

Long-term Fertilization and Mowing at WRC: Plant Community Characterization

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Project Description:

Initial Setup

Import Data

Simple Hypothesis Testing

```
#incorporating strata to restrict permutation within similar treatment
PCC.dist <- vegdist(PCC[, -c(1:9)], method="bray")

#adonis = adonis(PCC[, -c(1:9)] ~ Fertilizer*Mowing*Year+(1|BLOCK/QUADRAT..), strata = PCC$treatment, me
#adonis

#adonis2 = adonis(PCC[, -c(1:9)] ~ Fertilizer*Mowing*Year+(1|BLOCK/QUADRAT..), method = "bray", data = P
#adonis2

#adonis1 and adonis2 result in the same output

adonis3 = adonis(PCC[, -c(1:9)] ~ Fertilizer*Mowing*Year*Ditch+(1|BLOCK/QUADRAT..), method = "bray", dat
adonis3
```

```
##
## Call:
## adonis(formula = PCC[, -c(1:9)] ~ Fertilizer * Mowing * Year *      Ditch + (1 | BLOCK/QUADRAT..), d
##
## Permutation: free
## Number of permutations: 1000
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2
## Fertilizer      1    12.449 12.4493  74.789 0.04039
## Mowing          1    30.830 30.8297 185.210 0.10001
## Year           1    23.884 23.8842 143.484 0.07748
## Ditch          1    19.928 19.9283 119.719 0.06465
## Fertilizer:Mowing 1     3.455  3.4545  20.753 0.01121
## Fertilizer:Year   1     2.227  2.2267  13.377 0.00722
## Mowing:Year      1     7.208  7.2084  43.304 0.02338
## Fertilizer:Ditch  1     4.034  4.0337  24.233 0.01309
## Mowing:Ditch     1     4.546  4.5458  27.309 0.01475
## Year:Ditch       1     5.278  5.2781  31.708 0.01712
```

```

## Fertilizer:Mowing:Year      1      1.011  1.0111   6.074 0.00328
## Fertilizer:Mowing:Ditch     1      2.648  2.6476  15.905 0.00859
## Fertilizer:Year:Ditch       1      0.546  0.5460   3.280 0.00177
## Mowing:Year:Ditch           1      0.795  0.7945   4.773 0.00258
## Fertilizer:Mowing:Year:Ditch 1      0.323  0.3230   1.940 0.00105
## Residuals                   1136   189.097  0.1665       0.61344
## Total                       1151   308.258              1.00000
##                               Pr(>F)
## Fertilizer                   0.000999 ***
## Mowing                       0.000999 ***
## Year                         0.000999 ***
## Ditch                        0.000999 ***
## Fertilizer:Mowing            0.000999 ***
## Fertilizer:Year              0.000999 ***
## Mowing:Year                  0.000999 ***
## Fertilizer:Ditch             0.000999 ***
## Mowing:Ditch                 0.000999 ***
## Year:Ditch                   0.000999 ***
## Fertilizer:Mowing:Year       0.000999 ***
## Fertilizer:Mowing:Ditch      0.000999 ***
## Fertilizer:Year:Ditch        0.001998 **
## Mowing:Year:Ditch            0.001998 **
## Fertilizer:Mowing:Year:Ditch 0.043956 *
## Residuals
## Total
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Test for multivariate homogeneity of group dispersions (variances)

```

## Bray-Curtis distances between samples NEAR DITCH
PCC.ditch <-subset(PCC.trts, Ditch ==1)
PCC.dist.ditch <- vegdist(PCC.ditch[,-c(1:10)], method="bray")

