

Diversity Project Abundances

Joshua

4/1/2021

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

Importing data into R

```
site_species <- read.csv("alpine_ridge_data/OTU_table.csv", header = TRUE)
site_species.t <- t(site_species)
```

```
#Rarefaction
```

```
#Visualization of rarecurves for all samples
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 4.0.4
```

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

```
## Warning: package 'permute' was built under R version 4.0.4
```

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

```
## This is vegan 2.5-7
```

```
richness <- rowSums((site_species.t > 0) * 1)
print(richness)
```

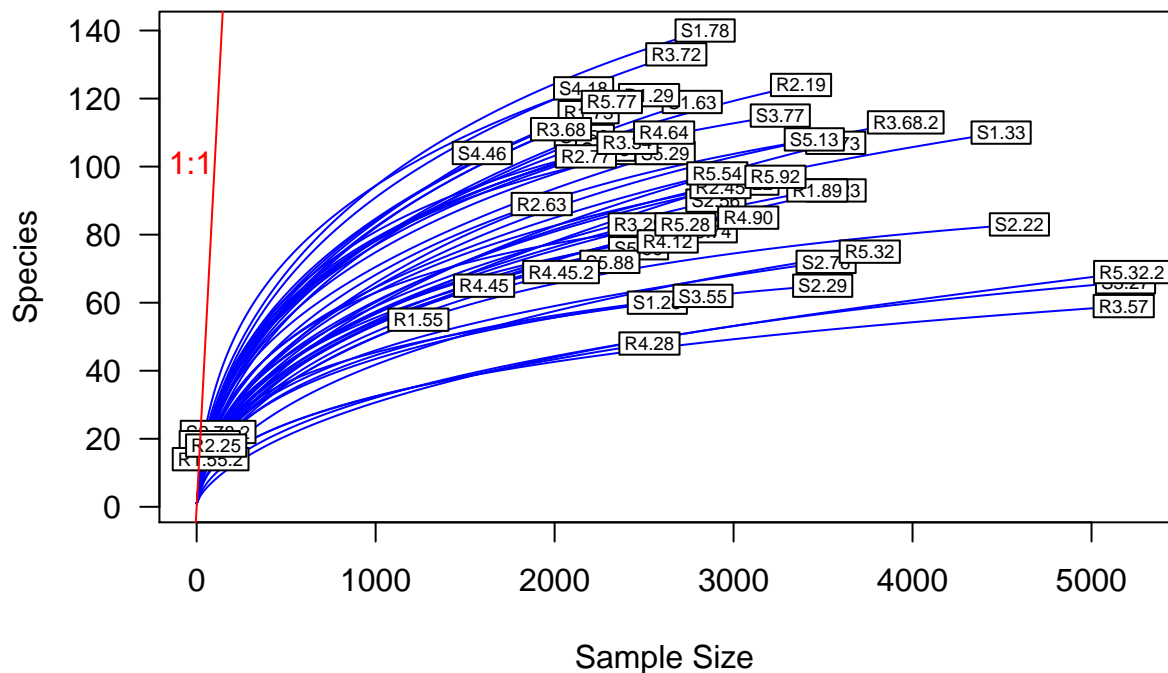
```
##  S1.28  S1.33  S1.56  S1.63  S1.78  S2.22  S2.29  S2.56  S2.73  S2.78
##      60    110    109    119    140     83     65     90    105     72
## S2.78.2 S3.23  S3.27  S3.55  S3.73  S3.77  S4.18  S4.22  S4.46  S4.68
##      22     93     66     62    107    115    123     95    104    104
##  S4.73  S5.13  S5.29  S5.56  S5.74  S5.88  R1.14  R1.29  R1.55 R1.55.2
##      105    108    104     76     81     72     19    121     55     14
##  R1.73  R1.89  R2.19  R2.25  R2.45  R2.63  R2.77  R3.29  R3.34  R3.57
##      116     93    124     18     94     89    103     83    107     59
##  R3.68 R3.68.2 R3.72  R4.12  R4.28  R4.45 R4.45.2 R4.64  R4.90  R5.28
##      111    113    133     78     48     65     69    110     85     83
##  R5.32 R5.32.2 R5.54  R5.77  R5.92
##      75     69     98    119     97
```

```

minimum.r <- min(rowSums(site_species.t))
rarefy <- rarefy(x = site_species.t, sample = minimum.r, se = TRUE)

rarecurve(x = site_species.t, step = 20, col = "blue", cex = .6, las = 1)
abline(0, 1, col = 'red')
text(200, 100, "1:1", pos = 2, col = 'red')

