

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 β -diversity. Now that you know how to formally quantify β -diversity, we will learn how to 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, 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 12th, 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] "C:/github/QB2026_Stancil/QB2026/Week4-Beta"
```

```
setwd("../Week4-Beta/") #change to wherever your wd is  
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 4.5.2
```

```
## Loading required package: permute
```

```
## Warning: package 'permute' was built under R version 4.5.2
```

```
library(ade4)
```

```
## Warning: package 'ade4' was built under R version 4.5.2
```

```
library(indicspecies)
```

```
## Warning: package 'indicspecies' was built under R version 4.5.2
```

2) LOADING DATA

Load dataset

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

```
# note, please do not print the dataset when submitting  
data(doubs)  
fish <- doubs$fish
```

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.

```

data(doubs)
fish <- doubs$fish
fish <- fish[-8, ]
# Create "Factors" vector
quality <- c(rep("HQ", 13), rep("MQ", 5), rep("LQ", 6), rep("MQ", 5))

# Run PERMANOVA with adonis function
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))
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  0.014 *
##
## Group HQ+MQ #sps. 2
##      stat p.value
## Satr 0.860  0.005 **
## Phph 0.859  0.011 *
##
## 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    0.006 **
## Titi 0.853    0.004 **
## Chto 0.829    0.001 ***
## Rham 0.829    0.002 **
## Anan 0.829    0.002 **
## Eslu 0.827    0.013 *
## Pefl 0.806    0.014 *
## Blbj 0.791    0.001 ***
## Scer 0.766    0.010 **
## Abbr 0.750    0.005 **
## Icme 0.661    0.023 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

fish.rel <- decostand(fish, method = "total")
phi <- multipatt(fish.rel, cluster = quality, func = "r.g",
  control = how(nperm=999))
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    0.001 ***
##
## Group LQ #sps. 2
##      stat p.value
## Alal 0.693    0.001 ***
## Ruru 0.473    0.034 *
##
## Group MQ #sps. 4
##      stat p.value
## Anan 0.571    0.007 **

```

```
## Spbi 0.557    0.007 **
## Chto 0.542    0.008 **
## Icme 0.475    0.035 *
##
## Group LQ+MQ #sps. 9
##      stat p.value
## Legi 0.658    0.004 **
## Baba 0.645    0.005 **
## Rham 0.600    0.005 **
## Acce 0.594    0.005 **
## Cyca 0.586    0.008 **
## Chna 0.571    0.003 **
## Blbj 0.571    0.011 *
## Gogo 0.523    0.010 **
## Abbr 0.499    0.027 *
## ---
## 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: Fish communities seemed to be obviously different depending on the quality (high, low, or medium) of the water! It was interesting to see such distinct separation. However, HQ actually had the fewest species, which was very interesting. I think so? We never created a good figure to show the environmental conditions of each site, so it is difficult to directly compare.

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.

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

#Mantel Test
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 0.133 0.154 0.202
## 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 high r value from the Mantel test suggests that the fish community differences and environmental differences are strongly positively correlated. So therefore, when the stream has more nutrients, more species tend to be present. This supports my hypothesis that higher nutrients supports more species.

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.

