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

## Madison Stoltz; Z620: Quantitative Biodiversity, Indiana University

### 08 February, 2023

**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, 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.pdf**).

The completed exercise is due on **Wednesday, February 8$^{\text{th}}$, 2023 before 12:00 PM (noon)**.

## 1) R SETUP

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

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

1. clear your R environment,
2. print your current working directory,
3. set your working directory to your "*/6.BetaDiversity*" folder, and

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

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

```
## [1] "/Users/madisonstoltz/GitHub/QB2023_Stoltz/2.Worksheets/6.BetaDiversity"
```

```
#setwd("~GitHub/QB2023_Stoltz/2.Worksheets/6.BetaDiversity")
library(vegan)
```

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

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

```
## This is vegan 2.6-4
```

```
library(viridis)
```

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

```
library(indicspecies)
library(gplots)
```

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

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

```
library(BiodiversityR)
```

```
## Loading required package: tcltk
```

```
## BiodiversityR 2.15-1: Use command BiodiversityRGUI() to launch the Graphical User Interface;
## to see changes use BiodiversityRGUI(changeLog=TRUE, backward.compatibility.messages=TRUE)
```

## 2) LOADING DATA

**Load dataset**

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

```
# note, pleae do not print the dataset when submitting
library(ade4)
data(doubs)
fish <- doubs$fish
fish <- fish[-8, ]
```

## 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.

```
quality <- c(rep("HQ", 13), rep("MQ", 5), rep("LQ", 6), rep("MQ", 5))
adonis(fish ~ quality, method="bray", permutations=999)
```

```
## 'adonis' will be deprecated: use 'adonis2' instead


## $aov.tab
## 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
##
## $call
## adonis(formula = fish ~ quality, permutations = 999, method = "bray")
##
## $coefficients
##                   Cogo       Satr       Phph       Neba       Thth       Teso
## (Intercept)  0.4384615  1.546154   1.941880   2.191453  0.4230769  0.5948718
## quality1     0.1769231  1.992308   1.750427   1.116239  0.3461538 -0.2102564
## quality2    -0.4384615 -1.546154  -1.608547  -1.524786 -0.4230769 -0.5948718
##                   Chna        Chto       Lele       Lece       Baba
## (Intercept)  0.7777778  1.000000e+00  1.5418803  2.0324786  1.7145299
## quality1    -0.7777778 -1.000000e+00 -0.8495726 -0.8017094 -1.6376068
## quality2     0.5555556 -1.135321e-16 -0.2085470  0.1341880  0.4521368
##                   Spbi       Gogo        Eslu       Pefl Rham      Legi
## (Intercept)  1.03333333  2.1649573  1.46410256  1.3461538  1.3  1.1444444
## quality1    -1.03333333 -1.7034188 -0.77179487 -0.8076923 -1.3 -1.1444444
## quality2    -0.03333333  0.6683761  0.03589744  0.1538462  0.2  0.1888889
##                   Scer       Cyca       Titi       Abbr       Icme       Acce
## (Intercept)  0.8401709  0.96666667  1.7128205  1.0444444  0.6666667  1.5333333
## quality1    -0.6863248 -0.96666667 -1.1743590 -1.0444444 -0.6666667 -1.5333333
## quality2     0.3264957  0.03333333  0.2871795  0.2888889 -0.1666667  0.4666667
##                   Ruru       Blbj        Alal       Anan
```

```
## (Intercept)   2.4452991  1.2555556   2.455556  1.03333333
## quality1      -1.6760684 -1.2555556  -2.455556 -1.03333333
## quality2       0.7213675  0.4111111   1.711111 -0.03333333
##
## $coef.sites
##                          1           2           3          4            5          6
## (Intercept)   0.8837625   0.7158590   0.6938684   0.6230418  0.593432800  0.5790159
## quality1     -0.1866775  -0.3635334  -0.3456333  -0.2543114  0.001651813 -0.2025678
## quality2      0.1162375   0.2564578   0.2548711   0.2057479  0.056023013  0.1732300
##                          7           9          10         11           12         13
## (Intercept)   0.6581737  0.71175827   0.6442621   0.7094992   0.6760632  0.7319489
## quality1     -0.3307310 -0.05986164  -0.2179352  -0.2948057  -0.3340042 -0.3052481
## quality2      0.2381097  0.04794668   0.1706838   0.2036504   0.2492646  0.2428243
##                         14          15          16         17           18         19
## (Intercept)   0.6625054   0.6126096  0.58629885  0.53831620   0.5265411  0.5207733
## quality1     -0.2452690  -0.1465108 -0.01793157  0.06448519   0.1353961  0.1853921
## quality2      0.2192664   0.2018642  0.14094735  0.08434935   0.0300669 -0.0183066
##                         20          21          22         23           24         25
## (Intercept)   0.5199318   0.5323960   0.5576307   0.8035439   0.6877772  0.6964587
## quality1      0.2948405   0.3155710   0.3206040   0.1145069   0.2110503  0.1691525
## quality2     -0.1191038  -0.1333993  -0.1281596  -0.1892430  -0.2071918 -0.1908893
##                         26          27          28         29           30
## (Intercept)   0.5546865   0.5573809   0.5683021  0.56565435   0.61089065
## quality1      0.2955016   0.3181323   0.3117246  0.28417790   0.30341313
## quality2     -0.1264475  -0.1150663  -0.1044695 -0.07583091  -0.09189382
##
## $f.perms
##             [,1]
##    [1,] 0.5847065
##    [2,] 1.2020173
##    [3,] 0.8785936
##    [4,] 0.4142252
##    [5,] 0.5632156
##    [6,] 0.6179875
##    [7,] 1.2779472
##    [8,] 1.3046613
##    [9,] 1.6282527
##   [10,] 0.5830050
##   [11,] 0.4202361
##   [12,] 1.8619412
##   [13,] 0.6179617
##   [14,] 1.0348477
##   [15,] 1.1407187
##   [16,] 0.9805584
##   [17,] 0.6981682
##   [18,] 1.2540561
##   [19,] 1.2140505
##   [20,] 3.1686437
##   [21,] 0.6529860
##   [22,] 1.5635037
##   [23,] 0.6423513
##   [24,] 0.9329652
##   [25,] 0.4545071
##   [26,] 1.3711028
```

