

7. Worksheet: Diversity Synthesis

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OVERVIEW

In this worksheet, you will conduct exercises that reinforce fundamental concepts of biodiversity. Specifically, you will construct a site-by-species matrix by sampling confectionery taxa. With this primary data structure, you will then answer questions and generate figures using tools from previous weeks, along with wrangling techniques that we learned about in class.

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. Refer to previous handouts to help with developing of questions and writing of code.
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 `7.DiversitySynthesis_Worskheet.Rmd` and the PDF output of Knitr (`DiversitySynthesis_Worskheet.pdf`).

CONFECTIONARY EXERCISE GOALS

We will construct a site-by-species matrix using confectionery taxa (i.e, gummies). The instructors have created distinct **sources communities** that vary in the composition of gummy taxa with even and uneven communities. It might be fun to consider them as distinct geographical regions experiencing different environmental regimes, or different experimental units under different treatments. Each student will sample a source community and then use a taxonomic key to identify gummies and their abundances.

In the end, students will use the site-by-species matrix to:

- 1) explore their sampling efforts and their effects on species richness using **coverage** and **rarefaction** concept,
- 2) measure **alpha diversity** for each sub-sample collated from data with their peers from the same source community,

- 3) examine **beta diversity** between each source community using the data generated across each source community, and
- 4) use **data wrangling** tools they have learned during the class to accomplish the above goals.

SAMPLING PROTOCOL TO CONSTRUCT A SITE-BY-SPECIES MATRIX

1. Instructors will assign you to sample confectionery taxa from one of the two designated source community bucket (A and B).
2. After randomly sampling one unit (imagine as an equal biomass) from the source community, each student will count the total number of individuals (N), identify the taxa using the species key and quantify the abundance of each taxon.
3. Work with other students in your group to assemble data into a site-by-species matrix on the white board. One person needs to create a .csv or .txt file and share your group's site-by-species matrix with the class using GitHub. Make sure that you include a sample identifier (student name) and what community you sampled from.

GROUP BRAINSTORM

In smaller groups, take 15 minutes to brainstorm questions, code, statistical tests, and “fantasy figures” using the site-by-species matrix the class generated.

1. Using this data, explore how well your sampling effort was. You can use rarefaction and coverage tools you have learned earlier.
2. Investigate alpha diversity based on the methods you have learned in the rest of the handout and accompanying worksheet. For example, you can measure richness, Shannon diversity and Simpson index. You can also convert them to effective number of species using the Hill numbers concept.
3. Measure beta diversity using ordination and multivariate statistical methods. For example, you can create a PCoA plot, based on Bray-Curtis dissimilarity, of sites and communities using different shape and color codes. Use Permanova to test if there are differences between communities.

DATA ANALYSIS

1) Sampling coverage and rarefaction curves

Question 1: Using this data, explore how well your sampling effort was. Compare your sampling efforts with other groups. Do you think that your samples cover the actual diversity found in each source community? You can use rarefaction and coverage tools you have learned earlier.

Answer 1: Use the space below to generate a rarefaction curve/sample coverage based on the data we collected in class for each community. Make sure to annotate your code using # symbols so others (including instructors) understand what you have done and why you have done it.

```
#load packages
library(readr)
setwd("~/Desktop/Research")
QB_Data_Wrangling_Lab_SP23_Sheet1 <- read_csv("QB Data Wrangling Lab SP23 - Sheet1.csv")
```

```
## Rows: 8 Columns: 32
## -- Column specification -----
## Delimiter: ","
## chr (2): Community, Name
## dbl (30): SP1, SP2, SP3, SP4, SP5, SP6, SP7, SP8, SP9, SP10, SP11, SP12, SP1...
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
View(QB_Data_Wrangling_Lab_SP23_Sheet1)
library(vegan)
```

```
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.6-4
```

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v dplyr 1.0.10
## v tibble 3.1.8       v stringr 1.5.0
## v tidyr 1.2.1        v forcats 1.0.0
## v purrr 1.0.1
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
```

```
library(ggplot2)
library(dplyr)
library(broom)
```

```
#Observed richness
```

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

```
#Look at B community
```

```
Bcommunityspecies <- QB_Data_Wrangling_Lab_SP23_Sheet1[5:8, 3:32]
as.matrix(Bcommunityspecies)
```

