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

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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 occurences 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

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

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

```r
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

```r
# First check the order
length(design$Management) == length(fisher)
```

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

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

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

```r
library(lme4)
```

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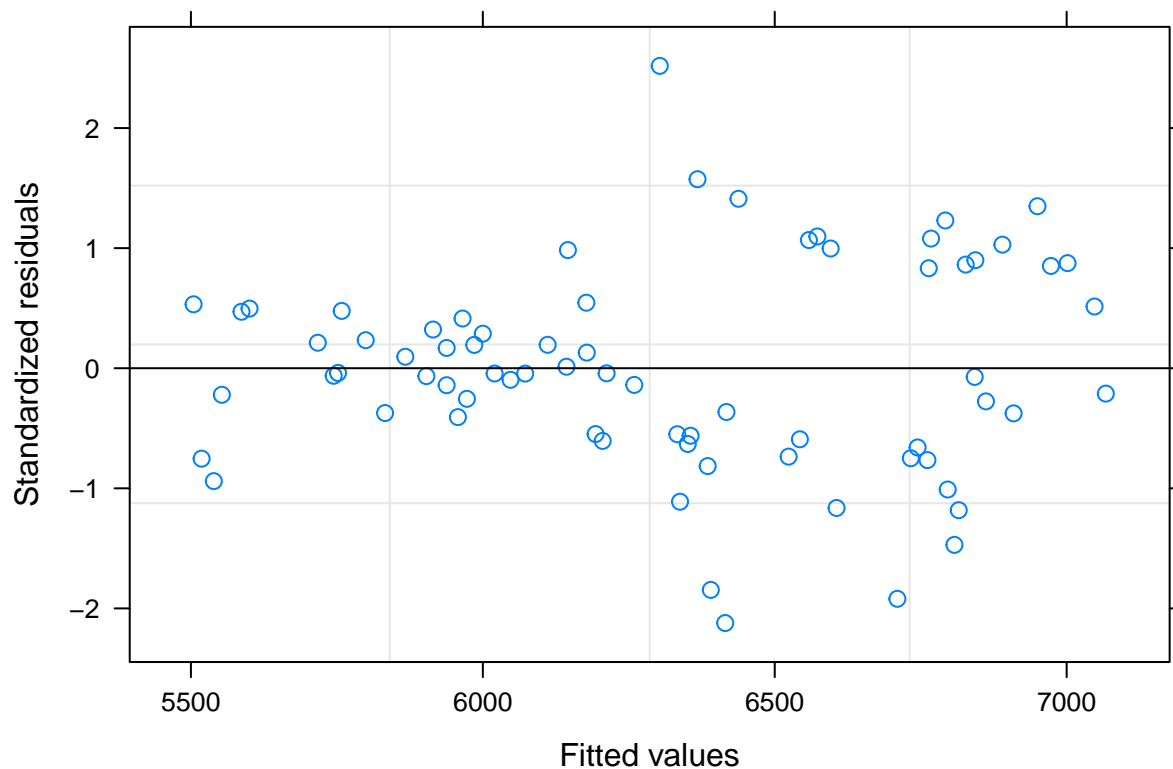
```
## Loading required package: Matrix
```

```
##
## 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
```

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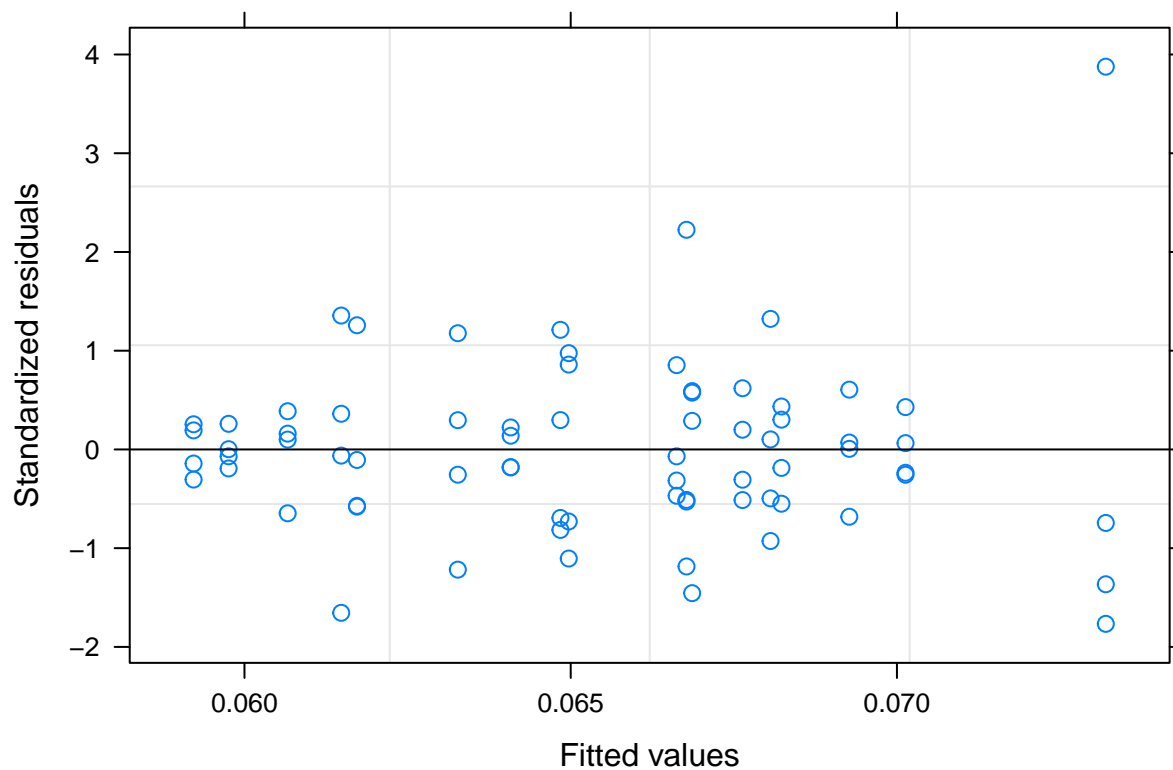