## Calculate multivariate dispersions
mod <- betadisper(PCC.dist.ditch, PCC.ditch$treatments)
mod

##
## Homogeneity of multivariate dispersions
##
## Call: betadisper(d = PCC.dist.ditch, group = PCC.ditch$treatments)
##
## No. of Positive Eigenvalues: 163
## No. of Negative Eigenvalues: 412
##
## Average distance to median:
##   UM/UF   UM/F   M/UF   M/F
## 0.4577 0.4615 0.3657 0.4024
##
## Eigenvalues for PCoA axes:
##   PCoA1   PCoA2   PCoA3   PCoA4   PCoA5   PCoA6   PCoA7   PCoA8

```

```
## 35.5307 22.1632 13.8661 10.1886 8.5768 6.6906 6.3087 5.6262
## Perform test
anova(mod)

## Analysis of Variance Table
##
## Response: Distances
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Groups      3 0.9204 0.306803  41.538 < 2.2e-16 ***
## Residuals 572 4.2248 0.007386
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

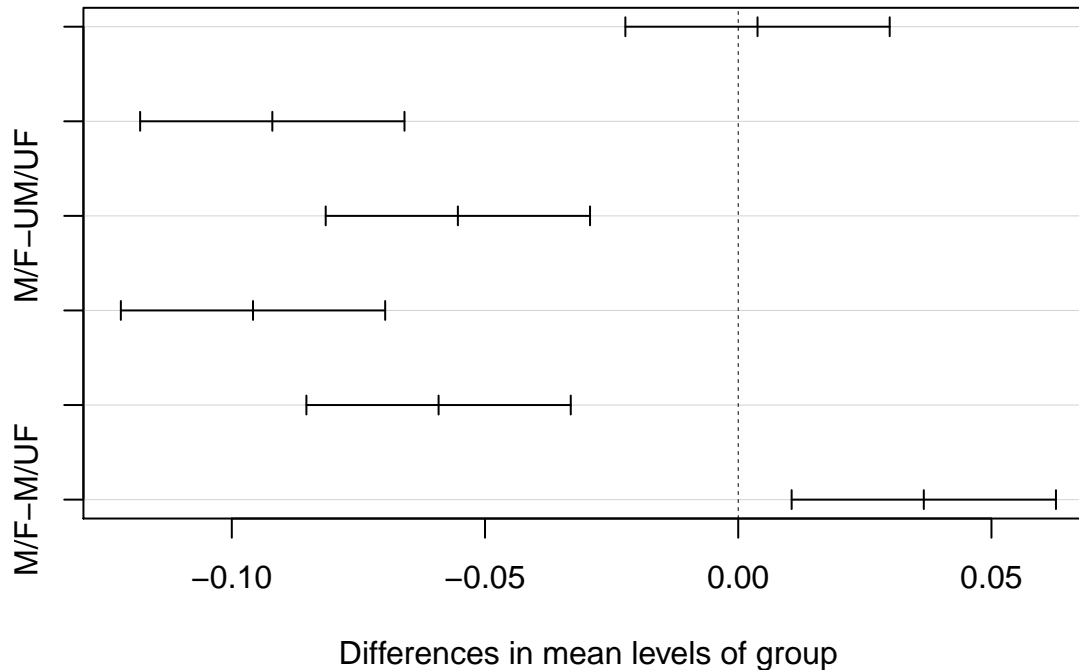
## Permutation test for F
permutest(mod, pairwise = TRUE)

##
## Permutation test for homogeneity of multivariate dispersions
## Permutation: free
## Number of permutations: 999
##
## Response: Distances
##           Df Sum Sq Mean Sq      F N.Perm Pr(>F)
## Groups      3 0.9204 0.306803 41.538   999 0.001 ***
## Residuals 572 4.2248 0.007386
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Pairwise comparisons:
## (Observed p-value below diagonal, permuted p-value above diagonal)
##           UM/UF      UM/F      M/UF      M/F
## UM/UF           7.0400e-01 1.0000e-03 0.001
## UM/F  7.4216e-01           1.0000e-03 0.001
## M/UF  1.0096e-18 7.7219e-18           0.001
## M/F   4.3260e-08 4.6350e-08 1.9620e-05
##
## Tukey's Honest Significant Differences
(mod.HSD <- TukeyHSD(mod))

