

# Trait-based approach in ecology

Aurele Toussaint (aurele.toussaint@cnrs.fr)

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## Species diversity

In this session we will learn how to estimate different indices to estimate species diversity. We will start by loading the data that we saved at the end of session 3 (remember that you have to set the working directory with the function `set.wd()` for R to be able to find the files!)

```
## total number of taxa

load("community.rda",verbose=T) # loading from previous
## Loading objects:
##   vas.plants
##   tree.counts
##   forest.types
##   xy
##   soil.data
##   tables.join
```

## Species richness

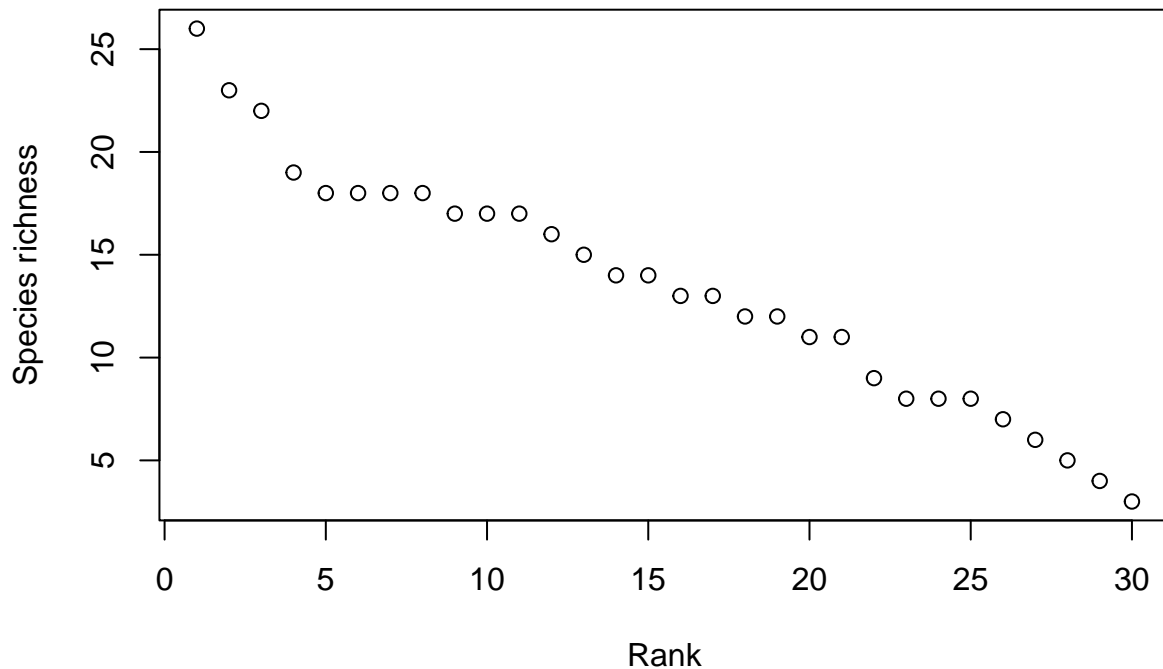
We are using the `vas.plants` table to find species richness: the number of taxa in a sample.

```
dim(vas.plants) # how many samples, how many taxa in the table
## [1] 30 79

rowSums(vas.plants) # total sum of rows (sites) colSums works for columns
##   X001Vapramae   X002Illli   X003Vitipalu   X004Konguta   X005Vehendi
##         18.5         15.0         25.5         29.0         12.5
##   X006.Erumae   X007Porgumae   X008Aardla   X009Kurepalu   X010Sarakuste
##         14.0         17.0         15.5          5.0         27.5
##   X011Kannu     X012Vonnu     X013Rookse   X014Kammeri   X015Kambja
##         21.5         17.5         31.5         23.5         24.0
##   X016Reola     X017Ignase     X018Unikula X019Haavametsa X020Kruusahaua
##         21.0         19.5         34.5          7.0         29.5
##   X021Aravu     X026Pedajamae     X027Miti     X028Puhaste   X031Pimmelaan
##         10.5         26.5          9.0         11.0         38.0
##   X032Logina   X033Voorepalu X036Taevaskoja   X044Savimae X073Pausakunnu
##         11.0         18.0         10.0         12.0         17.0
rowSums(vas.plants>0) # total count of rows (sums logical table if non-zero values)
##   X001Vapramae   X002Illli   X003Vitipalu   X004Konguta   X005Vehendi
```

```
##          14          11          18          23          5
##   X006.Erumae   X007Porgumae   X008Aardla   X009Kurepalu   X010Sarakuste
##          9          17          12          3          18
##   X011Kannu     X012Vonnu     X013Rookse   X014Kammeri   X015Kambja
##          18          12          19          15          14
##   X016Reola     X017Ignase    X018Unikula X019Haavametsa X020Kruusahaua
##          17          13          18          4          17
##   X021Aravu     X026Pedajamae   X027Miti   X028Puhaste   X031Pimmelaan
##          7          22          6          8          26
##   X032Logina    X033Voorepalu X036Taevaskoja   X044Savimae X073Pausakunnu
##          8          13          8          11          16
```

```
plot(sort(rowSums(vas.plants > 0), decreasing = T), ylab= "Species richness", xlab = "Rank") # making a
```



## Diversity indices

Often diversity indices are used which combine both richness and abundance differences (evenness). Just some examples below:

Shannon diversity:  $H = -\sum_{i=1}^S p_i \ln(p_i)$

Inverse Simpson diversity:  $D_2 = \frac{1}{\sum_{i=1}^S p_i^2}$

where  $p_i$  is the proportion (relative abundance) of species  $i$ , and  $S$  is the number of species.

We will use the package **vegan** for diversity calculations.

```

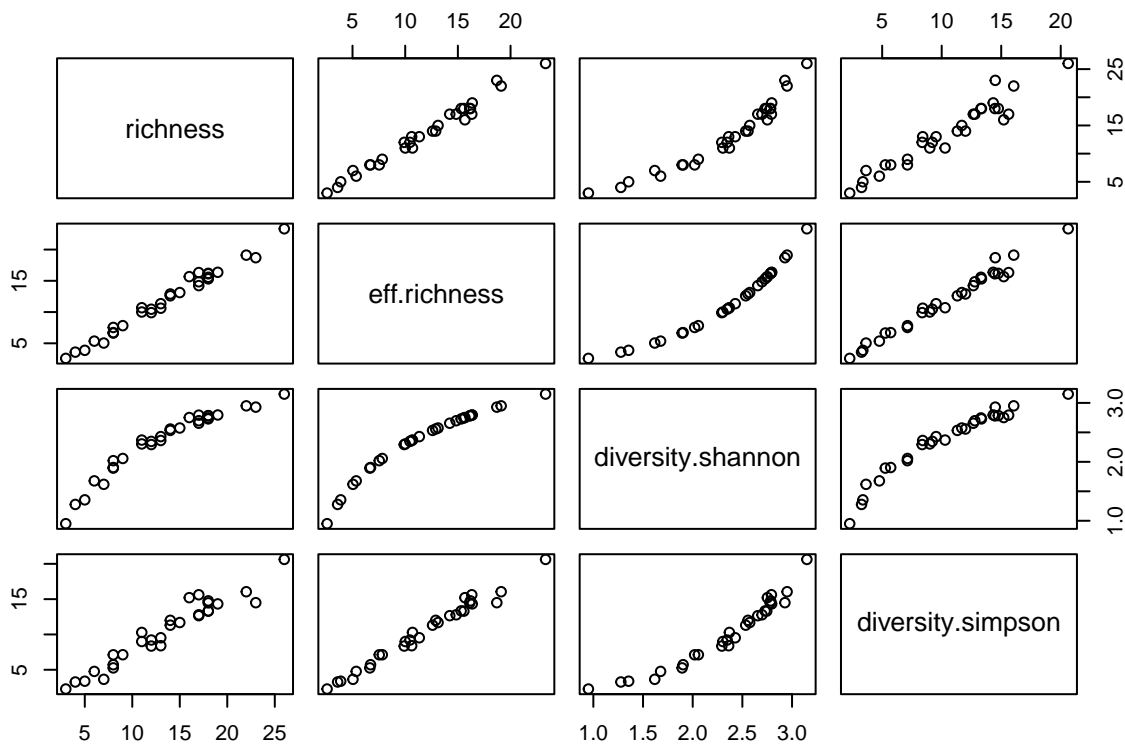
richness <- rowSums(vas.plants > 0) # definign richness for comparison as an object

library(vegan)

diversity.shannon <- diversity(vas.plants, "shannon")
eff.richness <- exp(diversity.shannon)
diversity.simpson <- diversity(vas.plants, "invsimpson")

pairs(data.frame(richness, eff.richness, diversity.shannon, diversity.simpson))

```



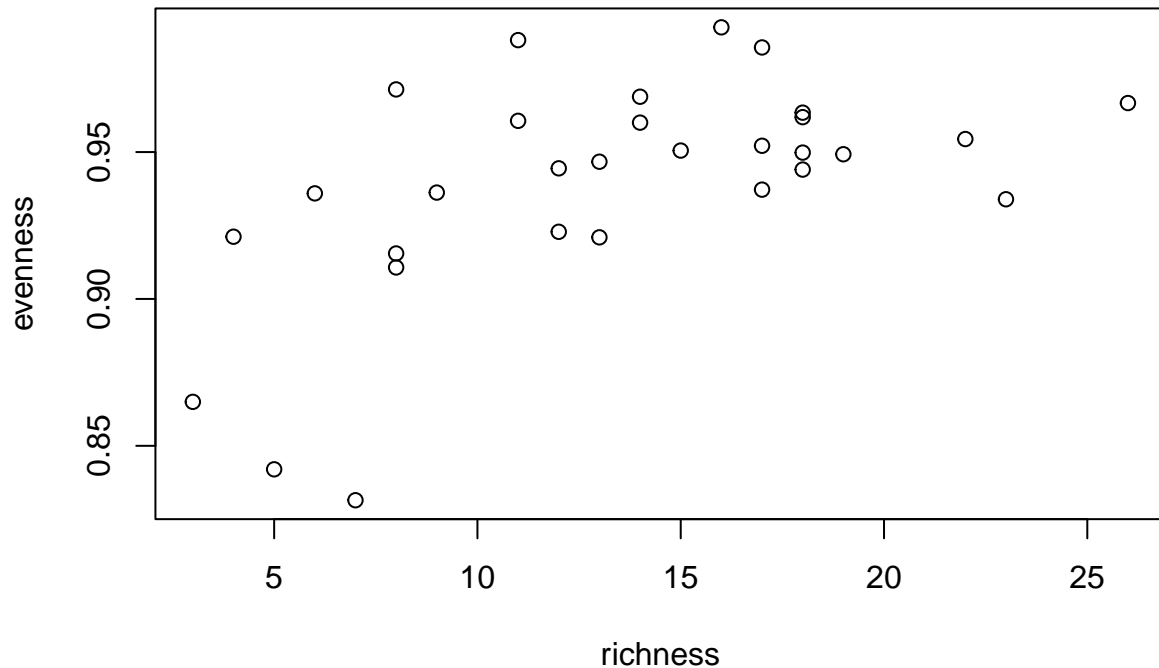
```

# Evenness -- a measure of abundance similarity, can be found by dividing Shannon diversity by ln(richness)

evenness <- diversity.shannon / log(richness)

plot(richness, evenness)

```

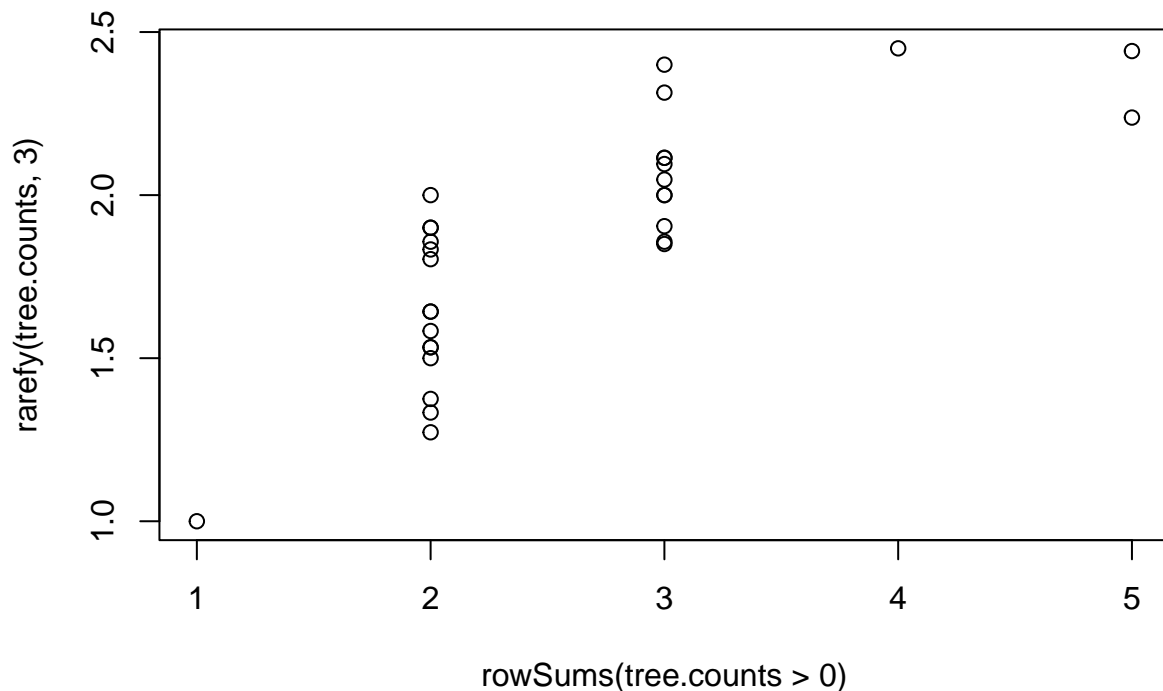


## Unequal sampling? Rarefaction and extrapolations

If sampling has been unequal between sites (e.g. different number of individuals have been considered), this sampling difference can be taken account by rarefaction and extrapolations. Rarefaction looks how many species we expect to find when sampling randomly  $n$  individuals

```
rarefy(tree.counts, 3) ## NB! Works with counts!
##      001Vapramäe      002Illi      003Vitipalu      004Konguta      005Vehendi
##      1.900000      2.000000      1.850000      1.533333      1.000000
##      006Erumäe      007Põrgumäe      008Aardla      009Kurepalu      010Sarakuste
##      1.533333      1.857143      2.441667      1.900000      1.904762
##      011Kannu      012Võnnu      013Rookse      014Kammeri      015Kambja
##      2.000000      2.047619      2.114286      2.000000      2.400000
##      016Reola      017Ignase      018Uniküla      019Haavametsa      020Kruusahaua
##      2.450000      2.114286      2.237762      1.333333      1.642857
##      021Aravu      026Pedajamäe      027Miti      028Puhaste      031Pimmelaan
##      2.314286      1.272727      1.803571      1.642857      1.500000
##      032Logina      033Voorepalu      036Taevaskoja      044Savimäe      073Sulaoja
##      1.857143      1.583333      2.095238      1.375000      1.833333
## attr(,"Subsample")
## [1] 3

plot(rowSums(tree.counts > 0), rarefy(tree.counts, 3)) # richness of trees vs. rarefied richness estima
```



```
## Sometimes it is nice to see species accumulation graphs from 2,3, ... n individuals
## First some max values
max.tree.count <- max(rowSums(tree.counts)) # max number of trees in a site

max.tree.rich <- max(rowSums(tree.counts > 0)) # max richness

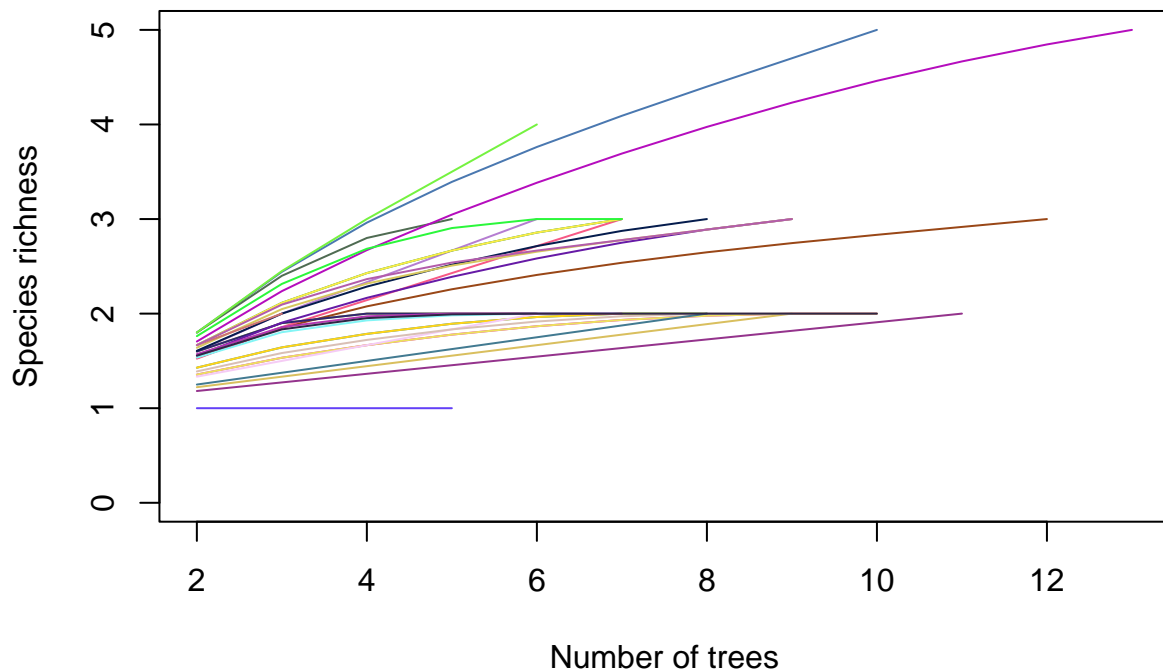
# Now plotting

plot(NA, xlim = c(2, max.tree.count), ylim = c(0, max.tree.rich),
     xlab="Number of trees", ylab="Species richness")

# Including all 30 sites!
for (i in 1:nrow(tree.counts)) {
  trees <- 2:rowSums(tree.counts[i, ])
  rar <- rarefy(tree.counts[i, ], trees)
  # Let's select colors randomly
  lines(x = trees, y = rar[1, ], pch = 16,
        col = rgb(red = sample(100, 1),
                  green = sample(100, 1),
                  blue = sample(100, 1),
                  maxColorValue = 100))
}

## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 3
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
```

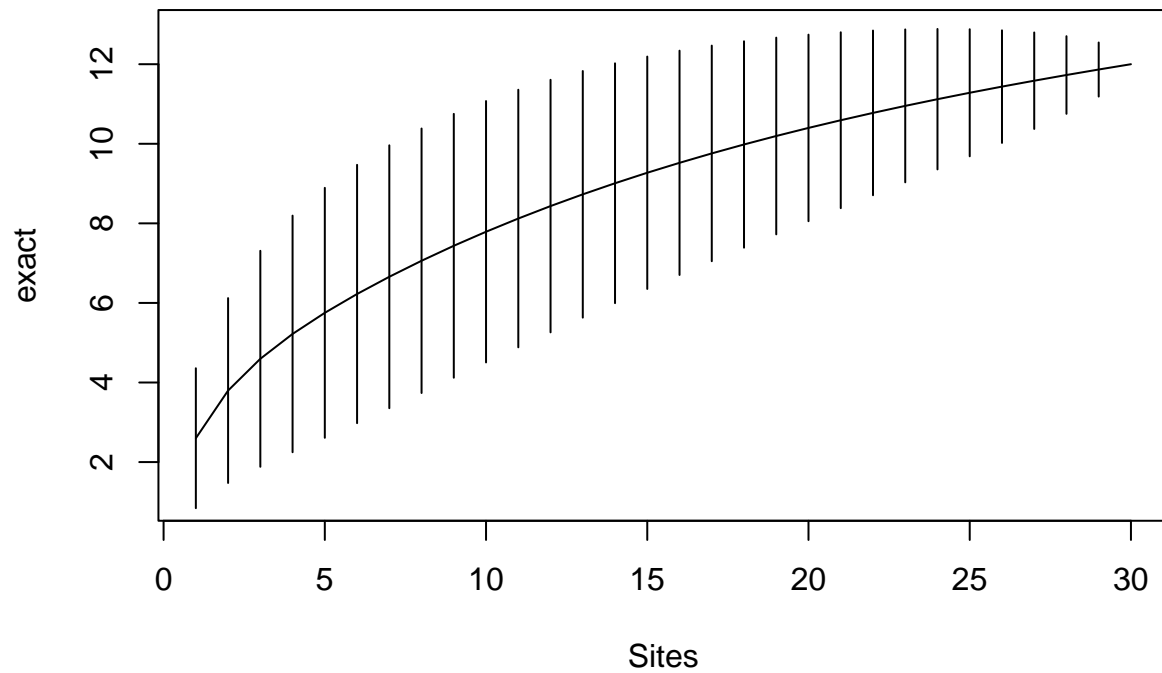
```
## counts 1, but smallest count is 2
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 5
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 2
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 3
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 2
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 2
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 3
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 2
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 3
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 2
## Warning in rarefy(tree.counts[i, ], trees): most observed count data have
## counts 1, but smallest count is 5
```



## Total estimated richness

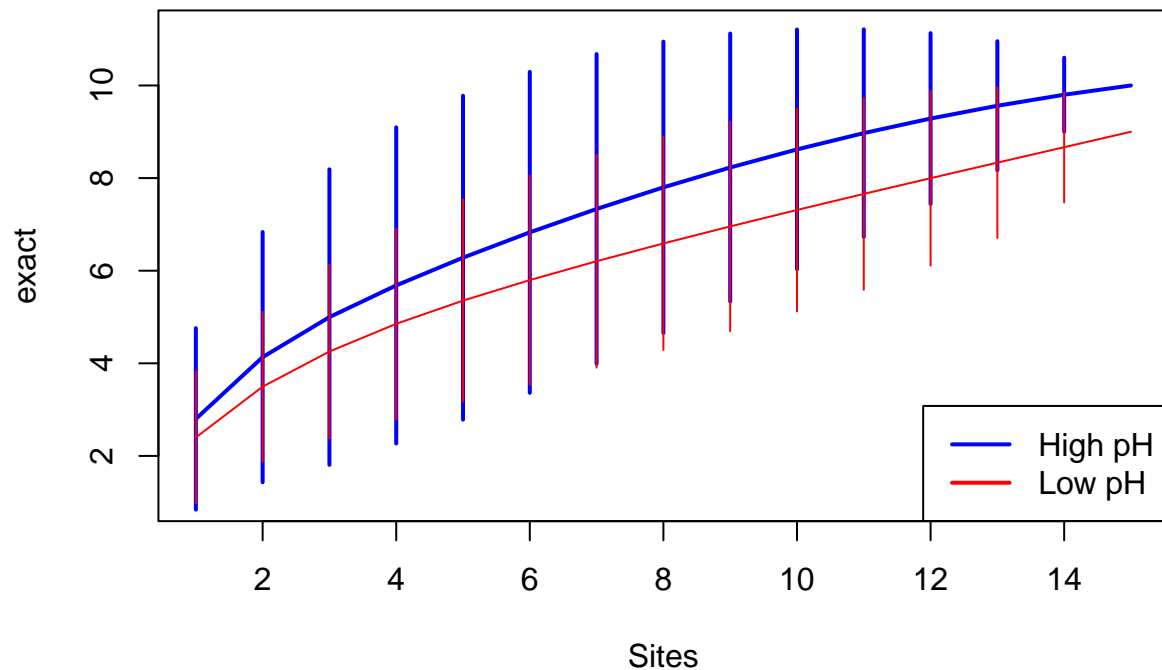
We might want to know what is the total expected richness (across all samples) when 1, 2, ..., n samples are included. There is a function `specaccum` which finds the mean and also error bars.

```
plot(specaccum(tree.counts)) ## specaccum only considers presences/absences!!
```



```
## Let's evaluate total richness separately for sites with low and sites with high soil pH:
high.pH <- soil.data$pH.KCl > median(soil.data$pH.KCl)
plot(specaccum(tree.counts[high.pH, ]), lwd = 2, col = "blue")
plot(specaccum(tree.counts[!high.pH, ]), col = "red", add=T)
legend("bottomright", legend = c("High pH", "Low pH"), col = c("blue", "red"), lwd = 2)
```





## Beta diversity

Beta diversity explores how much the different samples overlap in their species composition. Beta diversity can be defined through the difference between the mean richness across samples and the total richness over all samples in two ways: multiplicatively or additively.

```
# multiplicative beta diversity

ncol(vas.plants) / mean(rowSums(vas.plants > 0))
## [1] 5.895522

# additive beta diversity

ncol(vas.plants) - mean(rowSums(vas.plants > 0))
## [1] 65.6

# Comparing beta diversities between High vs. low pH soil subsamples

high.ph.gamma <- sum(colSums(vas.plants[high.pH,])>0)
low.ph.gamma <- sum(colSums(vas.plants[!high.pH,])>0)

high.ph.gamma
## [1] 74
```

```

low.ph.gamma
## [1] 47

high.ph.gamma / mean(rowSums(vas.plants[high.pH, ] > 0))
## [1] 4.302326
low.ph.gamma / mean(rowSums(vas.plants[!high.pH, ] > 0))
## [1] 4.895833

high.ph.gamma - mean(rowSums(vas.plants[high.pH, ] > 0))
## [1] 56.8
low.ph.gamma - mean(rowSums(vas.plants[!high.pH, ] > 0))
## [1] 37.4

