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

Atalanta Ritter; Z620: Quantitative Biodiversity, Indiana University

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## **OVERVIEW**

In this worksheet, we continue to explore concepts, statistics, and visualizations related to  $\beta$ -diversity. Now that you know how to formally quantify  $\beta$ -diversity, we will learn how to test hypotheses about  $\beta$ -diversity using multivariate statistics.

## **Directions:**

- 1. In the Markdown version of this document in your cloned repo, change "Student Name" on line 3 (above) with your name.
- 2. Complete as much of the worksheet as possible during class.
- 3. Use the handout as a guide; it contains a more complete description of data sets along with examples of proper scripting needed to carry out the exercises.
- 4. Answer questions in the worksheet. Space for your answers is provided in this document and is indicated by the ">" character. If you need a second paragraph be sure to start the first line with ">". You should notice that the answer is highlighted in green by RStudio (color may vary if you changed the editor theme).
- 5. Before you leave the classroom today, 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<sup>th</sup>, 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/Atalanta/GitHub/QB2023\_Ritter/2.Worksheets/6.BetaDiversity"

```
setwd("~/GitHub/QB2023_Ritter/2.Worksheets/6.BetaDiversity")
library(vegan)
```

```
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.6-4
```

# 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
require(ade4)
```

```
## Loading required package: 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.

```
fish <- doubs$fish
fish <- fish[-8, ] # remove site 8 from data bc no fish were observed
library(indicspecies)
# create factors vector
quality <- c(rep("HQ", 13), rep("MQ", 5), rep("LQ", 6), rep("MQ", 5))
# run PERMANOVA with adonis function
adonis(fish ~ quality, method = "bray", permutations = 999)</pre>
```

```
## '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)
                  3.0947 1.54733 10.97 0.45765 0.001 ***
## quality
             2
## Residuals 26
                  3.6674 0.14105
                                         0.54235
## Total
            28
                  6.7621
                                         1.00000
## ---
## Signif. codes: 0 '***' 0.001 '**' 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
            -0.4384615 -1.546154 -1.608547 -1.524786 -0.4230769 -0.5948718
## quality2
##
                 Chna
                             Chto
                                      Lele
                                                Lece
                                                         Baba
             0.7777778 1.000000e+00 1.5418803 2.0324786 1.7145299
## (Intercept)
## quality1
            -0.7777778 -1.000000e+00 -0.8495726 -0.8017094 -1.6376068
             0.5555556 -1.135321e-16 -0.2085470 0.1341880 0.4521368
## quality2
##
                  Spbi
                           Gogo
                                     Eslu
                                               Pefl Rham
## (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
            ##
                                     Titi
                                              Abbr
                                                       Icme
                 Scer
                           Cyca
                                                                Acce
            ## (Intercept)
            -0.6863248 -0.96666667 -1.1743590 -1.0444444 -0.6666667 -1.5333333
## quality1
             ## quality2
##
                 Ruru
                          Blbj
                                   Alal
                                             Anan
## (Intercept)
             2.4452991 1.2555556 2.455556 1.03333333
## quality1
            -1.6760684 -1.2555556 -2.455556 -1.03333333
             ## quality2
##
## $coef.sites
##
                    1
                             2
                                      3
                                                4
## (Intercept)
             -0.1866775 \ -0.3635334 \ -0.3456333 \ -0.2543114 \ 0.001651813 \ -0.2025678
## quality1
## quality2
             ##
                    7
                              9
                                      10
                                                11
                                                         12
## (Intercept)
            0.6581737  0.71175827  0.6442621  0.7094992  0.6760632  0.7319489
            -0.3307310 \ -0.05986164 \ -0.2179352 \ -0.2948057 \ -0.3340042 \ -0.3052481
## quality1
## quality2
                      0.2381097
                   14
                            15
                                      16
                                                17
                                                        18
                                                                 19
             0.6625054
                     0.6126096  0.58629885  0.53831620  0.5265411  0.5207733
## (Intercept)
## 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)
## quality1
             0.2948405 \quad 0.3155710 \quad 0.3206040 \quad 0.1145069 \quad 0.2110503 \quad 0.1691525
## quality2
            -0.1191038 -0.1333993 -0.1281596 -0.1892430 -0.2071918 -0.1908893
                   26
                            27
                                     28
                                                29
## (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,] 0.3961952
##
     [2,] 1.0158016
     [3,] 0.7470860
##
##
     [4,] 0.6101198
##
     [5,] 2.0917442
```

```
[6,] 0.8262515
##
##
      [7,] 0.9488474
##
      [8,] 0.3859601
##
      [9,] 0.4167597
##
     [10,] 1.1554895
##
     [11,] 1.0627465
##
     [12,] 0.6460444
     [13,] 0.4689881
##
##
     [14,] 0.8692392
##
     [15,] 1.0535139
##
     [16,] 0.4183034
##
     [17,] 1.2241074
##
     [18,] 2.0722672
##
     [19,] 0.3458036
##
     [20,] 0.6926822
     [21,] 2.2786212
##
##
     [22,] 0.5059592
     [23,] 1.5099255
##
##
     [24,] 0.8830375
     [25,] 1.0252494
##
##
     [26,] 1.4228950
##
     [27,] 1.5870565
##
     [28,] 1.1457366
##
     [29,] 0.7855130
##
     [30,] 0.9663488
##
     [31,] 0.8991970
##
     [32,] 1.7870352
##
     [33,] 0.5830621
##
     [34,] 0.7320197
##
     [35,] 1.8054136
##
     [36,] 1.4066201
##
     [37,] 0.3329782
##
     [38,] 0.8547046
##
     [39,] 0.6525534
     [40,] 0.8629764
##
##
     [41,] 0.9140763
##
     [42,] 0.4458694
##
     [43,] 0.3067033
     [44,] 1.3582117
##
##
     [45,] 0.9047073
##
     [46,] 1.2049440
##
     [47,] 0.4864204
##
     [48,] 1.3304821
##
     [49,] 0.9453845
##
     [50,] 1.3551881
##
     [51,] 0.7042144
##
     [52,] 0.6511803
##
     [53,] 0.7873555
##
     [54,] 1.9144219
##
     [55,] 0.3346153
##
     [56,] 0.4822610
##
     [57,] 2.4366871
##
     [58,] 0.5109562
```