4

```
##    [27,] 0.7126427
##    [28,] 0.5402182
##    [29,] 0.2649662
##    [30,] 0.2695014
##    [31,] 1.1764619
##    [32,] 0.6995890
##    [33,] 1.5035402
##    [34,] 0.9713681
##    [35,] 1.0776803
##    [36,] 0.7481204
##    [37,] 1.5345776
##    [38,] 0.6960119
##    [39,] 0.3490266
##    [40,] 0.6503848
##    [41,] 0.9243100
##    [42,] 1.6823728
##    [43,] 0.6090503
##    [44,] 1.4948448
##    [45,] 0.3608069
##    [46,] 0.5304474
##    [47,] 1.0157065
##    [48,] 1.8091319
##    [49,] 0.9652379
##    [50,] 0.9509899
##    [51,] 2.5518646
##    [52,] 0.2927491
##    [53,] 3.1055674
##    [54,] 1.1950382
##    [55,] 1.1348618
##    [56,] 0.7929830
##    [57,] 1.1236692
##    [58,] 0.4091814
##    [59,] 0.7387460
##    [60,] 1.0204167
##    [61,] 0.8110249
##    [62,] 0.4491011
##    [63,] 0.8754639
##    [64,] 1.3914586
##    [65,] 0.6070813
##    [66,] 2.5147792
##    [67,] 0.9220267
##    [68,] 0.5924798
##    [69,] 0.6390566
##    [70,] 0.6071092
##    [71,] 0.9026738
##    [72,] 1.6280619
##    [73,] 4.0324580
##    [74,] 0.5549420
##    [75,] 0.6242814
##    [76,] 0.8582922
##    [77,] 0.7605236
##    [78,] 1.1531256
##    [79,] 3.1997059
##    [80,] 0.8537147
```

```
##     [81,] 0.8832657
##     [82,] 1.7249910
##     [83,] 0.8462677
##     [84,] 1.5917192
##     [85,] 1.0759356
##     [86,] 0.7290535
##     [87,] 2.1471986
##     [88,] 0.6552266
##     [89,] 0.6352576
##     [90,] 0.7383426
##     [91,] 0.6646867
##     [92,] 1.3792217
##     [93,] 2.0748090
##     [94,] 0.7935639
##     [95,] 1.8843040
##     [96,] 1.0746811
##     [97,] 0.5387844
##     [98,] 0.4422245
##     [99,] 1.4769884
##    [100,] 3.1621649
##    [101,] 0.9921373
##    [102,] 1.2560547
##    [103,] 1.2567110
##    [104,] 3.0416764
##    [105,] 0.6776239
##    [106,] 0.7142007
##    [107,] 1.2666104
##    [108,] 0.6308934
##    [109,] 0.8215728
##    [110,] 1.0358457
##    [111,] 0.5110545
##    [112,] 0.8272313
##    [113,] 0.5461077
##    [114,] 1.1994503
##    [115,] 0.9125917
##    [116,] 0.8965795
##    [117,] 0.5314745
##    [118,] 0.4908737
##    [119,] 0.5546026
##    [120,] 1.2401818
##    [121,] 0.4029208
##    [122,] 2.9815145
##    [123,] 0.5803070
##    [124,] 1.0843782
##    [125,] 0.5064994
##    [126,] 1.6373507
##    [127,] 1.2113598
##    [128,] 0.6267024
##    [129,] 0.6927598
##    [130,] 1.3649118
##    [131,] 0.9821791
##    [132,] 2.2305559
##    [133,] 0.9736664
##    [134,] 0.4163003
```

```
## [135,] 0.7104550
## [136,] 0.5783353
## [137,] 0.8092514
## [138,] 1.3050400
## [139,] 0.7607758
## [140,] 1.1586639
## [141,] 0.3239070
## [142,] 3.2099249
## [143,] 1.3009306
## [144,] 1.2742443
## [145,] 1.1152764
## [146,] 0.3859546
## [147,] 0.4000538
## [148,] 0.8092438
## [149,] 0.6877514
## [150,] 1.0725353
## [151,] 0.6760640
## [152,] 0.7068730
## [153,] 0.6922203
## [154,] 1.2137493
## [155,] 1.6503827
## [156,] 0.9412190
## [157,] 0.5042375
## [158,] 0.9867739
## [159,] 1.0242232
## [160,] 0.4077899
## [161,] 0.5930698
## [162,] 0.6963900
## [163,] 0.7215568
## [164,] 1.2530114
## [165,] 2.3624459
## [166,] 0.9804357
## [167,] 0.6706726
## [168,] 0.5326614
## [169,] 1.2818390
## [170,] 0.4477585
## [171,] 0.6094712
## [172,] 0.4150703
## [173,] 0.9341849
## [174,] 0.7644991
## [175,] 0.6145583
## [176,] 2.2109222
## [177,] 0.8210497
## [178,] 0.4444100
## [179,] 1.2130746
## [180,] 0.6038915
## [181,] 0.8327712
## [182,] 2.5013541
## [183,] 2.8502487
## [184,] 1.3302623
## [185,] 0.7213515
## [186,] 0.9186235
## [187,] 1.4814444
## [188,] 1.0657971
```

```
## [189,] 0.7930075
## [190,] 1.2656317
## [191,] 1.1606494
## [192,] 0.4229054
## [193,] 0.2889546
## [194,] 2.7748836
## [195,] 0.4371622
## [196,] 1.1249236
## [197,] 0.6165355
## [198,] 0.5797782
## [199,] 1.2400736
## [200,] 0.2870775
## [201,] 1.0903833
## [202,] 0.8999697
## [203,] 1.5928956
## [204,] 1.0271828
## [205,] 0.5658159
## [206,] 1.4194570
## [207,] 0.7682610
## [208,] 1.3450822
## [209,] 0.3510487
## [210,] 0.3558485
## [211,] 1.5656820
## [212,] 0.9876423
## [213,] 1.4882471
## [214,] 0.4894519
## [215,] 0.5577396
## [216,] 0.6473919
## [217,] 0.4601133
## [218,] 0.7269681
## [219,] 3.0852119
## [220,] 0.9129246
## [221,] 0.9501360
## [222,] 3.5393847
## [223,] 1.3130226
## [224,] 1.1042686
## [225,] 1.2850906
## [226,] 3.4849331
## [227,] 1.2085229
## [228,] 1.4797022
## [229,] 0.4119191
## [230,] 1.4475098
## [231,] 0.8520875
## [232,] 2.8838026
## [233,] 0.9714207
## [234,] 2.1324802
## [235,] 1.3660983
## [236,] 1.8552528
## [237,] 0.8969178
## [238,] 1.1288153
## [239,] 1.5556044
## [240,] 1.7498266
## [241,] 1.7824645
## [242,] 0.8888609
```

```
##    [243,] 0.4905445
##    [244,] 0.8861411
##    [245,] 0.8028802
##    [246,] 1.2234024
##    [247,] 3.0641862
##    [248,] 0.5692950
##    [249,] 1.9762643
##    [250,] 4.8749480
##    [251,] 0.7314218
##    [252,] 0.9521170
##    [253,] 1.2388402
##    [254,] 0.9849897
##    [255,] 0.4283014
##    [256,] 0.2582767
##    [257,] 0.6780308
##    [258,] 0.3515463
##    [259,] 0.5178786
##    [260,] 0.4633684
##    [261,] 0.7616914
##    [262,] 0.5665198
##    [263,] 1.0539354
##    [264,] 1.6674633
##    [265,] 0.4714204
##    [266,] 0.5552995
##    [267,] 0.9701070
##    [268,] 0.6026952
##    [269,] 1.0613211
##    [270,] 0.4604652
##    [271,] 0.6779252
##    [272,] 1.3734610
##    [273,] 0.7085589
##    [274,] 0.8952533
##    [275,] 0.3994260
##    [276,] 0.6413794
##    [277,] 0.8929395
##    [278,] 0.4598726
##    [279,] 0.8518422
##    [280,] 0.4402958
##    [281,] 0.4324735
##    [282,] 1.6448647
##    [283,] 0.5897561
##    [284,] 1.6456656
##    [285,] 0.5081092
##    [286,] 0.7265069
##    [287,] 0.9726224
##    [288,] 3.2875505
##    [289,] 1.6709858
##    [290,] 1.0067934
##    [291,] 0.6464604
##    [292,] 2.2336466
##    [293,] 0.2766059
##    [294,] 0.8105550
##    [295,] 0.8693817
##    [296,] 0.8953994
```

```
## [297,] 0.7649821
## [298,] 1.0293356
## [299,] 1.0201202
## [300,] 0.2785494
## [301,] 0.4305218
## [302,] 0.9049716
## [303,] 0.7989911
## [304,] 1.0057440
## [305,] 0.3390386
## [306,] 0.3155635
## [307,] 0.8877937
## [308,] 2.3674782
## [309,] 0.7985145
## [310,] 0.9470064
## [311,] 0.8238079
## [312,] 0.2972749
## [313,] 1.2960838
## [314,] 1.4354282
## [315,] 1.3340226
## [316,] 1.0408766
## [317,] 0.9724012
## [318,] 0.7606312
## [319,] 0.4205473
## [320,] 1.4252706
## [321,] 0.5005642
## [322,] 0.3646662
## [323,] 0.3605052
## [324,] 2.1535599
## [325,] 0.7222023
## [326,] 0.8042948
## [327,] 0.8520672
## [328,] 0.5850182
## [329,] 0.5293449
## [330,] 1.0686062
## [331,] 1.1199799
## [332,] 0.9368769
## [333,] 0.7170925
## [334,] 0.4466007
## [335,] 1.4312682
## [336,] 0.9551150
## [337,] 1.3153664
## [338,] 1.0097750
## [339,] 0.3856271
## [340,] 1.1769390
## [341,] 0.5941082
## [342,] 1.2331395
## [343,] 0.5612369
## [344,] 1.9849816
## [345,] 0.7571131
## [346,] 0.6961969
## [347,] 2.3503085
## [348,] 1.5518246
## [349,] 0.8140042
## [350,] 2.0886205
```

```
## [351,] 1.2292967
## [352,] 0.5790002
## [353,] 0.3911795
## [354,] 0.5255543
## [355,] 0.4371940
## [356,] 1.0901499
## [357,] 0.7816147
## [358,] 1.9451456
## [359,] 1.2824910
## [360,] 2.3714742
## [361,] 1.3606797
## [362,] 1.2374270
## [363,] 0.8348307
## [364,] 1.3501836
## [365,] 0.7422167
## [366,] 0.7100246
## [367,] 0.5156040
## [368,] 0.2959406
## [369,] 0.9563345
## [370,] 1.7703320
## [371,] 0.9901847
## [372,] 0.7306040
## [373,] 0.9348226
## [374,] 0.6703181
## [375,] 1.3701841
## [376,] 1.0986134
## [377,] 0.8060586
## [378,] 2.0079251
## [379,] 0.6575183
## [380,] 1.8919063
## [381,] 0.4222175
## [382,] 0.7178384
## [383,] 1.1547607
## [384,] 1.0192614
## [385,] 0.6339274
## [386,] 3.6692034
## [387,] 0.4456736
## [388,] 1.0028115
## [389,] 1.0366372
## [390,] 1.1586530
## [391,] 0.8484290
## [392,] 1.4423895
## [393,] 2.1473279
## [394,] 1.0230781
## [395,] 1.0586598
## [396,] 1.2855432
## [397,] 0.6749115
## [398,] 0.8423028
## [399,] 1.0333413
## [400,] 2.1328832
## [401,] 0.8333308
## [402,] 1.4269135
## [403,] 1.0661243
## [404,] 1.9691511
```