```



```

#Rarefaction of samples
site_species.r <- rrarefy(site_species.t, 1000)

```

```

## Warning in rrarefy(site_species.t, 1000): some row sums < 'sample' and are not
## rarefied

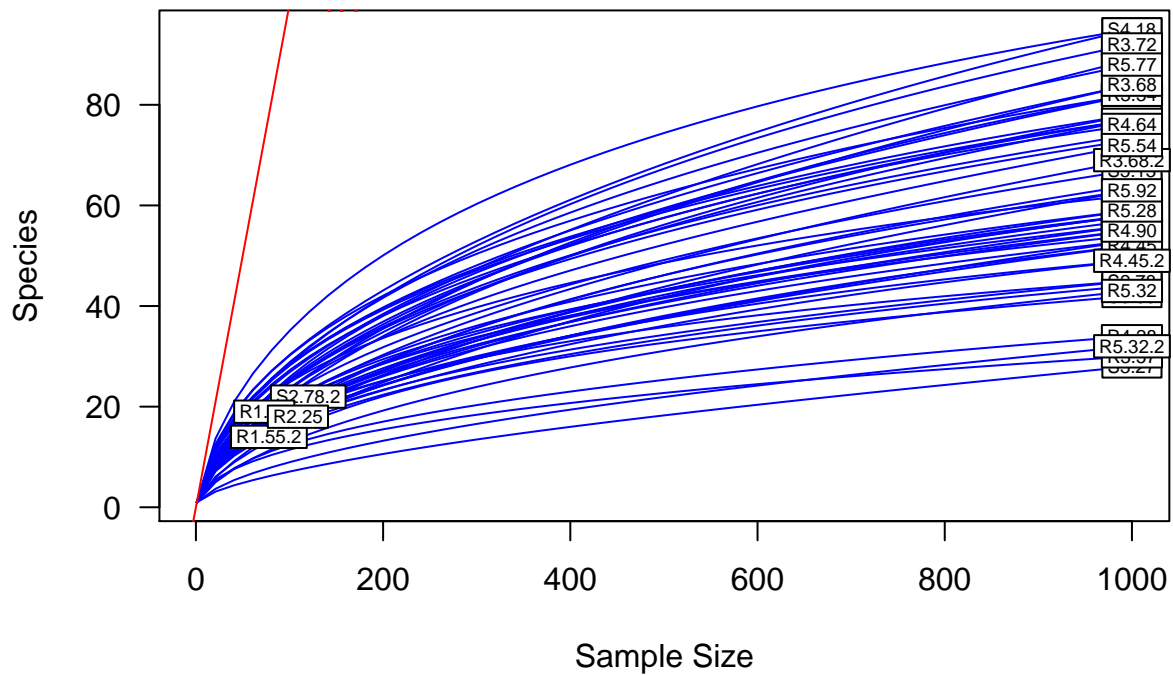
```

```

richness <- rowSums((site_species.r > 0) * 1)
minimum.r <- min(rowSums(site_species.r))
rarefy <- rarefy(x = site_species.r, sample = minimum.r, se = TRUE)

rarecurve(x = site_species.r, step = 20, col = "blue", cex = .6, las = 1)
abline(0, 1, col = 'red')
text(200, 100, "1:1", pos = 2, col = 'red')

