

All_analysis

Anna Lennon

2025-03-07

```
library(readxl)
library(dplyr)
library(tidyr)
library(vegan)
library(ggplot2)
library(tidyverse)
library(lattice)
library(ade4)
library(viridis)
library(gplots)
library(bios2mds)
library(Biostrings)
library(ape)
library(seqinr)
library(phylolm)
library(adephylo)
library(geiger)
library(picante)
library(stats)
library(RColorBrewer)
library(phylolm)
library(caper)
library(pmcl)
library(phangorn)
library(pander)

#tree data
tree <-read.csv("TREE.csv")

tree.species.df <-data.frame(Plot_ID = c(tree$PLOT),
                             SPCD =c(tree$SPCD))

tree.species.ss <-as.data.frame.matrix(table(tree.species.df$Plot_ID, tree.species.df$SPCD))
str(tree.species.df) #plot and species id

## 'data.frame':    43528 obs. of  2 variables:
##   $ Plot_ID: int  7242 7242 5662 7242 7242 7242 7307 5442 5442 5442 ...
##   $ SPCD   : int  318 318 541 318 318 762 931 621 621 ...
#print(tree.species.df)
#print(unique(tree.species.df$SPCD))
```

```

#Myco assocaitions
myco <-as.data.frame(read_xlsx("MycoType_ref2.xlsx"))

## New names:
## * `` -> `...6`
## * `` -> `...7`
myco<- myco[, -c(3:7)]
str(myco)

## 'data.frame': 107 obs. of 2 variables:
## $ SPCD : num 15 68 91 110 125 129 130 131 132 221 ...
## $ MycoType: num 1 2 1 1 1 1 1 1 1 2 ...
#print(unique(myco$SPCD))

#invasive
#invasive <-read_xlsx("INVASIVE.xlsx")
invasive <-read_xlsx("INVASIVE_SUBPLOT_SPP.xlsx")
str(invasive)

## tibble [1,231 x 21] (S3:tbl_df/tbl/data.frame)
## $ CN : chr [1:1231] "11370913000440" "11370914000440" "11370915000440" "11370916000440" ...
## $ PLT_CN : chr [1:1231] "782031931290487" "782031931290487" "782031931290487" "782031931290487" ...
## $ INVYR : num [1:1231] 2022 2022 2022 2022 2022 ...
## $ STATECD : num [1:1231] 18 18 18 18 18 18 18 18 18 18 ...
## $ UNITCD : num [1:1231] 1 1 1 1 1 1 1 1 1 1 ...
## $ COUNTYCD : num [1:1231] 153 153 153 153 153 153 153 153 153 153 ...
## $ PLOT : num [1:1231] 1477 1477 1477 1477 1477 ...
## $ SUBP : num [1:1231] 1 1 1 1 1 1 1 1 1 1 ...
## $ CON DID : num [1:1231] 1 1 1 1 1 1 1 1 1 1 ...
## $ VEG_FLDSPCD : chr [1:1231] "CEOR7" "LIVU" "LOJA" "LOMA6" ...
## $ UNIQUE_SP_NBR : num [1:1231] 1 1 1 1 1 1 1 1 1 1 ...
## $ VEG_SPCD : chr [1:1231] "CEOR7" "LIVU" "LOJA" "LOMA6" ...
## $ COVER_PCT : num [1:1231] 4 1 1 1 10 35 8 16 8 ...
## $ CREATED_BY : chr [1:1231] "FS_NIMS_IN_18" "FS_NIMS_IN_18" "FS_NIMS_IN_18" "FS_NIMS_IN_18" ...
## $ CREATED_DATE : POSIXct[1:1231], format: "2023-04-17 11:24:36" "2023-04-17 11:24:36" ...
## $ CREATED_IN_INSTANCE : chr [1:1231] "440" "440" "440" "440" ...
## $ MODIFIED_BY : logi [1:1231] NA NA NA NA NA ...
## $ MODIFIED_DATE : logi [1:1231] NA NA NA NA NA ...
## $ MODIFIED_IN_INSTANCE: logi [1:1231] NA NA NA NA NA ...
## $ CYCLE : num [1:1231] 3 3 3 3 3 3 3 3 3 ...
## $ SUBCYCLE : num [1:1231] 5 5 5 5 5 5 5 5 5 ...

#print(invasive)

#print(unique(invasive.df))

#References
#Plot ID Code
# plotID.master <-read_xlsx(path = "PLOT.xlsx")
# print(plotID.master)

#Clean- make sure has same species
untree.species <- unique(tree.species.df$SPCD)

```

```

unmyco.species <-unique(myco$SPCD)
length(untree.species)

## [1] 109
length(unmyco.species)

## [1] 107
#print(sort(untree.species))
#print(sort(unmyco.species))
setdiff(untree.species, unmyco.species)

## [1] 8421 999 998

tree.species.df <- tree.species.df %>%
  filter(!SPCD %in% c(999, 998))

#Filter if species has invasives

invasive_plots <- unique(invasive$PLOT)
invasive.plots.df <- tree.species.df[tree.species.df$Plot %in% invasive_plots, ]
ninvasive.plots.df <- tree.species.df[!tree.species.df$Plot %in% invasive_plots, ]

# invasive_plots <-as.data.frame(invasive$PLOT)
# invasive_plots <- unique(invasive_plots)
# #print(invasive_plots)
#
# invasive.plots.df <- data.frame()
# ninvasive.plots.df <- data.frame()
#
# for (i in seq_len(nrow(tree.species.df))) {
#   if (tree.species.df$Plot[i] %in% invasive_plots) {
#     invasive.plots.df <- rbind(invasive.plots.df, tree.species.df[i, ])
#   } else {
#     ninvasive.plots.df <- rbind(ninvasive.plots.df, tree.species.df[i, ])
#   }
# }
# invasive_plots <- unique(invasive.df$Plot_ID)
# print(invasive_plots)
# print(invasive.plots.df)
# print(ninvasive.plots.df)

#site by species invasive
invasive.df <-data.frame(Plot_ID= c(invasive$PLOT),
                         SPCD =c(invasive$VEG_SPCD))
invasive.ss <-as.data.frame.matrix(table(invasive.df$Plot_ID, invasive.df$SPCD))

#AM/ECM

ninvasive.myco.df <- merge(ninvasive.plots.df, myco, by="SPCD", all.x=TRUE, all.y=FALSE)
ninvasive.myco.ss <- as.data.frame.matrix(table(ninvasive.myco.df$Plot_ID, ninvasive.myco.df$MycoType))