```r
richness.lm
```

```
## Linear mixed-effects model fit by REML
##   Data: diversity
##   Log-restricted-likelihood: -436.9514
##   Fixed: richness ~ Date * Management * Plant
##                                  (Intercept)
##                                      5607.50
##                                    DateJun-12
##                                       419.75
##                                    DateJun-13
##                                       814.75
##                                ManagementLowN
##                                       -13.75
##                             ManagementOrganic
##                                       447.00
##                             PlantIntWheatgrass
```

```
##                                              385.00
##                       DateJun-12:ManagementLowN
##                                              378.75
##                       DateJun-13:ManagementLowN
##                                              488.50
##                    DateJun-12:ManagementOrganic
##                                             -207.75
##                    DateJun-13:ManagementOrganic
##                                              -18.50
##                  DateJun-12:PlantIntWheatgrass
##                                              200.75
##                  DateJun-13:PlantIntWheatgrass
##                                             -607.00
##              ManagementLowN:PlantIntWheatgrass
##                                             -172.25
##           ManagementOrganic:PlantIntWheatgrass
##                                             -517.75
##     DateJun-12:ManagementLowN:PlantIntWheatgrass
##                                             -360.75
##     DateJun-13:ManagementLowN:PlantIntWheatgrass
##                                              413.50
## DateJun-12:ManagementOrganic:PlantIntWheatgrass
##                                              464.75
## DateJun-13:ManagementOrganic:PlantIntWheatgrass
##                                              711.25
##
## Random effects:
##  Formula: ~1 | Block
##         (Intercept) Residual
## StdDev:    148.2683  615.123
##
## Number of Observations: 72
## Number of Groups: 4
```

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

```
##                      numDF denDF  F-value p-value
## (Intercept)              1    51 3706.609  <.0001
## Date                     2    51   12.190  <.0001
## Management               2    51    1.551  0.2218
## Plant                    1    51    1.159  0.2867
## Date:Management          4    51    0.689  0.6026
## Date:Plant               2    51    0.866  0.4265
## Management:Plant         2    51    0.107  0.8985
## Date:Management:Plant    4    51    0.401  0.8069
```

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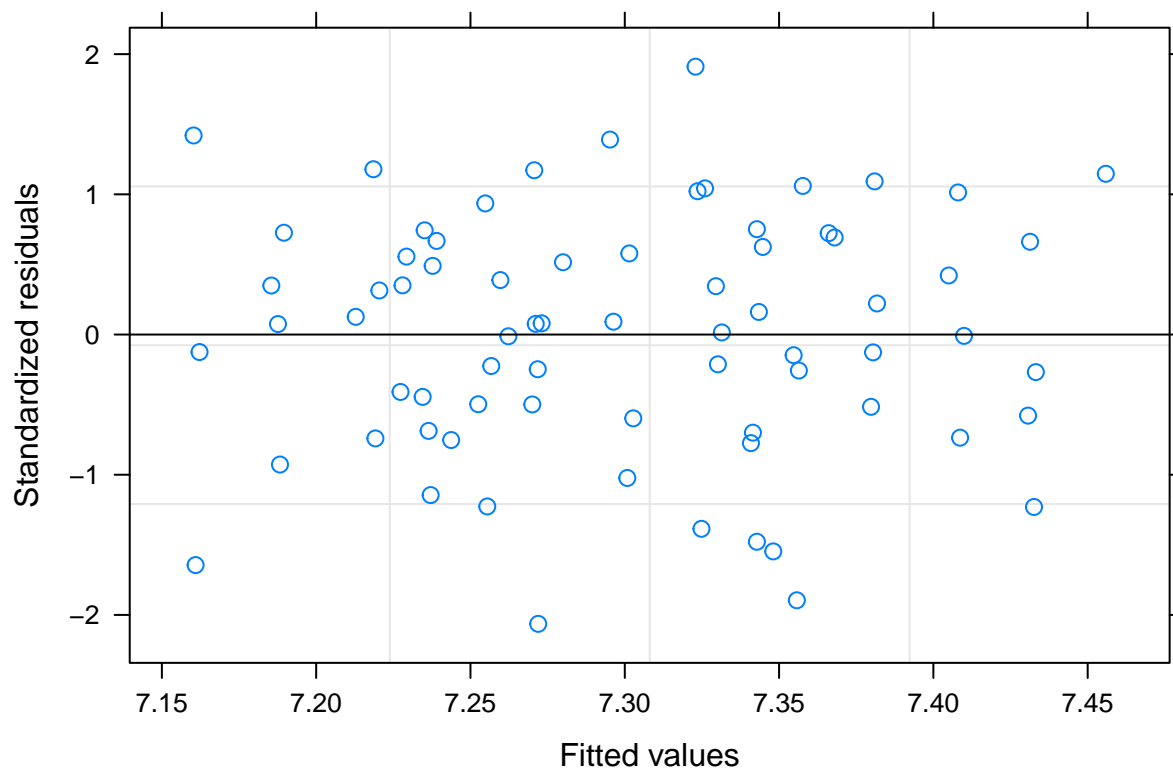
```
evenness.lm
```

