

Perenniality (and/or) management drives soil biological communities and functions

Christine D. Sprunger, Ariane L. Peralta, Steven Culman, Jay T. Lennon, Sieglinde S. Snapp

Last updated on 10 May, 2018

Project Description: Fill out

Initial Setup

Import Files

Environmental Data

```
# Import Environmental Data
design <- read.csv("../data/PWES_KBS_design.csv", header=TRUE)
```

Nematode Data

```
# Import Environmental Data
nema <- read.csv("../data/PWES_nema.csv", header=TRUE)
nema <- na.omit(nema)
dim(nema)

## [1] 65 61

nema.design <- nema[,c(1:9)]
nema.comm <- nema[, -c(1:9)]
dim(nema.comm)

## [1] 65 52

# Remove taxa with less than one occurrences across all sites
#nema.comm.a <- nema.comm[, which(colSums(nema.comm) >= 1)]
#dim(nema.comm.a)

# Make Relative Abundance Matrices removed xxx_sample = NA
dataRELnema <- nema.comm
for(i in 1:dim(nema.comm)[1]){
  dataRELnema[i,] <- nema.comm[i,]/sum(nema.comm[i,])
}

dim(dataRELnema)

## [1] 65 52

nemaREL <- cbind(nema.design, dataRELnema)
dim(nemaREL)
```

```
## [1] 65 61
```

Microbial Data

Diversity Metrics - Hypothesis Testing

```
# Rarefy Abundances (min abundance is 88033. We are sampling to 80000)  
min(rowSums(otus))
```

```
## [1] 88033
```

```
PWESdata.r <- rrarefy(otus, 80000)
```

```
# Fisher's Alpha
```

```
fisher <- fisher.alpha(PWESdata.r)
```

```
# Species Richness
```

```
richness <- rowSums((PWESdata.r >= 1))
```

```
# Shannon Diversity
```

```
shannon <- diversity(PWESdata.r, "shannon")
```

```
# Simpson's Evenness
```

```
simp.even <- apply(PWESdata.r, 1, simp_even)
```

```
#Pielou's evenness
```

```
J <- shannon/log(specnumber(PWESdata.r[, -c(1:1)]))
```

```
#combined richness, diversity, evenness
```

```
diversity <- cbind(design, richness, shannon, simp.even, J)
```

Diversity Metrics - Hypothesis Testing

```
# First check the order
```

```
length(design$Management) == length(fisher)
```

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

```
all.equal(gsub("-", "", rownames(design)), names(fisher))
```

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

```
library(lme4)
```

```
## Warning: package 'lme4' was built under R version 3.4.4
```

```
## Loading required package: Matrix
```

```
##
```

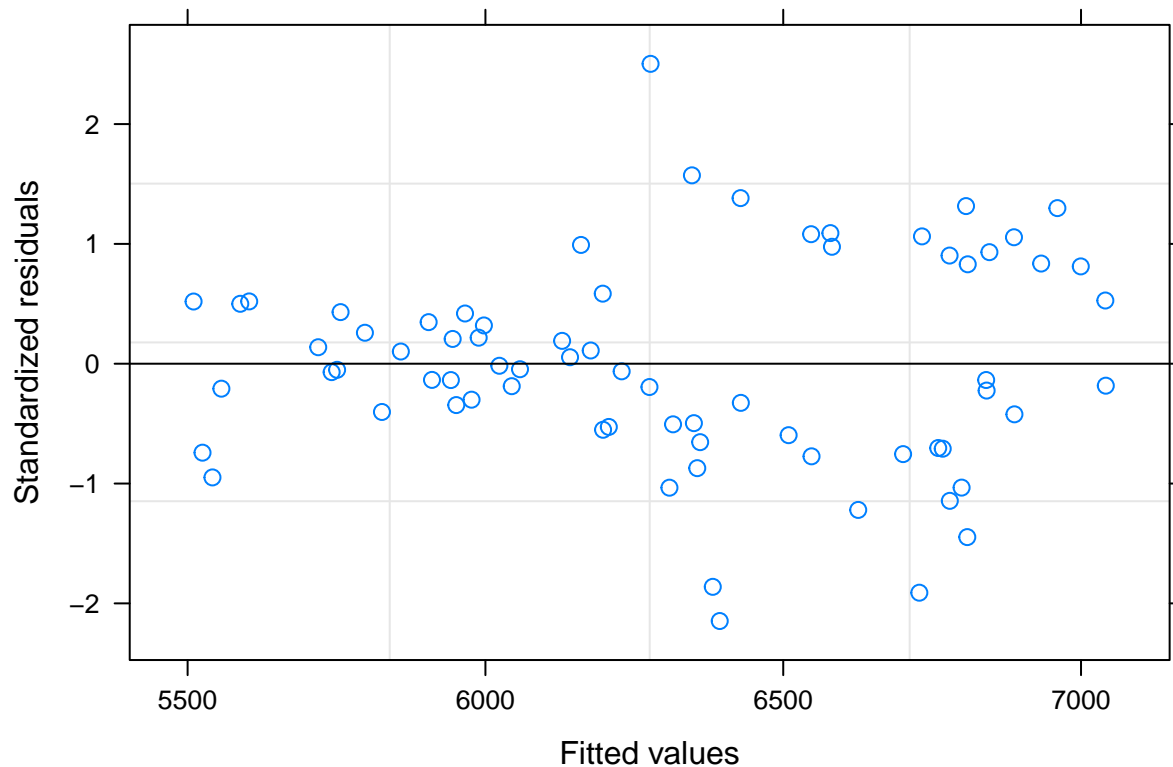
```
## Attaching package: 'Matrix'
```

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

```
##
```

```
## expand
```

```
## The following object is masked from 'package:reshape':
##
##   expand
##
## Attaching package: 'lme4'
##
## The following object is masked from 'package:nlme':
##
##   lmList
richness.lm <- lme(richness ~ Date*Management*Plant, random = ~1|Block, data = diversity)
plot(richness.lm)
```



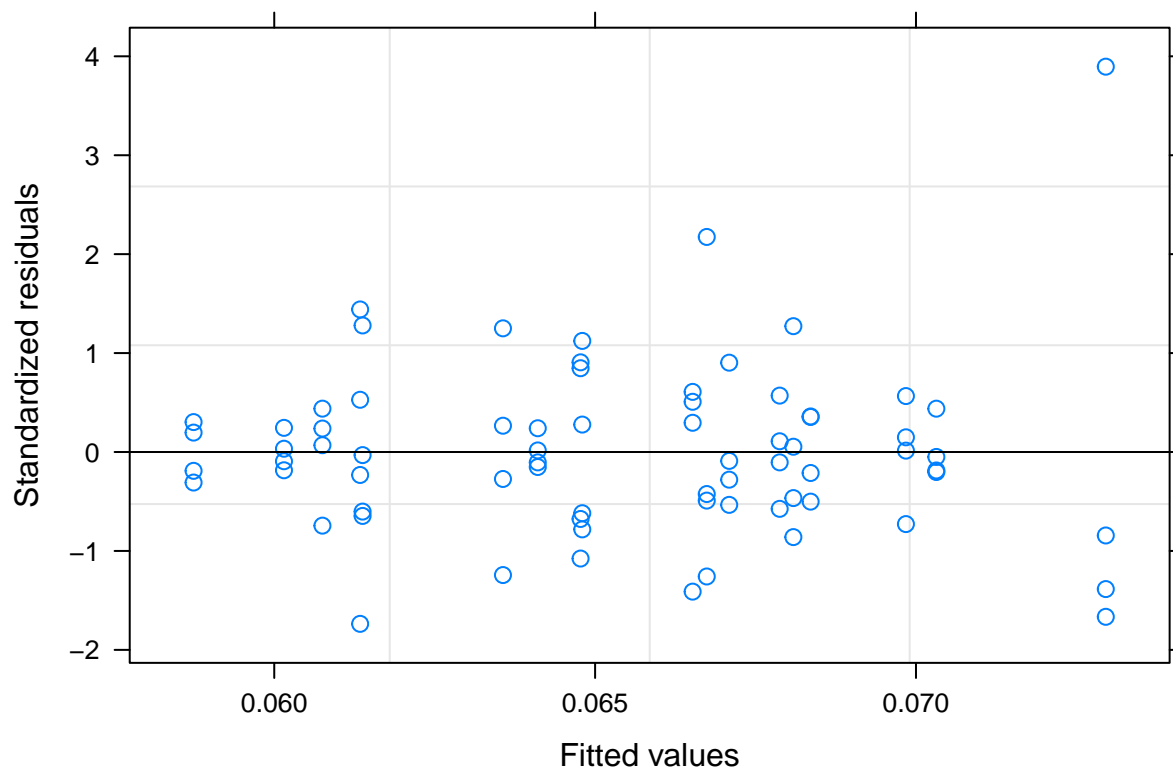
```
richness.lm
## Linear mixed-effects model fit by REML
## Data: diversity
## Log-restricted-likelihood: -436.3773
## Fixed: richness ~ Date * Management * Plant
##              (Intercept)
##              5610.50
##              DateJun-12
##              420.00
##              DateJun-13
##              790.00
##              ManagementLowN
##              -15.00
##              ManagementOrganic
##              440.75
##              PlantIntWheatgrass
```

```
##                               385.25
##           DateJun-12:ManagementLowN
##                               347.25
##           DateJun-13:ManagementLowN
##                               509.00
##           DateJun-12:ManagementOrganic
##                               -188.75
##           DateJun-13:ManagementOrganic
##                               12.00
##           DateJun-12:PlantIntWheatgrass
##                               217.25
##           DateJun-13:PlantIntWheatgrass
##                               -571.50
##           ManagementLowN:PlantIntWheatgrass
##                               -176.00
##           ManagementOrganic:PlantIntWheatgrass
##                               -524.75
##           DateJun-12:ManagementLowN:PlantIntWheatgrass
##                               -353.75
##           DateJun-13:ManagementLowN:PlantIntWheatgrass
##                               363.00
##           DateJun-12:ManagementOrganic:PlantIntWheatgrass
##                               453.75
##           DateJun-13:ManagementOrganic:PlantIntWheatgrass
##                               644.50
##
## Random effects:
## Formula: ~1 | Block
##           (Intercept) Residual
## StdDev:    144.6817  608.863
##
## Number of Observations: 72
## Number of Groups: 4
```

```
anova(richness.lm)
```

```
##           numDF denDF  F-value p-value
## (Intercept)      1    51 3834.584 <.0001
## Date           2    51  12.242 <.0001
## Management     2    51   1.504 0.2319
## Plant          1    51   1.191 0.2802
## Date:Management 4    51   0.702 0.5939
## Date:Plant      2    51   0.957 0.3908
## Management:Plant 2    51   0.149 0.8618
## Date:Management:Plant 4    51   0.365 0.8323
```

```
evenness.lm <- lme(simp.even ~ Date*Management*Plant, random = ~1|Block, data = diversity)
plot(evenness.lm)
```



```
evenness.lm
```

