# QB_Project_Group1

## 2025-03-02

## R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```r
library(vegan)
```

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

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

```r
library(gplots)
```

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

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

```r
library(maps)
library(mapdata)
library(ggplot2)
library(leaflet)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(RColorBrewer)
library(pheatmap)
```

```r
# World map for data collection sites
fish_data <- read.csv("/cloud/project/QB2025_Brown/Fish_Dataset.csv")

fish_data <- na.omit(fish_data)

lats <- as.numeric(fish_data[, 2])
lons <- as.numeric(fish_data[, 3])
```

```r
map_data <- data.frame(long = lons, lat = lats)

world_map <- map_data("world")

ggplot() +
  geom_polygon(data = world_map, aes(x = long, y = lat, group = group),
               fill = "lightgray", color = "black") +
  geom_point(data = map_data, aes(x = long, y = lat),
             color = "red", size = 2) +
  theme_minimal() +
  labs(title = "Fish Data Collection Sites",
       x = "Longitude", y = "Latitude")
```



Fish Data Collection Sites
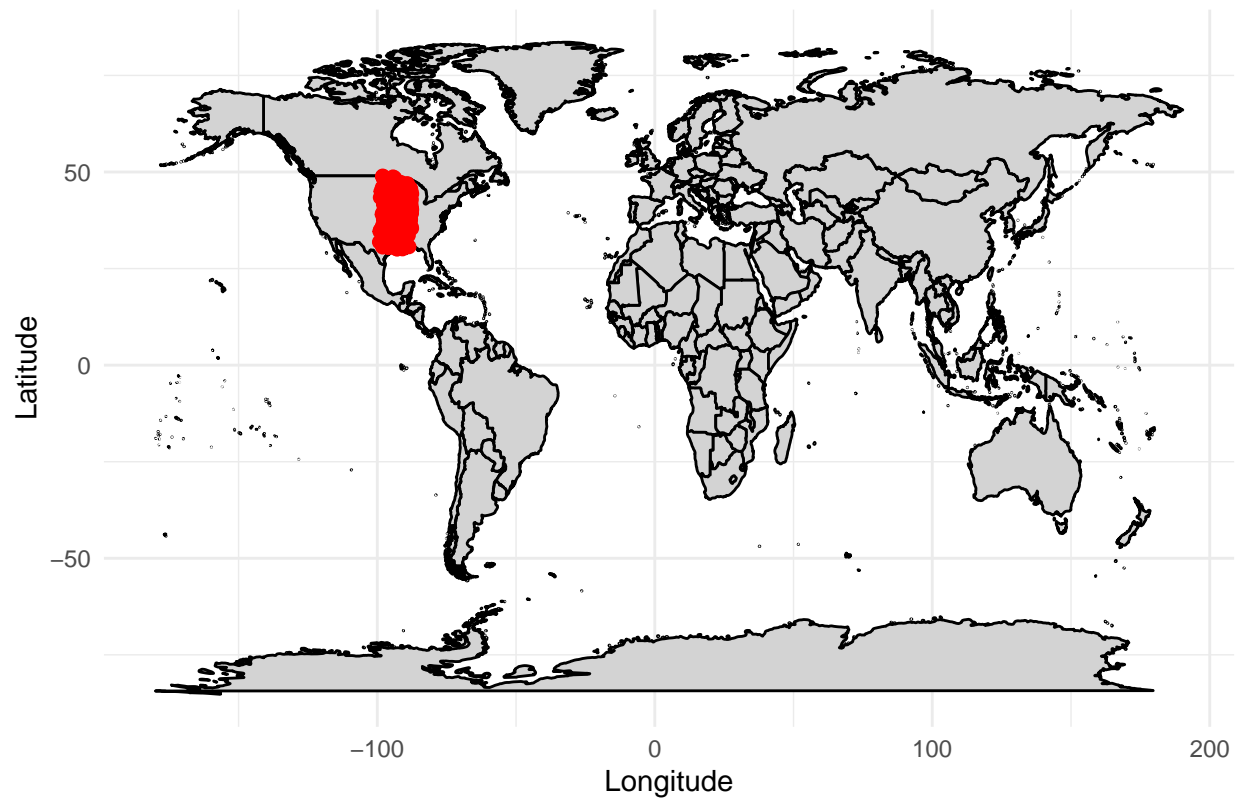
```r
fish_data$Lat_Zone <- recode(fish_data$Lat_Zone,
         "Two" = 1, "Three" = 2, "Four" = 3,
         "Five" = 4, "Six" = 5, "Seven" = 6, "Eight" = 7)



us_map <- map_data("state")


region_colors <- c("1" = "red", "2" = "blue", "3" = "green",
                   "4" = "purple", "5" = "orange", "6" = "yellow",
                   "7" = "pink")


ggplot() +
  geom_map(data = us_map, map = us_map, aes(x = long, y = lat, map_id = region),
           color = "black", fill = "lightgray", size = 0.2) +  # Map of the US
```

```
    geom_point(data = fish_data, aes(x = Longitude, y = Latitude, color = as.factor(Lat_Zone)),
                size = 3) +
    scale_color_manual(values = region_colors) +
    theme_minimal() +
    labs(title = "Fish Data Distribution on US Map", x = "Longitude", y = "Latitude") +
    theme(legend.position = "bottom")
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning in geom_map(data = us_map, map = us_map, aes(x = long, y = lat, :
## Ignoring unknown aesthetics: x and y
```



Fish Data Distribution on US Map
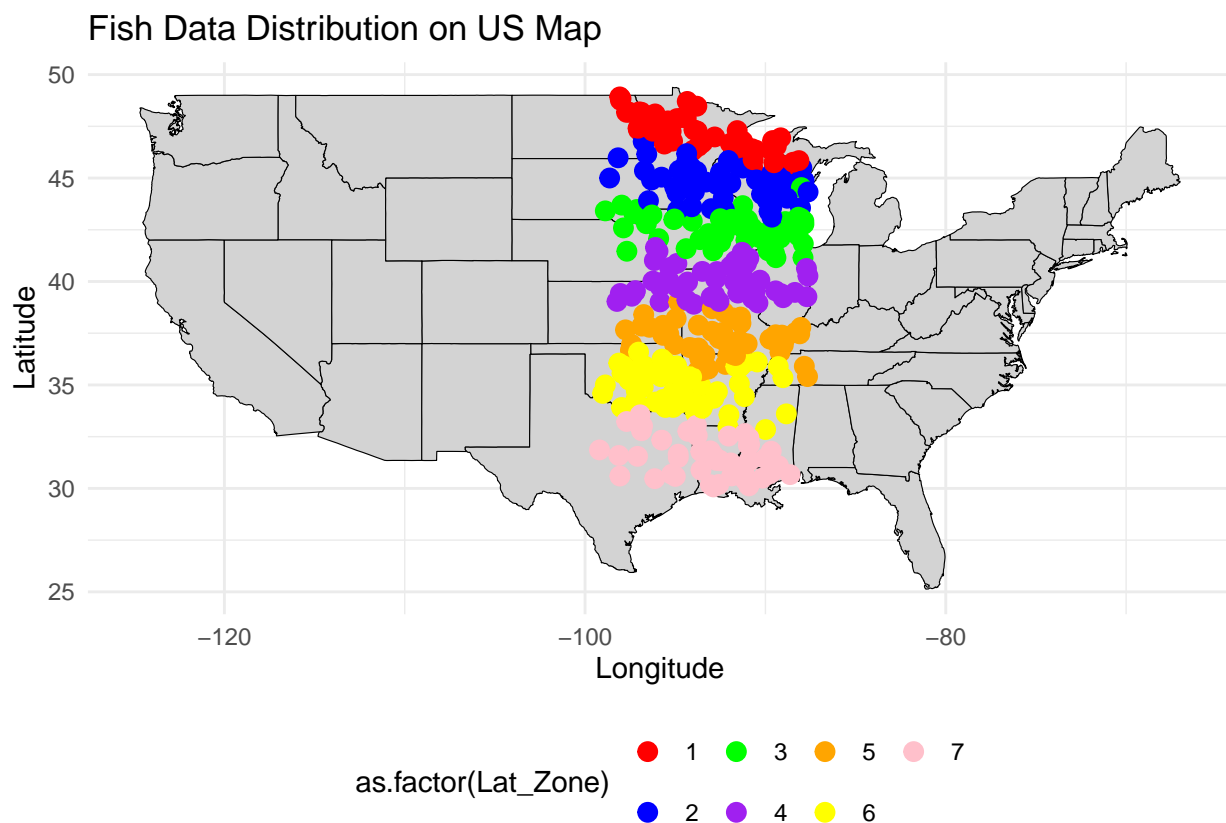
```
# Observed species richness for each zone
#fish_data

site <- fish_data$SiteID
site
```

```
##   [1] "FW08AR001"    "FW08AR007"    "FW08AR016"    "FW08AR017"
##   [5] "FW08AR020"    "FW08AR024"    "FW08AR028"    "FW08AR030"
##   [9] "FW08AR035"    "FW08AR037"    "FW08AR043"    "FW08AR052"
##  [13] "FW08AR060"    "FW08AR080"    "FW08AR084"    "FW08AR114"
##  [17] "FW08AR133"    "FW08AR192"    "FW08AR236"    "FW08IA002"
##  [21] "FW08IA003"    "FW08IA005"    "FW08IA008"    "FW08IA011"
##  [25] "FW08IA014"    "FW08IA016"    "FW08IA017"    "FW08IA042"
```

