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_Workshee**

The completed exercise is due on **Wednesday, February 6$^{\text{th}}$, 2019 before 12:00 PM (noon)**.

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/wolve/GitHub/QB2019_Crawley/2.Worksheets/8.BetaDiversity"

```
setwd("C:/Users/wolve/GitHub/QB2019_Crawley/2.Worksheets/8.BetaDiversity")
require(vegan)
```

Loading required package: vegan

Loading required package: permute

Loading required package: lattice

This is vegan 2.5-3

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
#install.packages("ade4")
require(ade4)
```

Loading required package: ade4

```
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?

   Answer 2a: Species richness is fairly low at the upstream sites; richness is highest downstream, with the exception of the 23-25 samples, and sites in the middle of the sampled reach. *Answer 2b*: Brown trout is largely absent from downstream and middle sites; abundance is highest upstream. *Answer 2c*: Species richness itself does not identify the species composition of each community. Using species richness alone as an estimate of brown trout abundance would be erroneous.

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(site.by.species = "", sitenum1 = "", sitenum2 = "", pairwise = FALSE){
  if (pairwise == TRUE){
    if (sitenum1 == "" | sitenum2 == ""){
      print("Error: please specify sites to compare")
      return(NA)}
    site1 = site.by.species[sitenum1,]
    site2 = site.by.species[sitenum2,]
    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)
    return(b.w)
  }
  else{
    SbyS.pa <- decostand(site.by.species, method = "pa")
    S <- ncol(SbyS.pa[,which(colSums(SbyS.pa) > 0)])
    a.bar <- mean(specnumber(SbyS.pa))
    b.w <- round(S/a.bar, 3)
    return(b.w)
  }
}
beta.w(doubs$fish, 1,2, pairwise=TRUE)
```

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

```
beta.w(doubs$fish, 1,10, pairwise=TRUE)
```

```
## [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: High turnover between sites increases regional diversity, but sites with low species richness . When the average richness of local sites is higher, and sites are dissimilar from one another, gamma diversity is greatest. ***Answer 3b***: Fish assemblage at site 1 is more similar to site 2 than to site 10. ***Answer 3c***: Defining beta additively changes the interpretation of beta to a measure of how many more species exist in a regional pool than in local sites.

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 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 SÃ¸rensen'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 = TRUE)
fish.ds
```

```
##             1          2          3          4          5          6
## 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
## 10 0.71428571 0.33333333 0.40000000 0.28571429 0.29411765 0.25000000
## 11 0.71428571 0.33333333 0.40000000 0.42857143 0.52941176 0.50000000
## 12 0.71428571 0.33333333 0.40000000 0.42857143 0.52941176 0.50000000
## 13 0.71428571 0.33333333 0.40000000 0.57142857 0.64705882 0.62500000
## 14 0.81818182 0.53846154 0.42857143 0.33333333 0.42857143 0.40000000
```

