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 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.

```r
# sourcing functions
source("/Users/ericanadolski/GitHub/QB2023_Nadolski/2.Worksheets/7.DiversitySynthesis/diversity_functio

package.list <- c("vegan", "viridis", "gplots", "indicspecies", "dplyr","ggplot2")
for (package in package.list) {
  if (!require(package, character.only = TRUE, quietly=TRUE)) {
    install.packages(package)
    library(package, character.only = TRUE)
  }
}
```

```
## This is vegan 2.6-4

##
## Attaching package: 'gplots'

## The following object is masked from 'package:stats':
##
##     lowess

##
## Attaching package: 'dplyr'

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

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

```
# read in data
gummy.total <- read.csv("/Users/ericanadolski/GitHub/QB2023_Nadolski/2.Worksheets/7.DiversitySynthesis/
# removing disturbance data
gummy.total <- gummy.total[-2,]
gummy.total <- gummy.total[-3,]

# remove community column so there are no characters
gummy <- gummy.total[-1]

### Coverage
coverage <- cbind(C(gummy))
max(coverage)
```

```
## [1] 0.9508197
```

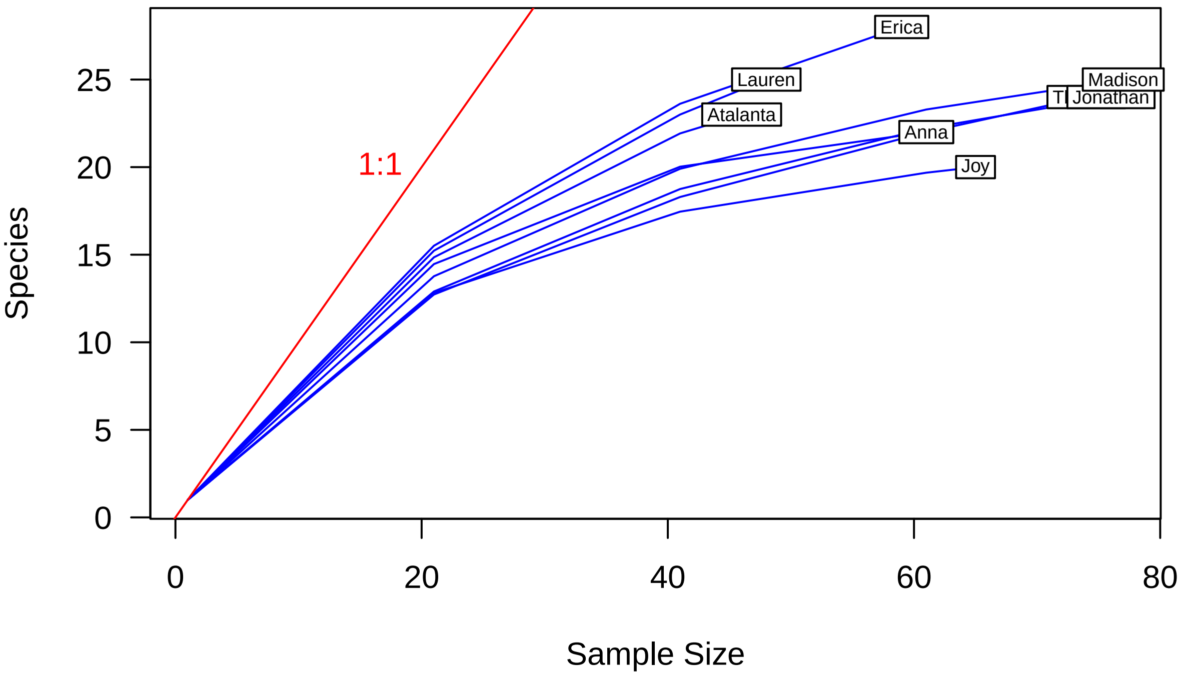
```
min(coverage)
```

```
## [1] 0.7291667
```

```
mean(coverage)
```

```
## [1] 0.8595187
```

```
### Rarefaction
# Calculate observed richness for all samples in gummy
gummy.Richness <- S.obs(gummy)
# Determine the size of the smallest sample
sample.sizes <- rowSums(gummy)
min.N <- min(sample.sizes)
# Use the `rarefy()` function to rarefy each sample to this level
gummy.rarefy <- rarefy(x = gummy, sample=min.N, se=TRUE)

# Plot the rarefaction results, add the 1:1 line and label
rarecurve(x = gummy, step=20, col="blue", cex=0.6, las=1);
abline(0, 1, col="red");
text(20, 20, "1:1", pos=2, col="red")
```



»

Answer 1: The overall rarefaction trend suggests that the sites from community one have greater species richness trends plotted over sample size and the sites from community 2 have lower richness trends plotted over sample size. Coverage ranged from 73% to 95% with a mean of 86%.

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.

