Add title of your project

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Directions:

1. Change "Add title of your project" on line 2 (above) to the name of your project.
2. Change "Add names of team members" on line 3 (above) to the names of team members in your project.
3. Write a <250 word Abstract describing your team's research.
4. Write a 1-2 paragraph Introduction providing some background and context for your project.
5. Set up your working enviroment (set directory, load packages) using the `/Week8-Projects` folder.
6. Provide a brief (~1 paragraph) description of the dataset.
7. Load the dataset and process in ways necessary for any initial analyses.
8. Use well annotated R chunks to analyze data, make figures, and peform statistics needed to address your quesstions and hypotheses.
9. Write a Discussion and Conclusion section to address the questions and hypotheses that you outlined in you outlined in your Abstract and Introuction.
10. Include citations in the Reference section.
11. Delete the text in this Directions section.
12. By Thursday March 9, 23:59, please submit the completed assignment by creating a **pull request** via GitHub. Your pull request should include this file *Project_assignment.Rmd* and the PDF output of `Knitr` (*Project_assignment.pdf*).

ABSTRACT

1) INTRODUCTION

2) SETUP

```
rm(list=ls())
getwd()
```

```
## [1] "C:/Users/matth/Documents/bin/QB2017_Gibson/Week8-Projects"
```

```
setwd("c:/Users/matth/Documents/bin/QB2017_Gibson/Week3-Beta")


package.list <- c('vegan', 'ade4', 'viridis', 'gplots', 'BiodiversityR', 'indicspecies')
for (package in package.list) {
  if (!require(package, character.only=T, quietly=T)){
    install.packages(package)
    library(package, character.only=T)
  }
}
```

```
## Warning: package 'vegan' was built under R version 3.2.5
```

```
## Warning: package 'permute' was built under R version 3.2.5
```

```
## This is vegan 2.4-2

## Warning: package 'ade4' was built under R version 3.2.5

##
## Attaching package: 'ade4'

## The following object is masked from 'package:vegan':
##
##     cca

## Warning: package 'viridis' was built under R version 3.2.5

## Warning: package 'gplots' was built under R version 3.2.5

##
## Attaching package: 'gplots'

## The following object is masked from 'package:stats':
##
##     lowess

## Warning: package 'BiodiversityR' was built under R version 3.2.5

## BiodiversityR 2.8-0: Use command BiodiversityRGUI() to launch the Graphical User Interface and to lea

## Warning: package 'indicspecies' was built under R version 3.2.5
```

```
package.list <- c('vegan', 'sp', 'gstat','raster', 'RgoogleMaps', 'maptools', 'rgdal',
                  'simba', 'gplots', 'rgeos', 'rgdal', "SoDA")
for (p in package.list){
  library(p, character.only = T)
  #install.packages(p)
}
```

```
## Warning: package 'sp' was built under R version 3.2.5

## Warning: package 'gstat' was built under R version 3.2.5

## Warning: package 'raster' was built under R version 3.2.5

## Warning: package 'RgoogleMaps' was built under R version 3.2.5

## Warning: package 'maptools' was built under R version 3.2.5

## Checking rgeos availability: TRUE

## Warning: package 'rgdal' was built under R version 3.2.5
```

```
## rgdal: version: 1.2-5, (SVN revision 648)
##  Geospatial Data Abstraction Library extensions to R successfully loaded
##  Loaded GDAL runtime: GDAL 2.0.1, released 2015/09/15
##  Path to GDAL shared files: C:/Users/matth/Documents/R/win-library/3.2/rgdal/gdal
##  GDAL does not use iconv for recoding strings.
##  Loaded PROJ.4 runtime: Rel. 4.9.1, 04 March 2015, [PJ_VERSION: 491]
##  Path to PROJ.4 shared files: C:/Users/matth/Documents/R/win-library/3.2/rgdal/proj
##  Linking to sp version: 1.2-4

## Warning: package 'simba' was built under R version 3.2.5

## This is simba 0.3-5

##
## Attaching package: 'simba'

## The following object is masked from 'package:stats':
##
##     mad

## Warning: package 'rgeos' was built under R version 3.2.5

## rgeos version: 0.3-22, (SVN revision 544)
##  GEOS runtime version: 3.5.0-CAPI-1.9.0 r4084
##  Linking to sp version: 1.2-4
##  Polygon checking: TRUE

## Warning: package 'SoDA' was built under R version 3.2.5
```

3) DESCRIPTION OF DATA

4) LOAD THE DATA

```
setwd("c:/Users/matth/Documents/bin/QB2017_Gibson/project")

myData <- read.table("speciesdata_clean.csv", sep=",", header=T, row.names = 1)
envData <- read.table("environmentaldata(1).csv", sep=",", header=T, row.names = 1)


##DATA TRANSFORMATIONS
envData$Topsoil.pH <- (1/(10^envData$Topsoil.pH))
envData$Subsoil.pH <- (1/(10^envData$Subsoil.pH))
envData$Topsoil.Ca <- log(envData$Topsoil.Ca+.01)
envData$Topsoil.Mg <- log(envData$Topsoil.Mg+.01)
envData$Topsoil.Mn <- log(envData$Topsoil.Mn+.01)
envData$Topsoil.Zn <- log(envData$Topsoil.Zn+.1)
envData$Topsoil.NO3 <- log(envData$Topsoil.NO3+.01)
envData$Topsoil.Ca <- log(envData$Topsoil.Ca+.01)
envData$Topsoil.N <- log(envData$Topsoil.N+.01)
envData$Topsoil.Fe <- log(envData$Topsoil.Fe+.01)
envData$Topsoil.Al <- log(envData$Topsoil.Al+.01)
```

5) ANALYSIS: FIGURES AND STATISTICS

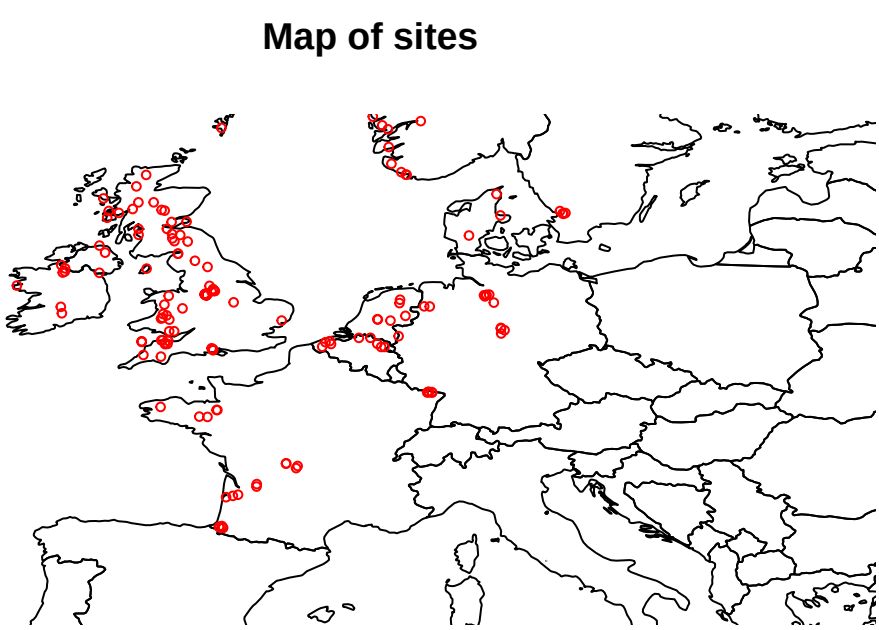
```
#PLOT OF SITES

library(rworldmap)
```

```
## Warning: package 'rworldmap' was built under R version 3.2.5
```

```
## ### Welcome to rworldmap ###
```

```
## For a short introduction type :   vignette('rworldmap')
```

```
newmap <- getMap(resolution="low")
#plot(newmap)
plot(newmap, xlim = c(-10, 20), ylim = c(40, 60), asp = 1, main="Map of sites")

points(envData$Latitude, envData$Longitude, col = "red", cex = .6)
```




```
S.obs <- function(x = ""){
  rowSums(x > 0) * 1
}

C <- function(x = ""){
```

```
  1 - (sum(x == 1) / rowSums(x))
}
d<- dim(myData)

#############################################################################################
#CALCULATE RICHNESS AND COVERAGE AT ALL SITES
s <- seq(2, d[1])
richness <- S.obs(myData[1, 4:ncol(myData)])
coverage <- C(myData[1, 4:ncol(myData)])
for (i in s) {
  coverage <- rbind(coverage, C(myData[i, 4:ncol(myData)]))
  richness <- rbind(richness, S.obs(myData[i, 4:ncol(myData)]))
}
```

Correlations of environmental variables with richness

```
#############################################################################################
#CORRELATIONS OF ENVIRONMENTAL VARIABLES WITH RICHNESS

#Remove plant chemical measurements
envData_reduced <- envData[, 1:23]
#Remove categorical variables
envData_reduced <- subset(envData_reduced, select=-c(Mangement.type, Grazing.intensity))
#Remove country and year
envData_reduced <- subset(envData_reduced, select=-c(Country, Survey.year))

bigFrame <- cbind(as.numeric(richness), envData_reduced[, 3:ncol(envData_reduced)])
colnames(bigFrame) <- c("richness", "Altitude", "Inclination", "vegetation.height", "Soil.depth", "Topso
 "Topsoil.Al",           "Topsoil.Ca",           "Topsoil.Fe",           "Topsoil.Mg",
"Topsoil.Mn",           "Topsoil.Zn",           "Topsoil.NO3",          "Topsoil.NH4",
"Topsoil.Olsen.P",      "Topsoil.C",            "Topsoil.N")
bigFrame2 <- cbind(as.numeric(richness), subset(envData, select= c(Mangement.type, Grazing.intensity, Co
colnames(bigFrame2) <- c("richness", "m.type", "g.type", "country")
#pairs(bigFrame)
cor1 <- cor(bigFrame)
par(mfrow=c(1,1))
library(psych)
```

```
## Warning: package 'psych' was built under R version 3.2.5
```

```
##
## Attaching package: 'psych'
```

```
## The following object is masked from 'package:simba':
##
##     sim
```

```
cor2 <- corr.test(bigFrame, method="pearson", adjust="BH")

#CORRELATIONS OF ENV VARIABLES WITH RICHNESS
cor2$r[,1]
```

```
##          richness          Altitude       Inclination vegetation.height
##       1.000000000      -0.293007022       0.002185831       0.295325791
##        Soil.depth        Topsoil.pH        Subsoil.pH        Topsoil.Al
##      -0.279287039      -0.544764375      -0.371704749      -0.382797381
##        Topsoil.Ca        Topsoil.Fe        Topsoil.Mg        Topsoil.Mn
##      -0.040417920      -0.428979906      -0.012043447       0.029818187
##        Topsoil.Zn       Topsoil.NO3       Topsoil.NH4   Topsoil.Olsen.P
##       0.265807502      -0.157906278      -0.233138436      -0.020855483
##         Topsoil.C         Topsoil.N
##      -0.275525740       0.039817137
```

Plots of richness vs. various environmental variables

```
##############################################################################################
#PLOT OF ENV VARIABLES VS RICHNESS

par(mfrow=c(2,2))

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.pH), data=bigFrame)
print(s <- summary(model1))
```

```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.pH), data = bigFrame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.4590  -5.8611  -0.3666   5.2523  24.4845
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)          3.405e+01  9.413e-01  36.170  < 2e-16 ***
## na.omit(Topsoil.pH) -1.215e+05  1.523e+04  -7.983 3.35e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.449 on 151 degrees of freedom
## Multiple R-squared:  0.2968, Adjusted R-squared:  0.2921
## F-statistic: 63.72 on 1 and 151 DF,  p-value: 3.349e-13
```

```
plot(bigFrame$Topsoil.pH, bigFrame$richness, ylab = "Richness", xlab = "[H+]", main="Richness vs. \n Hy
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = .00015, y = 50, labels = mylabel, cex=.9)
abline(model1)

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.Ca), data=bigFrame)
print(s <- summary(model1))
```

```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.Ca), data = bigFrame)
##
```

```
## Residuals:
##     Min      1Q  Median      3Q     Max
## -21.064  -8.321  -0.854   6.918  28.673
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)           31.290      4.924   6.354 2.34e-09 ***
## na.omit(Topsoil.Ca)   -1.501      3.019  -0.497     0.62
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.07 on 151 degrees of freedom
## Multiple R-squared:  0.001634,   Adjusted R-squared:  -0.004978
## F-statistic: 0.2471 on 1 and 151 DF,  p-value: 0.6199
```

```
plot(bigFrame$Topsoil.Ca, bigFrame$richness, ylab = "Richness", xlab = "Calcium", main = "Richness vs.\n
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = 1, y = 50, labels = mylabel, cex=.9)
abline(model1)

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.Mg), data=bigFrame)
print(s <- summary(model1))
```

