

Quantitative Biodiversity Final Project

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SETUP

CLEAR WORKING DIRECTORY, LOAD PACKAGES

```
rm(list = ls())

package.list <- c('vegan', 'dplyr', 'magrittr', 'ggplot2', 'BiodiversityR', 'indicspecies')
for(package in package.list){
  if(!require(package, character.only = TRUE, quietly = TRUE)){
    install.packages(package)
    library(package, character.only = TRUE)
  }
}
```

SET WORKING DIRECTORY, READ IN DATA

```
setwd("~/GitHub/QB19_IndependentProject/")

crawley.full <- read.csv("Crawley.csv")
crawley.site.factors <- read.csv("site_factors.csv")

crawley.df <- crawley.full[, -c(1:3)] # Get rid of non-incidence columns
```

SITE-BY-SPECIES MATRICES

sbs: full SbS; ordered by species name

```
# transpose data to create a site-by-species matrix, removing non-site columns
sbs <- t(crawley.full[1:292, 4:23])
sbs <- as.data.frame(sbs)
colnames(sbs) <- crawley.full[1:292, 1]
```

sbs.ns: SbS w/o species that occur in 0 or 1 sites; ordered by native status then species name

```
# sort by nativity status
cf.summed <- crawley.full[order(crawley.full$Nativity.Code), ]
# add rowsums column
cf.summed$sums <- rowSums(cf.summed[, 4:23])
# filter to remove species found in 0 or 1 site
cf.ns <- cf.summed[which(cf.summed$sums > 1), ]

# transpose data, add species names as column names
sbs.ns <- t(cf.ns[, 4:23])
```

```
sbs.ns <- as.data.frame(sbs.ns)
colnames(sbs.ns) <- cf.ns[ , 1]
```

sbs.factors: SbS plus environmental factors

```
sbs.factors <- read.csv("sbs_factors.csv", header = TRUE)
```

NUMBERS OF EACH TYPE OF SPECIES

Nativity codes are:

0 = native to Indiana

1 = native to the US

2 = exotic

3 = invasive

Check how many of each nativity code we have using dplyr

```
crawley.full %>%
  group_by(Nativity.Code) %>%
  summarize(grpcount = n())
```

```
## # A tibble: 6 x 2
##   Nativity.Code grpcount
##   <fct>          <int>
## 1 ""              8
## 2 0             175
## 3 1              2
## 4 2             69
## 5 3             24
## 6 UNK           22
```

Those 8 empty ones are just empty rows at the bottom of the df. Let's get rid of those, as well as the

```
crawley.full <- crawley.full[-c(293:300), -c(24, 25)]
crawley.df <- crawley.full[, -c(1:3)] # Get rid of non-incidence columns
crawley.species <- crawley.full$Species # Save species as a vector, in case we need it
crawley <- as.matrix(t(crawley.df))
```

```
crawley.sbsys <- matrix(crawley, ncol = ncol(crawley), dimnames = NULL)
```

SCATTER PLOTS

Richness vs. Invasive present / Invasive absent in community

Make site-by-species matrix where nativity code is "0" for Native, "1" for Invasive/Exotic

We want to separate into two df's: one for sites that have at least one invasive, and one for sites that

To do that, we make a vector of invasive species

```
crawley.inv <- crawley.full[crawley.full$ Nativity.Code == "3", ]
```

Every site has at least one invasive, so I can't make my plot!

Percent invasive species vs. species richness

```

# subset data into separate data frames for each nativity code
nativeIN <- subset(crawley.full, Nativity.Code == "0")
nativeUS <- subset(crawley.full, Nativity.Code == "1")
exotic <- subset(crawley.full, Nativity.Code == "2")
invasive <- subset(crawley.full, Nativity.Code == "3")
unknown <- subset(crawley.full, Nativity.Code == "UNK")

# sum columns to find observed species richness for each site; repeat for each nativity code
nativeIN.sr <- colSums(nativeIN[ , 4:23])
nativeUS.sr <- colSums(nativeUS[ , 4:23])
exotic.sr <- colSums(exotic[ , 4:23])
invasive.sr <- colSums(invasive[ , 4:23])
unknown.sr <- colSums(unknown[ , 4:23])

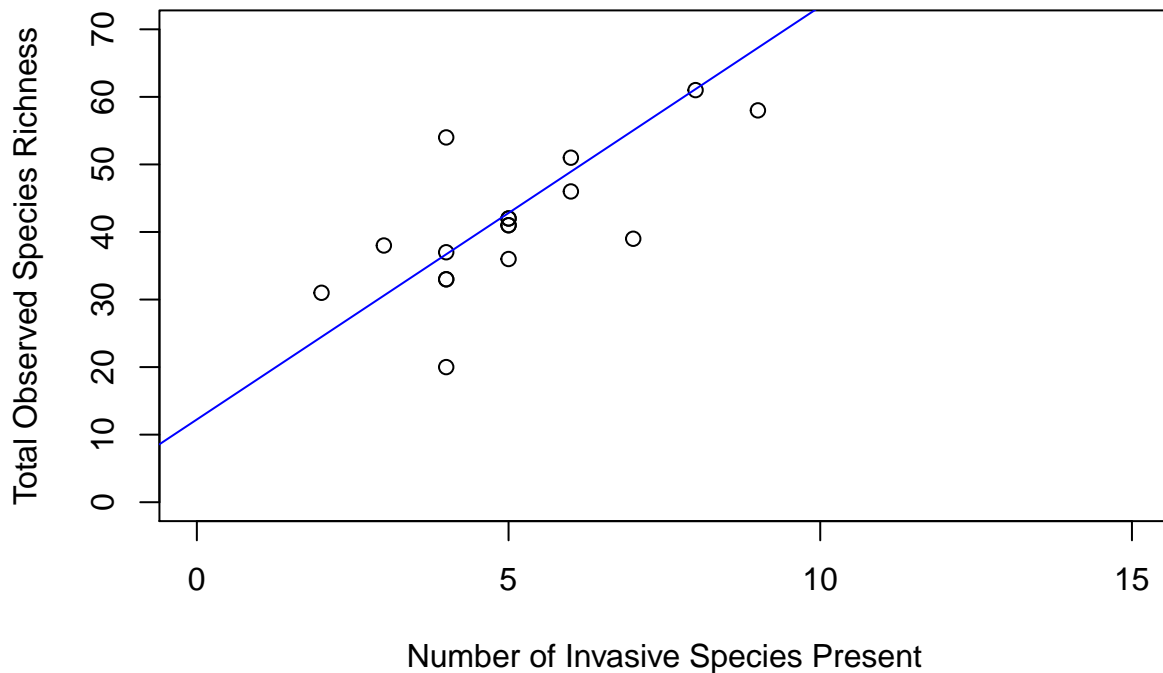
# calculate total native richness
native.sr <- nativeIN.sr + nativeUS.sr

# calculate total observed species richness
total.sr <- colSums(crawley.full[ , 4:23])

# this was a sanity check to make sure everything has worked so far
# total.osr <- nativeIN.sr + nativeUS.sr + exotic.sr + invasive.sr + unknown.sr
# total.sr == total.osr

# plot richness of invasive species vs total species richness
plot(invasive.sr, total.sr, ylim = range(0:70), xlim = range(0:15),
     xlab = "Number of Invasive Species Present", ylab = "Total Observed Species Richness")
# add fit lines
abline(lm(total.sr~invasive.sr), col="blue") # regression line (y~x)

```



```

# plot richness of invasive species vs native species richness
plot(invasive.sr, native.sr, ylim = range(0:70), xlim = range(0:15),

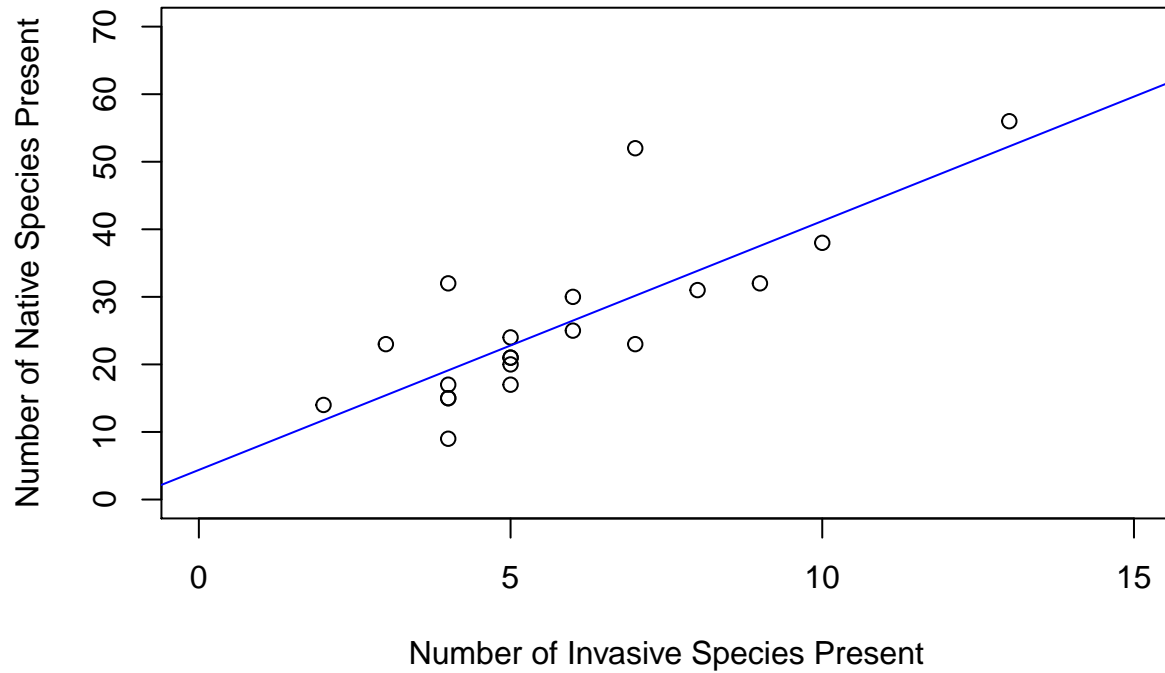
```

```

xlab = "Number of Invasive Species Present", ylab = "Number of Native Species Present", main = "Observed Richness of Native and Invasive Plants"
# add fit lines
abline(lm(native.sr~invasive.sr), col="blue") # regression line (y~x)

