9.Phylogenetic Diversity - Communities

Madison Stoltz; Z620: Quantitative Biodiversity, Indiana University

28 February, 2023

OVERVIEW

Complementing taxonomic measures of α- and β-diversity with evolutionary information yields insight into a broad range of biodiversity issues including conservation, biogeography, and community assembly. In this worksheet, you will be introduced to some commonly used methods in phylogenetic community ecology.

After completing this assignment you will know how to:

1. incorporate an evolutionary perspective into your understanding of community ecology
2. quantify and interpret phylogenetic α- and β-diversity
3. evaluate the contribution of phylogeny to spatial patterns of biodiversity

Directions:

1. In the Markdown version of this document in your cloned repo, change "Student Name" on line 3 (above) with 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 examples of proper scripting needed to carry out the exercises.
4. Answer questions in the worksheet. Space for your answers is provided in this document and is 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 today, it is *imperative* that you **push** this file to your GitHub repo, at whatever stage you are. This will enable you to pull your work onto your own computer.
6. When you have completed the worksheet, **Knit** the text and code into a single PDF file by pressing the `Knit` button in the RStudio scripting panel. This will save the PDF output in your '9.PhyloCom' folder.
7. After Knitting, please submit the worksheet by making a **push** to your GitHub repo and then create a **pull request** via GitHub. Your pull request should include this file *9.PhyloCom_Worksheet.Rmd* and the PDF output of `Knitr` (*9.PhyloCom_Worksheet.pdf*).

The completed exercise is due on **Wednesday, March 1st, 2023 before 12:00 PM (noon)**.

1) SETUP

Typically, the first thing you will do in either an R script or an RMarkdown file is setup your environment. This includes things such as setting the working directory and loading any packages that you will need.

In the R code chunk below, provide the code to:
1. clear your R environment,

2. print your current working directory,
3. set your working directory to your `/9.PhyloCom` folder,
4. load all of the required R packages (be sure to install if needed), and
5. load the required R source file.

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

```
## [1] "/Users/madisonstoltz/GitHub/QB2023_Stoltz/2.Worksheets/9.PhyloCom"
```

```
setwd("~/GitHub/QB2023_Stoltz/2.Worksheets/9.PhyloCom")

package.list <- c('picante', 'ape', 'seqinr', 'vegan', 'fossil',
                  'reshape', 'devtools', 'BiocManager', 'ineq',
                  'labdsv', 'matrixStats', 'pROC')
for (package in package.list) {
  if (!require(package, character.only = TRUE, quietly = TRUE)) {
    install.packages(package, repos = 'http://cran.us.r-project.org')
    library(package, character.only = TRUE)
  }
}
```

```
## This is vegan 2.6-4

##
## Attaching package: 'seqinr'

## The following object is masked from 'package:nlme':
##
##     gls

## The following object is masked from 'package:permute':
##
##     getType

## The following objects are masked from 'package:ape':
##
##     as.alignment, consensus

##
## Attaching package: 'shapefiles'

## The following objects are masked from 'package:foreign':
##
##     read.dbf, write.dbf

##
## Attaching package: 'devtools'

## The following object is masked from 'package:permute':
##
##     check
```

```
##
## Attaching package: 'BiocManager'

## The following object is masked from 'package:devtools':
##
##     install

## This is mgcv 1.8-41. For overview type 'help("mgcv-package")'.

## Registered S3 method overwritten by 'labdsv':
##   method       from
##   summary.dist ade4

## This is labdsv 2.0-1
## convert existing ordinations with as.dsvord()

##
## Attaching package: 'labdsv'

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

##
## Attaching package: 'matrixStats'

## The following object is masked from 'package:seqinr':
##
##     count

## Type 'citation("pROC")' for a citation.

##
## Attaching package: 'pROC'

## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
source("./bin/MothurTools.R")
```

2) DESCRIPTION OF DATA

need to discuss data set from spatial ecology!

