

Resource Heterogeneity Structures Microbial Communities

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Introduction

Much is already known about how spatial gradients in resource availability contribute to the structure and function of microbial communities. However, we are beginning to appreciate the molecular diversity within the resource pool. Resources can be just as diverse as consumers and differ in their quality and availability to consumers. As such, resource diversity represents a mechanism to understand spatial distributions of consumers. In this study, we explore how both the concentration and diversity of resources contribute to the structure and function of aquatic microbial communities.

We explore three hypotheses:

1. Is there a relationship between resource concentration and diversity?
 - Dilution Hypothesis: Arrieta et al. 2015 Science
2. Do the concentrations and diversity of resources explain differences between communities?
 - Resource Heterogeneity Hypothesis
3. Do concentration and diversity explain different aspects of diversity
 - Grinnellian (environmental habitat) vs. Eltonian (food habitat) Niche Hypothesis
 - Resource Substitution Hypothesis

Initial Setup

```
rm(list=ls())
getwd()
setwd("~/GitHub/ResourceHeterogeneity/analyses")

# Import Tools and Standard Functions
source("../bin/MothurTools.R")
se <- function(x, ...){sd(x, na.rm = TRUE)/sqrt(length(na.omit(x)))}

# Save Standard Plot Settings
opar <- par(no.readonly = TRUE) # Saves plot defaults

# Load Required Packages
require("xtable")
require("png")
```

```
require("grid")
require("vegan")
require("RgoogleMaps")
library("maps")
library("mapdata")
require("maptools")
require("picante")
```

Study System Map

We sampled 10 lakes in the Huron Mountains of Michigan. The Huron Mountains are located in the Superior Bedrock Uplands region of the Michigan Upper Peninsula (Schaetzl et al 2013).

The region is classified as Superior Bedrock Uplands The forests around the lakes are old-growth hemlock-nothern hardwoods (Kerry Woods) The lakes are part of the Pine River Watershed which drains into Lake Superior (see: www.co.marquette.mi.us/departments/plannings/docs/watershed.pdf)

Lake Information

Add Temperature Add Coordinates

```
lake.data <- read.csv("../data/lake_data.txt", row.names=1)
colnames(lake.data) <- c("depth", "pH", "DO1", "DO2")
lake.data$area <- rep(NA, dim(lake.data)[1])

# Shape file source: http://www.mcgi.state.mi.us/mgdl/?rel=ext&action=sext
shape <- readShapePoly("../data/lake_polygons_200403/lake_polygons_200403.shp",
                        IDvar = "UNIQUE_ID")

# Extract Areas
grp.opt <- shape$COUNTY == "Marquette" & shape$FMU == "LSW"
lake.data$area[1] <- shape$AREA[which(shape$NAME == "Lake Ann" & grp.opt)]
lake.data$area[2] <- shape$AREA[which(shape$NAME == "Canyon Lake" & grp.opt)]
lake.data$area[3] <- shape$AREA[which(shape$NAME == "Howe Lake" & grp.opt)]
lake.data$area[4] <- shape$AREA[which(shape$NAME == "Ives Lake" & grp.opt)]
lake.data$area[5] <- shape$AREA[which(shape$NAME == "Lily Pond" & grp.opt)]
lake.data$area[6] <- shape$AREA[which(shape$NAME == "Mountain Lake" & grp.opt)]
lake.data$area[7] <- 2000 # estimate...smallest and not in GIS dataset
lake.data$area[8] <- shape$AREA[which(shape$NAME == "Rush Lake" & grp.opt)]
lake.data$area[9] <- shape$AREA[which(shape$NAME == "Second Lake" & grp.opt)]
lake.data$area[10] <- shape$AREA[which(shape$NAME == "Third Lake" & grp.opt)]

# Convert sq m to sq km
lake.data$area <- lake.data$area / 1000000

# Notes on how to get shapefile info
# str(shape, max.level=4)
# Attempt to find Pony
# plot(shape[which(shape$LAKE_NAME == "no name" &
# shape$COUNTY == "Marquette" & shape$FMU == "LSW"), ])
```

```

# Plot from shapefile (just to check)
# grp.opts <- shape$COUNTY == "Marquette" & shape$FMU == "LSW"
# plot(shape[c(
#   which(shape$NAME == "Ives Lake" & grp.opts),
#   which(shape$NAME == "Mountain Lake" & grp.opts),
#   which(shape$NAME == "Howe Lake" & grp.opts),
#   which(shape$NAME == "Rush Lake" & grp.opts),
#   which(shape$NAME == "Lake Ann" & grp.opts),
#   which(shape$NAME == "Canyon Lake" & grp.opts),
#   which(shape$NAME == "Lily Pond" & grp.opts),
#   which(shape$NAME == "Second Lake" & grp.opts),
#   which(shape$NAME == "Third Lake" & grp.opts)),])

lake.data <- lake.data[sort(row.names(lake.data)), c("area", "pH")]

```

Table 1: Lake Physical Properties

```

addtorow <- list()
addtorow$pos <- list(0)
addtorow$command <- c("Lake & Area (Km2) & pH \\\n")
lake.tab <- xtable(lake.data, digits = c(0,1,3))
align(lake.tab) <- "ccc"
print(lake.tab, add.to.row = addtorow, include.colnames = FALSE,
      type= "latex", file="../tables/SuppTable1.tex",
      hline.after = c(-1, -1, 0, nrow(lake.tab)))
print(lake.tab, add.to.row = addtorow, include.colnames = FALSE,
      comment = FALSE, hline.after = c(-1, -1, 0, nrow(lake.tab)))

```

Lake	Area (Km ²)	pH
Ann	0.3	7.860
Canyon	0.0	7.020
Howe	0.7	7.780
Ives	1.9	8.100
Lily	0.0	5.510
Mountain	3.4	8.310
Pony	0.0	5.390
Rush	1.3	8.140
SecondPine	0.7	8.090
UpperPine	0.2	7.790

Supplemental Figure 1: Study System Map

```

png(filename="../figures/Supp1.png",
     width = 1800, height = 900, res = 96*2)
par(opar)
par(mfrow = c(1,1), mar = c(0, 0, 0, 0), oma = c(0, 0, 0, 0) + 0.5)

```

```

newmap1 <- GetMap(center = c(46.86, -87.93), zoom = 13,
  maptype = "terrain", GRAYSCALE = FALSE, frame = FALSE,
  path = "&style=feature:all|element:labels|visibility:off")
newmap2 <- GetMap(center = c(46.86, -87.82), zoom = 13,
  maptype = "terrain", GRAYSCALE = FALSE, frame = FALSE,
  path = "&style=feature:all|element:labels|visibility:off")

layout( matrix(c(1,1,1,1,1,1,
  1,1,1,1,1,1,
  1,1,1,1,1,1,
  2,2,2,2,2,2,
  2,2,2,3,3,3,
  2,2,2,3,3,3), 6, 6, byrow = FALSE),
  widths = rep(2, 6), heights = rep(2, 6))

# Left Side
PlotOnStaticMap(newmap1, zoom = 13, cex = 2, col = "blue")
text(-120, 270, "Howe", col="red", cex=1.2)
text(100, 255, "Rush", col="red", cex=1.2)
text(105, 55, "Mountain", col="red", cex=1.2)
arrows(10, 100, x1 = -10, y1 = 100, length=0.05, col = "red", lwd = 2, code = 1)
text(-36, 100, "Ann", col="red", cex=1.2)
arrows(60, 230, x1 = 40, y1 = 230, length=0.05, col = "red", lwd = 2, code = 1)
text(8, 230, "Pony", col="red", cex=1.2)
arrows(55, -230, x1 = 75, y1 = -230, length=0.05, col = "red", lwd = 2, code = 1)
text(120, -230, "Canyon", col="red", cex=1.2)

# Right Side
PlotOnStaticMap(newmap2, zoom = 13, cex = 2, col = "blue")
text(-180, -90, "Ives", col="red", cex=1.2)
arrows(-160, 20, x1 = -140, y1 = 20, length = 0.05, col = "red", lwd = 2, code = 1)
text(-75, 20, "Upper Pine", col="red", cex = 1.2)
arrows(-220, 80, x1 = -200, y1 = 80, length = 0.05, col = "red", lwd = 2, code = 1)
text(-125, 80, "Second Pine", col="red", cex = 1.2)
arrows(-55, -105, x1 = -35, y1 = -105, length = 0.05, col = "red", lwd = 2, code = 1)
text(-12, -105, "Lily", col="red", cex=1.2)

# Compass Arrow
arrows(280, 280, 280, 240, length = 0.1, col = "black", lwd = 3, code = 1)
text(280, 220, "N", col = "black", cex = 1.5)

# Inset
map("state", "Michigan", col = "gray80", fill = TRUE,
  xlim = c(-92,-82), ylim = c(41, 48))
points(-87.89, 46.8, pch = 20, col = "red")

dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)

```

This study system is known to have differences in the concentrations of growth limiting nutrients. Specifically, the concentrations of dissolved organic carbon and phosphorus differ between the lakes. We also have data for total nitrogen, but the values are odd and may not be reasonable for interpretation. The reason the nitrogen



Figure 1: Study System Map

values are odd is because many were at the lower detection level of the instrument.

Lake Nutrient Concentrations

```
# DOC
DOC2011 <- read.delim("../data/2011DOC_data.txt", header=T)
DOC2012 <- read.delim("../data/2012DOC_data.txt", header=T)
DOC <- rbind(DOC2011, DOC2012)
DOC <- DOC[grep("MEM*", DOC$Sample), ]
colnames(DOC) <- c("sample", "conc", "LCL", "UCL", "se")
DOCkey <- read.delim("../data/DOC_KEY_epi.txt", header=T)
DOC$code <- DOC$sample
DOC <- DOC[which(DOC$code %in% DOCkey$Sample.Name), ]
DOC$sample <- DOCkey$Site[match(DOCkey$Sample.Name, DOC$code)]
DOC$year <- substr(DOC$code, 4, 7)
DOC$conc <- pmax(DOC$conc, 0)
DOC2 <- data.frame("sample" = DOC$sample, "year" = DOC$year,
                   "conc" = DOC$conc)[order(DOC$sample, DOC$year), ]
DOC$sample[grep("Pony", DOC$sample)] <- "Pony"
DOC <- droplevels(DOC)

# Total Nitrogen
#TN2011 <- read.delim("../data/2011TN_data.txt", header=T)
#TN2012 <- read.delim("../data/2012TN_data.txt", header=T)
TN <- read.delim("../data/HMWF_TN.txt")
#TN <- TN[grep("MEM*", TN$Sample), ]
colnames(TN) <- c("sample", "year", "conc")
#TNkey <- read.delim("../data/DOC_KEY_epi.txt", header=T)
```

```

#TN$code <- TN$sample
#TN <- TN[which(TN$code %in% TNkey$Sample.Name), ]
#TN$sample <- TNkey$Site[match(TNkey$Sample.Name, TN$code)]
#TN$year <- substr(TN$code, 4, 7)
#TN$conc <- pmax(TN$conc, 0)
TN2 <- data.frame("sample" = TN$sample, "year" = TN$year,
                  "conc" = TN$conc)[order(TN$sample, TN$year), ]
#TN$sample[grep("Pony", TN$sample)] <- "Pony"
TN <- droplevels(TN)

# Total Phosphorus
TP2011 <- read.delim("../data/2011TP_data.txt")
TP2012 <- read.delim("../data/2012TP_data.txt")
TP2011$year <- rep("2011", dim(TP2011)[1])
TP2012$year <- rep("2012", dim(TP2012)[1])
TP <- rbind(TP2011, TP2012)
TP <- TP[grep("*iltered", TP$Sample), ]
colnames(TP) <- c("sample", "conc", "LCL", "UCL", "se", "year")
TP$code <- TP$sample
TDP <- TP[grep("*Filtered", TP$sample), ]
TP <- TP[grep("*Unfiltered", TP$sample), ]
TP$sample <- gsub(" Unfiltered", "", TP$sample)
TDP$sample <- gsub(" Filtered", "", TDP$sample)
TP[6, ] <- TDP[6, ]
TP <- TP[-c(which(TP$sample == "CanyonHypo" | TP$sample == "CanyonChemo")), ]
TP$sample <- gsub("CanyonEpi", "Canyon", TP$sample)
TP$sample <- as.factor(TP$sample)
TP$conc <- pmax(TP$conc, 0)
TP2 <- data.frame("sample" = TP$sample, "year" = TP$year,
                  "conc" = TP$conc)[order(TP$sample, TP$year), ]
TP$sample[grep("Pony", TP$sample)] <- "Pony"
TP <- droplevels(TP)

```

Organize Data Table

```

DOC2 <- aggregate(conc ~ sample + year, DOC2, mean)
TN2 <- aggregate(conc ~ sample + year, TN2, mean)
TP2 <- aggregate(conc ~ sample + year, TP2, mean)

nuts <- data.frame("sample" = DOC2$sample, "year" = DOC2$year,
                  "DOC" = DOC2$conc, "TP" = TP2$conc)

nuts <- data.frame(nuts[-which(nuts$sample == "Pony.N"), ])
nuts$sample[grep("Pony", nuts$sample)] <- "Pony"
nuts <- droplevels(nuts)
nuts$TN <- TN2$conc

```

Table 2: Lake Nutrients

```

nuts2 <- data.frame(matrix(NA, 10, 6))
row.names(nuts2) <- levels(nuts$sample)
colnames(nuts2) <- c("DOC11", "DOC12", "TP11", "TP12", "TN11", "TN12")
for (i in row.names(nuts2)){
  nuts2[i, 1] <- round(nuts[nuts$sample == i & nuts$year == "2011", 3], 2)
  nuts2[i, 2] <- round(nuts[nuts$sample == i & nuts$year == "2012", 3], 2)
  nuts2[i, 3] <- round(nuts[nuts$sample == i & nuts$year == "2011", 4], 2)
  nuts2[i, 4] <- round(nuts[nuts$sample == i & nuts$year == "2012", 4], 2)
  nuts2[i, 5] <- round(nuts[nuts$sample == i & nuts$year == "2011", 5], 2)
  nuts2[i, 6] <- round(nuts[nuts$sample == i & nuts$year == "2012", 5], 2)
}

addtorow <- list()
addtorow$pos <- list(0, 0)
addtorow$command <- c("& \\multicolumn{2}{c}{DOC (mg C L-1)} & \\multicolumn{2}{c}{TP ($\\mu$g P L-1)} & \\multicolumn{2}{c}{TN (mg N L-1)}\\\\\\n",
  "Lake & 2011 & 2012 & 2011 & 2012 & 2011 & 2012 \\\\\\n")
nut.tab <- xtable(nuts2)
align(nut.tab) <- "crrrrrr"
print(nut.tab, add.to.row = addtorow, include.colnames = FALSE,
  type= "latex", file="../tables/table1.tex",
  hline.after = c(-1, -1, 0, nrow(nut.tab)))
print(nut.tab, add.to.row = addtorow, include.colnames = FALSE,
  comment = FALSE, hline.after = c(-1, -1, 0, nrow(nut.tab)))

```

	DOC (mg C L ⁻¹)		TP (μg P L ⁻¹)		TN (mg N L ⁻¹)	
Lake	2011	2012	2011	2012	2011	2012
Ann	6.15	5.97	3.98	7.27	0.42	0.43
Canyon	7.62	7.23	2.45	2.64	0.44	0.38
Howe	6.88	7.04	1.86	5.21	0.56	0.57
Ives	9.54	6.91	1.35	9.15	0.42	0.38
Lily	13.36	14.35	4.74	11.55	0.82	0.93
Mountain	5.41	5.27	2.11	4.87	0.34	0.34
Pony	31.65	28.99	1.52	49.95	1.56	1.86
Rush	4.44	4.22	3.55	3.84	0.30	0.41
SecondPine	7.20	6.26	10.76	12.92	0.43	0.44
UpperPine	7.99	7.84	2.96	11.21	0.59	0.57

Supplemental Figure 2: Lake Nutrients

```

png(filename="../figures/Supp2.png",
  width = 1600, height =1200, res = 96*2)
par(opar)
par(mfrow = c(1,1), mar = c(0, 6, 0, 0) + 0.5, oma = c(4, 0, 1, 1) + 0.5)
layout(rbind(1, 2, 3), height = c(3, 3, 3))

```



```
labs <- c("Ann", "Canyon", "Howe", "Ives", "Lily", "Mountain", "Pony", "Rush",
         "Second\nPine", "Upper\nPine")
```

DOC Plot

```
plot(DOC$conc ~ DOC$sample, ylim = c(0, 35), las = 1,
     xaxt="n", xlab = "", yaxt="n", ylab = "")
axis(side=1, lwd.ticks = 2, tck = -0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=1, lwd.ticks = 2, tck = 0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=2, lwd.ticks = 2, labels = T, cex.axis = 1.2, las = 1,
     at = c(0, 10, 20, 30))
axis(side=2, lwd.ticks = 2, tck = 0.01, labels = F, cex.axis = 1,
     at = c(0, 10, 20, 30))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(0, 10, 20, 30))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0, 10, 20, 30))
mtext(side = 2, expression(paste("DOC (mg C L" ^-1, ")"), sep="")),
     line = 3.5, cex = 1)
legend("topleft", "A", bty = "n", x.intersp = 0, cex = 1.25)
box(lwd = 2)
```

Total Nitrogen Plot

```
plot(TN$conc ~ TN$sample, ylim = c(0,2), las = 1,
     xaxt="n", xlab = "", yaxt="n", ylab = "")
axis(side=1, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=1, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=2, lwd.ticks = 2, labels = T, cex.axis = 1.2, las = 1,
     at = c(0.0, 0.5, 1.0, 1.5))
axis(side=2, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0.0, 0.5, 1.0, 1.5))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(0.0, 0.5, 1.0, 1.5))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0.0, 0.5, 1.0, 1.5))
mtext(side = 2, expression(paste("TN (mg N L" ^-1, ")"), sep="")),
     line = 3.5, cex = 1)
legend("topleft", "B", bty = "n", x.intersp = 0, cex = 1.25)
box(lwd = 2)
```

Total Phosphorus Plot

```
plot(TP$sample, TP$conc, ylim = c(0,50), las = 1,
```



```

    xaxt="n", xlab = "", yaxt="n", ylab = "")
axis(side=1, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=1, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=2, lwd.ticks = 2, labels = T, cex.axis = 1.2, las = 1,
     at = c(0, 20, 40))
axis(side=2, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0, 20, 40))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(0, 20, 40))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0, 20, 40))
mtext(side = 2, expression(paste("TP (",mu, "g P L" ^-1, ")")),
     line = 3.5, cex = 1)
mtext(side = 1, text = labs, line = 1, at = seq(1:10), padj = 0.5, cex = 0.8)
legend("topleft", "C", bty = "n", x.intersp = 0, cex = 1.25)
box(lwd = 2)

dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)

```

But there are other differences between these lakes. For example, algal derived resources differ (as inferred from chlorophyll *a* concentrations). Additionally, bacterial respiration differs between lakes though there is also temperature dependence with these values as well (temperature between years of sampling).

Ecosystem and Microbial Processes

```

chla <- read.delim("../data/ChlorophyllA.txt")
resp <- read.delim("../data/Respiration.txt")
# npp
# CO2 flux
# EcoResp
# DO

```

Table 2: Ecosystem and Microbial Processes

```

eco <- data.frame(matrix(NA, 10, 4))
row.names(eco) <- levels(chla$Lake)
colnames(eco) <- c("Chl11", "Chl12", "Resp11", "Resp12")
for (i in row.names(eco)){
  eco[i, 1] <- round(mean(chla[chla$Lake == i & chla$Year == "2011", 3]), 2)
  eco[i, 2] <- round(mean(chla[chla$Lake == i & chla$Year == "2012", 3]), 2)
}

```

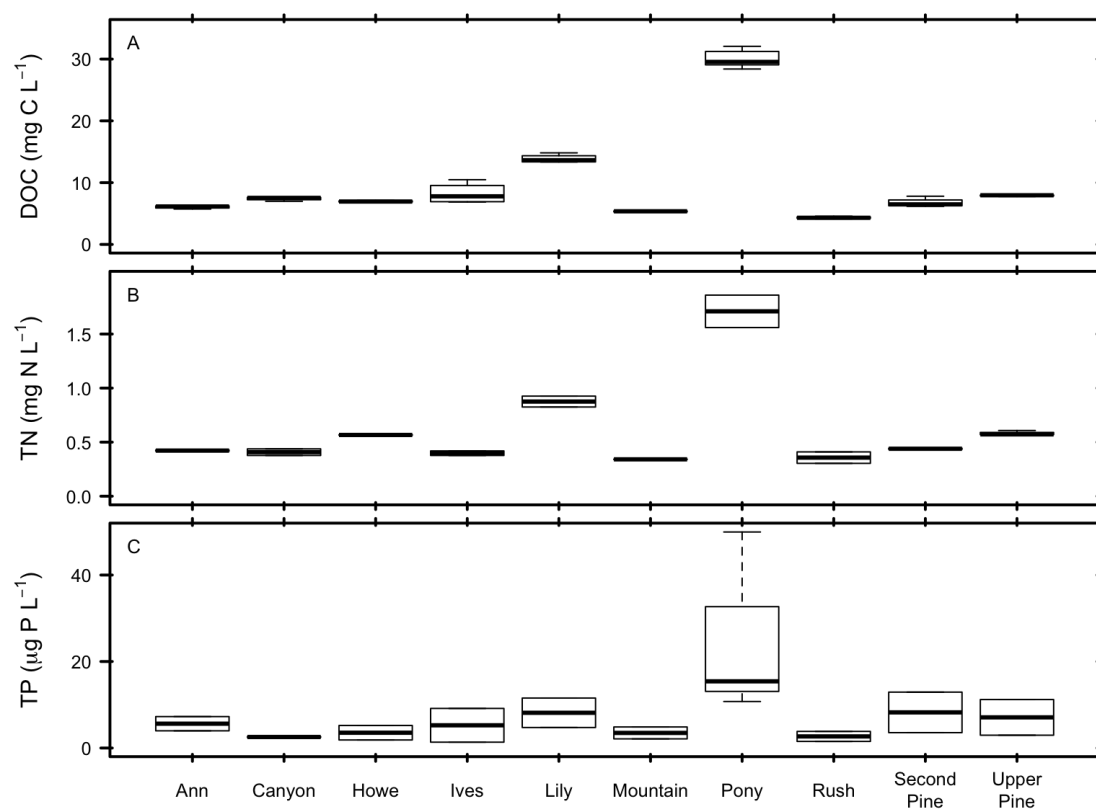


Figure 2: Lake Nutrients

```

eco[i, 3] <- round(mean(resp[resp$sample == i & resp$year == "2011", 4]), 3)
eco[i, 4] <- round(mean(resp[resp$sample == i & resp$year == "2012", 4]), 3)
}

addtorow <- list()
addtorow$pos <- list(0, 0, 0)
addtorow$command <- c("& \\multicolumn{2}{c}{Chl  $a$ } & \\multicolumn{2}{c}{Resp.} \\",
"& \\multicolumn{2}{c}{(\\mu g L-1)} & \\multicolumn{2}{c}{(\\mu M O2 Hr-1)} \\",
"Lake & 2011 & 2012 & 2011 & 2012 \\")
eco.tab <- xtable(eco)
align(eco.tab) <- c("c ", "r ", "r ", "r ", "r ")
print(eco.tab, add.to.row = addtorow, include.colnames = FALSE,
type= "latex", file= "../tables/table2.tex",
hline.after = c(-1, -1, 0, nrow(eco.tab)))
print(eco.tab, add.to.row = addtorow, include.colnames = FALSE,
comment = FALSE, hline.after = c(-1, -1, 0, nrow(eco.tab)))

```

Lake	Chl <i>a</i> ($\mu\text{g L}^{-1}$)		Resp. ($\mu\text{M O}_2 \text{ Hr}^{-1}$)	
	2011	2012	2011	2012
Ann	1.31	1.25	1.96	1.26
Canyon	3.70	1.63	1.78	1.32
Howe	0.75	1.85	1.48	0.97
Ives	2.03	1.39	1.42	0.80
Lily	5.77	3.55	2.06	0.94
Mountain	1.80	2.14	1.91	1.42
Pony	24.58	16.35	3.05	1.69
Rush	0.65	1.23	1.75	1.22
SecondPine	2.13	3.76	1.46	1.17
UpperPine	2.14	8.55	1.73	1.26

Supplemental Figure 3: Ecosystem and Microbial Processes

```

chla2 <- chla[chla$Year == "2012", ]
resp2 <- resp[resp$year == "2012", ]

png(filename= "../figures/Supp3.png",
width = 1600, height = 1200, res = 96*2)
par(opar)
par(mfrow = c(1,1), mar = c(0, 6, 0, 0) + 0.5, oma = c(4, 0, 1, 1) + 0.5)
layout(rbind(1, 2), height = c(4, 4))

labs <- c("Ann", "Canyon", "Howe", "Ives", "Lily", "Mountain", "Pony", "Rush",
"Second\nPine", "Upper\nPine")

# ChlaA Plot 2012
plot(chla2$ChlA ~ chla2$Lake, ylim = c(0, 20), las = 1,
xaxt="n", xlab = "", yaxt="n", ylab = "")

```

```

axis(side=1, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(1:10))
axis(side=1, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1:10))
axis(side=2, lwd.ticks = 2, labels = T, cex.axis = 1.2, las = 1,
     at = c(0, 10, 20))
axis(side=2, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0, 10, 20, 30))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(0, 10, 20, 30))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0, 10, 20, 30))
mtext(side = 2, expression(paste("Chl a (mg C L" ^-1, ")"), sep="")),
     line = 3.5, cex = 1)
legend("topleft", "A", bty = "n", x.intersp = 0, cex = 1.25)
box(lwd = 2)

# Bacterial Respiration
plot(resp2$rate ~ resp2$sample, ylim = c(0.5,2), las = 1,
     xaxt="n", xlab = "", yaxt="n", ylab = "")
axis(side=1, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=1, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=2, lwd.ticks = 2, labels = T, cex.axis = 1.2, las = 1,
     at = c(0, 1, 2))
axis(side=2, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0, 1, 2))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(1:10))
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1,
     at = c(0, 1, 2))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1,
     at = c(0, 1, 2))
mtext(side = 2, expression(paste("Resp. (", mu, "M O"[2], " Hr" ^-1, ")")),
     line = 3.5, cex = 1)
mtext(side = 1, text = labs, line = 1, at = seq(1:10), padj = 0.5, cex = 0.8)
legend("topleft", "B", bty = "n", x.intersp = 0, cex = 1.25)
box(lwd = 2)

dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)

```

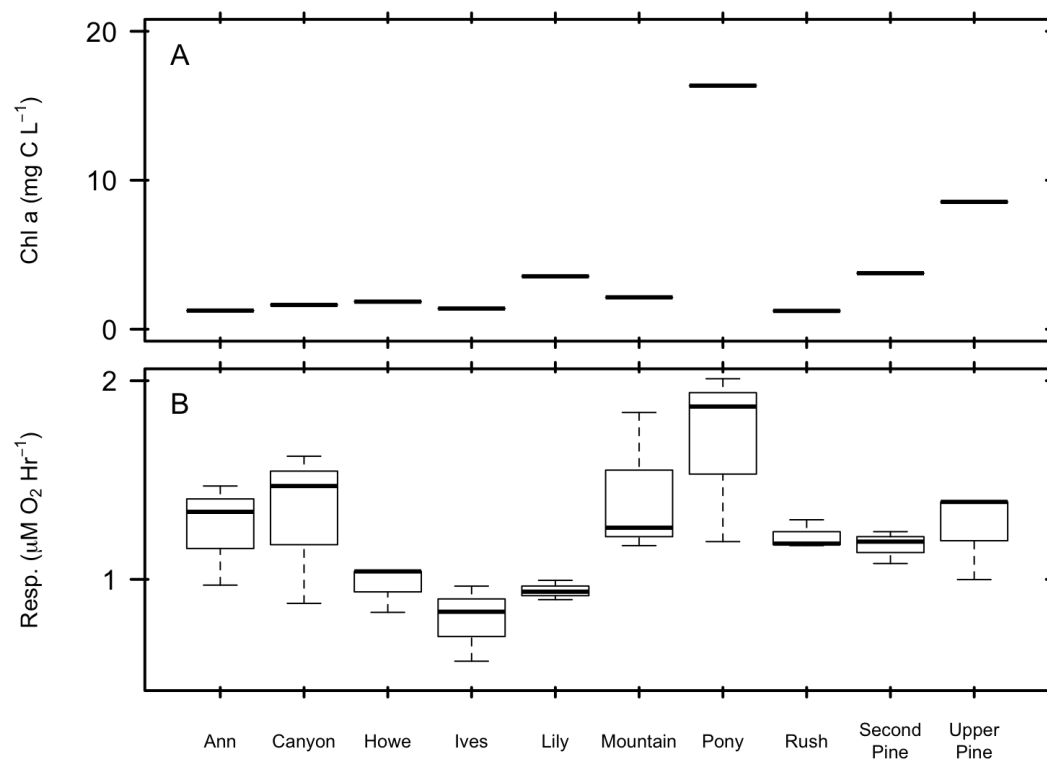


Figure 3: Ecosystem

Patterns of Bacterial Diversity

The major difference that we are interested in is bacterial diversity across the sites. We know that the lakes have different microbiomes. These microbiomes can be influenced by physical, chemical and biological interactions within each lake.

Import Raw Data

```
# Define Inputs
# Design = general design file for experiment
# shared = OTU table from mothur with sequence similarity clustering
# Taxonomy = Taxonomic information for each OTU
design.in <- "../data/design.txt"
shared <- "../data/HMWF.bac.final.shared"
taxon <- "../data/HMWF.bac.final.0.03.taxonomy"

# Import Design
design <- read.delim(design.in, header=T, row.names=1)

# Import Shared Files
OTUs.in <- read.otu(shared = shared, cutoff = "0.03") # 97% Similarity

# Import Taxonomy
OTU.tax <- read.tax(taxonomy = taxon, format = "rdp")
```

Data Transformations

```
# Reorder Site
OTUs.hmwf <- OTUs.in[rownames(design), ]

# Remove OTUs with less than two occurrences across all sites
# OTUs <- OTUs.hmwf[, which(colSums(OTUs.hmwf) >= 2)]
OTUs <- OTUs.hmwf[, colSums((OTUs.hmwf > 0) * 1) >= 2 | colSums(OTUs.hmwf >= 10)]

# Sequencing Coverage
coverage <- rowSums(OTUs)

# Good's Coverage
goods <- function(x = ""){
  1 - (sum(x == 1) / rowSums(x))
}
goods.c <- goods(OTUs)

# Make Presence Absence Matrix
OTUsPA <- (OTUs > 0) * 1

# Make Relative Abundance Matrices
OTUsREL <- OTUs
for(i in 1:dim(OTUs)[1]){
  OTUsREL[i,] <- OTUs[i,]/sum(OTUs[i,])
}
```

```

}

# Log Transform Relative Abundances
OTUsREL.log <- decostand(OTUs, method="log")

```

Calculate Alpha Diversity

```

# Observed Richness
S.obs <- rowSums((OTUs > 0) * 1)

# Simpson's Evenness
SimpE <- function(x = ""){
  x <- as.data.frame(x)
  D <- diversity(x, "inv")
  S <- sum((x > 0) * 1)
  E <- (D)/S
  return(E)
}
simpsE <- round(apply(OTUs, 1, SimpE), 3)

# Shannon's Diversity
H <- function(x = ""){
  x <- x[x>0]
  H = 0
  for (n_i in x){
    p = n_i / sum(x)
    H = H - p*log(p)
  }
  return(H)
}

shan <- round(apply(OTUs, 1, H), 2)
shan2 <- diversity(OTUs, index = "shannon")

# Rarefied Richness
S.rar <- round(rarefy(OTUs, min(rowSums(OTUs))), 0)

design <- droplevels(design)

alpha.div <- cbind(design, S.obs, simpsE, shan, S.rar)
alpha.div <- alpha.div[order(alpha.div$Lake, alpha.div$Year, alpha.div$Molecule), ]

```

Supplemental Figure 4: Lake Bacterial Alpha Diversity

```

png(filename="../figures/Supp4.png",
     width = 1600, height = 1100, res = 96*2)
par(opar)
par(mfrow = c(1,1), mar = c(0, 6, 0, 0) + 0.5, oma = c(3, 0, 1, 1) + 0.5)
layout(rbind(1, 2), height = c(3, 3))

```



```

labs <- c("Ann", "Canyon", "Howe", "Ives", "Lily", "Mountain", "Pony", "Rush",
          "Second\nPine", "Upper\nPine")

plot(alpha.div$S.obs ~ alpha.div$Lake, ylim = c(0,5000), las = 1,
      xaxt="n", xlab = "", yaxt="n", ylab = "")
axis(side=1, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(1:10))
axis(side=1, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1:10))
axis(side=2, lwd.ticks = 2, labels = T, cex.axis = 1, las = 1,
      at = c(1000, 3000, 5000))
axis(side=2, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1000, 3000, 5000, 7000))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(1:10))
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1:10))
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(1000, 3000, 5000, 7000))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1000, 3000, 5000, 7000))
mtext(side = 2, "Richness (S)", line = 4, cex = 1)
legend("topleft", "A", bty = "n", x.intersp = 0, cex = 1.25)
box(lwd = 2)

plot(alpha.div$simpsE ~ alpha.div$Lake, ylim = c(0,0.06), las = 1,
      xaxt="n", xlab = "", yaxt="n", ylab = "")
axis(side=1, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(1:10))
axis(side=1, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1:10))
axis(side=2, lwd.ticks = 2, labels = T, cex.axis = 1, las = 1,
      at = c(0, 0.02, 0.04, 0.06))
axis(side=2, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(0, 0.02, 0.04, 0.06))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(1:10))
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1:10))
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(0, 0.02, 0.04, 0.06))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(0, 0.02, 0.04, 0.06))
mtext(side = 2, "Simpson's Evenness (E)", line = 4, cex = 1)
mtext(side = 1, text = labs, line = 0.5, at = seq(1:10), padj = 0.5, cex = 0.8)
legend("topleft", "B", bty = "n", x.intersp = 0, cex = 1.25)
box(lwd = 2)

dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)

```

Alpha Diversity Statistics

```
alpha.div
```

##		Lake	Molecule	Year	S.obs	simpsE	shan	S.rar
##	Ann2011_DNA	Ann	DNA	2011	1622	0.015	4.02	765
##	Ann2011_RNA	Ann	RNA	2011	1332	0.018	4.38	860
##	Ann2012_DNA	Ann	DNA	2012	1232	0.031	4.43	678
##	Ann2012_RNA	Ann	RNA	2012	1111	0.028	4.45	705
##	Canyon2011_DNA	Canyon	DNA	2011	1392	0.016	3.92	709
##	Canyon2011_RNA	Canyon	RNA	2011	1469	0.013	4.07	907
##	Canyon2012_DNA	Canyon	DNA	2012	1311	0.020	4.06	727