```
## [405,] 0.6247730
## [406,] 0.9084891
## [407,] 0.9670379
## [408,] 0.8407416
## [409,] 1.0740622
## [410,] 0.8729295
## [411,] 0.2504011
## [412,] 1.4554960
## [413,] 0.5430029
## [414,] 0.3887929
## [415,] 0.7314797
## [416,] 1.5449255
## [417,] 1.1029942
## [418,] 0.9336289
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## [421,] 0.4501388
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## [423,] 1.0340750
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## [427,] 0.5003488
## [428,] 1.8789894
## [429,] 1.2245765
## [430,] 1.3189138
## [431,] 0.5047231
## [432,] 0.6060002
## [433,] 0.5687259
## [434,] 0.6545348
## [435,] 0.6440962
## [436,] 0.7068231
## [437,] 2.1845066
## [438,] 0.9762275
## [439,] 0.4275343
## [440,] 1.0992421
## [441,] 0.8328161
## [442,] 0.4069985
## [443,] 0.9387739
## [444,] 0.5895126
## [445,] 0.4097782
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## [448,] 1.9893141
## [449,] 0.6520669
## [450,] 1.1484824
## [451,] 0.9439867
## [452,] 0.4986665
## [453,] 0.5371064
## [454,] 2.4813800
## [455,] 3.2092523
## [456,] 1.1353306
## [457,] 1.4506478
## [458,] 0.9387798
```

```
## [459,] 0.5890718
## [460,] 1.5025320
## [461,] 1.1671514
## [462,] 0.9168368
## [463,] 0.8934668
## [464,] 0.6855930
## [465,] 0.8704782
## [466,] 0.8523462
## [467,] 1.7592712
## [468,] 0.9401208
## [469,] 0.6189110
## [470,] 2.6850352
## [471,] 1.4942018
## [472,] 0.5479516
## [473,] 1.2017555
## [474,] 2.2868814
## [475,] 2.7833768
## [476,] 0.5572746
## [477,] 0.2046145
## [478,] 0.9603799
## [479,] 0.8243006
## [480,] 0.7959566
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## [483,] 1.6787925
## [484,] 1.7909992
## [485,] 0.6269419
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## [489,] 0.9427533
## [490,] 0.6254767
## [491,] 0.5371398
## [492,] 0.5824645
## [493,] 3.2929492
## [494,] 1.9632462
## [495,] 0.9429580
## [496,] 1.4913521
## [497,] 0.4413291
## [498,] 0.6647294
## [499,] 0.5936485
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## [501,] 1.7588756
## [502,] 0.4969701
## [503,] 1.0172606
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## [509,] 0.9054321
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## [511,] 0.6072070
## [512,] 1.3237581
```

```
## [513,] 0.5373161
## [514,] 2.1464393
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## [516,] 1.1218216
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## [523,] 0.5367041
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## [557,] 0.7824590
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## [560,] 0.9987701
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## [562,] 1.8398756
## [563,] 0.8121672
## [564,] 1.1608374
## [565,] 1.1022941
## [566,] 0.8799473
```

```
## [567,] 0.8721289
## [568,] 1.8516780
## [569,] 0.5283250
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## [576,] 0.7827444
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## [578,] 0.8738874
## [579,] 0.5083574
## [580,] 0.6064388
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## [584,] 0.8985630
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## [593,] 0.5174847
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## [601,] 0.4013552
## [602,] 1.7340789
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## [608,] 0.4714894
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## [615,] 1.0006450
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## [618,] 1.3315384
## [619,] 0.7693137
## [620,] 0.5144924
```

```
## [621,] 0.6069993
## [622,] 1.2623730
## [623,] 0.5853191
## [624,] 0.6926715
## [625,] 1.3189509
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## [628,] 1.1746847
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## [642,] 1.2723100
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## [670,] 0.6060866
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## [672,] 1.6940927
## [673,] 0.5804154
## [674,] 1.8703743
```

```
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## [728,] 0.4455559
```

```
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## [746,] 0.2619544
## [747,] 1.1466079
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## [749,] 1.3601240
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## [754,] 0.9319287
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## [759,] 1.2533293
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## [763,] 1.0467144
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## [766,] 0.6867549
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## [774,] 0.6811568
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## [779,] 1.1988604
## [780,] 0.6496109
## [781,] 0.8968905
## [782,] 2.3134405
```

```
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## [785,] 0.5520104
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## [787,] 0.4938734
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## [791,] 0.8340723
## [792,] 1.4650478
## [793,] 2.1376844
## [794,] 1.6451128
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## [796,] 0.5375748
## [797,] 0.7874091
## [798,] 0.4373147
## [799,] 0.5689508
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## [801,] 0.7121225
## [802,] 0.8440260
## [803,] 0.7819908
## [804,] 0.9746342
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## [806,] 0.8239552
## [807,] 0.5485978
## [808,] 1.7260992
## [809,] 0.6477086
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## [814,] 0.9829002
## [815,] 2.1519212
## [816,] 0.7927319
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## [822,] 0.8051170
## [823,] 0.8900678
## [824,] 0.6261144
## [825,] 0.8101422
## [826,] 0.7067506
## [827,] 0.8128125
## [828,] 0.7442417
## [829,] 1.2984372
## [830,] 0.6785053
## [831,] 0.7285354
## [832,] 0.8521691
## [833,] 1.5619921
## [834,] 1.1788047
## [835,] 1.2587076
## [836,] 1.3982400
```

```
## [837,] 0.6858707
## [838,] 0.5796413
## [839,] 0.4017426
## [840,] 0.1981776
## [841,] 0.5393168
## [842,] 0.5743374
## [843,] 1.0163198
## [844,] 1.0293083
## [845,] 0.6462000
## [846,] 1.1730049
## [847,] 1.5632557
## [848,] 0.9532655
## [849,] 1.1538977
## [850,] 2.0440775
## [851,] 0.4733783
## [852,] 1.0651617
## [853,] 1.4002197
## [854,] 3.6073816
## [855,] 2.1749869
## [856,] 1.3775076
## [857,] 0.5682318
## [858,] 0.8759159
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## [860,] 0.5251833
## [861,] 0.4132734
## [862,] 0.4016781
## [863,] 1.0410844
## [864,] 0.6806905
## [865,] 1.2904108
## [866,] 0.9608119
## [867,] 0.4677283
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## [869,] 0.6879654
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## [878,] 0.4992975
## [879,] 1.0624299
## [880,] 0.8061555
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## [882,] 0.5350416
## [883,] 0.9288717
## [884,] 0.7937173
## [885,] 0.6649727
## [886,] 0.8805585
## [887,] 1.8111170
## [888,] 0.6035203
## [889,] 0.6695464
## [890,] 1.2076437
```

```
## [891,] 0.5492381
## [892,] 1.0963926
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## [903,] 0.9107340
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## [922,] 1.2117690
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## [925,] 0.8536210
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## [928,] 1.0911518
## [929,] 1.7832901
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## [944,] 2.5372682
```

