8. Worksheet: Among Site (Beta) Diversity – Part 1

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OVERVIEW

In this worksheet, we move beyond the investigation of within-site α-diversity. We will explore β-diversity, which is defined as the diversity that occurs among sites. This requires that we examine the compositional similarity of assemblages that vary in space or time.

After completing this exercise you will know how to:

1. formally quantify β-diversity
2. visualize β-diversity with heatmaps, cluster analysis, and ordination
3. test hypotheses about β-diversity using multivariate statistics

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. Ths 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 '8.BetaDiversity' 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 (**8.BetaDiversity_1_Worksheet.Rmd**) with all code blocks filled out and questions answered) and the PDF output of `Knitr` (**8.BetaDiversity_1_Worksheet.pdf**).

The completed exercise is due on **Friday, April 16$^{\text{th}}$, 2021 before 09:00 AM**.

1) R 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 "*/8.BetaDiversity*" folder, and

4. load the `vegan` R package (be sure to install if needed).

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

```
## [1] "C:/Users/fordf/OneDrive/Documents/GitHub/QB2021_Fishman/2.Worksheets/8.BetaDiversity"
```

```
setwd("~/GitHub/QB2021_Fishman/2.Worksheets/8.BetaDiversity/")
library('vegan')
```

```
## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.5-6
```

2) LOADING DATA

Load dataset

In the R code chunk below, do the following:

1. load the `doubs` dataset from the `ade4` package, and
2. explore the structure of the dataset.

```
# note, pleae do not print the dataset when submitting
library("ade4")
```

```
## Warning: package 'ade4' was built under R version 4.0.5
```

```
data(doubs)
str(doubs, max.level = 1)
```

```
## List of 4
##  $ env    :'data.frame': 30 obs. of  11 variables:
##  $ fish   :'data.frame': 30 obs. of  27 variables:
##  $ xy     :'data.frame': 30 obs. of  2 variables:
##  $ species:'data.frame': 27 obs. of  4 variables:
```

Question 1: Describe some of the attributes of the `doubs` dataset.

a. How many objects are in `doubs`?
b. How many fish species are there in the `doubs` dataset?
c. How many sites are in the `doubs` dataset?

> ***Answer 1a***: 4 ***Answer 1b***: 27 ***Answer 1c***: 30

Visualizing the Doubs River Dataset

Question 2: Answer the following questions based on the spatial patterns of richness (i.e., α-diversity) and Brown Trout (*Salmo trutta*) abundance in the Doubs River.

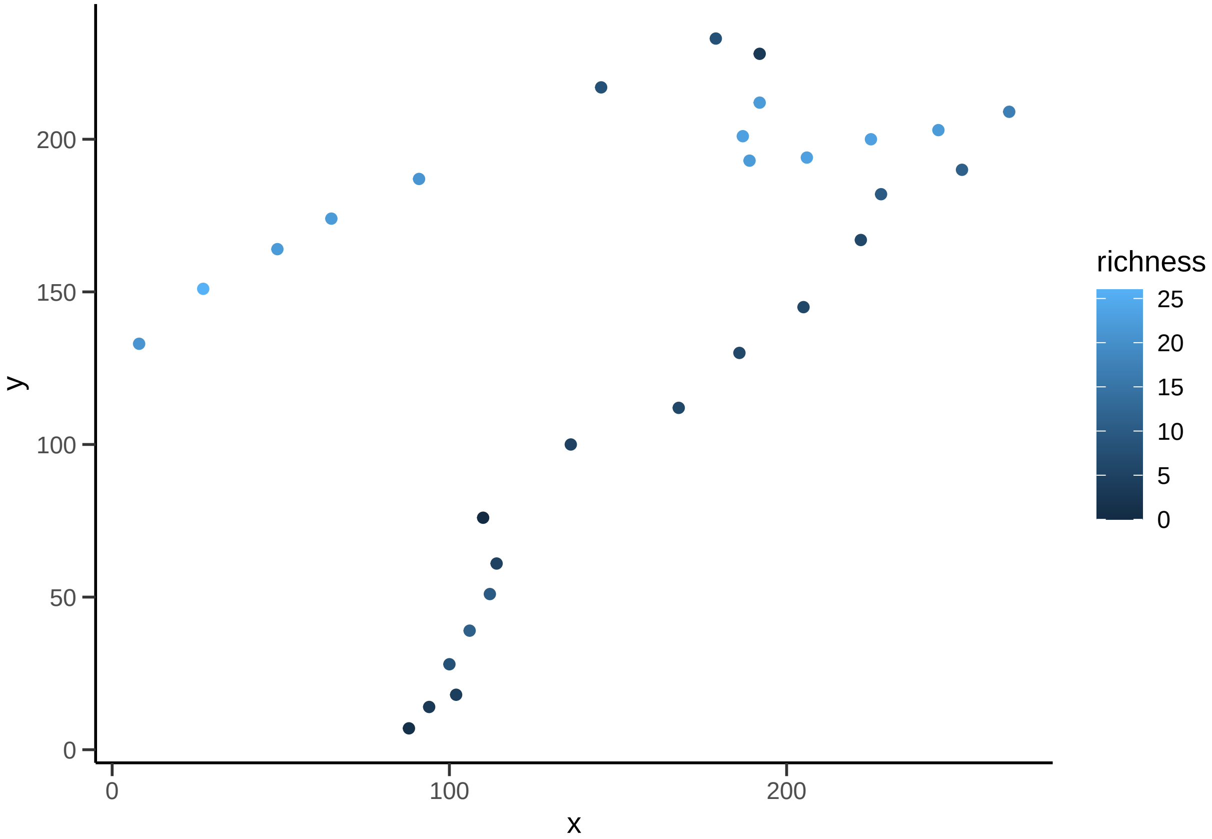
a. How does fish richness vary along the sampled reach of the Doubs River?
b. How does Brown Trout (*Salmo trutta*) abundance vary along the sampled reach of the Doubs River?
c. What do these patterns say about the limitations of using richness when examining patterns of biodiversity?

```
library('ggplot2')
```

```
## Warning: package 'ggplot2' was built under R version 4.0.5
```

```
richness <- specnumber(doubs$fish)
df1 <- cbind(doubs$xy, richness)

ggplot(df1, aes(x=x,y=y, color=richness)) +
  geom_point() +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(colour = "black"),
        axis.ticks.length = unit(5,"pt"),)
```



Answer 2a: Richness is greatest in the downstream region and also in this interior region. ***Answer 2b***: The brown trout aundance (not pictured here) is low in the downstream regions but higher in the upstream regions. ***Answer 2c***: The composition of different samples can be quite different even if they have similar richness or other alpha diversity measures.

