8. 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, it is *imperative* that you **push** this file to your GitHub repo, at whatever stage you are. This will enable you to pull your work onto your own computer.
6. When you have completed the worksheet, **Knit** the text and code into a single PDF file by pressing the `Knit` button in the RStudio scripting panel. This will save the PDF output in your '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_2_Worksheet.Rmd**) with all code blocks filled out and questions answered) and the PDF output of `Knitr` (**8.BetaDiversity_2_Worksheet**

The completed exercise is due on **Wednesday, February 13th, 2019 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 "*/8.BetaDiversity*" folder, and
4. load the `vegan` R package (be sure to install if needed).

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

```
## [1] "C:/Users/andjr/Github2/QB2019_Phillips/2.Worksheets/8.BetaDiversity"
```

```
install.packages("vegan", repos = "http://cran.us.r-project.org")
```

```
## Installing package into 'C:/Users/andjr/Documents/R/win-library/3.5'
## (as 'lib' is unspecified)
```

```
## package 'vegan' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
##  C:\Users\andjr\AppData\Local\Temp\Rtmpquls2r\downloaded_packages
```

```
require("vegan")
```

```
## Loading required package: vegan
```

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

```
## Loading required package: lattice
```

```
## This is vegan 2.5-4
```

```
#install.packages("OTUtable", repos = "http://cran.us.r-project.org")
require("OTUtable")
```

```
## Loading required package: OTUtable
```

```
#install.packages("ade4", repos = "http://cran.us.r-project.org")
require("ade4")
```

```
## Loading required package: ade4
```

```
#install.packages("indicspecies", repos = "http://cran.us.r-project.org")
require("indicspecies")
```

```
## Loading required package: indicspecies
```

```
require("tidyverse")
```

```
## Loading required package: tidyverse
```

```
## -- Attaching packages ---------------------------------------------------------------------------
```

```
## v ggplot2 3.1.0     v purrr   0.3.0
## v tibble  2.0.1     v dplyr   0.7.8
## v tidyr   0.8.2     v stringr 1.3.1
## v readr   1.3.1     v forcats 0.3.0
```

```
## -- Conflicts ------------------------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
require("vegan")
require("ggplot2")
require("OTUtable")
```