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## [976,] 3.2250963
## [977,] 0.4771815
## [978,] 1.2694736
## [979,] 0.8959387
## [980,] 0.4139215
## [981,] 1.5193320
## [982,] 1.3995576
## [983,] 0.9481892
## [984,] 0.8103944
## [985,] 0.9232032
## [986,] 0.9555174
## [987,] 0.9518013
## [988,] 0.6586874
## [989,] 0.8966655
## [990,] 1.0988094
## [991,] 0.7329402
## [992,] 0.6185545
## [993,] 0.6975576
## [994,] 0.7302477
## [995,] 0.7441974
## [996,] 0.5170188
## [997,] 0.9817035
## [998,] 2.2172398
```

```
## [999,] 0.4747904
##
## $model.matrix
##    (Intercept) quality1 quality2
## 1            1        1        0
## 2            1        1        0
## 3            1        1        0
## 4            1        1        0
## 5            1        1        0
## 6            1        1        0
## 7            1        1        0
## 8            1        1        0
## 9            1        1        0
## 10           1        1        0
## 11           1        1        0
## 12           1        1        0
## 13           1        1        0
## 14           1       -1       -1
## 15           1       -1       -1
## 16           1       -1       -1
## 17           1       -1       -1
## 18           1       -1       -1
## 19           1        0        1
## 20           1        0        1
## 21           1        0        1
## 22           1        0        1
## 23           1        0        1
## 24           1        0        1
## 25           1       -1       -1
## 26           1       -1       -1
## 27           1       -1       -1
## 28           1       -1       -1
## 29           1       -1       -1
##
## $terms
## fish ~ quality
## attr(,"variables")
## list(fish, quality)
## attr(,"factors")
##         quality
## fish          0
## quality       1
## attr(,"term.labels")
## [1] "quality"
## attr(,"order")
## [1] 1
## attr(,"intercept")
## [1] 1
## attr(,"response")
## [1] 1
## attr(,".Environment")
## <environment: R_GlobalEnv>
##
## attr(,"class")
```

```
## [1] "adonis"
```

```
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   0.021 *
##
##  Group HQ+MQ  #sps.  2
##       stat p.value
## Satr 0.860   0.004 **
## Phph 0.859   0.012 *
##
##  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   0.006 **
## Chto 0.829   0.001 ***
## Rham 0.829   0.001 ***
## Anan 0.829   0.002 **
## Eslu 0.827   0.017 *
## Pefl 0.806   0.011 *
## Blbj 0.791   0.001 ***
## Scer 0.766   0.007 **
## Abbr 0.750   0.006 **
## Icme 0.661   0.024 *
## ---
## 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   0.002 **
## Ruru 0.473   0.026 *
##
##  Group MQ  #sps.  4
##       stat p.value
## Anan 0.571   0.007 **
## Spbi 0.557   0.007 **
## Chto 0.542   0.006 **
## Icme 0.475   0.023 *
##
##  Group LQ+MQ  #sps.  9
##       stat p.value
## Legi 0.658   0.003 **
## Baba 0.645   0.004 **
## Rham 0.600   0.006 **
## Acce 0.594   0.007 **
## Cyca 0.586   0.001 ***
## Chna 0.571   0.005 **
## Blbj 0.571   0.009 **
## Gogo 0.523   0.011 *
## 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**: Based on the analyses, higher habitat quality has a lower amount of species. Specifically, higher habitat quality has some indicator species that can be useful to indicate if a habitat is of high quality or not. The analyses are not exactly the same, but there is some overlap with the indicator species. This could maybe mean variation in different definitions of a "high quality" habitat.

## 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%
## 0.108 0.145 0.179 0.224
## 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**: With an r value of 0.604 and a significance of 0.001, I can determine that there is a high correlation between fish diveristy and stream environmental conditions.