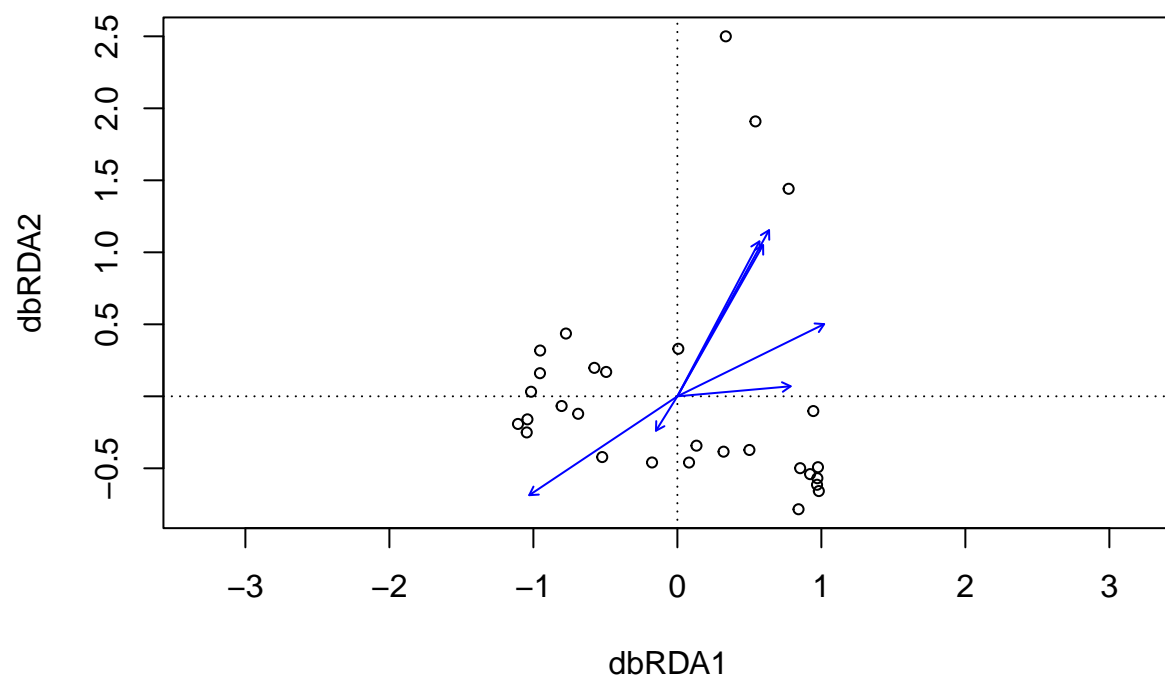
```
fish.dj <- vegdist(fish, method = "jaccard", binary = TRUE)

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

# Calculate Sørensen
fish.ds <- vegdist(fish, method = "bray", binary = TRUE)

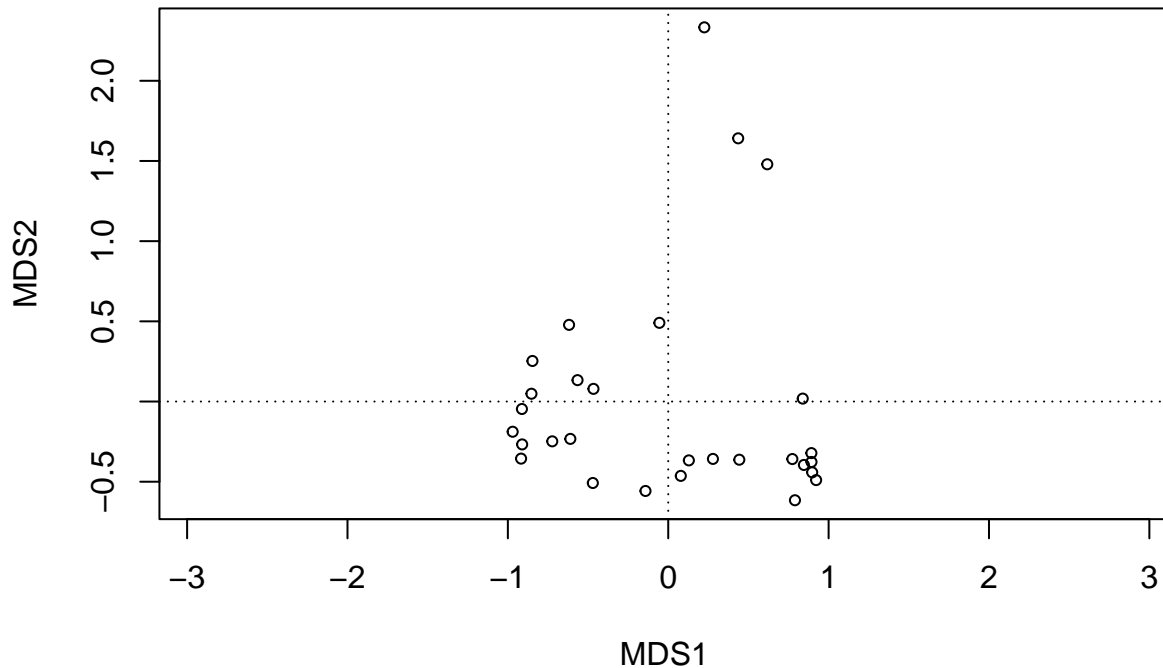
# Define environmental matrix
env.chem <- as.matrix(doubs$env[-8 , 5:11])

# Perform dbRDA
doubs.dbrda <- dbrda(fish.db ~ ., as.data.frame(env.chem))
ordiplot(doubs.dbrda)
```



```
# First, we will model only the intercept
doubts.dbrda.mod0 <- dbrda(fish.db ~ 1, as.data.frame(env.chem))

# Note there are no vectors here (we didn't constrain anything)
# Therefore, the axes suggest this is a simple MDS (i.e., PCoA)
ordiplot(doubts.dbrda.mod0)
```



```
# Define Plot Parameters
par(mar = c(5, 5, 4, 4) + 0.1)

# Calculate 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

# Initiate Plot
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)

# Add 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)

# Add Points & Labels
points(scores(doubs.dbrda, display = "wa"),
  pch = 19, cex = 3, bg = "gray", col = "gray")
text(scores(doubs.dbrda, display = "wa"),
```