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = distances ~ group, data = df)
##
## $group
##           diff           lwr           upr      p adj
## UM/F-UM/UF 0.00381131 -0.02228537 0.02990799 0.9818267
## M/UF-UM/UF -0.09200091 -0.11809758 -0.06590423 0.0000000
## M/F-UM/UF  -0.05535834 -0.08145502 -0.02926166 0.0000004
## M/UF-UM/F  -0.09581222 -0.12190889 -0.06971554 0.0000000
## M/F-UM/F   -0.05916965 -0.08526633 -0.03307297 0.0000001
## M/F-M/UF   0.03664256 0.01054589 0.06273924 0.0018327
```

```
plot(mod.HSD)
```

95% family-wise confidence level



```
#need to save plot
```

Indicator Species Analysis

```
#plant.ind - treatment-YES ditch  
library("labdsv")
```

```
## Loading required package: mgcv  
## This is mgcv 1.8-17. For overview type 'help("mgcv-package")'.  
## Loading required package: cluster  
##  
## Attaching package: 'labdsv'  
## The following object is masked from 'package:stats':  
##  
## density  
design.type <- PCC.ditch$treatments  
PCC.ditch.rel <- PCC.ditch[,-c(1:10)]  
dataREL <- PCC.ditch.rel[, colSums(PCC.ditch.rel) > 0.05]  
plant.ind <- indval(dataREL, design.type)  
levels(design.type)
```

```
## [1] "UM/UF" "UM/F" "M/UF" "M/F"
```

```
summary(plant.ind)
```

##	cluster	indicator_value	probability
## Smilax.glauca	1	0.3651	0.001
## Clethra.alnifolia	1	0.3450	0.001
## Smilax.rotundifolia	1	0.3086	0.001
## Prunus.serotina	1	0.2448	0.001
## Amelanchier.canadensis	1	0.1495	0.001
## Cyrilla.racemiflora	1	0.0999	0.001
## Rhus.radicans	1	0.0980	0.001
## Ilex.glabra	1	0.0976	0.001
## Aristida.virgata	1	0.0939	0.002
## Hypericum.sp.	1	0.0619	0.003
## Vaccinium.sp.	1	0.0582	0.005
## Crataegus.sp.	1	0.0278	0.021
## Sorbus.arbutifolia	2	0.5555	0.001
## Chasmanthium.laxum	2	0.3556	0.001
## Nyssa.sylvatica	2	0.3019	0.001
## Liquidambar.styraciflua	2	0.2851	0.001
## Itea.virginica	2	0.0976	0.001
## Acer.rubrum	2	0.0810	0.003
## Symplocos.tinctoria	2	0.0651	0.011
## Magnolia.virginica	2	0.0419	0.033
## Packera.tomentosa	3	0.4326	0.001
## Dichanthelium.scoparium	3	0.3971	0.001
## Arundinaria.tecta	3	0.3932	0.001
## Andropogon.virginica	3	0.3736	0.001
## Solidago.rugosa	3	0.3458	0.001
## Eupatorium.rotundifolium	3	0.3347	0.001
## Solidago.pinetorum	3	0.3338	0.001
## Dichanthelium.lucidum	3	0.3055	0.001
## Rhexia.mariana	3	0.2799	0.001
## Pycnanthemum.flexuosum	3	0.1784	0.001
## Solidago.stricta	3	0.1674	0.001
## Lespedeza.hirta	3	0.1493	0.001
## Rhynchospora.inexpansa	3	0.0915	0.003
## Viola.primulifolia	3	0.0830	0.001
## Lespedeza.capitata	3	0.0622	0.015
## Solidago.puberula	3	0.0391	0.002
## Gnaphaleum.purpureum	3	0.0347	0.003
## Bidens.bipinnata	3	0.0278	0.014
## Euthamia.caroliniana	4	0.5086	0.001
## Juncus.biflorus	4	0.4659	0.001
## Rhus.copallinum	4	0.3633	0.001
## Rubus.betulifolius	4	0.2020	0.002
## Eupatorium.semiserratum	4	0.1684	0.001
## Eupatorium.capillifolium	4	0.1256	0.001
## Juncus.effusus	4	0.0821	0.001
## Carex.glaucescens	4	0.0497	0.001
## Rhynchospora.chalarocephala	4	0.0322	0.035
##			
## Sum of probabilities	=	8.954	
##			
## Sum of Indicator Values	=	10.15	

