5. Worksheet: Alpha Diversity

Caroline Edwards; Z620: Quantitative Biodiversity, Indiana University

07 April, 2021

OVERVIEW

In this exercise, we will explore aspects of local or site-specific diversity, also known as alpha (α) diversity. First we will quantify two of the fundamental components of (α) 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 `5.AlphaDiversity` folder, and 4) Load the `vegan` R package (be sure to install first if you haven't already).

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

```
## [1] "/Users/carolineedwards/quant_bio/GitHub/QB2021_Edwards/2.Worksheets/5.AlphaDiversity"
```

```
setwd("~/quant_bio/GitHub/QB2021_Edwards/2.Worksheets/5.AlphaDiversity/")
require("vegan")
```

```
## Loading required package: vegan

## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.5-6
```

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  "Abarema.macradenium" "Acacia.melanoceras" "Acalypha.diversifolia
```

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,])
```

```
##  1
## 93
```

```
specnumber(BCI[1,])
```

```
##  1
## 93
```

```r
S.obs(BCI[1:4,])
```

```
##  1  2  3  4
## 93 84 90 94
```

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, site 1 has 93 species using both the S.obs and specnumber functions. The species richness of the first four sites of the BCI matrix 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.

```r
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
```

```r
site1<-BCI[1,]
1-C(site1)
```

```
##          1
## 0.06919643
```

```r
min(C(BCI))
```

```
## [1] 0.8705882
```

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 Good's Coverage (C) is 0 to 1.
>
> ***Answer 2b***: If n_i equalled N, then every sample sequenced at a site was a singleton, so we would get a C of zero and we could conclude that there is low coverage.
>
> ***Answer 2c***: 0.069
>
> ***Answer 2d***: The coverage of these plots are high, with most of the plots having coverage of C>0.9 and all having at least C> 0.87

Estimated richness

In the R code chunk below, do the following:

1. Load the microbial dataset (located in the `5.AlphaDiversity/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,]
S.obs(soilbac1)
```

```
## T1_1
## 1074
```

```
C(soilbac1)
```

```
##      T1_1
## 0.6479471
```

```
C(site1)
```

```
##         1
## 0.9308036
```

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: 13310

Answer 3b: 1074

Answer 3c: The coverage for the KBS sample is 0.648, so it is lower than the coverage for the BCI sample which is 0.931.

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`.

```r
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)
}
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)
}
S.chao1(site1)
```

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

```r
S.chao1(soilbac1)
```

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

```r
S.chao2(site = 1, SbyS = BCI)
```

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

```r
S.chao2(site = 1, SbyS = soilbac)
```

```
##   1
## NaN
```

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

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