[59,] 0.5635292

```
[60,] 0.5369006
##
##
     [61,] 1.4893240
##
     [62,] 0.7624209
##
     [63,] 0.5511569
##
     [64,] 0.8350679
##
     [65,] 0.5834352
##
     [66,] 0.8199769
##
     [67,] 0.8177388
##
     [68,] 0.7982297
##
     [69,] 0.7678917
##
     [70,] 0.6945469
##
     [71,] 1.0597561
##
     [72,] 0.5726041
##
     [73,] 1.1777948
##
     [74,] 0.6993450
##
     [75,] 1.7248851
##
     [76,] 0.8653041
##
     [77,] 2.2538065
##
     [78,] 1.5460759
##
     [79,] 0.9027364
##
     [80,] 0.8294556
##
     [81,] 1.1248746
##
     [82,] 2.3835431
##
     [83,] 0.9554778
##
     [84,] 0.6006015
##
     [85,] 0.5405376
##
     [86,] 0.9146308
##
     [87,] 0.8582499
##
     [88,] 0.5152263
##
     [89,] 0.3828730
##
     [90,] 1.7296783
##
     [91,] 0.3386072
##
     [92,] 0.5151054
##
     [93,] 1.0751006
##
     [94,] 0.5736453
##
     [95,] 0.6900142
##
     [96,] 0.9508894
##
     [97,] 0.4886737
##
     [98,] 0.7823396
##
     [99,] 0.6094296
    [100,] 0.7664962
##
    [101,] 0.5135764
    [102,] 0.6232584
##
    [103,] 0.7666292
    [104,] 1.8289849
##
    [105,] 1.2756705
##
    [106,] 0.5195929
##
    [107,] 0.5589332
   [108,] 1.7129923
##
    [109,] 2.2832254
##
    [110,] 0.5330042
##
   [111,] 1.7971060
##
   [112,] 0.8837842
## [113,] 1.0371467
```

```
[114,] 0.6954929
##
    [115,] 0.6350109
    [116,] 0.8528228
    [117,] 0.6019356
##
##
    [118,] 0.7529256
##
    [119,] 0.8216894
    [120,] 1.4785467
##
    [121,] 1.0422471
##
    [122,] 1.6755487
##
    [123,] 0.8105463
    [124,] 0.4127136
    [125,] 1.4517349
##
##
    [126,] 1.7829699
##
    [127,] 1.4365963
##
    [128,] 0.3453111
##
    [129,] 0.6805508
##
    [130,] 1.5803717
##
    [131,] 0.3130015
##
    [132,] 1.7713123
##
    [133,] 0.3567367
##
    [134,] 2.0267744
    [135,] 0.7292537
    [136,] 1.8903378
##
##
    [137,] 0.8914244
##
    [138,] 0.6993563
    [139,] 0.9140830
##
    [140,] 0.4024599
##
    [141,] 0.7946448
##
    [142,] 0.9634480
    [143,] 0.6033467
##
    [144,] 0.6781165
##
    [145,] 0.5168304
##
    [146,] 0.2421600
##
    [147,] 0.6466906
    [148,] 1.1504686
##
##
    [149,] 1.3743994
##
    [150,] 1.1649977
##
    [151,] 0.7768807
##
    [152,] 0.2527101
##
    [153,] 0.4619738
    [154,] 0.4393590
##
    [155,] 0.7371626
##
    [156,] 1.5400264
##
    [157,] 1.0308035
    [158,] 0.4270993
    [159,] 0.9002045
##
##
    [160,] 1.2192315
##
    [161,] 0.6424768
    [162,] 0.8862683
##
    [163,] 1.2807570
##
    [164,] 0.8793968
##
    [165,] 0.4632883
##
    [166,] 0.9188823
```