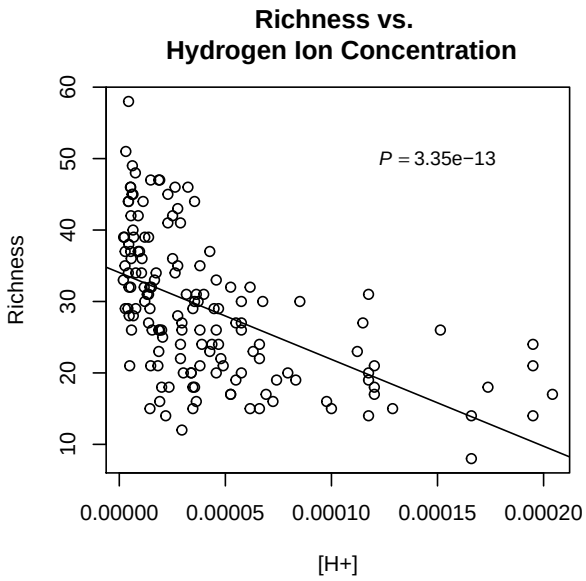
```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.Mg), data = bigFrame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.9624  -8.0143  -0.9364   7.0167  28.9844
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          29.3156     3.0809   9.515   <2e-16 ***
## na.omit(Topsoil.Mg)  -0.1142     0.7719  -0.148    0.883
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.07 on 151 degrees of freedom
## Multiple R-squared:  0.000145,   Adjusted R-squared:  -0.006477
## F-statistic: 0.0219 on 1 and 151 DF,  p-value: 0.8825
```

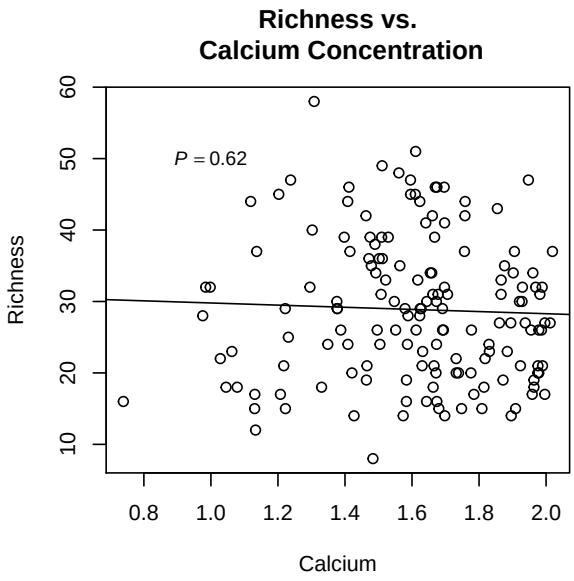
```
plot(bigFrame$Topsoil.Mg, bigFrame$richness, ylab = "Richness", xlab = "Magnesium",main = "Richness vs.
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = 6, y = 50, labels = mylabel, cex=.9)
abline(model1)

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.Mn), data=bigFrame)
print(s <- summary(model1))
```

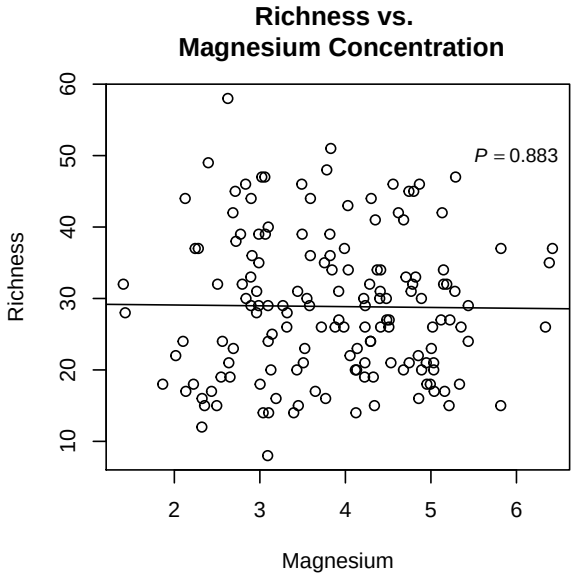
```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.Mn), data = bigFrame)
```

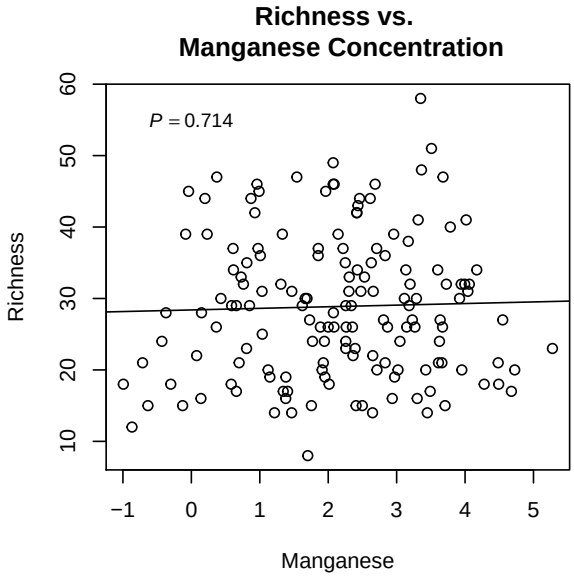
```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.7767  -8.4014  -0.3115   6.9695  28.8532
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          28.3948     1.5442  18.388   <2e-16 ***
## na.omit(Topsoil.Mn)   0.2245     0.6123   0.367    0.714
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.07 on 151 degrees of freedom
## Multiple R-squared:  0.0008891,  Adjusted R-squared:  -0.005728
## F-statistic: 0.1344 on 1 and 151 DF,  p-value: 0.7144
```

```
plot(bigFrame$Topsoil.Mn, bigFrame$richness, ylab = "Richness", xlab = "Manganese",main = "Richness vs.
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = .00015, y = 55, labels = mylabel, cex=.9)
abline(model1)
```










```
par(mfrow=c(2,2))

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.Zn), data=bigFrame)
print(s <- summary(model1))
```

```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.Zn), data = bigFrame)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -18.658  -7.767  -1.005   6.995  31.163
##
```

```
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)           28.6317     0.7885  36.312  < 2e-16 ***
## na.omit(Topsoil.Zn)    1.5749     0.4648   3.388 0.000897 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.712 on 151 degrees of freedom
## Multiple R-squared:  0.07065,    Adjusted R-squared:  0.0645
## F-statistic: 11.48 on 1 and 151 DF,  p-value: 0.0008975
```

```
plot(bigFrame$Topsoil.Zn, bigFrame$richness, ylab = "Richness", xlab = "Zinc",main = "Richness vs. \n Z
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = 3, y = 55, labels = mylabel, cex=.9)
abline(model1)

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.NO3), data=bigFrame)
print(s <- summary(model1))
```

```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.NO3), data = bigFrame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.5619  -8.1825  -0.9709   5.9915  29.5730
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)           29.9249     0.9654  30.999   <2e-16 ***
## na.omit(Topsoil.NO3)  -0.6961     0.3543  -1.965   0.0512 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.948 on 151 degrees of freedom
## Multiple R-squared:  0.02493,    Adjusted R-squared:  0.01848
## F-statistic: 3.861 on 1 and 151 DF,  p-value: 0.05124
```

```
plot(bigFrame$Topsoil.NO3, bigFrame$richness, ylab = "Richness", xlab = "Nitrates",main = "Richness vs.
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = -2, y = 54, labels = mylabel, cex=.9)
abline(model1)

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.N), data=bigFrame)
print(s <- summary(model1))
```

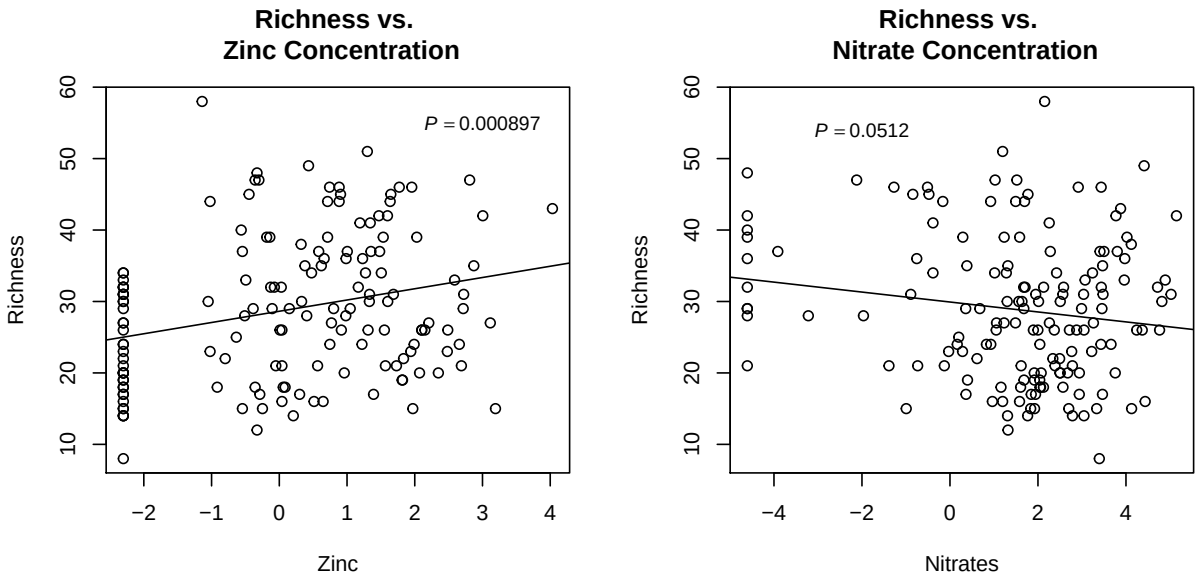
```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.N), data = bigFrame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -21.1447  -8.4746  -0.7482   6.2175  29.8375
```

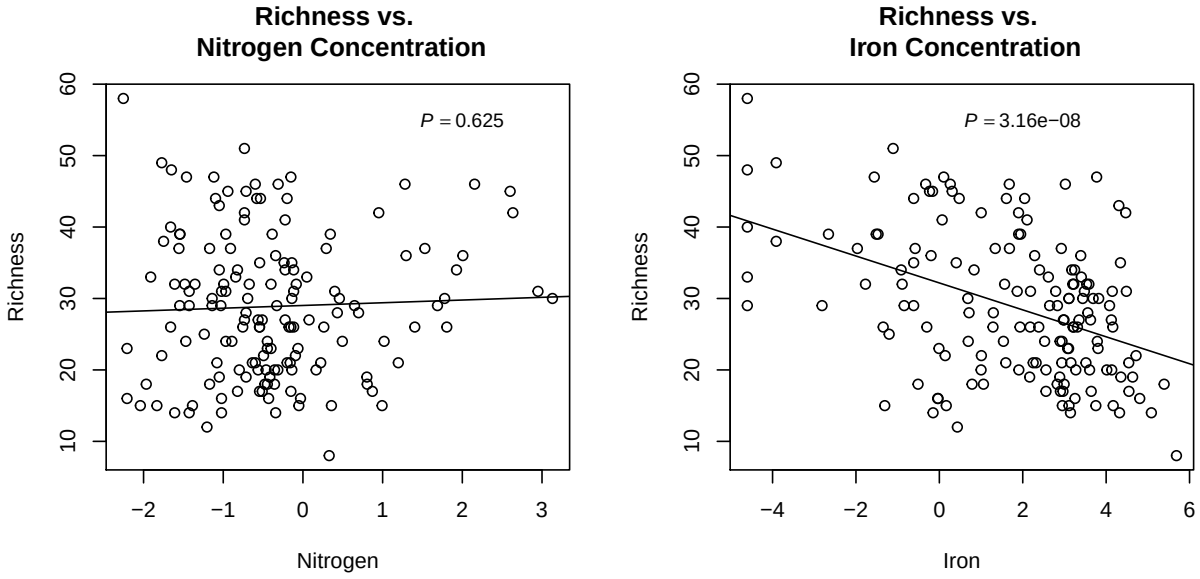
```
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)         29.0195     0.8651   33.55   <2e-16 ***
## na.omit(Topsoil.N)   0.3802     0.7765    0.49    0.625
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.07 on 151 degrees of freedom
## Multiple R-squared:  0.001585,   Adjusted R-squared:  -0.005027
## F-statistic: 0.2398 on 1 and 151 DF,  p-value: 0.6251
```

```
plot(bigFrame$Topsoil.N, bigFrame$richness, ylab = "Richness", xlab = "Nitrogen",main = "Richness vs. \n
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = 2, y = 55, labels = mylabel, cex=.9)
abline(model1)

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.Fe), data=bigFrame)
print(s <- summary(model1))
```

```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.Fe), data = bigFrame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.6429  -7.1156  -0.8555   6.4832  21.9358
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)          32.1749     0.9279  34.676  < 2e-16 ***
## na.omit(Topsoil.Fe)  -1.8850     0.3230  -5.836 3.16e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.101 on 151 degrees of freedom
## Multiple R-squared:  0.184,  Adjusted R-squared:  0.1786
## F-statistic: 34.05 on 1 and 151 DF,  p-value: 3.156e-08
```

```
plot(bigFrame$Topsoil.Fe, bigFrame$richness, ylab = "Richness", xlab = "Iron",main = "Richness vs. \n I
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = 2, y = 55, labels = mylabel, cex=.9)
abline(model1)
```






```
par(mfrow=c(2,2))

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.Al), data=bigFrame)
print(s <- summary(model1))
```