We sampled >50 forested ponds in Brown County State Park, Yellowood State Park, and Hoosier National Forest in southern Indiana. In addition to measuring a suite of geographic and environmental variables, we characterized the diversity of bacteria in the ponds using molecular-based approaches. Specifically, we amplified the 16S rRNA gene (i.e., the DNA sequence) and 16S rRNA transcripts (i.e., the RNA transcript of the gene) of bacteria. We used a program called `mothur` to quality-trim our data set and assign sequences to operational taxonomic units (OTUs), which resulted in a site-by-OTU matrix.
In this module we will focus on taxa that were present (i.e., DNA), but there will be a few steps where we need to parse out the transcript (i.e., RNA) samples. See the handout for a further description of this week's dataset.

3) LOAD THE DATA

In the R code chunk below, do the following:
1. load the environmental data for the Brown County ponds (*20130801_PondDataMod.csv*),
2. load the site-by-species matrix using the `read.otu()` function,
3. subset the data to include only DNA-based identifications of bacteria,
4. rename the sites by removing extra characters,
5. remove unnecessary OTUs in the site-by-species, and
6. load the taxonomic data using the `read.tax()` function from the source-code file.

```
env <- read.table("data/20130801_PondDataMod.csv", sep = ",", header = TRUE)
env <- na.omit(env)

comm <- read.otu(shared = "./data/INPonds.final.rdp.shared", cutoff = "1")

comm <- comm[grep("*-DNA", rownames(comm)), ]

rownames(comm) <- gsub("\\-DNA", "", rownames(comm))
rownames(comm) <- gsub("\\_", "", rownames(comm))

comm <- comm[rownames(comm) %in% env$Sample_ID, ]
comm <- comm[ , colSums(comm) > 0]
tax <- read.tax(taxonomy = "./data/INPonds.final.rdp.1.cons.taxonomy")
```

```
## Warning in type.convert.default(as.character(x)): 'as.is' should be specified
## by the caller; using TRUE

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```

Next, in the R code chunk below, do the following:
1. load the FASTA alignment for the bacterial operational taxonomic units (OTUs),
2. rename the OTUs by removing everything before the tab (\t) and after the bar (|),
3. import the *Methanosarcina* outgroup FASTA file,
4. convert both FASTA files into the DNAbin format and combine using `rbind()`,
5. visualize the sequence alignment,
6. using the alignment (with outgroup), pick a DNA substitution model, and create a phylogenetic distance matrix,
7. using the distance matrix above, make a neighbor joining tree,
8. remove any tips (OTUs) that are not in the community data set,
9. plot the rooted tree.

```r
#page 5
ponds.cons <- read.alignment(file = "./data/INPonds.final.rdp.1.rep.fasta",
                             format = "fasta")

ponds.cons$nam <- gsub("\\|.*$", "", gsub("^.*?\t", "", ponds.cons$nam))

outgroup <- read.alignment(file = "./data/methanosarcina.fasta", format = "fasta")

DNAbin <- rbind(as.DNAbin(outgroup),as.DNAbin(ponds.cons))

image.DNAbin(DNAbin, show.labels = T, cex.lab = 0.05, las = 1)
```

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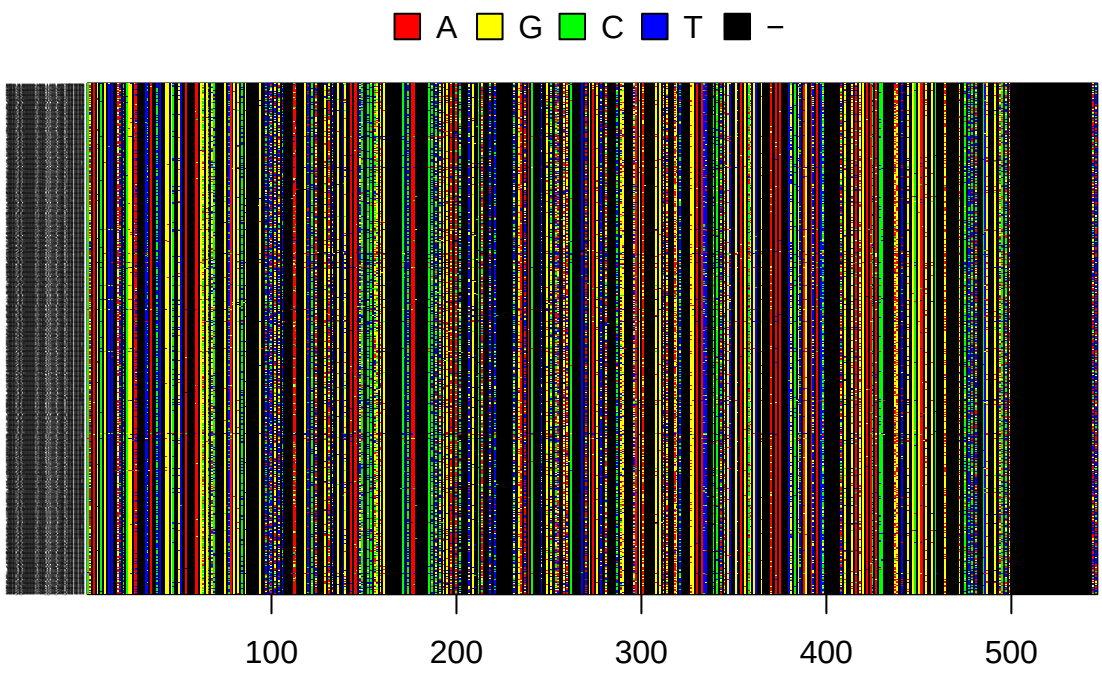


