

## 6. Worksheet: Among Site (Beta) Diversity – Part 2

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### OVERVIEW

In this worksheet, we continue to explore concepts, statistics, and visualizations related to  $\beta$ -diversity. Now that you know how to formally quantify  $\beta$ -diversity, we will learn how to 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, you should **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 Posit.cloud workspace: `/cloud/project/QB-2025/Week4-Beta/`
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\_2\_Worksheet.Rmd**) with all code blocks filled out and questions answered) and the PDF output of **Knitr** (**6.BetaDiversity\_2\_Worksheet.pdf**).

The completed exercise is due on **Wednesday, February 12<sup>th</sup>, 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, provide the code to:

1. clear your R environment,
2. print your current working directory,
3. set your working directory to your **Week4-Beta/** folder.
4. load the **vegan** R package (be sure to install if needed).

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

```
## [1] "/cloud/project/QB2025_Park/Week4-Beta"
```

```

setwd("/cloud/project/QB2025_Park/Week4-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)
  }
}

##
## 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)

install.packages("Rcmdr", dependencies = TRUE)

## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.4'
## (as 'lib' is unspecified)

```

## 2) LOADING DATA

### Load dataset

In the R code chunk below, load the `doubs` dataset from the `ade4` package

```
data(doubs)
```

## 3) HYPOTHESIS TESTING

### A. Multivariate Procedures for Categorical Designs

Earlier work done in the Doubs River suggested that the river has four distinct regions of habitat quality: the first region (sites 1-14) of “high quality”; the second (sites 15 - 19) and fourth (sites 26 - 30) of “moderate quality”; and the third (sites 20 - 25) of “low quality”.

In the code chunk below, test the hypothesis that fish community composition varies with river quality.

1. create a factor vector that categorizes habitat quality in the Doubs River,
2. use the multivariate analyses for categorical predictors to describe how fish community structure relates to habitat quality.

```

fish<-doubs$fish
fish<-fish[-8,]
quality<-c(rep("HQ", 13), rep("MQ", 5), rep("LQ", 6), rep("MQ", 5))
adonis2(fish~quality, method="bray", permutations=999)

## Permutation test for adonis under reduced model
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = fish ~ quality, permutations = 999, method = "bray")
##           Df SumOfSqs      R2      F Pr(>F)

```

```
## Model      2    3.0947 0.45765 10.97  0.001 ***
## Residual 26    3.6674 0.54235
## Total     28    6.7621 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
indval<-multipatt(fish, cluster=quality, func="IndVal.g",
  control=how(nperm=999))
fish.rel<-decostand(fish, method="total")
phi<-multipatt(fish.rel, cluster=quality, func="r.g",
  control=how(nperm=999))

summary(indval)
```

```
##
## Multilevel pattern analysis
## -----
##
## Association function: IndVal.g
## Significance level (alpha): 0.05
##
## Total number of species: 27
## Selected number of species: 23
## Number of species associated to 1 group: 1
## Number of species associated to 2 groups: 22
##
## List of species associated to each combination:
##
## Group MQ #sps. 1
##      stat p.value
## Teso 0.686  0.013 *
##
## Group HQ+MQ #sps. 2
##      stat p.value
## Satr 0.860  0.004 **
## Phph 0.859  0.015 *
##
## Group LQ+MQ #sps. 20
##      stat p.value
## Alal 0.935  0.001 ***
## Gogo 0.933  0.001 ***
## Ruru 0.916  0.001 ***
## Legi 0.901  0.001 ***
## Baba 0.895  0.001 ***
## Chna 0.866  0.001 ***
## Spbi 0.866  0.001 ***
## Cyca 0.866  0.001 ***
## Acce 0.866  0.001 ***
## Lele 0.863  0.003 **
## Titi 0.853  0.004 **
## Chto 0.829  0.001 ***
## Rham 0.829  0.001 ***
## Anan 0.829  0.001 ***
## Eslu 0.827  0.016 *
## Pefl 0.806  0.012 *
```

```
## Blbj 0.791 0.005 **
## Scer 0.766 0.006 **
## Abbr 0.750 0.005 **
## Icme 0.661 0.028 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(phi)
```

```
##
## Multilevel pattern analysis
## -----
##
## Association function: r.g
## Significance level (alpha): 0.05
##
## Total number of species: 27
## Selected number of species: 18
## Number of species associated to 1 group: 9
## Number of species associated to 2 groups: 9
##
## List of species associated to each combination:
##
## Group HQ #sps. 3
##      stat p.value
## Phph 0.802 0.001 ***
## Neba 0.734 0.001 ***
## Satr 0.650 0.002 **
##
## Group LQ #sps. 2
##      stat p.value
## Alal 0.693 0.001 ***
## Ruru 0.473 0.047 *
##
## Group MQ #sps. 4
##      stat p.value
## Anan 0.571 0.007 **
## Spbi 0.557 0.007 **
## Chto 0.542 0.007 **
## Icme 0.475 0.028 *
##
## Group LQ+MQ #sps. 9
##      stat p.value
## Legi 0.658 0.002 **
## Baba 0.645 0.001 ***
## Rham 0.600 0.004 **
## Acce 0.594 0.007 **
## Cyca 0.586 0.004 **
## Chna 0.571 0.004 **
## Blbj 0.571 0.008 **
## Gogo 0.523 0.018 *
## Abbr 0.499 0.017 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**Question 1:** Based on the PERMANOVA, IndVal, and phi coefficient analyses, what did you learn about the relationship between habitat quality and the fish species composition? Are the different analyses consistent with one another and do they agree with the visualizations (heat maps, cluster dendograms, ordinations) that you created?

**Answer 1:** The permanova shows us there is a significant correlation between fish species composition and habitat quality, with IndVal and phi coefficient analyses identifying different species that are significantly associated with different levels of quality. From the heat maps and ordinations we did, I noticed pockets of similarity among certain sites. When referring to the map of the Doubs River, these sites were located at different sections of the river (upstream, bend, and downstream), which are also associated with different qualities. These results support the hypothesis that fish species vary depending on habitat quality.

## B. Multivariate Procedures for Continuous Designs

### i. Mantel Test

In the R code chunk below, do the following:

1. create distance matrices for both fish communities and environmental factors, and
2. use a Mantel test to test the hypothesis that fish assemblages are correlated with stream environmental variables.