```

Observed Richness of Native and Invasive Plants

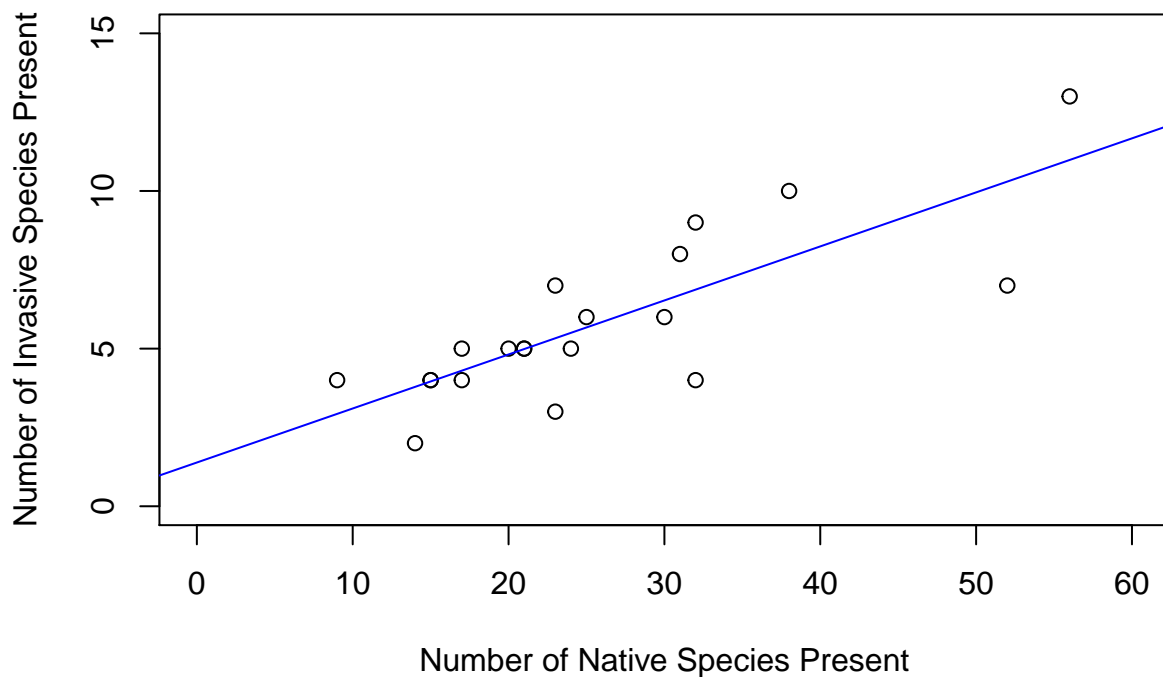


```

# plot richness of native species richness vs invasive species
plot(native.sr, invasive.sr, ylim = range(0:15), xlim = range(0:60),
      ylab = "Number of Invasive Species Present", xlab = "Number of Native Species Present", main = "Observed Richness of Native and Invasive Plants")
# add fit lines
abline(lm(invasive.sr~native.sr), col="blue") # regression line (y~x)

```

Observed Richness of Native and Invasive Plants



```
summary(lm(native.sr~invasive.sr))
```

```
##
## Call:
## lm(formula = native.sr ~ invasive.sr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.118  -4.118  -1.960   2.566  21.829
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.3816     4.2021   1.043   0.311
## invasive.sr     3.6842     0.6636   5.552 2.86e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.543 on 18 degrees of freedom
## Multiple R-squared:  0.6313, Adjusted R-squared:  0.6109
## F-statistic: 30.82 on 1 and 18 DF,  p-value: 2.857e-05
```

Ok, so there's a pretty clear positive trend for both graphs, which is pretty neat– so from this data, it looks like adding invasives simply adds species, and there isn't evidence that the invasives are decreasing native or total species richness (the opposite, in fact, which is logical for the first graph but really interesting for the second graph)

Planted species vs. volunteer species

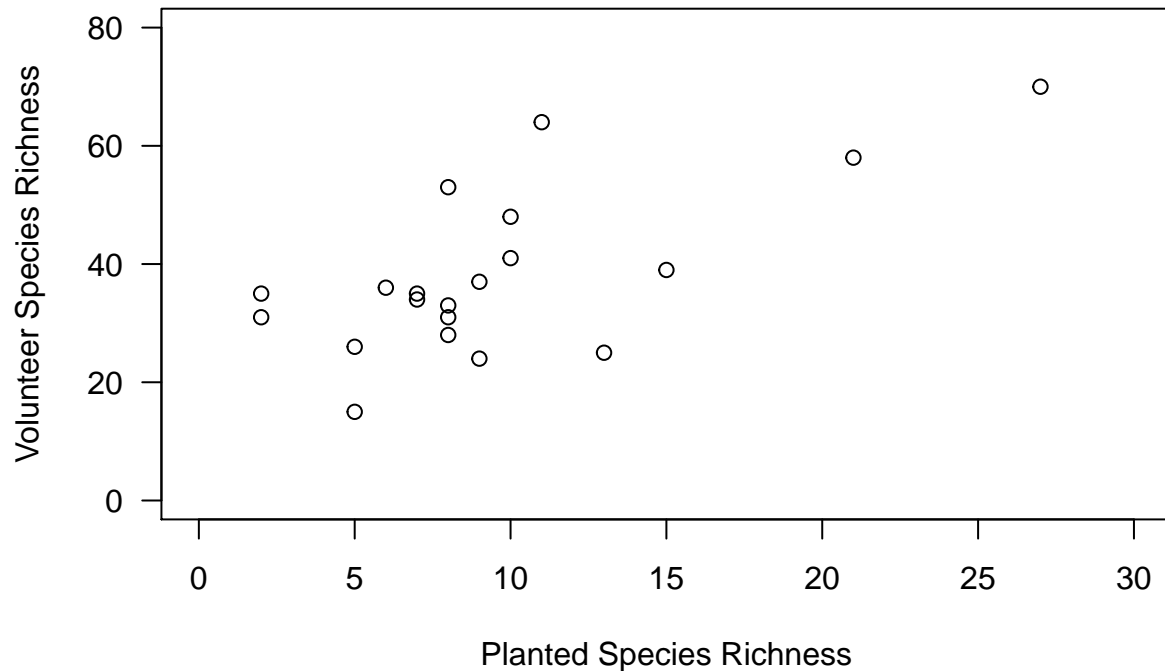
```
# ignore this for now, I'm just playin'
planted <- subset(crawley.full, Planted.or.Volunteer == "1")
volunteer <- subset(crawley.full, Planted.or.Volunteer == "2")
```

```

planted.SR <- colSums(planted[ , 4:23])
volunteer.SR <- colSums(volunteer[ , 4:23])

plot(planted.SR, volunteer.SR, ylim = c(0, 80), xlim = c(0, 30),
     xlab = "Planted Species Richness",
     ylab = "Volunteer Species Richness", las = 1)

```



Percent Invasive vs. Time Since Planting

```

crawley.full.1 <- crawley.full
time.since.planting <- crawley.site.factors$Years.between.planting.and.census # this is an integer, for

crawley.full.1 %>%
  group_by(Nativity.Code) %>%
  summarize(grpcount = n())

## # A tibble: 5 x 2
##   Nativity.Code grpcount
##   <fct>         <int>
## 1 0             175
## 2 1              2
## 3 2             69
## 4 3             24
## 5 UNK          22

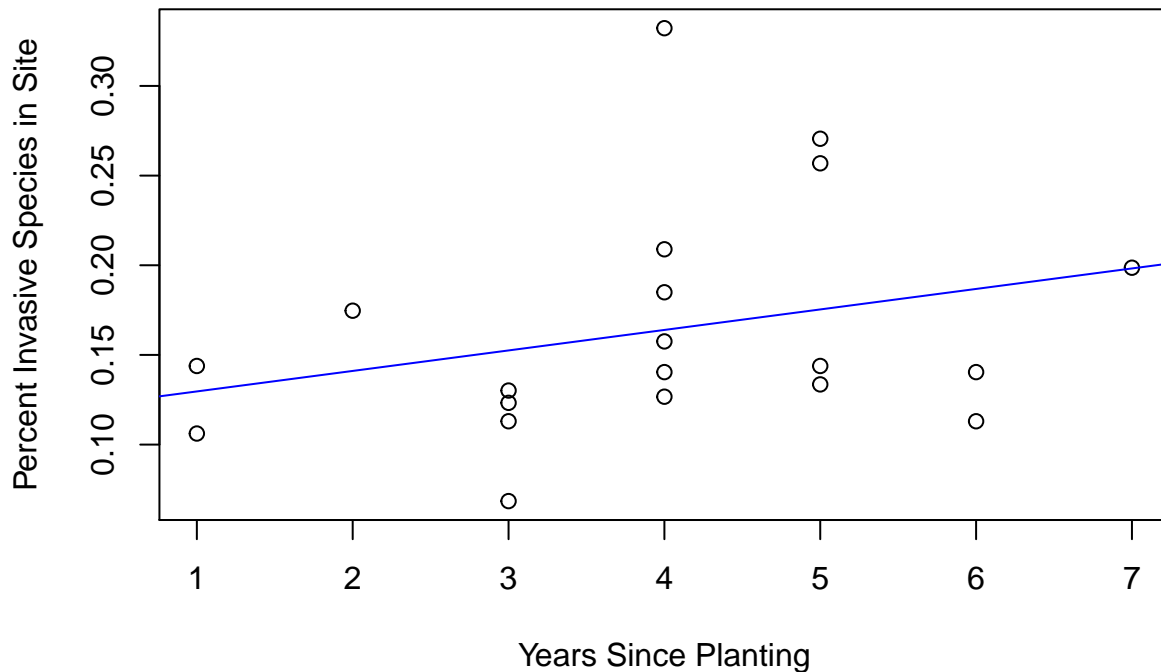
crawley.full.1 <- crawley.full.1[-c(293:300), -c(24, 25)]

# Calculate percent invasive for each site
percent.invasive <- colSums(crawley.df) / nrow(crawley.df)

plot(x = time.since.planting, y = percent.invasive,
     xlab = "Years Since Planting",
     ylab = "Percent Invasive Species in Site")