3) QUANTIFYING BETA-DIVERSITY

In the R code chunk below, do the following:

1. write a function (`beta.w()`) to calculate Whittaker's β-diversity (i.e., β_w) that accepts a site-by-species matrix with optional arguments to specify pairwise turnover between two sites, and
2. use this function to analyze various aspects of β-diversity in the Doubs River.

```
beta.w <- function(sbs, sitename1=NULL, sitename2=NULL, pairwise=F){
  if (pairwise){
    if ( is.null(sitename1) | is.null(sitename2) ){
      print("Please specify desired sites.")
      return(NULL)
    }

    site1 <- sbs[sitename1,]
    site2 <- sbs[sitename2,]
    site1 <- subset(site1, select=site1>0)
    site2 <- subset(site2, select=site2>0)
    gamma <- union(colnames(site1), colnames(site2))
    s <- length(gamma)
    a.bar <- mean(c(specnumber(site1), specnumber(site2)))
    b.w <- round(s/a.bar-1,3)

  } else{
    sbs.pa <- decostand(sbs, method = "pa")
    S <- ncol(sbs.pa[,which( colSums(sbs.pa) > 0 )])
    a.bar <- mean(specnumber(sbs.pa))
    b.w <- round(S/a.bar, 3)
  }

  return(b.w)
}

beta.w(doubs$fish)
```

```
## [1] 2.16
```

```
beta.w(doubs$fish, 1,2, T)
```

```
## [1] 0.5
```

```
beta.w(doubs$fish, 1,10, T)
```

```
## [1] 0.714
```

Question 3: Using your `beta.w()` function above, answer the following questions:

a. Describe how local richness (α) and turnover (β) contribute to regional (γ) fish diversity in the Doubs.
b. Is the fish assemblage at site 1 more similar to the one at site 2 or site 10?
c. Using your understanding of the equation $\beta_w = \gamma/\alpha$, how would your interpretation of β change if we instead defined beta additively (i.e., $\beta = \gamma - \alpha$)?

> ***Answer 3a***: On average, each site has half as much diversity as the region does. ***Answer 3b***: Site 1 is more similar to site 2, as beta diversity is lower between 1 and 2 than between 1 and 10. ***Answer 3c***: The modification would be there difference between the regional diversity and the average site diversity. Values would go from zero to positive infinity, instead of 1 to positive infinity, and would be more difficult to compare between regions of different diversity.

The Resemblance Matrix

In order to quantify β-diversity for more than two samples, we need to introduce a new primary ecological data structure: the **Resemblance Matrix**.

Question 4: How do incidence- and abundance-based metrics differ in their treatment of rare species?

> ***Answer 4***: In incidence metrics, all species that are present are treated equally, while in abundance-based approaches, rare species receive much less weight.

In the R code chunk below, do the following:

1. make a new object, `fish`, containing the fish abundance data for the Doubs River,
2. remove any sites where no fish were observed (i.e., rows with sum of zero),
3. construct a resemblance matrix based on Sørensen's Similarity ("fish.ds"), and
4. construct a resemblance matrix based on Bray-Curtis Distance ("fish.db").

```
fish <- doubs$fish

fish <- fish[-8,]

(fish.ds <- vegdist(fish, method = "bray", binary = T)) #sorensen
```

```
##             1          2          3          4          5          6          7
## 2  0.50000000                                                                  
## 3  0.60000000 0.14285714                                                       
## 4  0.77777778 0.45454545 0.33333333                                            
## 5  0.83333333 0.57142857 0.46666667 0.15789474                                 
## 6  0.81818182 0.53846154 0.42857143 0.11111111 0.04761905                      
## 7  0.66666667 0.25000000 0.33333333 0.38461538 0.37500000 0.33333333           
## 9  1.00000000 0.50000000 0.55555556 0.38461538 0.37500000 0.33333333 0.40000000
## 10 0.71428571 0.33333333 0.40000000 0.28571429 0.29411765 0.25000000 0.09090909
## 11 0.71428571 0.33333333 0.40000000 0.42857143 0.52941176 0.50000000 0.27272727
## 12 0.71428571 0.33333333 0.40000000 0.42857143 0.52941176 0.50000000 0.27272727
## 13 0.71428571 0.33333333 0.40000000 0.57142857 0.64705882 0.62500000 0.45454545
## 14 0.81818182 0.53846154 0.42857143 0.33333333 0.42857143 0.40000000 0.46666667
## 15 0.83333333 0.57142857 0.60000000 0.36842105 0.36363636 0.33333333 0.37500000
## 16 0.88888889 0.70000000 0.61904762 0.36000000 0.28571429 0.25925926 0.54545455
## 17 0.91304348 0.76000000 0.69230769 0.46666667 0.39393939 0.37500000 0.62962963
## 18 0.91666667 0.76923077 0.70370370 0.48387097 0.41176471 0.39393939 0.64285714
## 19 1.00000000 0.84615385 0.77777778 0.54838710 0.41176471 0.45454545 0.71428571
## 20 1.00000000 0.84000000 0.76923077 0.53333333 0.39393939 0.43750000 0.70370370
## 21 1.00000000 0.84615385 0.77777778 0.54838710 0.41176471 0.45454545 0.71428571
## 22 1.00000000 0.92000000 0.84615385 0.60000000 0.45454545 0.50000000 0.77777778
## 23 1.00000000 1.00000000 1.00000000 0.81818182 0.71428571 0.69230769 0.75000000
## 24 1.00000000 1.00000000 1.00000000 0.75000000 0.68421053 0.66666667 0.84615385
## 25 1.00000000 1.00000000 0.83333333 0.62500000 0.36842105 0.44444444 0.69230769
## 26 1.00000000 0.91666667 0.84000000 0.58620690 0.43750000 0.48387097 0.76923077
## 27 1.00000000 0.92000000 0.84615385 0.60000000 0.45454545 0.50000000 0.77777778
## 28 1.00000000 0.92000000 0.84615385 0.60000000 0.45454545 0.50000000 0.77777778
## 29 0.92592593 0.79310345 0.73333333 0.52941176 0.40540541 0.44444444 0.67741935
## 30 1.00000000 1.00000000 0.92000000 0.65517241 0.50000000 0.54838710 0.84615385
##             9         10         11         12         13         14         15
## 2                                                                              
## 3                                                                              
## 4                                                                              
## 5                                                                              
## 6                                                                              
## 7                                                                              
## 9                                                                              
## 10 0.45454545                                                                  
## 11 0.45454545 0.33333333                                                       
## 12 0.45454545 0.33333333 0.00000000                                            
## 13 0.63636364 0.50000000 0.16666667 0.16666667                                 
## 14 0.60000000 0.37500000 0.25000000 0.25000000 0.25000000                      
## 15 0.50000000 0.29411765 0.29411765 0.29411765 0.29411765 0.14285714
## 16 0.54545455 0.47826087 0.56521739 0.56521739 0.56521739 0.33333333 0.28571429
## 17 0.62962963 0.57142857 0.57142857 0.57142857 0.57142857 0.37500000 0.33333333
## 18 0.64285714 0.58620690 0.58620690 0.58620690 0.58620690 0.39393939 0.35294118
## 19 0.64285714 0.65517241 0.79310345 0.79310345 0.79310345 0.57575758 0.52941176
## 20 0.62962963 0.64285714 0.78571429 0.78571429 0.85714286 0.62500000 0.57575758
## 21 0.64285714 0.65517241 0.79310345 0.79310345 0.86206897 0.63636364 0.58823529
## 22 0.70370370 0.71428571 0.85714286 0.85714286 0.92857143 0.68750000 0.63636364
## 23 0.50000000 0.77777778 0.77777778 0.77777778 1.00000000 0.84615385 0.85714286
## 24 0.69230769 0.71428571 0.85714286 0.85714286 1.00000000 0.77777778 0.78947368
## 25 0.69230769 0.57142857 0.85714286 0.85714286 1.00000000 0.66666667 0.68421053
## 26 0.69230769 0.70370370 0.85185185 0.85185185 0.92592593 0.67741935 0.62500000
## 27 0.70370370 0.71428571 0.85714286 0.85714286 0.92857143 0.68750000 0.63636364
## 28 0.70370370 0.71428571 0.85714286 0.85714286 0.92857143 0.68750000 0.63636364
## 29 0.67741935 0.62500000 0.68750000 0.68750000 0.68750000 0.50000000 0.45945946
## 30 0.76923077 0.77777778 0.92592593 0.92592593 1.00000000 0.74193548 0.68750000
##            16         17         18         19         20         21         22
## 2
## 3
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## 5
## 6
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## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17 0.12820513
## 18 0.15000000 0.02222222
## 19 0.25000000 0.15555556 0.13043478
## 20 0.28205128 0.18181818 0.15555556 0.02222222
## 21 0.30000000 0.20000000 0.17391304 0.04347826 0.02222222
## 22 0.33333333 0.22727273 0.20000000 0.06666667 0.04545455 0.02222222
## 23 0.80000000 0.76000000 0.76923077 0.76923077 0.76000000 0.76923077 0.76000000
## 24 0.68000000 0.60000000 0.54838710 0.48387097 0.46666667 0.48387097 0.46666667
## 25 0.60000000 0.60000000 0.54838710 0.48387097 0.46666667 0.48387097 0.46666667
## 26 0.36842105 0.25581395 0.22727273 0.09090909 0.06976744 0.04545455 0.02325581
## 27 0.33333333 0.22727273 0.20000000 0.06666667 0.04545455 0.02222222 0.00000000
## 28 0.33333333 0.22727273 0.20000000 0.06666667 0.04545455 0.02222222 0.00000000
## 29 0.25581395 0.12500000 0.10204082 0.06122449 0.08333333 0.06122449 0.08333333
## 30 0.36842105 0.25581395 0.22727273 0.09090909 0.06976744 0.04545455 0.02325581
##            23         24         25         26         27         28         29
## 2
## 3
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## 10