```
## Linear mixed-effects model fit by REML
##   Data: diversity
##   Log-restricted-likelihood: 174.6814
##   Fixed: simp.even ~ Date * Management * Plant
##                              (Intercept)
##                             0.0680624888
##                                DateJun-12
##                             -0.0047926294
##                                DateJun-13
##                             -0.0083052977
##                            ManagementLowN
##                             -0.0004288674
##                         ManagementOrganic
##                             -0.0074000381
##                         PlantIntWheatgrass
##                             0.0020689074
##            DateJun-12:ManagementLowN
##                             -0.0013579755
##            DateJun-13:ManagementLowN
##                             -0.0001080651
##         DateJun-12:ManagementOrganic
##                             0.0107535048
##         DateJun-13:ManagementOrganic
##                             0.0124854419
##       DateJun-12:PlantIntWheatgrass
##                             -0.0036142818
##       DateJun-13:PlantIntWheatgrass
##                             0.0113744274
```

```
##           ManagementLowN:PlantIntWheatgrass
##                            -0.0028413179
##         ManagementOrganic:PlantIntWheatgrass
##                             0.0054982929
##     DateJun-12:ManagementLowN:PlantIntWheatgrass
##                             0.0096783773
##     DateJun-13:ManagementLowN:PlantIntWheatgrass
##                            -0.0057424623
## DateJun-12:ManagementOrganic:PlantIntWheatgrass
##                            -0.0056061485
## DateJun-13:ManagementOrganic:PlantIntWheatgrass
##                            -0.0145145032
##
## Random effects:
##  Formula: ~1 | Block
##         (Intercept)    Residual
## StdDev: 3.29331e-07 0.007560427
##
## Number of Observations: 72
## Number of Groups: 4
```

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

```
##                        numDF denDF  F-value p-value
## (Intercept)                1    51 5383.906  <.0001
## Date                       2    51    0.848  0.4342
## Management                 2    51    0.345  0.7101
## Plant                      1    51    4.412  0.0407
## Date:Management            4    51    1.019  0.4066
## Date:Plant                 2    51    1.291  0.2839
## Management:Plant           2    51    0.068  0.9341
## Date:Management:Plant      4    51    1.010  0.4112
```

```r
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: 41.15294
##   Fixed: shannon ~ Date * Management * Plant
##                               (Intercept)
##                                7.19457037
##                                 DateJun-12
##                                0.04687279
##                                 DateJun-13
##                                0.08239934
##                             ManagementLowN
##                               -0.02735185
##                          ManagementOrganic
##                                0.03092598
##                           PlantIntWheatgrass
##                                0.08351709
##              DateJun-12:ManagementLowN
##                                0.04765375
##              DateJun-13:ManagementLowN
##                                0.10013707
##           DateJun-12:ManagementOrganic
##                                0.06410087
##           DateJun-13:ManagementOrganic
##                                0.07885084
##         DateJun-12:PlantIntWheatgrass
##                               -0.01719822
##         DateJun-13:PlantIntWheatgrass
##                               -0.03061991
```

```
##          ManagementLowN:PlantIntWheatgrass
##                               -0.01646312
##        ManagementOrganic:PlantIntWheatgrass
##                               -0.06497648
##    DateJun-12:ManagementLowN:PlantIntWheatgrass
##                                0.03622626
##    DateJun-13:ManagementLowN:PlantIntWheatgrass
##                                0.02875638
## DateJun-12:ManagementOrganic:PlantIntWheatgrass
##                                0.02489509
## DateJun-13:ManagementOrganic:PlantIntWheatgrass
##                                0.06295298
##
## Random effects:
##  Formula: ~1 | Block
##         (Intercept)  Residual
## StdDev:  0.01839714 0.0882003
##
## Number of Observations: 72
## Number of Groups: 4
```

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