```
fish.dist<-vegdist(doubs$fish[-8,], method="bray")
env.dist<-vegdist(scale(doubs$env[-8,]),method="euclid")
mantel(fish.dist,env.dist)

##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = fish.dist, ydis = env.dist)
##
## Mantel statistic r: 0.604
##      Significance: 0.001
##
## Upper quantiles of permutations (null model):
##   90%   95%  97.5%  99%
## 0.104 0.142 0.172 0.200
## Permutation: free
## Number of permutations: 999
```

**Question 2:** What do the results from our Mantel test suggest about fish diversity and stream environmental conditions? How does this relate to your hypothesis about stream quality influencing fish communities?

**Answer 2:** The Mantel statistic is much higher than the statistic corresponding to the 99th percentile and the p value is small, suggesting fish diversity and environmental conditions are strongly correlated. These results support the hypothesis fish diversity is closely related to water quality.

### ii. Constrained Ordination

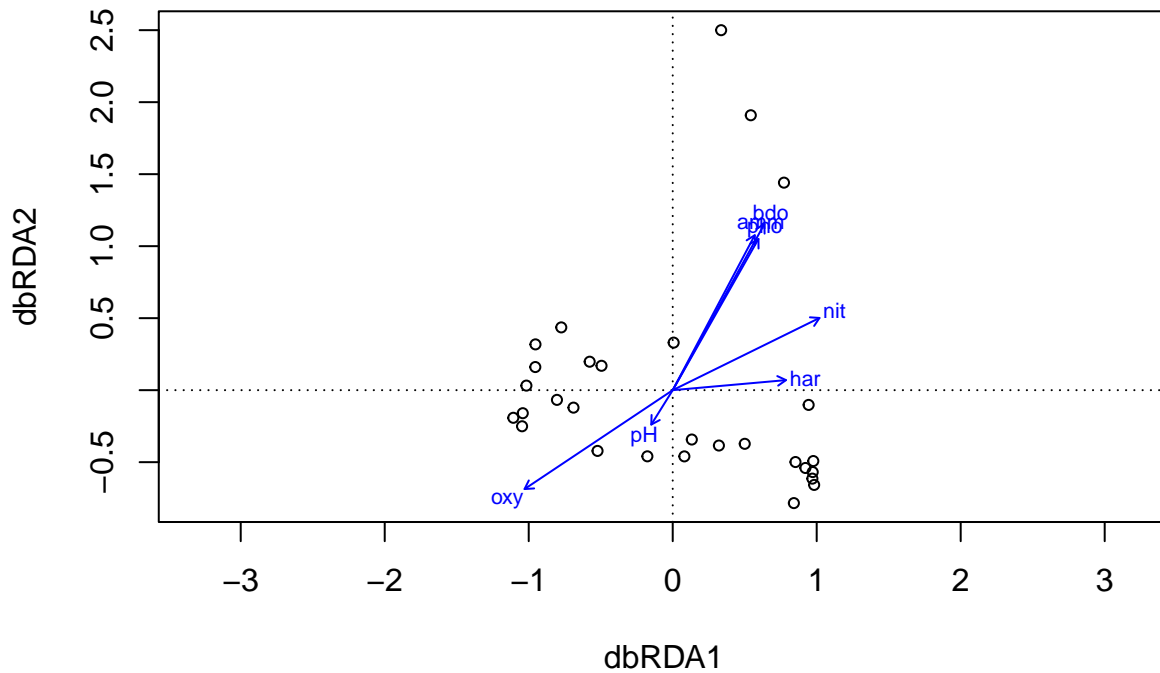
In the R code chunk below, do the following:

1. create an environmental matrix of the water chemistry data included in the `doubs` dataset using forward and reverse selection of variables,
2. conduct a redundancy analysis on the fish assemblages of the Doubs River,
3. use a permutation test to determine the significance of the constrained analysis,

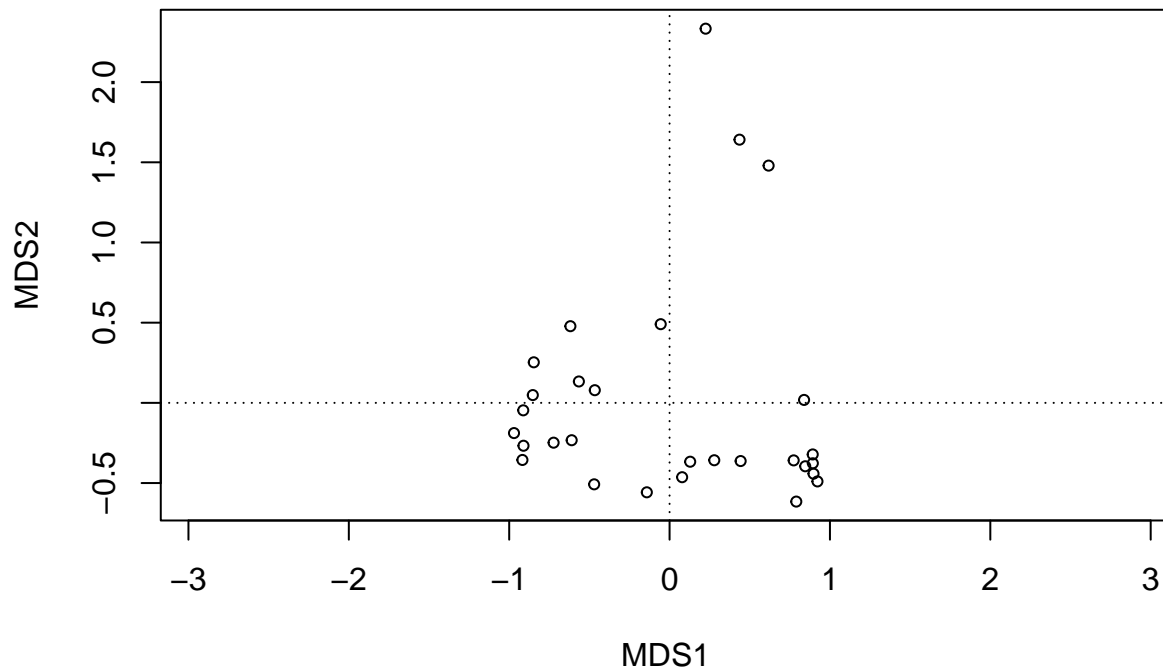
4. use a permutation test to determine the correlation of each environmental factor on the constrained axes,
5. calculate the explained variation on the first and second constrained axes,
6. plot the constrained ordination results including labeled points for each site, and
7. add vectors that demonstrate the influence of each environmental factor the constrained ordination.

