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

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01 February, 2023

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 '6.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 (**6.BetaDiversity_1_Worksheet.Rmd**) with all code blocks filled out and questions answered) and the PDF output of `Knitr` (**6.BetaDiversity_1_Worksheet.pdf**).

The completed exercise is due on **Wednesday, February 1st, 2023 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 "*/6.BetaDiversity*" folder, and
4. load the **vegan** R package (be sure to install if needed).

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

```
## [1] "/Users/annawerkowski/Documents/Github/QB2023_Werkowski/2.Worksheets/6.BetaDiversity"
```

```
setwd("~/Documents/Github/QB2023_Werkowski/2.Worksheets/6.BetaDiversity")
package.list <- c('vegan', 'ade4', 'viridis', 'gplots', 'BiodiversityR', 'indicspecies')
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
```

```
## BiodiversityR 2.15-1: Use command BiodiversityRGUI() to launch the Graphical User Interface;
## to see changes use BiodiversityRGUI(changeLog=TRUE, backward.compatibility.messages=TRUE)
```

```
`add.spec.scores.class` <-
  function(ordi,comm,method="cor.scores",multi=1,Rscale=F,scaling="1") {
    ordiscores <- scores(ordi,display="sites")
    n <- ncol(comm)
    p <- ncol(ordiscores)
    specscores <- array(NA,dim=c(n,p))
    rownames(specscores) <- colnames(comm)
    colnames(specscores) <- colnames(ordiscores)
    if (method == "cor.scores") {
      for (i in 1:n) {
        for (j in 1:p) {specscores[i,j] <- cor(comm[,i],ordiscores[,j],method="pearson")}
      }
    }
    if (method == "wa.scores") {specscores <- wascores(ordiscores,comm)}
    if (method == "pcoa.scores") {
      rownames(ordiscores) <- rownames(comm)
      eigenv <- ordi$eig
      accounted <- sum(eigenv)
      tot <- 2*(accounted/ordi$GOF[2])-(accounted/ordi$GOF[1])
      eigen.var <- eigenv/(nrow(comm)-1)
      neg <- length(eigenv[eigenv<0])
      pos <- length(eigenv[eigenv>0])
      tot <- tot/(nrow(comm)-1)
      eigen.percen <- 100*eigen.var/tot
      eigen.cumpercen <- cumsum(eigen.percen)
      constant <- ((nrow(comm)-1)*tot)^0.25
      ordiscores <- ordiscores * (nrow(comm)-1)^-0.5 * tot^-0.5 * constant
      p1 <- min(p, pos)
      for (i in 1:n) {
        for (j in 1:p1) {
          specscores[i,j] <- cor(comm[,i],ordiscores[,j])*sd(comm[,i])/sd(ordiscores[,j])
          if(is.na(specscores[i,j])) {specscores[i,j]<-0}
        }
      }
      if (Rscale==T && scaling=="2") {
        percen <- eigen.var/tot
        percen <- percen^0.5
        ordiscores <- sweep(ordiscores,2,percen,"/")
        specscores <- sweep(specscores,2,percen,"*")
      }
      if (Rscale==F) {
        specscores <- specscores / constant
        ordiscores <- ordi$points
      }
      ordi$points <- ordiscores
      ordi$eig <- eigen.var
      ordi$eig.percen <- eigen.percen
      ordi$eig.cumpercen <- eigen.cumpercen
      ordi$eigen.total <- tot
      ordi$R.constant <- constant
      ordi$Rscale <- Rscale
      ordi$scaling <- scaling
    }
    specscores <- specscores * multi
    ordi$cproj <- specscores
    return(ordi)
  }
```

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
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:
```

```
head(doubs$env)
```

```
##   dfs alt   slo flo pH har pho nit amm oxy bdo
## 1   3 934 6.176  84 79  45   1  20   0 122  27
## 2  22 932 3.434 100 80  40   2  20  10 103  19
## 3 102 914 3.638 180 83  52   5  22   5 105  35
## 4 185 854 3.497 253 80  72  10  21   0 110  13
## 5 215 849 3.178 264 81  84  38  52  20  80  62
## 6 324 846 3.497 286 79  60  20  15   0 102  53
```