```
## 15 0.83333333 0.57142857 0.60000000 0.36842105 0.36363636 0.33333333
## 16 0.88888889 0.70000000 0.61904762 0.36000000 0.28571429 0.25925926
## 17 0.91304348 0.76000000 0.69230769 0.46666667 0.39393939 0.37500000
## 18 0.91666667 0.76923077 0.70370370 0.48387097 0.41176471 0.39393939
## 19 1.00000000 0.84615385 0.77777778 0.54838710 0.41176471 0.45454545
## 20 1.00000000 0.84000000 0.76923077 0.53333333 0.39393939 0.43750000
## 21 1.00000000 0.84615385 0.77777778 0.54838710 0.41176471 0.45454545
## 22 1.00000000 0.92000000 0.84615385 0.60000000 0.45454545 0.50000000
## 23 1.00000000 1.00000000 1.00000000 0.81818182 0.71428571 0.69230769
## 24 1.00000000 1.00000000 1.00000000 0.75000000 0.68421053 0.66666667
## 25 1.00000000 1.00000000 0.83333333 0.62500000 0.36842105 0.44444444
## 26 1.00000000 0.91666667 0.84000000 0.58620690 0.43750000 0.48387097
## 27 1.00000000 0.92000000 0.84615385 0.60000000 0.45454545 0.50000000
## 28 1.00000000 0.92000000 0.84615385 0.60000000 0.45454545 0.50000000
## 29 0.92592593 0.79310345 0.73333333 0.52941176 0.40540541 0.44444444
## 30 1.00000000 1.00000000 0.92000000 0.65517241 0.50000000 0.54838710
##              7          9         10         11         12         13
## 2
## 3
## 4
## 5
## 6
## 7
## 9  0.40000000
## 10 0.09090909 0.45454545
## 11 0.27272727 0.45454545 0.33333333
## 12 0.27272727 0.45454545 0.33333333 0.00000000
## 13 0.45454545 0.63636364 0.50000000 0.16666667 0.16666667
## 14 0.46666667 0.60000000 0.37500000 0.25000000 0.25000000 0.25000000
## 15 0.37500000 0.50000000 0.29411765 0.29411765 0.29411765 0.29411765
## 16 0.54545455 0.54545455 0.47826087 0.56521739 0.56521739 0.56521739
## 17 0.62962963 0.62962963 0.57142857 0.57142857 0.57142857 0.57142857
## 18 0.64285714 0.64285714 0.58620690 0.58620690 0.58620690 0.58620690
## 19 0.71428571 0.64285714 0.65517241 0.79310345 0.79310345 0.79310345
## 20 0.70370370 0.62962963 0.64285714 0.78571429 0.78571429 0.85714286
## 21 0.71428571 0.64285714 0.65517241 0.79310345 0.79310345 0.86206897
## 22 0.77777778 0.70370370 0.71428571 0.85714286 0.85714286 0.92857143
## 23 0.75000000 0.50000000 0.77777778 0.77777778 0.77777778 1.00000000
## 24 0.84615385 0.69230769 0.71428571 0.85714286 0.85714286 1.00000000
## 25 0.69230769 0.69230769 0.57142857 0.85714286 0.85714286 1.00000000
## 26 0.76923077 0.69230769 0.70370370 0.85185185 0.85185185 0.92592593
## 27 0.77777778 0.70370370 0.71428571 0.85714286 0.85714286 0.92857143
## 28 0.77777778 0.70370370 0.71428571 0.85714286 0.85714286 0.92857143
## 29 0.67741935 0.67741935 0.62500000 0.68750000 0.68750000 0.68750000
## 30 0.84615385 0.76923077 0.77777778 0.92592593 0.92592593 1.00000000
##             14         15         16         17         18         19
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
```

```
## 11
## 12
## 13
## 14
## 15 0.14285714
## 16 0.33333333 0.28571429
## 17 0.37500000 0.33333333 0.12820513
## 18 0.39393939 0.35294118 0.15000000 0.02222222
## 19 0.57575758 0.52941176 0.25000000 0.15555556 0.13043478
## 20 0.62500000 0.57575758 0.28205128 0.18181818 0.15555556 0.02222222
## 21 0.63636364 0.58823529 0.30000000 0.20000000 0.17391304 0.04347826
## 22 0.68750000 0.63636364 0.33333333 0.22727273 0.20000000 0.06666667
## 23 0.84615385 0.85714286 0.80000000 0.76000000 0.76923077 0.76923077
## 24 0.77777778 0.78947368 0.68000000 0.60000000 0.54838710 0.48387097
## 25 0.66666667 0.68421053 0.60000000 0.60000000 0.54838710 0.48387097
## 26 0.67741935 0.62500000 0.36842105 0.25581395 0.22727273 0.09090909
## 27 0.68750000 0.63636364 0.33333333 0.22727273 0.20000000 0.06666667
## 28 0.68750000 0.63636364 0.33333333 0.22727273 0.20000000 0.06666667
## 29 0.50000000 0.45945946 0.25581395 0.12500000 0.10204082 0.06122449
## 30 0.74193548 0.68750000 0.36842105 0.25581395 0.22727273 0.09090909
##             20         21         22         23         24         25
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21 0.02222222
## 22 0.04545455 0.02222222
## 23 0.76000000 0.76923077 0.76000000
## 24 0.46666667 0.48387097 0.46666667 0.45454545
## 25 0.46666667 0.48387097 0.46666667 0.45454545 0.37500000
## 26 0.06976744 0.04545455 0.02325581 0.75000000 0.44827586 0.44827586
## 27 0.04545455 0.02222222 0.00000000 0.76000000 0.46666667 0.46666667
## 28 0.04545455 0.02222222 0.00000000 0.76000000 0.46666667 0.46666667
## 29 0.08333333 0.06122449 0.08333333 0.79310345 0.52941176 0.52941176
## 30 0.06976744 0.04545455 0.02325581 0.75000000 0.44827586 0.44827586
##             26         27         28         29
## 2
## 3
## 4
## 5
```

6