```
#1
env.chem <- as.matrix(doubs$env[-8 , 5:11])

#2 dbRDA
fish.db<-vegdist(fish, method="bray")
doubs.dbrda <- dbrda(fish.db ~ ., as.data.frame(env.chem))
ordiplot(doubs.dbrda)
```



```
doubs.dbrda.mod0 <- dbrda(fish.db ~ 1, as.data.frame(env.chem))
ordiplot(doubs.dbrda.mod0)
```



```
doubs.dbrda.mod1 <- dbrda(fish.db ~ ., as.data.frame(env.chem))
doubs.dbrda <- ordiR2step(doubs.dbrda.mod0, doubs.dbrda.mod1, perm.max = 200)
```

```
## Step: R2.adj= 0
## Call: fish.db ~ 1
##
##               R2.adjusted
## <All variables> 0.53032584
## + oxy          0.27727176
## + nit          0.25755208
## + bdo          0.17477787
## + pho          0.14568614
## + har          0.14174915
## + amm          0.14142804
## <none>         0.00000000
## + pH          -0.01827054
##
##      Df    AIC      F Pr(>F)
## + oxy  1 47.939 11.742 0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2772718
## Call: fish.db ~ oxy
##
##               R2.adjusted
## <All variables> 0.5303258
## + bdo          0.4009000
## + amm          0.3474192
## + pho          0.3452702
## + har          0.3331357
## + nit          0.3316120
## <none>         0.2772718
```

```

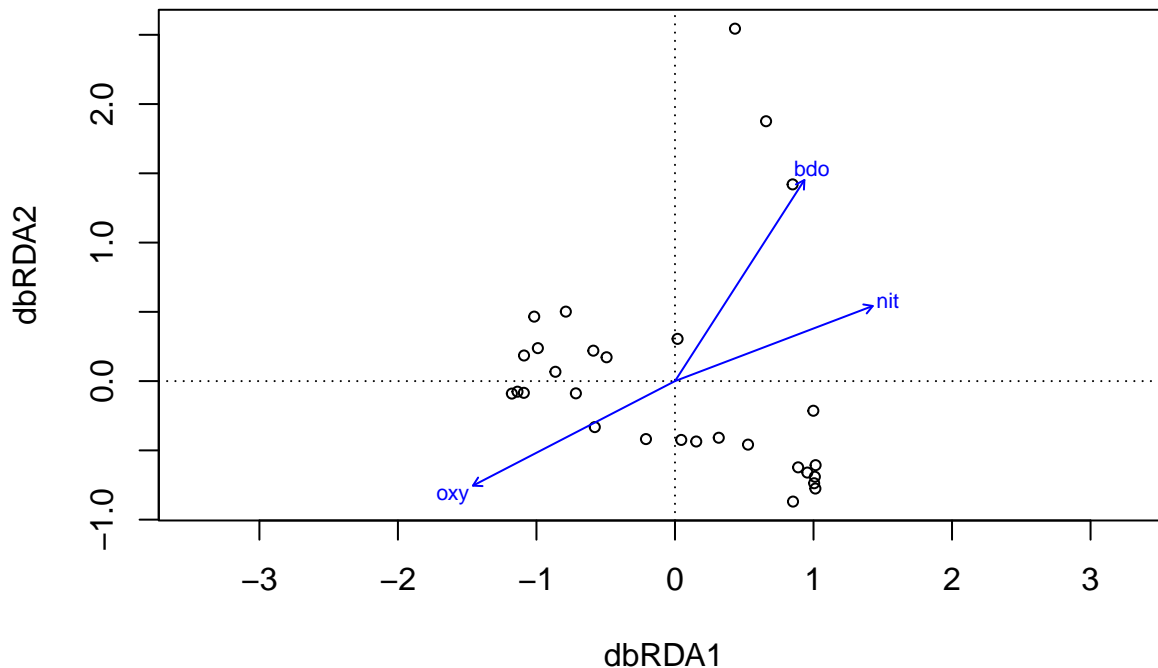
## + pH                0.2586983
##
##      Df      AIC      F Pr(>F)
## + bdo  1 43.404 6.5716 0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.4009
## Call: fish.db ~ oxy + bdo
##
##              R2.adjusted
## <All variables> 0.5303258
## + nit          0.4980793
## + har          0.4695121
## <none>         0.4009000
## + pho          0.3938042
## + amm          0.3869134
## + pH           0.3865240
##
##      Df      AIC      F Pr(>F)
## + nit  1 39.134 6.034 0.004 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.4980793
## Call: fish.db ~ oxy + bdo + nit
##
##              R2.adjusted
## + amm          0.5415705
## <All variables> 0.5303258
## + pho          0.5277128
## + har          0.5218852
## <none>         0.4980793
## + pH           0.4843267
doubts.dbrda$call