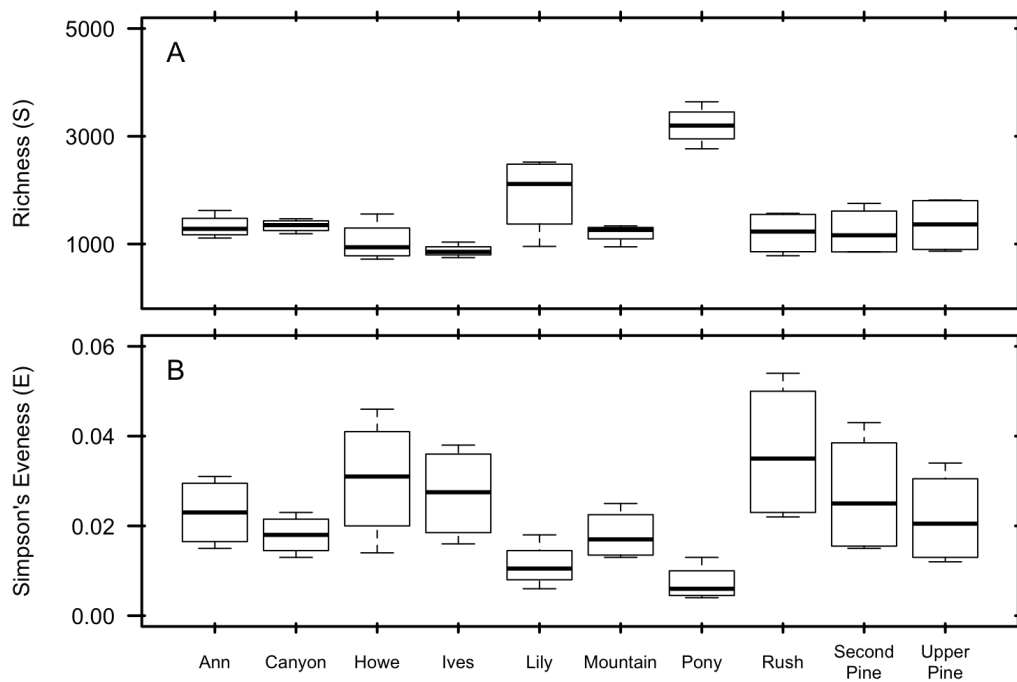


Figure 4: Lake Nutrients

## Canyon2012_RNA	Canyon	RNA	2012	1191	0.023	4.32	801
## Howe2011_DNA	Howe	DNA	2011	1557	0.014	3.99	736
## Howe2011_RNA	Howe	RNA	2011	720	0.036	4.35	720
## Howe2012_DNA	Howe	DNA	2012	1037	0.026	4.23	627
## Howe2012_RNA	Howe	RNA	2012	843	0.046	4.59	649
## Ives2011_DNA	Ives	DNA	2011	1036	0.016	3.70	544
## Ives2011_RNA	Ives	RNA	2011	747	0.034	4.14	562
## Ives2012_DNA	Ives	DNA	2012	861	0.021	3.90	521
## Ives2012_RNA	Ives	RNA	2012	850	0.038	4.41	589
## Lily2011_DNA	Lily	DNA	2011	1786	0.010	3.71	777
## Lily2011_RNA	Lily	RNA	2011	956	0.018	3.84	703
## Lily2012_DNA	Lily	DNA	2012	2443	0.006	3.80	1076
## Lily2012_RNA	Lily	RNA	2012	2521	0.011	4.33	1254
## Mountain2011_DNA	Mountain	DNA	2011	1336	0.014	3.88	707
## Mountain2011_RNA	Mountain	RNA	2011	1279	0.020	4.23	757
## Mountain2012_DNA	Mountain	DNA	2012	1243	0.013	3.70	690
## Mountain2012_RNA	Mountain	RNA	2012	948	0.025	4.12	653
## Pony2011_DNA	Pony	DNA	2011	3261	0.005	3.78	1337
## Pony2011_RNA	Pony	RNA	2011	2768	0.004	3.50	1154
## Pony2012_DNA	Pony	DNA	2012	3136	0.013	5.07	1956
## Pony2012_RNA	Pony	RNA	2012	3640	0.007	4.58	1863
## Rush2011_DNA	Rush	DNA	2011	1569	0.024	4.39	776
## Rush2011_RNA	Rush	RNA	2011	1531	0.022	4.33	822
## Rush2012_DNA	Rush	DNA	2012	931	0.054	4.48	575
## Rush2012_RNA	Rush	RNA	2012	783	0.046	4.35	560
## SecondPine2011_DNA	SecondPine	DNA	2011	1470	0.016	4.08	717

```
## SecondPine2011_RNA SecondPine      RNA 2011 1754 0.015 4.49 905
## SecondPine2012_DNA SecondPine      DNA 2012  854 0.034 4.21 530
## SecondPine2012_RNA SecondPine      RNA 2012  854 0.043 4.54 584
## UpperPine2011_DNA  UpperPine      DNA 2011 1795 0.014 4.17 745
## UpperPine2011_RNA  UpperPine      RNA 2011 1816 0.012 4.31 891
## UpperPine2012_DNA  UpperPine      DNA 2012  933 0.027 4.07 543
## UpperPine2012_RNA  UpperPine      RNA 2012  867 0.034 4.30 548
```

```
div.mod1 <- aov(S.obs ~ Lake, data = alpha.div)
TukeyHSD(div.mod1)
```

```
##      Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = S.obs ~ Lake, data = alpha.div)
##
## $Lake
##              diff              lwr              upr              p adj
## Canyon-Ann          16.50      -930.65678        963.6568 1.0000000
## Howe-Ann          -285.00     -1232.15678        662.1568 0.9880448
## Ives-Ann          -450.75     -1397.90678        496.4068 0.8265530
## Lily-Ann           602.25      -344.90678       1549.4068 0.4975400
## Mountain-Ann       -122.75     -1069.90678        824.4068 0.9999847
## Pony-Ann           1877.00       929.84322       2824.1568 0.0000069
## Rush-Ann          -120.75     -1067.90678        826.4068 0.9999867
## SecondPine-Ann      -91.25     -1038.40678        855.9068 0.9999988
## UpperPine-Ann        28.50      -918.65678       975.6568 1.0000000
## Howe-Canyon       -301.50     -1248.65678        645.6568 0.9825061
## Ives-Canyon        -467.25     -1414.40678        479.9068 0.7961358
## Lily-Canyon         585.75      -361.40678       1532.9068 0.5351853
## Mountain-Canyon    -139.25     -1086.40678        807.9068 0.9999553
## Pony-Canyon        1860.50       913.34322       2807.6568 0.0000081
## Rush-Canyon        -137.25     -1084.40678        809.9068 0.9999605
## SecondPine-Canyon  -107.75     -1054.90678        839.4068 0.9999950
## UpperPine-Canyon    12.00      -935.15678       959.1568 1.0000000
## Ives-Howe         -165.75     -1112.90678        781.4068 0.9998095
## Lily-Howe          887.25       -59.90678       1834.4068 0.0810592
## Mountain-Howe       162.25      -784.90678       1109.4068 0.9998402
## Pony-Howe         2162.00      1214.84322       3109.1568 0.0000005
## Rush-Howe          164.25      -782.90678       1111.4068 0.9998232
## SecondPine-Howe     193.75      -753.40678       1140.9068 0.9993278
## UpperPine-Howe      313.50      -633.65678       1260.6568 0.9773874
## Lily-Ives         1053.00       105.84322       2000.1568 0.0201203
## Mountain-Ives       328.00      -619.15678       1275.1568 0.9698002
## Pony-Ives         2327.75      1380.59322       3274.9068 0.0000001
## Rush-Ives          330.00      -617.15678       1277.1568 0.9686237
## SecondPine-Ives     359.50      -587.65678       1306.6568 0.9472188
## UpperPine-Ives      479.25      -467.90678       1426.4068 0.7726381
## Mountain-Lily      -725.00     -1672.15678        222.1568 0.2559131
## Pony-Lily          1274.75       327.59322       2221.9068 0.0025528
## Rush-Lily          -723.00     -1670.15678        224.1568 0.2591116
## SecondPine-Lily     -693.50     -1640.65678        253.6568 0.3094289
## UpperPine-Lily     -573.75     -1520.90678        373.4068 0.5628546
## Pony-Mountain      1999.75      1052.59322       2946.9068 0.0000021
```

```
## Rush-Mountain          2.00 -945.15678  949.1568 1.0000000
## SecondPine-Mountain    31.50 -915.65678  978.6568 1.0000000
## UpperPine-Mountain     151.25 -795.90678 1098.4068 0.9999107
## Rush-Pony             -1997.75 -2944.90678 -1050.5932 0.0000021
## SecondPine-Pony        -1968.25 -2915.40678 -1021.0932 0.0000028
## UpperPine-Pony         -1848.50 -2795.65678 -901.3432 0.0000091
## SecondPine-Rush         29.50 -917.65678  976.6568 1.0000000
## UpperPine-Rush         149.25 -797.90678 1096.4068 0.9999201
## UpperPine-SecondPine   119.75 -827.40678 1066.9068 0.9999876
```

```
div.mod2 <- aov(simpsE ~ Lake, data = alpha.div)
TukeyHSD(div.mod2)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = simpsE ~ Lake, data = alpha.div)
##
## $Lake
##              diff              lwr              upr              p adj
## Canyon-Ann      -5.000000e-03 -0.02915686 0.0191568604 0.9992621
## Howe-Ann         7.500000e-03 -0.01665686 0.0316568604 0.9852027
## Ives-Ann         4.250000e-03 -0.01990686 0.0284068604 0.9998010
## Lily-Ann        -1.175000e-02 -0.03590686 0.0124068604 0.8084834
## Mountain-Ann     -5.000000e-03 -0.02915686 0.0191568604 0.9992621
## Pony-Ann        -1.575000e-02 -0.03990686 0.0084068604 0.4633255
## Rush-Ann         1.350000e-02 -0.01065686 0.0376568604 0.6650546
## SecondPine-Ann    4.000000e-03 -0.02015686 0.0281568604 0.9998793
## UpperPine-Ann    -1.250000e-03 -0.02540686 0.0229068604 1.0000000
## Howe-Canyon      1.250000e-02 -0.01165686 0.0366568604 0.7504890
## Ives-Canyon      9.250000e-03 -0.01490686 0.0334068604 0.9444302
## Lily-Canyon     -6.750000e-03 -0.03090686 0.0174068604 0.9928815
## Mountain-Canyon -3.469447e-18 -0.02415686 0.0241568604 1.0000000
## Pony-Canyon     -1.075000e-02 -0.03490686 0.0134068604 0.8743931
## Rush-Canyon      1.850000e-02 -0.00565686 0.0426568604 0.2553416
## SecondPine-Canyon 9.000000e-03 -0.01515686 0.0331568604 0.9527154
## UpperPine-Canyon 3.750000e-03 -0.02040686 0.0279068604 0.9999295
## Ives-Howe       -3.250000e-03 -0.02740686 0.0209068604 0.9999790
## Lily-Howe       -1.925000e-02 -0.04340686 0.0049068604 0.2115360
## Mountain-Howe   -1.250000e-02 -0.03665686 0.0116568604 0.7504890
## Pony-Howe       -2.325000e-02 -0.04740686 0.0009068604 0.0668193
## Rush-Howe        6.000000e-03 -0.01815686 0.0301568604 0.9969909
## SecondPine-Howe -3.500000e-03 -0.02765686 0.0206568604 0.9999605
## UpperPine-Howe  -8.750000e-03 -0.03290686 0.0154068604 0.9601001
## Lily-Ives       -1.600000e-02 -0.04015686 0.0081568604 0.4418263
## Mountain-Ives   -9.250000e-03 -0.03340686 0.0149068604 0.9444302
## Pony-Ives       -2.000000e-02 -0.04415686 0.0041568604 0.1735473
## Rush-Ives        9.250000e-03 -0.01490686 0.0334068604 0.9444302
## SecondPine-Ives -2.500000e-04 -0.02440686 0.0239068604 1.0000000
## UpperPine-Ives  -5.500000e-03 -0.02965686 0.0186568604 0.9984463
## Mountain-Lily    6.750000e-03 -0.01740686 0.0309068604 0.9928815
## Pony-Lily       -4.000000e-03 -0.02815686 0.0201568604 0.9998793
## Rush-Lily        2.525000e-02  0.00109314 0.0494068604 0.0348567
## SecondPine-Lily  1.575000e-02 -0.00840686 0.0399068604 0.4633255
```

```
## UpperPine-Lily      1.050000e-02 -0.01365686 0.0346568604 0.8885348
## Pony-Mountain      -1.075000e-02 -0.03490686 0.0134068604 0.8743931
## Rush-Mountain       1.850000e-02 -0.00565686 0.0426568604 0.2553416
## SecondPine-Mountain 9.000000e-03 -0.01515686 0.0331568604 0.9527154
## UpperPine-Mountain  3.750000e-03 -0.02040686 0.0279068604 0.9999295
## Rush-Pony          2.925000e-02  0.00509314 0.0534068604 0.0085700
## SecondPine-Pony     1.975000e-02 -0.00440686 0.0439068604 0.1855774
## UpperPine-Pony      1.450000e-02 -0.00965686 0.0386568604 0.5749415
## SecondPine-Rush    -9.500000e-03 -0.03365686 0.0146568604 0.9352087
## UpperPine-Rush     -1.475000e-02 -0.03890686 0.0094068604 0.5522824
## UpperPine-SecondPine -5.250000e-03 -0.02940686 0.0189068604 0.9989170
```

```
div.mod3 <- aov(S.rar ~ Lake, data = alpha.div)
TukeyHSD(div.mod3)
```

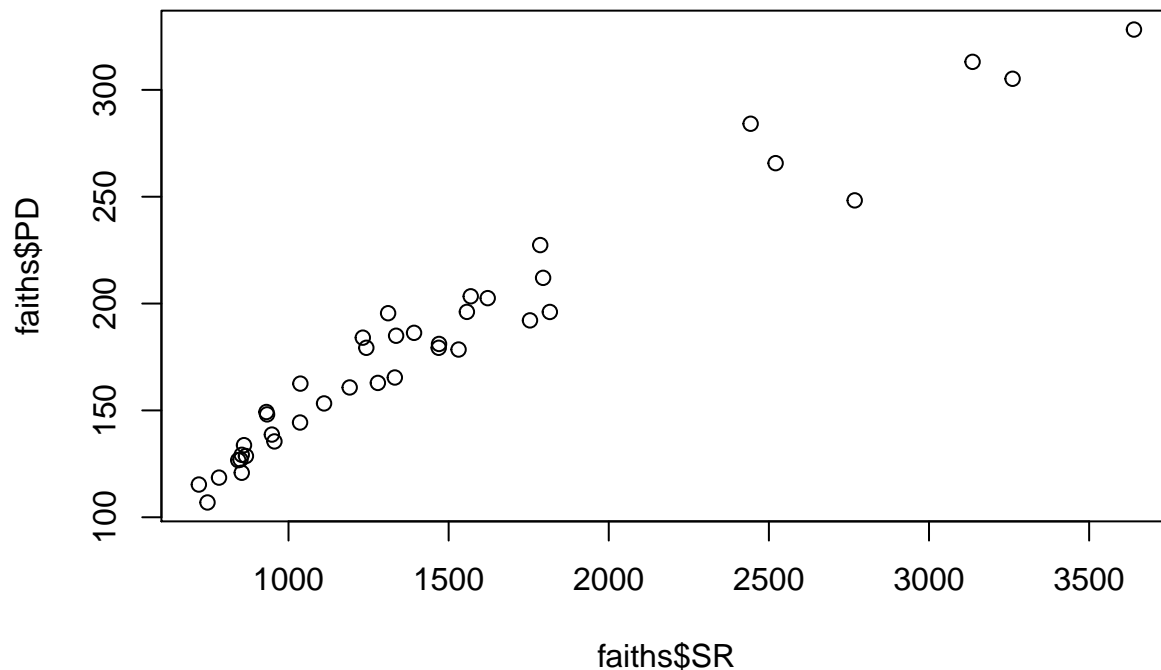
```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = S.rar ~ Lake, data = alpha.div)
##
## $Lake
##          diff          lwr          upr          p adj
## Canyon-Ann      34.00    -394.06434    462.0643 0.9999998
## Howe-Ann        -69.00    -497.06434    359.0643 0.9999034
## Ives-Ann       -198.00    -626.06434    230.0643 0.8482335
## Lily-Ann        200.50    -227.56434    628.5643 0.8389314
## Mountain-Ann    -50.25    -478.31434    377.8143 0.9999935
## Pony-Ann        825.50     397.43566   1253.5643 0.0000112
## Rush-Ann        -68.75    -496.81434    359.3143 0.9999063
## SecondPine-Ann  -68.00    -496.06434    360.0643 0.9999145
## UpperPine-Ann   -70.25    -498.31434    357.8143 0.9998879
## Howe-Canyon    -103.00    -531.06434    325.0643 0.9976302
## Ives-Canyon    -232.00    -660.06434    196.0643 0.7007346
## Lily-Canyon     166.50    -261.56434    594.5643 0.9391584
## Mountain-Canyon -84.25    -512.31434    343.8143 0.9995058
## Pony-Canyon     791.50     363.43566   1219.5643 0.0000235
## Rush-Canyon    -102.75    -530.81434    325.3143 0.9976734
## SecondPine-Canyon -102.00    -530.06434    326.0643 0.9977991
## UpperPine-Canyon -104.25    -532.31434    323.8143 0.9974042
## Ives-Howe      -129.00    -557.06434    299.0643 0.9879199
## Lily-Howe       269.50    -158.56434    697.5643 0.5110235
## Mountain-Howe    18.75    -409.31434    446.8143 1.0000000
## Pony-Howe       894.50     466.43566   1322.5643 0.0000026
## Rush-Howe        0.25    -427.81434    428.3143 1.0000000
## SecondPine-Howe   1.00    -427.06434    429.0643 1.0000000
## UpperPine-Howe   -1.25    -429.31434    426.8143 1.0000000
## Lily-Ives       398.50     -29.56434    826.5643 0.0846258
## Mountain-Ives    147.75    -280.31434    575.8143 0.9704225
## Pony-Ives      1023.50     595.43566   1451.5643 0.0000002
## Rush-Ives       129.25    -298.81434    557.3143 0.9877583
## SecondPine-Ives  130.00    -298.06434    558.0643 0.9872636
## UpperPine-Ives   127.75    -300.31434    555.8143 0.9887029
## Mountain-Lily   -250.75    -678.81434    177.3143 0.6066431
## Pony-Lily        625.00     196.93566   1053.0643 0.0008918
```

```
## Rush-Lily -269.25 -697.31434 158.8143 0.5122834
## SecondPine-Lily -268.50 -696.56434 159.5643 0.5160675
## UpperPine-Lily -270.75 -698.81434 157.3143 0.5047347
## Pony-Mountain 875.75 447.68566 1303.8143 0.0000038
## Rush-Mountain -18.50 -446.56434 409.5643 1.0000000
## SecondPine-Mountain -17.75 -445.81434 410.3143 1.0000000
## UpperPine-Mountain -20.00 -448.06434 408.0643 1.0000000
## Rush-Pony -894.25 -1322.31434 -466.1857 0.0000026
## SecondPine-Pony -893.50 -1321.56434 -465.4357 0.0000026
## UpperPine-Pony -895.75 -1323.81434 -467.6857 0.0000025
## SecondPine-Rush 0.75 -427.31434 428.8143 1.0000000
## UpperPine-Rush -1.50 -429.56434 426.5643 1.0000000
## UpperPine-SecondPine -2.25 -430.31434 425.8143 1.0000000
```

Lake Phylogenetic Diversity

```
# Import Tree with *ape*
hmf.tree <- read.tree("../fasttree/HMWF.bac.0.03.gg.tree")
# tips <- paste(rep("Otu", length(hmf.tree$tip.label)),
#               formatC(seq(1:length(hmf.tree$tip.label)),
#                       width = 6, format = "d", flag = "0"), sep = "")
# hmf.tree$tip.label <- tips
prunedTree <- prune.sample(OTUs,hmf.tree)

faiths <- pd(OTUs, prunedTree, include.root = FALSE)
# ses.pd(OTUs, prunedTree, include.root = FALSE, null.model = "independentswap", runs = 9, iterations =
# psr(OTUs, prunedTree)
plot(faiths$PD ~ faiths$SR)
```



Bacteria Diversity Table

```

bac.div <- cbind(alpha.div, faiths)

addtorow <- list()
addtorow$pos <- list(0, 0, 0)
addtorow$command <- c("& \\multicolumn{2}{c}{Chl  $\text{\emph{a}}$ } & \\multicolumn{2}{c}{Resp.} \\",
  "& \\multicolumn{2}{c}{( $\mu\text{g L}^{-1}$ )} & \\multicolumn{2}{c}{( $\mu\text{M O}_2 \text{ Hr}^{-1}$ )} \\",
  "Lake & 2011 & 2012 & 2011 & 2012 \\")
eco.tab <- xtable(eco)
align(eco.tab) <- c("c ", "r ", "r ", "r ", "r ")
print(eco.tab, add.to.row = addtorow, include.colnames = FALSE,
  type= "latex", file="../tables/table2.tex",
  hline.after = c(-1, -1, 0, nrow(eco.tab)))
print(eco.tab, add.to.row = addtorow, include.colnames = FALSE,
  comment = FALSE, hline.after = c(-1, -1, 0, nrow(eco.tab)))

```

Lake	Chl <i>a</i> ($\mu\text{g L}^{-1}$)		Resp. ($\mu\text{M O}_2 \text{ Hr}^{-1}$)	
	2011	2012	2011	2012
Ann	1.31	1.25	1.96	1.26
Canyon	3.70	1.63	1.78	1.32
Howe	0.75	1.85	1.48	0.97
Ives	2.03	1.39	1.42	0.80
Lily	5.77	3.55	2.06	0.94
Mountain	1.80	2.14	1.91	1.42
Pony	24.58	16.35	3.05	1.69
Rush	0.65	1.23	1.75	1.22
SecondPine	2.13	3.76	1.46	1.17
UpperPine	2.14	8.55	1.73	1.26

```

div.2011 <- bac.div[bac.div$Year == "2011", ]
div.2012 <- bac.div[bac.div$Year == "2012", ]
test <- t.test(div.2011$S.obs, div.2012$S.obs, paired = T)

div.D <- bac.div[bac.div$Molecule == "DNA", ]
div.R <- bac.div[bac.div$Molecule == "RNA", ]
test <- t.test(div.D$S.obs, div.R$S.obs, paired = T)

```

Calculate and Visualize Beta Diversity

```

beta.w <- function(site1 = "", site2 = ""){
  site1 = subset(site1, select = site1 > 0)      # Removes absences
  site2 = subset(site2, select = site2 > 0)      # Removes absences
  gamma = union(colnames(site1), colnames(site2)) # Gamma species pool
  s      = length(gamma)                        # Gamma richness
}

```



```

a.bar = mean(c(specnumber(site1), specnumber(site2))) # Mean sample richness
b.w   = round(s/a.bar - 1, 3)
return(b.w)
}

# Calculate Bray-Curtis
hmf.db <- vegdist(OTUsREL, method = "bray")

# Import UniFrac Distances
hmf.uni.in <- read.table("../fasttree/HMWF.bac.0.03.gg.tree1.weighted.phylip.dist", skip=1, row.names = )
hmf.uni <- as.dist(hmf.uni.in)

require(phyloseq)

```

```
## Loading required package: phyloseq
```

```
## Warning: replacing previous import by 'ggplot2::Position' when loading
## 'phyloseq'
```

```
## Warning: replacing previous import by 'scales::alpha' when loading
## 'phyloseq'
```

```

OTU.tab <- otu_table(OTUs, taxa_are_rows = F)
OTU.tab.l <- otu_table(OTUsREL, taxa_are_rows = F)
PHY.tree <- phy_tree(hmf.tree)
phylo.seq <- phyloseq(OTU.tab, PHY.tree)
phylo.seq.l <- phyloseq(OTU.tab.l, PHY.tree)
uni.frac.u <- UniFrac(phylo.seq, weighted = FALSE, normalized = TRUE)

```

```

## Warning in UniFrac(phylo.seq, weighted = FALSE, normalized = TRUE):
## Randomly assigning root as -- Otu002161 -- in the phylogenetic tree in the
## data you provided.

```

```
uni.frac.w <- UniFrac(phylo.seq, weighted = TRUE, normalized = TRUE)
```

```

## Warning in UniFrac(phylo.seq, weighted = TRUE, normalized = TRUE): Randomly
## assigning root as -- Otu012706 -- in the phylogenetic tree in the data you
## provided.

```

```
uni.frac.wl <- UniFrac(phylo.seq.l, weighted = TRUE, normalized = TRUE)
```

```

## Warning in UniFrac(phylo.seq.l, weighted = TRUE, normalized = TRUE):
## Randomly assigning root as -- Otu006404 -- in the phylogenetic tree in the
## data you provided.

```

Principal Coordinates Analysis: Bray Curtis

```

par(opar)
hmf.pcoa <- cmdscale(hmf.db, eig = TRUE, k = 3)
explainvar1 <- round(hmf.pcoa$eig[1] / sum(hmf.pcoa$eig), 3) * 100
explainvar2 <- round(hmf.pcoa$eig[2] / sum(hmf.pcoa$eig), 3) * 100
explainvar3 <- round(hmf.pcoa$eig[3] / sum(hmf.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

```

Principal Coordinates Analysis: UniFrac

```

par(opar)
hmf.pcoa.b <- cmdscale(uni.frac.w, eig = TRUE, k = 3)
explainvar1.b <- round(hmf.pcoa.b$eig[1] / sum(hmf.pcoa.b$eig), 3) * 100
explainvar2.b <- round(hmf.pcoa.b$eig[2] / sum(hmf.pcoa.b$eig), 3) * 100
explainvar3.b <- round(hmf.pcoa.b$eig[3] / sum(hmf.pcoa.b$eig), 3) * 100
sum.eig.b <- sum(explainvar1.b, explainvar2.b, explainvar3.b)

```

Eigenvalue Analysis Plots

```

png(filename="../figures/FigureS3.png",
     width = 1600, height = 1100, res = 96*2)
# Define Plot Parameters
layout(as.matrix(cbind(1,2)))
par(mar = c(1, 1.5, 3, 1.5) + 0.1, oma = c(5, 5, 0.5, 0.5))

# Bray Curtis Analysis
# Plot Eigenvalues
plot(hmf.pcoa$eig, main = "Bray Curtis",
     #xlab = "PCoA Axis", ylab = "Eigenvalue",
     las = 1, cex.lab = 1.5, pch = 16)

# Add Expectation based on Kaiser-Guttman criterion and Broken Stick Model
abline(h = mean(hmf.pcoa$eig), lty = 2, lwd = 2, col = "blue")
b.stick <- bstick(42, sum(hmf.pcoa$eig))
lines(1:42, b.stick, type = "l", lty = 4, lwd = 2, col = "red")

# Add Legend
legend("topright", legend = c("Avg Eigenvalue", "Broken-Stick"),
     lty = c(2, 4), bty = "n", col = c("blue", "red"))

axis(1, lwd=2, labels = F)
axis(2, lwd=2, labels = F)
#axis(3, lwd=2, tck=-0.01, labels = F)
#axis(4, lwd=2, tck=-0.01, labels = F)
axis(1, lwd=2, tck=0.01, labels = F)
axis(2, lwd=2, tck=0.01, labels = F)
#axis(3, lwd=2, tck=0.01, labels = F)
#axis(4, lwd=2, tck=0.01, labels = F)

box(lwd=2)

```

```

# UniFrac Analysis
# Plot Eigenvalues
plot(hmwf.pcoa.b$eig, main = "UniFrac",
     #xlab = "PCoA Axis", ylab = "Eigenvalue",
     las = 1, cex.lab = 1.5, pch = 16)

# Add Expectation based on Kaiser-Guttman criterion and Broken Stick Model
abline(h = mean(hmwf.pcoa.b$eig), lty = 2, lwd = 2, col = "blue")
b.stick <- bstick(42, sum(hmwf.pcoa.b$eig))
lines(1:42, b.stick, type = "l", lty = 4, lwd = 2, col = "red")

# Add Legend
legend("topright", legend = c("Avg Eigenvalue", "Broken-Stick"),
      lty = c(2, 4), bty = "n", col = c("blue", "red"))

axis(1, lwd=2, labels = F)
axis(2, lwd=2, labels = F)
#axis(3, lwd=2, tck=-0.01, labels = F)
#axis(4, lwd=2, tck=-0.01, labels = F)
axis(1, lwd=2, tck=0.01, labels = F)
axis(2, lwd=2, tck=0.01, labels = F)
#axis(3, lwd=2, tck=0.01, labels = F)
#axis(4, lwd=2, tck=0.01, labels = F)

box(lwd=2)
mtext("PCoA Axis", side = 1, outer = T, line = 2.5, cex = 2)
mtext("Eigenvalue", side = 2, outer = T, line = 2.5, cex = 2)

dev.off() # this writes plot to folder

## pdf
## 2

graphics.off() # shuts down open devices
par(opar)

```

Figure 4: Bacterial Community Composition Ordination Figure: Bray Curtis

```

design$Lake_Mol <- paste(design$Lake, design$Molecule, sep = "_")

png(filename="../figures/Figure4.png",
     width = 1200, height = 1200, res = 96*2)
par(opar)
# Define Plot Parameters
par(mar = c(5, 5, 1, 1) + 0.1)

# Define Plot Symbols
lake.pch <- rep(NA, length(design$Molecule))
for (i in 1:length(design$Molecule)){

```

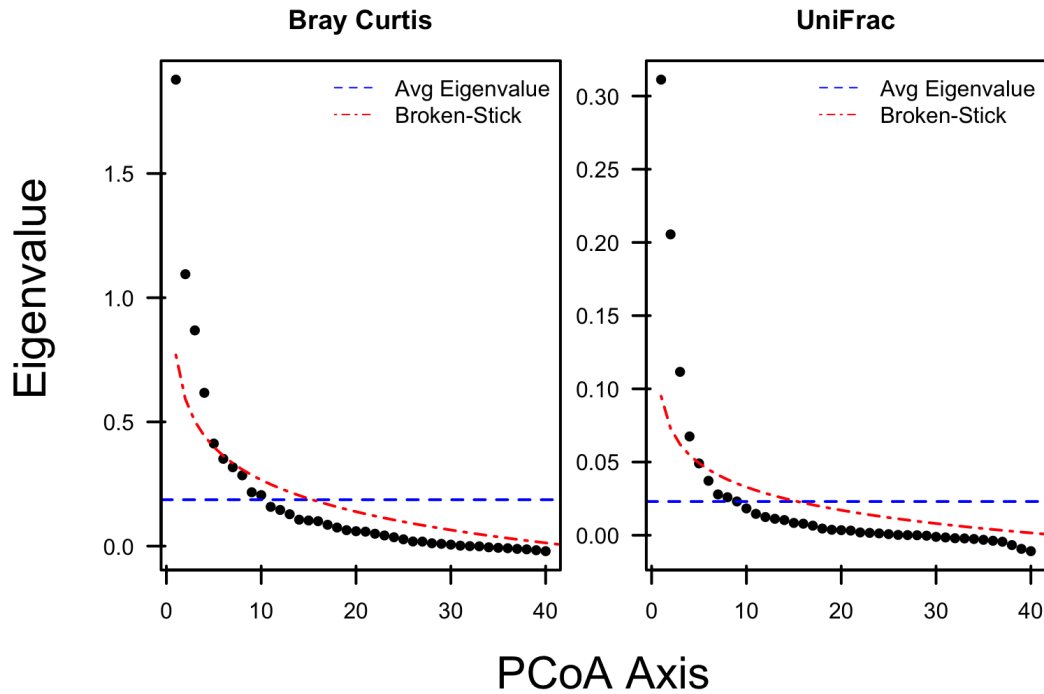


Figure 5: Eigenvalue Analysis

```
if (design$Molecule[i] == "DNA"){
  lake.pch[i] <- 16
}else{
  lake.pch[i] <- 17
}}

# Initiate Plot
plot(hmwf.pcoa$points[,1], hmwf.pcoa$points[,2],
     ylim = c(-0.31, 0.25), xlim = c(-0.3, 0.6),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     pch = lake.pch, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2,
     axes = FALSE)

# Add Axes
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
axis(side = 1, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 2, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)
```

```

# Add Points & Labels
points(hmwf.pcoa$points[,1], hmwf.pcoa$points[,2],
       pch = lake.pch, cex = 2.5, bg = "gray", col = "gray")

# ordiellipse(cbind(hmwf.pcoa$points[,1], hmwf.pcoa$points[,2]),
#             design$Lake, kind="sd", conf=0.95,
#             lwd=2, draw = "polygon", col="gray", border = "black", label=TRUE,
#             cex=1, bty = 'n')

#ordiellipse(cbind(hmwf.pcoa$points[,1], hmwf.pcoa$points[,2]),
#             design$Molecule,
#             lwd=2, draw = "polygon", col="gray", border = "black", label=TRUE,
#             cex=1, bty = 'n')

# Add Labels
# text(0.38, 0.13, "Lily")
# text(0.56, -0.11, "Pony")
# text(0.05, -0.19, "Upper Pine")
# text(-0.18, -0.29, "Second Pine")
# text(0, -0.05, "Mountain")
# text(-0.25, 0, "Ives")
# text(0.1, 0.1, "Canyon")
# text(-0.25, 0.1, "Howe")
# text(-0.2, 0.225, "Rush")
# text(-0.05, 0.2, "Ann")

dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)

```

Figure 4: Bacterial Community Composition Ordination Figure: Unifrac

```

png(filename="../figures/Figure4b.png",
     width = 1200, height = 1200, res = 96*2)
par(opar)
# Define Plot Parameters
par(mar = c(5, 5, 1, 1) + 0.1)

# Define Plot Symbols
lake.pch <- rep(NA, length(design$Molecule))
for (i in 1:length(design$Molecule)){
  if (design$Molecule[i] == "DNA"){
    lake.pch[i] <- 16
  }else{
    lake.pch[i] <- 17
  }
}

# Initiate Plot
plot(hmwf.pcoa.b$points[,1], hmwf.pcoa.b$points[,2],

```

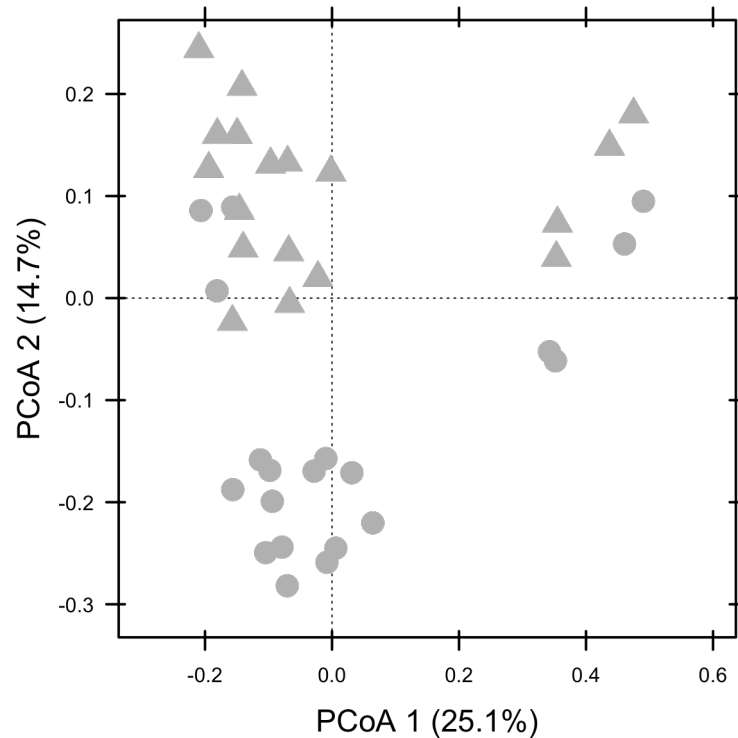


Figure 6: Lake Nutrients

```
ylim = c(-0.25, 0.25), xlim = c(-0.35, 0.25),
xlab = paste("PCoA 1 (", explainvar1.b, "%)", sep = ""),
ylab = paste("PCoA 2 (", explainvar2.b, "%)", sep = ""),
pch = lake.pch, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2,
axes = FALSE)

# Add Axes
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
axis(side = 1, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 2, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)

# Add Points & Labels
points(hmwf.pcoa.b$points[,1], hmwf.pcoa.b$points[,2],
       pch = lake.pch, cex = 2.5, bg = "gray", col = "gray")

ordiellipse(cbind(hmwf.pcoa.b$points[,1], hmwf.pcoa.b$points[,2]),
            design$Molecule, kind="sd", conf=0.95,
            lwd=2, draw = "polygon", col="gray", border = "black", label=TRUE,
            cex=1, bty = 'n')
```

```
dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)
```

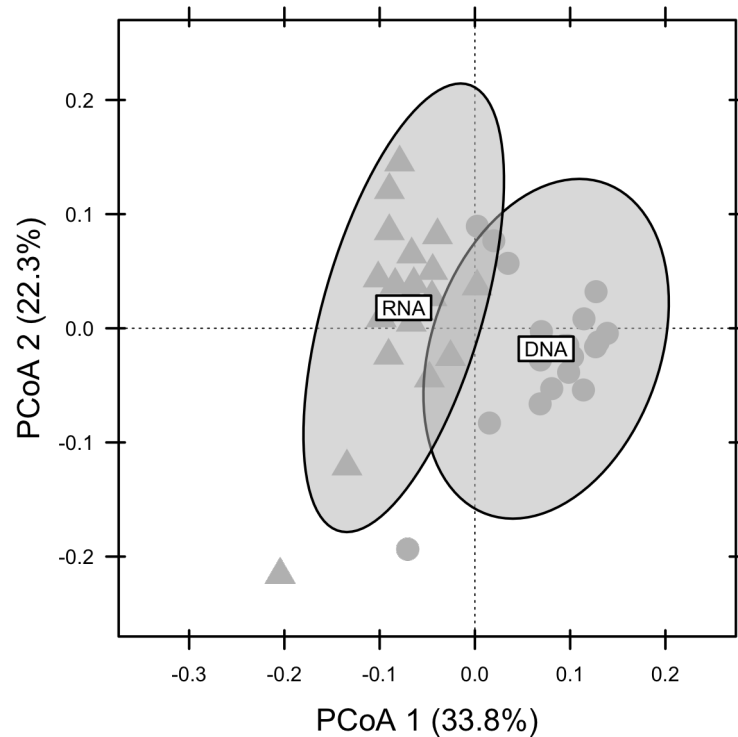


Figure 7: UniFrac Distances

PERMANOVA

```
per.bray <- adonis(OTUsREL ~ design$Lake + design$Molecule, method = "bray")
per.uni <- adonis(uni.frac.w ~ design$Lake + design$Molecule)
per.uni.u <- adonis(uni.frac.u ~ design$Lake + design$Molecule)
per.bray.l <- adonis(OTUsREL.log ~ design$Lake + design$Molecule, method = "bray")
per.bray.p <- adonis(OTUsPA ~ design$Lake + design$Molecule, method = "bray")
```

CCA Analysis

```
# Define Environmental Matrix
env.chem <- as.data.frame(scale(apply(nuts[,3:5], 2, log)))
row.names(env.chem) <- paste(nuts$sample, nuts$year, sep = "-")
env.chem <- as.matrix(env.chem[sort(row.names(env.chem)), ])

env.chem.L <- env.chem[nuts$sample != "Pony" & nuts$sample != "Lily", ]
```



```

# Define DNA Community
OTUsREL.D <- OTUsREL.log[design$Molecule == "DNA" , ]
OTUsREL.R <- OTUsREL[design$Molecule == "DNA" , ]

OTUsREL.D.L <- OTUsREL.log[design$Molecule == "DNA" &
                           design$Lake != "Pony" & design$Lake != "Lily", ]
OTUsREL.R.L <- OTUsREL.log[design$Molecule == "RNA" &
                           design$Lake != "Pony" & design$Lake != "Lily", ]

# Conduct CCA
hmf.bacD.cca <- vegan::cca(OTUsREL.D.L ~ env.chem.L, scale = T)
hmf.bacR.cca <- vegan::cca(OTUsREL.R.L ~ env.chem.L, scale = T)

# Permutation Tests
cca.ax <- anova(hmf.bacD.cca, by = "axis")
cca.ev <- anova(hmf.bacD.cca, by = "margin")
cca.fit <- envfit(hmf.bacD.cca, env.chem.L, perm = 999)
cca.R.fit <- envfit(hmf.bacR.cca, env.chem.L, perm = 999) # Only Phosphorus
cca.fit
cca.R.fit

RsquareAdj(hmf.bacD.cca)
RsquareAdj(hmf.bacR.cca)

# Calculate Explained Variation
cca.explainvar1 <- round(hmf.bacD.cca$CCA$eig[1] /
                        sum(c(hmf.bacD.cca$CCA$eig, hmf.bacD.cca$CA$eig)), 3) * 100
cca.explainvar2 <- round(hmf.bacD.cca$CCA$eig[2] /
                        sum(c(hmf.bacD.cca$CCA$eig, hmf.bacD.cca$CA$eig)), 3) * 100

# Define Plot Parameters
par(mar = c(5, 5, 4, 4) + 0.1)

# Initiate Plot
plot(scores(hmf.bacD.cca, display = "wa"), xlim = c(-3, 3), ylim = c(-4, 4),
     xlab = paste("CCA 1 (", cca.explainvar1, "%)", sep = ""),
     ylab = paste("CCA 2 (", cca.explainvar2, "%)", sep = ""),
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)

# Add Axes
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)

# Add Points & Labels
points(scores(hmf.bacD.cca, display = "wa"),
       pch = 19, cex = 2, bg = "gray", col = "gray")
#text(scores(hmf.bacD.cca, display = "wa"),
#      labels = row.names(scores(hmf.bacD.cca, display = "wa")))

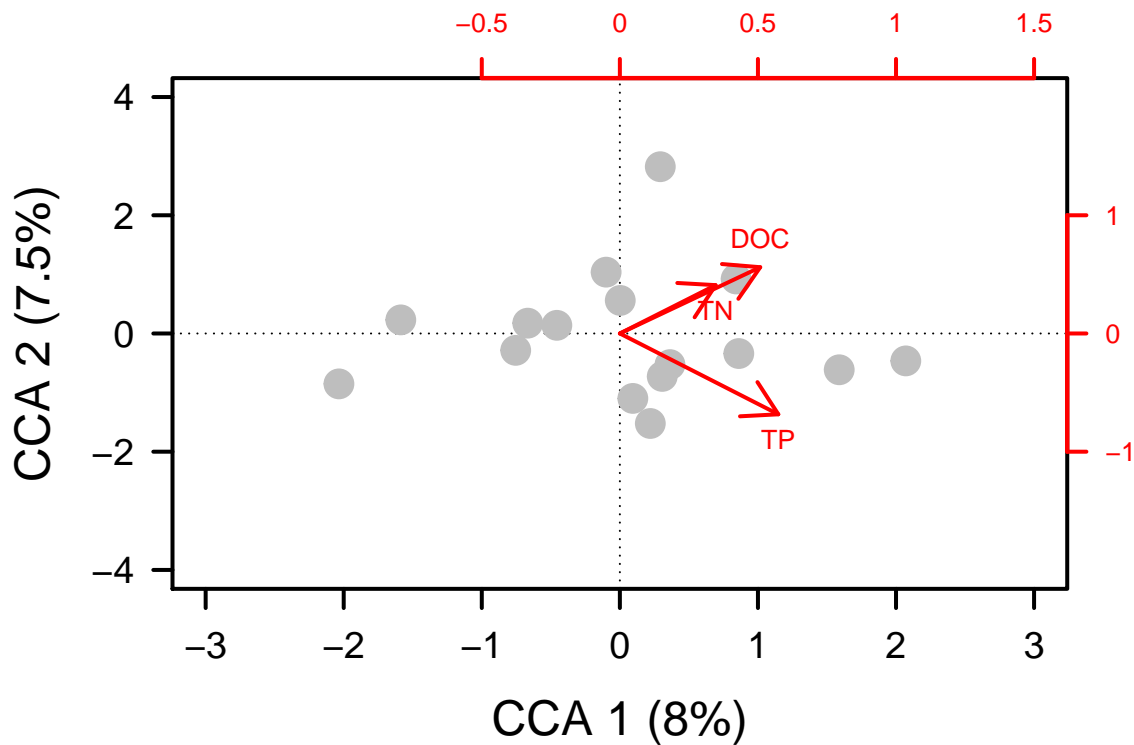
# Add Environmental Vectors
vectors <- scores(hmf.bacD.cca, display = "bp")

```

```

row.names(vectors) <- c("DOC", "TP", "TN")
arrows(0, 0, vectors[,1] * 2, vectors[, 2] * 2,
      lwd = 2, lty = 1, length = 0.2, col = "red")
text(vectors[,1] * 2, vectors[, 2] * 2, pos = c(3, 1, 1),
     labels = row.names(vectors), col = "red", cex = 0.8)
axis(side = 3, lwd.ticks=2, cex.axis= 0.8, las = 1, col = "red", lwd = 2.2,
     at = c(-0.5, 0, 0.5, 1, 1.5) * 2,
     labels = c(-0.5, 0, 0.5, 1, 1.5), col.axis = "red")
axis(side = 4, lwd.ticks=2, cex.axis = 0.8, las = 1, col = "red", lwd = 2.2,
     at = c(-1, 0, 1) * 2,
     labels = c(-1, 0, 1), col.axis = "red")