```
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21
## 22
## 23
## 24
## 25
## 26
## 27 0.02325581
## 28 0.02325581 0.00000000
## 29 0.10638298 0.08333333 0.08333333
## 30 0.04761905 0.02325581 0.02325581 0.10638298
```

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

```
##                    1          2          3          4          5          6
## 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
## 10  0.88235294 0.38461538 0.40000000 0.37142857 0.54166667 0.25714286
## 11  0.57142857 0.30434783 0.40740741 0.43750000 0.68888889 0.43750000
## 12  0.71428571 0.20000000 0.23529412 0.33333333 0.69230769 0.38461538
## 13  0.72727273 0.29032258 0.31428571 0.45000000 0.73584906 0.55000000
## 14  0.80645161 0.40000000 0.31818182 0.34693878 0.67741935 0.42857143
## 15  0.83333333 0.51111111 0.46938776 0.40740741 0.55223881 0.37037037
## 16  0.86046512 0.65384615 0.57142857 0.47540984 0.45945946 0.37704918
## 17  0.91489362 0.67857143 0.63333333 0.50769231 0.51282051 0.44615385
## 18  0.95555556 0.74074074 0.72413793 0.58730159 0.50000000 0.52380952
## 19  1.00000000 0.79310345 0.70967742 0.61194030 0.50000000 0.52238806
## 20  1.00000000 0.91176471 0.88888889 0.74025974 0.48888889 0.68831169
## 21  1.00000000 0.94594595 0.92307692 0.78313253 0.50000000 0.73493976
## 22  1.00000000 0.97619048 0.95454545 0.82795699 0.52830189 0.78494624
## 23  1.00000000 1.00000000 1.00000000 0.92000000 0.89473684 0.84000000
## 24  1.00000000 1.00000000 1.00000000 0.88888889 0.79591837 0.77777778
## 25  1.00000000 1.00000000 0.92592593 0.81250000 0.68888889 0.68750000
## 26  1.00000000 0.96363636 0.93220339 0.78125000 0.55844156 0.68750000
## 27  1.00000000 0.97333333 0.94936709 0.83333333 0.56701031 0.76190476
```