```
##
## Sum of Significant Indicator Values = 9.76
##
## Number of Significant Indicators = 47
##
## Significant Indicator Distribution
##
## 1 2 3 4
## 12 8 18 9

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

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

indicator.plant <- cbind(plant.indicators)

levels(design.type)

## [1] "UM/UF" "UM/F" "M/UF" "M/F"
# Export Plant Spp Indicator Table
write.table(indicator.plant, "../data/PlantIndicators_Ditch.txt",
            sep="\t", row.names = F, quote = F)
```

Test for multivariate homogeneity of group dispersions (variances)

```
## Bray-Curtis distances between samples FAR/NO DITCH
PCC.NOditch <- subset(PCC.trts, Ditch == 0)
PCC.dist.NOditch <- vegdist(PCC.NOditch[, -c(1:10)], method = "bray")

## Calculate multivariate dispersions
mod <- betadisper(PCC.dist.NOditch, PCC.NOditch$treatments)
mod

##
## Homogeneity of multivariate dispersions
##
## Call: betadisper(d = PCC.dist.NOditch, group =
## PCC.NOditch$treatments)
##
## No. of Positive Eigenvalues: 175
## No. of Negative Eigenvalues: 400
##
## Average distance to median:
## UM/UF UM/F M/UF M/F
## 0.4808 0.5250 0.3632 0.4349
##
## Eigenvalues for PCoA axes:
```

```

## PCoA1 PCoA2 PCoA3 PCoA4 PCoA5 PCoA6 PCoA7 PCoA8
## 34.6317 19.3911 13.1943 10.1261 9.7807 7.7500 6.6864 6.1280
## Perform test
anova(mod)

## Analysis of Variance Table
##
## Response: Distances
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Groups      3 2.0637 0.68790  103.34 < 2.2e-16 ***
## Residuals 572 3.8077 0.00666
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Permutation test for F
permutest(mod, pairwise = TRUE)