```r
# For loop version to generate alpha diversity metrics
for (site in 1:nrow(gummy)) {
  rich <- specnumber(gummy[site,])
  shan <- diversity(gummy[site,], "shannon")
  sim <- diversity(gummy[site,], "invsimpson")
  print(c(site,"Richness=",rich,"Shannon=",shan,"Inv Simpson=",sim))
}
```

```
##                                                    Erica
##                "1"        "Richness="               "28"         "Shannon="
##
## "3.16606289451938"     "Inv Simpson=" "20.3567251461988"
##                                                   Lauren
##                "2"        "Richness="               "25"         "Shannon="
##
## "3.05344343339234"     "Inv Simpson=" "18.2857142857143"
##                                                 Atalanta
##                "3"        "Richness="               "23"         "Shannon="
##
## "2.97532914169026"     "Inv Simpson="         "16.53125"
##                                                     Anna
##                "4"        "Richness="               "22"         "Shannon="
##
##  "2.9987214517061"     "Inv Simpson=" "18.6984924623116"
##                                                      Joy
##                "5"        "Richness="               "20"         "Shannon="
##
## "2.78779521532696"     "Inv Simpson=" "13.4984025559105"
##                                                   Thomas
##                "6"        "Richness="               "24"         "Shannon="
##
## "2.83494723217379"     "Inv Simpson=" "13.1634615384615"
##                                                 Jonathan
##                "7"        "Richness="               "24"         "Shannon="
##
## "2.83690585897294"     "Inv Simpson=" "12.0836820083682"
##                                                  Madison
##                "8"        "Richness="               "25"         "Shannon="
##
## "2.97819305760922"     "Inv Simpson=" "15.8106666666667"
```

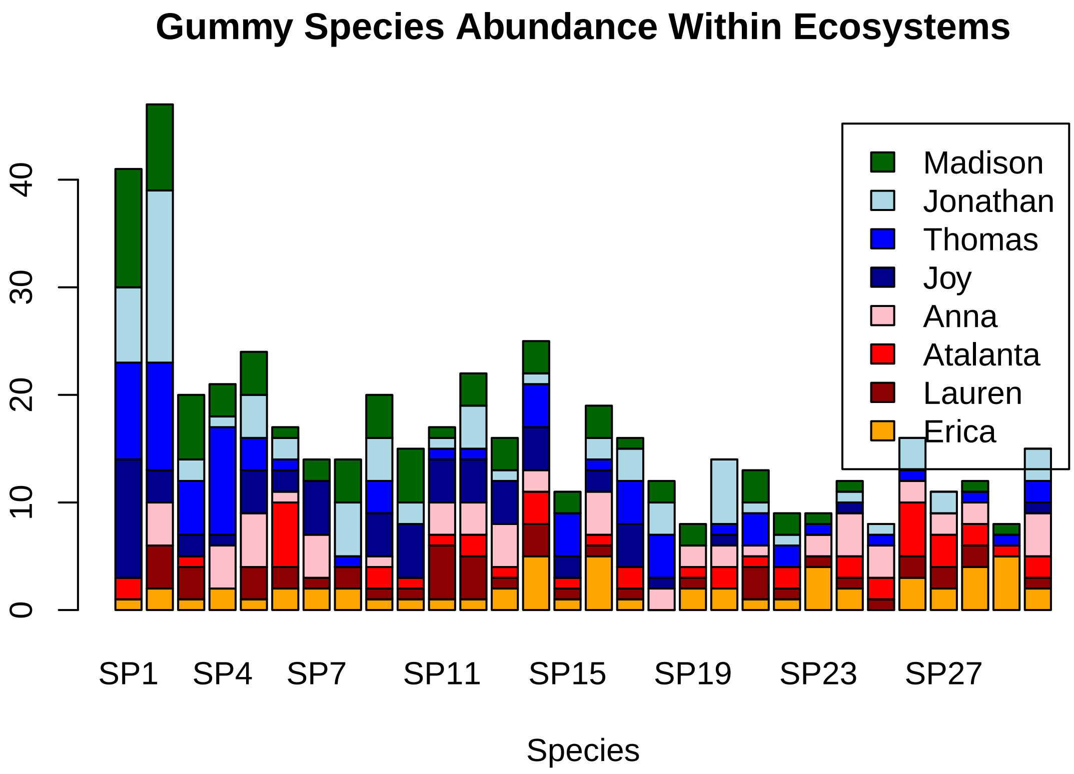
```r
# make numeric again
gummy[1,]<- as.numeric(gummy[1,])
gummy <- as.matrix(gummy)

# dplyr version to generate alpha diversity metrics
gummy2 <- as.data.frame(gummy)
gummy2 <- gummy2 %>% rowwise() %>% mutate(richness=specnumber(c_across(SP1:SP30)),
                                          shan = diversity(c_across(SP1:SP30), "shannon"),
                                          sim = diversity(c_across(SP1:SP30), "invsimpson"))