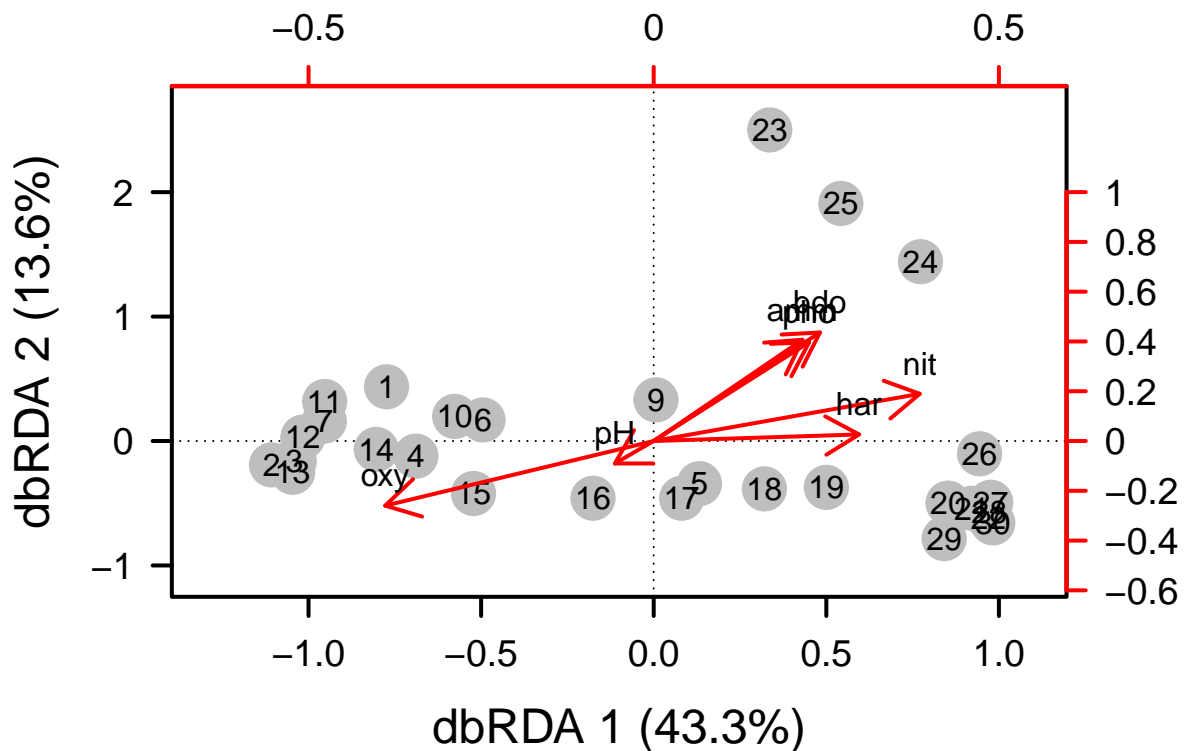


```

labels = row.names(scores(doubs.dbrda, display = "wa"))

# Add Environmental Vectors
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])))