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
#install.packages("ade4", repos = "http://cran.us.r-project.org")
#require("ade4")
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.

```
install.packages("vegan", repos = "http://cran.us.r-project.org")
```

```
## Installing package into 'C:/Users/andjr/Documents/R/win-library/3.5'
## (as 'lib' is unspecified)
```

```
## Warning: package 'vegan' is in use and will not be installed
```

```
require("vegan")
fish <- doubs$fish
fish <- fish[-8, ]

quality <- c(rep("HQ", 13), rep("MQ", 5), rep("LQ", 6), rep("MQ", 5))

adonis(fish ~ quality, method = "bray", permutations = 999)
```

```
##
## Call:
## adonis(formula = fish ~ quality, permutations = 999, method = "bray")
##
## Permutation: free
## Number of permutations: 999
```

```
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## quality    2    3.0947 1.54733   10.97 0.45765  0.001 ***
## Residuals 26    3.6674 0.14105         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   0.019 *
##
##  Group HQ+MQ  #sps.  2
##       stat p.value
## Satr 0.860   0.004 **
## Phph 0.859   0.013 *
##
##  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   0.002 **
## Titi 0.853   0.004 **
## Chto 0.829   0.001 ***
## Rham 0.829   0.001 ***
## Anan 0.829   0.001 ***
## Eslu 0.827   0.022 *
## Pefl 0.806   0.009 **
```

```
## Blbj 0.791   0.003 **
## Scer 0.766   0.009 **
## Abbr 0.750   0.005 **
## Icme 0.661   0.025 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
fish.rel <- decostand(fish, metho = "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   0.002 **
## Satr 0.650   0.001 ***
##
##  Group LQ  #sps.  2
##       stat p.value
## Alal 0.693   0.001 ***
## Ruru 0.473   0.032 *
##
##  Group MQ  #sps.  4
##       stat p.value
## Anan 0.571   0.009 **
## Spbi 0.557   0.007 **
## Chto 0.542   0.010 **
## Icme 0.475   0.030 *
##
##  Group LQ+MQ  #sps.  9
##       stat p.value
## Legi 0.658   0.002 **
## Baba 0.645   0.001 ***
## Rham 0.600   0.007 **
## Acce 0.594   0.002 **
## Cyca 0.586   0.003 **
## Chna 0.571   0.002 **
## Blbj 0.571   0.006 **
## Gogo 0.523   0.014 *
## Abbr 0.499   0.018 *
```

```
## ---
## 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 indicates that habitat quality and species composition are highly correlated, with a p-value of .001, and about 45% of the variation in one explained by the variation in the other. IndVal has varying significance depending on the species–some species have a p-value that rises to around .02, which is still considered significant. Most species show high correlation with habitat quality according to IndVal, however. Phi coefficient follows this pattern, with habitat quality and fish species correlated. I would say that this does agree with our previous visualizations–the patterns we saw point to certain quality indicator species, which in and of itself implies that habitat quality is going to make a difference when it comes to species composition.

B. Multivariate Procedures for Continuous Designs

i. Mantel Test

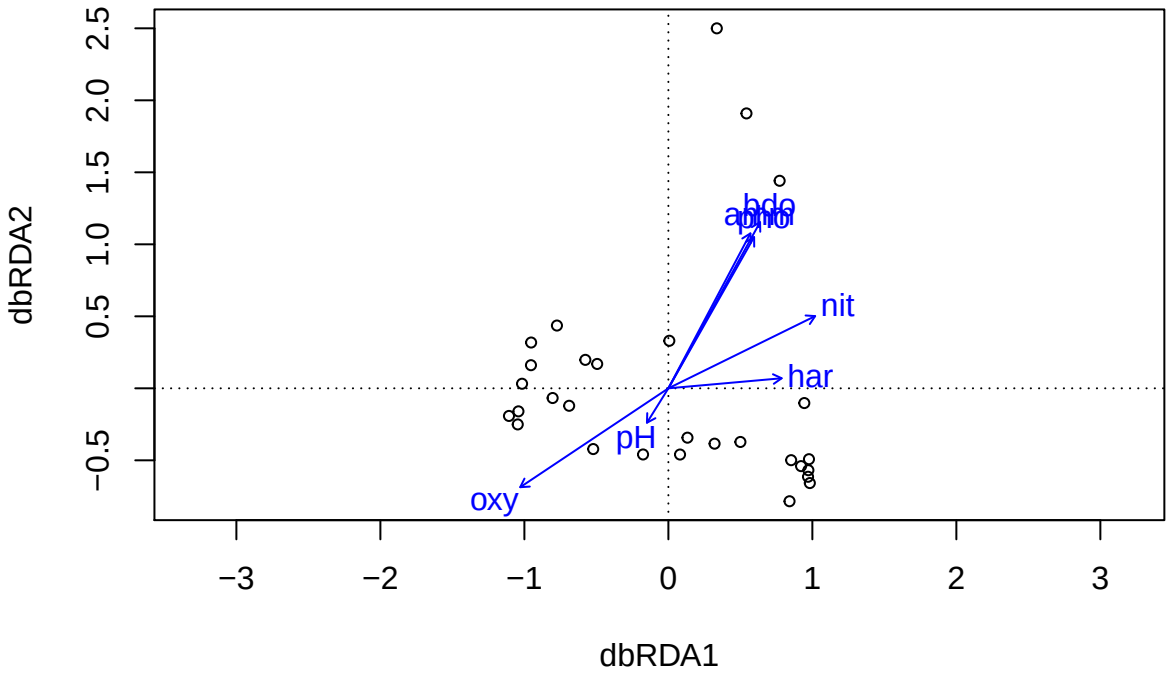
In the R code chunk below, do the following:

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.db <- vegdist(fish, method = "bray", diag = TRUE)
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%
## 0.111 0.149 0.181 0.200
## Permutation: free
## Number of permutations: 999
```

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

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



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?