```
##                         numDF denDF   F-value p-value
## (Intercept)                 1    51 276591.72  <.0001
## Date                        2    51     15.78  <.0001
## Management                  2    51      2.88  0.0653
## Plant                       1    51      7.63  0.0080
## Date:Management             4    51      1.12  0.3556
## Date:Plant                  2    51      0.00  0.9974
## Management:Plant            2    51      0.38  0.6843
## Date:Management:Plant       4    51      0.08  0.9873
```

```r
#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
```

```r
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.r
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               6422         534         7.28     0.0746
## 2 HighN      IntWheatgr~          6200         200         7.33     0.0726
## 3 LowN       Annual               6897         366         7.35     0.0481
## 4 LowN       IntWheatgr~          6916         159         7.41     0.0315
## 5 Organic    Annual               6851         359         7.39     0.0230
## 6 Organic    IntWheatgr~          6822         373         7.44     0.0526
```

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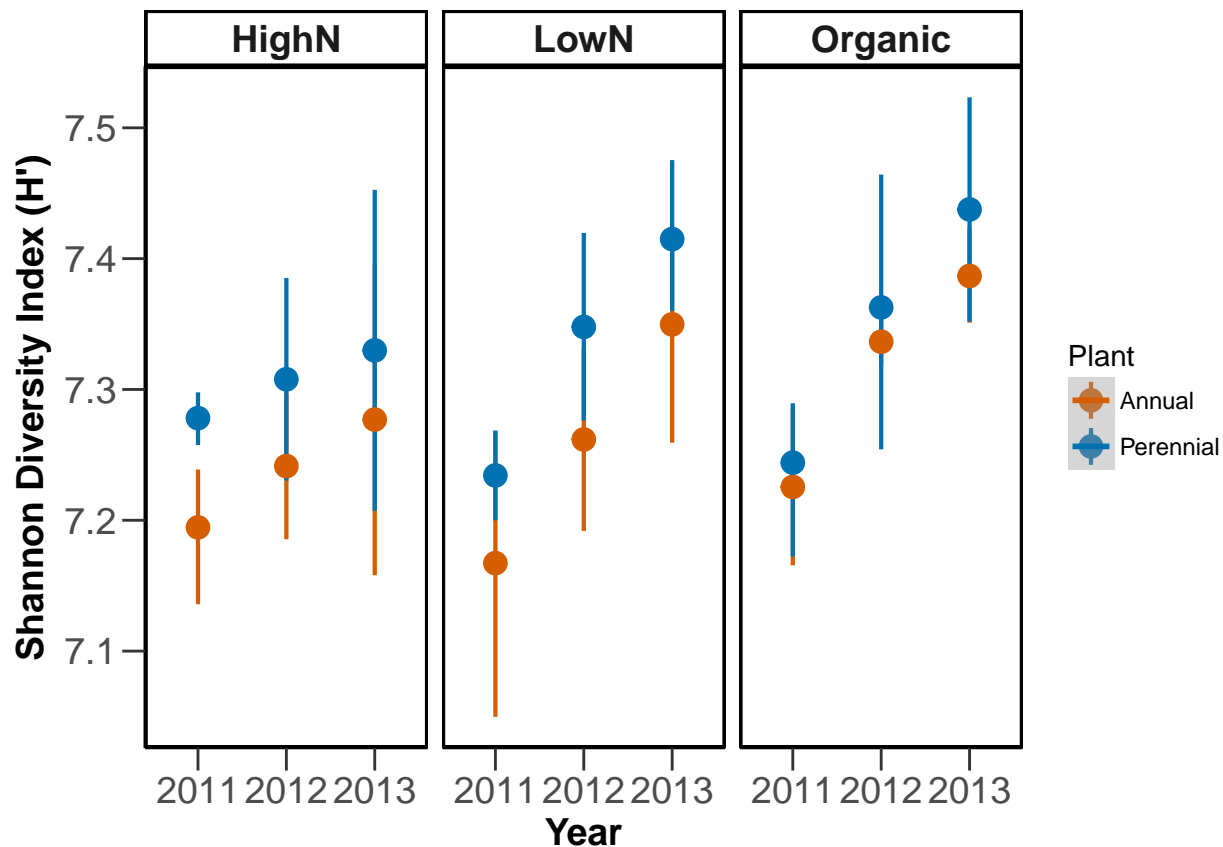
```
ggsave("../figures/shannon.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA
```

```
## 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, permu
##
## 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 0.100899
## Date              2    0.4027 0.201328  3.6942 0.09233 0.000999 ***
## Management        2    0.2698 0.134918  2.4756 0.06188 0.001998 **
## Plant             1    0.1084 0.108392  1.9889 0.02486 0.025974 *
## Date:Management   4    0.1796 0.044909  0.8241 0.04119 0.880120
```

```
## Date:Plant              2    0.1342 0.067076   1.2308 0.03076 0.148851
## Management:Plant         2    0.1323 0.066139   1.2136 0.03033 0.150849
## Date:Management:Plant    4    0.1673 0.041820   0.7674 0.03836 0.958042
## 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

```r
# 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
```

```r
explainvar2b #9.1
```

```
## [1] 9.1
```

