAT.B2.F	Russula_nitida/sphagnicola
##	260	MAT.B2.F	Russula_sp._1
##	261	MAT.B2.F	Russula_sp._2
##	262	MAT.B2.F	Russula_sp._3
##	263	MAT.B2.F	Russula_sp._4
##	264	MAT.B2.F	Russula_vinosa
##	265	MAT.B2.W	Alternaria_alternata
##	266	MAT.B2.W	Articulospora_tetracladia
##	267	MAT.B2.W	Cadophora_finlandica
##	268	MAT.B2.W	Cenococcum_geophilum
##	269	MAT.B2.W	Chalara_sp._1
##	270	MAT.B2.W	Cortinarius_sp._1
##	271	MAT.B2.W	Cortinarius_croceus_1
##	272	MAT.B2.W	Cortinarius_glandicolor
##	273	MAT.B2.W	Cortinarius_casimiri
##	274	MAT.B2.W	Cortinarius_croceus_2
##	275	MAT.B2.W	Cortinarius_herpeticus
##	276	MAT.B2.W	Cortinarius_tabularis
##	277	MAT.B2.W	Cortinarius_delibutus
##	278	MAT.B2.W	Cortinarius_sp._2
##	279	MAT.B2.W	Cortinarius_paragaudis
##	280	MAT.B2.W	Cortinarius_sp._3
##	281	MAT.B2.W	Helotiales_sp._1
##	282	MAT.B2.W	Laccaria_laccata
##	283	MAT.B2.W	Lactarius_vietus_1
##	284	MAT.B2.W	Lactarius_glyciosmus
##	285	MAT.B2.W	Lactarius_vietus_2
##	286	MAT.B2.W	Leccinum_holopus
##	287	MAT.B2.W	Leccinum_scabrum

## 288	MAT.B2.W	Leccinum_variicolor_1
## 289	MAT.B2.W	Leccinum_variicolor_2
## 290	MAT.B2.W	Leccinum_variicolor_3
## 291	MAT.B2.W	Leptodontidium_elatius
## 292	MAT.B2.W	Meliniomyces_variabilis
## 293	MAT.B2.W	Meliniomyces_bicolor
## 294	MAT.B2.W	Phialocephala_fortinii
## 295	MAT.B2.W	Pseudotomentella_sp._1
## 296	MAT.B2.W	Rhizoscyphus_ericae
## 297	MAT.B2.W	Thelephora_terrestris
## 298	MAT.B2.W	Tomentella_sublilacina
## 299	MAT.B2.W	Tomentella_sp._1
## 300	MAT.B2.W	Tomentellopsis_submollis
## 301	MAT.B2.W	Russula_chamiteae
## 302	MAT.B2.W	Russula_decolorans
## 303	MAT.B2.W	Russula_nitida/sphagnicola
## 304	MAT.B2.W	Russula_sp._1
## 305	MAT.B2.W	Russula_sp._2
## 306	MAT.B2.W	Russula_sp._3
## 307	MAT.B2.W	Russula_sp._4
## 308	MAT.B2.W	Russula_vinosa
## 309	MAT.B2.WF	Alternaria_alternata
## 310	MAT.B2.WF	Articulospora_tetracladia
## 311	MAT.B2.WF	Cadophora_finlandica
## 312	MAT.B2.WF	Cenococcum_geophilum
## 313	MAT.B2.WF	Chalara_sp._1
## 314	MAT.B2.WF	Cortinarius_sp._1
## 315	MAT.B2.WF	Cortinarius_croceus_1
## 316	MAT.B2.WF	Cortinarius_glandicolor
## 317	MAT.B2.WF	Cortinarius_casimiri
## 318	MAT.B2.WF	Cortinarius_croceus_2
## 319	MAT.B2.WF	Cortinarius_herpeticus
## 320	MAT.B2.WF	Cortinarius_tabularis
## 321	MAT.B2.WF	Cortinarius_delibutus
## 322	MAT.B2.WF	Cortinarius_sp._2
## 323	MAT.B2.WF	Cortinarius_paragaudis
## 324	MAT.B2.WF	Cortinarius_sp._3
## 325	MAT.B2.WF	Helotiales_sp._1
## 326	MAT.B2.WF	Laccaria_laccata
## 327	MAT.B2.WF	Lactarius_vietus_1
## 328	MAT.B2.WF	Lactarius_glyciosmus
## 329	MAT.B2.WF	Lactarius_vietus_2
## 330	MAT.B2.WF	Leccinum_holopus
## 331	MAT.B2.WF	Leccinum_scabrum
## 332	MAT.B2.WF	Leccinum_variicolor_1
## 333	MAT.B2.WF	Leccinum_variicolor_2
## 334	MAT.B2.WF	Leccinum_variicolor_3
## 335	MAT.B2.WF	Leptodontidium_elatius
## 336	MAT.B2.WF	Meliniomyces_variabilis
## 337	MAT.B2.WF	Meliniomyces_bicolor
## 338	MAT.B2.WF	Phialocephala_fortinii
## 339	MAT.B2.WF	Pseudotomentella_sp._1
## 340	MAT.B2.WF	Rhizoscyphus_ericae
## 341	MAT.B2.WF	Thelephora_terrestris