```

```

ninvasive.ECM.df <- subset(ninvasive.myco.df, ninvasive.myco.df$MycoType==1)
ninvasive.AM.df <- subset(ninvasive.myco.df, ninvasive.myco.df$MycoType==2)
ninvasive.both.df <- subset(ninvasive.myco.df, ninvasive.myco.df$MycoType==3)

invasive.myco.df <- merge(invasive.plots.df, myco, by="SPCD", all.x=TRUE, all.y=FALSE)

invasive.myco.ss <- as.data.frame.matrix(table(invasive.myco.df$Plot_ID, invasive.myco.df$MycoType))
invasive.ECM.df <- subset(invasive.myco.df, invasive.myco.df$MycoType==1)
invasive.AM.df <- subset(invasive.myco.df, invasive.myco.df$MycoType==2)
invasive.both.df <- subset(invasive.myco.df, invasive.myco.df$MycoType==3)

#Site by species noninvasive

ninvasive.AM.ss <- as.data.frame.matrix(table(ninvasive.AM.df$Plot_ID, ninvasive.AM.df$SPCD))
#ninvasive.AM.ss <- rownames_to_column(ninvasive.AM.ss, var = "Plot_ID")
#ninvasive.AM.ss.L <- ninvasive.AM.ss[,-1]

ninvasive.ECM.ss <- as.data.frame.matrix(table(ninvasive.ECM.df$Plot_ID, ninvasive.ECM.df$SPCD))
#ninvasive.ECM.ss <- rownames_to_column(ninvasive.ECM.ss, var = "Plot_ID")
#ninvasive.ECM.ss.L <- ninvasive.ECM.ss[,-1]

# ninvasive.both.ss <- as.data.frame.matrix(table(ninvasive.both.df$Plot_ID, ninvasive.both.df$SPCD))
# ninvasive.both.ss <- rownames_to_column(ninvasive.both.ss, var = "Plot_ID")

#Site by species: Invasive
invasive.AM.ss <- as.data.frame.matrix(table(invasive.AM.df$Plot_ID, invasive.AM.df$SPCD))
#invasive.AM.ss <- rownames_to_column(invasive.AM.ss, var = "Plot_ID")
#invasive.AM.ss <- ninvasive.AM.ss[,-1]

invasive.ECM.ss <- as.data.frame.matrix(table(invasive.ECM.df$Plot_ID, invasive.ECM.df$SPCD))
#invasive.ECM.ss <- rownames_to_column(invasive.ECM.ss, var = "Plot_ID")
#invasive.ECM.ss.L <- ninvasive.ECM.ss[,-1]

# invasive.both.ss <- as.data.frame.matrix(table(invasive.both.df$Plot_ID, invasive.both.df$SPCD))
#invasive.both.ss <- rownames_to_column(invasive.both.ss, var = "Plot_ID")

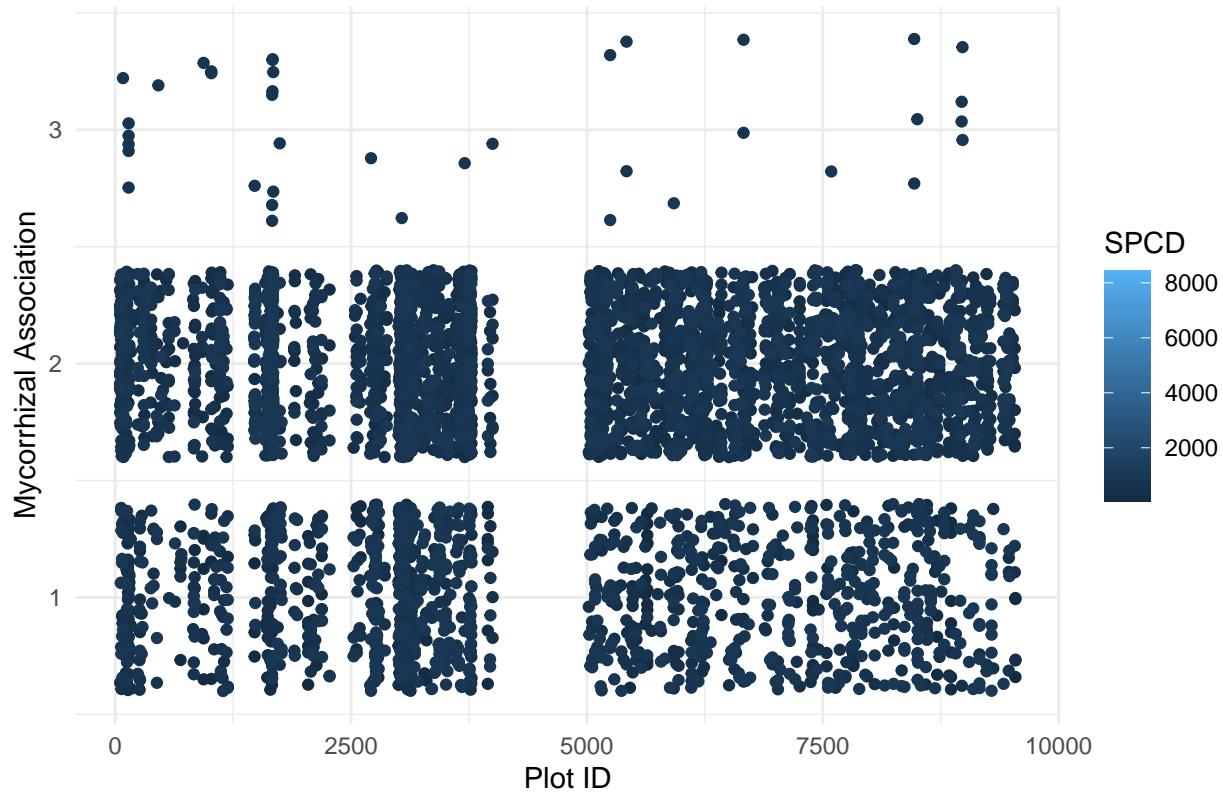
#Visualization of species present
#dim(tree.species.df)
myco.df.all <- rbind(invasive.myco.df, ninvasive.myco.df)

ggplot(invasive.myco.df) +
  aes(x = Plot_ID, y = MycoType, color = SPCD) +
  geom_jitter() +
  xlab("Plot ID") +
  ylab("Mycorrhizal Association") +
  ggtitle("Distribution of Mycorrhizal Type by Species in Invasive Plots") +
  theme_minimal()

## Warning: Removed 5 rows containing missing values or values outside the scale range
## (~geom_point()`).

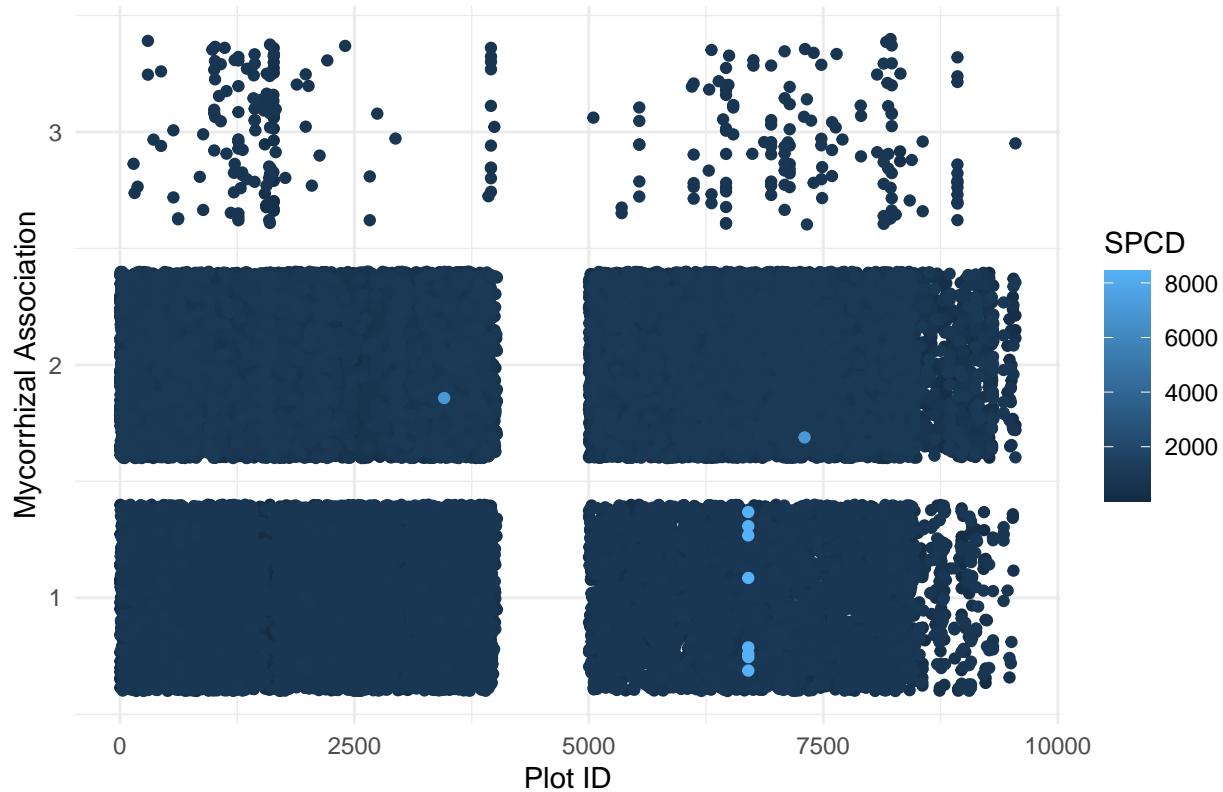
```

Distribution of Mycorrhizal Type by Species in Invasive Plots



```
ggplot(ninvasive.myco.df) +  
  aes(x = Plot_ID, y = MycoType, color = SPCD) +  
  geom_jitter() +  
  xlab("Plot ID") +  
  ylab("Mycorrhizal Association") +  
  ggtitle("Distribution of Mycorrhizal Type by Species in NonInvasive Plots") +  
  theme_minimal()
```

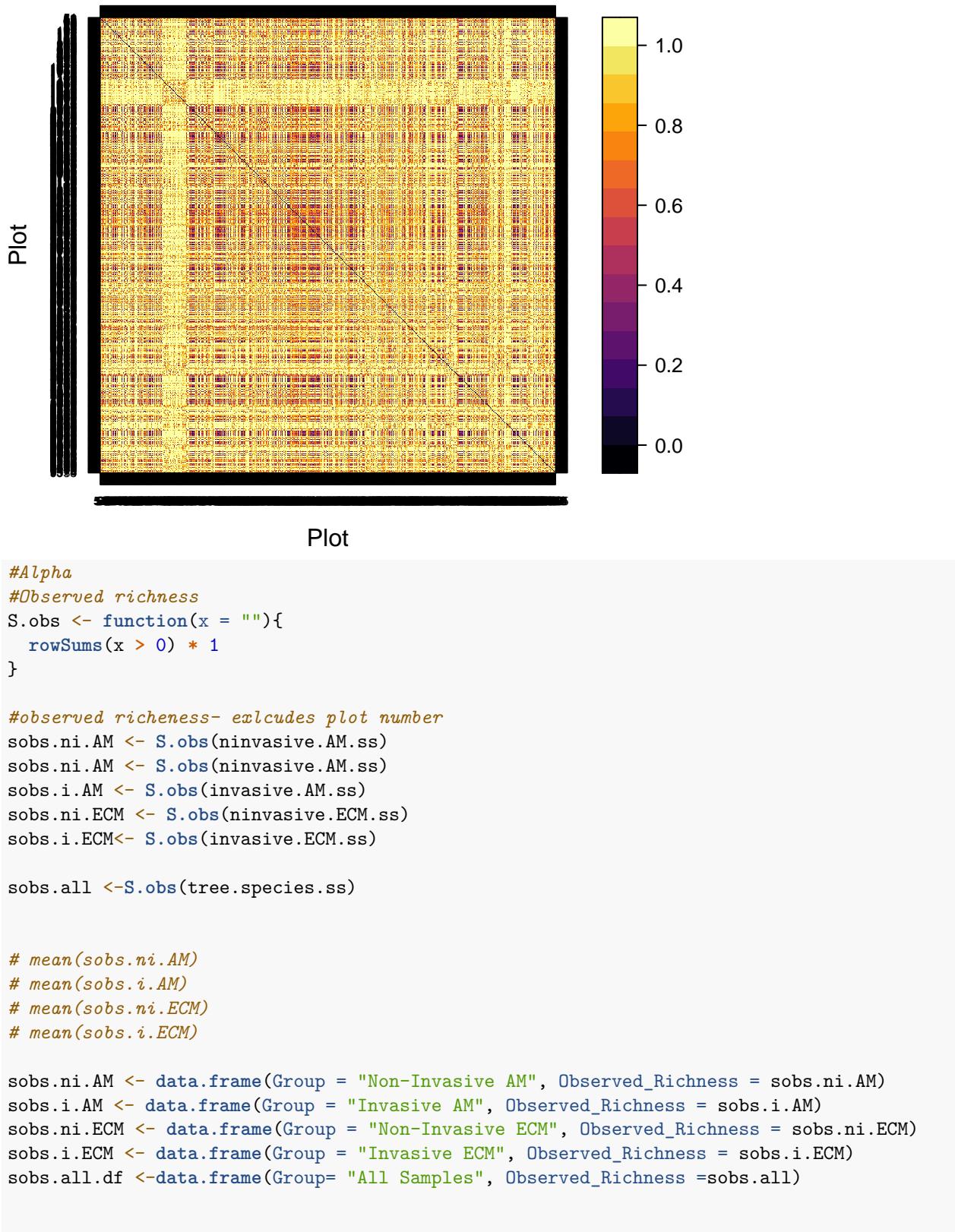
Distribution of Mycorrhizal Type by Species in NonInvasive Plots



```
tree.bray <- vegdist(invasive.AM.ss[1:643, 1:38], method = "bray")

order <- rev(attr(tree.bray, "Labels"))
levelplot(as.matrix(tree.bray)[,order], aspect = "iso", col.regions =inferno,
         xlab = "Plot", ylab = "Plot", scales =list(cex =.5),
         main = "Bray-Curtis Distance")
```