## 11
## 12
## 13
## 14
## 15
## 16
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## 18
## 19
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## 21
## 22
## 23
## 24 0.45454545
## 25 0.45454545 0.37500000
## 26 0.75000000 0.44827586 0.44827586
## 27 0.76000000 0.46666667 0.46666667 0.02325581
## 28 0.76000000 0.46666667 0.46666667 0.02325581 0.00000000
## 29 0.79310345 0.52941176 0.52941176 0.10638298 0.08333333 0.08333333
## 30 0.75000000 0.44827586 0.44827586 0.04761905 0.02325581 0.02325581 0.10638298
```

```
(fish.db <- vegdist(fish, method = "bray")) # braycurtis
```

```
##             1          2          3          4          5          6          7
## 2  0.60000000
## 3  0.68421053 0.14285714
## 4  0.75000000 0.33333333 0.18918919
## 5  0.89189189 0.69565217 0.68000000 0.49090909
## 6  0.75000000 0.39393939 0.29729730 0.19047619 0.41818182
## 7  0.68421053 0.14285714 0.12500000 0.24324324 0.64000000 0.24324324
## 9  1.00000000 0.69230769 0.73333333 0.65714286 0.58333333 0.54285714 0.66666667
## 10 0.88235294 0.38461538 0.40000000 0.37142857 0.54166667 0.25714286 0.26666667
## 11 0.57142857 0.30434783 0.40740741 0.43750000 0.68888889 0.43750000 0.33333333
## 12 0.71428571 0.20000000 0.23529412 0.33333333 0.69230769 0.38461538 0.17647059
## 13 0.72727273 0.29032258 0.31428571 0.45000000 0.73584906 0.55000000 0.37142857
## 14 0.80645161 0.40000000 0.31818182 0.34693878 0.67741935 0.42857143 0.36363636
## 15 0.83333333 0.51111111 0.46938776 0.40740741 0.55223881 0.37037037 0.38775510
## 16 0.86046512 0.65384615 0.57142857 0.47540984 0.45945946 0.37704918 0.53571429
## 17 0.91489362 0.67857143 0.63333333 0.50769231 0.51282051 0.44615385 0.60000000
## 18 0.95555556 0.74074074 0.72413793 0.58730159 0.50000000 0.52380952 0.68965517
## 19 1.00000000 0.79310345 0.70967742 0.61194030 0.50000000 0.52238806 0.67741935
## 20 1.00000000 0.91176471 0.88888889 0.74025974 0.48888889 0.68831169 0.86111111
## 21 1.00000000 0.94594595 0.92307692 0.78313253 0.50000000 0.73493976 0.89743590
## 22 1.00000000 0.97619048 0.95454545 0.82795699 0.52830189 0.78494624 0.93181818
## 23 1.00000000 1.00000000 1.00000000 0.92000000 0.89473684 0.84000000 0.90000000
## 24 1.00000000 1.00000000 1.00000000 0.88888889 0.79591837 0.77777778 0.93548387
## 25 1.00000000 1.00000000 0.92592593 0.81250000 0.68888889 0.68750000 0.85185185
## 26 1.00000000 0.96363636 0.93220339 0.78125000 0.55844156 0.68750000 0.89830508
## 27 1.00000000 0.97333333 0.94936709 0.83333333 0.56701031 0.76190476 0.92405063
## 28 1.00000000 0.97560976 0.95348837 0.82417582 0.57692308 0.78021978 0.93023256
## 29 0.97777778 0.93939394 0.92233010 0.81481481 0.53719008 0.77777778 0.90291262
## 30 1.00000000 1.00000000 0.98095238 0.87272727 0.59349593 0.83636364 0.96190476
##             9         10         11         12         13         14         15
## 2
## 3
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## 6
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## 9
## 10 0.57142857
## 11 0.76000000 0.44000000
## 12 0.68750000 0.37500000 0.24137931
## 13 0.81818182 0.57575758 0.33333333 0.18918919
## 14 0.76190476 0.47619048 0.43589744 0.21739130 0.19148936
## 15 0.65957447 0.40425532 0.50000000 0.33333333 0.38461538 0.24590164
## 16 0.70370370 0.51851852 0.64705882 0.55172414 0.59322034 0.44117647 0.26027397
## 17 0.68965517 0.51724138 0.63636364 0.58064516 0.61904762 0.50000000 0.40259740
## 18 0.64285714 0.57142857 0.69811321 0.66666667 0.70491803 0.60000000 0.46666667
## 19 0.66666667 0.63333333 0.82456140 0.75000000 0.81538462 0.67567568 0.56962025
## 20 0.68571429 0.77142857 0.91044776 0.89189189 0.92000000 0.83333333 0.70786517
## 21 0.76315789 0.81578947 0.91780822 0.92500000 0.95061728 0.86666667 0.76842105
## 22 0.76744186 0.86046512 0.95180723 0.95555556 0.97802198 0.90000000 0.77142857
## 23 0.77777778 0.88888889 0.86666667 0.90909091 1.00000000 0.93750000 0.94594595
## 24 0.72413793 0.79310345 0.92307692 0.93939394 1.00000000 0.90697674 0.87500000
## 25 0.84000000 0.76000000 0.90909091 0.93103448 1.00000000 0.84615385 0.81818182
## 26 0.71929825 0.82456140 0.92592593 0.93442623 0.96774194 0.85915493 0.76315789
## 27 0.76623377 0.84415584 0.94594595 0.95061728 0.97560976 0.89010989 0.77083333
## 28 0.76190476 0.85714286 0.95061728 0.95454545 0.97752809 0.89795918 0.78640777
## 29 0.78217822 0.84158416 0.89795918 0.90476190 0.90566038 0.84347826 0.73333333
## 30 0.84466019 0.90291262 0.98000000 0.98130841 1.00000000 0.93162393 0.81967213
##            16         17         18         19         20         21         22
## 2
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## 10
## 11
## 12
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## 15
## 16
## 17 0.26190476
## 18 0.34146341 0.13953488
## 19 0.39534884 0.31111111 0.25000000
## 20 0.58333333 0.42000000 0.32653061 0.23529412
## 21 0.62745098 0.49056604 0.40384615 0.29629630 0.10169492
## 22 0.66071429 0.55172414 0.47368421 0.38983051 0.18750000 0.10447761
## 23 0.90909091 0.83333333 0.82608696 0.84000000 0.86666667 0.87878788 0.89473684
## 24 0.81818182 0.69491525 0.64912281 0.63934426 0.57746479 0.61038961 0.65517241
## 25 0.76470588 0.74545455 0.66037736 0.61403509 0.67164179 0.69863014 0.73493976
## 26 0.63855422 0.54022989 0.45882353 0.32584270 0.21212121 0.20000000 0.25217391
## 27 0.66990291 0.57009346 0.48571429 0.37614679 0.19327731 0.13600000 0.12592593
## 28 0.69090909 0.57894737 0.50000000 0.41379310 0.22222222 0.16666667 0.12676056
## 29 0.65354331 0.51145038 0.44186047 0.41353383 0.24475524 0.18120805 0.11949686
## 30 0.72093023 0.57894737 0.52671756 0.48148148 0.29655172 0.23178808 0.18012422
##            23         24         25         26         27         28         29
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## 10
## 11
## 12
## 13
## 14
## 15
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## 22
## 23
## 24 0.57894737
## 25 0.46666667 0.46153846
## 26 0.82978723 0.48275862 0.59259259
## 27 0.88059701 0.61538462 0.70270270 0.18867925
## 28 0.89189189 0.64705882 0.72839506 0.23893805 0.09774436
## 29 0.91208791 0.70588235 0.77551020 0.33846154 0.18666667 0.14649682
## 30 0.91397849 0.71153846 0.78000000 0.36363636 0.19736842 0.15723270 0.14772727
```