## dbrda(formula = fish.db ~ oxy + bdo + nit, data = as.data.frame(env.chem))
doubts.dbrda$anova

##              R2.adj Df      AIC      F Pr(>F)
## + oxy          0.27727  1 47.939 11.7421 0.002 **
## + bdo          0.40090  1 43.404  6.5716 0.002 **
## + nit          0.49808  1 39.134  6.0340 0.004 **
## <All variables> 0.53033
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
ordiplot(doubts.dbrda)

```





```
#3/4 permutation/significance/corr
permutest(doubs.dbrda, permutations = 999)
```

```
##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = fish.db ~ oxy + bdo + nit, data =
## as.data.frame(env.chem))
## Permutation test for all constrained eigenvalues
##      Df Inertia      F Pr(>F)
## Model   3  3.7317 10.262  0.001 ***
## Residual 25  3.0304
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
envfit(doubs.dbrda, env.chem[,c(4,6,7)], perm = 999)
```

```
##
## ***VECTORS
##
##      dbRDA1  dbRDA2      r2 Pr(>r)
## nit  0.87724  0.48005 0.6431  0.001 ***
## oxy -0.82864 -0.55979 0.7656  0.001 ***
## bdo  0.55603  0.83116 0.8939  0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
```

```
#5 explained variation
dbrda.explainvar1 <- round(doubs.dbrda$CCA$eig[1] /
```

```

sum(c(doubs.dbrda$CCA$eig, doubs.dbrda$CA$eig)), 3) * 100
dbrda.explainvar2 <- round(doubs.dbrda$CCA$eig[2] /
sum(c(doubs.dbrda$CCA$eig, doubs.dbrda$CA$eig)), 3) * 100

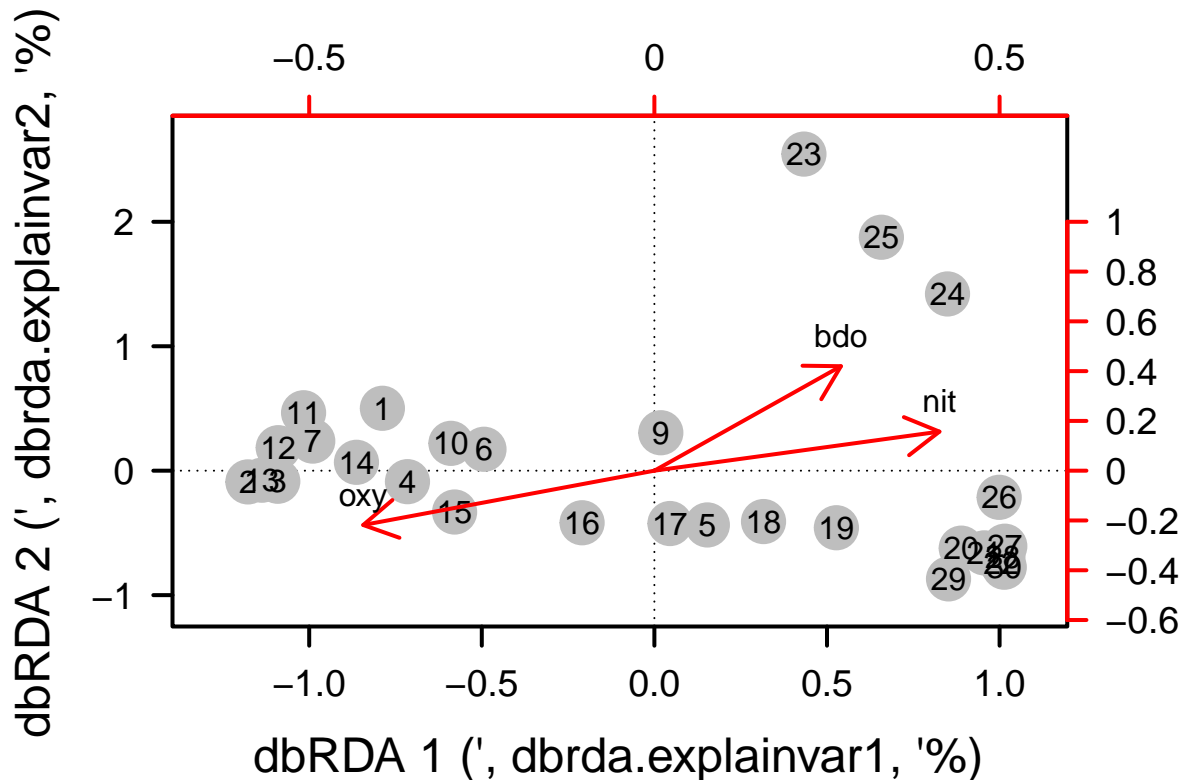
#6 plot ordination
par(mar = c(5, 5, 4, 4) + 0.1)
plot(scores(doubs.dbrda, display = "wa"), xlim = c(-1.3, 1.1),
      ylim = c(-1.1, 2.7), xlab = paste("dbRDA 1 ('", dbrda.explainvar1, '%)",
      sep = """, ylab = paste("dbRDA 2 ('", dbrda.explainvar2, '%)", sep = """,
      pch = 16, cex = 2.0, type = "n", cex.lab = 1.5,
      cex.axis = 1.2, axes = FALSE)