[167,] 1.6295804

```
[168,] 0.3532409
##
    [169,] 1.8390270
    [170,] 0.6831930
    [171,] 2.6077007
##
##
    [172,] 1.0538341
##
    [173,] 0.7594699
    [174,] 1.1536455
    [175,] 1.7932167
##
##
    [176,] 0.6257045
##
    [177,] 0.7809609
    [178,] 0.5718719
    [179,] 0.5101948
##
##
    [180,] 0.8659968
##
    [181,] 1.9705193
##
    [182,] 0.9481547
##
    [183,] 0.8154403
##
    [184,] 1.0519678
##
    [185,] 0.6577061
##
    [186,] 1.1323252
##
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##
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    [189,] 1.1807209
    [190,] 0.4226315
##
##
    [191,] 0.8200947
##
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    [193,] 1.5626273
##
    [194,] 1.2054996
##
    [195,] 2.0525080
##
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    [197,] 0.8127226
##
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##
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##
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##
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    [202,] 1.3630509
##
##
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##
    [204,] 0.3642000
##
    [205,] 1.7257033
    [206,] 1.4408313
##
##
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    [208,] 0.5211455
##
    [209,] 0.3662495
##
    [210,] 1.0426217
##
    [211,] 1.7500435
    [212,] 0.9598742
##
    [213,] 0.6717692
##
    [214,] 0.4831372
##
    [215,] 0.4616210
##
    [216,] 0.6987397
    [217,] 0.7017766
##
##
    [218,] 0.9972081
##
    [219,] 0.9432366
```

##

[220,] 2.0436291 [221,] 0.9470626

```
## [222,] 0.6552054
```

- ## [223,] 0.6490029
- ## [224,] 1.2545502
- ## [224,] 1.254550.
- ## [225,] 0.8786991
- ## [226,] 1.7773601
- ## [227,] 0.3880132
- **##** [228,] 0.7536954
- ## [229,] 0.8217746
- ## [230,] 3.1239858
- ## [231,] 1.3569115
- ## [232,] 1.2340462
- "" [202,] 1.2010102
- ## [233,] 0.6182700
- ## [234,] 0.9489453
- ## [235,] 1.9547866
- ## [236,] 0.4050634
- ## [237,] 1.6596916
- ## [238,] 1.1018602
- ## [239,] 0.7180308
- ## [240,] 0.4905225
- ## [241,] 0.8149162
- ## [242,] 0.8865428
- ## [243,] 1.1486378
- ... [210,] 1.1100070
- ## [244,] 0.7057061
- ## [245,] 1.7855172
- ## [246,] 0.5414973
- ## [247,] 0.4084763
- ## [248,] 0.3455123
- ## [249,] 1.0245318
- ## [250,] 1.1147603
- ## [251,] 0.9781204
- ## [252,] 0.8936066
- ## [253,] 0.4803072
- ## [254,] 0.6009331
- ## [255,] 1.2597840
- ## [256,] 0.8945053
- ## [257,] 0.4993548
- ## [258,] 0.7599007 ## [259,] 0.5528168
- ## [260,] 0.6215910
- ## [261,] 0.7846536
- **##** [262,] 1.1717176
- ## [263,] 1.4237803
- **##** [264,] 0.5978686
- ## [265,] 0.5700792
- ## [266,] 1.0062144
- ## [267,] 1.0091943
- ## [268,] 1.3299378
- ## [269,] 0.5709987
- ## [270,] 0.6044782
- ## [271,] 0.7871452
- **##** [272,] 0.9395619
- ## [273,] 0.6699829 ## [274,] 0.5198473
- ## [275,] 0.3024705

```
[276,] 1.1071218
##
    [277,] 0.8192570
    [278,] 0.7767848
    [279,] 0.6855885
##
##
    [280,] 0.2926372
##
    [281,] 0.9160037
    [282,] 0.6207288
##
    [283,] 0.8212622
##
    [284,] 2.4071411
##
    [285,] 0.6599403
    [286,] 2.6572447
    [287,] 1.2028249
##
    [288,] 0.8340276
##
##
    [289,] 0.5029041
##
    [290,] 1.4831486
##
    [291,] 0.7969941
##
    [292,] 0.4140945
##
    [293,] 0.7528903
##
    [294,] 2.4901422
    [295,] 1.5625454
##
##
    [296,] 0.3468070
    [297,] 0.9641384
    [298,] 0.8753118
##
##
    [299,] 0.3327731
##
    [300,] 0.6373756
    [301,] 1.5649724
##
    [302,] 0.4003649
    [303,] 2.2886133
##
    [304,] 1.5661547
    [305,] 0.2300339
    [306,] 1.1017991
##
##
    [307,] 0.3925001
##
    [308,] 0.7090384
##
    [309,] 0.9678178
##
    [310,] 0.8279685
##
    [311,] 0.8174267
##
    [312,] 1.9359438
##
    [313,] 0.5530586
##
    [314,] 1.2520485
##
    [315,] 0.4722325
    [316,] 0.9328003
##
    [317,] 0.7056124
##
    [318,] 0.5693447
##
    [319,] 1.0120271
    [320,] 0.7534260
##
    [321,] 0.4861985
##
    [322,] 0.9917903
##
    [323,] 0.9016455
##
    [324,] 2.5133676
```

