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

Timothy Biewer-Heisler; Z620: Quantitative Biodiversity, Indiana University

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OVERVIEW

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

After completing this exercise you will know how to:

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

Directions:

1. In the Markdown version of this document in your cloned repo, change "Student Name" on line 3 (above) with your name.
2. Complete as much of the worksheet as possible during class.
3. Use the handout as a guide; it contains a more complete description of data sets along with examples of proper scripting needed to carry out the exercises.
4. Answer questions in the worksheet. Space for your answers is provided in this document and is indicated by the ">" character. If you need a second paragraph be sure to start the first line with ">". You should notice that the answer is highlighted in green by RStudio (color may vary if you changed the editor theme).
5. Before you leave the classroom today, it is *imperative* that you **push** this file to your GitHub repo, at whatever stage you are. Ths will enable you to pull your work onto your own computer.
6. When you have completed the worksheet, **Knit** the text and code into a single PDF file by pressing the `Knit` button in the RStudio scripting panel. This will save the PDF output in your '8.BetaDiversity' folder.
7. After Knitting, please submit the worksheet by making a **push** to your GitHub repo and then create a **pull request** via GitHub. Your pull request should include this file (**8.BetaDiversity_1_Worksheet.Rmd**) with all code blocks filled out and questions answered) and the PDF output of `Knitr` (**8.BetaDiversity_1_Worksheet.pdf**).

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

1) R SETUP

Typically, the first thing you will do in either an R script or an RMarkdown file is setup your environment. This includes things such as setting the working directory and loading any packages that you will need.

In the R code chunk below, provide the code to:

1. clear your R environment,
2. print your current working directory,
3. set your working directory to your "*/8.BetaDiversity*" folder, and

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

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

```
## [1] "/Users/tbiewerh/GitHub/QB2021_Biewer-Heisler/2.Worksheets/8.BetaDiversity"
```

```
setwd("~/GitHub/QB2021_Biewer-Heisler/2.Worksheets/8.BetaDiversity")
#install.packages("vegan")
require("vegan")
```

```
## Loading required package: vegan

## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.5-7
```

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 = T, quietly = T)) {
    install.packages(package)
    library(package, character.only = T)
  }
}
```

```
##
## Attaching package: 'gplots'

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

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

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

```
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
```

```
e = 1
```

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***: Four lists are present. ***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***:There is a large amount of richness downstream and midstream (around the bend), with medium to low richness elsewhere.
> ***Answer 2b***:Brown Trout abundance is high upstream and at the start of the bend in the river.
> ***Answer 2c***:We shouldn't use them to make assumptions about any particular 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 =""){
  SbyS.pa <- decostand(site.by.species, method = "pa")
  S <- ncol(SbyS.pa[,which(colSums(SbyS.pa) > 0)])
  a.bar <- mean(specnumber(SbyS.pa))
  b.w <- round(S/a.bar, 3)
  return(b.w)
}
beta.w <- function(site.by.species = "", sitenum1 = "", sitenum2 = "", pairwise = FALSE) {
  if (pairwise == TRUE){
    if (sitenum1 == "" | sitenum2 == ""){
      print("Error: please specify sites to compare")
      return(NA)
    }
    site1 = site.by.species[sitenum1,]
    site2 = site.by.species[sitenum2,]
    site1 = subset(site1, select = site1 > 0)
    site2 = subset(site2, select = site2 > 0)
    gamma = union(colnames(site1), colnames(site2))
    s = length(gamma)
    a.bar = mean(c(specnumber(site1), specnumber(site2)))
    b.w = round(s/a.bar - 1, 3)
    return(b.w)
  }
  else{
    SbyS.pa <- decostand(site.by.species, method = "pa")
    S <- ncol(SbyS.pa[,which(colSums(SbyS.pa) > 0)])
    a.bar <- mean(specnumber(SbyS.pa))
    b.w <- round(S/a.bar, 3)
    return(b.w)
  }
}

beta.w(doubs$env)
```

```
## [1] 1.028
```

```
beta.w(doubs$fish)
```

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

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

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

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

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