Question 5: Using the distance matrices from above, answer the following questions:

a. Does the resemblance matrix (`fish.db`) represent similarity or dissimilarity? What information in the resemblance matrix led you to arrive at your answer?
b. Compare the resemblance matrices (`fish.db` or `fish.ds`) you just created. How does the choice of the Sørensen or Bray-Curtis distance influence your interpretation of site (dis)similarity?

   Answer 5a: It represents dissimilarity, as the values increase with increasing distance between sites. ***Answer 5b***: The two resemblance matrices seem pretty similar in their overall trends, though some of the values are slightly different. Sorensen uses only incidence instead of abundance.

4) VISUALIZING BETA-DIVERSITY

A. Heatmaps

In the R code chunk below, do the following:

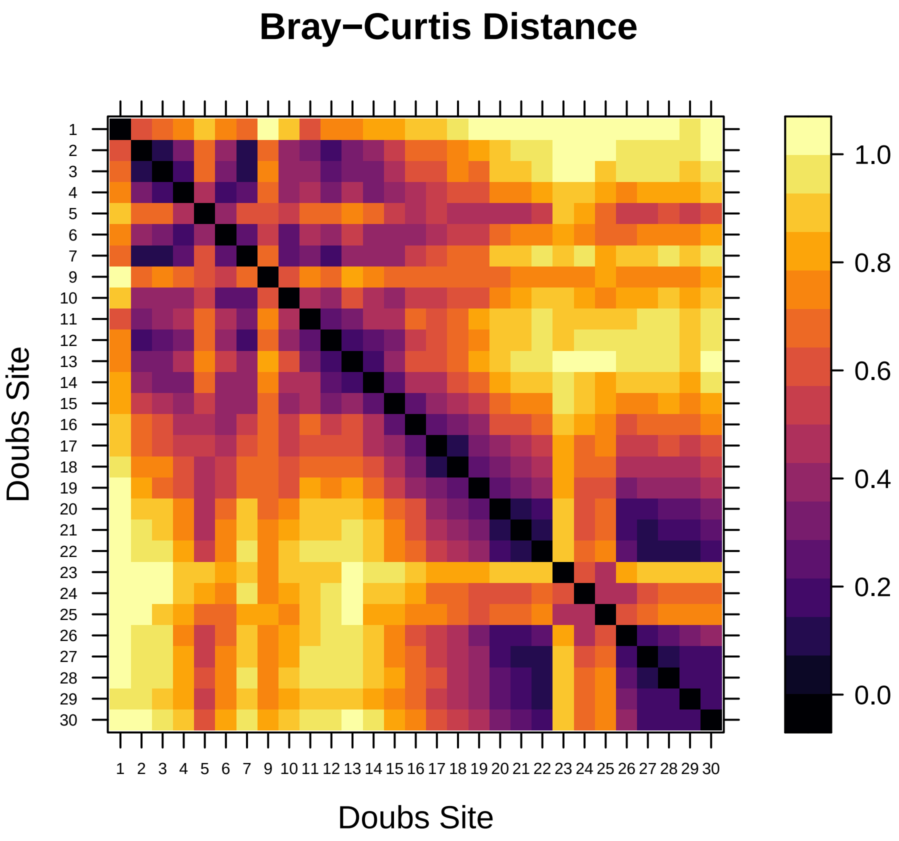
1. define a color palette,
2. define the order of sites in the Doubs River, and
3. use the `levelplot()` function to create a heatmap of fish abundances in the Doubs River.

```
library('viridis')
```

```
## Loading required package: viridisLite
```

```
order <- rev(attr(fish.db, "Labels"))
```

```
levelplot(as.matrix(fish.db)[,order], aspect="iso", col.regions=inferno,
          xlab="Doubs Site", ylab="Doubs Site", scales=list(cex=0.5),
          main="Bray-Curtis Distance")
```