# axes
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, labels, vectors
points(scores(doubs.dbrda, display = "wa"),
       pch = 19, cex = 3, bg = "gray", col = "gray")
text(scores(doubs.dbrda, display = "wa"),
     labels = row.names(scores(doubs.dbrda, display = "wa")))
vectors <- scores(doubs.dbrda, display = "bp")

row.names(vectors) <- rownames(vectors)
arrows(0, 0, vectors[,1], vectors[, 2],
      lwd = 2, lty = 1, length = 0.2, col = "red")
text(vectors[,1], vectors[, 2], pos = 3,
     labels = row.names(vectors))
axis(side = 3, lwd.ticks=2, cex.axis=1.2, las = 1, col = "red", lwd = 2.2,
     at = pretty(range(vectors[, 1])) * 2, labels = pretty(range(vectors[, 1])))
axis(side = 4, lwd.ticks=2, cex.axis=1.2, las = 1, col = "red", lwd = 2.2,
     at = pretty(range(vectors[, 2])) * 2, labels = pretty(range(vectors[, 2])))

```



**Question 3:** Based on the constrained ordination, what are the environmental variables (or groups of correlated variables) that seem to be contributing to variation in fish community structure?

**Answer 3:** According to the dbRDA plot, biological oxygen demand, nitrogen, and oxygen are the main contributors for fish diversity.

### iii. Variation Partitioning

In the code chunk below,

1. Create a matrix model of the selected environmental variables,
2. Create a matrix model of the selected PCNM axes,
3. Perform constrained and partial constrained ordinations using the spatial and environmental models you just created,
4. Test the significance of each of your constrained ordinations using permutation tests,
5. Partition the variation among sites into the relative importance of space, environment, spatially structured environment, and residuals,
6. Plot the variation partitioning output to visualize it.

```
doubs.dbrda$anova
```

```
##           R2.adj Df      AIC      F Pr(>F)
## + oxy       0.27727 1 47.939 11.7421 0.002 **
## + bdo       0.40090 1 43.404  6.5716 0.002 **
## + nit       0.49808 1 39.134  6.0340 0.004 **
## <All variables> 0.53033
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

env.mod <- model.matrix(~ oxy + bdo + nit, as.data.frame(env.chem))[, -1]
rs <- rowSums(fish)/sum(fish)
```

```
doubs.pcnmw <- pcnm(dist(doubs$xy[-8,]), w = rs, dist.ret = T)
doubs.pcnmw$values > 0
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [13] TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [25] FALSE FALSE
```

```
doubs.space <- as.data.frame(scores(doubs.pcnmw))
doubs.pcnm.mod0 <- dbrda(fish.db ~ 1, doubs.space)
doubs.pcnm.mod1 <- dbrda(fish.db ~ ., doubs.space)
step.pcnm <- ordiR2step(doubs.pcnm.mod0, doubs.pcnm.mod1, perm.max = 200)
```

```
## Step: R2.adj= 0
## Call: fish.db ~ 1
##
##               R2.adjusted
## <All variables> 0.626011301
## + PCNM2         0.235370423
## + PCNM3         0.078394885
## + PCNM13        0.065305668
## + PCNM5         0.046185074
## + PCNM6         0.032809156
## + PCNM16        0.030486700
## + PCNM14        0.029680999
## + PCNM9         0.020357410
## + PCNM15        0.013632610
## + PCNM8         0.009411968
## + PCNM1         0.003986221
## + PCNM17        0.002415012
## + PCNM10        0.001326442
## <none>          0.000000000
## + PCNM7         -0.001861430
## + PCNM11        -0.006841522
## + PCNM4         -0.007089863
## + PCNM12        -0.014396973
##
##           Df      AIC      F Pr(>F)
## + PCNM2   1 49.574 9.619 0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2353704
## Call: fish.db ~ PCNM2
##
##               R2.adjusted
## <All variables> 0.6260113
## + PCNM3         0.3429270
## + PCNM5         0.3057368
## + PCNM1         0.2885396
## + PCNM16        0.2786746
## + PCNM14        0.2744520
## + PCNM15        0.2692809
## + PCNM6         0.2659866
## + PCNM13        0.2636194
```