## 342 MAT.B2.WF Tomentella\_sublilacina  
 ## 343 MAT.B2.WF Tomentella\_sp.\_1  
 ## 344 MAT.B2.WF Tomentellopsis\_submollis  
 ## 345 MAT.B2.WF Russula\_chamiteae  
 ## 346 MAT.B2.WF Russula\_decolorans  
 ## 347 MAT.B2.WF Russula\_nitida/sphagnicola  
 ## 348 MAT.B2.WF Russula\_sp.\_1  
 ## 349 MAT.B2.WF Russula\_sp.\_2  
 ## 350 MAT.B2.WF Russula\_sp.\_3  
 ## 351 MAT.B2.WF Russula\_sp.\_4  
 ## 352 MAT.B2.WF Russula\_vinosa  
 ## 353 MAT.B3.C Alternaria\_alternata  
 ## 354 MAT.B3.C Articulospora\_tetracladia  
 ## 355 MAT.B3.C Cadophora\_finlandica  
 ## 356 MAT.B3.C Cenococcum\_geophilum  
 ## 357 MAT.B3.C Chalara\_sp.\_1  
 ## 358 MAT.B3.C Cortinarius\_sp.\_1  
 ## 359 MAT.B3.C Cortinarius\_croceus\_1  
 ## 360 MAT.B3.C Cortinarius\_glandicolor  
 ## 361 MAT.B3.C Cortinarius\_casimiri  
 ## 362 MAT.B3.C Cortinarius\_croceus\_2  
 ## 363 MAT.B3.C Cortinarius\_herpeticus  
 ## 364 MAT.B3.C Cortinarius\_tabularis  
 ## 365 MAT.B3.C Cortinarius\_delibutus  
 ## 366 MAT.B3.C Cortinarius\_sp.\_2  
 ## 367 MAT.B3.C Cortinarius\_paragaudis  
 ## 368 MAT.B3.C Cortinarius\_sp.\_3  
 ## 369 MAT.B3.C Helotiales\_sp.\_1  
 ## 370 MAT.B3.C Laccaria\_laccata  
 ## 371 MAT.B3.C Lactarius\_vietus\_1  
 ## 372 MAT.B3.C Lactarius\_glyciosmus  
 ## 373 MAT.B3.C Lactarius\_vietus\_2  
 ## 374 MAT.B3.C Leccinum\_holopus  
 ## 375 MAT.B3.C Leccinum\_scabrum  
 ## 376 MAT.B3.C Leccinum\_variicolor\_1  
 ## 377 MAT.B3.C Leccinum\_variicolor\_2  
 ## 378 MAT.B3.C Leccinum\_variicolor\_3  
 ## 379 MAT.B3.C Leptodontidium\_elatius  
 ## 380 MAT.B3.C Meliniomyces\_variabilis  
 ## 381 MAT.B3.C Meliniomyces\_bicolor  
 ## 382 MAT.B3.C Phialocephala\_fortinii  
 ## 383 MAT.B3.C Pseudotomentella\_sp.\_1  
 ## 384 MAT.B3.C Rhizoscyphus\_ericae  
 ## 385 MAT.B3.C Thelephora\_terrestris  
 ## 386 MAT.B3.C Tomentella\_sublilacina  
 ## 387 MAT.B3.C Tomentella\_sp.\_1  
 ## 388 MAT.B3.C Tomentellopsis\_submollis  
 ## 389 MAT.B3.C Russula\_chamiteae  
 ## 390 MAT.B3.C Russula\_decolorans  
 ## 391 MAT.B3.C Russula\_nitida/sphagnicola  
 ## 392 MAT.B3.C Russula\_sp.\_1  
 ## 393 MAT.B3.C Russula\_sp.\_2  
 ## 394 MAT.B3.C Russula\_sp.\_3  
 ## 395 MAT.B3.C Russula\_sp.\_4