Bray-Curtis Distance



```

sobs.i.am.box<- ggplot(sobs.i.AM, aes(y = sobs.i.AM)) +
  geom_boxplot(fill="azure2", alpha=0.2) +
  xlab("Observed Richness")

sobs.ni.am.box<- ggplot(sobs.ni.AM, aes(y = sobs.i.AM)) +
  geom_boxplot(fill="azure2", alpha=0.2) +
  xlab("Observed Richness")

sobs.i.ECM.box<- ggplot(sobs.i.ECM, aes(y = sobs.i.AM)) +
  geom_boxplot(fill="azure2", alpha=0.2) +
  xlab("Observed Richness")

sobs.ni.ECM.box<- ggplot(sobs.ni.ECM, aes(y = sobs.i.AM)) +
  geom_boxplot(fill="azure2", alpha=0.2) +
  xlab("Observed Richness")

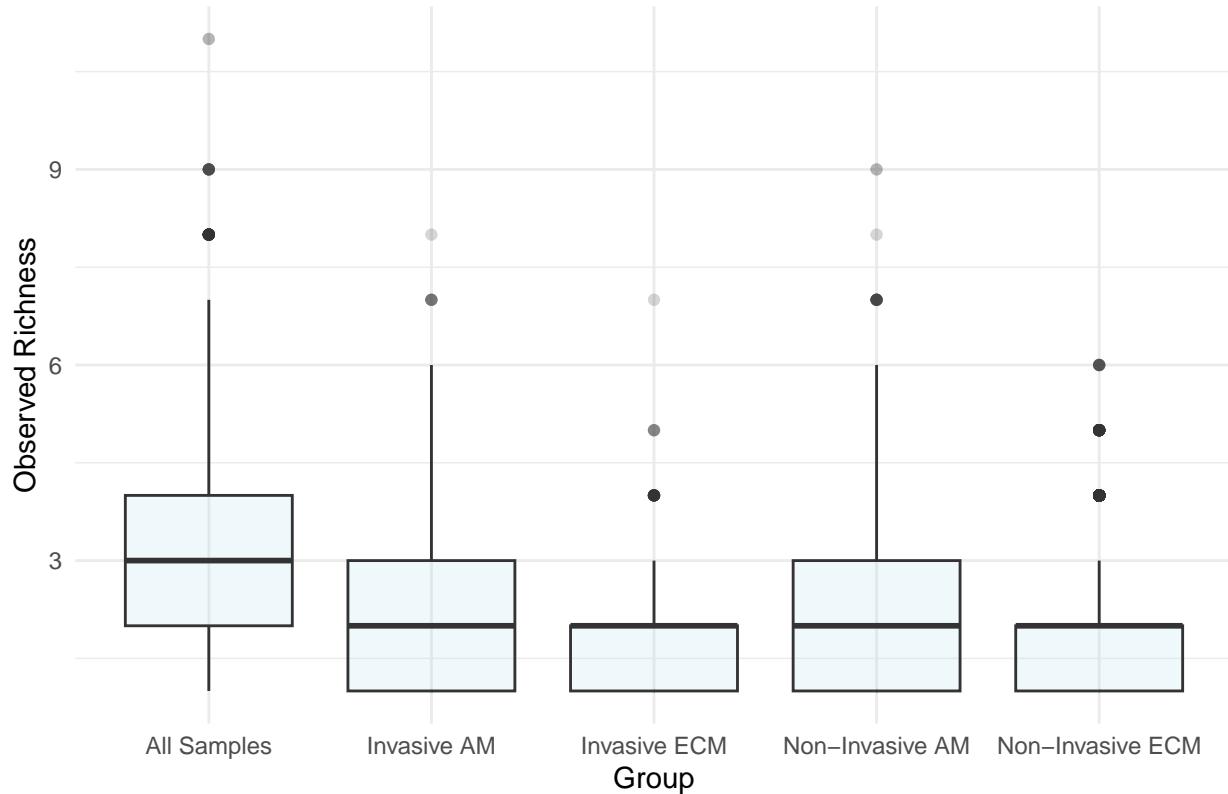
sobs_data <- bind_rows(sobs.ni.AM, sobs.i.AM, sobs.ni.ECM, sobs.i.ECM, sobs.all.df)

# # Perform clustering
# clusters <- kmeans(sobs_data$Observed_Richness, centers = 3, iter.max = 10, nstart = 1)
#
# centroids <- clusters$centers
#
# ordered_centroids <- order(centroids)
#
#
# sobs_data$Cluster <- factor(clusters$cluster, levels = ordered_centroids)
# sobs_data$Cluster <- as.numeric(sobs_data$Cluster)

# Boxplot visualization
ggplot(sobs_data, aes(x = Group, y = Observed_Richness)) +
  geom_boxplot(fill = "lightblue2", alpha = 0.2) +
  xlab("Group") +
  ylab("Observed Richness") +
  ggtitle("Observed Richness Across Groups") +
  theme_minimal()

```

Observed Richness Across Groups



```
#anova
sobs.aov <- aov(Observed_Richness ~ Group,
                  data = sobs_data)
summary(sobs.aov)
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## Group       4   8256   2064.0    1342 <2e-16 ***
## Residuals 17536   26962      1.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
TukeyHSD(sobs.aov)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Observed_Richness ~ Group, data = sobs_data)
##
## $Group
##          diff      lwr      upr     p adj
## Invasive AM-All Samples -0.98787238 -1.12763273 -0.8481120 0.0000000
## Invasive ECM-All Samples -1.65155011 -1.81973518 -1.4833650 0.0000000
## Non-Invasive AM-All Samples -1.25590486 -1.31783557 -1.1939742 0.0000000
## Non-Invasive ECM-All Samples -1.57288602 -1.63862885 -1.5071432 0.0000000
## Invasive ECM-Invasive AM -0.66367773 -0.87425874 -0.4530967 0.0000000
## Non-Invasive AM-Invasive AM -0.26803248 -0.40907701 -0.1269880 0.0000022
## Non-Invasive ECM-Invasive AM -0.58501364 -0.72777310 -0.4422542 0.0000000
## Non-Invasive AM-Invasive ECM  0.39564525  0.22639153  0.5648990 0.0000000
```

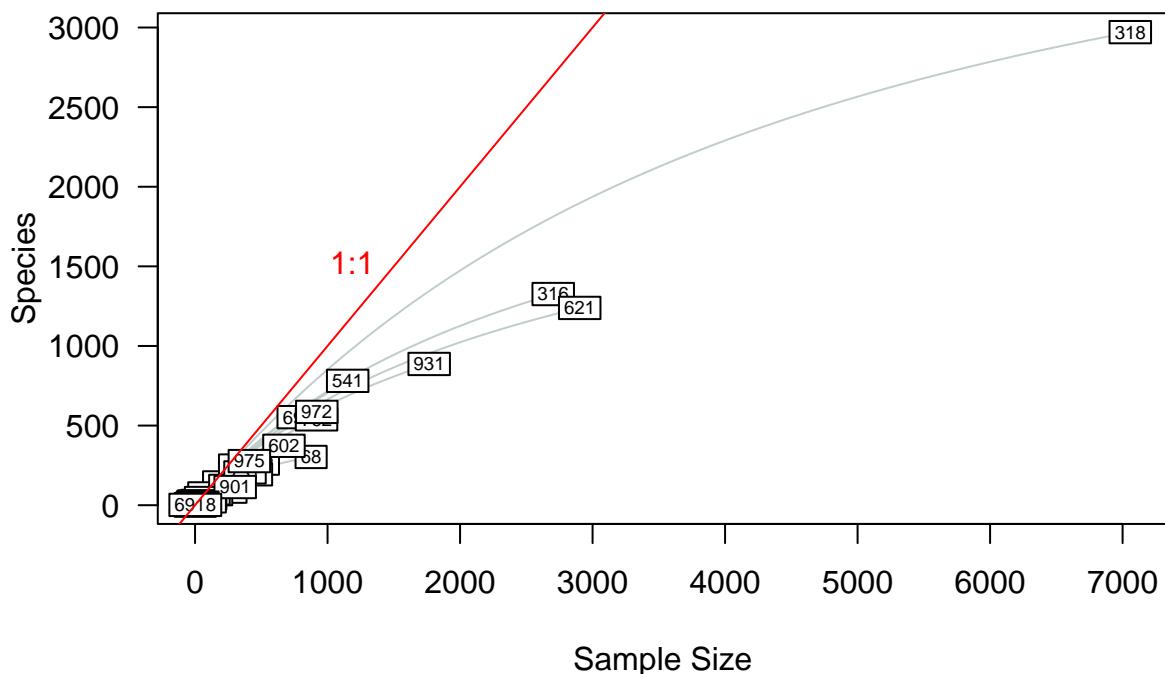
```

## Non-Invasive ECM-Invasive ECM      0.07866409 -0.09202138  0.2493496 0.7174548
## Non-Invasive ECM-Non-Invasive AM -0.31698116 -0.38541159 -0.2485507 0.0000000

#NI AM
ninvasive.AM.ss.t <- t(ninvasive.AM.ss)
ninvasive.AM.ss.S <- S.obs(ninvasive.AM.ss.t)
min.N <- min(rowSums(ninvasive.AM.ss.t))
S.rarefy <- rarefy(x = ninvasive.AM.ss.t , sample = min.N, se = TRUE)
rarecurve(x = ninvasive.AM.ss.t , step = 20, col = "azure3", cex = 0.6, las = 1)
abline(0, 1, col = 'red')
text(1500, 1500, "1:1", pos = 2, col = 'red')
title(main = "Rarefaction Curve of Non-Invasive AM Samples")