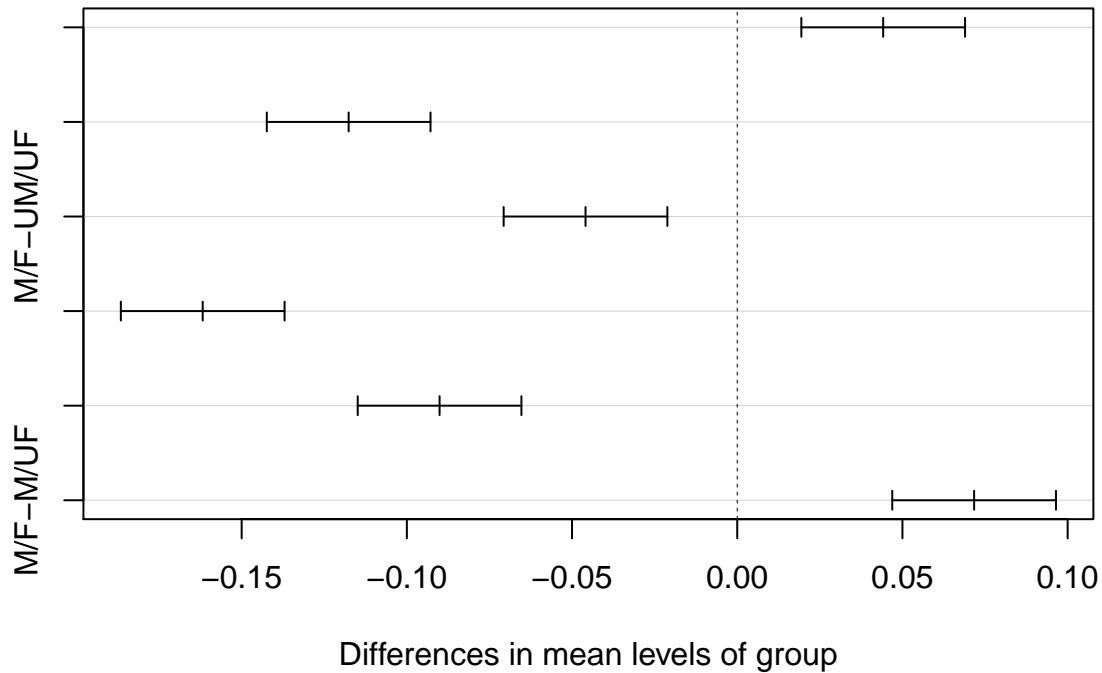
##
## Permutation test for homogeneity of multivariate dispersions
## Permutation: free
## Number of permutations: 999
##
## Response: Distances
##          Df Sum Sq Mean Sq      F N.Perm Pr(>F)
## Groups      3 2.0637 0.68790 103.34   999 0.001 ***
## Residuals 572 3.8077 0.00666
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Pairwise comparisons:
## (Observed p-value below diagonal, permuted p-value above diagonal)
##          UM/UF      UM/F      M/UF      M/F
## UM/UF          1.0000e-03 1.0000e-03 0.001
## UM/F  4.0087e-06          1.0000e-03 0.001
## M/UF  7.0144e-29 2.3266e-48          0.001
## M/F   8.5745e-06 8.8967e-18 3.0030e-12
## Tukey's Honest Significant Differences
(mod.HSD <- TukeyHSD(mod))

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = distances ~ group, data = df)
##
## $group
##          diff          lwr          upr      p adj
## UM/F-UM/UF  0.04417476 0.01939965 0.06894987 3.17e-05
## M/UF-UM/UF -0.11761293 -0.14238804 -0.09283782 0.00e+00
## M/F-UM/UF   -0.04592058 -0.07069569 -0.02114547 1.35e-05
## M/UF-UM/F   -0.16178770 -0.18656281 -0.13701259 0.00e+00
## M/F-UM/F    -0.09009534 -0.11487045 -0.06532023 0.00e+00
## M/F-M/UF     0.07169236 0.04691725 0.09646747 0.00e+00

plot(mod.HSD)

```

95% family-wise confidence level



##need to save plot

Indicator Species Analysis

```
#plant.ind - treatment-NO ditch
library("labdsv")
design.type <- PCC.NOditch$treatments
PCC.NOditch.rel <- PCC.NOditch[,-c(1:10)]
dataREL <- PCC.NOditch.rel[, colSums(PCC.NOditch.rel) > 0.05]
plant.ind <- indval(dataREL, design.type)
levels(design.type)
```