```
##  [29] "FW08IA044"    "FW08IA052"    "FW08IA053"    "FW08IA057"
##  [33] "FW08IL005"    "FW08IL010"    "FW08IL020"    "FW08IL029"
##  [37] "FW08IL044"    "FW08KS012"    "FW08KS038"    "FW08KS039"
##  [41] "FW08KS056"    "FW08KS063"    "FW08KY029"    "FW08KY033"
##  [45] "FW08LA029"    "FW08LA037"    "FW08LA040"    "FW08LA049"
##  [49] "FW08LA164"    "FW08LA173"    "FW08LA180"    "FW08MI005"
##  [53] "FW08MI013"    "FW08MN006"    "FW08MN010"    "FW08MN022"
##  [57] "FW08MN039"    "FW08MN049"    "FW08MN061"    "FW08MN080"
##  [61] "FW08MO006"    "FW08MO010"    "FW08MO029"    "FW08MO033"
##  [65] "FW08MO038"    "FW08MS002"    "FW08MS004"    "FW08MS048"
##  [69] "FW08MS069"    "FW08MS101"    "FW08ND004"    "FW08ND007"
##  [73] "FW08ND011"    "FW08ND016"    "FW08ND039"    "FW08ND071"
##  [77] "FW08NE035"    "FW08OK007"    "FW08OK009"    "FW08OK014"
##  [81] "FW08OK030"    "FW08OK039"    "FW08OK043"    "FW08OK047"
##  [85] "FW08OK050"    "FW08OK051"    "FW08OK057"    "FW08OK059"
##  [89] "FW08OK062"    "FW08SD005"    "FW08TN025"    "FW08TN032"
##  [93] "FW08TX001"    "FW08TX010"    "FW08TX014"    "FW08WI006"
##  [97] "FW08WI009"    "FW08WI013"    "FW08WI014"    "FW08WI017"
## [101] "FW08WI020"    "FW08WI039"    "FW08WI040"    "FW08WI044"
## [105] "FW08WI048"    "FW08WI049"    "FW08WI051"    "FW08WI053"
## [109] "FW08WI060"    "FW08WI075"    "FW08WI098"    "FW08WI100"
## [113] "FW08WI104"    "IALS-1049"    "IAR9-0901"    "IAR9-0902"
## [117] "IAR9-0904"    "IAR9-0906"    "IAR9-0908"    "IAR9-0909"
## [121] "IARM-1001"    "IARO-1017"    "IARO-1018"    "IAS9-0924"
## [125] "IAS9-0927"    "ILLS-1074"    "ILLS-1075"    "ILLS-1076"
## [129] "ILR9-0901"    "ILR9-0902"    "ILR9-0903"    "ILR9-0906"
## [133] "ILR9-0909"    "ILRF-0002"    "ILRM-1002"    "ILRM-1003"
## [137] "ILRO-1024"    "ILS9-0921"    "ILS9-0926"    "ILSS-1122"
## [141] "ILSS-1169"    "KSR9-0906"    "KSR9-0910"    "KSRS-1258"
## [145] "KSRS-1268"    "KSRS-1306"    "KSRS-1312"    "KSRS-1317"
## [149] "KSRS-1324"    "KSRS-1330"    "KSRS-1348"    "KSS9-0933"
## [153] "KSS9-0934"    "KYR9-0901"    "KYR9-0904"    "KYRO-1032"
## [157] "LAR9-0901"    "LAR9-0902"    "LAR9-0906"    "LAR9-0907"
## [161] "LARM-1002"    "LARM-1003"    "LAS9-0945"    "LAS9-0948"
## [165] "LAS9-0949"    "LAS9-0950"    "LASS-1049"    "LASS-1050"
## [169] "MILS-1057"    "MIRM-1002"    "MIS9-0936"    "MISS-1135"
## [173] "MNLS-1094"    "MNLS-1095"    "MNR9-0904"    "MNR9-0909"
## [177] "MNR9-0911"    "MNR9-0917"    "MNRF-0003"    "MNRF-0005"
## [181] "MNRF-0008"    "MNRF-0010"    "MNRM-1001"    "MNRM-1002"
## [185] "MNRO-1049"    "MNRO-1053"    "MNRO-1055"    "MNS9-0928"
## [189] "MNS9-0929"    "MNS9-0930"    "MNSS-1168"    "MOLS-1084"
## [193] "MOLS-1085"    "MOR9-0903"    "MOR9-0905"    "MOR9-0906"
## [197] "MOR9-0907"    "MOR9-0908"    "MOR9-0910"    "MORF-0005"
## [201] "MORF-0010"    "MORF-0011"    "MORO-1044"    "MORO-1045"
## [205] "MORO-1046"    "MORO-1047"    "MOS9-0934"    "MOS9-0937"
## [209] "MOS9-0938"    "MOSS-1159"    "MOSS-1163"    "MSR9-0904"
## [213] "MSR9-0906"    "MSRF-0003"    "MSRF-0004"    "MSRM-1001"
## [217] "MSRM-1003"    "MSRO-1021"    "NDR9-0904"    "NDR9-0918"
## [221] "NDRF-0008"    "NELS-1082"    "NERM-1001"    "NERM-1005"
## [225] "NERO-1037"    "NESS-1143"    "OKLS-1203"    "OKLS-1204"
## [229] "OKLS-1209"    "OKR9-0902"    "OKR9-0903"    "OKR9-0904"
## [233] "OKR9-0906"    "OKR9-0907"    "OKR9-0908"    "OKR9-0909"
## [237] "OKR9-0912"    "OKRF-0004"    "OKRM-1006"    "OKRO-1087"
## [241] "OKRO-1092"    "OKRO-1103"    "OKS9-0937"    "OKS9-0938"
```

```
## [245] "OKSS-1430"       "SDLS-1113"       "SDR9-0904"       "SDR9-0916"
## [249] "SDRM-1004"       "SDRO-1067"       "SDS9-0942"       "TNLS-1034"
## [253] "TXLS-1119"       "TXLS-1131"       "TXLS-1134"       "TXR9-0907"
## [257] "TXR9-0916"       "TXR9-0918"       "TXR9-0921"       "TXRO-1080"
## [261] "TXSS-1215"       "TXSS-1216"       "TXSS-1224"       "USGS-03338780"
## [265] "USGS-03603765"   "USGS-04063700"   "USGS-04071795"   "USGS-04085139"
## [269] "USGS-040863075"  "USGS-04087118"   "USGS-04087204"   "USGS-040872393"
## [273] "USGS-05030150"   "USGS-05051300"   "USGS-05062500"   "USGS-05066500"
## [277] "USGS-05086000"   "USGS-05200020"   "USGS-05201550"   "USGS-05220600"
## [281] "USGS-05227500"   "USGS-05261000"   "USGS-05267000"   "USGS-05270700"
## [285] "USGS-05276005"   "USGS-05304795"   "USGS-05316985"   "USGS-05317828"
## [289] "USGS-05330902"   "USGS-05331833"   "USGS-05406457"   "USGS-05451210"
## [293] "USGS-05451900"   "USGS-05458000"   "USGS-05464220"   "USGS-05465000"
## [297] "USGS-05465500"   "USGS-05467000"   "USGS-05470500"   "USGS-05474000"
## [301] "USGS-05525500"   "USGS-05531500"   "USGS-055437901"  "USGS-05548105"
## [305] "USGS-05556500"   "USGS-05558500"   "USGS-06483500"   "USGS-06805500"
## [309] "USGS-06923150"   "USGS-06927590"   "USGS-07050228"   "USGS-07053250"
## [313] "USGS-07057280"   "USGS-07058970"   "USGS-07060710"   "USGS-07060890"
## [317] "USGS-07060894"   "USGS-07065495"   "USGS-07067000"   "USGS-070692655"
## [321] "USGS-07069267"   "USGS-07186670"   "USGS-07188855"   "USGS-07196500"
## [325] "USGS-07288955"   "USGS-07375050"   "USGS-07379960"   "USGS-08012150"
## [329] "USGS-08012470"   "USGS-08044000"   "USGS-08050800"   "WILS-1087"
## [333] "WILS-1093"       "WIR9-0901"       "WIR9-0914"       "WIRF-0002"
## [337] "WIRF-0003"       "WIRF-0004"       "WIRF-0008"       "WIRF-0012"
## [341] "WIRF-0013"       "WIRF-0015"       "WIRM-1003"       "WIRO-1040"
## [345] "WIRO-1043"       "WIS9-0924"       "WIS9-0929"       "WIS9-0930"
## [349] "WIS9-0936"       "WISS-1168"
```

```r
species <- fish_data[ ,22:658]
```

```r
print(fish_data$Lat_Zone)
```

```
##    [1] 6 6 5 6 6 6 6 6 5 6 6 7 6 5 6 6 6 6 6 3 3 3 3 4 3 4 3 3 3 3 4 3 4 4 4 4 5
##   [38] 5 4 4 5 5 5 5 7 7 7 7 7 7 7 1 1 1 1 1 1 2 2 1 5 4 5 5 5 7 7 7 7 7 1 1 1 1
##   [75] 1 1 3 6 6 6 5 6 6 6 6 6 5 6 6 3 5 6 7 7 7 1 1 1 1 2 1 1 2 3 2 3 2 3 2 2 2
##  [112] 2 2 2 3 4 2 3 4 3 3 3 3 3 3 3 5 4 4 3 5 3 3 4 3 4 3 4 4 5 4 5 4 4 4 4 5 4
##  [149] 5 5 4 5 5 5 5 5 6 7 7 7 7 7 7 7 7 7 7 7 1 1 1 1 2 1 2 1 2 1 1 1 2 1 2 2 1
##  [186] 2 2 1 2 1 1 4 4 4 5 4 5 5 5 4 4 4 5 4 4 5 4 4 4 4 4 7 7 7 6 7 6 1 2 1 3
##  [223] 4 4 4 4 6 6 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 3 2 2 3 3 2 6 7 7 7 7 7 7 7
##  [260] 7 7 7 7 4 5 1 2 3 2 3 3 3 1 2 1 1 1 1 1 1 1 2 2 2 2 2 2 2 1 2 3 3 3 3 4
##  [297] 4 4 3 4 4 3 3 3 3 3 3 4 5 5 5 5 5 5 5 5 6 5 5 5 5 5 5 6 7 7 7 7 7 7 2 2
##  [334] 2 2 2 1 2 1 3 2 1 2 1 2 2 2 3 1 2
```