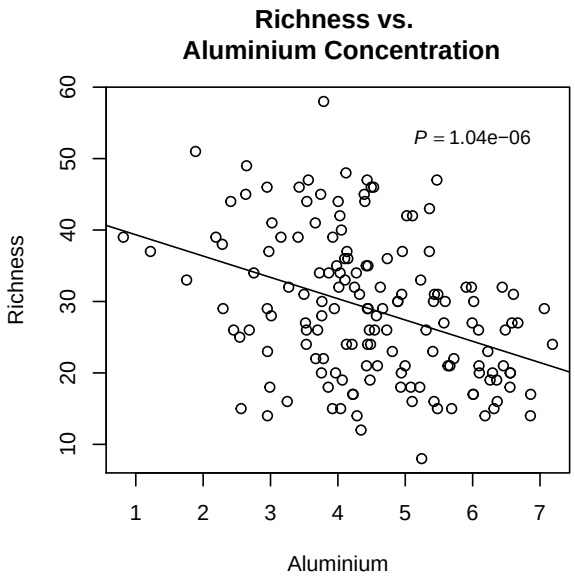
```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.Al), data = bigFrame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.6761  -7.3363  -0.6854   6.0489  26.9773
##
```

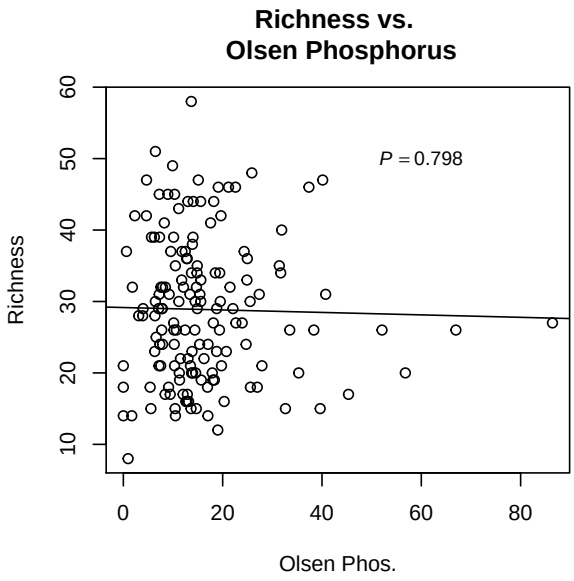
```
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)           42.3218     2.7459  15.413  < 2e-16 ***
## na.omit(Topsoil.Al)  -2.9826     0.5858  -5.092 1.04e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.307 on 151 degrees of freedom
## Multiple R-squared:  0.1465, Adjusted R-squared:  0.1409
## F-statistic: 25.93 on 1 and 151 DF,  p-value: 1.043e-06
```

```
plot(bigFrame$Topsoil.Al, bigFrame$richness, ylab = "Richness", xlab = "Aluminium",main = "Richness vs.
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = 6, y = 53, labels = mylabel, cex=.9)
abline(model1)

model1 <- lm(as.numeric(richness) ~ na.omit(Topsoil.Olsen.P), data=bigFrame)
print(s <- summary(model1))
```

```
##
## Call:
## lm(formula = as.numeric(richness) ~ na.omit(Topsoil.Olsen.P),
##     data = bigFrame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -21.1369  -8.1534  -0.6708   7.0652  29.0813
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               29.15341    1.35493  21.516   <2e-16 ***
## na.omit(Topsoil.Olsen.P) -0.01716    0.06694  -0.256    0.798
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.07 on 151 degrees of freedom
## Multiple R-squared:  0.000435,   Adjusted R-squared:  -0.006185
## F-statistic: 0.06571 on 1 and 151 DF,  p-value: 0.798
```

```
plot(bigFrame$Topsoil.Olsen.P, bigFrame$richness, ylab = "Richness", xlab = "Olsen Phos.",main = "Richn
mylabel = bquote(italic(P) == .(format(s$coefficients[2,4], digits = 3)))
text(x = 60, y = 50, labels = mylabel, cex=.9)
abline(model1)
```





Ordination of taxonomic diversity

```
par(mfrow=c(1,1))

myData <- myData[, 4:ncol(myData)]
spec.bray <- vegdist(myData, method = "bray")

spec.pcoa <- cmdscale(spec.bray, eig=T, k=3)
explainvar1 <- round(spec.pcoa$eig[1] / sum(spec.pcoa$eig), 3) * 100
explainvar2 <- round(spec.pcoa$eig[2] / sum(spec.pcoa$eig), 3) * 100
explainvar3 <- round(spec.pcoa$eig[3] / sum(spec.pcoa$eig), 3) * 100
sum.eig <- sum(explainvar1, explainvar2, explainvar3)
```

```
#Variance explained by first axis
explainvar1
```

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

```
#variance explained by second axis
explainvar2
```

```
## [1] 12.5
```

```
#variance explained by third axis
explainvar3
```

```
## [1] 7.7
```

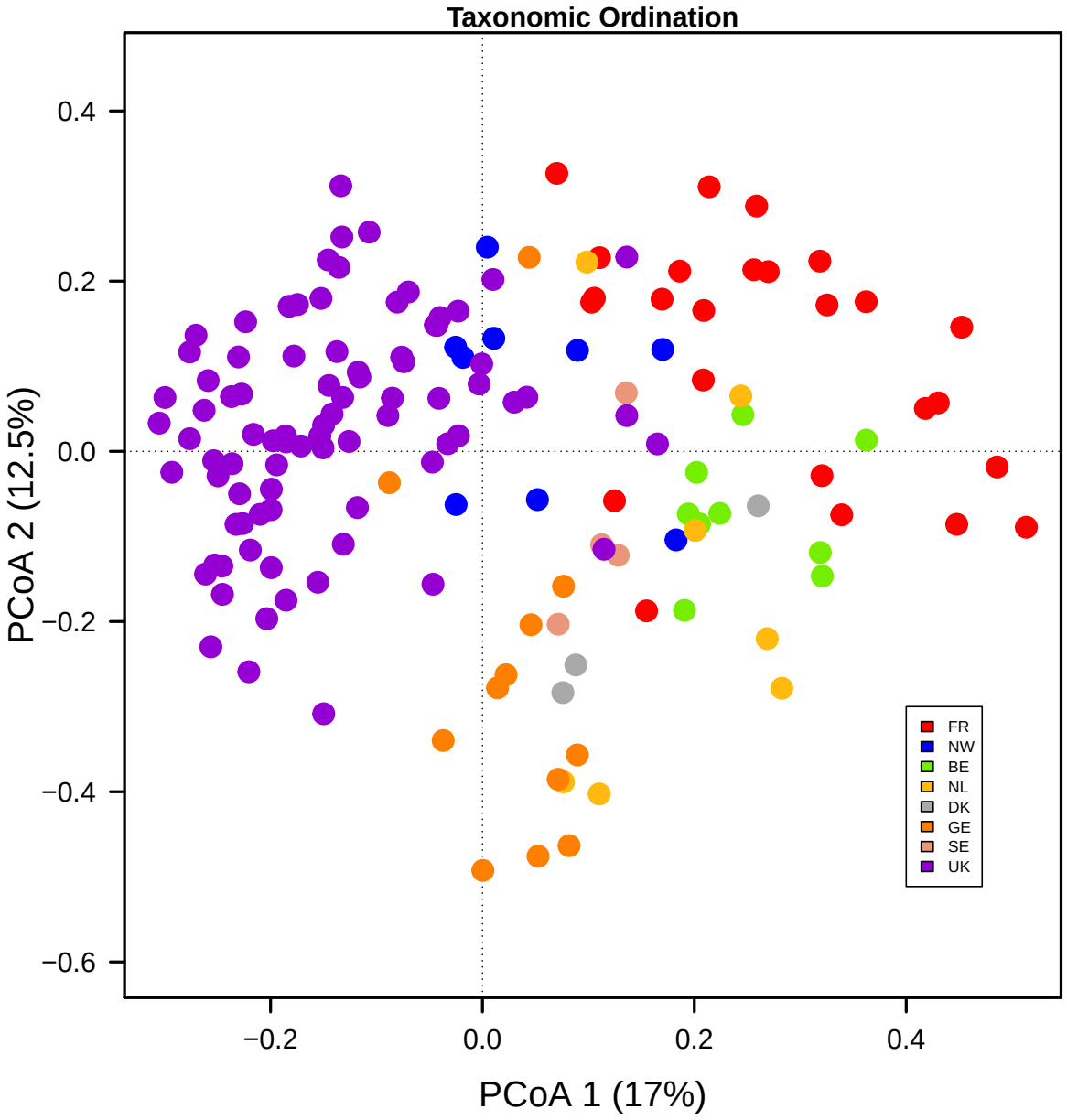
```
sum.eig
```

```
## [1] 37.2
```

```
par(mar = c(5, 5, 1, 2) + 0.1)

plot(spec.pcoa$points[ ,1], spec.pcoa$points[ ,2], ylim = c(-0.6, 0.45),
     xlab = paste("PCoA 1 (", explainvar1, "%)", sep = ""),
     ylab = paste("PCoA 2 (", explainvar2, "%)", sep = ""),
     main = "Taxonomic Ordination",
     pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = F)

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

```
data2 <- as.data.frame(spec.pcoa$points)
data2$cun <- substr(row.names(data2),1,2)
fr <- data2[which(data2$cun == "FR"),]
nw <- data2[which(data2$cun == "NW"),]
be <- data2[which(data2$cun == "BE"),]
nl <- data2[which(data2$cun == "NL"),]
dk <- data2[which(data2$cun == "DK"),]
ge <- data2[which(data2$cun == "GE"),]
se <- data2[which(data2$cun == "SE"),]
uk <- data2[which(data2$cun == "UK"),]


points(fr[,1], fr[,2] ,pch=19, cex=2, bg="red", col="red")
points(nw[,1], nw[,2],pch=19, cex=2, bg="blue", col="blue")
points(be[,1], be[,2],pch=19, cex=2, bg="chartreuse2", col="chartreuse2")
```

```
points(nl[,1], nl[,2],pch=19, cex=2, bg="darkgoldenrod1", col="darkgoldenrod1")
points(dk[,1], dk[,2],pch=19, cex=2, bg="darkgray", col="darkgray")
points(ge[,1], ge[,2],pch=19, cex=2, bg="darkorange1", col="darkorange1")
points(se[,1], se[,2],pch=19, cex=2, bg="darksalmon", col="darksalmon")
points(uk[,1], uk[,2],pch=19, cex=2, bg="darkviolet", col="darkviolet")

legend(.4,-.3,c("FR","NW", "BE", "NL", "DK", "GE", "SE", "UK"), cex = .7, col=c("red", "blue", "chartreu
                                                                    "darkgray", "darkorange1", "darksalmo
```




```
#I plotted just the country code...full site names were too long
#(spec.pcoa$points[ ,1], spec.pcoa$points[ ,2],
#       pch = 19, cex = 3, bg = "gray", col = "gray")
#text(spec.pcoa$points[ ,1], spec.pcoa$points[ ,2],
```

```
#     labels = substr(row.names(spec.pcoa$points),1,2))


specREL <- myData
  for(i in 1:nrow(myData)){
    specREL[i, ] = myData[i, ]/ sum(myData[i, ])
  }

spec.pcoa <- add.spec.scores(spec.pcoa, specREL, method = "pcoa.scores")
par(mfrow=c(1,1))
#Is just a mess.........