```

Rarefaction Curve of Non-Invasive AM Samples

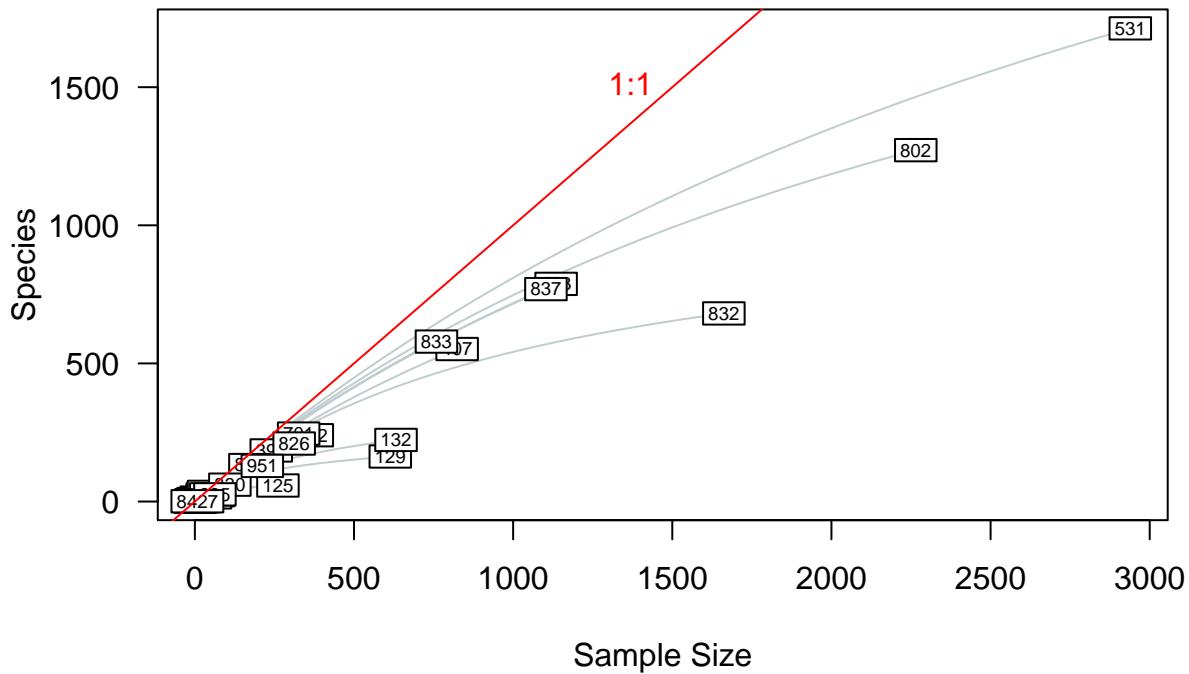


```

#NI ECM
ninvasive.ECM.ss.t <- t(ninvasive.ECM.ss)
ninvasive.ECM.ss.S <- S.obs(ninvasive.ECM.ss.t)
min.I.ecm <- min(rowSums(ninvasive.ECM.ss.t))
S.rarefy <- rarefy(x = ninvasive.ECM.ss.t , sample = min.I.ecm, se = TRUE)
rarecurve(x = ninvasive.ECM.ss.t , step = 20, col = "azure3", cex = 0.6, las = 1)
abline(0, 1, col = 'red')
text(1500, 1500, "1:1", pos = 2, col = 'red')
title(main = "Rarefaction Curve of Non-Invasive ECM Samples")

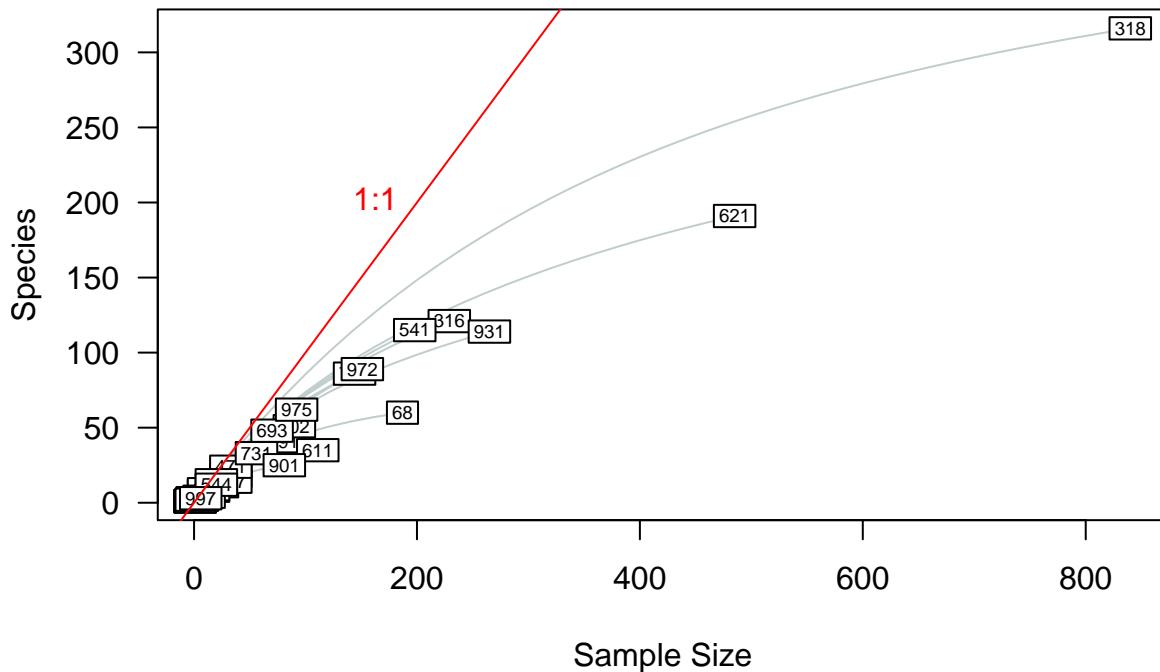
```

Rarefaction Curve of Non-Invasive ECM Samples



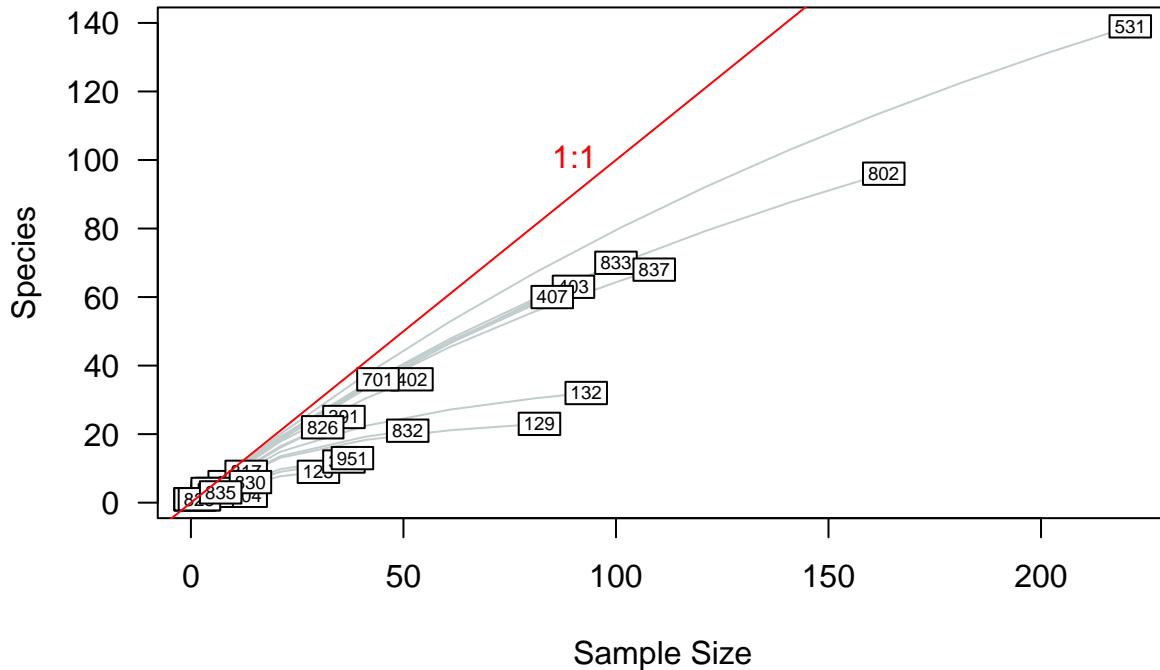
```
#I AM
invasive.AM.ss.t <- t(invasive.AM.ss)
invasive.AM.ss.S <- S.obs(invasive.AM.ss.t)
min.IAM <- min(rowSums(invasive.AM.ss.t))
S.rarefy <- rarefy(x = invasive.AM.ss.t , sample = min.IAM, se = TRUE)
rarecurve(x = invasive.AM.ss.t , step = 20, col = "azure3", cex = 0.6, las = 1)
abline(0, 1, col = 'red')
text(200, 200, "1:1", pos = 2, col = 'red')
title(main = "Rarefaction Curve of Invasive AM Samples")
```

Rarefaction Curve of Invasive AM Samples



```
#NI ECM
invasive.ECM.ss.t <- t(invasive.ECM.ss)
invasive.ECM.ss.S <- S.obs(invasive.ECM.ss.t)
min.IECM <- min(rowSums(invasive.ECM.ss.t))
S.rarefy <- rarefy(x = invasive.ECM.ss.t , sample = min.IECM, se = TRUE)
rarecurve(x = invasive.ECM.ss.t , step = 20, col = "azure3", cex = 0.6, las = 1)
abline(0, 1, col = 'red')
text(100, 100, "1:1", pos = 2, col = 'red')
title(main = "Rarefaction Curve of Invasive ECM Samples")
```