```
##      SP1 SP2 SP3 SP4 SP5 SP6 SP7 SP8 SP9 SP10 SP11 SP12 SP13 SP14 SP15 SP16
## [1,]  11  3  2  1  4  2  5  0  4  5  4  4  4  4  2  2
## [2,]  9 10  5 10  3  1  0  1  3  0  1  1  0  4  4  1
## [3,]  7 16  2  1  4  2  0  5  4  2  1  4  1  1  0  2
## [4,] 11  8  6  3  4  1  2  4  4  5  1  3  3  3  2  3
##      SP17 SP18 SP19 SP20 SP21 SP22 SP23 SP24 SP25 SP26 SP27 SP28 SP29 SP30
## [1,]  4  1  0  1  0  0  0  1  0  0  0  0  0  1
## [2,]  4  4  0  1  3  2  1  0  1  1  0  1  1  2
## [3,]  3  3  0  6  1  1  0  1  1  3  2  0  0  3
## [4,]  1  2  2  0  3  2  1  1  0  0  0  1  1  0
```

```
str(Bcommunityspecies)
```

```
## tibble [4 x 30] (S3: tbl_df/tbl/data.frame)
## $ SP1 : num [1:4] 11 9 7 11
## $ SP2 : num [1:4] 3 10 16 8
## $ SP3 : num [1:4] 2 5 2 6
## $ SP4 : num [1:4] 1 10 1 3
## $ SP5 : num [1:4] 4 3 4 4
## $ SP6 : num [1:4] 2 1 2 1
## $ SP7 : num [1:4] 5 0 0 2
## $ SP8 : num [1:4] 0 1 5 4
## $ SP9 : num [1:4] 4 3 4 4
## $ SP10: num [1:4] 5 0 2 5
## $ SP11: num [1:4] 4 1 1 1
## $ SP12: num [1:4] 4 1 4 3
## $ SP13: num [1:4] 4 0 1 3
## $ SP14: num [1:4] 4 4 1 3
## $ SP15: num [1:4] 2 4 0 2
## $ SP16: num [1:4] 2 1 2 3
## $ SP17: num [1:4] 4 4 3 1
## $ SP18: num [1:4] 1 4 3 2
## $ SP19: num [1:4] 0 0 0 2
## $ SP20: num [1:4] 1 1 6 0
## $ SP21: num [1:4] 0 3 1 3
## $ SP22: num [1:4] 0 2 1 2
## $ SP23: num [1:4] 0 1 0 1
## $ SP24: num [1:4] 1 0 1 1
## $ SP25: num [1:4] 0 1 1 0
## $ SP26: num [1:4] 0 1 3 0
## $ SP27: num [1:4] 0 0 2 0
## $ SP28: num [1:4] 0 1 0 1
## $ SP29: num [1:4] 0 1 0 1
## $ SP30: num [1:4] 1 2 3 0
```

```
Bcommunityspecies [1:30] = lapply(Bcommunityspecies[1:30], FUN= function(y){as.numeric(y)})
```

```
#generate a rarefaction curve/sample coverage
```

```
rf <- S.obs(Bcommunityspecies)
```

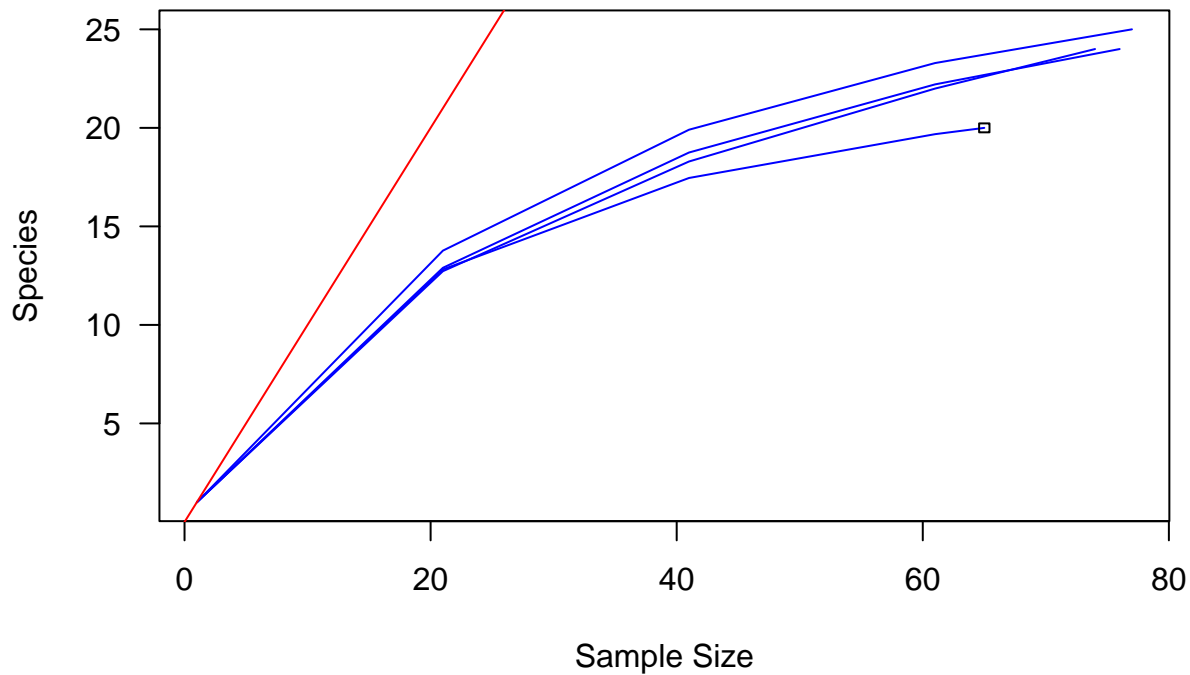
```
min.N <- min(rowSums(Bcommunityspecies))
```