# add community ID back in for plotting and testing hypotheses
gummy2 <- bind_cols(gummy2,gummy.total["Community"])
```

```r
rownames(gummy2) <- c("Erica","Lauren","Atalanta","Anna","Joy","Thomas","Jonathan","Madison")
```

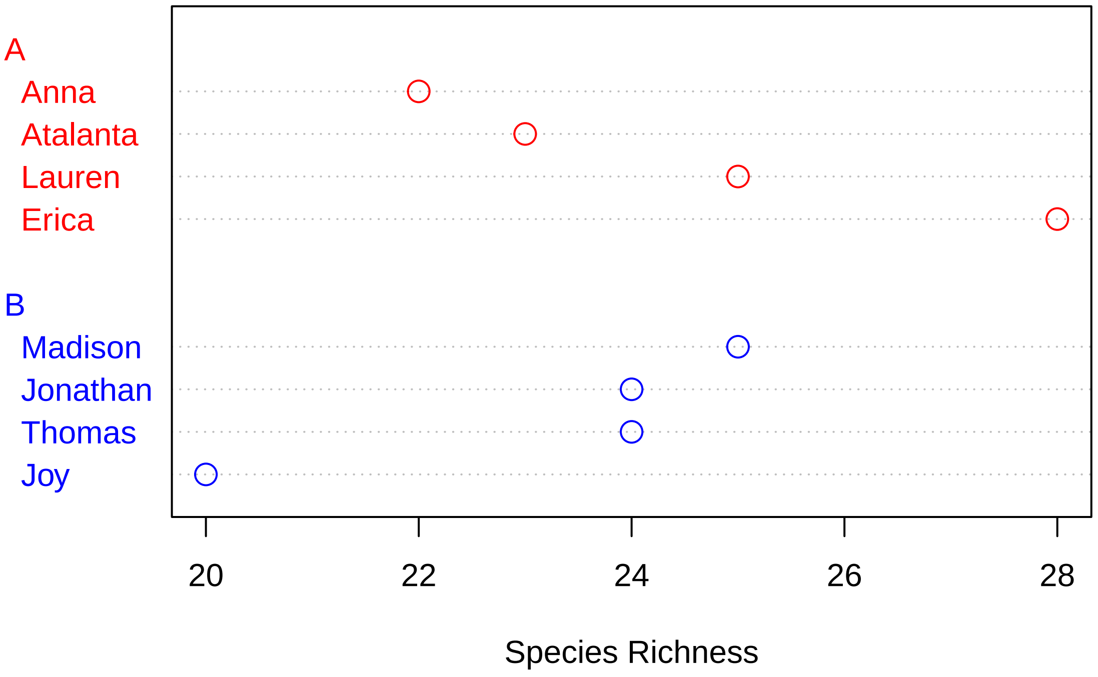
```
## Warning: Setting row names on a tibble is deprecated.
```

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

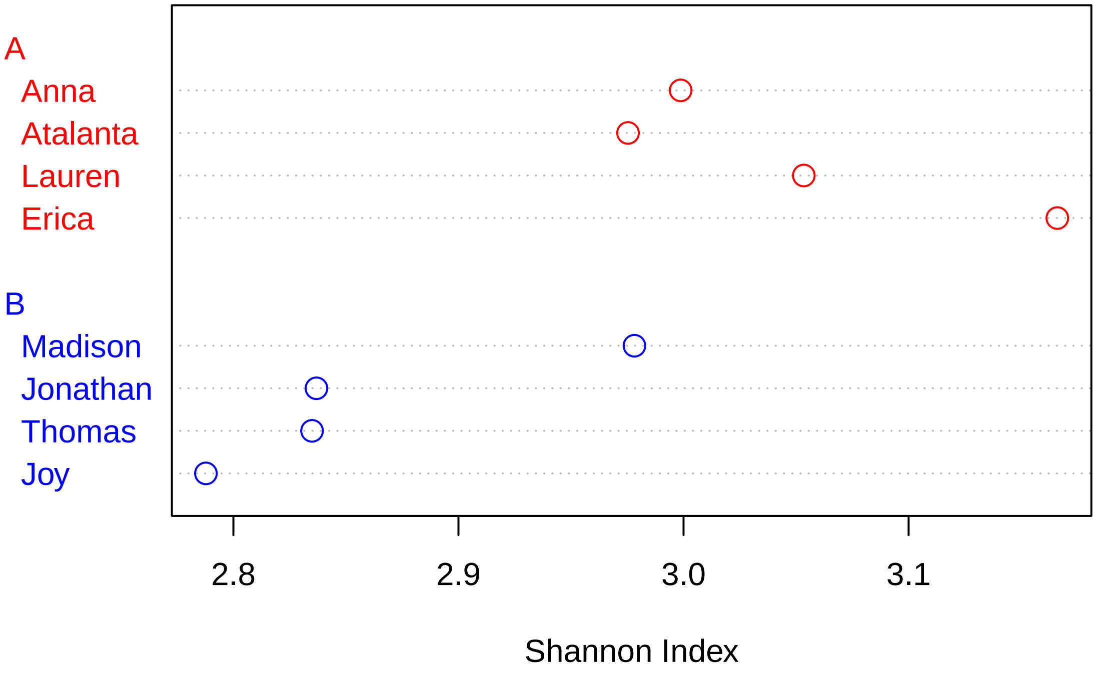
```r
# I figured out how to use mfrow() to generate a grid of plots but I cant get them to resize themselves

