6. 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, **push** this file to your GitHub repo.
6. For the assignment portion of the worksheet, follow the directions at the bottom of this file.
7. When you are done, **Knit** the text and code into a PDF file.
8. After Knitting, submit the completed exercise by creating a **pull request** via GitHub. Your pull request should include this file (**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 5$^{\text{th}}$, 2025 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, please provide the code to:

1) Clear your R environment,
2) Print your current working directory,
3) Set your working directory to your `Week3-Beta/` folder folder, and
4) Load the `vegan` R package (be sure to install first if you have not already).

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

```
## [1] "/cloud/project/QB2025_Park/Week3-Beta"
```

```r
setwd("/cloud/project/QB2025_Park/Week3-Beta")

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 2.6-8

##
## Attaching package: 'gplots'

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

## Warning in fun(libname, pkgname): couldn't connect to display ":0"

## BiodiversityR 2.17-1.1: Use command BiodiversityRGUI() to launch the Graphical User Interface;
## to see changes use BiodiversityRGUI(changeLog=TRUE, backward.compatibility.messages=TRUE)
```

```r
#install.packages("Rcmdr", dependencies = TRUE)
```

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.

```r
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:
```

```r
print(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
```

```r
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
```

```r
head(doubs$xy)
```

```
##     x  y
## 1  88  7
## 2  94 14
## 3 102 18
## 4 100 28
## 5 106 39
## 6 112 51
```

```r
print(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
```

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***: 26 ***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***: Fish richness is much higher in the bend and downstream of the Doubs River. ***Answer 2b***: Brown trout abundance is higher upstream. ***Answer 2c***: Even though richness is generally higher downstream, brown trout populations do not reflect the same pattern. This indicates that while richness tells us how diverse specific sites are, it lacks important details about abundance or distribution of species.

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){
      # Pairwise beta diversity
      site1=site.by.species[sitenum1,]
      site2=site.by.species[sitenum2,]
      # Remove absences
      site1=subset(site1, select=site1>0)
      site2=subset(site2, select=site2>0)

      gamma=union(colnames(site1), colnames(site2))
      # Gamma species pool
      s=length(gamma)
      # Gamma richness
      a.bar=mean(c(specnumber(site1), specnumber(site2)))
      # Mean sample richness
      b.w=round(s/a.bar-1, 3)
      return(b.w)
    }

  # OTHERWISE pairwise defaults to FALSE, so do this, like before:
  else{
      SbyS.pa<-decostand(site.by.species, method="pa")
      # Presence-absence
      S<-ncol(SbyS.pa[,which(colSums(SbyS.pa)>0)])
      # Number of species in region
      a.bar<-mean(specnumber(SbyS.pa))
      # Avg richness per site
      b.w<-round(S/a.bar, 3)
      return(b.w)
```

```
  }
}

beta.w(doubs$fish, sitenum1 = 1, sitenum2 = 2, pairwise = TRUE)
```

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

```
beta.w(doubs$fish, sitenum1 = 1, sitenum2 = 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***: Alpha diversity encompasses the richness and evenness of a single site, while beta diversity compares diversity between different sites. Both of these contribute to gamma diversity of the entire region, indicating species distribution and variance between different locations. ***Answer 3b***: Site 1 is more similar to site 2, indicated by the lower beta diversity (low turnover). ***Answer 3c***: If we do it additively, we would get an absolute number of species not shared between sites on average, while the multiplicative definition shows how much of the gamma diversity compares to the average diversity at each site, giving us an idea of the proportion of species rather than a direct number of species difference.

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 metrics give equal weight to rare species, treating all species as the same (since it's based only on presence-absence). Abundance-based metrics considers the number of individuals of each species, giving less weight to rare species.