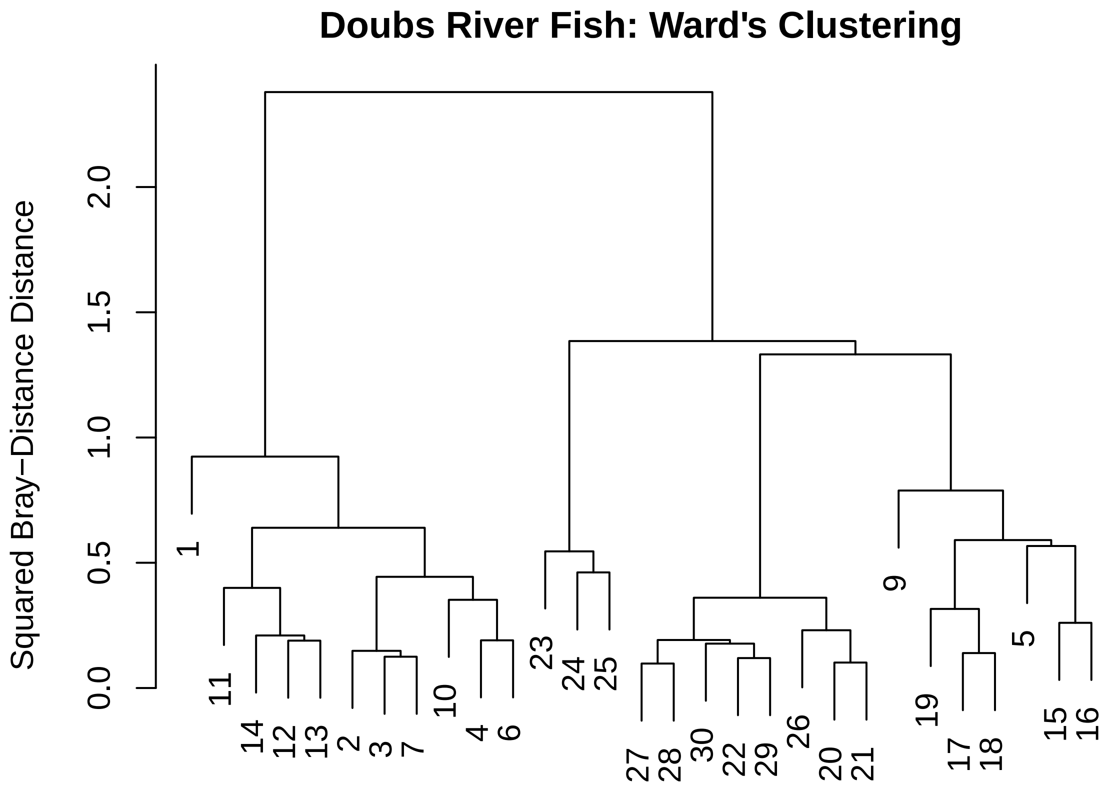


B. Cluster Analysis

In the R code chunk below, do the following:

1. perform a cluster analysis using Ward's Clustering, and
2. plot your cluster analysis (use either `hclust` or `heatmap.2`).

```
fish.ward <- hclust(fish.db, method="ward.D2")
par(mar=c(1,5,2,2)+0.1)
plot(fish.ward, main="Doubs River Fish: Ward's Clustering", ylab="Squared Bray-Distance Distance")
```



Question 6: Based on cluster analyses and the introductory plots that we generated after loading the data, develop an ecological hypothesis for fish diversity the `doubs` data set?

> ***Answer 6***: In general, sites closer to each other are more similar to each other. Community structure is very different after site 15, though a few sites before it cluser closely with earlier sites. Upstream and downstream communities appear to be quite different, and the environments in these locations may drive these differences.

C. Ordination

Principal Coordinates Analysis (PCoA)

In the R code chunk below, do the following:

1. perform a Principal Coordinates Analysis to visualize beta-diversity
2. calculate the variation explained by the first three axes in your ordination
3. plot the PCoA ordination,
4. label the sites as points using the Doubs River site number, and
5. identify influential species and add species coordinates to PCoA plot.

```
library(BiodiversityR)
```

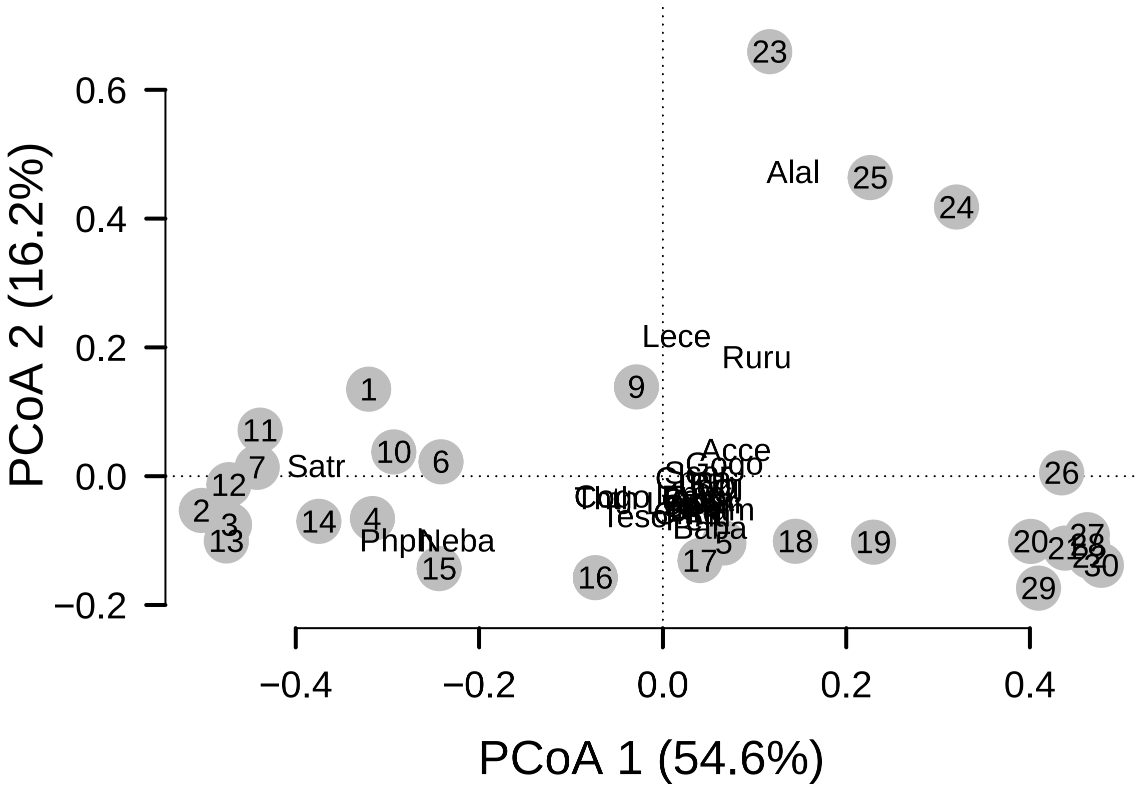
```
## Warning: package 'BiodiversityR' was built under R version 4.0.5
```

```
## Loading required package: tcltk
```

```
## Registered S3 methods overwritten by 'lme4':
##   method                          from
##   cooks.distance.influence.merMod car
##   influence.merMod                car
##   dfbeta.influence.merMod         car
##   dfbetas.influence.merMod        car
```

```
## BiodiversityR 2.12-3: Use command BiodiversityRGUI() to launch the Graphical User Interface;
## to see changes use BiodiversityRGUI(changeLog=TRUE, backward.compatibility.messages=TRUE)
```

```
fish.pcoa <- cmdscale(fish.db, eig=T, k=3)
eig.sum <- sum(fish.pcoa$eig)

explainvar1 <- round( fish.pcoa$eig[1]/eig.sum, 3)*100
explainvar2 <- round( fish.pcoa$eig[2]/eig.sum, 3)*100
explainvar3 <- round( fish.pcoa$eig[3]/eig.sum, 3)*100

sum.eig <- explainvar1+explainvar2+explainvar3

par(mar=c(5,5,1,2)+0.1)
plot(fish.pcoa$points[,1], fish.pcoa$points[,2], ylim=c(-0.2,0.7),
     xlab=paste0("PCoA 1 (", explainvar1,"%)"),
     ylab=paste0("PCoA 2 (", explainvar2,"%)"),
     pch=16, cex=2.0, type="n", cex.lab=1.5, cex.axis=1.2, axes=F)

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)

points(fish.pcoa$points[,1], fish.pcoa$points[,2], pch=19, cex=3, bg="grey",col="grey")
text(fish.pcoa$points[,1], fish.pcoa$points[,2], labels = row.names(fish.pcoa$points))

fishREL <- fish

for (i in 1:nrow(fish)){
  fishREL[i, ] <- fish[i,]/sum(fish[i,])
}

fish.pcoa <- add.spec.scores(fish.pcoa, fishREL, method = "pcoa.scores")
text(fish.pcoa$cproj[,1], fish.pcoa$cproj[,2],
     labels=row.names(fish.pcoa$cproj), col="black")
```