```



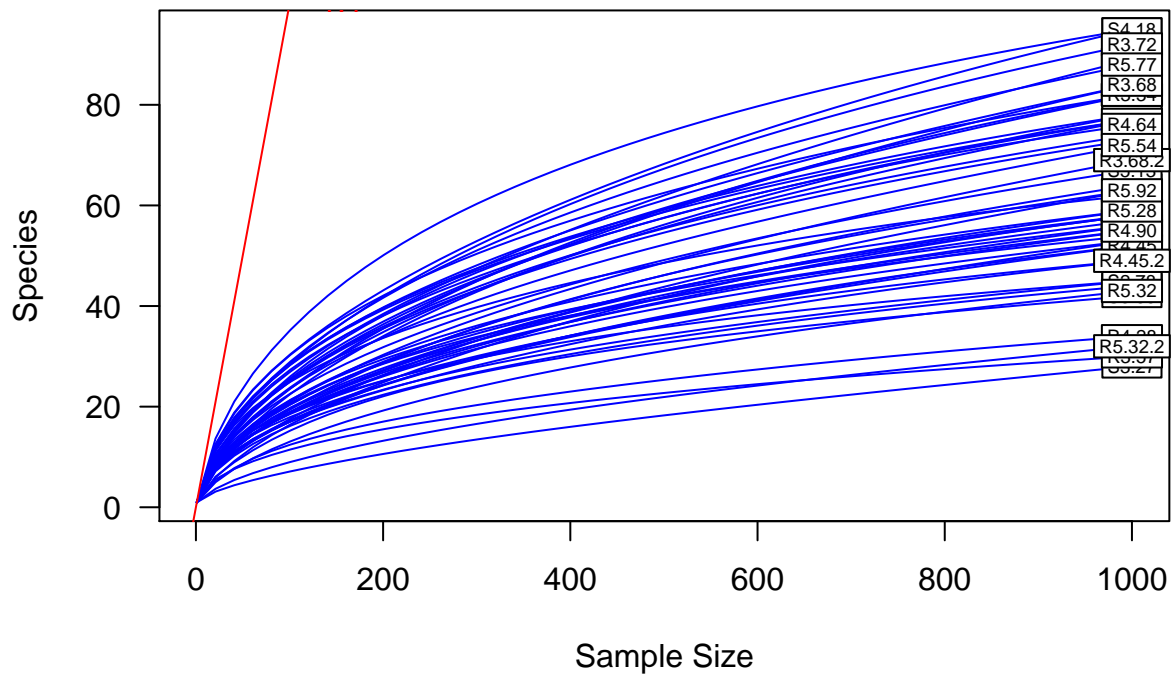
```
#Remove samples containing less than 1000 reads (R1.14, R1.55.2, R2.25, S2.78.2)

df.site_species.r <- as.data.frame(site_species.r)
rarefied_site_species <- data.frame()

for (i in 1:nrow(df.site_species.r)){
  if (rowSums(df.site_species.r[i,]) >= 1000){
    rarefied_site_species <- rbind(rarefied_site_species, df.site_species.r[i,])
  }
}

#Visualizing
richness <- rowSums((rarefied_site_species > 0) * 1)
minimum.r <- min(rowSums(rarefied_site_species))
rarefy <- rarefy(x = rarefied_site_species, sample = minimum.r, se = TRUE)

rarecurve(x = rarefied_site_species, step = 20, col = "blue", cex = .6, las = 1)
abline(0, 1, col = 'red')
text(200, 100, "1:1", pos = 2, col = 'red')
```



Calculating Bray-Curtis Beta-Diversity

```
funGalBC <- vegdist(rarefied_site_species, method = "bray")
```

Cluster Analysis of Fungal Communities

```
#Performing Cluster Analysis
funGal.ward <- hclust(funGalBC, method = "ward.D2")

#Plotting Cluster
par(mar = c(1,5,2,2) + .1)
plot(funGal.ward, main = "Doubs River Fish: Ward's Clustering",
      ylab = "Squared Bray-Curtis Distance")
```