```

```
abline(lm(percent.invasive ~ time.since.planting), col="blue")
```



```
summary(lm(percent.invasive ~ time.since.planting)) # P = 0.23
```

```
##
## Call:
## lm(formula = percent.invasive ~ time.since.planting)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.08400 -0.03778 -0.02292  0.02415  0.16826
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.118207   0.038735   3.052  0.00687 **
## time.since.planting 0.011430   0.009143   1.250  0.22724
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06265 on 18 degrees of freedom
## Multiple R-squared:  0.07989,    Adjusted R-squared:  0.02878
## F-statistic: 1.563 on 1 and 18 DF,  p-value: 0.2272
```

BETA DIVERSITY

Read in data, create SbS matrix

```
# loading transposed site by species matrix with nativity/planting codes removed
sbs.factors <- read.csv("sbs_factors.csv", header = TRUE)
sbs <- sbs.factors[, -c(1:7)]
```

Create distance matrices

```
# sorted data by site factors
mulch.sbs <- sbs.factors[order(sbs.factors$MULCH),]
litter.sbs <- sbs.factors[order(sbs.factors$LITTER),]
weediness.sbs <- sbs.factors[order(sbs.factors$WEEDINESS),]

# calculated Sorensen similarity
msbs.ds <- vegdist(mulch.sbs[ , -c(1:7)], method = "bray", binary = TRUE)
lsbs.ds <- vegdist(litter.sbs[ , -c(1:7)], method = "bray", binary = TRUE)
wsbs.ds <- vegdist(weediness.sbs[ , -c(1:7)], method = "bray", binary = TRUE)
```

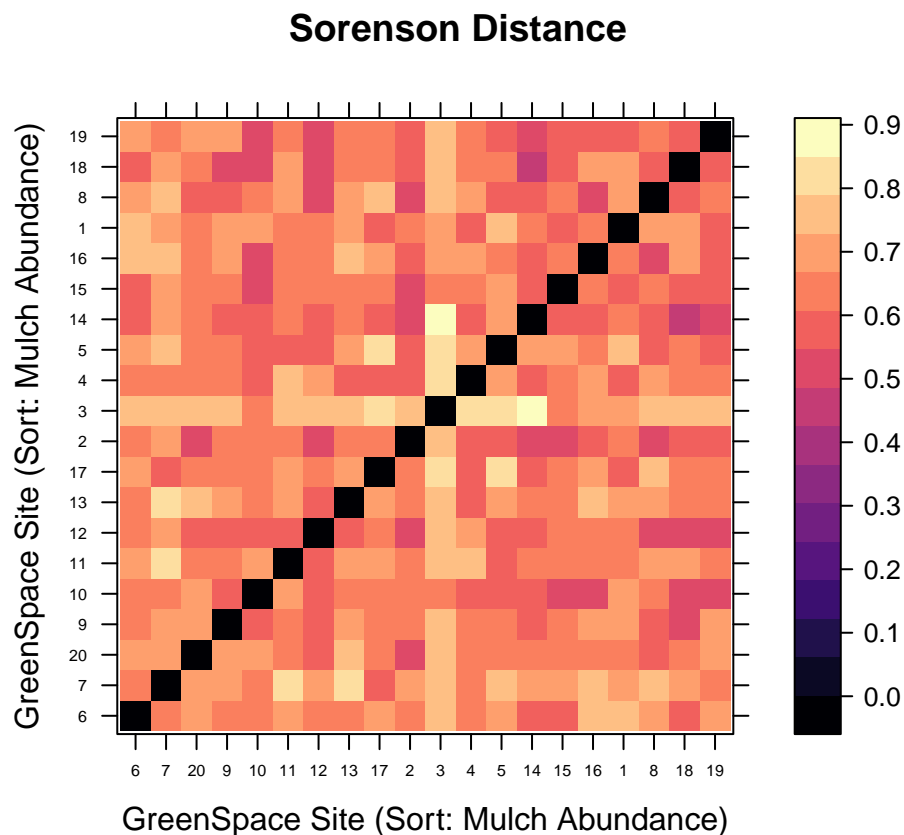
Heat maps

```
# heat maps of site similarity
require(viridis)
```

```
## Loading required package: viridis
```

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

```
levelplot(as.matrix(msbs.ds), aspect = "iso", col.regions = magma,
          xlab = "GreenSpace Site (Sort: Mulch Abundance)", ylab = "GreenSpace Site (Sort: Mulch Abundance)",
          main = "Sorensen Distance")
```



```
png(filename = "Mulch_heatmap.png")
```

```
levelplot(as.matrix(lsbs.ds), aspect = "iso", col.regions = magma,
          xlab = "GreenSpace Site (Sort: Litter Abundance)", ylab = "GreenSpace Site (Sort: Litter Abundance)",
          main = "Sorensen Distance")
```



```

levelplot(as.matrix(wsbs.ds), aspect = "iso", col.regions = magma,
          xlab = "GreenSpace Site (Sort: Weediness Index)", ylab = "GreenSpace Site (Sort: Weediness Index)",
          main = "Sorenson Distance")
png(filename = "Weediness_heatmap.png")

```

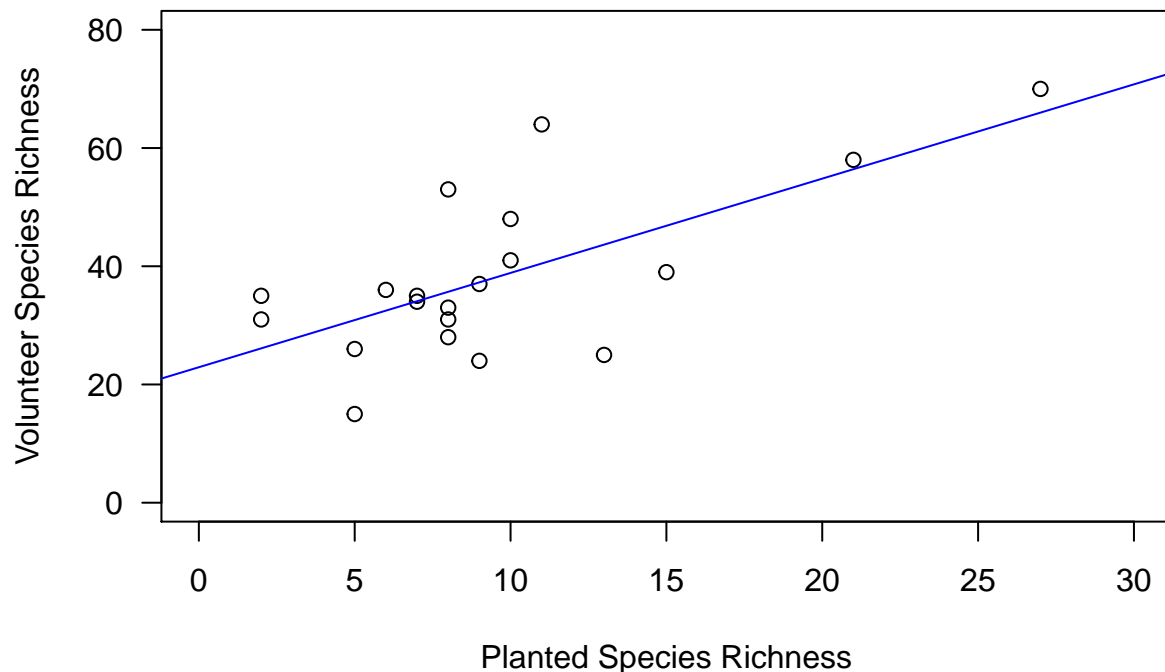
Not expecting to find any patterns with site similarity honestly (and it doesn't look like there are any!), but it's cool to see that they're overall pretty dissimilar. Wonder if that changes looking only at planted species? Not sure if the labels help, but the heat maps just differ based on the sorting of the dataset; the values are ascending, so right to left and down to up is least mulch/litter/weeds to most.

```

# subset initially planted vs volunteer species
planted <- subset(crawley.full, Planted.or.Volunteer == "1")
volunteer <- subset(crawley.full, Planted.or.Volunteer == "2")
planted.SR <- colSums(planted[, 4:23])
volunteer.SR <- colSums(volunteer[, 4:23])

plot(planted.SR, volunteer.SR, ylim = c(0, 80), xlim = c(0, 30),
     xlab = "Planted Species Richness",
     ylab = "Volunteer Species Richness", las = 1)
abline(lm(volunteer.SR~planted.SR), col="blue")