```

## Species diversity and environment

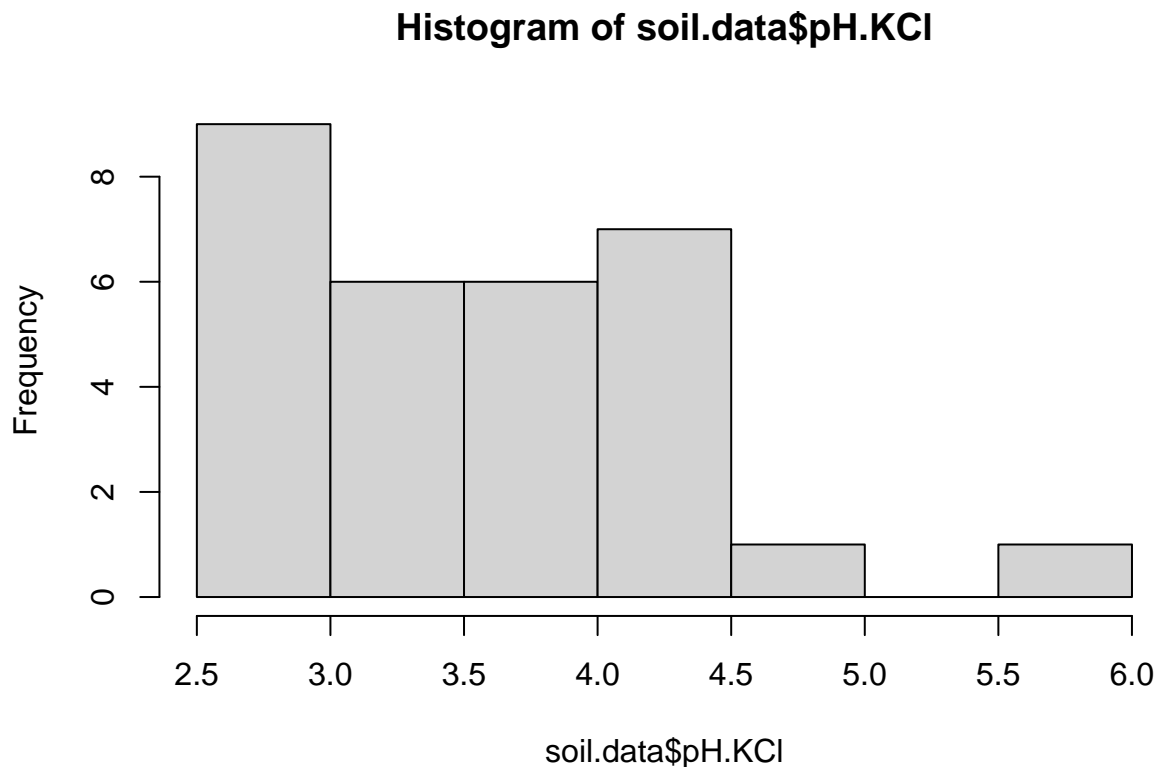
We will exploring the relationship between diversity and a soil parameter – soil pH.

```

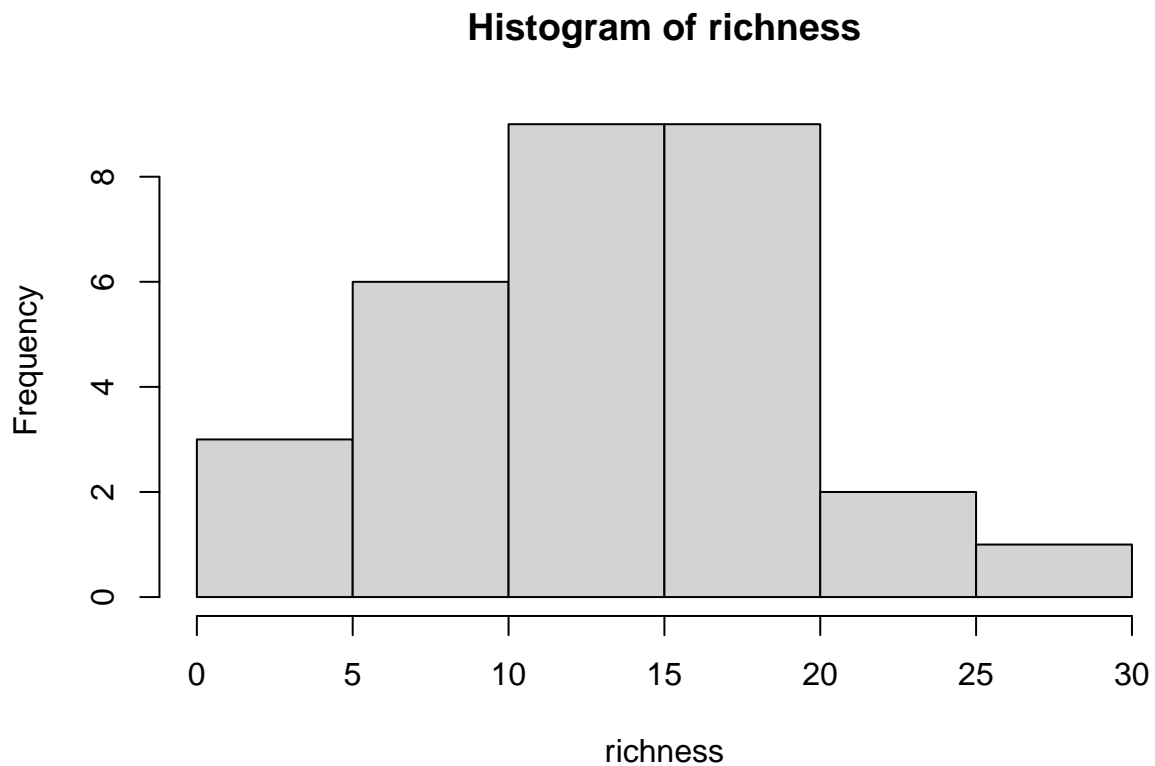
cor(soil.data$pH.KCl, richness) # just a correlation coefficient
## [1] 0.7247559

# Pearson correlation test requires normality of both variables and linearity
hist(soil.data$pH.KCl)

```



```
hist(richness)
```



```
# Normality test: Shapiro-Wilks test
```

```
shapiro.test(soil.data$pH.KCl)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: soil.data$pH.KCl
```

```
## W = 0.94732, p-value = 0.1432
```

```
shapiro.test(richness)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: richness
```

```
## W = 0.97798, p-value = 0.7696
```

```
# Linear fit
```

```
plot(soil.data$pH.KCl,richness)
```

```
# OK. If not ok, then try to transform data (e.g. log). If this does not help, use rank correlation (e.g. cor.test).
```

```
cor.o <- cor.test(soil.data$pH.KCl, richness) # recording output from a test as an object
```

```
cor.o
```

```
##
```

```

## Pearson's product-moment correlation
##
## data: soil.data$pH.KCl and richness
## t = 5.5661, df = 28, p-value = 5.919e-06
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.4932877 0.8603750
## sample estimates:
## cor
## 0.7247559

str(cor.o) ## data type for test output is a list as well (i.e. a mixture of different types of objects)
## List of 9
## $ statistic : Named num 5.57
## .. attr(*, "names")= chr "t"
## $ parameter : Named int 28
## .. attr(*, "names")= chr "df"
## $ p.value : num 5.92e-06
## $ estimate : Named num 0.725
## .. attr(*, "names")= chr "cor"
## $ null.value : Named num 0
## .. attr(*, "names")= chr "correlation"
## $ alternative: chr "two.sided"
## $ method : chr "Pearson's product-moment correlation"
## $ data.name : chr "soil.data$pH.KCl and richness"
## $ conf.int : num [1:2] 0.493 0.86
## .. attr(*, "conf.level")= num 0.95
## - attr(*, "class")= chr "htest"

cor.o$p.value # retrieving a component of the list (p-value)
## [1] 5.91914e-06

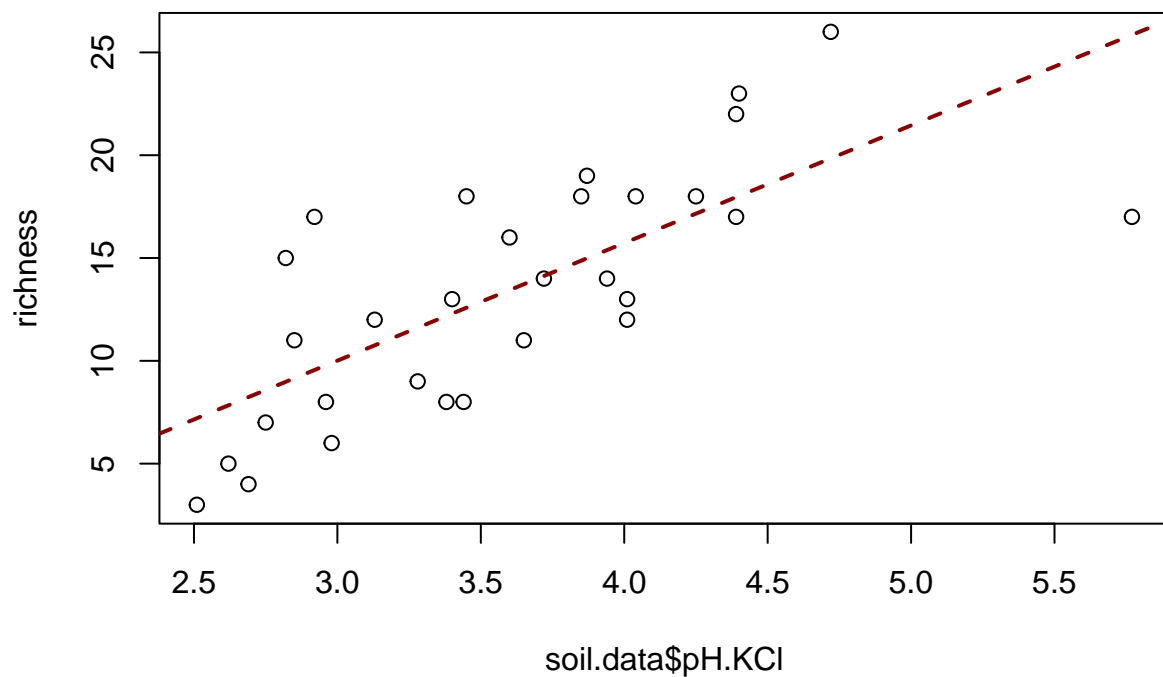
# Regression model -- we have hypothesis of dependent (richness) and independent (pH) variables
model <- lm(richness ~ soil.data$pH.KCl)

summary(model)
##
## Call:
## lm(formula = richness ~ soil.data$pH.KCl)
##
## Residuals:
## Min 1Q Median 3Q Max
## -8.8523 -2.8222 -0.5426 2.9875 7.4495
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) -7.152 3.766 -1.899 0.0679 .
## soil.data$pH.KCl 5.720 1.028 5.566 5.92e-06 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.066 on 28 degrees of freedom
## Multiple R-squared: 0.5253, Adjusted R-squared: 0.5083

```

```
## F-statistic: 30.98 on 1 and 28 DF, p-value: 5.919e-06
```

```
abline(model, col="darkred", lty = 2, lwd = 2) # adding regression line to the graph.
```



```
# Regression expects that model residuals are normally distributed (i.e. testing if there is a deviation)
shapiro.test(resid(model))
##
## Shapiro-Wilk normality test
##
## data:  resid(model)
## W = 0.96457, p-value = 0.403
# OK -- no deviation!
```

## Community (dis)similarity

Here we explore how similar ecological communities are. With this, we mean how much their species composition overlaps. Dissimilarity is just the opposite of similarity, both measures carry the same information.

## Reading and transforming community data

Let's read our community data and explore abundance data. Because abundance data tends to be skewed (few species have high abundance and many have low abundance), it is often reasonable to transform abundance

to get a better distribution.

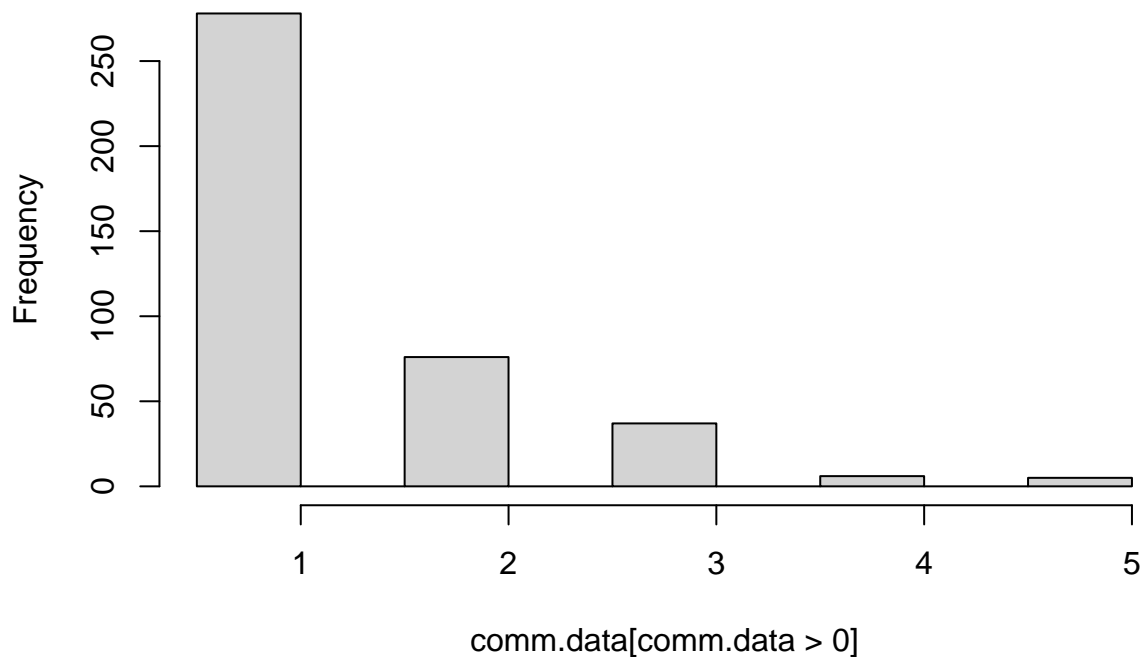
```
# Reading previously saved data
load("community.rda", verbose = T) # loading from previous
## Loading objects:
##   vas.plants
##   tree.counts
##   forest.types
##   xy
##   soil.data
##   tables.join
comm.data <- vas.plants # copy of a community data

# Most abundant species

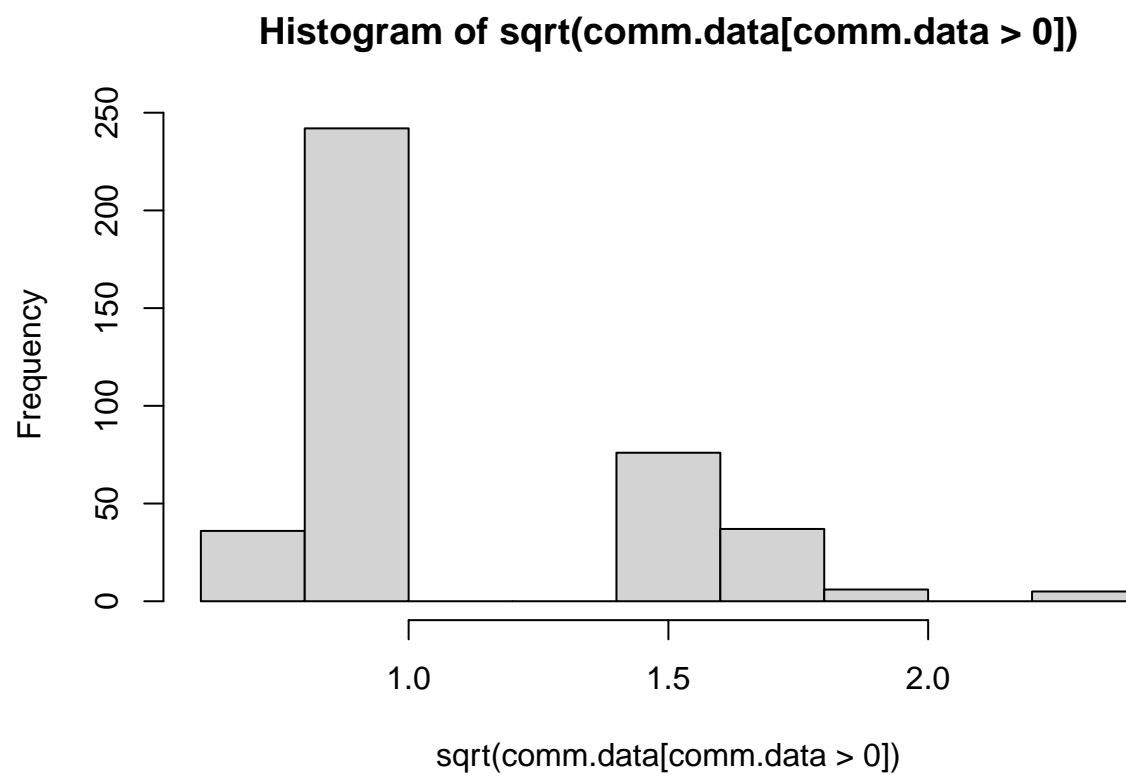
max.spp <- which.max(colSums(comm.data))
max.spp
## OXALacet
##      33

hist(comm.data[comm.data > 0]) # histogram of requeencies (other than 0)
```

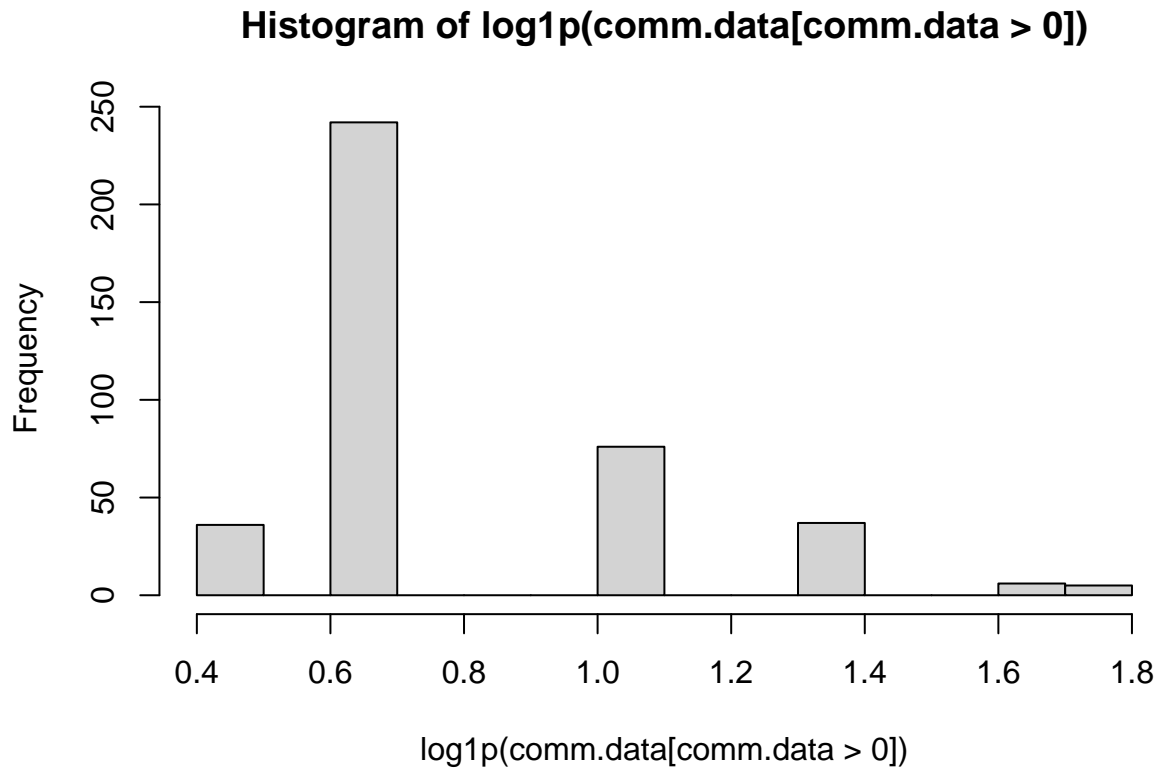
**Histogram of comm.data[comm.data > 0]**



```
hist(sqrt(comm.data[comm.data > 0])) # square root transformation
```



```
hist(log1p(comm.data[comm.data > 0])) # log (x+1) transformation
```



We can see that log-transformation gives approximately normal distribution, it downweights frequent taxa.

## Community distance matrix

We can measure dissimilarity by using several indices. Here are some examples.

Euclidean distance:

$$d_{jk} = \sqrt{\sum_{i=1}^n (x_{ij} - x_{ik})^2}$$

where  $x$  is abundance of species  $i$  in sites  $j$  and  $k$  and  $n$  is the total number of taxa.

Bray-Curtis distance:

$$d_{jk} = \frac{\sum_{i=1}^n |x_{ij} - x_{ik}|}{\sum_{i=1}^n (x_{ij} + x_{ik})}$$

Euclidean distance does not have an upper limit, whereas Bray-Curtis distance is bounded between 0 and 1.

With the `vegdist` function we can calculate various distance measures. It returns a triangular distance matrix, because distance from sample A to B is the same as from B to A.

```
library(vegan)

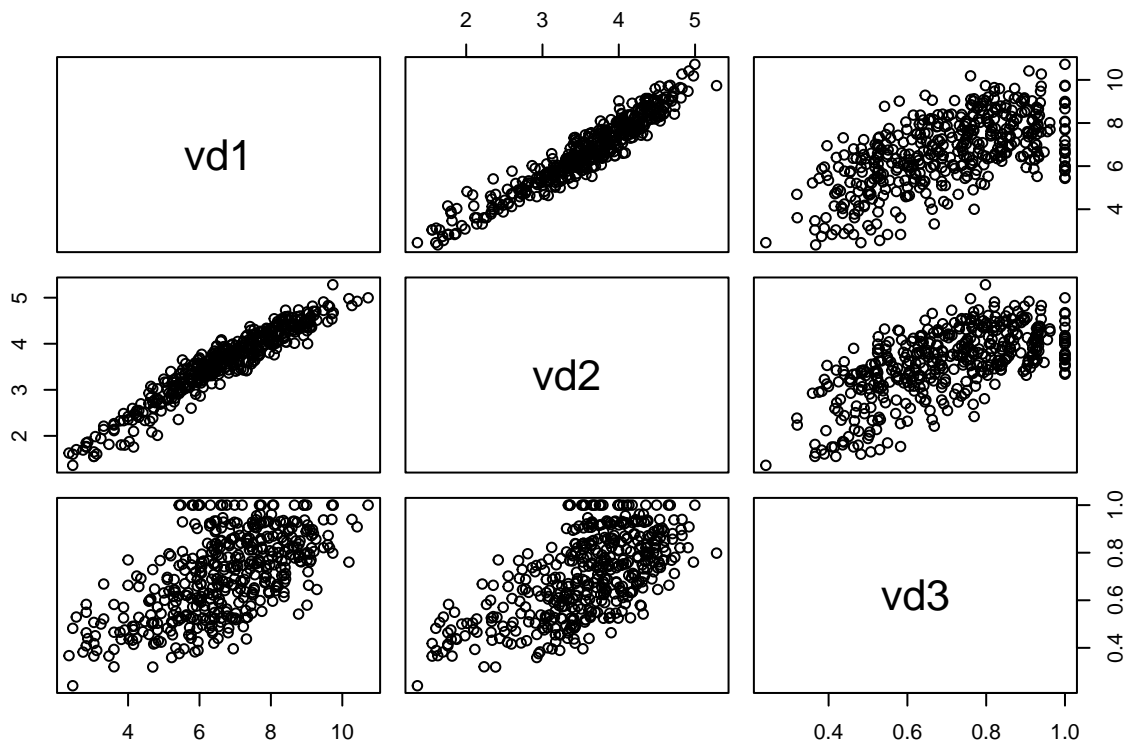
vegdist(comm.data[1:5, ], "euclidean") # triangular distance matrix
##           X001Vapraeae X002Illi X003Vitipalu X004Konguta
## X002Illi           6.422616
## X003Vitipalu       6.164414 7.729812
## X004Konguta       7.297260 8.544004 9.473648
```



```
## X005Vehendi      8.154753 5.766281      9.746794      9.708244

# Calculating some distances and plotting against each other.

vd1 <- vegdist(comm.data, "euclidean")
vd2 <- vegdist(log1p(comm.data), "euclidean") # log transformation
vd3 <- vegdist(log1p(comm.data), "bray")
pairs(cbind(vd1, vd2, vd3))
```



Explore other community (dis)similarity measures.

## Hierarchical clustering

Using a distance matrix we can perform a clustering of our samples. Initially all samples form their own clusters, then we start to join the most similar sites and form clustering trees.

Single linkage is based on the most similar members of two clusters. Complete linkage is based on the most dissimilar member of two clusters. Average linkage is based on calculating the average similarity between all members. Ward method is more complex, aiming to minimize the variance within clusters. You can check the Wildi book for more details.

If we have a hierarchical cluster tree, we can always cut this to any number of clusters.