Rarefaction Curve of Invasive ECM Samples



```

# ninvasive.ECM.ss
# invasive.AM.ss
# invasive.ECM.ss
# tree.species.ss

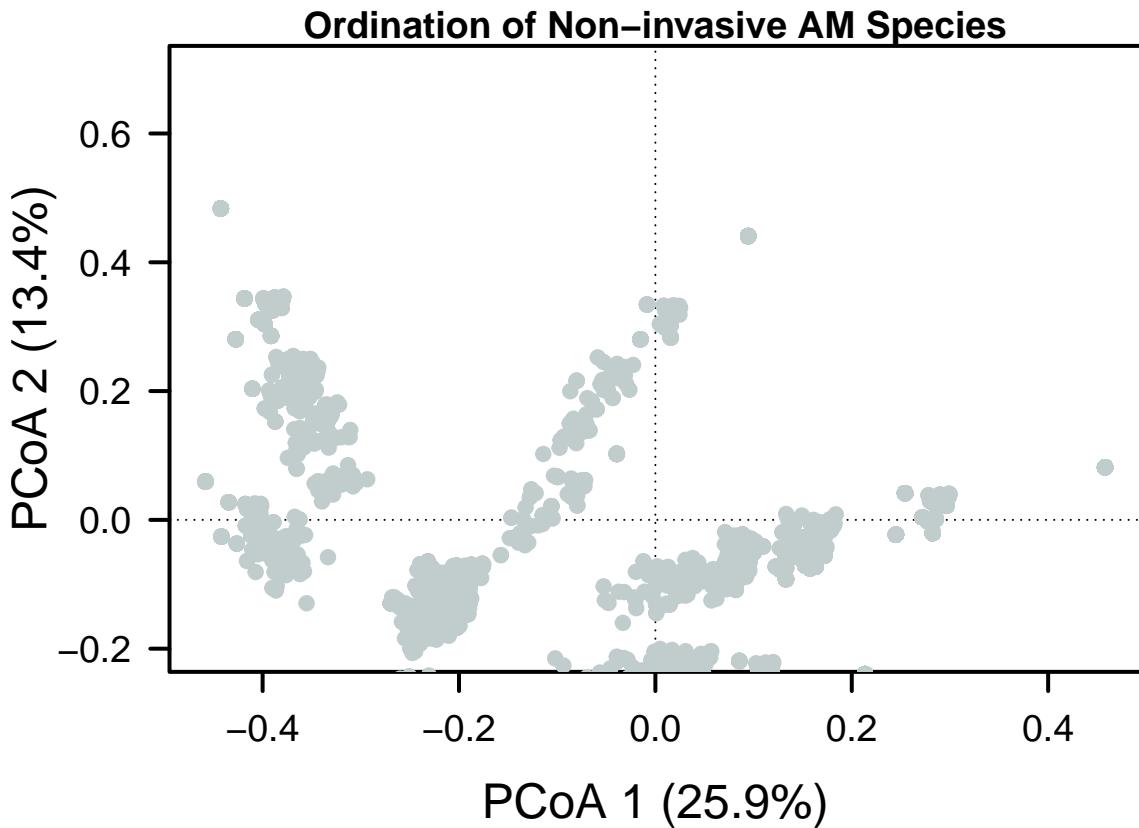
NI.AM.J <- vegdist(ninvasive.AM.ss, method = "jaccard", binary =TRUE)
NI.AM.pcoa <- cmdscale(NI.AM.J, eig =TRUE, k =3)
explainvar1 <- round(NI.AM.pcoa$eig[1] / sum(NI.AM.pcoa$eig), 3) * 100
explainvar2 <- round(NI.AM.pcoa$eig[2] / sum(NI.AM.pcoa$eig), 3) * 100
explainvar3 <- round(NI.AM.pcoa$eig[3] / sum(NI.AM.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)

#Plot
par(mar = c(5, 5, 1, 2) + 0.1)
plot(NI.AM.pcoa$points[,1], NI.AM.pcoa$points[,2], ylim = c(-0.2, 0.7),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)

axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 1.2, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)

points(NI.AM.pcoa$points[,1], NI.AM.pcoa$points[,2],
       pch = 19, cex = 1, bg = "gray", col = "azure3")
# text(jitter(NI.AM.pcoa$points[,1], amount = 0.02),
#       jitter(NI.AM.pcoa$points[,2], amount = 0.02))
#       #labels = row.names(NI.AM.pcoa$points), col = "black")
title("Ordination of Non-invasive AM Species")

```



```
#ninvasive.AM.ss.L <- ninvasive.AM.ss[,-1]
#ninvasive.ECM.ss.L <- ninvasive.AM.ss[,-1]
# invasive.AM.ss
# invasive.ECM.ss
# tree.species.ss

NI.ECM.J <- vegdist(ninvasive.ECM.ss, method = "jaccard", binary = TRUE)
NI.ECM.pcoa <- cmdscale(NI.ECM.J, eig = TRUE, k = 3)

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

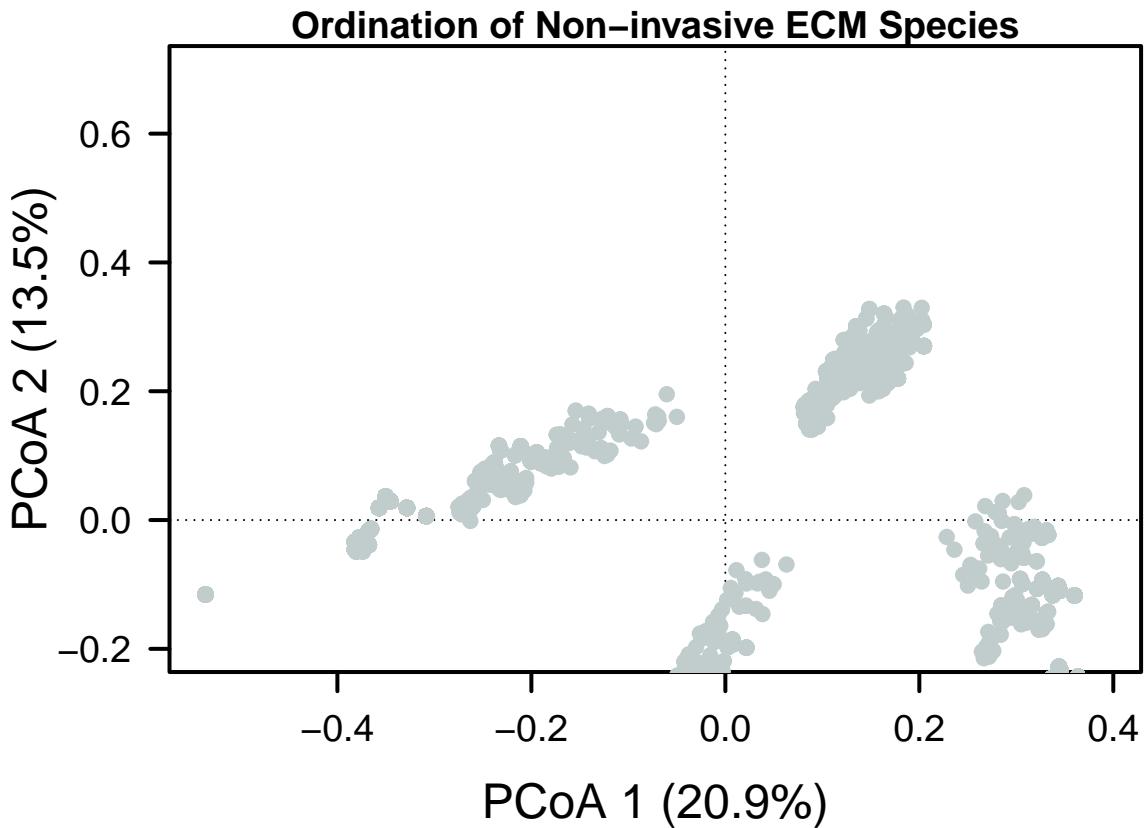
# Plot
par(mar = c(5, 5, 1, 2) + 0.1)
plot(NI.ECM.pcoa$points[,1], NI.ECM.pcoa$points[,2], ylim = c(-0.2, 0.7),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)

axis(side = 1, labels = TRUE, lwd.ticks = 2, cex.axis = 1.2, las = 1)
axis(side = 2, labels = TRUE, lwd.ticks = 2, cex.axis = 1.2, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)
points(NI.ECM.pcoa$points[,1], NI.ECM.pcoa$points[,2],
       pch = 19, cex = 1, bg = "gray", col = "azure3")
```

```

# text(jitter(NI.ECM.pcoa$points[,1], amount = 0.02),
#       jitter(NI.ECM.pcoa$points[,2], amount = 0.02),
#       labels = row.names(NI.ECM.pcoa$points), col = "black")
title("Ordination of Non-invasive ECM Species")

```



```

#ninvasive.AM.ss.L <- ninvasive.AM.ss[,-1]
#ninvasive.ECM.ss.L <- ninvasive.AM.ss[,-1]
#invasive.AM.ss.L <- invasive.AM.ss[,-1]
# invasive.ECM.ss
# tree.species.ss

I.AM.J <- vegdist(invasive.AM.ss, method = "jaccard", binary = TRUE)
I.AM.pcoa <- cmdscale(I.AM.J, eig = TRUE, k = 3)

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

par(mar = c(5, 5, 1, 2) + 0.1)
plot(I.AM.pcoa$points[,1], I.AM.pcoa$points[,2], ylim = c(-0.2, 0.7),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)

axis(side = 1, labels = TRUE, lwd.ticks = 2, cex.axis = 1.2, las = 1)
axis(side = 2, labels = TRUE, lwd.ticks = 2, cex.axis = 1.2, las = 1)