```



Statistical Analyses

What are the differences between lakes and does resource concentration explain differences

nuts

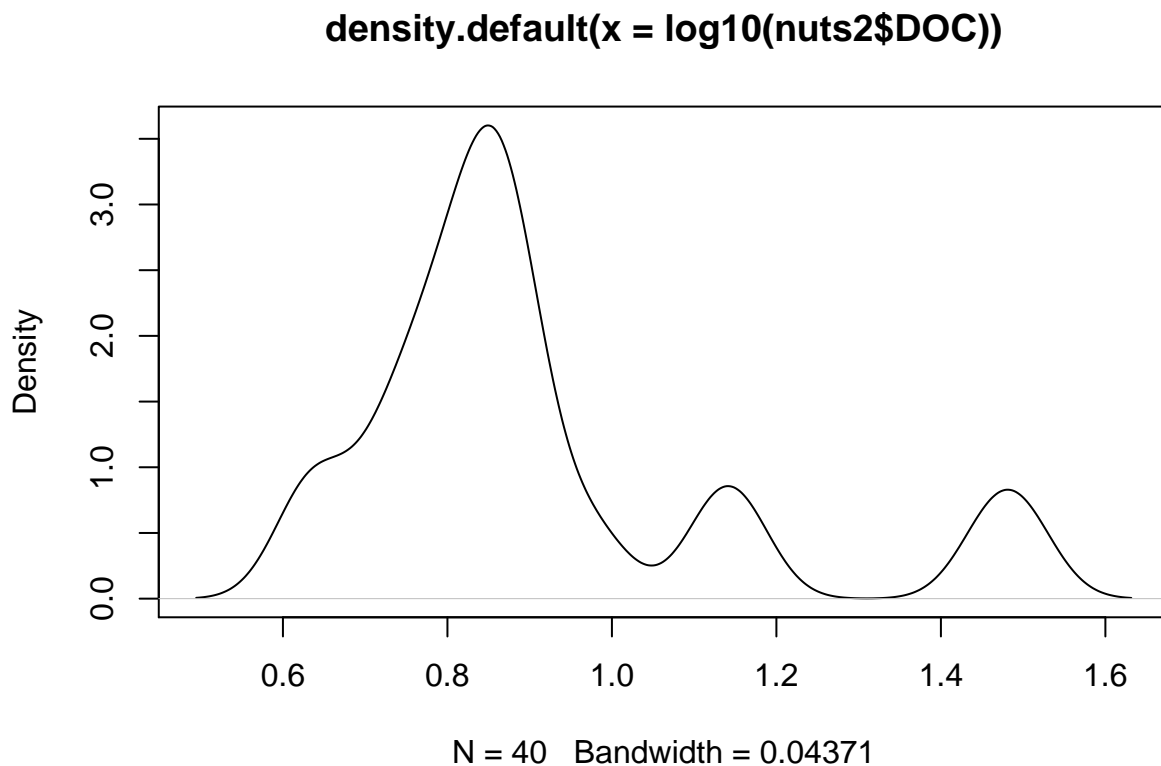
##	sample	year	DOC	TP	TN
## 1	Ann	2011	6.149285	3.977949	0.417
## 2	Canyon	2011	7.615331	2.452633	0.438
## 3	Howe	2011	6.875177	1.859455	0.564
## 4	Ives	2011	9.537734	1.351016	0.419
## 5	Lily	2011	13.358296	4.740607	0.825
## 6	Mountain	2011	5.411983	2.113674	0.343
## 8	Pony	2011	31.648222	1.520496	1.560
## 9	Rush	2011	4.437947	3.554250	0.304
## 10	SecondPine	2011	7.197479	10.757130	0.434

```
## 11 UpperPine 2011 7.990399 2.961072 0.590
## 12 Ann 2012 5.973806 7.267117 0.427
## 13 Canyon 2012 7.233826 2.638631 0.377
## 14 Howe 2012 7.037040 5.210013 0.569
## 15 Ives 2012 6.913681 9.152797 0.377
## 16 Lily 2012 14.351915 11.552753 0.926
## 17 Mountain 2012 5.270368 4.867162 0.339
## 18 Pony 2012 28.986069 49.952043 1.860
## 19 Rush 2012 4.223288 3.838609 0.410
## 20 SecondPine 2012 6.261643 12.924156 0.444
## 21 UpperPine 2012 7.840340 11.209902 0.567
```

```
nuts2 <- data.frame(nuts[rep(seq_len(nrow(nuts)), each=2),])
nuts2$molecule <- rep(c("DNA", "RNA"), 20)
nuts2 <- nuts2[order(nuts2$sample, nuts2$year, nuts2$molecule), ]
as.character(nuts2$sample) == as.character(design$Lake)
```

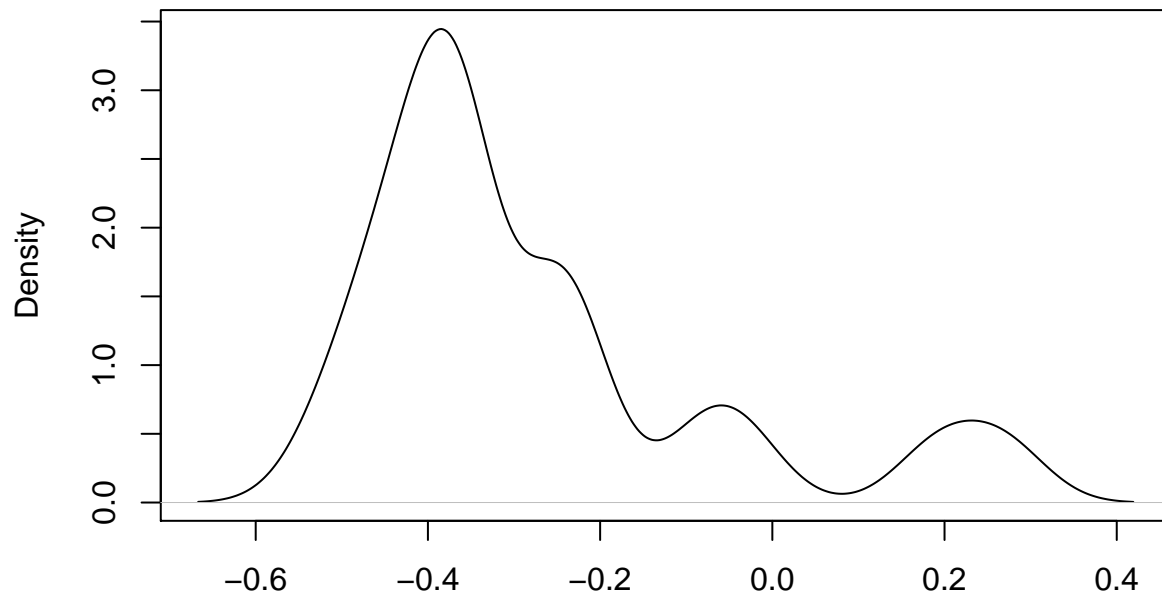
```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [15] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [29] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
plot(density(log10(nuts2$DOC)))
```



```
plot(density(log10(nuts2$TN)))
```

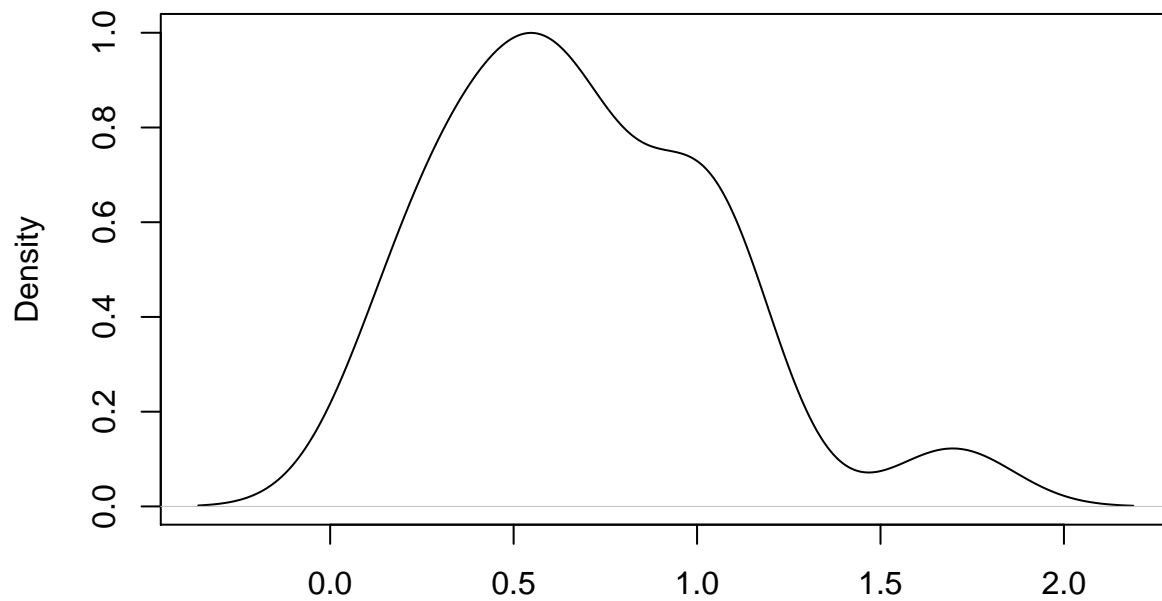
density.default(x = log10(nuts2\$TN))



N = 40 Bandwidth = 0.0499

```
plot(density(log10(nuts2$TP)))
```

density.default(x = log10(nuts2\$TP))



N = 40 Bandwidth = 0.1635

```
# Nutrient Z-Transformation
```

```
nuts2$DOC.z <- scale(log(nuts2$DOC))
```

```
nuts2$TP.z <- scale(log(nuts2$TP))
```

```
nuts2$TN.z <- scale(log1p(nuts2$TN))
```

```
beta.dis <- betadisper(vegdist(OTUsREL.log, "bray"), design$Lake)
```

```
permutest(beta.dis)
```

```
##
```

```
## Permutation test for homogeneity of multivariate dispersions
```

```
## Permutation: free
```

```
## Number of permutations: 999
```

```
##
```

```
## Response: Distances
```

```
##           Df  Sum Sq   Mean Sq      F N.Perm Pr(>F)
```

```
## Groups      9 0.018933 0.00210367 2.2111   999  0.053 .
```

```
## Residuals  30 0.028542 0.00095141
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
adonis(OTUsREL.log ~ design$Lake + design$Molecule, method = "bray", permutations = 999)
```

```
##
```

```
## Call:
```

```
## adonis(formula = OTUsREL.log ~ design$Lake + design$Molecule,      permutations = 999, method = "bray",
```

```
##
```

```
## Permutation: free
```

```
## Number of permutations: 999
```

```
##
```

```
## Terms added sequentially (first to last)
```

```
##
```

```
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
```

```
## design$Lake      9      5.0100 0.55666  5.2885 0.60066  0.001 ***
```

```
## design$Molecule  1      0.2783 0.27828  2.6438 0.03336  0.008 **
```

```
## Residuals       29      3.0525 0.10526      0.36598
```

```
## Total           39      8.3408      1.00000
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
adonis(OTUsREL ~ design$Lake + design$Molecule, method = "bray", permutations = 999)
```

```
##
```

```
## Call:
```

```
## adonis(formula = OTUsREL ~ design$Lake + design$Molecule, permutations = 999,      method = "bray")
```

```
##
```

```
## Permutation: free
```

```
## Number of permutations: 999
```

```
##
```

```
## Terms added sequentially (first to last)
```

```
##
```

```
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
```

```
## design$Lake      9      4.7954 0.53282  8.2834 0.64192  0.001 ***
```

```
## design$Molecule 1      0.8096 0.80965 12.5870 0.10838 0.001 ***
## Residuals        29      1.8654 0.06432          0.24970
## Total            39      7.4705          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lake.dbrda <- capscale(OTUsREL.log ~ design$Lake + design$Molecule, distance = "bray", add = T)
anova(lake.dbrda)
```

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = OTUsREL.log ~ design$Lake + design$Molecule, distance = "bray", add = T)
##           Df SumOfSqs      F Pr(>F)
## Model      10   5.2883 5.024 0.001 ***
## Residual   29   3.0525
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
RsquareAdj(lake.dbrda)
```

```
## $r.squared
## [1] 0.6340234
##
## $adj.r.squared
## [1] 0.5078246
```

```
coef(lake.dbrda)
```

```
##
##              CAP1      CAP2      CAP3      CAP4
## design$LakeCanyon    0.058983570 -0.026710999 -0.065150959 -0.29586081
## design$LakeHowe     -0.031908857 -0.031550606  0.009878469  0.19288298
## design$LakeIves      -0.047583959 -0.164510954 -0.039450945  0.24650289
## design$LakeLily       0.345756878 -0.067015736 -0.402022680  0.18682062
## design$LakeMountain -0.027017494 -0.241581598 -0.046129935  0.23325016
## design$LakePony       0.404237935 -0.257184545  0.268354258  0.10475110
## design$LakeRush       -0.031924314  0.008739798  0.040502029  0.18432042
## design$LakeSecondPine -0.031147085 -0.433400995 -0.132827379  0.04765915
## design$LakeUpperPine  0.014151701 -0.409085120 -0.098043095 -0.02758601
## design$MoleculeRNA  -0.005492991  0.007825409  0.020527984  0.03676786
##
##              CAP5      CAP6      CAP7      CAP8
## design$LakeCanyon    -0.15519305  0.24856586 -0.14379147 -0.07957525
## design$LakeHowe      -0.35132848 -0.11980294  0.08984451  0.02500773
## design$LakeIves      -0.38537092  0.36677724 -0.26087585 -0.04551835
## design$LakeLily       -0.12608418  0.06225551 -0.12486398 -0.10701185
## design$LakeMountain   0.15232442  0.30352653  0.07836315 -0.08455155
## design$LakePony       -0.15318445  0.10007661 -0.09805908 -0.10970120
## design$LakeRush       -0.02724796 -0.02707558 -0.33127111 -0.40842306
## design$LakeSecondPine -0.12793939 -0.03308583 -0.08503625 -0.14414891
## design$LakeUpperPine -0.17661791 -0.02892682 -0.21459352 -0.10880885
## design$MoleculeRNA   0.10104610 -0.05194362 -0.17629309  0.22257379
```

```
##              CAP9      CAP10
## design$LakeCanyon -0.53829958 -0.037211310
## design$LakeHowe -0.55855156  0.047151312
## design$LakeIves -0.23355540 -0.025284826
## design$LakeLily -0.36391418  0.013705496
## design$LakeMountain -0.49675891  0.094786786
## design$LakePony -0.36301286 -0.023493110
## design$LakeRush -0.43042229  0.001093753
## design$LakeSecondPine -0.36784014 -0.332414397
## design$LakeUpperPine -0.32891710  0.352092048
## design$MoleculeRNA -0.06047976 -0.030833694
```

```
chem.dbrda <- capscale(OTUsREL.log ~ nuts2$DOC.z + nuts2$TP.z + nuts2$TN.z,
                      add = T, distance = "bray")
anova(chem.dbrda)
```

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = OTUsREL.log ~ nuts2$DOC.z + nuts2$TP.z + nuts2$TN.z, distance = "bray", ad
##           Df SumOfSqs      F Pr(>F)
## Model      3   2.4522 4.9971 0.001 ***
## Residual  36   5.8886
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
RsquareAdj(chem.dbrda)
```

```
## $r.squared
## [1] 0.2939973
##
## $adj.r.squared
## [1] 0.2351637
```

```
coef(chem.dbrda)
```

```
##              CAP1      CAP2      CAP3
## nuts2$DOC.z 0.080766091 -0.10082615 -0.50472612
## nuts2$TP.z  0.002121103  0.15551144 -0.09170651
## nuts2$TN.z  0.080947760  0.05308542  0.53194566
```

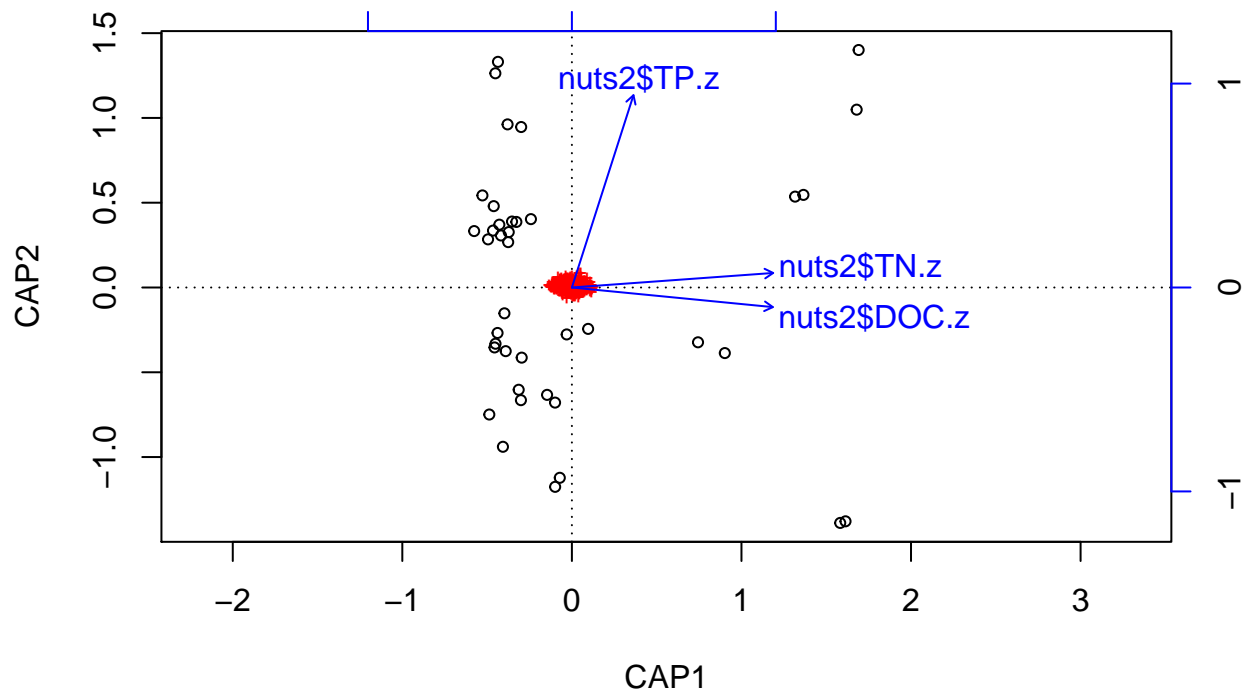
```
anova.cca(chem.dbrda, step=1000)
```

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = OTUsREL.log ~ nuts2$DOC.z + nuts2$TP.z + nuts2$TN.z, distance = "bray", ad
##           Df SumOfSqs      F Pr(>F)
## Model      3   2.4522 4.9971 0.001 ***
```



```
## Residual 36    5.8886
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(chem.dbrda)
```



```
lmod <- as.mlm(chem.dbrda)
# influence.measures(lmod)
lmod
```

```
##
## Call:
## lm(formula = x$CCA$wa ~ . - 1, data = as.data.frame(X))
##
## Coefficients:
##          CAP1          CAP2          CAP3
## `nuts2$DOC.z`  0.080766 -0.100826 -0.504726
## `nuts2$TP.z`   0.002121  0.155511 -0.091707
## `nuts2$TN.z`   0.080948  0.053085  0.531946
```

```
summary(lmod)
```

```
## Response CAP1 :
##
## Call:
## lm(formula = CAP1 ~ (`nuts2$DOC.z` + `nuts2$TP.z` + `nuts2$TN.z`) -
##    1, data = as.data.frame(X))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```

## -0.09554 -0.03390 -0.00413 0.03021 0.15497
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## `nuts2$DOC.z` 0.080766 0.029954 2.696 0.0105 *
## `nuts2$TP.z` 0.002121 0.010381 0.204 0.8392
## `nuts2$TN.z` 0.080948 0.031086 2.604 0.0132 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05749 on 37 degrees of freedom
## Multiple R-squared: 0.891, Adjusted R-squared: 0.882
## F-statistic: 100.8 on 3 and 37 DF, p-value: < 2.2e-16
##
##
## Response CAP2 :
##
## Call:
## lm(formula = CAP2 ~ (`nuts2$DOC.z` + `nuts2$TP.z` + `nuts2$TN.z`) -
## 1, data = as.data.frame(X))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.14468 -0.03998 0.01264 0.04889 0.11198
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## `nuts2$DOC.z` -0.10083 0.03559 -2.833 0.00743 **
## `nuts2$TP.z` 0.15551 0.01234 12.607 5.82e-15 ***
## `nuts2$TN.z` 0.05309 0.03694 1.437 0.15909
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06832 on 37 degrees of freedom
## Multiple R-squared: 0.8527, Adjusted R-squared: 0.8408
## F-statistic: 71.42 on 3 and 37 DF, p-value: 1.87e-15
##
##
## Response CAP3 :
##
## Call:
## lm(formula = CAP3 ~ (`nuts2$DOC.z` + `nuts2$TP.z` + `nuts2$TN.z`) -
## 1, data = as.data.frame(X))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.19555 -0.05668 0.02076 0.06570 0.13724
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## `nuts2$DOC.z` -0.50473 0.04717 -10.70 7.03e-13 ***
## `nuts2$TP.z` -0.09171 0.01635 -5.61 2.12e-06 ***
## `nuts2$TN.z` 0.53195 0.04895 10.87 4.54e-13 ***
## ---

```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09054 on 37 degrees of freedom
## Multiple R-squared:  0.7673, Adjusted R-squared:  0.7484
## F-statistic: 40.66 on 3 and 37 DF,  p-value: 8.453e-12
```

Species Distributions and Generalism

```
lake.yr <- paste(design$Lake[design$Molecule == "DNA"],
                design$Year[design$Molecule == "DNA"], sep = "")

total <- OTUs[design$Molecule == "DNA", ]
row.names(total) <- lake.yr
totalPA <- (total > 0) * 1

active.rna <- OTUs[design$Molecule == "RNA", ]
row.names(active.rna) <- lake.yr
activePA <- (active.rna > 0) * 1
active <- total * (activePA)
row.names(active) <- lake.yr

activePA.2 <- (active.rna > (total * 0.25)) * 1
active.2 <- total * (activePA.2)
row.names(active.2) <- lake.yr

per <- c(0.001, 0.005, 0.01, 0.02, 0.03, 0.04, 0.05, 0.075, 0.10)
per.act <- matrix(NA, dim(total)[1], length(per))
per.actT <- matrix(NA, dim(total)[1], length(per))
colnames(per.act) <- per
colnames(per.actT) <- per

for (i in 1:length(per)){
  activePA.temp <- (active.rna > (total * per[i])) * 1
  active.temp <- total * activePA.temp
  per.act[,i] <- rowSums(active.temp) / rowSums(total)
  per.actT[,i] <- rowSums(activePA.temp) / rowSums(totalPA)
}

mean.per.act <- colMeans(per.act)
se.per.act <- apply(per.act, 2, se)

mean.per.actT <- colMeans(per.actT)
se.per.actT <- apply(per.actT, 2, se)

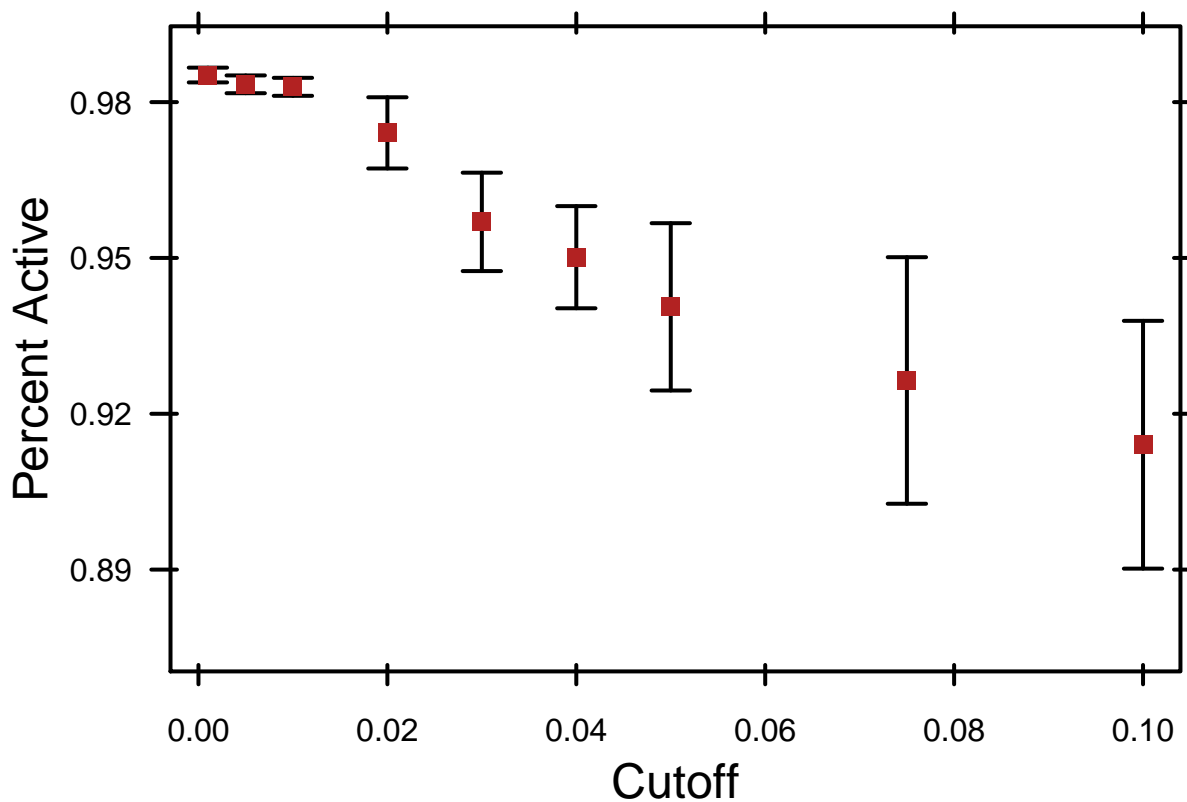
par(mar = c(4.5,5,1,1) + 0.1)
plot(mean.per.act ~ per, las = 1, type = "n",
     ylim = c(0.875, 0.99),
     xaxt = "n", yaxt = "n", xlab = "", ylab = "")

arrows(x0 = per, y0 = mean.per.act, y1 = mean.per.act + se.per.act, angle= 90, length = 0.1, lwd = 2)
arrows(x0 = per, y0 = mean.per.act, y1 = mean.per.act - se.per.act, angle= 90, length = 0.1, lwd = 2)
points(per, mean.per.act, pch = 15, col = "firebrick", cex = 1.25)
```

```

axis(side=1, lwd.ticks = 2, tck=-0.02, labels = T, cex.axis = 1)
axis(side=1, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1)
axis(side=2, lwd.ticks = 2, labels = T, cex.axis = 1, las = 1,
      at = c(0.89, 0.92, 0.95, 0.98))
axis(side=2, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(0.89, 0.92, 0.95, 0.98))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1)
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1)
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(0.89, 0.92, 0.95, 0.98))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(0.89, 0.92, 0.95, 0.98))
mtext(side = 2, "Percent Active", line = 3, cex = 1.5)
mtext(side = 1, "Cutoff", line = 2.5, cex = 1.5)
box(lwd = 2)

```



```

inactive <- total * (1 - activePA)
inactivePA <- (inactive > 0) * 1

gens <- data.frame(matrix(NA, 21, 3))
colnames(gens) <- c("sites", "taxaA", "taxaT")
gens$sites <- c(1:21)

for (i in 1:21){
  gens$taxaA[i] <- sum(colSums(activePA) == i)
  gens$taxaT[i] <- sum(colSums(totalPA) == i)
}

# Define Plot Parameters

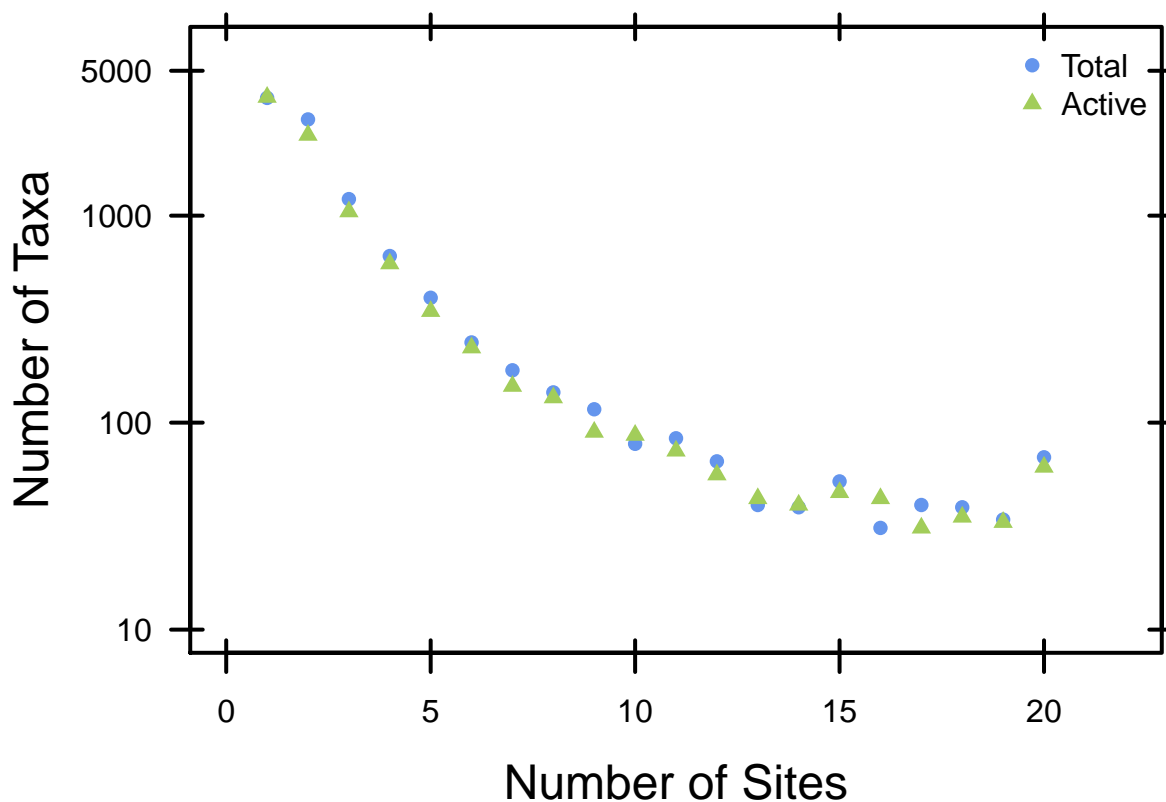
```

```

par(mar = c(5, 6, 1, 1) + 0.1)
plot(log10(gens$taxaT) ~ gens$sites,
     yaxt = "n", xaxt = "n", ylab = "", xlab = "", las = 1,
     pch = 16, col = "cornflowerblue", xlim = c(0, 22), ylim = c(1, 3.8))
points(log10(gens$taxaA) ~ gens$sites, pch = 17, col = "darkolivegreen3")

mtext(side = 1, "Number of Sites", line = 3, cex = 1.5)
mtext(side = 2, "Number of Taxa", line = 3.5, cex = 1.5)
axis(side = 1, lwd = 2, labels = T)
axis(side = 2, lwd = 2, at = c(1, 2, 3, 3.7), labels = c(10, 100, 1000, 5000), las = 1)
axis(side = 3, lwd = 2, tck = -0.02, labels = F)
axis(side = 4, lwd = 2, tck = -0.02, labels = F, at = c(1, 2, 3, 3.7))
axis(side = 1, lwd = 2, tck = 0.02, labels = F)
axis(side = 2, lwd = 2, tck = 0.02, labels = F, at = c(1, 2, 3, 3.7))
axis(side = 3, lwd = 2, tck = 0.02, labels = F)
axis(side = 4, lwd = 2, tck = 0.02, labels = F, at = c(1, 2, 3, 3.7))
legend("topright", pch = c(16, 17), c("Total", "Active"), bty = "n",
     col = c("cornflowerblue", "darkolivegreen3"))
box(lwd = 2)

```



```

# Inactive Taxa
inactivePA <- totalPA - activePA
inactive <- total * inactivePA

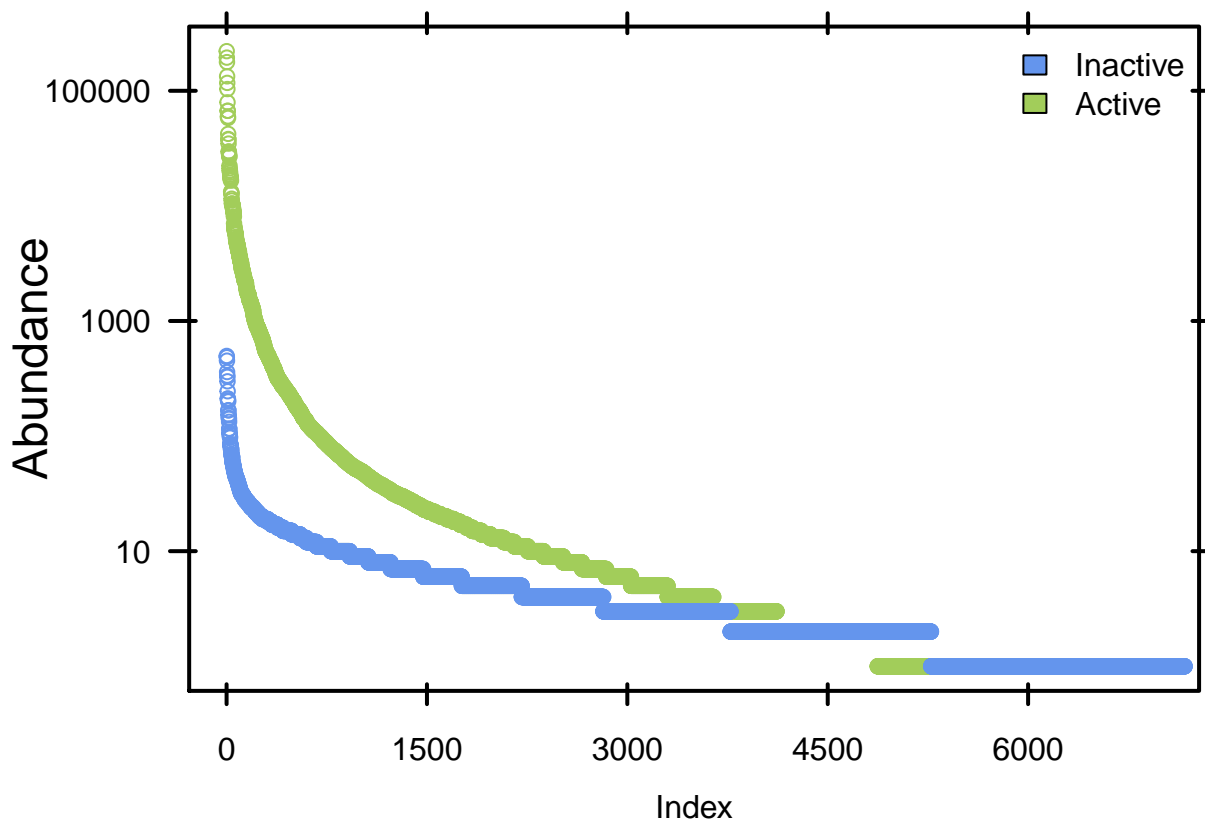
# Species Abundance Distributions for Active and Inactive Taxa
par(mar = c(4, 5, 1, 1) + 0.1)
plot(sort(log10(colSums(active))), decreasing = T, col = "darkolivegreen3",
     las = 1, yaxt="n", xlab = "", yaxt="n", ylab = "", xlim = c(0, 7000))

```

```

points(sort(log10(colSums(inactive)), decreasing = T), col = "cornflowerblue")
axis(side=1, lwd.ticks = 2, tck=-0.02, labels = T, cex.axis = 1, at = c(0, 1500, 3000, 4500, 6000))
axis(side=1, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(0, 1500, 3000, 4500, 6000))
axis(side=2, lwd.ticks = 2, labels = c("10", "1000", "100000"), cex.axis = 1, las = 1,
     at = c(1, 3, 5))
axis(side=2, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1, 3, 5))
axis(side=3, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(0, 1500, 3000, 4500, 6000))
axis(side=3, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(0, 1500, 3000, 4500, 6000))
axis(side=4, lwd.ticks = 2, tck=-0.02, labels = F, cex.axis = 1, at = c(1, 3, 5))
axis(side=4, lwd.ticks = 2, tck=0.01, labels = F, cex.axis = 1, at = c(1, 3, 5))
mtext(side = 2, "Abundance", line = 3.5, cex = 1.5)
mtext(side = 1, "Index", line = 2.5, cex = 1)
legend("topright", c("Inactive", "Active"), fill = c("cornflowerblue", "darkolivegreen3"), bty = "n")
box(lwd = 2)

```



```

pro.act <- rowSums(active)/rowSums(total)

rowSums(inactivePA)/rowSums(totalPA)

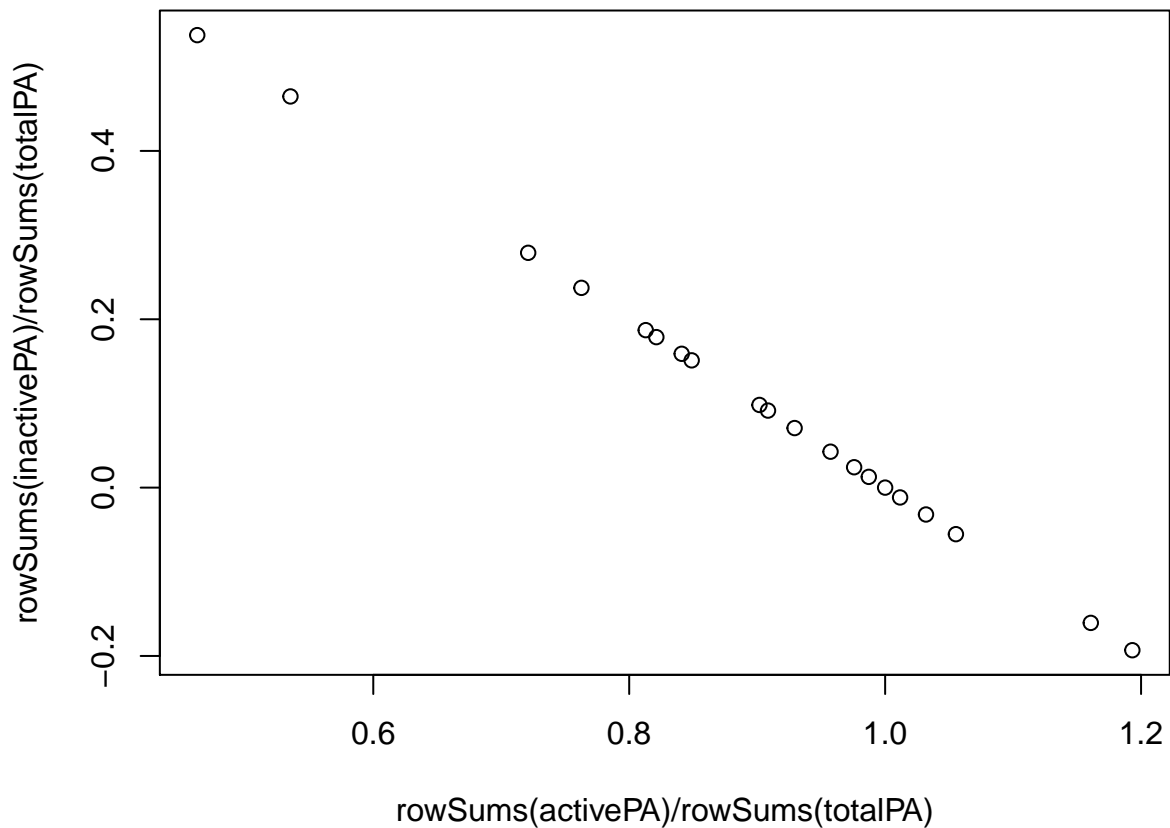
```

##	Ann2011	Ann2012	Canyon2011	Canyon2012	Howe2011
##	0.17879162	0.09821429	-0.05531609	0.09153318	0.53757225
##	Howe2012	Ives2011	Ives2012	Lily2011	Lily2012
##	0.18707811	0.27895753	0.01277584	0.46472564	-0.03192796
##	Mountain2011	Mountain2012	Pony2011	Pony2012	Rush2011
##	0.04266467	0.23732904	0.15118062	-0.16071429	0.02421925
##	Rush2012	SecondPine2011	SecondPine2012	UpperPine2011	UpperPine2012
##	0.15896885	-0.19319728	0.00000000	-0.01169916	0.07073955

```
rowSums(activePA)/rowSums(totalPA)
```

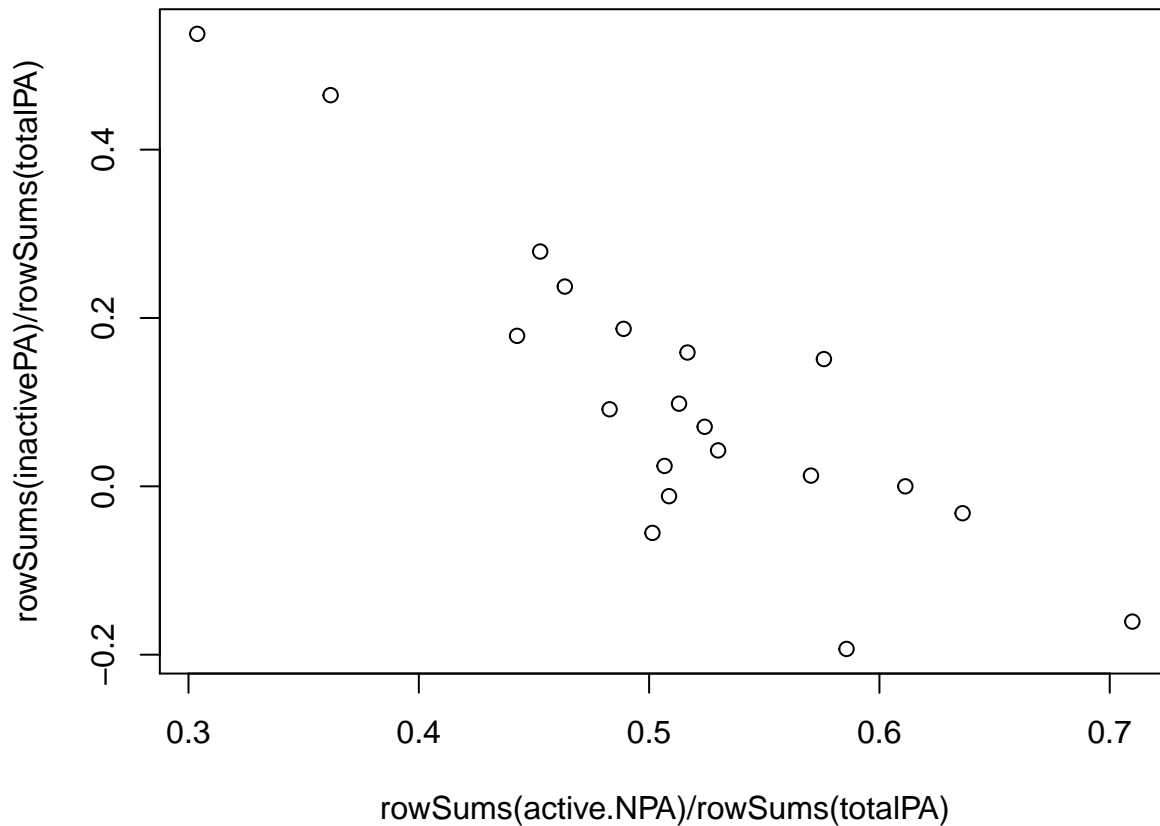
```
##      Ann2011      Ann2012      Canyon2011      Canyon2012      Howe2011
##      0.8212084      0.9017857      1.0553161      0.9084668      0.4624277
##      Howe2012      Ives2011      Ives2012      Lily2011      Lily2012
##      0.8129219      0.7210425      0.9872242      0.5352744      1.0319280
##      Mountain2011      Mountain2012      Pony2011      Pony2012      Rush2011
##      0.9573353      0.7626710      0.8488194      1.1607143      0.9757808
##      Rush2012      SecondPine2011      SecondPine2012      UpperPine2011      UpperPine2012
##      0.8410311      1.1931973      1.0000000      1.0116992      0.9292605
```

```
plot(rowSums(activePA)/rowSums(totalPA), rowSums(inactivePA)/rowSums(totalPA))
```



```
inactive <- total * inactivePA
active.N <- total * (1-inactivePA)
active.NPA <- (active.N > 0 ) * 1
```

```
plot(rowSums(active.NPA)/rowSums(totalPA), rowSums(inactivePA)/rowSums(totalPA))
```