# par(mfrow = c(2,2),
    # mar = c(0,0,2,1))

# plot of species abundance across sites
barplot(gummy, main="Gummy Species Abundance Within Ecosystems",
  xlab="Species", col=c("orange","darkred","red","pink", "darkblue", "blue", "lightblue","darkgreen"),
  legend = rownames(gummy))
```



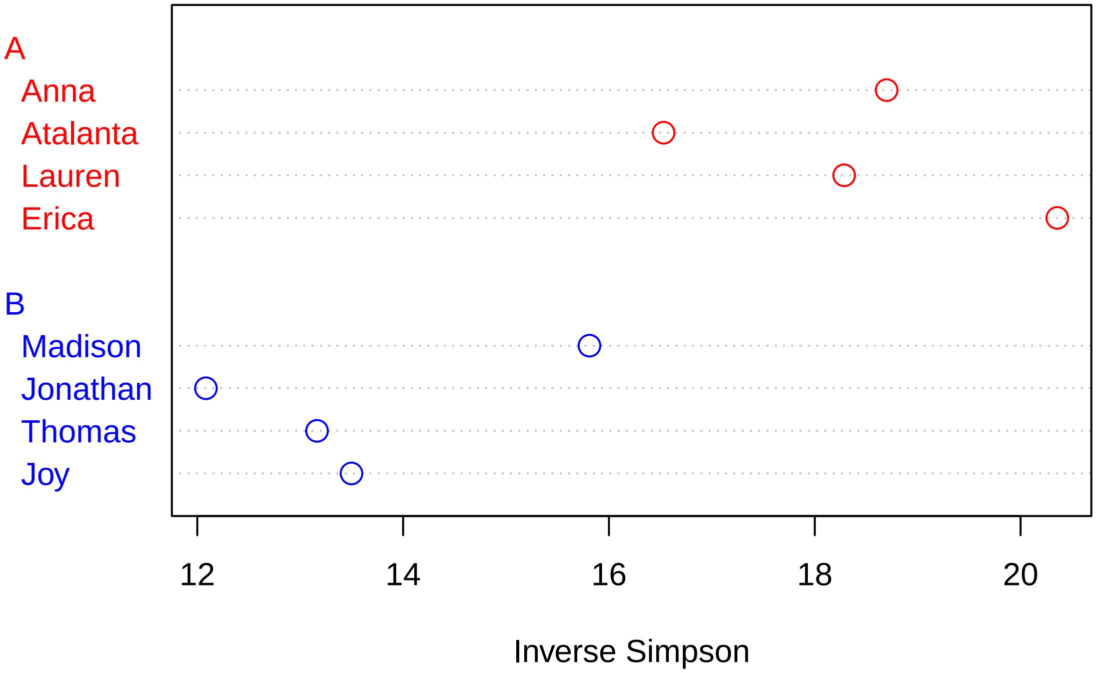
```r
# plot of species richness at each site
grps <- as.factor(gummy2$Community)
my_cols <- c("red", "blue") # Plot and color by groups Community
dotchart(gummy2$richness,
         labels = c("Erica","Lauren","Atalanta","Anna","Joy","Thomas","Jonathan","Madison"),
         groups = grps, gcolor = my_cols, color = my_cols[grps], pch = 21, pt.cex = 1.5,
         xlab = "Species Richness")
```



```r
# plot of shannon metric at each site - higher means high prob of new info with more sampling
dotchart(gummy2$shan,
         labels = c("Erica","Lauren","Atalanta","Anna","Joy","Thomas","Jonathan","Madison"),
         groups = grps, gcolor = my_cols, color = my_cols[grps], pch = 21, pt.cex = 1.5,
         xlab = "Shannon Index")
```