```



```

# Next, we will model the full model, with all explanatory variables
doubs.dbrda.mod1 <- dbrda(fish.db ~ ., as.data.frame(env.chem))

# Now we step through all combinations of explanatory variables in our model
# The function returns the model with the lowest AIC value
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
## <model>        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
## <model>        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
## <model>        0.4009000
## + pho          0.3938042
## + amm          0.3869134
## + pH           0.3865240
##
##           Df      AIC      F Pr(>F)
## + nit  1 39.134 6.034 0.002 **
## ---
## 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
## <model>         0.4980793
## + pH           0.4843267
```

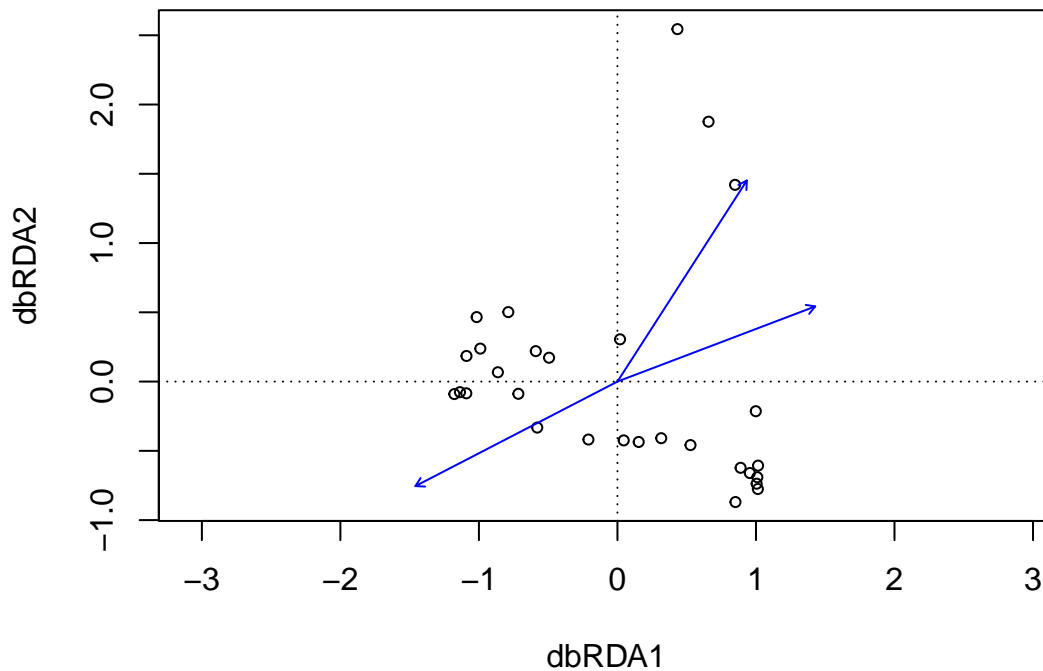
```
# Lets look at the model that was selected
doubts.dbrda$call
```

```
## 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 0.002 **
## <All variables> 0.53033
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ordiplot(doubts.dbrda)
```



```
# Permutation tests to evaluate significance
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
```

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: Oxygen and nitrogen seem to be important vectors that are contributing to the variation we observe. Dissolved chemicals.

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.

```
# Remember, our environmental model uses oxy, bdo, and nit and has R2 of 0.53
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  0.002 **
## <All variables> 0.53033
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Let's create a matrix model for our environmental data
env.mod <- model.matrix(~ oxy + bdo + nit, as.data.frame(env.chem))[, -1]
```

```
# First, we will weight each site by its relative abundance
rs <- rowSums(fish)/sum(fish)
```

```
# Next, we will perform PCNM
doubs.pcnmw <- pcnm(dist(doubs$xy[-8,]), w = rs, dist.ret = T)
```

```
# PCNM can return negative eigenvalues, but only the
# eigenvectors associated with the positive eigenvalues are meaningful
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
## <model>          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
## <model>         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
## <model>          0.3429270
## + PCNM11         0.3416399
## + PCNM12         0.3396547
## + PCNM4          0.3311509
##
##           Df      AIC      F Pr(>F)
## + PCNM5  1 43.941 3.8385 0.016 *
## ---
## 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
## <model>         0.4076020
## + PCNM4          0.3976526
##
##           Df      AIC      F Pr(>F)
## + PCNM1  1 41.411 4.057 0.01 **
## ---
## 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