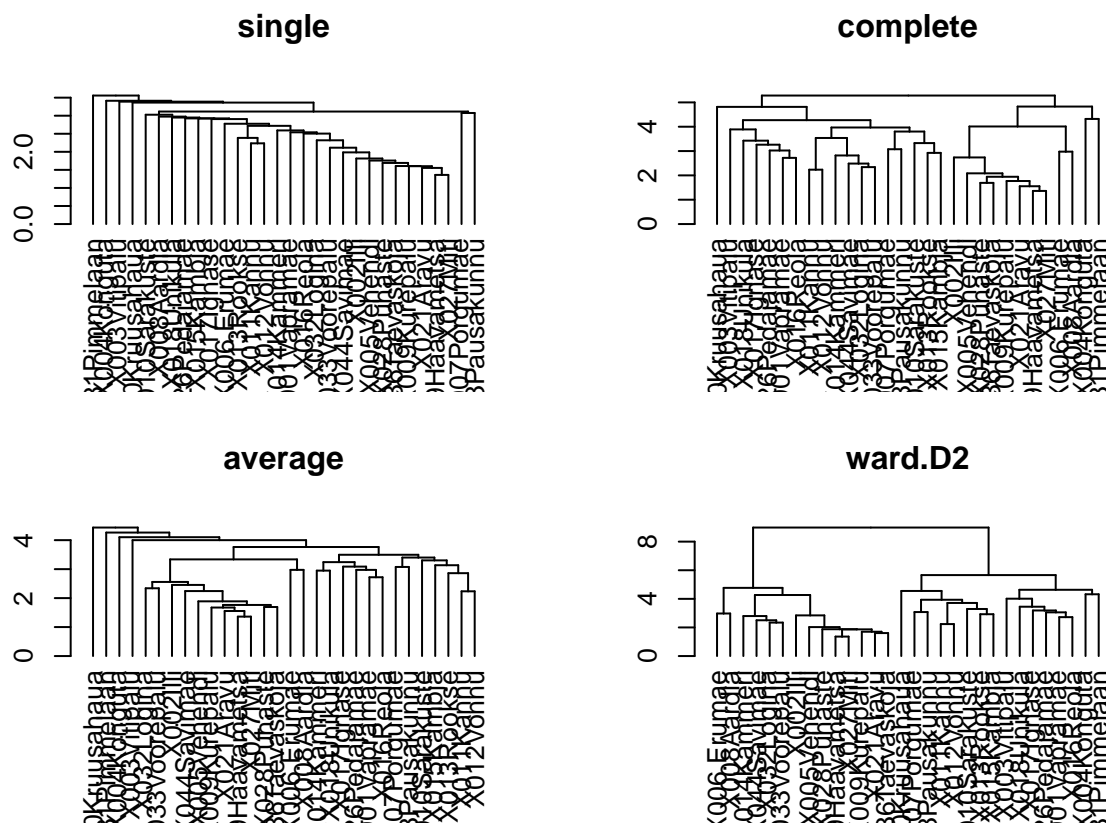
```

vd <- vd2 # selecting a distance matrix for future calculations
o.clu.s <- hclust(vd, method = "single")
o.clu.c <- hclust(vd, method = "complete")
o.clu.a <- hclust(vd, method = "average")
o.clu.w <- hclust(vd, method = "ward.D2")

par(mfrow = c(2, 2)) # several figures together 2 rows and 2 columns!

plot(as.dendrogram(o.clu.s), main = "single")
plot(as.dendrogram(o.clu.c), main = "complete")
plot(as.dendrogram(o.clu.a), main = "average")
plot(as.dendrogram(o.clu.w), main = "ward.D2")

```



```

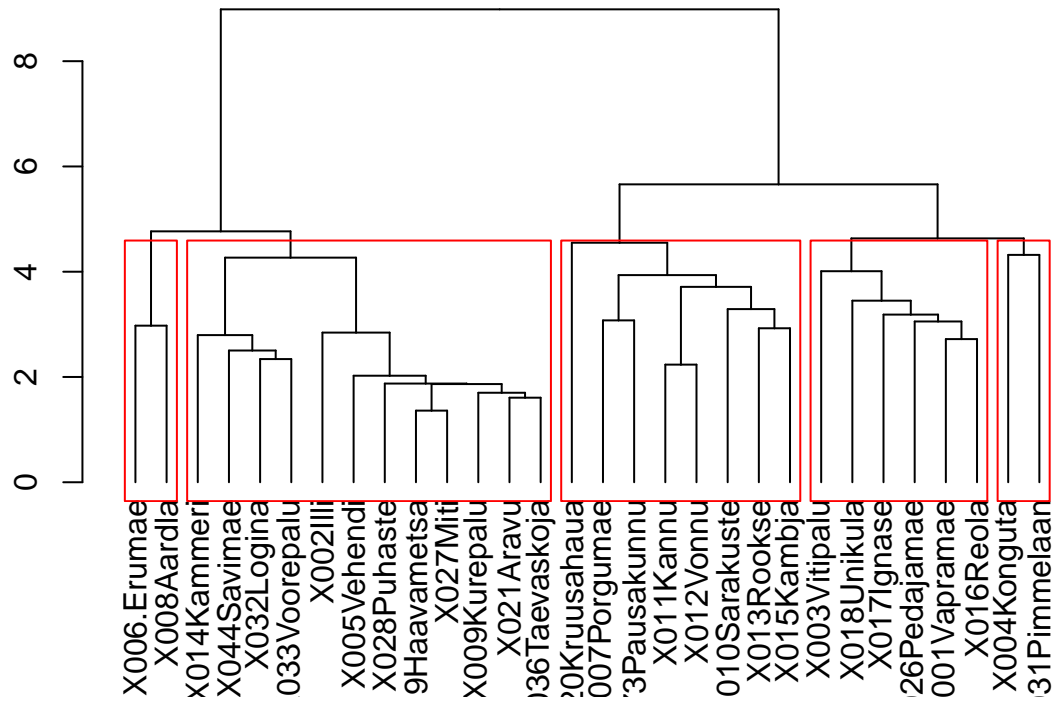
o.clu <- o.clu.w # selecting the most logical (Ward linkage)

par(mfrow = c(1, 1)) # single figure again.

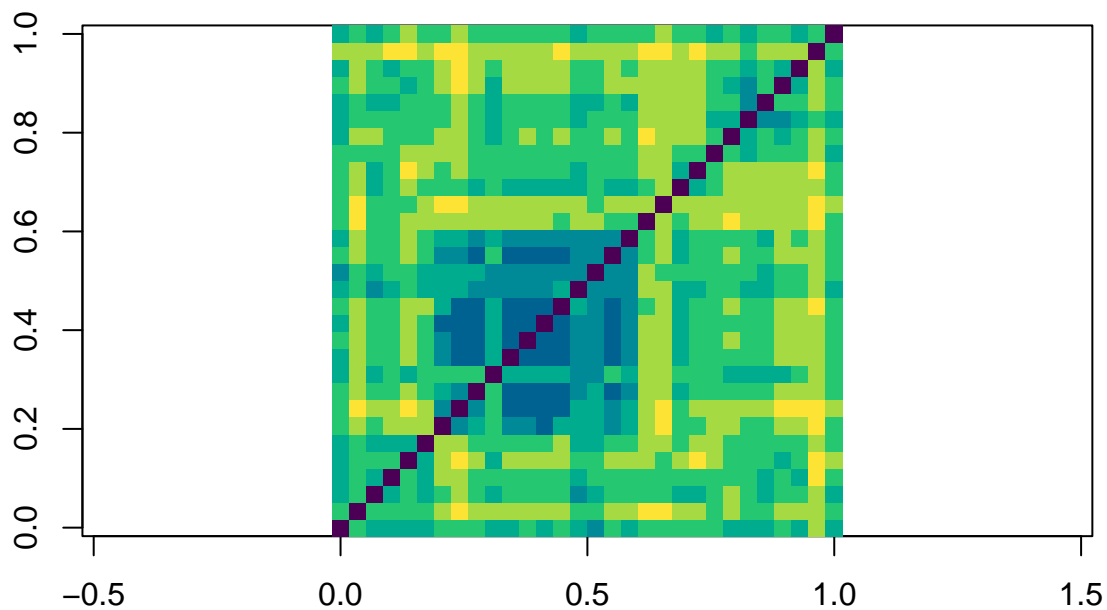
## Cutting tree to parts

o.grel <- cutree(o.clu, k = 5)
plot(as.dendrogram(o.clu))
rect.hclust(o.clu, 5, border = "red")

```



```
# Similarity between sites (colors), ordered along clusters
image(as.matrix(vd)[order(o.grel), order(o.grel)], asp = T,
      col = hcl.colors(8, palette = "viridis"))
```



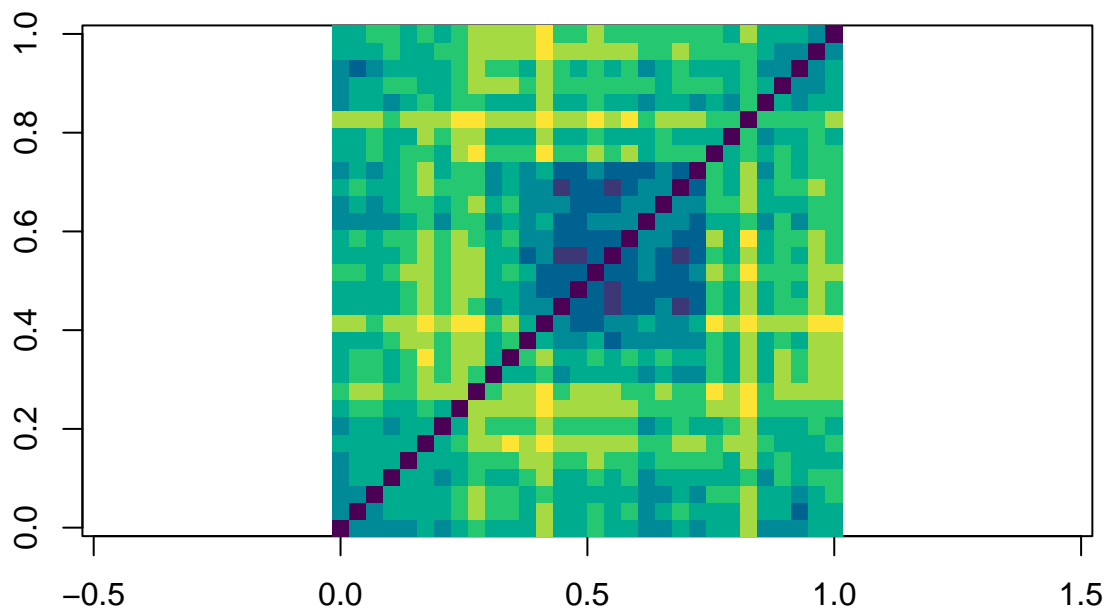
## k-means clustering

Not hierarchical – just give number of clusters needed. Computation is complex, based on machine learning and iterations.

```
k.o <- kmeans(comm.data, 5)
k.o$cluster
```

##	X001Vapramae	X002Illi	X003Vitipalu	X004Konguta	X005Vehendi
##	1	3	4	2	3
##	X006.Erumae	X007Porgumae	X008Aardla	X009Kurepalu	X010Sarakuste
##	2	4	2	3	5
##	X011Kannu	X012Vonnu	X013Rookse	X014Kammeri	X015Kambja
##	5	1	5	1	5
##	X016Reola	X017Ignase	X018Unikula	X019Haavametsa	X020Kruusahaua
##	1	1	1	3	4
##	X021Aravu	X026Pedajamae	X027Miti	X028Puhaste	X031Pimmelaan
##	3	1	3	3	1
##	X032Logina	X033Voorepalu	X036Taevaskoja	X044Savimae	X073Pausakunnu
##	3	3	3	3	4

```
image(as.matrix(vd1)[order(k.o$cluster), order(k.o$cluster)], asp = T,
      col = hcl.colors(8, palette = "viridis"))
```



## How many clusters?

Above we defined 5 clusters but can we find how many clusters are optimal? One method is to inspect at what number of groups the correlation between the real distance matrix between sites and the distance matrix between clusters maximizes. This distance in clusters can only include 0 (in different cluster) and 1 (in the same cluster) but we can still calculate the correlation.

```
# Lets define a vector for correlations
correls <- numeric() # making a numeric vector

for (i in 2:(nrow(comm.data) - 1)) {
  # loop for possible cluster numbers. We do not use 1 (all in the same cluster) and number of samples

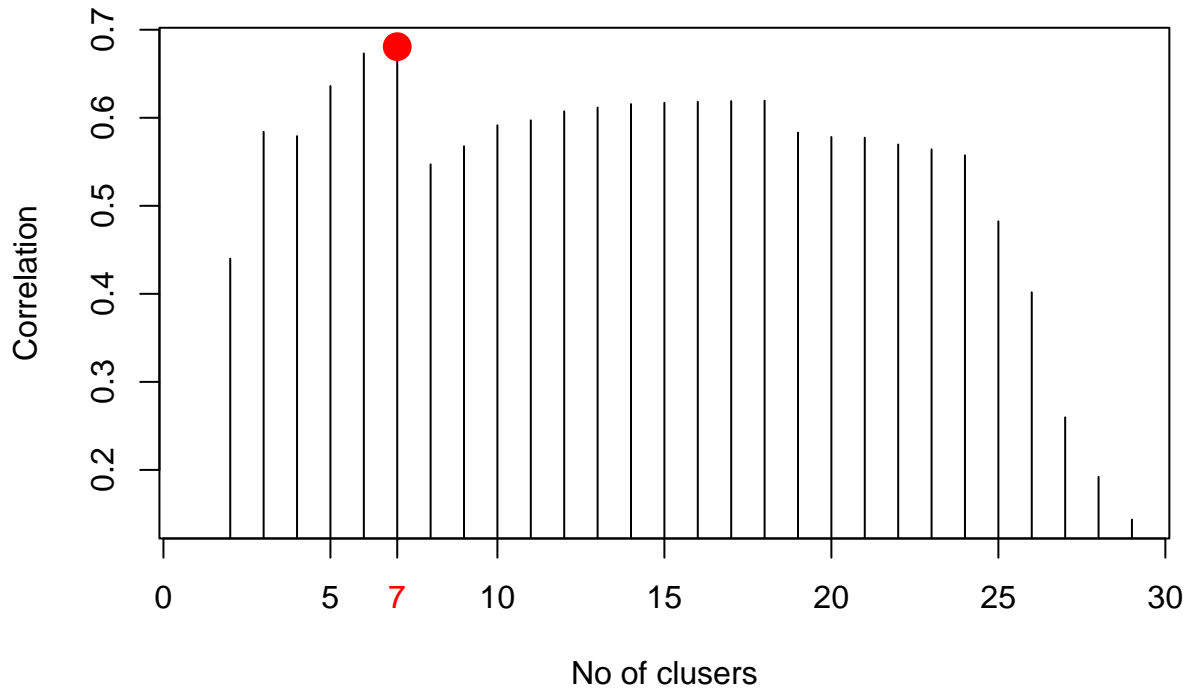
  clusters <- cutree(o.clu, k = i) # defining clusters
  clusdist <- vegdist(table(1:30, clusters), "bray") # dist calculates Bray distance
  # distance is 0 (in different cluster) or 1 (same cluster)

  # table(1:30,clusters) makes a table of 30 sites vs clusters, 1 if a site is in a cluster

  correls[i] <- cor(vd, clusdist) # correlation as a measure
}

plot(correls, type = "h", xlab = "No of clusers", ylab = "Correlation")
```

```
max.corr <- which.max(correls) # which is max correlation?
points(max.corr, correls[max.corr], pch = 16, col = "red", cex = 2)
axis(side = 1, at = max.corr, labels = max.corr, col.axis = "red")
```

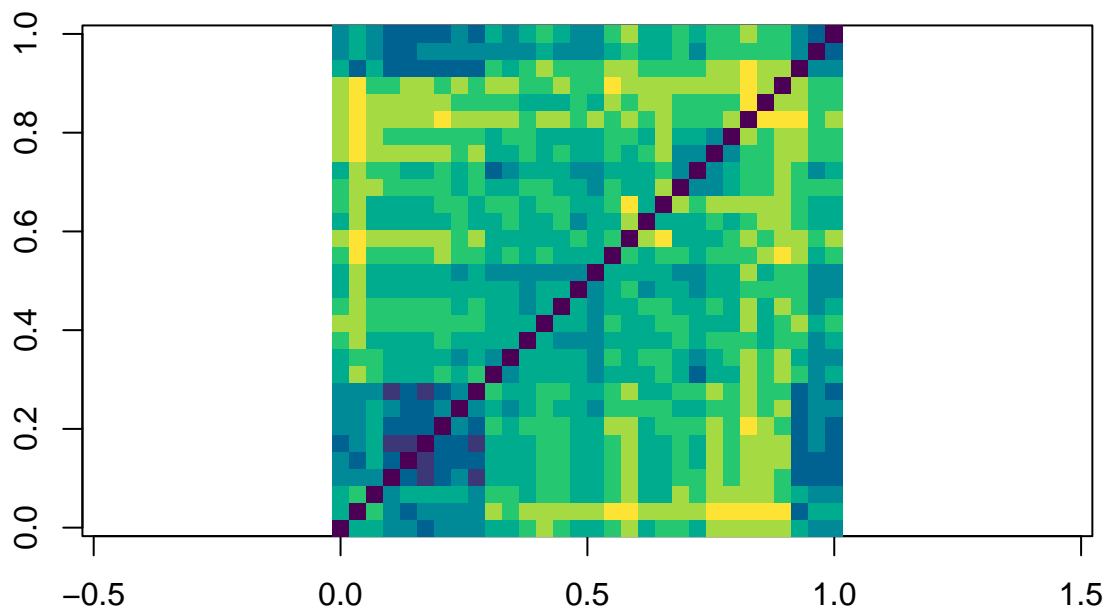


```
# A nice graph!
```

## Human-defined forest types vs. clusterings

Now we will compare how the clusters that we defined using maths are related to human-defined forest types.

```
forest.types # this vector contains the forest type each site is categorized as
## [1] "115" "113" "115" "151" "113" "113" "116" "116" "113" "116" "116" "114"
## [13] "116" "114" "116" "114" "114" "115" "113" "116" "151" "114" "113" "113"
## [25] "116" "151" "113" "113" "151" "114"
image(as.matrix(vd1)[order(forest.types), order(forest.types)], asp = T,
      col = hcl.colors(8, palette = "viridis"))
```



```
table(o.grel, forest.types) # cross-table
##      forest.types
## o.grel 113 114 115 116 151
##      1  0  3  3  0  0
##      2  8  1  0  0  3
##      3  0  0  0  1  1
##      4  1  0  0  1  0
##      5  0  2  0  6  0
table(k.o$cluster, forest.types)
##      forest.types
##      113 114 115 116 151
##      1  0  5  2  1  0
##      2  1  0  0  1  1
##      3  8  0  0  0  3
##      4  0  1  1  2  0
##      5  0  0  0  4  0
table(k.o$cluster, o.grel)
##      o.grel
##      1  2  3  4  5
##      1  5  1  1  0  1
##      2  0  0  1  2  0
##      3  0 11  0  0  0
##      4  1  0  0  0  3
##      5  0  0  0  0  4
```

```

# Fisher exact test of two groups
fisher.test(table(o.grel, forest.types))
##
## Fisher's Exact Test for Count Data
##
## data:  table(o.grel, forest.types)
## p-value = 6.84e-07
## alternative hypothesis: two.sided
fisher.test(table(k.o$cluster, forest.types))
##
## Fisher's Exact Test for Count Data
##
## data:  table(k.o$cluster, forest.types)
## p-value = 1.041e-06
## alternative hypothesis: two.sided
fisher.test(k.o$cluster, o.grel)
##
## Fisher's Exact Test for Count Data
##
## data:  k.o$cluster and o.grel
## p-value = 1.291e-09
## alternative hypothesis: two.sided

```

All tests are highly significant, but there are also some differences.

## Clustering also taxa

Sometimes we might want to cluster taxa which often co-occur. For that we need to transpose our *sites x taxa* matrix using the function `t`.

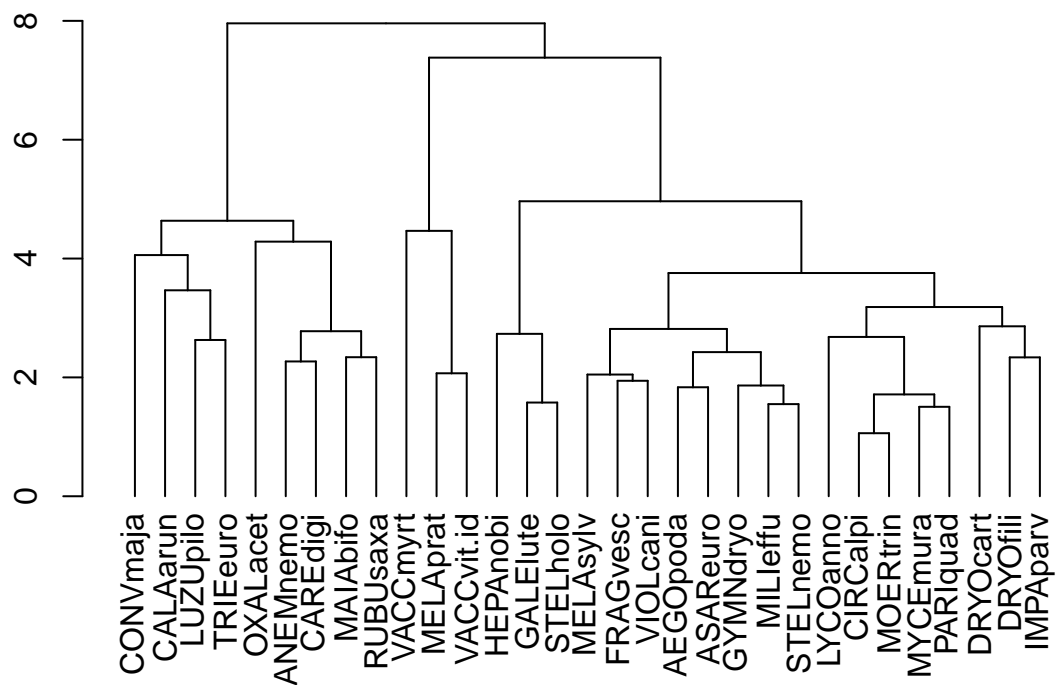
```

comm.data.2 <- log1p(comm.data[, colSums(comm.data > 0) > 3]) # omitting rare taxa which cannot co-occur

tdis <- vegdist(t(comm.data.2), "euclidean")
tdis.clus <- hclust(tdis, method = "ward.D2")
plot(as.dendrogram(tdis.clus))

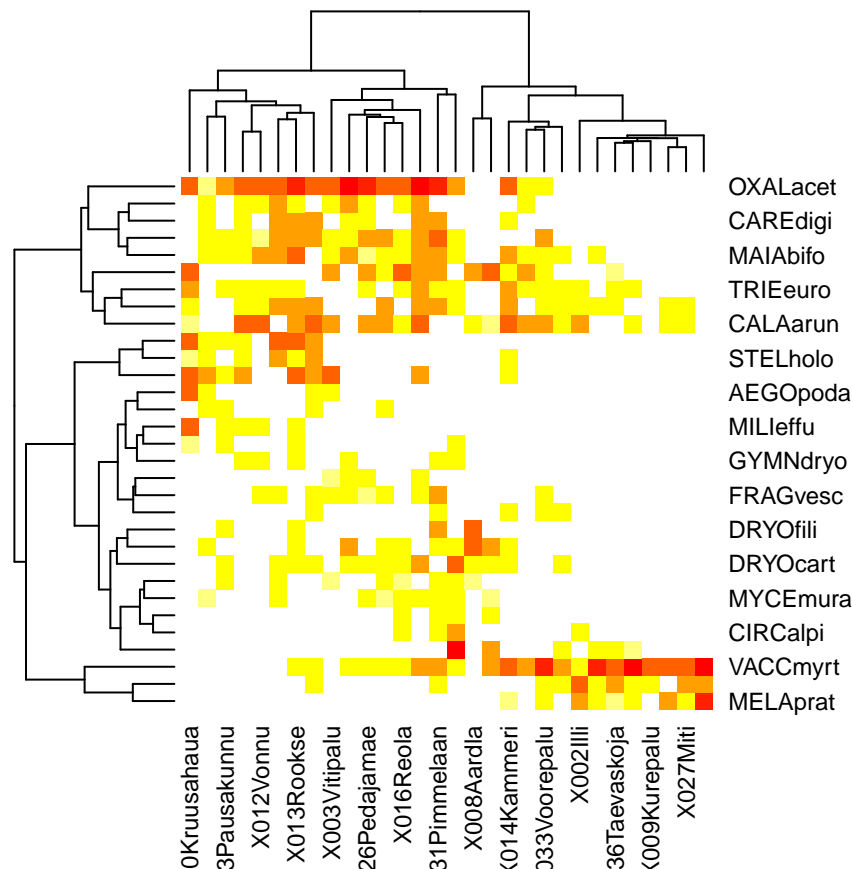
```





```
## Plotting both dendrograms together!
```

```
tabasco(comm.data.2, o.clu, tdis.clus)
```



```
## Saving for future!
save(o.grel, file = "clusters.rda")
```

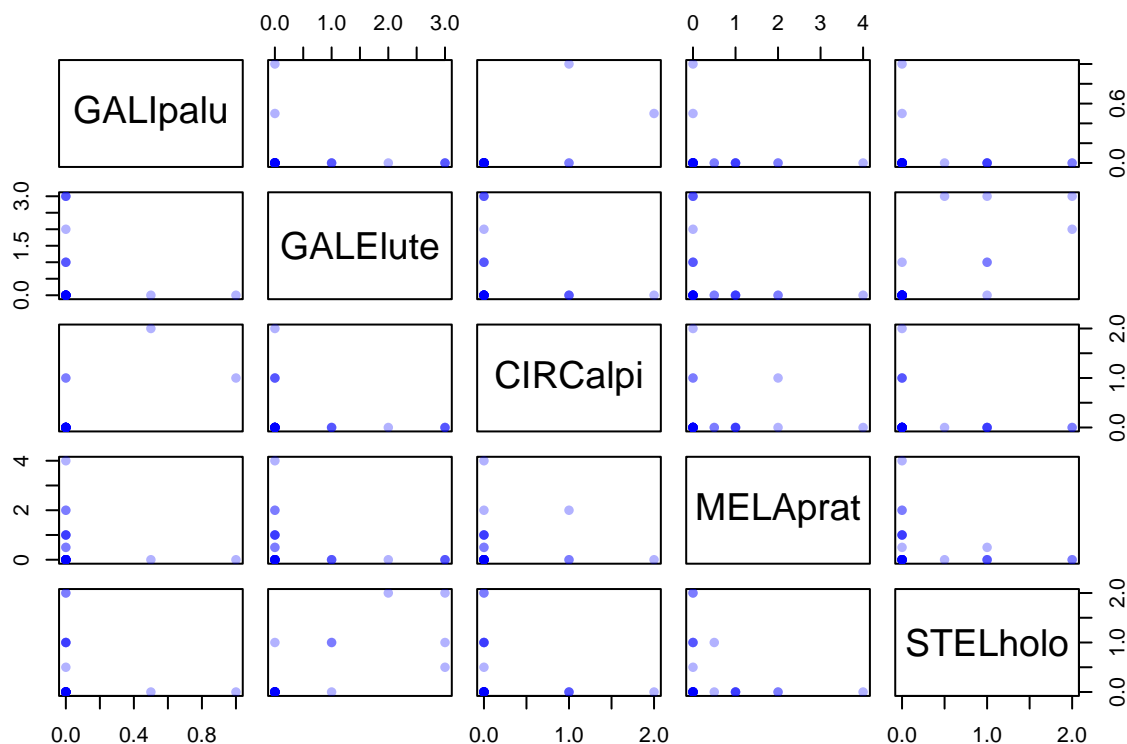
## Ordinations

Ordinations aim to put samples and taxa in order so that more similar items are close to each other. They help to visualize the similarity in structure between ecological communities.

### Taxa as axes

If we have just two taxa, we can plot samples on a 2-dimensional space where the axes reflect the abundance of each of these species. Then the distance between samples is the distance between points on the plot. We can imagine a 3-dimensional space (x, y and z). However, generally we have many more taxa. Let's select the 5 taxa with the highest IndVal value and make pairwise graphs!

```
load("community.rda") # loading from previous
load("clusters.rda")
comm.data <- log1p(vas.plants)
freq.spp <- c(58, 18, 10, 27, 38) # 5 most important spp from clusters
pairs(vas.plants[, freq.spp], pch = 16, col = rgb(0, 0, 1, 0.3))
```



Even with 5 taxa we have 10 pairwise graphs! Mathematically we can define as many axes as needed and put all points on this multi-dimensional space. Ordination allows to reduce the number of axes while keeping as much as possible of the original variation between sites.

## Principal Component Analysis (PCA)

Ordination of quantitative data, based on Euclidean distance between samples. There are different functions to perform PCA in different packages.