```
## 28 1.00000000 0.97560976 0.95348837 0.82417582 0.57692308 0.78021978
## 29 0.97777778 0.93939394 0.92233010 0.81481481 0.53719008 0.77777778
## 30 1.00000000 1.00000000 0.98095238 0.87272727 0.59349593 0.83636364
##                7          9         10         11         12         13
## 2
## 3
## 4
## 5
## 6
## 7
## 9  0.66666667
## 10 0.26666667 0.57142857
## 11 0.33333333 0.76000000 0.44000000
## 12 0.17647059 0.68750000 0.37500000 0.24137931
## 13 0.37142857 0.81818182 0.57575758 0.33333333 0.18918919
## 14 0.36363636 0.76190476 0.47619048 0.43589744 0.21739130 0.19148936
## 15 0.38775510 0.65957447 0.40425532 0.50000000 0.33333333 0.38461538
## 16 0.53571429 0.70370370 0.51851852 0.64705882 0.55172414 0.59322034
## 17 0.60000000 0.68965517 0.51724138 0.63636364 0.58064516 0.61904762
## 18 0.68965517 0.64285714 0.57142857 0.69811321 0.66666667 0.70491803
## 19 0.67741935 0.66666667 0.63333333 0.82456140 0.75000000 0.81538462
## 20 0.86111111 0.68571429 0.77142857 0.91044776 0.89189189 0.92000000
## 21 0.89743590 0.76315789 0.81578947 0.91780822 0.92500000 0.95061728
## 22 0.93181818 0.76744186 0.86046512 0.95180723 0.95555556 0.97802198
## 23 0.90000000 0.77777778 0.88888889 0.86666667 0.90909091 1.00000000
## 24 0.93548387 0.72413793 0.79310345 0.92307692 0.93939394 1.00000000
## 25 0.85185185 0.84000000 0.76000000 0.90909091 0.93103448 1.00000000
## 26 0.89830508 0.71929825 0.82456140 0.92592593 0.93442623 0.96774194
## 27 0.92405063 0.76623377 0.84415584 0.94594595 0.95061728 0.97560976
## 28 0.93023256 0.76190476 0.85714286 0.95061728 0.95454545 0.97752809
## 29 0.90291262 0.78217822 0.84158416 0.89795918 0.90476190 0.90566038
## 30 0.96190476 0.84466019 0.90291262 0.98000000 0.98130841 1.00000000
##               14         15         16         17         18         19
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15 0.24590164
## 16 0.44117647 0.26027397
## 17 0.50000000 0.40259740 0.26190476
## 18 0.60000000 0.46666667 0.34146341 0.13953488
## 19 0.67567568 0.56962025 0.39534884 0.31111111 0.25000000
## 20 0.83333333 0.70786517 0.58333333 0.42000000 0.32653061 0.23529412
## 21 0.86666667 0.76842105 0.62745098 0.49056604 0.40384615 0.29629630
## 22 0.90000000 0.77142857 0.66071429 0.55172414 0.47368421 0.38983051
## 23 0.93750000 0.94594595 0.90909091 0.83333333 0.82608696 0.84000000
```

```
## 24 0.90697674 0.87500000 0.81818182 0.69491525 0.64912281 0.63934426
## 25 0.84615385 0.81818182 0.76470588 0.74545455 0.66037736 0.61403509
## 26 0.85915493 0.76315789 0.63855422 0.54022989 0.45882353 0.32584270
## 27 0.89010989 0.77083333 0.66990291 0.57009346 0.48571429 0.37614679
## 28 0.89795918 0.78640777 0.69090909 0.57894737 0.50000000 0.41379310
## 29 0.84347826 0.73333333 0.65354331 0.51145038 0.44186047 0.41353383
## 30 0.93162393 0.81967213 0.72093023 0.57894737 0.52671756 0.48148148
##             20         21         22         23         24         25
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21 0.10169492
## 22 0.18750000 0.10447761
## 23 0.86666667 0.87878788 0.89473684
## 24 0.57746479 0.61038961 0.65517241 0.57894737
## 25 0.67164179 0.69863014 0.73493976 0.46666667 0.46153846
## 26 0.21212121 0.20000000 0.25217391 0.82978723 0.48275862 0.59259259
## 27 0.19327731 0.13600000 0.12592593 0.88059701 0.61538462 0.70270270
## 28 0.22222222 0.16666667 0.12676056 0.89189189 0.64705882 0.72839506
## 29 0.24475524 0.18120805 0.11949686 0.91208791 0.70588235 0.77551020
## 30 0.29655172 0.23178808 0.18012422 0.91397849 0.71153846 0.78000000
##             26         27         28         29
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
```

```
## 20
## 21
## 22
## 23
## 24
## 25
## 26
## 27 0.18867925
## 28 0.23893805 0.09774436
## 29 0.33846154 0.18666667 0.14649682
## 30 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 SÃ¸rensen or Bray-Curtis distance influence your interpretation of site (dis)similarity?