```r
S.ace(soilbac1)
```

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

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?

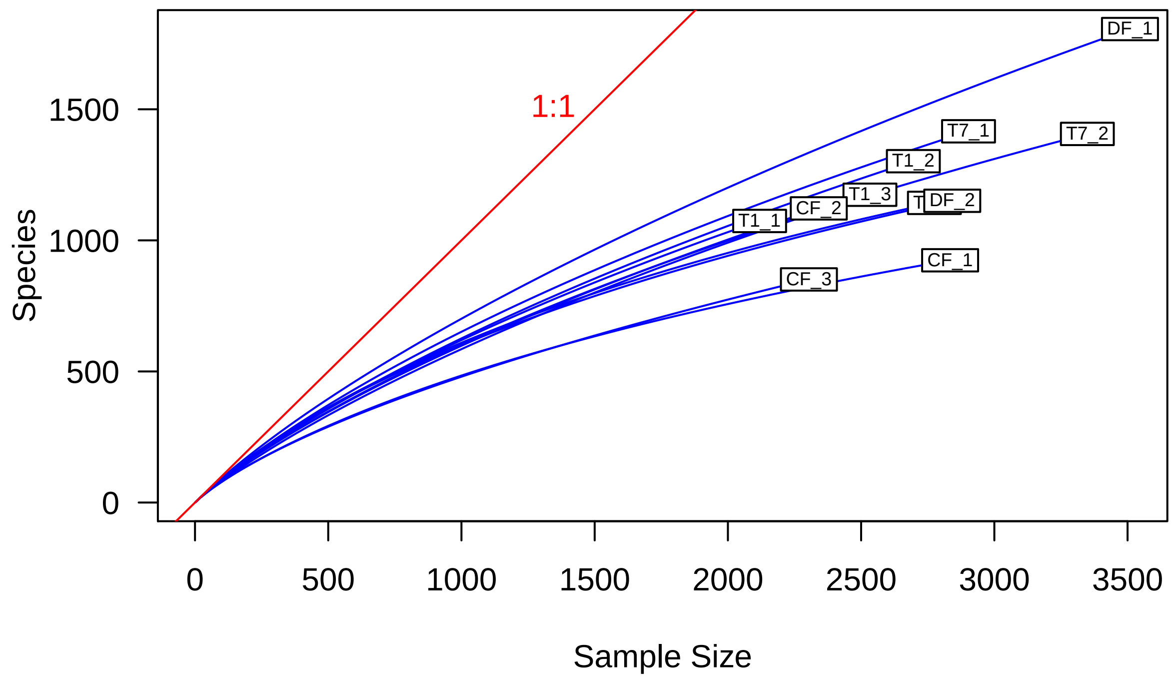
> ***Answer 4***: ACE stands for abundance-based coverage estimator and it estimates richness by looking at the abundance of other rare species, taxa with 10 or less individals, whereas Chao estimators make estimations of richness by looking at the number of singletons and doubletons. The estimators give different results, which for site1 from the BCI data was: Chao1=119.7, Chao2=104.6, ACE=159.3, however they are on the same magnitude, as is site1 from the soilbac data: Chao1=2628.5, ACE=4466. You should use the Chao esimators if you have many species with only a few individuals, otherwise you should use ACE to estimate richness.

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 EVENNESS 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

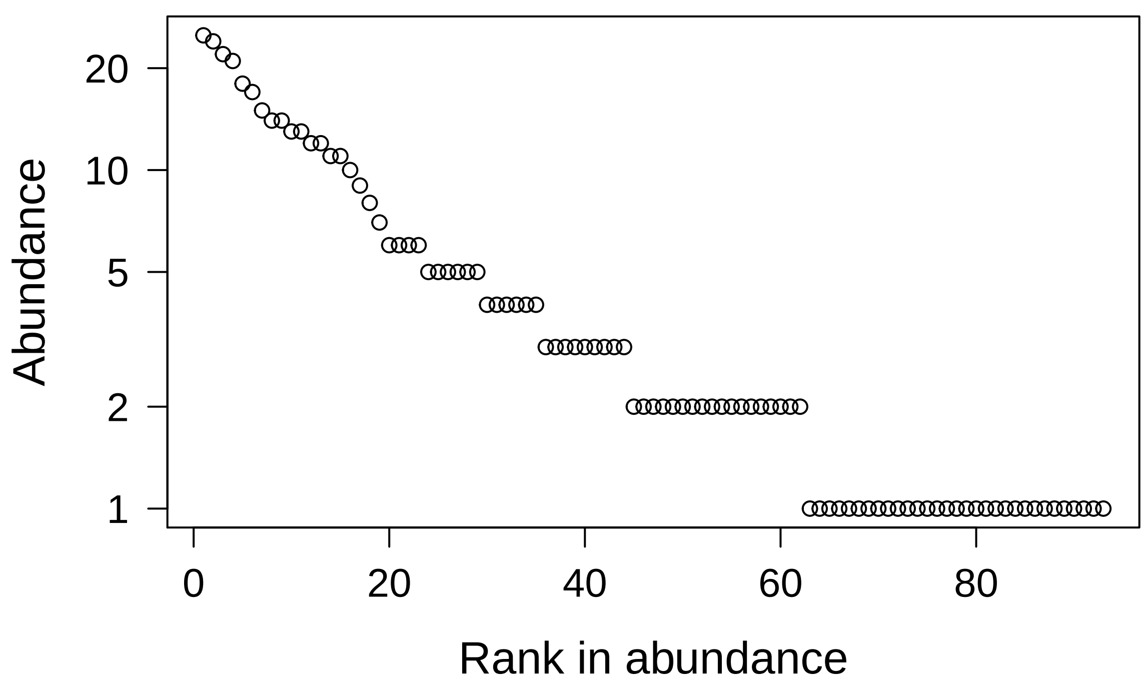
```
RAC <- function(x=""){
  x = as.vector(x)
  x.ab = x[x>0]
  x.ab.ranked = x.ab[order(x.ab, decreasing = TRUE)]
  return(x.ab.ranked)
}
```

Now, let's 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 = "Abundance", las = 1, ce
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)))
```



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***: When you log transform a dataset, it helps visualize the relationship and show a wide range of abundance data with abundances that are really high for a few species and many species that have very low abundances. The pattern shows that the abundance among species is unevenly distributed, which is a common pattern in ecology. Log transforming the data might also help with bias of very abundant species.