```
## [1] "UM/UF" "UM/F" "M/UF" "M/F"
```

```
summary(plant.ind)
```

```
##          cluster indicator_value probability
## Smilax.glauca          1         0.3638      0.001
## Cyrilla.racemiflora     1         0.3138      0.001
## Clethra.alnifolia       1         0.3069      0.001
## Nyssa.sylvatica         1         0.2622      0.001
## Amelanchier.canadensis  1         0.1976      0.001
## Pteridium.aquilinum     1         0.1738      0.001
## Pinus.taeda             1         0.1111      0.001
## Vaccinium.sp.           1         0.1086      0.001
## Symplocos.tinctoria     1         0.0773      0.004
## Hypericum.sp.           1         0.0766      0.018
```


## Itea.virginica	1	0.0478	0.003
## Sorbus.arbutifolia	2	0.3857	0.001
## Rubus.betulifolius	2	0.3477	0.001
## Smilax.rotundifolia	2	0.3049	0.001
## Scirpus.cyperinus	2	0.1863	0.001
## Rhexia.mariana	2	0.1759	0.027
## Pycnanthemum.flexuosum	2	0.1390	0.004
## Dichanthelium.scabriusculum	2	0.1063	0.009
## Eupatorium.semiserratum	2	0.0973	0.001
## Liquidambar.styraciflua	2	0.0950	0.034
## Acer.rubrum	2	0.0937	0.006
## Viburnum.nudum	2	0.0751	0.001
## Rhus.radicans	2	0.0577	0.001
## Saccharum.giganteum	2	0.0486	0.001
## Sphagnum.sp	2	0.0309	0.012
## Solidago.stricta	3	0.5607	0.001
## Andropogon.virginica	3	0.5009	0.001
## Rhynchospora.inexpansa	3	0.4854	0.001
## Scleria.minor	3	0.4371	0.001
## Aristida.virgata	3	0.4362	0.001
## Packera.tomentosa	3	0.3899	0.001
## Eupatorium.rotundifolium	3	0.3483	0.001
## Polygala.cruciata	3	0.3115	0.001
## Lobelia.nuttallii	3	0.1978	0.001
## Solidago.rugosa	3	0.1776	0.001
## Rhynchospora.chalarocephala	3	0.1051	0.006
## Gratiola.pilosa	3	0.0905	0.002
## Rhexia.virginica	3	0.0877	0.001
## Viola.primulifolia	3	0.0799	0.002
## Amphicarpum.purshii	3	0.0654	0.001
## Ilex.glabra	3	0.0559	0.008
## Polygala.lutea	3	0.0453	0.025
## Lycopodium	3	0.0265	0.011
## Juncus.biflorus	4	0.6465	0.001
## Euthamia.caroliniana	4	0.4321	0.001
## Arundinaria.tecta	4	0.3731	0.001
## Dichanthelium.lucidum	4	0.3269	0.001
## Chasmanthium.laxum	4	0.3089	0.001
## Dichanthelium.scoparium	4	0.2586	0.001
## Carex.glaucescens	4	0.1984	0.001
## Eupatorium.recurvans	4	0.1288	0.037
## Eupatorium.capillifolium	4	0.1239	0.001
## Calamagrostis.coarctata	4	0.1132	0.001
## Juncus.canadensis	4	0.1004	0.001
## Juncus.effusus	4	0.0841	0.003
## Ludwigia.alternifolia	4	0.0672	0.001
## Lespedeza.capitata	4	0.0582	0.028
##			
## Sum of probabilities	=	7.822	
##			
## Sum of Indicator Values	=	12.26	
##			
## Sum of Significant Indicator Values	=	11.81	
##			

```

## Number of Significant Indicators      = 57
##
## Significant Indicator Distribution
##
## 1  2  3  4
## 11 14 18 14

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

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

indicator.plant <- cbind(plant.indicators)

levels(design.type)

## [1] "UM/UF" "UM/F" "M/UF" "M/F"
# Export Plant Spp Indicator Table
write.table(indicator.plant, "../data/PlantIndicators_NOditch.txt",
            sep="\t", row.names = F, quote = F)

```

Plot Plant Community Composition

```

sampleREL.dist <- vegdist(PCC[, -c(1:9)], method="bray")
WRC_pcoa <- cmdscale(sampleREL.dist, k=3, eig=TRUE, add=FALSE)
explainvar1 <- round(WRC_pcoa$eig[1]/sum(WRC_pcoa$eig)*100, 1)
explainvar2 <- round(WRC_pcoa$eig[2]/sum(WRC_pcoa$eig)*100, 1)
explainvar3 <- round(WRC_pcoa$eig[3]/sum(WRC_pcoa$eig)*100, 1)
explainvar1