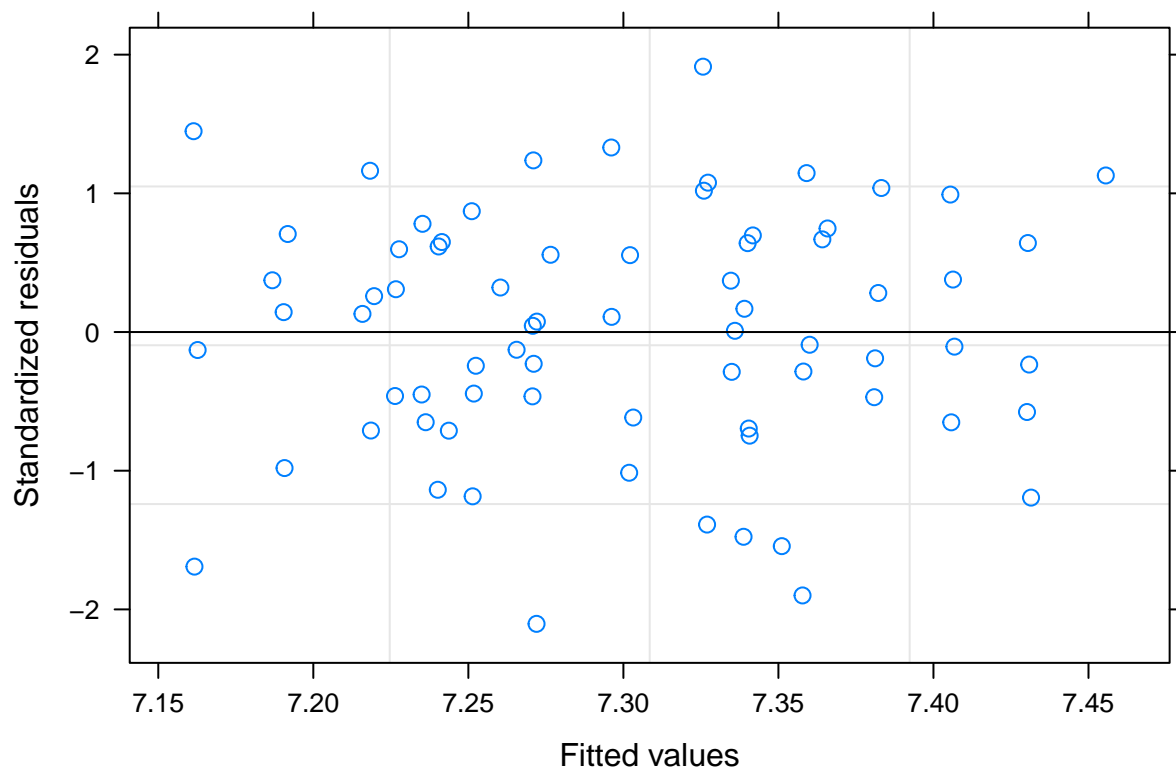
```
## Linear mixed-effects model fit by REML
## Data: diversity
## Log-restricted-likelihood: 175.4137
## Fixed: simp.even ~ Date * Management * Plant
##              (Intercept)
##              0.0680895525
##              DateJun-12
##              -0.0045253894
##              DateJun-13
##              -0.0079377327
##              ManagementLowN
##              -0.0002131479
##              ManagementOrganic
##              -0.0073385438
##              PlantIntWheatgrass
##              0.0022282215
##              DateJun-12:ManagementLowN
##              -0.0020123419
##              DateJun-13:ManagementLowN
##              -0.0011955642
##              DateJun-12:ManagementOrganic
##              0.0108640883
##              DateJun-13:ManagementOrganic
##              0.0119866101
##              DateJun-12:PlantIntWheatgrass
##              -0.0044156925
##              DateJun-13:PlantIntWheatgrass
##              0.0105777968
```

```
##           ManagementLowN:PlantIntWheatgrass
##                                     -0.0035845699
##           ManagementOrganic:PlantIntWheatgrass
##                                     0.0053789153
##   DateJun-12:ManagementLowN:PlantIntWheatgrass
##                                     0.0111731396
##   DateJun-13:ManagementLowN:PlantIntWheatgrass
##                                     -0.0038581531
## DateJun-12:ManagementOrganic:PlantIntWheatgrass
##                                     -0.0055076511
## DateJun-13:ManagementOrganic:PlantIntWheatgrass
##                                     -0.0131414793
##
## Random effects:
## Formula: ~1 | Block
##      (Intercept)      Residual
## StdDev: 2.53607e-07 0.007458585
##
## Number of Observations: 72
## Number of Groups: 4
```

```
anova(evenness.lm)
```

| | numDF | denDF | F-value | p-value |
|--------------------------|-------|-------|----------|---------|
| ## (Intercept) | 1 | 51 | 5537.593 | <.0001 |
| ## Date | 2 | 51 | 0.900 | 0.4129 |
| ## Management | 2 | 51 | 0.461 | 0.6336 |
| ## Plant | 1 | 51 | 4.243 | 0.0445 |
| ## Date:Management | 4 | 51 | 1.116 | 0.3593 |
| ## Date:Plant | 2 | 51 | 1.543 | 0.2236 |
| ## Management:Plant | 2 | 51 | 0.038 | 0.9628 |
| ## Date:Management:Plant | 4 | 51 | 1.045 | 0.3934 |

```
shannon.lm <- lme(shannon ~ Date*Management*Plant, random = ~1|Block, data = diversity)
plot(shannon.lm)
```



```
shannon.lm
```

```
## Linear mixed-effects model fit by REML
## Data: diversity
## Log-restricted-likelihood: 42.20046
## Fixed: shannon ~ Date * Management * Plant
##                                     (Intercept)
##                                     7.19719150
##                                     DateJun-12
##                                     0.04449267
##                                     DateJun-13
##                                     0.08024436
##                                     ManagementLowN
##                                     -0.02905364
##                                     ManagementOrganic
##                                     0.02785834
##                                     PlantIntWheatgrass
##                                     0.08034726
##                                     DateJun-12:ManagementLowN
##                                     0.04522275
##                                     DateJun-13:ManagementLowN
##                                     0.09712720
##                                     DateJun-12:ManagementOrganic
##                                     0.07186876
##                                     DateJun-13:ManagementOrganic
##                                     0.08235038
##                                     DateJun-12:PlantIntWheatgrass
##                                     -0.01341175
##                                     DateJun-13:PlantIntWheatgrass
##                                     -0.02535187
```

```
##           ManagementLowN:PlantIntWheatgrass
##                               -0.01538313
##           ManagementOrganic:PlantIntWheatgrass
##                               -0.05849819
##   DateJun-12:ManagementLowN:PlantIntWheatgrass
##                               0.03778050
##   DateJun-13:ManagementLowN:PlantIntWheatgrass
##                               0.02708823
## DateJun-12:ManagementOrganic:PlantIntWheatgrass
##                               0.01468254
## DateJun-13:ManagementOrganic:PlantIntWheatgrass
##                               0.05277437
##
## Random effects:
## Formula: ~1 | Block
##      (Intercept)   Residual
## StdDev:  0.01851619 0.08644907
##
## Number of Observations: 72
## Number of Groups: 4
```

```
anova(shannon.lm)
```

| | numDF | denDF | F-value | p-value |
|--------------------------|-------|-------|-----------|---------|
| ## (Intercept) | 1 | 51 | 281204.47 | <.0001 |
| ## Date | 2 | 51 | 16.14 | <.0001 |
| ## Management | 2 | 51 | 3.10 | 0.0536 |
| ## Plant | 1 | 51 | 7.96 | 0.0068 |
| ## Date:Management | 4 | 51 | 1.13 | 0.3526 |
| ## Date:Plant | 2 | 51 | 0.00 | 0.9965 |
| ## Management:Plant | 2 | 51 | 0.42 | 0.6608 |
| ## Date:Management:Plant | 4 | 51 | 0.08 | 0.9891 |

```
#calculate mean and se
```

```
library(reshape2)
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
## The following object is masked from 'package:nlme':
##
##   collapse
## The following object is masked from 'package:reshape':
##
##   rename
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
```

```
diversity.1 <- subset(diversity, Year == 2013)
```

```
dim(diversity.1)
```