```
doubs$species
```

```
##                     Scientific             French           English code
## 1                 Cottus gobio             chabot european bullhead Cogo
## 2           Salmo trutta fario       truite fario       brown trout Satr
## 3            Phoxinus phoxinus             vairon            minnow Phph
## 4       Nemacheilus barbatulus      loche franche       stone loach Neba
## 5          Thymallus thymallus              ombre          grayling Thth
## 6     Telestes soufia agassizi            blageon           blageon Teso
## 7           Chondrostoma nasus               hotu              nase Chna
## 8       Chondostroma toxostoma          toxostome         toxostoma Chto
## 9          Leuciscus leuciscus           vandoise       common dace Lele
## 10 Leuciscus cephalus cephalus           chevaine              chub Lece
## 11               Barbus barbus barbeau fluviatile            barbel Baba
## 12       Spirlinus bipunctatus            spirlin           spirlin Spbi
## 13                 Gobio gobio             goujon           gudgeon Gogo
## 14                 Esox lucius            brochet              pike Eslu
## 15           Perca fluviatilis  perche fluviatile             perch Pefl
## 16              Rhodeus amarus           bouviere        bitterling Rham
## 17            Lepomis gibbosus      perche-soleil       pumpkinseed Legi
## 18  Scardinius erythrophtalmus           rotengle              rudd Scer
## 19             Cyprinus carpio              carpe              carp Cyca
## 20                 Tinca tinca             tanche             tench Titi
## 21               Abramis brama              breme  freshwater bream Abbr
## 22             Ictalurus melas       poisson chat    black bullhead Icme
## 23              Acerina cernua           gremille             ruffe Acce
## 24             Rutilus rutilus             gardon             roach Ruru
## 25             Blicca bjoerkna   breme bordeliere      silver bream Blbj
## 26           Alburnus alburnus            ablette             bleak Alal
## 27           Anguilla anguilla           anguille               eel Anan
```

```
doubs$fish
```

```
##    Cogo Satr Phph Neba Thth Teso Chna Chto Lele Lece Baba Spbi Gogo Eslu Pefl
## 1     0    3    0    0    0    0    0    0    0    0    0    0    0    0    0
## 2     0    5    4    3    0    0    0    0    0    0    0    0    0    0    0
## 3     0    5    5    5    0    0    0    0    0    0    0    0    0    1    0
## 4     0    4    5    5    0    0    0    0    0    1    0    0    1    2    2
## 5     0    2    3    2    0    0    0    0    5    2    0    0    2    4    4
## 6     0    3    4    5    0    0    0    0    1    2    0    0    1    1    1
## 7     0    5    4    5    0    0    0    0    1    1    0    0    0    0    0
## 8     0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
## 9     0    0    1    3    0    0    0    0    0    5    0    0    0    0    0
## 10    0    1    4    4    0    0    0    0    2    2    0    0    1    0    0
## 11    1    3    4    1    1    0    0    0    0    1    0    0    0    0    0
## 12    2    5    4    4    2    0    0    0    0    1    0    0    0    0    0
## 13    2    5    5    2    3    2    0    0    0    0    0    0    0    0    0
## 14    3    5    5    4    4    3    0    0    0    1    1    0    1    1    0
## 15    3    4    4    5    2    4    0    0    3    3    2    0    2    0    0
## 16    2    3    3    5    0    5    0    4    5    2    2    1    2    1    1
## 17    1    2    4    4    1    2    1    4    3    2    3    4    1    1    2
## 18    1    1    3    3    1    1    1    3    2    3    3    3    2    1    3
## 19    0    0    3    5    0    1    2    3    2    1    2    2    4    1    1
## 20    0    0    1    2    0    0    2    2    2    3    4    3    4    2    2
## 21    0    0    1    1    0    0    2    2    2    2    4    2    5    3    3
## 22    0    0    0    1    0    0    3    2    3    4    5    1    5    3    4
## 23    0    0    0    0    0    0    0    0    0    1    0    0    0    0    0
## 24    0    0    0    0    0    0    1    0    0    2    0    0    1    0    0
## 25    0    0    0    0    0    0    0    0    1    1    0    0    2    1    0
## 26    0    0    0    1    0    0    1    0    1    2    2    1    3    2    1
## 27    0    0    0    1    0    0    1    1    2    3    4    1    4    4    1
## 28    0    0    0    1    0    0    1    1    2    4    3    1    4    3    2
## 29    0    1    1    1    1    1    2    2    3    4    5    3    5    5    4
## 30    0    0    0    0    0    0    1    2    3    3    3    5    5    4    5
##    Rham Legi Scer Cyca Titi Abbr Icme Acce Ruru Blbj Alal Anan
## 1     0    0    0    0    0    0    0    0    0    0    0    0
## 2     0    0    0    0    0    0    0    0    0    0    0    0
## 3     0    0    0    0    0    0    0    0    0    0    0    0
## 4     0    0    0    0    1    0    0    0    0    0    0    0
## 5     0    0    2    0    3    0    0    0    5    0    0    0
## 6     0    0    0    0    2    0    0    0    1    0    0    0
## 7     0    0    0    0    0    0    0    0    0    0    0    0
## 8     0    0    0    0    0    0    0    0    0    0    0    0
## 9     0    0    0    0    1    0    0    0    4    0    0    0
## 10    0    0    0    0    0    0    0    0    0    0    0    0
## 11    0    0    0    0    0    0    0    0    0    0    0    0
## 12    0    0    0    0    0    0    0    0    0    0    0    0
## 13    0    0    0    0    0    0    0    0    0    0    0    0
## 14    0    0    0    0    0    0    0    0    0    0    0    0
## 15    0    0    0    0    1    0    0    0    0    0    0    0
## 16    0    1    0    1    1    0    0    0    1    0    0    0
## 17    1    1    0    1    1    0    0    0    2    0    2    1
## 18    2    1    0    1    1    0    0    1    2    0    2    1
## 19    2    1    1    1    2    1    0    1    5    1    3    1
## 20    3    2    2    1    4    1    0    2    5    2    5    2
## 21    3    2    2    2    4    3    1    3    5    3    5    2
## 22    3    3    2    3    4    4    2    4    5    4    5    2
## 23    0    0    0    0    0    0    0    0    1    0    2    0
## 24    0    1    0    0    0    0    0    2    2    1    5    0
## 25    0    0    1    0    0    0    0    1    1    0    3    0
## 26    2    2    1    1    3    2    1    4    4    2    5    2
## 27    3    3    1    2    5    3    2    5    5    4    5    3
## 28    4    4    2    4    4    3    3    5    5    5    5    4
## 29    5    5    2    3    3    4    4    5    5    4    5    4
## 30    5    3    5    5    5    5    5    5    5    5    5    5
```