```r
# plot of inverse simpsons metric at each site
dotchart(gummy2$sim,
         labels = c("Erica","Lauren","Atalanta","Anna","Joy","Thomas","Jonathan","Madison"),
         groups = grps, gcolor = my_cols, color = my_cols[grps], pch = 21, pt.cex = 1.5,
         xlab = "Inverse Simpson")
```



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.

Figure 1: Biodiversity of Gummy Species Across Two Communities. A: Bar plot showing abundance of each of thirty species across all sites, with sites colored within each bar. Community A sites in warm colors; Community B sites in cool colors. B. Dot plot of species richness for each site, grouped by Community. C. Dot plot of Shannon's diversity metric for each site, grouped by Community. D. Dot plot of inverse Simpson's diversity metric for each site, grouped by Community.

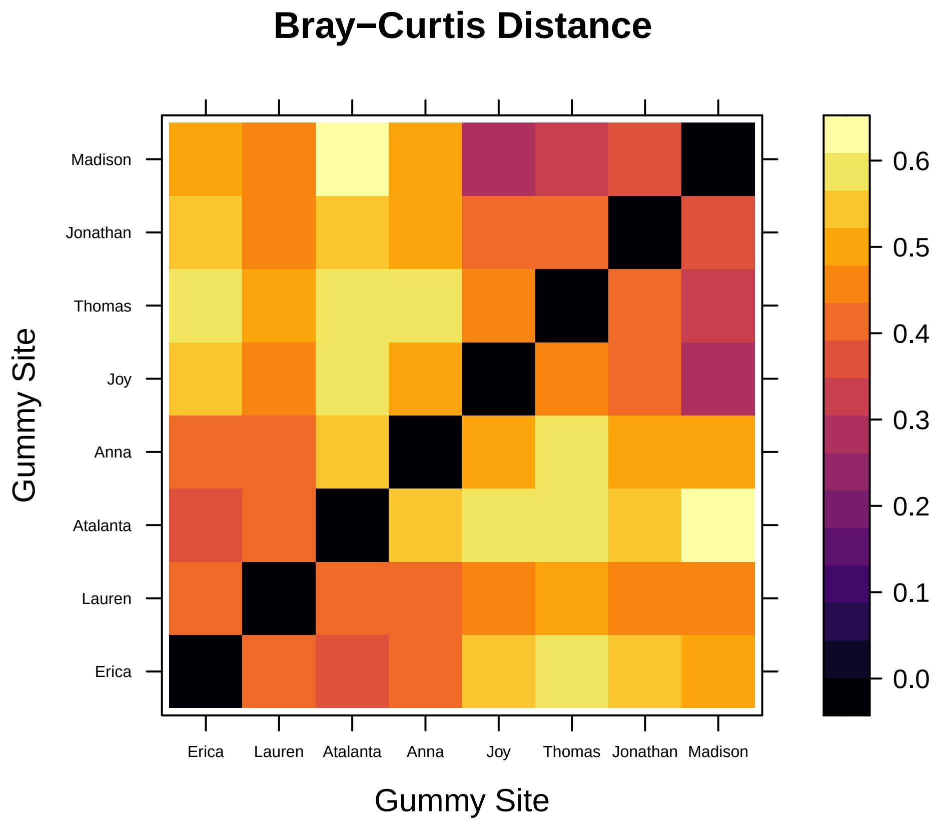
3) Beta diversity

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 dissimilarity
gummy.db <- vegdist(gummy[,1:30], method="bray")

# Heatmap to visualize similarity
levelplot(as.matrix(gummy.db), aspect="iso", col.regions=inferno,
          xlab="Gummy Site", ylab= "Gummy Site", scales=list(cex=0.5),
          main= "Bray-Curtis Distance")
```



```
# looks like community 1 sites are more similar to each other, and community 2 sites are more similar t

#PERMANOVA
# to test for difference associated with community 1 vs 2
gummy <- gummy[,1:30]
community <- c(rep("A", 4), rep("B", 4))
adonis(gummy ~ community, method="bray", permutations=999)
```

```
## 'adonis' will be deprecated: use 'adonis2' instead
```

```
## $aov.tab
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## community  1   0.31895 0.31895  3.8605 0.39151  0.033 *
## Residuals  6   0.49571 0.08262         0.60849
## Total      7   0.81466                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $call
## adonis(formula = gummy ~ community, permutations = 999, method = "bray")
##
## $coefficients
##                SP1    SP2   SP3    SP4   SP5   SP6           SP7   SP8   SP9
## (Intercept)  5.125  5.875  2.50  2.625  3.00 2.125  1.750000e+00  1.75  2.50
## community1  -4.375 -3.375 -1.25 -1.125 -0.75 0.625 -1.342437e-16 -0.75 -1.25
##               SP10  SP11  SP12         SP13  SP14   SP15  SP16 SP17 SP18 SP19
## (Intercept)  1.875 2.125  2.75  2.00000e+00 3.125  1.375 2.375    2  1.5  1.0
## community1  -1.125 0.375 -0.25 -1.21731e-16 0.125 -0.625 0.375   -1 -1.0  0.5
##              SP20   SP21   SP22  SP23 SP24 SP25 SP26  SP27 SP28 SP29  SP30
## (Intercept)  1.75  1.625  1.125 1.125 1.50  1.0    2 1.375  1.5  1.0 1.875
## community1  -0.25 -0.125 -0.125 0.625 0.75  0.5    1 0.875  1.0  0.5 0.375
##
## $coef.sites
##                  Erica      Lauren   Atalanta        Anna       Joy    Thomas
## (Intercept)  0.4220687  0.39065129  0.4587502  0.42922560 0.4120827 0.4275198
## community1  -0.1239824 -0.08059001 -0.1215706 -0.09283702 0.1202197 0.1363959
##              Jonathan   Madison
## (Intercept) 0.4069227 0.3793954
## community1  0.1059075 0.1312320
##
## $f.perms
##              [,1]
##    [1,] 0.3802881
##    [2,] 1.3564416
##    [3,] 1.3573663
##    [4,] 1.2095051
##    [5,] 1.1495976
##    [6,] 0.8636075
##    [7,] 0.8320900
##    [8,] 0.5325287
##    [9,] 0.5679079
##   [10,] 0.7385108
##   [11,] 0.6687867
##   [12,] 1.2643171
##   [13,] 1.8393788
##   [14,] 1.3564416
##   [15,] 0.6747114
##   [16,] 0.6723741
##   [17,] 0.5325287
##   [18,] 1.2450232
##   [19,] 0.7315165
##   [20,] 0.5325287
##   [21,] 0.4774510
##   [22,] 0.4244291
##   [23,] 0.5980672
##   [24,] 1.2643171
##   [25,] 1.8393788
##   [26,] 0.3276923
##   [27,] 0.6687867
##   [28,] 0.7827233
##   [29,] 1.2450232
##   [30,] 0.3802881
##   [31,] 0.3276923
##   [32,] 1.2643171
##   [33,] 0.6747114
##   [34,] 1.3564416
##   [35,] 0.7385108
##   [36,] 0.8636075
##   [37,] 0.6069838
##   [38,] 0.6723741
##   [39,] 1.1229696
##   [40,] 0.7448797
##   [41,] 1.3564416
##   [42,] 0.8636075
##   [43,] 1.1229696
##   [44,] 0.6687867
##   [45,] 1.1229696
##   [46,] 0.7827233
##   [47,] 1.5268480
##   [48,] 1.1229696
##   [49,] 0.7315165
##   [50,] 0.7827233
##   [51,] 1.3349363
##   [52,] 1.2095051
##   [53,] 0.7385108
##   [54,] 1.1411912
##   [55,] 0.7448797
##   [56,] 1.5386435
##   [57,] 1.3564416
##   [58,] 1.2643171
##   [59,] 1.1411912
##   [60,] 1.2304356
##   [61,] 0.8320900
##   [62,] 0.4774510
##   [63,] 0.6069838
##   [64,] 0.6687867
##   [65,] 0.7448797
##   [66,] 0.8636075
##   [67,] 1.3349363
##   [68,] 0.6069838
##   [69,] 1.5386435
##   [70,] 1.8393788
##   [71,] 1.5386435
##   [72,] 1.1411912
##   [73,] 0.8805548
##   [74,] 1.2095051
##   [75,] 1.5386435
##   [76,] 1.2643171
##   [77,] 1.2643171
##   [78,] 0.7827233
##   [79,] 0.7827233
##   [80,] 0.6069838
##   [81,] 0.3802881
##   [82,] 0.8592754
##   [83,] 0.8592754
##   [84,] 1.3564416
##   [85,] 0.3802881
##   [86,] 1.1229696
##   [87,] 1.2643171
##   [88,] 1.8251915
##   [89,] 1.3349363
##   [90,] 1.2304356
##   [91,] 0.3276923
##   [92,] 0.8592754
##   [93,] 1.1229696
##   [94,] 1.8251915
##   [95,] 0.6069838
##   [96,] 0.4244291
##   [97,] 1.2304356
##   [98,] 1.3573663
##   [99,] 1.3349363
##  [100,] 0.5980672
##  [101,] 1.2304356
##  [102,] 0.5325287
##  [103,] 0.3802881
##  [104,] 0.6723741
##  [105,] 0.8636075
##  [106,] 1.3573663
##  [107,] 1.3573663
##  [108,] 0.6723741
##  [109,] 0.7315165
##  [110,] 0.7385108
##  [111,] 0.3802881
##  [112,] 0.8805548
##  [113,] 1.2095051
##  [114,] 0.3802881
##  [115,] 0.7827233
##  [116,] 0.3802881
##  [117,] 0.8805548
##  [118,] 0.4244291
##  [119,] 0.8636075
##  [120,] 