```



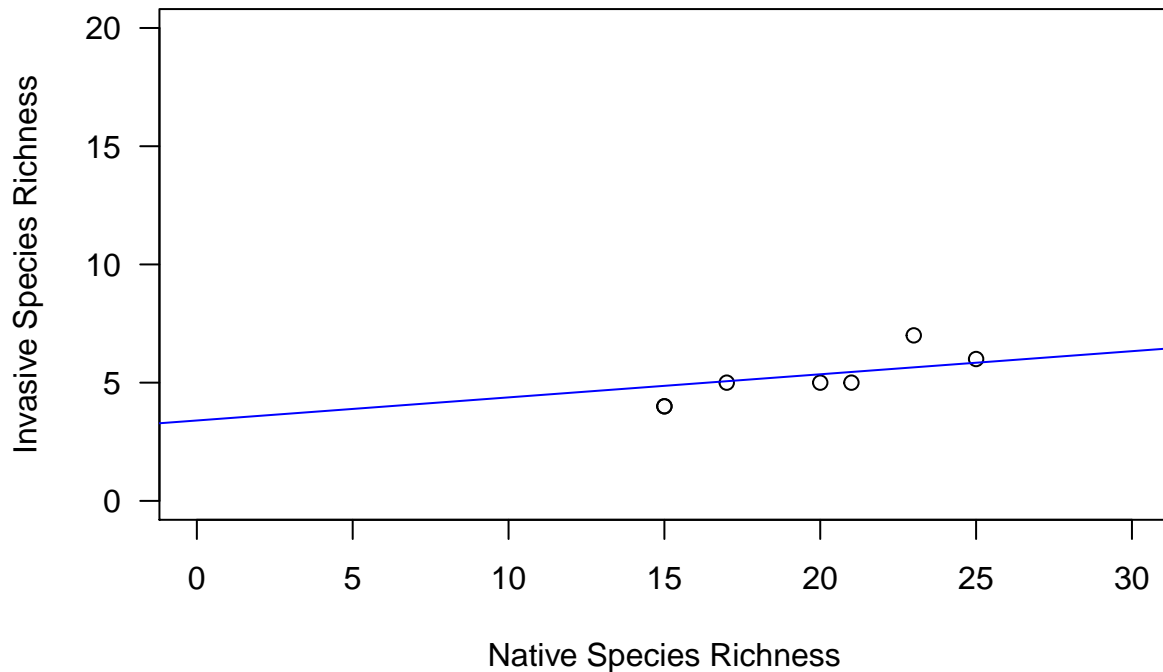
```

# What about planted v volunteer in low mulch sites? Native v invasive?
# rationale: low mulch as a measure of open niche space (high mulch = lots of open space?)
# lowmulch <- subset(sbs.factors, MULCH %in% c("0", "1"))
nativeLM <- nativeIN[, c(9, 10, 12, 13, 14, 15, 16, 20, 23)]
invasiveLM <- invasive[, c(9, 10, 12, 13, 14, 15, 16, 20, 23)]
nativeLM.SR <- colSums(nativeLM)
invasiveLM.SR <- colSums(invasiveLM)

plot(nativeLM.SR, invasiveLM.SR, ylim = c(0, 20), xlim = c(0, 30),
     xlab = "Native Species Richness",
     ylab = "Invasive Species Richness", las = 1)

```

```
abline(lm(invasiveLM.SR~nativeLM.SR), col="blue")
```



```
summary(lm(invasiveLM.SR~nativeLM.SR))
```

```
##
## Call:
## lm(formula = invasiveLM.SR ~ nativeLM.SR)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3840 -0.8656 -0.3543  0.1571  2.4729
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.39957    1.07155   3.173  0.0157 *
## nativeLM.SR   0.09773    0.04031   2.424  0.0458 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.294 on 7 degrees of freedom
## Multiple R-squared:  0.4564, Adjusted R-squared:  0.3788
## F-statistic: 5.878 on 1 and 7 DF, p-value: 0.04579
```

PERMANOVA

Using site types and locations

```
# site type (i.e. school, residential, etc.)
site.type <- c(rep("Business", 1), rep("Residential", 1), rep("School", 1), rep("Residential", 1), rep("School", 1))
adonis(sbs ~ site.type, method = "bray", permutations = 999)
```

```
##
```

```
## Call:
## adonis(formula = sbs ~ site.type, permutations = 999, method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## site.type  3      0.6393 0.21310 0.99864 0.15771 0.509
## Residuals 16      3.4142 0.21339      0.84229
## Total     19      4.0535      1.00000

# median income classification
region.SES <- c(rep("Mid", 1), rep("Low", 1), rep("Mid", 1), rep("Low", 2), rep("Mid", 1), rep("Low", 1), rep("Mid", 1), rep("Low", 1))
adonis(sbs ~ region.SES, method = "bray", permutations = 999)

##
## Call:
## adonis(formula = sbs ~ region.SES, permutations = 999, method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## region.SES  2      0.4242 0.21210 0.99349 0.10465 0.482
## Residuals 17      3.6293 0.21349      0.89535
## Total     19      4.0535      1.00000

# weediness
weediness <- c(rep("Absent", 2), rep("Low", 6), rep("Medium", 10), rep("High", 2))
adonis(sbs ~ weediness, method = "bray", permutations = 999)

##
## Call:
## adonis(formula = sbs ~ weediness, permutations = 999, method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## weediness  3      0.5676 0.18920 0.86843 0.14003 0.802
## Residuals 16      3.4859 0.21787      0.85997
## Total     19      4.0535      1.00000

# mulch
mulch <- c(rep("None", 3), rep("Low", 6), rep("Medium", 7), rep("High", 4))
adonis(sbs ~ mulch, method = "bray", permutations = 999)

##
## Call:
## adonis(formula = sbs ~ mulch, permutations = 999, method = "bray")
```

```
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model    R2 Pr(>F)
## mulch      3    0.6899 0.22997  1.0939 0.1702  0.246
## Residuals 16    3.3636 0.21022        0.8298
## Total     19    4.0535          1.0000

# didn't do litter- realized that only two sites had any litter at all. Explains why the heat map looks
# also neither of the PERMANOVAs were significant
```

ORDINATION

PCoA, full Sbs

```
sbs.ds <- vegdist(sbs, method = "bray", binary = TRUE)
sbs.pcoa <- cmdscale(sbs.ds, eig = TRUE, k = 3)
explainvar1.sbs <- round(sbs.pcoa$eig[1] / sum(sbs.pcoa$eig), 3) * 100
explainvar2.sbs <- round(sbs.pcoa$eig[2] / sum(sbs.pcoa$eig), 3) * 100
explainvar3.sbs <- round(sbs.pcoa$eig[3] / sum(sbs.pcoa$eig), 3) * 100
sum.eigsbs <- sum(explainvar1.sbs, explainvar2.sbs, explainvar3.sbs)
sum.eigsbs

## [1] 36.2

plot full PCoA

par(mar = c(4, 4, 1, 1) + 0.1)
plot(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2],
     ylim = c(-1.2, 2), xlim = c(-2.5, 2.5),
     xlab = paste("PCoA 1 (", explainvar1.sbs, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2.sbs, "%)", sep = ""),
     pch = 16, cex = 0.8, type = "n", cex.lab = 0.8, cex.axis = 0.8, axes = FALSE)
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 0.8, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 0.8, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)
points(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2],
       pch = 19, cex = 2, bg = "gray", col = "gray")
text(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2], cex = 0.8,
     labels = rownames(sbs))

# add species labels to PCoA
sbs.pcoa <- add.spec.scores(sbs.pcoa, sbs, method = "pcoa.scores")
```

```
## Warning in cor(comm[, i], ordiscores[, j]): the standard deviation is zero
```

```
## Warning in cor(comm[, i], ordiscores[, j]): the standard deviation is zero
```

```
## Warning in cor(comm[, i], ordiscores[, j]): the standard deviation is zero
```

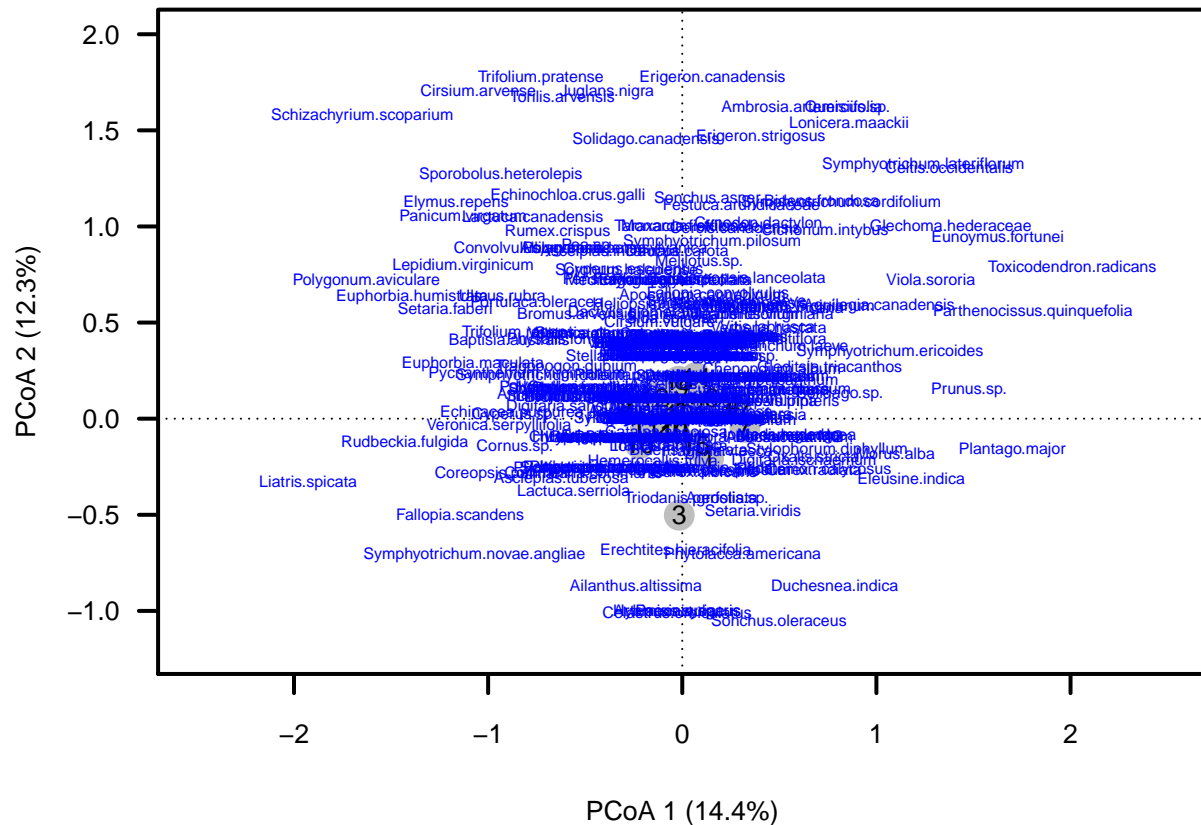
```
## Warning in cor(comm[, i], ordiscores[, j]): the standard deviation is zero
```

[illegible]

[illegible]