Phosphorus Contributes to Activity

```
png(filename="../figures/Figure6.png",
      width = 1200, height = 1000, res = 96*2)
par(opar)
par(mar=c(5, 5, 1, 1) + 0.1)
plot(rowSums(active.NPA)/rowSums(totalIPA) ~ log10(nuts$TP[c(order(nuts$sample))]),
      xlab = expression(paste("Total Phosphorus (", mu , "g L"-1, ")")),
      ylab = "Proportion of Active Taxa",
      las = 1, cex.lab = 1.5, xlim = c(0, 1.8), ylim = c(0.25, 0.75), xaxt = "n",
      pch = 15, col = "darkorchid4", cex = 1.5)
axis(side = 1, lwd = 2, at = c(0, 0.7, 1.7), labels = c(0, 5, 50))
axis(side = 2, lwd = 2, labels = F)
axis(side = 3, lwd = 2, tck = 0.02, labels = F, at = c(0, 0.7, 1.7))
axis(side = 4, lwd = 2, tck = 0.02, labels = F)
axis(side = 1, lwd = 2, tck = -0.02, labels = F, at = c(0, 0.7, 1.7))
axis(side = 2, lwd = 2, tck = -0.02, labels = F)
axis(side = 3, lwd = 2, tck = -0.02, labels = F, at = c(0, 0.7, 1.7))
axis(side = 4, lwd = 2, tck = -0.02, labels = F)
box(lwd = 2)
phos <- lm(rowSums(active.NPA)/rowSums(totalIPA) ~ log10(nuts$TP[c(order(nuts$sample))]))
nitro <- lm(rowSums(active.NPA)/rowSums(totalIPA) ~ log10(nuts$TN[c(order(nuts$sample))]))
carb <- lm(rowSums(active.NPA)/rowSums(totalIPA) ~ log10(nuts$DOC[c(order(nuts$sample))]))
mod1 <- summary(phos)
abline(phos, lty = 2, lwd = 4, col = "darkred")
```



```

Rsq <- round(mod1$r.squared, 2)
Pv <- round(mod1$coefficients[2,4], 3)
text(1.5, 0.35, bquote(italic(R)^2 == .(format(Rsq, digits = 3))))
text(1.5, 0.3, bquote(italic(p) == .(format(Pv, digits = 3))))
dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)

```

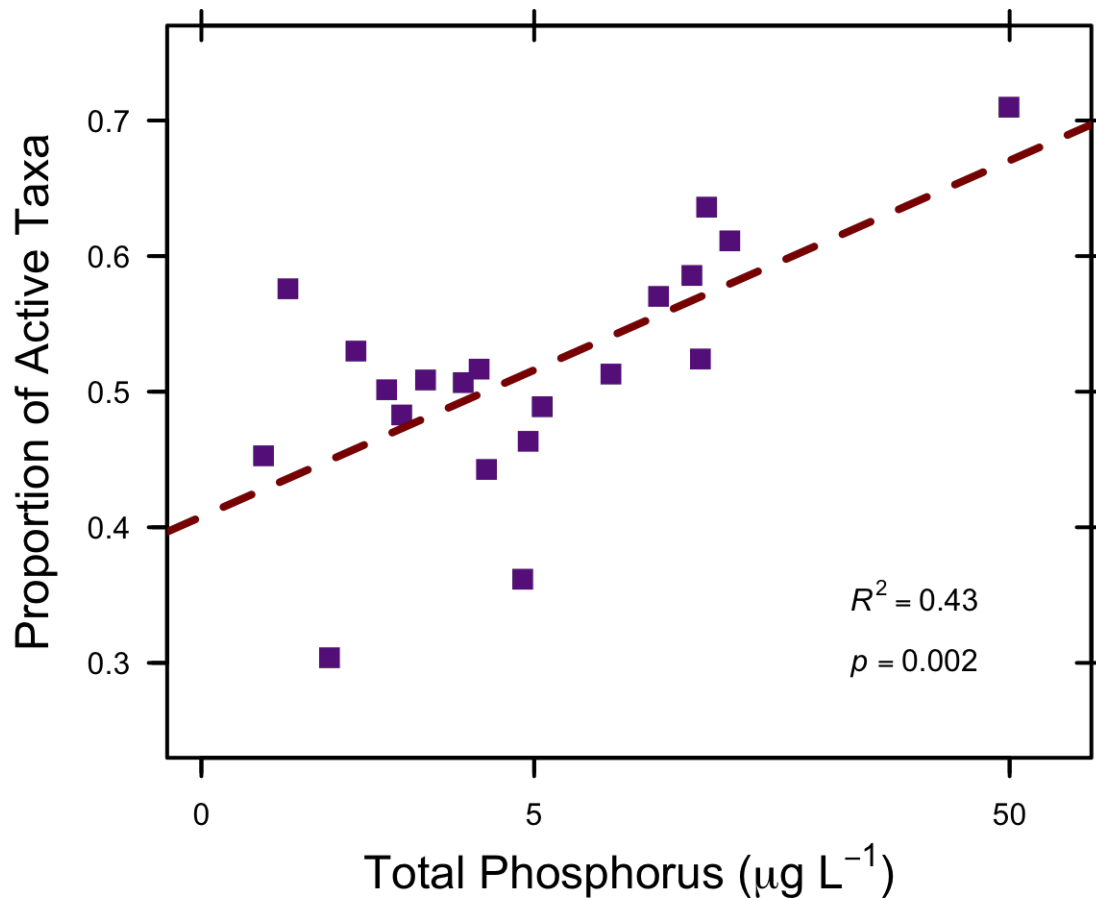


Figure 8: Resource Alpha Diversity

Patterns of Resource Diversity

```

# Define Inputs
# Resource = raw site-by-resource matrix
resource.pos <- "../data/SpecAbundAvePos.csv"
resource.neg <- "../data/SpecAbundAveNeg.csv"

# Import Resources
res.in <- read.csv(resource.neg, header=T, row.names=1)

```

```
rownames(res.in)
```

```
## [1] "Ann_Lake-5.1906"      "blank-5.7312"        "Canyon_Chemo-NA"
## [4] "Canyon_Epi-8.0847"    "Canyon_Hypo-5.2494"   "Canyon_I-8.72"
## [7] "Canyon_II-5.4808"     "Canyon_III-7.392"     "Canyon_IV-5.41395"
## [10] "Cowe_Lake-5.39"       "Ives_Lake-7.512"      "Jordan_River-0"
## [13] "Lily_Pond-7.6638"     "Mountain_lake-12.915" "Pony_Lake-8.9376"
## [16] "Rush-16.299"          "Second_Pine-9.0368"   "Upper_Pine-13.9104"
```

```
rownames(res.in) <- c("Ann", "blank", "CanyonChemo", "Canyon", "CanyonHypo",
                      "CanyonI", "CanyonII", "CanyonIII", "CanyonIV", "Howe",
                      "Ives", "Jordan", "Lily", "Mountain", "Pony", "Rush",
                      "SecondPine", "UpperPine")
```

```
blank <- unlist(res.in["blank", ])
res.hmwf <- res.in[-c(which(rownames(res.in) %in% c("blank", "CanyonChemo",
                                                    "CanyonHypo", "CanyonI", "CanyonII",
                                                    "CanyonIII", "CanyonIV", "Jordan"))), ]
```

Remove Major Peaks from Blanks

```
summary(blank)
```

```
##      Min.   1st Qu.   Median     Mean   3rd Qu.    Max.
##  21.25    641.80   1744.00   2729.00   3106.00  151500.00
```

```
blank[which(blank > 2 * sd(blank))]
```

```
##      C2      C5      C31      C83      C123      C124      C179
## 22847.63 92992.79 151455.84 38813.41 19059.45 24546.52 19593.59
##      C182      C185      C272      C273      C282      C284      C482
## 37004.20 16470.29 32986.92 16930.44 13222.98 56068.87 16735.12
##      C486      C487      C488      C489
## 17168.74 13282.27 29717.08 23246.62
```

```
# res.hmwf <- res.hmwf[, -c(which(blank > sd(blank)))]
```

```
# What other peaks should be removed
for (i in 1:dim(res.hmwf)[1]){
  res.hmwf[i, ] <- res.hmwf[i, ] - blank * 1.1
}
```

```
res.hmwf[res.hmwf < 50] <- 0
res.hmwf <- res.hmwf[, colSums(res.hmwf) > 0]
```

Data Transformations

```

# Remove OTUs with less than two occurrences across all sites
res <- res.hmwf

# Sequencing Coverage
coverage <- rowSums(res)

# # Remove Low Coverage Samples (This code removes two sites: Site 5DNA, Site 6cDNA)
# lows <- which(coverage < 10000)
# OTUs <- OTUs[-which(coverage < 10000), ]
# design <- design[-which(coverage < 10000), ]

# Make Relative Abundance Matrices
resREL <- res
for(i in 1:dim(res)[1]){
  resREL[i,] <- res[i,]/sum(res[i,])
}

# Log Transform Relative Resource Abundance
resREL.log <- decostand(resREL, method="log")

```

```
## Warning: non-integer data: divided by smallest positive value
```

Calculate Alpha Diversity

```

# Observed Richness
S.res <- rowSums((res > 0) * 1)

# Simpson's Evenness
res.simpE <- round(apply(res, 1, SimpE), 3)

# Shannon's Diversity
res.shan <- round(apply(res, 1, H), 2)
res.shan2 <- round(diversity(res, index = "shannon"), 2)

res.div <- as.data.frame(cbind(S.res, res.simpE, res.shan2))

```

Figure 5: Resource Diversity

```

png(filename="../figures/Figure5.png",
     width = 1600, height = 1200, res = 96*2)
par(opar)
par(mfrow = c(1,1), mar = c(0, 9, 0, 0) + 0.5, oma = c(5, 0, 1, 1) + 0.5)
layout(rbind(1, 2, 3), height = c(3, 3, 3))
labs <- c("Ann", "Canyon", "Howe", "Ives", "Lily", "Mountain", "Pony", "Rush",
         "Second\nPine", "Upper\nPine")
rich <- barplot(res.div$S.res, names.arg = NULL, las = 1, ylim=c(0, 750),
               xlab = "", ylab = "")
mtext(side = 2, text = "Resource\nRichness", cex.lab = 1.2, line = 4.5)

```

```

even <- barplot(res.div$res.simpsE, names.arg = NULL, las = 1, ylim=c(0, 0.27),
  xlab = "", ylab = "")
mtext(side = 2, text = "Simpson's\nEvenness", cex.lab = 1.2, line = 4.5)
shan <- barplot(res.div$res.shan, names.arg = NULL, las = 1, ylim = c(0, 9),
  xlab = "", ylab = "")
mtext(side = 2, text = "Shannon\nDiversity", cex.lab = 1.2, line = 4.5)
mtext(side = 1, text = labs, line = 2, at = shan, padj = 0.5, cex = 0.8)

dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)

```

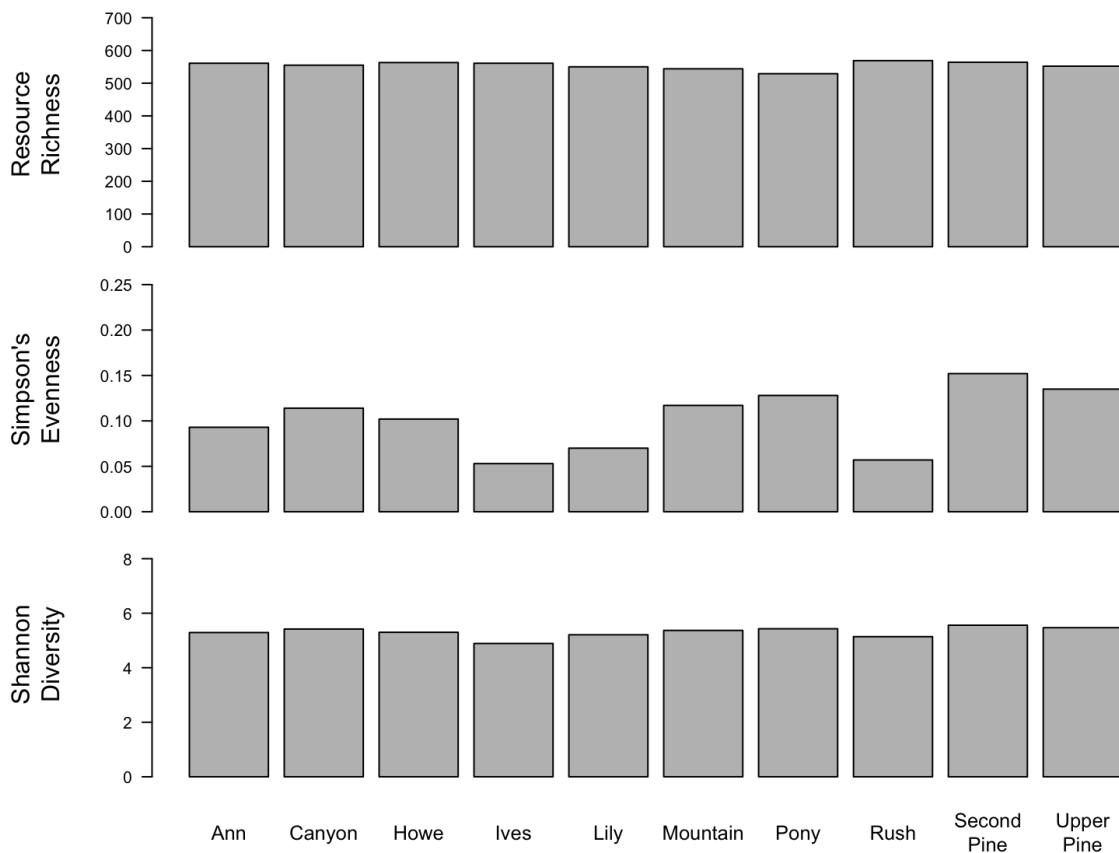


Figure 9: Resource Alpha Diversity

Hypothesis that resource diversity is related to nutrient concentration

```

nuts2012 <- nuts2[nuts2$year == "2012" & nuts2$molecule == "DNA", ]
evenmod <- lm(res.div$res.simpsE ~ nuts2012$DOC*nuts2012$TN*nuts2012$TP)
richmod <- lm(res.div$res.s ~ nuts2012$DOC*nuts2012$TN*nuts2012$TP)
summary(evenmod)

```

```
##
## Call:
## lm(formula = res.div$res.simpsE ~ nuts2012$DOC * nuts2012$TN *
##     nuts2012$TP)
##
## Residuals:
##      1      2      3      4      5      6
## -1.813e-02 -6.178e-03  9.835e-03 -3.627e-04 -9.911e-04  2.039e-02
##      7      8      9     10
##  1.556e-05 -8.306e-03  9.749e-04  2.753e-03
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.065357   0.148589   0.440   0.703
## nuts2012$DOC      0.048555   0.018108   2.681   0.115
## nuts2012$TN     -0.812639   0.388092  -2.094   0.171
## nuts2012$TP      0.021483   0.028268   0.760   0.527
## nuts2012$DOC:nuts2012$TN  0.015957   0.030662   0.520   0.655
## nuts2012$DOC:nuts2012$TP -0.011941   0.004487  -2.661   0.117
## nuts2012$TN:nuts2012$TP   0.128851   0.049515   2.602   0.121
## nuts2012$DOC:nuts2012$TN:nuts2012$TP 0.001319   0.001794   0.735   0.539
##
## Residual standard error: 0.02189 on 2 degrees of freedom
## Multiple R-squared:  0.9057, Adjusted R-squared:  0.5758
## F-statistic: 2.745 on 7 and 2 DF, p-value: 0.2929
```

```
summary(richmod)
```

```
##
## Call:
## lm(formula = res.div$S.res ~ nuts2012$DOC * nuts2012$TN * nuts2012$TP)
##
## Residuals:
##      1      2      3      4      5      6
##  0.661982  5.280093 -3.805515  0.625775  0.552656 -11.061751
##      7      8      9     10
## -0.007862  6.743308  3.489548 -2.478234
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      504.96385   72.74284   6.942   0.0201
## nuts2012$DOC     -2.91918    8.86492  -0.329   0.7732
## nuts2012$TN     175.33883  189.99368   0.923   0.4535
## nuts2012$TP      8.34626   13.83889   0.603   0.6077
## nuts2012$DOC:nuts2012$TN -1.60981   15.01096  -0.107   0.9244
## nuts2012$DOC:nuts2012$TP  0.04267    2.19670   0.019   0.9863
## nuts2012$TN:nuts2012$TP -22.83781   24.24059  -0.942   0.4456
## nuts2012$DOC:nuts2012$TN:nuts2012$TP 0.56162    0.87835   0.639   0.5880
##
## (Intercept) *
## nuts2012$DOC
## nuts2012$TN
## nuts2012$TP
## nuts2012$DOC:nuts2012$TN
```

```
## nuts2012$DOC:nuts2012$TP
## nuts2012$TN:nuts2012$TP
## nuts2012$DOC:nuts2012$TN:nuts2012$TP
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.72 on 2 degrees of freedom
## Multiple R-squared:  0.8153, Adjusted R-squared:  0.169
## F-statistic: 1.261 on 7 and 2 DF,  p-value: 0.5106
```

```
evenmod <- lm(res.div$res.simpsE ~ log(nuts2012$DOC))
richmod <- lm(res.div$S.res ~ log(nuts2012$DOC))
summary(evenmod)
```

```
##
## Call:
## lm(formula = res.div$res.simpsE ~ log(nuts2012$DOC))
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.047506	-0.029684	0.005882	0.018026	0.052670

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.07755	0.04479	1.732	0.122
log(nuts2012\$DOC)	0.01187	0.02099	0.566	0.587

```
##
## Residual standard error: 0.03495 on 8 degrees of freedom
## Multiple R-squared:  0.03845,    Adjusted R-squared:  -0.08174
## F-statistic: 0.3199 on 1 and 8 DF,  p-value: 0.5872
```

```
summary(richmod)
```

```
##
## Call:
## lm(formula = res.div$S.res ~ log(nuts2012$DOC))
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-17.612	-2.531	2.580	4.893	6.242

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	589.520	9.733	60.566	6.14e-12 ***
log(nuts2012\$DOC)	-16.791	4.562	-3.681	0.00621 **

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.597 on 8 degrees of freedom
## Multiple R-squared:  0.6288, Adjusted R-squared:  0.5824
## F-statistic: 13.55 on 1 and 8 DF,  p-value: 0.00621
```

```
xtable(summary(evenmod))
```

```
## % latex table generated in R 3.2.3 by xtable 1.8-2 package
## % Thu Mar 31 21:05:23 2016
## \begin{table}[ht]
## \centering
## \begin{tabular}{rrrrr}
## \hline
## & Estimate & Std. Error & t value & Pr(>|t|) & \\
## \hline
## (Intercept) & 0.0776 & 0.0448 & 1.73 & 0.1216 & \\
## log(nuts2012\DOC) & 0.0119 & 0.0210 & 0.57 & 0.5872 & \\
## \hline
## \end{tabular}
## \end{table}
```

Hypothesis that resource diversity influences consumer diversity

```
alpha.div2012 <- alpha.div[alpha.div$Year == "2012" & alpha.div$Molecule == "RNA", c(1, 4:6)]
rownames(alpha.div2012) <- alpha.div2012[, 1]
alpha.div2012 <- alpha.div2012[, -1]
rownames(res.div) == rownames(alpha.div2012)
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
cor(res.div, alpha.div2012)
```

```
##           S.obs      simpsE      shan
## S.res      -0.79777446  0.8464796 0.09607441
## res.simpsE  0.08866852 -0.1099914 0.15291370
## res.shan2   0.14004230 -0.1763717 0.09211756
```

```
rich.mod1 <- lm(alpha.div2012$S.obs ~ res.div$S.res)
rich.mod2 <- lm(alpha.div2012$S.obs ~ res.div$res.simpsE)
summary(rich.mod1)
```

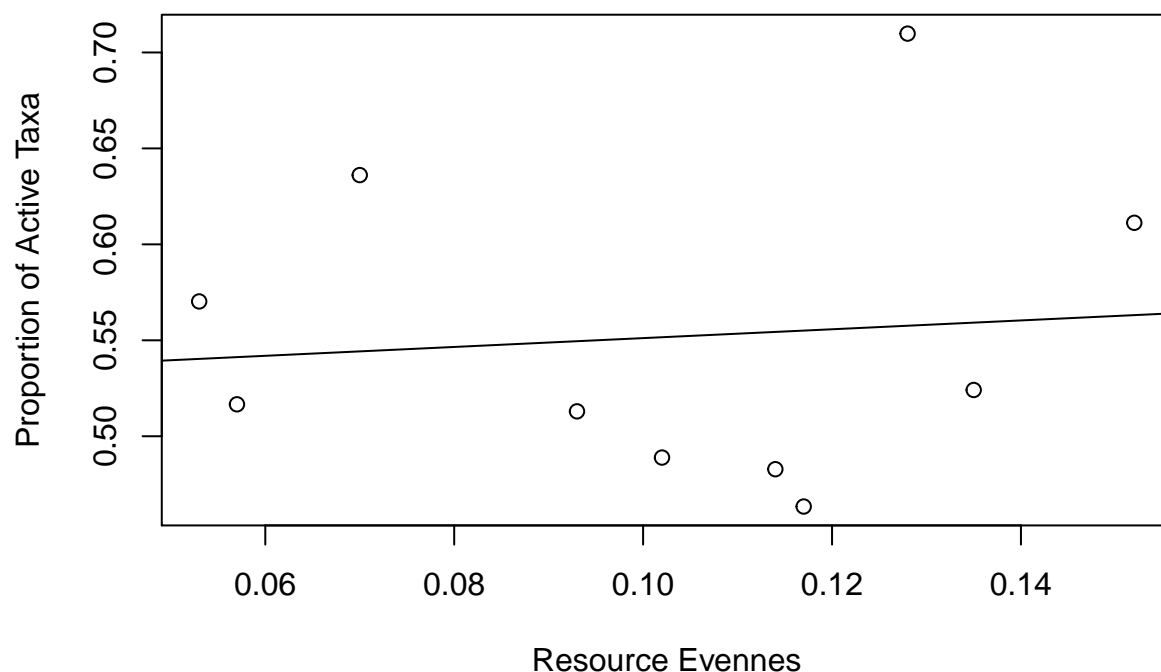
```
##
## Call:
## lm(formula = alpha.div2012$S.obs ~ res.div$S.res)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1110.98  -145.15    50.12   292.89   849.90
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  37226.68   9585.83   3.884  0.00465 **
## res.div$S.res   -64.65    17.27  -3.742  0.00569 **
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 609.2 on 8 degrees of freedom
## Multiple R-squared:  0.6364, Adjusted R-squared:  0.591
## F-statistic:    14 on 1 and 8 DF,  p-value: 0.005687
```

```
summary(rich.mod2)
```

```
##
## Call:
## lm(formula = alpha.div2012$S.obs ~ res.div$res.simpsE)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -632.2  -504.3  -418.8  -206.5   2214.1
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         1104      1068   1.034   0.331
## res.div$res.simpsE     2513       9982   0.252   0.808
##
## Residual standard error: 1006 on 8 degrees of freedom
## Multiple R-squared:  0.007862, Adjusted R-squared:  -0.1162
## F-statistic: 0.0634 on 1 and 8 DF,  p-value: 0.8076
```

```
plot((rowSums(active.NPA)/rowSums(totalPA))[seq(2, 20, by = 2)] ~ res.div$res.simpsE,
     xlab = "Resource Evennes", ylab = "Proportion of Active Taxa")
res.ev <- lm((rowSums(active.NPA)/rowSums(totalPA))[seq(2, 20, by = 2)] ~ res.div$res.simpsE)
abline(res.ev)
```



Between site comparisons of resources

```
# Calculate Bray-Curtis
res.db <- vegdist(resREL, method = "bray")

res.pcoa <- cmdscale(res.db, eig = TRUE, k = 3)
explainvar1 <- round(res.pcoa$eig[1] / sum(res.pcoa$eig), 3) * 100
explainvar2 <- round(res.pcoa$eig[2] / sum(res.pcoa$eig), 3) * 100
explainvar3 <- round(res.pcoa$eig[3] / sum(res.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

# Define Plot Parameters
par(mar = c(5, 5, 1, 2) + 0.1)

# Plot Eigenvalues
plot(res.pcoa$eig, xlab = "PCoA Axis", ylab = "Eigenvalue",
     las = 1, cex.lab = 1.5, pch = 16)

# Add Expectation based on Kaiser-Guttman criterion and Broken Stick Model
abline(h = mean(res.pcoa$eig), lty = 2, lwd = 2, col = "blue")
b.stick <- bstick(10, sum(res.pcoa$eig))
lines(1:10, b.stick, type = "l", lty = 4, lwd = 2, col = "red")

# Add Legend
legend("topright", legend = c("Avg Eigenvalue", "Broken-Stick"),
     lty = c(2, 4), bty = "n", col = c("blue", "red"))
```

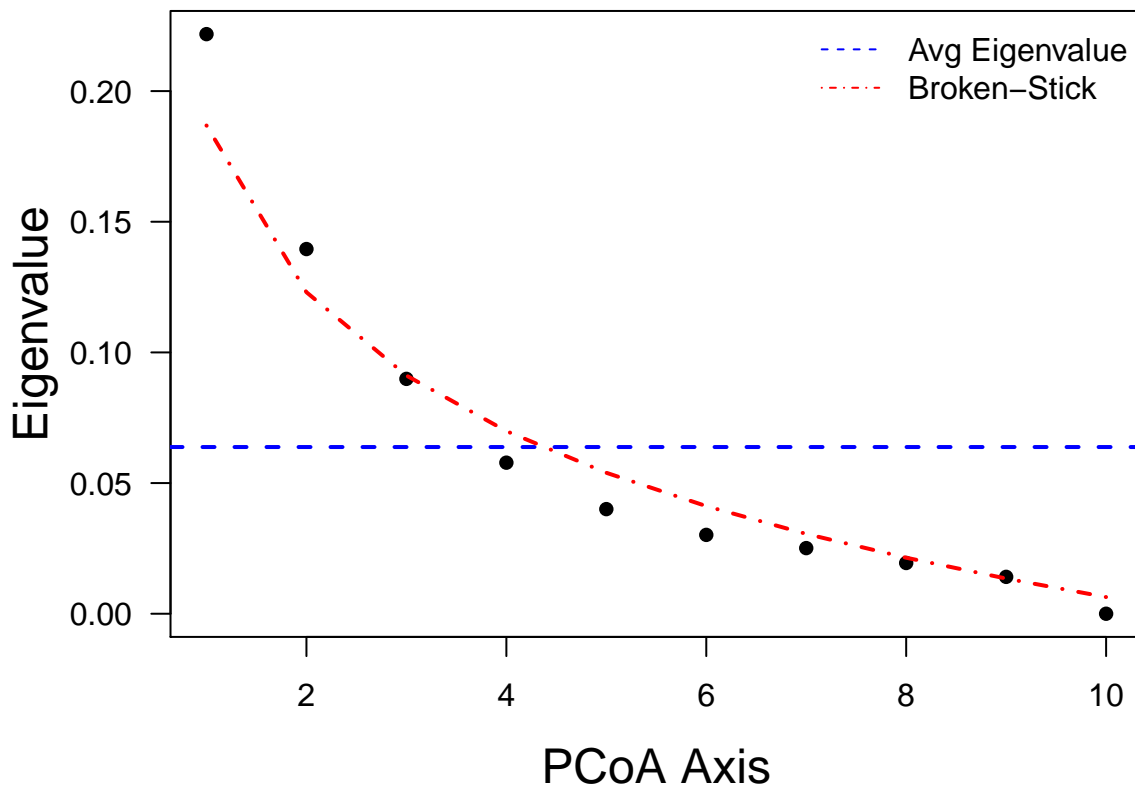


Figure 6: Resource Differences Across Sites

```
png(filename="../figures/Figure6.png",
      width = 1200, height = 1200, res = 96*2)

# Define Plot Parameters
par(mar = c(5, 5, 1, 1) + 0.1)

# Initiate Plot
plot(res.pcoa$points[,1], res.pcoa$points[,2], ylim = c(-0.25, 0.3),
      xlim = c(-0.4, 0.4),
      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)

# Add Axes
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)

# Add Points & Labels
points(res.pcoa$points[,1], res.pcoa$points[,2],
       pch = 19, cex = 3, bg = "gray", col = "gray")
text(res.pcoa$points[,1], res.pcoa$points[,2],
     labels = row.names(res.pcoa$points))
dev.off() # this writes plot to folder
graphics.off() # shuts down open devices
par(opar)
```

Resource Explanations of Differences

```
OTUsREL2012.DNA <- OTUsREL[which(design$Year == "2012" & design$Molecule == "DNA"), ]
OTUsREL2012.DNA <- OTUsREL2012.DNA[, colSums(OTUsREL2012.DNA > 0)]
OTUsREL2012.RNA <- OTUsREL[which(design$Year == "2012" & design$Molecule == "RNA"), ]
OTUsREL2012.RNA <- OTUsREL2012.RNA[, colSums(OTUsREL2012.RNA > 0)]
active.N2012 <- active.N[grep("2012", rownames(active.N)), ]
rownames(OTUsREL2012.DNA) <- design$Lake[which(design$Year == "2012" & design$Molecule == "DNA")]
rownames(OTUsREL2012.RNA) <- design$Lake[which(design$Year == "2012" & design$Molecule == "RNA")]
rownames(active.N2012) <- design$Lake[which(design$Year == "2012" & design$Molecule == "DNA")]

# DNA
dbrda2012 <- capscale(OTUsREL2012.DNA ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, add = T, distance = "br")

## Warning in cmdscale(X, k = k, eig = TRUE, add = add): only 8 of the first 9
## eigenvalues are > 0

anova(dbrda2012)
```

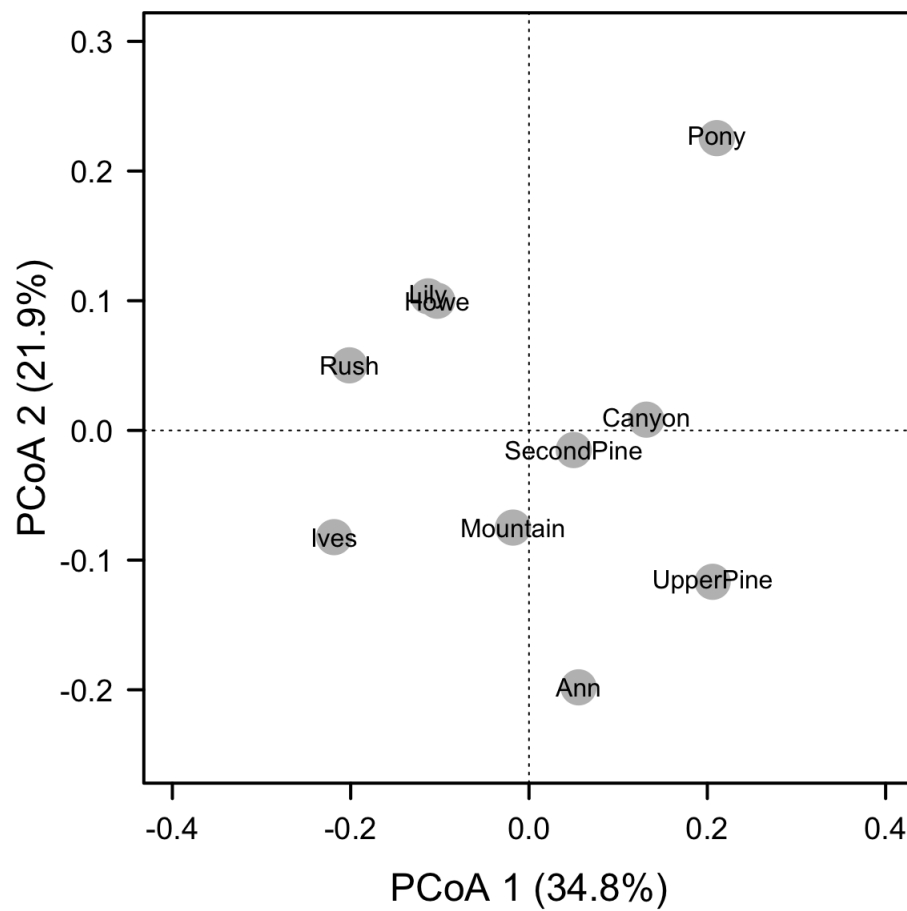


Figure 10: Resource Ordination

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = OTUsREL2012.DNA ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, distance = "br
##           Df SumOfSqs      F Pr(>F)
## Model      3  0.18760 1.9167  0.088 .
## Residual   6  0.19575
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
RsquareAdj(dbrda2012)
```

```
## $r.squared
## [1] 0.4893716
##
## $adj.r.squared
## [1] 0.2340574
```

```
coef(dbrda2012)
```

```
##           CAP1      CAP2      CAP3
## nuts2012$DOC -0.08665049 -0.20602323 -0.20832737
## nuts2012$TN   3.32155319  2.23604603  2.80303220
## nuts2012$TP  -0.06574191  0.01700405  0.03371554
```

```
# RNA
```

```
dbrda2012 <- capscale(OTUsREL2012.RNA ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, add = T, distance = "br
```

```
## Warning in cmdscale(X, k = k, eig = TRUE, add = add): only 8 of the first 9
## eigenvalues are > 0
```

```
anova(dbrda2012)
```

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = OTUsREL2012.RNA ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, distance = "br
##           Df SumOfSqs      F Pr(>F)
## Model      3  0.18760 1.9167  0.093 .
## Residual   6  0.19575
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
RsquareAdj(dbrda2012)
```

```
## $r.squared
## [1] 0.4893716
##
## $adj.r.squared
## [1] 0.2340574
```

```
coef(dbrda2012)
```

```
##              CAP1          CAP2          CAP3
## nuts2012$DOC -0.08665049 -0.20602323 -0.20832737
## nuts2012$TN   3.32155319  2.23604603  2.80303220
## nuts2012$TP  -0.06574191  0.01700405  0.03371554
```

```
# Active
```

```
dbrda2012 <- capscale(active.N2012 ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, add =T, distance = "bray")
anova(dbrda2012)
```

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = active.N2012 ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, distance = "bray")
##           Df SumOfSqs      F Pr(>F)
## Model      3  0.75254 1.9712  0.019 *
## Residual    6  0.76353
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
RsquareAdj(dbrda2012)
```

```
## $r.squared
## [1] 0.496375
##
## $adj.r.squared
## [1] 0.2445625
```

```
coef(dbrda2012)
```

```
##              CAP1          CAP2          CAP3
## nuts2012$DOC  0.08055203 -0.003445359  0.294709469
## nuts2012$TN   0.13440004 -1.707176730 -4.577891568
## nuts2012$TP  -0.02643324  0.070566186 -0.008340943
```

```
# Resoruces
```

```
chem.dbrda <- capscale(resREL ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, add =T, distance = "bray")
anova(chem.dbrda)
```

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = resREL ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, distance = "bray", add =T)
##           Df SumOfSqs      F Pr(>F)
## Model      3  0.25058 1.294   0.18
## Residual    6  0.38728
```

```
RsquareAdj(chem.dbrda)
```

```
## $r.squared  
## [1] 0.392843  
##  
## $adj.r.squared  
## [1] 0.08926447
```

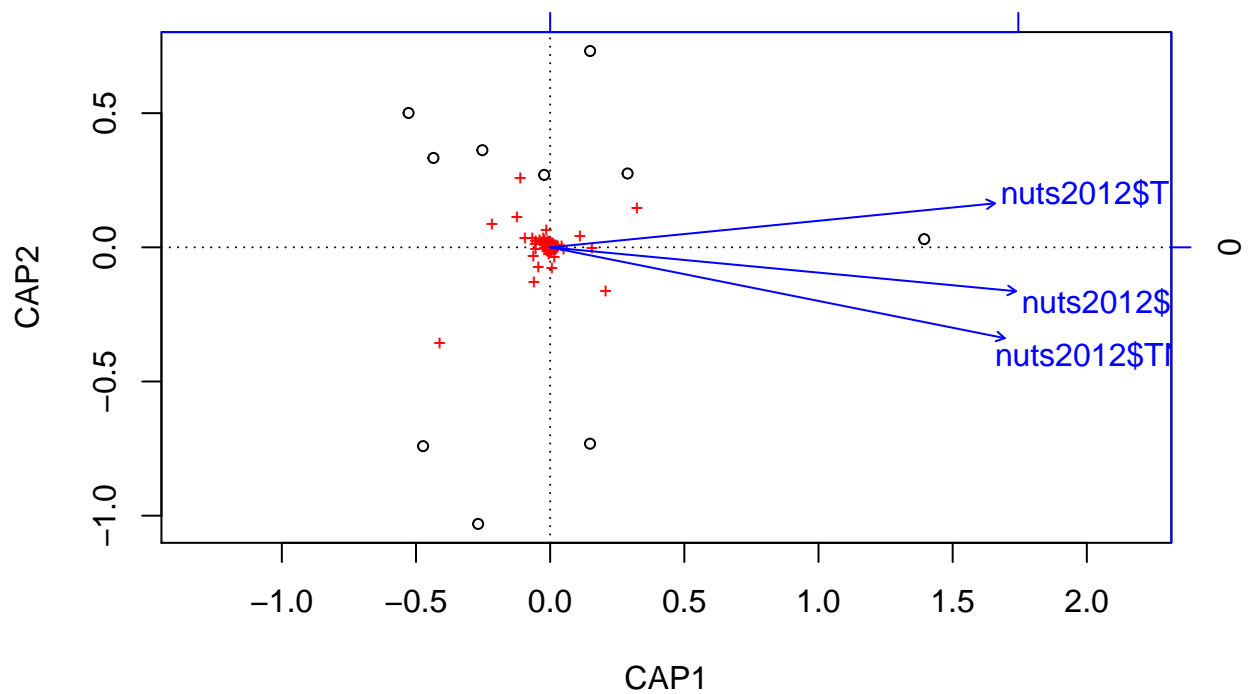
```
coef(chem.dbrda)
```

```
##           CAP1      CAP2      CAP3  
## nuts2012$DOC 0.066586751 0.1474111 0.25921101  
## nuts2012$TN  -0.457552304 -4.0261543 -2.73319131  
## nuts2012$TP   0.003780914 0.0557068 -0.05128675
```

```
anova.cca(chem.dbrda, step=1000)
```

```
## Permutation test for capscale under reduced model  
## Permutation: free  
## Number of permutations: 999  
##  
## Model: capscale(formula = resREL ~ nuts2012$DOC + nuts2012$TN + nuts2012$TP, distance = "bray", add = 1)  
##           Df SumOfSqs      F Pr(>F)  
## Model      3  0.25058 1.294 0.183  
## Residual   6  0.38728
```

```
plot(chem.dbrda)
```



```
lmod <- as.mlm(chem.dbrda)
lmod
```

```
##
## Call:
## lm(formula = x$CCA$wa ~ . - 1, data = as.data.frame(X))
##
## Coefficients:
##          CAP1          CAP2          CAP3
## `nuts2012$DOC`  0.066587   0.147411   0.259211
## `nuts2012$TN`  -0.457552  -4.026154  -2.733191
## `nuts2012$TP`   0.003781   0.055707  -0.051287
```