1.3573663
##  [121,] 1.8251915
##  [122,] 1.2304356
##  [123,] 1.1229696
##  [124,] 1.5386435
##  [125,] 1.5268480
##  [126,] 1.2450232
##  [127,] 0.5980672
##  [128,] 0.3802881
##  [129,] 0.8320900
##  [130,] 0.4244291
##  [131,] 1.3564416
##  [132,] 0.8592754
##  [133,] 1.2304356
##  [134,] 1.2450232
##  [135,] 0.7827233
##  [136,] 0.5679079
##  [137,] 0.5325287
##  [138,] 0.5980672
##  [139,] 0.7448797
##  [140,] 0.6687867
##  [141,] 0.3276923
##  [142,] 0.4774510
##  [143,] 1.1229696
##  [144,] 1.1411912
##  [145,] 1.5386435
##  [146,] 0.6687867
##  [147,] 0.4244291
##  [148,] 1.2095051
##  [149,] 0.4774510
##  [150,] 0.5679079
##  [151,] 1.2095051
##  [152,] 0.6723741
##  [153,] 0.5980672
##  [154,] 1.2457273
##  [155,] 1.3349363
##  [156,] 0.8592754
##  [157,] 1.1411912
##  [158,] 1.1411912
##  [159,] 0.7315165
##  [160,] 1.3349363
##  [161,] 0.6723741
##  [162,] 1.1411912
##  [163,] 1.5268480
##  [164,] 1.8393788
##  [165,] 0.3802881
##  [166,] 1.2450232
##  [167,] 1.8251915
##  [168,] 0.8320900
##  [169,] 1.3564416
##  [170,] 0.5980672
##  [171,] 0.6723741
##  [172,] 0.7385108
##  [173,] 3.8605106
##  [174,] 0.4244291
##  [175,] 0.6069838
##  [176,] 1.8393788
##  [177,] 1.2304356
##  [178,] 0.7315165
##  [179,] 0.7315165
##  [180,] 1.2304356
##  [181,] 0.5980672
##  [182,] 1.2095051
##  [183,] 0.7448797
##  [184,] 0.4244291
##  [185,] 0.3802881
##  [186,] 0.6747114
##  [187,] 3.8605106
##  [188,] 0.5679079
##  [189,] 0.4244291
##  [190,] 1.2450232
##  [191,] 1.3349363
##  [192,] 1.1229696
##  [193,] 0.6723741
##  [194,] 0.3276923
##  [195,] 1.2457273
##  [196,] 1.2457273
## [197,] 1.2457273
## [198,] 0.3276923
## [199,] 0.8592754
## [200,] 3.8605106
## [201,] 0.6687867
## [202,] 1.2304356
## [203,] 1.8251915
## [204,] 0.6069838
## [205,] 1.2095051
## [206,] 0.3802881
## [207,] 1.8393788
## [208,] 0.6687867
## [209,] 1.3573663
## [210,] 0.4244291
## [211,] 0.8320900
## [212,] 0.3276923
## [213,] 0.6747114
## [214,] 0.5980672
## [215,] 1.2450232
## [216,] 1.8393788
## [217,] 1.5386435
## [218,] 1.8251915
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##  [869,] 0.6747114
##  [870,] 0.5980672
##  [871,] 0.7827233
##  [872,] 1.3564416
##  [873,] 0.5980672
##  [874,] 0.7827233
##  [875,] 1.2457273
##  [876,] 0.8320900
##  [877,] 1.8251915
##  [878,] 0.6747114
##  [879,] 0.3802881
##  [880,] 0.7827233
##  [881,] 1.3573663
##  [882,] 0.4774510
##  [883,] 0.7385108
##  [884,] 1.1229696
##  [885,] 1.8251915
##  [886,] 1.8251915
##  [887,] 0.6687867
##  [888,] 1.2304356
##  [889,] 0.6723741
##  [890,] 0.5325287
##  [891,] 0.6069838
##  [892,] 0.5325287
##  [893,] 1.2095051
##  [894,] 0.8320900
##  [895,] 0.8636075
##  [896,] 1.8393788
##  [897,] 1.1411912
##  [898,] 1.2457273
## [899,] 1.1411912
## [900,] 0.7827233
## [901,] 0.8636075
## [902,] 1.1229696
## [903,] 1.1229696
## [904,] 3.8605106
## [905,] 1.1229696
## [906,] 1.5268480
## [907,] 1.2450232
## [908,] 0.7827233
## [909,] 0.7385108
## [910,] 1.2095051
## [911,] 0.7315165
## [912,] 1.1495976
## [913,] 1.2457273
## [914,] 1.5268480
## [915,] 0.4774510
## [916,] 0.6747114
## [917,] 1.1411912
## [918,] 1.3349363
## [919,] 0.4244291
## [920,] 0.8320900
## [921,] 0.8805548
## [922,] 1.1495976
## [923,] 0.4244291
## [924,] 0.8636075
## [925,] 0.4774510
## [926,] 0.6747114
## [927,] 0.7315165
## [928,] 1.5386435
## [929,] 3.8605106
## [930,] 0.5325287
## [931,] 3.8605106
## [932,] 3.8605106
## [933,] 3.8605106
## [934,] 0.6069838
## [935,] 1.2304356
## [936,] 1.2095051
## [937,] 0.4774510
## [938,] 1.2643171
## [939,] 0.8320900
## [940,] 1.1495976
## [941,] 1.3349363
## [942,] 0.6723741
## [943,] 0.8805548
## [944,] 0.8592754
## [945,] 0.3276923
## [946,] 0.3276923
## [947,] 1.3564416
## [948,] 0.3802881
## [949,] 0.3276923
## [950,] 0.5679079
## [951,] 0.7385108
## [952,] 0.4774510
##  [953,] 1.5268480
##  [954,] 0.7315165
##  [955,] 0.7448797
##  [956,] 0.7827233
##  [957,] 0.3802881
##  [958,] 0.4774510
##  [959,] 1.3349363
##  [960,] 1.5268480
##  [961,] 1.2304356
##  [962,] 1.2304356
##  [963,] 0.5679079
##  [964,] 1.2450232
##  [965,] 0.7448797
##  [966,] 0.8592754
##  [967,] 1.2450232
##  [968,] 1.1411912
##  [969,] 1.3573663
##  [970,] 0.7315165
##  [971,] 0.6687867
##  [972,] 1.8393788
##  [973,] 0.7385108
##  [974,] 1.8251915
##  [975,] 0.8805548
##  [976,] 1.3564416
##  [977,] 0.6747114
##  [978,] 1.2095051
##  [979,] 1.2095051
##  [980,] 0.5325287
##  [981,] 1.2643171
##  [982,] 0.3802881
##  [983,] 1.2457273
##  [984,] 1.2304356
##  [985,] 0.5325287
##  [986,] 0.6723741
##  [987,] 0.6069838
##  [988,] 0.6687867
##  [989,] 0.6069838
##  [990,] 1.8251915
##  [991,] 0.6723741
##  [992,] 1.1229696
##  [993,] 3.8605106
##  [994,] 0.5325287
##  [995,] 1.1495976
##  [996,] 0.8320900
##  [997,] 1.8393788
##  [998,] 0.6069838
##  [999,] 0.7448797
##
## $model.matrix
##   (Intercept) community1
## 1           1          1
## 2           1          1
## 3           1          1
## 4           1          1
## 5           1         -1
## 6           1         -1
## 7           1         -1
## 8           1         -1
##
## $terms
## gummy ~ community
## attr(,"variables")
## list(gummy, community)
## attr(,"factors")
##           community
## gummy             0
## community         1
## attr(,"term.labels")
## [1] "community"
## attr(,"order")
## [1] 1
## attr(,"intercept")
## [1] 1
## attr(,"response")
## [1] 1
## attr(,".Environment")
## <environment: R_GlobalEnv>
##
## attr(,"class")
## [1] "adonis"
```

```
# Indicator values
indval <- multipatt(gummy, cluster=community,func="IndVal.g",control=how(nperm=999))
summary(indval)
```