```
doubs$xy
```

```
##      x   y
## 1   88   7
## 2   94  14
## 3  102  18
## 4  100  28
## 5  106  39
## 6  112  51
## 7  114  61
## 8  110  76
## 9  136 100
## 10 168 112
## 11 186 130
## 12 205 145
## 13 222 167
## 14 228 182
## 15 252 190
## 16 266 209
## 17 245 203
## 18 225 200
## 19 206 194
## 20 189 193
## 21 187 201
## 22 192 212
## 23 192 228
## 24 179 233
## 25 145 217
## 26  91 187
## 27  65 174
## 28  49 164
## 29  27 151
## 30   8 133
```

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***: There are 4 objects - env, fish, xy, and species. ***Answer 1b***: There are 27 fish species. ***Answer 1c***: There are 30 sites.

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***: The further downstream the fish are sampled, the higher the richness is. ***Answer 2b***: There is a higher abundance of Brown Trout in the upstream portion of the stream. ***Answer 2c***: This indicates that there is not a positive correlation between the richness of the stream and the abundance of Brown Trout. These patterns show that we cannot only depend on richness values to tell us everything about a sample site.

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.

```r
beta.w <- function(site.by.species = ""){
  SbyS.pa <- decostand(site.by.species, method = "pa")
  #convert to presence-absence
  S <- ncol(SbyS.pa[, which(colSums(SbyS.pa) > 0)])
  #number of species in the region
  a.bar <- mean(specnumber(SbyS.pa))
  #average richness at each site
  b.w <- round(S/a.bar, 3)
  #round to 3 decimal places
  return(b.w)
}


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 = base::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)
  }
}

#in order to also look at alpha diversity, create the observed richness function
S.obs <- function(x = ""){
  rowSums(x > 0) * 1
}
#creating subsets of the Doubs dataset for easier access
fish <- doubs$fish
location <- doubs$xy
species <- doubs$species
enviro <- doubs$env
#using the beta.w function created above to see the results

beta.w(fish,1,2,pairwise=TRUE) #value is 0.5
```

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

```
beta.w(fish,1,10,pairwise = TRUE) #value is 0.714
```

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

```
beta.w(fish,2,10,pairwise = TRUE) #value is 0.333
```

```
## [1] 0.333
```

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: Both local richness (alpha diversity) and turnover (beta diversity) are part of the regional makeup (gamma diversity) in the Doubs. Alpha diversity is observed at the local site level, Beta diversity is observed at the regional level, and Gamma diversity is observed on the global level. Like Russian nesting dolls, all of the levels are part of each other and contribute to the larger picture. ***Answer 3b***: The fish assemblage at site 1 is more similar to those at site 10 because when the beta value was calculated, the comparison between 1&2 was 0.5 while 1&10 was 0.714. Since this value is closer to 1.0, it shows that they have more overlap than the other two sites. ***Answer 3c***: If you defined beta additively, then you would be evaluating turnover between two sites, a combined richness of the two sites being compared. The normal multiplicative model quantifies how many times more diverse the regional species pool is than the average richness at each site within the region.

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***: Incidence based metrics place emphasis on species that are shared or not shared between sites. Abundance-based metrics place emphasis on overall sample differences.

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").