#text(spec.pcoa$cproj[ ,1], spec.pcoa$cproj[ ,2],
#     labels = row.names(spec.pcoa$cproj), col = "black")


spe.corr <- add.spec.scores(spec.pcoa, specREL, method = "cor.scores")$cproj
corrcut <- 0.8
imp.spp <- spe.corr[abs(spe.corr[, 1]) >= corrcut | abs(spe.corr[, 2]) >= corrcut, ]

#As expected, this takes quite a long time...

fit <- envfit(spec.pcoa, specREL, perm = 999)
```

Constrained Ordination

```
#Isolating the environmental chemical data (removing categorical variables and other plant chemical mea
env.chem <- na.omit(envData_reduced[, 7:19])
env.chem <- as.matrix(env.chem)
#is.na(env.chem) <- do.call(cbind,lapply(env.chem, is.infinite))


###REMOVING SITES WITH MISSING DATA
myData <- myData[rownames(myData) != "GE712", ]
myData <- myData[rownames(myData) != "GE713", ]
myData <- myData[rownames(myData) != "GE715", ]

spec.db <- vegdist(myData, method = "bray", diag=T)
eu.dbrda <- dbrda(spec.db ~ ., as.data.frame(env.chem), na.action=na.omit)
#ordiplot(eu.dbrda)
eu.dbrda.mod0 <- dbrda(spec.db ~ 1, as.data.frame(env.chem), na.action=na.omit)

#ordiplot(eu.dbrda.mod0)
eu.dbrda.mod1 <- dbrda(spec.db ~ ., as.data.frame(env.chem), na.action=na.omit)
#Model selection
eu.dbrda <- ordiR2step(eu.dbrda.mod0, eu.dbrda.mod1, perm.max= 200)
```

```
## Step: R2.adj= 0
## Call: spec.db ~ 1
##
```

```
##                   R2.adjusted
## <All variables>   0.233072065
## + Topsoil.Fe      0.075624279
## + Topsoil.Ca      0.065833552
## + Topsoil.pH      0.064150290
## + Topsoil.Mn      0.060049384
## + Topsoil.Mg      0.055727100
## + Topsoil.C       0.050388134
## + Topsoil.NO3     0.047068612
## + Topsoil.Al      0.046614164
## + Topsoil.NH4     0.027716821
## + Subsoil.pH      0.026762163
## + Topsoil.Zn      0.014471709
## + Topsoil.N       0.011048427
## + Topsoil.Olsen.P 0.005914765
## <none>            0.000000000
##
##              Df    AIC     F Pr(>F)
## + Topsoil.Fe  1 522.36 13.19  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.07562428
## Call: spec.db ~ Topsoil.Fe
##
##                   R2.adjusted
## <All variables>    0.23307206
## + Topsoil.Mn       0.12732460
## + Topsoil.Ca       0.11681302
## + Topsoil.Mg       0.11078257
## + Topsoil.NO3      0.11030513
## + Topsoil.pH       0.09960237
## + Topsoil.N        0.09262335
## + Topsoil.C        0.09247877
## + Topsoil.Zn       0.08860550
## + Topsoil.Al       0.08562377
## + Subsoil.pH       0.08525023
## + Topsoil.NH4      0.08101239
## + Topsoil.Olsen.P  0.07733366
## <none>             0.07562428
## - Topsoil.Fe       0.00000000
##
##              Df    AIC     F Pr(>F)
## + Topsoil.Mn  1 514.71 9.768  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.1273246
## Call: spec.db ~ Topsoil.Fe + Topsoil.Mn
##
##                   R2.adjusted
## <All variables>    0.23307206
## + Topsoil.NO3      0.15169404
## + Topsoil.pH       0.15150635
```

```
## + Topsoil.C        0.14337982
## + Topsoil.N        0.14279249
## + Topsoil.Zn       0.14189425
## + Topsoil.Al       0.14184523
## + Topsoil.Mg       0.14001400
## + Topsoil.Ca       0.13890345
## + Subsoil.pH       0.13729855
## + Topsoil.NH4      0.13253609
## <none>             0.12732460
## + Topsoil.Olsen.P  0.12625317
## - Topsoil.Mn       0.07562428
## - Topsoil.Fe       0.06004938
##
##               Df    AIC      F Pr(>F)
## + Topsoil.NO3  1 511.44 5.2229  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.151694
## Call: spec.db ~ Topsoil.Fe + Topsoil.Mn + Topsoil.NO3
##
##                   R2.adjusted
## <All variables>    0.23307206
## + Topsoil.pH       0.17676623
## + Topsoil.Zn       0.16677750
## + Topsoil.C        0.16671856
## + Topsoil.N        0.16640736
## + Topsoil.Al       0.16448259
## + Topsoil.Mg       0.16425426
## + Topsoil.Ca       0.16190450
## + Subsoil.pH       0.16178178
## + Topsoil.NH4      0.15712883
## <none>             0.15169404
## + Topsoil.Olsen.P  0.15050505
## - Topsoil.NO3      0.12732460
## - Topsoil.Mn       0.11030513
## - Topsoil.Fe       0.09009497
##
##              Df    AIC      F Pr(>F)
## + Topsoil.pH  1 507.91 5.4465  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.1767662
## Call: spec.db ~ Topsoil.Fe + Topsoil.Mn + Topsoil.NO3 + Topsoil.pH
##
##                   R2.adjusted
## <All variables>     0.2330721
## + Topsoil.Mg        0.1877969
## + Topsoil.N         0.1877436
## + Topsoil.Al        0.1877387
## + Topsoil.C         0.1870879
## + Topsoil.Zn        0.1869582
## + Topsoil.Ca        0.1866070
```

```
## + Topsoil.NH4       0.1790030
## <none>              0.1767662
## + Topsoil.Olsen.P   0.1756853
## + Subsoil.pH        0.1743496
## - Topsoil.pH        0.1516940
## - Topsoil.NO3       0.1515063
## - Topsoil.Fe        0.1502700
## - Topsoil.Mn        0.1350870
##
##              Df    AIC      F Pr(>F)
## + Topsoil.Mg  1 506.85 2.9693  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.1877969
## Call: spec.db ~ Topsoil.Fe + Topsoil.Mn + Topsoil.NO3 + Topsoil.pH +      Topsoil.Mg
##
##                   R2.adjusted
## <All variables>     0.2330721
## + Topsoil.Ca        0.1994352
## + Topsoil.Al        0.1989927
## + Topsoil.N         0.1984216
## + Topsoil.Zn        0.1965825
## + Topsoil.C         0.1952748
## + Topsoil.NH4       0.1902348
## <none>              0.1877969
## + Topsoil.Olsen.P   0.1866656
## + Subsoil.pH        0.1855067
## - Topsoil.Mg        0.1767662
## - Topsoil.Fe        0.1699456
## - Topsoil.pH        0.1642543
## - Topsoil.NO3       0.1629218
## - Topsoil.Mn        0.1622390
##
##              Df    AIC      F Pr(>F)
## + Topsoil.Ca  1 505.64 3.0934  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.1994352
## Call: spec.db ~ Topsoil.Fe + Topsoil.Mn + Topsoil.NO3 + Topsoil.pH +      Topsoil.Mg + Topsoil.Ca
##
##                   R2.adjusted
## <All variables>     0.2330721
## + Topsoil.N         0.2104360
## + Topsoil.Al        0.2100873
## + Topsoil.Zn        0.2090907
## + Topsoil.C         0.2068020
## + Topsoil.NH4       0.2025284
## <none>              0.1994352
## + Topsoil.Olsen.P   0.1982575
## + Subsoil.pH        0.1971121
## - Topsoil.Ca        0.1877969
## - Topsoil.Mg        0.1866070
```

```
## - Topsoil.Fe        0.1822691
## - Topsoil.Mn        0.1810869
## - Topsoil.NO3       0.1751459
## - Topsoil.pH        0.1751232
##
##             Df    AIC      F Pr(>F)
## + Topsoil.N  1 504.51 2.9924  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.210436
## Call: spec.db ~ Topsoil.Fe + Topsoil.Mn + Topsoil.NO3 + Topsoil.pH +      Topsoil.Mg + Topsoil.Ca + T
##
##                   R2.adjusted
## <All variables>     0.2330721
## + Topsoil.Al        0.2214184
## + Topsoil.Zn        0.2181452
## + Topsoil.C         0.2173624
## + Topsoil.NH4       0.2144296
## <none>              0.2104360
## + Topsoil.Olsen.P   0.2099301
## + Subsoil.pH        0.2081573
## - Topsoil.N         0.1994352
## - Topsoil.Ca        0.1984216
## - Topsoil.Mg        0.1975323
## - Topsoil.Mn        0.1937521
## - Topsoil.Fe        0.1914406
## - Topsoil.pH        0.1888177
## - Topsoil.NO3       0.1871851
##
##              Df    AIC     F Pr(>F)
## + Topsoil.Al  1 503.35 3.003  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2214184
## Call: spec.db ~ Topsoil.Fe + Topsoil.Mn + Topsoil.NO3 + Topsoil.pH +      Topsoil.Mg + Topsoil.Ca + T
##
##                   R2.adjusted
## <All variables>     0.2330721
## + Topsoil.C         0.2283626
## + Topsoil.Zn        0.2266993
## + Topsoil.NH4       0.2237910
## <none>              0.2214184
## + Topsoil.Olsen.P   0.2209549
## + Subsoil.pH        0.2192024
## - Topsoil.Al        0.2104360
## - Topsoil.N         0.2100873
## - Topsoil.Ca        0.2099196
## - Topsoil.Mg        0.2083460
## - Topsoil.Fe        0.2045175
## - Topsoil.Mn        0.2026679
## - Topsoil.pH        0.2010439
## - Topsoil.NO3       0.1996790
```

```
##
##             Df    AIC      F Pr(>F)
## + Topsoil.C  1 502.94 2.2689  0.004 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2283626
## Call: spec.db ~ Topsoil.Fe + Topsoil.Mn + Topsoil.NO3 + Topsoil.pH +      Topsoil.Mg + Topsoil.Ca + T
##
##                   R2.adjusted
## + Topsoil.Zn        0.2337449
## <All variables>     0.2330721
## + Topsoil.NH4       0.2305760
## <none>              0.2283626
## + Topsoil.Olsen.P   0.2283209
## + Subsoil.pH        0.2258360
## - Topsoil.C         0.2214184
## - Topsoil.Mg        0.2176699
## - Topsoil.N         0.2175420
## - Topsoil.Al        0.2173624
## - Topsoil.Ca        0.2167750
## - Topsoil.pH        0.2152465
## - Topsoil.Fe        0.2112044
## - Topsoil.Mn        0.2088409
## - Topsoil.NO3       0.2062968
```

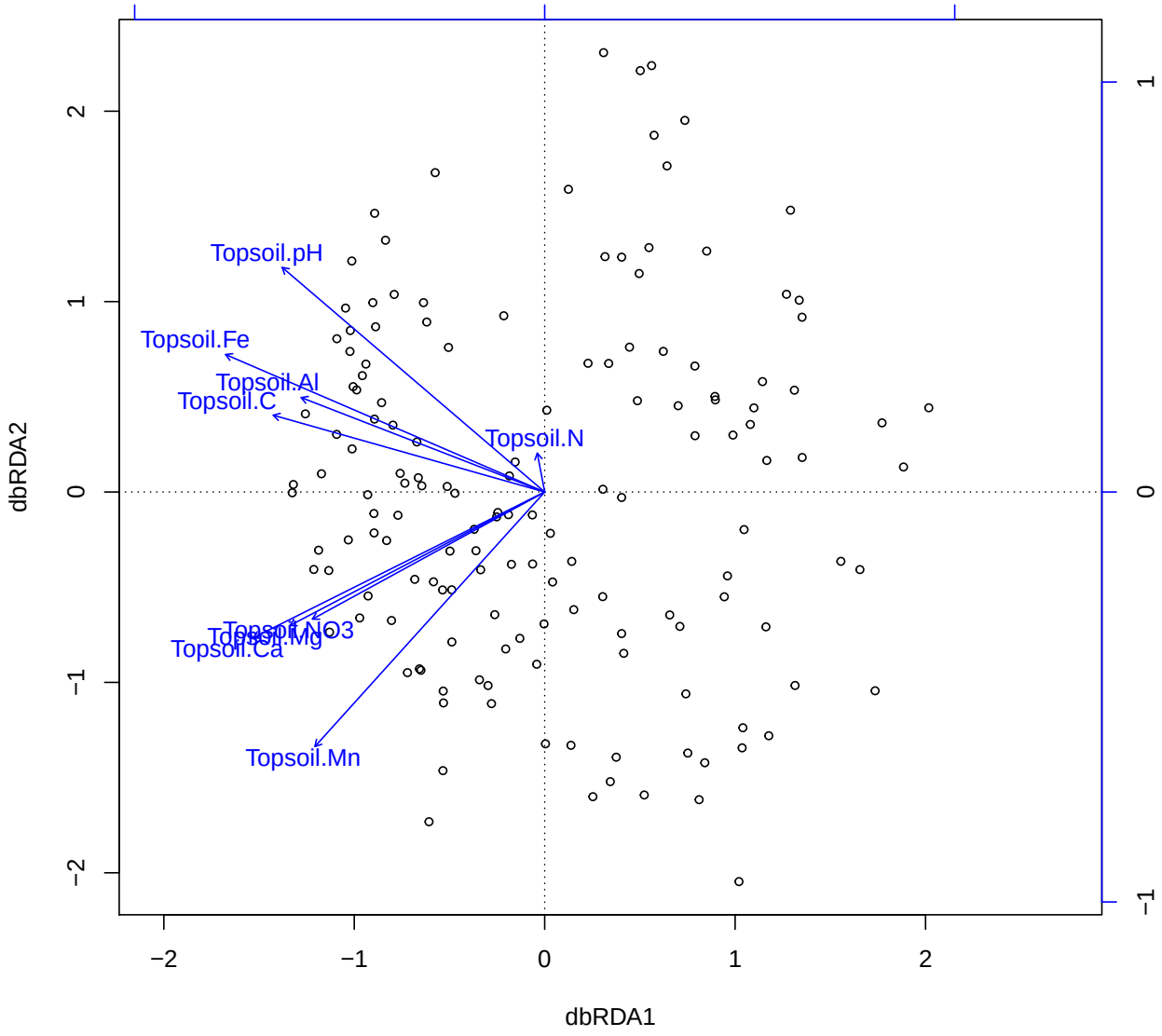
```
eu.dbrda$call
```

```
## dbrda(formula = spec.db ~ Topsoil.Fe + Topsoil.Mn + Topsoil.NO3 +
##     Topsoil.pH + Topsoil.Mg + Topsoil.Ca + Topsoil.N + Topsoil.Al +
##     Topsoil.C, data = as.data.frame(env.chem), na.action = na.omit)
```