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,]

#Sorensen, incidence based
fish.ds<-vegdist(fish, method="bray", binary=TRUE)

#Bray-Curtis, abundance based
fish.db<-vegdist(fish, method="bray")

print(fish.ds)
```

```
##            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
```

```r
print(fish.db)
```

```
##             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
## 4
## 5
## 6
## 7
## 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
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 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
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
```

```
## 16
## 17
## 18
## 19
## 20
## 21
## 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 0 is completely similar and 1 is dissimilar. We can tell because the matrix compares every site to every site and the diagonals where one site would be compared to itself are 0. ***Answer 5b***: They're both really similar, but the Bray-Curtis values are a little higher, potentially indicating that just the presence of rare species is contributing to the higher dissimilarity of the Sorensen matrix. Removing the weight of these rare species allows us to get a more inclusive view of how rare species in one site may contribute more to a different site.

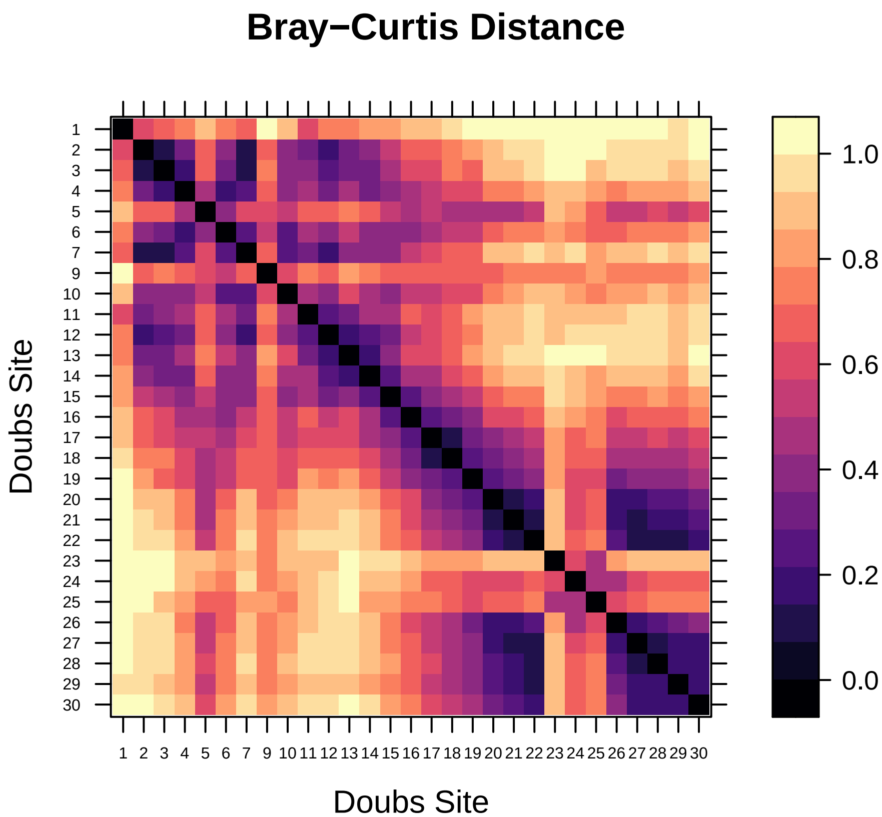
4) VISUALIZING BETA-DIVERSITY

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"))
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")
```

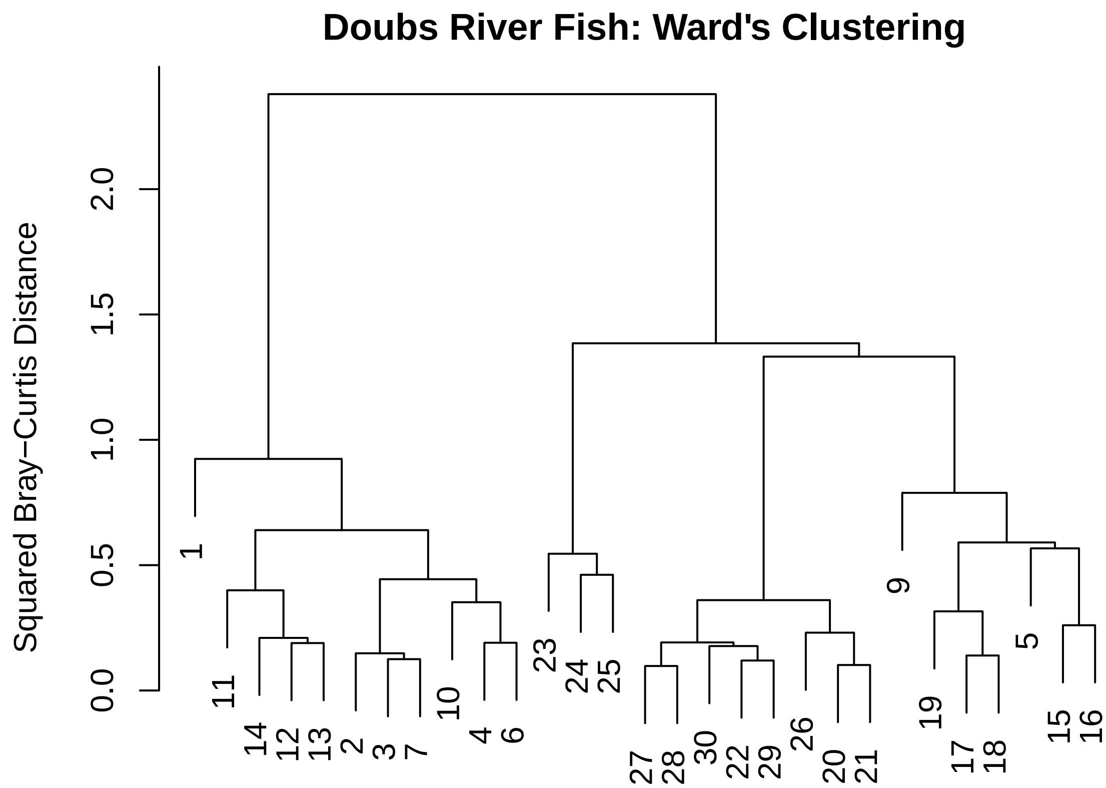


B. Cluster Analysis

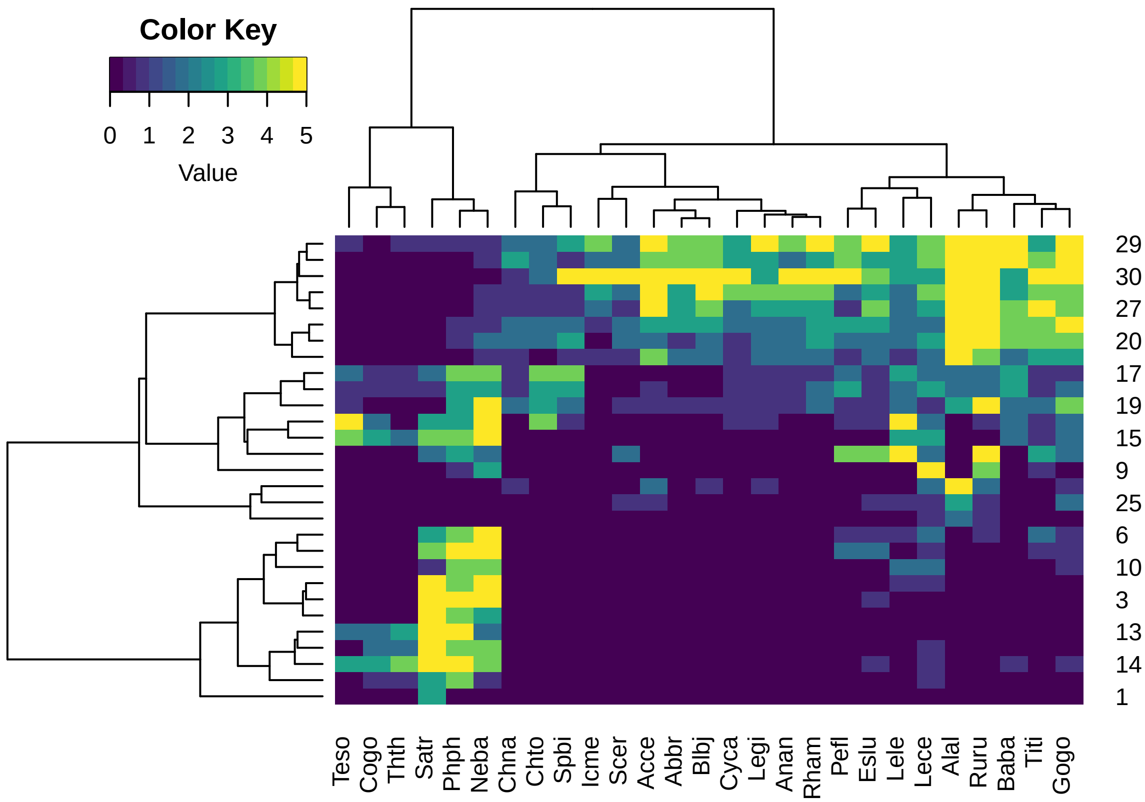
In the R code chunk below, do the following:

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-Curtis Distance")
```




```
gplots::heatmap.2(as.matrix(fish),
          distfun=function(x) vegdist(x, method="bray"),
          hclustfun=function(x) hclust(x, method="ward.D2"),
          col=viridis, trace="none", density.info="none")
```



