

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

Jonathan Enriquez Madrid; Z620: Quantitative Biodiversity, Indiana University

01 February, 2023

### OVERVIEW

In this worksheet, we move beyond the investigation of within-site  $\alpha$ -diversity. We will explore  $\beta$ -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  $\beta$ -diversity
2. visualize  $\beta$ -diversity with heatmaps, cluster analysis, and ordination
3. test hypotheses about  $\beta$ -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. This will enable you to pull your work onto your own computer.
6. When you have completed the worksheet, **Knit** the text and code into a single PDF file by pressing the **Knit** button in the RStudio scripting panel. This will save the PDF output in your ‘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 1<sup>st</sup>, 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] "C:/Users/jonat/GitHub/QB2023_Enriquez_Madrid/2.Worksheets/6.BetaDiversity"
```

```
setwd("C:/Users/jonat/GitHub/QB2023_Enriquez_Madrid/2.Worksheets/6.BetaDiversity")
```

## 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, please do not print the dataset when submitting
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)
```

```
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)#environmental factors (pH, ammon, etc)
```

```
##   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
```

```
head(doubs$fish)#number of fish in each species
```

```
##   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
##   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   0
## 2   0   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   0
## 4   0   0   0   0   1   0   0   0   0   0   0   0   0
## 5   0   0   2   0   3   0   0   0   5   0   0   0   0
## 6   0   0   0   0   2   0   0   0   1   0   0   0   0
```

```
head(doubs$species)#species present
```

##	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

```
head(doubs$xy)#sites?
```

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

```
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
```

```
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	Chondrostoma 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	Spiralinus bipunctatus	spiralin	spiralin 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 erythrophthalmus	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	gremlille	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.

- How many objects are in doubs?
- How many fish species are there in the doubs dataset?
- How many sites are in the doubs dataset?

**Answer 1a:** There are four objects in the doubs data set. These objects are environment, fish, xy, and species.

**Answer 1b:** There are 27 species.

**Answer 1c:** There seems to be 30 sites.

## Visualizing the Doubs River Dataset

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

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

**Answer 2a:** I can see some patterns, but I'm not sure if they are significant. I see that high richness is seen at medium to high Y-coordinate values, in addition to high richness seen at low and high X-coordinate values. I also see low richness ranging from high to low Y-coordinate values, and low richness ranging from medium to high X-coordinate values.

**Answer 2b:** Brown trout abundance seems to be richest at medium and high X-coordinate values, in addition to high richness at low and medium Y-coordinate values. The richest abundance of brown trout does not coincide with the richest sites when including all species. There is low evenness among sites as some sites are represented more by some species than others, as can be seen from comparing the fish richness and brown trout richness.

**Answer 2c:** These patterns show us that species richness is not equivalent to species evenness in terms of how many individuals of one species there is at a specific site. For example, richness for one site could be 12. This is indicating there are 12 different species at this site, but it does not say how much of each species there is at that site. 80% of the site could be occupied by 4 species, while the rest of the 20% is occupied by the 8 other species. Yes there are 12 different species at a site, but is biodiversity high being that the majority of individuals at that site belong to one of the 4 most represented species, and not the other 8 rare species?

## 3) QUANTIFYING BETA-DIVERSITY

In the R code chunk below, do the following:

1. write a function (`beta.w()`) to calculate Whittaker's  $\beta$ -diversity (i.e.,  $\beta_w$ ) 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  $\beta$ -diversity in the Doubs River.

```
beta.w1 <- function(site.by.species = ""){
  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.w1(doubs$fish)#2.16
```

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

```
beta.w2 <- 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.w2(doubs$fish)#2.16
```

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

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

- a. Describe how local richness ( $\alpha$ ) and turnover ( $\beta$ ) contribute to regional ( $\gamma$ ) 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  $\beta$  change if we instead defined beta additively (i.e.,  $\beta = \gamma - \alpha$ )?

**Answer 3a:** Local richness describes the number of species at one site while turnover describes how species composition among sites differs. Beta diversity shows how many times more the

regional fish diversity is than the average richness at each site within the region (alpha diversity).

**Answer 3b:**The line of code does not provide values in such a way that I could compare the diversity between site 1, site 2 and site 10. Instead 'beta.w()' gives out a single value.

**Answer 3c:**If we defined beta as additive rather than multiplicative we would be interpreting Beta diversity as how many more species exist in the regional area than in the local sites compared to how many times more diverse the regional area is than the local sites.

## The Resemblance Matrix

In order to quantify  $\beta$ -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 give more weight to rare species than abundance-metrics do. Incidence metrics just identify if a species is present or not, they do not identify how much of that species is present, and thus give the same weight to abundant and rare species. An Incidence-based metric will report a rare species as present, even if there is one or two individuals in the whole species. An abundance-based metric will let us know how many of the rare species there is.

In the R code chunk below, do the following:

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