A dendrogram illustrating the hierarchical clustering of 36 samples based on Squared Bray-Curtis Distance. The y-axis represents the distance, ranging from 0.0 to 2.0. The samples are labeled with codes such as S3.27, R3.32, R5.36, R1.55, R4.90, S2.26, S1.73, S3.56, R1.89, R1.73, R2.29, R5.19, S1.23, R3.22, R3.13, R4.64, S4.18, S3.77, S1.78, S1.56, S1.36, S5.74, R4.45, R4.52, S4.46, and S4.73. The dendrogram shows that the samples are grouped into several distinct clusters, with the most significant split occurring at a distance of approximately 1.8, separating a group of samples on the left from a larger group on the right.

```

fungal.pcoa <- cmdscale(fungalBC, eig = TRUE, k = 3)

explainvar1 <- round(fungal.pcoa$eig[1]/sum(fungal.pcoa$eig), 3) * 100
explainvar2 <- round(fungal.pcoa$eig[2]/sum(fungal.pcoa$eig), 3) * 100
explainvar3 <- round(fungal.pcoa$eig[3]/sum(fungal.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

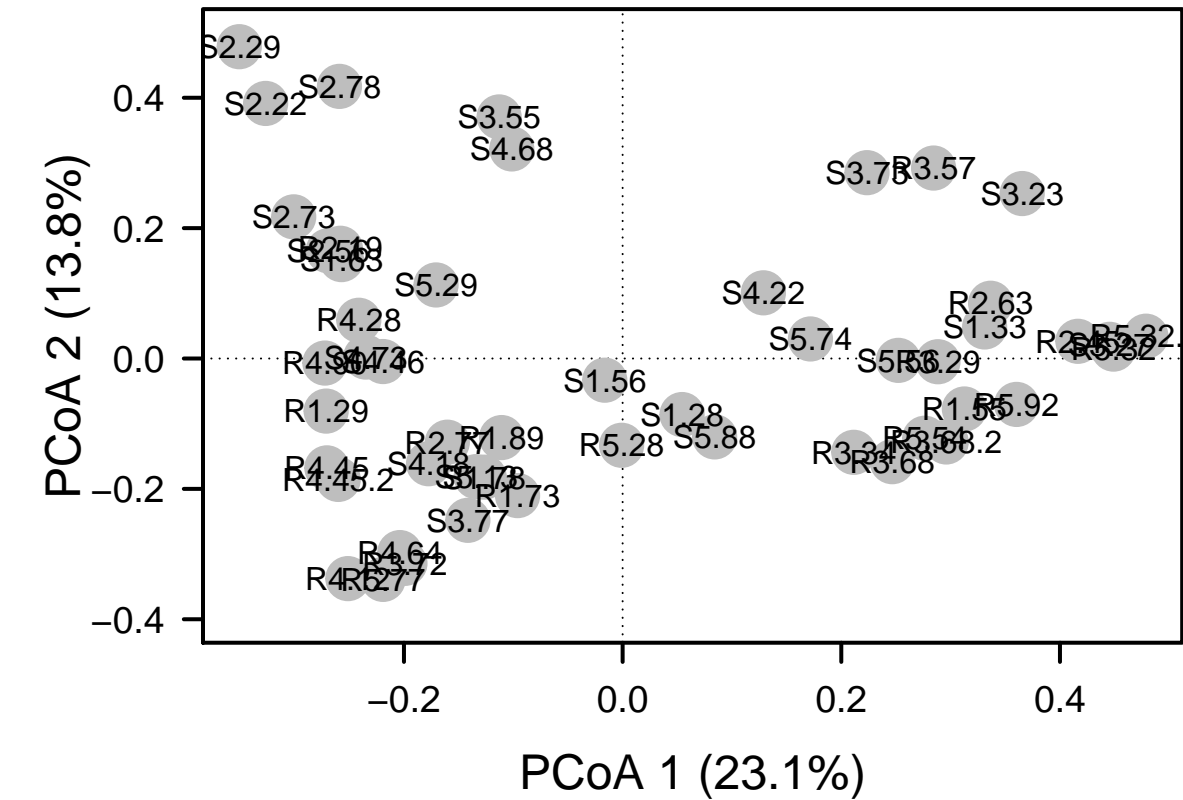
#Define Plot Parameters
par(mar = c(5,5,1,2), .1)

#Initiate Plot
plot(fungal.pcoa$points[,1], fungal.pcoa$points[,2], ylim = c(-.4, .5),
     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 axis
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(fungal.pcoa$points[,1], fungal.pcoa$points[,2],
       pch = 19, cex = 3, bg = "gray", col = "gray")
text(fungal.pcoa$points[,1], fungal.pcoa$points[,2],
      labels = row.names(fungal.pcoa$points))
```