> *Answer 5a*: Dissimilarity; the value calculated for sites 1 and 2 is lower than the value calculated for sites 1 and 10. Previous comparison of these sites using Whittaker's beta diversity showed that sites 1 and 2 are more similar than sites 1 and 10. *Answer 5b*: Sorensen distance is based on incidence rather than abundance data, and produces lower values than Bray-Curtis distance. Since all species present at a site are given equal weight, the sites are interpreted as more similar than using Bray-Curtis distance.

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.

```
require(viridis)
```

```
## Loading required package: viridis
```

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

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

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Bray–Curtis Distance
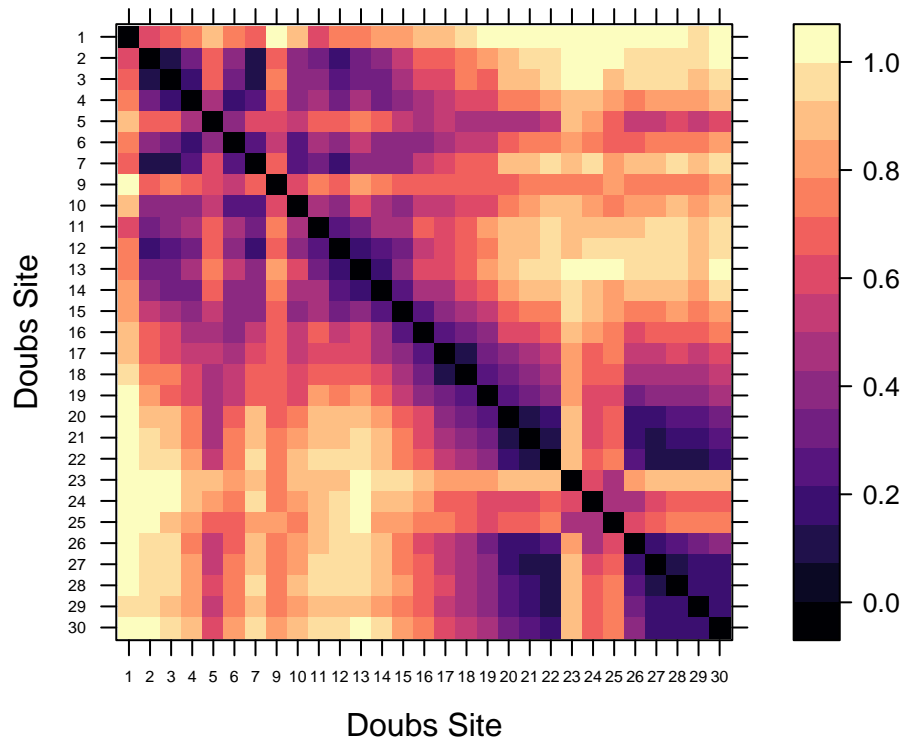
B. Cluster Analysis

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`).

```r
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-Curtis Distance")
```