### 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.

```
#page 14
fish.db <- vegdist(fish, method="bray")

env.chem <- as.matrix(doubs$env[-8 , 5:11])
doubs.dbrda <- dbrda(fish.db ~ ., as.data.frame(env.chem))
ordiplot(doubs.dbrda)
```
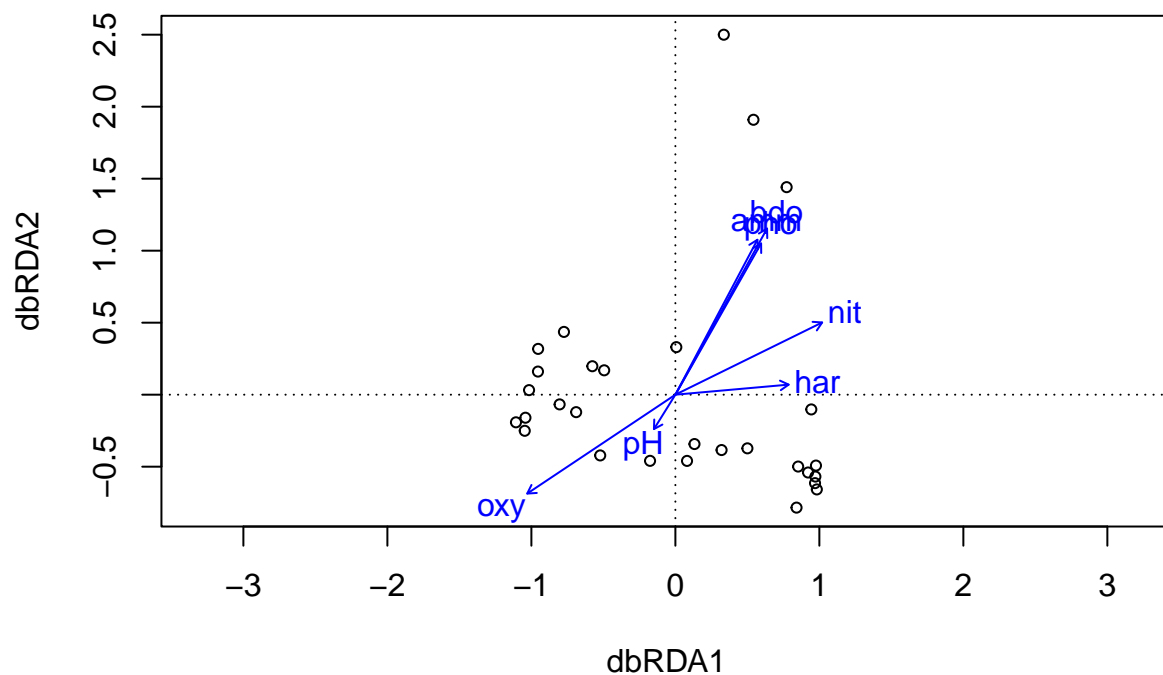


```
#page 15
doubs.dbrda.mod0 <- dbrda(fish.db ~ 1, as.data.frame(env.chem))
ordiplot(doubs.dbrda.mod0)
```
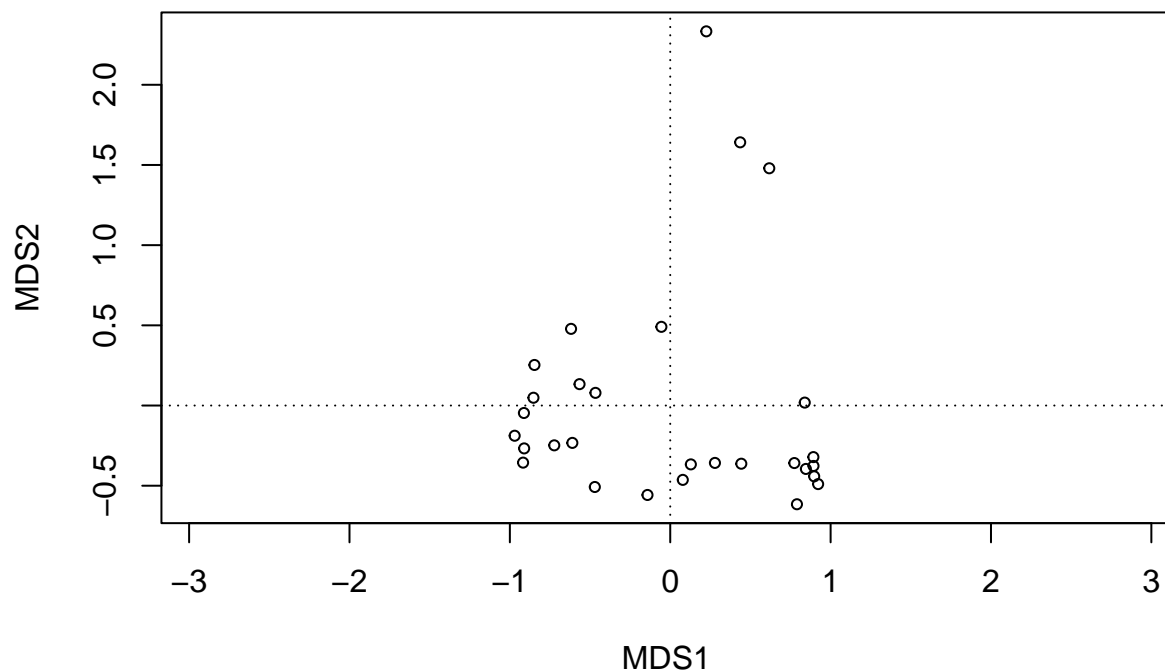
```r
doubs.dbrda.mod1 <- dbrda(fish.db ~ ., as.data.frame(env.chem))
doubs.dbrda <- ordiR2step(doubs.dbrda.mod0, doubs.dbrda.mod1, perm.max = 200)
```

```
## 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)
```
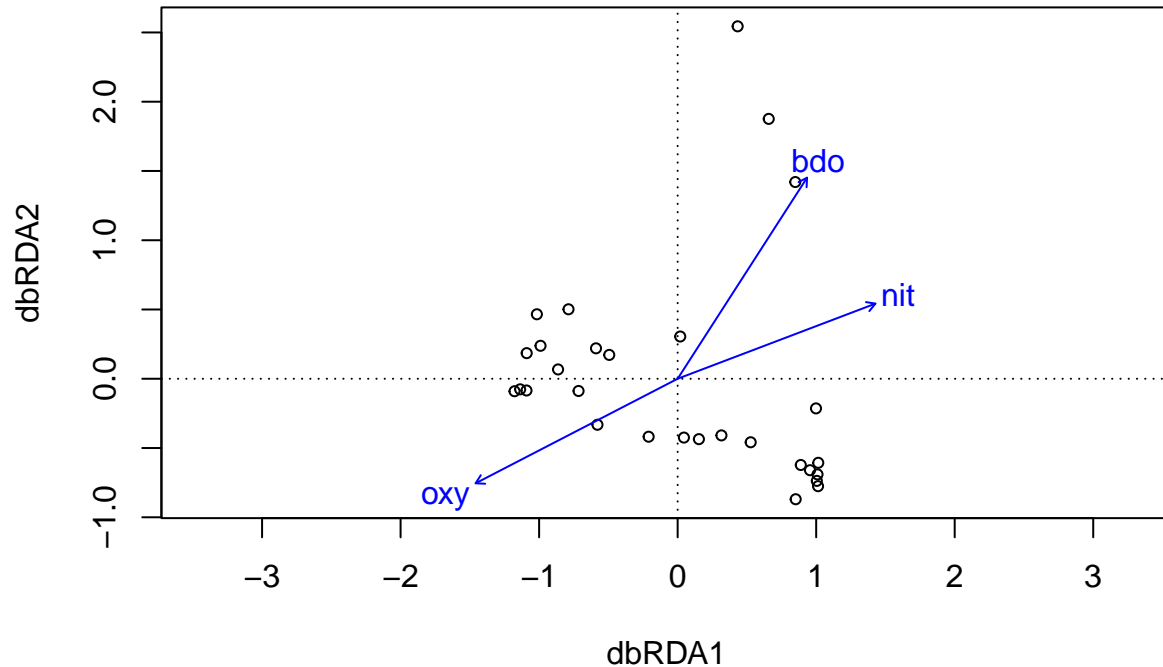


```
permutest(doubs.dbrda, permutations = 999)
```

```
##
## 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
```

```
#Page 16
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

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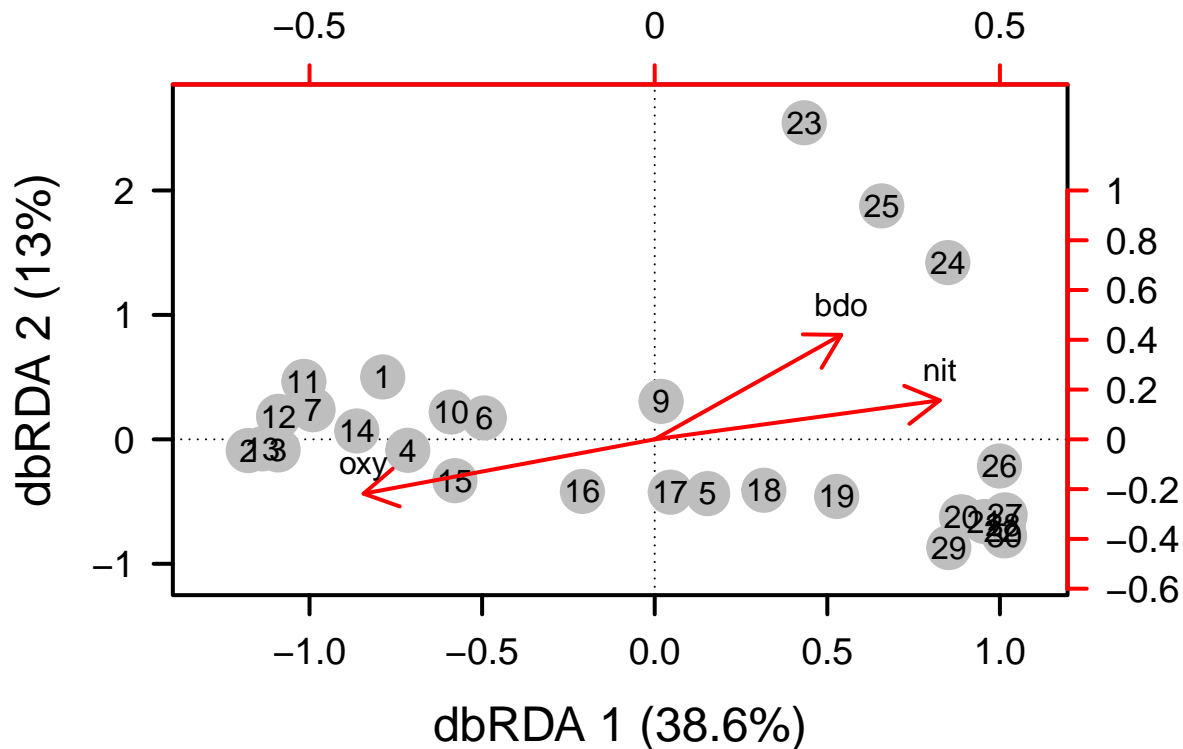
**Question 3**: Based on the constrained ordination, what are the environmental variables (or groups of correlated variables) that seem to be contributing to variation in fish community structure?

