

Temporal_Cluster

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Temporal Cluster Analysis of Juvenile Sockeye Diets

The following is a collection of the scripts run to generate and analyse the data for temporal cluster analyses of the juvenile sockeye diet data collected in 2015 and 2016.

Abundance Data

Preparing the Data

```
library(tidyverse)
```

```
## -- Attaching packages -----  
## v ggplot2 3.0.0      v purrr  0.2.5  
## v tibble  1.4.2      v dplyr  0.7.7  
## v tidyr   0.8.1      v stringr 1.3.1  
## v readr   1.1.1      v forcats 0.3.0  
  
## -- Conflicts -----  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()    masks stats::lag()
```

```
library(vegan)
```

```
## Loading required package: permute  
## Loading required package: lattice  
## This is vegan 2.5-2
```

```
library(lubridate)
```

```
##  
## Attaching package: 'lubridate'  
  
## The following object is masked from 'package:base':  
##  
##     date
```

```
library(dendextend)
```

```
##  
## -----  
## Welcome to dendextend version 1.8.0  
## Type citation('dendextend') for how to cite the package.  
##  
## Type browseVignettes(package = 'dendextend') for the package vignette.  
## The github page is: https://github.com/talgalili/dendextend/  
##  
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues  
## Or contact: <tal.galili@gmail.com>  
##
```

```

## To suppress this message use: suppressPackageStartupMessages(library(dendextend))
## -----

##
## Attaching package: 'dendextend'

## The following object is masked from 'package:permute':
##
##     shuffle

## The following object is masked from 'package:stats':
##
##     cutree
library(here)

## here() starts at C:/Users/Sam/Documents/Academic/UBC/Grad/My Research/R/sockeye_diets
##
## Attaching package: 'here'

## The following object is masked from 'package:lubridate':
##
##     here
#Import files
temp <- read_csv(here("raw", "Temporal.csv"))

## Warning: Duplicated column names deduplicated: 'species' =>
## 'species_1' [31]

## Parsed with column specification:
## cols(
##   .default = col_character(),
##   sam.id = col_integer(),
##   sam.proc.date = col_date(format = ""),
##   lab.proc.date = col_date(format = ""),
##   date = col_date(format = ""),
##   year = col_integer(),
##   day = col_integer(),
##   sample.int = col_integer(),
##   species.no = col_integer(),
##   stomtray = col_integer(),
##   forklength = col_integer(),
##   fishweight = col_double(),
##   wet.content.w = col_double(),
##   corrected.ww = col_double(),
##   fullness.mean = col_double(),
##   fullness.est = col_integer(),
##   DI = col_integer(),
##   count = col_integer(),
##   length.max = col_double(),
##   group.weight = col_double()
## )

## See spec(...) for full column specifications.

## Warning in rbind(names(probs), probs_f): number of columns of result is not
## a multiple of vector length (arg 1)

```

```

## Warning: 12 parsing failures.
## row # A tibble: 5 x 5 col      row col      expected actual file
## ... .....
## See problems(...) for more details.

meta <- read_csv(here("processed", "temp_meta.csv"))

## Parsed with column specification:
## cols(
##   semsp_id = col_character(),
##   site = col_character(),
##   location = col_character(),
##   survey_id = col_character(),
##   year = col_integer(),
##   month = col_character(),
##   day = col_character(),
##   set_time = col_time(format = ""),
##   set_time.adj = col_integer(),
##   lat = col_double(),
##   lon = col_double(),
##   forklength = col_integer(),
##   fishweight = col_double(),
##   meantemp = col_double(),
##   meansal = col_double(),
##   secchi = col_double(),
##   z.abundance = col_double(),
##   z.biomass = col_double(),
##   stock_1 = col_character()
## )

#Data wrangling:-----#

#using detailed level of taxonomy (plot.taxon.d), for coarser resolution use plot.taxon
#setting up the data and apply an sqrt arcsine transformation to rel abund data
#Calculating abundance data at the individual sample level
temp_abund1 <- temp %>%
  select(semssp_id = semssp.no, ufn, date, sample.int, location, site, fullness.est, plot.taxon.d,
  separate(date, c("year", "month", "day"), sep = "-") %>%
  unite(ID, c(year, sample.int), remove = FALSE) %>%
  filter(count != "Na", !plot.taxon.d %in% c('NA', 'Digested', 'Anisakis'), fullness.est >5) %>%
  group_by(semssp_id, ID, year, month, sample.int, site, location, plot.taxon.d) %>%
  summarise(total = sum(count)) %>%
  mutate(relabund = (total/sum(total))) %>%
  mutate(arcsin = ((2/pi)*asin(sqrt(relabund)))) %>%
  select(semssp_id, ID, year, month, sample.int, site, location, plot.taxon.d, arcsin)

#save
write_csv(temp_abund1, "./processed/temp_relabund_transformed.csv")

#rearranging rows of taxonomic data into columns by plot taxon, making all NA's = 0, selecting only tax
temp_clusdata_abund<- spread(temp_abund1, key = plot.taxon.d, value = arcsin)
temp_clusdata_abund[is.na(temp_clusdata_abund)] <- 0

#converting it to a dataframe and setting rownames as the first column and then only selecting the taxon
# as part of the data prep for Bray-Curtis

```

```
temp_clusdata_abund <- data.frame(temp_clusdata_abund)
rownames(temp_clusdata_abund)=temp_clusdata_abund[,1]
temp_bc_abund <- temp_clusdata_abund[8:77]

#edit metadata to only contain same ID's as in the temporal fish data
metadata1 <- semi_join(meta, temp_clusdata_abund, by = "semsp_id")
metadata <- merge(metadata1, temp_clusdata_abund[,c("semsp_id", "ID", "sample.int")], by = "semsp_id")
select(1, 4, 2:3, 20:21, 5:19)
```

Cluster Analyses

Code to run the Bray-Curtis Analysis, then test for significant clusters using SIMPROF, then look for significance between clusters using ANOSIM and see which species contribute to significant differences using SIMPER.