```
beta.w(doubs$fish, 2, 10, pairwise = TRUE)
```

```
## [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: Regional fish diversity is determined by multiplying local richness and turnover. ***Answer 3b***: It seems that 1 and 10 are more similar than 1 and 2 due to the values 0.714 and 0.5 for each comparison respectively. ***Answer 3c***: I think we would no longer be able to compare richness as well, since it would be completely dependent on how large the richness is instead of as a ratio.

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 would likely overestimate the presence of rare species compared to abundance-based metrics and would not well reflect their true states.

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, methods = "jaccard", binary = TRUE)

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

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



fish.db <- vegdist(fish, method = "bray", upper = TRUE, diag = TRUE)

fish.db
```

```
##             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
```

```
fish.ds
```

```
##             1          2          3          4          5          6          7
## 1  0.00000000
## 2  0.50000000 0.00000000
## 3  0.60000000 0.14285714 0.00000000
## 4  0.77777778 0.45454545 0.33333333 0.00000000
## 5  0.83333333 0.57142857 0.46666667 0.15789474 0.00000000
## 6  0.81818182 0.53846154 0.42857143 0.11111111 0.04761905 0.00000000
## 7  0.66666667 0.25000000 0.33333333 0.38461538 0.37500000 0.33333333 0.00000000
## 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
## 1
## 2
## 3
## 4
## 5
## 6
## 7
## 9  0.00000000
## 10 0.45454545 0.00000000
## 11 0.45454545 0.33333333 0.00000000
## 12 0.45454545 0.33333333 0.00000000 0.00000000
## 13 0.63636364 0.50000000 0.16666667 0.16666667 0.00000000
## 14 0.60000000 0.37500000 0.25000000 0.25000000 0.25000000 0.00000000
## 15 0.50000000 0.29411765 0.29411765 0.29411765 0.29411765 0.14285714 0.00000000
## 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
## 1
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16 0.00000000
## 17 0.12820513 0.00000000
## 18 0.15000000 0.02222222 0.00000000
## 19 0.25000000 0.15555556 0.13043478 0.00000000
## 20 0.28205128 0.18181818 0.15555556 0.02222222 0.00000000
## 21 0.30000000 0.20000000 0.17391304 0.04347826 0.02222222 0.00000000
## 22 0.33333333 0.22727273 0.20000000 0.06666667 0.04545455 0.02222222 0.00000000
## 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
## 1
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21
## 22
## 23 0.00000000
## 24 0.45454545 0.00000000
## 25 0.45454545 0.37500000 0.00000000
## 26 0.75000000 0.44827586 0.44827586 0.00000000
## 27 0.76000000 0.46666667 0.46666667 0.02325581 0.00000000
## 28 0.76000000 0.46666667 0.46666667 0.02325581 0.00000000 0.00000000
## 29 0.79310345 0.52941176 0.52941176 0.10638298 0.08333333 0.08333333 0.00000000
## 30 0.75000000 0.44827586 0.44827586 0.04761905 0.02325581 0.02325581 0.10638298
##            30
## 1
## 2
## 3
## 4
## 5
## 6
## 7
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21
## 22
## 23
## 24
## 25
## 26
## 27
## 28
## 29
## 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***: The resemblance matrix measures dissimilarity, with increasing numbers being more dissimilar up to 1. I know this by looking at the diagonal which is comparing sites to themselves which gives a value of 0. ***Answer 5b***: Bray-Curtis seems to have an increased estimate of dissimilarity compared to the Sorensen.