```r
fish <- doubs$fish
fish <- fish[-8, ]
fish.dj <- vegdist(fish, method = "jaccard", binary = TRUE) #jaccard calculation
fish.db <- vegdist(fish, method = "bray") #bray-curtis calculation
fish.ds <- vegdist(fish, method = "bray", binary = TRUE) #sorenson calculation
print(fish.ds) #construct a resemblance matrix based on sorenson
```

```
##             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
## 4
## 5
## 6
## 7
## 9
## 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
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 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", upper = TRUE, diag = TRUE)
print(fish.db) #construct a resemblance matrix based on bray-curtis
```

```
##             1          2          3          4          5          6          7
## 1  0.00000000 0.60000000 0.68421053 0.75000000 0.89189189 0.75000000 0.68421053
## 2  0.60000000 0.00000000 0.14285714 0.33333333 0.69565217 0.39393939 0.14285714
## 3  0.68421053 0.14285714 0.00000000 0.18918919 0.68000000 0.29729730 0.12500000
## 4  0.75000000 0.33333333 0.18918919 0.00000000 0.49090909 0.19047619 0.24324324
## 5  0.89189189 0.69565217 0.68000000 0.49090909 0.00000000 0.41818182 0.64000000
## 6  0.75000000 0.39393939 0.29729730 0.19047619 0.41818182 0.00000000 0.24324324
## 7  0.68421053 0.14285714 0.12500000 0.24324324 0.64000000 0.24324324 0.00000000
## 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
## 1  1.00000000 0.88235294 0.57142857 0.71428571 0.72727273 0.80645161 0.83333333
## 2  0.69230769 0.38461538 0.30434783 0.20000000 0.29032258 0.40000000 0.51111111
## 3  0.73333333 0.40000000 0.40740741 0.23529412 0.31428571 0.31818182 0.46938776
## 4  0.65714286 0.37142857 0.43750000 0.33333333 0.45000000 0.34693878 0.40740741
## 5  0.58333333 0.54166667 0.68888889 0.69230769 0.73584906 0.67741935 0.55223881
## 6  0.54285714 0.25714286 0.43750000 0.38461538 0.55000000 0.42857143 0.37037037
## 7  0.66666667 0.26666667 0.33333333 0.17647059 0.37142857 0.36363636 0.38775510
## 9  0.00000000 0.57142857 0.76000000 0.68750000 0.81818182 0.76190476 0.65957447
## 10 0.57142857 0.00000000 0.44000000 0.37500000 0.57575758 0.47619048 0.40425532
## 11 0.76000000 0.44000000 0.00000000 0.24137931 0.33333333 0.43589744 0.50000000
## 12 0.68750000 0.37500000 0.24137931 0.00000000 0.18918919 0.21739130 0.33333333
## 13 0.81818182 0.57575758 0.33333333 0.18918919 0.00000000 0.19148936 0.38461538
## 14 0.76190476 0.47619048 0.43589744 0.21739130 0.19148936 0.00000000 0.24590164
## 15 0.65957447 0.40425532 0.50000000 0.33333333 0.38461538 0.24590164 0.00000000
## 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
## 1  0.86046512 0.91489362 0.95555556 1.00000000 