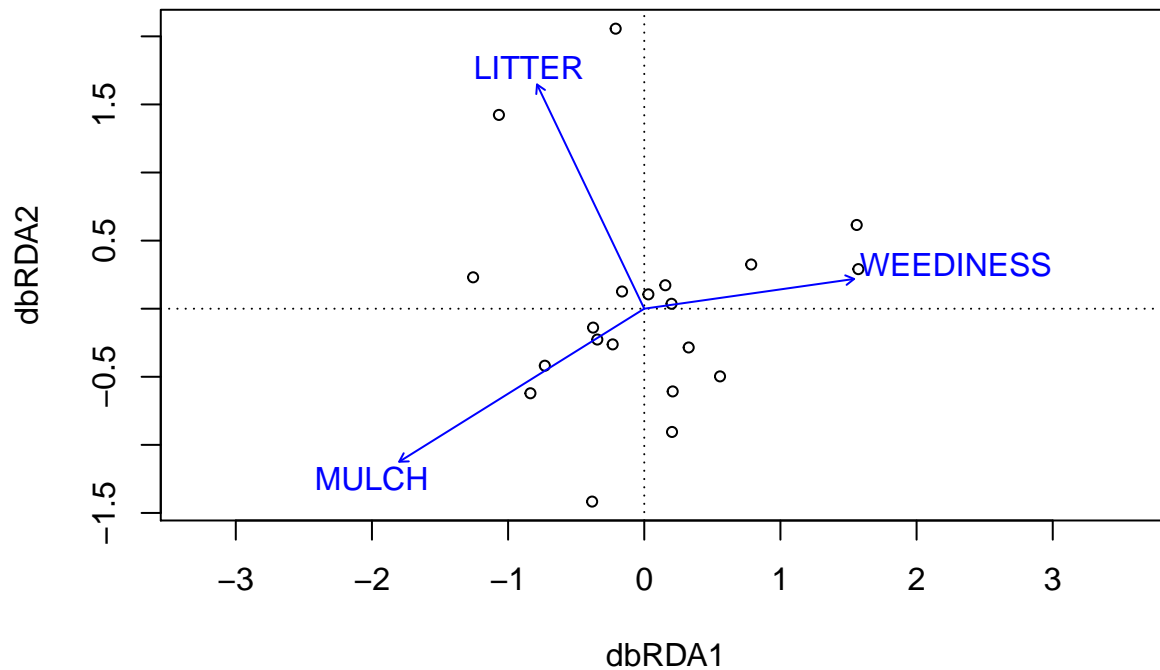
[illegible]

```
text(sbs.pcoa$cproj[, 1], sbs.pcoa$cproj[, 2], cex = 0.5,
     labels = row.names(sbs.pcoa$cproj), col = "blue")
```



dbRDA

```
#dbRDA plot with site factors
site.factors <- sbs.factors[, 2:4]
sbs.dbrda <- dbRDA(sbs.ds ~ ., as.data.frame(site.factors))
ordiplot(sbs.dbrda)
```

```
png(filename="dbRDA.png")
```

```
# changed site.factors to character data... dbrda won't run anymore? sitefactors reads as three vectors
# is a dbrda possible with categorical data?
# sitefactors <- as.factor(site.factors)
# as.data.frame(sitefactors)
# sbs.dbrda <- dbrda(sbs.ds ~ ., as.data.frame(sitefactors))
# ordiplot(sbs.dbrda)
```

```
permutest(sbs.dbrda, permutations = 999)
```

```
##
## Permutation test for dbrda under reduced model
##
## Permutation: free
## Number of permutations: 999
##
## Model: dbrda(formula = sbs.ds ~ MULCH + LITTER + WEEDINESS, data =
## as.data.frame(site.factors))
## Permutation test for all constrained eigenvalues
##      Df Inertia      F Pr(>F)
## Model   3  0.6862 1.0868  0.279
## Residual 16  3.3673
```

```
envfit(sbs.dbrda, site.factors, perm = 999)
```

```
##
## ***VECTORS
##
##      dbRDA1  dbRDA2    r2 Pr(>r)
## MULCH   -0.86765 -0.49718 0.7966  0.001 ***
## LITTER   -0.46666  0.88444 0.6022  0.006 **
## WEEDINESS 0.99446  0.10512 0.4430  0.012 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
```

```
#mantel test? not sure if done right.
```

```
sitefact.ds <- vegdist(site.factors, method = "euclidean")
mantel(sbs.ds,sitefact.ds)
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = sbs.ds, ydis = sitefact.ds)
##
## Mantel statistic r: 0.01239
##      Significance: 0.443
##
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%  99%
## 0.173 0.213 0.248 0.290
## Permutation: free
## Number of permutations: 999
```

PCoA, not including species in 1/0 sites

```
sbs.ds <- vegdist(sbs.ns, method = "bray", binary = TRUE)
sbs.pcoa <- cmdscale(sbs.ds, eig = TRUE, k = 3)
explainvar1.sbs <- round(sbs.pcoa$eig[1] / sum(sbs.pcoa$eig), 3) * 100
explainvar2.sbs <- round(sbs.pcoa$eig[2] / sum(sbs.pcoa$eig), 3) * 100
explainvar3.sbs <- round(sbs.pcoa$eig[3] / sum(sbs.pcoa$eig), 3) * 100
sum.eigsbs <- sum(explainvar1.sbs, explainvar2.sbs, explainvar3.sbs)
```

plot PCoA, color-coding by native status, adding text for richness indicator species

```
# plot
par(mar = c(4, 4, 1, 1) + 0.1)
plot(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2],
     ylim = c(-1.1, 1.9), xlim = c(-2.2, 2),
     xlab = paste("PCoA 1 (", explainvar1.sbs, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2.sbs, "%)", sep = ""),
     pch = 16, cex = 0.8, type = "n", cex.lab = 0.8, cex.axis = 0.8, axes = FALSE)
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 0.8, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 0.8, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)
points(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2],
       pch = 19, cex = 1.5, bg = "gray", col = "gray")
text(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2], cex = 0.6,
     # labels = rownames(sbs.ns)      # these made the graph very messy (well... even more messy)
     col = "black")

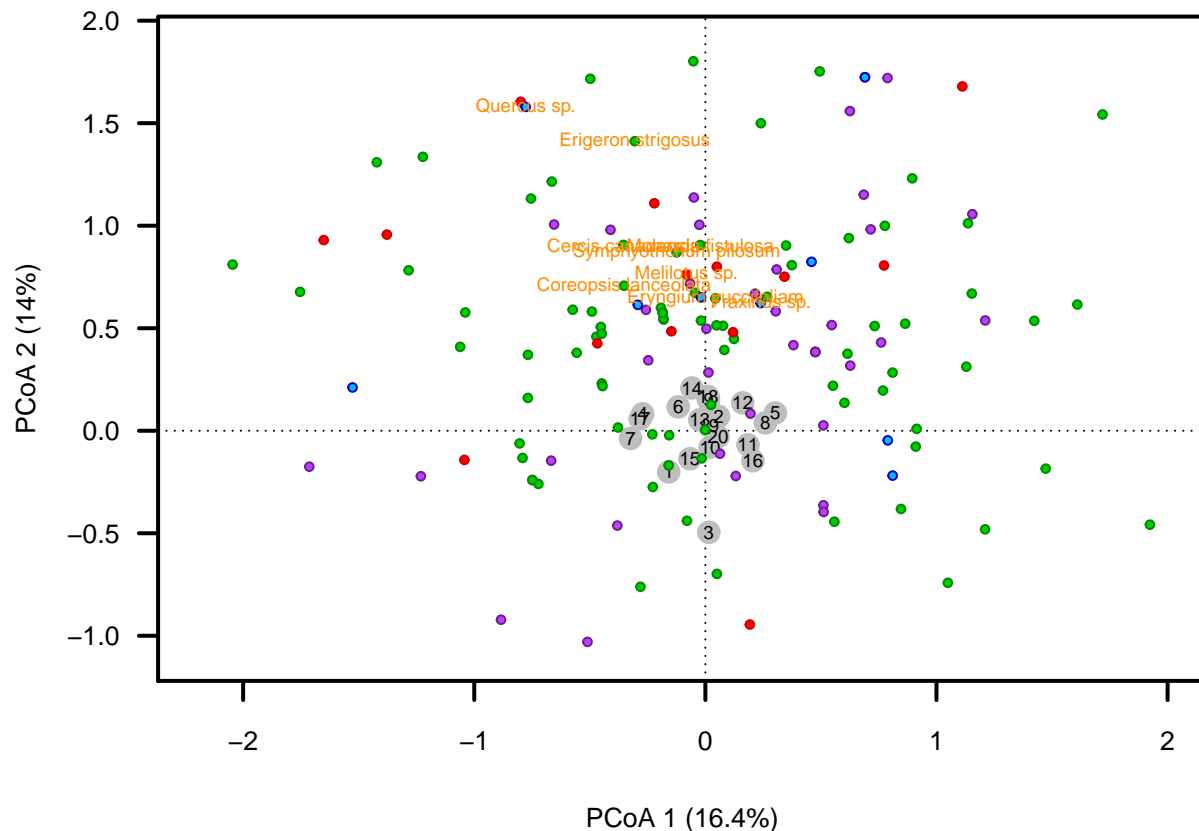
# add species labels to PCoA (I had to separate them manually, not sure how to do it better)
sbs.pcoa <- add.spec.scores(sbs.pcoa, sbs.ns, method = "pcoa.scores")
# native species (IN or US)
points(sbs.pcoa$cproj[1:84, 1], sbs.pcoa$cproj[1:84, 2],
```

```

    pch = 21, cex = 0.6, bg = "green3", col = "green4")
#text(sbs.pcoa$cproj[1:84, 1], sbs.pcoa$cproj[1:84, 2], cex = 0.4,
#      labels = row.names(sbs.pcoa$cproj[1:84, ]),
#      col = "darkgreen")
# exotic species
points(sbs.pcoa$cproj[85:120, 1], sbs.pcoa$cproj[85:120, 2],
       pch = 21, cex = 0.6, bg = "darkorchid1", col = "darkorchid4")
#text(sbs.pcoa$cproj[85:120, 1], sbs.pcoa$cproj[85:120, 2], cex = 0.4,
#      labels = row.names(sbs.pcoa$cproj[85:120, ]),
#      col = "purple")
# invasive species
points(sbs.pcoa$cproj[121:135, 1], sbs.pcoa$cproj[121:135, 2],
       pch = 21, cex = 0.6, bg = "red1", col = "red3")
#text(sbs.pcoa$cproj[121:135, 1], sbs.pcoa$cproj[121:135, 2], cex = 0.4,
#      labels = row.names(sbs.pcoa$cproj[121:135, ]),
#      col = "red")
# unknown nativity status species
points(sbs.pcoa$cproj[135:143, 1], sbs.pcoa$cproj[135:143, 2],
       pch = 21, cex = 0.6, bg = "deepskyblue", col = "blue3")
#text(sbs.pcoa$cproj[135:143, 1], sbs.pcoa$cproj[135:143, 2], cex = 0.4,
#      labels = row.names(sbs.pcoa$cproj[135:143, ]),
#      col = "blue")

# indicator species: high richness sites
text(sbs.pcoa$cproj[c(45, 29, 19, 143, 30, 131, 76, 140, 22), 1],
     sbs.pcoa$cproj[c(45, 29, 19, 143, 30, 131, 76, 140, 22), 2], cex = 0.6,
     labels = row.names(sbs.pcoa$cproj[c(45, 29, 19, 143, 30, 131, 76, 140, 22), ]),
     col = "darkorange")