```
eu.dbrda$anova
```

```
##                   R2.adj Df    AIC       F Pr(>F)
## + Topsoil.Fe    0.075624  1 522.36 13.1899  0.002 **
## + Topsoil.Mn    0.127325  1 514.71  9.7680  0.002 **
## + Topsoil.NO3   0.151694  1 511.44  5.2229  0.002 **
## + Topsoil.pH    0.176766  1 507.91  5.4465  0.002 **
## + Topsoil.Mg    0.187797  1 506.85  2.9693  0.002 **
## + Topsoil.Ca    0.199435  1 505.64  3.0934  0.002 **
## + Topsoil.N     0.210436  1 504.51  2.9924  0.002 **
## + Topsoil.Al    0.221418  1 503.35  3.0030  0.002 **
## + Topsoil.C     0.228363  1 502.94  2.2689  0.004 **
## <All variables> 0.233072
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ordiplot(eu.dbrda)
```




```
par(mfrow=c(1,1))

#3. use a permutation test to determine the significance of the constrained analysis,
permutest(eu.dbrda, permutations = 999)
```

```
##
## Permutation test for dbrda
##
## Permutation: free
## Number of permutations: 999
##
## Call: dbrda(formula = spec.db ~ Topsoil.Fe + Topsoil.Mn +
## Topsoil.NO3 + Topsoil.pH + Topsoil.Mg + Topsoil.Ca + Topsoil.N +
```

```
## Topsoil.Al + Topsoil.C, data = as.data.frame(env.chem), na.action
## = na.omit)
## Permutation test for all constrained eigenvalues
## Pseudo-F:     5.899541 (with 9, 140 Degrees of Freedom)
## Significance:     0.001
```

```
#4 use a permutation test to determine the correlation of each environmental factor on the constrained
envfit(eu.dbrda, env.chem[,c(1,3,4,5,6,7,9,12,13)], perm = 999)
```

```
##
## ***VECTORS
##
##               dbRDA1   dbRDA2     r2 Pr(>r)
## Topsoil.pH  -0.80907  0.58772 0.4518  0.001 ***
## Topsoil.Al  -0.95215  0.30563 0.2711  0.001 ***
## Topsoil.Ca  -0.91650 -0.40002 0.4249  0.001 ***
## Topsoil.Fe  -0.94148  0.33707 0.4777  0.001 ***
## Topsoil.Mg  -0.90968 -0.41530 0.3304  0.001 ***
## Topsoil.Mn  -0.72660 -0.68706 0.4471  0.001 ***
## Topsoil.NO3 -0.90289 -0.42988 0.2795  0.001 ***
## Topsoil.C   -0.97439  0.22485 0.3196  0.001 ***
## Topsoil.N   -0.20596  0.97856 0.0055  0.681
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
```

```
#5
dbrda.explainvar1 <- round(eu.dbrda$CCA$eig[1] /
                           sum(c(eu.dbrda$CCA$eig, eu.dbrda$CA$eig)), 3) * 100
dbrda.explainvar2 <- round(eu.dbrda$CCA$eig[2] /
                           sum(c(eu.dbrda$CCA$eig, eu.dbrda$CA$eig)), 3) * 100
dbrda.explainvar1
```

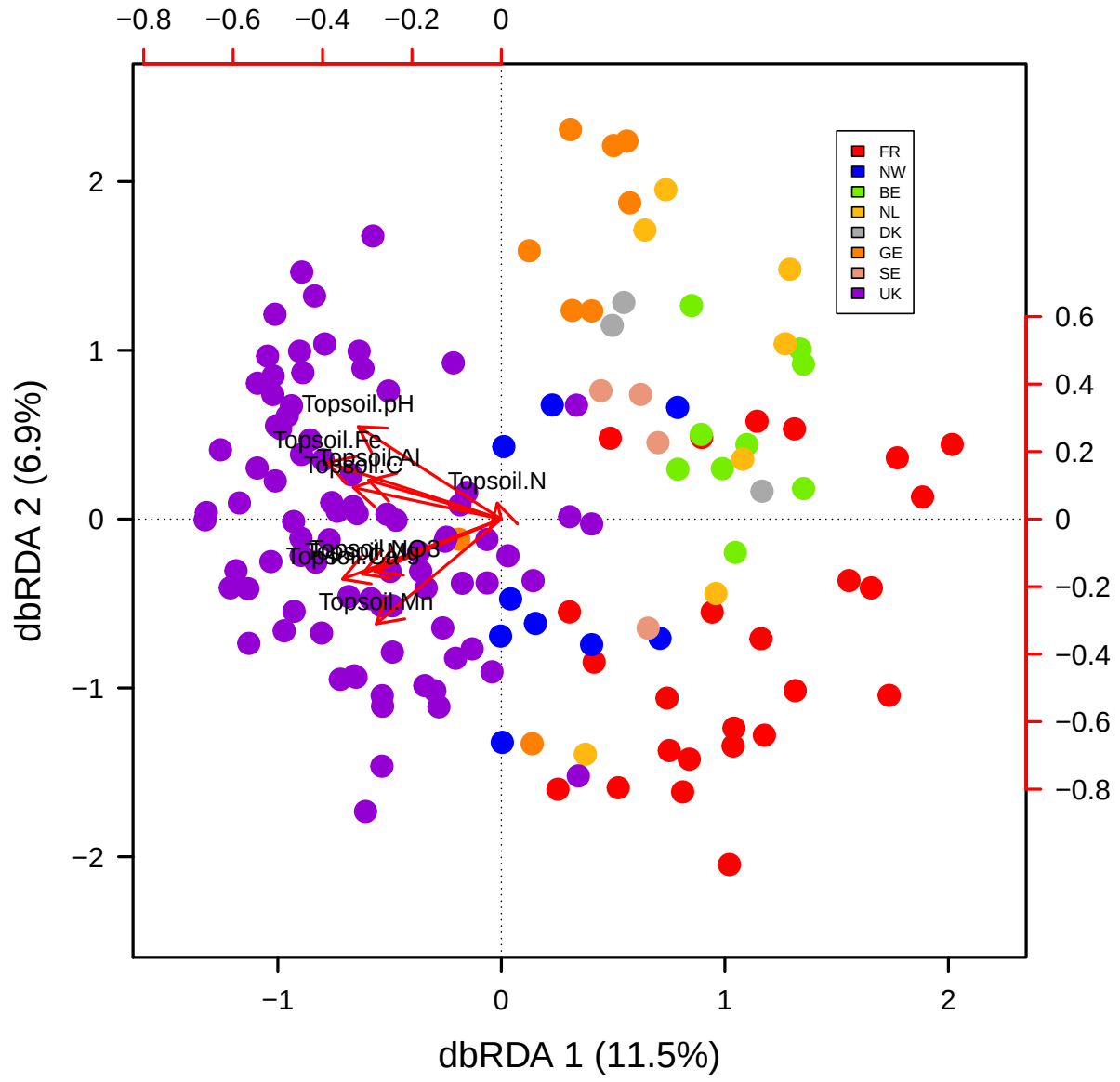
```
## dbRDA1
##   11.5
```

```
dbrda.explainvar2
```

```
## dbRDA2
##    6.9
```

```
#6
par(mar = c(5, 5, 4, 4) + 0.1)

plot(scores(eu.dbrda, display = "wa"), xlim = c(-1.5, 2.2), ylim = c(-2.4, 2.5),
xlab = paste("dbRDA 1 (", dbrda.explainvar1, "%)", sep = ""),
ylab = paste("dbRDA 2 (", dbrda.explainvar2, "%)", sep = ""),
pch = 16, cex = 2.0, type = "n", cex.lab = 1.5, cex.axis = 1.2, axes = FALSE)

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

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

data <- as.data.frame(scores(eu.dbrda)$sites)
data$cun <- substr(row.names(data),1,2)
fr <- data[which(data$cun == "FR"),]
nw <- data[which(data$cun == "NW"),]
be <- data[which(data$cun == "BE"),]
nl <- data[which(data$cun == "NL"),]
dk <- data[which(data$cun == "DK"),]
ge <- data[which(data$cun == "GE"),]
se <- data[which(data$cun == "SE"),]
uk <- data[which(data$cun == "UK"),]


points(fr$dbRDA1, fr$dbRDA2,pch=19, cex=2, bg="red", col="red")
points(nw$dbRDA1, nw$dbRDA2,pch=19, cex=2, bg="blue", col="blue")
points(be$dbRDA1, be$dbRDA2,pch=19, cex=2, bg="chartreuse2", col="chartreuse2")
points(nl$dbRDA1, nl$dbRDA2,pch=19, cex=2, bg="darkgoldenrod1", col="darkgoldenrod1")
points(dk$dbRDA1, dk$dbRDA2,pch=19, cex=2, bg="darkgray", col="darkgray")
points(ge$dbRDA1, ge$dbRDA2,pch=19, cex=2, bg="darkorange1", col="darkorange1")
points(se$dbRDA1, se$dbRDA2,pch=19, cex=2, bg="darksalmon", col="darksalmon")
points(uk$dbRDA1, uk$dbRDA2,pch=19, cex=2, bg="darkviolet", col="darkviolet")

legend(1.5,2.3,c("FR","NW", "BE", "NL", "DK", "GE", "SE", "UK"), cex = .7, col=c("red", "blue", "chartr
                                                                    "darkgray", "darkorange1", "darksalm
#text(scores(eu.dbrda, display = "wa"),
 # labels = substr(row.names(scores(eu.dbrda, display = "wa")),1,2))

vectors <- scores(eu.dbrda, display = "bp")

#row.names(vectors) <- c("pH", "har", "pho", "nit", "amm", "oxy", "bdo")

arrows(0, 0, vectors[,1], vectors[, 2],
  lwd = 2, lty = 1, length = 0.2, col = "red")
text(vectors[,1], vectors[, 2], pos = 3,
  labels = row.names(vectors))

axis(side = 3, lwd.ticks=2, cex.axis=1.2, las = 1, col = "red", lwd = 2.2,
at = pretty(range(vectors[, 1])) * 2, labels = pretty(range(vectors[, 1])))
axis(side = 4, lwd.ticks=2, cex.axis=1.2, las = 1, col = "red", lwd = 2.2,
at = pretty(range(vectors[, 2])) * 2, labels = pretty(range(vectors[, 2])))
```




```
par(mfrow=c(1,1))
```

Variance Partitioning

```
#Remove plant measurements
envData_reduced <- envData[, 1:23]
#Remove categorical variables
envData_reduced <- subset(envData_reduced, select=-c(Mangement.type, Grazing.intensity))
#Remove country and year
envData_reduced <- subset(envData_reduced, select=-c(Country, Survey.year))
envData_reduced <- envData_reduced[rownames(envData_reduced) != "GE712", ]
envData_reduced <- envData_reduced[rownames(envData_reduced) != "GE713", ]
envData_reduced <- envData_reduced[rownames(envData_reduced) != "GE715", ]
```

```r
#Remove unneeded data
myData <- myData[, 4:ncol(myData)]
XY_soda <- as.data.frame(geoXY(envData_reduced$Latitude, envData_reduced$Longitude))
#XY_soda <- cbind(row.names((envData_reduced)), XY_soda)
#colnames(XY_soda) <- c("site", "X", "Y")
#Begin DISTANCE DECAY CODE
xy <- data.frame(site.name = row.names(envData_reduced), lats = envData_reduced$Latitude, lons = envDat
#coordinates(xy) <- ~lats+lons
comm.dist <- 1 - vegdist(myData)
#proj4string(xy) <- CRS("+proj=longlat +datum=NAD83")
#UTM <- spTransform(xy, CRS("+proj=utm + zone=51 ellps=WGS84"))
#UTM <- as.data.frame(UTM)
xy$lats_utm <- XY_soda$Y
xy$lons_utm <- XY_soda$X

#lats <- as.numeric(xy$lats_utm)
#lons <- as.numeric(xy$lons_utm)

lats <- XY_soda$Y
lons <- XY_soda$X

# 3) Calculate geographic distance between plots and assign to the variable 'coord.dist'
coord.dist <- dist(as.matrix(lats, lons))




par(mfrow=c(1,1))

eu.dbrda$anova
```

```
##                   R2.adj Df    AIC       F Pr(>F)
## + Topsoil.Fe    0.075624  1 522.36 13.1899  0.002 **
## + Topsoil.Mn    0.127325  1 514.71  9.7680  0.002 **
## + Topsoil.NO3   0.151694  1 511.44  5.2229  0.002 **
## + Topsoil.pH    0.176766  1 507.91  5.4465  0.002 **
## + Topsoil.Mg    0.187797  1 506.85  2.9693  0.002 **
## + Topsoil.Ca    0.199435  1 505.64  3.0934  0.002 **
## + Topsoil.N     0.210436  1 504.51  2.9924  0.002 **
## + Topsoil.Al    0.221418  1 503.35  3.0030  0.002 **
## + Topsoil.C     0.228363  1 502.94  2.2689  0.004 **
## <All variables> 0.233072
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
env.mod <- model.matrix(~ Topsoil.pH + Topsoil.Ca + Topsoil.Mn + Topsoil.C + Topsoil.NO3 + Topsoil.N + 
rs <- rowSums(myData)/sum(myData)

xy <- as.data.frame(xy)