```r
fish_data$Lat_Zone <- recode(fish_data$Lat_Zone,
        "Two" = 1, "Three" = 2, "Four" = 3,
        "Five" = 4, "Six" = 5, "Seven" = 6, "Eight" = 7)
```

```
## Warning in recode.numeric(fish_data$Lat_Zone, Two = 1, Three = 2, Four = 3, :
## NAs introduced by coercion
```

```r
as.numeric(fish_data$Lat_Zone)
```

```
##    [1] 6 6 5 6 6 6 6 6 5 6 6 7 6 5 6 6 6 6 6 3 3 3 3 4 3 4 3 3 3 3 4 3 4 4 4 4 5
##   [38] 5 4 4 5 5 5 5 7 7 7 7 7 7 7 1 1 1 1 1 1 2 2 1 5 4 5 5 5 7 7 7 7 7 1 1 1 1
##   [75] 1 1 3 6 6 6 5 6 6 6 6 6 5 6 6 3 5 6 7 7 7 1 1 1 1 2 1 1 2 3 2 3 2 3 2 2 2
```

```
## [112] 2 2 2 3 4 2 3 4 3 3 3 3 3 3 3 5 4 4 3 5 3 3 4 3 4 3 4 4 5 4 5 4 4 4 4 5 4
## [149] 5 5 4 5 5 5 5 5 6 7 7 7 7 7 7 7 7 7 7 7 1 1 1 1 2 1 2 1 2 1 1 1 2 1 2 2 1
## [186] 2 2 1 2 1 1 4 4 4 5 4 5 5 5 4 4 4 5 4 4 5 4 4 4 4 4 7 7 7 7 6 7 6 1 2 1 3
## [223] 4 4 4 4 6 6 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 3 2 2 3 3 2 6 7 7 7 7 7 7 7
## [260] 7 7 7 7 4 5 1 2 3 2 3 3 3 1 2 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 1 2 3 3 3 3 4
## [297] 4 4 3 4 4 3 3 3 3 3 3 4 5 5 5 5 5 5 5 5 6 5 5 5 5 5 5 6 7 7 7 7 7 7 7 2 2
## [334] 2 2 2 1 2 1 3 2 1 2 1 2 2 2 3 1 2
```

```r
S.obs <- function(x = ""){
  rowSums(x > 0) * 1
}

lat1 <- subset(species, Lat_Zone == 1)
richness1 <- S.obs(lat1)
lat2 <- subset(species, Lat_Zone == 2)
richness2 <-S.obs(lat2)
lat3 <- subset(species, Lat_Zone == 3)
richness3 <-S.obs(lat3)
lat4 <- subset(species, Lat_Zone == 4)
richness4 <-S.obs(lat4)
lat5 <- subset(species, Lat_Zone == 5)
richness5 <-S.obs(lat5)
lat6 <- subset(species, Lat_Zone == 6)
richness6 <-S.obs(lat6)
lat7 <- subset(species, Lat_Zone == 7)
richness7 <-S.obs(lat7)

richness_df <- data.frame(
  Lat_Zone = factor(1:7),  # Convert to factor for discrete x-axis
  Observed_Richness = c(richness1, richness2, richness3, richness4, richness5, richness6, richness7)
)


ggplot(richness_df, aes(x = Lat_Zone, y = Observed_Richness, fill = Lat_Zone)) +
  geom_boxplot() +
  labs(x = "Lat_Zone", y = "Observed Richness", title = "Species Richness by Latitudinal Zone") +
  theme_minimal() +
  scale_fill_brewer(palette = "Set3")
```

## Species Richness by Latitudinal Zone
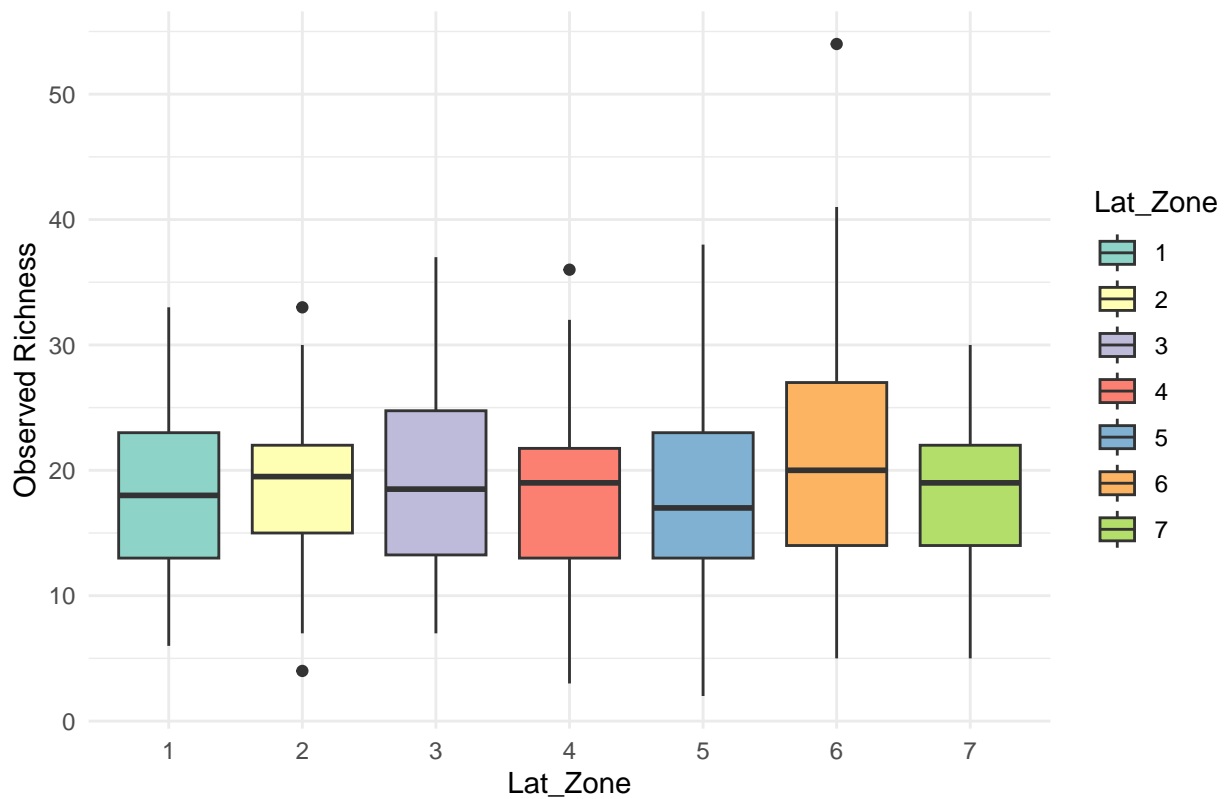


```r
#Shannon's Diversity for each zone

ShanH <- function(x = ""){
  H = 0
  for (n_i in x){
    if(n_i > 0) {
      p = n_i / sum(x)
      H = H - p*log(p)
    }
  }
  return(H)
}

diversity(lat1, index = "shannon")
```

```
##         52         53         54         55         56         57         60
## 1.99429012 1.44064366 1.68236169 2.40827852 1.61580760 1.43026592 2.01763911
##         71         72         73         74         75         76         96
## 1.63808095 1.61970118 1.86834551 0.47750400 0.04786485 0.70423031 1.83628018
##         97         98         99        101        102        169        170
## 1.85367143 2.26445973 1.86148986 2.01597228 1.52398035 2.38599473 2.17689801
##        171        172        174        176        178        179        180
## 1.18940357 1.60195094 1.83126845 0.33424256 1.89609691 2.04276343 1.83882496
##        182        185        188        190        191        219        221
## 1.45471100 1.93293034 0.60285680 1.85323149 1.81502285 2.01731557 1.86187289
##        266        273        275        276        277        278        279
## 1.97698518 1.55765241 2.33039727 1.95203836 0.64690074 1.75720267 1.92705852
```

```
##        280        281        290        337        339        342        344
## 2.43466169 1.86900420 1.61089491 2.55284886 2.31832108 1.93782397 2.03463156
##        349
## 1.38382030
```

```r
Shan1 <- diversity(lat1, index = "shannon")
Shan2 <- diversity(lat2, index = "shannon")
Shan3 <- diversity(lat3, index = "shannon")
Shan4 <- diversity(lat4, index = "shannon")
Shan5 <- diversity(lat5, index = "shannon")
Shan6 <- diversity(lat6, index = "shannon")
Shan7 <- diversity(lat7, index = "shannon")