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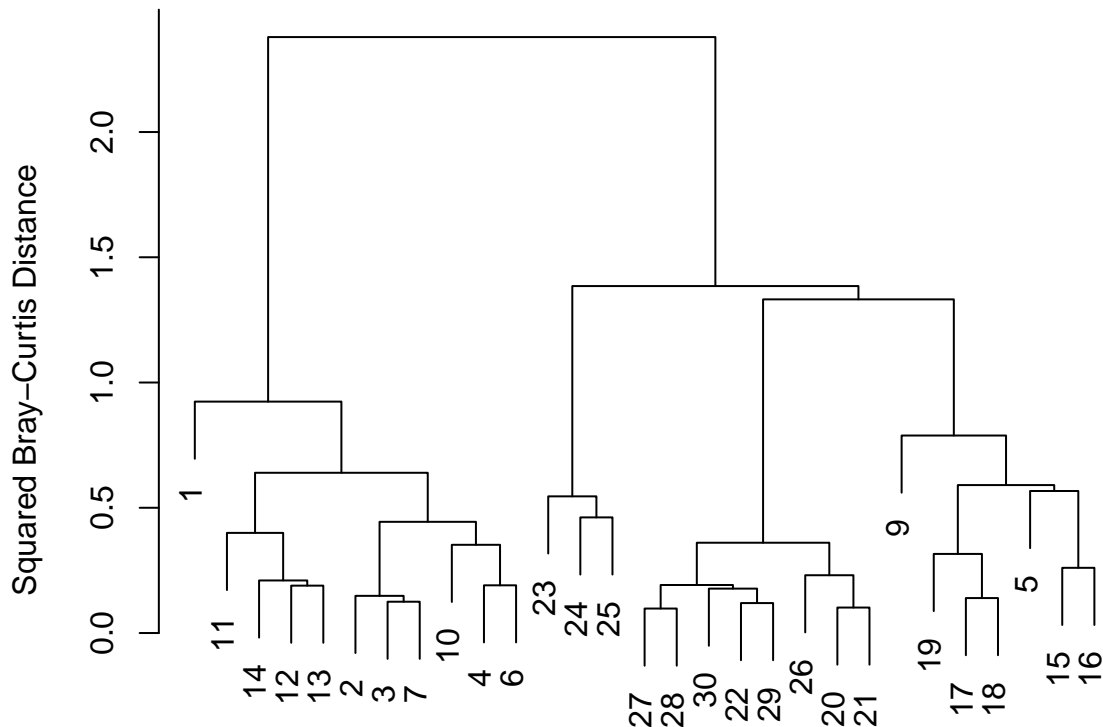
Question 6: Based on cluster analyses and the introductory plots that we generated after loading the data, develop an ecological hypothesis for fish diversity the `doubs` data set?

> **Answer 6**: Species diversity differs across sampling sites due to environmental factors.

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.

```
fish.pcoa <- cmdscale(fish.db, eig = TRUE, k =3)
explainvar1 <- round(fish.pcoa$eig[1] / sum(fish.pcoa$eig), 3) * 100
explainvar2 <- round(fish.pcoa$eig[2] / sum(fish.pcoa$eig), 3) * 100
explainvar3 <- round(fish.pcoa$eig[3] / sum(fish.pcoa$eig), 3) * 100
sum.eig <- sum(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 = 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(fish.pcoa$points[ ,1], fish.pcoa$points[ ,2],
    pch = 19, cex = 3, bg = "gray", col = "gray")
text(fish.pcoa$points[ ,1], fish.pcoa$points[ ,2],
    labels = row.names(fish.pcoa$points))
require("BiodiversityR")
```

```
## Loading required package: BiodiversityR
```