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***:

C. Ordination

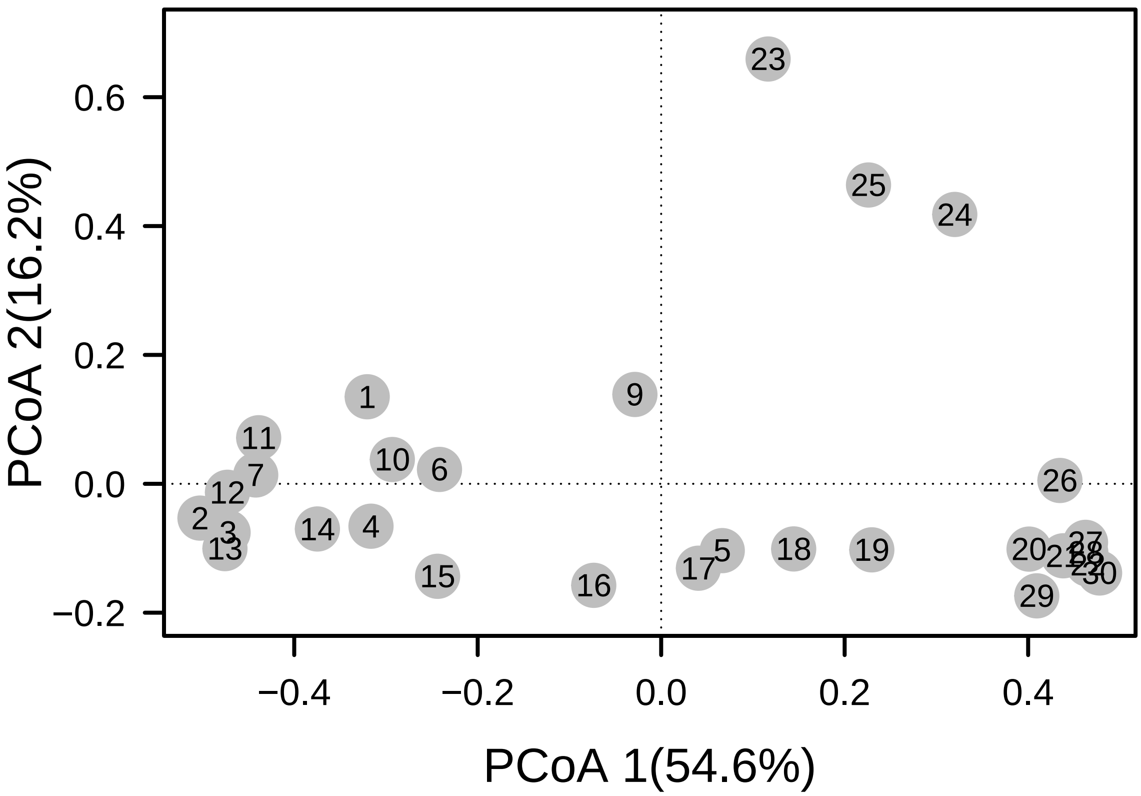
Principal Coordinates Analysis (PCoA)