```
summary(lmod)
```

```
## Response CAP1 :
##
## Call:
## lm(formula = CAP1 ~ (`nuts2012$DOC` + `nuts2012$TN` + `nuts2012$TP`) -
##     1, data = as.data.frame(X))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.280107 -0.079988 -0.006128  0.083630  0.250485
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## `nuts2012$DOC`  0.066587   0.052926   1.258   0.249
## `nuts2012$TN`  -0.457552   0.846653  -0.540   0.606
## `nuts2012$TP`   0.003781   0.013133   0.288   0.782
##
## Residual standard error: 0.1732 on 7 degrees of freedom
## Multiple R-squared:  0.8264, Adjusted R-squared:  0.752
## F-statistic: 11.11 on 3 and 7 DF,  p-value: 0.004718
##
##
## Response CAP2 :
##
## Call:
## lm(formula = CAP2 ~ (`nuts2012$DOC` + `nuts2012$TN` + `nuts2012$TP`) -
##     1, data = as.data.frame(X))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.18966 -0.16391 -0.01948  0.05003  0.48816
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## `nuts2012$DOC`  0.14741   0.07189   2.051  0.07946 .
## `nuts2012$TN`  -4.02615   1.14998  -3.501  0.00998 **
## `nuts2012$TP`   0.05571   0.01784   3.123  0.01677 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.2353 on 7 degrees of freedom
## Multiple R-squared: 0.7207, Adjusted R-squared: 0.601
## F-statistic: 6.022 on 3 and 7 DF, p-value: 0.0237
##
##
## Response CAP3 :
##
## Call:
## lm(formula = CAP3 ~ (`nuts2012$DOC` + `nuts2012$TN` + `nuts2012$TP`) -
## 1, data = as.data.frame(X))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3227 -0.2485 -0.0477  0.1862  0.4466
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## `nuts2012$DOC`  0.25921    0.09768   2.654  0.0328 *
## `nuts2012$TN`  -2.73319    1.56266  -1.749  0.1238
## `nuts2012$TP`  -0.05129    0.02424  -2.116  0.0722 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3197 on 7 degrees of freedom
## Multiple R-squared: 0.5829, Adjusted R-squared: 0.4042
## F-statistic: 3.261 on 3 and 7 DF, p-value: 0.08954

chem.dbrda <- capscale(resREL ~ log(nuts2012$DOC), add = T, distance = "bray")
anova(chem.dbrda)

## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = resREL ~ log(nuts2012$DOC), distance = "bray", add = T)
##           Df SumOfSqs      F Pr(>F)
## Model      1  0.12420 1.9343  0.043 *
## Residual    8  0.51366
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

RsquareAdj(chem.dbrda)

## $r.squared
## [1] 0.1947118
##
## $adj.r.squared
## [1] 0.09405081

coef(chem.dbrda)
```

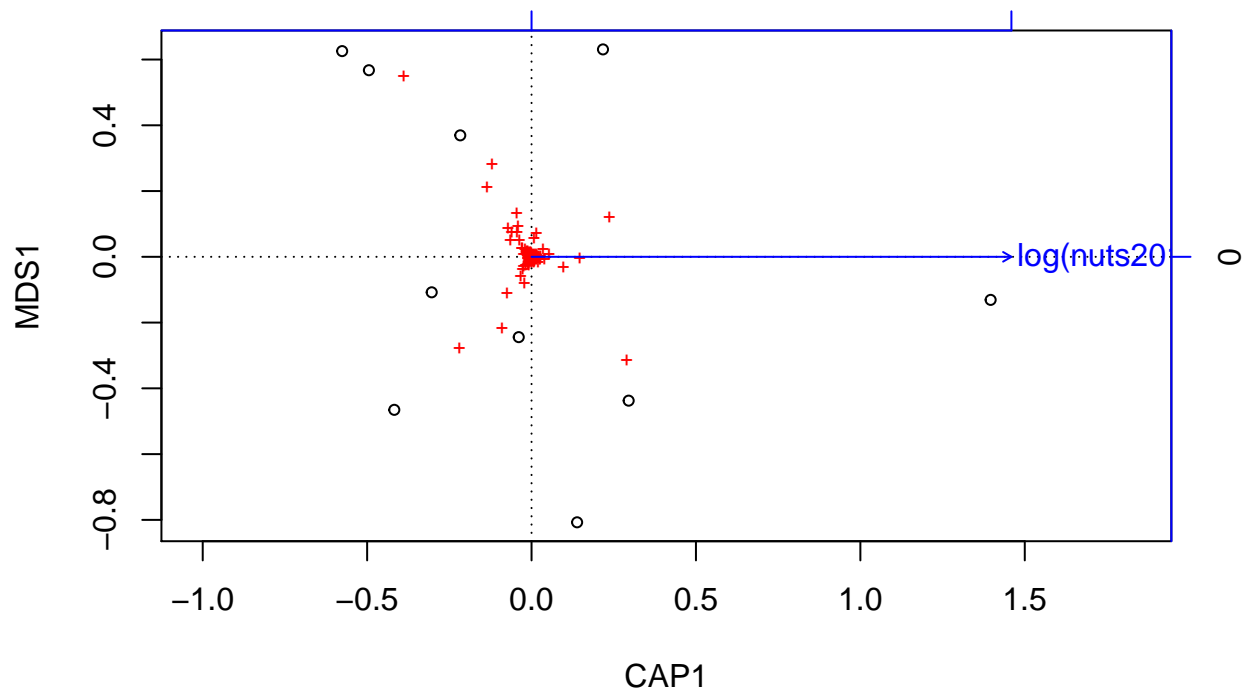


```
## CAP1
## log(nuts2012$DOC) 0.6004698
```

```
anova.cca(chem.dbrda, step=1000)
```

```
## Permutation test for capscale under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = resREL ~ log(nuts2012$DOC), distance = "bray", add = T)
##      Df SumOfSqs      F Pr(>F)
## Model   1  0.12420 1.9343 0.034 *
## Residual 8  0.51366
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(chem.dbrda)
```



```
lmod <- as.mlm(chem.dbrda)
lmod
```

```
##
## Call:
## lm(formula = x$CCA$wa ~ . - 1, data = as.data.frame(X))
##
## Coefficients:
## `log(nuts2012$DOC)`
##      0.6005
```

```
summary(lmod)
```

```
##
## Call:
## lm(formula = x$CCA$wa ~ . - 1, data = as.data.frame(X))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.29143 -0.09346  0.05226  0.10989  0.24425
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## `log(nuts2012$DOC)`    0.6005     0.1000   6.004 0.000201 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1666 on 9 degrees of freedom
## Multiple R-squared:  0.8002, Adjusted R-squared:  0.778
## F-statistic: 36.05 on 1 and 9 DF,  p-value: 0.0002015
```

```
require(cocorresp)
```

```
## Loading required package: cocorresp
```

```
#test1 <- coca(OTUsREL2012.RNA, resREL, n.axes = 4)

# Variance Partitioning

nuts3 <- cbind(scale(log(nuts2012$DOC)), scale(log1p(nuts2012$TP)))
# nuts3 <- scale(log(nuts2012$DOC))
rownames(nuts3) <- nuts2012$sample

res.db <- vegdist(resREL, method = "altGower")
res.pcoa <- cmdscale(res.db, eig = TRUE, k = 5)

OTUsREL.log2012 <- OTUsREL.log[design$Year == "2012" & design$Molecule == "RNA", ]
OTUsREL2012 <- OTUsREL[design$Year == "2012" & design$Molecule == "RNA", ]
spe.pcoa <- cmdscale(vegdist(OTUsREL2012, method="bray"), eig = TRUE, k = 5)

# Active
HMFvarpart <- varpart(spe.pcoa$points[, 1:2], nuts3, res.pcoa$points[, 1:2])
HMFvarpart <- varpart(OTUsREL.log2012, nuts3, res.pcoa$points)
HMFvarpart
```

```
##
## Partition of variation in RDA
##
## Call: varpart(Y = OTUsREL.log2012, X = nuts3, res.pcoa$points)
##
## Explanatory tables:
```

```
## X1:  nuts3
## X2:  res.pcoa$points
##
## No. of explanatory tables: 2
## Total variation (SS): 112296
##           Variance: 12477
## No. of observations: 10
##
## Partition table:
##           Df R.squared Adj.R.squared Testable
## [a+b] = X1      2  0.43386      0.27210      TRUE
## [b+c] = X2      5  0.69171      0.30634      TRUE
## [a+b+c] = X1+X2  7  0.84950      0.32274      TRUE
## Individual fractions
## [a] = X1|X2      2              0.01640      TRUE
## [b]              0              0.25570      FALSE
## [c] = X2|X1      5              0.05064      TRUE
## [d] = Residuals              0.67726      FALSE
## ---
## Use function 'rda' to test significance of fractions of interest
```

```
png(filename="../figures/Figure7.png",
     width = 1200, height = 1200, res = 96*2)
```

```
plot(HMWFvarpart)
```

```
dev.off() # this writes plot to folder
```

```
## pdf
## 2
```

```
graphics.off() # shuts down open devices
par(opar)
```

```
anova.cca(rda(spe.pcoa$points, nuts3), step=1000) #[a+b]
```

```
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: rda(X = spe.pcoa$points, Y = nuts3)
##           Df Variance      F Pr(>F)
## Model      2 0.073408 2.8109 0.004 **
## Residual   7 0.091404
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova.cca(rda(spe.pcoa$points, res.pcoa$points), step=1000) #[b+c]
```

```
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
```

```
##
## Model: rda(X = spe.pcoa$points, Y = res.pcoa$points)
##           Df Variance      F Pr(>F)
## Model      5 0.112439 1.7175 0.069 .
## Residual   4 0.052373
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova.cca(rda(spe.pcoa$points, cbind(nuts3, res.pcoa$points)), step=1000) #[a+b+c]
```

```
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: rda(X = spe.pcoa$points, Y = cbind(nuts3, res.pcoa$points))
##           Df Variance      F Pr(>F)
## Model      7 0.134654 1.2757 0.319
## Residual   2 0.030158
```

```
anova.cca(rda(spe.pcoa$points, res.pcoa$points, nuts3), step=1000) # [a]
```

```
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: rda(X = spe.pcoa$points, Y = res.pcoa$points, Z = nuts3)
##           Df Variance      F Pr(>F)
## Model      5 0.061246 0.8123 0.682
## Residual   2 0.030158
```

```
anova.cca(rda(spe.pcoa$points, nuts3, res.pcoa$points), step=1000) # [c]
```

```
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: rda(X = spe.pcoa$points, Y = nuts3, Z = res.pcoa$points)
##           Df Variance      F Pr(>F)
## Model      2 0.022215 0.7366 0.645
## Residual   2 0.030158
```

Phylogenetic Approach

Resource distribution is not able to explain the distribution of all organisms combined. But why should we expect this assumption?

Remove Cyanobacteria

Microbial Functional Groups

Define RDP microbial groups Test each along with resource differences Who are the generalist taxa (which are active everywhere) Are generalists more abundant when resource concentration is higher?

Can we group resources

What are the similar groups of resources: cluster resources based on abundance Can we cluster based on chemical data?

```
res.dist <- vegdist(t(resREL), "bray")

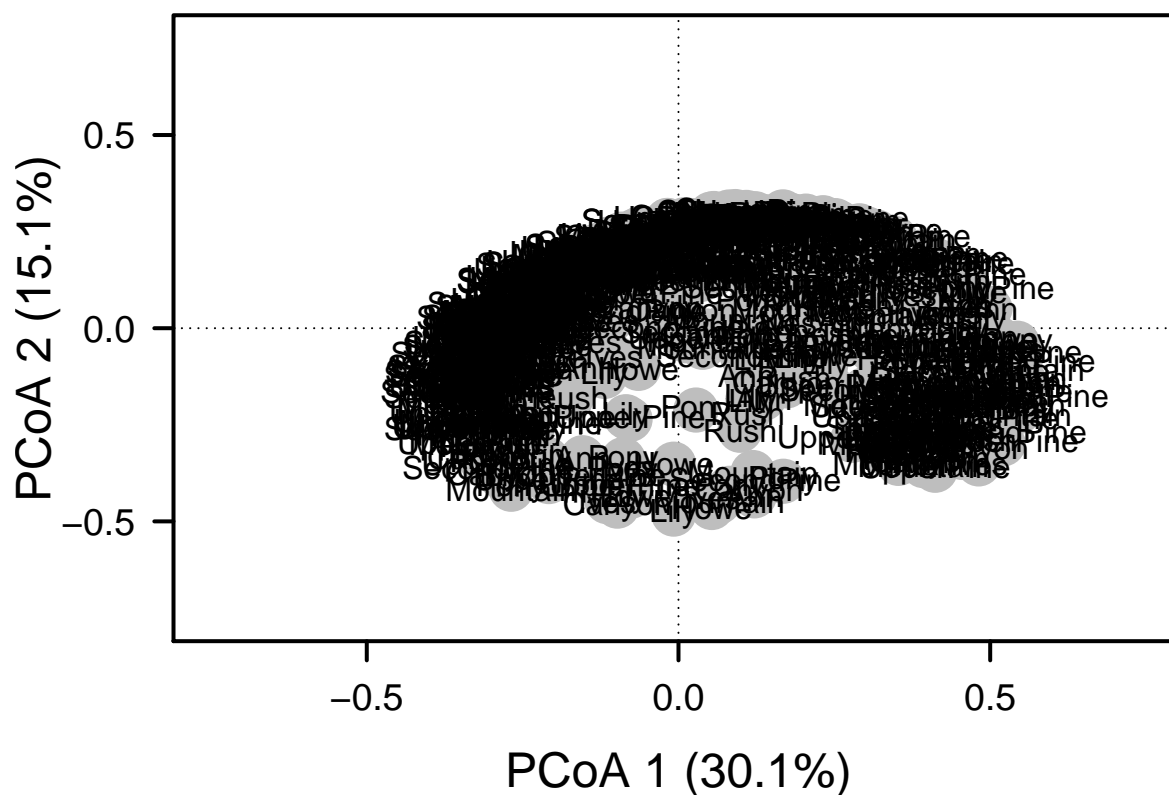
res2.pcoa <- cmdscale(res.dist, eig = TRUE, k = 3)
explainvar1 <- round(res2.pcoa$eig[1] / sum(res2.pcoa$eig), 3) * 100
explainvar2 <- round(res2.pcoa$eig[2] / sum(res2.pcoa$eig), 3) * 100
explainvar3 <- round(res2.pcoa$eig[3] / sum(res2.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

# Define Plot Parameters
par(mar = c(5, 5, 1, 1) + 0.1)

# Initiate Plot
plot(res2.pcoa$points[,1], res2.pcoa$points[,2], ylim = c(-0.75, 0.75),
      xlim = c(-0.75, 0.75),
      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)

# Add Axes
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)

# Add Points & Labels
points(res2.pcoa$points[,1], res2.pcoa$points[,2],
       pch = 19, cex = 3, bg = "gray", col = "gray")
text(res2.pcoa$points[,1], res2.pcoa$points[,2],
     labels = row.names(res.pcoa$points))
```