1.00000000 1.00000000 1.00000000
## 2  0.65384615 0.67857143 0.74074074 0.79310345 0.91176471 0.94594595 0.97619048
## 3  0.57142857 0.63333333 0.72413793 0.70967742 0.88888889 0.92307692 0.95454545
## 4  0.47540984 0.50769231 0.58730159 0.61194030 0.74025974 0.78313253 0.82795699
## 5  0.45945946 0.51282051 0.50000000 0.50000000 0.48888889 0.50000000 0.52830189
## 6  0.37704918 0.44615385 0.52380952 0.52238806 0.68831169 0.73493976 0.78494624
## 7  0.53571429 0.60000000 0.68965517 0.67741935 0.86111111 0.89743590 0.93181818
## 9  0.70370370 0.68965517 0.64285714 0.66666667 0.68571429 0.76315789 0.76744186
## 10 0.51851852 0.51724138 0.57142857 0.63333333 0.77142857 0.81578947 0.86046512
## 11 0.64705882 0.63636364 0.69811321 0.82456140 0.91044776 0.91780822 0.95180723
## 12 0.55172414 0.58064516 0.66666667 0.75000000 0.89189189 0.92500000 0.95555556
## 13 0.59322034 0.61904762 0.70491803 0.81538462 0.92000000 0.95061728 0.97802198
## 14 0.44117647 0.50000000 0.60000000 0.67567568 0.83333333 0.86666667 0.90000000
## 15 0.26027397 0.40259740 0.46666667 0.56962025 0.70786517 0.76842105 0.77142857
## 16 0.00000000 0.26190476 0.34146341 0.39534884 0.58333333 0.62745098 0.66071429
## 17 0.26190476 0.00000000 0.13953488 0.31111111 0.42000000 0.49056604 0.55172414
## 18 0.34146341 0.13953488 0.00000000 0.25000000 0.32653061 0.40384615 0.47368421
## 19 0.39534884 0.31111111 0.25000000 0.00000000 0.23529412 0.29629630 0.38983051
## 20 0.58333333 0.42000000 0.32653061 0.23529412 0.00000000 0.10169492 0.18750000
## 21 0.62745098 0.49056604 0.40384615 0.29629630 0.10169492 0.00000000 0.10447761
## 22 0.66071429 0.55172414 0.47368421 0.38983051 0.18750000 0.10447761 0.00000000
## 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
## 1  1.00000000 1.00000000 1.00000000 1.00000000 1.00000000 1.00000000 0.97777778
## 2  1.00000000 1.00000000 1.00000000 0.96363636 0.97333333 0.97560976 0.93939394
## 3  1.00000000 1.00000000 0.92592593 0.93220339 0.94936709 0.95348837 0.92233010
## 4  0.92000000 0.88888889 0.81250000 0.78125000 0.83333333 0.82417582 0.81481481
## 5  0.89473684 0.79591837 0.68888889 0.55844156 0.56701031 0.57692308 0.53719008
## 6  0.84000000 0.77777778 0.68750000 0.68750000 0.76190476 0.78021978 0.77777778
## 7  0.90000000 0.93548387 0.85185185 0.89830508 0.92405063 0.93023256 0.90291262
## 9  0.77777778 0.72413793 0.84000000 0.71929825 0.76623377 0.76190476 0.78217822
## 10 0.88888889 0.79310345 0.76000000 0.82456140 0.84415584 0.85714286 0.84158416
## 11 0.86666667 0.92307692 0.90909091 0.92592593 0.94594595 0.95061728 0.89795918
## 12 0.90909091 0.93939394 0.93103448 0.93442623 0.95061728 0.95454545 0.90476190
## 13 1.00000000 1.00000000 1.00000000 