> **Answer 3**: Oxy, bdo, and nit are the three main environmental variables that seem to be contributing to variation in fish community structure. Oxy seems to be more indepedent and bdo and nit are closer/more related.

### 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  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  0.016 *
## ---
## 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  0.004 **
## ---
## 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  0.014 *
## ---
## 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  0.044 *
## ---
## 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
## <none>            0.6043089
```
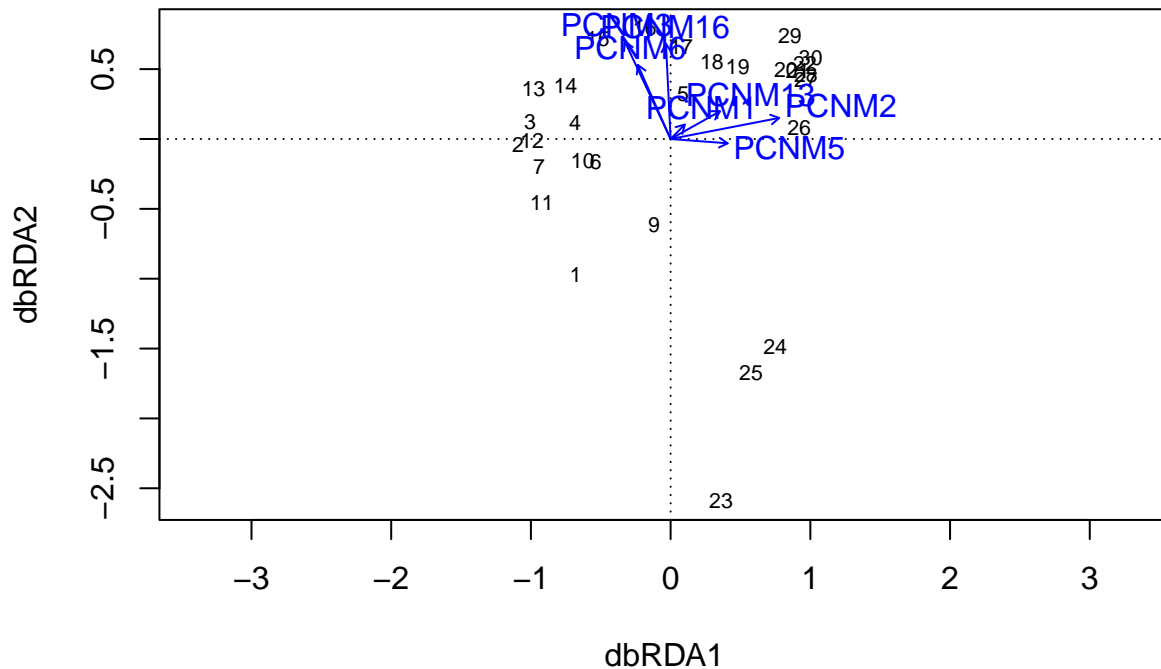
```
## + PCNM17         0.6037430
## + PCNM11         0.5978305
## + PCNM4          0.5963667
## + PCNM14         0.5932113
##
##          Df    AIC     F Pr(>F)
## + PCNM8   1 34.219 2.151  0.094 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
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  0.002 **
## + PCNM5         0.40760  1 43.941 3.8385  0.016 *
## + 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  0.014 *
## + 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
```