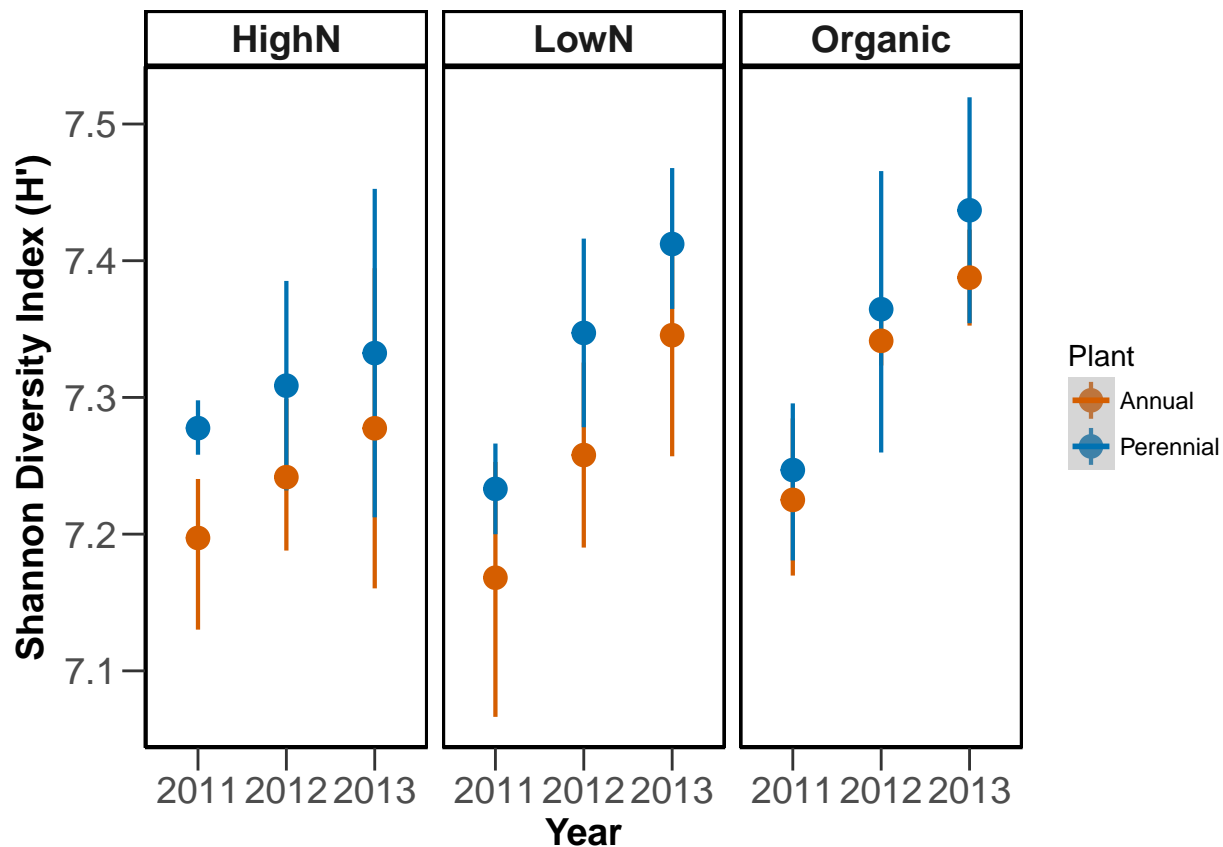
```
## [1] 24 13
```

```
summary <- diversity.1 %>% group_by(Management, Plant) %>% summarise(mean.richness=mean(richness), se.richness=sd(richness)/sqrt(n()),  
print(summary)
```

```
## # A tibble: 6 x 6  
## # Groups:   Management [?]  
##   Management Plant      mean.richness se.richness mean.shannon se.shannon  
##   <fct>      <fct>          <dbl>         <dbl>         <dbl>         <dbl>  
## 1 HighN      Annual             6400           528           7.28          0.0738  
## 2 HighN      IntWheatgr~       6214           199           7.33          0.0712  
## 3 LowN       Annual             6894           362           7.35          0.0470  
## 4 LowN      IntWheatgr~       6895           154           7.41          0.0294  
## 5 Organic   Annual             6853           349           7.39          0.0219  
## 6 Organic   IntWheatgr~       6787           362           7.44          0.0508
```

Plot shannon diversity

```
date_1 <- as.factor(diversity$Date)  
labels <- c("Jun-11"="2011", "Jun-12"="2012", "Jun-13"="2013")  
  
# Graphing Shannon Diversity - Date x Plant over Mgmt  
p <- ggplot(diversity, aes(x=Date, y=shannon, color=as.factor(Plant)))+ scale_color_manual(name="Plant", values=c("HighN"="red", "LowN"="blue", "Organic"="green"))  
p1=p+geom_smooth(method="lm")+facet_wrap(~Management)+facet_grid(. ~ Management)  
p1 + theme_bw() +  
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) +  
  theme(axis.title=element_text(vjust=1,size=14,face="bold"),  
        axis.text=element_text(size=14), axis.text.x = element_text(vjust=0.65, hjust=0.5, size=14), panel.border = element_rect(colour = "black",size=1)) +  
  theme(axis.ticks.length=unit(0.3,"cm")) + labs(x = "Year", y = "Shannon Diversity Index (H')") +  
  theme(strip.text.x = element_text(size=14, face="bold"), strip.text.y = element_text(size=14, face="bold"), strip.background = element_rect(colour="black", fill="white", size=1)) +  
  scale_x_discrete(breaks=c("Jun-11", "Jun-12", "Jun-13"), labels=c("2011", "2012", "2013"))
```



```
ggsave("../figures/shannon.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)
```

```
## Saving 6.5 x 4.5 in image
```

Simple Hypothesis Testing - Microbes

```
#PERMANOVA Date/Plant/Management
new.data <- cbind(design, dataREL)
adonis = adonis(new.data[, -c(1:9)] ~ Block + Date * Management * Plant, method = "bray", data = new.data, perm=
adonis
```

```
##
## Call:
## adonis(formula = new.data[, -c(1:9)] ~ Block + Date * Management * Plant, data = new.data, perm=
##
## Permutation: free
## Number of permutations: 1000
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2    Pr(>F)
## Block          1   0.0783  0.078300   1.4367 0.01795 0.089910 .
## Date           2   0.4027  0.201328   3.6942 0.09233 0.000999 ***
## Management     2   0.2698  0.134918   2.4756 0.06188 0.000999 ***
## Plant          1   0.1084  0.108392   1.9889 0.02486 0.026973 *
## Date:Management 4   0.1796  0.044909   0.8241 0.04119 0.881119
```

```
## Date:Plant          2      0.1342 0.067076  1.2308 0.03076 0.137862
## Management:Plant    2      0.1323 0.066139  1.2136 0.03033 0.159840
## Date:Management:Plant 4      0.1673 0.041820  0.7674 0.03836 0.939061
## Residuals           53      2.8884 0.054498      0.66234
## Total               71      4.3609      1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Microbial Ordinations

Principal Coordinates Ordination

```
# Principal Coordinates Analysis
dataREL.dist <- vegdist(dataREL, method="bray")

pcoa <- cmdscale(dataREL.dist, k=3, eig=TRUE, add=FALSE)
# Classical (Metric) Multidimensional Scaling; returns PCoA coordinates
# eig=TRUE returns eigenvalues; k = # of dimensions to calculate

explainvar1b <- round(pcoa$eig[1] / sum(pcoa$eig), 3) * 100
explainvar2b <- round(pcoa$eig[2] / sum(pcoa$eig), 3) * 100
sum.eigb <- sum(explainvar1b, explainvar2b)

explainvar1b #23.1

## [1] 23.1
explainvar2b #9.1

## [1] 9.1

# Principal Coordinates Analysis Mgmt*Date
all.equal(rownames(design), rownames(dataREL))

## [1] TRUE

pcoa.groups <- paste(new.data$Management, new.data$Date, sep = "_")
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)

# Calculate Centroids (mean and SE)
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)

# Combine
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)

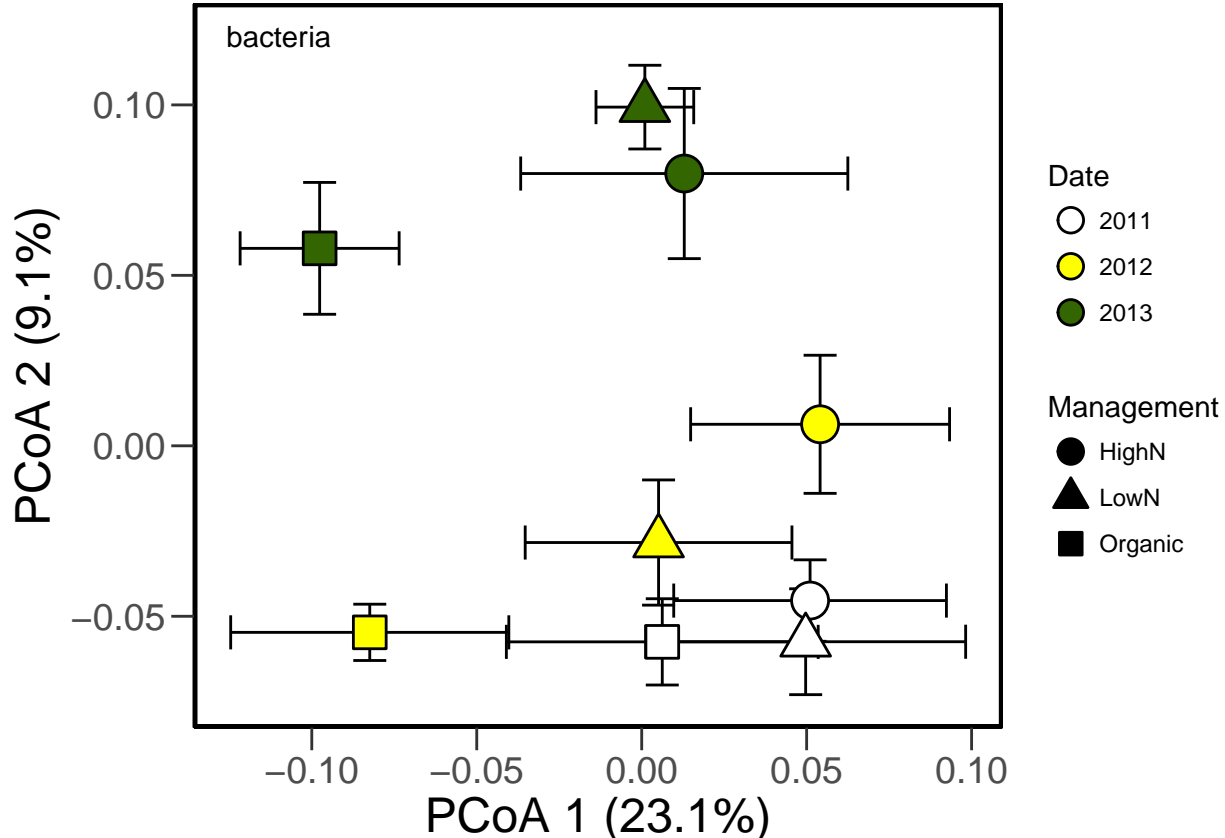
pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `\[`, 2)) # Management
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `\[`, 1)) # Date

# Principal Coordinates Analysis (Mgmt*Date)
```

```

df1a <- as.data.frame(pcoa.cent.dataframe)
plot1a <- ggplot(df1a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
  group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
plot1a + theme(panel.grid.major = element_blank(),
  panel.grid.minor = element_blank(),
  axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("2011", "2012", "2013"),
    values = c("#FFFFFF", "#FFFF00", "#336600")) +
  scale_fill_manual(labels = c("2011", "2012", "2013"),
    values = c("#FFFFFF", "#FFFF00", "#336600")) +
  scale_shape_manual(labels = c("HighN", "LowN", "Organic"),
    values = c(21, 24, 22)) +
  #coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
  theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
    axis.text.x = element_text(size=14),
    panel.border = element_rect(colour = "black", size=1.25)) +
  theme(axis.ticks.length=unit(0.3,"cm")) +
  xlab("PCoA 1 (23.1%)") + ylab("PCoA 2 (9.1%)") +
  labs(fill = "Date", shape = "Management") +
  guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
    shape = guide_legend(override.aes = list(size = 4, fill="black"))) +
  annotate("text", x = -0.11, y = 0.12, label = "bacteria")

```