```



plot PCoA, color-coding by native status, adding text for percent volunteer indicator species

```
# plot
par(mar = c(4, 4, 1, 1) + 0.1)
plot(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2],
     ylim = c(-1.1, 1.9), xlim = c(-2.2, 2),
     xlab = paste("PCoA 1 (", explainvar1.sbs, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2.sbs, "%)", sep = ""),
     pch = 16, cex = 0.8, type = "n", cex.lab = 0.8, cex.axis = 0.8, axes = FALSE)
axis(side = 1, labels = T, lwd.ticks = 2, cex.axis = 0.8, las = 1)
axis(side = 2, labels = T, lwd.ticks = 2, cex.axis = 0.8, las = 1)
abline(h = 0, v = 0, lty = 3)
box(lwd = 2)
points(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2],
       pch = 19, cex = 1.5, bg = "gray", col = "gray")
text(sbs.pcoa$points[, 1], sbs.pcoa$points[, 2], cex = 0.6,
     # labels = rownames(sbs.ns)      # these made the graph very messy (well... even more messy)
     col = "black")

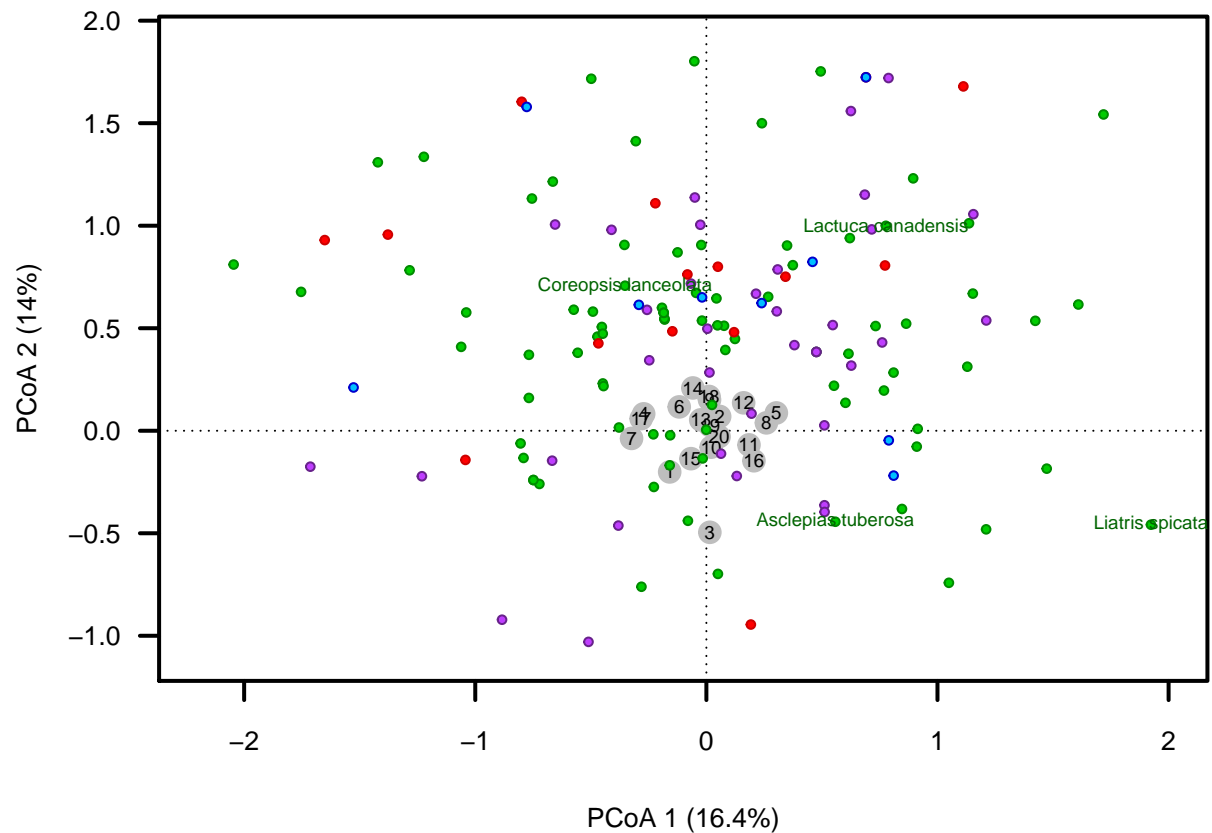
# add species labels to PCoA (I had to separate them manually, not sure how to do it better)
sbs.pcoa <- add.spec.scores(sbs.pcoa, sbs.ns, method = "pcoa.scores")
# native species (IN or US)
points(sbs.pcoa$cproj[1:84, 1], sbs.pcoa$cproj[1:84, 2],
       pch = 21, cex = 0.6, bg = "green3", col = "green4")
#text(sbs.pcoa$cproj[1:84, 1], sbs.pcoa$cproj[1:84, 2], cex = 0.4,
#     labels = row.names(sbs.pcoa$cproj[1:84, ]),
#     col = "darkgreen")
# exotic species
```

```

points(sbs.pcoa$cproj[85:120, 1], sbs.pcoa$cproj[85:120, 2],
       pch = 21, cex = 0.6, bg = "darkorchid1", col = "darkorchid4")
#text(sbs.pcoa$cproj[85:120, 1], sbs.pcoa$cproj[85:120, 2], cex = 0.4,
#      labels = row.names(sbs.pcoa$cproj[85:120, ]),
#      col = "purple")
# invasive species
points(sbs.pcoa$cproj[121:135, 1], sbs.pcoa$cproj[121:135, 2],
       pch = 21, cex = 0.6, bg = "red1", col = "red3")
#text(sbs.pcoa$cproj[121:135, 1], sbs.pcoa$cproj[121:135, 2], cex = 0.4,
#      labels = row.names(sbs.pcoa$cproj[121:135, ]),
#      col = "red")
# unknown nativity status species
points(sbs.pcoa$cproj[135:143, 1], sbs.pcoa$cproj[135:143, 2],
       pch = 21, cex = 0.6, bg = "deepskyblue", col = "blue3")
#text(sbs.pcoa$cproj[135:143, 1], sbs.pcoa$cproj[135:143, 2], cex = 0.4,
#      labels = row.names(sbs.pcoa$cproj[135:143, ]),
#      col = "blue")

# indicator species: low percent volunteer sites
text(sbs.pcoa$cproj[c(12, 42, 22, 40), 1], sbs.pcoa$cproj[c(12, 42, 22, 40), 2], cex = 0.6,
     labels = row.names(sbs.pcoa$cproj[c(12, 42, 22, 40), ]),
     col = "darkgreen")
# indicator species: high/low percent volunteer sites
text(sbs.pcoa$cproj[107, 1], sbs.pcoa$cproj[107, 2], cex = 0.6,
     labels = row.names(sbs.pcoa$cproj[107, ]),
     col = "grey")
# indicator species: high percent volunteer sites
text(sbs.pcoa$cproj[99, 1], sbs.pcoa$cproj[99, 2], cex = 0.6,
     labels = row.names(sbs.pcoa$cproj[99, ]),
     col = "darkorange")

```



INDICATOR SPECIES

Indicator species: site richness

```
# test hypothesis: there are relatively few species driving community differences
```

```
# create "factors" vector
richness <- rowSums(sbs)
```

```
min(richness) + ((max(richness) - min(richness)) / 3)
```

```
## [1] 45.33333
```

```
max(richness) - ((max(richness) - min(richness)) / 3)
```

```
## [1] 70.66667
```

```
levels <- function(x){
  if(x <= 45){
    return("L")
  } else if(x > 45 & x <= 70){
    return("M")
  } else{
    return("H")
  }
}
```

```
richness.level <- sapply(richness, levels)
```

```

# run PERMANOVA with adonis function
adonis(sbs ~ richness, method = "bray", permutations = 999)

##
## Call:
## adonis(formula = sbs ~ richness, permutations = 999, method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model        R2 Pr(>F)
## richness      1    0.3744 0.37444    1.832 0.09238 0.005 **
## Residuals    18    3.6790 0.20439          0.90762
## Total        19    4.0535          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# identify indicator species
indval <- multipatt(sbs, cluster = richness.level, func = "IndVal.g", control = how(nperm = 999))
summary(indval)

##
## Multilevel pattern analysis
## -----
##
## Association function: IndVal.g
## Significance level (alpha): 0.05
##
## Total number of species: 289
## Selected number of species: 17
## Number of species associated to 1 group: 9
## Number of species associated to 2 groups: 8
##
## List of species associated to each combination:
##
## Group H  #sps.  8
##
##              stat p.value
## Monarda.fistulosa    0.964  0.004 **
## Erigeron.strigosus    0.868  0.009 **
## Cynodon.dactylon      0.827  0.041 *
## Eryngium.yuccifoliam  0.816  0.016 *
## Melilotus.sp.         0.816  0.015 *
## Fraxinus.sp.          0.773  0.037 *
## Symphyotrichum.pilosum 0.773  0.043 *
## Asclepias.incarnata   0.696  0.044 *
##
## Group M  #sps.  1
##
##              stat p.value
## Symphyotrichum.oolentangiense 0.707  0.043 *
##
## Group H+M  #sps.  8