```

```

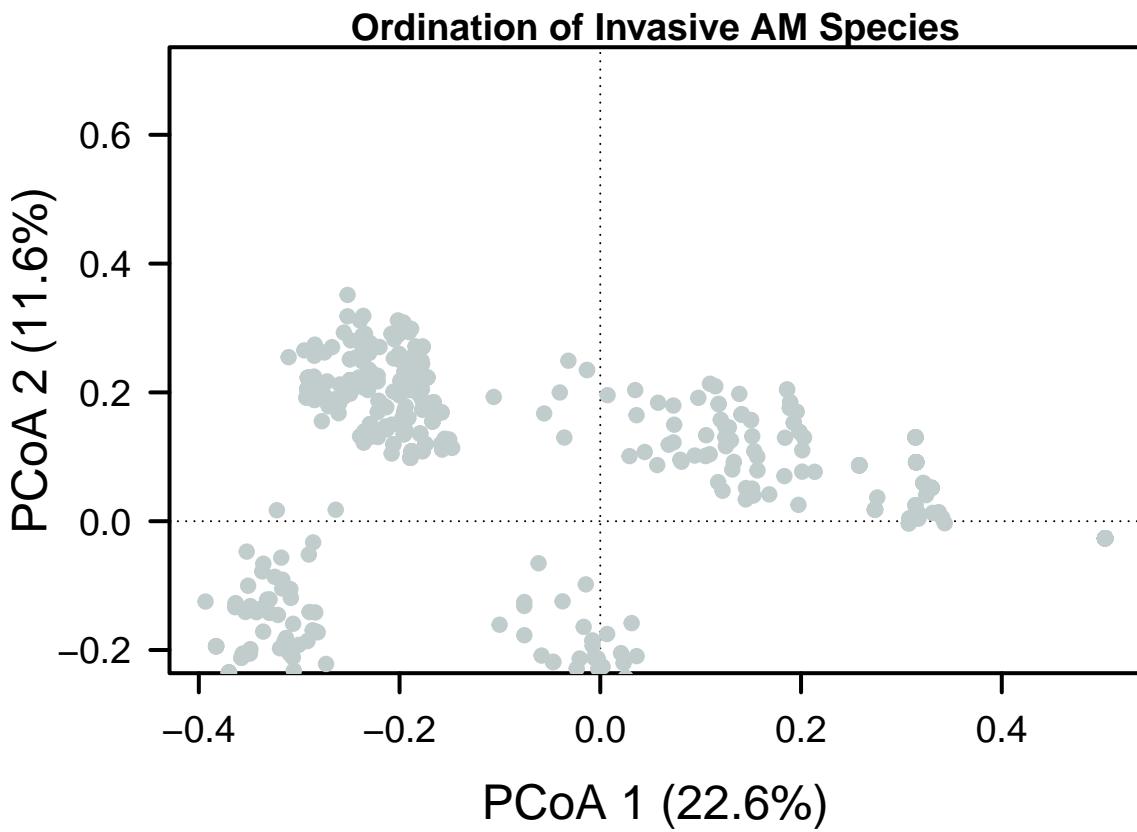
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)

points(I.AM.pcoa$points[,1], I.AM.pcoa$points[,2],
       pch = 19, cex = 1, bg = "gray", col = "azure3")

# text(jitter(I.AM.pcoa$points[,1], amount = 0.02),
#       jitter(I.AM.pcoa$points[,2], amount = 0.02),
#       labels = row.names(I.AM.pcoa$points), col = "black")

title("Ordination of Invasive AM Species")

```



```

#constraintd ordiance

#ninvasive.AM.ss.L <- ninvasive.AM.ss[,-1]
#ninvasive.ECM.ss.L <- ninvasive.AM.ss[,-1]
#invasive.AM.ss.L <- invasive.AM.ss[,-1]
#invasive.ECM.ss <- invasive.ECM.ss[,-1]
# tree.species.ss

I.ECM.J <- vegdist(invasive.ECM.ss, method = "jaccard", binary = TRUE)
I.ECM.pcoa <- cmdscale(I.ECM.J, eig = TRUE, k = 3)

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

```

```

par(mar = c(5, 5, 1, 2) + 0.1)
plot(I.ECM.pcoa$points[,1], I.ECM.pcoa$points[,2], ylim = c(-0.2, 0.7),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)

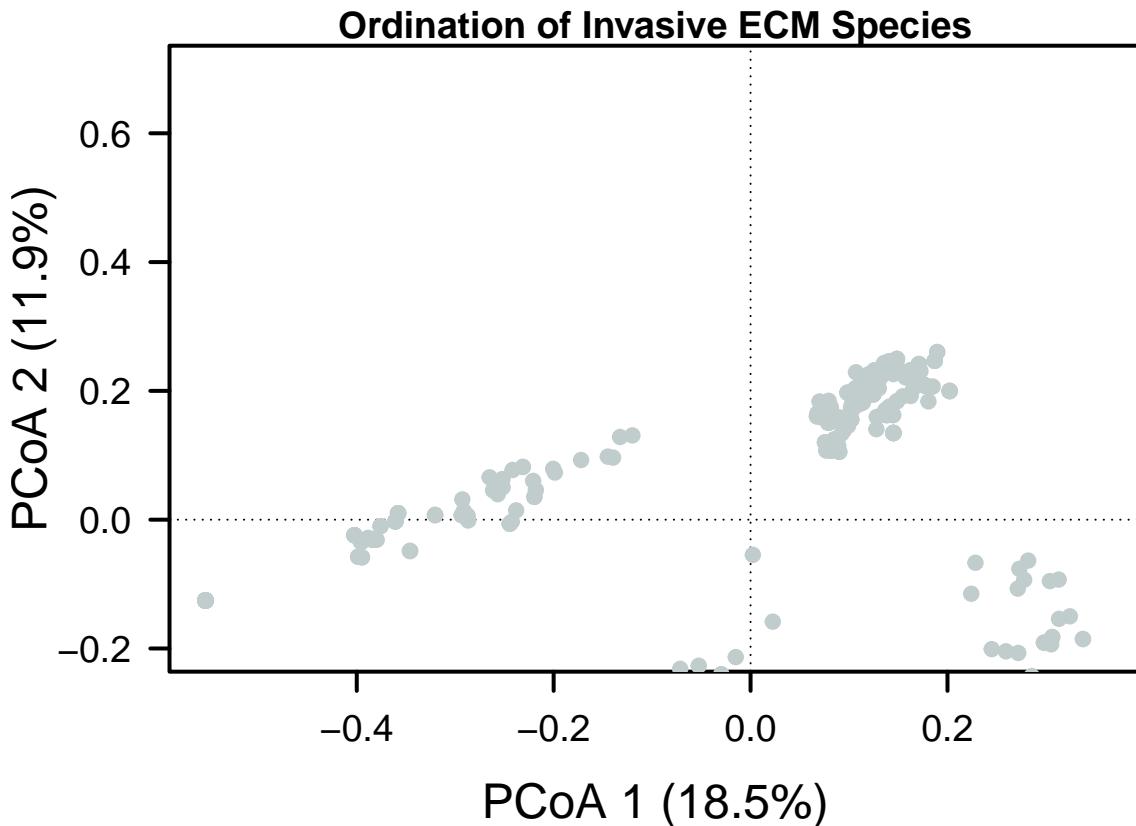
axis(side = 1, labels = TRUE, lwd.ticks = 2, cex.axis = 1.2, las = 1)
axis(side = 2, labels = TRUE, lwd.ticks = 2, cex.axis = 1.2, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)

points(I.ECM.pcoa$points[,1], I.ECM.pcoa$points[,2],
       pch = 19, cex = 1, bg = "gray", col = "azure3")

# text(jitter(I.ECM.pcoa$points[,1], amount = 0.02),
#       jitter(I.ECM.pcoa$points[,2], amount = 0.02),
#       labels = row.names(I.ECM.pcoa$points), col = "black")

title("Ordination of Invasive ECM Species")

```



```

#SS to use: ninvasive.AM.ss ninvasive.ECM.ss invasive.AM.ss invasive.ECM.ss
#variable matrix: invasive.ss
# NI.AM.db <- vegdist(ninvasive.AM.ss, method = "bray", binary =TRUE)
# I.AM.db <- vegdist(invasive.AM.ss, method = "bray", binary =TRUE)
# NI.ECM.db <- vegdist(ninvasive.ECM.ss, method = "bray", binary =TRUE)
# I.ECM.db <- vegdist(invasive.ECM.ss, method = "bray", binary =TRUE)
# tree.db <- vegdist(tree.species.ss, method = "bray")

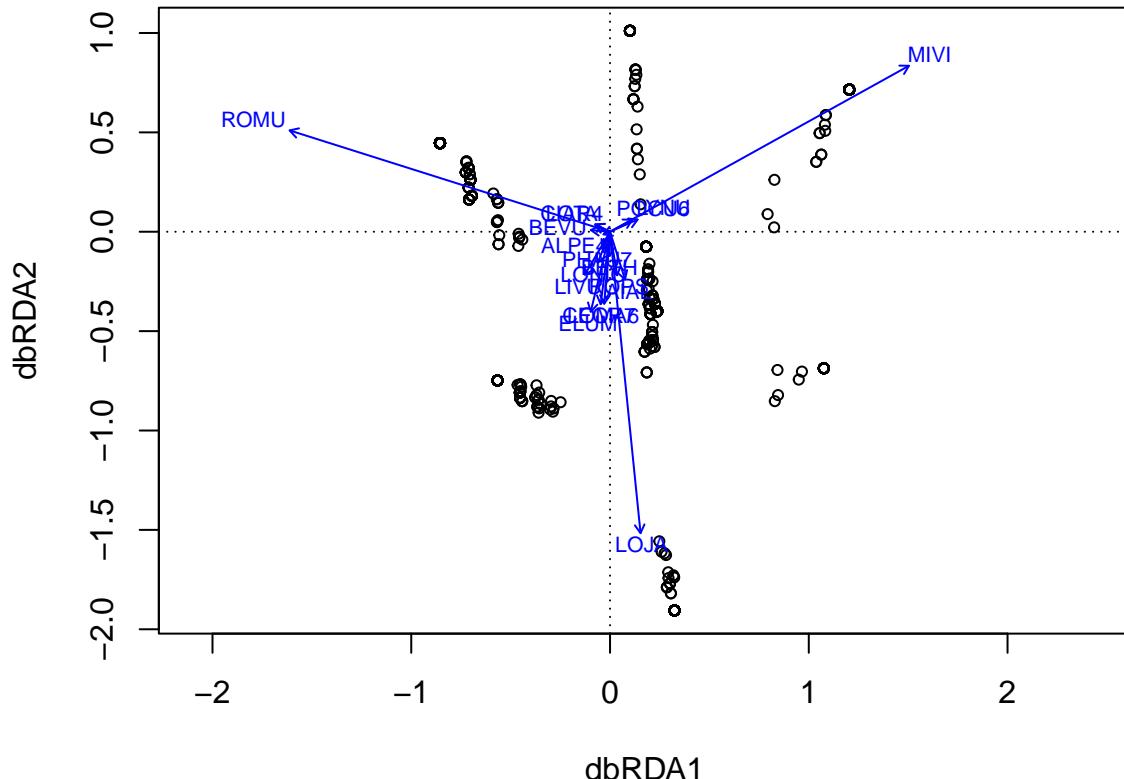
```

```

invasive.db <- vegdist(invasive.ss, method = "bray", binary = TRUE)

tree.dbra <- dbrda(invasive.db ~ ., as.data.frame(invasive.ss))
ordiplot(tree.dbra)

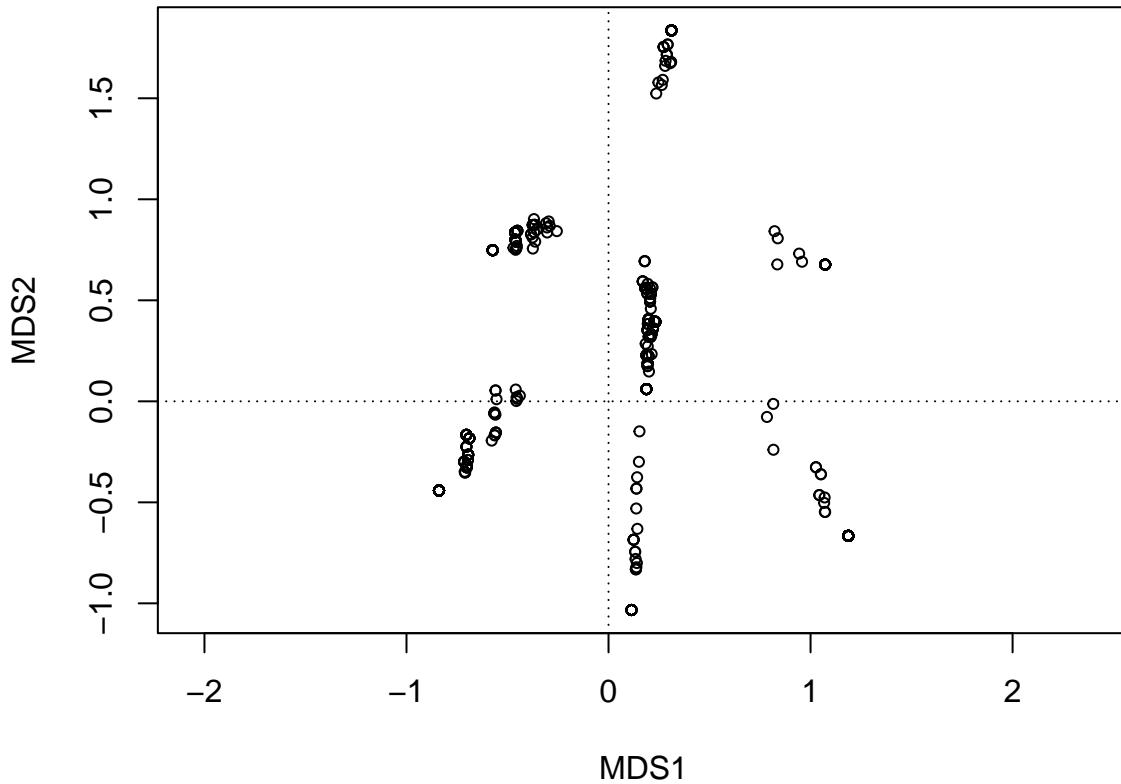
```



```

invasive.dbrda.mod0 <- dbrda(invasive.db ~1, as.data.frame(invasive.ss))
ordiplot(invasive.dbrda.mod0)