```
fish <- doubs$fish
fish <- fish[-8,]
fish.dj <- vegdist(fish, method = "jaccard", binary = TRUE)
fish.dj
```

```
##           1           2           3           4           5           6           7
## 2  0.66666667
## 3  0.75000000 0.25000000
## 4  0.87500000 0.62500000 0.50000000
## 5  0.90909091 0.72727273 0.63636364 0.27272727
## 6  0.90000000 0.70000000 0.60000000 0.20000000 0.09090909
## 7  0.80000000 0.40000000 0.50000000 0.55555556 0.54545455 0.50000000
## 9  1.00000000 0.66666667 0.71428571 0.55555556 0.54545455 0.50000000 0.57142857
## 10 0.83333333 0.50000000 0.57142857 0.44444444 0.45454545 0.40000000 0.16666667
## 11 0.83333333 0.50000000 0.57142857 0.60000000 0.69230769 0.66666667 0.42857143
## 12 0.83333333 0.50000000 0.57142857 0.60000000 0.69230769 0.66666667 0.42857143
## 13 0.83333333 0.50000000 0.57142857 0.72727273 0.78571429 0.76923077 0.62500000
## 14 0.90000000 0.70000000 0.60000000 0.50000000 0.60000000 0.57142857 0.63636364
## 15 0.90909091 0.72727273 0.75000000 0.53846154 0.53333333 0.50000000 0.54545455
## 16 0.94117647 0.82352941 0.76470588 0.52941176 0.44444444 0.41176471 0.70588235
## 17 0.95454545 0.86363636 0.81818182 0.63636364 0.56521739 0.54545455 0.77272727
## 18 0.95652174 0.86956522 0.82608696 0.65217391 0.58333333 0.56521739 0.78260870
## 19 1.00000000 0.91666667 0.87500000 0.70833333 0.58333333 0.62500000 0.83333333
## 20 1.00000000 0.91304348 0.86956522 0.69565217 0.56521739 0.60869565 0.82608696
```

```

## 21 1.00000000 0.91666667 0.87500000 0.70833333 0.58333333 0.62500000 0.83333333
## 22 1.00000000 0.95833333 0.91666667 0.75000000 0.62500000 0.66666667 0.87500000
## 23 1.00000000 1.00000000 1.00000000 0.90000000 0.83333333 0.81818182 0.85714286
## 24 1.00000000 1.00000000 1.00000000 0.85714286 0.81250000 0.80000000 0.91666667
## 25 1.00000000 1.00000000 0.90909091 0.76923077 0.53846154 0.61538462 0.81818182
## 26 1.00000000 0.95652174 0.91304348 0.73913043 0.60869565 0.65217391 0.86956522
## 27 1.00000000 0.95833333 0.91666667 0.75000000 0.62500000 0.66666667 0.87500000
## 28 1.00000000 0.95833333 0.91666667 0.75000000 0.62500000 0.66666667 0.87500000
## 29 0.96153846 0.88461538 0.84615385 0.69230769 0.57692308 0.61538462 0.80769231
## 30 1.00000000 1.00000000 0.95833333 0.79166667 0.66666667 0.70833333 0.91666667
##          9          10          11          12          13          14          15
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10 0.62500000
## 11 0.62500000 0.50000000
## 12 0.62500000 0.50000000 0.00000000
## 13 0.77777778 0.66666667 0.28571429 0.28571429
## 14 0.75000000 0.54545455 0.40000000 0.40000000 0.40000000
## 15 0.66666667 0.45454545 0.45454545 0.45454545 0.45454545 0.25000000
## 16 0.70588235 0.64705882 0.72222222 0.72222222 0.72222222 0.50000000 0.44444444
## 17 0.77272727 0.72727273 0.72727273 0.72727273 0.72727273 0.54545455 0.50000000
## 18 0.78260870 0.73913043 0.73913043 0.73913043 0.73913043 0.56521739 0.52173913
## 19 0.78260870 0.79166667 0.88461538 0.88461538 0.88461538 0.73076923 0.69230769
## 20 0.77272727 0.78260870 0.88000000 0.88000000 0.92307692 0.76923077 0.73076923
## 21 0.78260870 0.79166667 0.88461538 0.88461538 0.92592593 0.77777778 0.74074074
## 22 0.82608696 0.83333333 0.92307692 0.92307692 0.96296296 0.81481481 0.77777778
## 23 0.66666667 0.87500000 0.87500000 0.87500000 1.00000000 0.91666667 0.92307692
## 24 0.81818182 0.83333333 0.92307692 0.92307692 1.00000000 0.87500000 0.88235294
## 25 0.81818182 0.72727273 0.92307692 0.92307692 1.00000000 0.80000000 0.81250000
## 26 0.81818182 0.82608696 0.92000000 0.92000000 0.96153846 0.80769231 0.76923077
## 27 0.82608696 0.83333333 0.92307692 0.92307692 0.96296296 0.81481481 0.77777778
## 28 0.82608696 0.83333333 0.92307692 0.92307692 0.96296296 0.81481481 0.77777778
## 29 0.80769231 0.76923077 0.81481481 0.81481481 0.81481481 0.66666667 0.62962963
## 30 0.86956522 0.87500000 0.96153846 0.96153846 1.00000000 0.85185185 0.81481481
##          16          17          18          19          20          21          22
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16

```