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

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

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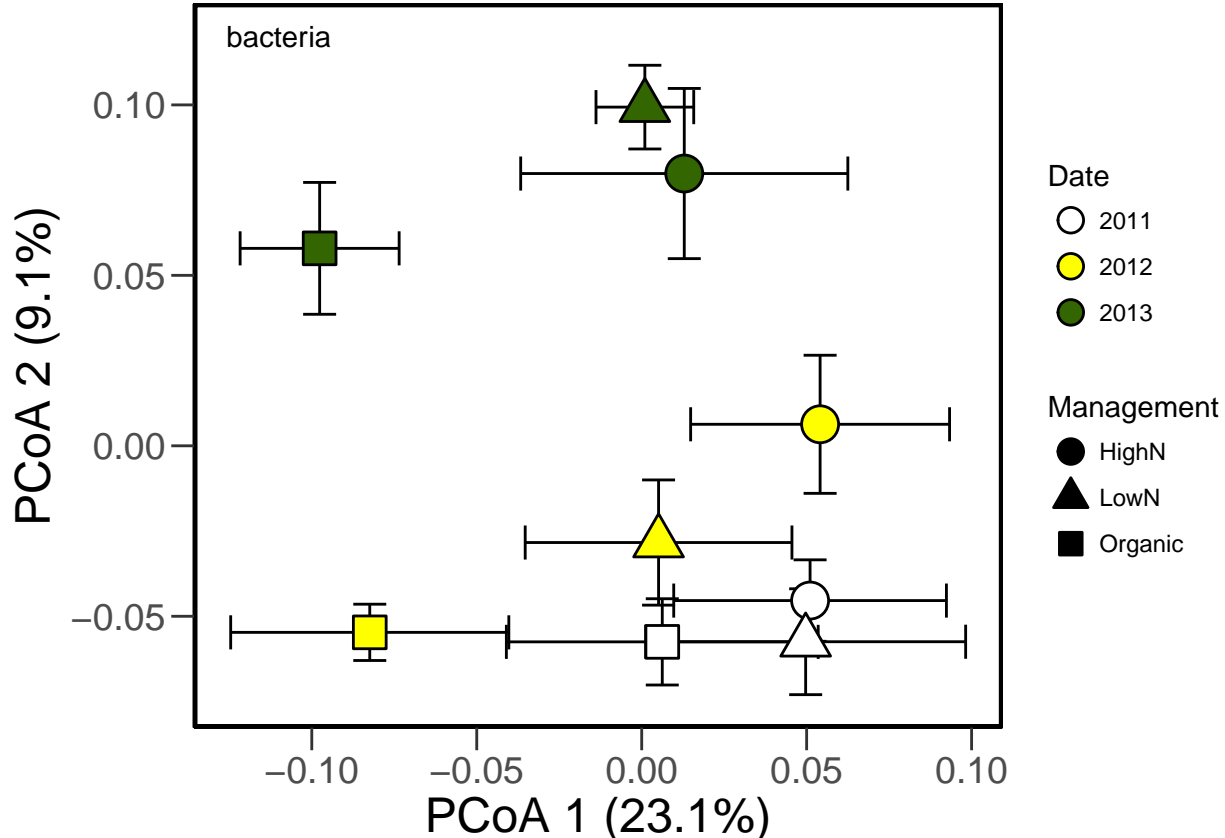
```r
ggsave("../figures/16SrRNA_PWES_YrMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=N
```

Saving 6.5 x 4.5 in image

```r
# Principal Coordinates Analysis (Mgmt*Plant)
all.equal(rownames(design), rownames(dataREL))
```