## [1] 20.1
explainvar2

## [1] 11.5
explainvar3

## [1] 11.2

pcoap <- merge(as.data.frame(WRC_pcoa$points), PCC$treatment, by=0, all.x=T)
rownames(pcoap) <- rownames(WRC_pcoa$points)
pcoap <- merge(pcoap[, -1], PCC$Year, by=0, all.x=T)
rownames(pcoap) <- rownames(WRC_pcoa$points)
treatments <- PCC$treatment
year <- PCC$Year
ditch <- as.factor(PCC$Ditch)
levels(treatments) <- c("UM/UF", "UM/F", "M/UF", "M/F")
points <- cbind(as.data.frame(WRC_pcoa$points), treatments, year, ditch)
L.centroids <- melt(points, id=c("treatments", "year", "ditch"), measure.vars = c("V1", "V2", "V3"))

```

```

centroids <- cast(L.centroids, ... ~ variable, mean)
centroids <- cast(L.centroids, ... ~ variable, fun.aggregate=c(mean,se))

pdf(file="../figures/Plant_PCoA.pdf", width = 9, height = 3, bg = "white")
#ggsave("../figures/Plant_Rplot.pdf", plot=last_plot(), device=NULL, path=NULL, scale=1, width=NA, height=NA)

par(opar)
layout(matrix(1:4, 1))

par(mar=c(0.5,1,1,0.5), oma=c(5,5,1,1)+0.1)
x.dim <- c((min(centroids$V1_mean)-(max(centroids$V1_mean)*0.15)) ,
           (max(centroids$V1_mean)+(max(centroids$V1_mean)*0.15)))

y.dim <- c((min(centroids$V2_mean)-(max(centroids$V2_mean*0.15))),
           (max(centroids$V2_mean)+(max(centroids$V2_mean)*0.15)+0.05))

trt.arrows <- function(trt = "", col.trt = ""){
  trt.yr <- centroids[which(centroids$treatments == trt), ]$year
  cex.yr <- 1.2 + (as.numeric(trt.yr) - 2000) * 0.1
  arrows(centroids[which(centroids$treatments == trt), ]$V1_mean,
         y1 = centroids[which(centroids$treatments == trt), ]$V2_mean -
               centroids[which(centroids$treatments == trt), ]$V2_se,
         y0 = centroids[which(centroids$treatments == trt), ]$V2_mean +
               centroids[which(centroids$treatments == trt), ]$V2_se,
         angle = 90,length=0.025, lwd = 2, code = 3)
  arrows(centroids[which(centroids$treatments == trt), ]$V2_mean,
         x1 = centroids[which(centroids$treatments == trt), ]$V1_mean -
               centroids[which(centroids$treatments == trt), ]$V1_se,
         x0 = centroids[which(centroids$treatments == trt), ]$V1_mean +
               centroids[which(centroids$treatments == trt), ]$V1_se,
         angle = 90, length=0.025, lwd = 2, code = 3)
  trt.pch <- as.character(centroids[which(centroids$treatments == trt), ]$ditch)
  trt.pch[which(trt.pch == 0)] <- 21; trt.pch[which(trt.pch == 1)] <- 24
  trt.pch <- as.numeric(trt.pch)
  points(centroids[which(centroids$treatments == trt), ]$V1_mean,
         centroids[which(centroids$treatments == trt), ]$V2_mean,
         pch=trt.pch, cex=cex.yr, col="gray10", bg=col.trt)
  pos.yr <- as.character(centroids[which(centroids$treatments == trt), ]$ditch)
  pos.yr[which(pos.yr == 0)] <- 3; pos.yr[which(pos.yr == 1)] <- 1
  pos.yr <- as.numeric(pos.yr)
  offset.yr <- pos.yr
  offset.yr[which(offset.yr == 1)] <- -1; offset.yr[which(offset.yr == 3)] <- 1
  text(centroids[which(centroids$treatments == trt), ]$V1_mean +
       (centroids[which(centroids$treatments == trt), ]$V1_se * offset.yr),
       centroids[which(centroids$treatments == trt), ]$V2_mean +
       (centroids[which(centroids$treatments == trt), ]$V2_se * offset.yr),
       labels=centroids[which(centroids$treatments == trt), ]$year,
       pos=pos.yr, cex = 0.6, srt = 45, offset = 0.5)
}