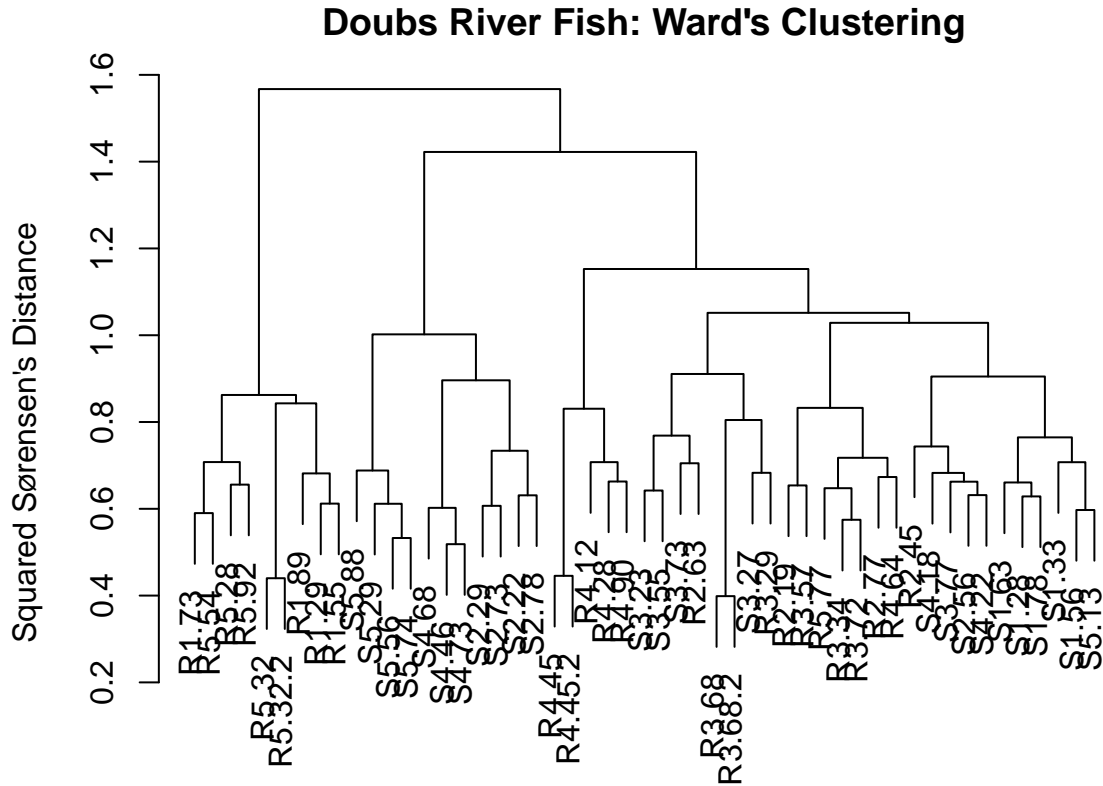
#Calculating Sorensen Beta-Diversity

```
fungalBC <- vegdist(rarefied_site_species, method = "bray", binary = "TRUE")
```

Cluster Analysis of Fungal Communities

```
#Performing Cluster Analysis
funga1.ward <- hclust(funga1BC, method = "ward.D2")

#Plotting Cluster
par(mar = c(1,5,2,2) + .1)
plot(funga1.ward, main = "Doubs River Fish: Ward's Clustering",
      ylab = "Squared Sørensen's Distance")
```