[1] TRUE

```r
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")
```
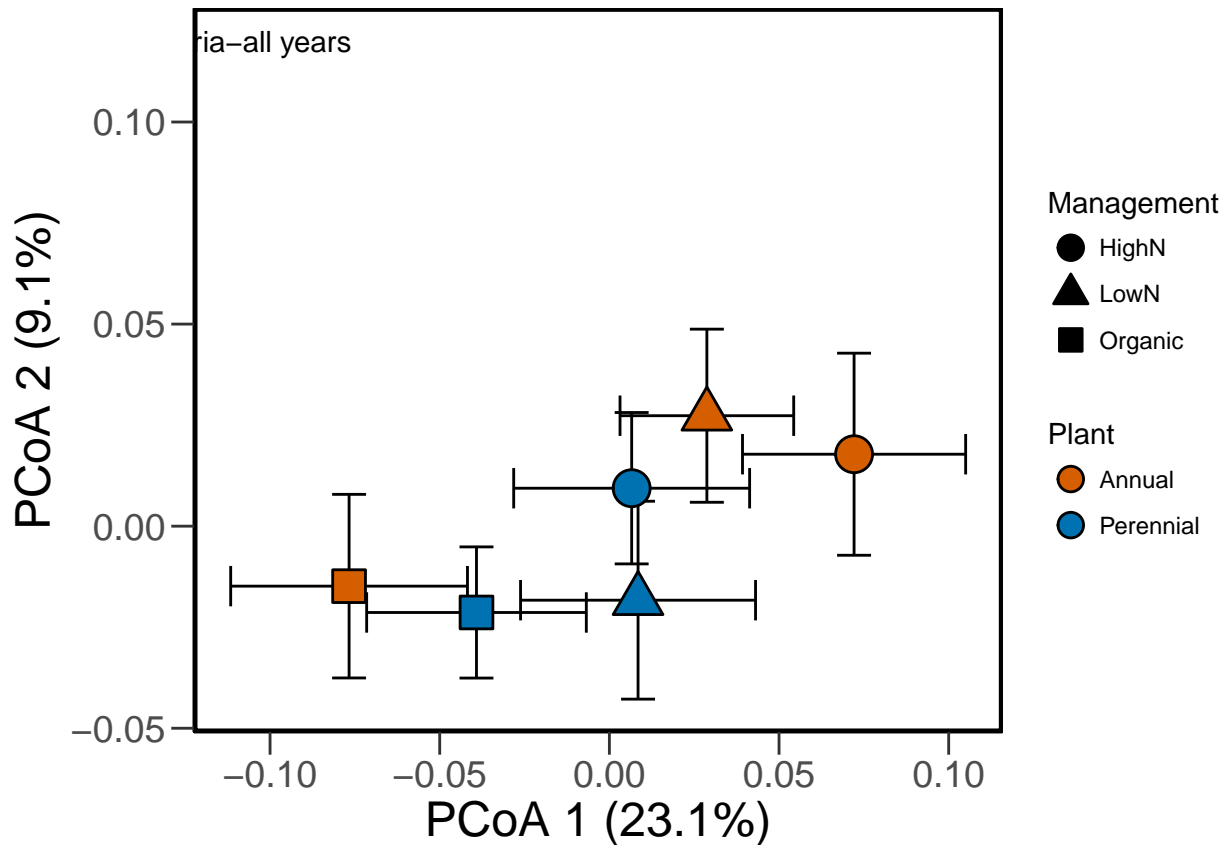
ria–all years

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

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

Principal Coordinates Ordination -BACTERIA seaparate 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.
adonis.2011
```

```
##
## Call:
## adonis(formula = new.data.2011[, -c(1:9)] ~ Block + Management *      Plant, data = new.data.2011, pe
##
## 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 0.4525
## Management        2   0.07623 0.038117 0.72092 0.06545 0.8032
## Plant             1   0.04778 0.047775 0.90359 0.04102 0.4456
## Management:Plant  2   0.09531 0.047653 0.90127 0.08183 0.4935
## Residuals        17   0.89884 0.052873         0.77174
```

```
## Total             23   1.16469                1.00000
```

```r
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
```

```r
explainvar2b #8.9
```

```
## [1] 8.9
```

```r
# 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)) +
```

```r
    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
```

```r
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.
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 0.097902 .
## Management       2   0.18090 0.090448 1.62803 0.12694 0.008991 **
## Plant            1   0.11567 0.115672 2.08206 0.08117 0.004995 **
## Management:Plant 2   0.10355 0.051775 0.93193 0.07266 0.525475
## 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
```

```r
# 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.
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 0.63736
## Management       2   0.19234 0.096172 1.71997 0.14055 0.04695 *
## Plant            1   0.07910 0.079096 1.41459 0.05780 0.14286
## Management:Plant 2   0.10070 0.050351 0.90050 0.07359 0.56344
```

```
## 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
```

```r
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
```

```r
explainvar2b #10.0
```

```
## [1] 10
```

```r
# 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.
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 0.077922 .
## Management         2   0.18090 0.090448 1.62803 0.12694 0.013986 *
## Plant              1   0.11567 0.115672 2.08206 0.08117 0.006993 **
## Management:Plant   2   0.10355 0.051775 0.93193 0.07266 0.553447
## 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 ...
##  $ Prismatolaimus  : 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 0.00629 ...
##  $ 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, permuta
##
## 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 0.014985 *
## 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 0.991009
## Date:Plant             2    0.2199 0.10997  1.3068 0.03260 0.174825
## Management:Plant       2    0.2650 0.13251  1.5746 0.03928 0.055944 .
## Date:Management:Plant  4    0.2319 0.05798  0.6889 0.03437 0.914086
## 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
```

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

explainvar1b #19.8
```

```
## [1] 19.8
```

```r
explainvar2b #18.3
```

```
## [1] 18.3
```