```

## 17 0.22727273
## 18 0.26086957 0.04347826
## 19 0.40000000 0.26923077 0.23076923
## 20 0.44000000 0.30769231 0.26923077 0.04347826
## 21 0.46153846 0.33333333 0.29629630 0.08333333 0.04347826
## 22 0.50000000 0.37037037 0.33333333 0.12500000 0.08695652 0.04347826
## 23 0.88888889 0.86363636 0.86956522 0.86956522 0.86363636 0.86956522 0.86363636
## 24 0.80952381 0.75000000 0.70833333 0.65217391 0.63636364 0.65217391 0.63636364
## 25 0.75000000 0.75000000 0.70833333 0.65217391 0.63636364 0.65217391 0.63636364
## 26 0.53846154 0.40740741 0.37037037 0.16666667 0.13043478 0.08695652 0.04545455
## 27 0.50000000 0.37037037 0.33333333 0.12500000 0.08695652 0.04347826 0.00000000
## 28 0.50000000 0.37037037 0.33333333 0.12500000 0.08695652 0.04347826 0.00000000
## 29 0.40740741 0.22222222 0.18518519 0.11538462 0.15384615 0.11538462 0.15384615
## 30 0.53846154 0.40740741 0.37037037 0.16666667 0.13043478 0.08695652 0.04545455
##          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 0.62500000
## 25 0.62500000 0.54545455
## 26 0.85714286 0.61904762 0.61904762
## 27 0.86363636 0.63636364 0.63636364 0.04545455
## 28 0.86363636 0.63636364 0.63636364 0.04545455 0.00000000
## 29 0.88461538 0.69230769 0.69230769 0.19230769 0.15384615 0.15384615
## 30 0.85714286 0.61904762 0.61904762 0.09090909 0.04545455 0.04545455 0.19230769

```

```

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

```
fish.ds <- vegdist(fish, method = "bray", binary = TRUE)
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
```

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

- Does the resemblance matrix (`fish.db`) represent similarity or dissimilarity? What information in the resemblance matrix led you to arrive at your answer?
- 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:** The resemblance matrix ‘fish.db’ represents dissimilarity. Numbers near 1 indicate total dissimilarity, while numbers near 0 indicate low dissimilarity (or high similarity). Areas in the matrix where the two sites that are being compared are the same are blank as these sites have 0 dissimilarity.

**Answer 5b:** Sørensen checks for similarity between two sites while Bray-Curtis distance checks for dissimilarity between two sites. For Sørensen, values of 0 indicate no similarity while values of 1 indicate complete similarity. As for Bray-Curtis distance, values of 0 indicate complete similarity and values of 1 indicate complete dissimilarity.