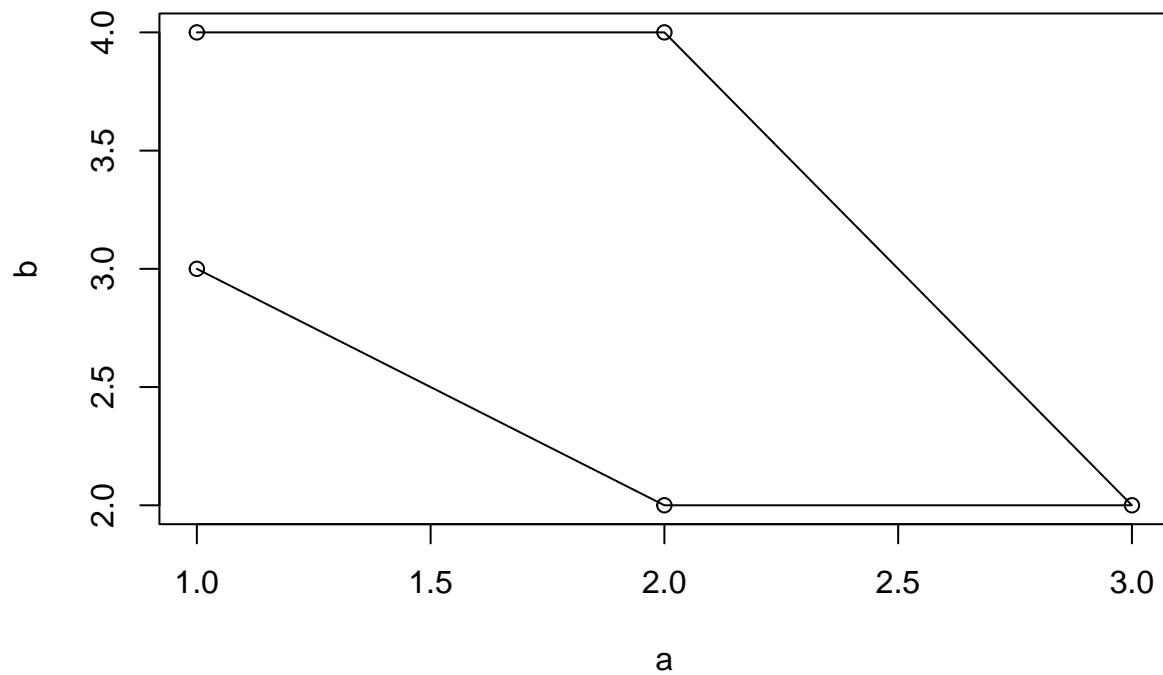
PCA first examines the cloud of points in the multidimensional matrix and puts the first axis along the largest variation; the following axis is the one that is perpendicular to the first one and describes the largest proportion of the variation left. This process is done (finding perpendicular axes to those previously selected), until no information is left to be explained.

This method assumes that abundance of taxa are linearly related to some gradients (just increasing or decreasing). It might be true for short environmental gradient but for longer gradients unimodal responses are more likely.

NB! Ordination axes does not have meaningful direction, they only show variation. You can always multiply some axis by -1 to reverse its direction!

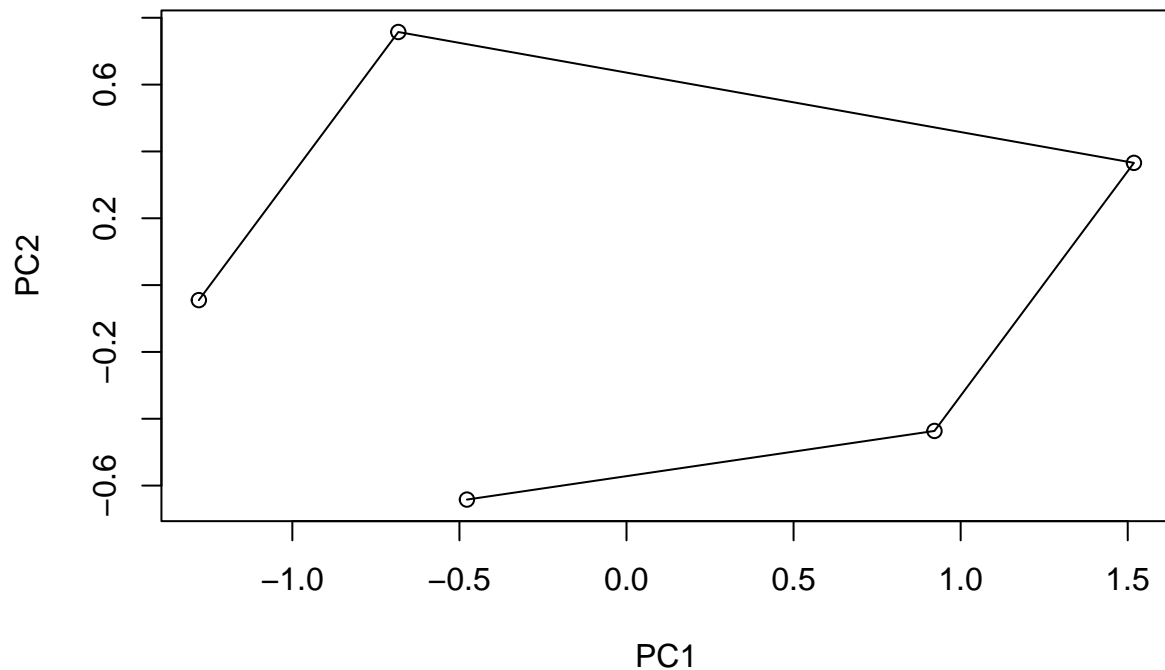
```
library(dave)
## Warning: replacing previous import 'labdsv::scores' by 'vegan::scores' when
## loading 'dave'
## Warning: replacing previous import 'labdsv::pca' by 'vegan::pca' when loading
## 'dave'
```

```
## Warning: replacing previous import 'labdsv::pco' by 'vegan::pco' when loading
## 'dave'
## Warning: replacing previous import 'labdsv::calibrate' by 'vegan::calibrate'
## when loading 'dave'
# Let's make an artificial table with 2 taxa a and b
test <- data.frame(a = c(1, 2, 3, 2, 1), b = c(3, 2, 2, 4, 4))
plot(test, type = "o")
```



```
# How the same data looks in PCA axes?

o.pca <- prcomp(test)
plot(o.pca$x[,1:2], asp = 1, type = "o")
```



*# since we had originally 2 dimensions then we have the same shape but PC1 is describing the most variation*

```
summary(o.pca)
```

```
## Importance of components:
```

```
##           PC1    PC2
## Standard deviation  1.1713 0.5727
## Proportion of Variance 0.8071 0.1929
## Cumulative Proportion 0.8071 1.0000
```

*# how much of total variation is described by the principal components.*

*# Now, using real community data*

```
o.pca <- prcomp(comm.data)
```

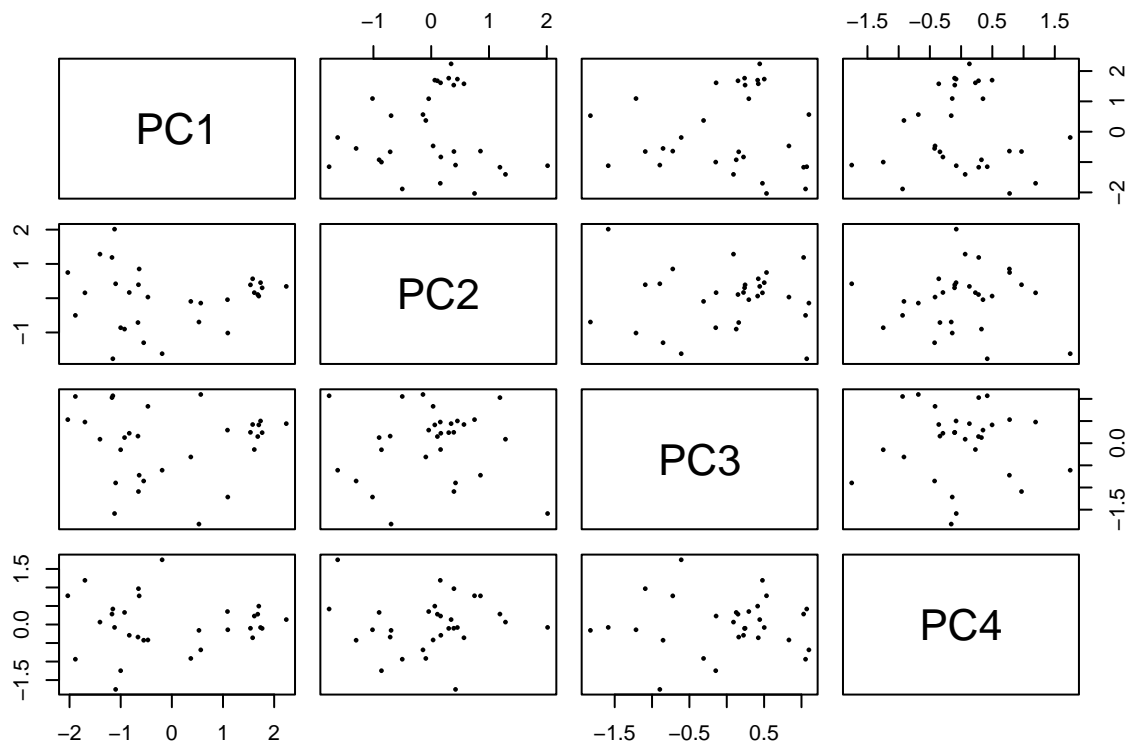
```
summary(o.pca) # How much our principal components describe
```

```
## Importance of components:
```

```
##           PC1    PC2    PC3    PC4    PC5    PC6    PC7
## Standard deviation  1.3064 0.8512 0.78620 0.72071 0.62673 0.57314 0.54010
## Proportion of Variance 0.2555 0.1085 0.09254 0.07777 0.05881 0.04918 0.04367
## Cumulative Proportion 0.2555 0.3640 0.45655 0.53431 0.59312 0.64230 0.68597
##           PC8    PC9    PC10    PC11    PC12    PC13    PC14
## Standard deviation  0.52109 0.49162 0.45124 0.41312 0.39359 0.37787 0.35786
## Proportion of Variance 0.04065 0.03618 0.03048 0.02555 0.02319 0.02138 0.01917
## Cumulative Proportion 0.72662 0.76281 0.79329 0.81885 0.84204 0.86341 0.88259
##           PC15    PC16    PC17    PC18    PC19    PC20    PC21
## Standard deviation  0.35043 0.31108 0.30573 0.27529 0.27072 0.23740 0.21337
```

```
## Proportion of Variance 0.01838 0.01449 0.01399 0.01135 0.01097 0.00844 0.00682
## Cumulative Proportion 0.90097 0.91546 0.92945 0.94080 0.95177 0.96021 0.96703
##                      PC22  PC23  PC24  PC25  PC26  PC27  PC28
## Standard deviation    0.21089 0.1917 0.18782 0.16537 0.15206 0.1484 0.14236
## Proportion of Variance 0.00666 0.0055 0.00528 0.00409 0.00346 0.0033 0.00303
## Cumulative Proportion 0.97368 0.9792 0.98447 0.98856 0.99202 0.9953 0.99836
##                      PC29  PC30
## Standard deviation    0.10480 5.802e-16
## Proportion of Variance 0.00164 0.000e+00
## Cumulative Proportion 1.00000 1.000e+00
```

```
pairs(o.pca$x[, 1:4], pch = 16, cex = 0.5) # ordination plots
```



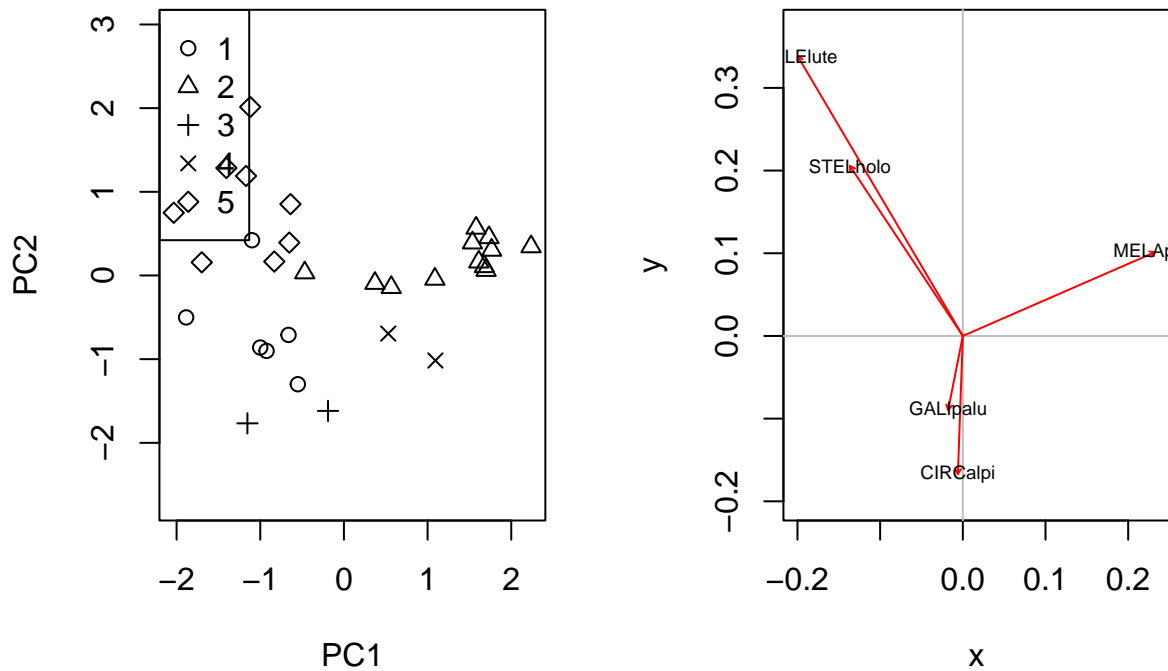
```
# mostly, however, just PC1 vs. PC2 are used
```

```
par(mfrow = c(1, 2))
plot(o.pca$x[, 1:2], asp = 1, pch = o.grel) # clusters
legend("topleft", legend = unique(o.grel), pch = unique(o.grel))
```

```
# Eigenvectors of frequent species -- describing their contribution to principal components, can be vis
```

```
x <- o.pca$rotation[freq.spp, 1]
y <- o.pca$rotation[freq.spp, 2]
plot(x, y, type = "n", asp = 1)
```

```
abline(h = 0, v = 0, col = "gray")
arrows(0, 0, x, y, length = 0.03, col = "red")
text(x, y, colnames(comm.data)[freq.spp], cex = 0.6)
```



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

## Principal Coordinates Analysis

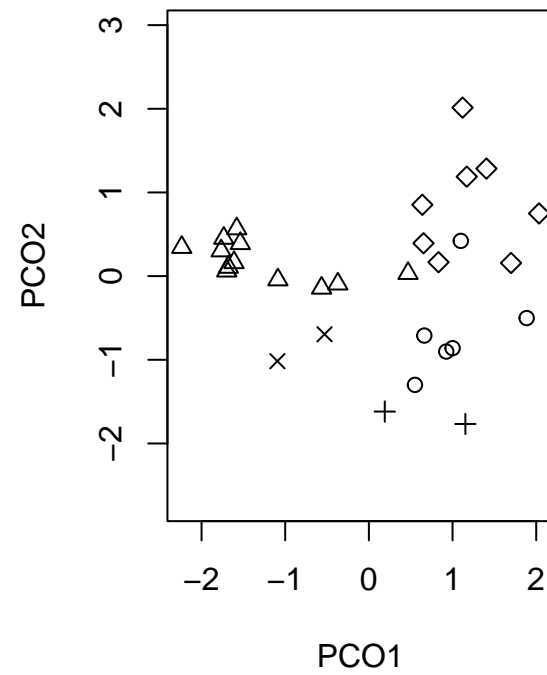
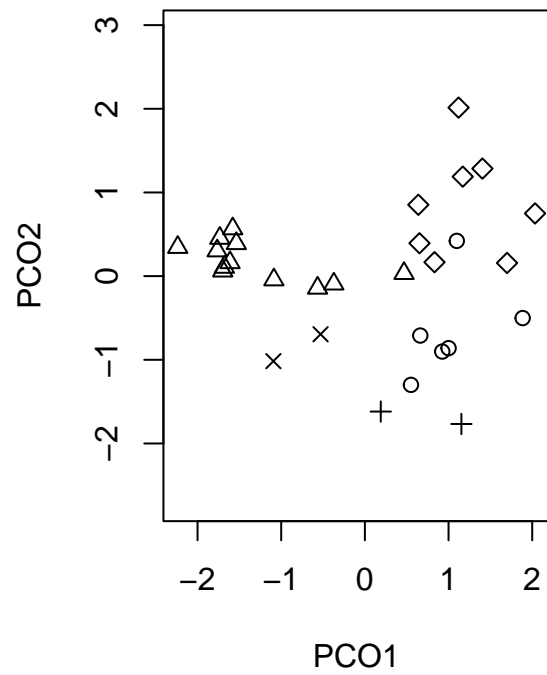
Ordination based on eigenvalues and any distance matrix. If you select Euclidean distance, it is equal to PCA.

```
vegdist <- vegdist(comm.data, "euclidean")
o.pco <- pco(vegdist)
par(mfrow = c(1, 2))
plot(o.pco$points[, 1:2], asp = 1, pch = o.grel, xlab = "PC01", ylab = "PC02")

## Should be identical (NB! axis direction does not have meaning)

# Now using Bray-Curtis distance

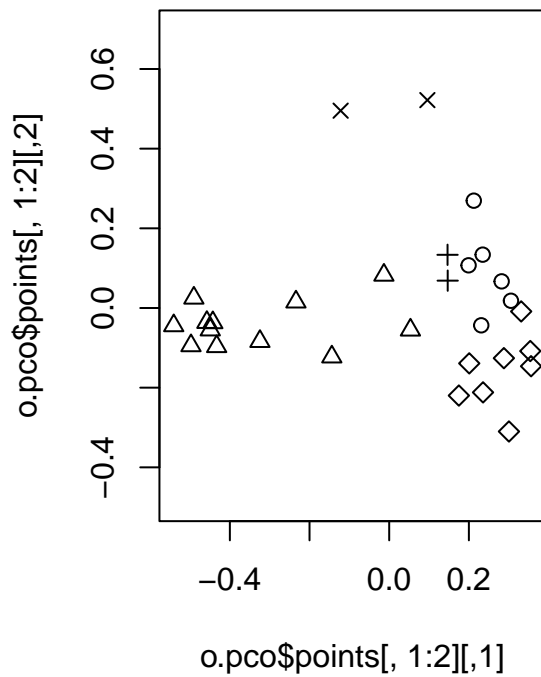
plot(o.pco$points[, 1:2], asp = 1, pch = o.grel, xlab = "PC01", ylab = "PC02")
```



```
vegdist <- vegdist(comm.data, "bray")
o.pco <- pco(vegdist)
plot(o.pco$points[, 1:2], asp = 1, pch = o.grel)

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





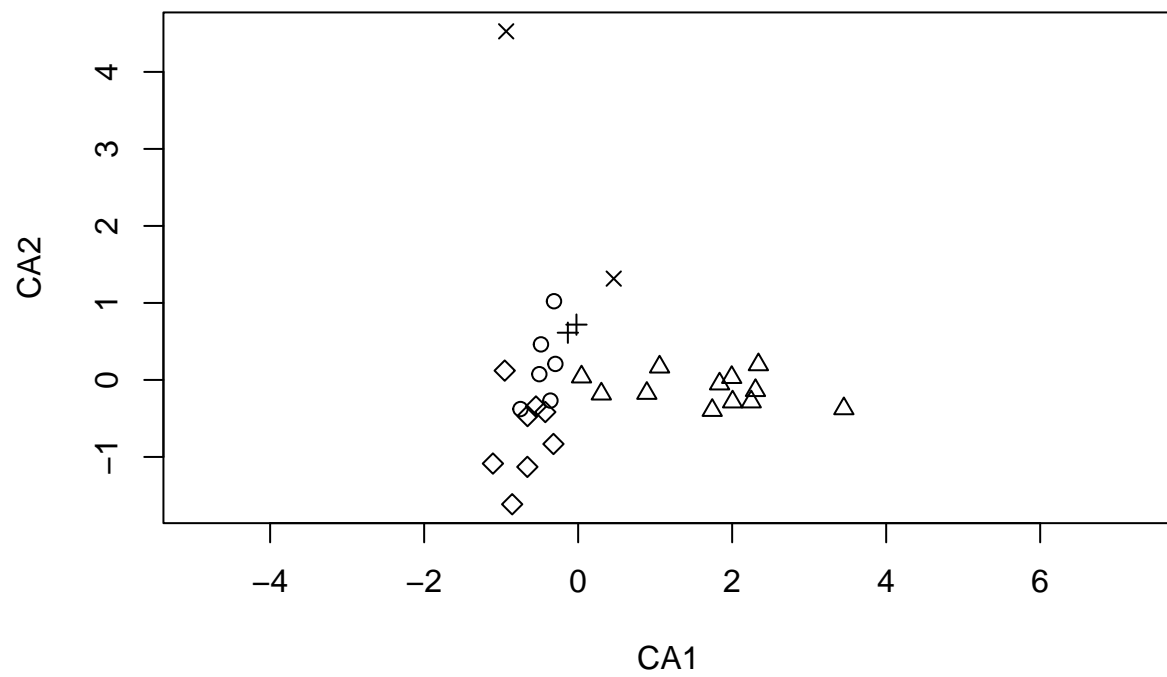
## Correspondence Analysis

This technique tries to ordinate both samples and taxa in parallel. It expects unimodal response curves of taxa and aims to find the weighted averages for taxa and sites (the synonym to Correspondence Analysis is Reciprocal Averaging).

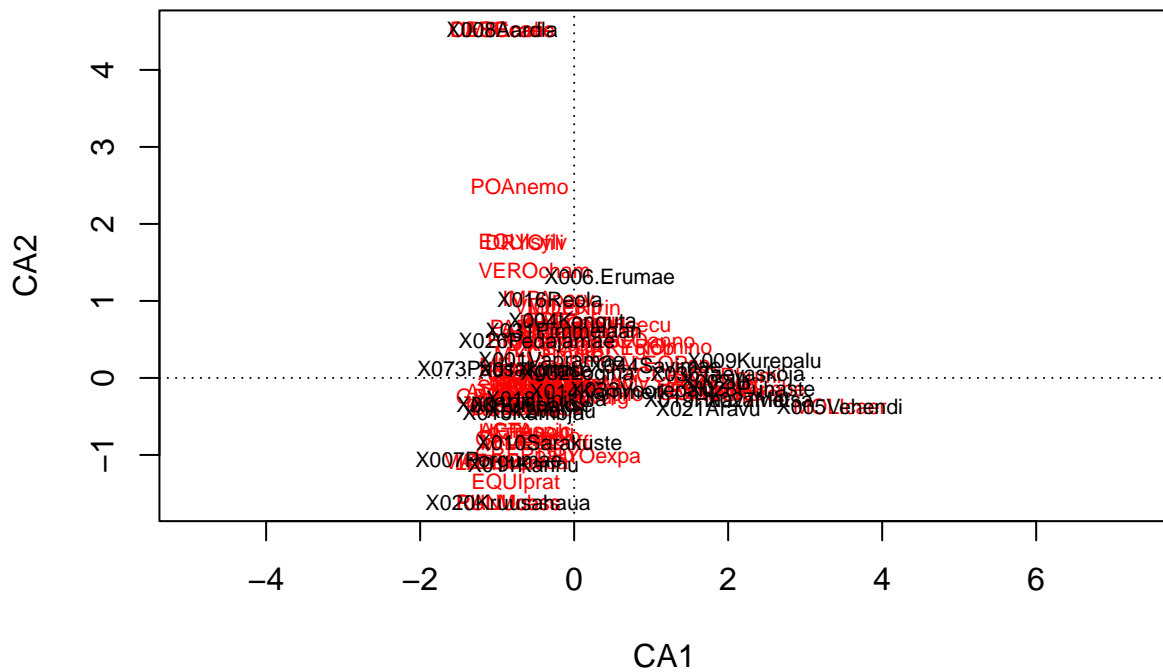
```
o.ca <- cca(comm.data)

summary(o.ca)$cont$importance[, 1:3]
##                CA1          CA2          CA3
## Eigenvalue      0.5392631 0.39437464 0.33141756
## Proportion Explained 0.1258140 0.09201047 0.07732213
## Cumulative Proportion 0.1258140 0.21782447 0.29514660