0.96774194 0.97560976 0.97752809 0.90566038
## 14 0.93750000 0.90697674 0.84615385 0.85915493 0.89010989 0.89795918 0.84347826
## 15 0.94594595 0.87500000 0.81818182 0.76315789 0.77083333 0.78640777 0.73333333
## 16 0.90909091 0.81818182 0.76470588 0.63855422 0.66990291 0.69090909 0.65354331
## 17 0.83333333 0.69491525 0.74545455 0.54022989 0.57009346 0.57894737 0.51145038
## 18 0.82608696 0.64912281 0.66037736 0.45882353 0.48571429 0.50000000 0.44186047
## 19 0.84000000 0.63934426 0.61403509 0.32584270 0.37614679 0.41379310 0.41353383
## 20 0.86666667 0.57746479 0.67164179 0.21212121 0.19327731 0.22222222 0.24475524
## 21 0.87878788 0.61038961 0.69863014 0.20000000 0.13600000 0.16666667 0.18120805
## 22 0.89473684 0.65517241 0.73493976 0.25217391 0.12592593 0.12676056 0.11949686
## 23 0.00000000 0.57894737 0.46666667 0.82978723 0.88059701 0.89189189 0.91208791
## 24 0.57894737 0.00000000 0.46153846 0.48275862 0.61538462 0.64705882 0.70588235
## 25 0.46666667 0.46153846 0.00000000 0.59259259 0.70270270 0.72839506 0.77551020
## 26 0.82978723 0.48275862 0.59259259 0.00000000 0.18867925 0.23893805 0.33846154
## 27 0.88059701 0.61538462 0.70270270 0.18867925 0.00000000 0.09774436 0.18666667
## 28 0.89189189 0.64705882 0.72839506 0.23893805 0.09774436 0.00000000 0.14649682
## 29 0.91208791 0.70588235 0.77551020 0.33846154 0.18666667 0.14649682 0.00000000
## 30 0.91397849 0.71153846 0.78000000 0.36363636 0.19736842 0.15723270 0.14772727
##            30
## 1  1.00000000
## 2  1.00000000
## 3  0.98095238
## 4  0.87272727
## 5  0.59349593
## 6  0.83636364
## 7  0.96190476
## 9  0.84466019
## 10 0.90291262
## 11 0.98000000
## 12 0.98130841
## 13 1.00000000
## 14 0.93162393
## 15 0.81967213
## 16 0.72093023
## 17 0.57894737
## 18 0.52671756
## 19 0.48148148
## 20 0.29655172
## 21 0.23178808
## 22 0.18012422
## 23 0.91397849
## 24 0.71153846
## 25 0.78000000
## 26 0.36363636
## 27 0.19736842
## 28 0.15723270
## 29 0.14772727
## 30 0.00000000
```

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***: I believe that the Bray-Curtis resemblance matrix represents more similarity in the data. I reason I believe this to be so is because the print out not only shows a full square of values, but in the heatmap that was created down below, the color values reflect that. ***Answer 5b***: Well, Sorenson and Bray-Curtis are quite similar aside from the fact that Bray-Curtis is a quantitative version of Sorenson. Based on the fact that Bray-Curtis is more quantitative, I would be influnced to trust the results of that distance more than the other.

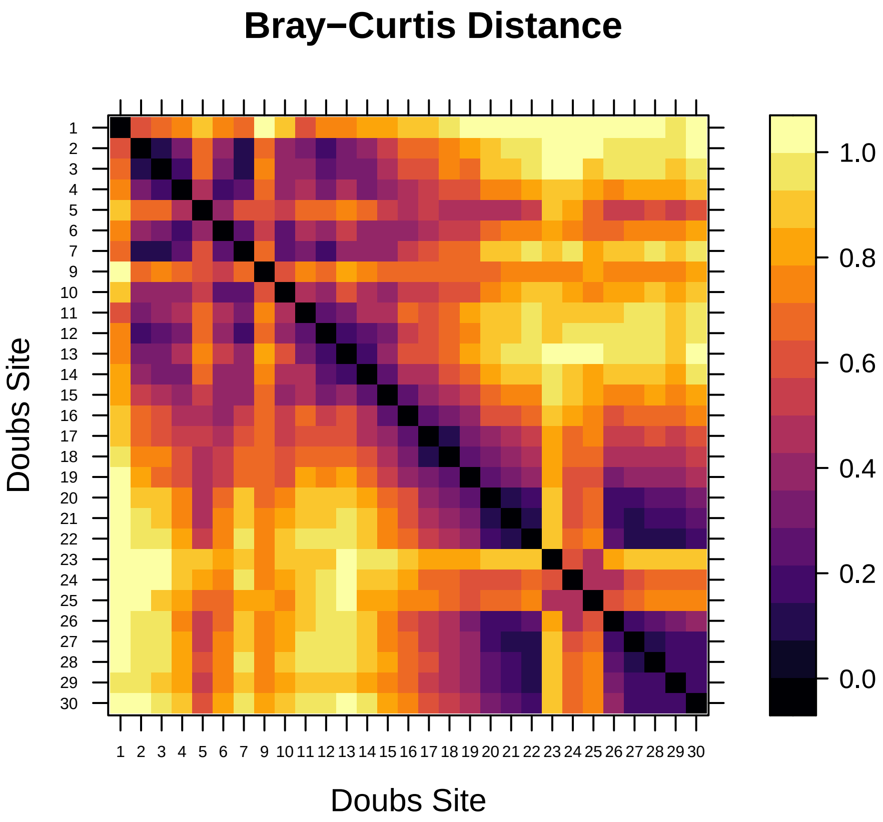
4) VISUALIZING BETA-DIVERSITY

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.