```

## + PCNM9          0.2517847
## + PCNM8          0.2496240
## + PCNM10         0.2434688
## + PCNM7          0.2431476
## + PCNM17         0.2404343
## + PCNM11         0.2366833
## <none>           0.2353704
## + PCNM12         0.2288789
## + PCNM4          0.2189522
##
##           Df      AIC      F Pr(>F)
## + PCNM3    1 46.083 5.4196 0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.342927
## Call: fish.db ~ PCNM2 + PCNM3
##
##           R2.adjusted
## <All variables> 0.6260113
## + PCNM5          0.4076020
## + PCNM1          0.3970300
## + PCNM16         0.3853210
## + PCNM15         0.3828748
## + PCNM14         0.3781827
## + PCNM13         0.3770376
## + PCNM6          0.3595644
## + PCNM8          0.3556885
## + PCNM7          0.3541631
## + PCNM10         0.3526775
## + PCNM17         0.3513683
## + PCNM9          0.3433672
## <none>           0.3429270
## + PCNM11         0.3416399
## + PCNM12         0.3396547
## + PCNM4          0.3311509
##
##           Df      AIC      F Pr(>F)
## + PCNM5    1 43.941 3.8385 0.008 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.407602
## Call: fish.db ~ PCNM2 + PCNM3 + PCNM5
##
##           R2.adjusted
## <All variables> 0.6260113
## + PCNM1          0.4721469
## + PCNM16         0.4631976
## + PCNM15         0.4589111
## + PCNM14         0.4535248
## + PCNM13         0.4511582
## + PCNM6          0.4305640
## + PCNM7          0.4261965

```

```

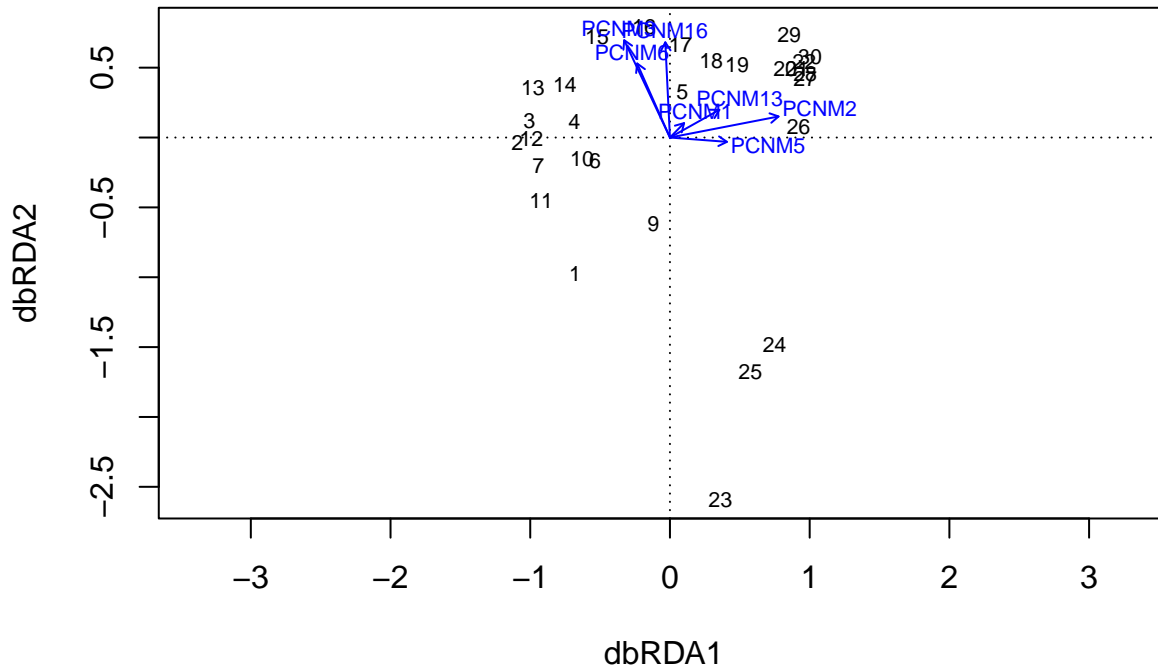
## + PCNM8          0.4224505
## + PCNM17         0.4181666
## + PCNM10         0.4154485
## + PCNM11         0.4112178
## + PCNM9          0.4111995
## + PCNM12         0.4087602
## <none>           0.4076020
## + PCNM4          0.3976526
##
##           Df      AIC      F Pr(>F)
## + PCNM1  1 41.411 4.057  0.004 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.4721469
## Call: fish.db ~ PCNM2 + PCNM3 + PCNM5 + PCNM1
##
##           R2.adjusted
## <All variables>  0.6260113
## + PCNM13         0.5212427
## + PCNM16         0.5208668
## + PCNM15         0.5161770
## + PCNM14         0.5147355
## + PCNM6          0.4999020
## + PCNM7          0.4936559
## + PCNM8          0.4904113
## + PCNM17         0.4856884
## + PCNM10         0.4835952
## + PCNM11         0.4760087
## + PCNM9          0.4751424
## + PCNM12         0.4747221
## <none>           0.4721469
## + PCNM4          0.4651218
##
##           Df      AIC      F Pr(>F)
## + PCNM13  1 39.346 3.4612  0.016 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.5212427
## Call: fish.db ~ PCNM2 + PCNM3 + PCNM5 + PCNM1 + PCNM13
##
##           R2.adjusted
## <All variables>  0.6260113
## + PCNM16         0.5767968
## + PCNM15         0.5715331
## + PCNM14         0.5698343
## + PCNM6          0.5475140
## + PCNM7          0.5392074
## + PCNM8          0.5379134
## + PCNM11         0.5281106
## + PCNM9          0.5267003
## + PCNM10         0.5265029
## + PCNM12         0.5255581

```