```

```

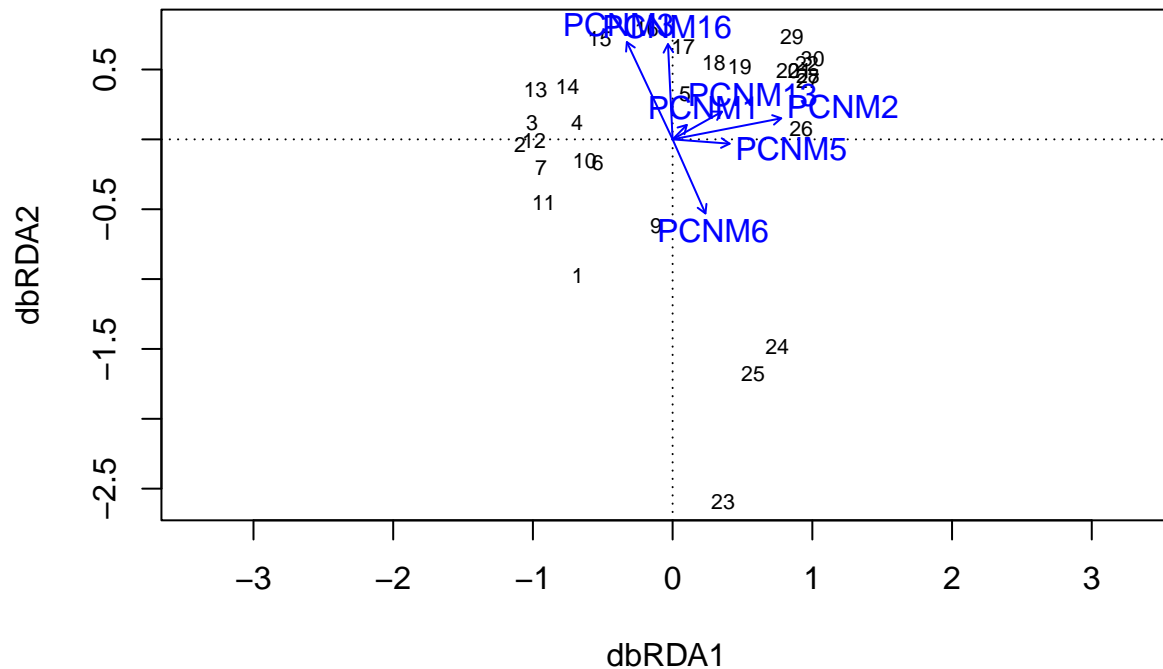
## <model>          0.4721469
## + PCNM4          0.4651218
##
##           Df      AIC      F Pr(>F)
## + PCNM13  1 39.346 3.4612 0.008 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.5212427
## Call: fish.db ~ PCNM2 + PCNM3 + PCNM5 + PCNM1 + PCNM13
##
##           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
## <model>          0.5212427
## + PCNM17          0.5171800
## + PCNM4           0.5152311
##
##           Df      AIC      F Pr(>F)
## + PCNM16  1 36.48 4.0192 0.002 **
## ---
## 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
## <model>          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 0.044 *
## ---
## 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
## <model>        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  0.102
```

```
# Because this is another dbRDA, we could visualize the biplot
# showing how each vector explains variation across sites
plot(step.pcnm)
```



```
# The object `step.pcnm` now contains the selected model.
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 0.016 *
## + PCNM1         0.47215 1 41.411 4.0570 0.010 **
## + PCNM13        0.52124 1 39.346 3.4612 0.008 **
## + PCNM16        0.57680 1 36.480 4.0192 0.002 **
## + PCNM6         0.60431 1 35.182 2.5296 0.044 *
## <All variables> 0.62601
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# We can now construct a spatial model using only the selected PCNM axes.
space.mod <- model.matrix(~ PCNM2 + PCNM3 + PCNM5 + PCNM1 +
                          PCNM13 + PCNM16 + PCNM6, doubts.space)[-1]
```

```
# First conduct constrained ordinations
doubts.total.env <- dbrda(fish.db ~ env.mod)
doubts.total.space <- dbrda(fish.db ~ space.mod)
```

```
# Next construct partial constrained ordinations
doubts.env.cond.space <- dbrda(fish.db ~ env.mod + Condition(space.mod))
doubts.space.cond.env <- dbrda(fish.db ~ space.mod + Condition(env.mod))
```

```
# Next test for significance of the dbRDA fractions.
permutest(doubts.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(doubts.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
```

```
# Using the built-in varpart() function
doubs.varpart <- varpart(fish.db, env.mod, space.mod)
doubs.varpart
```