```
order <- rev(attr(fish.db, "Labels")) #define order of sites
levelplot(as.matrix(fish.db)[, order], aspect = "iso", col.regions = inferno, xlab ="Doubs Site", ylab =
```

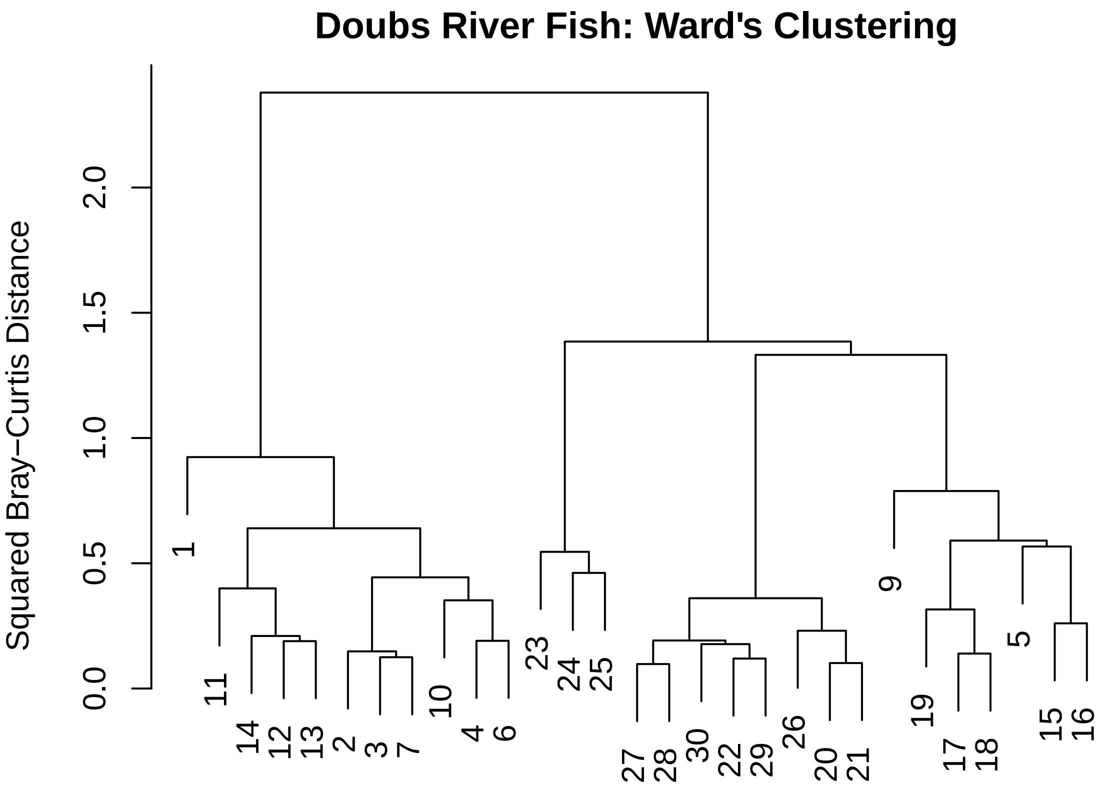


B. Cluster Analysis

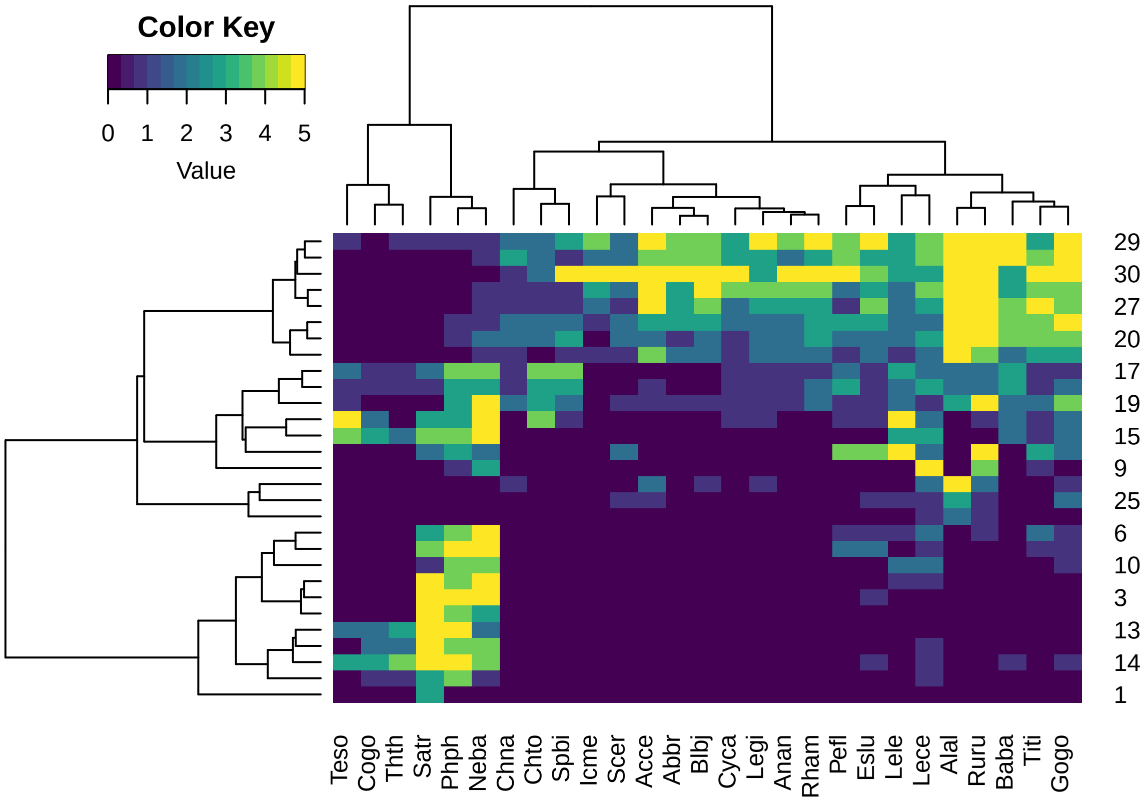
In the R code chunk below, do the following:

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") #perform cluster analysis
par(mar = c(1, 5, 2, 2) + 0.1)
plot(fish.ward, main = "Doubs River Fish: Ward's Clustering", ylab = "Squared Bray-Curtis Distance")
```



```
gplots::heatmap.2(as.matrix(fish), distfun = function(x)  vegdist(x, method = "bray"), hclustfun = func
```