## 396	MAT.B3.C	Russula_vinosa
## 397	MAT.B3.F	Alternaria_alternata
## 398	MAT.B3.F	Articulospora_tetracladia
## 399	MAT.B3.F	Cadophora_finlandica
## 400	MAT.B3.F	Cenococcum_geophilum
## 401	MAT.B3.F	Chalara_sp._1
## 402	MAT.B3.F	Cortinarius_sp._1
## 403	MAT.B3.F	Cortinarius_croceus_1
## 404	MAT.B3.F	Cortinarius_glandicolor
## 405	MAT.B3.F	Cortinarius_casimiri
## 406	MAT.B3.F	Cortinarius_croceus_2
## 407	MAT.B3.F	Cortinarius_herpeticus
## 408	MAT.B3.F	Cortinarius_tabularis
## 409	MAT.B3.F	Cortinarius_delibutus
## 410	MAT.B3.F	Cortinarius_sp._2
## 411	MAT.B3.F	Cortinarius_paragaudis
## 412	MAT.B3.F	Cortinarius_sp._3
## 413	MAT.B3.F	Helotiales_sp._1
## 414	MAT.B3.F	Laccaria_laccata
## 415	MAT.B3.F	Lactarius_vietus_1
## 416	MAT.B3.F	Lactarius_glyciosmus
## 417	MAT.B3.F	Lactarius_vietus_2
## 418	MAT.B3.F	Leccinum_holopus
## 419	MAT.B3.F	Leccinum_scabrum
## 420	MAT.B3.F	Leccinum_variicolor_1
## 421	MAT.B3.F	Leccinum_variicolor_2
## 422	MAT.B3.F	Leccinum_variicolor_3
## 423	MAT.B3.F	Leptodontidium_elatius
## 424	MAT.B3.F	Meliniomyces_variabilis
## 425	MAT.B3.F	Meliniomyces_bicolor
## 426	MAT.B3.F	Phialocephala_fortinii
## 427	MAT.B3.F	Pseudotomentella_sp._1
## 428	MAT.B3.F	Rhizoscyphus_ericae
## 429	MAT.B3.F	Thelephora_terrestris
## 430	MAT.B3.F	Tomentella_sublilacina
## 431	MAT.B3.F	Tomentella_sp._1
## 432	MAT.B3.F	Tomentellopsis_submollis
## 433	MAT.B3.F	Russula_chamiteae
## 434	MAT.B3.F	Russula_decolorans
## 435	MAT.B3.F	Russula_nitida/sphagnicola
## 436	MAT.B3.F	Russula_sp._1
## 437	MAT.B3.F	Russula_sp._2
## 438	MAT.B3.F	Russula_sp._3
## 439	MAT.B3.F	Russula_sp._4
## 440	MAT.B3.F	Russula_vinosa
## 441	MAT.B3.W	Alternaria_alternata
## 442	MAT.B3.W	Articulospora_tetracladia
## 443	MAT.B3.W	Cadophora_finlandica
## 444	MAT.B3.W	Cenococcum_geophilum
## 445	MAT.B3.W	Chalara_sp._1
## 446	MAT.B3.W	Cortinarius_sp._1
## 447	MAT.B3.W	Cortinarius_croceus_1
## 448	MAT.B3.W	Cortinarius_glandicolor
## 449	MAT.B3.W	Cortinarius_casimiri