```

## <none>          0.5212427
## + PCNM17        0.5171800
## + PCNM4         0.5152311
##
##           Df      AIC      F Pr(>F)
## + PCNM16  1 36.48 4.0192  0.01 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.5767968
## Call: fish.db ~ PCNM2 + PCNM3 + PCNM5 + PCNM1 + PCNM13 + PCNM16
##
##           R2.adjusted
## <All variables>  0.6260113
## + PCNM6         0.6043089
## + PCNM8         0.5970286
## + PCNM12        0.5946888
## + PCNM7         0.5946475
## + PCNM9         0.5883735
## + PCNM10        0.5851333
## + PCNM15        0.5846468
## <none>          0.5767968
## + PCNM17        0.5748533
## + PCNM4         0.5733749
## + PCNM11        0.5711176
## + PCNM14        0.5652509
##
##           Df      AIC      F Pr(>F)
## + PCNM6  1 35.182 2.5296  0.036 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.6043089
## Call: fish.db ~ PCNM2 + PCNM3 + PCNM5 + PCNM1 + PCNM13 + PCNM16 + PCNM6
##
##           R2.adjusted
## <All variables>  0.6260113
## + PCNM8         0.6248697
## + PCNM12        0.6208788
## + PCNM10        0.6170988
## + PCNM7         0.6142419
## + PCNM15        0.6140369
## + PCNM9         0.6107110
## <none>          0.6043089
## + PCNM17        0.6037430
## + PCNM11        0.5978305
## + PCNM4         0.5963667
## + PCNM14        0.5932113
##
##           Df      AIC      F Pr(>F)
## + PCNM8  1 34.219 2.151  0.104
plot(step.pcnm)

```



```
step.pcnm$anova
```

```
##           R2.adj Df      AIC      F Pr(>F)
## + PCNM2      0.23537  1 49.574  9.6190  0.002 **
## + PCNM3      0.34293  1 46.083  5.4196  0.002 **
## + PCNM5      0.40760  1 43.941  3.8385  0.008 **
## + PCNM1      0.47215  1 41.411  4.0570  0.004 **
## + PCNM13     0.52124  1 39.346  3.4612  0.016 *
## + PCNM16     0.57680  1 36.480  4.0192  0.010 **
## + PCNM6      0.60431  1 35.182  2.5296  0.036 *
## <All variables> 0.62601
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

space.mod <- model.matrix(~ PCNM2 + PCNM3 + PCNM5 + PCNM1 +
                           PCNM13 + PCNM16 + PCNM6, dous.space)[-1]

# first conduct constrained ordinations
dous.total.env <- dbrda(fish.db ~ env.mod)
dous.total.space <- dbrda(fish.db ~ space.mod)

# partial constrained ordinations
dous.env.cond.space <- dbrda(fish.db ~ env.mod + Condition(space.mod))
dous.space.cond.env <- dbrda(fish.db ~ space.mod + Condition(env.mod))

# dbRDA fraction significance
permutest(dous.env.cond.space, permutations = 999)

##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 999
##
```



```

## Model: dbrda(formula = fish.db ~ env.mod + Condition(space.mod))
## Permutation test for all constrained eigenvalues
##           Df Inertia      F Pr(>F)
## Model      3 0.85158 4.423  0.001 ***
## Residual 18 1.15519
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

permutest(doubs.space.cond.env, permutations = 999)

##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = fish.db ~ space.mod + Condition(env.mod))
## Permutation test for all constrained eigenvalues
##           Df Inertia      F Pr(>F)
## Model      7 1.8752 4.1741  0.001 ***
## Residual 18 1.1552
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

permutest(doubs.total.env, permutations = 999)

##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = fish.db ~ env.mod)
## Permutation test for all constrained eigenvalues
##           Df Inertia      F Pr(>F)
## Model      3 3.7317 10.262  0.001 ***
## Residual 25 3.0304
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

permutest(doubs.total.space, permutations = 999)

##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = fish.db ~ space.mod)
## Permutation test for all constrained eigenvalues
##           Df Inertia      F Pr(>F)
## Model      7 4.7553 7.1089  0.001 ***
## Residual 21 2.0068
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

# varpart() function
doubs.varpart <- varpart(fish.db, env.mod, space.mod)
doubs.varpart

##
## Partition of squared Bray distance in dbRDA
##
## Call: varpart(Y = fish.db, X = env.mod, space.mod)
##
## Explanatory tables:
## X1:  env.mod
## X2:  space.mod
##
## No. of explanatory tables: 2
## Total variation (SS): 6.7621
## No. of observations: 29
##
## Partition table:
##


|                    | Df | R.squared | Adj.R.squared | Testable |
|--------------------|----|-----------|---------------|----------|
| ## [a+c] = X1      | 3  | 0.55186   | 0.49808       | TRUE     |
| ## [b+c] = X2      | 7  | 0.70323   | 0.60431       | TRUE     |
| ## [a+b+c] = X1+X2 | 10 | 0.82917   | 0.73426       | TRUE     |