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***: Fish that have a shorter Bray-Curtis distance will be more diverse than those with a higher Bray-Curtis distance.

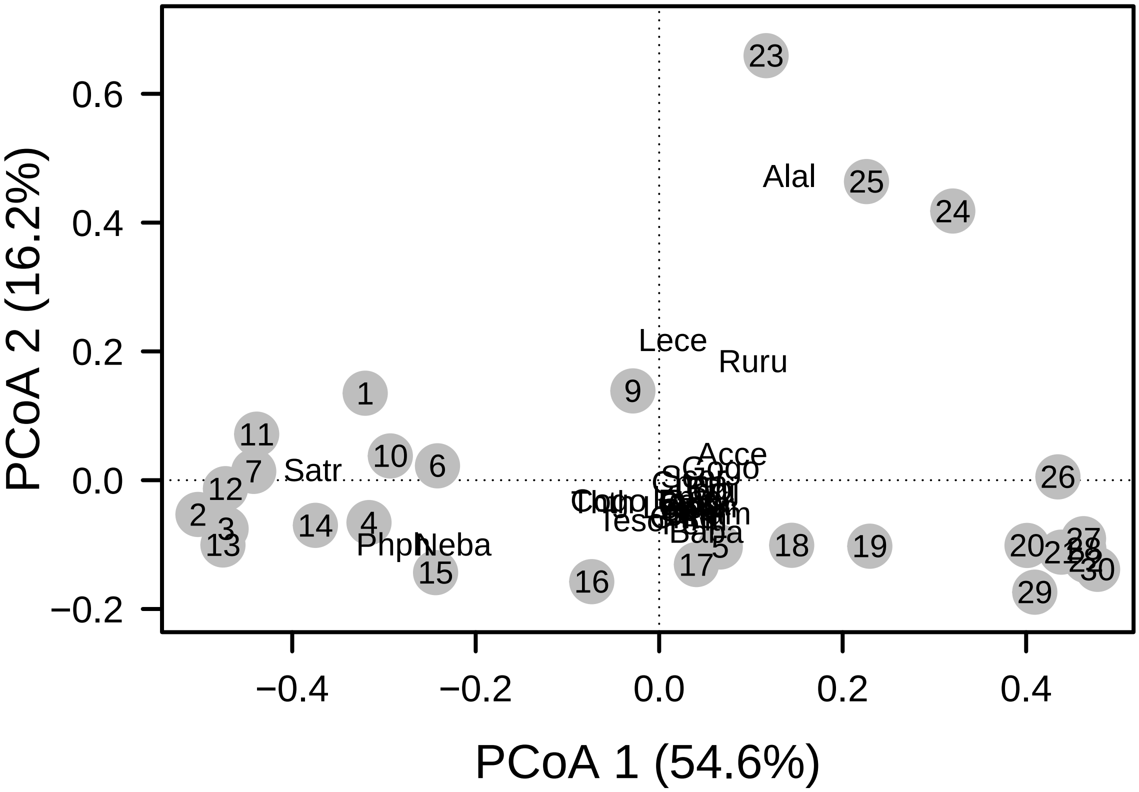
C. Ordination

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.

```r
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)
#define plot parameters
par(mar = c(5, 5, 1, 2) + 0.1)
#initiate plot
plot(fish.pcoa$points[ ,1], fish.pcoa$points[ ,2], ylim = c(-0.2, 0.7), xlab = paste("PCoA 1 (", explai
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$points))
fishREL <- fish
for (i in 1:nrow(fish)){
  fishREL[i, ] = fish[i, ] / sum(fish[i, ])
}
fish.pcoa <- add.spec.scores.class(fish.pcoa, fishREL, method = "pcoa.scores")
text(fish.pcoa$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.class(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***: Sites with higher fish community composition were found in the lower right-hand quadrant of the graph, ranging between the 0.0 and 0.4 values on the PCoA 1 axis. Nearly all of the sites were clustered between the 0.0 and -0.2 values on the PCoA 2 axis, making the two bottom quadrants the most populated. ***Answer 7b***: Due to their skewness from the other fish species/sites, the Alal species would most likely be a good potential indicator of river quality.

SYNTHESIS

Load the dataset from that you and your partner are using for the team project. Use one of the tools introduced in the beta diversity module to visualize your data. Describe any interesting patterns and identify a hypothesis is relevant to the principles of biodiversity.

```
#this is actively being worked on - John and Canan can vouch for me!
```