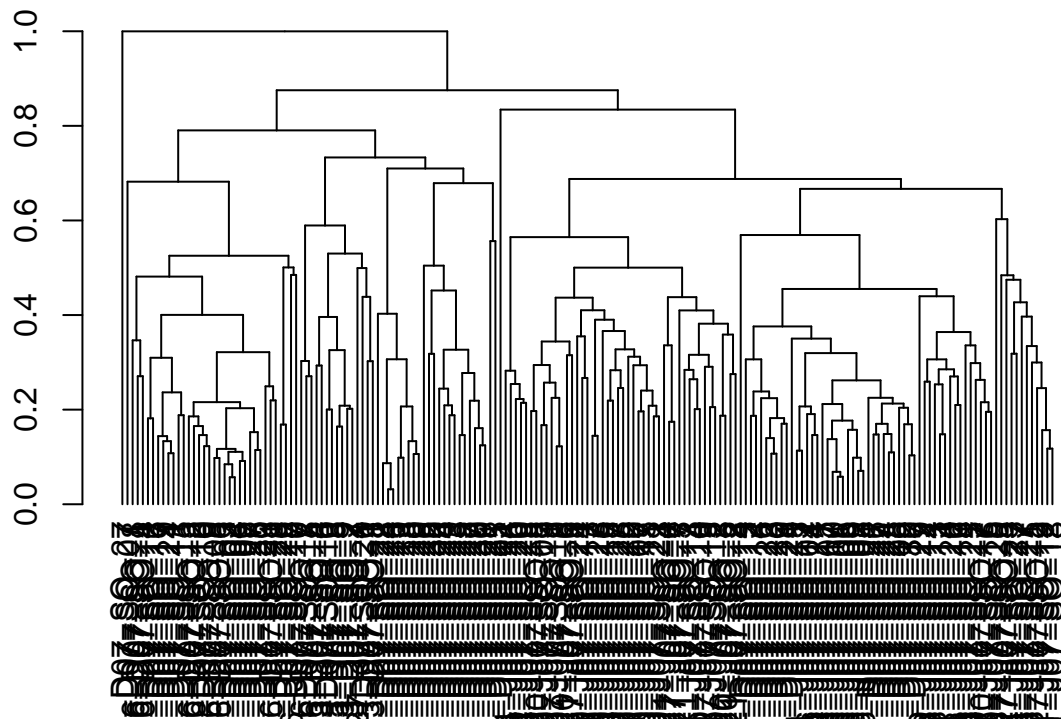
```
#-----Bray-Curtis-----#

#vegdist uses the vegan package to calculate the distances between variables
temp_bc_dist <- vegdist(temp_bc_abund, method = "bray")

#hclust creates the dendrogram by calculating the amount of dissimilarity between clusters,
# average calculates the distance between all the different values in each group and then averages them
temp_bc_clust <- hclust(temp_bc_dist, method = "average")

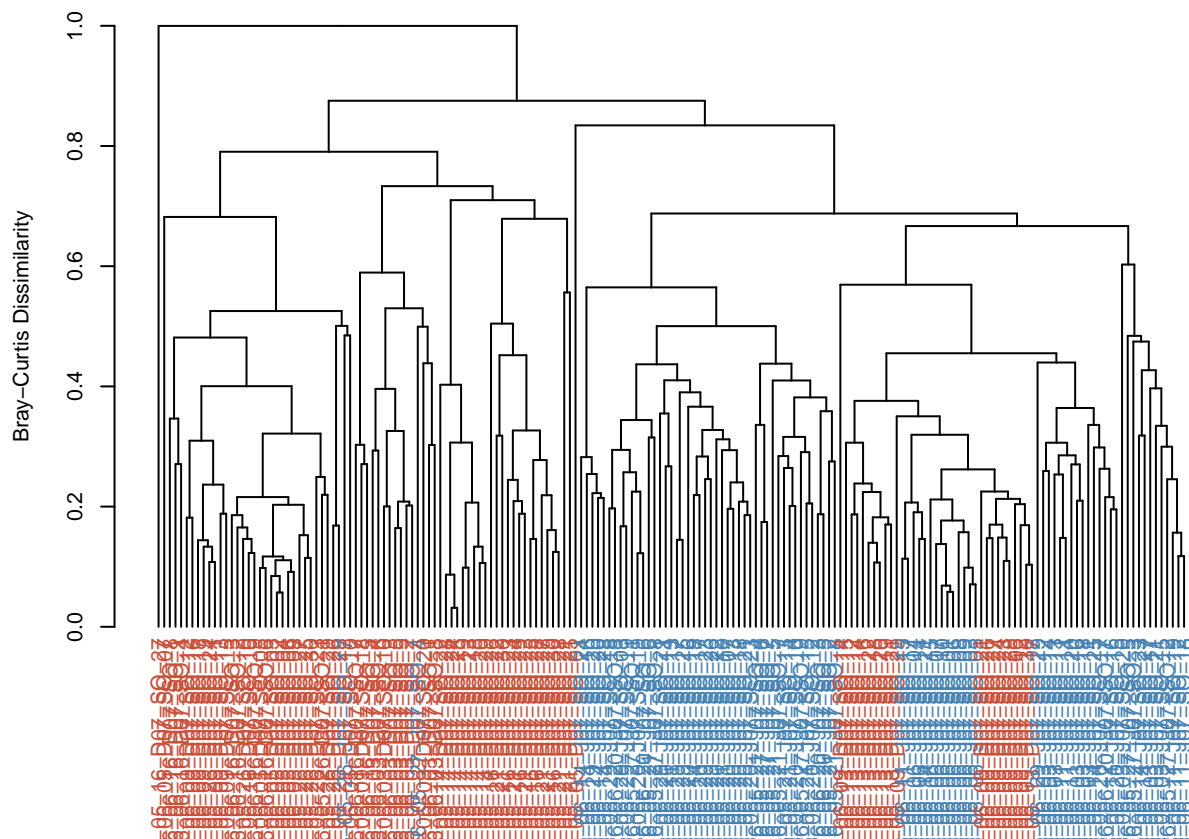
#-----Plotting-----#

# plotting the Bray-Curtis dissimilarity, I made it as a dendrogram to flatten out the bottom
den_temp_clust = as.dendrogram(temp_bc_clust)
plot(den_temp_clust)
```



```
#Colouring (from https://rstudio-pubs-static.s3.amazonaws.com/68544\_06343669257d4f35aaca449f9ff1e6f7.html)
#creating a colour palette with dif colours for DI and JS
cbPalette <- c("tomato3", "steelblue")
colorCode <- c(DI=cbPalette[1], JS = cbPalette[2])

labels_colors(den_temp_clust) <- colorCode[temp_clusdata_abund$location][order.dendrogram(den_temp_clust)]
par(cex = 0.7, mar=c(7,4,1,1))
plot(den_temp_clust, ylab = "Bray-Curtis Dissimilarity")
```



```
##-----SIMPROF TEST-----##
```

```
##
```

```
library(clustsig)
```

```
#Calculates number of significant clusters using average linkage method
```

```
simprof_test <- simprof(temp_bc_abund, num.expected=200, num.simulated=100,  
  method.cluster="average", method.distance="czekanowski",  
  method.transform="identity", alpha=0.01, sample.orientation = "row",  
  const = 1 ,silent=FALSE, increment=10, undef.zero=T,  
  warn.braycurtis = F)
```