#xy <- xy[xy$site.name != "GE712", ]
#xy <- xy[xy$site.name != "GE713", ]
#xy <- xy[xy$site.name != "GE715", ]
```

```
coord.mat <- as.matrix(xy[,4:5])

doubs.pcnmw <- pcnm(dist(coord.mat), w = rs, dist.ret = T)

doubs.pcnmw$values > 0
```

```
##   [1]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [12]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [23]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [34]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [45]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [56]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [67]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [78]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE
##  [89] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [100] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [111] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [122] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [133] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [144] FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
doubs.space <- as.data.frame(scores(doubs.pcnmw))
doubs.pcnm.mod0 <- dbrda(spec.db ~ 1, doubs.space)
doubs.pcnm.mod1 <- dbrda(spec.db ~ ., doubs.space)
step.pcnm <- ordiR2step(doubs.pcnm.mod0, doubs.pcnm.mod1, perm.max = 200)
```

```
## Step: R2.adj= 0
## Call: spec.db ~ 1
##
##                   R2.adjusted
## <All variables>  2.918731e-01
## + PCNM1          1.016273e-01
## + PCNM6          3.610363e-02
## + PCNM2          3.442265e-02
## + PCNM3          3.439273e-02
## + PCNM4          2.752947e-02
## + PCNM9          1.866204e-02
## + PCNM10         1.757677e-02
## + PCNM5          1.241833e-02
## + PCNM8          6.526548e-03
## + PCNM7          3.317421e-03
## + PCNM38         2.406063e-03
## + PCNM18         8.989146e-04
## + PCNM27         8.629368e-04
## + PCNM46         8.301070e-04
## + PCNM26         7.003689e-04
## + PCNM12         6.862519e-04
## + PCNM49         5.449833e-04
## + PCNM47         3.050463e-04
## <none>           0.000000e+00
## + PCNM11        -7.623141e-05
```

```
## + PCNM34        -1.012485e-04
## + PCNM24        -3.859401e-04
## + PCNM20        -4.345229e-04
## + PCNM25        -4.402215e-04
## + PCNM17        -5.352488e-04
## + PCNM15        -5.904304e-04
## + PCNM16        -6.852381e-04
## + PCNM32        -7.452453e-04
## + PCNM23        -8.121311e-04
## + PCNM60        -8.306764e-04
## + PCNM14        -8.371541e-04
## + PCNM56        -9.866668e-04
## + PCNM66        -1.011360e-03
## + PCNM43        -1.129803e-03
## + PCNM41        -1.152784e-03
## + PCNM29        -1.230324e-03
## + PCNM40        -1.273457e-03
## + PCNM19        -1.332624e-03
## + PCNM22        -1.392065e-03
## + PCNM13        -1.426682e-03
## + PCNM30        -1.441060e-03
## + PCNM54        -1.514160e-03
## + PCNM80        -1.539456e-03
## + PCNM55        -1.833391e-03
## + PCNM31        -2.014929e-03
## + PCNM28        -2.115215e-03
## + PCNM44        -2.151982e-03
## + PCNM64        -2.192573e-03
## + PCNM62        -2.232253e-03
## + PCNM37        -2.313985e-03
## + PCNM58        -2.366037e-03
## + PCNM59        -2.419075e-03
## + PCNM21        -2.496898e-03
## + PCNM45        -2.503849e-03
## + PCNM42        -2.505483e-03
## + PCNM33        -2.730645e-03
## + PCNM39        -2.738112e-03
## + PCNM53        -2.879785e-03
## + PCNM71        -2.940335e-03
## + PCNM82        -3.023909e-03
## + PCNM52        -3.030643e-03
## + PCNM36        -3.206509e-03
## + PCNM57        -3.229240e-03
## + PCNM85        -3.238024e-03
## + PCNM67        -3.264833e-03
## + PCNM35        -3.405024e-03
## + PCNM75        -3.656464e-03
## + PCNM48        -4.058909e-03
## + PCNM63        -4.082231e-03
## + PCNM79        -4.082556e-03
## + PCNM50        -4.084553e-03
## + PCNM77        -4.087416e-03
## + PCNM84        -4.120699e-03
## + PCNM69        -4.127541e-03
```

```
## + PCNM83        -4.157285e-03
## + PCNM74        -4.158496e-03
## + PCNM86        -4.206517e-03
## + PCNM78        -4.340406e-03
## + PCNM68        -4.340885e-03
## + PCNM76        -4.495923e-03
## + PCNM72        -4.587021e-03
## + PCNM81        -4.642168e-03
## + PCNM61        -5.149019e-03
## + PCNM70        -5.216329e-03
## + PCNM73        -5.415176e-03
## + PCNM51        -5.697853e-03
## + PCNM65        -5.716235e-03
##
##         Df    AIC      F Pr(>F)
## + PCNM1  1 518.08 17.855  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.1016273
## Call: spec.db ~ PCNM1
##
##                 R2.adjusted
## <All variables>  0.29187313
## + PCNM2          0.14116893
## + PCNM6          0.13895269
## + PCNM3          0.13615924
## + PCNM4          0.12985725
## + PCNM9          0.12110907
## + PCNM10         0.11942193
## + PCNM5          0.11496558
## + PCNM8          0.10939982
## + PCNM7          0.10537946
## + PCNM38         0.10420731
## + PCNM27         0.10344046
## + PCNM46         0.10326272
## + PCNM26         0.10325542
## + PCNM18         0.10324738
## + PCNM12         0.10294832
## + PCNM49         0.10291377
## + PCNM47         0.10273830
## + PCNM34         0.10222485
## + PCNM11         0.10201758
## + PCNM24         0.10192489
## + PCNM25         0.10177654
## + PCNM17         0.10172568
## + PCNM15         0.10167161
## + PCNM32         0.10166534
## <none>           0.10162727
## + PCNM20         0.10159965
## + PCNM56         0.10154070
## + PCNM16         0.10147374
## + PCNM23         0.10139727
## + PCNM14         0.10136139
```

```
## + PCNM60         0.10120758
## + PCNM43         0.10118946
## + PCNM41         0.10117888
## + PCNM13         0.10117727
## + PCNM29         0.10103897
## + PCNM19         0.10102498
## + PCNM66         0.10101425
## + PCNM22         0.10087938
## + PCNM54         0.10081413
## + PCNM30         0.10079756
## + PCNM80         0.10076062
## + PCNM40         0.10075650
## + PCNM55         0.10032447
## + PCNM44         0.10019801
## + PCNM28         0.10012701
## + PCNM37         0.10009625
## + PCNM64         0.10004555
## + PCNM42         0.09991887
## + PCNM59         0.09986127
## + PCNM45         0.09982441
## + PCNM21         0.09978089
## + PCNM58         0.09974842
## + PCNM62         0.09964967
## + PCNM33         0.09959004
## + PCNM39         0.09955581
## + PCNM31         0.09945937
## + PCNM53         0.09945215
## + PCNM71         0.09943421
## + PCNM82         0.09927652
## + PCNM52         0.09920482
## + PCNM57         0.09908688
## + PCNM85         0.09904532
## + PCNM67         0.09899010
## + PCNM35         0.09887472
## + PCNM36         0.09881035
## + PCNM75         0.09865356
## + PCNM48         0.09824742
## + PCNM50         0.09823368
## + PCNM84         0.09821059
## + PCNM63         0.09820921
## + PCNM79         0.09820362
## + PCNM77         0.09819647
## + PCNM83         0.09812405
## + PCNM74         0.09812123
## + PCNM86         0.09801854
## + PCNM78         0.09794566
## + PCNM69         0.09793591
## + PCNM68         0.09792825
## + PCNM76         0.09779158
## + PCNM72         0.09768231
## + PCNM81         0.09761118
## + PCNM61         0.09713275
## + PCNM70         0.09705483
## + PCNM73         0.09685810
```

```
## + PCNM51         0.09664314
## + PCNM65         0.09663074
## - PCNM1          0.00000000
##
##         Df    AIC      F Pr(>F)
## + PCNM2  1 512.31 7.8141  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.1411689
## Call: spec.db ~ PCNM1 + PCNM2
##
##                 R2.adjusted
## <All variables>  0.29187313
## + PCNM6          0.17881353
## + PCNM3          0.17631372
## + PCNM4          0.17156509
## + PCNM9          0.16102194
## + PCNM10         0.15899411
## + PCNM5          0.15618931
## + PCNM8          0.14928592
## + PCNM7          0.14522121
## + PCNM38         0.14411092
## + PCNM18         0.14346120
## + PCNM27         0.14313371
## + PCNM26         0.14310505
## + PCNM46         0.14285333
## + PCNM12         0.14280428
## + PCNM49         0.14273416
## + PCNM47         0.14251486
## + PCNM34         0.14217839
## + PCNM17         0.14189997
## + PCNM15         0.14180690
## + PCNM24         0.14179781
## + PCNM11         0.14178810
## + PCNM25         0.14163838
## + PCNM16         0.14153410
## + PCNM20         0.14146116
## + PCNM32         0.14144737
## + PCNM56         0.14137321
## + PCNM23         0.14121263
## <none>           0.14116893
## + PCNM14         0.14115585
## + PCNM41         0.14101556
## + PCNM43         0.14099972
## + PCNM60         0.14095969
## + PCNM66         0.14090042
## + PCNM29         0.14083740
## + PCNM19         0.14077994
## + PCNM13         0.14062496
## + PCNM30         0.14059272
## + PCNM40         0.14059193
## + PCNM80         0.14055996
## + PCNM54         0.14052160
```

```
## + PCNM22         0.14036767
## + PCNM55         0.14017631
## + PCNM44         0.13999855
## + PCNM28         0.13997847
## + PCNM37         0.13990479
## + PCNM64         0.13984252
## + PCNM59         0.13965857
## + PCNM45         0.13962654
## + PCNM42         0.13958076
## + PCNM39         0.13956042
## + PCNM58         0.13954807
## + PCNM62         0.13945870
## + PCNM21         0.13943167
## + PCNM33         0.13939926
## + PCNM53         0.13926594
## + PCNM71         0.13924240
## + PCNM31         0.13923168
## + PCNM82         0.13907511
## + PCNM52         0.13900507
## + PCNM57         0.13890922
## + PCNM85         0.13885381
## + PCNM67         0.13884185
## + PCNM35         0.13864771
## + PCNM36         0.13859376
## + PCNM75         0.13843389
## + PCNM48         0.13803465
## + PCNM84         0.13800075
## + PCNM63         0.13799822
## + PCNM79         0.13799039
## + PCNM77         0.13798335
## + PCNM50         0.13793766
## + PCNM83         0.13791820
## + PCNM74         0.13790559
## + PCNM86         0.13780409
## + PCNM78         0.13773415
## + PCNM68         0.13770258
## + PCNM69         0.13769928
## + PCNM76         0.13757643
## + PCNM72         0.13746791
## + PCNM81         0.13739683
## + PCNM61         0.13691357
## + PCNM70         0.13683136
## + PCNM73         0.13663801
## + PCNM65         0.13641606
## + PCNM51         0.13639261
## - PCNM2          0.10162727
## - PCNM1          0.03442265
##
##         Df    AIC      F Pr(>F)
## + PCNM6  1 506.57 7.7387  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.1788135
```

```
## Call: spec.db ~ PCNM1 + PCNM2 + PCNM6
##
##                 R2.adjusted
## <All variables>  0.29187313
## + PCNM3          0.21399936
## + PCNM4          0.20834976
## + PCNM9          0.19847742
## + PCNM10         0.19695618
## + PCNM5          0.19358897
## + PCNM8          0.18719327
## + PCNM7          0.18316255
## + PCNM38         0.18214114
## + PCNM46         0.18144766
## + PCNM18         0.18136120
## + PCNM27         0.18110293
## + PCNM26         0.18104300
## + PCNM12         0.18072567
## + PCNM49         0.18052178
## + PCNM47         0.18042123
## + PCNM34         0.18009004
## + PCNM17         0.17982324
## + PCNM24         0.17971743
## + PCNM15         0.17967519
## + PCNM11         0.17961714
## + PCNM56         0.17957176
## + PCNM25         0.17953988
## + PCNM16         0.17943819
## + PCNM32         0.17939373
## + PCNM20         0.17936631
## + PCNM23         0.17913281
## + PCNM14         0.17907296
## + PCNM41         0.17891907
## + PCNM60         0.17886432
## <none>           0.17881353
## + PCNM66         0.17881126
## + PCNM43         0.17876309
## + PCNM29         0.17872114
## + PCNM19         0.17868188
## + PCNM13         0.17852826
## + PCNM40         0.17851350
## + PCNM30         0.17851209
## + PCNM80         0.17848792
## + PCNM54         0.17841516
## + PCNM22         0.17832280
## + PCNM55         0.17806679
## + PCNM44         0.17791136
## + PCNM28         0.17785054
## + PCNM37         0.17777957
## + PCNM64         0.17764558
## + PCNM59         0.17755197
## + PCNM39         0.17751108
## + PCNM45         0.17750467
## + PCNM58         0.17744514
## + PCNM42         0.17740220
```