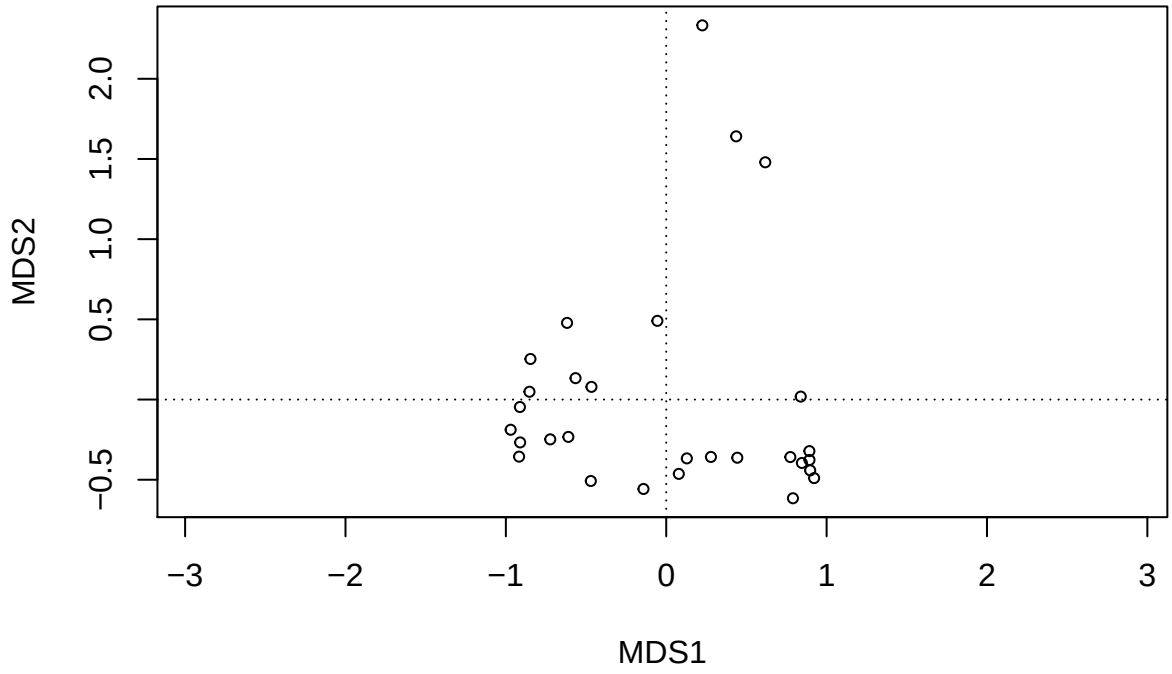
> ***Answer 2***: Once again, with a p-value of .001, the Mantel test shows that stream quality and fish species diversity are highly correlated, supporting my previous hypothesis. Specifically, about half the species are negatively correlated with har and nit, and the other half negatively correlated with oxy and pH. The remaining environmental indicators are mostly negatively correlated with species diversity.

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.

```
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  0.002 **
## ---
## 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
## <none>            0.4980793
## + pH              0.4843267
```

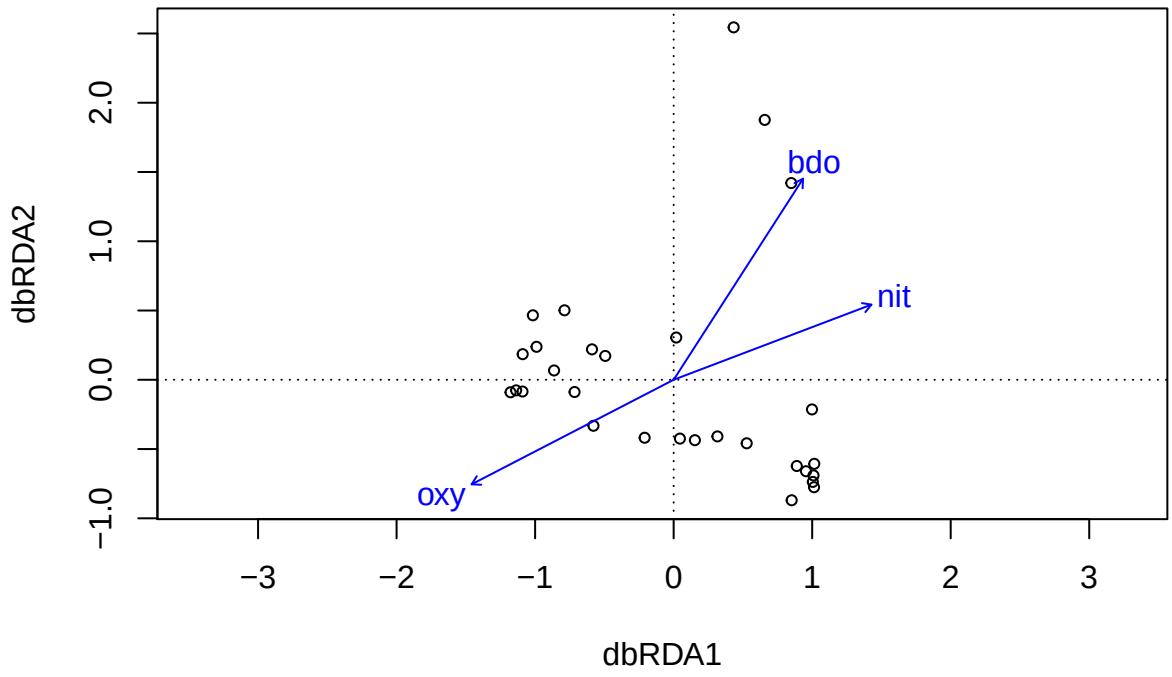
```
doubs.dbrda$call
```

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

```
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
```

```
ordiplot(doubs.dbrda)
```




```
permutest(doubs.dbrda, permutations = 999)
```