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## [1] "Expected iteration 20"
## [1] "Expected iteration 30"
## [1] "Expected iteration 40"
## [1] "Expected iteration 50"
## [1] "Expected iteration 60"
## [1] "Expected iteration 70"
## [1] "Expected iteration 80"
## [1] "Expected iteration 90"
## [1] "Expected iteration 100"
## [1] "Expected iteration 110"
## [1] "Expected iteration 120"
## [1] "Expected iteration 130"
## [1] "Expected iteration 140"
## [1] "Expected iteration 150"
```

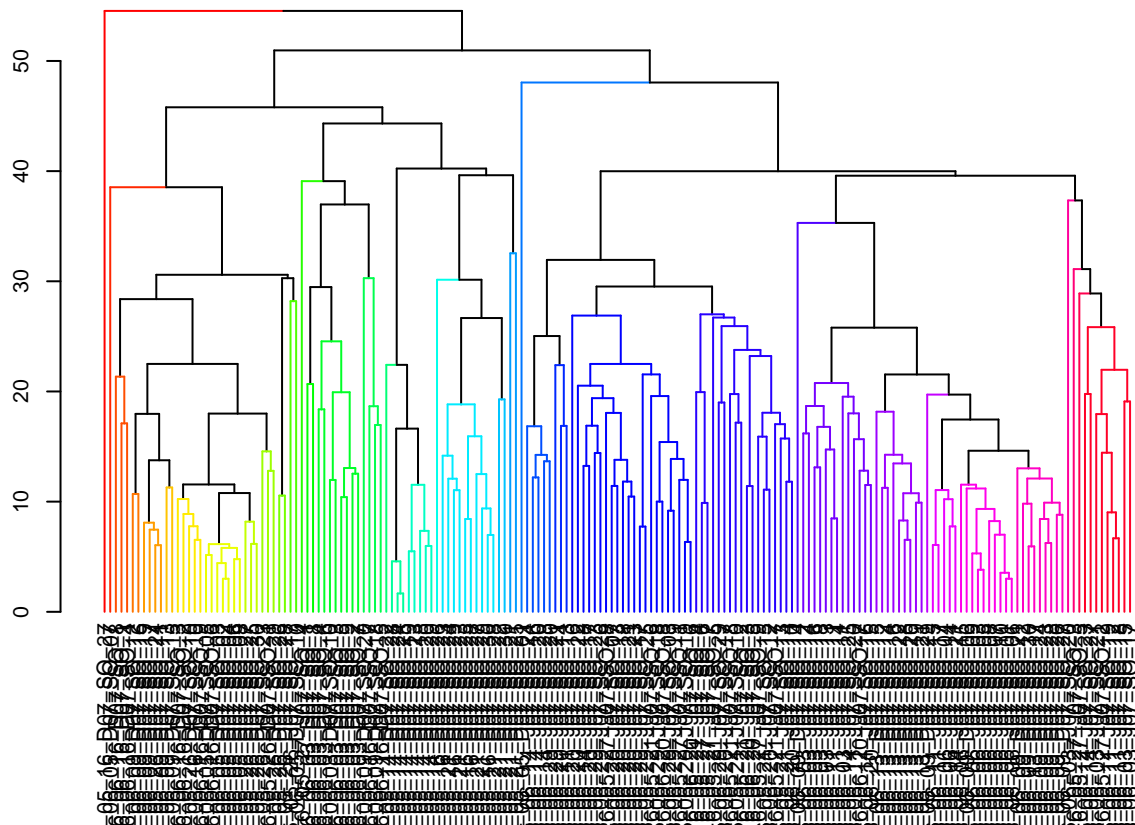
```
## [1] "Expected iteration 160"
## [1] "Expected iteration 170"
## [1] "Expected iteration 180"
## [1] "Expected iteration 190"
## [1] "Expected iteration 200"
## [1] "Simulated iteration 10"
## [1] "Simulated iteration 20"
## [1] "Simulated iteration 30"
## [1] "Simulated iteration 40"
## [1] "Simulated iteration 50"
## [1] "Simulated iteration 60"
## [1] "Simulated iteration 70"
## [1] "Simulated iteration 80"
## [1] "Simulated iteration 90"
## [1] "Simulated iteration 100"
## [1] "Expected iteration 10"
## [1] "Expected iteration 20"
## [1] "Expected iteration 30"
## [1] "Expected iteration 40"
## [1] "Expected iteration 50"
## [1] "Expected iteration 60"
## [1] "Expected iteration 70"
## [1] "Expected iteration 80"
## [1] "Expected iteration 90"
## [1] "Expected iteration 100"
## [1] "Expected iteration 110"
## [1] "Expected iteration 120"
## [1] "Expected iteration 130"
## [1] "Expected iteration 140"
## [1] "Expected iteration 150"
## [1] "Expected iteration 160"
## [1] "Expected iteration 170"
## [1] "Expected iteration 180"
## [1] "Expected iteration 190"
## [1] "Expected iteration 200"
## [1] "Simulated iteration 10"
## [1] "Simulated iteration 20"
## [1] "Simulated iteration 30"
## [1] "Simulated iteration 40"
## [1] "Simulated iteration 50"
## [1] "Simulated iteration 60"
## [1] "Simulated iteration 70"
## [1] "Simulated iteration 80"
## [1] "Simulated iteration 90"
## [1] "Simulated iteration 100"
## [1] "Expected iteration 10"
## [1] "Expected iteration 20"
## [1] "Expected iteration 30"
## [1] "Expected iteration 40"
## [1] "Expected iteration 50"
## [1] "Expected iteration 60"
## [1] "Expected iteration 70"
## [1] "Expected iteration 80"
## [1] "Expected iteration 90"
```