## 4) VISUALIZING BETA-DIVERSITY

### A. Heatmaps

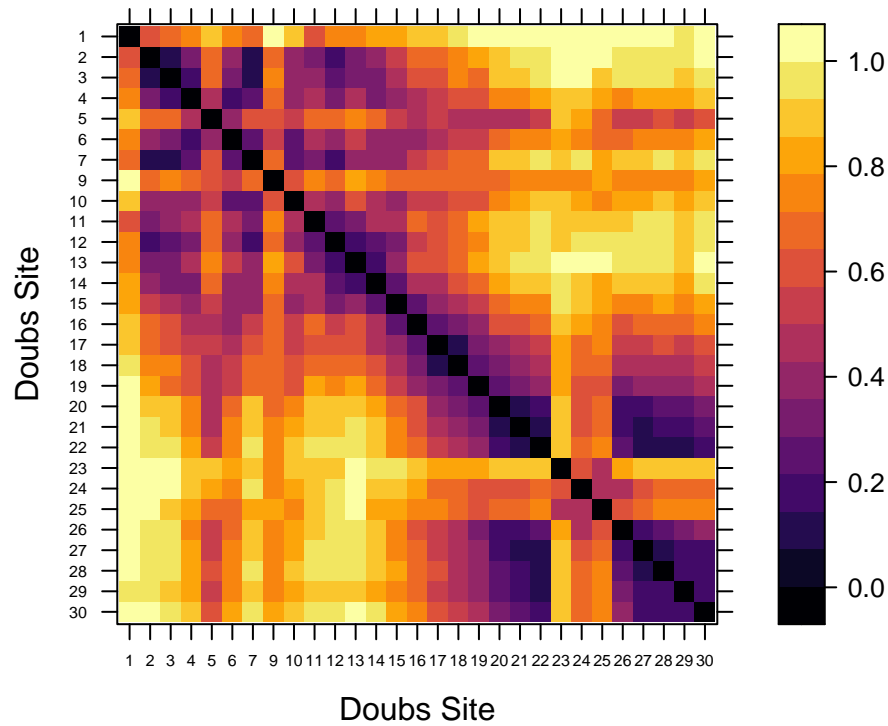
In the R code chunk below, do the following:

- define a color palette,
- define the order of sites in the Doubs River, and
- 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 = inferno,
          xlab = "Doubs Site", ylab = "Doubs Site", scales = list(cex = 0.5),
          main = "Bray-Curtis Distance")
```

## Bray–Curtis Distance



### B. Cluster Analysis

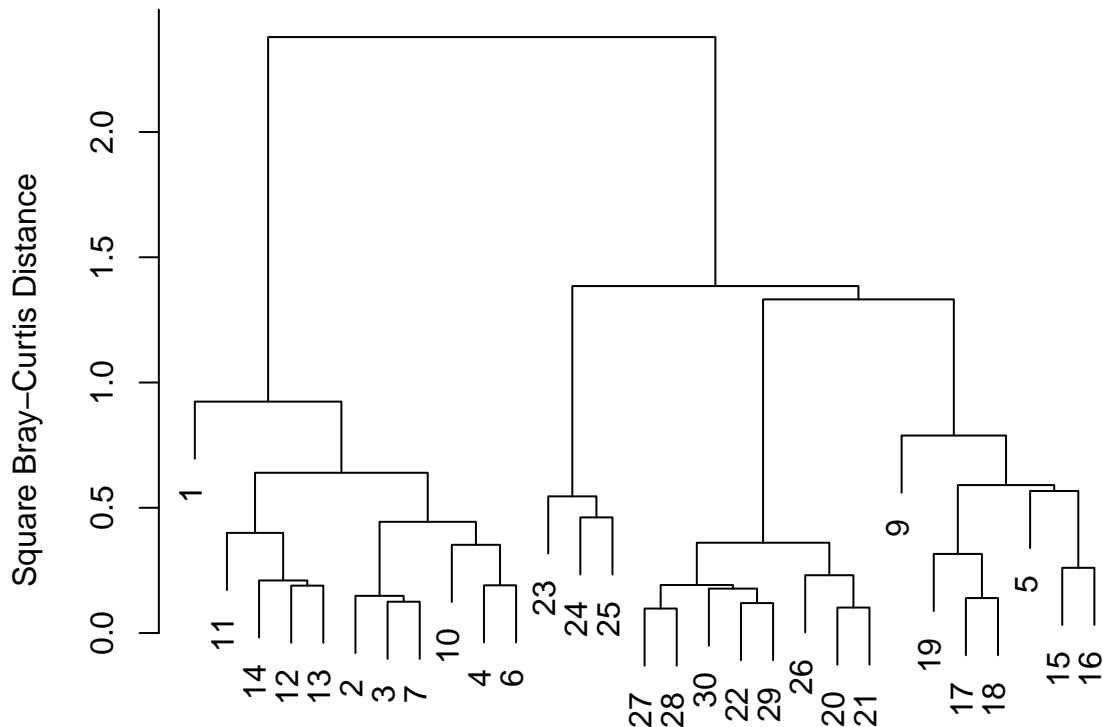
In the R code chunk below, do the following:

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") #Ward's Cluster

par(mar = c(1, 5, 2, 2) + 0.1)
plot(fish.ward, main = "Doubs River Fish: Ward's Clustering",
     ylab = "Square 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:** A general trend I notice from the heat map is that as sites increase in distance from one another, their similarity decreases. We could hypothesize that as distance between two sites increases, so does the dissimilarity between those two sites. In general, sites closer to each other will have higher similarity than sites further from each other.

## 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, axis = FALSE)

## Warning in plot.window(...): "axis" is not a graphical parameter

## Warning in plot.xy(xy, type, ...): "axis" is not a graphical parameter

## Warning in axis(side = side, at = at, labels = labels, ...): "axis" is not a
## graphical parameter

## Warning in axis(side = side, at = at, labels = labels, ...): "axis" is not a
## graphical parameter

## Warning in box(...): "axis" is not a graphical parameter

## Warning in title(...): "axis" is not a graphical parameter

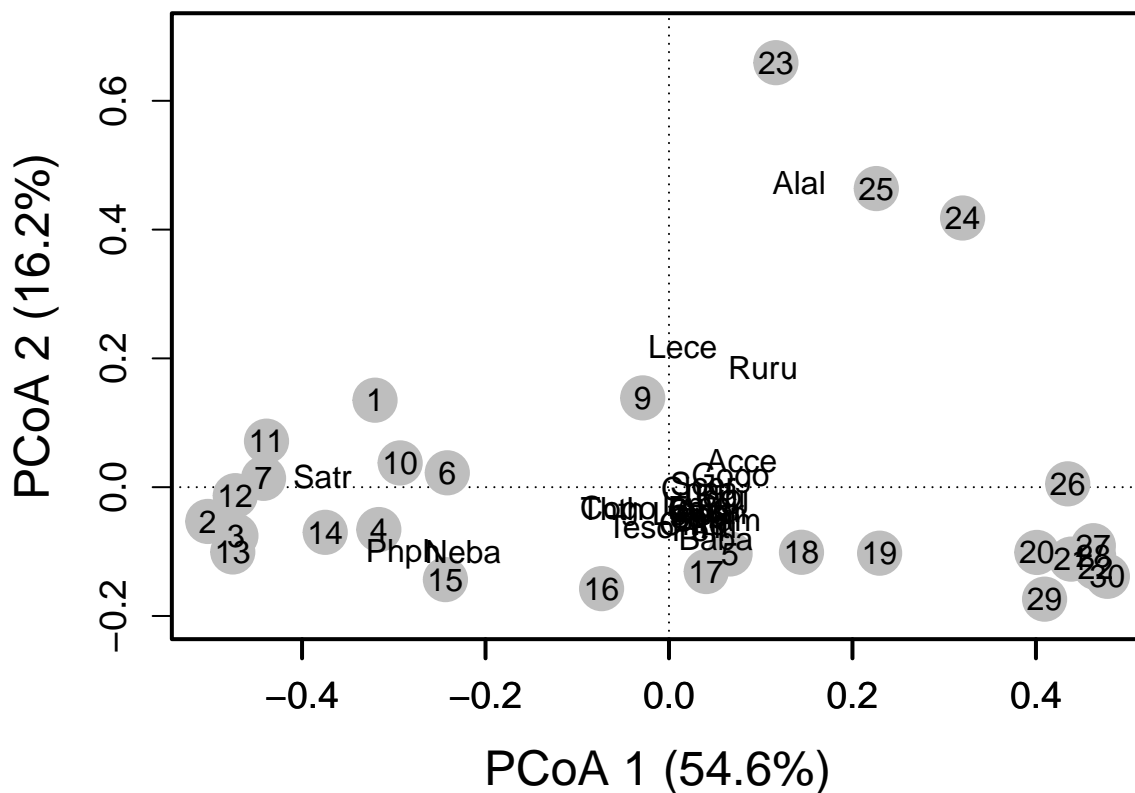
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)

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(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:** There seems to be four different groups displayed on the PCoA plot. One group is positioned from -0.6 to -0.2 on the X-axis and -0.2 to 0.2 on the Y-axis. The second group is positioned -0.1 to 0.2 on the X-axis and -0.2 to 0.2 on the Y-axis, the third group is 0.1 to 0.4 on the X-axis and 0.4 to 0.7 on the Y-axis. The fourth group is positioned 0.4 to 0.5 on the X-axis and -0.2 to 0.1 on the Y-axis. The PCoA groups objects based on similarity, so in this case Lece and Ruru fish are more similar to each other than Alal is to either of them. Satr, Phph, and Neba fish are more similar to one another than they are to Lece and Ruru, and Alal.

**Answer 7b:** Fish species that are indicators of river quality should be grouped together in the PCoA plot as they are species that are similar in their importance of maintaining 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.