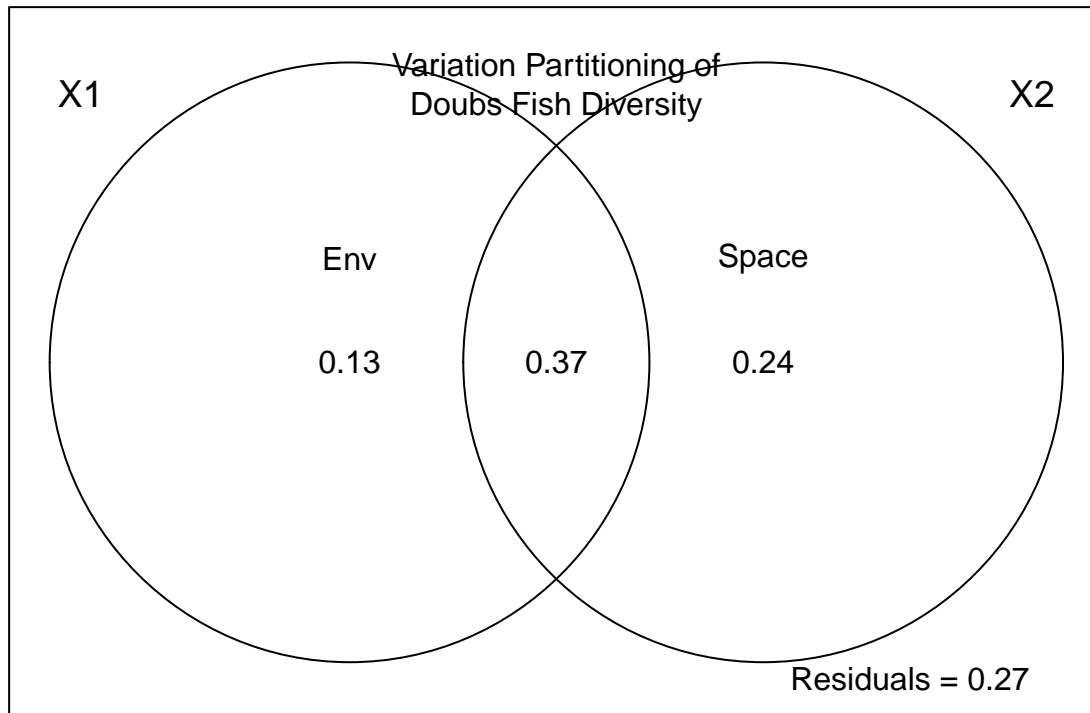

## Individual fractions


|                    |   |  |         |       |
|--------------------|---|--|---------|-------|
| ## [a] = X1 X2     | 3 |  | 0.12995 | TRUE  |
| ## [b] = X2 X1     | 7 |  | 0.23618 | TRUE  |
| ## [c]             | 0 |  | 0.36813 | FALSE |
| ## [d] = Residuals |   |  | 0.26574 | FALSE |


## ---
## Use function 'dbrda' to test significance of fractions of interest

par(mar = c(2,2,2,2))
plot(doubs.varpart)
text(1, 0.25, "Space")
text(0, 0.25, "Env")
mtext("Variation Partitioning of\nDoubs Fish Diversity", side = 3, line = -3)

```



**Question 4:** Interpret the variation partitioning results.

**Answer 4:** A total of 74% of fish diversity variation is explained by environmental and spatial factors. 37% is attributed to integration of both spatial and environmental factors, meaning there is a close relationship between the two factors. Biologically, this makes sense, as two sites closer in proximity are more likely to be similar in habitat.

## SYNTHESIS

Load the dataset from that you and your partner are using for the team project. Use one of the hypothesis-testing tools introduced in the beta diversity module. Interpret the findings of your data with respect to principles of biodiversity.

```
#couldn't get this to work, will try again
zoobs<-read.csv('/cloud/project/QB2025_Park/Week4-Beta/merged_data_full.csv')
zoobsA<-read.csv('/cloud/project/QB2025_Park/Week4-Beta/SbS_full.csv',
header = TRUE)
zoobs.db<-vegdist(zoobsA, method="bray")
zoobs.dbrda.mod0 <- dbrda(zoobs.db ~ 1,
as.data.frame(zoobs[,11-25]))
ordiplot(doubs.dbrda.mod0)
```

```
permutation/significance/corr permutest(zoobs.dbrda, permutations = 999)
envfit(doubs.dbrda, env.chem[,c(4,6,7)], perm = 999)
```

```
#5 explained variation
dbrda.explainvar1 <- round(doubs.dbrdaCCAeig[1] / sum(c(doubs.dbrdaCCAeig,
doubs.dbrdaCAeig)), 3) * 100
dbrda.explainvar2 <- round(doubs.dbrdaCCAeig[2] / sum(c(doubs.dbrdaCCAeig,
doubs.dbrdaCAeig)), 3) * 100
```

```
#6 plot ordination
par(mar = c(5, 5, 4, 4) + 0.1)
plot(scores(doubs.dbrda, display = "wa"), xlim = c(-1.3, 1.1), ylim = c(-1.1, 2.7),
xlab = paste("dbRDA 1 ('", dbrda.explainvar1, "%)", sep = ""), ylab = paste("dbRDA 2 ('",
dbrda.explainvar2, "%)", sep = ""), pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)
```

## axes

```
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, labels, vectors

```
points(scores(doubs.dbrda, display = "wa"), pch = 19, cex = 3, bg = "gray", col = "gray")
text(scores(doubs.dbrda, display = "wa"), labels = row.names(scores(doubs.dbrda, display = "wa"))) vectors
<- scores(doubs.dbrda, display = "bp")
```

```
row.names(vectors) <- rownames(vectors) arrows(0, 0, vectors[,1], vectors[, 2], lwd = 2, lty = 1, length
= 0.2, col = "red") text(vectors[,1], vectors[, 2], pos = 3, labels = row.names(vectors)) axis(side = 3,
lwd.ticks=2, cex.axis=1.2, las = 1, col = "red", lwd = 2.2, at = pretty(range(vectors[, 1])) * 2, labels =
pretty(range(vectors[, 1]))) axis(side = 4, lwd.ticks=2, cex.axis=1.2, las = 1, col = "red", lwd = 2.2, at =
pretty(range(vectors[, 2])) * 2, labels = pretty(range(vectors[, 2]))) ““
```