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

#bottompage18
doubs.total.env <- dbrda(fish.db ~ env.mod)
doubs.total.space <- dbrda(fish.db ~ space.mod)

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

permutest(doubs.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
```

```r
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
```

```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)
```

```
## 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
```

```
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)
```
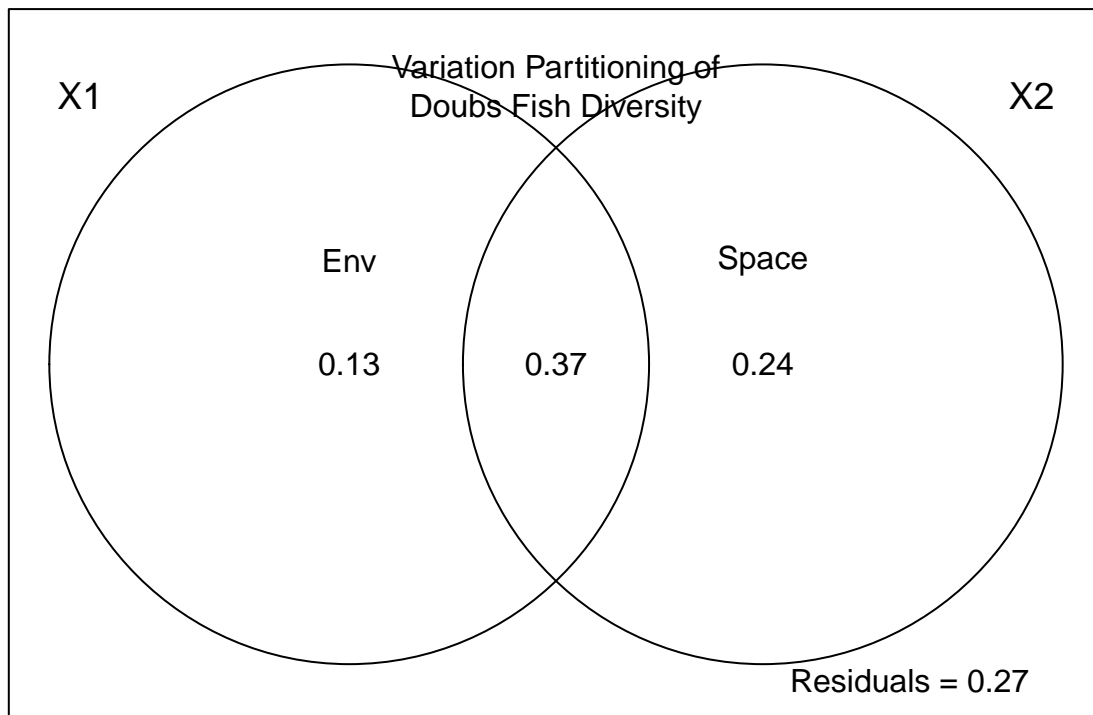


```
fish <- doubs$fish[-8,]
fish.hel <- decostand(fish, method="hellinger")
fish.dh <- vegdist(fish.hel, method="euclidean")

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

par(mar=c(5,5,1,2)+0.1)
plot(fish.pcoa$eig, xlab="PCoA Axis", ylab="Eigenvalue",
     las = 1, cex.lab = 1.5, pch =16)

abline(h=mean(fish.pcoa$eig), lty=2, lwd=2, col="blue")
b.stick <- bstick(29, sum(fish.pcoa$eig))
lines(1:29, b.stick, type="l", lty=4, lwd=2, col="red")

legend("topright", legend=c("Avg Eigenvalue", "Broken=Stick"),
       lty= c(2, 4), bty="n", col= c("blue", "red"))
```
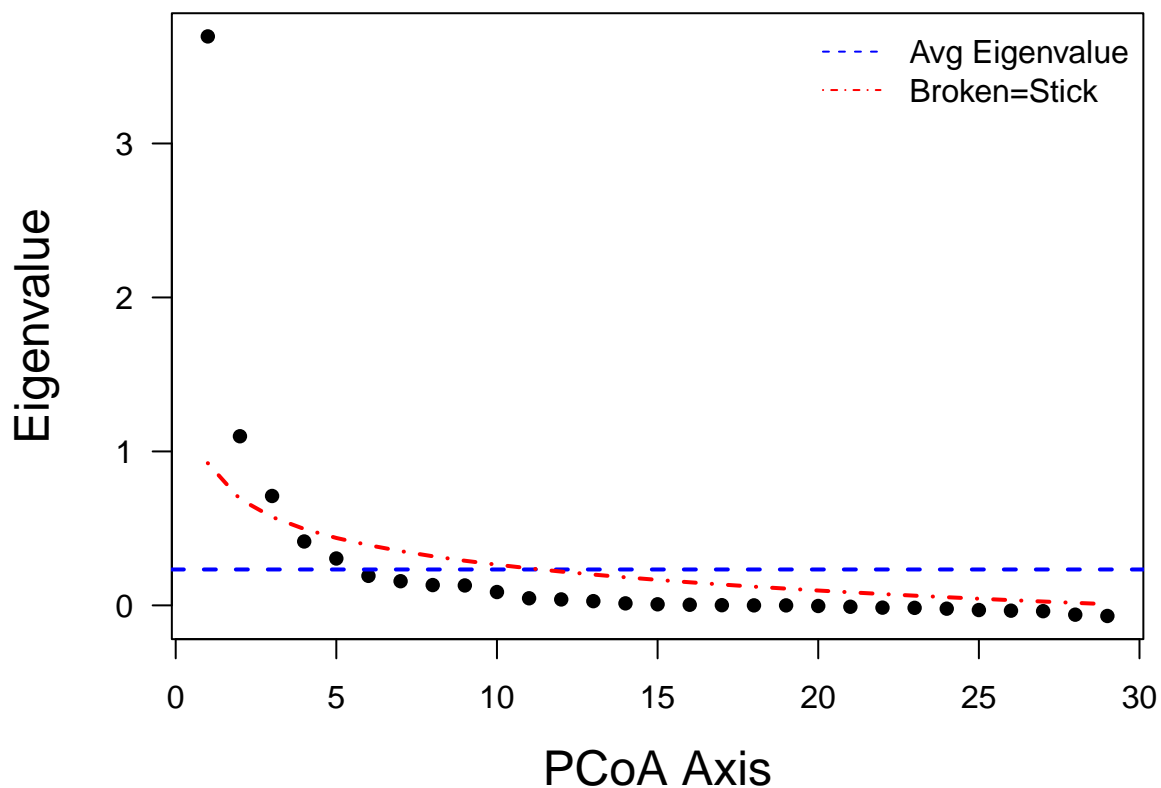
```r
env.chem <- as.matrix(doubs$env[-8 , 5:11])
doubs.cca <- vegan::cca(fish ~ env.chem)
anova(doubs.cca, by="axis")
```