```



```

tree.dbra.mod1 <- dbrda(invasive.db ~., as.data.frame(invasive.ss))

#takes a minute
library(future)
library(furrr)
plan(multisession)
tree.dbrda <- ordiR2step(invasive.dbrda.mod0, tree.dbra.mod1, perm.max =100)

## Step: R2.adj= 0
## Call: invasive.db ~ 1
##
##          R2.adjusted
## <All variables> 1.2045952453
## + ROMU           0.3349717213
## + MIVI           0.3235073586
## + LOJA            0.1852073977
## + LOMA6           0.0870011084
## + ELUM            0.0839849345
## + LONIC            0.0798980859
## + CEOR7            0.0480821244
## + ALPE4            0.0476119589
## + BETH             0.0331653069
## + AIAL              0.0325040344
## + ROPS              0.0299337638
## + LIVU              0.0235653477
## + BEVU              0.0109800593
## + LYNU              0.0027309205
## + POCU6             0.0007393595
## <none>            0.0000000000

```

```

## + CIAR4      -0.0001323416
## + LOTA       -0.0001323416
## + PHAU7      -0.0003562652
##
##          Df      AIC      F Pr(>F)
## + ROMU    1 3320.7 343.51  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.3349717
## Call: invasive.db ~ ROMU
##
##          R2.adjusted
## <All variables> 1.2045952
## + MIVI        0.5710185
## + LOJA        0.5248955
## + LOMA6       0.4221448
## + ELUM        0.4213467
## + LONIC       0.4152132
## + CEOR7       0.3850496
## + ALPE4       0.3829772
## + BETH        0.3682664
## + AIAL         0.3652129
## + ROPS        0.3649916
## + LIVU        0.3584087
## + BEVU        0.3460806
## + PHAU7       0.3377622
## + LYNU        0.3362509
## + POCU6       0.3351381
## <none>        0.3349717
## + CIAR4       0.3347585
## + LOTA        0.3347585
##
##          Df      AIC      F Pr(>F)
## + MIVI    1 3023.1 374.62  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.5710185
## Call: invasive.db ~ ROMU + MIVI
##
##          R2.adjusted
## <All variables> 1.2045952
## + LOJA        0.7637653
## + ELUM        0.6550543
## + LOMA6       0.6529086
## + LONIC       0.6451986
## + CEOR7       0.6207132
## + ALPE4       0.6172509
## + BETH        0.6023282
## + ROPS        0.6007479
## + AIAL         0.5956248
## + LIVU        0.5927510
## + BEVU        0.5813670

```

```

## + PHAU7      0.5741382
## + LYNU       0.5723368
## + CIAR4      0.5711243
## + LOTA       0.5711243
## + POCU6      0.5710660
## <none>      0.5710185
##
##          Df     AIC      F Pr(>F)
## + LOJA    1 2617.9 554.19  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.7637653
## Call: invasive.db ~ ROMU + MIVI + LOJA
##
##          R2.adjusted
## <All variables> 1.2045952
## + ELUM        0.8467287
## + LOMA6       0.8463006
## + LONIC       0.8369665
## + CEOR7       0.8090214
## + ALPE4       0.8076907
## + BETH        0.7953703
## + ROPS        0.7932448
## + AIAL        0.7887972
## + LIVU        0.7846964
## + BEVU        0.7736169
## + PHAU7       0.7668344
## + LYNU        0.7650875
## + LOTA        0.7640509
## + CIAR4       0.7640509
## + POCU6       0.7639722
## <none>       0.7637653
##
##          Df     AIC      F Pr(>F)
## + ELUM    1 2324.2 367.45  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.8467287
## Call: invasive.db ~ ROMU + MIVI + LOJA + ELUM
##
##          R2.adjusted
## <All variables> 1.2045952
## + LOMA6       0.9277917
## + LONIC       0.9200041
## + CEOR7       0.8921896
## + ALPE4       0.8904707
## + BETH        0.8775659
## + ROPS        0.8750887
## + AIAL        0.8716459
## + LIVU        0.8671189
## + BEVU        0.8566631
## + PHAU7       0.8491265

```

```

## + LYNU          0.8481718
## + LOTA          0.8471176
## + CIAR4         0.8471176
## + POCU6         0.8470537
## <none>          0.8467287
##
##           Df      AIC      F Pr(>F)
## + LOMA6    1 1812.7 759.9  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.9277917
## Call: invasive.db ~ ROMU + MIVI + LOJA + ELUM + LOMA6
##
##           R2.adjusted
## <All variables> 1.2045952
## + LONIC          0.9999757
## + CEOR7          0.9728730
## + ALPE4          0.9716869
## + BETH           0.9583737
## + ROPS           0.9548098
## + AIAL           0.9527996
## + LIVU           0.9482627
## + BEVU           0.9377558
## + PHAU7          0.9304542
## + LYNU           0.9293394
## + LOTA           0.9282929
## + CIAR4          0.9282929
## + POCU6          0.9282322
## <none>          0.9277917
##
##           Df      AIC      F Pr(>F)
## + LONIC    1 -3633.4 2008779  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.9999757
## Call: invasive.db ~ ROMU + MIVI + LOJA + ELUM + LOMA6 + LONIC
##
##           R2.adjusted
## <All variables> 1.2045952
## + CEOR7          1.0432786
## + ALPE4          1.0408887
## + BETH           1.0304439
## + ROPS           1.0269545
## + AIAL           1.0250853
## + LIVU           1.0204496
## + BEVU           1.0094676
## + PHAU7          1.0027801
## + LYNU           1.0011425
## + LOTA           1.0005669
## + CIAR4          1.0005669
## + POCU6          1.0005158
## <none>          0.9999757

```

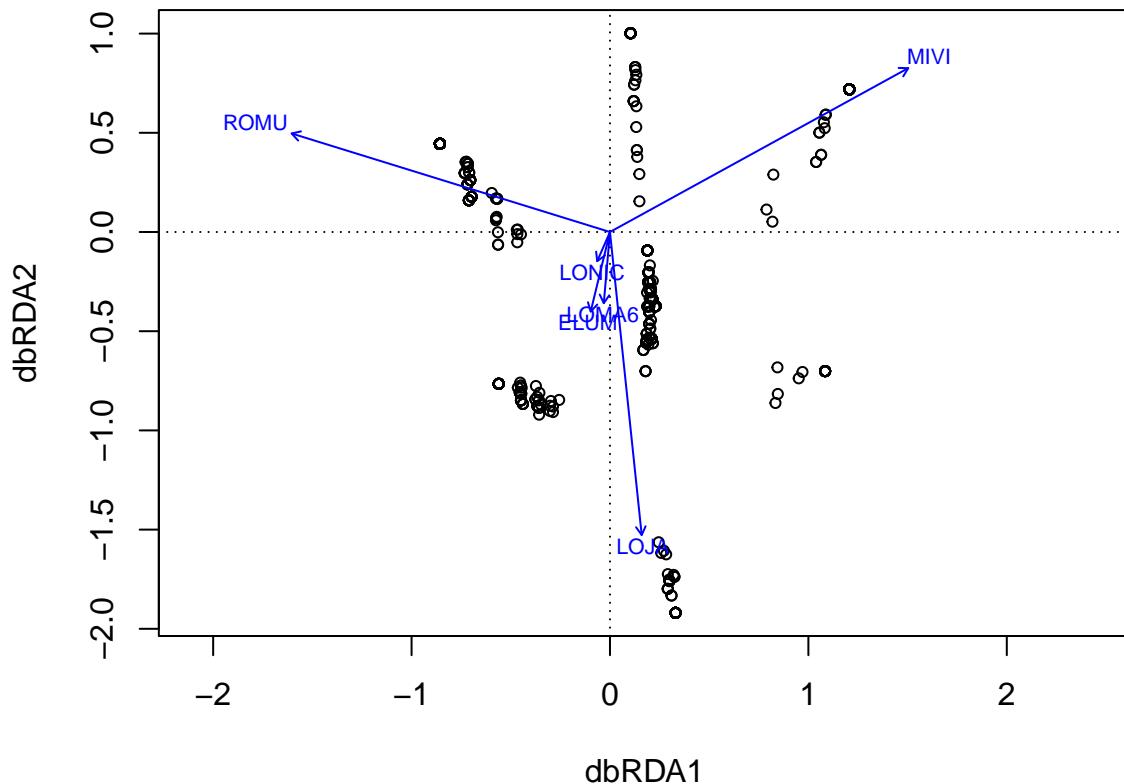
```

## Warning in log(RSS/n): NaNs produced
##          Df AIC      F Pr(>F)
## + CEOR7  1 NaN -673.38  0.878
tree.dbrda$call

## dbrda(formula = invasive.db ~ ROMU + MIVI + LOJA + ELUM + LOMA6 +
##       LONIC, data = as.data.frame(invasive.ss))
tree.dbrda$anova

##          R2.adj Df      AIC      F Pr(>F)
## + ROMU    0.33497  1 3320.7 343.51 0.002 **
## + MIVI    0.57102  1 3023.1 374.62 0.002 **
## + LOJA    0.76377  1 2617.9 554.19 0.002 **
## + ELUM    0.84673  1 2324.2 367.45 0.002 **
## + LOMA6   0.92779  1 1812.7 759.90 0.002 **
## + LONIC   0.99998  1 -3633.4 2008779.33 0.002 **
## <All variables> 1.20460
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
ordiplot(tree.dbrda)