Shan_df <- data.frame(
  Lat_Zone = factor(1:7),
  Shannon_div = c(Shan1, Shan2, Shan3, Shan4, Shan5, Shan6, Shan7)
)


ggplot(Shan_df, aes(x = Lat_Zone, y = Shannon_div, fill = Lat_Zone)) +
  geom_boxplot() +
  labs(
    x = "Latitudinal Zone",
    y = "Shannon Diversity",
    title = "Shannon's Diversity by Latitudinal Zone"
  ) +
  theme_minimal() +
  scale_fill_brewer(palette = "Set3")
```

## Shannon's Diversity by Latitudinal Zone
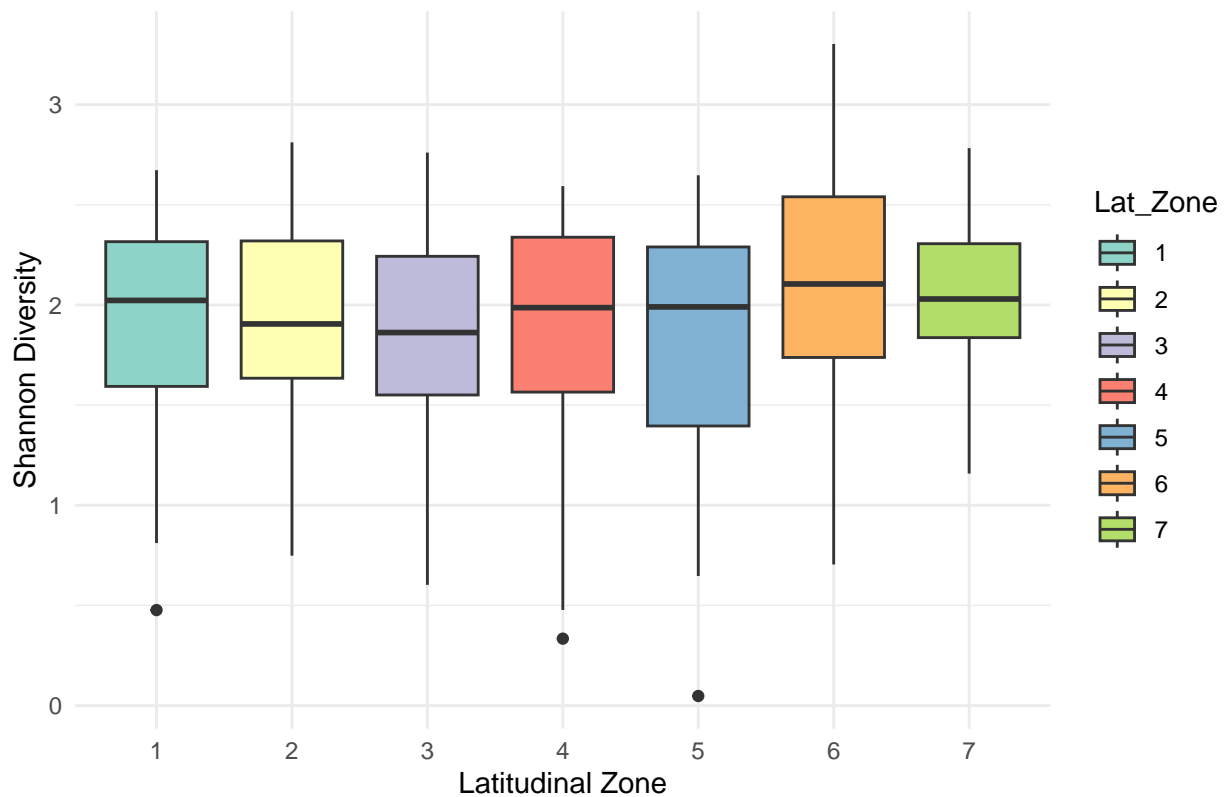


```r
#Simpson's Diversity of each zone

SimpD <- function(x = ""){
  D = 0
  N = sum(x)
  for (n_i in x){
    D = D + (n_i^2)/(N^2)
  }
  return(D)
}


D.inv <- 1/SimpD(lat1)

Simp1 <- diversity(lat1, index = "inv")
Simp2 <- diversity(lat2, index = "inv")
Simp3 <- diversity(lat3, index = "inv")
Simp4 <- diversity(lat4, index = "inv")
Simp5 <- diversity(lat5, index = "inv")
Simp6 <- diversity(lat6, index = "inv")
Simp7 <- diversity(lat7, index = "inv")


Simp_df <- data.frame(
  Lat_Zone = factor(1:7),
  Simp_div = c(Simp1, Simp2, Simp3, Simp4, Simp5, Simp6, Simp7)
)
```

```
ggplot(Simp_df, aes(x = Lat_Zone, y = Simp_div, fill = Lat_Zone)) +
  geom_boxplot() +
  labs(
    x = "Latitudinal Zone",
    y = "Simpson's Diversity",
    title = "Simpsons's Diversity by Latitudinal Zone"
  ) +
  theme_minimal() +
  scale_fill_brewer(palette = "Set3")
```



Simpsons's Diversity by Latitudinal Zone
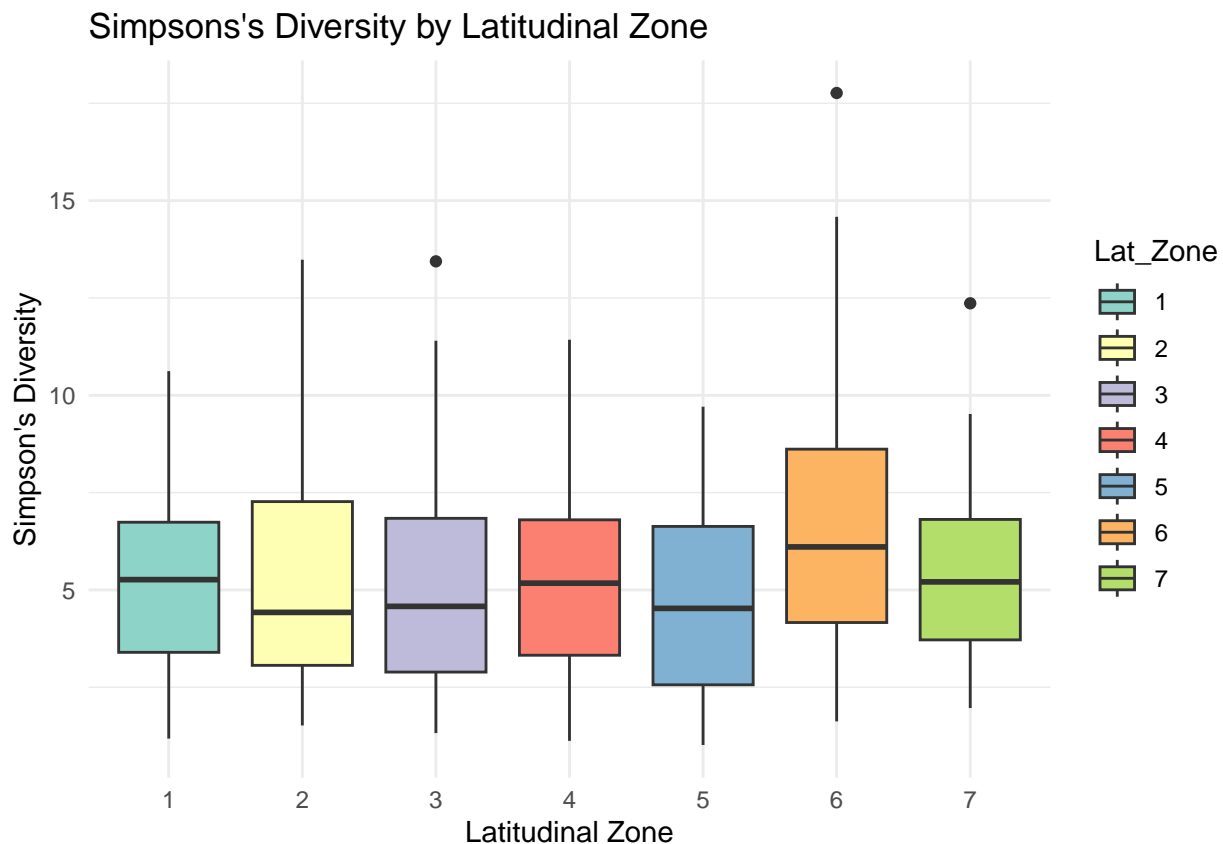
```
#Beta Diversity- Heatmap
```

```
library(lattice)
library(viridis)
```

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

```
##
## Attaching package: 'viridis'
```

```
## The following object is masked from 'package:maps':
##
##     unemp
```

```
as.numeric(fish_data$Lat_Zone)
```

```
##    [1] 6 6 5 6 6 6 6 6 5 6 6 7 6 5 6 6 6 6 6 3 3 3 3 4 3 4 3 3 3 3 4 3 4 4 4 4 5
##   [38] 5 4 4 5 5 5 5 7 7 7 7 7 7 7 1 1 1 1 1 1 2 2 1 5 4 5 5 5 7 7 7 7 7 1 1 1 1
```

```
##   [75] 1 1 3 6 6 6 5 6 6 6 6 6 5 6 6 3 5 6 7 7 7 1 1 1 1 2 1 1 2 3 2 3 2 3 2 2 2
## [112] 2 2 2 3 4 2 3 4 3 3 3 3 3 3 3 5 4 4 3 5 3 3 4 3 4 3 4 4 5 4 5 4 4 4 4 5 4
## [149] 5 5 4 5 5 5 5 5 6 7 7 7 7 7 7 7 7 7 7 7 1 1 1 1 2 1 2 1 2 1 1 1 2 1 2 2 1
## [186] 2 2 1 2 1 1 4 4 4 5 4 5 5 5 4 4 4 5 4 4 5 4 4 4 4 4 7 7 7 7 6 7 6 1 2 1 3
## [223] 4 4 4 4 6 6 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 3 2 2 3 3 2 6 7 7 7 7 7 7 7
## [260] 7 7 7 7 4 5 1 2 3 2 3 3 3 1 2 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 1 2 3 3 3 3 4
## [297] 4 4 3 4 4 3 3 3 3 3 3 4 5 5 5 5 5 5 5 5 6 5 5 5 5 5 5 6 7 7 7 7 7 7 7 2 2
## [334] 2 2 2 1 2 1 3 2 1 2 1 2 2 2 3 1 2
```