```

ggsave("../figures/16SrRNA_PWES_YrMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=N

## Saving 6.5 x 4.5 in image
# Principal Coordinates Analysis (Mgmt*Plant)
all.equal(rownames(design), rownames(dataREL))

## [1] TRUE

pcoa.groups <- paste(new.data$Management, new.data$Plant, sep = "_")
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)

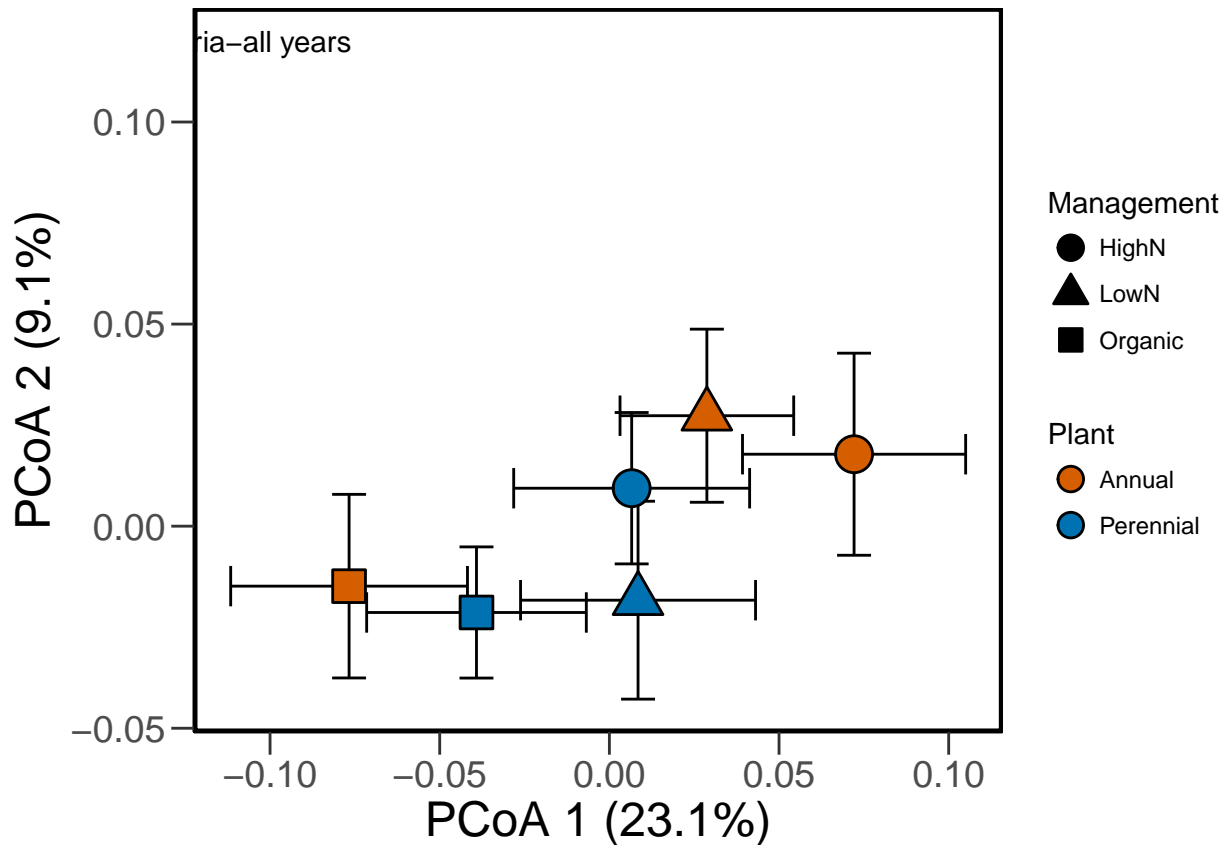
# Calculate Centroids (mean and SE)
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)

# Combine
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)

pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 2)) # Management
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 1)) # Plant

#Plot
df2a <- as.data.frame(pcoa.cent.dataframe)
plot2a <- ggplot(df2a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
                          group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
plot2a + theme(panel.grid.major = element_blank(),
               panel.grid.minor = element_blank(),
               axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("Annual", "Perennial"),
                      values = c("#D55E00", "#0072B2")) +
  scale_fill_manual(labels = c("Annual", "Perennial"),
                    values = c("#D55E00", "#0072B2")) +
  scale_shape_manual(labels = c("HighN", "LowN", "Organic"),
                     values = c(21, 24, 22)) +
  #coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
  theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
        axis.text.x = element_text(size=14),
        panel.border = element_rect(colour = "black", size=1.25)) +
  theme(axis.ticks.length=unit(0.3,"cm")) +
  xlab("PCoA 1 (23.1%)") + ylab("PCoA 2 (9.1%)") +
  labs(fill = "Plant", shape = "Management") +
  guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
         shape = guide_legend(override.aes = list(size = 4, fill="black"))) +
  annotate("text", x = -0.11, y = 0.12, label = "bacteria-all years")

```



```
ggsave("../figures/16SrRNA_PWES_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=
```

```
## Saving 6.5 x 4.5 in image
```

Principal Coordinates Ordination -BACTERIA seaprate years

```
# PERMANOVA - 2011 only
new.data.2011 <- subset(new.data, Year == 2011)
adonis.2011 = adonis(new.data.2011[, -c(1:9)] ~Block+Management*Plant, method = "bray", data = new.data.2011)
adonis.2011
```

```
##
## Call:
## adonis(formula = new.data.2011[, -c(1:9)] ~ Block + Management * Plant, data = new.data.2011, p
##
## Permutation: free
## Number of permutations: 1000
##
## Terms added sequentially (first to last)
##
##          Df SumsOfSqs  MeanSqs F.Model    R2 Pr(>F)
## Block      1   0.04654  0.046544  0.88030 0.03996 0.4695
## Management 2   0.07623  0.038117  0.72092 0.06545 0.8422
## Plant       1   0.04778  0.047775  0.90359 0.04102 0.4466
## Management:Plant 2  0.09531  0.047653  0.90127 0.08183 0.5005
## Residuals  17  0.89884  0.052873          0.77174
```

```
## Total          23    1.16469          1.00000
dataREL.dist <- vegdist(new.data.2011[, -c(1:9)], method="bray")

pcoa <- cmdscale(dataREL.dist, k=3, eig=TRUE, add=FALSE)
# Classical (Metric) Multidimensional Scaling; returns PCoA coordinates
# eig=TRUE returns eigenvalues; k = # of dimensions to calculate

explainvar1b <- round(pcoa$eig[1] / sum(pcoa$eig), 3) * 100
explainvar2b <- round(pcoa$eig[2] / sum(pcoa$eig), 3) * 100
sum.eigb <- sum(explainvar1b, explainvar2b)

explainvar1b #35.7

## [1] 35.7
explainvar2b #8.9

## [1] 8.9
# Principal Coordinates Analysis (Mgmt*Plant) - 2011 only
pcoa.groups <- paste(new.data.2011$Management, new.data.2011$Plant, sep = "_")
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)

# Calculate Centroids (mean and SE)
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)

# Combine
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)

pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 2)) # Management
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 1)) # Plant

#Plot
df8a <- as.data.frame(pcoa.cent.dataframe)
plot8a <- ggplot(df8a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
                          group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
bact.2011<- plot8a + theme(panel.grid.major = element_blank(),
                          panel.grid.minor = element_blank(),
                          axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("Annual", "Perennial"),
                      values = c("#D55E00", "#0072B2")) +
  scale_fill_manual(labels = c("Annual", "Perennial"),
                    values = c("#D55E00", "#0072B2")) +
  scale_shape_manual(labels = c("HighN", "LowN", "Organic"),
                     values = c(21, 24, 22)) +
  #coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
```

```

theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
      axis.text.x = element_text(size=14),
      panel.border = element_rect(colour = "black", size=1.25)) +
theme(axis.ticks.length=unit(0.3,"cm")) +
xlab("PCoA 1 (35.7%)") + ylab("PCoA 2 (8.9%)") +
labs(fill = "Plant", shape = "Management") +
guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
       shape = guide_legend(override.aes = list(size = 4, fill="black")))) +
annotate("text", x = -0.12, y = 0.31, label = "bacteria-2011")

ggsave("../figures/bact.2011_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=N

## Saving 6.5 x 4.5 in image

new.data.2013 <- subset(new.data, Year == 2013)
adonis.2013 = adonis(new.data.2013[, -c(1:9)] ~Block+Management*Plant, method = "bray", data = new.data.2013)
adonis.2013

##
## Call:
## adonis(formula = new.data.2013[, -c(1:9)] ~ Block + Management * Plant, data = new.data.2013, p
##
## Permutation: free
## Number of permutations: 1000
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2  Pr(>F)
## Block          1   0.08052 0.080516 1.44926 0.05650 0.090909 .
## Management      2   0.18090 0.090448 1.62803 0.12694 0.010989 *
## Plant           1   0.11567 0.115672 2.08206 0.08117 0.006993 **
## Management:Plant 2   0.10355 0.051775 0.93193 0.07266 0.547453
## Residuals      17   0.94446 0.055557           0.66274
## Total          23   1.42510           1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# PERMANOVA - 2012 only
new.data.2012 <- subset(new.data, Year == 2012)
adonis.2012 = adonis(new.data.2012[, -c(1:9)] ~Block+Management*Plant, method = "bray", data = new.data.2012)
adonis.2012

##
## Call:
## adonis(formula = new.data.2012[, -c(1:9)] ~ Block + Management * Plant, data = new.data.2012, p
##
## Permutation: free
## Number of permutations: 1000
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2  Pr(>F)
## Block          1   0.04580 0.045801 0.81911 0.03347 0.65235
## Management      2   0.19234 0.096172 1.71997 0.14055 0.03796 *
## Plant           1   0.07910 0.079096 1.41459 0.05780 0.14286
## Management:Plant 2   0.10070 0.050351 0.90050 0.07359 0.57043

```



```
## Residuals      17    0.95055 0.055915      0.69460
## Total         23    1.36850      1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

dataREL.dist <- vegdist(new.data.2012[,-c(1:9)], method="bray")

pcoa <- cmdscale(dataREL.dist, k=3, eig=TRUE, add=FALSE)
# Classical (Metric) Multidimensional Scaling; returns PCoA coordinates
# eig=TRUE returns eigenvalues; k = # of dimensions to calculate

explainvar1b <- round(pcoa$eig[1] / sum(pcoa$eig), 3) * 100
explainvar2b <- round(pcoa$eig[2] / sum(pcoa$eig), 3) * 100
sum.eigb <- sum(explainvar1b, explainvar2b)

explainvar1b #28.9

## [1] 28.9

explainvar2b #10.0

## [1] 10

# Principal Coordinates Analysis (Mgmt*Plant) - 2012 only
pcoa.groups <- paste(new.data.2012$Management, new.data.2012$Plant, sep = "_")
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)