```

## [1] "Expected iteration 100"
## [1] "Expected iteration 110"
## [1] "Expected iteration 120"
## [1] "Expected iteration 130"
## [1] "Expected iteration 140"
## [1] "Expected iteration 150"
## [1] "Expected iteration 160"
## [1] "Expected iteration 170"
## [1] "Expected iteration 180"
## [1] "Expected iteration 190"
## [1] "Expected iteration 200"
## [1] "Simulated iteration 10"
## [1] "Simulated iteration 20"
## [1] "Simulated iteration 30"
## [1] "Simulated iteration 40"
## [1] "Simulated iteration 50"
## [1] "Simulated iteration 60"
## [1] "Simulated iteration 70"
## [1] "Simulated iteration 80"
## [1] "Simulated iteration 90"
## [1] "Simulated iteration 100"

```

```
simprof.plot(simprof_test)
```



```
## 'dendrogram' with 2 branches and 183 members total, at height 54.54177
```

```
##
##-----ANOSIM/SIMPER-----##
##

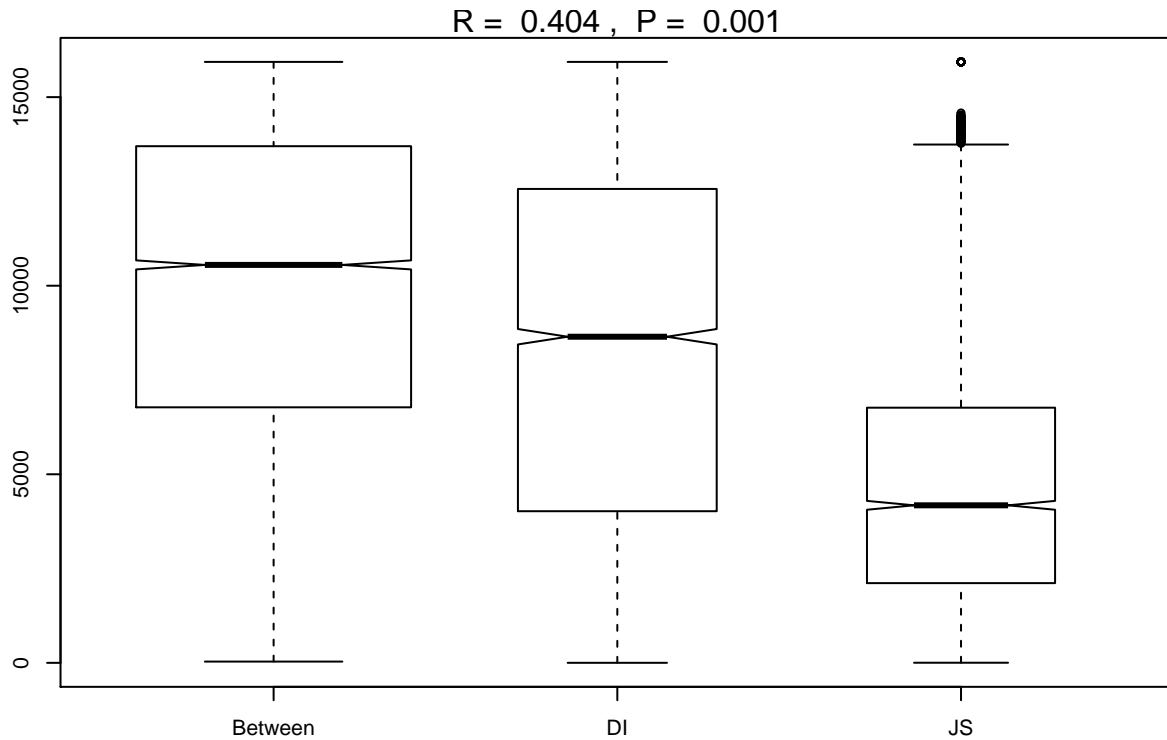
#create the BC dissimilarity matrix
temp_bc_dist <- vegdist(temp_bc_abund, method = "bray")