```r
set.seed(123)

fish_data_lat_fix <- fish_data %>%
  group_by(Lat_Zone) %>%
  mutate(SiteID = sample(
    seq((unique(Lat_Zone) - 1) * 50 + 1, unique(Lat_Zone) * 50),
    size = n(),
    replace = FALSE
  )) %>%
  ungroup()


result <- cbind(fish_data_lat_fix[, 1], fish_data_lat_fix[, 23:658])

result.db <- vegdist(result, method = "bray", upper = TRUE, diag = TRUE)
result.db.mat <- as.matrix(result.db)

order1 <- rev(rownames(result.db.mat))

zone_labels <- rep(1:7, each = 50)

zone_boundaries <- seq(50, 350, by = 50)

levelplot(result.db.mat[order1, order1],
          aspect = "iso",
          col.regions = viridis::inferno(256),
          xlab = "Latitude Group",
          ylab = "Latitude Group",
          scales = list(cex = 0.1),
          main = "Bray-Curtis Distance",
          panel = function(...) {
            panel.levelplot(...)
            for (boundary in zone_boundaries) {
              panel.abline(h = boundary, col = "white", lwd = 2)
              panel.abline(v = boundary, col = "white", lwd = 2)
            }
          })
```

## Bray–Curtis Distance
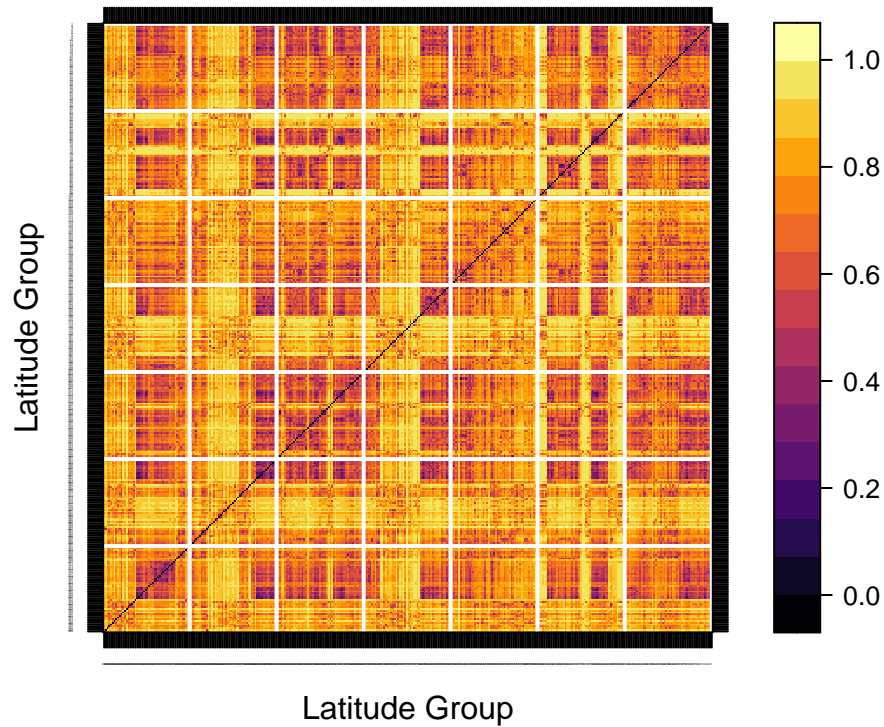


```r
# Beta Diversity Dispersion

result.db <- vegdist(result, method = "bray", upper = TRUE, diag = TRUE)

betadisper_result <- betadisper(result.db, group = fish_data_lat_fix$Lat_Zone)

boxplot(betadisper_result,
        main = "Beta Diversity Dispersion by Latitudinal Zone",
        xlab = "Latitudinal Zones",
        ylab = "Beta Diversity Dispersion")
```

## Beta Diversity Dispersion by Latitudinal Zone
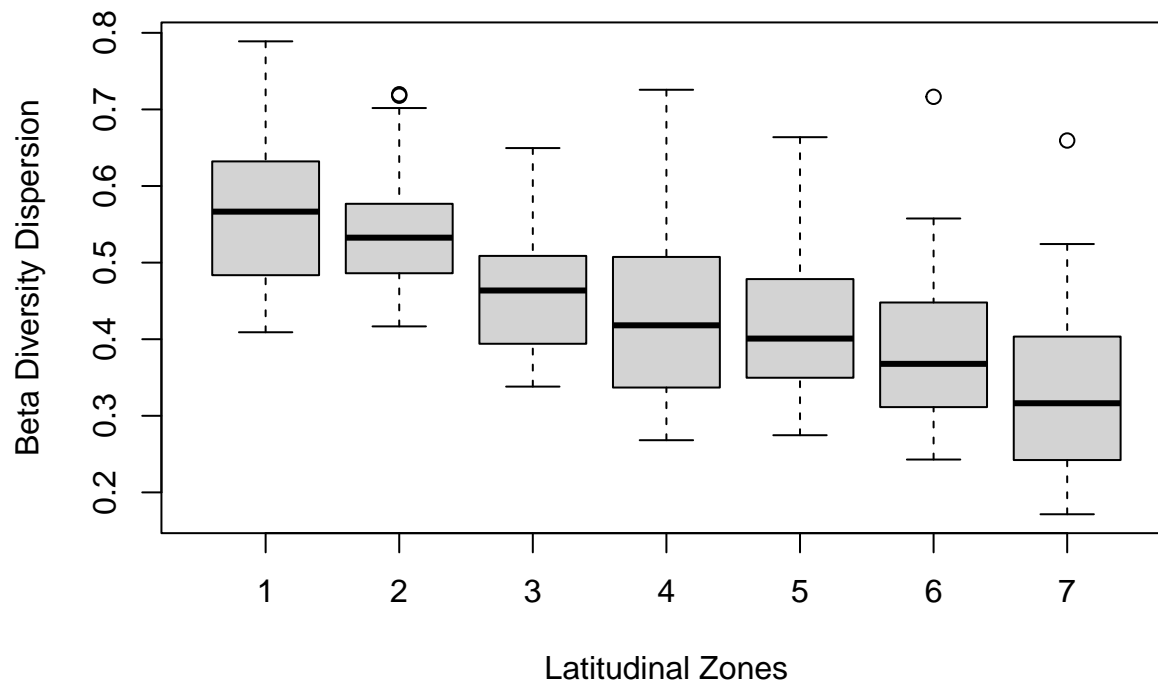


```r
permanova_result <- adonis2(result.db ~ fish_data_lat_fix$Lat_Zone, method = "bray")
summary(permanova_result)
```

```
##        Df              SumOfSqs           R2                F
##  Min.   :  1.0   Min.   : 18.46   Min.   :0.1792   Min.   :75.95
##  1st Qu.:174.5   1st Qu.: 51.52   1st Qu.:0.5000   1st Qu.:75.95
##  Median :348.0   Median : 84.58   Median :0.8208   Median :75.95
##  Mean   :232.7   Mean   : 68.69   Mean   :0.6667   Mean   :75.95
##  3rd Qu.:348.5   3rd Qu.: 93.81   3rd Qu.:0.9104   3rd Qu.:75.95
##  Max.   :349.0   Max.   :103.04   Max.   :1.0000   Max.   :75.95
##                                                    NA's   :2
##      Pr(>F)
##  Min.   :0.001
##  1st Qu.:0.001
##  Median :0.001
##  Mean   :0.001
##  3rd Qu.:0.001
##  Max.   :0.001
##  NA's   :2
```

```r
# Influential Species

add.spec.scores.class <-
  function(ordi,comm,method="cor.scores",multi=1,Rscale=F,scaling="1") {
    ordiscores <- scores(ordi,display="sites")
    n <- ncol(comm)
    p <- ncol(ordiscores)
    specscores <- array(NA,dim=c(n,p))
    rownames(specscores) <- colnames(comm)
    colnames(specscores) <- colnames(ordiscores)
```