# Calculate Centroids (mean and SE)
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)

# Combine
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)

pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 2)) # Management
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 1)) # Plant

#Plot
df9a <- as.data.frame(pcoa.cent.dataframe)
plot9a <- ggplot(df9a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
  group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
bact.2012<- plot9a + theme(panel.grid.major = element_blank(),
  panel.grid.minor = element_blank(),
  axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("Annual", "Perennial"),
    values = c("#D55E00", "#0072B2")) +
  scale_fill_manual(labels = c("Annual", "Perennial"),
    values = c("#D55E00", "#0072B2")) +
```

```

scale_shape_manual(labels = c("HighN", "LowN", "Organic"),
                    values = c(21, 24, 22)) +
#coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
      axis.text.x = element_text(size=14),
      panel.border = element_rect(colour = "black", size=1.25)) +
theme(axis.ticks.length=unit(0.3, "cm")) +
xlab("PCoA 1 (28.9%)") + ylab("PCoA 2 (10.0%)") +
labs(fill = "Plant", shape = "Management") +
guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
      shape = guide_legend(override.aes = list(size = 4, fill="black"))) +
annotate("text", x = -0.15, y = 0.31, label = "bacteria-2012")

ggsave("../figures/bact.2012_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=N

## Saving 6.5 x 4.5 in image
# PERMANOVA - 2013 only
new.data.2013 <- subset(new.data, Year == 2013)
adonis.2013 = adonis(new.data.2013[, -c(1:9)] ~ Block + Management * Plant, method = "bray", data = new.data.2013)
adonis.2013

##
## Call:
## adonis(formula = new.data.2013[, -c(1:9)] ~ Block + Management * Plant, data = new.data.2013, p
##
## Permutation: free
## Number of permutations: 1000
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2  Pr(>F)
## Block          1   0.08052 0.080516 1.44926 0.05650 0.101898
## Management     2   0.18090 0.090448 1.62803 0.12694 0.015984 *
## Plant          1   0.11567 0.115672 2.08206 0.08117 0.008991 **
## Management:Plant 2   0.10355 0.051775 0.93193 0.07266 0.554446
## Residuals     17   0.94446 0.055557          0.66274
## Total         23   1.42510          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

dataREL.dist <- vegdist(new.data.2013[, -c(1:9)], method="bray")

pcoa <- cmdscale(dataREL.dist, k=3, eig=TRUE, add=FALSE)
# Classical (Metric) Multidimensional Scaling; returns PCoA coordinates
# eig=TRUE returns eigenvalues; k = # of dimensions to calculate

explainvar1b <- round(pcoa$eig[1] / sum(pcoa$eig), 3) * 100
explainvar2b <- round(pcoa$eig[2] / sum(pcoa$eig), 3) * 100
sum.eigb <- sum(explainvar1b, explainvar2b)

explainvar1b #26.2

## [1] 26.2

```

```
explainvar2b #13.8
```

```
## [1] 13.8
```

```
# Principal Coordinates Analysis (Mgmt*Plant) - 2013 only
```

```
pcoa.groups <- paste(new.data.2013$Management, new.data.2013$Plant, sep = "_")
```

```
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)
```

```
# Calculate Centroids (mean and SE)
```

```
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
```

```
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
```

```
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
```

```
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)
```

```
# Combine
```

```
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
```

```
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
```

```
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)
```

```
pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 2)) # Management
```

```
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 1)) # Plant
```

```
#Plot
```

```
df10a <- as.data.frame(pcoa.cent.dataframe)
```

```
plot10a <- ggplot(df10a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,  
  group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
```

```
bact.2013<- plot10a + theme(panel.grid.major = element_blank(),
```

```
  panel.grid.minor = element_blank(),
```

```
  axis.line = element_line(colour = "black")) +
```

```
theme(panel.background = element_blank()) +
```

```
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
```

```
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
```

```
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
```

```
  scale_colour_manual(labels = c("Annual","Perennial"),
```

```
    values = c("#D55E00", "#0072B2")) +
```

```
  scale_fill_manual(labels = c("Annual","Perennial"),
```

```
    values = c("#D55E00", "#0072B2")) +
```

```
  scale_shape_manual(labels = c("HighN","LowN","Organic"),
```

```
    values = c(21, 24, 22)) +
```

```
#coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
```

```
theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
```

```
  axis.text.x = element_text(size=14),
```

```
  panel.border = element_rect(colour = "black", size=1.25)) +
```

```
theme(axis.ticks.length=unit(0.3,"cm")) +
```

```
xlab("PCoA 1 (26.2%)") + ylab("PCoA 2 (13.8%)") +
```

```
labs(fill = "Plant", shape = "Management") +
```

```
guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
```

```
  shape = guide_legend(override.aes = list(size = 4, fill="black")))) +
```

```
  annotate("text", x = -0.1, y = 0.31, label = "bacteria-2013")
```

```
ggsave("../figures/bact.2013_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=N
```

```
## Saving 6.5 x 4.5 in image
```

Simple Hypothesis Testing - Nematodes

```
#PERMANOVA Date/Plant/Management
str(nemaREL)
```

```
## 'data.frame': 65 obs. of 61 variables:
## $ Year : int 2011 2011 2011 2011 2011 2011 2011 2011 2011 2011 ...
## $ Micro_ID : Factor w/ 72 levels "micro-1","micro-10",...: 1 12 23 34 45 56 67 71 5 6 ...
## $ Field.ID : int 1 16 31 46 61 76 91 106 11 26 ...
## $ Date : Factor w/ 3 levels "11-Jun","12-Jun",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ Sample : Factor w/ 24 levels "1-HA1","1-HA2",...: 17 9 1 18 10 2 19 11 21 13 ...
## $ Depth : Factor w/ 1 level "0-10cm": 1 1 1 1 1 1 1 1 1 1 ...
## $ Management : Factor w/ 3 levels "HighN","LowN",...: 3 2 1 3 2 1 3 2 3 2 ...
## $ Plant : Factor w/ 2 levels "Annual","IntWheatgrass": 1 1 1 1 1 1 1 1 2 2 ...
## $ Block : int 1 1 1 2 2 2 3 3 1 1 ...
## $ Monhysteridae : num 0.0233 0 0.0201 0.0228 0.0881 ...
## $ Monhysteridae.. : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Panagrolaimus : num 0.00465 0 0.00503 0.02283 0.05031 ...
## $ Rhabditidae : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Rhabditis : num 0 0 0.0101 0.0137 0.0881 ...
## $ Dauerlarvae : num 0.0558 0 0 0.0685 0.0252 ...
## $ Mesorhabditis : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Diploscapter : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Diplogasteridae : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Acrobeles : num 0 0 0 0.06849 0.00629 ...
## $ Acrobeloides : num 0.1721 0.1393 0.1357 0.1279 0.0881 ...
## $ Chiloplacus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Cephalobidae : num 0.00465 0.01639 0.00503 0.03196 0.01887 ...
## $ Metacrolobus : num 0 0 0 0.00457 0 ...
## $ Plectus : num 0 0.0082 0.0201 0 0 ...
## $ AnaPlectus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Wilsonema : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Pristomatolaimus : num 0 0 0.00503 0.04566 0 ...
## $ Alaimus : num 0.00465 0 0.00503 0.0137 0.01887 ...
## $ Aphelenchus : num 0.1023 0.0738 0.0955 0.0228 0.044 ...
## $ Aphelenchoides : num 0 0 0 0.0457 0.0314 ...
## $ Aprutides : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Tylenchidae : num 0.335 0.082 0.397 0.1 0.27 ...
## $ Diphterophora : num 0.00465 0.03279 0.0201 0 0.00629 ...
## $ Tylencholaimus : num 0.01395 0 0 0.00913 0 ...
## $ Tylencholaimellus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Gracilacus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Paratylenchus : num 0 0.0082 0 0.0183 0 ...
## $ Pratylenchus : num 0.1163 0.4672 0.1407 0.3196 0.0629 ...
## $ Meloigogyne : num 0 0 0 0 0.00629 ...
## $ Mesocriconema : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Hopolaimus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Tylenchorhynchus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Helicotylenchus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Paratrichodorus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Xiphinema : num 0 0.01639 0.00503 0 0 ...
## $ Chromadoridae : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Achromadora : num 0 0 0 0 0 ...
```

```
## $ Dorylaimidae : num 0.1163 0.1148 0.0804 0.0502 0.1761 ...
## $ Qudsianematidae : num 0 0 0.0101 0 0 ...
## $ Thornematidae : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Aporcelaimidae : num 0.0186 0.03279 0.04523 0.00457 0.01258 ...
## $ Mesodorylaimus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Tripyla : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Tripylina : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Mylonchulus : num 0.00465 0 0 0 0 ...
## $ Mononchus : num 0.02326 0.0082 0 0.00913 0.00629 ...
## $ Clarkus : num 0 0 0 0 0 ...
## $ Mononchidae : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Granonchulus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Anatonchus : num 0 0 0 0 0 0 0 0 0 0 ...
## $ Discolaimus : num 0 0 0 0 0 ...
```

```
adonis2 = adonis(nemaREL[, -c(1:9)] ~ Block + Date * Management * Plant, method = "bray", data = nemaREL, perm=
adonis2
```

```
##
## Call:
## adonis(formula = nemaREL[, -c(1:9)] ~ Block + Date * Management *      Plant, data = nemaREL, permut=
##
## Permutation: free
## Number of permutations: 1000
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2    Pr(>F)
## Block          1    0.1843 0.18426  2.1896 0.02731 0.026973 *
## Date            2    0.9286 0.46428  5.5170 0.13761 0.000999 ***
## Management      2    0.4542 0.22708  2.6983 0.06731 0.000999 ***
## Plant           1    0.4169 0.41694  4.9544 0.06179 0.000999 ***
## Date:Management  4    0.1756 0.04391  0.5218 0.02603 0.990010
## Date:Plant       2    0.2199 0.10997  1.3068 0.03260 0.168831
## Management:Plant  2    0.2650 0.13251  1.5746 0.03928 0.069930 .
## Date:Management:Plant 4    0.2319 0.05798  0.6889 0.03437 0.932068
## Residuals       46    3.8711 0.08416          0.57371
## Total           64    6.7476          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Nematode Ordinations