## 450	MAT.B3.W	Cortinarius_croceus_2
## 451	MAT.B3.W	Cortinarius_herpeticus
## 452	MAT.B3.W	Cortinarius_tabularis
## 453	MAT.B3.W	Cortinarius_delibutus
## 454	MAT.B3.W	Cortinarius_sp._2
## 455	MAT.B3.W	Cortinarius_paragaudis
## 456	MAT.B3.W	Cortinarius_sp._3
## 457	MAT.B3.W	Helotiales_sp._1
## 458	MAT.B3.W	Laccaria_laccata
## 459	MAT.B3.W	Lactarius_vietus_1
## 460	MAT.B3.W	Lactarius_glyciosmus
## 461	MAT.B3.W	Lactarius_vietus_2
## 462	MAT.B3.W	Leccinum_holopus
## 463	MAT.B3.W	Leccinum_scabrum
## 464	MAT.B3.W	Leccinum_variicolor_1
## 465	MAT.B3.W	Leccinum_variicolor_2
## 466	MAT.B3.W	Leccinum_variicolor_3
## 467	MAT.B3.W	Leptodontidium_elatius
## 468	MAT.B3.W	Meliniumyces_variabilis
## 469	MAT.B3.W	Meliniumyces_bicolor
## 470	MAT.B3.W	Phialocephala_fortinii
## 471	MAT.B3.W	Pseudotomentella_sp._1
## 472	MAT.B3.W	Rhizoscyphus_ericae
## 473	MAT.B3.W	Thelephora_terrestris
## 474	MAT.B3.W	Tomentella_sublilacina
## 475	MAT.B3.W	Tomentella_sp._1
## 476	MAT.B3.W	Tomentellopsis_submollis
## 477	MAT.B3.W	Russula_chamiteae
## 478	MAT.B3.W	Russula_decolorans
## 479	MAT.B3.W	Russula_nitida/sphagnicola
## 480	MAT.B3.W	Russula_sp._1
## 481	MAT.B3.W	Russula_sp._2
## 482	MAT.B3.W	Russula_sp._3
## 483	MAT.B3.W	Russula_sp._4
## 484	MAT.B3.W	Russula_vinosa
## 485	MAT.B3.WF	Alternaria_alternata
## 486	MAT.B3.WF	Articulospora_tetracladia
## 487	MAT.B3.WF	Cadophora_finlandica
## 488	MAT.B3.WF	Cenococcum_geophilum
## 489	MAT.B3.WF	Chalara_sp._1
## 490	MAT.B3.WF	Cortinarius_sp._1
## 491	MAT.B3.WF	Cortinarius_croceus_1
## 492	MAT.B3.WF	Cortinarius_glandicolor
## 493	MAT.B3.WF	Cortinarius_casimiri
## 494	MAT.B3.WF	Cortinarius_croceus_2
## 495	MAT.B3.WF	Cortinarius_herpeticus
## 496	MAT.B3.WF	Cortinarius_tabularis
## 497	MAT.B3.WF	Cortinarius_delibutus
## 498	MAT.B3.WF	Cortinarius_sp._2
## 499	MAT.B3.WF	Cortinarius_paragaudis
## 500	MAT.B3.WF	Cortinarius_sp._3
## 501	MAT.B3.WF	Helotiales_sp._1
## 502	MAT.B3.WF	Laccaria_laccata
## 503	MAT.B3.WF	Lactarius_vietus_1