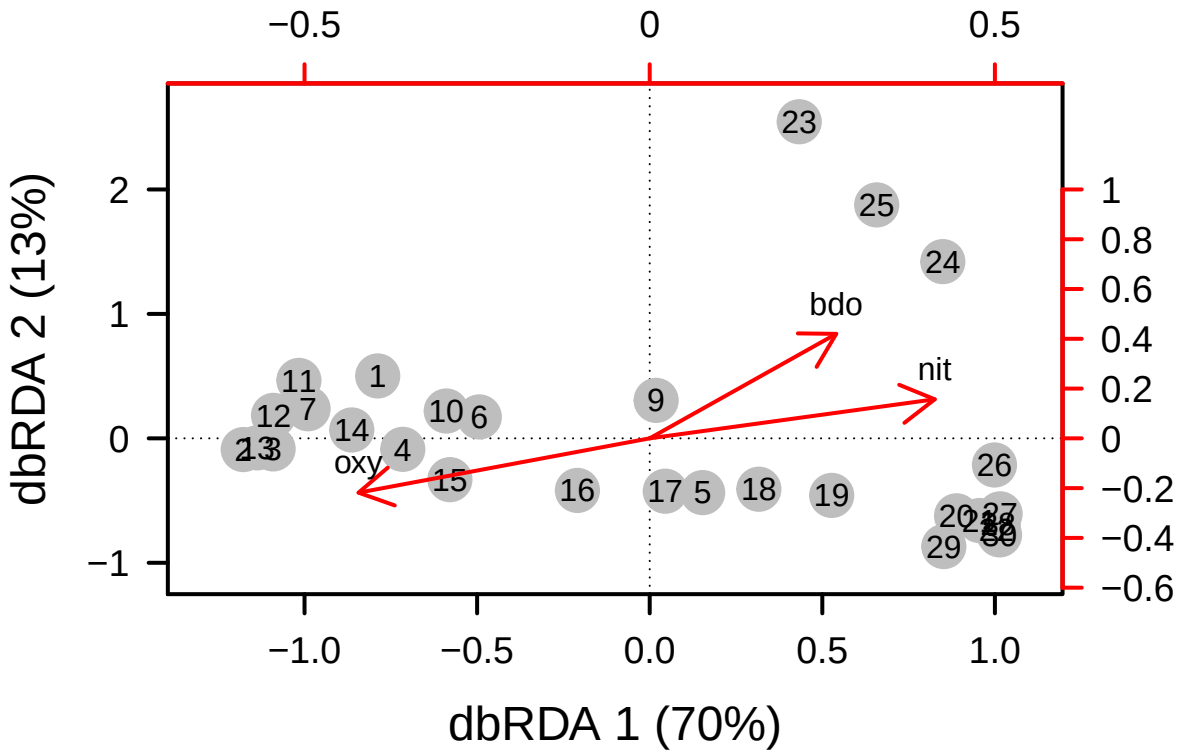
```
##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = fish.db ~ oxy + bdo + nit, data =
## as.data.frame(env.chem))
## Permutation test for all constrained eigenvalues
##          Df Inertia      F Pr(>F)
```

```
## 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
```

```
dbrda.explainvar1 <- round(doubs.dbrda$CCA$eig[1] /
                           sum(c(doubs.dbrda$CCA$eig)), 3) * 100
dbrda.explainvar2 <- round(doubs.dbrda$CCA$eig[2] /
                           sum(c(doubs.dbrda$CCA$eig, doubs.dbrda$CA$eig)), 3) * 100

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)

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(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")

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***: It appears that bdo and nit are contributing most to variation in fish community structure–they follow those sites that vary most from the composition of the majority of sites, bdo more so than nit.

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  0.002 **
## <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
## [12]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE
## [23] FALSE FALSE 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
##
```