Principal Coordinates Ordination

```
# Principal Coordinates Analysis - all years
dataREL.dist <- vegdist(dataRELnema, method="bray")

pcoa <- cmdscale(dataREL.dist, k=3, eig=TRUE, add=FALSE)
# Classical (Metric) Multidimensional Scaling; returns PCoA coordinates
# eig=TRUE returns eigenvalues; k = # of dimensions to calculate

explainvar1b <- round(pcoa$eig[1] / sum(pcoa$eig), 3) * 100
```

```

explainvar2b <- round(pcoa$eig[2] / sum(pcoa$eig), 3) * 100
sum.eigb <- sum(explainvar1b, explainvar2b)

explainvar1b #19.8

## [1] 19.8

explainvar2b #18.3

## [1] 18.3

# Principal Coordinates Analysis Mgmt*Date
pcoa.groups <- paste(nemaREL$Management, nemaREL$Date, sep = "_")
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)

# Calculate Centroids (mean and SE)
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)

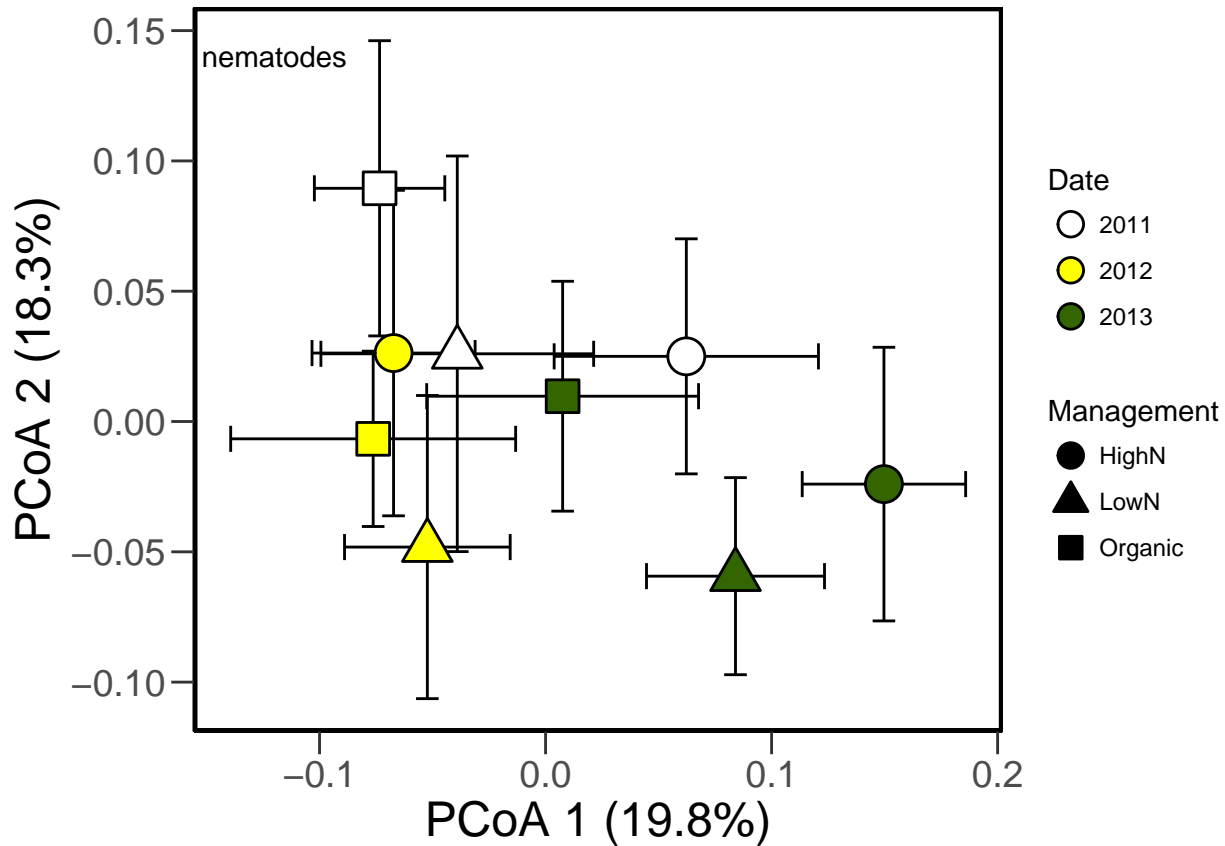
# Combine
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)

pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 2)) # Management
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 1)) # Date

# Principal Coordinates Analysis (Mgmt*Date)
df3a <- as.data.frame(pcoa.cent.dataframe)
plot3a <- ggplot(df3a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
  group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
plot3a + theme(panel.grid.major = element_blank(),
  panel.grid.minor = element_blank(),
  axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("2011", "2012", "2013"),
    values = c("#FFFFFF", "#FFFF00", "#336600")) +
  scale_fill_manual(labels = c("2011", "2012", "2013"),
    values = c("#FFFFFF", "#FFFF00", "#336600")) +
  scale_shape_manual(labels = c("HighN", "LowN", "Organic"),
    values = c(21, 24, 22)) +
  #coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
  theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
    axis.text.x = element_text(size=14),
    panel.border = element_rect(colour = "black", size=1.25)) +
  theme(axis.ticks.length=unit(0.3,"cm")) +
  xlab("PCoA 1 (19.8%)") + ylab("PCoA 2 (18.3%)") +
  labs(fill = "Date", shape = "Management") +
  guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
    shape = guide_legend(override.aes = list(size = 4, fill="black"))) +

```

```
annotate("text", x = -0.12, y = 0.14, label = "nematodes")
```



```
ggsave("../figures/nema_PWES_YrMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)
```

```
## Saving 6.5 x 4.5 in image
```

```
# Principal Coordinates Analysis (Mgmt*Plant)
```

```
pcoa.groups <- paste(nemaREL$Management, nemaREL$Plant, sep = "_")
```

```
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)
```

```
# Calculate Centroids (mean and SE)
```

```
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
```

```
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
```

```
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
```

```
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)
```

```
# Combine
```

```
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
```

```
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
```

```
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)
```

```
pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 2)) # Management
```

```
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 1)) # Plant
```

```
#Plot
```

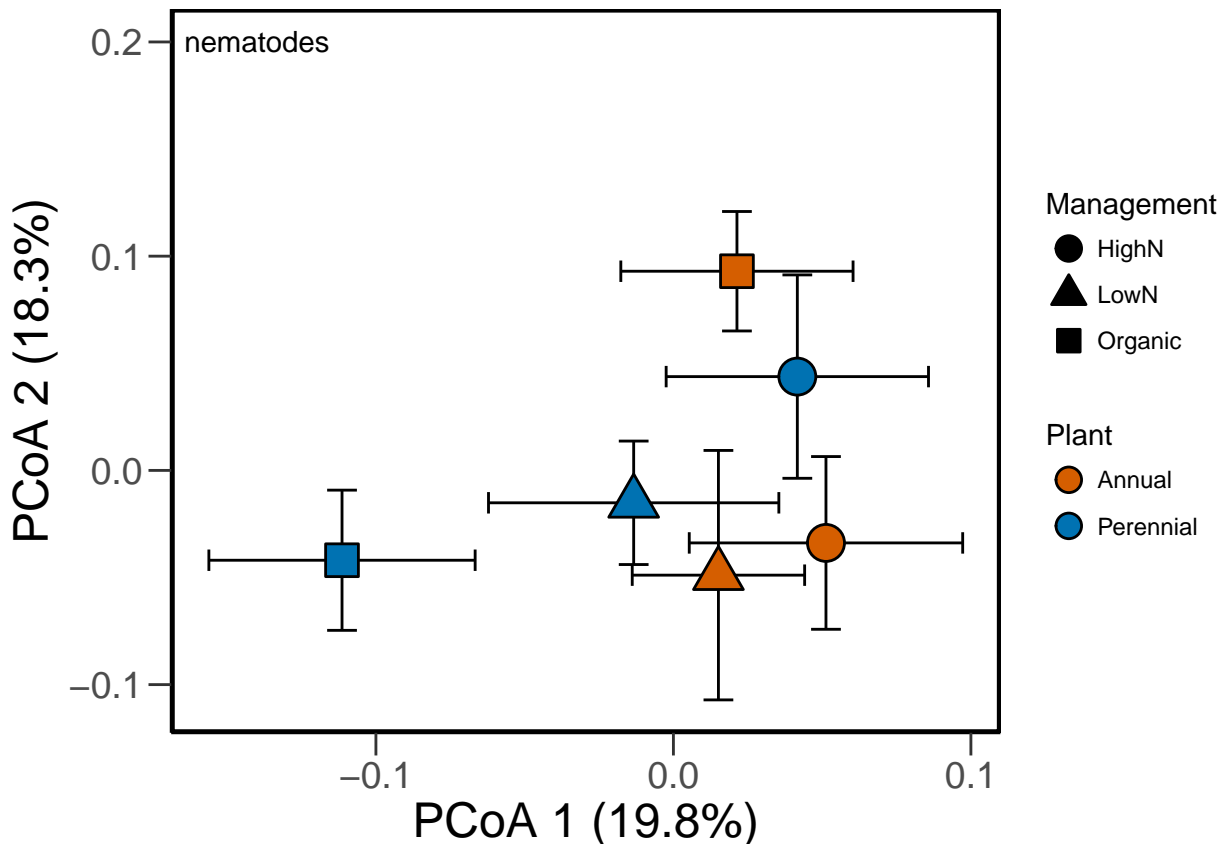
```
df4a <- as.data.frame(pcoa.cent.dataframe)
```

```
plot4a <- ggplot(df4a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
```

```

group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
plot4a + theme(panel.grid.major = element_blank(),
  panel.grid.minor = element_blank(),
  axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("Annual","Perennial"),
    values = c("#D55E00", "#0072B2")) +
  scale_fill_manual(labels = c("Annual","Perennial"),
    values = c("#D55E00", "#0072B2")) +
  scale_shape_manual(labels = c("HighN","LowN","Organic"),
    values = c(21, 24, 22)) +
  #coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
  theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
    axis.text.x = element_text(size=14),
    panel.border = element_rect(colour = "black", size=1.25)) +
  theme(axis.ticks.length=unit(0.3,"cm")) +
  xlab("PCoA 1 (19.8%)") + ylab("PCoA 2 (18.3%)") +
  labs(fill = "Plant", shape = "Management") +
  guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
    shape = guide_legend(override.aes = list(size = 4, fill="black"))) +
  annotate("text", x = -0.14, y = 0.2, label = "nematodes")