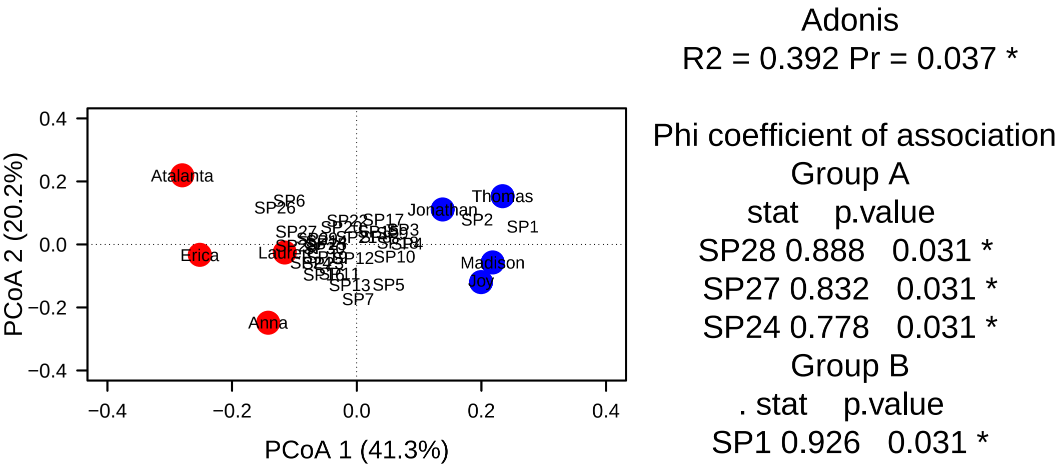
```
##
##  Multilevel pattern analysis
##  ---------------------------
##
##  Association function: IndVal.g
##  Significance level (alpha): 0.05
##
##  Total number of species: 30
##  Selected number of species: 2
##  Number of species associated to 1 group: 2
##
##  List of species associated to each combination:
##
##  Group A  #sps.  1
##       stat p.value
## SP28 0.913   0.033 *
##
##  Group B  #sps.  1
##      stat p.value
## SP1 0.963   0.033 *
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
# phi coefficient of association
gummy.rel <- decostand(gummy, method="total")
phi <- multipatt(gummy.rel, cluster=community, func="r.g", control=how(nperm=999))
summary(phi)
```

```
##
##  Multilevel pattern analysis
##  ---------------------------
##
##  Association function: r.g
##  Significance level (alpha): 0.05
##
##  Total number of species: 30
##  Selected number of species: 5
##  Number of species associated to 1 group: 5
##
##  List of species associated to each combination:
##
##  Group A  #sps.  4
##       stat p.value
## SP28 0.888   0.032 *
## SP27 0.832   0.032 *
## SP24 0.778   0.032 *
## SP26 0.688   0.050 *
##
##  Group B  #sps.  1
##      stat p.value
## SP1 0.926   0.032 *
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

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