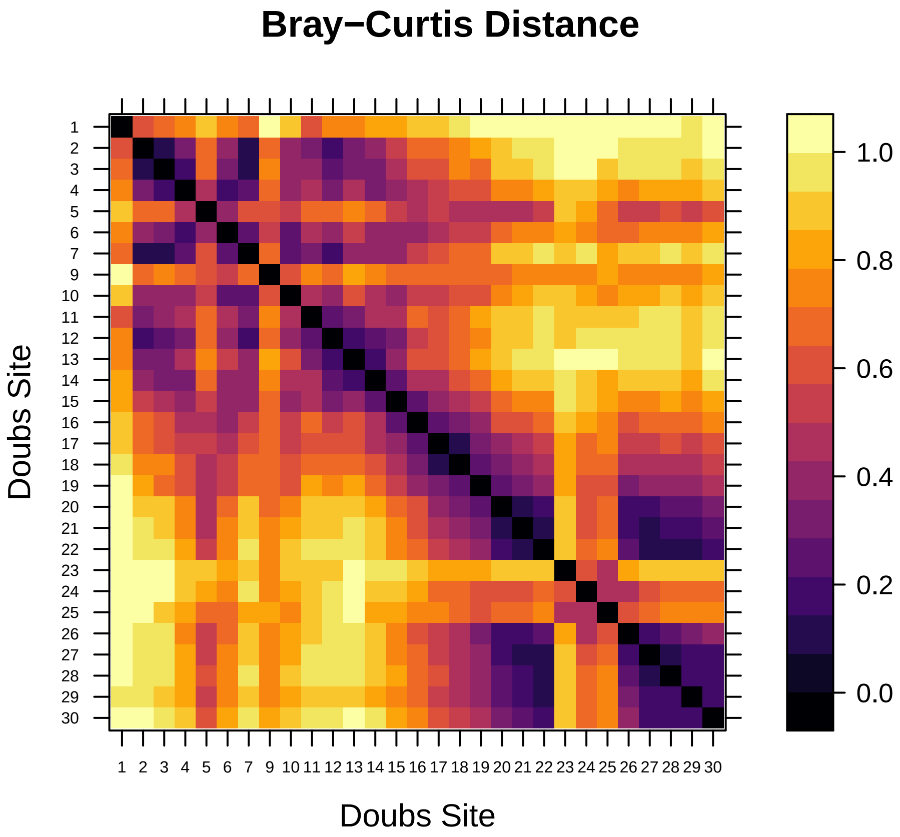
4) VISUALIZING BETA-DIVERSITY

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 = inferno, xlab = "Doubs Site", ylab
```

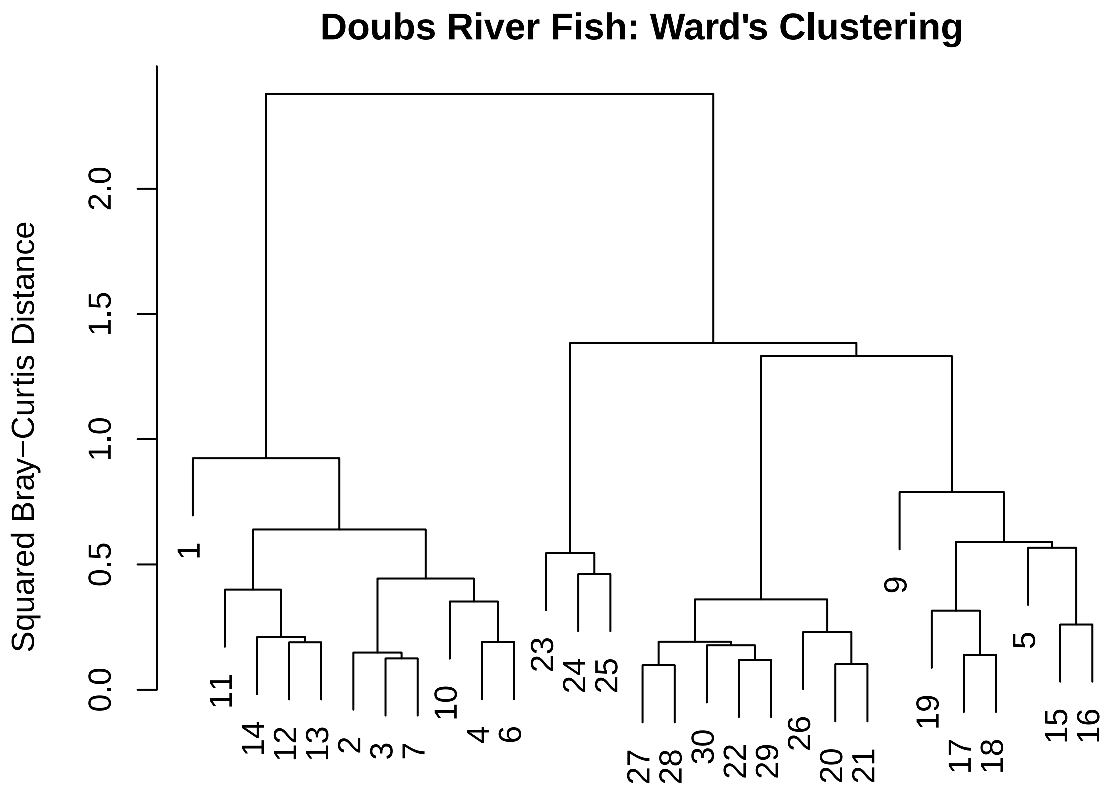


B. Cluster Analysis

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")

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