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

```
## BiodiversityR 2.11-1: Use command BiodiversityRGUI() to launch the Graphical User Interface;
## to see changes use BiodiversityRGUI(changeLog=TRUE, backward.compatibility.messages=TRUE)
```

```
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")
```
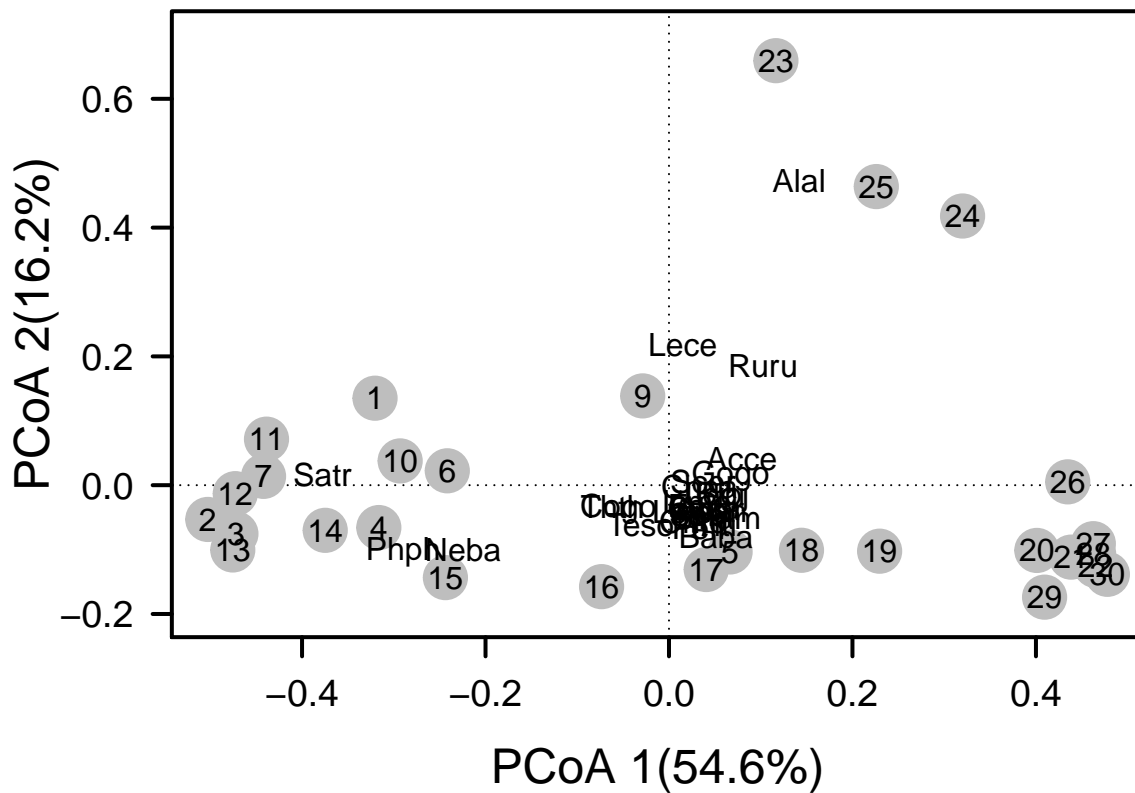
In the R code chunk below, do the following:

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, method = "cor.scores")$cproj
corrcut <- 0.7
imp.spp <- spe.corr[abs(spe.corr[, 1]) >= corrcut | abs(spe.corr[, 2]) >= corrcut, ]
fit <- envfit(fish.pcoa, fishREL, perm = 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***:
> ***Answer 7b***:

SYNTHESIS

Using the jelly bean data from class (i.e., JellyBeans.Source.txt and JellyBeans.txt):

1) Compare the average pairwise similarity among subsamples in group A to the average pairswise similarity among subsamples in group B. Use a t-test to determine whether compositional similarity was affected by the "vicariance" event. Finally, compare the compositional similarity of jelly beans in group A and group B to the source community?

2) Create a cluster diagram or ordination using the jelly bean data. Are there any visual trends that would suggest a difference in composition between group A and group B?

```
setwd("C:/Users/wolve/GitHub/QB2019_Crawley/2.Worksheets/6.DiversitySampling")
jellybeans <- read.table("JellyBeans.txt", sep = "\t", header = TRUE)
jellybeans.source <- read.table("JellyBeans.Source.txt", sep = "\t", header = TRUE)
jellybeans$GreenTrans <- c(1, 5, 5, 4, 7, 3, 4, 2, 4)
jellybeans$Rainbow <- c(2, 2, 1, 3, 1, 3, 1, 2, 0)
jellybeans.new <- jellybeans[ , -c(1, 2, 15, 30)]
jbsource.new <- t(jellybeans.source[-c(1, 2, 5)])

groupA <- jellybeans.new[c(1:3, 6, 8), ]
groupB <- jellybeans.new[c(4,5, 7, 9), ]
beta.w(groupA)
```

```
## [1] 1.182
```

```
beta.w(groupB)
```

```
## [1] 1.253
```

```
t.test(groupA, groupB)
```

```
##
##  Welch Two Sample t-test
##
## data:  groupA and groupB
## t = 0.48046, df = 229.63, p-value = 0.6314
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.6798338  1.1182953
## sample estimates:
## mean of x mean of y
##  2.969231  2.750000
```

```
beta.w(jbsource.new)
```

```
## Warning in decostand(site.by.species, method = "pa"): input data contains negative entries: result ma
```

```
## [1] 1.793
```

```
jellybeans.db <- vegdist(jellybeans.new, method = "bray")
jellybeans.ward <- hclust(jellybeans.db, method = "ward.D2")
par(mar = c(1, 5, 2, 2) + 0.1)
plot(jellybeans.ward, main = "Jellybean Counts: Ward's Clustering", ylab = "Squared Bray-Curtis Distance
```