```
S.rarefy <- rarefy(x = Bcommunityspecies, sample = min.N, se = TRUE)
```

```
rarecurve(x = Bcommunityspecies, step = 20, col = "blue", cex = 0.6, las = 1)
```

```
abline(0, 1, col = 'red')
```

```
text(1500, 1500, "1:1", pos = 2, col = 'red')
```



2) Alpha diversity

Question 2: Compare alpha diversity measures within sites and among communities. You can calculate and plot richness, Shannon diversity, and Simpson index. You can also convert these indices to effective number of species using the Hill numbers concept by generating a diversity profile, which will make comparisons easier across sites.

What is the variation among the samples in your group and between the communities of other groups for the alpha diversity indices? Generate a hypothesis around the diversity metrics you chose and test your hypothesis. Interpret your findings.

Answer 2a - Analysis: Use the space below for code that is being used to analyze your data and test your hypotheses on your chosen alpha diversity tool. Make sure to annotate your code using # symbols so others (including instructors) understand what you have done and why you have done it.

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

SimpE(Bcommunityspecies)
```

```
## [1] 0.6749201 0.5484776 0.5034868 0.6324267
```

```
#Shannon's Diversity
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(Bcommunityspecies, index= "shannon")
```

```
## [1] 2.787795 2.834947 2.836906 2.978193
```

Answer 2b - Plot: With your analysis, create one (and only one, although it can have multiple panels) publication-quality figure.

```
#RAC function
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)
}

#plot RAC
plot.new()

Bcommunityspecies <- QB_Data_Wrangling_Lab_SP23_Sheet1[5:8, 3:32]
as.matrix(Bcommunityspecies)
```

```
##      SP1 SP2 SP3 SP4 SP5 SP6 SP7 SP8 SP9 SP10 SP11 SP12 SP13 SP14 SP15 SP16
## [1,]  11  3  2  1  4  2  5  0  4  5  4  4  4  4  2  2
## [2,]  9 10  5 10  3  1  0  1  3  0  1  1  0  4  4  1
## [3,]  7 16  2  1  4  2  0  5  4  2  1  4  1  1  0  2
## [4,] 11  8  6  3  4  1  2  4  4  5  1  3  3  3  2  3
##      SP17 SP18 SP19 SP20 SP21 SP22 SP23 SP24 SP25 SP26 SP27 SP28 SP29 SP30
## [1,]  4  1  0  1  0  0  0  1  0  0  0  0  0  1
## [2,]  4  4  0  1  3  2  1  0  1  1  0  1  1  2
## [3,]  3  3  0  6  1  1  0  1  1  3  2  0  0  3
## [4,]  1  2  2  0  3  2  1  1  0  0  0  1  1  0
```

```
str(Bcommunityspecies)
```