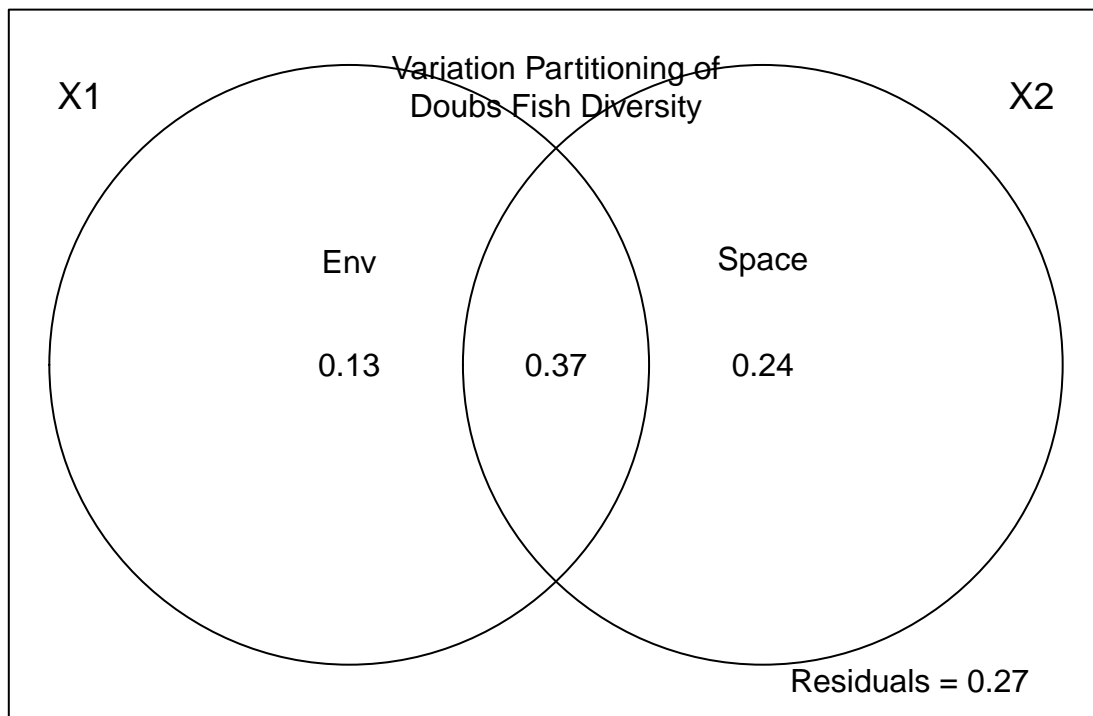
```
##
## Partition of squared Bray distance in dbRDA
##
## Call: varpart(Y = fish.db, X = env.mod, space.mod)
##
## Explanatory tables:
## X1:  env.mod
## X2:  space.mod
```

```
##
## 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: Most of the variation in the fish data is explained by both Environmental and the Space variation. Space alone seems to also explain a large chunk of the fish variation. This means that there are differences along the river that are not directly tied to factors like dissolved oxygen, nitrogen, etc.