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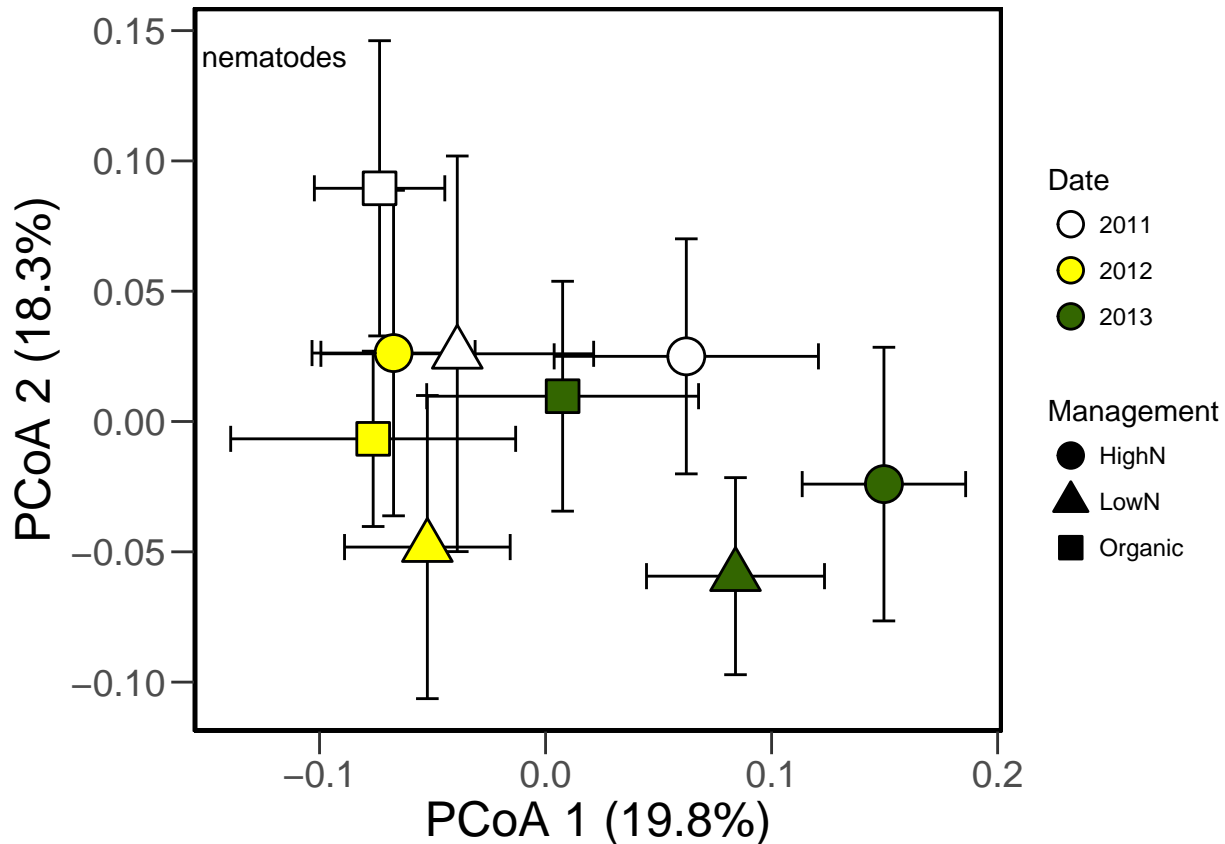
```
ggsave("../figures/nema_PWES_YrMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA,
```

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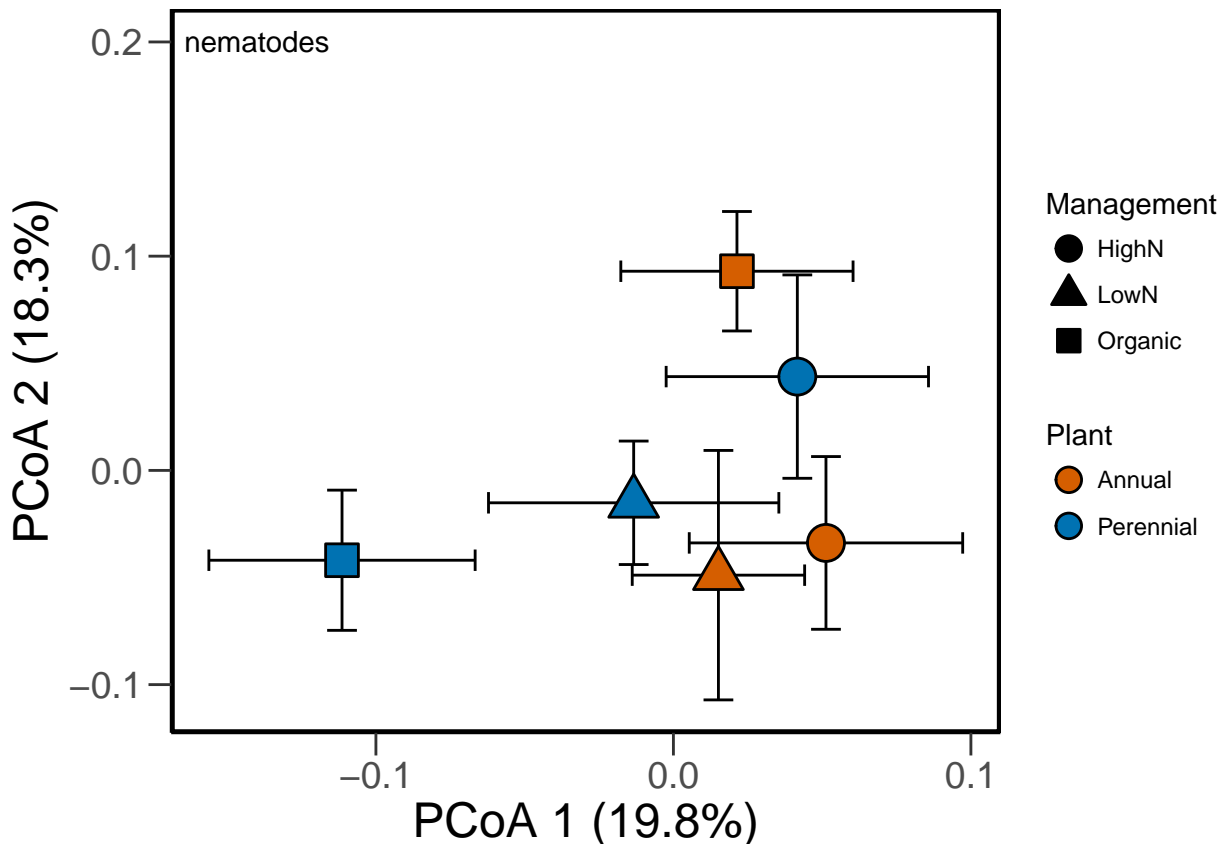
```
ggsave("../figures/nema_PlantMgmt.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, he
```