##

##

##

##

[325,] 0.6570464

[326,] 0.4519799

[327,] 1.2137234

[328,] 1.4087193

[329,] 0.6574384

```
[330,] 1.0327940
##
    [331,] 1.0362081
##
    [332,] 1.6304822
    [333,] 1.0253153
##
##
    [334,] 0.6511102
##
    [335,] 0.9447247
##
    [336,] 0.8825338
    [337,] 0.7101515
##
##
    [338,] 0.5936397
##
    [339,] 0.5882003
    [340,] 0.2564475
##
    [341,] 1.1526147
##
    [342,] 1.1997892
##
    [343,] 0.7071229
##
    [344,] 1.5694738
##
    [345,] 0.5737570
##
    [346,] 0.6787211
##
    [347,] 0.8952393
##
    [348,] 0.7066311
##
    [349,] 0.5029680
##
    [350,] 0.5943948
##
    [351,] 0.7235344
    [352,] 1.2475975
##
##
    [353,] 1.5484137
##
    [354,] 0.8648503
    [355,] 2.1520323
##
    [356,] 1.4448391
##
    [357,] 2.1397414
##
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##
    [359,] 1.1039020
##
    [360,] 0.4715394
##
    [361,] 2.0038514
##
    [362,] 0.9990421
##
    [363,] 0.7616653
##
    [364,] 2.2872970
##
    [365,] 0.5492067
##
    [366,] 0.6341355
##
    [367,] 0.4773141
##
    [368,] 0.4587000
##
    [369,] 1.1463353
    [370,] 0.6516614
##
    [371,] 0.5863014
    [372,] 1.6507766
##
##
    [373,] 1.2414130
    [374,] 1.5246371
##
    [375,] 1.4464940
##
    [376,] 0.9115082
##
##
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    [925,] 0.4331592
    [926,] 0.5872526
    [927,] 1.1435807
##
##
    [928,] 0.6890990
##
    [929,] 4.4867676
    [930,] 2.5740782
##
    [931,] 1.3496112
##
    [932,] 1.1485776
##
    [933,] 0.6262605
    [934,] 0.5452745
    [935,] 0.6845948
##
    [936,] 0.3551586
##
##
    [937,] 0.4106725
##
    [938,] 0.4149936
##
    [939,] 1.8468096
##
    [940,] 0.7426420
##
    [941,] 0.7427564
##
    [942,] 0.7371693
##
    [943,] 1.6172909
    [944,] 1.5184425
##
    [945,] 0.9079921
    [946,] 0.6099168
##
##
    [947,] 0.6520944
##
    [948,] 0.6139978
    [949,] 0.6071297
##
    [950,] 0.5087039
##
    [951,] 1.6317957
##
    [952,] 0.6942519
    [953,] 0.5529455
##
    [954,] 0.4553919
##
    [955,] 0.7427274
##
    [956,] 0.9124645
##
    [957,] 1.0569766
##
    [958,] 0.7355105
##
    [959,] 0.8971954
##
    [960,] 0.4849972
##
    [961,] 0.3195363
##
    [962,] 1.0268636
##
    [963,] 0.6541974
    [964,] 0.5391689
##
    [965,] 1.9129599
##
    [966,] 0.7635590
##
    [967,] 0.5606903
    [968,] 1.6871873
##
    [969,] 1.4222286
##
    [970,] 0.4145074
##
    [971,] 0.8220428
    [972,] 1.0528752
    [973,] 1.0790987
##
##
    [974,] 1.1792080
##
    [975,] 1.1382983
##
    [976,] 0.6398419
##
    [977,] 1.5954647
```

```
[978,] 0.3594811
##
    [979,] 1.3130404
    [980,] 0.4308180
##
   [981,] 0.9756420
    [982,] 0.8629311
##
   [983,] 0.8836908
    [984,] 0.6771933
    [985,] 1.4600820
##
##
    [986,] 0.9932179
##
    [987,] 1.7449229
    [988,] 0.8422944
##
    [989,] 0.7628666
    [990,] 0.6976432
##
   [991,] 1.4530632
    [992,] 0.5652891
    [993,] 2.0314070
##
##
    [994,] 0.5586794
##
    [995,] 0.6361191
   [996,] 1.9417376
##
##
   [997,] 0.8051047
##
  [998,] 0.8895697
##
   [999,] 1.4893333
##
## $model.matrix
##
      (Intercept) quality1 quality2
## 1
              1
                     1
## 2
                1
                          1
                                   0
## 3
                1
                         1
                                   0
## 4
                         1
                                   0
                1
## 5
                1
                         1
## 6
                         1
                                   0
                1
## 7
                1
                         1
                                   0
## 8
                1
                         1
                                   0
## 9
                                   0
                1
                         1
## 10
                1
                         1
                                   0
## 11
                         1
                                   0
                1
## 12
                1
                         1
                                   0
## 13
                1
                         1
                                   0
## 14
                1