```
# Distances between molecules given sites
summary(resREL) # the data
```

##	C1	C2	C3
##	Min. :0.0000000	Min. :0.00000	Min. :0.001349
##	1st Qu.:0.0006769	1st Qu.:0.01021	1st Qu.:0.001874
##	Median :0.0021680	Median :0.02382	Median :0.002522
##	Mean :0.0017680	Mean :0.03596	Mean :0.002322
##	3rd Qu.:0.0025300	3rd Qu.:0.06352	3rd Qu.:0.002664
##	Max. :0.0034959	Max. :0.09267	Max. :0.003047
##	C4	C6	C8
##	Min. :0.0000000	Min. :0.000000	Min. :0.0000000
##	1st Qu.:0.0006889	1st Qu.:0.008753	1st Qu.:0.0004477
##	Median :0.0019029	Median :0.011175	Median :0.0014253
##	Mean :0.0023593	Mean :0.015287	Mean :0.0016791
##	3rd Qu.:0.0034990	3rd Qu.:0.021488	3rd Qu.:0.0027515
##	Max. :0.0062077	Max. :0.034030	Max. :0.0036636
##	C9	C10	C12
##	Min. :0.0000000	Min. :0.001596	Min. :0.00000
##	1st Qu.:0.0008124	1st Qu.:0.001784	1st Qu.:0.00000
##	Median :0.0020051	Median :0.002065	Median :0.00000
##	Mean :0.0025981	Mean :0.002571	Mean :0.01207
##	3rd Qu.:0.0041760	3rd Qu.:0.002461	3rd Qu.:0.01055
##	Max. :0.0065816	Max. :0.006766	Max. :0.07706
##	C15	C16	C17
##	Min. :0.0007315	Min. :0.001196	Min. :0.0006099
##	1st Qu.:0.0009698	1st Qu.:0.001904	1st Qu.:0.0014167
##	Median :0.0012655	Median :0.002072	Median :0.0017960

## Mean :0.0013874	Mean :0.002297	Mean :0.0017094
## 3rd Qu.:0.0016481	3rd Qu.:0.002393	3rd Qu.:0.0019740
## Max. :0.0025889	Max. :0.004384	Max. :0.0024360
## C18	C21	C22
## Min. :0.0007549	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0008615	1st Qu.:0.0000000	1st Qu.:0.0001666
## Median :0.0009738	Median :0.0000000	Median :0.0003782
## Mean :0.0012026	Mean :0.0007879	Mean :0.0004249
## 3rd Qu.:0.0013444	3rd Qu.:0.0007414	3rd Qu.:0.0005896
## Max. :0.0025072	Max. :0.0033198	Max. :0.0010642
## C23	C24	C25
## Min. :0.0005187	Min. :0.0008872	Min. :0.0005300
## 1st Qu.:0.0006114	1st Qu.:0.0012307	1st Qu.:0.0009237
## Median :0.0007896	Median :0.0012514	Median :0.0014235
## Mean :0.0009253	Mean :0.0014909	Mean :0.0013972
## 3rd Qu.:0.0010573	3rd Qu.:0.0015984	3rd Qu.:0.0017669
## Max. :0.0017919	Max. :0.0030045	Max. :0.0021955
## C26	C27	C30
## Min. :0.0007041	Min. :0.0005791	Min. :0.0000000
## 1st Qu.:0.0008437	1st Qu.:0.0007552	1st Qu.:0.0000000
## Median :0.0010062	Median :0.0010735	Median :0.002619
## Mean :0.0011499	Mean :0.0012338	Mean :0.002481
## 3rd Qu.:0.0014643	3rd Qu.:0.0016358	3rd Qu.:0.003420
## Max. :0.0019654	Max. :0.0023398	Max. :0.009302
## C34	C35	C36
## Min. :0.000e+00	Min. :0.0004700	Min. :0.001923
## 1st Qu.:0.000e+00	1st Qu.:0.0007526	1st Qu.:0.002162
## Median :0.000e+00	Median :0.0009726	Median :0.002765
## Mean :9.269e-05	Mean :0.0009933	Mean :0.002983
## 3rd Qu.:1.068e-04	3rd Qu.:0.0011147	3rd Qu.:0.003508
## Max. :4.312e-04	Max. :0.0019407	Max. :0.004929
## C37	C39	C40
## Min. :0.0008008	Min. :0.0006464	Min. :0.000872
## 1st Qu.:0.0013065	1st Qu.:0.0011249	1st Qu.:0.001251
## Median :0.0015571	Median :0.0013664	Median :0.001323
## Mean :0.0016492	Mean :0.0014357	Mean :0.001772
## 3rd Qu.:0.0019003	3rd Qu.:0.0016469	3rd Qu.:0.002170
## Max. :0.0030991	Max. :0.0027018	Max. :0.003942
## C41	C43	C45
## Min. :0.0005675	Min. :0.000e+00	Min. :0.0002968
## 1st Qu.:0.0006183	1st Qu.:8.346e-05	1st Qu.:0.0003817
## Median :0.0007413	Median :2.716e-04	Median :0.0004246
## Mean :0.0008867	Mean :5.360e-04	Mean :0.0004563
## 3rd Qu.:0.0008489	3rd Qu.:8.657e-04	3rd Qu.:0.0005194
## Max. :0.0023745	Max. :1.885e-03	Max. :0.0007426
## C48	C51	C52
## Min. :0.000e+00	Min. :0.0009345	Min. :0.001120
## 1st Qu.:0.000e+00	1st Qu.:0.0019101	1st Qu.:0.001460
## Median :0.000e+00	Median :0.0029662	Median :0.001662
## Mean :9.741e-05	Mean :0.0031205	Mean :0.002010
## 3rd Qu.:0.000e+00	3rd Qu.:0.0039750	3rd Qu.:0.002701
## Max. :6.006e-04	Max. :0.0064976	Max. :0.003164
## C53	C54	C55
## Min. :0.0002193	Min. :0.001273	Min. :0.0004134

## 1st Qu.:0.0006245	1st Qu.:0.002034	1st Qu.:0.0009660
## Median :0.0010364	Median :0.002218	Median :0.0010965
## Mean :0.0012340	Mean :0.002231	Mean :0.0013457
## 3rd Qu.:0.0016400	3rd Qu.:0.002580	3rd Qu.:0.0015344
## Max. :0.0032822	Max. :0.002973	Max. :0.0030224
## C56	C57	C58
## Min. :0.001189	Min. :0.0009858	Min. :0.001117
## 1st Qu.:0.001639	1st Qu.:0.0014930	1st Qu.:0.001461
## Median :0.001902	Median :0.0016593	Median :0.002148
## Mean :0.002050	Mean :0.0018152	Mean :0.002110
## 3rd Qu.:0.002107	3rd Qu.:0.0018626	3rd Qu.:0.002477
## Max. :0.004055	Max. :0.0030216	Max. :0.003729
## C59	C63	C64
## Min. :0.001688	Min. :0.0009083	Min. :0.0001369
## 1st Qu.:0.002780	1st Qu.:0.0013450	1st Qu.:0.0007349
## Median :0.002963	Median :0.0016361	Median :0.0010733
## Mean :0.003140	Mean :0.0015248	Mean :0.0010186
## 3rd Qu.:0.003632	3rd Qu.:0.0017835	3rd Qu.:0.0013766
## Max. :0.004464	Max. :0.0019122	Max. :0.0017041
## C65	C66	C67
## Min. :0.0006838	Min. :0.001441	Min. :0.0009683
## 1st Qu.:0.0010515	1st Qu.:0.001682	1st Qu.:0.0010593
## Median :0.0011644	Median :0.001926	Median :0.0012783
## Mean :0.0013102	Mean :0.002085	Mean :0.0015913
## 3rd Qu.:0.0013685	3rd Qu.:0.002161	3rd Qu.:0.0017875
## Max. :0.0028256	Max. :0.004083	Max. :0.0039310
## C68	C69	C72
## Min. :0.0000000	Min. :0.0007864	Min. :0.0000000
## 1st Qu.:0.0001247	1st Qu.:0.0010588	1st Qu.:0.0000000
## Median :0.0002230	Median :0.0011316	Median :0.0000000
## Mean :0.0003940	Mean :0.0013036	Mean :0.0002051
## 3rd Qu.:0.0003821	3rd Qu.:0.0013292	3rd Qu.:0.0000000
## Max. :0.0016939	Max. :0.0028517	Max. :0.0019273
## C74	C76	C78
## Min. :0.0006201	Min. :0.0000671	Min. :0.000e+00
## 1st Qu.:0.0008305	1st Qu.:0.0003063	1st Qu.:0.000e+00
## Median :0.0009772	Median :0.0004837	Median :0.000e+00
## Mean :0.0010205	Mean :0.0007027	Mean :2.654e-05
## 3rd Qu.:0.0011286	3rd Qu.:0.0008449	3rd Qu.:0.000e+00
## Max. :0.0017580	Max. :0.0026257	Max. :2.654e-04
## C81	C82	C86
## Min. :0.0003159	Min. :0.0000000	Min. :0.000000
## 1st Qu.:0.0006907	1st Qu.:0.0002574	1st Qu.:0.002807
## Median :0.0008923	Median :0.0037626	Median :0.007846
## Mean :0.0010575	Mean :0.0066804	Mean :0.008590
## 3rd Qu.:0.0014611	3rd Qu.:0.0082167	3rd Qu.:0.013323
## Max. :0.0022194	Max. :0.0221693	Max. :0.019905
## C87	C88	C89
## Min. :0.0000000	Min. :7.543e-05	Min. :0.001114
## 1st Qu.:0.0000000	1st Qu.:5.540e-04	1st Qu.:0.001465
## Median :0.0000000	Median :1.085e-03	Median :0.001947
## Mean :0.0001133	Mean :1.049e-03	Mean :0.001992
## 3rd Qu.:0.0000000	3rd Qu.:1.478e-03	3rd Qu.:0.002376
## Max. :0.0010061	Max. :2.014e-03	Max. :0.003237

##	C90	C91	C92
##	Min. :0.0002552	Min. :0.0003913	Min. :0.001532
##	1st Qu.:0.0005255	1st Qu.:0.0008213	1st Qu.:0.001796
##	Median :0.0006114	Median :0.0011167	Median :0.002070
##	Mean :0.0006082	Mean :0.0011378	Mean :0.002101
##	3rd Qu.:0.0006947	3rd Qu.:0.0013243	3rd Qu.:0.002435
##	Max. :0.0009990	Max. :0.0019275	Max. :0.002763
##	C93	C94	C95
##	Min. :0.0004021	Min. :0.001079	Min. :0.0002646
##	1st Qu.:0.0009305	1st Qu.:0.001738	1st Qu.:0.0011197
##	Median :0.0010819	Median :0.002168	Median :0.0014824
##	Mean :0.0012279	Mean :0.002373	Mean :0.0014754
##	3rd Qu.:0.0014568	3rd Qu.:0.002849	3rd Qu.:0.0020812
##	Max. :0.0023505	Max. :0.003942	Max. :0.0022901
##	C96	C97	C99
##	Min. :0.0004647	Min. :0.001048	Min. :0.001967
##	1st Qu.:0.0007220	1st Qu.:0.001180	1st Qu.:0.002442
##	Median :0.0009420	Median :0.001368	Median :0.002760
##	Mean :0.0010435	Mean :0.001407	Mean :0.002681
##	3rd Qu.:0.0012413	3rd Qu.:0.001603	3rd Qu.:0.002925
##	Max. :0.0021508	Max. :0.001911	Max. :0.003301
##	C101	C102	C103
##	Min. :0.001010	Min. :0.001707	Min. :0.0006557
##	1st Qu.:0.001156	1st Qu.:0.002036	1st Qu.:0.0011064
##	Median :0.001472	Median :0.002538	Median :0.0014048
##	Mean :0.001775	Mean :0.002653	Mean :0.0014927
##	3rd Qu.:0.002029	3rd Qu.:0.003056	3rd Qu.:0.0017457
##	Max. :0.004384	Max. :0.004592	Max. :0.0028412
##	C104	C105	C106
##	Min. :0.0001818	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.0007646	1st Qu.:0.0002549	1st Qu.:0.000529
##	Median :0.0016225	Median :0.0004128	Median :0.001062
##	Mean :0.0016078	Mean :0.0004856	Mean :0.001115
##	3rd Qu.:0.0022646	3rd Qu.:0.0008025	3rd Qu.:0.001620
##	Max. :0.0033858	Max. :0.0009414	Max. :0.002454
##	C107	C108	C111
##	Min. :0.0004344	Min. :0.0001302	Min. :0.001401
##	1st Qu.:0.0006998	1st Qu.:0.0006446	1st Qu.:0.002096
##	Median :0.0009511	Median :0.0007066	Median :0.002404
##	Mean :0.0013134	Mean :0.0007464	Mean :0.002316
##	3rd Qu.:0.0018916	3rd Qu.:0.0009138	3rd Qu.:0.002738
##	Max. :0.0031489	Max. :0.0012402	Max. :0.003026
##	C112	C115	C117
##	Min. :0.0009737	Min. :0.000e+00	Min. :0.0005762
##	1st Qu.:0.0011885	1st Qu.:0.000e+00	1st Qu.:0.0008774
##	Median :0.0015258	Median :5.584e-05	Median :0.0011996
##	Mean :0.0015552	Mean :2.192e-04	Mean :0.0012523
##	3rd Qu.:0.0017009	3rd Qu.:4.100e-04	3rd Qu.:0.0015011
##	Max. :0.0027301	Max. :7.136e-04	Max. :0.0022778
##	C118	C120	C127
##	Min. :0.0004198	Min. :0.000000	Min. :0.0000000
##	1st Qu.:0.0005646	1st Qu.:0.000000	1st Qu.:0.0000000
##	Median :0.0006073	Median :0.000000	Median :0.0000000
##	Mean :0.0007512	Mean :0.001352	Mean :0.0001751

##	3rd Qu.:0.0008341	3rd Qu.:0.001003	3rd Qu.:0.0000000
##	Max. :0.0016220	Max. :0.008922	Max. :0.0017509
##	C129	C130	C131
##	Min. :0.0000000	Min. :0.001054	Min. :0.0004572
##	1st Qu.:0.0000000	1st Qu.:0.002862	1st Qu.:0.0012015
##	Median :0.0000000	Median :0.003327	Median :0.0016111
##	Mean :0.0001768	Mean :0.003884	Mean :0.0016956
##	3rd Qu.:0.0000000	3rd Qu.:0.004095	3rd Qu.:0.0017781
##	Max. :0.0017678	Max. :0.010672	Max. :0.0039623
##	C132	C133	C134
##	Min. :0.001314	Min. :0.0003817	Min. :0.0005342
##	1st Qu.:0.001703	1st Qu.:0.0003991	1st Qu.:0.0007317
##	Median :0.002083	Median :0.0004367	Median :0.0014657
##	Mean :0.002042	Mean :0.0004748	Mean :0.0012646
##	3rd Qu.:0.002371	3rd Qu.:0.0005229	3rd Qu.:0.0016090
##	Max. :0.002763	Max. :0.0006821	Max. :0.0021862
##	C135	C136	C140
##	Min. :0.0006133	Min. :0.001381	Min. :0.001878
##	1st Qu.:0.0008894	1st Qu.:0.002705	1st Qu.:0.002450
##	Median :0.0010229	Median :0.003202	Median :0.002929
##	Mean :0.0009906	Mean :0.003077	Mean :0.002805
##	3rd Qu.:0.0011581	3rd Qu.:0.003617	3rd Qu.:0.003144
##	Max. :0.0013017	Max. :0.004160	Max. :0.003848
##	C141	C142	C143
##	Min. :0.0008382	Min. :0.001034	Min. :0.0004503
##	1st Qu.:0.0012592	1st Qu.:0.001283	1st Qu.:0.0008539
##	Median :0.0014575	Median :0.001683	Median :0.0014301
##	Mean :0.0015294	Mean :0.001895	Mean :0.0014560
##	3rd Qu.:0.0019495	3rd Qu.:0.002538	3rd Qu.:0.0019110
##	Max. :0.0022383	Max. :0.003143	Max. :0.0029519
##	C144	C145	C146
##	Min. :0.001450	Min. :0.0002372	Min. :0.0001942
##	1st Qu.:0.001631	1st Qu.:0.0005694	1st Qu.:0.0003917
##	Median :0.001946	Median :0.0007362	Median :0.0006803
##	Mean :0.002302	Mean :0.0007693	Mean :0.0008982
##	3rd Qu.:0.002755	3rd Qu.:0.0009528	3rd Qu.:0.0011035
##	Max. :0.004480	Max. :0.0014154	Max. :0.0029378
##	C147	C148	C151
##	Min. :0.0006189	Min. :0.0006330	Min. :0.0002005
##	1st Qu.:0.0007153	1st Qu.:0.0007487	1st Qu.:0.0004396
##	Median :0.0008282	Median :0.0008858	Median :0.0007182
##	Mean :0.0009235	Mean :0.0010061	Mean :0.0007716
##	3rd Qu.:0.0009001	3rd Qu.:0.0010577	3rd Qu.:0.0009615
##	Max. :0.0018752	Max. :0.0022391	Max. :0.0018462
##	C153	C154	C156
##	Min. :0.0002197	Min. :0.0000000	Min. :0.0004883
##	1st Qu.:0.0003277	1st Qu.:0.0005227	1st Qu.:0.0007088
##	Median :0.0004733	Median :0.0007816	Median :0.0011432
##	Mean :0.0005972	Mean :0.0007407	Mean :0.0013475
##	3rd Qu.:0.0007011	3rd Qu.:0.0010587	3rd Qu.:0.0015200
##	Max. :0.0015042	Max. :0.0013663	Max. :0.0033185
##	C157	C158	C160
##	Min. :0.000e+00	Min. :0.001143	Min. :0.0008353
##	1st Qu.:0.000e+00	1st Qu.:0.001291	1st Qu.:0.0011903

## Median :7.388e-05	Median :0.001484	Median :0.0012682
## Mean :2.688e-04	Mean :0.001715	Mean :0.0012965
## 3rd Qu.:3.149e-04	3rd Qu.:0.002125	3rd Qu.:0.0012926
## Max. :1.538e-03	Max. :0.002640	Max. :0.0018058
## C163	C165	C168
## Min. :0.001172	Min. :0.0000000	Min. :0.0002310
## 1st Qu.:0.001333	1st Qu.:0.0000000	1st Qu.:0.0002445
## Median :0.001443	Median :0.0000000	Median :0.0002701
## Mean :0.001595	Mean :0.0003151	Mean :0.0002820
## 3rd Qu.:0.001582	3rd Qu.:0.0004247	3rd Qu.:0.0003175
## Max. :0.002559	Max. :0.0017895	Max. :0.0003686
## C169	C170	C171
## Min. :0.0000000	Min. :0.000000	Min. :0.01180
## 1st Qu.:0.0000000	1st Qu.:0.000000	1st Qu.:0.02433
## Median :0.0000000	Median :0.002784	Median :0.04311
## Mean :0.0002668	Mean :0.003643	Mean :0.04346
## 3rd Qu.:0.0000000	3rd Qu.:0.006558	3rd Qu.:0.05796
## Max. :0.0013957	Max. :0.011180	Max. :0.08241
## C172	C173	C183
## Min. :0.001136	Min. :0.0000000	Min. :0.000000
## 1st Qu.:0.003310	1st Qu.:0.0000000	1st Qu.:0.000749
## Median :0.009710	Median :0.0001166	Median :0.001689
## Mean :0.010141	Mean :0.0006674	Mean :0.006471
## 3rd Qu.:0.016703	3rd Qu.:0.0007269	3rd Qu.:0.006971
## Max. :0.020794	Max. :0.0043533	Max. :0.029451
## C187	C188	C191
## Min. :0.000e+00	Min. :0.000e+00	Min. :0.000000
## 1st Qu.:2.428e-05	1st Qu.:9.449e-05	1st Qu.:0.000000
## Median :4.870e-04	Median :2.168e-04	Median :0.000000
## Mean :5.273e-04	Mean :2.699e-04	Mean :0.000813
## 3rd Qu.:1.009e-03	3rd Qu.:4.776e-04	3rd Qu.:0.000000
## Max. :1.196e-03	Max. :5.570e-04	Max. :0.007466
## C192	C193	C194
## Min. :0.0007061	Min. :0.001356	Min. :0.0001423
## 1st Qu.:0.0009792	1st Qu.:0.001626	1st Qu.:0.0003202
## Median :0.0011633	Median :0.002009	Median :0.0006634
## Mean :0.0012454	Mean :0.002125	Mean :0.0008859
## 3rd Qu.:0.0013746	3rd Qu.:0.002362	3rd Qu.:0.0012260
## Max. :0.0021506	Max. :0.003859	Max. :0.0027165
## C195	C196	C197
## Min. :0.0000000	Min. :0.001118	Min. :0.001095
## 1st Qu.:0.0002092	1st Qu.:0.001459	1st Qu.:0.001429
## Median :0.0004926	Median :0.001759	Median :0.001597
## Mean :0.0004361	Mean :0.001701	Mean :0.001624
## 3rd Qu.:0.0005562	3rd Qu.:0.001868	3rd Qu.:0.001724
## Max. :0.0009816	Max. :0.002400	Max. :0.002762
## C199	C200	C201
## Min. :0.0009078	Min. :0.0007464	Min. :0.002205
## 1st Qu.:0.0011283	1st Qu.:0.0008827	1st Qu.:0.002421
## Median :0.0014061	Median :0.0011689	Median :0.002827
## Mean :0.0015118	Mean :0.0013307	Mean :0.003021
## 3rd Qu.:0.0018515	3rd Qu.:0.0017677	3rd Qu.:0.003235
## Max. :0.0024839	Max. :0.0021324	Max. :0.005184
## C202	C203	C204

##	Min. :0.0006979	Min. :0.0006971	Min. :0.001323
##	1st Qu.:0.0008663	1st Qu.:0.0012309	1st Qu.:0.001814
##	Median :0.0012513	Median :0.0017699	Median :0.002414
##	Mean :0.0012154	Mean :0.0017068	Mean :0.002395
##	3rd Qu.:0.0015239	3rd Qu.:0.0020505	3rd Qu.:0.002848
##	Max. :0.0016801	Max. :0.0026799	Max. :0.003450
##	C207	C208	C209
##	Min. :0.000e+00	Min. :0.0007106	Min. :0.000e+00
##	1st Qu.:0.000e+00	1st Qu.:0.0007423	1st Qu.:0.000e+00
##	Median :0.000e+00	Median :0.0007869	Median :0.000e+00
##	Mean :1.395e-05	Mean :0.0008208	Mean :1.389e-05
##	3rd Qu.:0.000e+00	3rd Qu.:0.0008753	3rd Qu.:0.000e+00
##	Max. :8.692e-05	Max. :0.0010469	Max. :7.987e-05
##	C213	C214	C215
##	Min. :0.0000000	Min. :0.0006308	Min. :0.001148
##	1st Qu.:0.0000000	1st Qu.:0.0007496	1st Qu.:0.002157
##	Median :0.0000000	Median :0.0007859	Median :0.002323
##	Mean :0.0000675	Mean :0.0008276	Mean :0.002324
##	3rd Qu.:0.0001137	3rd Qu.:0.0008816	3rd Qu.:0.002684
##	Max. :0.0003387	Max. :0.0010457	Max. :0.003474
##	C216	C217	C218
##	Min. :0.0009356	Min. :0.0001513	Min. :0.0008466
##	1st Qu.:0.0013085	1st Qu.:0.0005234	1st Qu.:0.0015788
##	Median :0.0014670	Median :0.0009236	Median :0.0018952
##	Mean :0.0014220	Mean :0.0007995	Mean :0.0020981
##	3rd Qu.:0.0016311	3rd Qu.:0.0009941	3rd Qu.:0.0023242
##	Max. :0.0018545	Max. :0.0013135	Max. :0.0039627
##	C219	C220	C221
##	Min. :0.000e+00	Min. :0.0003035	Min. :0.0007427
##	1st Qu.:5.721e-05	1st Qu.:0.0005979	1st Qu.:0.0014119
##	Median :6.583e-05	Median :0.0009257	Median :0.0016004
##	Mean :6.723e-05	Mean :0.0008724	Mean :0.0017040
##	3rd Qu.:7.857e-05	3rd Qu.:0.0011560	3rd Qu.:0.0021333
##	Max. :1.133e-04	Max. :0.0013340	Max. :0.0027892
##	C222	C223	C224
##	Min. :0.002956	Min. :0.000e+00	Min. :0.0006256
##	1st Qu.:0.003246	1st Qu.:7.689e-05	1st Qu.:0.0008998
##	Median :0.004013	Median :4.037e-04	Median :0.0011900
##	Mean :0.004720	Mean :4.065e-04	Mean :0.0011264
##	3rd Qu.:0.005544	3rd Qu.:6.366e-04	3rd Qu.:0.0012652
##	Max. :0.009032	Max. :9.678e-04	Max. :0.0015851
##	C225	C226	C227
##	Min. :0.0008237	Min. :0.002182	Min. :0.001989
##	1st Qu.:0.0023913	1st Qu.:0.002556	1st Qu.:0.002244
##	Median :0.0028524	Median :0.003260	Median :0.002291
##	Mean :0.0029438	Mean :0.003507	Mean :0.002586
##	3rd Qu.:0.0035533	3rd Qu.:0.003984	3rd Qu.:0.002532
##	Max. :0.0048156	Max. :0.006667	Max. :0.004029
##	C231	C232	C233
##	Min. :0.0000000	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.0009113	1st Qu.:0.0000000	1st Qu.:0.0001515
##	Median :0.0015770	Median :0.0001128	Median :0.0001753
##	Mean :0.0017306	Mean :0.0003216	Mean :0.0004226
##	3rd Qu.:0.0024079	3rd Qu.:0.0004624	3rd Qu.:0.0005211

## Max. :0.0036741	Max. :0.0016200	Max. :0.0017185
## C234	C235	C236
## Min. :0.0000000	Min. :0.000e+00	Min. :0.0003314
## 1st Qu.:0.0000000	1st Qu.:0.000e+00	1st Qu.:0.0007162
## Median :0.0000000	Median :0.000e+00	Median :0.0010564
## Mean :0.0001822	Mean :1.395e-05	Mean :0.0010370
## 3rd Qu.:0.0002313	3rd Qu.:0.000e+00	3rd Qu.:0.0013632
## Max. :0.0011322	Max. :1.395e-04	Max. :0.0017783
## C237	C238	C239
## Min. :0.0004658	Min. :0.0001933	Min. :0.0003441
## 1st Qu.:0.0011642	1st Qu.:0.0005539	1st Qu.:0.0005041
## Median :0.0012937	Median :0.0008196	Median :0.0005241
## Mean :0.0015525	Mean :0.0010231	Mean :0.0005108
## 3rd Qu.:0.0021172	3rd Qu.:0.0015842	3rd Qu.:0.0005457
## Max. :0.0031252	Max. :0.0019186	Max. :0.0006849
## C240	C241	C242
## Min. :0.0004628	Min. :0.0007017	Min. :0.001371
## 1st Qu.:0.0010675	1st Qu.:0.0008367	1st Qu.:0.001466
## Median :0.0013203	Median :0.0010237	Median :0.002035
## Mean :0.0014442	Mean :0.0011573	Mean :0.002051
## 3rd Qu.:0.0017297	3rd Qu.:0.0012284	3rd Qu.:0.002541
## Max. :0.0029728	Max. :0.0021162	Max. :0.003011
## C243	C244	C247
## Min. :0.0004764	Min. :0.0008321	Min. :0.0003487
## 1st Qu.:0.0009372	1st Qu.:0.0011085	1st Qu.:0.0004870
## Median :0.0011809	Median :0.0011946	Median :0.0005370
## Mean :0.0012912	Mean :0.0012193	Mean :0.0006054
## 3rd Qu.:0.0016491	3rd Qu.:0.0012493	3rd Qu.:0.0007368
## Max. :0.0024285	Max. :0.0018532	Max. :0.0010257
## C248	C249	C250
## Min. :0.0004346	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0004456	1st Qu.:0.0000000	1st Qu.:0.0000000
## Median :0.0005228	Median :0.0000000	Median :0.0000000
## Mean :0.0005425	Mean :0.0001459	Mean :0.0014805
## 3rd Qu.:0.0006249	3rd Qu.:0.0000000	3rd Qu.:0.0007405
## Max. :0.0007008	Max. :0.0009861	Max. :0.0080851
## C252	C253	C256
## Min. :0.000e+00	Min. :0.0002128	Min. :0.0000000
## 1st Qu.:5.989e-05	1st Qu.:0.0002721	1st Qu.:0.0001004
## Median :3.893e-04	Median :0.0002948	Median :0.0001673
## Mean :4.591e-04	Mean :0.0002957	Mean :0.0001605
## 3rd Qu.:7.979e-04	3rd Qu.:0.0003141	3rd Qu.:0.0002537
## Max. :1.167e-03	Max. :0.0003935	Max. :0.0002850
## C257	C258	C260
## Min. :0.0002292	Min. :0.001724	Min. :0.0000000
## 1st Qu.:0.0002878	1st Qu.:0.002642	1st Qu.:0.0001223
## Median :0.0003483	Median :0.003617	Median :0.0003092
## Mean :0.0003534	Mean :0.006329	Mean :0.0005255
## 3rd Qu.:0.0004177	3rd Qu.:0.004697	3rd Qu.:0.0006359
## Max. :0.0004619	Max. :0.031214	Max. :0.0021979
## C261	C264	C265
## Min. :0.000363	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:0.001310	1st Qu.:0.000e+00	1st Qu.:2.374e-05
## Median :0.001509	Median :5.193e-05	Median :1.089e-04

## Mean :0.001489	Mean :3.891e-03	Mean :1.255e-04
## 3rd Qu.:0.001860	3rd Qu.:1.948e-03	3rd Qu.:1.605e-04
## Max. :0.002330	Max. :2.711e-02	Max. :4.209e-04
## C266	C267	C268
## Min. :0.000000	Min. :0.000000	Min. :0.0000000
## 1st Qu.:0.001549	1st Qu.:0.01217	1st Qu.:0.0000000
## Median :0.008304	Median :0.01414	Median :0.0004294
## Mean :0.008330	Mean :0.02355	Mean :0.0030648
## 3rd Qu.:0.011790	3rd Qu.:0.01791	3rd Qu.:0.0035487
## Max. :0.021954	Max. :0.12171	Max. :0.0118815
## C269	C286	C288
## Min. :0.0000000	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0000000	1st Qu.:0.0005317	1st Qu.:0.0000000
## Median :0.0000000	Median :0.0027747	Median :0.001554
## Mean :0.0004394	Mean :0.0023169	Mean :0.005210
## 3rd Qu.:0.0000000	3rd Qu.:0.0038848	3rd Qu.:0.007550
## Max. :0.0043944	Max. :0.0045192	Max. :0.023915
## C290	C291	C292
## Min. :0.0004500	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0005640	1st Qu.:0.001588	1st Qu.:0.0002463
## Median :0.0005993	Median :0.002339	Median :0.0003202
## Mean :0.0006913	Mean :0.001996	Mean :0.0003296
## 3rd Qu.:0.0008228	3rd Qu.:0.002442	3rd Qu.:0.0004637
## Max. :0.0012220	Max. :0.003964	Max. :0.0005245
## C293	C294	C296
## Min. :0.0000000	Min. :0.0000000	Min. :0.001017
## 1st Qu.:0.001798	1st Qu.:0.0000000	1st Qu.:0.001252
## Median :0.011945	Median :0.0000000	Median :0.001528
## Mean :0.017434	Mean :0.0002096	Mean :0.001563
## 3rd Qu.:0.033954	3rd Qu.:0.0000000	3rd Qu.:0.001650
## Max. :0.044610	Max. :0.0020960	Max. :0.002354
## C297	C300	C301
## Min. :0.001734	Min. :0.0009093	Min. :0.0008364
## 1st Qu.:0.002028	1st Qu.:0.0015137	1st Qu.:0.0018925
## Median :0.002546	Median :0.0016319	Median :0.0021733
## Mean :0.002593	Mean :0.0017145	Mean :0.0024579
## 3rd Qu.:0.002990	3rd Qu.:0.0020743	3rd Qu.:0.0031493
## Max. :0.003858	Max. :0.0025052	Max. :0.0042289
## C303	C304	C305
## Min. :0.0000000	Min. :0.0000000	Min. :0.0007066
## 1st Qu.:0.0000822	1st Qu.:0.0006477	1st Qu.:0.0008303
## Median :0.0003116	Median :0.0011323	Median :0.0010481
## Mean :0.0005473	Mean :0.0009965	Mean :0.0010779
## 3rd Qu.:0.0006114	3rd Qu.:0.0013911	3rd Qu.:0.0013256
## Max. :0.0025734	Max. :0.0020951	Max. :0.0015463
## C306	C307	C308
## Min. :0.000e+00	Min. :0.0004612	Min. :0.0009186
## 1st Qu.:0.000e+00	1st Qu.:0.0007798	1st Qu.:0.0019643
## Median :0.000e+00	Median :0.0009700	Median :0.0023146
## Mean :1.115e-05	Mean :0.0009454	Mean :0.0025767
## 3rd Qu.:0.000e+00	3rd Qu.:0.0011367	3rd Qu.:0.0023773
## Max. :1.115e-04	Max. :0.0012924	Max. :0.0070375
## C309	C310	C312
## Min. :0.0000000	Min. :0.001619	Min. :0.000e+00

##	1st Qu.:0.0000000	1st Qu.:0.001742	1st Qu.:2.012e-05
##	Median :0.0000000	Median :0.001878	Median :1.061e-04
##	Mean :0.0002204	Mean :0.002280	Mean :1.221e-04
##	3rd Qu.:0.0002389	3rd Qu.:0.002657	3rd Qu.:1.485e-04
##	Max. :0.0013539	Max. :0.004192	Max. :3.673e-04
##	C313	C314	C315
##	Min. :0.0000000	Min. :0.001805	Min. :0.0009766
##	1st Qu.:0.0000000	1st Qu.:0.002438	1st Qu.:0.0018505
##	Median :0.0000000	Median :0.002892	Median :0.0026521
##	Mean :0.0000493	Mean :0.003083	Mean :0.0024921
##	3rd Qu.:0.0000000	3rd Qu.:0.003398	3rd Qu.:0.0031030
##	Max. :0.0003034	Max. :0.005030	Max. :0.0040858
##	C316	C317	C318
##	Min. :0.0005592	Min. :0.000e+00	Min. :0.0005150
##	1st Qu.:0.0005945	1st Qu.:0.000e+00	1st Qu.:0.0005921
##	Median :0.0006680	Median :0.000e+00	Median :0.0006093
##	Mean :0.0008016	Mean :7.633e-05	Mean :0.0007185
##	3rd Qu.:0.0008533	3rd Qu.:0.000e+00	3rd Qu.:0.0008257
##	Max. :0.0015814	Max. :4.303e-04	Max. :0.0011148
##	C319	C320	C322
##	Min. :0.001514	Min. :0.0006455	Min. :4.758e-05
##	1st Qu.:0.002053	1st Qu.:0.0008031	1st Qu.:7.476e-05
##	Median :0.002184	Median :0.0008683	Median :1.474e-04
##	Mean :0.002383	Mean :0.0009330	Mean :1.564e-04
##	3rd Qu.:0.002564	3rd Qu.:0.0010054	3rd Qu.:2.255e-04
##	Max. :0.003685	Max. :0.0015020	Max. :3.369e-04
##	C323	C325	C326
##	Min. :0.000000	Min. :9.245e-05	Min. :0.0003762
##	1st Qu.:0.001195	1st Qu.:1.055e-03	1st Qu.:0.0003867
##	Median :0.002402	Median :1.362e-03	Median :0.0004561
##	Mean :0.002269	Mean :1.454e-03	Mean :0.0004599
##	3rd Qu.:0.003637	3rd Qu.:2.048e-03	3rd Qu.:0.0004894
##	Max. :0.004698	Max. :2.748e-03	Max. :0.0006446
##	C327	C328	C329
##	Min. :0.000e+00	Min. :0.0003975	Min. :0.000568
##	1st Qu.:1.724e-05	1st Qu.:0.0008343	1st Qu.:0.001269
##	Median :3.830e-04	Median :0.0011037	Median :0.002139
##	Mean :5.019e-04	Mean :0.0009817	Mean :0.002212
##	3rd Qu.:6.489e-04	3rd Qu.:0.0011523	3rd Qu.:0.003103
##	Max. :2.092e-03	Max. :0.0012774	Max. :0.003967
##	C330	C331	C332
##	Min. :0.0007711	Min. :0.0000000	Min. :0.001571
##	1st Qu.:0.0009777	1st Qu.:0.0000000	1st Qu.:0.002157
##	Median :0.0010670	Median :0.0001637	Median :0.002659
##	Mean :0.0011872	Mean :0.0005383	Mean :0.002572
##	3rd Qu.:0.0012795	3rd Qu.:0.0010162	3rd Qu.:0.002800
##	Max. :0.0018430	Max. :0.0022180	Max. :0.003570
##	C333	C334	C335
##	Min. :0.0001937	Min. :0.0009573	Min. :0.0009396
##	1st Qu.:0.0001974	1st Qu.:0.0018863	1st Qu.:0.0014215
##	Median :0.0002377	Median :0.0022530	Median :0.0017303
##	Mean :0.0002549	Mean :0.0024272	Mean :0.0021504
##	3rd Qu.:0.0003115	3rd Qu.:0.0029362	3rd Qu.:0.0027207
##	Max. :0.0003582	Max. :0.0040743	Max. :0.0048883

##	C336	C337	C339
##	Min. :0.001066	Min. :0.0001386	Min. :0.000e+00
##	1st Qu.:0.001175	1st Qu.:0.0017538	1st Qu.:0.000e+00
##	Median :0.001399	Median :0.0024330	Median :2.691e-05
##	Mean :0.001513	Mean :0.0023546	Mean :5.007e-05
##	3rd Qu.:0.001730	3rd Qu.:0.0028081	3rd Qu.:6.744e-05
##	Max. :0.002325	Max. :0.0050151	Max. :1.988e-04
##	C340	C341	C342
##	Min. :0.000890	Min. :0.000e+00	Min. :0.0000000
##	1st Qu.:0.001266	1st Qu.:0.000e+00	1st Qu.:0.0001940
##	Median :0.001984	Median :0.000e+00	Median :0.0011645
##	Mean :0.001871	Mean :3.244e-05	Mean :0.0009562
##	3rd Qu.:0.002396	3rd Qu.:0.000e+00	3rd Qu.:0.0015639
##	Max. :0.002810	Max. :2.359e-04	Max. :0.0018297
##	C343	C344	C345
##	Min. :0.001147	Min. :0.003442	Min. :0.000e+00
##	1st Qu.:0.001492	1st Qu.:0.004604	1st Qu.:0.000e+00
##	Median :0.002034	Median :0.005082	Median :0.000e+00
##	Mean :0.002060	Mean :0.005247	Mean :2.943e-05
##	3rd Qu.:0.002282	3rd Qu.:0.005753	3rd Qu.:0.000e+00
##	Max. :0.003428	Max. :0.007688	Max. :2.291e-04
##	C347	C348	C349
##	Min. :0.0007094	Min. :0.0007266	Min. :0.0000000
##	1st Qu.:0.0008520	1st Qu.:0.0008171	1st Qu.:0.0000000
##	Median :0.0010456	Median :0.0011175	Median :0.0003458
##	Mean :0.0011707	Mean :0.0011530	Mean :0.0005165
##	3rd Qu.:0.0011648	3rd Qu.:0.0012636	3rd Qu.:0.0007979
##	Max. :0.0026540	Max. :0.0023345	Max. :0.0021360
##	C350	C351	C352
##	Min. :0.0000000	Min. :0.0000000	Min. :0.000838
##	1st Qu.:0.0005550	1st Qu.:0.0002055	1st Qu.:0.001293
##	Median :0.0006741	Median :0.0002919	Median :0.001532
##	Mean :0.0008043	Mean :0.0002469	Mean :0.001535
##	3rd Qu.:0.0012877	3rd Qu.:0.0003463	3rd Qu.:0.001832
##	Max. :0.0015127	Max. :0.0003859	Max. :0.002192
##	C353	C354	C356
##	Min. :0.0003735	Min. :0.000e+00	Min. :0.000e+00
##	1st Qu.:0.0004732	1st Qu.:0.000e+00	1st Qu.:0.000e+00
##	Median :0.0005353	Median :0.000e+00	Median :0.000e+00
##	Mean :0.0006254	Mean :5.476e-05	Mean :2.621e-05
##	3rd Qu.:0.0006310	3rd Qu.:8.467e-05	3rd Qu.:0.000e+00
##	Max. :0.0013635	Max. :2.723e-04	Max. :2.621e-04
##	C359	C360	C361
##	Min. :0.0000000	Min. :0.000000	Min. :7.495e-05
##	1st Qu.:0.0003293	1st Qu.:0.001060	1st Qu.:9.250e-04
##	Median :0.0003860	Median :0.001331	Median :1.646e-03
##	Mean :0.0005070	Mean :0.001290	Mean :1.828e-03
##	3rd Qu.:0.0007316	3rd Qu.:0.001670	3rd Qu.:2.475e-03
##	Max. :0.0012884	Max. :0.002374	Max. :5.051e-03
##	C362	C364	C365
##	Min. :0.0000000	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.0000000	1st Qu.:0.0005024	1st Qu.:0.0009945
##	Median :0.0001379	Median :0.0007686	Median :0.0030244
##	Mean :0.0003360	Mean :0.0009140	Mean :0.0027882

## 3rd Qu.:0.0006820	3rd Qu.:0.0011898	3rd Qu.:0.0041879
## Max. :0.0010437	Max. :0.0023209	Max. :0.0057159
## C366	C367	C368
## Min. :0.0000000	Min. :0.0005098	Min. :0.0004768
## 1st Qu.:0.0007335	1st Qu.:0.0014861	1st Qu.:0.0005676
## Median :0.0011053	Median :0.0020198	Median :0.0012793
## Mean :0.0012799	Mean :0.0018125	Mean :0.0011923
## 3rd Qu.:0.0013097	3rd Qu.:0.0022186	3rd Qu.:0.0016109
## Max. :0.0043397	Max. :0.0027089	Max. :0.0020150
## C369	C374	C375
## Min. :0.001183	Min. :0.0000000	Min. :0.000e+00
## 1st Qu.:0.001410	1st Qu.:0.0000000	1st Qu.:2.245e-05
## Median :0.001717	Median :0.0000000	Median :1.970e-04
## Mean :0.002157	Mean :0.0002164	Mean :1.900e-04
## 3rd Qu.:0.002606	3rd Qu.:0.0000000	3rd Qu.:3.318e-04
## Max. :0.004139	Max. :0.0019057	Max. :4.148e-04
## C376	C377	C378
## Min. :0.001543	Min. :0.0004918	Min. :0.0003574
## 1st Qu.:0.002281	1st Qu.:0.0011680	1st Qu.:0.0006439
## Median :0.002783	Median :0.0017431	Median :0.0010643
## Mean :0.003029	Mean :0.0017066	Mean :0.0015399
## 3rd Qu.:0.003748	3rd Qu.:0.0022113	3rd Qu.:0.0014499
## Max. :0.004886	Max. :0.0028173	Max. :0.0056218
## C379	C380	C381
## Min. :0.0004798	Min. :0.001442	Min. :0.0000000
## 1st Qu.:0.0009407	1st Qu.:0.001613	1st Qu.:0.0002496
## Median :0.0016515	Median :0.001845	Median :0.0011171
## Mean :0.0014527	Mean :0.001893	Mean :0.0013298
## 3rd Qu.:0.0020034	3rd Qu.:0.002092	3rd Qu.:0.0014697
## Max. :0.0022055	Max. :0.002449	Max. :0.0049392
## C382	C383	C384
## Min. :0.001527	Min. :9.272e-05	Min. :6.209e-05
## 1st Qu.:0.001772	1st Qu.:5.446e-04	1st Qu.:2.174e-04
## Median :0.001945	Median :8.216e-04	Median :2.703e-04
## Mean :0.002255	Mean :8.436e-04	Mean :3.152e-04
## 3rd Qu.:0.002614	3rd Qu.:1.198e-03	3rd Qu.:4.144e-04
## Max. :0.003884	Max. :1.479e-03	Max. :6.157e-04
## C385	C386	C387
## Min. :0.001430	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:0.001604	1st Qu.:5.596e-05	1st Qu.:0.000e+00
## Median :0.001767	Median :7.863e-05	Median :0.000e+00
## Mean :0.001869	Mean :8.995e-05	Mean :1.005e-05
## 3rd Qu.:0.002152	3rd Qu.:1.232e-04	3rd Qu.:0.000e+00
## Max. :0.002446	Max. :1.977e-04	Max. :1.005e-04
## C388	C389	C390
## Min. :0.0000000	Min. :0.000e+00	Min. :0.0006941
## 1st Qu.:0.0002896	1st Qu.:0.000e+00	1st Qu.:0.0012387
## Median :0.0004932	Median :0.000e+00	Median :0.0019725
## Mean :0.0007627	Mean :3.648e-05	Mean :0.0018121
## 3rd Qu.:0.0011139	3rd Qu.:0.000e+00	3rd Qu.:0.0024477
## Max. :0.0023592	Max. :3.011e-04	Max. :0.0028624
## C391	C392	C393
## Min. :0.0000000	Min. :0.0000000	Min. :0.0009236
## 1st Qu.:0.002075	1st Qu.:0.0002517	1st Qu.:0.0014737

## Median :0.002507	Median :0.0005189	Median :0.0016633
## Mean :0.002433	Mean :0.0004897	Mean :0.0017348
## 3rd Qu.:0.003100	3rd Qu.:0.0007477	3rd Qu.:0.0019924
## Max. :0.004048	Max. :0.0010019	Max. :0.0026486
## C394	C395	C400
## Min. :0.0008084	Min. :0.000e+00	Min. :0.0004026
## 1st Qu.:0.0013816	1st Qu.:0.000e+00	1st Qu.:0.0008451
## Median :0.0020463	Median :0.000e+00	Median :0.0017352
## Mean :0.0023521	Mean :8.572e-05	Mean :0.0016668
## 3rd Qu.:0.0029535	3rd Qu.:1.664e-04	3rd Qu.:0.0020720
## Max. :0.0050417	Max. :3.246e-04	Max. :0.0037149
## C401	C402	C404
## Min. :0.0006796	Min. :0.0008877	Min. :0.000e+00
## 1st Qu.:0.0012319	1st Qu.:0.0010609	1st Qu.:0.000e+00
## Median :0.0015096	Median :0.0011859	Median :0.000e+00
## Mean :0.0014344	Mean :0.0016930	Mean :3.581e-05
## 3rd Qu.:0.0017381	3rd Qu.:0.0019638	3rd Qu.:0.000e+00
## Max. :0.0019829	Max. :0.0041280	Max. :2.980e-04
## C408	C409	C411
## Min. :0.0002379	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:0.0004764	1st Qu.:5.493e-05	1st Qu.:0.000e+00
## Median :0.0008504	Median :3.708e-04	Median :0.000e+00
## Mean :0.0007911	Mean :3.594e-04	Mean :4.214e-05
## 3rd Qu.:0.0010042	3rd Qu.:5.404e-04	3rd Qu.:0.000e+00
## Max. :0.0013377	Max. :9.736e-04	Max. :2.538e-04
## C415	C417	C418
## Min. :0.000e+00	Min. :0.0009492	Min. :0.0000000
## 1st Qu.:9.966e-05	1st Qu.:0.0010729	1st Qu.:0.0003203
## Median :3.207e-04	Median :0.0012829	Median :0.0004703
## Mean :3.707e-04	Mean :0.0012656	Mean :0.0006044
## 3rd Qu.:5.808e-04	3rd Qu.:0.0013986	3rd Qu.:0.0009302
## Max. :9.113e-04	Max. :0.0016126	Max. :0.0013466
## C420	C421	C424
## Min. :7.838e-05	Min. :0.0002804	Min. :0.000e+00
## 1st Qu.:1.330e-04	1st Qu.:0.0005840	1st Qu.:0.000e+00
## Median :1.788e-04	Median :0.0009267	Median :0.000e+00
## Mean :2.006e-04	Mean :0.0009168	Mean :2.687e-05
## 3rd Qu.:2.623e-04	3rd Qu.:0.0011862	3rd Qu.:0.000e+00
## Max. :3.833e-04	Max. :0.0016065	Max. :2.687e-04
## C426	C427	C428
## Min. :0.000e+00	Min. :0.0000000	Min. :0.001283
## 1st Qu.:0.000e+00	1st Qu.:0.0003383	1st Qu.:0.001500
## Median :0.000e+00	Median :0.0005971	Median :0.001691
## Mean :3.393e-05	Mean :0.0007505	Mean :0.001668
## 3rd Qu.:4.792e-05	3rd Qu.:0.0012317	3rd Qu.:0.001871
## Max. :1.837e-04	Max. :0.0016667	Max. :0.001944
## C431	C434	C435
## Min. :0.000e+00	Min. :0.0001466	Min. :0.0001068
## 1st Qu.:0.000e+00	1st Qu.:0.0002896	1st Qu.:0.0002669
## Median :0.000e+00	Median :0.0005457	Median :0.0010587
## Mean :3.687e-05	Mean :0.0005862	Mean :0.0008166
## 3rd Qu.:5.185e-05	3rd Qu.:0.0007329	3rd Qu.:0.0011058
## Max. :2.296e-04	Max. :0.0012589	Max. :0.0017208
## C436	C437	C439

## Min. :0.0003901	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0006706	1st Qu.:0.0000000	1st Qu.:0.0000000
## Median :0.0007600	Median :0.0000000	Median :0.0001543
## Mean :0.0008251	Mean :0.0001014	Mean :0.0003792
## 3rd Qu.:0.0010242	3rd Qu.:0.0000000	3rd Qu.:0.0005378
## Max. :0.0012949	Max. :0.0005691	Max. :0.0013688
## C441	C442	C443
## Min. :0.0000000	Min. :0.0007588	Min. :6.263e-05
## 1st Qu.:0.0004033	1st Qu.:0.0009079	1st Qu.:7.642e-04
## Median :0.0005999	Median :0.0010248	Median :1.134e-03
## Mean :0.0008897	Mean :0.0012915	Mean :1.041e-03
## 3rd Qu.:0.0013373	3rd Qu.:0.0017296	3rd Qu.:1.279e-03
## Max. :0.0025965	Max. :0.0021982	Max. :1.889e-03
## C444	C447	C448
## Min. :0.0000000	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0000000	1st Qu.:0.0000000	1st Qu.:0.0000000
## Median :0.0000000	Median :0.0000000	Median :0.0000000
## Mean :0.0002107	Mean :0.005518	Mean :0.007856
## 3rd Qu.:0.0000000	3rd Qu.:0.0000000	3rd Qu.:0.014884
## Max. :0.0018851	Max. :0.045796	Max. :0.032917
## C449	C450	C451
## Min. :0.000e+00	Min. :0.0003065	Min. :0.0003051
## 1st Qu.:0.000e+00	1st Qu.:0.0003589	1st Qu.:0.0004588
## Median :0.000e+00	Median :0.0004630	Median :0.0006187
## Mean :3.889e-04	Mean :0.0004794	Mean :0.0005920
## 3rd Qu.:8.436e-05	3rd Qu.:0.0005966	3rd Qu.:0.0007082
## Max. :3.663e-03	Max. :0.0006928	Max. :0.0008671
## C453	C454	C455
## Min. :0.000e+00	Min. :0.0003518	Min. :0.0000000
## 1st Qu.:1.922e-05	1st Qu.:0.0004190	1st Qu.:0.01087
## Median :1.224e-04	Median :0.0004473	Median :0.01690
## Mean :9.402e-05	Mean :0.0005141	Mean :0.02208
## 3rd Qu.:1.521e-04	3rd Qu.:0.0005524	3rd Qu.:0.02417
## Max. :1.615e-04	Max. :0.0009188	Max. :0.07799
## C456	C457	C459
## Min. :0.0000000	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:0.0000000	1st Qu.:5.343e-05	1st Qu.:0.000e+00
## Median :0.0000000	Median :4.021e-04	Median :9.123e-05
## Mean :0.0001732	Mean :1.267e-03	Mean :5.581e-04
## 3rd Qu.:0.0000000	3rd Qu.:1.398e-03	3rd Qu.:3.527e-04
## Max. :0.0008926	Max. :5.455e-03	Max. :3.598e-03
## C460	C461	C496
## Min. :0.007891	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.048626	1st Qu.:0.0001515	1st Qu.:0.0001210
## Median :0.074999	Median :0.0007644	Median :0.0004024
## Mean :0.077108	Mean :0.0018114	Mean :0.0003687
## 3rd Qu.:0.091516	3rd Qu.:0.0022415	3rd Qu.:0.0005895
## Max. :0.157810	Max. :0.0071185	Max. :0.0007603
## C498	C499	C500
## Min. :0.0000000	Min. :0.0003360	Min. :0.000e+00
## 1st Qu.:0.0000000	1st Qu.:0.0009629	1st Qu.:5.874e-05
## Median :0.002579	Median :0.0012400	Median :1.289e-04
## Mean :0.005347	Mean :0.0010790	Mean :1.950e-04
## 3rd Qu.:0.010600	3rd Qu.:0.0013676	3rd Qu.:2.970e-04

## Max. :0.015529	Max. :0.0013935	Max. :6.266e-04
## C506	C508	C509
## Min. :0.0000000	Min. :0.000e+00	Min. :0.0000000
## 1st Qu.:0.0001172	1st Qu.:0.000e+00	1st Qu.:0.0000000
## Median :0.0001515	Median :3.188e-05	Median :0.0000000
## Mean :0.0001483	Mean :1.150e-04	Mean :0.0001871
## 3rd Qu.:0.0001680	3rd Qu.:2.538e-04	3rd Qu.:0.0000000
## Max. :0.0002851	Max. :3.696e-04	Max. :0.0018705
## C510	C511	C512
## Min. :0.0008048	Min. :0.0000000	Min. :0.001614
## 1st Qu.:0.0014433	1st Qu.:0.0002706	1st Qu.:0.002007
## Median :0.0015969	Median :0.0003979	Median :0.002161
## Mean :0.0016933	Mean :0.0004716	Mean :0.002350
## 3rd Qu.:0.0019651	3rd Qu.:0.0005726	3rd Qu.:0.002743
## Max. :0.0026455	Max. :0.0014750	Max. :0.003215
## C513	C514	C516
## Min. :0.000000	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.001244	1st Qu.:0.0000000	1st Qu.:0.0000000
## Median :0.001735	Median :0.0000000	Median :0.0000000
## Mean :0.001561	Mean :0.0004843	Mean :0.0001751
## 3rd Qu.:0.002057	3rd Qu.:0.0009115	3rd Qu.:0.0000000
## Max. :0.002663	Max. :0.0018642	Max. :0.0010692
## C517	C518	C519
## Min. :0.0001717	Min. :0.0001938	Min. :0.000e+00
## 1st Qu.:0.0004397	1st Qu.:0.0005208	1st Qu.:0.000e+00
## Median :0.0007667	Median :0.0006362	Median :9.403e-05
## Mean :0.0007093	Mean :0.0006335	Mean :1.519e-04
## 3rd Qu.:0.0009949	3rd Qu.:0.0006977	3rd Qu.:1.931e-04
## Max. :0.0011133	Max. :0.0012130	Max. :6.537e-04
## C520	C521	C523
## Min. :0.0004864	Min. :0.001968	Min. :0.002486
## 1st Qu.:0.0006309	1st Qu.:0.002643	1st Qu.:0.002841
## Median :0.0007636	Median :0.002841	Median :0.003344
## Mean :0.0008269	Mean :0.002922	Mean :0.003600
## 3rd Qu.:0.0010545	3rd Qu.:0.003443	3rd Qu.:0.004092
## Max. :0.0012095	Max. :0.003791	Max. :0.006049
## C525	C526	C527
## Min. :0.001431	Min. :0.0002665	Min. :0.0002602
## 1st Qu.:0.001886	1st Qu.:0.0003108	1st Qu.:0.0008664
## Median :0.002095	Median :0.0003987	Median :0.0014514
## Mean :0.002547	Mean :0.0004098	Mean :0.0014809
## 3rd Qu.:0.003061	3rd Qu.:0.0004609	3rd Qu.:0.0018815
## Max. :0.004321	Max. :0.0006951	Max. :0.0028312
## C528	C529	C530
## Min. :0.001150	Min. :0.0008069	Min. :0.001340
## 1st Qu.:0.001966	1st Qu.:0.0012396	1st Qu.:0.001565
## Median :0.002517	Median :0.0016767	Median :0.001979
## Mean :0.003087	Mean :0.0022148	Mean :0.002004
## 3rd Qu.:0.004315	3rd Qu.:0.0034490	3rd Qu.:0.002209
## Max. :0.005667	Max. :0.0039788	Max. :0.003013
## C531	C532	C535
## Min. :0.000e+00	Min. :0.000e+00	Min. :0.0006721
## 1st Qu.:7.247e-05	1st Qu.:7.768e-05	1st Qu.:0.0007753
## Median :1.495e-04	Median :1.212e-04	Median :0.0009430

## Mean :1.265e-04	Mean :1.338e-04	Mean :0.0009608
## 3rd Qu.:2.008e-04	3rd Qu.:1.965e-04	3rd Qu.:0.0011576
## Max. :2.144e-04	Max. :2.791e-04	Max. :0.0013548
## C536	C537	C538
## Min. :0.0001813	Min. :0.000000	Min. :0.0003788
## 1st Qu.:0.0003323	1st Qu.:0.001086	1st Qu.:0.0015247
## Median :0.0003771	Median :0.001784	Median :0.0018546
## Mean :0.0003965	Mean :0.001603	Mean :0.0017837
## 3rd Qu.:0.0004830	3rd Qu.:0.002216	3rd Qu.:0.0020395
## Max. :0.0007051	Max. :0.002905	Max. :0.0028634
## C539	C540	C541
## Min. :0.001691	Min. :0.0003205	Min. :9.074e-05
## 1st Qu.:0.001921	1st Qu.:0.0013016	1st Qu.:4.333e-04
## Median :0.002211	Median :0.0020202	Median :5.110e-04
## Mean :0.002349	Mean :0.0017997	Mean :5.430e-04
## 3rd Qu.:0.002871	3rd Qu.:0.0021950	3rd Qu.:6.812e-04
## Max. :0.003207	Max. :0.0027817	Max. :1.130e-03
## C542	C543	C544
## Min. :0.0000000	Min. :0.000000	Min. :0.0004151
## 1st Qu.:0.0001325	1st Qu.:0.001817	1st Qu.:0.0006404
## Median :0.0006517	Median :0.002185	Median :0.0016211
## Mean :0.0005962	Mean :0.001903	Mean :0.0017365
## 3rd Qu.:0.0007114	3rd Qu.:0.002479	3rd Qu.:0.0027282
## Max. :0.0014427	Max. :0.002961	Max. :0.0034514
## C545	C546	C549
## Min. :0.000000	Min. :0.000e+00	Min. :0.0005958
## 1st Qu.:0.000832	1st Qu.:3.601e-05	1st Qu.:0.0006719
## Median :0.001128	Median :5.676e-04	Median :0.0007867
## Mean :0.001083	Mean :6.703e-04	Mean :0.0008869
## 3rd Qu.:0.001539	3rd Qu.:8.834e-04	3rd Qu.:0.0010620
## Max. :0.001724	Max. :2.393e-03	Max. :0.0014234
## C550	C551	C552
## Min. :0.000000	Min. :0.002144	Min. :0.0000000
## 1st Qu.:0.001008	1st Qu.:0.003066	1st Qu.:0.0001728
## Median :0.001289	Median :0.003649	Median :0.0002438
## Mean :0.001410	Mean :0.003496	Mean :0.0002221
## 3rd Qu.:0.001999	3rd Qu.:0.003897	3rd Qu.:0.0003111
## Max. :0.002341	Max. :0.005084	Max. :0.0003512
## C553	C554	C555
## Min. :0.000558	Min. :0.0007843	Min. :6.510e-05
## 1st Qu.:0.001188	1st Qu.:0.0011232	1st Qu.:8.909e-05
## Median :0.001276	Median :0.0016170	Median :9.574e-05
## Mean :0.001319	Mean :0.0015492	Mean :9.796e-05
## 3rd Qu.:0.001582	3rd Qu.:0.0018808	3rd Qu.:1.145e-04
## Max. :0.002037	Max. :0.0024737	Max. :1.235e-04
## C556	C557	C558
## Min. :0.000e+00	Min. :0.0000000	Min. :0.0002809
## 1st Qu.:7.475e-05	1st Qu.:0.0000000	1st Qu.:0.0008200
## Median :7.842e-05	Median :0.0000000	Median :0.0009183
## Mean :8.848e-05	Mean :0.0002282	Mean :0.0009380
## 3rd Qu.:1.025e-04	3rd Qu.:0.0002293	3rd Qu.:0.0011774
## Max. :1.864e-04	Max. :0.0011761	Max. :0.0014475
## C559	C560	C561
## Min. :0.0000000	Min. :0.0006459	Min. :0.001388

## 1st Qu.:0.0000000	1st Qu.:0.0010610	1st Qu.:0.002959
## Median :0.0000000	Median :0.0015043	Median :0.004854
## Mean :0.0001682	Mean :0.0015306	Mean :0.004340
## 3rd Qu.:0.0003080	3rd Qu.:0.0019906	3rd Qu.:0.005447
## Max. :0.0007649	Max. :0.0025459	Max. :0.007310
## C562	C563	C566
## Min. :0.0000000	Min. :0.000475	Min. :0.0000000
## 1st Qu.:0.0002848	1st Qu.:0.001170	1st Qu.:0.0004345
## Median :0.0004691	Median :0.001388	Median :0.0005898
## Mean :0.0007216	Mean :0.001595	Mean :0.0006700
## 3rd Qu.:0.0009600	3rd Qu.:0.001995	3rd Qu.:0.0007734
## Max. :0.0022667	Max. :0.003043	Max. :0.0015840
## C568	C569	C570
## Min. :0.0004817	Min. :0.0003922	Min. :0.0002518
## 1st Qu.:0.0006111	1st Qu.:0.0005105	1st Qu.:0.0003225
## Median :0.0007102	Median :0.0005998	Median :0.0003690
## Mean :0.0007142	Mean :0.0006432	Mean :0.0004040
## 3rd Qu.:0.0008040	3rd Qu.:0.0007071	3rd Qu.:0.0005175
## Max. :0.0010147	Max. :0.0010418	Max. :0.0005587
## C573	C574	C575
## Min. :0.001275	Min. :0.0000000	Min. :0.000e+00
## 1st Qu.:0.001374	1st Qu.:0.0003783	1st Qu.:0.000e+00
## Median :0.001542	Median :0.0012646	Median :0.000e+00
## Mean :0.001594	Mean :0.0014855	Mean :2.898e-05
## 3rd Qu.:0.001695	3rd Qu.:0.0024552	3rd Qu.:0.000e+00
## Max. :0.002296	Max. :0.0035953	Max. :2.898e-04
## C576	C577	C579
## Min. :0.0001085	Min. :0.000e+00	Min. :9.705e-05
## 1st Qu.:0.0001492	1st Qu.:5.548e-05	1st Qu.:6.414e-04
## Median :0.0001927	Median :1.575e-04	Median :1.400e-03
## Mean :0.0002020	Mean :1.329e-04	Mean :1.239e-03
## 3rd Qu.:0.0002143	3rd Qu.:2.144e-04	3rd Qu.:1.628e-03
## Max. :0.0003579	Max. :2.541e-04	Max. :2.510e-03
## C580	C582	C583
## Min. :0.000e+00	Min. :0.001001	Min. :0.0000000
## 1st Qu.:0.000e+00	1st Qu.:0.002128	1st Qu.:0.0005606
## Median :3.663e-05	Median :0.002584	Median :0.0008431
## Mean :7.385e-05	Mean :0.002583	Mean :0.0008351
## 3rd Qu.:1.348e-04	3rd Qu.:0.003131	3rd Qu.:0.0010012
## Max. :2.699e-04	Max. :0.003917	Max. :0.0022144
## C584	C586	C587
## Min. :0.000000	Min. :0.000e+00	Min. :0.0001375
## 1st Qu.:0.001962	1st Qu.:0.000e+00	1st Qu.:0.0003145
## Median :0.003368	Median :0.000e+00	Median :0.0003853
## Mean :0.003068	Mean :9.289e-06	Mean :0.0003746
## 3rd Qu.:0.004070	3rd Qu.:0.000e+00	3rd Qu.:0.0004439
## Max. :0.006007	Max. :9.289e-05	Max. :0.0005714
## C588	C589	C590
## Min. :0.0001246	Min. :0.0007788	Min. :0.0000000
## 1st Qu.:0.0005998	1st Qu.:0.0012176	1st Qu.:0.0008237
## Median :0.0008487	Median :0.0016482	Median :0.0031378
## Mean :0.0007675	Mean :0.0017681	Mean :0.0027637
## 3rd Qu.:0.0009717	3rd Qu.:0.0022207	3rd Qu.:0.0042393
## Max. :0.0011775	Max. :0.0029508	Max. :0.0060612

##	C591	C592	C593
##	Min. :0.0000000	Min. :0.0000000	Min. :0.000e+00
##	1st Qu.:0.0003518	1st Qu.:0.0000000	1st Qu.:0.000e+00
##	Median :0.0005140	Median :0.0001121	Median :0.000e+00
##	Mean :0.0005836	Mean :0.0003804	Mean :5.984e-05
##	3rd Qu.:0.0008492	3rd Qu.:0.0006997	3rd Qu.:5.971e-05
##	Max. :0.0012806	Max. :0.0013749	Max. :3.627e-04
##	C595	C596	C597
##	Min. :0.0005436	Min. :0.001350	Min. :0.0000000
##	1st Qu.:0.0015999	1st Qu.:0.001596	1st Qu.:0.0008843
##	Median :0.0022694	Median :0.001717	Median :0.0010167
##	Mean :0.0023710	Mean :0.001805	Mean :0.0011252
##	3rd Qu.:0.0032403	3rd Qu.:0.002033	3rd Qu.:0.0011765
##	Max. :0.0042207	Max. :0.002401	Max. :0.0030778
##	C598	C599	C600
##	Min. :5.283e-05	Min. :0.0004267	Min. :0.0000000
##	1st Qu.:6.120e-05	1st Qu.:0.0013110	1st Qu.:0.0000000
##	Median :7.264e-05	Median :0.0018149	Median :0.0001123
##	Mean :7.223e-05	Mean :0.0019532	Mean :0.0001882
##	3rd Qu.:8.441e-05	3rd Qu.:0.0024578	3rd Qu.:0.0002495
##	Max. :9.061e-05	Max. :0.0037068	Max. :0.0006871
##	C601	C602	C603
##	Min. :0.0009163	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.0015019	1st Qu.:0.0009356	1st Qu.:0.0000174
##	Median :0.0017332	Median :0.0014632	Median :0.0002781
##	Mean :0.0018895	Mean :0.0015814	Mean :0.0003580
##	3rd Qu.:0.0022080	3rd Qu.:0.0023456	3rd Qu.:0.0006733
##	Max. :0.0035689	Max. :0.0035600	Max. :0.0008550
##	C604	C605	C606
##	Min. :0.0000000	Min. :0.000e+00	Min. :0.000e+00
##	1st Qu.:0.0004676	1st Qu.:0.000e+00	1st Qu.:0.000e+00
##	Median :0.0006541	Median :0.000e+00	Median :6.597e-05
##	Mean :0.0006951	Mean :7.824e-06	Mean :7.442e-05
##	3rd Qu.:0.0010206	3rd Qu.:0.000e+00	3rd Qu.:1.308e-04
##	Max. :0.0013431	Max. :7.824e-05	Max. :2.034e-04
##	C608	C609	C610
##	Min. :0.0002435	Min. :0.0000000	Min. :0.0004706
##	1st Qu.:0.0003778	1st Qu.:0.0008393	1st Qu.:0.0005861
##	Median :0.0007403	Median :0.0013469	Median :0.0006805
##	Mean :0.0007678	Mean :0.0017605	Mean :0.0008365
##	3rd Qu.:0.0010820	3rd Qu.:0.0019853	3rd Qu.:0.0008983
##	Max. :0.0015050	Max. :0.0062583	Max. :0.0021530
##	C611	C612	C613
##	Min. :0.0003704	Min. :0.0000000	Min. :0.0002913
##	1st Qu.:0.0005566	1st Qu.:0.0000000	1st Qu.:0.0006744
##	Median :0.0006287	Median :0.0000000	Median :0.0007644
##	Mean :0.0007511	Mean :0.0001796	Mean :0.0007957
##	3rd Qu.:0.0007235	3rd Qu.:0.0000000	3rd Qu.:0.0009487
##	Max. :0.0018890	Max. :0.0015839	Max. :0.0012289
##	C614	C618	C620
##	Min. :0.0003278	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.0004503	1st Qu.:0.0006718	1st Qu.:0.0000000
##	Median :0.0005242	Median :0.0011971	Median :0.0000000
##	Mean :0.0006022	Mean :0.0013725	Mean :0.0001660

## 3rd Qu.:0.0005772	3rd Qu.:0.0018826	3rd Qu.:0.0002893
## Max. :0.0015055	Max. :0.0028833	Max. :0.0006189
## C621	C622	C623
## Min. :0.0000000	Min. :0.0002119	Min. :0.0001944
## 1st Qu.:0.0004616	1st Qu.:0.0002409	1st Qu.:0.0003798
## Median :0.0007677	Median :0.0002787	Median :0.0010025
## Mean :0.0008917	Mean :0.0002915	Mean :0.0010892
## 3rd Qu.:0.0015101	3rd Qu.:0.0003358	3rd Qu.:0.0014639
## Max. :0.0018110	Max. :0.0004362	Max. :0.0030372
## C624	C625	C626
## Min. :0.000e+00	Min. :8.942e-05	Min. :0.000e+00
## 1st Qu.:3.669e-05	1st Qu.:2.401e-04	1st Qu.:0.000e+00
## Median :1.977e-04	Median :4.280e-04	Median :0.000e+00
## Mean :1.804e-04	Mean :3.842e-04	Mean :2.734e-05
## 3rd Qu.:2.708e-04	3rd Qu.:5.320e-04	3rd Qu.:5.197e-05
## Max. :3.992e-04	Max. :6.009e-04	Max. :1.073e-04
## C627	C628	C629
## Min. :0.0000000	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0000000	1st Qu.:0.0004338	1st Qu.:0.0004200
## Median :0.0000000	Median :0.0008786	Median :0.0006259
## Mean :0.0002173	Mean :0.0010514	Mean :0.0010016
## 3rd Qu.:0.0001189	3rd Qu.:0.0016001	3rd Qu.:0.0016675
## Max. :0.0017088	Max. :0.0025046	Max. :0.0025161
## C630	C631	C632
## Min. :0.001126	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:0.001970	1st Qu.:0.000e+00	1st Qu.:0.000e+00
## Median :0.002408	Median :0.000e+00	Median :0.000e+00
## Mean :0.002379	Mean :1.706e-05	Mean :4.828e-05
## 3rd Qu.:0.002580	3rd Qu.:3.987e-05	3rd Qu.:0.000e+00
## Max. :0.003845	Max. :6.292e-05	Max. :3.002e-04
## C633	C634	C638
## Min. :0.0000000	Min. :0.000e+00	Min. :0.0000000
## 1st Qu.:0.0002392	1st Qu.:0.000e+00	1st Qu.:0.0004038
## Median :0.0006448	Median :0.000e+00	Median :0.0008511
## Mean :0.0006844	Mean :2.316e-05	Mean :0.0009239
## 3rd Qu.:0.0008319	3rd Qu.:0.000e+00	3rd Qu.:0.0013312
## Max. :0.0017289	Max. :2.316e-04	Max. :0.0020706
## C639	C640	C641
## Min. :0.0004230	Min. :0.0005909	Min. :0.000e+00
## 1st Qu.:0.0008871	1st Qu.:0.0011606	1st Qu.:0.000e+00
## Median :0.0015638	Median :0.0012798	Median :0.000e+00
## Mean :0.0013989	Mean :0.0014373	Mean :1.586e-05
## 3rd Qu.:0.0018012	3rd Qu.:0.0016218	3rd Qu.:0.000e+00
## Max. :0.0022456	Max. :0.0027629	Max. :8.813e-05
## C644	C645	C646
## Min. :0.0001360	Min. :0.000e+00	Min. :0.0006056
## 1st Qu.:0.0002282	1st Qu.:0.000e+00	1st Qu.:0.0009732
## Median :0.0002331	Median :0.000e+00	Median :0.0013585
## Mean :0.0002319	Mean :2.864e-05	Mean :0.0013879
## 3rd Qu.:0.0002562	3rd Qu.:0.000e+00	3rd Qu.:0.0015678
## Max. :0.0002905	Max. :2.864e-04	Max. :0.0028489
## C647	C648	C649
## Min. :5.396e-05	Min. :6.438e-05	Min. :0.0004612
## 1st Qu.:7.370e-05	1st Qu.:8.596e-04	1st Qu.:0.0008754

## Median :1.008e-04	Median :1.197e-03	Median :0.0010281
## Mean :1.060e-04	Mean :1.176e-03	Mean :0.0009769
## 3rd Qu.:1.226e-04	3rd Qu.:1.543e-03	3rd Qu.:0.0011445
## Max. :1.740e-04	Max. :2.337e-03	Max. :0.0013240
## C650	C651	C652
## Min. :0.000e+00	Min. :0.000e+00	Min. :0.0003392
## 1st Qu.:0.000e+00	1st Qu.:0.000e+00	1st Qu.:0.0010500
## Median :0.000e+00	Median :0.000e+00	Median :0.0015406
## Mean :2.175e-05	Mean :2.320e-05	Mean :0.0014288
## 3rd Qu.:0.000e+00	3rd Qu.:3.807e-05	3rd Qu.:0.0018963
## Max. :2.175e-04	Max. :9.897e-05	Max. :0.0020997
## C653	C654	C655
## Min. :0.0003446	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0008572	1st Qu.:0.0001475	1st Qu.:0.0001170
## Median :0.0011880	Median :0.0002714	Median :0.0002229
## Mean :0.0011463	Mean :0.0002609	Mean :0.0002988
## 3rd Qu.:0.0015078	3rd Qu.:0.0003569	3rd Qu.:0.0005025
## Max. :0.0017312	Max. :0.0005853	Max. :0.0007471
## C656	C663	C664
## Min. :0.0000000	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0000000	1st Qu.:0.000730	1st Qu.:0.0000000
## Median :0.0000000	Median :0.001327	Median :0.0000000
## Mean :0.0001099	Mean :0.001598	Mean :0.0002455
## 3rd Qu.:0.0001438	3rd Qu.:0.002559	3rd Qu.:0.0002583
## Max. :0.0007004	Max. :0.003841	Max. :0.0011924
## C665	C666	C667
## Min. :0.0000000	Min. :0.0004767	Min. :0.0000000
## 1st Qu.:0.0006311	1st Qu.:0.0014731	1st Qu.:0.000304
## Median :0.0014072	Median :0.0027053	Median :0.001273
## Mean :0.0013227	Mean :0.0023097	Mean :0.001137
## 3rd Qu.:0.0018448	3rd Qu.:0.0031264	3rd Qu.:0.001900
## Max. :0.0026161	Max. :0.0034670	Max. :0.002218
## C668	C669	C670
## Min. :0.000e+00	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:7.452e-05	1st Qu.:0.0000000	1st Qu.:0.0000000
## Median :5.170e-04	Median :0.0000000	Median :0.0002718
## Mean :6.548e-04	Mean :0.0001193	Mean :0.0004047
## 3rd Qu.:7.347e-04	3rd Qu.:0.0000000	3rd Qu.:0.0006177
## Max. :2.426e-03	Max. :0.0006642	Max. :0.0014479
## C671	C672	C673
## Min. :0.000e+00	Min. :0.001268	Min. :0.001725
## 1st Qu.:0.000e+00	1st Qu.:0.001856	1st Qu.:0.002336
## Median :0.000e+00	Median :0.002382	Median :0.003188
## Mean :1.615e-05	Mean :0.002375	Mean :0.003123
## 3rd Qu.:0.000e+00	3rd Qu.:0.002706	3rd Qu.:0.003729
## Max. :1.615e-04	Max. :0.003777	Max. :0.004725
## C674	C677	C678
## Min. :0.0000000	Min. :0.0009087	Min. :0.000e+00
## 1st Qu.:0.0000000	1st Qu.:0.0012486	1st Qu.:0.000e+00
## Median :0.0000000	Median :0.0013019	Median :0.000e+00
## Mean :0.0001724	Mean :0.0013433	Mean :4.665e-05
## 3rd Qu.:0.0002194	3rd Qu.:0.0015250	3rd Qu.:7.651e-05
## Max. :0.0009136	Max. :0.0017495	Max. :2.167e-04
## C679	C680	C681

##	Min. :0.0001217	Min. :0.0000000	Min. :0.000e+00
##	1st Qu.:0.0002507	1st Qu.:0.0000000	1st Qu.:0.000e+00
##	Median :0.0003136	Median :0.0002430	Median :0.000e+00
##	Mean :0.0004430	Mean :0.0004548	Mean :1.072e-05
##	3rd Qu.:0.0003989	3rd Qu.:0.0006455	3rd Qu.:0.000e+00
##	Max. :0.0013170	Max. :0.0018236	Max. :1.072e-04
##	C682	C684	C685
##	Min. :0.000e+00	Min. :0.000e+00	Min. :0.0000000
##	1st Qu.:0.000e+00	1st Qu.:0.000e+00	1st Qu.:0.0000000
##	Median :0.000e+00	Median :0.000e+00	Median :0.0001639
##	Mean :1.139e-05	Mean :2.259e-05	Mean :0.0002369
##	3rd Qu.:0.000e+00	3rd Qu.:0.000e+00	3rd Qu.:0.0004109
##	Max. :1.139e-04	Max. :2.259e-04	Max. :0.0007359
##	C686	C687	C688
##	Min. :0.0000000	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.0001458	1st Qu.:0.0000000	1st Qu.:0.0003627
##	Median :0.0003753	Median :0.0000000	Median :0.0004700
##	Mean :0.0003948	Mean :0.0003587	Mean :0.0004726
##	3rd Qu.:0.0006831	3rd Qu.:0.0006355	3rd Qu.:0.0006609
##	Max. :0.0007883	Max. :0.0017698	Max. :0.0008852
##	C689	C690	C691
##	Min. :0.0000000	Min. :0.0001201	Min. :0.0003127
##	1st Qu.:0.0003611	1st Qu.:0.0001550	1st Qu.:0.0004632
##	Median :0.0013692	Median :0.0001864	Median :0.0005225
##	Mean :0.0010379	Mean :0.0001763	Mean :0.0005187
##	3rd Qu.:0.0015128	3rd Qu.:0.0001905	3rd Qu.:0.0005454
##	Max. :0.0018785	Max. :0.0002338	Max. :0.0007281
##	C692	C693	C694
##	Min. :0.000e+00	Min. :0.000e+00	Min. :0.000e+00
##	1st Qu.:6.872e-05	1st Qu.:0.000e+00	1st Qu.:0.000e+00
##	Median :1.025e-04	Median :0.000e+00	Median :0.000e+00
##	Mean :1.101e-04	Mean :2.540e-05	Mean :2.633e-05
##	3rd Qu.:1.483e-04	3rd Qu.:5.093e-05	3rd Qu.:0.000e+00
##	Max. :2.335e-04	Max. :8.729e-05	Max. :2.633e-04
##	C695	C697	C700
##	Min. :0.0000000	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.0000000	1st Qu.:0.0000000	1st Qu.:0.0001059
##	Median :0.0000000	Median :0.0000000	Median :0.0005421
##	Mean :0.0000950	Mean :0.0001966	Mean :0.0005786
##	3rd Qu.:0.0001535	3rd Qu.:0.0000000	3rd Qu.:0.0006297
##	Max. :0.0004509	Max. :0.0016381	Max. :0.0015791
##	C701	C702	C704
##	Min. :0.001442	Min. :0.0003847	Min. :0.0000000
##	1st Qu.:0.001755	1st Qu.:0.0008009	1st Qu.:0.0004812
##	Median :0.002046	Median :0.0009353	Median :0.0009514
##	Mean :0.002167	Mean :0.0009265	Mean :0.0009455
##	3rd Qu.:0.002464	3rd Qu.:0.0011227	3rd Qu.:0.0012834
##	Max. :0.003122	Max. :0.0014933	Max. :0.0021297
##	C705	C706	C708
##	Min. :0.000e+00	Min. :0.000e+00	Min. :0.000e+00
##	1st Qu.:0.000e+00	1st Qu.:0.000e+00	1st Qu.:0.000e+00
##	Median :3.738e-05	Median :0.000e+00	Median :0.000e+00
##	Mean :3.873e-04	Mean :9.481e-05	Mean :2.372e-05
##	3rd Qu.:1.566e-04	3rd Qu.:0.000e+00	3rd Qu.:0.000e+00

## Max. :2.399e-03	Max. :9.481e-04	Max. :1.369e-04
## C709	C710	C711
## Min. :0.0000000	Min. :0.0006208	Min. :0.002773
## 1st Qu.:0.0001654	1st Qu.:0.0009822	1st Qu.:0.002964
## Median :0.0014218	Median :0.0014096	Median :0.004161
## Mean :0.0011843	Mean :0.0015701	Mean :0.004082
## 3rd Qu.:0.0019786	3rd Qu.:0.0017944	3rd Qu.:0.004632
## Max. :0.0023890	Max. :0.0035091	Max. :0.006041
## C712	C714	C716
## Min. :0.0004204	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:0.0010733	1st Qu.:0.000e+00	1st Qu.:0.000e+00
## Median :0.0014070	Median :0.000e+00	Median :0.000e+00
## Mean :0.0013124	Mean :5.043e-05	Mean :5.222e-06
## 3rd Qu.:0.0015884	3rd Qu.:7.159e-05	3rd Qu.:0.000e+00
## Max. :0.0018388	Max. :2.547e-04	Max. :5.222e-05
## C717	C718	C720
## Min. :0.000e+00	Min. :0.000e+00	Min. :0.0005928
## 1st Qu.:0.000e+00	1st Qu.:0.000e+00	1st Qu.:0.0010513
## Median :0.000e+00	Median :0.000e+00	Median :0.0014886
## Mean :1.095e-05	Mean :2.897e-05	Mean :0.0014429
## 3rd Qu.:0.000e+00	3rd Qu.:6.522e-05	3rd Qu.:0.0019624
## Max. :1.095e-04	Max. :1.102e-04	Max. :0.0021490
## C721	C722	C723
## Min. :0.000e+00	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:7.578e-05	1st Qu.:5.988e-05	1st Qu.:0.000e+00
## Median :1.563e-04	Median :8.606e-05	Median :6.622e-05
## Mean :1.849e-04	Mean :1.228e-04	Mean :5.227e-05
## 3rd Qu.:2.639e-04	3rd Qu.:2.027e-04	3rd Qu.:8.457e-05
## Max. :5.531e-04	Max. :3.442e-04	Max. :1.143e-04
## C724	C725	C726
## Min. :0.0004527	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0010494	1st Qu.:0.0000000	1st Qu.:0.0000000
## Median :0.0013662	Median :0.0000000	Median :0.0002456
## Mean :0.0012633	Mean :0.0001883	Mean :0.0004891
## 3rd Qu.:0.0014228	3rd Qu.:0.0001657	3rd Qu.:0.0006475
## Max. :0.0017986	Max. :0.0009824	Max. :0.0018191
## C727	C728	C729
## Min. :0.0000000	Min. :0.0001508	Min. :0.0008313
## 1st Qu.:0.0000000	1st Qu.:0.0006907	1st Qu.:0.0013544
## Median :0.0000000	Median :0.0009524	Median :0.0016855
## Mean :0.0001153	Mean :0.0014983	Mean :0.0017386
## 3rd Qu.:0.0001935	3rd Qu.:0.0023821	3rd Qu.:0.0018956
## Max. :0.0005642	Max. :0.0034216	Max. :0.0031154
## C730	C731	C732
## Min. :0.0000000	Min. :0.001806	Min. :0.0003063
## 1st Qu.:0.0000000	1st Qu.:0.002624	1st Qu.:0.0006937
## Median :0.0004667	Median :0.003787	Median :0.0014658
## Mean :0.0006752	Mean :0.003725	Mean :0.0013194
## 3rd Qu.:0.0013733	3rd Qu.:0.004887	3rd Qu.:0.0018417
## Max. :0.0017598	Max. :0.005564	Max. :0.0022617
## C733	C734	C735
## Min. :0.003632	Min. :0.0001994	Min. :0.001084
## 1st Qu.:0.004775	1st Qu.:0.0002872	1st Qu.:0.001762
## Median :0.004944	Median :0.0004073	Median :0.002136

## Mean :0.005281	Mean :0.0004386	Mean :0.002015
## 3rd Qu.:0.006088	3rd Qu.:0.0005420	3rd Qu.:0.002267
## Max. :0.006684	Max. :0.0008040	Max. :0.002723
## C737	C742	C743
## Min. :0.0000000	Min. :0.000e+00	Min. :0.0006467
## 1st Qu.:0.0004998	1st Qu.:0.000e+00	1st Qu.:0.0019751
## Median :0.0021222	Median :6.477e-05	Median :0.0023612
## Mean :0.0023997	Mean :8.359e-05	Mean :0.0023518
## 3rd Qu.:0.0037495	3rd Qu.:1.195e-04	3rd Qu.:0.0027143
## Max. :0.0073219	Max. :3.280e-04	Max. :0.0038128
## C744	C745	C746
## Min. :0.0000000	Min. :0.000e+00	Min. :0.0000000
## 1st Qu.:0.0001711	1st Qu.:0.000e+00	1st Qu.:0.0003865
## Median :0.0003101	Median :0.000e+00	Median :0.0006701
## Mean :0.0003244	Mean :3.707e-05	Mean :0.0006954
## 3rd Qu.:0.0004854	3rd Qu.:0.000e+00	3rd Qu.:0.0008130
## Max. :0.0006013	Max. :1.870e-04	Max. :0.0022507
## C747	C748	C749
## Min. :0.001760	Min. :5.480e-05	Min. :0.000649
## 1st Qu.:0.003631	1st Qu.:6.163e-05	1st Qu.:0.002832
## Median :0.005148	Median :7.471e-05	Median :0.004178
## Mean :0.004922	Mean :8.218e-05	Mean :0.003993
## 3rd Qu.:0.005932	3rd Qu.:1.044e-04	3rd Qu.:0.004741
## Max. :0.007769	Max. :1.243e-04	Max. :0.007371
## C750	C751	C752
## Min. :0.0000000	Min. :0.0001743	Min. :0.0005994
## 1st Qu.:0.0002546	1st Qu.:0.0004393	1st Qu.:0.0015569
## Median :0.0003939	Median :0.0005810	Median :0.0020411
## Mean :0.0003835	Mean :0.0006443	Mean :0.0018786
## 3rd Qu.:0.0004733	3rd Qu.:0.0008080	3rd Qu.:0.0022939
## Max. :0.0008408	Max. :0.0012218	Max. :0.0025837
## C753	C755	C756
## Min. :0.000919	Min. :0.0000000	Min. :0.000e+00
## 1st Qu.:0.001627	1st Qu.:0.0000000	1st Qu.:0.000e+00
## Median :0.002043	Median :0.0000000	Median :4.847e-05
## Mean :0.002319	Mean :0.0005168	Mean :7.683e-05
## 3rd Qu.:0.003050	3rd Qu.:0.0008637	3rd Qu.:1.253e-04
## Max. :0.004002	Max. :0.0025505	Max. :2.385e-04
## C757	C760	C761
## Min. :0.00e+00	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:0.00e+00	1st Qu.:0.000e+00	1st Qu.:0.000e+00
## Median :0.00e+00	Median :0.000e+00	Median :0.000e+00
## Mean :7.77e-06	Mean :6.454e-05	Mean :6.222e-05
## 3rd Qu.:0.00e+00	3rd Qu.:1.514e-04	3rd Qu.:7.495e-05
## Max. :7.77e-05	Max. :2.027e-04	Max. :2.622e-04
## C762	C763	C764
## Min. :0.0008758	Min. :0.0005945	Min. :0.0006571
## 1st Qu.:0.0012132	1st Qu.:0.0011436	1st Qu.:0.0008827
## Median :0.0017223	Median :0.0015925	Median :0.0012062
## Mean :0.0015828	Mean :0.0017394	Mean :0.0013722
## 3rd Qu.:0.0019247	3rd Qu.:0.0023497	3rd Qu.:0.0013376
## Max. :0.0022181	Max. :0.0029231	Max. :0.0031712
## C765	C766	C767
## Min. :0.0000000	Min. :0.0004497	Min. :0.000e+00

## 1st Qu.:0.0000000	1st Qu.:0.0010980	1st Qu.:0.000e+00
## Median :0.0003050	Median :0.0013768	Median :0.000e+00
## Mean :0.0004201	Mean :0.0015095	Mean :1.961e-05
## 3rd Qu.:0.0006666	3rd Qu.:0.0020768	3rd Qu.:0.000e+00
## Max. :0.0015867	Max. :0.0024338	Max. :1.064e-04
## C768	C771	C772
## Min. :0.000e+00	Min. :8.688e-05	Min. :0.000e+00
## 1st Qu.:0.000e+00	1st Qu.:1.609e-04	1st Qu.:5.041e-05
## Median :0.000e+00	Median :1.951e-04	Median :5.962e-05
## Mean :9.987e-06	Mean :2.169e-04	Mean :7.759e-05
## 3rd Qu.:0.000e+00	3rd Qu.:2.738e-04	3rd Qu.:8.845e-05
## Max. :9.987e-05	Max. :3.798e-04	Max. :2.015e-04
## C774	C775	C776
## Min. :0.0000000	Min. :0.0003561	Min. :0.0000000
## 1st Qu.:0.0000000	1st Qu.:0.0004697	1st Qu.:0.0001095
## Median :0.0001209	Median :0.0006837	Median :0.0009297
## Mean :0.0002388	Mean :0.0006910	Mean :0.0011882
## 3rd Qu.:0.0002043	3rd Qu.:0.0008728	3rd Qu.:0.0015822
## Max. :0.0009317	Max. :0.0011443	Max. :0.0039737
## C777	C778	C779
## Min. :9.107e-05	Min. :0.0008308	Min. :0.0005031
## 1st Qu.:2.555e-04	1st Qu.:0.0015700	1st Qu.:0.0008285
## Median :2.734e-04	Median :0.0018316	Median :0.0014701
## Mean :3.772e-04	Mean :0.0018509	Mean :0.0013563
## 3rd Qu.:4.801e-04	3rd Qu.:0.0020749	3rd Qu.:0.0016425
## Max. :8.497e-04	Max. :0.0029662	Max. :0.0021995
## C780	C781	C782
## Min. :0.0001439	Min. :0.000e+00	Min. :0.0000000
## 1st Qu.:0.0010781	1st Qu.:0.000e+00	1st Qu.:0.0002261
## Median :0.0015728	Median :0.000e+00	Median :0.0014616
## Mean :0.0015052	Mean :5.703e-05	Mean :0.0016241
## 3rd Qu.:0.0019583	3rd Qu.:0.000e+00	3rd Qu.:0.0028604
## Max. :0.0027981	Max. :5.703e-04	Max. :0.0037940
## C786	C787	C788
## Min. :0.0000000	Min. :0.0001145	Min. :0.0006920
## 1st Qu.:0.0001323	1st Qu.:0.0001844	1st Qu.:0.0008434
## Median :0.0008908	Median :0.0002068	Median :0.0013602
## Mean :0.0008673	Mean :0.0002055	Mean :0.0014193
## 3rd Qu.:0.0010708	3rd Qu.:0.0002403	3rd Qu.:0.0018405
## Max. :0.0022591	Max. :0.0002763	Max. :0.0024527
## C789	C790	C791
## Min. :0.000e+00	Min. :0.002846	Min. :0.0000911
## 1st Qu.:1.315e-05	1st Qu.:0.003329	1st Qu.:0.0001844
## Median :2.745e-04	Median :0.004253	Median :0.0002511
## Mean :3.263e-04	Mean :0.004237	Mean :0.0002521
## 3rd Qu.:5.296e-04	3rd Qu.:0.004799	3rd Qu.:0.0003168
## Max. :1.022e-03	Max. :0.006823	Max. :0.0004077
## C792	C793	C794
## Min. :0.0000000	Min. :0.002395	Min. :0.0007528
## 1st Qu.:0.0002549	1st Qu.:0.003465	1st Qu.:0.0022069
## Median :0.0003908	Median :0.004280	Median :0.0026243
## Mean :0.0003702	Mean :0.003963	Mean :0.0025241
## 3rd Qu.:0.0004859	3rd Qu.:0.004480	3rd Qu.:0.0029794
## Max. :0.0007198	Max. :0.005134	Max. :0.0040810

##	C795	C796	C797
##	Min. :0.0000000	Min. :0.0000000	Min. :0.0003395
##	1st Qu.:0.0001338	1st Qu.:0.0000000	1st Qu.:0.0006723
##	Median :0.0002868	Median :0.0003900	Median :0.0008675
##	Mean :0.0003134	Mean :0.0005193	Mean :0.0008601
##	3rd Qu.:0.0003725	3rd Qu.:0.0009603	3rd Qu.:0.0010732
##	Max. :0.0008866	Max. :0.0014182	Max. :0.0013384
##	C798	C799	C800
##	Min. :0.0002878	Min. :0.0006842	Min. :0.000e+00
##	1st Qu.:0.0004590	1st Qu.:0.0008754	1st Qu.:0.000e+00
##	Median :0.0005023	Median :0.0010165	Median :0.000e+00
##	Mean :0.0005869	Mean :0.0013195	Mean :6.434e-05
##	3rd Qu.:0.0007083	3rd Qu.:0.0015766	3rd Qu.:1.549e-04
##	Max. :0.0009928	Max. :0.0024877	Max. :1.906e-04
##	C801	C802	C803
##	Min. :7.186e-05	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:7.939e-04	1st Qu.:0.0000000	1st Qu.:0.0004122
##	Median :1.010e-03	Median :0.0005459	Median :0.0009187
##	Mean :1.066e-03	Mean :0.0006201	Mean :0.0009072
##	3rd Qu.:1.469e-03	3rd Qu.:0.0009589	3rd Qu.:0.0013134
##	Max. :1.775e-03	Max. :0.0020693	Max. :0.0018136
##	C804	C805	C806
##	Min. :0.0002579	Min. :0.0002219	Min. :0.000e+00
##	1st Qu.:0.0002800	1st Qu.:0.0003386	1st Qu.:0.000e+00
##	Median :0.0003429	Median :0.0003729	Median :0.000e+00
##	Mean :0.0003949	Mean :0.0004198	Mean :2.357e-05
##	3rd Qu.:0.0005060	3rd Qu.:0.0005016	3rd Qu.:4.691e-05
##	Max. :0.0006811	Max. :0.0007332	Max. :7.495e-05
##	C807	C809	C810
##	Min. :0.0000000	Min. :0.000e+00	Min. :0.000e+00
##	1st Qu.:0.0001542	1st Qu.:0.000e+00	1st Qu.:0.000e+00
##	Median :0.0004011	Median :0.000e+00	Median :0.000e+00
##	Mean :0.0004919	Mean :1.793e-05	Mean :3.523e-05
##	3rd Qu.:0.0009150	3rd Qu.:0.000e+00	3rd Qu.:6.201e-05
##	Max. :0.0009807	Max. :1.148e-04	Max. :1.678e-04
##	C812	C813	C814
##	Min. :0.000e+00	Min. :0.0005016	Min. :0.0006304
##	1st Qu.:0.000e+00	1st Qu.:0.0008329	1st Qu.:0.0007184
##	Median :0.000e+00	Median :0.0009885	Median :0.0008206
##	Mean :6.752e-05	Mean :0.0010199	Mean :0.0009239
##	3rd Qu.:1.455e-04	3rd Qu.:0.0012448	3rd Qu.:0.0010473
##	Max. :2.206e-04	Max. :0.0014469	Max. :0.0015460
##	C815	C816	C817
##	Min. :0.0001317	Min. :0.0004253	Min. :0.0000000
##	1st Qu.:0.0002972	1st Qu.:0.0006197	1st Qu.:0.0000520
##	Median :0.0009624	Median :0.0012712	Median :0.0005041
##	Mean :0.0009305	Mean :0.0014094	Mean :0.0009269
##	3rd Qu.:0.0015329	3rd Qu.:0.0018317	3rd Qu.:0.0009567
##	Max. :0.0017088	Max. :0.0033397	Max. :0.0035471
##	C818	C819	C820
##	Min. :0.0000000	Min. :0.0007773	Min. :0.001908
##	1st Qu.:0.002736	1st Qu.:0.0010837	1st Qu.:0.002194
##	Median :0.003208	Median :0.0013032	Median :0.002548
##	Mean :0.003191	Mean :0.0014365	Mean :0.002657

## 3rd Qu.:0.003780	3rd Qu.:0.0019354	3rd Qu.:0.003032
## Max. :0.005134	Max. :0.0021714	Max. :0.003825
## C821	C822	C823
## Min. :0.000e+00	Min. :0.0002546	Min. :0.0008873
## 1st Qu.:0.000e+00	1st Qu.:0.0012160	1st Qu.:0.0010022
## Median :0.000e+00	Median :0.0013216	Median :0.0010797
## Mean :2.621e-05	Mean :0.0013796	Mean :0.0010969
## 3rd Qu.:0.000e+00	3rd Qu.:0.0016699	3rd Qu.:0.0011994
## Max. :2.100e-04	Max. :0.0021265	Max. :0.0013517
## C824	C825	C826
## Min. :0.0001036	Min. :0.0001207	Min. :0.000e+00
## 1st Qu.:0.0001138	1st Qu.:0.0001636	1st Qu.:0.000e+00
## Median :0.0001267	Median :0.0002034	Median :0.000e+00
## Mean :0.0001400	Mean :0.0002144	Mean :2.339e-05
## 3rd Qu.:0.0001474	3rd Qu.:0.0002471	3rd Qu.:0.000e+00
## Max. :0.0002099	Max. :0.0003572	Max. :2.339e-04
## C827	C828	C829
## Min. :0.0000000	Min. :0.000e+00	Min. :0.0e+00
## 1st Qu.:0.0002591	1st Qu.:0.000e+00	1st Qu.:0.0e+00
## Median :0.0003480	Median :5.710e-05	Median :0.0e+00
## Mean :0.0003601	Mean :8.764e-05	Mean :8.4e-06
## 3rd Qu.:0.0004407	3rd Qu.:1.755e-04	3rd Qu.:0.0e+00
## Max. :0.0007792	Max. :2.204e-04	Max. :8.4e-05
## C831	C832	C833
## Min. :0.000e+00	Min. :0.0005889	Min. :0.0007868
## 1st Qu.:0.000e+00	1st Qu.:0.0007188	1st Qu.:0.0009130
## Median :0.000e+00	Median :0.0008331	Median :0.0010070
## Mean :8.876e-05	Mean :0.0008665	Mean :0.0010242
## 3rd Qu.:0.000e+00	3rd Qu.:0.0009523	3rd Qu.:0.0010478
## Max. :6.495e-04	Max. :0.0012994	Max. :0.0013951
## C835	C840	C841
## Min. :0.0002231	Min. :0.0003981	Min. :0.0003462
## 1st Qu.:0.0004869	1st Qu.:0.0007147	1st Qu.:0.0004809
## Median :0.0006470	Median :0.0010874	Median :0.0005559
## Mean :0.0006216	Mean :0.0009690	Mean :0.0005996
## 3rd Qu.:0.0007714	3rd Qu.:0.0012070	3rd Qu.:0.0007210
## Max. :0.0010212	Max. :0.0014189	Max. :0.0009303
## C842	C843	C844
## Min. :0.0004503	Min. :5.668e-05	Min. :0.000e+00
## 1st Qu.:0.0006046	1st Qu.:1.331e-04	1st Qu.:0.000e+00
## Median :0.0007731	Median :3.145e-04	Median :0.000e+00
## Mean :0.0007299	Mean :3.186e-04	Mean :7.548e-05
## 3rd Qu.:0.0008053	3rd Qu.:4.971e-04	3rd Qu.:0.000e+00
## Max. :0.0009879	Max. :6.263e-04	Max. :6.627e-04
## C846	C848	C849
## Min. :0.000e+00	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.000e+00	1st Qu.:0.0000000	1st Qu.:0.0001927
## Median :0.000e+00	Median :0.0002411	Median :0.0002756
## Mean :1.275e-05	Mean :0.0002685	Mean :0.0002791
## 3rd Qu.:0.000e+00	3rd Qu.:0.0003990	3rd Qu.:0.0004104
## Max. :7.346e-05	Max. :0.0008935	Max. :0.0004452
## C850	C851	C853
## Min. :0.000e+00	Min. :5.868e-05	Min. :0.000e+00
## 1st Qu.:0.000e+00	1st Qu.:7.995e-05	1st Qu.:0.000e+00

## Median :0.000e+00	Median :8.413e-05	Median :0.000e+00
## Mean :4.040e-05	Mean :8.796e-05	Mean :1.260e-05
## 3rd Qu.:5.011e-05	3rd Qu.:9.765e-05	3rd Qu.:0.000e+00
## Max. :2.171e-04	Max. :1.205e-04	Max. :6.634e-05
## C856	C857	C858
## Min. :0.0003880	Min. :0.0002621	Min. :0.0001509
## 1st Qu.:0.0004661	1st Qu.:0.0004501	1st Qu.:0.0004376
## Median :0.0005859	Median :0.0005088	Median :0.0005445
## Mean :0.0005444	Mean :0.0005835	Mean :0.0006040
## 3rd Qu.:0.0006069	3rd Qu.:0.0005602	3rd Qu.:0.0008848
## Max. :0.0006465	Max. :0.0014523	Max. :0.0010006
## C859	C860	C861
## Min. :0.000e+00	Min. :0.00e+00	Min. :0.000e+00
## 1st Qu.:0.000e+00	1st Qu.:0.00e+00	1st Qu.:0.000e+00
## Median :0.000e+00	Median :0.00e+00	Median :6.647e-05
## Mean :4.923e-05	Mean :1.16e-05	Mean :9.709e-05
## 3rd Qu.:0.000e+00	3rd Qu.:0.00e+00	3rd Qu.:1.300e-04
## Max. :3.176e-04	Max. :1.16e-04	Max. :3.442e-04
## C862	C864	C866
## Min. :0.00e+00	Min. :0.0004662	Min. :0.000e+00
## 1st Qu.:0.00e+00	1st Qu.:0.0005307	1st Qu.:0.000e+00
## Median :0.00e+00	Median :0.0006591	Median :4.291e-05
## Mean :9.04e-06	Mean :0.0006422	Mean :2.160e-04
## 3rd Qu.:0.00e+00	3rd Qu.:0.0007168	3rd Qu.:3.850e-04
## Max. :9.04e-05	Max. :0.0008807	Max. :8.790e-04
## C867	C868	C870
## Min. :0.0000000	Min. :0.0003074	Min. :0.000e+00
## 1st Qu.:0.0001507	1st Qu.:0.0004221	1st Qu.:0.000e+00
## Median :0.0003423	Median :0.0004884	Median :0.000e+00
## Mean :0.0005599	Mean :0.0005071	Mean :5.710e-05
## 3rd Qu.:0.0009662	3rd Qu.:0.0006166	3rd Qu.:4.763e-05
## Max. :0.0015535	Max. :0.0007088	Max. :3.609e-04
## C871	C874	C878
## Min. :0.000e+00	Min. :0.0000000	Min. :0.000e+00
## 1st Qu.:3.005e-05	1st Qu.:0.0000000	1st Qu.:0.000e+00
## Median :3.725e-04	Median :0.0000000	Median :5.704e-05
## Mean :4.214e-04	Mean :0.0001016	Mean :5.715e-05
## 3rd Qu.:6.069e-04	3rd Qu.:0.0000000	3rd Qu.:9.239e-05
## Max. :1.161e-03	Max. :0.0010160	Max. :1.802e-04
## C882	C885	C886
## Min. :0.000e+00	Min. :0.0001850	Min. :0.000e+00
## 1st Qu.:5.137e-05	1st Qu.:0.0002454	1st Qu.:0.000e+00
## Median :5.959e-05	Median :0.0004039	Median :0.000e+00
## Mean :5.463e-05	Mean :0.0005527	Mean :7.001e-05
## 3rd Qu.:7.635e-05	3rd Qu.:0.0008393	3rd Qu.:0.000e+00
## Max. :8.865e-05	Max. :0.0013136	Max. :7.001e-04
## C887	C889	C890
## Min. :0.0006338	Min. :0.000e+00	Min. :0.0001725
## 1st Qu.:0.0007992	1st Qu.:0.000e+00	1st Qu.:0.0002678
## Median :0.0010932	Median :0.000e+00	Median :0.0003626
## Mean :0.0010780	Mean :6.306e-05	Mean :0.0003367
## 3rd Qu.:0.0012222	3rd Qu.:0.000e+00	3rd Qu.:0.0003962
## Max. :0.0015988	Max. :3.634e-04	Max. :0.0004686
## C891	C892	C894

##	Min. :0.001093	Min. :0.0001021	Min. :0.000e+00
##	1st Qu.:0.001191	1st Qu.:0.0003134	1st Qu.:9.958e-05
##	Median :0.001488	Median :0.0003987	Median :1.282e-04
##	Mean :0.001585	Mean :0.0005563	Mean :1.508e-04
##	3rd Qu.:0.001823	3rd Qu.:0.0007977	3rd Qu.:2.082e-04
##	Max. :0.002537	Max. :0.0015440	Max. :2.906e-04
##	C895	C896	C898
##	Min. :0.000e+00	Min. :0.0005360	Min. :4.213e-05
##	1st Qu.:3.319e-05	1st Qu.:0.0007752	1st Qu.:6.178e-05
##	Median :2.664e-04	Median :0.0010141	Median :7.363e-05
##	Mean :4.238e-04	Mean :0.0010531	Mean :7.550e-05
##	3rd Qu.:5.808e-04	3rd Qu.:0.0013157	3rd Qu.:8.748e-05
##	Max. :1.609e-03	Max. :0.0016528	Max. :1.062e-04
##	C899	C900	C901
##	Min. :0.0001036	Min. :0.0000000	Min. :0.000e+00
##	1st Qu.:0.0002575	1st Qu.:0.0000000	1st Qu.:0.000e+00
##	Median :0.0002921	Median :0.0001844	Median :0.000e+00
##	Mean :0.0003030	Mean :0.0002812	Mean :2.039e-05
##	3rd Qu.:0.0003423	3rd Qu.:0.0003767	3rd Qu.:0.000e+00
##	Max. :0.0005114	Max. :0.0009687	Max. :2.039e-04
##	C903	C904	C907
##	Min. :0.0000000	Min. :0.0002889	Min. :0.000e+00
##	1st Qu.:0.0000000	1st Qu.:0.0003593	1st Qu.:0.000e+00
##	Median :0.0004234	Median :0.0004197	Median :0.000e+00
##	Mean :0.0005121	Mean :0.0004141	Mean :3.829e-05
##	3rd Qu.:0.0009152	3rd Qu.:0.0004646	3rd Qu.:6.992e-05
##	Max. :0.0013330	Max. :0.0005219	Max. :1.601e-04
##	C908	C909	C910
##	Min. :0.000e+00	Min. :0.0004125	Min. :0.0000000
##	1st Qu.:0.000e+00	1st Qu.:0.0008163	1st Qu.:0.0001464
##	Median :0.000e+00	Median :0.0010361	Median :0.0003235
##	Mean :3.045e-04	Mean :0.0010862	Mean :0.0003303
##	3rd Qu.:7.169e-05	3rd Qu.:0.0012822	3rd Qu.:0.0003795
##	Max. :2.062e-03	Max. :0.0019412	Max. :0.0009012
##	C911	C912	C913
##	Min. :0.0001589	Min. :0.0001774	Min. :0.000e+00
##	1st Qu.:0.0002136	1st Qu.:0.0004241	1st Qu.:0.000e+00
##	Median :0.0003066	Median :0.0005750	Median :0.000e+00
##	Mean :0.0002988	Mean :0.0005607	Mean :1.763e-05
##	3rd Qu.:0.0003716	3rd Qu.:0.0006868	3rd Qu.:0.000e+00
##	Max. :0.0004588	Max. :0.0011276	Max. :1.763e-04
##	C914	C919	C920
##	Min. :0.0002685	Min. :0.000e+00	Min. :0.0003425
##	1st Qu.:0.0007161	1st Qu.:0.000e+00	1st Qu.:0.0004704
##	Median :0.0011870	Median :0.000e+00	Median :0.0004920
##	Mean :0.0012213	Mean :1.463e-05	Mean :0.0004989
##	3rd Qu.:0.0015383	3rd Qu.:0.000e+00	3rd Qu.:0.0005236
##	Max. :0.0022868	Max. :9.100e-05	Max. :0.0006736
##	C921	C922	C923
##	Min. :0.000e+00	Min. :0.0001548	Min. :0.0000000
##	1st Qu.:4.617e-05	1st Qu.:0.0002388	1st Qu.:0.0000000
##	Median :6.560e-04	Median :0.0002435	Median :0.0000000
##	Mean :5.253e-04	Mean :0.0004021	Mean :0.0002314
##	3rd Qu.:7.515e-04	3rd Qu.:0.0005068	3rd Qu.:0.0003906

## Max. :1.152e-03	Max. :0.0011691	Max. :0.0008641
## C925	C926	C927
## Min. :0.0002871	Min. :0.0000000	Min. :9.952e-05
## 1st Qu.:0.0003844	1st Qu.:0.0000000	1st Qu.:1.315e-04
## Median :0.0007132	Median :0.0000000	Median :1.612e-04
## Mean :0.0006828	Mean :0.0001416	Mean :1.683e-04
## 3rd Qu.:0.0009126	3rd Qu.:0.0002514	3rd Qu.:1.783e-04
## Max. :0.0012914	Max. :0.0005555	Max. :2.710e-04
## C929	C930	C931
## Min. :0.000e+00	Min. :0.000e+00	Min. :0.0001567
## 1st Qu.:0.000e+00	1st Qu.:6.903e-05	1st Qu.:0.0003288
## Median :5.275e-05	Median :7.284e-05	Median :0.0003813
## Mean :3.713e-05	Mean :7.857e-05	Mean :0.0005801
## 3rd Qu.:6.364e-05	3rd Qu.:1.039e-04	3rd Qu.:0.0005188
## Max. :7.098e-05	Max. :1.390e-04	Max. :0.0017529
## C932	C933	C934
## Min. :0.000e+00	Min. :0.0001319	Min. :0.000e+00
## 1st Qu.:0.000e+00	1st Qu.:0.0003659	1st Qu.:4.849e-05
## Median :5.214e-05	Median :0.0005215	Median :4.484e-04
## Mean :8.303e-05	Mean :0.0005752	Mean :5.156e-04
## 3rd Qu.:1.356e-04	3rd Qu.:0.0006988	3rd Qu.:6.806e-04
## Max. :2.913e-04	Max. :0.0012054	Max. :1.780e-03
## C935	C936	C937
## Min. :0.0001415	Min. :0.0004919	Min. :0.0000000
## 1st Qu.:0.0002205	1st Qu.:0.0007204	1st Qu.:0.0003406
## Median :0.0002881	Median :0.0008135	Median :0.0005439
## Mean :0.0002653	Mean :0.0007766	Mean :0.0005733
## 3rd Qu.:0.0003114	3rd Qu.:0.0008833	3rd Qu.:0.0008897
## Max. :0.0003373	Max. :0.0010007	Max. :0.0013053
## C938	C939	C940
## Min. :0.000e+00	Min. :9.921e-05	Min. :0.0000000
## 1st Qu.:0.000e+00	1st Qu.:1.429e-04	1st Qu.:0.0000000
## Median :5.317e-05	Median :1.834e-04	Median :0.0000000
## Mean :4.098e-05	Mean :1.919e-04	Mean :0.0000849
## 3rd Qu.:7.114e-05	3rd Qu.:2.294e-04	3rd Qu.:0.0001162
## Max. :8.672e-05	Max. :3.287e-04	Max. :0.0003831
## C941	C942	C943
## Min. :0.000e+00	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:3.437e-05	1st Qu.:0.000e+00	1st Qu.:0.000e+00
## Median :2.044e-04	Median :0.000e+00	Median :6.473e-05
## Mean :6.165e-04	Mean :4.726e-05	Mean :1.060e-04
## 3rd Qu.:6.581e-04	3rd Qu.:4.078e-05	3rd Qu.:1.334e-04
## Max. :2.974e-03	Max. :2.151e-04	Max. :3.995e-04
## C944	C945	C946
## Min. :0.001160	Min. :0.0009684	Min. :0.0002579
## 1st Qu.:0.001409	1st Qu.:0.0010738	1st Qu.:0.0005217
## Median :0.001808	Median :0.0012733	Median :0.0008408
## Mean :0.002094	Mean :0.0013895	Mean :0.0008860
## 3rd Qu.:0.002915	3rd Qu.:0.0014731	3rd Qu.:0.0012928
## Max. :0.003257	Max. :0.0026154	Max. :0.0014317
## C947	C948	C949
## Min. :0.0002191	Min. :0.0000000	Min. :0.0000000
## 1st Qu.:0.0003201	1st Qu.:0.0000000	1st Qu.:0.0000000
## Median :0.0005247	Median :0.0001444	Median :0.0002421

## Mean :0.0005216	Mean :0.0006337	Mean :0.0004638
## 3rd Qu.:0.0005859	3rd Qu.:0.0010342	3rd Qu.:0.0009638
## Max. :0.0010793	Max. :0.0028130	Max. :0.0012577
## C952	C955	C956
## Min. :0.0000000	Min. :0.0001141	Min. :0.0001799
## 1st Qu.:0.0000000	1st Qu.:0.0002114	1st Qu.:0.0002227
## Median :0.0000000	Median :0.0002602	Median :0.0002830
## Mean :0.0002444	Mean :0.0002634	Mean :0.0004656
## 3rd Qu.:0.0003206	3rd Qu.:0.0003175	3rd Qu.:0.0006292
## Max. :0.0009459	Max. :0.0003819	Max. :0.0012485
## C957	C959	C960
## Min. :0.000e+00	Min. :0.000e+00	Min. :0.0000000
## 1st Qu.:3.004e-05	1st Qu.:0.000e+00	1st Qu.:0.0002555
## Median :2.322e-04	Median :0.000e+00	Median :0.0003098
## Mean :3.837e-04	Mean :1.630e-05	Mean :0.0003157
## 3rd Qu.:4.426e-04	3rd Qu.:0.000e+00	3rd Qu.:0.0003827
## Max. :1.348e-03	Max. :9.799e-05	Max. :0.0006326
## C961	C962	C967
## Min. :0.0003159	Min. :0.000e+00	Min. :0.000e+00
## 1st Qu.:0.0005833	1st Qu.:0.000e+00	1st Qu.:0.000e+00
## Median :0.0008420	Median :0.000e+00	Median :3.039e-05
## Mean :0.0008071	Mean :4.570e-05	Mean :5.906e-05
## 3rd Qu.:0.0010227	3rd Qu.:7.912e-05	3rd Qu.:1.180e-04
## Max. :0.0011907	Max. :1.834e-04	Max. :1.812e-04
## C968	C970	C971
## Min. :0.0000000	Min. :0.0008595	Min. :0.0005279
## 1st Qu.:0.0006941	1st Qu.:0.0009883	1st Qu.:0.0011342
## Median :0.0012607	Median :0.0014584	Median :0.0011964
## Mean :0.0012889	Mean :0.0033103	Mean :0.0013455
## 3rd Qu.:0.0016856	3rd Qu.:0.0024248	3rd Qu.:0.0015994
## Max. :0.0028818	Max. :0.0172678	Max. :0.0023718
## C972	C973	C974
## Min. :0.0000000	Min. :0.0002439	Min. :0.000624
## 1st Qu.:0.0000000	1st Qu.:0.0004896	1st Qu.:0.001583
## Median :0.0000000	Median :0.0009232	Median :0.001903
## Mean :0.0002199	Mean :0.0009414	Mean :0.001905
## 3rd Qu.:0.0004649	3rd Qu.:0.0012682	3rd Qu.:0.002350
## Max. :0.0008062	Max. :0.0019409	Max. :0.002922
## C975	C980	C981
## Min. :0.0003466	Min. :0.0000000	Min. :0.000e+00
## 1st Qu.:0.0004368	1st Qu.:0.0000000	1st Qu.:5.076e-05
## Median :0.0007460	Median :0.0006445	Median :2.831e-04
## Mean :0.0008137	Mean :0.0007875	Mean :2.810e-04
## 3rd Qu.:0.0011603	3rd Qu.:0.0011804	3rd Qu.:4.787e-04
## Max. :0.0014487	Max. :0.0026199	Max. :5.736e-04
## C984	C986	C987
## Min. :0.0002064	Min. :0.000e+00	Min. :0.0006492
## 1st Qu.:0.0002604	1st Qu.:0.000e+00	1st Qu.:0.0007283
## Median :0.0003401	Median :0.000e+00	Median :0.0008623
## Mean :0.0003766	Mean :4.539e-05	Mean :0.0009134
## 3rd Qu.:0.0004136	3rd Qu.:9.335e-05	3rd Qu.:0.0009889
## Max. :0.0006563	Max. :1.615e-04	Max. :0.0015257
## C988	C989	C990
## Min. :0.000e+00	Min. :0.0004503	Min. :0.000e+00

##	1st Qu.:0.000e+00	1st Qu.:0.0006437	1st Qu.:0.000e+00
##	Median :0.000e+00	Median :0.0007467	Median :0.000e+00
##	Mean :2.138e-05	Mean :0.0007326	Mean :3.152e-05
##	3rd Qu.:0.000e+00	3rd Qu.:0.0008450	3rd Qu.:5.346e-05
##	Max. :1.474e-04	Max. :0.0010185	Max. :1.611e-04
##	C991	C992	C994
##	Min. :0.0000000	Min. :0.0005245	Min. :0.000e+00
##	1st Qu.:0.0001793	1st Qu.:0.0007193	1st Qu.:1.426e-05
##	Median :0.0002643	Median :0.0007999	Median :8.088e-05
##	Mean :0.0002821	Mean :0.0007795	Mean :1.949e-04
##	3rd Qu.:0.0003627	3rd Qu.:0.0008937	3rd Qu.:3.114e-04
##	Max. :0.0007103	Max. :0.0009767	Max. :6.474e-04
##	C995	C996	C999
##	Min. :0.0000000	Min. :0.0005284	Min. :0.0002109
##	1st Qu.:0.0000000	1st Qu.:0.0005560	1st Qu.:0.0003531
##	Median :0.0000000	Median :0.0006026	Median :0.0004592
##	Mean :0.0001381	Mean :0.0006462	Mean :0.0004612
##	3rd Qu.:0.0000000	3rd Qu.:0.0007051	3rd Qu.:0.0005336
##	Max. :0.0010254	Max. :0.0008844	Max. :0.0007113
##	C1000	C1001	C1002
##	Min. :0.0000000	Min. :8.103e-05	Min. :0.000e+00
##	1st Qu.:0.0000000	1st Qu.:1.792e-04	1st Qu.:0.000e+00
##	Median :0.0000000	Median :2.278e-04	Median :0.000e+00
##	Mean :0.0001595	Mean :5.914e-04	Mean :1.450e-05
##	3rd Qu.:0.0000000	3rd Qu.:5.948e-04	3rd Qu.:0.000e+00
##	Max. :0.0015954	Max. :2.776e-03	Max. :7.512e-05
##	C1003	C1004	C1005
##	Min. :0.000e+00	Min. :0.000e+00	Min. :0.000e+00
##	1st Qu.:0.000e+00	1st Qu.:0.000e+00	1st Qu.:0.000e+00
##	Median :0.000e+00	Median :3.056e-05	Median :0.000e+00
##	Mean :3.642e-05	Mean :7.192e-05	Mean :4.011e-05
##	3rd Qu.:0.000e+00	3rd Qu.:1.211e-04	3rd Qu.:0.000e+00
##	Max. :3.642e-04	Max. :2.547e-04	Max. :4.011e-04
##	C1007	C1008	C1009
##	Min. :0.0001818	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.0003675	1st Qu.:0.0000000	1st Qu.:0.0000000
##	Median :0.0025029	Median :0.0001973	Median :0.0000000
##	Mean :0.0027261	Mean :0.0002795	Mean :0.0003482
##	3rd Qu.:0.0041291	3rd Qu.:0.0004015	3rd Qu.:0.0003282
##	Max. :0.0065129	Max. :0.0009726	Max. :0.0016513
##	C1010	C1011	C1012
##	Min. :0.000e+00	Min. :0.000e+00	Min. :0.0000000
##	1st Qu.:0.000e+00	1st Qu.:2.936e-05	1st Qu.:0.0001374
##	Median :4.805e-05	Median :3.782e-04	Median :0.0002674
##	Mean :5.139e-04	Mean :1.186e-03	Mean :0.0003418
##	3rd Qu.:2.742e-04	3rd Qu.:1.925e-03	3rd Qu.:0.0005591
##	Max. :2.650e-03	Max. :5.450e-03	Max. :0.0008542
##	C1013	C1014	C1015
##	Min. :0.000e+00	Min. :0.0000000	Min. :0.0000000
##	1st Qu.:0.000e+00	1st Qu.:0.0002555	1st Qu.:0.0000511
##	Median :8.205e-05	Median :0.0007817	Median :0.0027266
##	Mean :8.735e-04	Mean :0.0012365	Mean :0.0029672
##	3rd Qu.:6.373e-04	3rd Qu.:0.0011683	3rd Qu.:0.0042328
##	Max. :3.862e-03	Max. :0.0061008	Max. :0.0094291