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)

# Plot
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)
```

```r
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))
```



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.

```r
require("vegan")
fishREL<-fish
  for(i in 1:nrow(fish)){
  fishREL[i,]=fish[i,]/sum(fish[i,])
}
fish.pcoa1 <- add.spec.scores.class(fish.pcoa,fishREL, method = "pcoa.scores")
#text(fish.pcoa1$cproj[,1], fish.pcoa1$cproj[,2],
#     labels = row.names(fish.pcoa1$cproj), col = "black")

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

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.

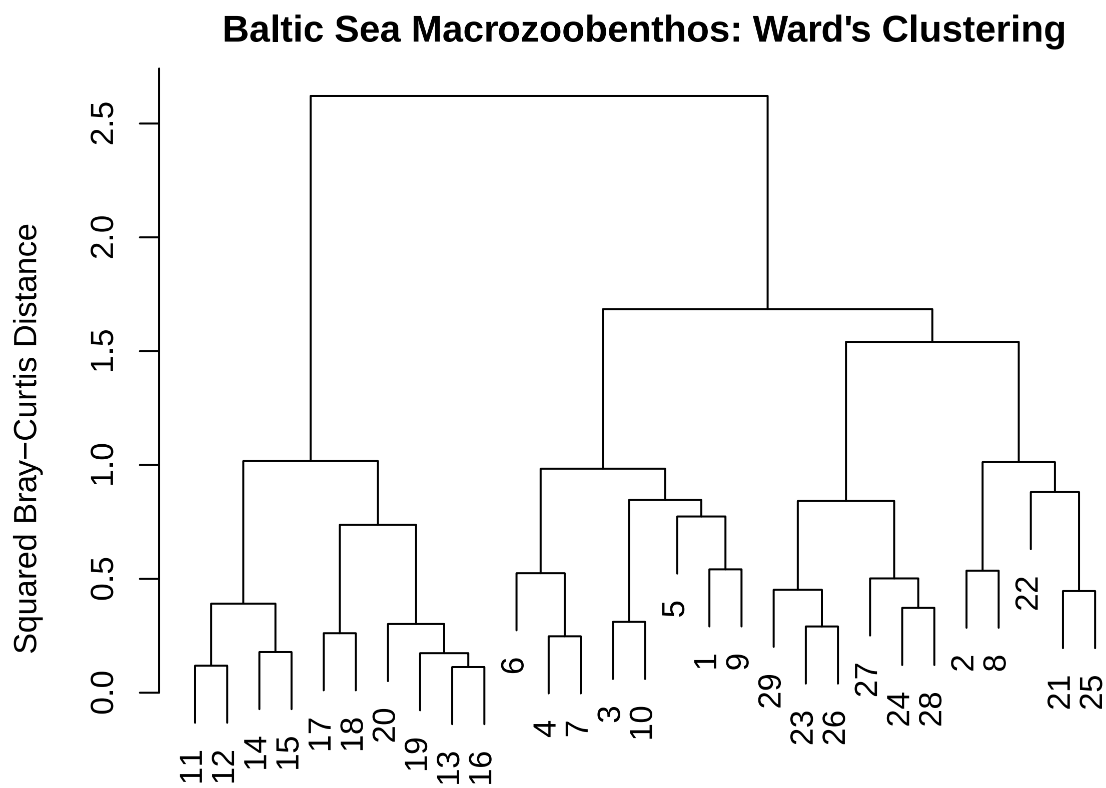
```
MZB<-read.csv("SbS_full.csv")
mzb<-MZB[,-1]

mzb.db<-vegdist(mzb, method="bray")
print(mzb.db)
```

```
##            1         2         3         4         5         6         7
## 2  0.7667699
## 3  0.6264179 0.8818363
## 4  0.6354009 0.8881789 0.4202515
## 5  0.7559932 0.7254005 0.7271788 0.5920055
## 6  0.8039272 0.9531479 0.7125317 0.4959957 0.8034800
## 7  0.6555922 0.8943974 0.5064302 0.2477268 0.6116707 0.4446378
## 8  0.9135317 0.5360502 0.9344123 0.9343843 0.7852162 0.9713586 0.9337349
## 9  0.5417559 0.7777778 0.7119228 0.7793864 0.6884343 0.9047944 0.8130646
## 10 0.6261735 0.8626400 0.3111220 0.5751041 0.8033456 0.7980401 0.6540168
## 11 0.9713631 0.9901487 0.9638752 0.9627776 0.9905001 0.9766320 0.9711712
## 12 0.9766465 0.9915759 0.9077471 0.9215659 0.9918342 0.9575437 0.9511928
## 13 0.9569632 0.9793654 0.9508792 0.9508723 0.9841012 0.9764938 0.9666760
## 14 0.9691172 0.9858194 0.9661195 0.9644323 0.9898387 0.9815454 0.9753165
## 15 0.9738606 0.9897297 0.9206478 0.9164305 0.9901110 0.9525769 0.9436963
## 16 0.9630643 0.9758322 0.9625877 0.9575928 0.9778428 0.9825048 0.9740260
## 17 0.9766731 0.9719495 0.9716891 0.9673626 0.9818683 0.9957907 0.9937259
## 18 0.9473517 0.9396807 0.9478495 0.9429954 0.9636190 0.9844288 0.9713203
## 19 0.9709771 0.9784810 0.9686808 0.9666076 0.9852083 0.9878701 0.9822090
## 20 0.9521587 0.9711957 0.9499037 