Jellybean Counts: Ward's Clustering
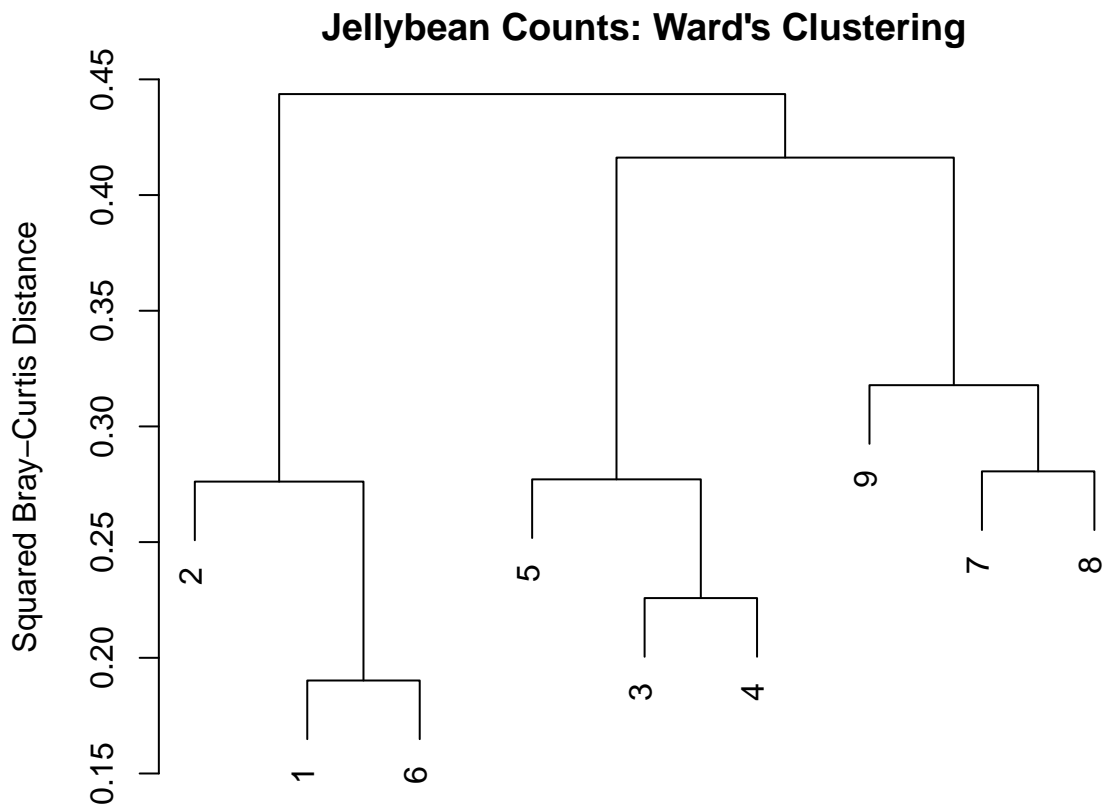
Cluster analysis indicates that samples from different groups are more similar in some cases than sites within the same group (i.e. 3 and 4, 7 and 8 clump together)