```

```

##                                stat p.value
## Trifolium.pratense            0.931  0.003 **
## Erigeron.canadensis          0.838  0.043 *
## Toxicodendron.radicans       0.838  0.045 *
## Cercis.canadensis            0.824  0.020 *
## Quercus.sp.                  0.824  0.023 *
## Solidago.canadensis          0.803  0.048 *
## Symphyotrichum.cordifolium   0.756  0.019 *
## Daucus.carota                0.732  0.036 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# calculate phi coefficient of association to examine habitat preference
sbs.rel <- decostand(sbs, method = "total")
phi <- multipatt(sbs, cluster = richness.level, func = "r.g", control = how(nperm = 999))
summary(phi)

##
## Multilevel pattern analysis
## -----
##
## Association function: r.g
## Significance level (alpha): 0.05
##
## Total number of species: 289
## Selected number of species: 11
## Number of species associated to 1 group: 10
## Number of species associated to 2 groups: 1
##
## List of species associated to each combination:
##
## Group H  #sps.  10
##
##                                stat p.value
## Monarda.fistulosa            0.945  0.003 **
## Erigeron.strigosus           0.794  0.013 *
## Eryngium.yuccifoliam         0.756  0.012 *
## Melilotus.sp.                0.756  0.025 *
## Cynodon.dactylon             0.725  0.024 *
## Fraxinus.sp.                 0.686  0.045 *
## Symphyotrichum.pilosum       0.686  0.043 *
## Cercis.canadensis            0.672  0.020 *
## Quercus.sp.                  0.672  0.022 *
## Echinochloa.crus.galli       0.646  0.046 *
##
## Group H+M  #sps.  1
##
##                                stat p.value
## Trifolium.pratense           0.775  0.006 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Indicator species: richness (no absent/single species)

# create "factors" vector
richness.ns <- rowSums(sbs.ns)

min(richness.ns) + ((max(richness.ns) - min(richness.ns)) / 3)

```



```
## [1] 37.33333
max(richness.ns) - ((max(richness.ns) - min(richness.ns)) / 3)

## [1] 58.66667
levels.ns <- function(x){
  if(x <= 37){
    return("L")
  } else if(x > 37 & x <= 58){
    return("M")
  } else{
    return("H")
  }
}

# make qualitative
richness.level.ns <- sapply(richness.ns, levels.ns)

# run PERMANOVA with adonis function
adonis(sbs.ns ~ richness.ns, method = "bray", permutations = 999)

##
## Call:
## adonis(formula = sbs.ns ~ richness.ns, permutations = 999, method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## richness.ns  1    0.3542 0.35421  2.0195 0.10088 0.002 **
## Residuals   18    3.1571 0.17539          0.89912
## Total       19    3.5113          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# identify indicator species
indval <- multipatt(sbs.ns, cluster = richness.level.ns, func = "IndVal.g", control = how(nperm = 999))
summary(indval)

##
## Multilevel pattern analysis
## -----
##
## Association function: IndVal.g
## Significance level (alpha): 0.05
##
## Total number of species: 143
## Selected number of species: 16
## Number of species associated to 1 group: 10
## Number of species associated to 2 groups: 6
##
## List of species associated to each combination:
##
```

```

## Group H #sps. 10
##
##          stat p.value
## Monarda fistulosa    0.935  0.007 **
## Erigeron strigosus   0.897  0.009 **
## Cercis canadensis    0.849  0.018 *
## Quercus sp.          0.849  0.019 *
## Eryngium yuccifoliam 0.816  0.014 *
## Melilotus sp.        0.816  0.023 *
## Symphyotrichum pilosum 0.761  0.040 *
## Fraxinus sp.         0.761  0.029 *
## Asclepias incarnata   0.741  0.048 *
## Coreopsis lanceolata 0.716  0.041 *
##
## Group H+M #sps. 6
##
##          stat p.value
## Erigeron canadensis  0.825  0.044 *
## Toxicodendron radicans 0.825  0.027 *
## Glechoma hederaceae   0.811  0.009 **
## Lonicera maackii      0.788  0.028 *
## Cyperus esculentus    0.707  0.035 *
## Daucus carota         0.707  0.035 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# calculate phi coefficient of association to examine habitat preference
sbs.rel <- decostand(sbs.ns, method = "total")
phi <- multipatt(sbs.ns, cluster = richness.level.ns, func = "r.g", control = how(nperm = 999))
summary(phi)

##
## Multilevel pattern analysis
## -----
##
## Association function: r.g
## Significance level (alpha): 0.05
##
## Total number of species: 143
## Selected number of species: 11
## Number of species associated to 1 group: 10
## Number of species associated to 2 groups: 1
##
## List of species associated to each combination:
##
## Group H #sps. 10
##
##          stat p.value
## Monarda fistulosa    0.901  0.007 **
## Erigeron strigosus   0.841  0.011 *
## Cercis canadensis    0.763  0.019 *
## Quercus sp.          0.763  0.021 *
## Eryngium yuccifoliam 0.756  0.019 *
## Melilotus sp.        0.756  0.016 *
## Symphyotrichum pilosum 0.666  0.033 *
## Fraxinus sp.         0.666  0.029 *
## Asclepias incarnata   0.632  0.045 *
## Coreopsis lanceolata 0.589  0.043 *

```

```
##
## Group H+M #sps. 1
##          stat p.value
## Glechoma hederaceae 0.651 0.043 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Indicator species: percent volunteer

# Change volunteer species to be coded as "0"
crawley.full$Planted.or.Volunteer[crawley.full$Planted.or.Volunteer == "2"] <- 0
Planted.or.Volunteer <- crawley.full$Planted.or.Volunteer
# Volunteer species only
crawley.volunteer <- crawley.full[crawley.full$Planted.or.Volunteer == "0", ]
# Remove non-incidence columns
crawley.volunteer.sbs <- crawley.volunteer[, -c(1:3)]

percent.volunteer <- colSums(crawley.volunteer.sbs) / colSums(crawley.full[, -c(1:3)])

#determine range
min(percent.volunteer) + ((max(percent.volunteer) - min(percent.volunteer)) / 3)

## [1] 0.7539118
max(percent.volunteer) - ((max(percent.volunteer) - min(percent.volunteer)) / 3)

## [1] 0.8499289

levels.vol <- function(x){
  if(x <= 0.7539){
    return("L")
  } else if(x > 0.7539 & x <= 0.8499){
    return("M")
  } else{
    return("H")
  }
}

# make qualitative
volunteer.level <- sapply(percent.volunteer, levels.vol)

# run PERMANOVA with adonis function
adonis(sbs ~ percent.volunteer, method = "bray", permutations = 999)

##
## Call:
## adonis(formula = sbs ~ percent.volunteer, permutations = 999,          method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##          Df SumsOfSqs MeanSqs F.Model    R2 Pr(>F)
## percent.volunteer  1    0.2639 0.26393  1.2537 0.06511 0.159
## Residuals        18    3.7895 0.21053          0.93489
## Total            19    4.0535          1.00000
```

```
# identify indicator species
indval <- multipatt(sbs, cluster = volunteer.level, func = "IndVal.g", control = how(nperm = 999))
summary(indval)
```

```
##
## Multilevel pattern analysis
## -----
##
## Association function: IndVal.g
## Significance level (alpha): 0.05
##
## Total number of species: 289
## Selected number of species: 5
## Number of species associated to 1 group: 3
## Number of species associated to 2 groups: 2
##
## List of species associated to each combination:
##
## Group H #sps. 1
##               stat p.value
## Festuca.arundinaceae 0.734 0.024 *
##
## Group L #sps. 2
##               stat p.value
## Liatris.spicata 0.839 0.006 **
## Asclepias.tuberosa 0.756 0.009 **
##
## Group H+L #sps. 2
##               stat p.value
## Elymus.repens 0.849 0.022 *
## Panicum.virgatum 0.798 0.014 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# calculate phi coefficient of association to examine habitat preference
sbs.rel <- decostand(sbs, method = "total")
phi <- multipatt(sbs, cluster = volunteer.level, func = "r.g", control = how(nperm = 999))
summary(phi)
```

```
##
## Multilevel pattern analysis
## -----
##
## Association function: r.g
## Significance level (alpha): 0.05
##
## Total number of species: 289
## Selected number of species: 7
## Number of species associated to 1 group: 5
## Number of species associated to 2 groups: 2
##
## List of species associated to each combination:
##
## Group H #sps. 3
##               stat p.value
```

```
## Juglans.nigra          0.632  0.022 *
## Ambrosia.artemisiifolia 0.586  0.049 *
## Stellaria.media       0.555  0.043 *
##
## Group L  #sps.  2
##              stat p.value
## Liatris.spicata  0.745  0.003 **
## Asclepias.tuberosa 0.657  0.023 *
##
## Group H+L  #sps.  1
##              stat p.value
## Panicum.virgatum 0.618  0.015 *
##
## Group L+M  #sps.  1
##              stat p.value
## Echinacea.purpurea 0.604  0.02 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Indicator species: percent volunteer (no single/absent species)

```
# Change volunteer species to be coded as "0"
cf.1 <- crawley.full
cf.1$Planted.or.Volunteer[cf.1$Planted.or.Volunteer == "2"] <- 0
# add sum column
cf.1$sums <- rowSums(cf.1[, 4:23])
# filter to remove species found in 0 or 1 site
cf.1.ns <- cf.1[which(cf.1$sums > 1), ]

# Volunteer species only, remove non-incidence columns
cf.1.ns.vol <- cf.1.ns[cf.1.ns$Planted.or.Volunteer == "0", 4:23]

percent.volunteer.ns <- colSums(cf.1.ns.vol) / rowSums(sbs.ns)

#determine range
min(percent.volunteer.ns) + ((max(percent.volunteer.ns) - min(percent.volunteer.ns)) / 3)

## [1] 0.772619
max(percent.volunteer.ns) - ((max(percent.volunteer.ns) - min(percent.volunteer.ns)) / 3)

## [1] 0.8577381

levels.vol.ns <- function(x){
  if(x <= 0.7726){
    return("L")
  } else if(x > 0.7726 & x <= 0.8577){
    return("M")
  } else{
    return("H")
  }
}