```r
    if (method == "cor.scores") {
      for (i in 1:n) {
        for (j in 1:p) {specscores[i,j] <- cor(comm[,i],ordiscores[,j],method="pearson")}
      }
    }
    if (method == "wa.scores") {specscores <- wascores(ordiscores,comm)}
    if (method == "pcoa.scores") {
      rownames(ordiscores) <- rownames(comm)
      eigenv <- ordi$eig
      accounted <- sum(eigenv)
      tot <- 2*(accounted/ordi$GOF[2])-(accounted/ordi$GOF[1])
      eigen.var <- eigenv/(nrow(comm)-1)
      neg <- length(eigenv[eigenv<0])
      pos <- length(eigenv[eigenv>0])
      tot <- tot/(nrow(comm)-1)
      eigen.percen <- 100*eigen.var/tot
      eigen.cumpercen <- cumsum(eigen.percen)
      constant <- ((nrow(comm)-1)*tot)^0.25
      ordiscores <- ordiscores * (nrow(comm)-1)^-0.5 * tot^-0.5 * constant
      p1 <- min(p, pos)
      for (i in 1:n) {
        for (j in 1:p1) {
          specscores[i,j] <- cor(comm[,i],ordiscores[,j])*sd(comm[,i])/sd(ordiscores[,j])
          if(is.na(specscores[i,j])) {specscores[i,j]<-0}
        }
      }
      if (Rscale==T && scaling=="2") {
        percen <- eigen.var/tot
        percen <- percen^0.5
        ordiscores <- sweep(ordiscores,2,percen,"/")
        specscores <- sweep(specscores,2,percen,"*")
      }
      if (Rscale==F) {
        specscores <- specscores / constant
        ordiscores <- ordi$points
      }
      ordi$points <- ordiscores
      ordi$eig <- eigen.var
      ordi$eig.percen <- eigen.percen
      ordi$eig.cumpercen <- eigen.cumpercen
      ordi$eigen.total <- tot
      ordi$R.constant <- constant
      ordi$Rscale <- Rscale
      ordi$scaling <- scaling
    }
    specscores <- specscores * multi
    ordi$cproj <- specscores
    return(ordi)
  }


species_1 <- species[, -1]
```

```r
fish.pcoa <- cmdscale(result.db, eig = TRUE, k = 3)
explainvar1 <- round(fish.pcoa$eig[1] / sum(fish.pcoa$eig), 3) * 100
explainvar2 <- round(fish.pcoa$eig[2] / sum(fish.pcoa$eig), 3) * 100
explainvar3 <- round(fish.pcoa$eig[3] / sum(fish.pcoa$eig), 3) * 100
par(mar = c(5, 5, 1, 2) + 0.1)
plot(fish.pcoa$points[ ,1], fish.pcoa$points[ ,2], ylim = c(-0.2, 0.7),
     xlab = paste("PcoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PcoA 2 (", 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(fish.pcoa$points[ ,1], fish.pcoa$points[ ,2],
       pch = 19, cex = 3, bg = "gray", col = "gray")
text(fish.pcoa$points[ ,1], fish.pcoa$points[ ,2],
     labels = row.names(fish.pcoa$points))

fishREL <- species_1
for(i in 1:nrow(species_1)){
  fishREL[i, ] = species_1[i, ] / sum(species_1[i, ])
}
fish.pcoa <- add.spec.scores.class(fish.pcoa,fishREL,method = "pcoa.scores")
```

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```

```r
text(fish.pcoa$cproj[ ,1], fish.pcoa$cproj[ ,2],
     labels = row.names(fish.pcoa$cproj), col = "black")
```
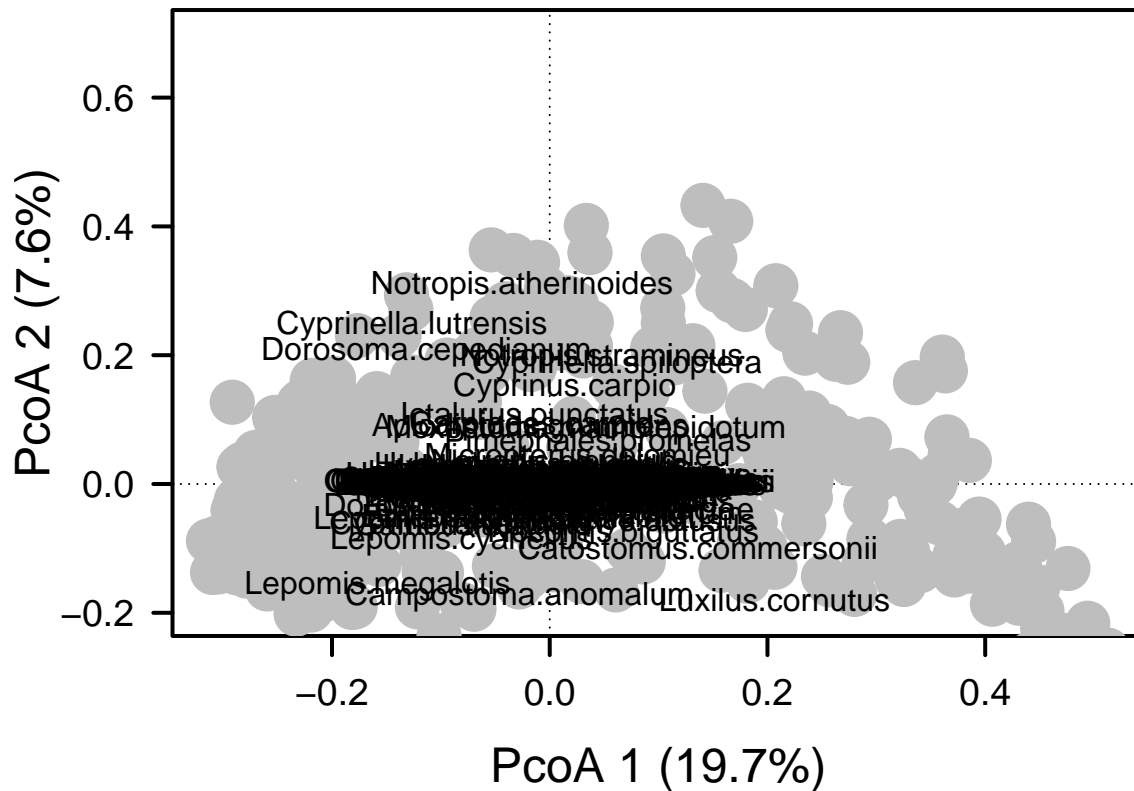


```r
# Constrained Ordination Plot

env.chem <- cbind(fish_data_lat_fix[, 2:3], fish_data_lat_fix[, 5:20])


fish.dbrda <- dbrda(result.db ~., as.data.frame(env.chem))
ordiplot(fish.dbrda)
```
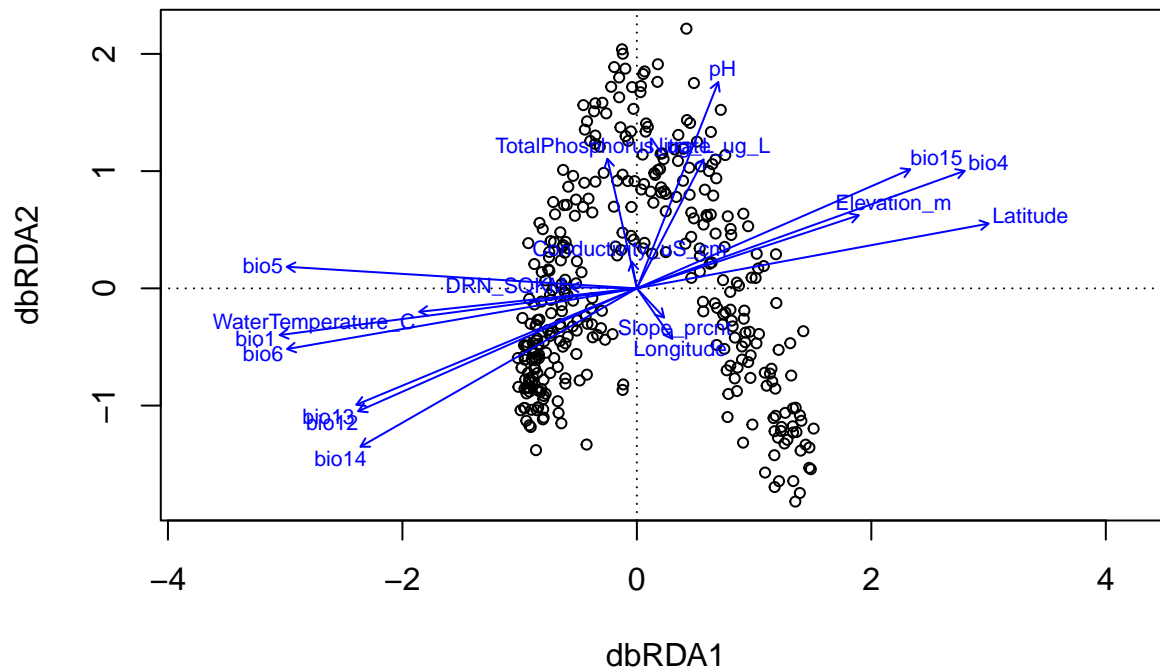
```
fish.dbrda.mod0 <- dbrda(result.db ~ 1, as.data.frame(env.chem))
ordiplot(fish.dbrda.mod0)
```
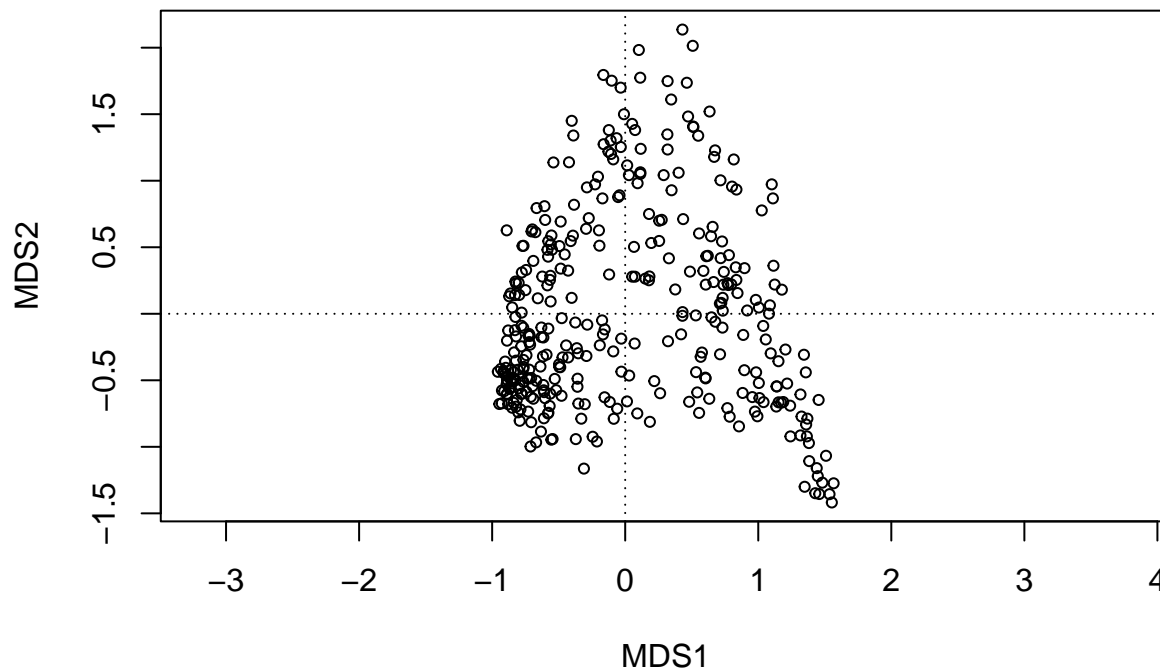