```
## + PCNM62         0.17733489
## + PCNM21         0.17732154
## + PCNM33         0.17730527
## + PCNM53         0.17722874
## + PCNM71         0.17713314
## + PCNM31         0.17711044
## + PCNM82         0.17697428
## + PCNM52         0.17693310
## + PCNM57         0.17678015
## + PCNM67         0.17673748
## + PCNM85         0.17671764
## + PCNM35         0.17654354
## + PCNM36         0.17648113
## + PCNM75         0.17631661
## + PCNM48         0.17591282
## + PCNM63         0.17589310
## + PCNM84         0.17588933
## + PCNM79         0.17587065
## + PCNM77         0.17585653
## + PCNM50         0.17582659
## + PCNM83         0.17579960
## + PCNM74         0.17579355
## + PCNM86         0.17565972
## + PCNM78         0.17562390
## + PCNM68         0.17557729
## + PCNM69         0.17554988
## + PCNM76         0.17545671
## + PCNM72         0.17534685
## + PCNM81         0.17525234
## + PCNM61         0.17493305
## + PCNM70         0.17458744
## + PCNM73         0.17449171
## + PCNM51         0.17423862
## + PCNM65         0.17423211
## - PCNM6          0.14116893
## - PCNM2          0.13895269
## - PCNM1          0.07088726
##
##         Df    AIC      F Pr(>F)
## + PCNM3  1 500.97 7.5358  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2139994
## Call: spec.db ~ PCNM1 + PCNM2 + PCNM6 + PCNM3
##
##                 R2.adjusted
## <All variables>   0.2918731
## + PCNM4           0.2440992
## + PCNM9           0.2341311
## + PCNM10          0.2319854
## + PCNM5           0.2291556
## + PCNM8           0.2224604
## + PCNM7           0.2186240
```

```
## + PCNM38          0.2176871
## + PCNM18          0.2168516
## + PCNM27          0.2167685
## + PCNM46          0.2162943
## + PCNM12          0.2161759
## + PCNM26          0.2161422
## + PCNM47          0.2158841
## + PCNM49          0.2158359
## + PCNM34          0.2154467
## + PCNM17          0.2152649
## + PCNM24          0.2151238
## + PCNM56          0.2151068
## + PCNM15          0.2150064
## + PCNM11          0.2149330
## + PCNM25          0.2149014
## + PCNM16          0.2148539
## + PCNM20          0.2148016
## + PCNM32          0.2146866
## + PCNM14          0.2145873
## + PCNM23          0.2144963
## + PCNM41          0.2143233
## + PCNM66          0.2142496
## + PCNM43          0.2141844
## + PCNM60          0.2141758
## + PCNM29          0.2141491
## + PCNM19          0.2140981
## + PCNM40          0.2140237
## <none>            0.2139994
## + PCNM13          0.2139562
## + PCNM30          0.2139422
## + PCNM80          0.2139187
## + PCNM54          0.2138118
## + PCNM22          0.2137100
## + PCNM55          0.2134972
## + PCNM44          0.2134546
## + PCNM28          0.2133379
## + PCNM64          0.2131018
## + PCNM59          0.2130125
## + PCNM37          0.2129458
## + PCNM58          0.2129216
## + PCNM45          0.2129183
## + PCNM42          0.2128848
## + PCNM39          0.2128651
## + PCNM62          0.2127531
## + PCNM21          0.2127240
## + PCNM33          0.2126642
## + PCNM53          0.2126121
## + PCNM71          0.2125577
## + PCNM31          0.2124847
## + PCNM82          0.2123904
## + PCNM52          0.2123035
## + PCNM57          0.2122079
## + PCNM85          0.2121544
## + PCNM67          0.2121514
```

```
## + PCNM35          0.2119853
## + PCNM36          0.2119086
## + PCNM75          0.2117513
## + PCNM63          0.2113022
## + PCNM84          0.2113013
## + PCNM48          0.2112948
## + PCNM79          0.2112884
## + PCNM77          0.2112663
## + PCNM50          0.2112209
## + PCNM74          0.2112124
## + PCNM83          0.2112069
## + PCNM86          0.2110591
## + PCNM78          0.2110357
## + PCNM68          0.2109595
## + PCNM76          0.2108636
## + PCNM69          0.2107947
## + PCNM72          0.2107492
## + PCNM81          0.2106599
## + PCNM61          0.2102923
## + PCNM70          0.2099694
## + PCNM73          0.2098952
## + PCNM65          0.2096309
## + PCNM51          0.2094643
## - PCNM3           0.1788135
## - PCNM6           0.1763137
## - PCNM2           0.1735237
## - PCNM1           0.1059469
##
##         Df    AIC      F Pr(>F)
## + PCNM4  1 496.07 6.7739  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2440992
## Call: spec.db ~ PCNM1 + PCNM2 + PCNM6 + PCNM3 + PCNM4
##
##                 R2.adjusted
## <All variables>   0.2918731
## + PCNM9           0.2645228
## + PCNM10          0.2629907
## + PCNM5           0.2599510
## + PCNM8           0.2528087
## + PCNM7           0.2490472
## + PCNM38          0.2480509
## + PCNM18          0.2471123
## + PCNM27          0.2470984
## + PCNM46          0.2467008
## + PCNM12          0.2464944
## + PCNM26          0.2464170
## + PCNM47          0.2462651
## + PCNM49          0.2461802
## + PCNM34          0.2457141
## + PCNM17          0.2455751
## + PCNM11          0.2454316
```

```
## + PCNM56          0.2454231
## + PCNM24          0.2453356
## + PCNM15          0.2452493
## + PCNM25          0.2451818
## + PCNM20          0.2451605
## + PCNM16          0.2451151
## + PCNM14          0.2450799
## + PCNM32          0.2449534
## + PCNM23          0.2447956
## + PCNM41          0.2446284
## + PCNM43          0.2445961
## + PCNM66          0.2445855
## + PCNM29          0.2445125
## + PCNM19          0.2444019
## + PCNM60          0.2443454
## + PCNM40          0.2442765
## + PCNM30          0.2442319
## + PCNM80          0.2442258
## + PCNM13          0.2442069
## <none>            0.2440992
## + PCNM22          0.2440093
## + PCNM54          0.2439480
## + PCNM55          0.2438070
## + PCNM28          0.2436391
## + PCNM44          0.2435289
## + PCNM64          0.2434089
## + PCNM59          0.2433155
## + PCNM37          0.2432735
## + PCNM42          0.2431861
## + PCNM39          0.2431771
## + PCNM58          0.2431675
## + PCNM21          0.2431374
## + PCNM45          0.2430563
## + PCNM62          0.2430534
## + PCNM33          0.2429881
## + PCNM71          0.2428581
## + PCNM53          0.2428490
## + PCNM31          0.2427888
## + PCNM82          0.2426914
## + PCNM52          0.2426109
## + PCNM57          0.2425588
## + PCNM85          0.2424596
## + PCNM67          0.2424322
## + PCNM35          0.2423396
## + PCNM36          0.2422032
## + PCNM75          0.2420472
## + PCNM84          0.2416009
## + PCNM63          0.2415966
## + PCNM48          0.2415931
## + PCNM79          0.2415554
## + PCNM77          0.2415517
## + PCNM50          0.2415271
## + PCNM83          0.2414985
## + PCNM74          0.2414837
```

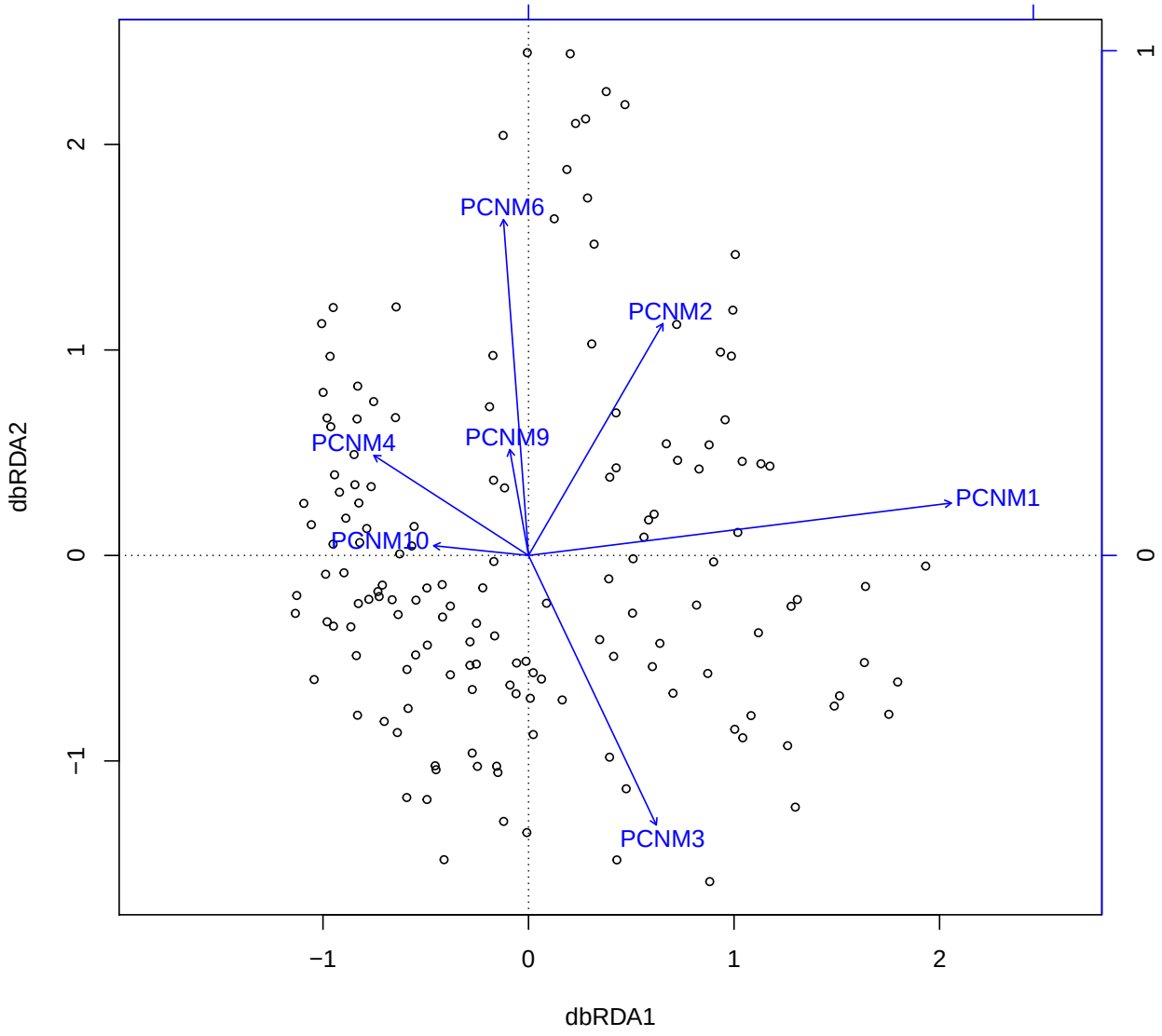
```
## + PCNM86          0.2413474
## + PCNM78          0.2413294
## + PCNM68          0.2411875
## + PCNM76          0.2411401
## + PCNM72          0.2410373
## + PCNM69          0.2409540
## + PCNM81          0.2409468
## + PCNM61          0.2405799
## + PCNM70          0.2402515
## + PCNM73          0.2401777
## + PCNM65          0.2398975
## + PCNM51          0.2397665
## - PCNM4           0.2139994
## - PCNM3           0.2083498
## - PCNM6           0.2072667
## - PCNM2           0.2013784
## - PCNM1           0.1352628
##
##         Df    AIC      F Pr(>F)
## + PCNM9  1 492.92 4.9988  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2645228
## Call: spec.db ~ PCNM1 + PCNM2 + PCNM6 + PCNM3 + PCNM4 + PCNM9
##
##                 R2.adjusted
## <All variables>   0.2918731
## + PCNM10          0.2837784
## + PCNM5           0.2806397
## + PCNM8           0.2732740
## + PCNM7           0.2696557
## + PCNM38          0.2685536
## + PCNM18          0.2678197
## + PCNM27          0.2676726
## + PCNM46          0.2672273
## + PCNM12          0.2670779
## + PCNM26          0.2669497
## + PCNM47          0.2668489
## + PCNM49          0.2666595
## + PCNM34          0.2662971
## + PCNM17          0.2661677
## + PCNM24          0.2659115
## + PCNM11          0.2658492
## + PCNM25          0.2658096
## + PCNM15          0.2657818
## + PCNM56          0.2657794
## + PCNM20          0.2657287
## + PCNM16          0.2656887
## + PCNM14          0.2656615
## + PCNM32          0.2655409
## + PCNM23          0.2654191
## + PCNM43          0.2652530
## + PCNM41          0.2651913
```