                         -1
                                  -1
## 15
                1
                        -1
                                  -1
## 16
                        -1
                                  -1
## 17
                1
                         -1
                                  -1
## 18
                1
                         -1
                                  -1
## 19
                1
                         0
                                   1
## 20
                1
                         0
                                   1
## 21
                         0
                1
                                   1
## 22
                1
                         0
                                   1
                1
                         0
## 23
                                   1
## 24
                1
                         0
                                   1
## 25
                1
                         -1
                                  -1
## 26
                1
                        -1
                                  -1
## 27
               1
                        -1
                                  -1
## 28
                1
                        -1
                                  -1
## 29
                         -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"
# indicator value (IndVal)
indval <- multipatt(fish, cluster = quality, func = "IndVal.g", control = how(nperm = 999))</pre>
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 0.011 *
##
## Group HQ+MQ #sps. 2
        stat p.value
## Satr 0.860 0.004 **
              0.011 *
## Phph 0.859
##
  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
              0.003 **
## Cyca 0.866
               0.003 **
## Acce 0.866
              0.002 **
## Lele 0.863
              0.003 **
## Titi 0.853
              0.006 **
## Chto 0.829
              0.003 **
## Rham 0.829
              0.004 **
## Anan 0.829
              0.004 **
## Eslu 0.827
              0.025 *
## Pefl 0.806
              0.017 *
## Blbj 0.791
               0.004 **
## Scer 0.766
               0.014 *
## Abbr 0.750
              0.013 *
## Icme 0.661
              0.037 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# phi coefficient of association
fish.rel <- decostand(fish, method = "total")</pre>
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 ***
              0.001 ***
## Neba 0.734
## Satr 0.650
              0.002 **
##
##
   Group LQ #sps. 2
##
        stat p.value
## Alal 0.693
              0.001 ***
## Ruru 0.473
               0.034 *
##
##
  Group MQ #sps. 4
        stat p.value
## Anan 0.571
              0.006 **
## Spbi 0.557
              0.008 **
## Chto 0.542 0.016 *
```

```
## Icme 0.475
                0.033 *
##
##
   Group LQ+MQ
                 #sps.
##
         stat p.value
## Legi 0.658
                0.001 ***
## Baba 0.645
                0.001 ***
## Rham 0.600
                0.004 **
## Acce 0.594
                0.004 **
## Cyca 0.586
                0.004 **
## Chna 0.571
                0.004 **
## Blbj 0.571
                0.005 **
## Gogo 0.523
                0.019 *
## Abbr 0.499
                0.021 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 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 tells us that there is a significant difference in fish community composition across river quality groups (df = 2, F = 10.92, P = 0.001). IndVal gives us 3 species of fish as indicators of high and medium quality: Teso (Blageon), Satr (Brown trout), and Phph (minnow). The phi coefficient analysis tells us that 3 species prefer high quality sites: Satr and Phph again, as well as Neba (stone loach). I would say that these results are pretty consistent with each other. Both IndVal and phi coefficient analysis identify the brown trout and minnow as associated with higher quality sites, which is also what I inferred from the PCoA analysis.

## B. Multivariate Procedures for Continuous Designs

#### i. Mantel Test

In the R code chunk below, do the following:

## 0.113 0.156 0.175 0.208

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