```
fish.dbrda.mod1 <- dbrda(result.db ~., as.data.frame(env.chem))
fish.dbrda <- ordiR2step(fish.dbrda.mod0, fish.dbrda.mod1, perm.max = 200)
```

```
## Step: R2.adj= 0
## Call: result.db ~ 1
##
##                        R2.adjusted
## <All variables>        0.297955894
## + bio1                 0.173991954
```

```
## + Latitude             0.169463722
## + bio6                 0.167598895
## + bio5                 0.167129296
## + bio4                 0.150696285
## + bio14                0.113412305
## + bio12                0.112150651
## + bio13                0.111271514
## + bio15                0.109243928
## + Elevation_m          0.075893711
## + WaterTemperature_C   0.068660014
## + pH                   0.025760144
## + Nitrate_ug_L         0.015220987
## + Longitude            0.013311856
## + TotalPhosphorus_ug_L 0.012496268
## + DRN_SQKM             0.011498770
## + Slope_prcnt          0.007188645
## + Conductivity_uS_cm   0.003939742
## <none>                 0.000000000
##
##        Df    AIC      F Pr(>F)
## + bio1  1 1557.4 74.514  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.173992
## Call: result.db ~ bio1
##
##                        R2.adjusted
## <All variables>          0.2979559
## + bio4                   0.1975777
## + bio5                   0.1940328
## + bio14                  0.1935926
## + pH                     0.1923151
## + Latitude               0.1901579
## + bio15                  0.1893379
## + Elevation_m            0.1879219
## + bio12                  0.1872199
## + Longitude              0.1863973
## + TotalPhosphorus_ug_L   0.1861358
## + bio6                   0.1854063
## + Nitrate_ug_L           0.1835446
## + WaterTemperature_C     0.1811624
## + bio13                  0.1810889
## + Slope_prcnt            0.1808251
## + DRN_SQKM               0.1801633
## + Conductivity_uS_cm     0.1785979
## <none>                   0.1739920
##
##        Df    AIC      F Pr(>F)
## + bio4  1 1548.2 11.229  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.1975777
```

```
## Call: result.db ~ bio1 + bio4
##
##                          R2.adjusted
## <All variables>            0.2979559
## + Longitude                0.2155298
## + bio6                     0.2122977
## + Elevation_m              0.2105895
## + bio15                    0.2096281
## + bio5                     0.2076524
## + Nitrate_ug_L             0.2065597
## + pH                       0.2056088
## + bio14                    0.2044093
## + WaterTemperature_C       0.2043425
## + TotalPhosphorus_ug_L     0.2040601
## + Slope_prcnt              0.2039209
## + DRN_SQKM                 0.2038972
## + Latitude                 0.2038281
## + bio12                    0.2028872
## + Conductivity_uS_cm       0.2019992
## + bio13                    0.1996908
## <none>                     0.1975777
##
##              Df    AIC      F Pr(>F)
## + Longitude   1 1541.3 8.9409  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2155298
## Call: result.db ~ bio1 + bio4 + Longitude
##
##                          R2.adjusted
## <All variables>            0.2979559
## + Elevation_m              0.2308862
## + bio6                     0.2261795
## + bio5                     0.2261022
## + bio14                    0.2251522
## + Slope_prcnt              0.2233024
## + Nitrate_ug_L             0.2232283
## + WaterTemperature_C       0.2227446
## + bio15                    0.2226614
## + pH                       0.2221563
## + TotalPhosphorus_ug_L     0.2221173
## + Latitude                 0.2220238
## + DRN_SQKM                 0.2212205
## + Conductivity_uS_cm       0.2192443
## + bio12                    0.2186935
## + bio13                    0.2174892
## <none>                     0.2155298
##
##                Df    AIC      F Pr(>F)
## + Elevation_m   1 1535.4 7.9084  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Step: R2.adj= 0.2308862
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m
##
##                          R2.adjusted
## <All variables>           0.2979559
## + bio6                    0.2419257
## + bio15                   0.2397774
## + bio14                   0.2390502
## + pH                      0.2376421
## + Nitrate_ug_L            0.2375460
## + TotalPhosphorus_ug_L    0.2374329
## + Latitude               0.2372287
## + WaterTemperature_C      0.2370789
## + Slope_prcnt             0.2363925
## + bio5                    0.2363535
## + DRN_SQKM                0.2351621
## + Conductivity_uS_cm      0.2349345
## + bio12                   0.2344382
## + bio13                   0.2328913
## <none>                    0.2308862
##
##        Df    AIC      F Pr(>F)
## + bio6  1 1531.3 6.0241  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2419257
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6
##
##                          R2.adjusted
## <All variables>           0.2979559
## + bio15                   0.2506100
## + Latitude               0.2488605
## + bio14                   0.2484180
## + pH                      0.2482101
## + WaterTemperature_C      0.2478207
## + Slope_prcnt             0.2473368
## + TotalPhosphorus_ug_L    0.2470921
## + bio5                    0.2469264
## + Nitrate_ug_L            0.2468700
## + Conductivity_uS_cm      0.2464664
## + DRN_SQKM                0.2461904
## + bio12                   0.2453756
## + bio13                   0.2430272
## <none>                    0.2419257
##
##        Df    AIC      F Pr(>F)
## + bio15  1 1528.2 4.9864  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.25061
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15
##
```

```
##                            R2.adjusted
## <All variables>              0.2979559
## + pH                         0.2568336
## + Latitude                   0.2568312
## + WaterTemperature_C         0.2565704
## + Nitrate_ug_L               0.2554881
## + bio14                      0.2553735
## + bio5                       0.2553099
## + Conductivity_uS_cm         0.2550252
## + TotalPhosphorus_ug_L       0.2549607
## + DRN_SQKM                   0.2549433
## + Slope_prcnt                0.2548745
## + bio12                      0.2539259
## + bio13                      0.2524986
## <none>                       0.2506100
##
##       Df    AIC      F Pr(>F)
## + pH   1 1526.3 3.8724  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2568336
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +      pH
##
##                            R2.adjusted
## <All variables>              0.2979559
## + Latitude                   0.2623905
## + Nitrate_ug_L               0.2618268
## + WaterTemperature_C         0.2617860
## + Conductivity_uS_cm         0.2612047
## + Slope_prcnt                0.2611254
## + bio5                       0.2607947
## + DRN_SQKM                   0.2605384
## + bio14                      0.2602490
## + TotalPhosphorus_ug_L       0.2601431
## + bio12                      0.2591609
## + bio13                      0.2580048
## <none>                       0.2568336
##
##           Df    AIC      F Pr(>F)
## + Latitude  1 1524.7 3.5765  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2623905
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +      pH + Latitude
##
##                            R2.adjusted
## <All variables>              0.2979559
## + Slope_prcnt                0.2670264
## + WaterTemperature_C         0.2670171
## + Conductivity_uS_cm         0.2667555
## + DRN_SQKM                   0.2661433
## + Nitrate_ug_L               0.2660036
```

```
## + bio5                      0.2654310
## + TotalPhosphorus_ug_L    0.2653464
## + bio14                     0.2650370
## + bio12                     0.2638457
## + bio13                     0.2634783
## <none>                      0.2623905
##
##                Df    AIC      F Pr(>F)
## + Slope_prcnt  1 1523.4 3.1568  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2670264
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +      pH + Latitude + Slope_
##
##                          R2.adjusted
## <All variables>          0.2979559
## + Conductivity_uS_cm     0.2712788
## + WaterTemperature_C     0.2712744
## + DRN_SQKM               0.2707343
## + Nitrate_ug_L           0.2702999
## + bio5                   0.2700683
## + TotalPhosphorus_ug_L   0.2698145
## + bio14                  0.2696245
## + bio12                  0.2684047
## + bio13                  0.2680513
## <none>                   0.2670264
##
##                        Df    AIC      F Pr(>F)
## + Conductivity_uS_cm    1 1522.3 2.9841  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2712788
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +      pH + Latitude + Slope_
##
##                          R2.adjusted
## <All variables>          0.2979559
## + WaterTemperature_C     0.2755818
## + DRN_SQKM               0.2750166
## + bio5                   0.2749403
## + Nitrate_ug_L           0.2745042
## + bio14                  0.2741816
## + TotalPhosphorus_ug_L   0.2738794
## + bio12                  0.2724841
## + bio13                  0.2723295
## <none>                   0.2712788
##
##                        Df    AIC      F Pr(>F)
## + WaterTemperature_C    1 1521.2 3.0136  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2755818
```