PCoA of Fungal Communities

```

fungal.pcoa <- cmdscale(fungalBC, eig = TRUE, k = 3)

explainvar1 <- round(fungal.pcoa$eig[1]/sum(fungal.pcoa$eig), 3) * 100
explainvar2 <- round(fungal.pcoa$eig[2]/sum(fungal.pcoa$eig), 3) * 100
explainvar3 <- round(fungal.pcoa$eig[3]/sum(fungal.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

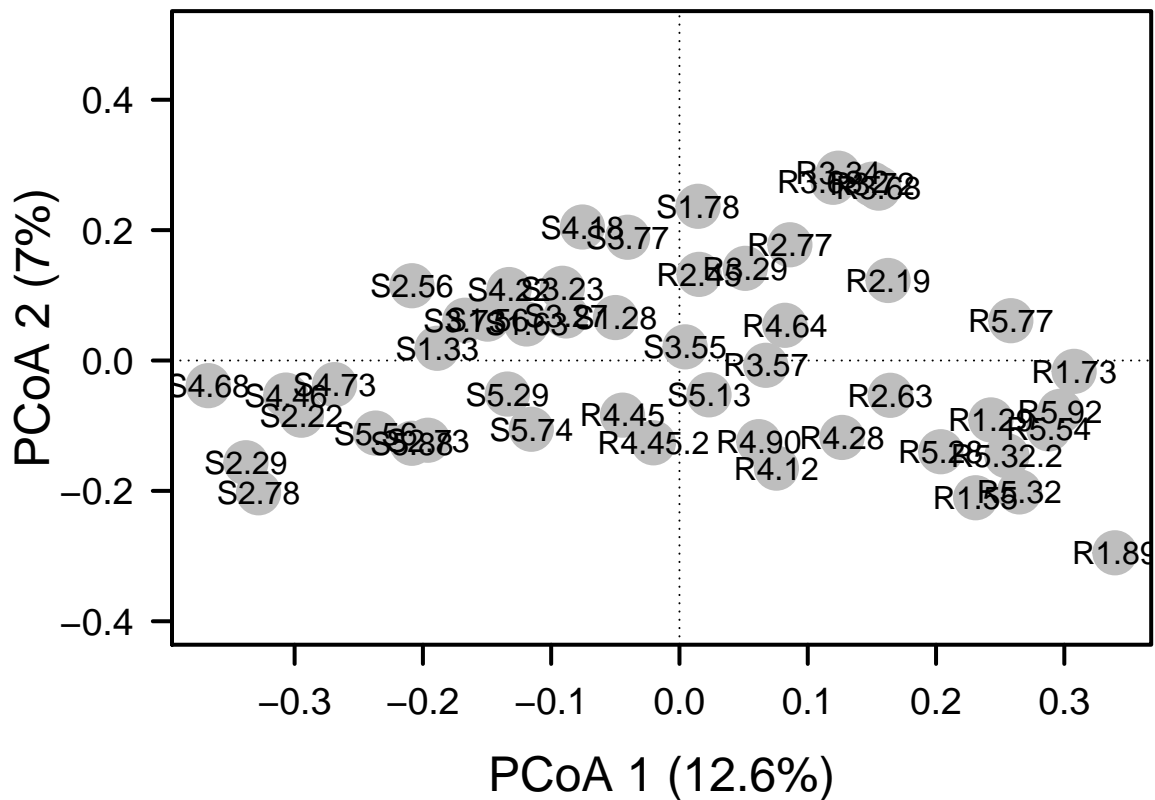
#Define Plot Parameters
par(mar = c(5,5,1,2), .1)

#Initiate Plot
plot(fungal.pcoa$points[,1], fungal.pcoa$points[,2], ylim = c(-.4, .5),
     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 axis
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(fungal.pcoa$points[,1], fungal.pcoa$points[,2],
      pch = 19, cex = 3, bg = "gray", col = "gray")
text(fungal.pcoa$points[,1], fungal.pcoa$points[,2],
     labels = row.names(fungal.pcoa$points))
```