```
##      C1016      C1017      C1018
## Min.   :0.0000000 Min.   :0.0000000 Min.   :0.0001700
## 1st Qu.:0.0000000 1st Qu.:0.0000000 1st Qu.:0.0004441
## Median :0.0000000 Median :0.0004401 Median :0.0013016
## Mean   :0.0003617 Mean   :0.0038891 Mean   :0.0017151
## 3rd Qu.:0.0004476 3rd Qu.:0.0053870 3rd Qu.:0.0020647
## Max.   :0.0023955 Max.   :0.0187287 Max.   :0.0071077
##      C1019      C1020      C1021
## Min.   :0.0000000 Min.   :0.000e+00 Min.   :0.0000000
## 1st Qu.:0.0000000 1st Qu.:0.000e+00 1st Qu.:0.0000000
## Median :0.0003566 Median :0.000e+00 Median :0.000816
## Mean   :0.0006591 Mean   :7.048e-05 Mean   :0.002347
## 3rd Qu.:0.0009389 3rd Qu.:0.000e+00 3rd Qu.:0.005059
## Max.   :0.0023944 Max.   :7.048e-04 Max.   :0.007382
##      C1022
## Min.   :0.000e+00
## 1st Qu.:0.000e+00
## Median :0.000e+00
## Mean   :8.731e-05
## 3rd Qu.:1.032e-04
## Max.   :4.004e-04
```

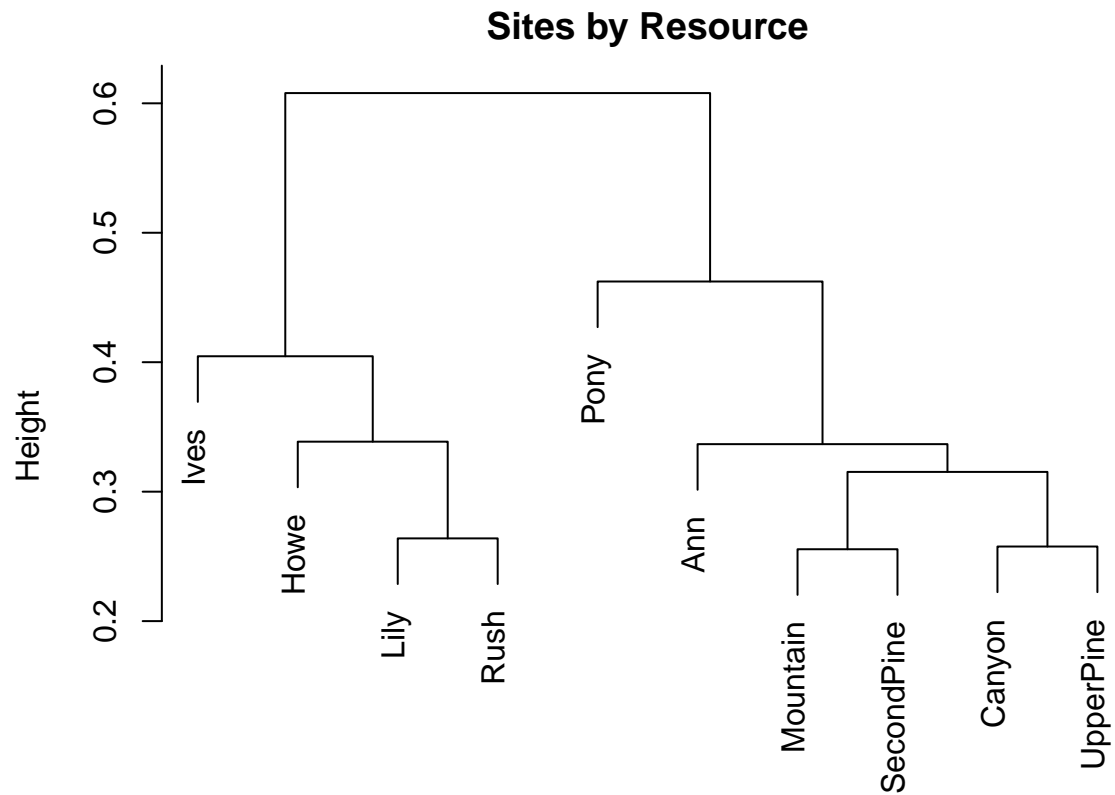
```
# Calculate distances
res.dist <- vegdist(resREL, method = "bray")
res.dist2 <- vegdist(t(resREL), method = "bray")