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

> ***Answer 6***: Generally the closer the sites are in distance the more similar they are, with exceptions for 1, 5, 9, and 23-25.

C. Ordination

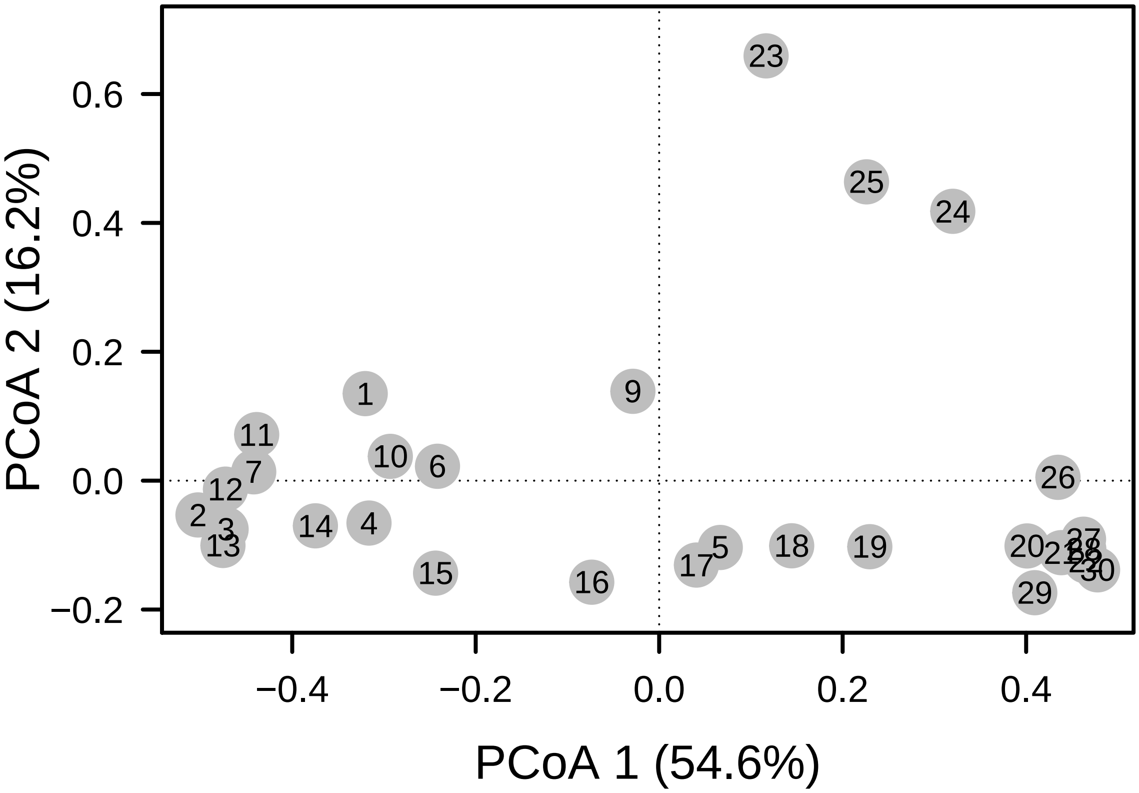
Principal Coordinates Analysis (PCoA)

In the R code chunk below, do the following:

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