## 504	MAT.B3.WF	Lactarius_glyciosmus
## 505	MAT.B3.WF	Lactarius_vietus_2
## 506	MAT.B3.WF	Leccinum_holopus
## 507	MAT.B3.WF	Leccinum_scabrum
## 508	MAT.B3.WF	Leccinum_variicolor_1
## 509	MAT.B3.WF	Leccinum_variicolor_2
## 510	MAT.B3.WF	Leccinum_variicolor_3
## 511	MAT.B3.WF	Leptodontidium_elatius
## 512	MAT.B3.WF	Meliniomyces_variabilis
## 513	MAT.B3.WF	Meliniomyces_bicolor
## 514	MAT.B3.WF	Phialocephala_fortinii
## 515	MAT.B3.WF	Pseudotomentella_sp._1
## 516	MAT.B3.WF	Rhizoscyphus_ericae
## 517	MAT.B3.WF	Thelephora_terrestris
## 518	MAT.B3.WF	Tomentella_sublilacina
## 519	MAT.B3.WF	Tomentella_sp._1
## 520	MAT.B3.WF	Tomentellopsis_submollis
## 521	MAT.B3.WF	Russula_chamiteae
## 522	MAT.B3.WF	Russula_decolorans
## 523	MAT.B3.WF	Russula_nitida/sphagnicola
## 524	MAT.B3.WF	Russula_sp._1
## 525	MAT.B3.WF	Russula_sp._2
## 526	MAT.B3.WF	Russula_sp._3
## 527	MAT.B3.WF	Russula_sp._4
## 528	MAT.B3.WF	Russula_vinosa
## 529	MAT.B4.C	Alternaria_alternata
## 530	MAT.B4.C	Articulospora_tetracladia
## 531	MAT.B4.C	Cadophora_finlandica
## 532	MAT.B4.C	Cenococcum_geophilum
## 533	MAT.B4.C	Chalara_sp._1
## 534	MAT.B4.C	Cortinarius_sp._1
## 535	MAT.B4.C	Cortinarius_croceus_1
## 536	MAT.B4.C	Cortinarius_glandicolor
## 537	MAT.B4.C	Cortinarius_casimiri
## 538	MAT.B4.C	Cortinarius_croceus_2
## 539	MAT.B4.C	Cortinarius_herpeticus
## 540	MAT.B4.C	Cortinarius_tabularis
## 541	MAT.B4.C	Cortinarius_delibutus
## 542	MAT.B4.C	Cortinarius_sp._2
## 543	MAT.B4.C	Cortinarius_paragaudis
## 544	MAT.B4.C	Cortinarius_sp._3
## 545	MAT.B4.C	Helotiales_sp._1
## 546	MAT.B4.C	Laccaria_laccata
## 547	MAT.B4.C	Lactarius_vietus_1
## 548	MAT.B4.C	Lactarius_glyciosmus
## 549	MAT.B4.C	Lactarius_vietus_2
## 550	MAT.B4.C	Leccinum_holopus
## 551	MAT.B4.C	Leccinum_scabrum
## 552	MAT.B4.C	Leccinum_variicolor_1
## 553	MAT.B4.C	Leccinum_variicolor_2
## 554	MAT.B4.C	Leccinum_variicolor_3
## 555	MAT.B4.C	Leptodontidium_elatius
## 556	MAT.B4.C	Meliniomyces_variabilis
## 557	MAT.B4.C	Meliniomyces_bicolor

## 558	MAT.B4.C	Phialocephala_fortinii
## 559	MAT.B4.C	Pseudotomentella_sp._1
## 560	MAT.B4.C	Rhizoscyphus_ericae
## 561	MAT.B4.C	Thelephora_terrestris
## 562	MAT.B4.C	Tomentella_sublilacina
## 563	MAT.B4.C	Tomentella_sp._1
## 564	MAT.B4.C	Tomentellopsis_submollis
## 565	MAT.B4.C	Russula_chamiteae
## 566	MAT.B4.C	Russula_decolorans
## 567	MAT.B4.C	Russula_nitida/sphagnicola
## 568	MAT.B4.C	Russula_sp._1
## 569	MAT.B4.C	Russula_sp._2
## 570	MAT.B4.C	Russula_sp._3
## 571	MAT.B4.C	Russula_sp._4
## 572	MAT.B4.C	Russula_vinosa
## 573	MAT.B4.F	Alternaria_alternata
## 574	MAT.B4.F	Articulospora_tetracladia
## 575	MAT.B4.F	Cadophora_finlandica
## 576	MAT.B4.F	Cenococcum_geophilum
## 577	MAT.B4.F	Chalara_sp._1
## 578	MAT.B4.F	Cortinarius_sp._1
## 579	MAT.B4.F	Cortinarius_croceus_1
## 580	MAT.B4.F	Cortinarius_glandicolor
## 581	MAT.B4.F	Cortinarius_casimiri
## 582	MAT.B4.F	Cortinarius_croceus_2
## 583	MAT.B4.F	Cortinarius_herpeticus
## 584	MAT.B4.F	Cortinarius_tabularis
## 585	MAT.B4.F	Cortinarius_delibutus
## 586	MAT.B4.F	Cortinarius_sp._2
## 587	MAT.B4.F	Cortinarius_paragaudis
## 588	MAT.B4.F	Cortinarius_sp._3
## 589	MAT.B4.F	Helotiales_sp._1
## 590	MAT.B4.F	Laccaria_laccata
## 591	MAT.B4.F	Lactarius_vietus_1
## 592	MAT.B4.F	Lactarius_glyciosmus
## 593	MAT.B4.F	Lactarius_vietus_2
## 594	MAT.B4.F	Leccinum_holopus
## 595	MAT.B4.F	Leccinum_scabrum
## 596	MAT.B4.F	Leccinum_variicolor_1
## 597	MAT.B4.F	Leccinum_variicolor_2
## 598	MAT.B4.F	Leccinum_variicolor_3
## 599	MAT.B4.F	Leptodontidium_elatius
## 600	MAT.B4.F	Meliniomyces_variabilis
## 601	MAT.B4.F	Meliniomyces_bicolor
## 602	MAT.B4.F	Phialocephala_fortinii
## 603	MAT.B4.F	Pseudotomentella_sp._1
## 604	MAT.B4.F	Rhizoscyphus_ericae
## 605	MAT.B4.F	Thelephora_terrestris
## 606	MAT.B4.F	Tomentella_sublilacina
## 607	MAT.B4.F	Tomentella_sp._1
## 608	MAT.B4.F	Tomentellopsis_submollis
## 609	MAT.B4.F	Russula_chamiteae
## 610	MAT.B4.F	Russula_decolorans
## 611	MAT.B4.F	Russula_nitida/sphagnicola