```
#page 6
seq.dist.jc <- dist.dna(DNAbin, model = "JC", pairwise.deletion = FALSE)

phy.all <- bionj(seq.dist.jc)

phy <- drop.tip(phy.all, phy.all$tip.label[!phy.all$tip.label %in%
              c(colnames(comm), "Methanosarcina")])

outgroup <- match("Methanosarcina", phy$tip.label)

phy <- root(phy, outgroup, resolve.root = TRUE)

par(mar = c(1, 1, 2, 1) + 0.1)
plot.phylo(phy, main = "Neighbor Joining Tree", "phylogram",
      show.tip.label = FALSE, use.edge.length = FALSE,
      direction = "right", cex = 0.6, label.offset = 1)
```

```
## Warning in plot.phylo(phy, main = "Neighbor Joining Tree", "phylogram", : found
## fewer than 2 tips in the tree
```

```
## NULL
```

4) PHYLOGENETIC ALPHA DIVERSITY

A. Faith's Phylogenetic Diversity (PD)

In the R code chunk below, do the following:
1. calculate Faith's D using the `pd()` function.

```
pd <- pd(comm, phy, include.root = FALSE)
```

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In the R code chunk below, do the following:
1. plot species richness (S) versus phylogenetic diversity (PD),
2. add the trend line, and
3. calculate the scaling exponent.

```
#par(mar = c(5, 5, 4, 1) + 0.1)

#plot(log(pd$S), log(pd$PD),
#     pch = 20, col = "red", las = 1,
#     xlab = "ln(S)", ylab = "ln(PD)", cex.main = 1,
#     main="Phylodiversity (PD) vs. Taxonomic richness (S)")

#fit <- lm('log(pd$PD) ~ log(pd$S)')
#abline(fit, col = "red", lw = 2)
#exponent <- round(coefficients(fit)[2], 2)
#legend("topleft", legend=paste("Scaling exponent = ", exponent, sep = ""),
#       bty = "n", lw = 2, col = "red")
```

Question 1: Answer the following questions about the PD-S pattern.
a. Based on how PD is calculated, why should this metric be related to taxonomic richness? b. Describe the relationship between taxonomic richness and phylodiversity. c. When would you expect these two estimates of diversity to deviate from one another? d. Interpret the significance of the scaling PD-S scaling exponent.

> ***Answer 1a***: PD sums the branch lengths for each species found in a sample from the root to the tip of the phylogenetic tree. A higher PD means that in the assemblage, there is a more evolutionary divergent taxa. This could correlate then to a higher taxonomic richness. ***Answer 1b***: A higher phylodiversity is more diversity in a tree and more diversity means higher taxonomic richess. ***Answer 1c***: Maybe a deviation like this could occur if there is high diversity in the tree but the taxa themselves are not as diverse. ***Answer 1d***: I assume the scaling aspect is to understand how PD and S correlate with eachother on a visually appealing, linear scale that is easier to understand and accurate

i. Randomizations and Null Models

In the R code chunk below, do the following:
1. estimate the standardized effect size of PD using the `richness` randomization method.