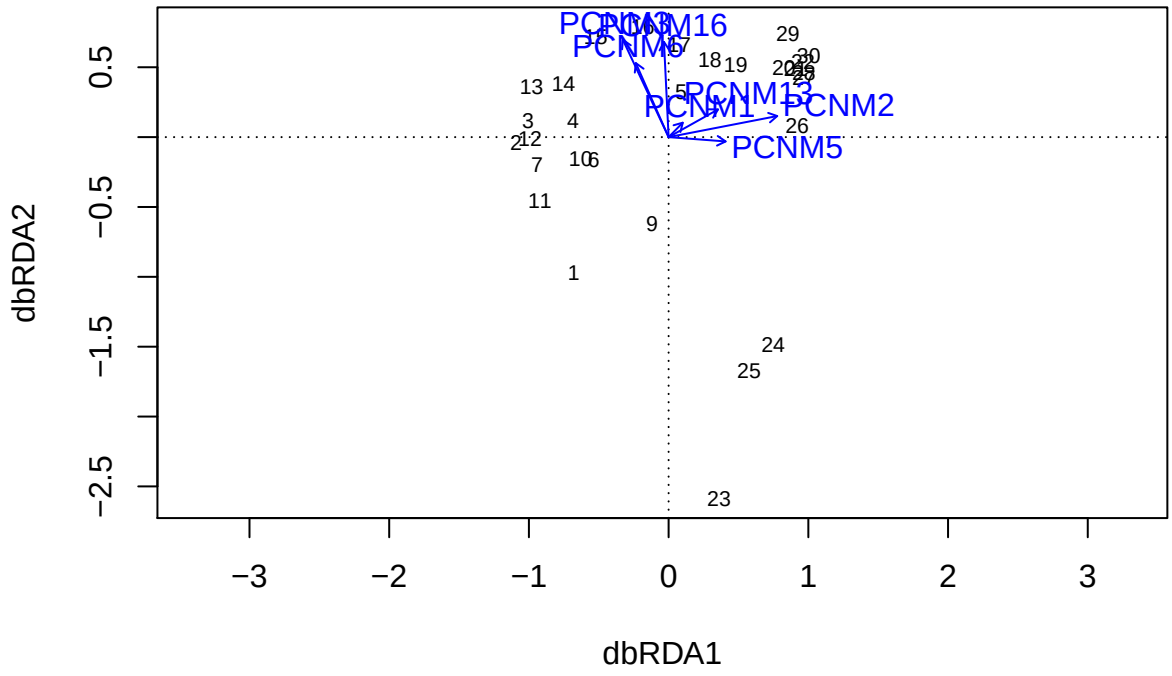
```
##                 R2.adjusted
## <All variables>   0.6260113
## + PCNM3           0.3429270
## + PCNM5           0.3057368
## + PCNM1           0.2885396
## + PCNM16          0.2786746
## + PCNM14          0.2744520
## + PCNM15          0.2692809
## + PCNM6           0.2659866
## + PCNM13          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  0.004 **
## ---
## 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  0.016 *
## ---
## 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
## <none>            0.4076020
## + PCNM4           0.3976526
##
##         Df    AIC     F Pr(>F)
## + PCNM1  1 41.411 4.057  0.008 **
## ---
## 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  0.018 *
## ---
## 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  0.018 *
## ---
## 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  0.024 *
## ---
## 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  0.072 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
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  0.004 **
## + PCNM5         0.40760  1 43.941 3.8385  0.016 *
## + PCNM1         0.47215  1 41.411 4.0570  0.008 **
## + PCNM13        0.52124  1 39.346 3.4612  0.018 *
## + PCNM16        0.57680  1 36.480 4.0192  0.018 *
## + PCNM6         0.60431  1 35.182 2.5296  0.024 *
## <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, doubs.space)[,-1]

doubs.total.env <- dbrda(fish.db ~ env.mod + Condition(space.mod))
doubs.space.cond.env <- dbrda(fish.db ~ space.mod + Condition(env.mod))

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.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 + 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
```

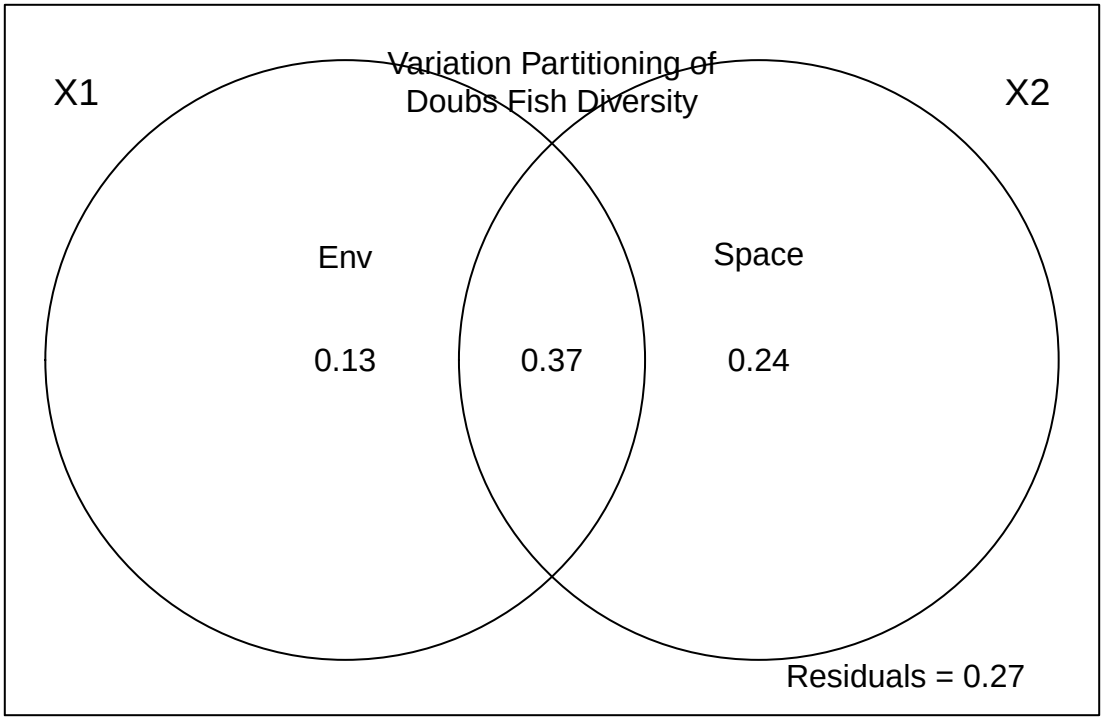
```r
permutest(doubs.total.env, permutations = 999)
```

```
##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = fish.db ~ env.mod + 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
```

```r
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+b] = 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]                    0                 0.36813    FALSE
## [c] = X2|X1            7                 0.23618     TRUE
## [d] = Residuals                          0.26574    FALSE
## ---
## Use function 'dbrda' to test significance of fractions of interest
```

```r
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***: I believe this is showing that 13% of the variation among sites is due to environmental variables, and 24% of the variation among sites is explained by distance between the sites. So, this doesn't necessarily support the earlier hypothesis that site quality is contributing a ton to fish diversity. Isn't this also saying that 37% of the variation is due to a combination of environmental variables and distance? So maybe quality does make a difference, but only as the site is also distant.

SYNTHESIS

1) Using the jelly bean data from class (i.e., JellyBeans.txt), perform a PERMANOVA to test whether or not the vicariance event (random splitting of source community) had an affect on jelly bean composition. Based on your previous analyses with this data set, what are your thoughts about the importance of stochastic vs. deterministic factors on estimates of biodiversity?