```
fish.pcoa <- cmdscale(fish.db, eig = TRUE, k = 3)

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

```
par(mar = c(5, 5, 1, 2) + 0.1)

plot(fish.pcoa$points[ ,1], fish.pcoa$points[ ,2], ylim = c(-0.2, 0.7),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)

axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)

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

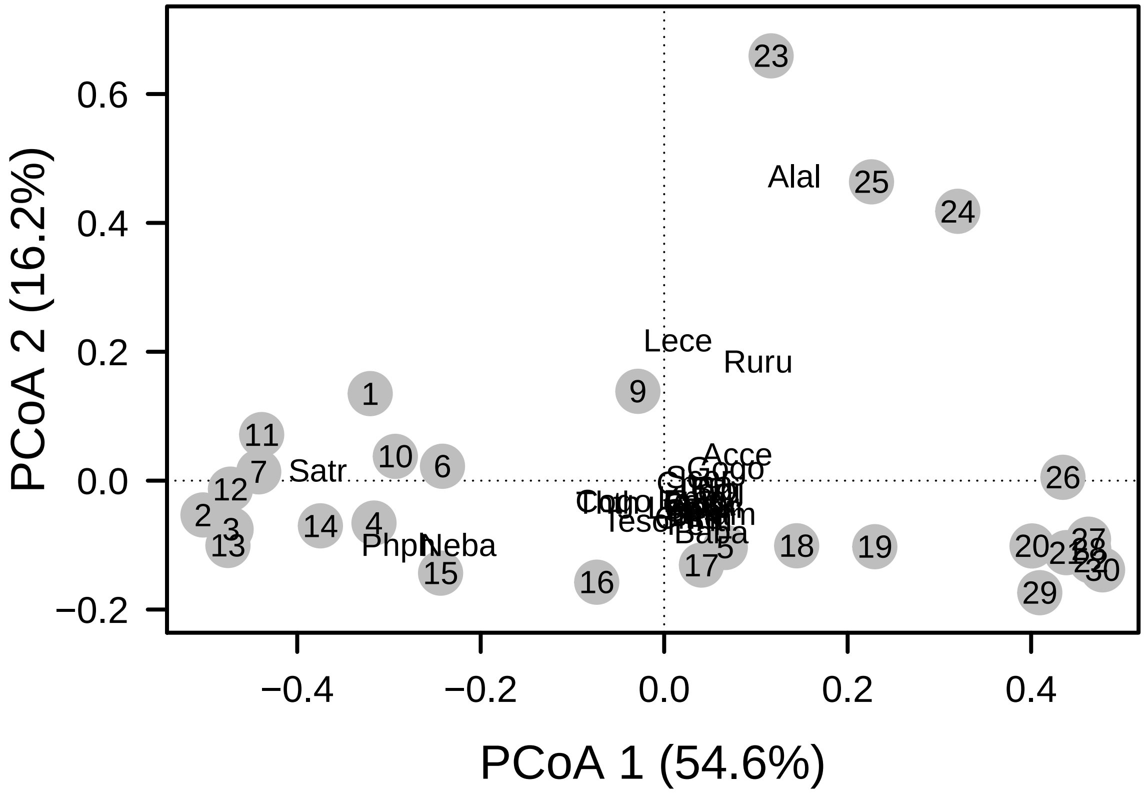


In the R code chunk below, do the following:

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.