## 612	MAT.B4.F	Russula_sp._1
## 613	MAT.B4.F	Russula_sp._2
## 614	MAT.B4.F	Russula_sp._3
## 615	MAT.B4.F	Russula_sp._4
## 616	MAT.B4.F	Russula_vinosa
## 617	MAT.B4.W	Alternaria_alternata
## 618	MAT.B4.W	Articulospora_tetracladia
## 619	MAT.B4.W	Cadophora_finlandica
## 620	MAT.B4.W	Cenococcum_geophilum
## 621	MAT.B4.W	Chalara_sp._1
## 622	MAT.B4.W	Cortinarius_sp._1
## 623	MAT.B4.W	Cortinarius_croceus_1
## 624	MAT.B4.W	Cortinarius_glandicolor
## 625	MAT.B4.W	Cortinarius_casimiri
## 626	MAT.B4.W	Cortinarius_croceus_2
## 627	MAT.B4.W	Cortinarius_herpeticus
## 628	MAT.B4.W	Cortinarius_tabularis
## 629	MAT.B4.W	Cortinarius_delibutus
## 630	MAT.B4.W	Cortinarius_sp._2
## 631	MAT.B4.W	Cortinarius_paragaudis
## 632	MAT.B4.W	Cortinarius_sp._3
## 633	MAT.B4.W	Helotiales_sp._1
## 634	MAT.B4.W	Laccaria_laccata
## 635	MAT.B4.W	Lactarius_vietus_1
## 636	MAT.B4.W	Lactarius_glyciosmus
## 637	MAT.B4.W	Lactarius_vietus_2
## 638	MAT.B4.W	Leccinum_holopus
## 639	MAT.B4.W	Leccinum_scabrum
## 640	MAT.B4.W	Leccinum_variicolor_1
## 641	MAT.B4.W	Leccinum_variicolor_2
## 642	MAT.B4.W	Leccinum_variicolor_3
## 643	MAT.B4.W	Leptodontidium_elatius
## 644	MAT.B4.W	Meliniomyces_variabilis
## 645	MAT.B4.W	Meliniomyces_bicolor
## 646	MAT.B4.W	Phialocephala_fortinii
## 647	MAT.B4.W	Pseudotomentella_sp._1
## 648	MAT.B4.W	Rhizoscyphus_ericae
## 649	MAT.B4.W	Thelephora_terrestris
## 650	MAT.B4.W	Tomentella_sublilacina
## 651	MAT.B4.W	Tomentella_sp._1
## 652	MAT.B4.W	Tomentellopsis_submollis
## 653	MAT.B4.W	Russula_chamiteae
## 654	MAT.B4.W	Russula_decolorans
## 655	MAT.B4.W	Russula_nitida/sphagnicola
## 656	MAT.B4.W	Russula_sp._1
## 657	MAT.B4.W	Russula_sp._2
## 658	MAT.B4.W	Russula_sp._3
## 659	MAT.B4.W	Russula_sp._4
## 660	MAT.B4.W	Russula_vinosa
## 661	MAT.B4.WF	Alternaria_alternata
## 662	MAT.B4.WF	Articulospora_tetracladia
## 663	MAT.B4.WF	Cadophora_finlandica
## 664	MAT.B4.WF	Cenococcum_geophilum
## 665	MAT.B4.WF	Chalara_sp._1

```

## 666 MAT.B4.WF      Cortinarius_sp._1
## 667 MAT.B4.WF      Cortinarius_croceus_1
## 668 MAT.B4.WF      Cortinarius_glandicolor
## 669 MAT.B4.WF      Cortinarius_casimiri
## 670 MAT.B4.WF      Cortinarius_croceus_2
## 671 MAT.B4.WF      Cortinarius_herpeticus
## 672 MAT.B4.WF      Cortinarius_tabularis
## 673 MAT.B4.WF      Cortinarius_delibutus
## 674 MAT.B4.WF      Cortinarius_sp._2
## 675 MAT.B4.WF      Cortinarius_paragaudis
## 676 MAT.B4.WF      Cortinarius_sp._3
## 677 MAT.B4.WF      Helotiales_sp._1
## 678 MAT.B4.WF      Laccaria_laccata
## 679 MAT.B4.WF      Lactarius_vietus_1
## 680 MAT.B4.WF      Lactarius_glyciosmus
## 681 MAT.B4.WF      Lactarius_vietus_2
## 682 MAT.B4.WF      Leccinum_holopus
## 683 MAT.B4.WF      Leccinum_scabrum
## 684 MAT.B4.WF      Leccinum_variicolor_1
## 685 MAT.B4.WF      Leccinum_variicolor_2
## 686 MAT.B4.WF      Leccinum_variicolor_3
## 687 MAT.B4.WF      Leptodontidium_elatius
## 688 MAT.B4.WF      Meliniomyces_variabilis
## 689 MAT.B4.WF      Meliniomyces_bicolor
## 690 MAT.B4.WF      Phialocephala_fortinii
## 691 MAT.B4.WF      Pseudotomentella_sp._1
## 692 MAT.B4.WF      Rhizoscyphus_ericae
## 693 MAT.B4.WF      Thelephora_terrestris
## 694 MAT.B4.WF      Tomentella_sublilacina
## 695 MAT.B4.WF      Tomentella_sp._1
## 696 MAT.B4.WF      Tomentellopsis_submollis
## 697 MAT.B4.WF      Russula_chamiteae
## 698 MAT.B4.WF      Russula_decolorans
## 699 MAT.B4.WF      Russula_nitida/sphagnicola
## 700 MAT.B4.WF      Russula_sp._1
## 701 MAT.B4.WF      Russula_sp._2
## 702 MAT.B4.WF      Russula_sp._3
## 703 MAT.B4.WF      Russula_sp._4
## 704 MAT.B4.WF      Russula_vinosa