```
ses.pd <- ses.pd(comm[1:2,], phy, null.model = "richness", runs = 25,
                 include.root = FALSE)
```

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```

Question 2: Using `help()` and the table above, run the `ses.pd()` function using two other null models and answer the following questions:

a. What are the null and alternative hypotheses you are testing via randomization when calculating `ses.pd`?
b. How did your choice of null model influence your observed ses.pd values? Explain why this choice affected or did not affect the output.

> ***Answer 2a***: The null would be that the community patterns are no different from a random community. The alternative is that the patterns found are different from a random community.
> ***Answer 2b***: If I chose to understand the null as being no different from a randomly chosen community, my output (which had the same values) would be accepting the null.

B. Phylogenetic Dispersion Within a Sample

Another way to assess phylogenetic α-diversity is to look at dispersion within a sample.

i. Phylogenetic Resemblance Matrix

In the R code chunk below, do the following:
1. calculate the phylogenetic resemblance matrix for taxa in the Indiana ponds data set.

```
#phydist <- cophenetic.phylo(phy)
```

ii. Net Relatedness Index (NRI)

In the R code chunk below, do the following:
1. Calculate the NRI for each site in the Indiana ponds data set.

```
#ses.mpd <- ses.mpd(comm, phydist, null.model = "taxa.labels",
#                    abundance.weighted = FALSE, runs = 25)

#NRI <- as.matrix(-1 * ((ses.mpd[,2] - ses.mpd[,3]) / ses.mpd[,4]))
#rownames(NRI) <- row.names(ses.mpd)
#colnames(NRI) <- "NRI"
```

iii. Nearest Taxon Index (NTI)

In the R code chunk below, do the following: 1. Calculate the NTI for each site in the Indiana ponds data set.

```
#ses.mntd <- ses.mntd(comm, phydist, null.model = "taxa.labels",
#                      abundance.weighted = FALSE, runs = 25)

#NTI <- as.matrix(-1 * ((ses.mntd[,2] - ses.mntd[,3]) / ses.mntd[,4]))
#rownames(NTI) <- row.names(ses.mntd)
#colnames(NTI) <- "NTI"
```

Question 3:

a. In your own words describe what you are doing when you calculate the NRI.
b. In your own words describe what you are doing when you calculate the NTI.
c. Interpret the NRI and NTI values you observed for this dataset.
d. In the NRI and NTI examples above, the arguments "abundance.weighted = FALSE" means that the indices were calculated using presence-absence data. Modify and rerun the code so that NRI and NTI are calculated using abundance data. How does this affect the interpretation of NRI and NTI?

Answer 3a: NRI (Net Relatedness Index) is used to evaluate the phylogenetic structure of communities. It measures the standardized effect size of the mean phylogenetic distance (MPD). This distance is used to look at relatedness between all taxa in the community. ***Answer 3b***: NTI (Nearest Taxon Index) is used to test for phylogenetic clustering and overdispersion. It measures the mean nearest phylogenetic neighbor distance (MNND, instead of MPD with NRI). ***Answer 3c***: I kept getting an error for both saying subscript out of bounds. I think this was the issue we were trying to fix in class on Friday. However, I know that negative NRI values indicate that a sample is phylogenetically overdispersed and positive NRI values indicate that a sample is phylogenetically underdispersed, or clustered, such that taxa are more closely related to one another than expected under the null model. ***Answer 3d***: I can't seem to figure out why the number of species would matter when making a tree. Especially looking at NRI and NTI, they measure distances between species and not the species themselves.

5) PHYLOGENETIC BETA DIVERSITY

A. Phylogenetically Based Community Resemblance Matrix

In the R code chunk below, do the following:
1. calculate the phylogenetically based community resemblance matrix using Mean Pair Distance, and
2. calculate the phylogenetically based community resemblance matrix using UniFrac distance.

```
#Bottom of page 11
#dist.mp <- comdist(comm, phydist)
#dist.uf <- unifrac(comm, phy)
```

In the R code chunk below, do the following:
1. plot Mean Pair Distance versus UniFrac distance and compare.