plot(pcoap$V1, pcoap$V2, xlab="",
     ylab="",

```

```

      xlim=x.dim, ylim=y.dim, pch=16, cex=2.0, type="n",xaxt="n",yaxt="n",
      cex.lab=1.5, cex.axis=1.2)
axis(side=1, labels = T, las=1, cex = 0.8)
axis(side=2, las=1, cex = 0.8)
abline(h=0, lty="dotted")
abline(v=0, lty="dotted")
box(lwd=2)
trt.arrows(trt = "UM/UF", col.trt = "gray90")
text(0.45, -0.35, "Unmowed\nUnfertilized", adj = 1)

plot(pcoap$V1, pcoap$V2, xlab="",
      ylab="",
      xlim=x.dim, ylim=y.dim, pch=16, cex=2.0, type="n",xaxt="n",yaxt="n",
      cex.lab=1.5, cex.axis=1.2)
axis(side=1, labels = T, las=1, cex = 0.8)
axis(side=2, labels = F, las=1, cex = 0.8)
abline(h=0, lty="dotted")
abline(v=0, lty="dotted")
box(lwd=2)
trt.arrows(trt = "UM/F", col.trt = "forestgreen")
text(0.45, -0.35, "Unmowed\nFertilized", adj = 1)

plot(pcoap$V1, pcoap$V2, xlab="",
      ylab="",
      xlim=x.dim, ylim=y.dim, pch=16, cex=2.0, type="n",xaxt="n",yaxt="n",
      cex.lab=1.5, cex.axis=1.2)
axis(side=1, labels = T, las=1, cex = 0.8)
axis(side=2, labels = F, las=1, cex = 0.8)
abline(h=0, lty="dotted")
abline(v=0, lty="dotted")
box(lwd=2)
trt.arrows(trt = "M/UF", col.trt = "gray90")
text(0.45, -0.35, "Mowed\nUnfertilized", adj = 1)

plot(pcoap$V1, pcoap$V2, xlab="",
      ylab="",
      xlim=x.dim, ylim=y.dim, pch=16, cex=2.0, type="n",xaxt="n",yaxt="n",
      cex.lab=1.5, cex.axis=1.2)
axis(side=1, las=1, cex = 0.8)
axis(side=2, labels = F, las=1, cex = 0.8)
abline(h=0, lty="dotted")
abline(v=0, lty="dotted")
box(lwd=2)
trt.arrows(trt = "M/F", col.trt = "forestgreen")
text(0.45, -0.35, "Mowed\nFertilized", adj = 1)

legend("topright", c("+ Ditch Effect", "- Ditch Effect"),
      bty = "n", pch = c(24, 21),
      col = "gray10", pt.bg = "gray90", pt.cex = 1.5)
usr <- par("usr")
clip(0.05, 0.0905, 0.2, 0.4)

```

```

legend("topright", c("+ Ditch Effect", "- Ditch Effect"),
      bty = "n", pch = c(24, 21),
      col = "gray10", pt.bg = "forestgreen", pt.cex = 1.5)
do.call("clip", as.list(usr))

mtext(paste("PCoA Axis 1 (",explainvar1, "%)", sep=""), side = 1,
      line = 2.5, outer = T, cex = 1.25)

mtext(paste("PCoA Axis 2 (",explainvar2, "%)", sep=""), side = 2,
      line = 2.5, outer = T, cex = 1.25)

dev.off() # this writes plot to folder

## pdf
## 2
graphics.off() # shuts down open devices

```