```

```

unique_plots <- data.frame(Plot = unique(Synthdata_reform$Plot))
unique_plots

```

```

##      Plot
## 1  MAT.B1.C
## 2  MAT.B1.F
## 3  MAT.B1.W
## 4  MAT.B1.WF
## 5  MAT.B2.C
## 6  MAT.B2.F
## 7  MAT.B2.W
## 8  MAT.B2.WF
## 9  MAT.B3.C
## 10 MAT.B3.F
## 11 MAT.B3.W

```

```
## 12 MAT.B3.WF
## 13 MAT.B4.C
## 14 MAT.B4.F
## 15 MAT.B4.W
## 16 MAT.B4.WF
```

```
unique_species <- data.frame(Species = unique(Synthdata_reform$Species))
unique_species
```

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



it seems as there are a total 16 plots or sites in this specific dataset. There are 44 unique species. Since I am low on time due to issues with the .Rmd file, I am out of time to look at further interesting observations based on what we've learned this week.

## SUBMITTING YOUR ASSIGNMENT

Use Knitr to create a PDF of your completed 5.AlphaDiversity\_Worksheet.Rmd document, push it to GitHub, and create a pull request. Please make sure your updated repo include both the pdf and RMarkdown files.

Unless otherwise noted, this assignment is due on **Wednesday, January 29<sup>th</sup>, 2025 at 12:00 PM (noon)**.