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  0.106
## Management        2   0.16951 0.084756 0.94256 0.11421  0.534
## Plant             1   0.16219 0.162185 1.80362 0.10928  0.077 .
## Management:Plant  2   0.10552 0.052761 0.58675 0.07110  0.894
## 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

```r
# 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

```r
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  0.024 *
## Management       2   0.15376 0.076880 0.85587 0.07050  0.645
## Plant            1   0.15116 0.151159 1.68277 0.06931  0.099 .
## Management:Plant 2   0.16217 0.081086 0.90269 0.07436  0.606
## 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")
```

```r
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
```

```r
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  0.049 *
## Management    2   0.31947 0.15973  2.3238 0.14815  0.009 **
```

```
## Plant              1    0.30920 0.30920  4.4981 0.14338  0.001 ***
## Management:Plant   2    0.21851 0.10925  1.5894 0.10133  0.080 .
## 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
```

```r
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
```

```r
explainvar2b #24.2
```

```
## [1] 24.2
```

```r
# 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"
```

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

```
##          cluster indicator_value probability
## Otu00034       1          0.5811       0.024
## Otu00028       1          0.5741       0.032
## Otu00015       1          0.5722       0.001
## Otu00011       1          0.5694       0.006
## Otu00054       1          0.5690       0.010
## Otu00044       1          0.5672       0.024
## Otu00005       1          0.5628       0.001
## Otu00048       1          0.5433       0.013
## Otu00029       1          0.5289       0.028
## Otu00050       2          0.6347       0.003
## Otu00062       2          0.5830       0.003
## Otu00022       2          0.5644       0.006
##
## Sum of probabilities              =   21.405
##
## 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
```

```r
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
```

```r
table(indicator.bac$Phylum)
```

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

```
##                  1                4                1                1
##     Proteobacteria
##                  5
```

```r
table(indicator.bac$Cluster)
```

```
##
## 1 2
## 9 3
```

```r
levels(design.type)
```

```
## [1] "Annual"        "IntWheatgrass"
```

```r
# 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"
```

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

```
##          cluster indicator_value probability
## Otu00008       3          0.1343       0.002
## Otu00022       3          0.1341       0.004
## Otu00007       3          0.1310       0.041
## Otu00016       3          0.1263       0.003
##
## Sum of probabilities                =  19.419
##
## Sum of Indicator Values             =  6.66
##
## Sum of Significant Indicator Values =  0.53
##
## Number of Significant Indicators    =  4
##
## Significant Indicator Distribution
##
## 3
## 4
```

```r
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       0.002
## Paratylenchus       1          0.6953       0.018
## Pratylenchus        1          0.6526       0.019
```

```
## Plectus              2         0.9385        0.001
## Monhysteridae        2         0.7899        0.001
##
## Sum of probabilities                  =   6.623
##
## 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
```

```r
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
```

```r
table(indicators$taxa)
```

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

```r
table(indicators$Cluster)
```

```
##
## 1 2
## 3 2
```

```r
levels(design.type)
```

```
## [1] "Annual"        "IntWheatgrass"
```

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

#bac.ind - by management
```

```r
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"
```

```r
summary(nema.ind)
```

```
##                 cluster indicator_value probability
## Dauerlarvae           3          0.9316       0.001
## Qudsianematidae       3          0.4711       0.043
##
## Sum of probabilities                 =  9.404
##
## Sum of Indicator Values              =  8.58
##
## Sum of Significant Indicator Values  =  1.4
##
## Number of Significant Indicators     =  2
##
## Significant Indicator Distribution
##
## 3
## 2
```

```r
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
```

```r
table(indicators$taxa)
```

```
##
##     Dauerlarvae Qudsianematidae
##               1               1
```

```r
table(indicators$Cluster)
```

```
##
## 3
## 2
```

```r
levels(design.type)
```

```
## [1] "HighN"   "LowN"    "Organic"
```

```r
# Export Bacteria Indicator Table
write.table(indicators, "../data/NemaIndicators_Mgmt.txt",
            sep="\t", row.names = F, quote = F)
```