Now that we have visualized unevennes, 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 two estimates do not agree, however they both show site1 to be moderately even: E_{1/D}=0.423 and E_{var}=0.507. Simpson's evenness measures the variance of the rank abundance curve, and can be biased by abundant species. Smith and Wilson's Evenness is a more robust metric of evenness and log transforms abundances, which decreases the bias of abundant species.

##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".

```r
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)
}

ShanH(site1)
```

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

```r
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)
}
SimpD(site1)
```

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

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

diversity(site1, "inv")
```

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

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

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

Fisher's $\boldsymbol{\alpha}$

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

1. Provide the code for calculating Fisher's $\boldsymbol{\alpha}$,
2. Calculate Fisher's $\boldsymbol{\alpha}$ 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 $\boldsymbol{\alpha}$ different from $E_{H'}$ and E_{var}? What does Fisher's $\boldsymbol{\alpha}$ take into account that $E_{H'}$ and E_{var} do not?

> ***Answer 7***: Fisher's alpha is different from E_H' and E_var because it estimates diversity, instead of just calculating a diversity metric, so it accounts for sampling error, whereas the other two metrics don't.

##6) MOVING BEYOND UNIVARIATE METRICS OF α 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

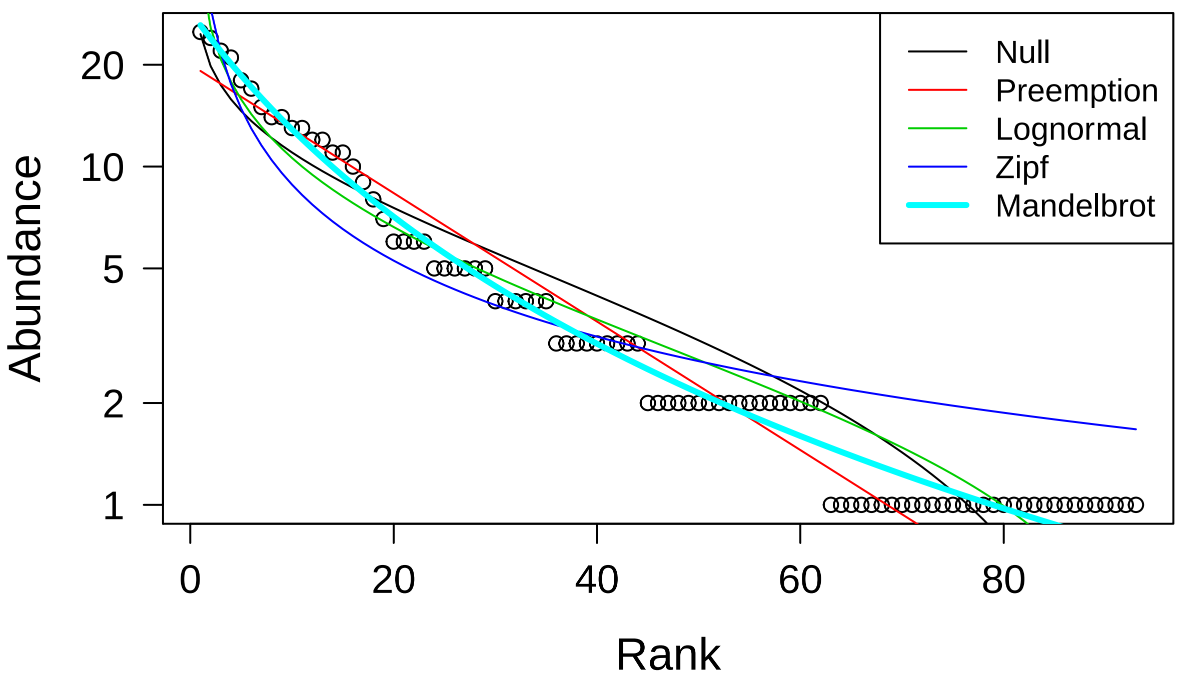
The RAC is a simple data structure that is both a vector of abundances. It is also a row in the site-by-species matrix (minus the zeros, i.e., absences).

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 8: 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 8a***: The model that best fits the data is the Mandelbrot model. ***Answer 8b***: The Zipf-Mandelbrot model has an evenness parameter, which the other models do not, so it could be that evenness is very important in explaining the abundance patterns of these data.

Question 9: 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 preemtion model assumes there is a negative linear relationship between total abundance and total resources. ***Answer 10b***: THe niche preemption models looks like a straight line in the RAD plot because in the model, each new species that occupies an environment takes alpha resources away from the species already there. Because alpha is constant, the resulting relationship is linear.

Question 10: 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***: It is important to account for the number of parameters a model uses becuase models with lots and lots of parameters might be able to explain data better, but not represent true patterns underlying. This is model overfitting and it makes the patterns and relationships found not generalizable. So, it is important to have a penalty for too many parameters when choosing a model.

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
```