```




```
ggsave("../figures/nema_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)
```

```
## Saving 6.5 x 4.5 in image
```

Principal Coordinates Ordination - NEMATODES seaparate years

```
nemaREL.2011 <- subset(nemaREL, Year == 2011)
dim(nemaREL)
```

```
## [1] 65 61
```

```
dim(nemaREL.2011)
```

```
## [1] 17 61
```

```
# PERMANOVA - 2011 only
```

```
adonis(nemaREL.2011[, -c(1:9)] ~ Block + Management * Plant, data=nemaREL.2011)
```

```
##
```

```
## Call:
```

```
## adonis(formula = nemaREL.2011[, -c(1:9)] ~ Block + Management * Plant, data = nemaREL.2011)
```

```
##
```

```
## Permutation: free
```

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

```
##
```

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

```
##
```

```
##
```

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
|---------------------|----|-----------|----------|---------|---------|--------|
| ## Block | 1 | 0.14772 | 0.147722 | 1.64279 | 0.09953 | 0.110 |
| ## Management | 2 | 0.16951 | 0.084756 | 0.94256 | 0.11421 | 0.508 |
| ## Plant | 1 | 0.16219 | 0.162185 | 1.80362 | 0.10928 | 0.082 |
| ## Management:Plant | 2 | 0.10552 | 0.052761 | 0.58675 | 0.07110 | 0.899 |
| ## Residuals | 10 | 0.89922 | 0.089922 | | 0.60588 | |
| ## Total | 16 | 1.48416 | | | 1.00000 | |

```
## ---
```

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

```
dataREL.dist <- vegdist(nemaREL.2011[, -c(1:9)], method="bray")
```

```
pcoa <- cmdscale(dataREL.dist, k=3, eig=TRUE, add=FALSE)
```

```
# Classical (Metric) Multidimensional Scaling; returns PCoA coordinates
```

```
# eig=TRUE returns eigenvalues; k = # of dimensions to calculate
```

```
explainvar1b <- round(pcoa$eig[1] / sum(pcoa$eig), 3) * 100
```

```
explainvar2b <- round(pcoa$eig[2] / sum(pcoa$eig), 3) * 100
```

```
sum.eigb <- sum(explainvar1b, explainvar2b)
```

```
explainvar1b #28.6
```

```
## [1] 28.6
```

```
explainvar2b #22.0
```

```
## [1] 22
```

```

# Principal Coordinates Analysis (Mgmt*Plant) - 2011 only
pcoa.groups <- paste(nemaREL.2011$Management, nemaREL.2011$Plant, sep = "_")
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)

# Calculate Centroids (mean and SE)
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)

# Combine
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)

pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 2)) # Management
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 1)) # Plant

#Plot
df7a <- as.data.frame(pcoa.cent.dataframe)
plot7a <- ggplot(df7a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
                          group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
nema.2011<- plot7a + theme(panel.grid.major = element_blank(),
                          panel.grid.minor = element_blank(),
                          axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("Annual", "Perennial"),
                      values = c("#D55E00", "#0072B2")) +
  scale_fill_manual(labels = c("Annual", "Perennial"),
                    values = c("#D55E00", "#0072B2")) +
  scale_shape_manual(labels = c("HighN", "LowN", "Organic"),
                     values = c(21, 24, 22)) +
#coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
      axis.text.x = element_text(size=14),
      panel.border = element_rect(colour = "black", size=1.25)) +
theme(axis.ticks.length=unit(0.3,"cm")) +
xlab("PCoA 1 (28.6%)") + ylab("PCoA 2 (22.0%)") +
labs(fill = "Plant", shape = "Management") +
guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
       shape = guide_legend(override.aes = list(size = 4, fill="black"))) +
annotate("text", x = -0.15, y = 0.31, label = "nematodes-2011")

ggsave("../figures/nema.2011_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=N

## Saving 6.5 x 4.5 in image
nemaREL.2012 <- subset(nemaREL, Year == 2012)
dim(nemaREL)

## [1] 65 61

```

```

dim(nemaREL.2012)

## [1] 24 61

# PERMANOVA - 2012 only
adonis(nemaREL.2012[, -c(1:9)] ~ Block + Management * Plant, data = nemaREL.2012)

##
## Call:
## adonis(formula = nemaREL.2012[, -c(1:9)] ~ Block + Management * Plant, data = nemaREL.2012)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Block          1   0.18669 0.186692 2.07835 0.08561 0.036 *
## Management     2   0.15376 0.076880 0.85587 0.07050 0.647
## Plant          1   0.15116 0.151159 1.68277 0.06931 0.101
## Management:Plant 2   0.16217 0.081086 0.90269 0.07436 0.592
## Residuals     17   1.52706 0.089827          0.70022
## Total         23   2.18084          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

dataREL.dist <- vegdist(nemaREL.2012[, -c(1:9)], method = "bray")

pcoa <- cmdscale(dataREL.dist, k = 3, eig = TRUE, add = FALSE)
# Classical (Metric) Multidimensional Scaling; returns PCoA coordinates
# eig = TRUE returns eigenvalues; k = # of dimensions to calculate

explainvar1b <- round(pcoa$eig[1] / sum(pcoa$eig), 3) * 100
explainvar2b <- round(pcoa$eig[2] / sum(pcoa$eig), 3) * 100
sum.eigb <- sum(explainvar1b, explainvar2b)

explainvar1b #25.8

## [1] 25.8

explainvar2b #17.6

## [1] 17.6

# Principal Coordinates Analysis (Mgmt*Plant) - 2012 only
pcoa.groups <- paste(nemaREL.2012$Management, nemaREL.2012$Plant, sep = "_")
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)

# Calculate Centroids (mean and SE)
pcoa.L.centroids <- melt(pcoa.points, id = "group", measure.vars = c("X1", "X2"))
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)

# Combine
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")

```

```

pcoa.cent.treats <- rownames(pcoa.cent.dataframe)

pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `\[`, 2)) # Management
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `\[`, 1)) # Plant

#Plot
df6a <- as.data.frame(pcoa.cent.dataframe)
plot6a <- ggplot(df6a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
                          group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
nema.2012<- plot6a + theme(panel.grid.major = element_blank(),
                          panel.grid.minor = element_blank(),
                          axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("Annual","Perennial"),
                      values = c("#D55E00", "#0072B2")) +
  scale_fill_manual(labels = c("Annual","Perennial"),
                    values = c("#D55E00", "#0072B2")) +
  scale_shape_manual(labels = c("HighN","LowN","Organic"),
                     values = c(21, 24, 22)) +
  #coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
  theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
        axis.text.x = element_text(size=14),
        panel.border = element_rect(colour = "black", size=1.25)) +
  theme(axis.ticks.length=unit(0.3,"cm")) +
  xlab("PCoA 1 (25.8%)") + ylab("PCoA 2 (17.6%)") +
  labs(fill = "Plant", shape = "Management") +
  guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
         shape = guide_legend(override.aes = list(size = 4, fill="black"))) +
  annotate("text", x = -0.15, y = 0.31, label = "nematodes-2012")

ggsave("../figures/nema.2012_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=N

## Saving 6.5 x 4.5 in image
nemaREL.2013 <- subset(nemaREL, Year == 2013)

# PERMANOVA - 2013 only
adonis(nemaREL.2013[, -c(1:9)] ~ Block + Management * Plant, data=nemaREL.2013)

##
## Call:
## adonis(formula = nemaREL.2013[, -c(1:9)] ~ Block + Management * Plant, data = nemaREL.2013)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Block          1   0.14070 0.14070   2.0469 0.06525  0.054 .
## Management     2   0.31947 0.15973   2.3238 0.14815  0.008 **

```

```
## Plant          1    0.30920 0.30920  4.4981 0.14338  0.001 ***
## Management:Plant 2    0.21851 0.10925  1.5894 0.10133  0.074 .
## Residuals      17    1.16858 0.06874          0.54190
## Total          23    2.15646          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

dataREL.dist <- vegdist(nemaREL.2013[,-c(1:9)], method="bray")

pcoa <- cmdscale(dataREL.dist, k=3, eig=TRUE, add=FALSE)
# Classical (Metric) Multidimensional Scaling; returns PCoA coordinates
# eig=TRUE returns eigenvalues; k = # of dimensions to calculate

explainvar1b <- round(pcoa$eig[1] / sum(pcoa$eig), 3) * 100
explainvar2b <- round(pcoa$eig[2] / sum(pcoa$eig), 3) * 100
sum.eigb <- sum(explainvar1b, explainvar2b)

explainvar1b #27.0

## [1] 27
explainvar2b #24.2

## [1] 24.2

# Principal Coordinates Analysis (Mgmt*Plant) - 2013 only
pcoa.groups <- paste(nemaREL.2013$Management, nemaREL.2013$Plant, sep = "_")
pcoa.points <- data.frame(pcoa$points, group = pcoa.groups)

# Calculate Centroids (mean and SE)
pcoa.L.centroids <- melt(pcoa.points, id="group", measure.vars = c("X1", "X2"))
pcoa.centroids <- acast(pcoa.L.centroids, variable ~ group, mean)
pcoa.centroids.se <- acast(pcoa.L.centroids, variable ~ group, se)
pcoa.centroids.sd <- acast(pcoa.L.centroids, variable ~ group, sd)

# Combine
pcoa.cent.dataframe <- cbind(t(pcoa.centroids), t(pcoa.centroids.se))
colnames(pcoa.cent.dataframe) <- c("V1", "V2", "V1e", "V2e")
pcoa.cent.treats <- rownames(pcoa.cent.dataframe)

pcoa.col <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 2)) # Management
pcoa.shape <- as.factor(sapply(strsplit(pcoa.cent.treats, "_"), `[`, 1)) # Plant

#Plot
df5a <- as.data.frame(pcoa.cent.dataframe)
plot5a <- ggplot(df5a, aes(x=V1, y=V2, colour=pcoa.col, shape = pcoa.shape,
  group = interaction(pcoa.col, pcoa.shape))) + theme_bw()
nema.2013<- plot5a + theme(panel.grid.major = element_blank(),
  panel.grid.minor = element_blank(),
  axis.line = element_line(colour = "black")) +
theme(panel.background = element_blank()) +
  geom_errorbarh(aes(xmax=V1+V1e, xmin=V1-V1e, height=0.01), colour="black") +
  geom_errorbar(aes(ymax=V2+V2e, ymin=V2-V2e, width=0.01), colour="black") +
  geom_point(aes(fill=pcoa.col), colour = "black", size=6, stroke = 0.75) +
  scale_colour_manual(labels = c("Annual", "Perennial"),
    values = c("#D55E00", "#0072B2")) +
```

```

scale_fill_manual(labels = c("Annual","Perennial"),
                  values = c("#D55E00", "#0072B2")) +
scale_shape_manual(labels = c("HighN","LowN","Organic"),
                  values = c(21, 24, 22)) +
#coord_cartesian(xlim = c(-0.25, 0.5), ylim = c(-0.35, 0.3)) +
theme(axis.title = element_text(size=18), axis.text=element_text(size=14),
      axis.text.x = element_text(size=14),
      panel.border = element_rect(colour = "black", size=1.25)) +
theme(axis.ticks.length=unit(0.3,"cm")) +
xlab("PCoA 1 (27.0%)") + ylab("PCoA 2 (24.2%)") +
labs(fill = "Plant", shape = "Management") +
guides(fill = guide_legend(override.aes = list(pch=21, size = 4, colour="black")),
       shape = guide_legend(override.aes = list(size = 4, fill="black"))) +
annotate("text", x = -0.1, y = 0.31, label = "nematodes-2013")

ggsave("../figures/nema.2013_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=N
## Saving 6.5 x 4.5 in image