```



```
permuteTest(tree.dbrda, permutations = 999)
```

```

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

```

```

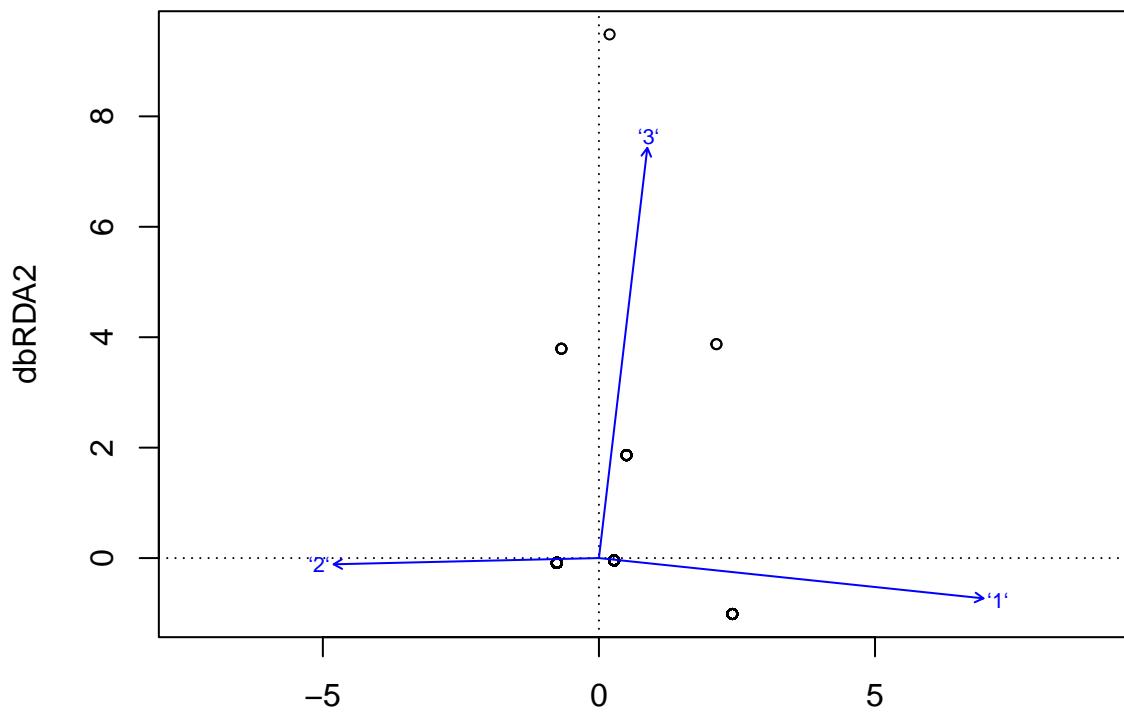
## 
## Model: dbrda(formula = invasive.db ~ ROMU + MIVI + LOJA + ELUM + LOMA6
## + LONIC, data = as.data.frame(invasive.ss))
## Permutation test for all constrained eigenvalues
##          Df Inertia      F Pr(>F)
## Model      6 196.604 4672335  0.001 ***
## Residual 674   0.005
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
envfit(tree.dbrda, invasive.ss, perm = 999)

## 
## ***VECTORS
##
##          dbRDA1    dbRDA2      r2 Pr(>r)
## AIAL     0.31485 -0.94914 0.0147  0.008 **
## ALPE4   -0.99320  0.11643 0.0003  0.866
## BETH    -0.03595 -0.99935 0.0033  0.318
## BEVU    -0.99296  0.11848 0.0025  0.447
## CEOR7   -0.13561 -0.99076 0.0316  0.001 ***
## CIAR4   -0.90107  0.43368 0.0017  0.691
## ELUM    -0.23509 -0.97197 0.0420  0.001 ***
## LIVU    -0.51954 -0.85445 0.0156  0.007 **
## LOJA    0.11473 -0.99340 0.5855  0.001 ***
## LOMA6   -0.08122 -0.99670 0.0321  0.001 ***
## LONIC   -0.40559 -0.91406 0.0064  0.100 .
## LOTA    -0.90107  0.43368 0.0017  0.679
## LYNU    0.91457  0.40442 0.0058  0.119
## MIVI    0.88395  0.46759 0.7398  0.001 ***
## PHAU7   -0.40853 -0.91275 0.0021  0.670
## POCU6   0.88600  0.46369 0.0040  0.294
## ROMU   -0.95570  0.29434 0.7199  0.001 ***
## ROPS    0.17011 -0.98543 0.0116  0.017 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
dbrda.explainvar1 <- round(tree.dbrda$CCA$eig[1] /
                           sum(c(tree.dbrda$CCA$eig, tree.dbrda$CA$eig)), 3) * 100
dbrda.explainvar2 <- round(tree.dbrda$CCA$eig[2] /
                           sum(c(tree.dbrda$CCA$eig, tree.dbrda$CA$eig)), 3) * 100

invasive.myco.db <- vegdist(invasive.myco.ss, method ="bray", binary = TRUE)

tree.dbra <- dbrda(invasive.myco.db ~ ., as.data.frame(invasive.myco.ss))
ordiplot(tree.dbra)

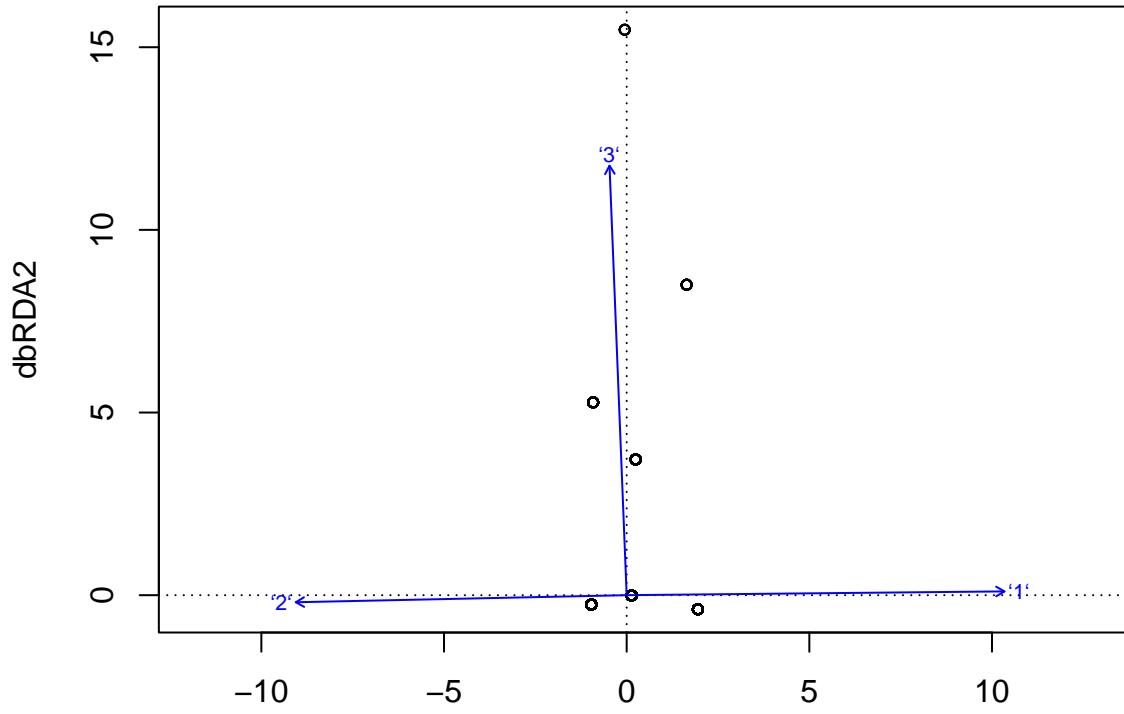
```



dbRDA1

```
ninvasive.myco.db <- vegdist(ninvasive.myco.ss, method = "bray", binary = TRUE)
```

```
ntree.dbra <- dbrda(ninvasive.myco.db ~ ., as.data.frame(ninvasive.myco.ss))
ordiplot(ntree.dbra)
```



dbRDA1

#Supple-

mentary code:

```
SPCDinfo <- read.csv("cloud/project/QB_biodiversity_project_EH/SPCDinfo.csv")
treesp <- SPCDinfo[c("Scientific.Name", "Genus", "Family")] #extract relevant cols
treephylo <- phylo.maker(treesp, scenarios = "S3", nodes = nodes.info.1) #make tree
plot.phylo(treephylo, scenario.3, cex = .2)
treephyloscenario.3
```