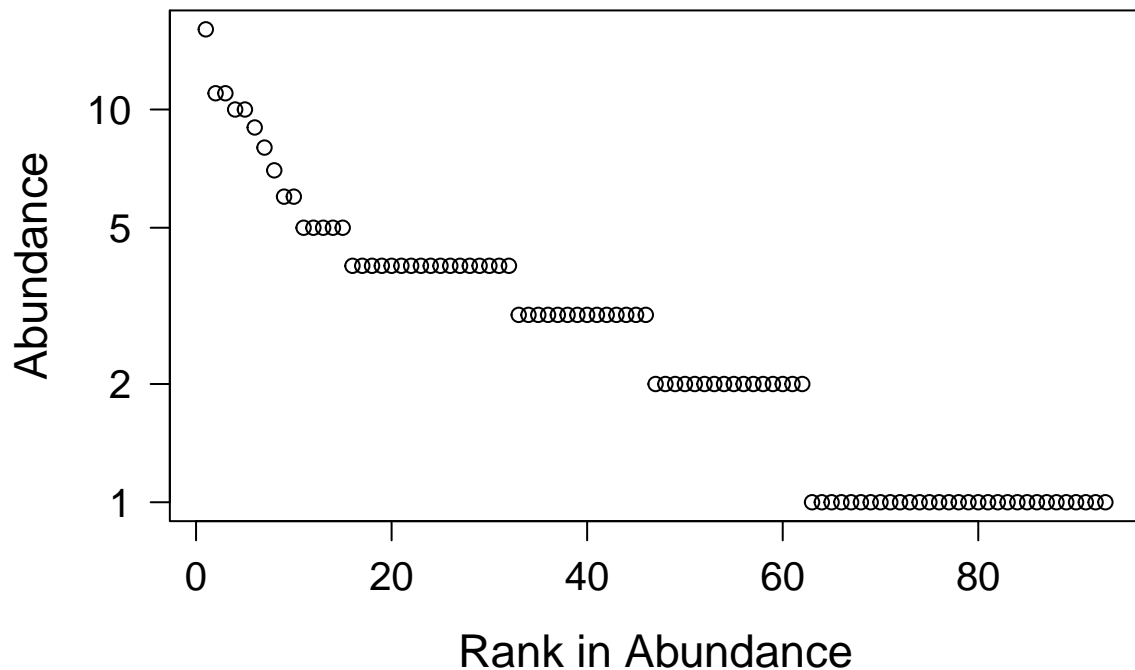
```
## tibble [4 x 30] (S3: tbl_df/tbl/data.frame)
## $ SP1 : num [1:4] 11 9 7 11
## $ SP2 : num [1:4] 3 10 16 8
## $ SP3 : num [1:4] 2 5 2 6
```

```
## $ SP4 : num [1:4] 1 10 1 3
## $ SP5 : num [1:4] 4 3 4 4
## $ SP6 : num [1:4] 2 1 2 1
## $ SP7 : num [1:4] 5 0 0 2
## $ SP8 : num [1:4] 0 1 5 4
## $ SP9 : num [1:4] 4 3 4 4
## $ SP10: num [1:4] 5 0 2 5
## $ SP11: num [1:4] 4 1 1 1
## $ SP12: num [1:4] 4 1 4 3
## $ SP13: num [1:4] 4 0 1 3
## $ SP14: num [1:4] 4 4 1 3
## $ SP15: num [1:4] 2 4 0 2
## $ SP16: num [1:4] 2 1 2 3
## $ SP17: num [1:4] 4 4 3 1
## $ SP18: num [1:4] 1 4 3 2
## $ SP19: num [1:4] 0 0 0 2
## $ SP20: num [1:4] 1 1 6 0
## $ SP21: num [1:4] 0 3 1 3
## $ SP22: num [1:4] 0 2 1 2
## $ SP23: num [1:4] 0 1 0 1
## $ SP24: num [1:4] 1 0 1 1
## $ SP25: num [1:4] 0 1 1 0
## $ SP26: num [1:4] 0 1 3 0
## $ SP27: num [1:4] 0 0 2 0
## $ SP28: num [1:4] 0 1 0 1
## $ SP29: num [1:4] 0 1 0 1
## $ SP30: num [1:4] 1 2 3 0
```

```
Bcommunityspecies [1:30] = lapply(Bcommunityspecies[1:30], FUN= function(y){as.numeric(y)})

rac <- RAC(x = Bcommunityspecies)
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, 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)))
```



Answer 2c - Interpret results: Write an informative yet succinct (~5 sentences) caption that creates a “stand-alone” figure. Take a peek at figures and figure captions in a paper published in your favorite journal for inspiration.