```
## Permutation test for cca under reduced model
## Forward tests for axes
## Permutation: free
## Number of permutations: 999
##
## Model: cca(formula = fish ~ env.chem)
##          Df ChiSquare       F Pr(>F)
## CCA1      1   0.47139 20.1023  0.001 ***
## CCA2      1   0.10410  4.4394  0.003 **
## CCA3      1   0.05302  2.2608  0.412
## CCA4      1   0.02446  1.0430  0.954
## CCA5      1   0.01103  0.4702  1.000
## CCA6      1   0.00723  0.3081  1.000
## CCA7      1   0.00325  0.1385  1.000
## Residual 21   0.49244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
cca.fit <- envfit(doubs.cca, env.chem, perm=999)
cca.fit
```

```
##
```

```
## ***VECTORS
##
##          CCA1      CCA2      r2 Pr(>r)
## pH   -0.48829   0.87268 0.0957   0.233
## har   0.69849   0.71562 0.5347   0.001 ***
## pho   0.99867  -0.05164 0.1812   0.066 .
## nit   0.95037   0.31113 0.4560   0.001 ***
## amm   0.96060  -0.27792 0.1828   0.065 .
## oxy  -0.94012   0.34085 0.6369   0.001 ***
## bdo   0.93937  -0.34292 0.2335   0.030 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
```

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

#page23
par(mar = c(5,5,4,4) + 0.1)

plot(scores(doubs.cca, display = "wa"), xlim = c(-3.5, 2), ylim = c(-3.2, 3.2),
     xlab = paste("CCA 1 (", cca.explainvar1, "%)", sep = ""),
     ylab = paste("CCA 2 (", cca.explainvar1, "%)", 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.cca, display="wa"),
       pch = 19, cex = 3, bg = "gray", col = "gray")
text(scores(doubs.cca, display = "wa"),
     labels = row.names(scores(doubs.cca, display="wa")))

vectors <- scores(doubs.cca, display = "bp")
row.names(vectors) <- c("pH", "har", "pho", "nit", "amm", "oxy", "bdo")
arrows(0, 0, vectors[,1] * 2, vectors[, 2] * 2,
       lwd = 2, lty = 1, length=0.2, col = "red")
text(vectors[,1] * 2, vectors[, 2]*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])))
```
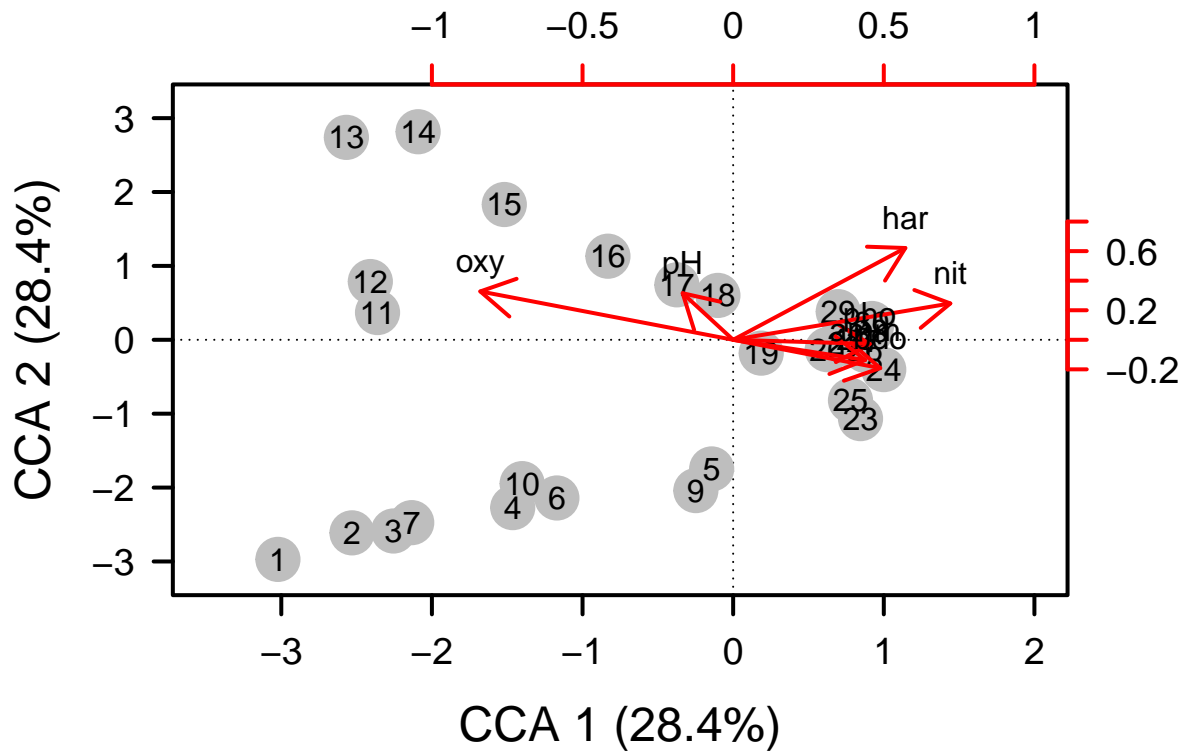
```r
doubs.ca <- dbrda(fish.db ~ 1)
total.var <- sum(doubs.ca$CA$eig)

step.1 <- sum(doubs.total.env$CCA$eig) * 100/ total.var
step.2 <- sum(doubs.total.space$CCA$eig) * 100/ total.var
step.3 <- sum(doubs.env.cond.space$CCA$eig) * 100/ total.var
step.4 <- sum(doubs.space.cond.env$CCA$eig) * 100/ total.var

sum(step.1 + step.4)
```

```
## [1] 82.91657
```

```r
sum(step.2 + step.3)
```

```
## [1] 82.91657
```

```r
pure.env <- step.3

env.space <- step.1 - step.3
space.env <- step.2 - step.4

pure.space <- step.4

resid.var <- 100 - sum(step.1 + step.4)
```

```
sum(c(pure.env, env.space, pure.space, resid.var))
```

```
## [1] 100
```

*Question 4*: Interpret the variation partitioning results.

> *Answer 4*: There is high overlap between most of the environmental factors, meaning that they are highly correlated to eachother. However, there are some env. factors such as oxy, pH, har, and nit that are more "alone" and therefore less correlated with other env. factors.

## 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.

```
#QB_Seabird_Data <- read_csv("~/Desktop/Research/QB Seabird Data.csv")
#Make matrices for species and env factors
#dataspecies <- QB_Seabird_Data[ ,2:5]
#View(dataspecies)
#dataenvironment <- QB_Seabird_Data[ ,14:17]
#View(dataenvironment)

#mantel(dataspecies,dataenvironment)
```

> Synthesis Answer: I ran the above code but it did not work. I plan to ask about this in class on Friday. I attached below my warning message.

> "Warning: non-square matrixWarning: non-square matrixWarning: number of items to replace is not a multiple of replacement lengthError in dimnames(df) <- if (is.null(labels)) list(seq_len(size), seq_len(size)) else list(labels, : length of 'dimnames' [1] not equal to array extent"