```
# define matrices
fish.dist <- vegdist(doubs$fish[-8,], method = "bray")</pre>
env.dist <- vegdist(scale(doubs$env[-8,]), method = "euclid")</pre>
#mantel test
mantel(fish.dist, env.dist)
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = fish.dist, ydis = env.dist)
##
## Mantel statistic r: 0.604
##
         Significance: 0.001
## Upper quantiles of permutations (null model):
     90%
           95% 97.5%
                        99%
```

```
## Permutation: free
## Number of permutations: 999
```

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

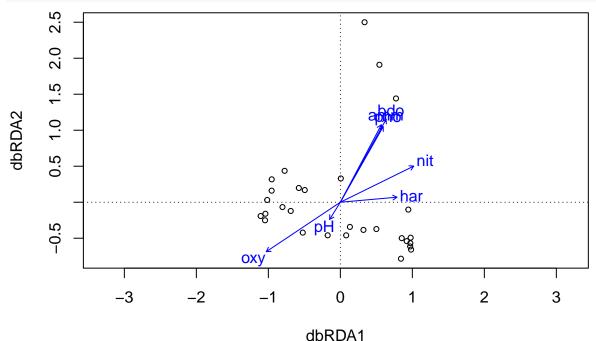
**Answer 2**: The r statistic is pretty high (0.604) and the p-value is significant (0.001), so fish diversity does appear correlated with stream environmental conditions. This supports my hypothesis that fish diversity is influenced by water quality, with species like brown trout and minnow preferring high quality sites.

#### ii. Constrained Ordination

In the R code chunk below, do the following:

- 1. create an environmental matrix of the water chemistry data included in the doubs dataset using forward and reverse selection of variables,
- 2. conduct a redundancy analysis on the fish assemblages of the Doubs River,
- 3. use a permutation test to determine the significance of the constrained analysis,
- 4. use a permutation test to determine the correlation of each environmental factor on the constrained axes,
- 5. calculate the explained variation on the first and second constrained axes,
- 6. plot the constrained ordination results including labeled points for each site, and
- 7. add vectors that demonstrate the influence of each environmental factor the constrained ordination.

```
fish.db <- vegdist(fish, method = "bray")
# define environmental matrix
env.chem <- as.matrix(doubs$env[-8, 5:11])
# perform dbRDA
doubs.dbrda <- dbrda(fish.db ~ ., as.data.frame(env.chem))
ordiplot(doubs.dbrda)</pre>
```

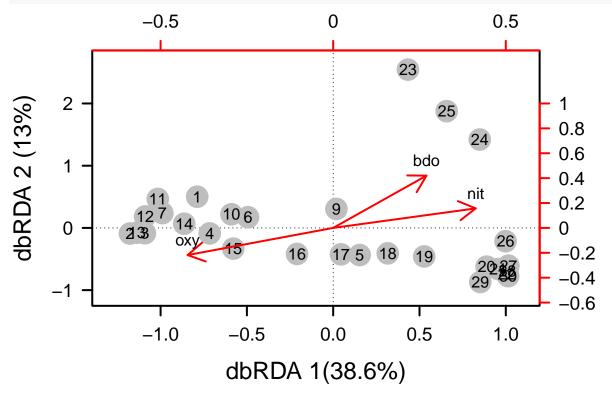


```
doubs.dbrda.mod0 <- dbrda(fish.db ~ 1, as.data.frame(env.chem))
doubs.dbrda.mod1 <- dbrda(fish.db ~ ., as.data.frame(env.chem))
doubs.dbrda <- ordiR2step(doubs.dbrda.mod0, doubs.dbrda.mod1, perm.max = 200)</pre>
```

```
## 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
                   0.00000000
## <none>
                  -0.01827054
## + pH
##
##
       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
##
##
                       F Pr(>F)
        Df
              AIC
## + bdo 1 43.404 6.5716 0.002 **
## Signif. codes: 0 '***' 0.001 '**' 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
                    0.3938042
## + pho
                    0.3869134
## + amm
## + pH
                    0.3865240
##
                    F Pr(>F)
##
        Df AIC
## + nit 1 39.134 6.034 0.002 **
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
```

```
## Step: R2.adj = 0.4980793
## Call: fish.db ~ oxy + bdo + nit
##
##
                   R2.adjusted
## + amm
                     0.5415705
                     0.5303258
## <All variables>
## + pho
                     0.5277128
## + har
                     0.5218852
## <none>
                     0.4980793
## + pH
                     0.4843267
# permutation test to determine the significance of the constrained analysis
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)
           3 3.7317 10.262 0.001 ***
## Model
## Residual 25 3.0304
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# permutation test to determine the correlation of each environmental factor on the constrained axes
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 '**' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
# calculate explained variation on the first and second constrained axes
dbrda.explainvar1 <- round(doubs.dbrda$CCA$eig[1] / sum(c(doubs.dbrda$CCA$eig, doubs.dbrda$CA$eig)), 3)
dbrda.explainvar2 <- round(doubs.dbrda$CCA$eig[2] / sum(c(doubs.dbrda$CCA$eig, doubs.dbrda$CA$eig)), 3)
# plot the constrained ordination results including labeled points for each site
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)
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(1wd = 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")))
```

```
# add vectors that demonstrate the influence of each environmental factor the constrained
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])))</pre>
```



**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**: Three environmental variables stand out as predictors of fish community structure: bdo, nit, and oxy. bdo seems to be part of a group of correlated variables, including amm and pho.

#### 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.