attach(metadata)

#anosim using our dissimilarity matrix and our grouping variable: location
temp.ano <- anosim(temp_bc_dist, location)
summary(temp.ano)

##
## Call:
## anosim(x = temp_bc_dist, grouping = location)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.4037
##      Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##      90%      95%     97.5%     99%
## 0.00931 0.01407 0.01914 0.02636
##
## Dissimilarity ranks between and within classes:
##           0%      25%      50%      75% 100%   N
## Between 33 6775.25 10551.5 13697.50 15934 8366
## DI       1 4020.50  8647.0 12565.50 15934 4371
## JS       3 2113.75  4177.0  6765.25 15934 3916

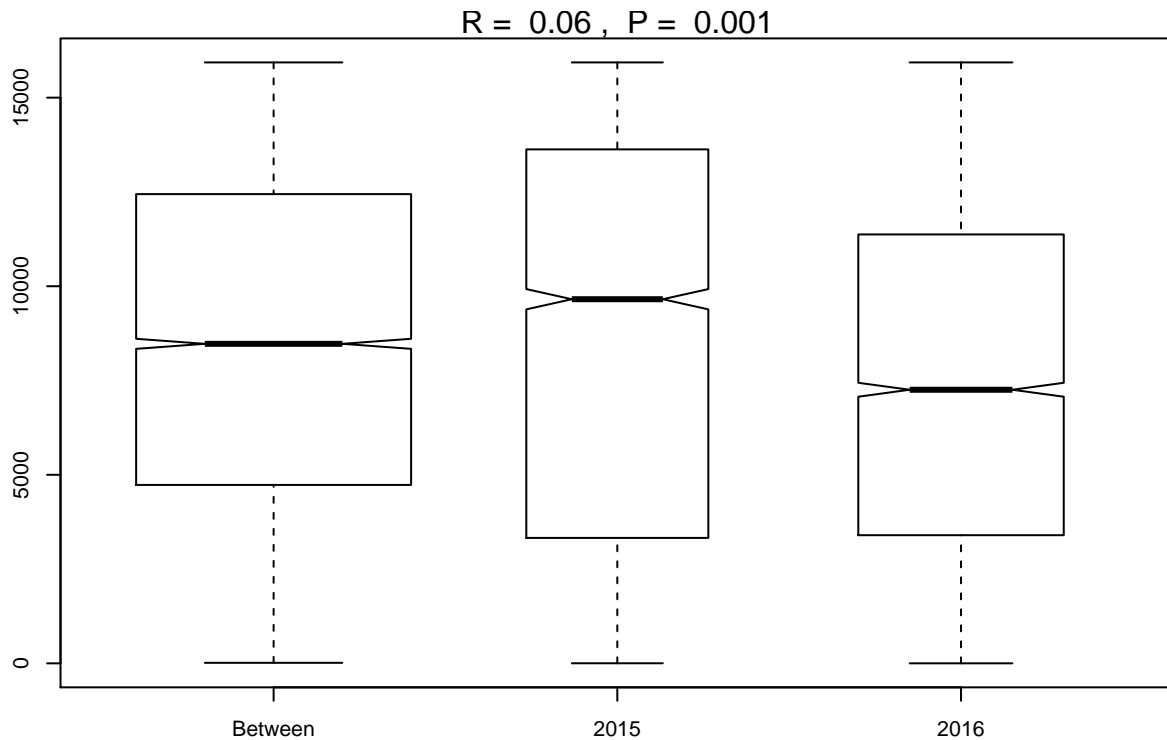
plot(temp.ano)
```



```
#anosim using our dissimilarity matrix and our grouping variable: year
temp.ano <- anosim(temp_bc_dist, year)
summary(temp.ano)
```