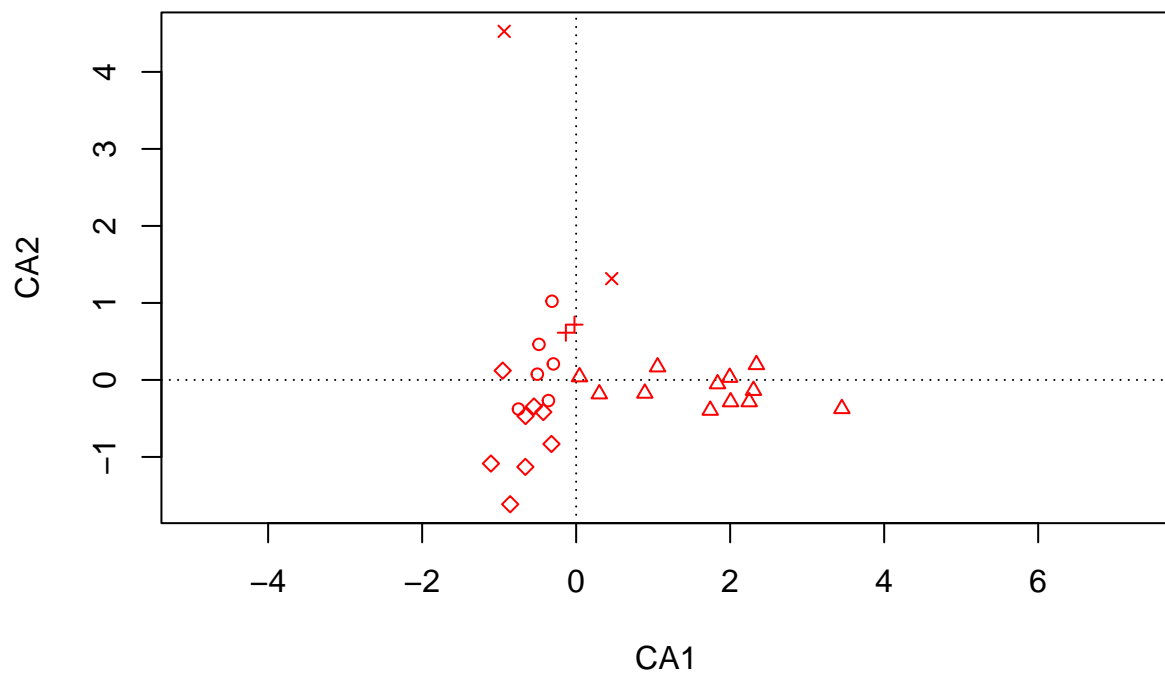
plot(o.ca$CA$u[, 1:2], pch = o.grel, asp = 1)
```



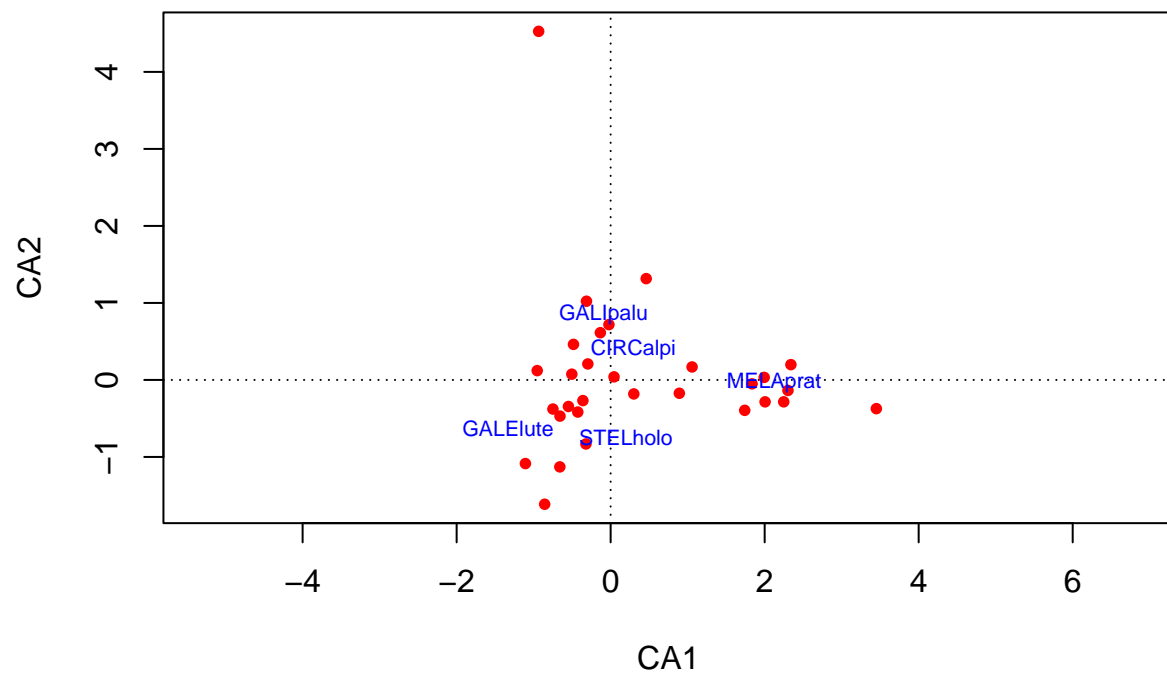
```
plot(o.ca) # Biplot where both sites and taxa are given (their averaged locations)
```



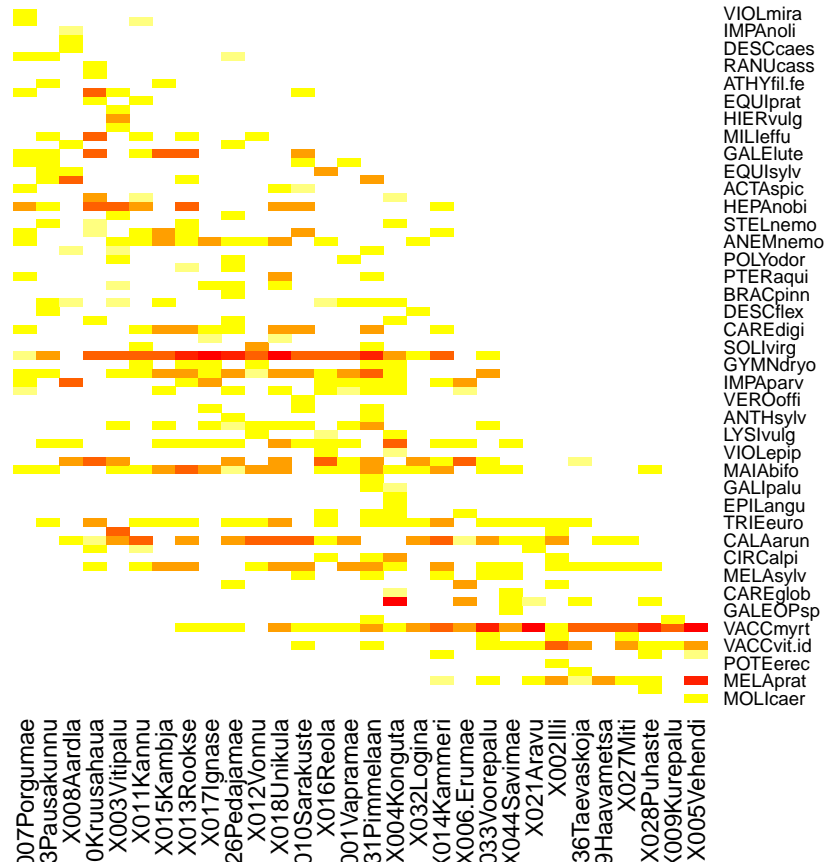
```
# Adding manually sites and species to obtain a more clean image
plot(o.ca, type = "n")
points(o.ca, display = "sites", cex = 0.8, pch = o.grel, col = "red")
text(o.ca, display = "spec", cex = 0.7, col = "blue",
     select = freq.spp)
```



```
plot(o.ca, type = "n", xlim = c(-2, 3.5))
points(o.ca, display = "sites", cex = 0.8, pch = 16, col = "red")
ordipointlabel(o.ca, cex = 0.7, display = "species", col = "blue", add = T,
               select = freq.spp) ## Tries to optimize the location of the text labels to avoid overlap
```



```
tabasco(comm.data, o.ca) # ordering tables using CA for both samples and taxa.
```



## Nonmetric Multidimensional Scaling (NMDS)

Not based on maximum variation but on shifting iteratively of objects within a low number of axes so that the distance between samples is maximally kept. The algorithm starts from a random order or PCA. Compares the difference between real distance and the distance within the ordination space (this difference is called “stress”). Often used nowadays because computing is not limiting any more. A rule of thumb: stress ca 0.05 means an excellent representation in reduced dimensions, 0.1 is great, 0.2 is satisfactory, and stress >0.3 means a poor representation.

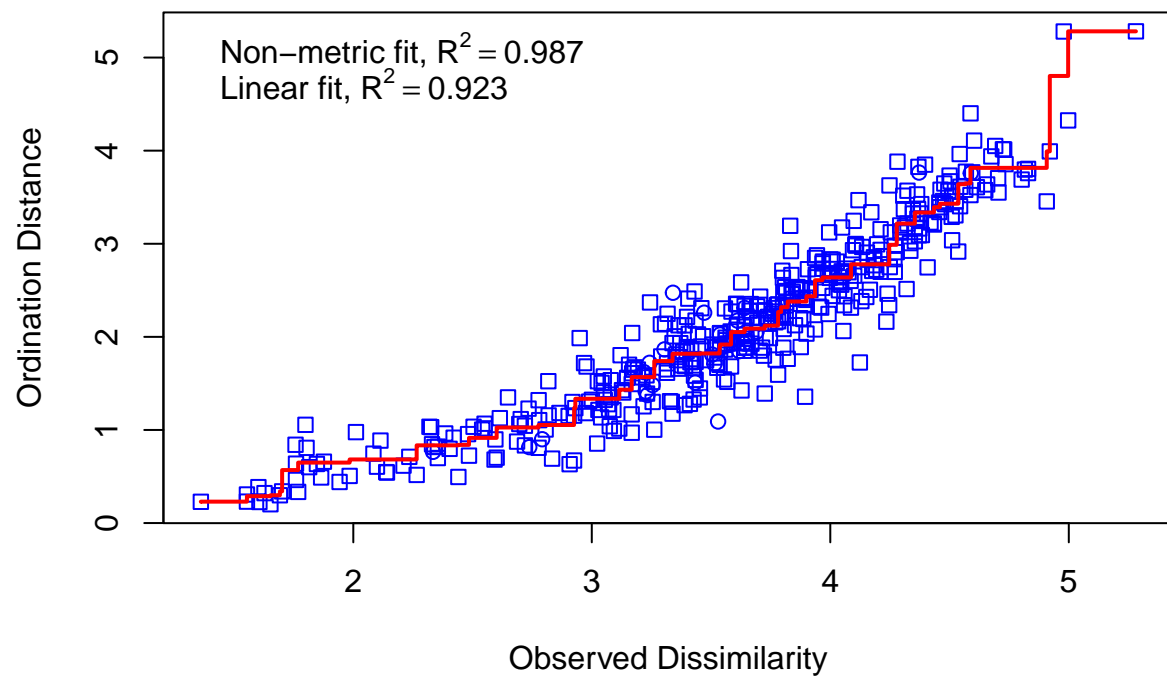
We also explore how to limit clusters and draw species richness on the ordination graph.

```
o.mds <- metaMDS(comm.data, distance = "euclidean", k = 3)
## Run 0 stress 0.1125173
## Run 1 stress 0.1125167
## ... New best solution
## ... Procrustes: rmse 0.0004085559 max resid 0.001505128
## ... Similar to previous best
## Run 2 stress 0.1122944
## ... New best solution
## ... Procrustes: rmse 0.02093857 max resid 0.08352378
## Run 3 stress 0.1125209
## ... Procrustes: rmse 0.01964965 max resid 0.07996769
## Run 4 stress 0.1184548
## Run 5 stress 0.1122949
## ... Procrustes: rmse 0.0004730182 max resid 0.001852725
```

```

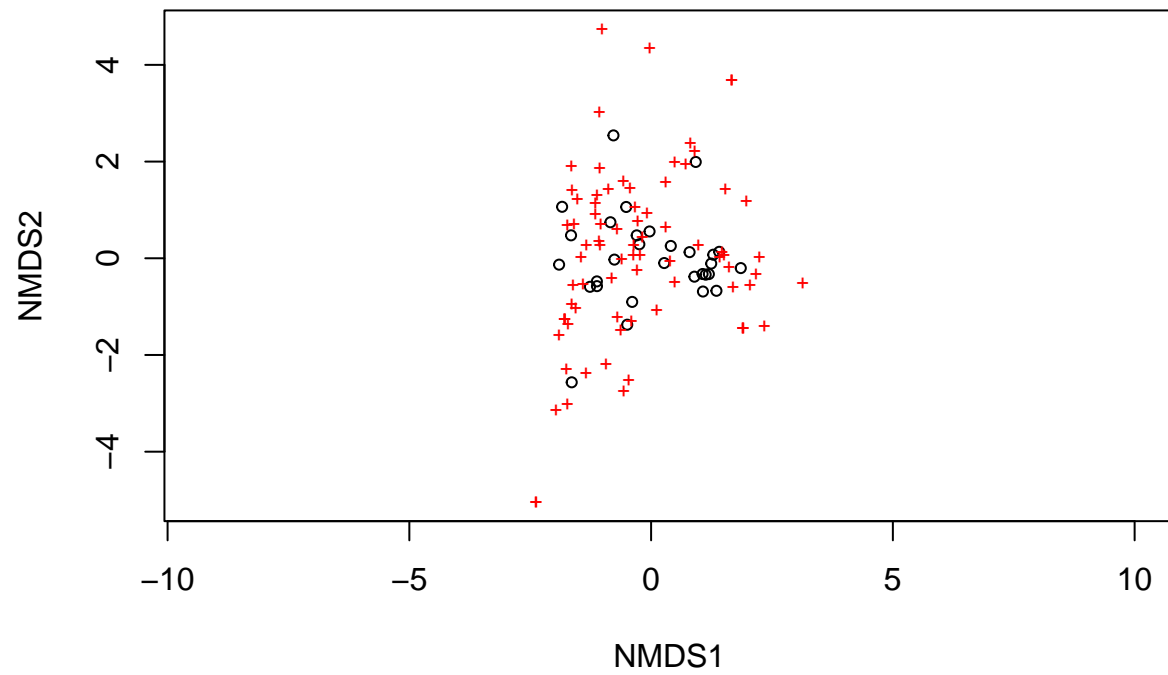
## ... Similar to previous best
## Run 6 stress 0.1184553
## Run 7 stress 0.1122948
## ... Procrustes: rmse 0.0002472672 max resid 0.0009298979
## ... Similar to previous best
## Run 8 stress 0.1124119
## ... Procrustes: rmse 0.005967248 max resid 0.01832438
## Run 9 stress 0.1122999
## ... Procrustes: rmse 0.00141392 max resid 0.004483972
## ... Similar to previous best
## Run 10 stress 0.1122945
## ... Procrustes: rmse 0.0001955405 max resid 0.0007660798
## ... Similar to previous best
## Run 11 stress 0.1184549
## Run 12 stress 0.1270614
## Run 13 stress 0.1122946
## ... Procrustes: rmse 0.0003297681 max resid 0.001290142
## ... Similar to previous best
## Run 14 stress 0.1125174
## ... Procrustes: rmse 0.02140294 max resid 0.08481692
## Run 15 stress 0.1125167
## ... Procrustes: rmse 0.02062548 max resid 0.08273438
## Run 16 stress 0.1197972
## Run 17 stress 0.1184602
## Run 18 stress 0.1122947
## ... Procrustes: rmse 0.0002251873 max resid 0.0007605293
## ... Similar to previous best
## Run 19 stress 0.1122944
## ... Procrustes: rmse 9.206646e-05 max resid 0.0003618954
## ... Similar to previous best
## Run 20 stress 0.1187897
## *** Best solution repeated 7 times
stressplot(o.mds, vegdist) # stress is the distance of points from the line! Looks fine!

```

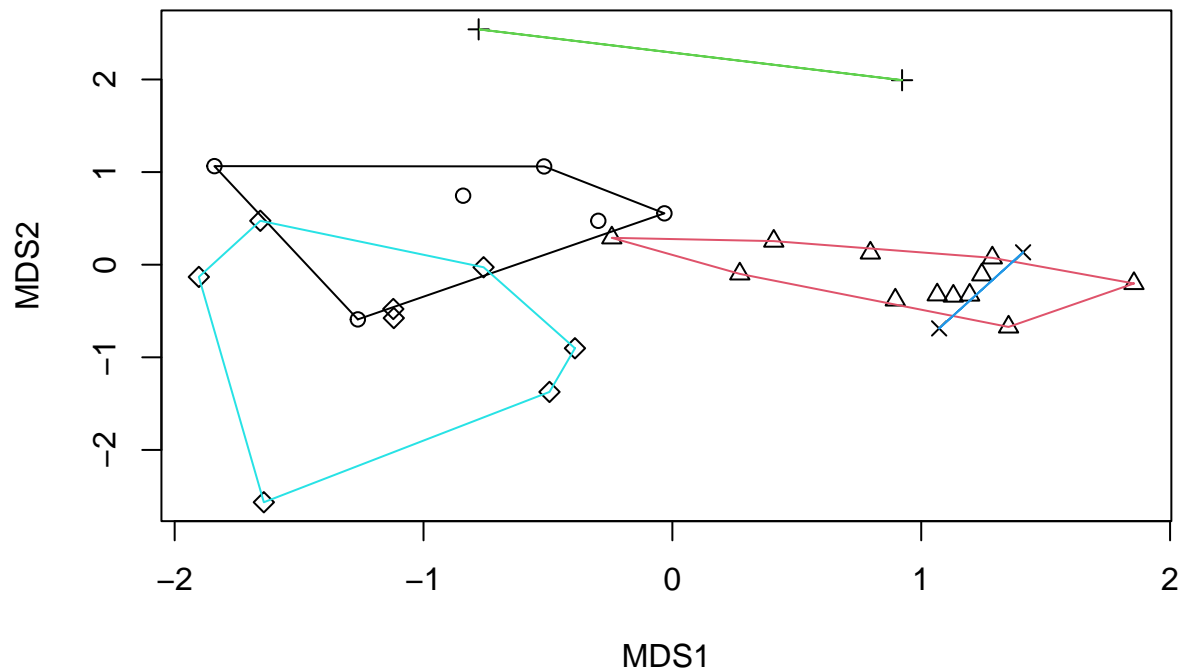


```
plot(o.mds) # biplot, samples taxa
```





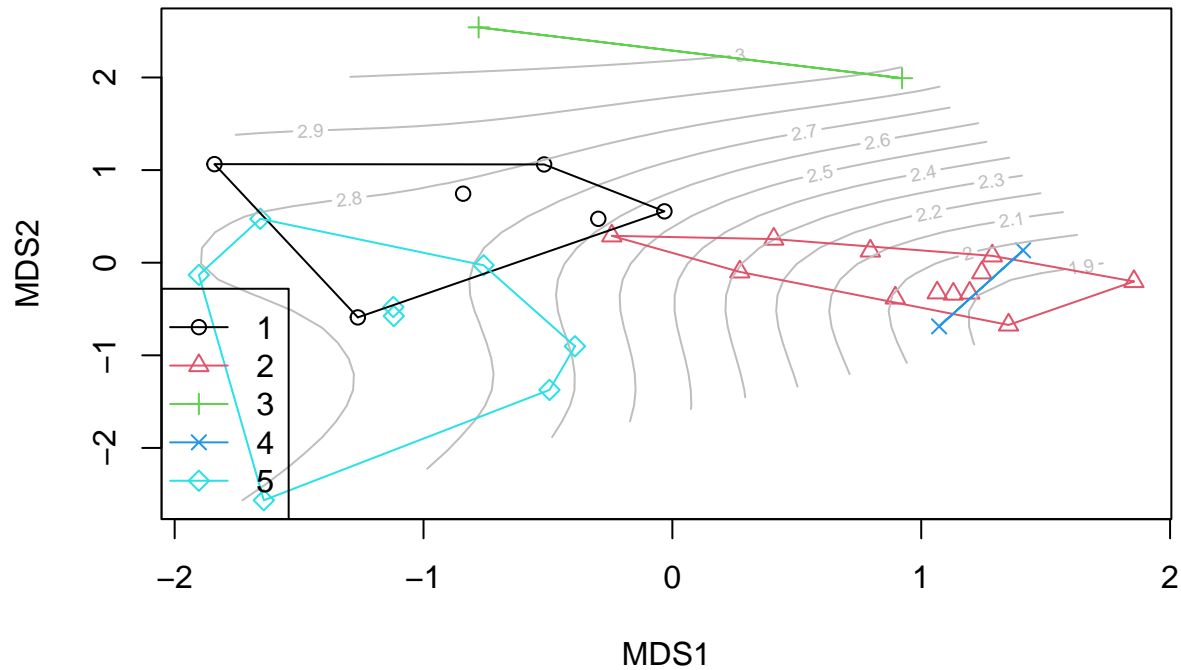
```
plot(o.mds$points, pch = o.grel) # only samples  
ordihull(o.mds, o.grel, col = 1:5) # connecting clusters
```



```
## Adding species diversity to plot
plot(o.mds$points, pch = o.grel, col = o.grel)
ordisurf(o.mds, diversity(comm.data), col = "grey", main = "Shannon diversity",
        add = T)

##
## Family: gaussian
## Link function: identity
##
## Formula:
## y ~ s(x1, x2, k = 10, bs = "tp", fx = FALSE)
##
## Estimated degrees of freedom:
## 5.1 total = 6.1
##
## REML score: 15.15061
ordihull(o.mds, o.grel, col = 1:5)
legend("bottomleft", legend = unique(o.grel), col = unique(o.grel),
      pch = unique(o.grel), lwd = 1)
```

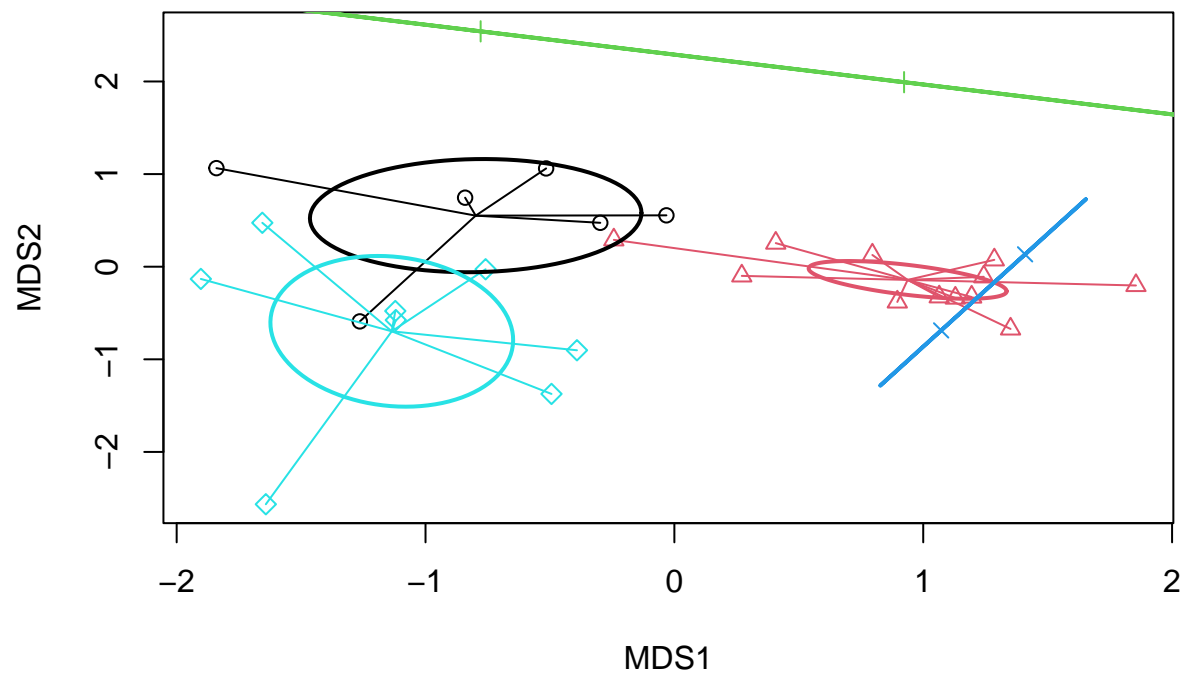
## Shannon diversity



Try also `ordispider` and `ordiellipse` functions

Answer

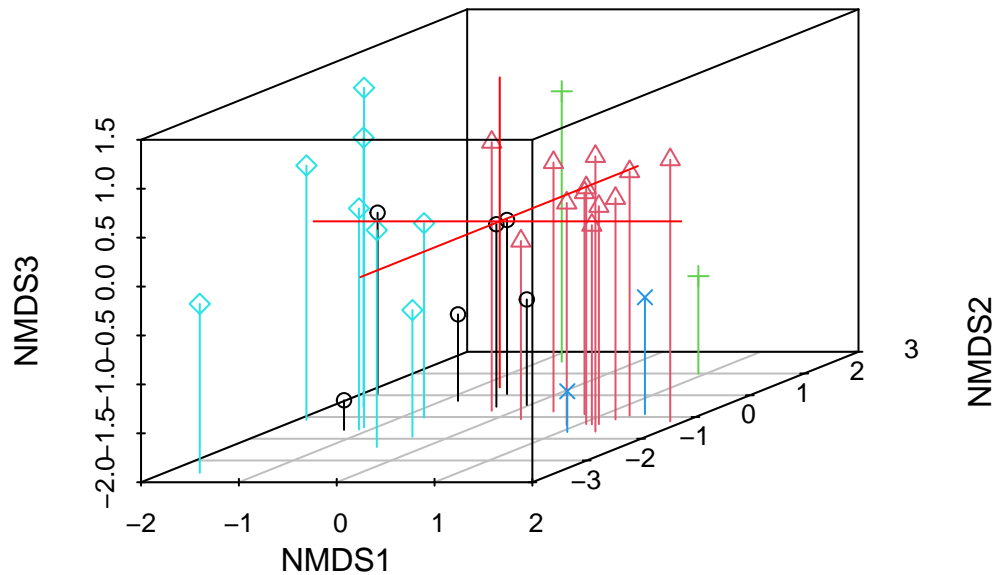
```
plot(o.mds$points, pch = o.grel, col = o.grel)
ordispider(o.mds, o.grel, col = unique(o.grel))
ordiellipse(o.mds, o.grel, col = unique(o.grel),
  kind="se", lwd=2, con = 0.95)
## Warning in chol.default(cov, pivot = TRUE): the matrix is either rank-deficient
## or not positive definite
## Warning in chol.default(cov, pivot = TRUE): the matrix is either rank-deficient
## or not positive definite
```



### 3D visualizations

```
library(vegan3d)

ordiplot3d(o.mds, type = "h", pch = o.grel,
           , col = o.grel)
```



```
ordirgl(o.mds, col = o.grel, pch = o.grel) # Should open a new window!

save(o.mds, file = "ordi.rda")
```

## Combining community and environmental data

The main aim of this lesson is to examine how the community structure (i.e. species richness and composition) is linked to environmental variables.

### Reading data from previous days

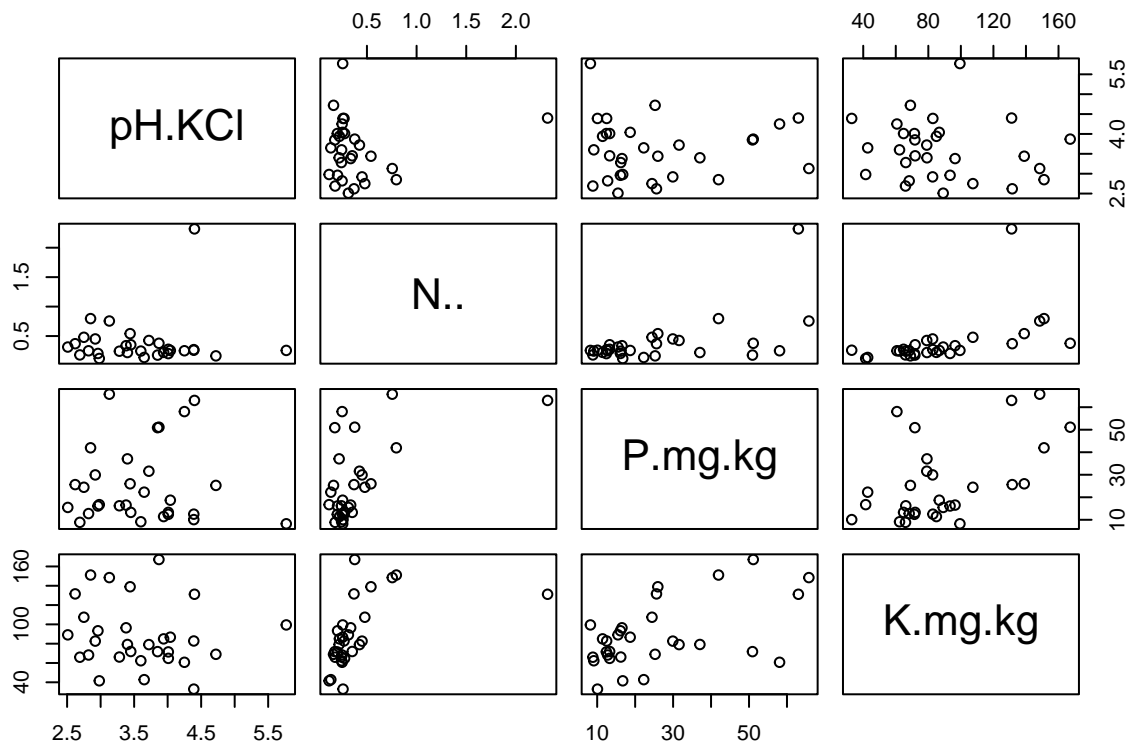
```
library(dave)
load("community.rda") # loading from previous
load("clusters.rda")
load("ordi.rda")
```

### Exploring and combining similar soil data

In the previous class, we used ordination methods to put samples and taxa in order, so that similar items are close to each other. Ordination methods can also be used with correlated environmental data, so that we

obtained a combined measurement of some environmental variable. An alternative method is to standardize and average measures. Let's look at soil chemistry.

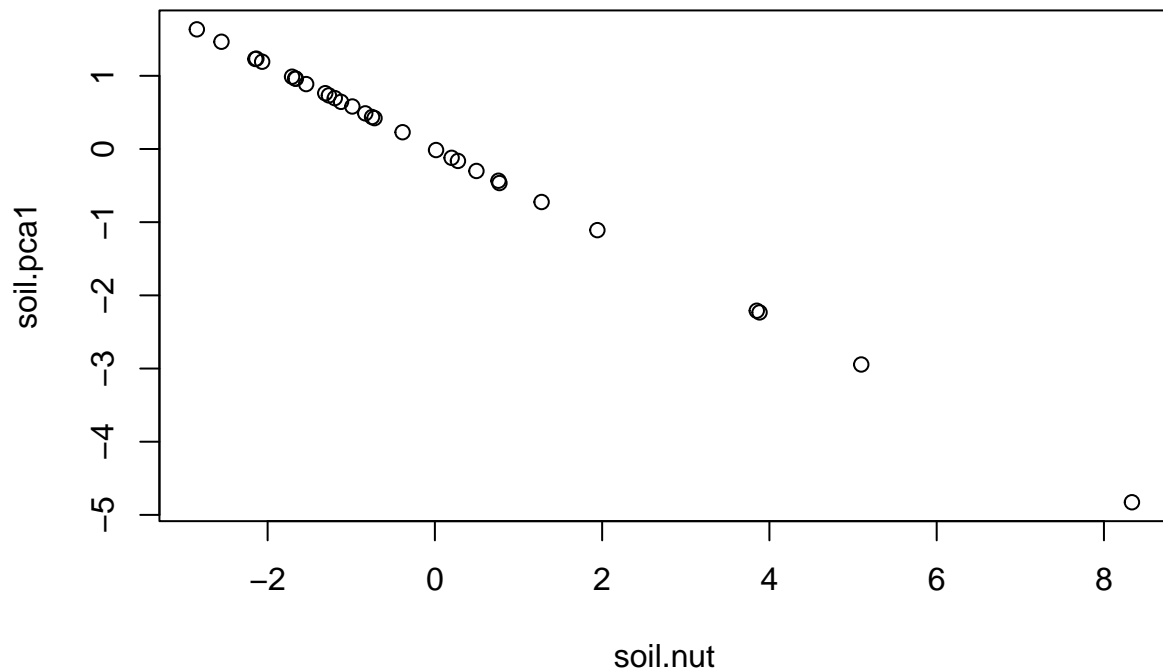
```
cor(soil.data[,-5]) # N, P and K strongly correlated
##           pH.KCl      N..      P.mg.kg      K.mg.kg
## pH.KCl      1.0000000  0.06737856  0.01357602 -0.1420262
## N..         0.06737856  1.00000000  0.56044799  0.5161510
## P.mg.kg     0.01357602  0.56044799  1.00000000  0.5283704
## K.mg.kg    -0.14202617  0.51615100  0.52837042  1.0000000
pairs(soil.data[,-5])
```