```
# matrix model for environmental data
env.mod <- model.matrix(~ oxy + bdo + nit, as.data.frame(env.chem))[, -1]
# weight each site by its relative abundance</pre>
```

```
rs <- rowSums(fish)/sum(fish)</pre>
# perform PCNM
doubs.pcnmw <- pcnm(dist(doubs$xy[-8,]), w = rs, dist.ret = T)</pre>
# get only positive eigenvalues
doubs.pcnmw$values > 0
  Г1]
        ## [13] TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE
## [25] FALSE FALSE
doubs.space <- as.data.frame(scores(doubs.pcnmw))</pre>
doubs.pcnm.mod0 <- dbrda(fish.db ~ 1, doubs.space)</pre>
doubs.pcnm.mod1 <- dbrda(fish.db ~ ., doubs.space)</pre>
step.pcnm <- ordiR2step(doubs.pcnm.mod0, doubs.pcnm.mod1, perm.max = 200)</pre>
## 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 '**' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj = 0.2353704
## Call: fish.db ~ PCNM2
##
                  R2.adjusted
                    0.6260113
## <All variables>
## + 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 '**' 0.05 '.' 0.1 ' ' 1
## Step: R2.adj = 0.342927
## Call: fish.db ~ PCNM2 + PCNM3
##
##
                  R2.adjusted
## <All variables> 0.6260113
## + PCNM5
                    0.4076020
## + PCNM1
                    0.3970300
## + PCNM16
                    0.3853210
## + PCNM15
                    0.3828748
## + PCNM14
                    0.3781827
## + PCNM13
                    0.3770376
## + PCNM6
                    0.3595644
## + PCNM8
                    0.3556885
## + PCNM7
                    0.3541631
## + PCNM10
                   0.3526775
## + PCNM17
                    0.3513683
## + PCNM9
                    0.3433672
## <none>
                    0.3429270
## + PCNM11
                    0.3416399
## + PCNM12
                    0.3396547
## + PCNM4
                    0.3311509
##
         Df AIC
                         F Pr(>F)
## + PCNM5 1 43.941 3.8385 0.008 **
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 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
```

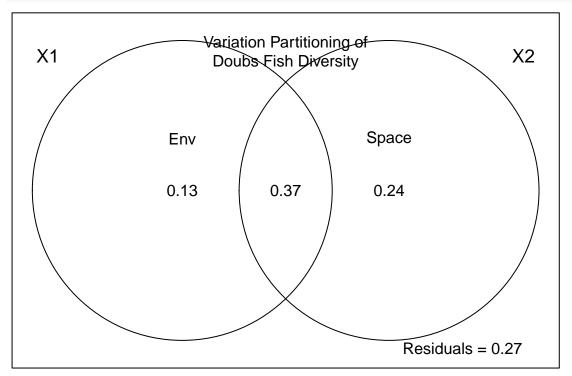
```
## + PCNM13
                    0.4511582
## + PCNM6
                    0.4305640
## + PCNM7
                    0.4261965
## + PCNM8
                    0.4224505
## + PCNM17
                    0.4181666
## + PCNM10
                    0.4154485
## + PCNM11
                    0.4112178
## + PCNM9
                    0.4111995
## + PCNM12
                    0.4087602
## <none>
                    0.4076020
## + PCNM4
                    0.3976526
##
          Df AIC F Pr(>F)
##
## + PCNM1 1 41.411 4.057 0.01 **
## Signif. codes: 0 '***' 0.001 '**' 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 '**' 0.05 '.' 0.1 ' ' 1
## Step: R2.adj = 0.5212427
## Call: fish.db ~ PCNM2 + PCNM3 + PCNM5 + PCNM1 + PCNM13
##
                  R2.adjusted
                    0.6260113
## <All variables>
## + PCNM16
                    0.5767968
## + PCNM15
                    0.5715331
## + PCNM14
                    0.5698343
## + PCNM6
                    0.5475140
## + PCNM7
                    0.5392074
## + PCNM8
                    0.5379134
## + PCNM11
                    0.5281106
```