Answer: Figure 1. The rank in abundance against species abundance. The rank of abundance depicts the ranking of species from the most to least abundant. The species abundance is the measure of prevalence of a species. Here, the rank in abundance increases as the abundance decreases. Contrastingly, the rank in abundance decreases as the abundance increases. Rank in abundance and species abundance present an inverse relationship.

3) Beta diversity

Question 3: Measure beta diversity using ordination and multivariate statistics methods. You can create a PCoA plot, based on Bray-Curtis dissimilarity, of sites and communities using different shape and color codes. Then, you can use a Permanova to test if there are differences between communities. Generate a hypothesis around your chosen analysis and test your hypothesis. Interpret your findings.

Can you detect compositional differences between each source community sampled?

Answer 3a - Analysis: Use the space below for code that is being used to analyze your data and test your hypotheses on your chosen beta diversity tool. Make sure to annotate your code using # symbols so others (including instructors) understand what you have done and why you have done it.

```
#Bray-Curtis
Bcommunityspecies <- QB_Data_Wrangling_Lab_SP23_Sheet1[5:8, 3:32]
as.matrix(Bcommunityspecies)
```



```
##      SP1 SP2 SP3 SP4 SP5 SP6 SP7 SP8 SP9 SP10 SP11 SP12 SP13 SP14 SP15 SP16
## [1,]  11  3  2  1  4  2  5  0  4  5  4  4  4  4  2  2
## [2,]  9 10  5 10  3  1  0  1  3  0  1  1  0  4  4  1
## [3,]  7 16  2  1  4  2  0  5  4  2  1  4  1  1  0  2
## [4,] 11  8  6  3  4  1  2  4  4  5  1  3  3  3  2  3
##      SP17 SP18 SP19 SP20 SP21 SP22 SP23 SP24 SP25 SP26 SP27 SP28 SP29 SP30
## [1,]    4    1    0    1    0    0    0    1    0    0    0    0    0    1
## [2,]    4    4    0    1    3    2    1    0    1    1    0    1    1    2
## [3,]    3    3    0    6    1    1    0    1    1    3    2    0    0    3
## [4,]    1    2    2    0    3    2    1    1    0    0    0    1    1    0
```

```
str(Bcommunityspecies)
```

```
## tibble [4 x 30] (S3: tbl_df/tbl/data.frame)
```

```
## $ SP1 : num [1:4] 11 9 7 11
## $ SP2 : num [1:4] 3 10 16 8
## $ SP3 : num [1:4] 2 5 2 6
## $ SP4 : num [1:4] 1 10 1 3
## $ SP5 : num [1:4] 4 3 4 4
## $ SP6 : num [1:4] 2 1 2 1
## $ SP7 : num [1:4] 5 0 0 2
## $ SP8 : num [1:4] 0 1 5 4
## $ SP9 : num [1:4] 4 3 4 4
## $ SP10: num [1:4] 5 0 2 5
## $ SP11: num [1:4] 4 1 1 1
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## $ SP13: num [1:4] 4 0 1 3
## $ SP14: num [1:4] 4 4 1 3
## $ SP15: num [1:4] 2 4 0 2
## $ SP16: num [1:4] 2 1 2 3
## $ SP17: num [1:4] 4 4 3 1
## $ SP18: num [1:4] 1 4 3 2
## $ SP19: num [1:4] 0 0 0 2
## $ SP20: num [1:4] 1 1 6 0
## $ SP21: num [1:4] 0 3 1 3
## $ SP22: num [1:4] 0 2 1 2
## $ SP23: num [1:4] 0 1 0 1
## $ SP24: num [1:4] 1 0 1 1
## $ SP25: num [1:4] 0 1 1 0
## $ SP26: num [1:4] 0 1 3 0
## $ SP27: num [1:4] 0 0 2 0
## $ SP28: num [1:4] 0 1 0 1
## $ SP29: num [1:4] 0 1 0 1
## $ SP30: num [1:4] 1 2 3 0
```

```
Bcommunityspecies [1:30] = lapply(Bcommunityspecies[1:30], FUN= function(y){as.numeric(y)})
speciesbc <- vegdist(Bcommunityspecies, method="bray")
```