```
# An option to use PCA for soils
soil.pca = prcomp(soil.data[,2:4], scale.=T) # scale.=T standardizes units
soil.pca1=soil.pca$x[,1]

# Averaging all three after rescaling
npk.scale=scale(soil.data[,2:4]) # rescaling mean 0 and sd 1
soil.nut=rowSums(npk.scale)

plot(soil.nut,soil.pca1) # NB! PCA axes can be changed!
```



```
soil.pca1=soil.pca1*-1
```

Make PCA with all soil variables found in `envir.txt` and examine how well the PC scores are correlated with the initial soil variables.

Answer

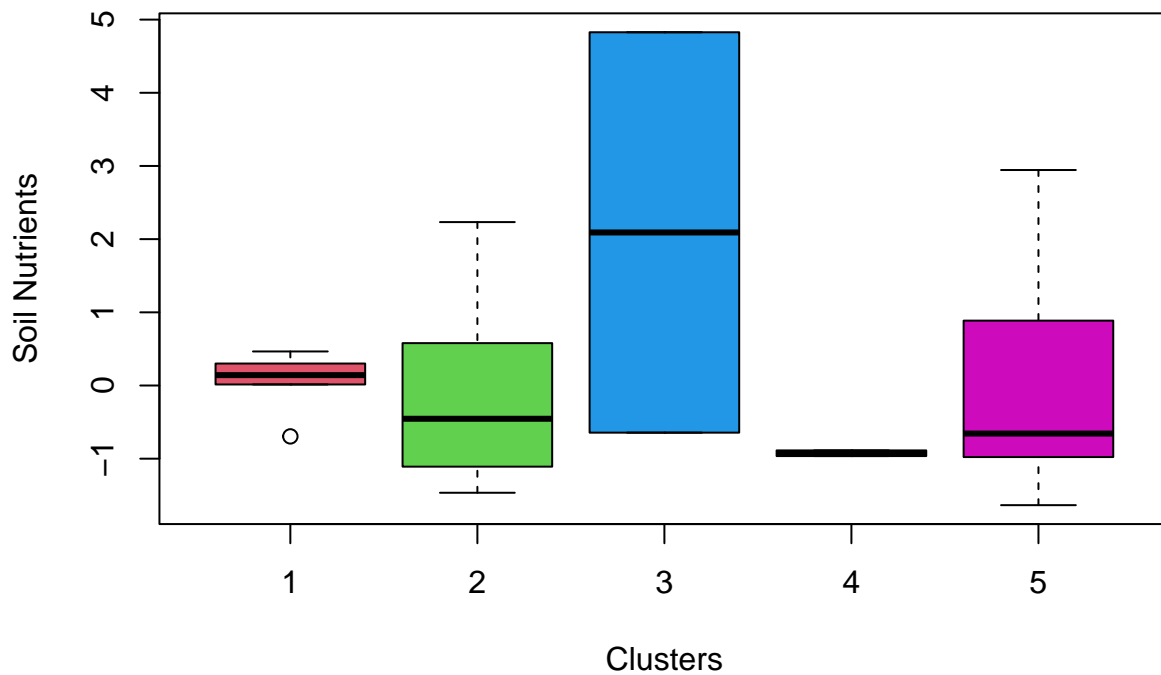
```
envir=read.table("envir.txt")
names(envir)
## [1] "lon"      "lat"      "forest.types" "Jrk..nr." "Proovi.nimi"
## [6] "pH.KCl"   "N.."      "P.mg.kg"      "K.mg.kg"   "Ca.mg.kg"
## [11] "Mg.mg.kg" "OA.."
env.pca = prcomp(envir[,6:12], scale.=T)
all.soil.pca1=scores(env.pca$x)[,1]
## Error in UseMethod("scores"): no applicable method for 'scores' applied to an object of class "c('ma
cor(all.soil.pca1,envir[,6:12])
## Error in eval(expr, envir, enclos): object 'all.soil.pca1' not found
```

## Environment within clusters

Instead of working with the original environmental data, we are going to use our new variable 'soil.pca1' as a synthetic variable that reflects nutrient availability in our sites. We will test whether environment differs between samples representing different clusters. For this, we will first make some box plots, then we will perform an anova test and then we will examine whether the assumptions of anova are met.

```
## Using clusters and soil data (Soil pH as an example)
```

```
boxplot(soil.pca1 ~as.factor(o.grel),col=2:6,ylab="Soil Nutrients",xlab="Clusters")
```



```
# ANOVA test
```

```
o.anova=aov(soil.pca1 ~ as.factor(o.grel))
```

```
anova(o.anova)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: soil.pca1
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(o.grel)  4 11.015   2.7538   1.4044 0.2614
## Residuals        25 49.020   1.9608
```

```
# testing anova assumptions:
```

```
# 1. residuls of the model must be normally distributed
```

```
shapiro.test(resid(o.anova)) # p > 0.05
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data:  resid(o.anova)
```



```
## W = 0.92643, p-value = 0.03951

# 2. homogeneity of variances among groups

bartlett.test(soil.pca1, as.factor(o.grel)) # p > 0.05
##
## Bartlett test of homogeneity of variances
##
## data: soil.pca1 and as.factor(o.grel)
## Bartlett's K-squared = 16.131, df = 4, p-value = 0.002848

## If ANOVA assumptions are not met, we can make non-parametric test
## for example Kruskal-Wallis rank sum test

kruskal.test(soil.pca1 ~ as.factor(o.grel)) ## Not significantly different
##
## Kruskal-Wallis rank sum test
##
## data: soil.pca1 by as.factor(o.grel)
## Kruskal-Wallis chi-squared = 4.05, df = 4, p-value = 0.3993

## Same with soil pH

o.anova=aov(soil.data$pH.KCl ~ as.factor(o.grel))
shapiro.test(resid(o.anova)) # OK
##
## Shapiro-Wilk normality test
##
## data: resid(o.anova)
## W = 0.93286, p-value = 0.05851
bartlett.test(soil.data$pH.KCl, as.factor(o.grel)) # OK
##
## Bartlett test of homogeneity of variances
##
## data: soil.data$pH.KCl and as.factor(o.grel)
## Bartlett's K-squared = 3.2945, df = 4, p-value = 0.5098

anova(o.anova) # significance
## Analysis of Variance Table
##
## Response: soil.data$pH.KCl
##           Df Sum Sq Mean Sq F value    Pr(>F)
## as.factor(o.grel)  4  6.9907  1.74769    5.042 0.004048 **
## Residuals        25  8.6657  0.34663
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
TukeyHSD(o.anova) # comparison of pairs, Tukey test
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = soil.data$pH.KCl ~ as.factor(o.grel))
##
```

```
## $`as.factor(o.grel)`
##      diff      lwr      upr      p adj
## 2-1 -0.70000 -1.5645426 0.1645426 0.1545794
## 3-1  0.80500 -0.6067922 2.2167922 0.4667457
## 4-1 -0.11000 -1.5217922 1.3017922 0.9993478
## 5-1  0.26875 -0.6650628 1.2025628 0.9137158
## 3-2  1.50500  0.1843893 2.8256107 0.0198753
## 4-2  0.59000 -0.7306107 1.9106107 0.6864372
## 5-2  0.96875  0.1795342 1.7579658 0.0108067
## 4-3 -0.91500 -2.6440853 0.8140853 0.5388419
## 5-3 -0.53625 -1.9032119 0.8307119 0.7775773
## 5-4  0.37875 -0.9882119 1.7457119 0.9239282
```

Parametric tests (e.g. ANOVA) are usually more powerful than non-parametric tests (e.g. Kruskal-Wallis) but results are often similar. Test how soil pH is related to clusters using Kruskal-Wallis test.

Answer

```
kruskal.test(soil.data$pH.KCl ~ as.factor(o.grel))
##
##  Kruskal-Wallis rank sum test
##
## data:  soil.data$pH.KCl by as.factor(o.grel)
## Kruskal-Wallis chi-squared = 14.634, df = 4, p-value = 0.005524
```

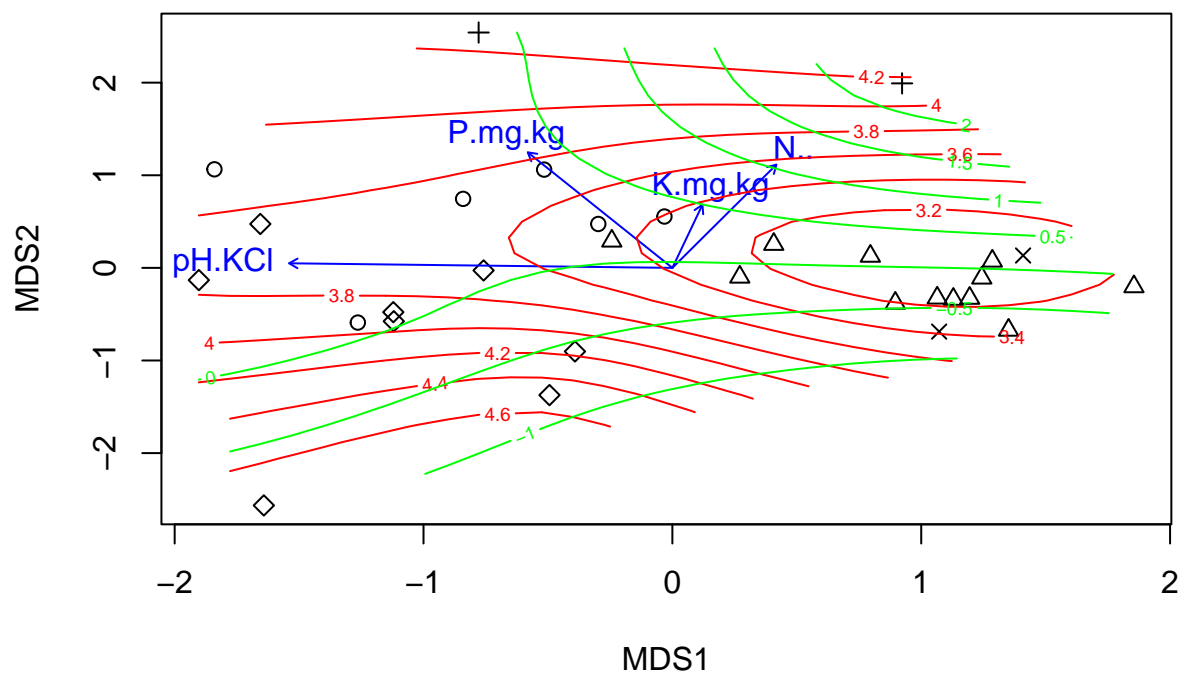
## Environment related ordination

We can use the function `envfit` to visually explore the correlation of ordination results with environmental parameters.

```
o.ev=envfit(o.mds,soil.data[,5])
o.ev
##
## ***VECTORS
##
##      NMDS1      NMDS2      r2 Pr(>r)
## pH.KCl -0.99948  0.03214 0.2577 0.027 *
## N.      0.35104  0.93636 0.1539 0.088 .
## P.mg.kg -0.42223  0.90649 0.2055 0.048 *
## K.mg.kg  0.17443  0.98467 0.0521 0.464
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Permutation: free
## Number of permutations: 999
plot(o.mds$points,pch=o.grel)
plot(o.ev,add=T) # Adding correlations to graph

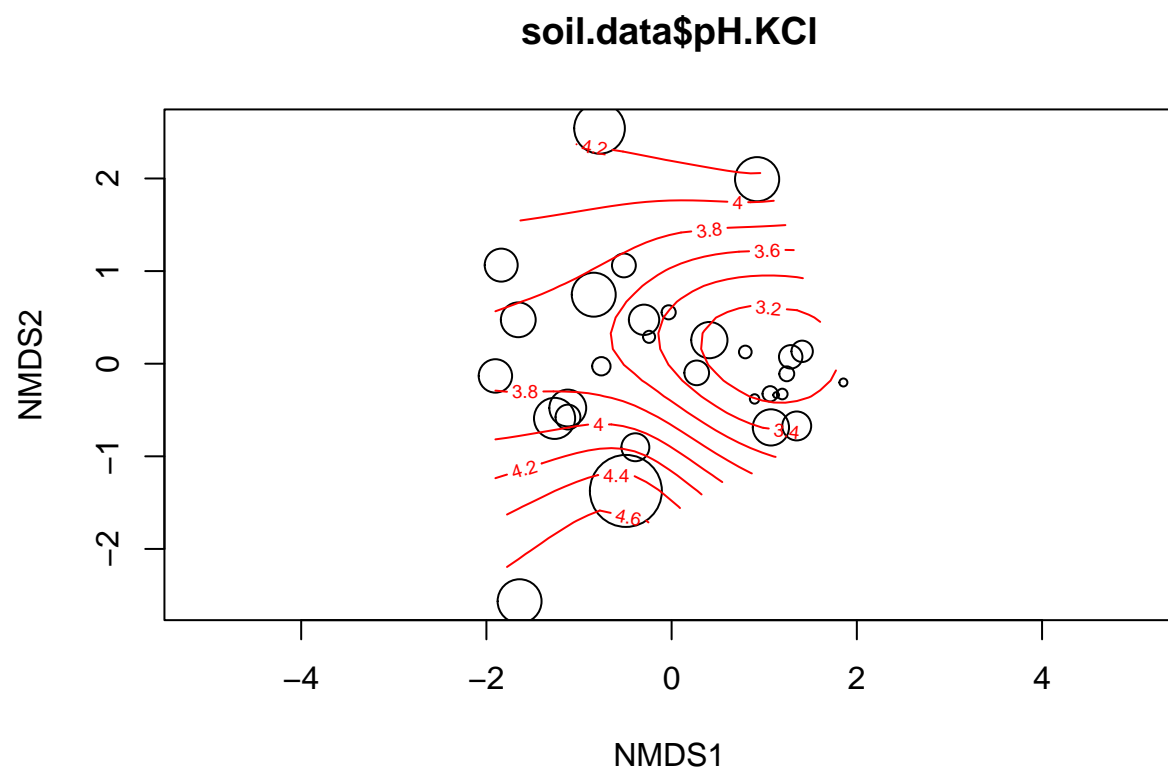
ordisurf(o.mds,soil.data$pH.KCl,add=T)
##
## Family: gaussian
```

```
## Link function: identity
##
## Formula:
## y ~ s(x1, x2, k = 10, bs = "tp", fx = FALSE)
##
## Estimated degrees of freedom:
## 4.66 total = 5.66
##
## REML score: 29.02159
ordisurf(o.mds,soil.pca1,add=T,col="green")
```

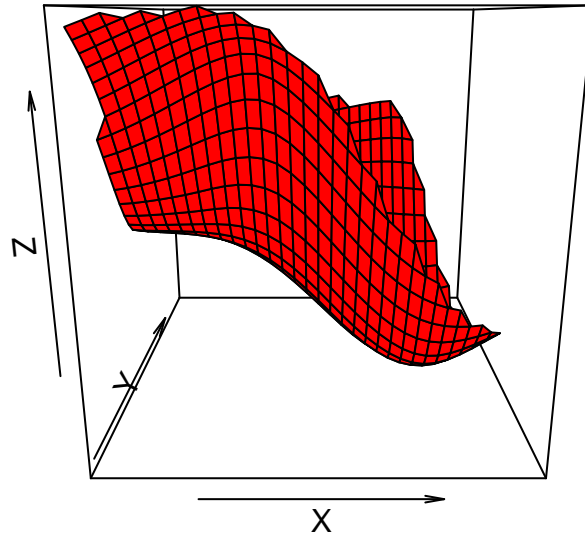


```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## y ~ s(x1, x2, k = 10, bs = "tp", fx = FALSE)
##
## Estimated degrees of freedom:
## 4.52 total = 5.52
##
## REML score: 52.69282

oo=ordisurf(o.mds,soil.data$pH.KCl,bubble=5) # visualizing environment with circle size
```



```
plot(oo,what="persp") # 3D image of study variable (z) along ordination axes (x and y)
```

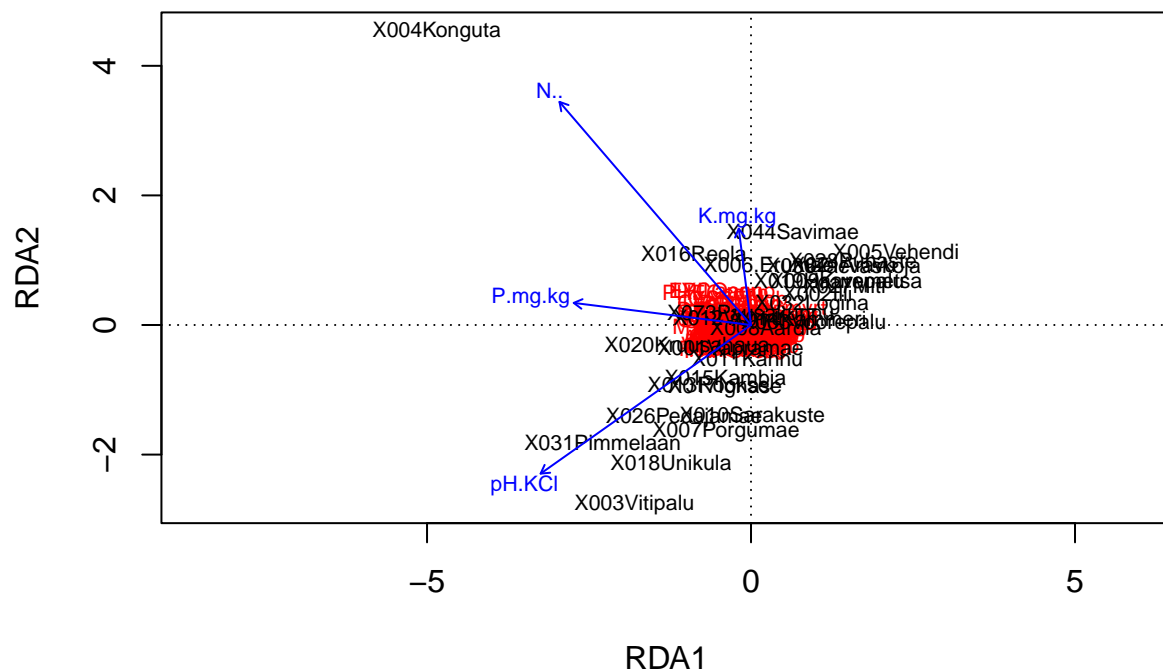


## Constrained ordination

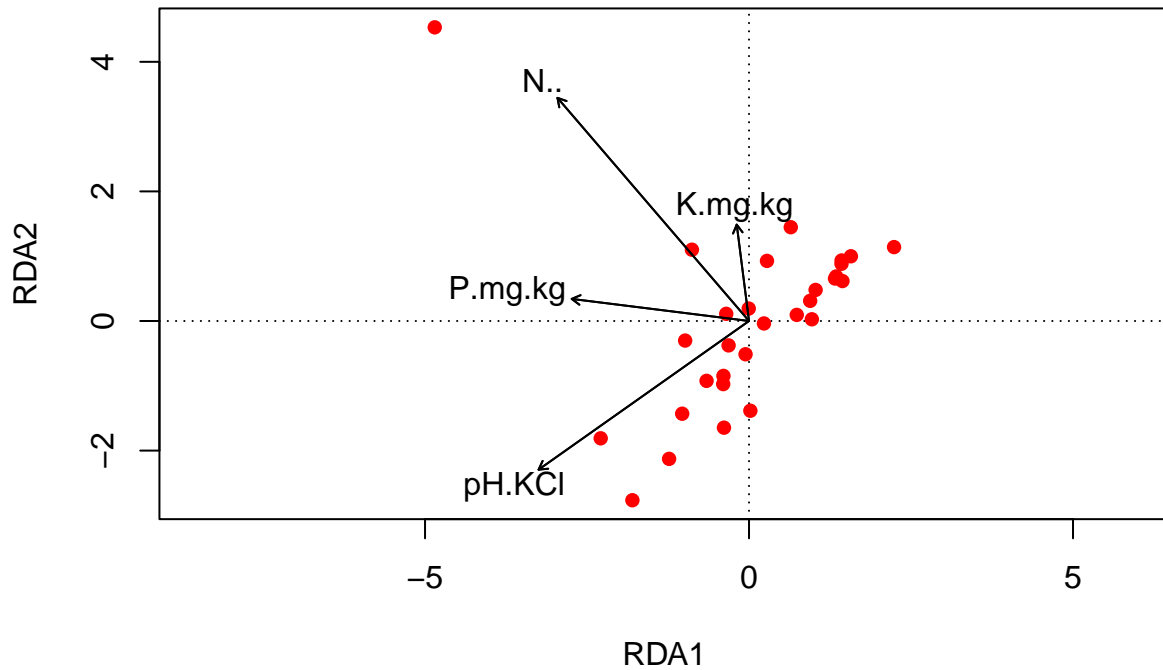
Exploring only variation that can be explained by the selected environmental variables (=constraints). Comparing the taxonomic space vs. environmental space.

```
## Linear relationships (similar to PCA)
```

```
o.rda=rda(vas.plants~pH.KCl+N..+P.mg.kg+K.mg.kg,data=soil.data,scale=T) # here formulas are suggested,
plot(o.rda)
```



```
# More simple graph
plot(o.rda,type="n")
points(o.rda,"sites",col="red",pch=16)
points(o.rda,"cn") # constraints arrow
text(o.rda,"cn")
```



```
anova(o.rda) # overall significance by randomizations
## Permutation test for rda under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data, scale = T)
##           Df Variance      F Pr(>F)
## Model      4   18.204 1.8714 0.001 ***
## Residual  25   60.796
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(o.rda,by="mar") # each parameter separately
## Permutation test for rda under reduced model
## Marginal effects of terms
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data, scale = T)
##           Df Variance      F Pr(>F)
## pH.KCl      1    5.202 2.1391 0.001 ***
## N..          1    5.844 2.4033 0.003 **
## P.mg.kg      1    4.311 1.7728 0.017 *
## K.mg.kg      1    2.587 1.0636 0.366
## Residual  25   60.796
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(o.rda,by="axis") # significance along axes
## Permutation test for rda under reduced model
## Forward tests for axes
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data, scale = T)
##           Df Variance      F Pr(>F)
## RDA1       1    6.397 2.6306 0.013 *
## RDA2       1    6.331 2.6033 0.013 *
## RDA3       1    3.454 1.4202 0.225
## RDA4       1    2.022 0.8313 0.695
## Residual 25    60.796
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

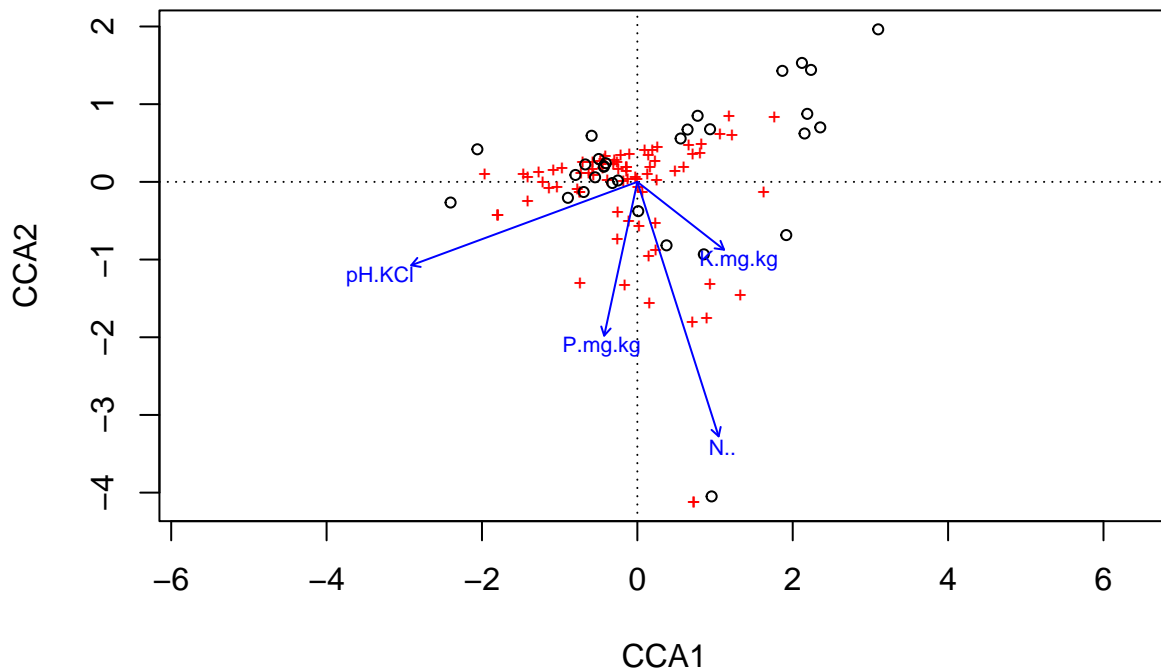
## Canonical Correspondence Analysis is similar but expect unimodal responses
o.cca=cca(vas.plants~pH.KCl+N..+P.mg.kg+K.mg.kg,data=soil.data)
anova(o.cca)
## Permutation test for cca under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: cca(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data)
##           Df ChiSquare      F Pr(>F)
## Model      4    0.8410 1.5721 0.007 **
## Residual 25    3.3434
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Plot cca figure and test the overall model, each soil parameter separately and along axes.