```
##
## Call:
## anosim(x = temp_bc_dist, grouping = year)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.05975
##      Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##      90%      95%     97.5%      99%
## 0.0103 0.0152 0.0190 0.0262
##
## Dissimilarity ranks between and within classes:
##           0%      25%      50%      75%     100%      N
## Between 14 4731.50 8472.5 12441.50 15934 8342
## 2015      2 3326.00 9655.0 13628.50 15934 3655
## 2016      1 3398.75 7254.5 11372.25 15934 4656
```

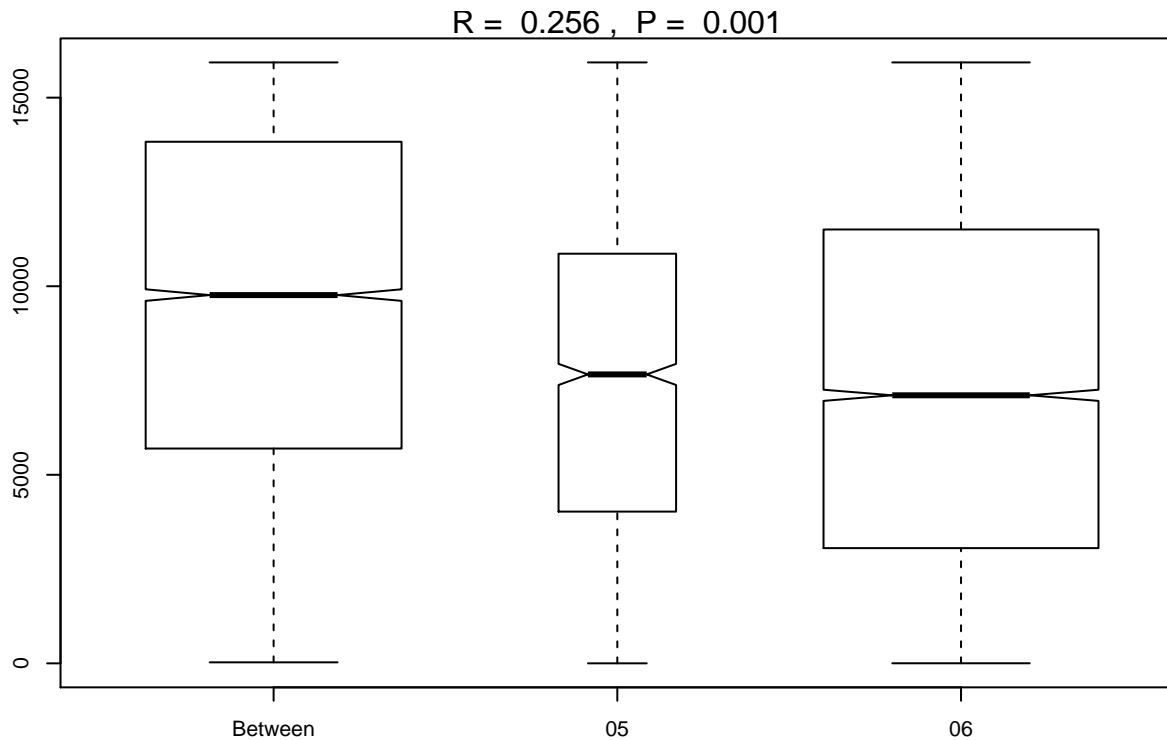
```
plot(temp.ano)
```



```
#anosim using our dissimilarity matrix and our grouping variable: month
temp.ano <- anosim(temp_bc_dist, month)
summary(temp.ano)
```

```
##
## Call:
## anosim(x = temp_bc_dist, grouping = month)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.2557
##      Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##      90%   95%  97.5%   99%
## 0.0356 0.0465 0.0558 0.0761
##
## Dissimilarity ranks between and within classes:
##      0%    25%    50%    75%   100%    N
## Between 27 5696.50 9765.0 13830.25 15934 7040
## 05      1 4024.00 7661.0 10862.00 15934 1485
## 06      2 3055.75 7107.5 11504.25 15934 8128
```