In the R code chunk below, do the following:

1. identify influential species based on correlations along each PCoA axis (use a cutoff of 0.70), and
2. use a permutation test (999 permutations) to test the correlations of each species along each axis.

```
spe.corr <- add.spec.scores(fish.pcoa, fishREL)$cproj
corrcut <- 0.7
imp.spp <- spe.corr[abs(spe.corr[,1]) >= corrcut | abs(spe.corr[,2]) >=corrcut]
envfit(fish.pcoa, fishREL, perm=999)
```

```
##
## ***VECTORS
##
##           Dim1     Dim2     r2 Pr(>r)
## Cogo -0.83884 -0.54438 0.2982  0.015 *
## Satr -0.99904  0.04371 0.4326  0.005 **
## Phph -0.94110 -0.33813 0.7814  0.001 ***
## Neba -0.91413 -0.40543 0.6234  0.001 ***
## Thth -0.87692 -0.48063 0.2634  0.028 *
## Teso -0.44704 -0.89452 0.1700  0.098 .
## Chna  0.99707 -0.07644 0.4612  0.003 **
## Chto  0.42032 -0.90738 0.2579  0.021 *
## Lele  0.33041 -0.94384 0.0495  0.531
## Lece  0.06856  0.99765 0.3399  0.010 **
## Baba  0.54118 -0.84091 0.6752  0.001 ***
## Spbi  0.57341 -0.81927 0.4138  0.004 **
## Gogo  0.97507  0.22188 0.3753  0.005 **
## Eslu  0.72044 -0.69352 0.1673  0.088 .
## Pefl  0.43762 -0.89916 0.3048  0.011 *
## Rham  0.72476 -0.68901 0.8301  0.001 ***
## Legi  0.93461 -0.35568 0.7016  0.001 ***
## Scer  0.98569  0.16858 0.3533  0.011 *
## Cyca  0.68181 -0.73153 0.7743  0.001 ***
## Titi  0.64378 -0.76521 0.4586  0.002 **
## Abbr  0.77254 -0.63497 0.7128  0.001 ***
## Icme  0.75626 -0.65427 0.5270  0.003 **
## Acce  0.88799  0.45986 0.6294  0.001 ***
## Ruru  0.48379  0.87518 0.5177  0.002 **
## Blbj  0.95802 -0.28671 0.6766  0.001 ***
## Alal  0.28755  0.95777 0.8592  0.001 ***
## Anan  0.74277 -0.66954 0.7894  0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
```

Question 7: Address the following questions about the ordination results of the doubs data set:

a. Describe the grouping of sites in the Doubs River based on fish community composition.
b. Generate a hypothesis about which fish species are potential indicators of river quality.

> ***Answer 7a***: There are 4 defined clusters based on community composition. One site is differentiated by the presense of Alal, another is differentiated by the presence of Satr, Phph, and Neba, and a third has many associated species. A fourth cluster is differentiated by having none of these species. ***Answer 7b***: Alal, Satr, Phph, and Neba may be able to differentiate river quality, as here they are shown to be able to differentiate these clusters the best.

SYNTHESIS

Using the mobsim package from the DataWrangling module last week, simulate two local communities each containing 1000 individuals (N) and 25 species (S), but with one having a random spatial distribution and the other having a patchy spatial distribution. Take ten (10) subsamples from each site using the quadrat function and answer the following questions:

1) Compare the average pairwise similarity among subsamples in site 1 (random spatial distribution) to the average pairswise similarity among subsamples in site 2 (patchy spatial distribution). Use a t-test to determine whether compositional similarity was affected by the spatial distribution. Finally, compare the compositional similarity of site 1 and site 2 to the source community?

```
library(mobsim)
```

```
## Warning: package 'mobsim' was built under R version 4.0.4
```

```
com.ran <- sim_poisson_community(s_pool = 25, n_sim = 1000, sad_type = "lnorm",
        sad_coef = list("meanlog" = 2, "sdlog" = 1))
comm_mat.ran <- sample_quadrats(com.ran, n_quadrats = 10, quadrat_area = 0.1,
               method = "random", avoid_overlap = T,plot = F)
```

```
## Warning in sample_quadrats(com.ran, n_quadrats = 10, quadrat_area = 0.1, : Cannot find a sampling la
##                                              Install the package spatstat for an improved method for
##                                              Use less quadrats or smaller quadrat area, or set avoid_
```

```
# obtain site by species
sbs.ran <- comm_mat.ran$spec_dat
```

```r
com.clust <- sim_thomas_community(s_pool = 25, n_sim = 1000, sad_type = "lnorm",
        sad_coef = list("meanlog" = 2, "sdlog" = 1))

comm_mat.clust <- sample_quadrats(com.clust, n_quadrats = 10, quadrat_area = 0.1,
               method = "random", avoid_overlap = T,plot = F)
```

```
## Warning in sample_quadrats(com.clust, n_quadrats = 10, quadrat_area = 0.1, : Cannot find a sampling
##                                              Install the package spatstat for an improved method for
##                                              Use less quadrats or smaller quadrat area, or set avoid_
```

```r
# obtain site by species
sbs.clust <- comm_mat.clust$spec_dat
```