```
## + PCNM66          0.2651656
## + PCNM29          0.2650860
## + PCNM19          0.2649807
## + PCNM60          0.2649162
## + PCNM40          0.2649003
## + PCNM13          0.2648167
## + PCNM30          0.2648020
## + PCNM80          0.2647893
## + PCNM22          0.2646246
## <none>            0.2645228
## + PCNM54          0.2645108
## + PCNM55          0.2643728
## + PCNM28          0.2641910
## + PCNM64          0.2641285
## + PCNM44          0.2641177
## + PCNM42          0.2639961
## + PCNM59          0.2638763
## + PCNM37          0.2638477
## + PCNM39          0.2637989
## + PCNM21          0.2637505
## + PCNM58          0.2637349
## + PCNM62          0.2636122
## + PCNM45          0.2635980
## + PCNM33          0.2635314
## + PCNM71          0.2634354
## + PCNM53          0.2634103
## + PCNM31          0.2633612
## + PCNM82          0.2632490
## + PCNM52          0.2631663
## + PCNM57          0.2631223
## + PCNM85          0.2630229
## + PCNM67          0.2629881
## + PCNM35          0.2629211
## + PCNM36          0.2627637
## + PCNM75          0.2625997
## + PCNM48          0.2621576
## + PCNM84          0.2621509
## + PCNM63          0.2621102
## + PCNM79          0.2621085
## + PCNM77          0.2620993
## + PCNM50          0.2620765
## + PCNM83          0.2620393
## + PCNM74          0.2620352
## + PCNM78          0.2618998
## + PCNM86          0.2618992
## + PCNM68          0.2617345
## + PCNM76          0.2616873
## + PCNM72          0.2615855
## + PCNM69          0.2615011
## + PCNM81          0.2614917
## + PCNM61          0.2612460
## + PCNM70          0.2607565
## + PCNM73          0.2607099
## + PCNM65          0.2604428
```

```
## + PCNM51          0.2602942
## - PCNM9           0.2440992
## - PCNM4           0.2341311
## - PCNM3           0.2282981
## - PCNM6           0.2278559
## - PCNM2           0.2213850
## - PCNM1           0.1548088
##
##          Df    AIC      F Pr(>F)
## + PCNM10  1 489.89 4.8446  0.002 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Step: R2.adj= 0.2837784
## Call: spec.db ~ PCNM1 + PCNM2 + PCNM6 + PCNM3 + PCNM4 + PCNM9 + PCNM10
##
##                 R2.adjusted
## + PCNM5           0.3004875
## + PCNM8           0.2928001
## <All variables>   0.2918731
## + PCNM7           0.2896059
## + PCNM38          0.2879104
## + PCNM18          0.2871135
## + PCNM27          0.2871112
## + PCNM46          0.2866392
## + PCNM12          0.2864710
## + PCNM26          0.2862751
## + PCNM47          0.2861650
## + PCNM49          0.2860577
## + PCNM34          0.2856697
## + PCNM17          0.2855724
## + PCNM15          0.2855601
## + PCNM24          0.2853139
## + PCNM25          0.2852044
## + PCNM11          0.2851970
## + PCNM56          0.2851572
## + PCNM20          0.2850962
## + PCNM16          0.2850845
## + PCNM14          0.2850617
## + PCNM32          0.2849185
## + PCNM23          0.2847747
## + PCNM43          0.2846497
## + PCNM66          0.2845920
## + PCNM41          0.2845836
## + PCNM29          0.2844113
## + PCNM19          0.2843946
## + PCNM13          0.2843230
## + PCNM40          0.2843136
## + PCNM80          0.2842142
## + PCNM30          0.2841884
## + PCNM60          0.2840729
## + PCNM22          0.2840452
## + PCNM54          0.2838986
## + PCNM55          0.2838664
```

```
## <none>           0.2837784
## + PCNM64         0.2835409
## + PCNM28         0.2835399
## + PCNM44         0.2835079
## + PCNM42         0.2833851
## + PCNM59         0.2833579
## + PCNM37         0.2832583
## + PCNM58         0.2832420
## + PCNM21         0.2831999
## + PCNM39         0.2831420
## + PCNM62         0.2829975
## + PCNM45         0.2829770
## + PCNM33         0.2829183
## + PCNM71         0.2828449
## + PCNM53         0.2827943
## + PCNM31         0.2827878
## + PCNM82         0.2826334
## + PCNM52         0.2825515
## + PCNM85         0.2823995
## + PCNM67         0.2823608
## + PCNM57         0.2823411
## + PCNM35         0.2822453
## + PCNM36         0.2821431
## + PCNM75         0.2820319
## + PCNM84         0.2815265
## + PCNM79         0.2814893
## + PCNM63         0.2814852
## + PCNM48         0.2814838
## + PCNM77         0.2814766
## + PCNM50         0.2814434
## + PCNM83         0.2814211
## + PCNM74         0.2814096
## + PCNM78         0.2812750
## + PCNM86         0.2812629
## + PCNM68         0.2811197
## + PCNM76         0.2810640
## + PCNM72         0.2809528
## + PCNM69         0.2808909
## + PCNM81         0.2808629
## + PCNM61         0.2806398
## + PCNM70         0.2801778
## + PCNM73         0.2800647
## + PCNM65         0.2798047
## + PCNM51         0.2796794
## - PCNM10         0.2645228
## - PCNM9          0.2629907
## - PCNM4          0.2524684
## - PCNM3          0.2477224
## - PCNM6          0.2467728
## - PCNM2          0.2406098
## - PCNM1          0.1738131
```

```
plot(step.pcnm)
```




```
step.pcnm$anova
```

```
##                  R2.adj Df    AIC       F Pr(>F)
## + PCNM1         0.10163  1 518.08 17.8554  0.002 **
## + PCNM2         0.14117  1 512.31  7.8141  0.002 **
## + PCNM6         0.17881  1 506.57  7.7387  0.002 **
## + PCNM3         0.21400  1 500.97  7.5358  0.002 **
## + PCNM4         0.24410  1 496.07  6.7739  0.002 **
## + PCNM9         0.26452  1 492.92  4.9988  0.002 **
## + PCNM10        0.28378  1 489.89  4.8446  0.002 **
## <All variables> 0.29187
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
space.mod <- model.matrix(~ PCNM1 + PCNM3 + PCNM2 + PCNM6 + PCNM4 + PCNM9 + PCNM7 + PCNM11 + PCNM8 + PCN


doubs.total.env <- dbrda(spec.db ~ env.mod)
doubs.total.space <- dbrda(spec.db ~ space.mod)

doubs.env.cond.space <- dbrda(spec.db ~ env.mod + Condition(space.mod))
doubs.space.cond.env <- dbrda(spec.db ~ space.mod + Condition(space.mod))


permutest(doubs.env.cond.space, permutations = 999)
```

```
##
## Permutation test for dbrda
##
## Permutation: free
## Number of permutations: 999
##
## Call: dbrda(formula = spec.db ~ env.mod + Condition(space.mod))
## Permutation test for all constrained eigenvalues
## Pseudo-F:     2.667353 (with 8, 131 Degrees of Freedom)
## Significance:     0.001
```

```
permutest(doubs.space.cond.env, permutations = 999)
```

```
##
## Permutation test for dbrda
##
##
## Call: dbrda(formula = spec.db ~ space.mod + Condition(space.mod))
## Permutation test for all constrained eigenvalues
## Pseudo-F:     NA (with 0, 139 Degrees of Freedom)
## Significance:     NA
```

```
permutest(doubs.total.env, permutations = 999)
```

```
##
## Permutation test for dbrda
##
## Permutation: free
## Number of permutations: 999
##
## Call: dbrda(formula = spec.db ~ env.mod)
## Permutation test for all constrained eigenvalues
## Pseudo-F:     5.816973 (with 8, 141 Degrees of Freedom)
## Significance:     0.001
```

```
permutest(doubs.total.space, permutations = 999)
```

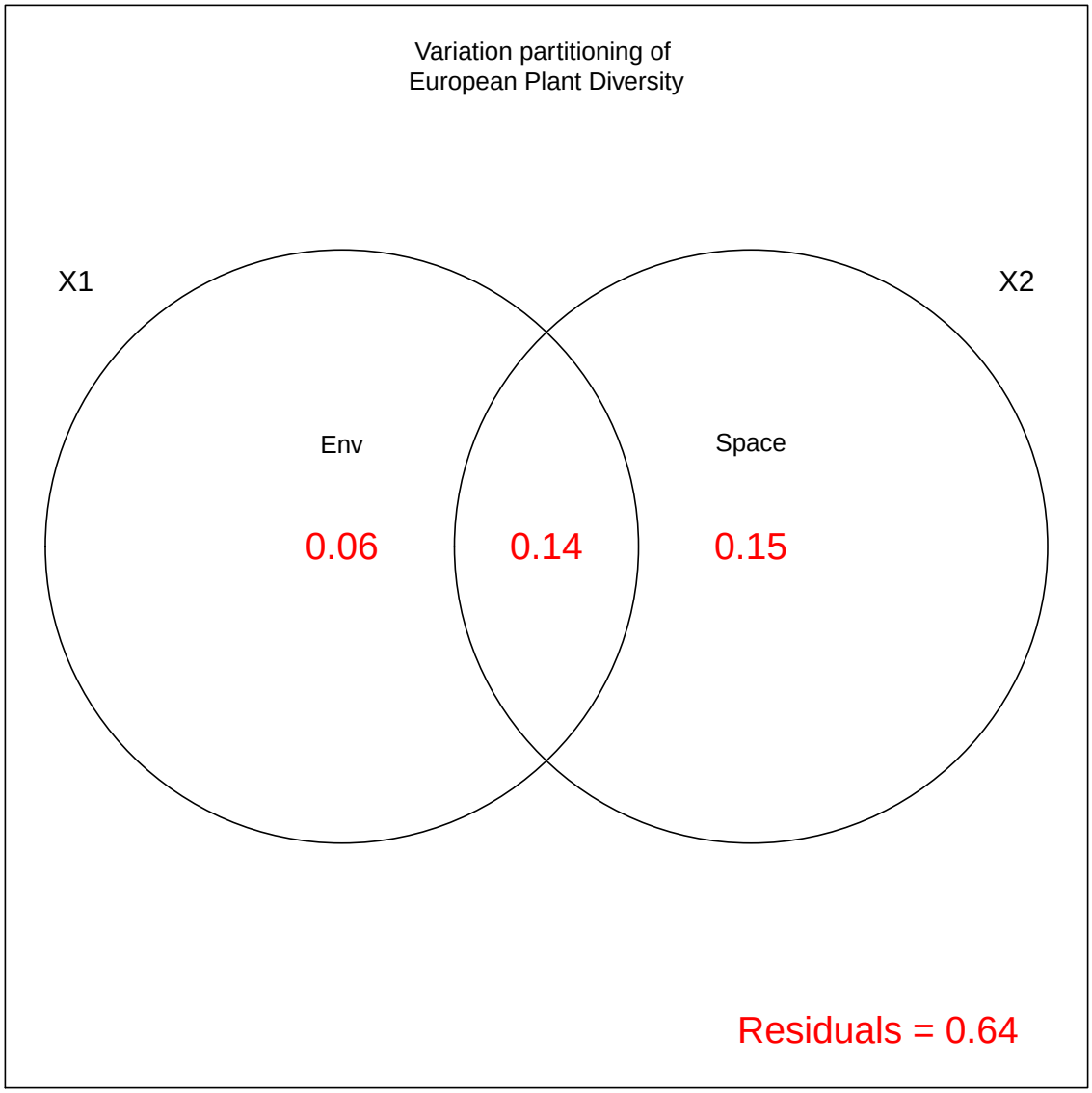
```
##
## Permutation test for dbrda
```

```
##
## Permutation: free
## Number of permutations: 999
##
## Call: dbrda(formula = spec.db ~ space.mod)
## Permutation test for all constrained eigenvalues
## Pseudo-F:     7.287653 (with 10, 139 Degrees of Freedom)
## Significance:     0.001
```

```
doubs.varpart <- varpart(spec.db, env.mod, space.mod)
doubs.varpart
```

```
##
## Partition of squared Bray distance in dbRDA
##
## Call: varpart(Y = spec.db, X = env.mod, space.mod)
##
## Explanatory tables:
## X1:  env.mod
## X2:  space.mod
##
## No. of explanatory tables: 2
## Total variation (SS): 34.737
## No. of observations: 150
##
## Partition table:
##                       Df R.squared Adj.R.squared Testable
## [a+b] = X1             8   0.24814       0.20548     TRUE
## [b+c] = X2            10   0.34396       0.29676     TRUE
## [a+b+c] = X1+X2       18   0.43585       0.35834     TRUE
## Individual fractions
## [a] = X1|X2            8                 0.06158     TRUE
## [b]                    0                 0.14391    FALSE
## [c] = X2|X1           10                 0.15285     TRUE
## [d] = Residuals                          0.64166    FALSE
## ---
## Use function 'capscale' to test significance of fractions of interest
```

```
par(mar = c(2,2,2,2))
plot(doubs.varpart, col ="red", cex = 1.5)
text(1, 0.25, "Space")
text(0, 0.25, "Env")
mtext("Variation partitioning of \nEuropean Plant Diversity", side = 3, line = -3)
```



6) DISCUSSION AND CONCLUSION

7) REFERENCES