```
fish.pcoa <- cmdscale(fish.db, eig = TRUE, k = 3)

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

```
par(mar = c(5, 5, 1, 2) + 0.1)

plot(fish.pcoa$points[ ,1], fish.pcoa$points[ ,2], ylim = c(-0.2, 0.7),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)

axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)

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

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")
```



```
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: Many of the sites 20-22 & 26-30 are clustered together with much different composition than 1-15, with 16-19 and 23 -25 in their own cluster. ***Answer 7b***: Because there is such a high density of species in 16-19 those species are in an area with high quality. The presence of Satr in 1-15 with the exception of 9 may make Satr an indicator of lower quality. Alal may be another indicator of poor quality, with those regions having fewer species which may be indicative of river quality.

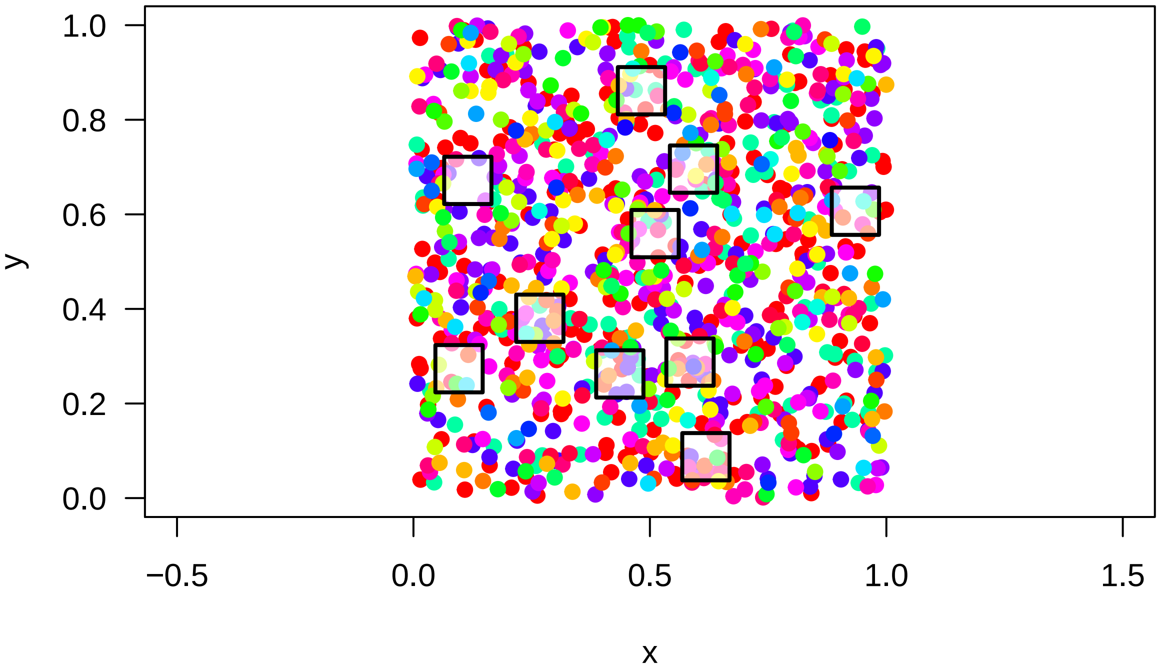
SYNTHESIS

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

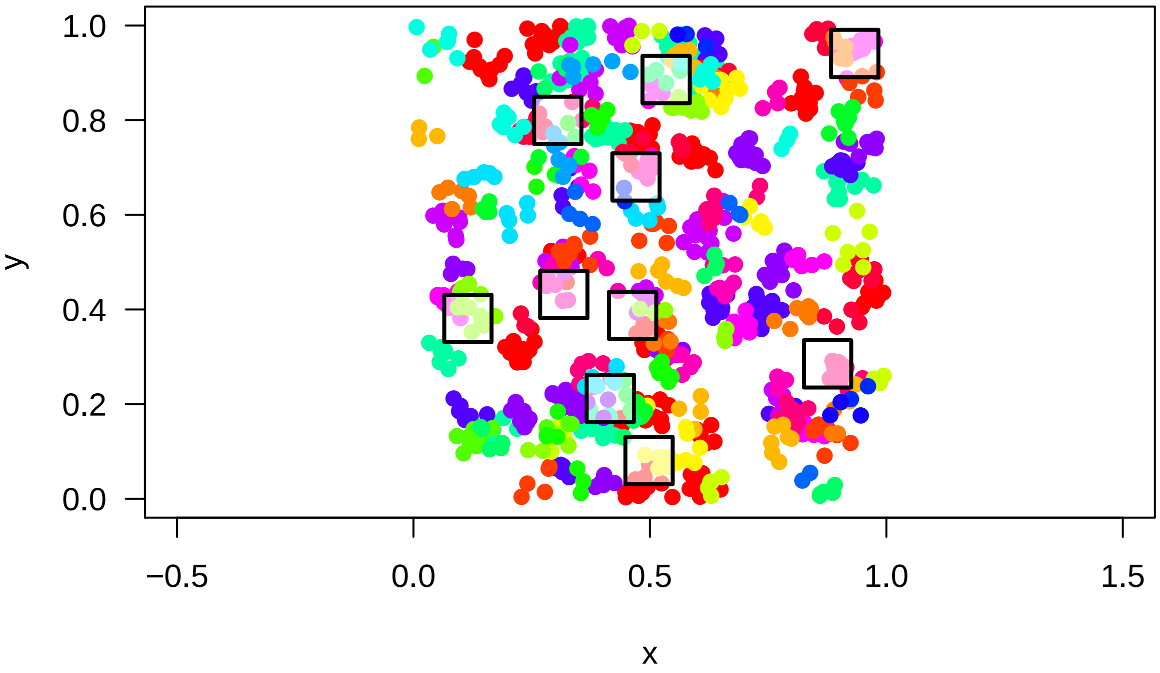
```
package.list <- c('mobsim', 'knitr', 'vegan', 'tidyr', 'dplyr', 'ggplot2', 'formatR')
for (package in package.list) {
  if (!require(package, character.only = TRUE, quietly = TRUE)) {
    install.packages(package)
    library(package, character.only = TRUE)
  }
}
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
# set page dimensions for printing
opts_chunk$set(tidy.opts = list(width.cutoff = 70),
        tidy = TRUE, fig.width = 5, fig.height = 5)