```
plot(temp.ano)
```

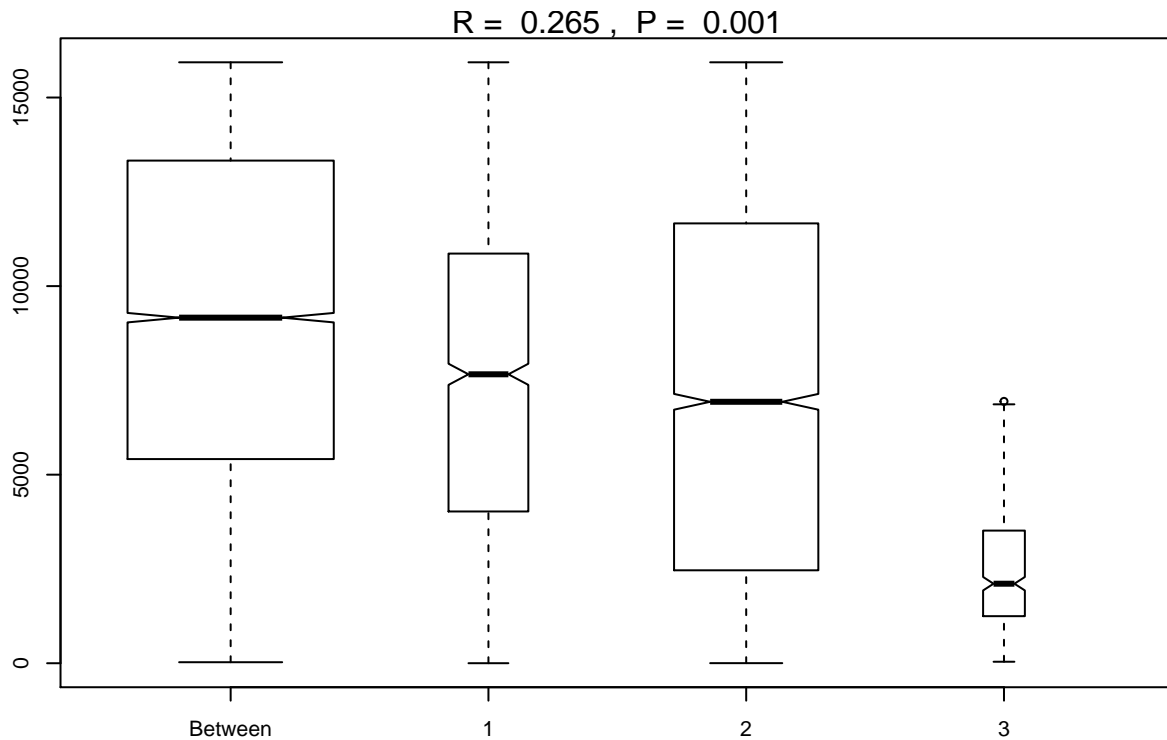


```
#anosim using our dissimilarity matrix and our grouping variable: sample.int (interval from 1-3, with 1
temp.ano <- anosim(temp_bc_dist, sample.int)
summary(temp.ano)
```

```
##
## Call:
## anosim(x = temp_bc_dist, grouping = sample.int)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.2645
##      Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##   90%   95%  97.5%   99%
## 0.0293 0.0380 0.0511 0.0665
##
## Dissimilarity ranks between and within classes:
##      0%   25%   50%   75%  100%   N
## Between 27 5413.50 9163.0 13328.0 15934 9911
## 1       1 4024.00 7661.0 10862.0 15934 1485
## 2       2 2464.00 6932.0 11662.5 15934 4851
```

```
## 3      40 1248.25 2108.5 3515.0 6943 406
```

```
plot(temp.ano)
```



```
#simper analysis using the BC dissimilarity matrix and grouping variable
```

```
sim <- with(metadata, simper(temp_bc_abund, location))
```

```
summary(sim) #produces table with average contribution to dissimilarity, avg abundances in groups a and b
```