0.9477926 0.9769495 0.9787725 0.9672823
## 21 0.9495413 0.7588652 0.9671138 0.9645022 0.8970588 0.9878558 0.9720157
## 22 0.9746690 0.8836364 0.9835069 0.9834998 0.9435364 0.9939198 0.9859649
## 23 0.8410405 0.8534202 0.7548241 0.8046934 0.8695652 0.9232417 0.7983963
## 24 0.8417330 0.8425000 0.7589254 0.8422914 0.8898164 0.9429855 0.8424242
## 25 0.9366516 0.7581699 0.9417559 0.9468723 0.8664773 0.9799773 0.9567287
## 26 0.8301983 0.7900990 0.7924230 0.7962890 0.8560354 0.9260877 0.8270916
## 27 0.9103178 0.8850299 0.8058659 0.8847363 0.8961882 0.9670273 0.8915493
## 28 0.8433420 0.8923445 0.7221640 0.7716480 0.8735818 0.9175824 0.8106301
## 29 0.8408644 0.7944251 0.7618133 0.7601845 0.7942387 0.9097447 0.8045754
##            8         9        10        11        12        13        14
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9  0.8826816
## 10 0.9388186 0.6024490
```

```
## 11 0.9981137 0.9826118 0.9622274
## 12 0.9983905 0.9804314 0.9035311 0.1187300
## 13 0.9959839 0.9732562 0.9499553 0.3891447 0.4365576
## 14 0.9969937 0.9819614 0.9639859 0.3468101 0.3604331 0.2185234
## 15 0.9978355 0.9779810 0.9166246 0.2314487 0.2196362 0.3520224 0.1785219
## 16 0.9947978 0.9615304 0.9567332 0.4647580 0.5116716 0.1126340 0.2783487
## 17 0.9889001 0.9668770 0.9671690 0.7179425 0.7412607 0.4535294 0.5959729
## 18 0.9856584 0.9339080 0.9394125 0.7655115 0.7953327 0.5579345 0.6745685
## 19 0.9951997 0.9731361 0.9696058 0.4251864 0.4736155 0.1551963 0.2711475
## 20 0.9937553 0.9602649 0.9471181 0.5750501 0.6084120 0.2919314 0.4587508
## 21 0.8880000 0.9057437 0.9591178 0.9958357 0.9964485 0.9935262 0.9967037
## 22 0.7966102 0.9345238 0.9794816 0.9964012 0.9967695 0.9923015 0.9953258
## 23 0.9431072 0.8021761 0.7909630 0.9638466 0.9691848 0.9446445 0.9653225
## 24 0.9377916 0.7961571 0.8485486 0.9709491 0.9750523 0.9494598 0.9687139
## 25 0.7852349 0.8321479 0.9405204 0.9922568 0.9933940 0.9883229 0.9931554
## 26 0.8850575 0.8093126 0.8001921 0.9629252 0.9701871 0.9399923 0.9608209
## 27 0.9557522 0.8506494 0.9137645 0.9832719 