Answer

```
plot(o.cca,type="points")
```





```
anova(o.cca) # overall significance by randomizations
## Permutation test for cca under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: cca(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data)
##      Df ChiSquare      F Pr(>F)
## Model    4    0.8410 1.5721 0.007 **
## Residual 25    3.3434
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(o.cca,by="mar") # each parameter separately
## Permutation test for cca under reduced model
## Marginal effects of terms
## Permutation: free
## Number of permutations: 999
##
## Model: cca(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data)
##      Df ChiSquare      F Pr(>F)
## pH.KCl    1    0.2659 1.9879 0.003 **
## N..        1    0.2371 1.7726 0.050 *
## P.mg.kg    1    0.1970 1.4730 0.068 .
## K.mg.kg    1    0.1319 0.9862 0.503
## Residual 25    3.3434
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

anova(o.cca,by="axis")
## Permutation test for cca under reduced model
## Forward tests for axes
## Permutation: free
## Number of permutations: 999
##
## Model: cca(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data)
##           Df ChiSquare      F Pr(>F)
## CCA1       1    0.3092 2.3123 0.046 *
## CCA2       1    0.2572 1.9229 0.205
## CCA3       1    0.1727 1.2915 0.886
## CCA4       1    0.1019 0.7618 1.000
## Residual 25    3.3434
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

## Multivariate ANOVA based on dissimilarities

Partition dissimilarities among different sources of variation. No ordination is used; instead the multivariate space is considered. Significance values are obtained from permutation tests. Also known as PERMANOVA (function `adonis`).

```

o.adonis=adonis(vas.plants~pH.KCl+N..+P.mg.kg+K.mg.kg,data=soil.data,method="manhattan",by="mar")
## Warning in adonis(vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data, : 'adonis' is deprecated
## Use 'adonis2' instead.
## See help("Deprecated") and help("vegan-deprecated").
o.adonis
## $aov.tab
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## pH.KCl     1    1041.1 1041.11 3.06903 0.08982 0.005 **
## N..        1     902.7  902.67 2.66094 0.07787 0.019 *
## P.mg.kg    1     917.2  917.16 2.70365 0.07912 0.011 *
## K.mg.kg    1     249.7  249.68 0.73603 0.02154 0.678
## Residuals 25    8480.7  339.23      0.73164
## Total     29   11591.4      1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $call
## adonis(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg,
##       data = soil.data, method = "manhattan", by = "mar")
##
## $coefficients
##           ACTAspic      AEGOpoda      ANEMnemo      ASAREuro      ATHYfil.fe
## (Intercept) -0.649387587 -0.6027499398 -0.948180533 -0.526318964 0.0630297931
## pH.KCl       0.183948992  0.3334725959  0.257401024  0.188683322  0.0239258861
## N..         -0.203542766 -0.0117574158 -0.842201725 -0.036207162  0.0254001971

```

## P.mg.kg	0.001951280	0.0001594375	0.020039495	-0.005244977	-0.0041148486
## K.mg.kg	0.001132885	-0.0044902636	0.003414033	0.001468718	0.0001462588
##	BRACpinn	CALAarun	CALLvulg	CAREdigi	CIRCcalpi
## (Intercept)	-0.1662993541	1.064086651	0.03011184	-1.746880416	0.015747660
## pH.KCl	0.0559854468	-0.036856491	0.08631801	0.509780817	0.063848113
## N..	-0.0076362347	-0.977117068	-0.39739190	-0.956781144	0.925238107
## P.mg.kg	-0.0021368644	0.031850897	0.02442177	0.007122152	0.002774729
## K.mg.kg	0.0006349172	-0.001943363	-0.00770594	0.006803343	-0.005706051
##	CONVmaja	DESCflex	DRYUcart	DRYUexpa	EPILangu
## (Intercept)	0.76186042	0.003591954	0.024649610	0.302717528	-0.0963394383
## pH.KCl	0.25023842	0.001863890	0.098099982	-0.020063924	0.0239223225
## N..	-0.30166345	0.027228514	1.048008818	0.121548956	0.4912953162
## P.mg.kg	0.01461693	-0.003997893	0.008098180	-0.002822480	-0.0004532061
## K.mg.kg	-0.01252558	0.001681238	-0.004733619	-0.001383407	-0.0015009045
##	FESTovin	FRAGvesc	GALElute	GERAsylv	GYMNdryo
## (Intercept)	0.5104946465	-0.668337982	-1.738258628	-0.557434176	-0.524713143
## pH.KCl	-0.0320186494	0.271600519	0.535808959	0.180134994	0.091435403
## N..	-0.0108761690	-0.612938450	-0.462439855	-0.014875286	0.122877405
## P.mg.kg	0.0009161362	0.019393128	-0.011559692	-0.006686985	0.009125762
## K.mg.kg	-0.0035769415	-0.002479698	0.008533768	0.001928550	0.001327123
##	HEPAnobi	IMPAnoli	LATHvern	LUZUpilo	LYCOanno
## (Intercept)	-1.8530393877	0.0058388462	-0.531533111	0.2704660343	0.208982235
## pH.KCl	0.6575270172	0.0116873117	0.149373481	0.1283381757	-0.036990896
## N..	-1.0360293055	0.0124034402	-0.023611786	-0.2637922901	2.506668647
## P.mg.kg	0.0233405098	-0.0006719019	-0.004571104	0.0104928562	-0.007251952
## K.mg.kg	-0.0008644401	-0.0002133519	0.001936431	-0.0007403069	-0.005648483
##	MAIAbifo	MELAprat	MELInuta	MILIEffu	MOLICAer
## (Intercept)	-1.410491945	2.232493884	-0.2122232388	-0.0418672875	0.099471129
## pH.KCl	0.338427808	-0.462967680	0.0730932225	0.1182714544	-0.048563988
## N..	-0.824036975	-0.101662276	-0.0740677452	0.0204821680	-0.044403104
## P.mg.kg	0.025721391	-0.010007000	0.0011055914	0.0006758232	-0.001227371
## K.mg.kg	0.008371583	0.001797213	-0.0001933523	-0.0019868944	0.001779788
##	MYCEmura	ORTHsecu	OXALacet	PARIquad	PTERAqui
## (Intercept)	-0.480664519	0.396639670	-1.463910011	-0.100587029	-0.8148286545
## pH.KCl	0.209848013	-0.001552336	0.810771081	0.126862374	0.2517587104
## N..	0.275903910	0.011821777	-1.331703525	0.412844690	-0.3998149220
## P.mg.kg	0.001889293	-0.001681138	0.063777821	0.001451912	0.0096633571
## K.mg.kg	-0.002008230	-0.002493950	-0.008151248	-0.003785052	-0.0005715594
##	RANUcass	RUBUsaxa	STELholo	STELnemo	TRIEeuro
## (Intercept)	0.0476646378	-2.208656447	-0.838203129	-0.3338606366	0.602480711
## pH.KCl	0.0376335186	0.746050213	0.273750968	0.0836492185	0.027422571
## N..	0.0656569007	-0.680523500	-0.215321448	0.3642241401	0.171491179
## P.mg.kg	-0.0009256143	0.015561302	-0.011137916	-0.0004739158	0.004138613
## K.mg.kg	-0.0017163995	0.002359786	0.005728462	0.0002637021	-0.001953828
##	VACCmyrt	VACCvit.id	VEROcham	VIOLmira	ANGESylv
## (Intercept)	5.452495582	1.9773498274	-0.231171440	-0.601149062	-0.215873449
## pH.KCl	-1.097130038	-0.3269270530	0.100450306	0.155949867	0.087324991
## N..	-0.007957104	-0.1906607196	-0.125359186	-0.050648915	-0.135025998
## P.mg.kg	-0.025527183	-0.0045794188	0.004229433	-0.003702368	0.005454622
## K.mg.kg	0.009584858	-0.0009089737	-0.001399225	0.002135206	-0.001350125
##	ANTHsylv	CAMPpers	CAREcane	CAREglob	
## (Intercept)	-0.3785225929	0.0474235608	0.0116776925	-0.0364551492	
## pH.KCl	0.1290786693	-0.0017004134	0.0233746234	-0.0252870012	

```

## N.. -0.0817039799 -0.1079095085 0.0248068803 0.2682529444
## P.mg.kg -0.0010312730 0.0046172966 -0.0013438037 -0.0003117127
## K.mg.kg 0.0004415649 -0.0009608731 -0.0004267038 0.0009433797
## CHIMumbe CREPpalu DESCcaes DRYOfili EQUIprat
## (Intercept) 0.0487197915 0.116775508 0.0116776925 -0.6507669173 0.186896541
## pH.KCl -0.0087098070 0.080651812 0.0233746234 0.2572204518 0.024480746
## N.. 0.0055113712 0.403998588 0.0248068803 -0.2336144759 0.119731158
## P.mg.kg -0.0018544933 -0.002946568 -0.0013438037 -0.0013781309 -0.002663086
## K.mg.kg 0.0006942737 -0.004382027 -0.0004267038 0.0009559903 -0.002113950
## EQUIsylv GALEOPsp GALIalbu. GALIpalu GOODrepe
## (Intercept) 0.622173556 1.171457e-02 -0.049574095 -0.2603929579 0.4042660812
## pH.KCl -0.079211229 -3.724816e-02 0.031339544 0.0850543837 -0.0876046424
## N.. 0.128274291 2.260529e-02 -0.127389763 0.1715799129 0.0209879293
## P.mg.kg -0.001403502 -8.510967e-05 0.007591486 0.0008789883 -0.0037587237
## K.mg.kg -0.002470969 1.693832e-03 -0.001985042 -0.0009438046 0.0009279642
## HIERvulg IMPAparv LYSIvulg MELAnemo MELAsylv
## (Intercept) -0.099148189 -0.097028642 -0.0381712005 -0.3604083944 -0.017124671
## pH.KCl 0.062679088 0.187709039 -0.0231587069 0.0783443135 0.042109412
## N.. -0.254779526 0.194804167 0.4366010671 -0.1073819211 -0.052245143
## P.mg.kg 0.015182973 0.001258470 0.0047589559 -0.0009577235 -0.002721555
## K.mg.kg -0.003970084 -0.002467795 -0.0009438936 0.0022083778 0.001384334
## MOERtrin PHEGconn POAnemo POLYodor POTEerec
## (Intercept) 0.1253054221 -0.0963394383 -0.1546216616 -0.172887218 0.178834126
## pH.KCl 0.0227078393 0.0239223225 0.0793600702 0.090583414 -0.007700627
## N.. 0.4665057155 0.4912953162 0.0171706456 -0.129486551 -0.015222613
## P.mg.kg 0.0009848375 -0.0004532061 -0.0034806681 0.006781035 0.001647307
## K.mg.kg -0.0031433585 -0.0015009045 0.0002082134 -0.002001269 -0.001750814
## PULMobsc PYROmino RANUauri. SCORhumi SOLIvirg
## (Intercept) 0.0476646378 0.0934841192 -0.049574095 0.1534216980 -0.198470510
## pH.KCl 0.0376335186 0.0038235203 0.031339544 -0.0352468546 0.015167519
## N.. 0.0656569007 -0.0448676996 -0.127389763 -0.0270326796 -0.161319818
## P.mg.kg -0.0009256143 -0.0005009939 0.007591486 -0.0013406729 0.008864201
## K.mg.kg -0.0017163995 -0.0001214159 -0.001985042 0.0005801034 0.001283194
## URTIdioi VEROfffi VIOLcani VIOLepip VIOLrivi.
## (Intercept) -0.214974155 -0.0950206963 -0.09623928 0.1936459309 -0.2116686368
## pH.KCl 0.117541288 0.0332826284 0.06825439 -0.0374279665 0.0916172138
## N.. 0.549315982 -0.0306894404 -0.28715013 0.2775854902 -0.1830270715
## P.mg.kg -0.003515685 -0.0009528379 0.01089347 0.0007016396 0.0032572797
## K.mg.kg -0.002582387 0.0005087706 -0.00227935 -0.0015105274 -0.0003496213
##
## $coef.sites
## X001Vapramae X002Illli X003Vitipalu X004Konguta X005Vehendi
## (Intercept) 17.01923314 -8.13046110 31.66123890 26.7178704 -13.63644865
## pH.KCl 1.71686200 8.48100718 -0.16378668 2.9275852 10.74660541
## N.. 2.53586762 -1.33802664 9.32260358 -20.9399601 -1.35853802
## P.mg.kg -0.02896474 0.18025759 -0.24092191 0.1082539 0.33158782
## K.mg.kg -0.01534406 -0.01090618 0.03198507 0.0244864 -0.07703152
## X006.Erumae X007Porgumae X008Aardla X009Kurepalu X010Sarakuste
## (Intercept) -2.959641560 35.0548591 7.173357846 -13.44163842 34.19500205
## pH.KCl 6.995929065 -1.3783346 4.977581471 8.95618962 -0.62189505
## N.. -5.088658570 3.7055043 -1.428743575 -1.77794087 9.26188281
## P.mg.kg 0.217441225 0.1936495 0.189559380 0.28971385 0.01734453
## K.mg.kg -0.006201037 -0.1006153 -0.007706228 -0.05961616 -0.07503080

```

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##          X011Kannu   X012Vonnu   X013Rookse X014Kammeri   X015Kambja
## (Intercept) 27.435468022 16.59552901 47.25889306 8.85071429 36.309852855
## pH.KCl      0.530306878 3.43179004 -2.28742365 4.64815435 -1.114274533
## N. .        4.463686162 3.61642306 10.22316184 4.21429255 5.994241675
## P.mg.kg     0.005797764 -0.09146147 -0.09796434 0.05123078 0.006497922
## K.mg.kg     -0.063929222 -0.04782278 -0.11868871 -0.04809291 -0.080981998
##          X016Reola   X017Ignase X018Unikula X019Haavametsa X020Kruusahaua
## (Intercept) 13.954773204 23.35752988 39.30684014 -16.71757338 27.98526048
## pH.KCl      3.064031573 1.79479564 -1.05381981 9.57829546 0.87746316
## N. .        -3.240707380 5.94571305 12.71555909 -1.70475152 -0.47333092
## P.mg.kg     0.007772311 -0.09741163 -0.26629718 0.26194008 0.10939787
## K.mg.kg     0.011067182 -0.04384381 -0.02517021 -0.04384486 0.02751942
##          X021Aravu X026Pedajamae   X027Miti X028Puhaste X031Pimmelaan
## (Intercept) -15.41367943 31.10168558 -18.09747591 -12.37820176 44.30900973
## pH.KCl      10.14048714 -0.13285415 10.04402464 9.59236081 -1.32818416
## N. .        -2.38825962 5.64645061 -1.38901450 -3.08650914 5.35939170
## P.mg.kg     0.30577451 -0.05304346 0.26993840 0.30648321 -0.08662929
## K.mg.kg     -0.06635892 -0.02794632 -0.03949889 -0.07073083 -0.03151242
##          X032Logina X033Voorepalu X036Taevaskoja X044Savimae X073Pausakunnu
## (Intercept) 0.2031479 -1.30969726 -14.87056513 -6.38854343 20.59354864
## pH.KCl      5.7291805 6.50125545 9.67884593 8.14566446 1.86522219
## N. .        1.6080951 2.19414002 -3.23225499 -3.56488232 -2.37220968
## P.mg.kg     0.1168450 0.13976135 0.29459617 0.22827519 0.18809719
## K.mg.kg     -0.0539511 -0.05018532 -0.05322259 -0.06939645 -0.05742741
##
## $f.perms
##          [,1]          [,2]          [,3]          [,4]
## [1,] 0.8918716 0.5278073806 2.29141640 1.4816360
## [2,] 0.7502888 0.9343951065 0.31193960 0.4841544
## [3,] 0.6014890 0.5914929430 0.24456788 1.3127477
## [4,] 0.4999123 0.6820079659 1.20324585 0.6138787
## [5,] 1.0124176 0.5576282260 0.76330825 0.6462396
## [6,] 0.7844545 1.0395838902 0.91900847 1.0913004
## [7,] 0.3991100 0.6602350528 0.74930302 0.9349831
## [8,] 1.4371593 0.8397038307 1.11380494 0.6948049
## [9,] 0.9850503 0.5024723294 1.26155259 0.9056112
## [10,] 0.9205653 0.5879486791 1.24332578 0.8144495
## [11,] 0.9652523 0.9240970231 0.68524812 1.0343037
## [12,] 0.9603699 0.2364374468 0.53536076 0.2297331
## [13,] 0.8176076 1.7655892595 0.74470936 0.8690604
## [14,] 0.5592049 1.0075752273 1.52824427 0.4481566
## [15,] 0.9553778 1.3760418751 0.65306876 2.0207720
## [16,] 1.1602326 0.8641927990 0.61420444 0.9057282
## [17,] 0.8452875 0.5569397211 0.64879738 1.5055293
## [18,] 1.4460958 0.7334026072 1.11169046 1.3546722
## [19,] 1.0822501 2.1974643378 0.71308839 0.5052060
## [20,] 0.8472120 0.2145280021 0.98977594 0.7299622
## [21,] 0.7324707 1.3993093368 1.36399766 0.5172815
## [22,] 2.1770963 2.7082660486 0.82634135 0.6928620
## [23,] 0.7060042 1.3494662901 1.40028591 0.7820549
## [24,] 0.3150660 1.1498712119 2.05489400 0.7575576
## [25,] 1.1519329 0.5969120671 0.91709540 1.3590485
## [26,] 1.5827003 0.7595721159 0.70697638 0.7412563

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```

## [27,] 2.3967447 0.5607160359 0.58907167 1.3107553
## [28,] 0.9485007 0.9627157109 0.62324937 1.6860529
## [29,] 0.4600113 1.7174698696 0.83145683 1.4701514
## [30,] 0.8925715 0.3749899527 0.39810246 1.0644474
## [31,] 1.0529343 1.4002584892 1.39924327 1.2971150
## [32,] 0.8556772 1.1348578198 1.45818261 0.7575503
## [33,] 1.7543753 0.1300508936 1.15649186 0.7178005
## [34,] 0.9104458 1.6759468548 2.49976466 0.9348925
## [35,] 2.0892697 1.0568280434 1.21334857 1.0058614
## [36,] 2.3208857 0.2036412900 2.06229237 0.4917179
## [37,] 0.8692979 0.7954803360 0.69072091 1.1933365
## [38,] 1.4344221 0.5208484226 1.42835259 2.2335938
## [39,] 1.0731490 0.6087705772 0.98733807 0.8557859
## [40,] 1.1582004 2.4533709763 0.65711785 0.3998486
## [41,] 1.5713791 1.9088171134 1.38134528 1.2825138
## [42,] 0.7393509 1.3135613310 0.69843399 0.8697891
## [43,] 1.5923816 2.4681889085 0.54596862 1.9812683
## [44,] 0.7322696 0.3164719531 1.09862274 1.3611762
## [45,] 0.3073077 0.8377324935 0.96126480 2.0013396
## [46,] 0.2630415 0.3175122559 0.60525139 0.8592604
## [47,] 1.2730389 1.0308518712 1.19701871 0.6888107
## [48,] 0.8960732 1.0823173090 0.69712751 1.1647686
## [49,] 1.1199127 0.1597783311 0.69733481 0.5190833
## [50,] 0.3218956 0.8951439717 0.52144908 2.4806171
## [51,] 1.2768785 0.5332076441 0.41337120 0.3982882
## [52,] 1.2633889 1.4827918815 0.51153036 1.2594867
## [53,] 0.8760636 0.5843749305 0.51157043 1.7608687
## [54,] 0.8360442 0.6480377137 2.69623759 0.8171680
## [55,] 0.4548956 0.4908602048 0.61477303 0.4078539
## [56,] 0.7652346 0.4621446278 0.60608342 1.2616407
## [57,] 0.6382410 0.4152845596 0.72335866 0.7682504
## [58,] 0.9617554 1.0692620881 0.69146029 1.2649013
## [59,] 1.8009686 1.2372812823 0.72122765 0.4903939
## [60,] 0.6689070 1.4005857526 1.27864984 0.6454276
## [61,] 0.7322133 1.8527403388 0.60654134 0.8639681
## [62,] 0.7842531 1.3142774234 0.20310765 1.0116386
## [63,] 0.9053774 1.1997272926 0.49433849 1.1612347
## [64,] 0.5967810 0.5825602118 1.49412883 0.6533376
## [65,] 0.6303871 1.3115682970 0.32006264 0.8752962
## [66,] 0.3547301 0.3551898105 1.06171714 1.0113857
## [67,] 1.1198825 2.0623366192 0.53256487 0.7768313
## [68,] 1.9087155 0.3134945109 0.91856789 0.1902469
## [69,] 0.8466718 0.8675774129 0.65789711 0.3496677
## [70,] 0.6225819 0.5629901835 1.11046101 0.5201609
## [71,] 1.6460893 0.3868819113 1.30586714 1.1638549
## [72,] 2.1016543 1.1030923191 1.14618403 0.8587654
## [73,] 1.1782424 0.3917249928 0.81143750 0.8590153
## [74,] 1.1169455 0.6601158800 0.82850125 1.1136271
## [75,] 3.2756914 0.3766660283 0.98312307 2.0344038
## [76,] 1.6715066 0.1238917604 0.90532624 1.3500015
## [77,] 1.9132734 0.3753580605 0.53584542 0.8397393
## [78,] 0.7472077 0.4617812542 1.12008546 0.4870267
## [79,] 0.8396324 1.4540248996 1.94649119 0.7529903

```



```

## [80,] 0.5228463 1.6342088018 1.18000878 1.4604946
## [81,] 0.7799188 0.4122943667 0.73420862 0.6854246
## [82,] 0.4480986 0.2859420137 0.40183709 1.3057337
## [83,] 1.0416351 0.5866135159 0.94335460 0.6327250
## [84,] 0.6720316 0.4499184301 0.16617885 1.0486939
## [85,] 0.9708986 1.2193476646 0.46794379 0.8338157
## [86,] 0.6517287 1.1380509207 1.55936631 0.8829347
## [87,] 1.7647023 1.0824026390 0.79065817 1.5353296
## [88,] 1.6547783 0.6119971732 0.56347124 0.6014331
## [89,] 0.8697230 0.2258803824 0.62019345 0.4659995
## [90,] 1.1337665 1.1329309675 0.72832296 1.0755761
## [91,] 0.8866842 0.3171383836 1.90085740 0.9179701
## [92,] 0.3542172 0.3272100879 0.35273624 1.5655695
## [93,] 0.7671657 0.3967684135 1.02095162 0.5443075
## [94,] 0.6949348 0.8060061777 0.89791343 0.8505400
## [95,] 0.8388871 0.7084386585 0.64958718 0.7003162
## [96,] 0.7256275 0.1601040186 1.57465764 0.5580785
## [97,] 0.4310561 1.7729396517 0.99082680 0.8967896
## [98,] 1.1397020 1.2398674057 2.97945693 0.9499059
## [99,] 0.9920760 1.0967426784 0.74815923 0.6589266
## [100,] 2.1865651 0.8199495005 0.83348745 0.8244986
## [101,] 2.1697455 0.4325807833 1.31972286 1.3377976
## [102,] 0.3545988 0.5457229154 0.81721076 1.0320223
## [103,] 1.0294305 1.4410910524 1.25521239 0.9033916
## [104,] 0.9834844 0.2142355119 1.06073684 0.5493321
## [105,] 0.6208783 1.2490715032 1.88166446 1.0644413
## [106,] 0.5026666 2.3030576105 1.22074003 1.5293157
## [107,] 0.2696255 0.6502852298 2.43195237 0.6518620
## [108,] 1.5825978 0.7873623771 0.87736929 0.7776372
## [109,] 0.9524317 0.9647927759 0.85228610 0.9637805
## [110,] 0.8267423 0.5510199484 0.78172359 1.3092585
## [111,] 1.4681775 0.7356874545 0.51113216 0.7549669
## [112,] 0.7612186 1.1177051714 0.59148247 1.9781946
## [113,] 1.6138345 1.2470610444 1.37500725 0.7684521
## [114,] 0.8467320 1.1507087419 2.59324866 0.8235834
## [115,] 0.5990388 0.5897216150 0.72948619 1.2004744
## [116,] 2.3242867 1.8475815128 0.83137523 1.0897790
## [117,] 1.7883918 0.8387250435 0.41695194 0.7588187
## [118,] 1.6607874 0.5915762905 1.03729963 0.6144525
## [119,] 0.9960791 0.8189891305 0.79693894 0.2766724
## [120,] 1.3488384 1.0425599664 2.48697148 0.9332512
## [121,] 0.8700005 0.4701209914 0.64505495 0.8167366
## [122,] 0.4418139 0.2238084980 1.77820153 0.8482871
## [123,] 2.9807959 1.9783012838 1.19069444 1.3373713
## [124,] 0.6632287 0.3342735383 0.74698220 0.5166030
## [125,] 0.6494710 1.0163546840 1.32198264 0.9206514
## [126,] 0.5390759 0.9058826196 2.12096719 0.6211293
## [127,] 0.7998932 2.1360213070 1.98886374 1.2235341
## [128,] 1.7161194 1.1452667421 0.82067385 0.9721168
## [129,] 1.0779355 0.5893231997 1.63097144 1.1294279
## [130,] 0.7940295 0.7375686945 0.73750319 0.8834282
## [131,] 0.5852186 0.3294600520 1.06926119 0.5475300
## [132,] 0.9006542 0.7473475241 1.49506414 0.8680992

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## [133,] 2.0991462 1.9666966530 0.41574214 0.9332637
## [134,] 2.9311880 0.6816795422 1.71728851 0.8886766
## [135,] 0.6732399 0.8962334784 0.16528608 2.3982215
## [136,] 1.0238495 0.5409197223 0.48542699 0.9727176
## [137,] 0.6604568 0.3157306834 1.57429673 0.5568441
## [138,] 0.3362625 1.6156910812 0.73214609 1.5210691
## [139,] 1.9968078 0.6340076276 1.77481122 0.8816709
## [140,] 0.4363644 0.9235851654 0.36960445 1.5655608
## [141,] 1.6180160 0.7474971814 0.46593623 1.0427988
## [142,] 0.8381004 1.2217601445 0.49413839 1.2843833
## [143,] 0.9012151 0.5547796578 0.76527076 0.5335792
## [144,] 0.6139684 0.8527415428 0.89856244 0.9142761
## [145,] 0.9483295 1.8426077340 1.39562306 1.0804871
## [146,] 0.7957493 1.3989458145 1.52688443 0.8369224
## [147,] 0.7207064 1.4440139880 0.68550161 1.4459604
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## [149,] 1.6552837 2.0448637913 0.65723615 1.9702723
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## [154,] 0.2900315 0.4461587401 1.55755979 1.7825500
## [155,] 2.0105435 0.3284906664 1.59549830 1.2776458
## [156,] 1.3293106 0.4665079921 1.96528080 0.7246359
## [157,] 0.9602894 2.3023034354 0.76613242 1.5473036
## [158,] 0.7113122 0.7098057873 1.47666791 1.3853758
## [159,] 0.6185651 1.3139437614 0.33365611 0.4409039
## [160,] 0.5273073 0.6392501554 1.45154501 0.7554860
## [161,] 1.6042459 0.8056602738 1.22426626 0.4148399
## [162,] 1.1246586 0.4488713941 1.79336243 1.2028728
## [163,] 0.4743634 0.9842407717 0.92119962 0.4120631
## [164,] 1.9976477 0.5338948054 1.31810178 0.6702173
## [165,] 0.4385074 1.3052387837 1.00656239 1.1944110
## [166,] 0.5932186 1.3324830942 0.67735028 0.6503563
## [167,] 0.9989121 2.6707601249 0.67463492 0.8411720
## [168,] 1.5117796 0.4309897039 0.65426971 0.7559577
## [169,] 1.6408772 0.5005595597 0.60644785 0.6120280
## [170,] 1.6771001 2.0364852295 3.91655892 0.8371352
## [171,] 1.4822600 0.8735708470 1.32662327 1.5136305
## [172,] 1.0956988 0.8491853499 0.91452793 1.5324144
## [173,] 0.5564912 2.2961823680 1.21728808 0.6572799
## [174,] 0.3225929 2.1906314578 0.70781309 2.3377753
## [175,] 1.4007809 0.3658140362 0.92701774 1.1431881
## [176,] 1.2542330 2.9353305767 2.40723648 0.7618870
## [177,] 0.5435758 0.2845887515 1.21742428 1.3157585
## [178,] 1.2830611 0.3298037678 0.55117202 1.2852664
## [179,] 0.8240218 0.6627366508 1.61899121 1.0389882
## [180,] 2.3039539 0.9860525955 1.88578428 1.0431857
## [181,] 2.5031826 1.3294803297 1.09583644 0.7008691
## [182,] 0.5321530 0.8277945396 0.92142016 1.0045470
## [183,] 0.9306894 1.2207390343 0.48851737 0.7462736
## [184,] 0.9650175 0.5751691136 0.56548989 1.0597786
## [185,] 1.4723122 0.6705031159 1.21283775 0.7919372

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## [186,] 0.9845621 0.4873995594 1.00834777 0.2272243
## [187,] 0.9278602 0.8336086962 0.57019711 1.4400907
## [188,] 0.6613845 1.4122745840 0.81549266 0.7503495
## [189,] 0.7827379 1.0394269095 1.70630371 0.7338846
## [190,] 0.7525126 0.8737622740 1.12373981 0.9202438
## [191,] 0.7762748 2.8013138779 1.11810410 0.2326633
## [192,] 0.9958117 0.8686197976 0.63088649 0.4513846
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## [194,] 1.0819801 2.9414106469 0.90436408 1.1677348
## [195,] 1.7776971 0.3220251420 0.74535032 1.4794622
## [196,] 1.7743339 1.0336745281 0.74159348 0.8033216
## [197,] 0.5436728 0.8803499658 1.14157300 1.1129466
## [198,] 2.1219143 0.2991763428 3.01835954 1.4448195
## [199,] 0.8451078 0.2295196007 0.63610348 0.3732587
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## [761,] 1.4128152 0.7691590240 0.91521022 1.0879057
## [762,] 0.7265656 1.2227415335 0.89305213 1.2234672
## [763,] 0.9081266 0.8086101535 1.19623310 0.5919935
## [764,] 1.3222636 0.8893296237 0.87608235 1.1934378
## [765,] 0.2930878 0.6694642497 0.71297589 0.9348021
## [766,] 1.2505851 1.6729763725 1.32387987 1.2288191
## [767,] 0.5002224 2.5729828069 1.36556940 2.2395062
## [768,] 1.1694880 0.1295830197 0.83520458 0.5875091