```
getwd()
```

```
## [1] "C:/Users/andjr/Github2/QB2019_Phillips/2.Worksheets/8.BetaDiversity"
```

```
jellybeanpops <- read.table("JellyBeans.txt", sep = "\t", header = TRUE)
jellybeansource <- read.table("JellyBeans.Source.txt", sep="\t", header = TRUE)
jellybeancategory<-jellybeanpops$Group
jellybeanpops<-jellybeanpops[,3:30]
```

```
adonis(jellybeanpops ~ jellybeancategory, method = "bray", permutations = 999)
```

```
##
## Call:
## adonis(formula = jellybeanpops ~ jellybeancategory, permutations = 999,      method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##                   Df SumsOfSqs  MeanSqs F.Model      R2 Pr(>F)
## jellybeancategory  1   0.09247 0.092468  2.0401 0.22568   0.05 *
## Residuals          7   0.31727 0.045324         0.77432
## Total              8   0.40974                  1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANSWER: Stochastic models are a lot more complicated, but they do factor in the randomness that we see when we're working with natural populations. We can't predict everything, which makes deterministic models a little less accurate. However, they are simpler and give us a good idea. I think deterministic models are good for a snapshot view of what's going on in a population or between populations, but if you need a better understanding of the variation that could/does exist with the communities, or if you need to be sure you're accounting for all possible situations (like with policy decisions or something), stochastic is probably the way to go.

2) Load the dataset you are using for your Team Project. Perform an ordination to visualize your dataset. Using this ordination, develop some hypotheses relevant to β-diversity. Use a statistic to test one of these hypotheses. Succinctly explain the finding and its relevance to your system.

```
#require("vegan")
#install.packages("OTUtable", repos = "http://cran.us.r-project.org")
#require("OTUtable")
require("viridis")
```

```
## Loading required package: viridis
```

```
## Loading required package: viridisLite
```

```
bog_loc <- read.table("NTL_MO_bogs_location.txt", header = TRUE, sep = "\t", row.names = 1)
data(otu_table)
str(otu_table, max.level=0)
```

```
## 'data.frame':    6208 obs. of  1387 variables:
```

```
first <- c("E01JUL07", "E02JUL07", "E03JUL07", "E04JUL07")
otu_JUL07 <- otu_table[,grep(paste(first, collapse = "|"), colnames(otu_table))]
CB <- c("CB", "JUL")
otu_CB <- otu_table[,grep(CB, colnames(otu_table))]
```

```
## Warning in grep(CB, colnames(otu_table)): argument 'pattern' has length > 1
## and only the first element will be used
```