Answer 3b - Plot: With your analysis, create one (and only one, although it can have multiple panels) *publication-quality* figure.

```

#PCoA
library(viridis)

## Loading required package: viridisLite

library(lattice)

order <- rev(attr(Bcommunityspecies, "Labels"))

speciesbc <- as.matrix(speciesbc)

gummy.pcoa <- cmdscale(speciesbc, eig = TRUE, k = 3)
# Quantify percent variation explained by the first three axes
explainvar1 <- round(gummy.pcoa$eig[1] / sum(gummy.pcoa$eig), 3) * 100
explainvar2<- round(gummy.pcoa$eig[2] / sum(gummy.pcoa$eig), 3) * 100
explainvar3 <- round(gummy.pcoa$eig[3] / sum(gummy.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

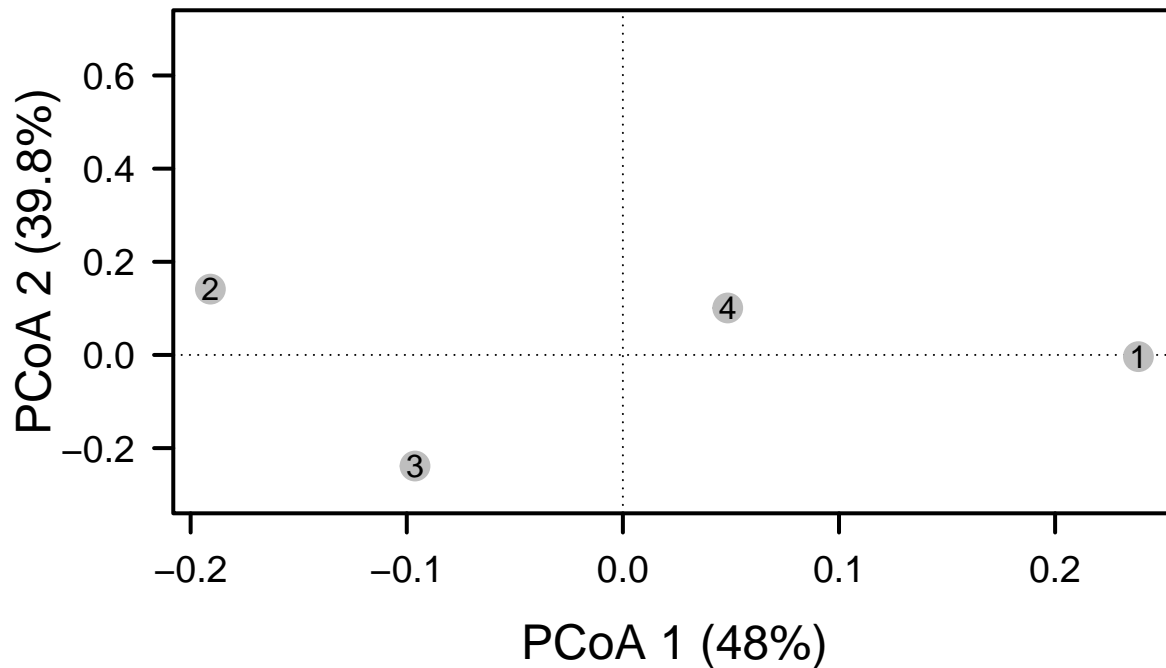
# Define plot parameters
par(mar = c(5.1, 4.1, 4.1, 2.1) + 0.1)

# Initiate plot
plot(gummy.pcoa$points[,1], gummy.pcoa$points[,2], ylim = c(-0.3, 0.7),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5,
     cex.axis = 1.2, axes = FALSE)

# Add axes
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)

# Add points and labels
points(gummy.pcoa$points[,1], gummy.pcoa$points[,2],
       pch = 19, cex = 2, bg = "gray", col = "gray")
text(gummy.pcoa$points[,1], gummy.pcoa$points[,2],
     labels = row.names(gummy.pcoa$points))

```



Answer 3c - Interpret results: Write an informative yet succinct (~5 sentences) caption that creates a “stand-alone” figure. Take a peek at figures and figure captions in a paper published in your favorite journal for inspiration.

Answer: Figure 2. PCoA basic ordination plot of species within community B. PCoA presents variation among the 4 species. PCoA 1 accounts for 48% of the variation amongst species. PCoA 2 accounts for 39.8% of the variation amongst species. The species are clearly diverged on both PCoA 1 and PCoA 2.

SUBMITTING YOUR ASSIGNMENT

Use Knitr to create a PDF of your completed 7.DiversitySynthesis_Worksheet.Rmd document, push it to GitHub, and create a pull request. Please make sure your updated repo includes both the pdf and RMarkdown files.

Unless otherwise noted, this assignment is due on **Wednesday, February 15th, 2023 at 12:00 PM (noon)**.