```
#par(mar = c(5, 5, 2, 1) + 0.1)
#plot(dist.mp, dist.uf,
#     pch = 20, col = "red", las = 1, asp = 1, xlim = c(0.15, 0.5), ylim = #c(0.15, 0.5),
#     xlab = "Mean Pair Distance", ylab = "UniFrac Distance")
#abline(b = 1, a = 0, lty = 2)
#text(0.5, 0.47, "1:1")
```

Question 4:

a. In your own words describe Mean Pair Distance, UniFrac distance, and the difference between them.
b. Using the plot above, describe the relationship between Mean Pair Distance and UniFrac distance. Note: we are calculating unweighted phylogenetic distances (similar to incidence based measures). That means that we are not taking into account the abundance of each taxon in each site.
c. Why might MPD show less variation than UniFrac?

> ***Answer 4a***: Mean pair distance is the mean distance between taxa. The UniFrac distance is the shared and unshared branch lengths between taxa. These differ based on what distance they consider. ***Answer 4b***: Based on the plot, as UniFrac distance increases, Mean pair distance stays the same. ***Answer 4c***: I think MPD shows less variation because it is not accounting for unshared branches between taxa.

B. Visualizing Phylogenetic Beta-Diversity

Now that we have our phylogenetically based community resemblance matrix, we can visualize phylogenetic diversity among samples using the same techniques that we used in the β-diversity module from earlier in the course.

In the R code chunk below, do the following:
1. perform a PCoA based on the UniFrac distances, and
2. calculate the explained variation for the first three PCoA axes.

```
#page 12
#pond.pcoa <- cmdscale(dist.uf, eig = T, k = 3)
#explainvar1 <- round(pond.pcoa$eig[1] / sum(pond.pcoa$eig), 3) * 100
#explainvar2 <- round(pond.pcoa$eig[2] / sum(pond.pcoa$eig), 3) * 100
#explainvar3 <- round(pond.pcoa$eig[3] / sum(pond.pcoa$eig), 3) * 100
#sum.eig <- sum(explainvar1, explainvar2, explainvar3)
```

Now that we have calculated our PCoA, we can plot the results.

In the R code chunk below, do the following:
1. plot the PCoA results using either the R base package or the `ggplot` package,
2. include the appropriate axes,
3. add and label the points, and
4. customize the plot.

```
#par(mar = c(5, 5, 1, 2) + 0.1)
#plot(pond.pcoa$points[ ,1], pond.pcoa$points[ ,2],
#xlim = c(-0.2, 0.2), ylim = c(-.16, 0.16),
#     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(pond.pcoa$points[ ,1], pond.pcoa$points[ ,2],
#       pch = 19, cex = 3, bg = "gray", col = "gray")
#text(pond.pcoa$points[ ,1], pond.pcoa$points[ ,2],
#     labels = row.names(pond.pcoa$points))
```

In the following R code chunk: 1. perform another PCoA on taxonomic data using an appropriate measure of dissimilarity, and 2. calculate the explained variation on the first three PCoA axes.

Question 5: Using a combination of visualization tools and percent variation explained, how does the phylogenetically based ordination compare or contrast with the taxonomic ordination? What does this tell you about the importance of phylogenetic information in this system?

> ***Answer 5***: In a taxonomic ordination, you are looking at the taxa alone and no considering their evolutionary history. Contranstingly, the phylogenetically based ordination has multiple taxa and considers evolutionary history among the taxa. I would consider phylogenetic information important when considering multiple taxa.

C. Hypothesis Testing

i. Categorical Approach

In the R code chunk below, do the following:
1. test the hypothesis that watershed has an effect on the phylogenetic diversity of bacterial communities.

```
#watershed <- env$Location

#phylo.adonis <- adonis2(dist.uf ~ watershed, permutations = 999)

#tax.adonis <- adonis2(
#  vegdist(
#    decostand(comm, method = "log"),
#    method = "bray") ~ watershed,
#  permutations = 999)
```

ii. Continuous Approach

In the R code chunk below, do the following: 1. from the environmental data matrix, subset the variables related to physical and chemical properties of the ponds, and
2. calculate environmental distance between ponds based on the Euclidean distance between sites in the environmental data matrix (after transforming and centering using `scale()`).