```
##
```

```
## Contrast: DI_JS
```

```
##
```

##	average	sd	ratio	ava	avb	cumsum
## Calanus	1.249e-01	0.0944535	1.3220	0.0531475	0.3795457	0.1533
## Oikopleura	1.151e-01	0.1235498	0.9320	0.3164040	0.0547833	0.2947
## Metridia	1.132e-01	0.0980030	1.1553	0.1967923	0.3021392	0.4337
## Pseudocalanus	5.357e-02	0.0679391	0.7886	0.0048627	0.1551356	0.4995
## Barnacle	5.335e-02	0.0588220	0.9070	0.1569782	0.0351501	0.5650
## Digested.Calanoid	4.470e-02	0.0367484	1.2165	0.0540864	0.1451071	0.6199
## Podonidae	3.406e-02	0.0671565	0.5072	0.0895156	0.0119468	0.6617
## Euphausia	2.845e-02	0.0377914	0.7529	0.0183521	0.0771616	0.6966
## Other	2.741e-02	0.0737951	0.3714	0.0704498	0.0024653	0.7303
## Gastropoda	1.900e-02	0.0429794	0.4422	0.0553717	0.0048792	0.7536
## Corycaeus	1.673e-02	0.0186509	0.8971	0.0483918	0.0080400	0.7741
## Chaetognatha	1.576e-02	0.0268301	0.5872	0.0342182	0.0165251	0.7935
## Centropages	1.365e-02	0.0227747	0.5993	0.0333587	0.0145937	0.8102
## Hyperiididae	1.340e-02	0.0277823	0.4824	0.0324580	0.0132036	0.8267
## Epilabidocera	1.322e-02	0.0197315	0.6699	0.0204457	0.0283632	0.8429

## Asteroidea	1.300e-02	0.0419147	0.3102	0.0391777	0.0000000	0.8589
## Eucalanus	8.813e-03	0.0128815	0.6842	0.0082630	0.0214303	0.8697
## Bivalvia	8.786e-03	0.0173278	0.5070	0.0245923	0.0000000	0.8805
## Brachyura	6.926e-03	0.0117297	0.5905	0.0151382	0.0080717	0.8890
## Porcellanidae	6.728e-03	0.0128098	0.5253	0.0181488	0.0030143	0.8973
## Tortanus	5.383e-03	0.0131138	0.4105	0.0013708	0.0144644	0.9039
## Digested.Decapod	5.203e-03	0.0140459	0.3704	0.0059134	0.0105151	0.9103
## Aetideus	5.100e-03	0.0235874	0.2162	0.0007826	0.0145756	0.9165
## Limacina	4.741e-03	0.0112806	0.4203	0.0051871	0.0088360	0.9223
## Thysanoessa	4.603e-03	0.0431376	0.1067	0.0111001	0.0000000	0.9280
## Calanoida	4.206e-03	0.0097969	0.4293	0.0011711	0.0112729	0.9332
## Tomopteris	4.044e-03	0.0109360	0.3698	0.0114348	0.0000000	0.9381
## Paracalanus	4.032e-03	0.0074976	0.5377	0.0095779	0.0036744	0.9431
## Acartia	3.976e-03	0.0125895	0.3158	0.0013051	0.0110435	0.9480
## Diptera	3.607e-03	0.0088512	0.4075	0.0017441	0.0093440	0.9524
## Digested.Amphipod	3.014e-03	0.0182645	0.1650	0.0073470	0.0010738	0.9561
## Evadne	2.985e-03	0.0160261	0.1863	0.0067002	0.0023340	0.9598
## Polychaeta	2.712e-03	0.0073797	0.3676	0.0052634	0.0031072	0.9631
## Harpacticoida	2.559e-03	0.0067955	0.3766	0.0022448	0.0058942	0.9662
## Grapsidae	2.541e-03	0.0066669	0.3812	0.0077149	0.0000000	0.9693
## Paraeuchaeta	2.395e-03	0.0066254	0.3614	0.0052241	0.0019747	0.9723
## Actinopterygii	2.246e-03	0.0067637	0.3320	0.0000000	0.0069049	0.9750
## Cancridae	2.223e-03	0.0141129	0.1575	0.0056098	0.0013615	0.9778
## Bryozoa	1.845e-03	0.0048969	0.3767	0.0048763	0.0005382	0.9800
## Siphonophorae	1.445e-03	0.0063157	0.2288	0.0035585	0.0012149	0.9818
## Spionidae	1.406e-03	0.0041947	0.3352	0.0037568	0.0007596	0.9835
## Neocalanus	1.377e-03	0.0061235	0.2248	0.0003788	0.0036402	0.9852
## Phrosinidae	1.180e-03	0.0051186	0.2305	0.0021803	0.0011217	0.9867
## Pinnotheridae	1.164e-03	0.0042721	0.2724	0.0036319	0.0000000	0.9881
## Cumacea	9.845e-04	0.0053271	0.1848	0.0000000	0.0029772	0.9893
## Arthropoda	9.140e-04	0.0043690	0.2092	0.0015792	0.0010951	0.9904
## Candacia	8.466e-04	0.0038778	0.2183	0.0015430	0.0008895	0.9915
## Majidae	7.421e-04	0.0046823	0.1585	0.0003833	0.0020132	0.9924
## Anomura	6.852e-04	0.0040010	0.1713	0.0009792	0.0010049	0.9932
## Digested.Insect	6.579e-04	0.0032939	0.1997	0.0002237	0.0016914	0.9940
## Oncaea	5.956e-04	0.0028590	0.2083	0.0000000	0.0017192	0.9948
## Coleoptera	5.820e-04	0.0041803	0.1392	0.0000000	0.0016995	0.9955
## Cyclopoida	4.278e-04	0.0029298	0.1460	0.0011744	0.0000000	0.9960
## Cnidaria	4.161e-04	0.0039152	0.1063	0.0000000	0.0011978	0.9965
## Portunidae	3.737e-04	0.0020951	0.1784	0.0006955	0.0004545	0.9970
## Heterorhabdus	3.533e-04	0.0023386	0.1511	0.0000000	0.0011396	0.9974
## Caprellidae	3.351e-04	0.0020763	0.1614	0.0003765	0.0006432	0.9978
## Arachnida	3.075e-04	0.0028903	0.1064	0.0000000	0.0010951	0.9982
## Isopoda	2.430e-04	0.0022856	0.1063	0.0000000	0.0007512	0.9985
## Insecta	2.074e-04	0.0019521	0.1063	0.0000000	0.0005886	0.9988
## Gaetanus	1.468e-04	0.0013809	0.1063	0.0000000	0.0004582	0.9989
## Callianassidae	1.321e-04	0.0012419	0.1064	0.0000000	0.0004465	0.9991
## Clausocalanus	1.321e-04	0.0012419	0.1064	0.0000000	0.0004465	0.9993
## Monstrilloida	1.298e-04	0.0012570	0.1033	0.0003542	0.0000000	0.9994
## Upogebiidae	1.118e-04	0.0010813	0.1034	0.0003418	0.0000000	0.9996
## Hippolytidae	9.076e-05	0.0008780	0.1034	0.0002803	0.0000000	0.9997
## Xanthidae	9.076e-05	0.0008780	0.1034	0.0002803	0.0000000	0.9998
## Clytia	6.928e-05	0.0006700	0.1034	0.0002280	0.0000000	0.9999
## Gammaridae	5.874e-05	0.0005684	0.1034	0.0001771	0.0000000	0.9999

```
## Caridea          5.312e-05 0.0005139 0.1034 0.0001643 0.0000000 1.0000
## Permutation: free
## Number of permutations: 0
```

```
sim #lists most influential species and their cumulative contributions
```

```
## cumulative contributions of most influential species:
```

```
##
```

```
## $DI_JS
```

```
##          Calanus          Oikopleura          Metridia          Pseudocalanus
```

```
##          0.1533147          0.2946837          0.4336995          0.4994762
```

```
##          Barnacle Digated.Calanoid          Podonidae          Euphausia
```

```
##          0.5649787          0.6198641          0.6616830          0.6966179
```

```
##          Other
```

```
##          0.7302691
```

```
#to get the overall dissimilarity between the clusters
```

```
lapply(sim, FUN = function(x){x$overall})
```

```
## $DI_JS
```

```
## [1] 0.8144824
```

Ordination

Then conduct BIOENV model to find best correlated environmental variables. Then run NMDS and ordinate with environmental parameters as vectors.