0.9871735 0.9748908 0.9851927
## 28 0.9558174 0.7712895 0.8101948 0.9579137 0.9615236 0.9315991 0.9553287
## 29 0.8752998 0.8331617 0.7619712 0.9651870 0.9623058 0.9361987 0.9580087
##           15        16        17        18        19        20        21
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16 0.4294147
## 17 0.6864152 0.3833692
## 18 0.7543343 0.4925906 0.2611807
## 19 0.4128214 0.1655491 0.5067937 0.5761545
## 20 0.5612569 0.2382082 0.4534905 0.4463739 0.2479859
## 21 0.9956552 0.9895038 0.9897172 0.9866399 0.9956005 0.9890993
## 22 0.9966403 0.9918757 0.9855521 0.9785235 0.9925094 0.9902271 0.9259259
## 23 0.9640501 0.9610964 0.9754062 0.9245489 0.9688397 0.9397590 0.8857143
## 24 0.9718178 0.9507431 0.9634592 0.9156328 0.9620853 0.9340659 0.9174917
## 25 0.9925131 0.9819734 0.9796851 0.9697567 0.9899344 0.9817664 0.4464286
## 26 0.9650242 0.9551529 0.9594096 0.9023256 0.9618369 0.9320572 0.8778135
## 27 0.9855805 0.9688093 0.9599680 0.9453659 0.9780349 0.9648428 0.8907956
## 28 0.9546859 0.9401601 0.9423770 0.8907850 0.9533333 0.9217822 0.9376947
## 29 0.9535464 0.9531668 0.9508270 0.8926775 0.9574204 0.9295924 0.9526316
##           22        23        24        25        26        27        28
## 2
## 3
## 4
## 5
## 6
```

```
## 7
## 8
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21
## 22
## 23 0.9225182
## 24 0.9332220 0.4179104
## 25 0.6380952 0.8018018 0.8031746
## 26 0.8750000 0.2908243 0.5295537 0.7074627
## 27 0.9463722 0.6300103 0.5289042 0.8105263 0.6967593
## 28 0.9370079 0.3203285 0.3724138 0.8498498 0.4265896 0.4092050
## 29 0.8981233 0.4578652 0.6971047 0.8762376 0.3731343 0.8520900 0.5588865
```

```r
mzbw<-hclust(mzb.db, method="ward.D2")
par(mar=c(1, 5, 2, 2)+0.1)
plot(mzbw, main="Baltic Sea Macrozoobenthos: Ward's Clustering",
     ylab="Squared Bray-Curtis Distance")
```



```
gplots::heatmap.2(as.matrix(mzb),
          distfun=function(x) vegdist(x, method="bray"),
          hclustfun=function(x) hclust(x, method="ward.D2"),
          col=magma, trace="none", density.info="none")
```