```
#envs <- env[, 5:19]

#envs <- envs[, -which(names(envs) %in% c("TDS", "Salinity", "Cal_Volume"))]

#env.dist <- vegdist(scale(envs), method = "euclid")
```

In the R code chunk below, do the following:
1. conduct a Mantel test to evaluate whether or not UniFrac distance is correlated with environmental variation.

```
#mantel(dist.uf, env.dist)
```

Last, conduct a distance-based Redundancy Analysis (dbRDA).

In the R code chunk below, do the following:
1. conduct a dbRDA to test the hypothesis that environmental variation effects the phylogenetic diversity of bacterial communities,
2. use a permutation test to determine significance, and 3. plot the dbRDA results

```
#ponds.dbrda <- vegan::dbrda(dist.uf ~ ., data = as.data.frame(scale(envs)))

#anova(ponds.dbrda, by = "axis")
#ponds.fit <- envfit(ponds.dbrda, envs, perm = 999)
#ponds.fit

#dbrda.explainvar1 <- round(ponds.dbrda$CCA$eig[1] /
#                     sum(c(ponds.dbrda$CCA$eig, ponds.dbrda$CA$eig)), 3) * 100
#dbrda.explainvar2 <- round(ponds.dbrda$CCA$eig[2] /
#                     sum(c(ponds.dbrda$CCA$eig, ponds.dbrda$CA$eig)), 3) * 100

#par(mar = c(5, 5, 4, 4) + 0.1)

#plot(scores(ponds.dbrda, display = "wa"), xlim = c(-2, 2), ylim = c(-2, 2),
#  xlab = paste("dbRDA 1 (", dbrda.explainvar1, "%)", sep = ""),
#  ylab = paste("dbRDA 2 (", dbrda.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(scores(ponds.dbrda, display = "wa"),
#       pch = 19, cex = 3, bg = "gray", col = "gray")
#text(scores(ponds.dbrda, display = "wa"),
#    labels = row.names(scores(ponds.dbrda, display = "wa")), cex = 0.5)
```

```
#vectors <- scores(ponds.dbrda, display = "bp")

#arrows(0, 0, vectors[,1] * 2, vectors[, 2] * 2,
#       lwd = 2, lty = 1, length = 0.2, col = "red")
#text(vectors[,1] * 2, vectors[, 2] * 2, pos = 3,
#     labels = row.names(vectors))
#axis(side = 3, lwd.ticks = 2, cex.axis = 1.2, las = 1, col = "red", lwd = 2.2,
#     at = pretty(range(vectors[, 1])) * 2, labels = pretty(range(vectors[, 1])))
#axis(side = 4, lwd.ticks = 2, cex.axis = 1.2, las = 1, col = "red", lwd = 2.2,
#     at = pretty(range(vectors[, 2])) * 2, labels = pretty(range(vectors[, 2])))
```

Question 6: Based on the multivariate procedures conducted above, describe the phylogenetic patterns of β-diversity for bacterial communities in the Indiana ponds.

> ***Answer 6***: Looking at the PCoA, we can see the amount of explained variation for each phylogenetically informed PCoA axis, where PCoA1 is 9.5% and PCoA2 is 6%. Both of these values explain a small amount of variation. Maybe this means there is not much phylogenetic diversity among samples.

6) SPATIAL PHYLOGENETIC COMMUNITY ECOLOGY

A. Phylogenetic Distance-Decay (PDD)

A distance decay (DD) relationship reflects the spatial autocorrelation of community similarity. That is, communities located near one another should be more similar to one another in taxonomic composition than distant communities. (This is analagous to the isolation by distance (IBD) pattern that is commonly found when examining genetic similarity of a populations as a function of space.) Historically, the two most common explanations for the taxonomic DD are that it reflects spatially autocorrelated environmental variables and the influence of dispersal limitation. However, if phylogenetic diversity is also spatially autocorrelated, then evolutionary history may also explain some of the taxonomic DD pattern. Here, we will construct the phylogenetic distance-decay (PDD) relationship

First, calculate distances for geographic data, taxonomic data, and phylogenetic data among all unique pair-wise combinations of ponds.

In the R code chunk below, do the following:
1. calculate the geographic distances among ponds,
2. calculate the taxonomic similarity among ponds,
3. calculate the phylogenetic similarity among ponds, and
4. create a dataframe that includes all of the above information.