```

Bacterial community indicator species analysis 2013 only - plant

```

new.data <- cbind(design,dataREL)
library("labdsv")

## Loading required package: mgcv
## This is mgcv 1.8-23. For overview type 'help("mgcv-package")'.
## Loading required package: MASS
##
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##   select
## Loading required package: cluster
##
## Attaching package: 'labdsv'
## The following object is masked from 'package:stats':
##
##   density
new.data.2013 <- subset(new.data, Year == 2013)
design.type <- new.data.2013$Plant
dataREL.2013 <- new.data.2013[,-c(1:9)]

dataREL <- dataREL.2013[, colSums(dataREL.2013) > 0.05]
bac.ind <- indval(dataREL, design.type)
levels(design.type)

## [1] "Annual"          "IntWheatgrass"

```

```
summary(bac.ind)
```

```
##           cluster indicator_value probability
## Otu00034      1           0.5811         0.020
## Otu00028      1           0.5741         0.023
## Otu00015      1           0.5722         0.003
## Otu00011      1           0.5694         0.007
## Otu00054      1           0.5690         0.012
## Otu00044      1           0.5672         0.037
## Otu00005      1           0.5628         0.003
## Otu00048      1           0.5433         0.025
## Otu00029      1           0.5289         0.030
## Otu00050      2           0.6347         0.002
## Otu00062      2           0.5830         0.002
## Otu00022      2           0.5644         0.010
##
## Sum of probabilities                = 21.494
##
## Sum of Indicator Values              = 28.81
##
## Sum of Significant Indicator Values  = 6.85
##
## Number of Significant Indicators     = 12
##
## Significant Indicator Distribution
##
## 1 2
## 9 3
```

```
inds <- which(bac.ind$pval <= 0.05)
bac.indicators <- as.data.frame(matrix(NA, nrow = length(inds), ncol = 4))
colnames(bac.indicators) <- c("OTU", "Cluster", "IndVal", "Prob")

bac.indicators$OTU <- names(inds)
bac.indicators$Cluster <- bac.ind$maxcls[inds]
bac.indicators$IndVal <- bac.ind$indcls[inds]
bac.indicators$Prob <- bac.ind$pval[inds]

ind.tax <- otu.tax[which(as.character(otu.tax$OTU) %in% bac.indicators$OTU), ]
ind.tax <- ind.tax[match(ind.tax$OTU, bac.indicators$OTU), ]

indicator.bac <- cbind(bac.indicators, ind.tax[, -c(1)])

indicator.bac <- indicator.bac[order(as.numeric(indicator.bac$Cluster)), ]

table(indicator.bac$Cluster)

##
## 1 2
## 9 3

table(indicator.bac$Phylum)
```

```
##
## Acidobacteria Actinobacteria Firmicutes Gemmatimonadetes
```

```

##           1           4           1           1
## Proteobacteria
##           5
table(indicator.bac$Cluster)

##
## 1 2
## 9 3
levels(design.type)

## [1] "Annual"      "IntWheatgrass"
# Export Bacteria Indicator Table
write.table(indicator.bac, "../data/BacterialIndicators_Plant.txt",
            sep="\t", row.names = F, quote = F)

#bac.ind - by management
design.type <- design$Management

dataREL <- dataREL.2013[, colSums(dataREL.2013) > 0.05]
bac.ind <- indval(dataREL, design.type)
levels(design.type)

## [1] "HighN"      "LowN"      "Organic"
summary(bac.ind)

##      cluster indicator_value probability
## Otu00008      3          0.1343      0.003
## Otu00022      3          0.1341      0.008
## Otu00007      3          0.1310      0.035
## Otu00016      3          0.1263      0.004
##
## Sum of probabilities              = 19.547
##
## Sum of Indicator Values           = 6.66
##
## Sum of Significant Indicator Values = 0.53
##
## Number of Significant Indicators   = 4
##
## Significant Indicator Distribution
##
## 3
## 4
inds <- which(bac.ind$pval <= 0.05)
bac.indicators <- as.data.frame(matrix(NA, nrow = length(inds), ncol = 4))
colnames(bac.indicators) <- c("OTU", "Cluster", "IndVal", "Prob")

bac.indicators$OTU <- names(inds)
bac.indicators$Cluster <- bac.ind$maxcls[inds]
bac.indicators$IndVal <- bac.ind$indcls[inds]
bac.indicators$Prob <- bac.ind$pval[inds]

```



```

ind.tax <- otu.tax[which(as.character(otu.tax$OTU) %in% bac.indicators$OTU), ]
ind.tax <- ind.tax[match(ind.tax$OTU, bac.indicators$OTU), ]

indicator.bac <- cbind(bac.indicators, ind.tax[, -c(1)])

indicator.bac <- indicator.bac[order(as.numeric(indicator.bac$Cluster)), ]

table(indicator.bac$Cluster)

##
## 3
## 4

table(indicator.bac$Phylum)

##
##  Acidobacteria Proteobacteria
##           1           3

table(indicator.bac$Cluster)

##
## 3
## 4

levels(design.type)

## [1] "HighN" "LowN" "Organic"
# Export Bacteria Indicator Table
write.table(indicator.bac, "../data/BacterialIndicators_Mgmt.txt",
            sep="\t", row.names = F, quote = F)

```

Nematode community indicator species analysis 2013 only - plant and mgmt

```

nemaREL <- cbind(nema.design, dataRELnema)
library("labdsv")

new.data.2013 <- subset(nemaREL, Year == 2013)
design.type <- new.data.2013$Plant
dataREL.2013 <- new.data.2013[, -c(1:9)]

dataREL <- dataREL.2013[, colSums(dataREL.2013) > 0.05]
nema.ind <- indval(dataREL, design.type)
levels(design.type)

## [1] "Annual" "IntWheatgrass"

summary(nema.ind)

##           cluster indicator_value probability
## Aphelenchus      1           0.7878         0.001
## Paratylenchus     1           0.6953         0.007
## Pratylenchus      1           0.6526         0.010

```

```

## Plectus                2            0.9385      0.001
## Monhysteridae          2            0.7899      0.001
##
## Sum of probabilities                = 6.689
##
## Sum of Indicator Values              = 11.11
##
## Sum of Significant Indicator Values  = 3.86
##
## Number of Significant Indicators     = 5
##
## Significant Indicator Distribution
##
## 1 2
## 3 2

inds <- which(nema.ind$pval <= 0.05)
nema.indicators <- as.data.frame(matrix(NA, nrow = length(inds), ncol = 4))
colnames(nema.indicators) <- c("taxa", "Cluster", "IndVal", "Prob")

nema.indicators$taxa <- names(inds)
nema.indicators$Cluster <- nema.ind$maxcls[inds]
nema.indicators$IndVal <- nema.ind$indcls[inds]
nema.indicators$Prob <- nema.ind$pval[inds]

#ind.tax <- otu.tax[which(as.character(otu.tax$OTU) %in% bac.indicators$OTU), ]
#ind.tax <- ind.tax[match(ind.tax$OTU, bac.indicators$OTU), ]
#indicator.bac <- cbind(bac.indicators, ind.tax[, -c(1)])

indicators <- nema.indicators[order(as.numeric(nema.indicators$Cluster)), ]

table(indicators$Cluster)

##
## 1 2
## 3 2

table(indicators$taxa)

##
## Aphelenchus Monhysteridae Paratylenchus Plectus Pratylenchus
## 1 1 1 1 1

table(indicators$Cluster)

##
## 1 2
## 3 2

levels(design.type)

## [1] "Annual" "IntWheatgrass"

# Export Nematod Indicator Table
write.table(indicators, "../data/NemaIndicators_Plant.txt",
            sep="\t", row.names = F, quote = F)

#nema.ind - by management

```

```

design.type <- new.data.2013$Management
dataREL.2013 <- new.data.2013[, -c(1:9)]

dataREL <- dataREL.2013[, colSums(dataREL.2013) > 0.05]
nema.ind <- indval(dataREL, design.type)
levels(design.type)

## [1] "HighN"    "LowN"     "Organic"
summary(nema.ind)

##              cluster indicator_value probability
## Dauerlarvae          3           0.9316      0.001
## Qudsianematidae       3           0.4711      0.048
##
## Sum of probabilities                = 9.423
##
## Sum of Indicator Values              = 8.58
##
## Sum of Significant Indicator Values  = 1.4
##
## Number of Significant Indicators     = 2
##
## Significant Indicator Distribution
##
## 3
## 2

inds <- which(nema.ind$pval <= 0.05)
nema.indicators <- as.data.frame(matrix(NA, nrow = length(inds), ncol = 4))
colnames(nema.indicators) <- c("taxa", "Cluster", "IndVal", "Prob")

nema.indicators$taxa <- names(inds)
nema.indicators$Cluster <- nema.ind$maxcls[inds]
nema.indicators$IndVal <- nema.ind$indcls[inds]
nema.indicators$Prob <- nema.ind$pval[inds]

indicators <- nema.indicators[order(as.numeric(nema.indicators$Cluster)), ]

table(indicators$Cluster)

##
## 3
## 2

table(indicators$taxa)

##
## Dauerlarvae Qudsianematidae
##           1           1

table(indicators$Cluster)

##
## 3
## 2

```

```
levels(design.type)

## [1] "HighN"    "LowN"     "Organic"
# Export Nematod Indicator Table
write.table(indicators, "../data/NemaIndicators_Plant.txt",
            sep="\t", row.names = F, quote = F)
```