```
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +      pH + Latitude + Slope_
##
##                         R2.adjusted
## <All variables>           0.2979559
## + bio5                    0.2792622
## + DRN_SQKM                0.2791336
## + bio14                   0.2785077
## + TotalPhosphorus_ug_L    0.2780517
## + Nitrate_ug_L            0.2779327
## + bio12                   0.2767413
## + bio13                   0.2766171
## <none>                    0.2755818
##
##        Df    AIC      F Pr(>F)
## + bio5  1 1520.4 2.726  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2792622
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +      pH + Latitude + Slope_
##
##                         R2.adjusted
## <All variables>           0.2979559
## + DRN_SQKM                0.2828146
## + bio14                   0.2817732
## + TotalPhosphorus_ug_L    0.2817245
## + Nitrate_ug_L            0.2816413
## + bio12                   0.2808022
## + bio13                   0.2801292
## <none>                    0.2792622
##
##            Df    AIC      F Pr(>F)
## + DRN_SQKM  1 1519.7 2.6692  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2828146
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +      pH + Latitude + Slope_
##
##                         R2.adjusted
## <All variables>           0.2979559
## + TotalPhosphorus_ug_L    0.2852847
## + bio14                   0.2852267
## + Nitrate_ug_L            0.2852157
## + bio12                   0.2842743
## + bio13                   0.2839029
## <none>                    0.2828146
##
##                         Df    AIC      F Pr(>F)
## + TotalPhosphorus_ug_L   1 1519.4 2.1612  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2852847
```

```
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +     pH + Latitude + Slope_
##
##                    R2.adjusted
## <All variables>    0.2979559
## + Nitrate_ug_L     0.2879107
## + bio14            0.2877111
## + bio12            0.2867725
## + bio13            0.2862067
## <none>             0.2852847
##
##                Df    AIC      F Pr(>F)
## + Nitrate_ug_L  1 1519.1 2.2354  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2879107
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +     pH + Latitude + Slope_
##
##                    R2.adjusted
## <All variables>    0.2979559
## + bio14            0.2903113
## + bio12            0.2894635
## + bio13            0.2888629
## <none>             0.2879107
##
##          Df    AIC      F Pr(>F)
## + bio14   1 1518.8 2.1298  0.004 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2903113
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +     pH + Latitude + Slope_
##
##                    R2.adjusted
## <All variables>    0.2979559
## + bio12            0.2942547
## + bio13            0.2923837
## <none>             0.2903113
##
##          Df    AIC      F Pr(>F)
## + bio12   1 1517.8 2.8607  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2942547
## Call: result.db ~ bio1 + bio4 + Longitude + Elevation_m + bio6 + bio15 +     pH + Latitude + Slope_
##
##                    R2.adjusted
## + bio13            0.2979559
## <All variables>    0.2979559
## <none>             0.2942547
```

```r
fish.dbrda$call
```

```
## dbrda(formula = result.db ~ bio1 + bio4 + Longitude + Elevation_m +
```

```
##       bio6 + bio15 + pH + Latitude + Slope_prcnt + Conductivity_uS_cm +
##       WaterTemperature_C + bio5 + DRN_SQKM + TotalPhosphorus_ug_L +
##       Nitrate_ug_L + bio14 + bio12, data = as.data.frame(env.chem))
```

`fish.dbrda$anova`

```
##                             R2.adj Df    AIC       F Pr(>F)
## + bio1                     0.17399  1 1557.4 74.5140  0.002 **
## + bio4                     0.19758  1 1548.2 11.2288  0.002 **
## + Longitude                0.21553  1 1541.3  8.9409  0.002 **
## + Elevation_m              0.23089  1 1535.4  7.9084  0.002 **
## + bio6                     0.24193  1 1531.3  6.0241  0.002 **
## + bio15                    0.25061  1 1528.2  4.9864  0.002 **
## + pH                       0.25683  1 1526.3  3.8724  0.002 **
## + Latitude                 0.26239  1 1524.7  3.5765  0.002 **
## + Slope_prcnt              0.26703  1 1523.4  3.1568  0.002 **
## + Conductivity_uS_cm       0.27128  1 1522.3  2.9841  0.002 **
## + WaterTemperature_C       0.27558  1 1521.2  3.0136  0.002 **
## + bio5                     0.27926  1 1520.4  2.7260  0.002 **
## + DRN_SQKM                 0.28281  1 1519.7  2.6692  0.002 **
## + TotalPhosphorus_ug_L     0.28529  1 1519.4  2.1612  0.002 **
## + Nitrate_ug_L             0.28791  1 1519.1  2.2354  0.002 **
## + bio14                    0.29031  1 1518.8  2.1298  0.004 **
## + bio12                    0.29425  1 1517.8  2.8607  0.002 **
## <All variables>           0.29796
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**`ordiplot`**`(fish.dbrda)`
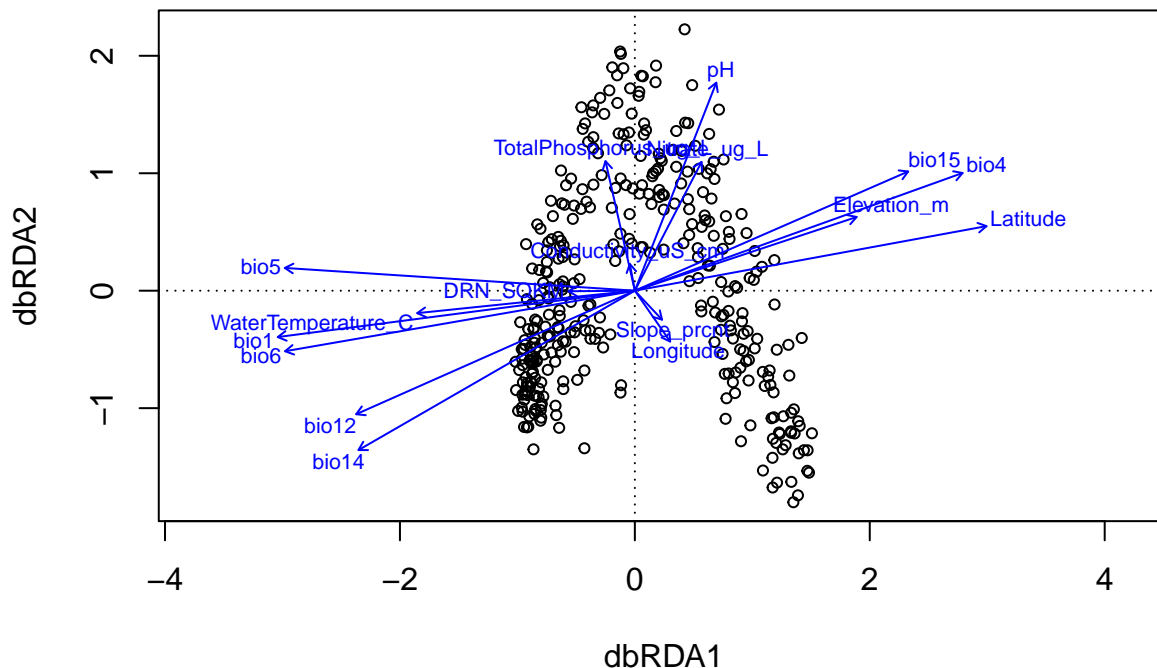


**`permutest`**`(fish.dbrda, `**`permutations = `**`999)`

```
##
## Permutation test for dbrda under reduced model
```

```
##
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = result.db ~ bio1 + bio4 + Longitude +
## Elevation_m + bio6 + bio15 + pH + Latitude + Slope_prcnt +
## Conductivity_uS_cm + WaterTemperature_C + bio5 + DRN_SQKM +
## TotalPhosphorus_ug_L + Nitrate_ug_L + bio14 + bio12, data =
## as.data.frame(env.chem))
## Permutation test for all constrained eigenvalues
##           Df Inertia      F Pr(>F)
## Model     17  33.862 9.5596  0.001 ***
## Residual 332  69.178
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
fish.team.env <- env.chem[, c(1, 2, 4, 7, 9, 11)]
fish.team.db <- dbrda(result.db ~ ., as.data.frame(fish.team.env))

envfit(fish.team.db, fish.team.env, perm = 999)
```

```
##
## ***VECTORS
##
##                        dbRDA1   dbRDA2     r2 Pr(>r)
## Latitude              0.99422  0.10732 0.9063  0.001 ***
## Longitude             0.33332 -0.94281 0.1013  0.001 ***
## Conductivity_uS_cm    0.01123  0.99994 0.0359  0.002 **
## TotalPhosphorus_ug_L -0.12757  0.99183 0.2244  0.001 ***
## Slope_prcnt           0.43685 -0.89954 0.0397  0.002 **
## bio1                 -0.99757 -0.06970 0.9177  0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
```

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

par(mar = c(5, 5, 4, 4) + 0.1)
plot(scores(fish.team.db, display = "wa"),
     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, axe = 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(fish.team.db, display = "wa"),
       pch = 10, cex = 1, bg = "gray", col = "gray")
```

```r
text(scores(fish.team.db, display = "wa"),
     labels = row.names(scores(fish.team.db, display = "wa")), cex = 0.5)


vectors <- scores(fish.team.db, 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,
     label = row.names(vectors), col = "blue", cex = 1)
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])))
```