```
#Page 17
#long.lat <- as.matrix(cbind(env$long, env$lat))
#coord.dist <- earth.dist(long.lat, dist = TRUE)

#bray.curtis.dist <- 1 - vegdist(comm)

#unifrac.dist <- 1 - dist.uf

#unifrac.dist.mlt <- melt(as.matrix(unifrac.dist))[melt(upper.tri(as.matrix(unifrac.dist)))$value,]

#bray.curtis.dist.mlt <- melt(as.matrix(bray.curtis.dist))[melt(upper.tri(as.matrix(bray.curtis.dist)))
```

```
#coord.dist.mlt <- melt(as.matrix(coord.dist))[melt(upper.tri(as.matrix(coord.dist)))$value,]

#env.dist.mlt <- melt(as.matrix(env.dist))[melt(upper.tri(as.matrix(env.dist)))$value,]

#df <- data.frame(coord.dist.mlt, bray.curtis.dist.mlt[, 3], unifrac.dist.mlt[, 3],
#                 env.dist.mlt[, 3])
#names(df)[3:6] <- c("geo.dist","bray.curtis", "unifrac", "env.dist")
```

Now, let's plot the DD relationships:
In the R code chunk below, do the following:
1. plot the taxonomic distance decay relationship,
2. plot the phylogenetic distance decay relationship, and
3. add trend lines to each.

```
#par(mfrow=c(2, 1), mar = c(1, 5, 2, 1) + 0.1, oma = c(2, 0, 0, 0))

#plot(df$geo.dist, df$bray.curtis, xlab = "", xaxt = "n", las = 1, ylim = c(0.1, 0.9),
#     ylab="Bray-Curtis Similarity",
#     main = "Distance Decay", col = "SteelBlue")

#DD.reg.bc <- lm(df$bray.curtis ~ df$geo.dist)
#summary(DD.reg.bc)
#abline(DD.reg.bc , col = "red4", lwd = 2)

#par(mar = c(2, 5, 1, 1) + 0.1)

#plot(df$geo.dist, df$unifrac, xlab = "", las = 1, ylim = c(0.1, 0.9),
#     ylab = "Unifrac Similarity", col = "darkorchid4")

#DD.reg.uni <- lm(df$unifrac ~ df$geo.dist)
#summary(DD.reg.uni)
#abline(DD.reg.uni, col = "red4", lwd = 2)

#mtext("Geographic Distance (km)", side = 1, adj = 0.55,
#      line = 0.5, outer = TRUE)
```

In the R code chunk below, test if the trend lines in the above distance decay relationships are different from one another.

```
#source("./bin/diffslope.R")
#diffslope(df$geo.dist, df$unifrac, df$geo.dist, df$bray.curtis)
```

Question 7: Interpret the slopes from the taxonomic and phylogenetic DD relationships. If there are differences, hypothesize why this might be.

> ***Answer 7***: The slopes differ from eachother. This could be because UniFrac is the phylogenetic similarity among ponds and Bray-Curtis is the taxonomic similarity among ponds.

SYNTHESIS

Ignoring technical or methodological constraints, discuss how phylogenetic information could be useful in your own research. Specifically, what kinds of phylogenetic data would you need? How could you use it to answer

important questions in your field? In your response, feel free to consider not only phylogenetic approaches related to phylogenetic community ecology, but also those we discussed last week in the PhyloTraits module, or any other concepts that we have not covered in this course.

Answer: In our data set (team 3) we have 4 seabird species we are looking at. Last week when making a tree with the 4 birds, the tree came out very small. Our team thought to add more seabirds to the tree to expand it out. Upon relooking at the original paper, we found that the researchers found many other seabirds in the region. The 4 seabirds that were chosen were picked because they were the top 4 most abundant. Having other seabird species included could expand our understanding of seabird presence and environmental sea factors or rat infestation on islands. Maybe abundant seabirds have a different relationship to these factors than not so abundant seabirds.