com <- sim_poisson_community(s_pool = 25, n_sim = 1000, sad_type = "lnorm",
        sad_coef = list("meanlog" = 2, "sdlog" = 1))
comm_mat <- sample_quadrats(com, n_quadrats = 10, quadrat_area = 0.01,
             method = "random", avoid_overlap = T)
```



```
comRan <- sim_thomas_community(s_pool = 25, n_sim = 1000, sad_type = "lnorm",
        sad_coef = list("meanlog" = 2, "sdlog" = 1))
comRan_mat <- sample_quadrats(comRan, n_quadrats = 10, quadrat_area = 0.01,
             method = "random", avoid_overlap = T)
```



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

```
fullspec <- bind_rows(comm_mat$spec_dat, comRan_mat$spec_dat)
```

```
beta.w(fullspec, 1, 12, pairwise = T)
```

```
## [1] 0.857
```

```
i = 0
matlist <- c()
ranlist <- c()
while (i < 50) {
    comm_mat <- sample_quadrats(com, n_quadrats = 10, quadrat_area = 0.01,
        method = "random", avoid_overlap = T, plot = F)
    matlist <- c(matlist, beta.w(comm_mat$spec_dat))
    comRan_mat <- sample_quadrats(comRan, n_quadrats = 10, quadrat_area = 0.01,
        method = "random", avoid_overlap = T, plot = F)
    ranlist <- c(ranlist, beta.w(comRan_mat$spec_dat))
    i = i + 1
}

t.test(matlist, ranlist)
```

```
##
##  Welch Two Sample t-test
##
## data:  matlist and ranlist
## t = -27.526, df = 60.111, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -3.332301 -2.880819
## sample estimates:
## mean of x mean of y
##   2.97560   6.08216
```

```
site12mat <- comm_mat$spec_dat[1:2, ]
site12ran <- comRan_mat$spec_dat[1:2, ]
beta.w(site12mat)
```

```
## [1] 1.286
```

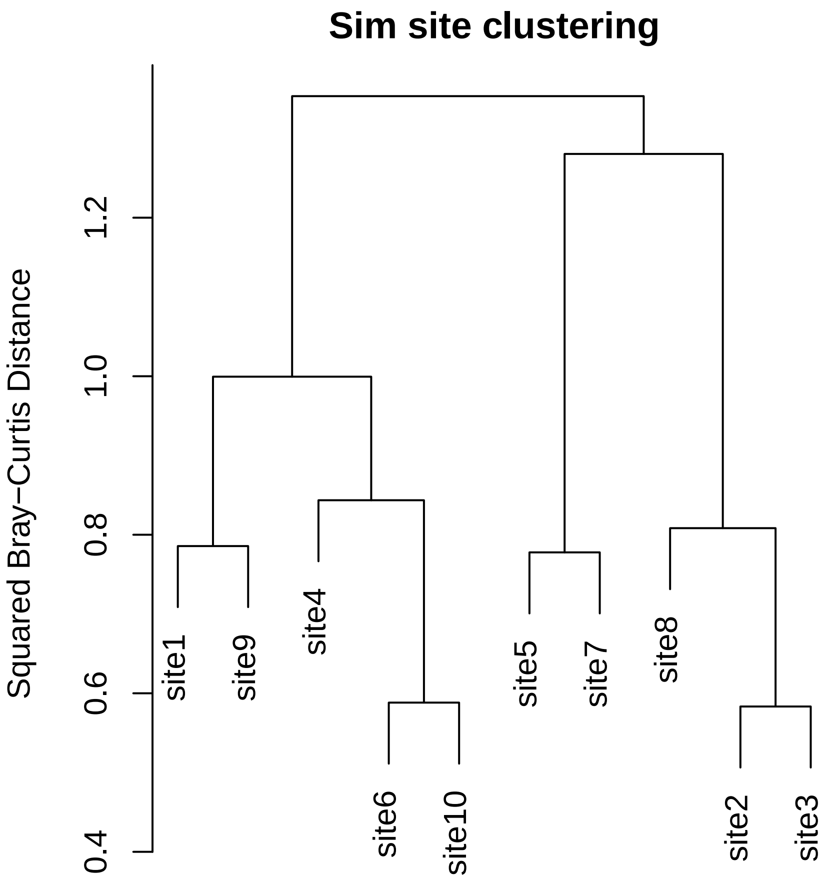
```
beta.w(site12ran)
```

```
## [1] 2
```

In regards to the differences in beta diversity between random and patchy communities, it seems that patchy has a much higher diversity than random. For the site 1 and 2 compared to the total they do seems to have a much lower value, ~1.5 compared to the total vs much higher values.

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

```
fish.db <- vegdist(comRan_mat$spec_dat, method = "bray", upper = TRUE,
    diag = TRUE)
fish.ward <- hclust(fish.db, method = "ward.D2")

par(mar = c(1, 5, 2, 2) + 0.1)
plot(fish.ward, main = "Sim site clustering", ylab = "Squared Bray-Curtis Distance")
```



>It does seem that site 1 and site 2 are rather different due to their distances on the clustering.