```
## + PCNM9
                    0.5267003
## + PCNM10
                    0.5265029
## + PCNM12
                   0.5255581
## <none>
                    0.5212427
## + PCNM17
                    0.5171800
## + PCNM4
                    0.5152311
          Df AIC F Pr(>F)
##
## + PCNM16 1 36.48 4.0192 0.01 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Step: R2.adj = 0.5767968
## Call: fish.db ~ PCNM2 + PCNM3 + PCNM5 + PCNM1 + PCNM13 + PCNM16
##
##
                  R2.adjusted
## <All variables> 0.6260113
## + PCNM6
                    0.6043089
## + PCNM8
                    0.5970286
## + PCNM12
                    0.5946888
## + PCNM7
                    0.5946475
## + PCNM9
                   0.5883735
## + PCNM10
                   0.5851333
## + PCNM15
                   0.5846468
## <none>
                    0.5767968
## + PCNM17
                  0.5748533
## + PCNM4
                    0.5733749
## + PCNM11
                    0.5711176
## + PCNM14
                    0.5652509
##
##
         Df AIC
                       F Pr(>F)
## + PCNM6 1 35.182 2.5296 0.032 *
## Signif. codes: 0 '***' 0.001 '**' 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 '**' 0.05 '.' 0.1 ' ' 1
step.pcnm$anova # this tells us the selected PCNM axes are 2, 3, 5, 1, 13, 16
                   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 **
                  0.40760 1 43.941 3.8385 0.008 **
## + PCNM5
## + PCNM1
                  0.47215 1 41.411 4.0570 0.010 **
                  0.52124 1 39.346 3.4612 0.018 *
## + PCNM13
## + PCNM16
                  0.57680 1 36.480 4.0192 0.010 **
## + PCNM6
                  0.60431 1 35.182 2.5296 0.032 *
## <All variables> 0.62601
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# construct matrix model of the selected PCNM axes
space.mod <- model.matrix(~ PCNM2 + PCNM3 + PCNM5 + PCNM1 + PCNM13 + PCNM16 + PCNM6, doubs.space)[, -1]
# constrained ordinations
doubs.total.env <- dbrda(fish.db ~ env.mod)</pre>
doubs.total.space <- dbrda(fish.db ~ space.mod)</pre>
# partial constrained ordinations
doubs.env.cond.space <- dbrda(fish.db ~ env.mod + Condition(space.mod))</pre>
doubs.space.cond.env <- dbrda(fish.db ~ space.mod + Condition(env.mod))</pre>
# Test the significance of each of your constrained ordinations using permutation tests
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)
            3 0.85158 4.423 0.001 ***
## Model
## Residual 18 1.15519
## Signif. codes: 0 '***' 0.001 '**' 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)
            7 1.8752 4.1741 0.001 ***
## Model
## Residual 18 1.1552
## ---
```

```
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
permutest(doubs.total.env, permutations = 999)
##
## Permutation test for dbrda under reduced model
## Permutation: free
## Number of permutations: 999
## Model: dbrda(formula = fish.db ~ env.mod)
## Permutation test for all constrained eigenvalues
           Df Inertia
                           F Pr(>F)
           3 3.7317 10.262 0.001 ***
## Model
## Residual 25 3.0304
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
permutest(doubs.total.space, permiutations = 999)
##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 99
## Model: dbrda(formula = fish.db ~ space.mod)
## Permutation test for all constrained eigenvalues
           Df Inertia
                           F Pr(>F)
           7 4.7553 7.1089 0.01 **
## Model
## Residual 21 2.0068
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# Partition the variation among sites into the relative importance of space, environment, spatially st
doubs.varpart <- varpart(fish.db, env.mod, space.mod)</pre>
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
                            0.82917
                                          0.73426
                       10
                                                      TRUE
```

```
## Individual fractions
\# [a] = X1|X2
                         3
                                            0.12995
                                                        TRUE
                         7
## [b] = X2|X1
                                            0.23618
                                                        TRUE
                         0
                                                       FALSE
## [c]
                                            0.36813
## [d] = Residuals
                                            0.26574
                                                       FALSE
## ---
## Use function 'dbrda' to test significance of fractions of interest
# plot the variation partitioning output to visualize it
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**: The results tell us that 13% of variation among sites can be explained by environment alone, 24% by space alone, 37% by both environment and space, and 27% by neither environment nor space.

## **SYNTHESIS**

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

We decided to conduct a Mantel test to see if seabird abundances are correlated with 4 oceanographic variables: sea surface temperature (SST), chlorophyll a (CHL) concentration, sea-level anomaly (SLA), and net primary productivity (NPP).

```
# loading in dataset
seabirds <- read.csv("/Users/Atalanta/Downloads/Data_DRYAD_Seabirds.csv")</pre>
```

```
# removing sites where no observations were made of any species
# mantel test comparing site-by-species matrix with site-by-environment matrix
dataspecies <- seabirds.lite[ ,2:5]</pre>
dataenv <- seabirds.lite[, 14:17]</pre>
seabird.dist <- vegdist(dataspecies, method = "bray")</pre>
## Warning in vegdist(dataspecies, method = "bray"): you have empty rows: their dissimilarities may be
##
                  meaningless in method "bray"
ocean.dist <- vegdist(dataenv, method = "euclid")</pre>
mantel(seabird.dist, ocean.dist)
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = seabird.dist, ydis = ocean.dist)
## Mantel statistic r: 0.04782
##
        Significance: 0.012
##
## Upper quantiles of permutations (null model):
##
     90%
            95% 97.5%
                         99%
## 0.0280 0.0367 0.0424 0.0487
## Permutation: free
## Number of permutations: 999
```

It seems like the correlation value isn't very high (only 0.04782) but the p-value is significant (0.017) – I also tried rerunning it a few more times just to make sure it wasn't a chance result of the permutations but I consistently get p-values in the 0.015 - 0.025 range. So there seems to be a correlation between abundances of the seabird species and oceanographic variables.