```
### PCoA with species score
gummy.pcoa <- cmdscale(gummy.db, eig=TRUE, k=3)

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)

# add spec scores
gummyREL <- gummy[,1:30]
gummy.num <- gummy[,1:30]
for(i in 1:nrow(gummy.num)){
  gummyREL[i, ] = gummy.num[i, ] / sum(gummy.num[i, ])
}
gummy.pcoa <- add.spec.scores.class(gummy.pcoa,gummyREL, method = "pcoa.scores")

#plot pcoa plus spec scores
pcoa <- plot(gummy.pcoa$points[ ,1], gummy.pcoa$points[ ,2], ylim = c(-0.4, 0.4), xlim = c(-0.4, 0.4),
     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);
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);
points(gummy.pcoa$points[1:4,1], gummy.pcoa$points[1:4,2],
       pch = 19, cex = 3, bg = "red", col = "red");
points(gummy.pcoa$points[5:8,1], gummy.pcoa$points[5:8,2],
       pch = 19, cex = 3, bg = "blue", col = "blue");
text(gummy.pcoa$points[ ,1], gummy.pcoa$points[ ,2],
     labels = row.names(gummy.pcoa$points));
text(gummy.pcoa$cproj[ ,1], gummy.pcoa$cproj[ ,2],
     labels = row.names(gummy.pcoa$cproj), col = "black")

par(mar = c(0, 0, 0, 0))

plot(x = 0:10, y = 0:10, ann = F,bty = "n",type = "n",
     xaxt = "n", yaxt = "n");
text(x = 5,y = 5,"Adonis\n R2 = 0.392 Pr = 0.037 * \n \n Phi coefficient of association\nGroup A\nstat
```



Adonis
R2 = 0.392 Pr = 0.037 *

Phi coefficient of association
Group A
stat p.value
SP28 0.888 0.031 *
SP27 0.832 0.031 *
SP24 0.778 0.031 *
Group B
. stat p.value
SP1 0.926 0.031 *

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.

Figure 2: Comparison of beta diversity at sites between and among two gummy communities. A. Principal component analysis of four sites each from two communities. PC1 captures 41.3% of the variation across sites and maps onto the split between Community A and B. PC2 captures another 20.2% of the variation across sites and maps onto variation among sites within each larger community. Permutational multivariate analysis of variance using distance matrices was performed using the adonis R package. Community identity explains 39% of the variation with a marginally significant P value. Calculation of the Phi coefficient of association using multi-level pattern analysis indicated that SP1 was a strong indicator of Community A identity, while Spp. 24, 27, and 28 were indicators of Community B identity.

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 15$^{\text{th}}$, 2023 at 12:00 PM (noon)**.