Relative Abundance Visualization

```
genus <- read.csv("alpine_ridge_data/genus_table.csv", header = TRUE)
#convert rownames into column
library(data.table)
```

```
## Warning: package 'data.table' was built under R version 4.0.5
```

```
genus.1 <- as.data.frame(t(rarefied_site_species))
setDT(genus.1, keep.rownames = TRUE)[,]
```

```
##      rn S1.28 S1.33 S1.56 S1.63 S1.78 S2.22 S2.29 S2.56 S2.73 S2.78 S3.23
##  1:  V1      0      0      0      0      0      0      0      0      0      0      0
##  2:  V2      0      0      0      0      0      0      0      0      0      0      0
##  3:  V3      0      0      0      0      0      0      0      0      0      0      0
```



```

## 4: V4 0 0 0 1 0 0 0 0 0 0 0 0
## 5: V5 0 0 0 0 0 0 0 0 0 0 0 0
## ---
## 803: V803 1 0 0 0 1 0 1 3 0 0 1
## 804: V804 0 0 0 0 0 0 0 0 5 0 0
## 805: V805 0 0 0 0 0 0 0 0 0 0 0
## 806: V806 0 0 0 0 0 0 0 0 0 0 0
## 807: V807 0 0 0 0 0 0 0 0 0 0 0
## S3.27 S3.55 S3.73 S3.77 S4.18 S4.22 S4.46 S4.68 S4.73 S5.13 S5.29 S5.56
## 1: 0 0 0 0 0 0 0 0 1 0 0 0
## 2: 0 0 0 0 8 0 27 0 0 0 16 14
## 3: 0 0 0 0 0 0 0 0 0 0 0 0
## 4: 0 0 0 0 0 0 0 0 0 0 0 0
## 5: 0 0 0 0 0 0 1 0 0 0 0 0
## ---
## 803: 0 0 0 2 8 2 1 4 0 0 0 0
## 804: 0 1 0 1 0 0 0 0 0 0 0 0
## 805: 0 0 0 0 0 0 0 0 0 0 0 0
## 806: 0 0 0 0 0 0 0 0 0 0 0 0
## 807: 0 0 0 0 0 0 0 0 0 0 0 0
## S5.74 S5.88 R1.29 R1.55 R1.73 R1.89 R2.19 R2.45 R2.63 R2.77 R3.29 R3.34
## 1: 0 0 0 0 0 0 0 0 0 0 0 0
## 2: 7 3 0 0 0 0 0 0 0 0 0 0
## 3: 0 0 0 0 0 0 0 0 0 0 0 0
## 4: 0 0 0 0 0 0 0 0 0 0 0 0
## 5: 0 0 0 0 0 0 0 0 0 0 0 0
## ---
## 803: 0 0 0 0 0 0 0 4 0 1 0 1
## 804: 0 0 5 1 3 0 0 0 0 0 0 0
## 805: 0 0 0 0 0 0 0 1 0 0 0 0
## 806: 0 0 0 0 0 0 0 0 0 0 0 0
## 807: 0 0 0 0 0 0 0 0 0 0 0 0
## R3.57 R3.68 R3.68.2 R3.72 R4.12 R4.28 R4.45 R4.45.2 R4.64 R4.90 R5.28
## 1: 0 0 0 0 0 0 0 0 0 0 0
## 2: 0 0 0 0 0 0 0 0 0 0 0
## 3: 0 0 0 0 1 0 0 0 0 0 0
## 4: 0 0 0 0 0 0 0 0 0 0 0
## 5: 0 0 0 0 0 0 0 0 0 0 0
## ---
## 803: 0 0 0 3 0 0 0 0 1 0 0
## 804: 0 0 0 0 0 0 0 5 2 6 13
## 805: 0 0 0 0 0 0 0 0 0 0 0
## 806: 0 0 0 0 0 0 0 0 0 0 2
## 807: 0 0 1 0 0 0 0 0 0 0 0
## R5.32 R5.32.2 R5.54 R5.77 R5.92
## 1: 0 0 0 0 0
## 2: 0 0 0 0 0
## 3: 0 0 0 0 0
## 4: 0 0 0 0 0
## 5: 0 0 0 0 0
## ---
## 803: 3 0 0 0 0
## 804: 1 0 18 17 2
## 805: 0 0 0 0 0

```