```
Zoopn <- read.csv("C:\\Users\\jonat\\OneDrive\\Documents\\Quantitative Biodiversity\\Semester_Project; 1  
str(Zoopn) #Numbers are characters
```

```
## 'data.frame': 1923 obs. of 14 variables:  
## $ Lake_Name: int 1 1 1 1 1 1 1 1 1 ...  
## $ dent : chr "62,436.84" "118,327.89" "200,150.36" "39,442.63" ...  
## $ cerio : chr "1,007.05" "2,517.61" "8,811.65" "1,678.41" ...  
## $ pulic : chr "114,299.70" "275,678.80" "281,972.84" "228,263.73" ...  
## $ Bosmina : chr "0" "0" "0" "839.2" ...  
## $ parv : chr "0" "0" "0" "0" ...  
## $ ambig : chr "0" "0" "0" "0" ...  
## $ diaph : chr "0" "0" "0" "0" ...  
## $ scaph : chr "0" "0" "0" "0" ...  
## $ alona : chr "0" "0" "0" "0" ...  
## $ chaob : chr "31" "19" "82" "52" ...  
## $ ostr : chr "" "" "" "" ...  
## $ cal : chr "" "" "" "" ...  
## $ cyc : chr "" "" "" "" ...
```

```
new_zoopSbyS <- gsub(",", "", Zoopn) #Deletes commas from numbers  
new2_zoopSbyS <- gsub("log(", "", Zoopn, fixed=TRUE) #didn't remove quotation marks  
new3_zoopSbyS <- gsub(paste(c("[(", "[)"])", collapse = "|"), "", Zoopn) #didn't remove quotation marks.  
zoopSbyS <- as.numeric(as.character(new2_zoopSbyS)) #converts characters to numeric. Gives all NAs.
```

```
## Warning: NAs introduced by coercion
```

```
vegdist(zoopSbyS, method = "bray", binary = TRUE, na.rm = TRUE)
```

```
## Warning in vegdist(zoopSbyS, method = "bray", binary = TRUE, na.rm = TRUE): you have empty rows: the  
## meaningless in method "bray"
```

```
## Warning in vegdist(zoopSbyS, method = "bray", binary = TRUE, na.rm = TRUE):  
## missing values in results
```

```
## 1 2 3 4 5 6 7 8 9 10 11 12 13  
## 2 NA  
## 3 NA NA  
## 4 NA NA NA  
## 5 NA NA NA NA  
## 6 NA NA NA NA NA  
## 7 NA NA NA NA NA NA  
## 8 NA NA NA NA NA NA NA  
## 9 NA NA NA NA NA NA NA NA  
## 10 NA NA NA NA NA NA NA NA NA
```

```
## 11 NA NA NA NA NA NA NA NA NA NA NA
## 12 NA NA NA NA NA NA NA NA NA NA NA NA
## 13 NA NA NA NA NA NA NA NA NA NA NA NA NA
## 14 NA NA NA NA NA NA NA NA NA NA NA NA NA NA
```

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