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

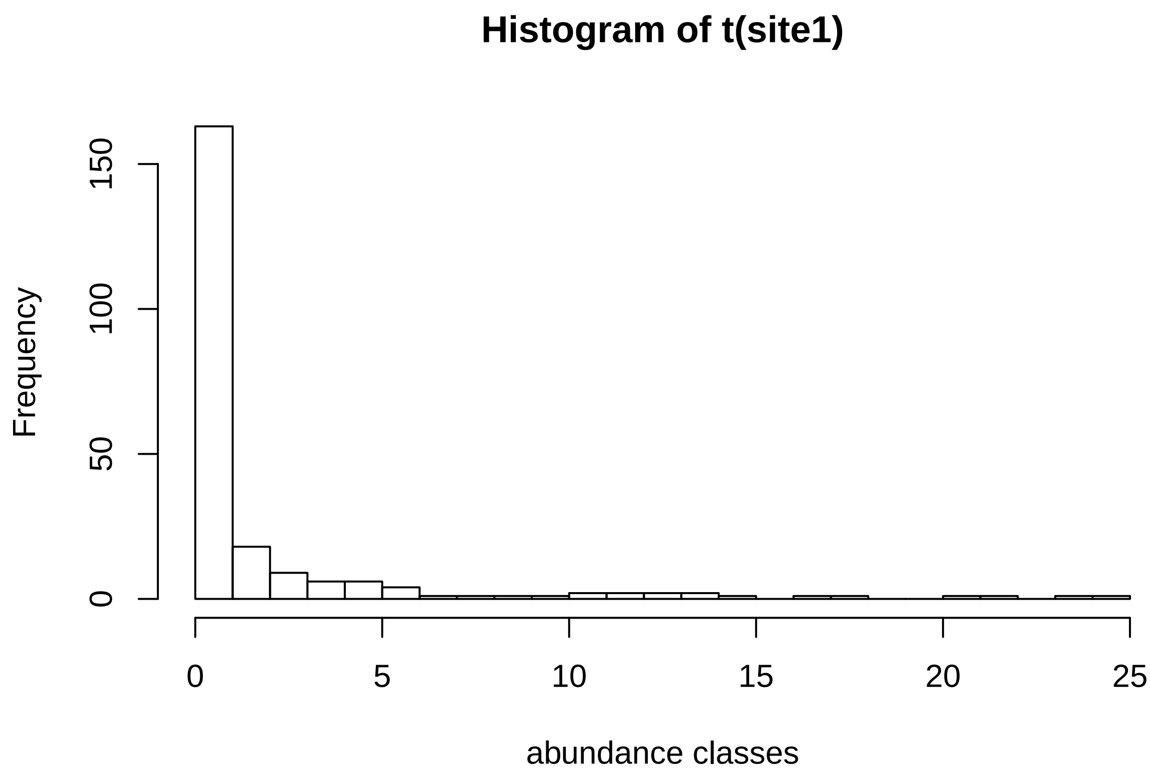
```
## [1] 39.41555
```

```
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.

```r
hist(t(site1), xlab = "abundance classes", breaks = 25)
```



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?

   There are two types of sites, ridge and snowbed, and there are 5 sites per type, but 55 total "sites" in the site by species matrix because of sampling more than once at each site. There 808 OTUs in the site-by-species matrix.

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, April 7th, 2021 at 12:00 PM (noon)**.