# make qualitative
volunteer.level.ns <- sapply(percent.volunteer.ns, levels.vol.ns)
```

```

# run PERMANOVA with adonis function
adonis(sbs.ns ~ percent.volunteer.ns, method = "bray", permutations = 999)

##
## Call:
## adonis(formula = sbs.ns ~ percent.volunteer.ns, permutations = 999,      method = "bray")
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## percent.volunteer.ns  1    0.2763 0.27632  1.5375 0.07869  0.044 *
## Residuals            18    3.2350 0.17972      0.92131
## Total                19    3.5113      1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# identify indicator species
indval <- multipatt(sbs.ns, cluster = volunteer.level.ns, func = "IndVal.g", control = how(nperm = 999))
summary(indval)

##
## Multilevel pattern analysis
## -----
##
## Association function: IndVal.g
## Significance level (alpha): 0.05
##
## Total number of species: 143
## Selected number of species: 3
## Number of species associated to 1 group: 2
## Number of species associated to 2 groups: 1
##
## List of species associated to each combination:
##
## Group H  #sps.  1
##              stat p.value
## Eleusine indica 0.73   0.041 *
##
## Group L  #sps.  1
##              stat p.value
## Asclepias tuberosa 0.851   0.008 **
##
## Group H+L  #sps.  1
##              stat p.value
## Plantago lanceolata 0.877   0.012 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# calculate phi coefficient of association to examine habitat preference
sbs.rel <- decostand(sbs.ns, method = "total")
phi <- multipatt(sbs.ns, cluster = volunteer.level.ns, func = "r.g", control = how(nperm = 999))
summary(phi)

```

```
##
## Multilevel pattern analysis
## -----
##
## Association function: r.g
## Significance level (alpha): 0.05
##
## Total number of species: 143
## Selected number of species: 5
## Number of species associated to 1 group: 4
## Number of species associated to 2 groups: 1
##
## List of species associated to each combination:
##
## Group L #sps. 4
##               stat p.value
## Asclepias tuberosa 0.784 0.017 *
## Liatris spicata    0.669 0.017 *
## Coreopsis lanceolata 0.628 0.031 *
## Lactuca canadensis 0.628 0.037 *
##
## Group H+L #sps. 1
##               stat p.value
## Plantago lanceolata 0.659 0.027 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Invasive species colonization by year

```
time.since.planting <- crawley.site.factors$Years.between.planting.and.census # this is an integer, for

crawley.full.2 <- crawley.full

crawley.full.2 %>%
  group_by(Nativity.Code) %>%
  summarize(grpcount = n())

## # A tibble: 5 x 2
##   Nativity.Code grpcount
##   <fct>         <int>
## 1 0             175
## 2 1              2
## 3 2             69
## 4 3             24
## 5 UNK          22

crawley.full.2 <- crawley.full.2[-c(293:300), -c(24, 25)]

sites <- c("Athenaeum", "Bauman.Park", "Center.for.Inquiry", "Chinqpın.Oak.Park",
"Community.Caring...Sharing", "Cottage.Home", "Englewood", "Fletcher.Gateway",
"Fletcher.Park", "Historic.Meridian.Park", "Jonathan.Jennings",
"Lynhurst", "Merrill.Street", "Paramount.Charter", "Purpose.Park",
"Ransom.Place", "Skiles.Test", "University.Park", "Westminster",
```

```

"Willard.Park")

# number of invasive species per site
crawley.invasives <- crawley.full.2[crawley.full.2$Nativity.Code == "3", ]
n.invasives <- colSums(crawley.invasives[, 4:ncol(crawley.invasives)])

# make df
df <- data.frame(site = sites, n.inv = n.invasives)

# Get list of invasive species in each site
for (i in 4:ncol(crawley.invasives)) {
  species <- crawley.invasives[crawley.invasives[, i] == 1, ]$Species
  site <- colnames(crawley.invasives)[i]
  print(data.frame(site, species))
}

```

```

##           site           species
## 1 Athenaeum Ailanthus altissima
## 2 Athenaeum      Morus alba
##           site           species
## 1 Bauman.Park Ailanthus altissima
## 2 Bauman.Park  Centaurea stoebe
## 3 Bauman.Park  Cirsium vulgare
## 4 Bauman.Park Convolvulus arvensis
## 5 Bauman.Park  Lonicera maackii
## 6 Bauman.Park  Melilotus alba
## 7 Bauman.Park      Morus alba
## 8 Bauman.Park  Torilis arvensis
##           site           species
## 1 Center.for.Inquiry Ailanthus altissima
## 2 Center.for.Inquiry  Artemisia vulgaris
## 3 Center.for.Inquiry Celastrus orbiculatus
## 4 Center.for.Inquiry      Morus alba
##           site           species
## 1 Chinqpin.Oak.Park Convolvulus arvensis
## 2 Chinqpin.Oak.Park  Eunymus fortunei
## 3 Chinqpin.Oak.Park  Glechoma hederaceae
## 4 Chinqpin.Oak.Park  Lonicera maackii
## 5 Chinqpin.Oak.Park      Morus alba
## 6 Chinqpin.Oak.Park  Torilis arvensis
##           site           species
## 1 Community.Caring...Sharing Cirsium arvense
## 2 Community.Caring...Sharing Convolvulus arvensis
## 3 Community.Caring...Sharing  Humulus japonicus
## 4 Community.Caring...Sharing  Sorghum halepense
## 5 Community.Caring...Sharing  Torilis arvensis
##           site           species
## 1 Cottage.Home      Daucus carota
## 2 Cottage.Home      Eunymus fortunei
## 3 Cottage.Home  Festuca arundinaceae
## 4 Cottage.Home  Glechoma hederaceae
## 5 Cottage.Home      Melilotus alba
## 6 Cottage.Home      Morus alba
## 7 Cottage.Home  Sorghum halepense

```



```

## 8 Cottage.Home      Torilis arvensis
## 9 Cottage.Home Vincetoxicum rossicum
##      site              species
## 1 Englewood      Eunonymus fortunei
## 2 Englewood Festuca arundicaceae
## 3 Englewood  Glechoma hederaceae
## 4 Englewood      Morus alba
##      site              species
## 1 Fletcher.Gateway  Cirsium arvense
## 2 Fletcher.Gateway  Daucus carota
## 3 Fletcher.Gateway  Pyrus callerya
## 4 Fletcher.Gateway Torilis arvensis
##      site              species
## 1 Fletcher.Park Ailanthus altissima
## 2 Fletcher.Park  Cirsium arvense
## 3 Fletcher.Park  Eunonymus fortunei
## 4 Fletcher.Park  Glechoma hederaceae
## 5 Fletcher.Park  Lonicera maackii
## 6 Fletcher.Park  Morus alba
## 7 Fletcher.Park  Rosa multiflora
##      site              species
## 1 Historic.Meridian.Park Ailanthus altissima
## 2 Historic.Meridian.Park Convolvulus arvensis
## 3 Historic.Meridian.Park Eunonymus fortunei
## 4 Historic.Meridian.Park Glechoma hederaceae
## 5 Historic.Meridian.Park Lonicera tatarica
## 6 Historic.Meridian.Park Torilis arvensis
##      site              species
## 1 Jonathan.Jennings      Cirsium arvense
## 2 Jonathan.Jennings Convolvulus arvensis
## 3 Jonathan.Jennings Festuca arundicaceae
## 4 Jonathan.Jennings Hesperis matronalis
## 5 Jonathan.Jennings      Morus alba
##      site              species
## 1 Lynhurst      Cirsium arvense
## 2 Lynhurst Festuca arundicaceae
## 3 Lynhurst      Lonicera maackii
## 4 Lynhurst      Morus alba
## 5 Lynhurst      Torilis arvensis
##      site              species
## 1 Merrill.Street      Cirsium arvense
## 2 Merrill.Street Convolvulus arvensis
## 3 Merrill.Street      Lonicera maackii
## 4 Merrill.Street      Melilotus alba
## 5 Merrill.Street      Morus alba
## 6 Merrill.Street      Torilis arvensis
## 7 Merrill.Street      Ulmus pumila
##      site              species
## 1 Paramount.Charter Ailanthus altissima
## 2 Paramount.Charter  Cirsium arvense
## 3 Paramount.Charter Convolvulus arvensis
## 4 Paramount.Charter  Daucus carota
## 5 Paramount.Charter Festuca arundicaceae
## 6 Paramount.Charter  Glechoma hederaceae

```

```

## 7 Paramount.Charter      Lonicera maackii
## 8 Paramount.Charter      Melilotus sp.
## 9 Paramount.Charter      Morus alba
## 10 Paramount.Charter     Torilis arvensis
##           site           species
## 1 Purpose.Park Ailanthus altissima
## 2 Purpose.Park   Daucus carota
## 3 Purpose.Park Glechoma hederaceae
## 4 Purpose.Park   Lonicera maackii
## 5 Purpose.Park   Morus alba
##           site           species
## 1 Ransom.Place  Ailanthus altissima
## 2 Ransom.Place  Convolvulus arvensis
## 3 Ransom.Place   Morus alba
##           site           species
## 1 Skiles.Test   Cirsium arvense
## 2 Skiles.Test   Eunonymus fortunei
## 3 Skiles.Test   Lonicera maackii
## 4 Skiles.Test   Morus alba
## 5 Skiles.Test   Rosa multiflora
##           site           species
## 1 University.Park Ailanthus altissima
## 2 University.Park   Cirsium arvense
## 3 University.Park   Cirsium vulgare
## 4 University.Park Convolvulus arvensis
## 5 University.Park   Daucus carota
## 6 University.Park   Eunonymus fortunei
## 7 University.Park Festuca arundinaceae
## 8 University.Park Glechoma hederaceae
## 9 University.Park   Lonicera maackii
## 10 University.Park   Melilotus sp.
## 11 University.Park   Morus alba
## 12 University.Park   Sorghum halepense
## 13 University.Park   Torilis arvensis
##           site           species
## 1 Westminster  Ailanthus altissima
## 2 Westminster   Cirsium arvense
## 3 Westminster  Convolvulus arvensis
## 4 Westminster  Festuca arundinaceae
##           site           species
## 1 Willard.Park Ailanthus altissima
## 2 Willard.Park   Cirsium arvense
## 3 Willard.Park   Morus alba
## 4 Willard.Park   Torilis arvensis

```