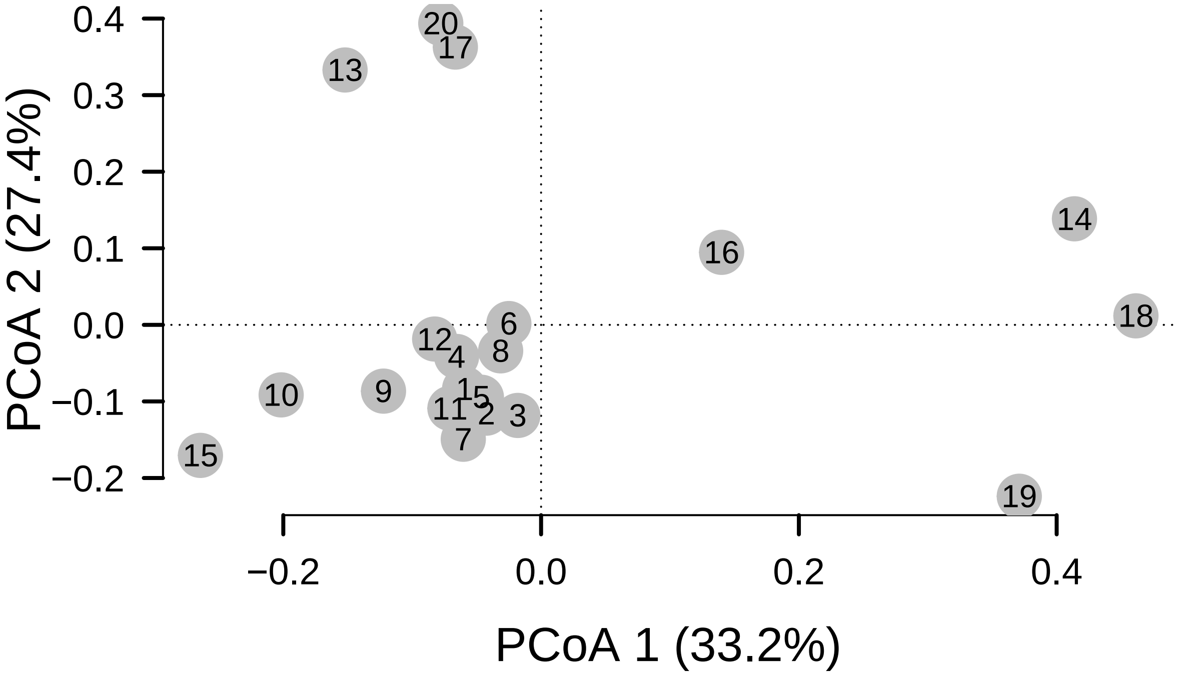
```r
pairwise <- function(sbs){

  vals <- c() # initialize empty values

  # all possible pairwise comparisons
  for (i in 1:10){
    for (j in 2:10){

      if (i<=j){ # don't compare samples to themselves or repeat comparisons
        next
      }

      val <- beta.w(sbs, i, j, T)
      vals <- c(vals, val)

    }
  }
  return(vals)
}

beta.w.ran <- pairwise(sbs.ran)

beta.w.clust <- pairwise(sbs.clust)

(results <- t.test(beta.w.ran, beta.w.clust, alternative="two.sided"))
```

```
##
##  Welch Two Sample t-test
##
## data:  beta.w.ran and beta.w.clust
## t = -9.1843, df = 41.037, p-value = 1.663e-11
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.3495989 -0.2235677
## sample estimates:
## mean of x mean of y
## 0.1852778 0.4718611
```

: There is a significant difference between the two sites' average pairwise beta diversity. Samples from the patchy simulations have higher beta diversity than from the random communities. This is likely because patchiness makes it less likely to sample the same species in the one quadrat than the random assemblage.

2) Create a cluster diagram or ordination using your simulated data. Are there any visual trends that would suggest a difference in composition between site 1 and site 2? Describe.

```r
sbs.all <- rbind(sbs.ran, sbs.clust)
rownames(sbs.all) <- 1:20 # re-number samples

sim.db <- vegdist(sbs.all, method="bray") # braycurtis distance

sim.pcoa <- cmdscale(sim.db, eig=T, k=3)

eig.sum <- sum(sim.pcoa$eig)

explainvar1 <- round( sim.pcoa$eig[1]/eig.sum, 3)*100
explainvar2 <- round( sim.pcoa$eig[2]/eig.sum, 3)*100
explainvar3 <- round( sim.pcoa$eig[3]/eig.sum, 3)*100
sum.eig <- explainvar1+explainvar2+explainvar3

# plot
# par(mar=c(5,5,1,2)+0.1)
plot(sim.pcoa$points[,1], sim.pcoa$points[,2],
     xlab=paste0("PCoA 1 (", explainvar1,"%)"),
     ylab=paste0("PCoA 2 (", explainvar2,"%)"),
     pch=16, cex=2.0, type="n", cex.lab=1.5, cex.axis=1.2, axes=F)

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)

points(sim.pcoa$points[,1], sim.pcoa$points[,2], pch=19, cex=3, bg="grey",col="grey")
text(sim.pcoa$points[,1], sim.pcoa$points[,2], labels = row.names(sim.pcoa$points))
```



>: In the above plot, the random samples are 1-10, and the patchy samples are 11-20. After running simulations a few times to account for stochasticity, I have noticed a few trends. The random samples tend to cluster together fairly tightly. This cluster may contain some patchy samples, but not always. The patchy samples have much higher spread/variance and often consist of several clusters that are quite distant from each other. This makes some sense, as some samples of the patchy communities will be fairly similar, but others will be quite different from each other.