res.pcoa <- cmdscale(res.dist2, eig = TRUE, k = 3)

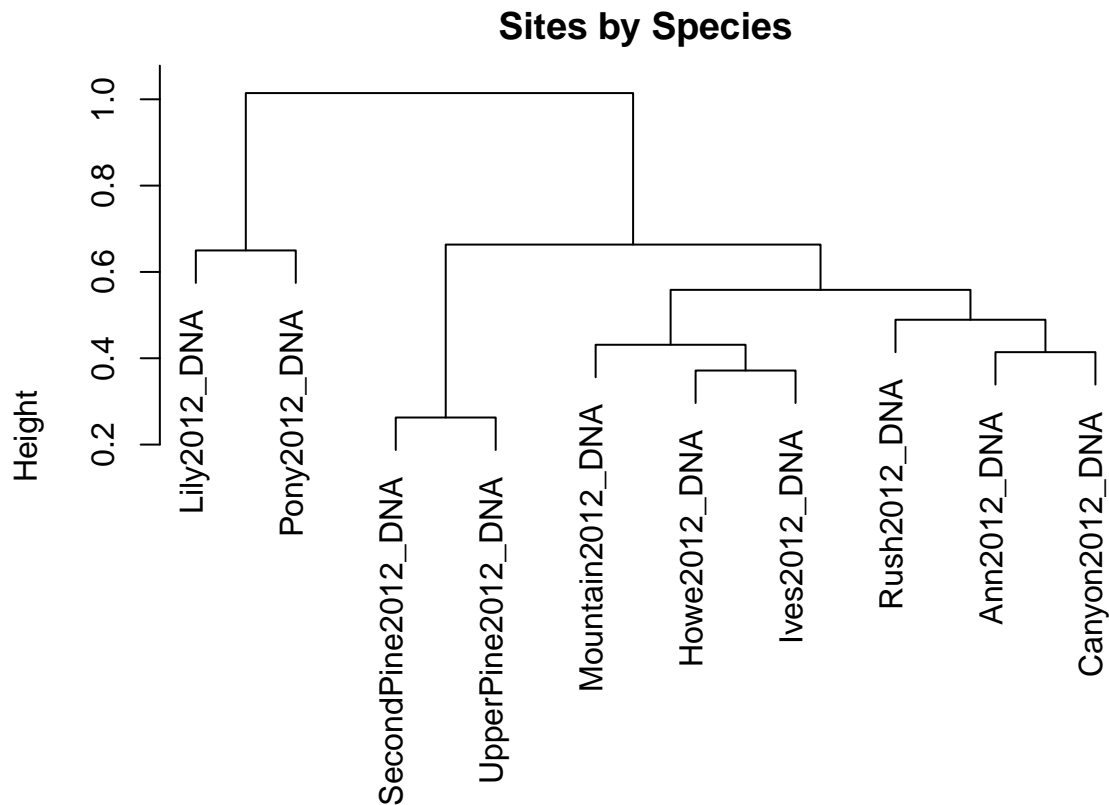
# Clustering
res.k <- kmeans(resREL, 5, iter.max = 10)

# plot(resREL, col = res.k$cluster)

# Perform Cluster Analysis
res.ward <- hclust(res.dist, method = "ward.D2")
# Plot Cluster
par(mar = c(1, 5, 2, 2) + 0.1)
plot(res.ward, main = "Sites by Resource")
```



```
bac.dist <- vegdist(OTUsREL[design$Year == "2012" &  
                      design$Molecule == "DNA", ], method="bray")  
bac.ward <- hclust(bac.dist, method = "ward.D2")  
plot(bac.ward, main = "Sites by Species")
```



Co-Occurance Analysis

```
require("bioDist")
```

```
## Loading required package: bioDist
```

```
## Loading required package: Biobase
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: parallel
```

```
##
```

```
## Attaching package: 'BiocGenerics'
```

```
## The following objects are masked from 'package:parallel':
```

```
##
```

```
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,  
##   clusterExport, clusterMap, parApply, parCapply, parLapply,  
##   parLapplyLB, parRapply, parSapply, parSapplyLB
```

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

```
##
```

```
##   IQR, mad, xtabs
```

```
## The following objects are masked from 'package:base':
##
##   anyDuplicated, append, as.data.frame, as.vector, cbind,
##   colnames, do.call, duplicated, eval, evalq, Filter, Find, get,
##   grep, grepl, intersect, is.unsorted, lapply, lengths, Map,
##   mapply, match, mget, order, paste, pmax, pmax.int, pmin,
##   pmin.int, Position, rank, rbind, Reduce, rownames, sapply,
##   setdiff, sort, table, tapply, union, unique, unlist, unsplit
##
## Welcome to Bioconductor
##
##   Vignettes contain introductory material; view with
##   'browseVignettes()'. To cite Bioconductor, see
##   'citation("Biobase")', and for packages 'citation("pkgname)".
##
## Attaching package: 'Biobase'
##
## The following object is masked from 'package:phyloseq':
##
##   sampleNames
##
## Loading required package: KernSmooth
##
## KernSmooth 2.23 loaded
## Copyright M. P. Wand 1997-2009
```

```
# Subset OTUs for to remove very rare taxa
OTUsREL2 <- OTUsREL[,which(colSums(as.matrix(OTUsREL)) > 0.05)]
resREL2 <- resREL[,which(colSums(as.matrix(resREL)) > 0.022)]

rownames(OTUsREL)
```

```
## [1] "Ann2011_DNA"      "Ann2011_RNA"      "Ann2012_DNA"
## [4] "Ann2012_RNA"      "Canyon2011_DNA"    "Canyon2011_RNA"
## [7] "Canyon2012_DNA"    "Canyon2012_RNA"    "Howe2011_DNA"
## [10] "Howe2011_RNA"      "Howe2012_DNA"      "Howe2012_RNA"
## [13] "Ives2011_DNA"      "Ives2011_RNA"      "Ives2012_DNA"
## [16] "Ives2012_RNA"      "Lily2011_DNA"      "Lily2011_RNA"
## [19] "Lily2012_DNA"      "Lily2012_RNA"      "Mountain2011_DNA"
## [22] "Mountain2011_RNA"  "Mountain2012_DNA"  "Mountain2012_RNA"
## [25] "Pony2011_DNA"      "Pony2011_RNA"      "Pony2012_DNA"
## [28] "Pony2012_RNA"      "Rush2011_DNA"      "Rush2011_RNA"
## [31] "Rush2012_DNA"      "Rush2012_RNA"      "SecondPine2011_DNA"
## [34] "SecondPine2011_RNA" "SecondPine2012_DNA" "SecondPine2012_RNA"
## [37] "UpperPine2011_DNA" "UpperPine2011_RNA" "UpperPine2012_DNA"
## [40] "UpperPine2012_RNA"
```

```
rownames(resREL)
```

```
## [1] "Ann"      "Canyon"    "Howe"      "Ives"      "Lily"
## [6] "Mountain" "Pony"      "Rush"      "SecondPine" "UpperPine"
```



```

OTUsREL3 <- OTUsREL2[grepl("2012_RNA", rownames(OTUsREL)),]
OTUsREL3 <- OTUsREL3[,order(colSums(as.matrix(OTUsREL3)), decreasing = T)[1:100]]
resREL3 <- resREL2[,order(colSums(as.matrix(resREL2)), decreasing = T)[1:100]]
ConRes1 <- cbind(as.matrix(OTUsREL3), as.matrix(resREL3))
ConRes2 <- cbind(as.matrix(resREL3), as.matrix(OTUsREL3))
ConRes <- rbind(ConRes1, ConRes2)

# Calculate 1 - Spearman Correlation Coefficients: Spearman Distance
spear.bac <- spearman.dist(t(OTUsREL2), abs = FALSE)
spear.res <- spearman.dist(t(as.matrix(resREL2)), abs = FALSE)
spear.ConRes <- spearman.dist(t(as.matrix(ConRes)), abs = FALSE, diag = F, upper = F)

spear.bac2 <- spear.bac - 1
spear.bac3 <- spear.bac2
spear.bac3[which(spear.bac2 < 0.5 & spear.bac2 > -0.5)] <- NA

spear.res2 <- spear.res - 1
spear.res3 <- spear.res2
spear.res3[which(spear.res2 < 0.5 & spear.res2 > -0.5)] <- NA

spear.ConRes2 <- spear.ConRes - 1
spear.ConRes3 <- spear.ConRes2
spear.ConRes3[which(spear.ConRes2 < 0.5 & spear.ConRes2 > -0.5)] <- NA
spear.ConRes4 <- as.matrix(spear.ConRes3) # [1:100, 101:200]

# Custome Color Palette
jet.colors <- colorRampPalette(c("#00007F", "blue", "#007FFF", "cyan",
                                "#7FFF7F", "yellow", "#FF7F00", "red",
                                "#7F0000"))

layout(rbind(c(1,2)))

require(gridExtra)

```

```
## Loading required package: gridExtra
```

```
##
```

```
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:Biobase':
```

```
##
```

```
## combine
```

```
## The following object is masked from 'package:BiocGenerics':
```

```
##
```

```
## combine
```

```

order <- rev(attr(spear.bac3, "Labels"))
plot1 <- levelplot(as.matrix(spear.bac3)[,order], aspect = "iso", col.regions = jet.colors,
  xlab = list(label = "OTU", cex = 1.2), ylab = list(label = "OTU", cex = 1.2),
  scales = list(cex = 0.3, x = list(rot=90)),
  main = "Species Co-Occurrence")

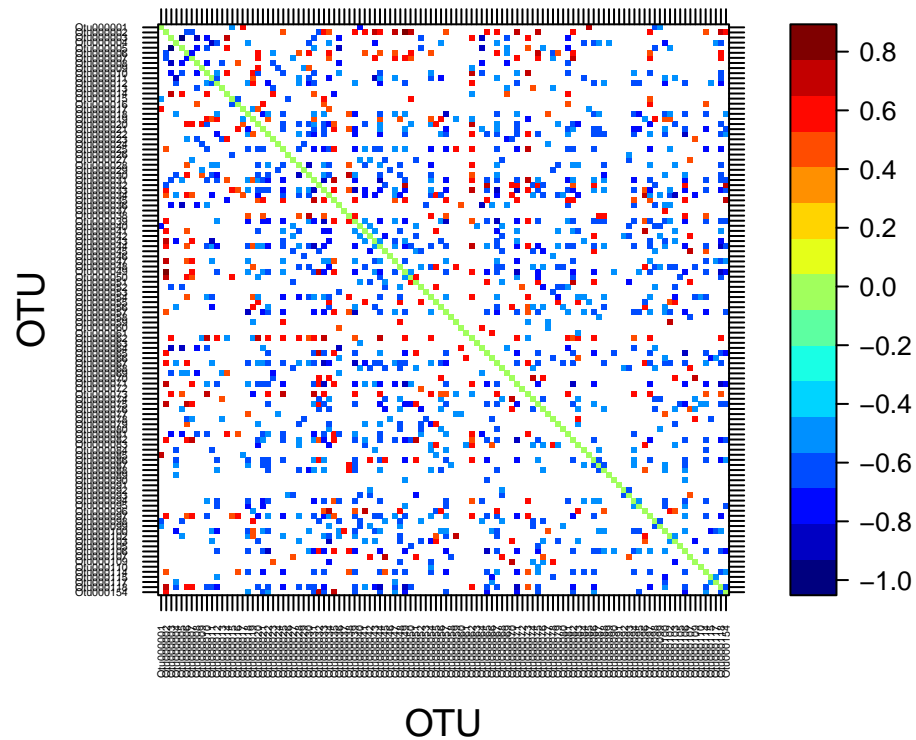
```

```

order <- rev(attr(spear.res3, "Labels"))
plot2 <- levelplot(as.matrix(spear.res3)[,order], aspect = "iso", col.regions = jet.colors,
  xlab = list(label = "Resource", cex = 1.2), ylab = list(label = "Resource", cex = 1.2),
  scales = list(cex = 0.3, x = list(rot=90)),
  main = "Resource Co-Occurrence")
plot1

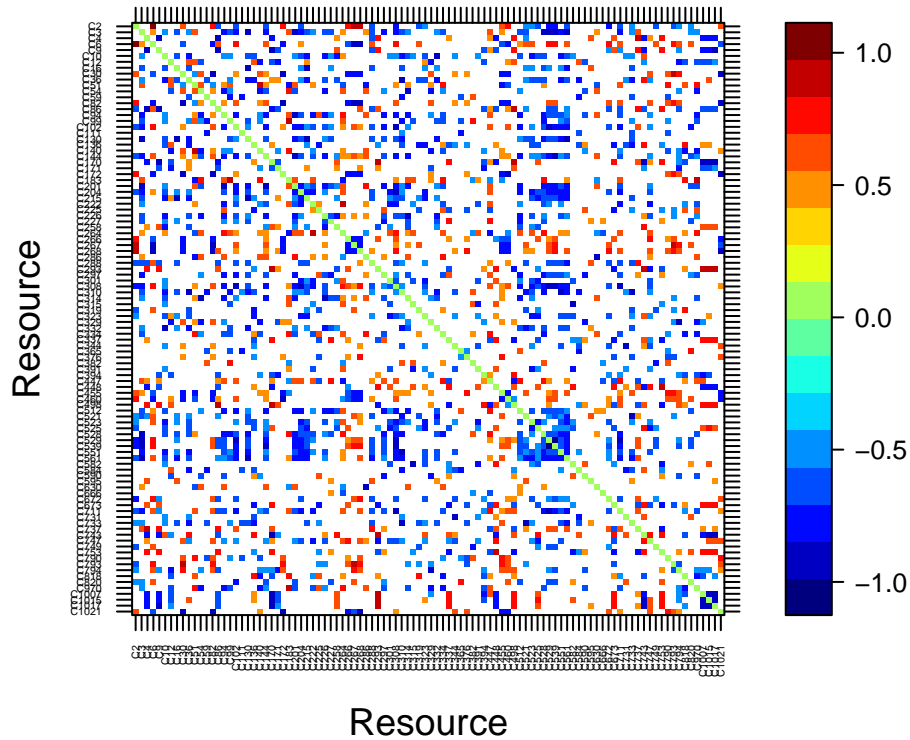
```

Species Co-Occurrence



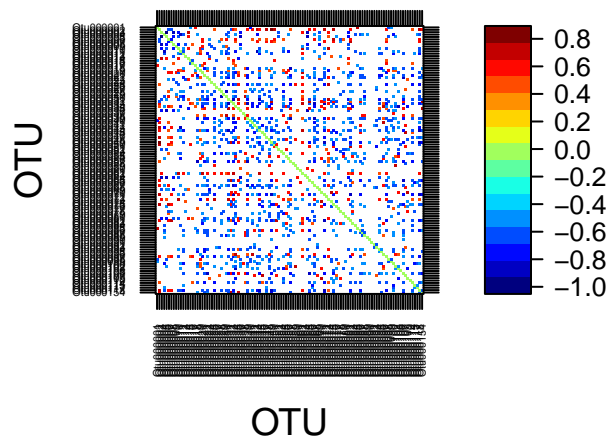
plot2

Resource Co-Occurrence

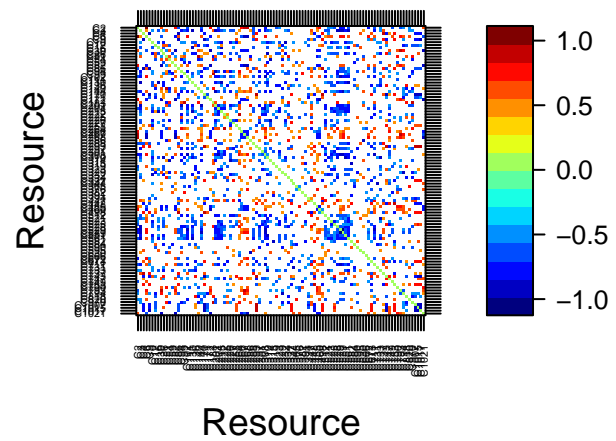


```
grid.arrange(plot1, plot2, ncol = 2)
```

Species Co-Occurrence



Resource Co-Occurrence

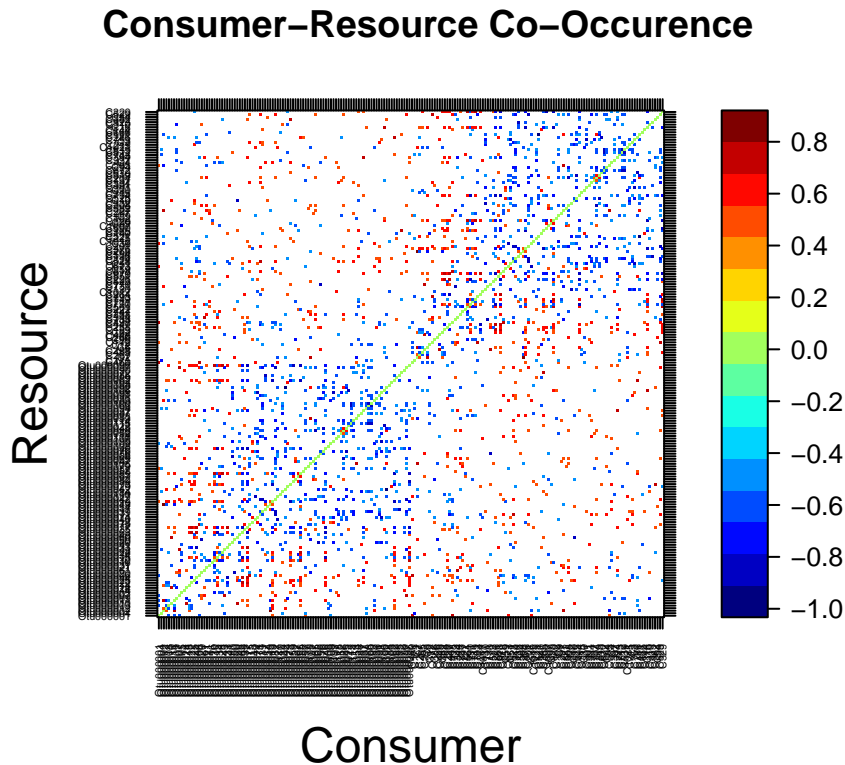


```
plot3 <- levelplot(spear.ConRes4, aspect = "iso", col.regions = jet.colors,
  xlab = list(label = "Consumer", cex = 1.5),
  ylab = list(label = "Resource", cex = 1.5),
  scales = list(cex = 0.3, tck = 0.75,
    #x = list(labels=colnames(ConRes)[1:100], rot=90),
    #y = list(labels=colnames(ConRes)[101:200])),
  x = list(rot=90),
```

```

y = list(),
main = list(label = "Consumer-Resource Co-Occurrence", line = 1),
par.settings=list(layout.heights=list(top.padding=3, bottom.padding=3)))
plot3

```



```

spearB.pcoa <- cmdscale(spear.bac, eig = TRUE, k = 3)
explainvar1 <- round(spearB.pcoa$eig[1] / sum(spearB.pcoa$eig), 3) * 100
explainvar2 <- round(spearB.pcoa$eig[2] / sum(spearB.pcoa$eig), 3) * 100
explainvar3 <- round(spearB.pcoa$eig[3] / sum(spearB.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

par(mar = c(5, 5, 1, 1) + 0.1)

# Define Plot Symbols
lake.pch <- rep(NA, length(design$Molecule))
for (i in 1:length(design$Molecule)){
  if (design$Molecule[i] == "DNA"){
    lake.pch[i] <- 16
  }else{
    lake.pch[i] <- 17
  }}

# Initiate Plot
plot(spearB.pcoa$points[,1], spearB.pcoa$points[,2],
     ylim = c(-0.4, 0.8), xlim = c(-0.5, 0.6),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),

```

```

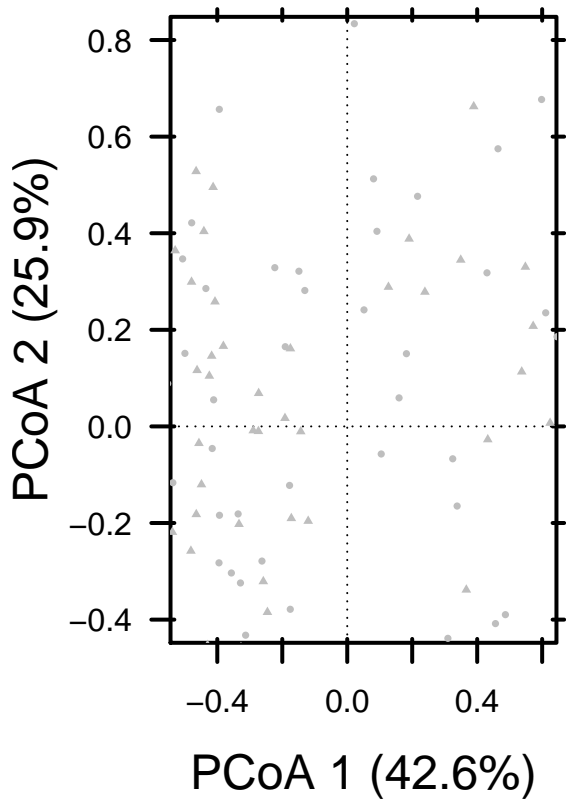
pch = lake.pch, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2,
axes = FALSE)

# Add Axes
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1, las = 1)
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=-0.02)
axis(side = 1, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 2, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 3, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
axis(side = 4, labels = F, lwd.ticks = 2, cex.axis = 1, las = 1, tck=0.01)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)

# Add Points & Labels
points(spearB.pcoa$points[,1], spearB.pcoa$points[,2],
       pch = lake.pch, cex = 0.5, bg = "gray", col = "gray")

#ordiellipse(cbind(spearB.pcoa$points[,1], spearB.pcoa$points[,2]),
#  design$Lake, kind="sd", conf=0.95,
#  lwd=2, draw = "polygon", col="gray", border = "black", label=TRUE,
#  cex=1, bty = 'n')

```



Cluster Lakes by Nutrients

```
# nuts.m <- nuts[,3:5]
# row.names(nuts.m) <- paste(nuts[,1], nuts[,2], sep = "-")
# nuts.s <- t(scale(nuts.m))
#
# # Determine number of clusters
# wss <- (nrow(nuts.s)-1)*sum(apply(nuts.s,2,var))
# for (i in 2:3) wss[i] <- sum(kmeans(nuts.s,
#   centers=i)$withinss)
# plot(1:15, wss, type="b", xlab="Number of Clusters",
#   ylab="Within groups sum of squares")
#
# # K-Means Cluster Analysis
# fit <- kmeans(nuts.s, 2) # 4 cluster solution
# # get cluster means
# aggregate(nuts.s,by=list(fit$cluster),FUN=mean)
# # append cluster assignment
# mydata <- data.frame(nuts.s, fit$cluster)
#
#
# test <- hclust(dist(t(nuts.s)), method = "ward.D2")
#
# # Ward Hierarchical Clustering with Bootstrapped p values
# library(pvclust)
# fit <- pvclust(t(nuts.s), method.hclust="ward.D2", method.dist = "euclidean")
# plot(fit) # dendrogram with p values
# # add rectangles around groups highly supported by the data
# purrect(fit, alpha=.95)
```