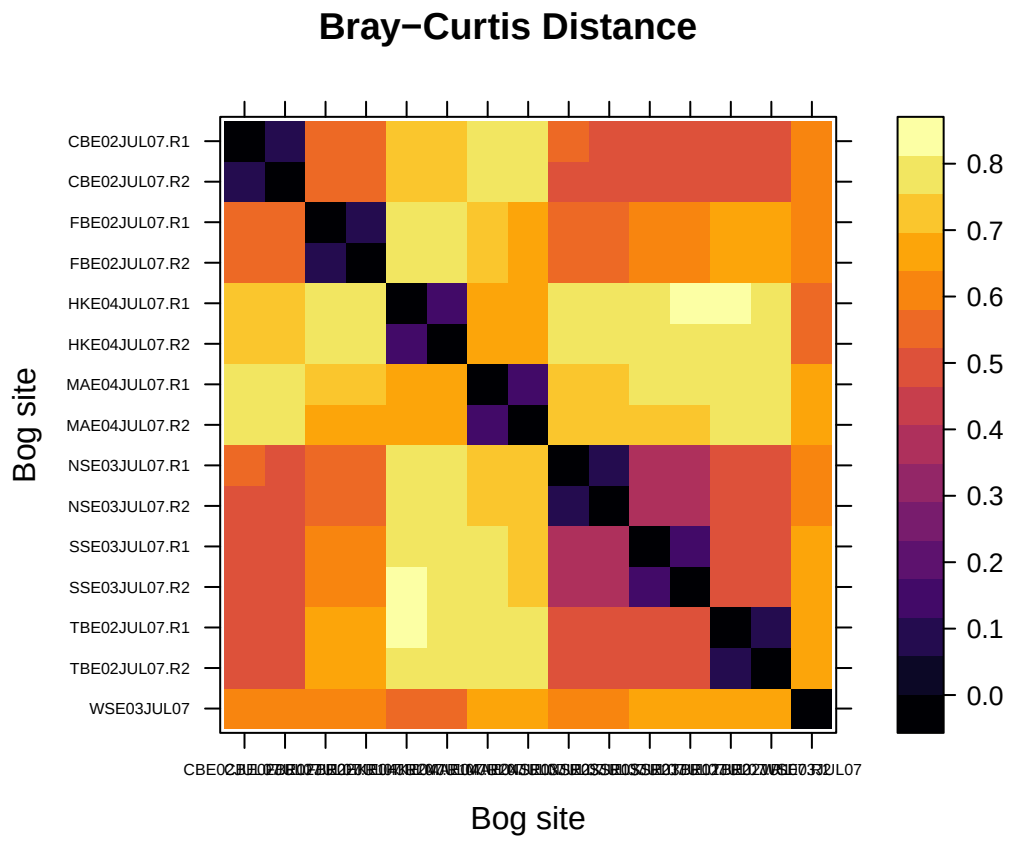
```
print(colnames(otu_JUL07))
```

```
##  [1] "CBE02JUL07.R1" "CBE02JUL07.R2" "FBE02JUL07.R1" "FBE02JUL07.R2"
##  [5] "HKE04JUL07.R1" "HKE04JUL07.R2" "MAE04JUL07.R1" "MAE04JUL07.R2"
##  [9] "NSE03JUL07.R1" "NSE03JUL07.R2" "SSE03JUL07.R1" "SSE03JUL07.R2"
## [13] "TBE02JUL07.R1" "TBE02JUL07.R2" "WSE03JUL07"
```

```
print(colnames(otu_CB))
```

```
##   [1] "CBU01JUL05"    "CBU02AUG05"    "CBU03JUN05"    "CBU05AUG05"
##   [5] "CBU05JUL05"    "CBU07JUN05"    "CBU08JUL05"    "CBU10AUG05"
##   [9] "CBU10JUN05"    "CBU12JUL05"    "CBU12JUN05"    "CBU14JUL05"
##  [13] "CBU14JUN05"    "CBU17JUN05"    "CBU19JUL05"    "CBU21JUN05"
##  [17] "CBU24JUN05"    "CBU24MAY05"    "CBU27MAY05"    "CBU28JUL05"
##  [21] "CBU28JUN05"    "CBU30AUG05"    "CBU31MAY05"    "CBE01OCT07.R1"
##  [25] "CBE01OCT07.R2" "CBE02AUG07.R1" "CBE02AUG07.R2" "CBE02AUG09"
##  [29] "CBE02JUL07.R1" "CBE02JUL07.R2" "CBE03JUN09"    "CBE05JUL07.R1"
##  [33] "CBE05JUL07.R2" "CBE06AUG07"    "CBE06NOV07.R1" "CBE06NOV07.R2"
##  [37] "CBE07JUL09"    "CBE08JUN09"    "CBE09AUG07.R1" "CBE09AUG07.R2"
##  [41] "CBE10JUL07.R1" "CBE10JUL07.R2" "CBE10SEP07.R1" "CBE10SEP07.R2"
##  [45] "CBE12AUG09"    "CBE12JUL07.R1" "CBE12JUL07.R2" "CBE13JUL09"
##  [49] "CBE15JUN09"    "CBE16JUL07.R1" "CBE16JUL07.R2" "CBE16OCT07.R1"
##  [53] "CBE16OCT07.R2" "CBE17SEP07.R1" "CBE17SEP07.R2" "CBE18AUG09"
##  [57] "CBE18JUL07.R1" "CBE18JUL07.R2" "CBE19JUN07.R1" "CBE19JUN07.R2"
##  [61] "CBE20AUG07"    "CBE21JUL09"    "CBE21JUN07.R1" "CBE21JUN07.R2"
##  [65] "CBE23AUG07.R1" "CBE23AUG07.R2" "CBE23JUN09"    "CBE23OCT07.R1"
##  [69] "CBE23OCT07.R2" "CBE24AUG09"    "CBE25JUL07.R1" "CBE25JUL07.R2"
##  [73] "CBE25SEP07.R1" "CBE25SEP07.R2" "CBE27AUG07.R1" "CBE27AUG07.R2"
##  [77] "CBE27JUL07.R1" "CBE27JUL07.R2" "CBE27JUL09"    "CBE27JUN07.R1"
##  [81] "CBE27JUN07.R2" "CBE29JUN07.R1" "CBE29JUN07.R2" "CBE29JUN09"
##  [85] "CBE29MAY09"    "CBE29OCT07"    "CBE31JUL07.R1" "CBE31JUL07.R2"
##  [89] "CBH01OCT07.R1" "CBH01OCT07.R2" "CBH02AUG09"    "CBH02JUL07.R1"
##  [93] "CBH02JUL07.R2" "CBH03JUN09"    "CBH05JUL07.R1" "CBH05JUL07.R2"
##  [97] "CBH06AUG07.R1" "CBH06AUG07.R2" "CBH06NOV07.R1" "CBH06NOV07.R2"
## [101] "CBH07JUL09"    "CBH08JUN09"    "CBH09AUG07.R1" "CBH09AUG07.R2"
## [105] "CBH10JUL07.R1" "CBH10JUL07.R2" "CBH10SEP07.R1" "CBH10SEP07.R2"
## [109] "CBH12AUG09"    "CBH12JUL07.R1" "CBH12JUL07.R2" "CBH13JUL09"
## [113] "CBH15JUN09"    "CBH16JUL07.R1" "CBH16JUL07.R2" "CBH16OCT07.R1"
## [117] "CBH16OCT07.R2" "CBH17SEP07.R1" "CBH17SEP07.R2" "CBH18AUG09"
## [121] "CBH18JUL07.R1" "CBH18JUL07.R2" "CBH19JUN07.R1" "CBH19JUN07.R2"
## [125] "CBH20AUG07.R1" "CBH20AUG07.R2" "CBH21JUL09"    "CBH21JUN07.R1"
## [129] "CBH21JUN07.R2" "CBH23AUG07.R1" "CBH23AUG07.R2" "CBH23JUN09"
## [133] "CBH23OCT07.R1" "CBH23OCT07.R2" "CBH24AUG09"    "CBH25JUL07.R1"
## [137] "CBH25JUL07.R2" "CBH25SEP07.R1" "CBH25SEP07.R2" "CBH27AUG07.R1"
## [141] "CBH27AUG07.R2" "CBH27JUL07.R1" "CBH27JUL07.R2" "CBH27JUL09"
## [145] "CBH27JUN07.R1" "CBH27JUN07.R2" "CBH29JUN07.R1" "CBH29JUN07.R2"
## [149] "CBH29JUN09"    "CBH29MAY09"    "CBH29OCT07.R1" "CBH29OCT07.R2"
## [153] "CBH31JUL07"
```

```
otu_JUL07 <- as.data.frame(t(otu_JUL07))

otu_JUL07.db <- vegdist(otu_JUL07, method = "bray", upper = TRUE, diag = TRUE)
order <- rev(attr(otu_JUL07.db, "Labels"))
levelplot(as.matrix(otu_JUL07.db)[, order], aspect = "iso", col.regions = inferno, xlab = "Bog site", yl
```




```
#CBE27JUN07 and MAE27JUN07

(cor(otu_table[[80]], otu_table[[444]]))^2
```

```
## [1] 0.4001371
```

```
#CBE01OCT07 and MAE01OCT07

(cor(otu_table[[24]], otu_table[[372]]))^2
```

```
## [1] 0.0882046
```

ANSWER: Based on the Bray-curtis Distance matrix above, (and considering our map of the bog placement, not shown here), I would hypothesize that distance impacts the similarity of the species composition between bogs, specifically that as bogs get further apart, their species composition differs more. The statistic I can use to quickly test this hypothesis are simple r^2 calculations, to see how much of the variation between bogs is explained by distance between them. Looking at Crystal Bog and Mary Lake, two of the most distant bogs, I can calculate r^2

between the values. This calculation results in a value of 0.4 for the bogs on June 27 of the same year, and of .09 for the bogs on October first later that year. This supports my hypothesis that distance is correlated with difference in species composition.