```

```

## [769,] 1.4558474 1.8032421793 0.44364757 0.7623781
## [770,] 0.8368905 1.8489319606 0.85796410 0.2876020
## [771,] 1.1586691 0.2304393663 0.89428115 1.0336396
## [772,] 0.3222950 0.8333324105 1.24990658 0.6946129
## [773,] 1.9091391 0.3933562389 0.98357219 2.1919405
## [774,] 0.7919664 0.4930342938 0.80738355 1.4731386
## [775,] 0.8101380 0.8665391205 1.14366236 0.3441674
## [776,] 1.2671851 1.7589283228 1.17210974 1.0305126
## [777,] 0.8737489 1.1880323008 0.36488298 1.5542517
## [778,] 1.0702268 0.5200067230 1.05406858 0.5370161
## [779,] 0.7703784 0.4255500109 0.50220667 0.7708351
## [780,] 0.3384159 0.5573260756 1.38384622 0.9376959
## [781,] 0.9205543 0.4051076386 0.80300497 0.7567006
## [782,] 0.5058075 0.6069902062 2.19806282 1.1290927
## [783,] 1.3612529 0.2761821087 1.25814814 0.8180370
## [784,] 0.9680408 2.7612555755 1.58203983 0.9918871
## [785,] 1.4627104 2.1079366496 1.71806645 0.3168963
## [786,] 0.9740079 0.8370793746 1.16936784 1.9009601
## [787,] 0.9032048 0.8809343914 0.28017107 0.8843147
## [788,] 1.4323584 1.3619223732 0.62138309 0.7859923
## [789,] 0.8005213 0.1395725209 4.67446940 1.3428705
## [790,] 0.5423720 1.0668382346 0.82020461 0.5752457
## [791,] 1.5189310 1.7510150724 1.19111974 2.0834368
## [792,] 1.8708349 0.4588501219 0.73437228 0.5671544
## [793,] 1.1837785 1.4487820322 0.81258865 1.3074311
## [794,] 0.2634974 0.6506435983 0.44851597 0.4090913
## [795,] 0.7501339 1.1131512938 0.58493625 0.9908138
## [796,] 1.0658168 0.6619269138 1.69020506 0.7654031
## [797,] 1.3041127 0.7450743711 2.09877317 0.7742430
## [798,] 1.9312601 1.1898111630 0.49692665 1.0103028
## [799,] 0.5159509 0.1412900479 0.44543668 1.0543904
## [800,] 2.9469209 0.9571424226 1.00375029 1.3728319
## [801,] 0.9613096 0.5869082536 1.55990924 1.0203912
## [802,] 1.6792886 0.6044671446 0.56461697 1.6922363
## [803,] 0.5857005 1.0501234339 1.49039324 1.4809968
## [804,] 0.7674906 0.6725591778 0.33879699 0.5807939
## [805,] 0.7811687 0.3432845264 0.84586412 0.3980069
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## [807,] 2.2788769 1.7317419876 1.84417838 1.5148346
## [808,] 0.8907860 1.4762293475 0.57731572 0.6683549
## [809,] 1.8115050 2.8880611835 1.39574486 0.4860599
## [810,] 0.6947202 1.8226177485 0.60705786 0.4886010
## [811,] 1.6567555 0.5372465239 0.56695494 0.9130976
## [812,] 0.5145699 0.4581657706 1.24696729 0.5519465
## [813,] 1.3529609 0.4082542304 1.86193957 0.8774015
## [814,] 0.8128185 0.3382690677 1.09192980 0.4727041
## [815,] 1.3385044 1.3406475210 0.27702842 1.1100809
## [816,] 2.0820986 1.7173697393 0.94138431 1.6964384
## [817,] 0.2004342 0.7237892021 1.86421791 1.6647737
## [818,] 0.3870833 1.4025570053 0.57619180 1.0551341
## [819,] 1.0221682 1.1781289051 1.45839013 0.7673737
## [820,] 0.4195431 0.7495420433 1.93613881 0.3815998
## [821,] 0.6733009 1.0767166010 0.92330806 0.5540581

```

```

## [822,] 0.9771232 1.1227794047 0.47947944 2.2462890
## [823,] 2.5582240 1.8318890861 0.55345238 0.8580364
## [824,] 1.1623805 0.4482573655 0.99968980 1.5806418
## [825,] 0.6431776 0.4124951872 0.38903331 0.4663374
## [826,] 0.5760622 1.4946979400 0.69983935 1.1065864
## [827,] 2.2927318 1.9334111503 0.66173753 1.7380584
## [828,] 1.6445419 2.3602941783 0.58196951 0.8202115
## [829,] 0.4614876 0.3493320380 1.56696587 1.5978535
## [830,] 0.5035122 1.0303152150 1.40036885 1.0805869
## [831,] 1.2153274 0.3194007585 0.74489008 1.1101178
## [832,] 0.6235931 1.5461150507 0.37152831 0.5245962
## [833,] 1.5225105 0.5555218666 0.64713067 1.1549859
## [834,] 0.8560858 0.1759852472 0.53161114 1.2707576
## [835,] 1.4190673 2.1318362891 1.09357382 1.5485562
## [836,] 1.0380758 0.3583835997 1.16387233 0.7215487
## [837,] 0.6378462 0.6867732894 1.06824813 0.3830501
## [838,] 0.2664727 0.5529387372 0.48317989 0.4731289
## [839,] 1.9693654 0.6082230992 0.60554154 1.4362257
## [840,] 0.5787188 1.1249256338 0.88295801 0.9646370
## [841,] 1.1391975 1.3750393017 1.05947261 0.5722175
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## [844,] 1.4078304 0.2560902259 1.50998677 1.0725260
## [845,] 0.8401602 0.8515526225 0.59382644 1.8215721
## [846,] 0.4557129 1.7042968333 1.02419450 0.5588651
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## [848,] 0.5568269 0.4998418297 0.37645708 0.7317214
## [849,] 2.0611530 1.0334099507 1.30602883 1.5764174
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## [856,] 0.9299307 2.2386268318 0.73383702 0.8625015
## [857,] 0.6954884 1.7372737294 1.15129768 1.0187039
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## [873,] 0.3284725 0.7023317055 1.08073621 0.7917802
## [874,] 1.5112061 3.3586711192 1.49832901 1.0948872

```



```

## [875,] 1.4512488 1.4385935292 1.76336828 1.2952300
## [876,] 0.9042247 0.6675029342 0.60370997 0.5101446
## [877,] 0.3442794 0.4462334024 0.93748544 0.6064719
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## [884,] 0.5082732 0.7855177857 0.98927708 1.0678790
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## [887,] 0.8631782 1.8549793466 1.20230848 1.2366007
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## [902,] 1.0726894 2.4665490096 1.40482551 1.3279069
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## [904,] 0.7454620 1.6611552257 0.53313213 0.4572069
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## [907,] 0.3800360 1.8352846708 1.06252021 0.6467175
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## [911,] 0.5240428 0.8772636330 0.43078569 0.3037868
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## [913,] 0.6507571 0.2082832843 0.76350459 0.6898294
## [914,] 0.6118722 1.3050169988 0.68032445 0.6415382
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## [916,] 0.3633582 0.4183602940 1.58332625 1.0474057
## [917,] 0.5063245 0.5529316786 0.56248824 0.5779530
## [918,] 0.7607024 2.5823853510 0.62584107 1.7289824
## [919,] 1.5600702 0.8545161490 1.59211800 0.3999054
## [920,] 0.8039690 0.7910116198 1.41588478 0.4732899
## [921,] 1.1340208 2.2994138322 2.12014894 1.0471629
## [922,] 1.6011124 1.3214291409 0.54091446 1.7098664
## [923,] 0.7764037 1.0191144893 1.37872180 1.4293216
## [924,] 1.3137073 2.5423789996 0.61825275 0.9505267
## [925,] 0.5655846 0.1157512161 0.61349664 1.3667812
## [926,] 0.6457051 0.2552428049 1.31074724 1.1682190
## [927,] 1.0649086 2.0200545780 0.57595408 0.5119385

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```

## [928,] 0.9410880 0.1926922369 1.08129275 0.6447507
## [929,] 0.6585686 0.6223333162 1.30835017 0.8544170
## [930,] 0.5955509 0.3854993447 0.57432927 1.0849653
## [931,] 1.7255555 1.1340468160 0.73044416 0.6958163
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## [933,] 1.1077966 0.7563325386 1.65261733 0.6098637
## [934,] 2.0569906 0.6443179602 0.25464633 0.3759593
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## [938,] 0.7200973 1.9736708880 1.45746744 0.7134566
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## [942,] 0.9109148 0.3489584856 0.78363375 0.5269161
## [943,] 0.2984008 0.2709868850 0.64599714 0.4301909
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## [954,] 1.0268636 0.3772331409 0.86254742 1.6936370
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## [960,] 1.6561847 0.7324299687 1.50954686 1.3531152
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## [963,] 0.6657521 0.7555581981 1.19701479 0.8625082
## [964,] 0.5113516 1.1534040202 0.98287206 0.6499456
## [965,] 1.4537433 1.3720891990 0.61519102 0.7616396
## [966,] 1.6177272 0.5727264547 0.56146477 0.9652821
## [967,] 0.7686044 0.4021140540 2.56530102 0.5448449
## [968,] 0.2542878 2.1921815717 0.73631187 1.0504330
## [969,] 0.7394145 0.4877946531 0.94509336 0.9405993
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## [972,] 0.9096793 1.0247649942 0.90845262 1.0241351
## [973,] 1.7638380 0.3232659823 1.23271337 0.8663880
## [974,] 1.2076849 1.6327487039 0.92753062 0.6722474
## [975,] 1.9483233 2.2069517267 0.58914765 1.2935839
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## [981,] 1.2943810 1.5601791978 1.54305761 0.5833456
## [982,] 2.3953299 0.6263455098 0.89644121 1.3706236
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## [984,] 0.6890950 0.5225389529 0.75077710 1.2033917
## [985,] 0.5563671 0.1160774190 0.78617916 0.6773236
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## [991,] 0.7875159 0.8700166911 0.49696369 0.6384989
## [992,] 1.2464133 1.0634404168 0.91939190 1.4845853
## [993,] 0.9432425 1.6553492980 0.42247655 0.4716079
## [994,] 0.5560838 0.6115748542 0.35173134 1.2198500
## [995,] 0.5442187 0.5883452283 1.05771233 1.8588805
## [996,] 1.0022116 1.0039297543 0.36930818 0.7258685
## [997,] 0.8616872 0.8177286374 0.70041140 1.2962402
## [998,] 0.7563874 1.6532177729 0.61491531 1.0033338
## [999,] 1.2965731 2.0791455454 0.78288967 2.1081955
##
## $model.matrix
##      (Intercept) pH.KCl      N..      P.mg.kg      K.mg.kg
## 1              1    3.72 0.4246261 31.571334 79.04454
## 2              1    3.65 0.1364021 22.264589 42.73691
## 3              1    4.25 0.2500752 58.047875 60.71264
## 4              1    4.40 2.3192906 63.004453 131.18302
## 5              1    2.62 0.3698321 25.623389 131.56542
## 6              1    3.28 0.2426881 16.215942 66.16427
## 7              1    5.77 0.2557405 8.214731 99.41711
## 8              1    4.01 0.2749614 13.283927 64.78593
## 9              1    2.51 0.3133842 15.479056 89.14338
## 10             1    4.04 0.2550077 18.696151 86.72334
## 11             1    3.45 0.3518922 13.284533 71.89113
## 12             1    3.13 0.7552086 65.774300 148.45346
## 13             1    3.87 0.3768197 51.118770 167.18983
## 14             1    2.82 0.2495660 12.757784 68.25374
## 15             1    3.94 0.2228461 11.421171 84.96703
## 16             1    2.92 0.4507300 29.924303 82.64504
## 17             1    3.40 0.2200201 37.057869 79.17404
## 18             1    3.85 0.1762699 50.911118 71.75413
## 19             1    2.69 0.1794443 8.860196 65.97427
## 20             1    4.39 0.2592368 10.073987 32.93117
## 21             1    2.75 0.4787677 24.440573 107.38674
## 22             1    4.39 0.2691432 12.495427 82.79072
## 23             1    2.98 0.1188524 16.727024 41.51526
## 24             1    3.38 0.3361435 16.531787 96.44632
## 25             1    4.72 0.1634929 25.261675 68.99408
## 26             1    3.44 0.5404526 25.979380 138.94642
## 27             1    4.01 0.2014326 12.415253 71.46143
## 28             1    2.96 0.2040349 16.122918 93.36687
## 29             1    2.85 0.7959958 41.964598 151.10819
## 30             1    3.60 0.2448960 9.110415 62.30611
##

```



```
## $terms
## vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg
## attr("variables")
## list(vas.plants, pH.KCl, N.., P.mg.kg, K.mg.kg)
## attr("factors")
##           pH.KCl N.. P.mg.kg K.mg.kg
## vas.plants      0  0         0       0
## pH.KCl          1  0         0       0
## N..             0  1         0       0
## P.mg.kg         0  0         1       0
## K.mg.kg         0  0         0       1
## attr("term.labels")
## [1] "pH.KCl" "N.." "P.mg.kg" "K.mg.kg"
## attr("order")
## [1] 1 1 1 1
## attr("intercept")
## [1] 1
## attr("response")
## [1] 1
## attr(".Environment")
## <environment: R_GlobalEnv>
##
## attr("class")
## [1] "adonis"
```

Use another community distance measure and look if you can get same results.

Answer

```
o.adonis=adonis(vas.plants~pH.KCl+N..+P.mg.kg+K.mg.kg,data=soil.data,method="bray",by="mar")
## Warning in adonis(vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg, data = soil.data, : 'adonis' is deprecated
## Use 'adonis2' instead.
## See help("Deprecated") and help("vegan-deprecated").
o.adonis
## $aov.tab
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## pH.KCl      1    1.3009 1.30085   5.7324 0.16493 0.001 ***
## N..          1    0.3108 0.31079   1.3696 0.03940 0.194
## P.mg.kg      1    0.4370 0.43704   1.9259 0.05541 0.080 .
## K.mg.kg      1    0.1654 0.16541   0.7289 0.02097 0.639
## Residuals   25    5.6732 0.22693         0.71928
## Total       29    7.8873         1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $call
## adonis(formula = vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg,
##        data = soil.data, method = "bray", by = "mar")
```

```

##
## $coefficients
##      ACTAspic      AEGOpoda      ANEMnemo      ASAREuro      ATHYfil.fe
## (Intercept) -0.649387587 -0.6027499398 -0.948180533 -0.526318964 0.0630297931
## pH.KCl      0.183948992 0.3334725959 0.257401024 0.188683322 0.0239258861
## N..         -0.203542766 -0.0117574158 -0.842201725 -0.036207162 0.0254001971
## P.mg.kg      0.001951280 0.0001594375 0.020039495 -0.005244977 -0.0041148486
## K.mg.kg      0.001132885 -0.0044902636 0.003414033 0.001468718 0.0001462588
##      BRACpinn      CALAarun      CALLvulg      CAREdigi      CIRCaldi
## (Intercept) -0.1662993541 1.064086651 0.03011184 -1.746880416 0.015747660
## pH.KCl      0.0559854468 -0.036856491 0.08631801 0.509780817 0.063848113
## N..         -0.0076362347 -0.977117068 -0.39739190 -0.956781144 0.925238107
## P.mg.kg      -0.0021368644 0.031850897 0.02442177 0.007122152 0.002774729
## K.mg.kg      0.0006349172 -0.001943363 -0.00770594 0.006803343 -0.005706051
##      CONVmaja      DESCflex      DRYOcart      DRYOexpa      EPILangu
## (Intercept) 0.76186042 0.003591954 0.024649610 0.302717528 -0.0963394383
## pH.KCl      0.25023842 0.001863890 0.098099982 -0.020063924 0.0239223225
## N..         -0.30166345 0.027228514 1.048008818 0.121548956 0.4912953162
## P.mg.kg      0.01461693 -0.003997893 0.008098180 -0.002822480 -0.0004532061
## K.mg.kg      -0.01252558 0.001681238 -0.004733619 -0.001383407 -0.0015009045
##      FESTovin      FRAGvesc      GALElute      GERAsylv      GYMNdryo
## (Intercept) 0.5104946465 -0.668337982 -1.738258628 -0.557434176 -0.524713143
## pH.KCl      -0.0320186494 0.271600519 0.535808959 0.180134994 0.091435403
## N..         -0.0108761690 -0.612938450 -0.462439855 -0.014875286 0.122877405
## P.mg.kg      0.0009161362 0.019393128 -0.011559692 -0.006686985 0.009125762
## K.mg.kg      -0.0035769415 -0.002479698 0.008533768 0.001928550 0.001327123
##      HEPAnobi      IMPAnoli      LATHvern      LUZUpilo      LYCOanno
## (Intercept) -1.8530393877 0.0058388462 -0.531533111 0.2704660343 0.208982235
## pH.KCl      0.6575270172 0.0116873117 0.149373481 0.1283381757 -0.036990896
## N..         -1.0360293055 0.0124034402 -0.023611786 -0.2637922901 2.506668647
## P.mg.kg      0.0233405098 -0.0006719019 -0.004571104 0.0104928562 -0.007251952
## K.mg.kg      -0.0008644401 -0.0002133519 0.001936431 -0.0007403069 -0.005648483
##      MAIAbifo      MELAprat      MELInuta      MILIeffu      MOLicaer
## (Intercept) -1.410491945 2.232493884 -0.2122232388 -0.0418672875 0.099471129
## pH.KCl      0.338427808 -0.462967680 0.0730932225 0.1182714544 -0.048563988
## N..         -0.824036975 -0.101662276 -0.0740677452 0.0204821680 -0.044403104
## P.mg.kg      0.025721391 -0.010007000 0.0011055914 0.0006758232 -0.001227371
## K.mg.kg      0.008371583 0.001797213 -0.0001933523 -0.0019868944 0.001779788
##      MYCEmura      ORTHsecu      OXALacet      PARIquad      PTERaqui
## (Intercept) -0.480664519 0.396639670 -1.463910011 -0.100587029 -0.8148286545
## pH.KCl      0.209848013 -0.001552336 0.810771081 0.126862374 0.2517587104
## N..         0.275903910 0.011821777 -1.331703525 0.412844690 -0.3998149220
## P.mg.kg      0.001889293 -0.001681138 0.063777821 0.001451912 0.0096633571
## K.mg.kg      -0.002008230 -0.002493950 -0.008151248 -0.003785052 -0.0005715594
##      RANUcass      RUBUsaxa      STELholo      STELnemo      TRIEeuro
## (Intercept) 0.0476646378 -2.208656447 -0.838203129 -0.3338606366 0.602480711
## pH.KCl      0.0376335186 0.746050213 0.273750968 0.0836492185 0.027422571
## N..         0.0656569007 -0.680523500 -0.215321448 0.3642241401 0.171491179
## P.mg.kg      -0.0009256143 0.015561302 -0.011137916 -0.0004739158 0.004138613
## K.mg.kg      -0.0017163995 0.002359786 0.005728462 0.0002637021 -0.001953828
##      VACCmyrt      VACCvit.id      VEROcham      VIOLmira      ANGESylv
## (Intercept) 5.452495582 1.9773498274 -0.231171440 -0.601149062 -0.215873449
## pH.KCl      -1.097130038 -0.3269270530 0.100450306 0.155949867 0.087324991

```

```

## N.. -0.007957104 -0.1906607196 -0.125359186 -0.050648915 -0.135025998
## P.mg.kg -0.025527183 -0.0045794188 0.004229433 -0.003702368 0.005454622
## K.mg.kg 0.009584858 -0.0009089737 -0.001399225 0.002135206 -0.001350125
## ANTHsylv CAMPpers CAREcane CAREglob
## (Intercept) -0.3785225929 0.0474235608 0.0116776925 -0.0364551492
## pH.KCl 0.1290786693 -0.0017004134 0.0233746234 -0.0252870012
## N.. -0.0817039799 -0.1079095085 0.0248068803 0.2682529444
## P.mg.kg -0.0010312730 0.0046172966 -0.0013438037 -0.0003117127
## K.mg.kg 0.0004415649 -0.0009608731 -0.0004267038 0.0009433797
## CHIMumbe CREPpalu DESCcaes DRYOfili EQUIprat
## (Intercept) 0.0487197915 0.116775508 0.0116776925 -0.6507669173 0.186896541
## pH.KCl -0.0087098070 0.080651812 0.0233746234 0.2572204518 0.024480746
## N.. 0.0055113712 0.403998588 0.0248068803 -0.2336144759 0.119731158
## P.mg.kg -0.0018544933 -0.002946568 -0.0013438037 -0.0013781309 -0.002663086
## K.mg.kg 0.0006942737 -0.004382027 -0.0004267038 0.0009559903 -0.002113950
## EQUIsylv GALEOPsp GALIalbu. GALIpalu GOODrepe
## (Intercept) 0.622173556 1.171457e-02 -0.049574095 -0.2603929579 0.4042660812
## pH.KCl -0.079211229 -3.724816e-02 0.031339544 0.0850543837 -0.0876046424
## N.. 0.128274291 2.260529e-02 -0.127389763 0.1715799129 0.0209879293
## P.mg.kg -0.001403502 -8.510967e-05 0.007591486 0.0008789883 -0.0037587237
## K.mg.kg -0.002470969 1.693832e-03 -0.001985042 -0.0009438046 0.0009279642
## HIERvulg IMPAparv LYSIvulg MELAnemo MELAsylv
## (Intercept) -0.099148189 -0.097028642 -0.0381712005 -0.3604083944 -0.017124671
## pH.KCl 0.062679088 0.187709039 -0.0231587069 0.0783443135 0.042109412
## N.. -0.254779526 0.194804167 0.4366010671 -0.1073819211 -0.052245143
## P.mg.kg 0.015182973 0.001258470 0.0047589559 -0.0009577235 -0.002721555
## K.mg.kg -0.003970084 -0.002467795 -0.0009438936 0.0022083778 0.001384334
## MOERtrin PHEGconn POAnemo POLYodor POTEerec
## (Intercept) 0.1253054221 -0.0963394383 -0.1546216616 -0.172887218 0.178834126
## pH.KCl 0.0227078393 0.0239223225 0.0793600702 0.090583414 -0.007700627
## N.. 0.4665057155 0.4912953162 0.0171706456 -0.129486551 -0.015222613
## P.mg.kg 0.0009848375 -0.0004532061 -0.0034806681 0.006781035 0.001647307
## K.mg.kg -0.0031433585 -0.0015009045 0.0002082134 -0.002001269 -0.001750814
## PULMobsc PYROmino RANUauri. SCORhumi SOLIvirg
## (Intercept) 0.0476646378 0.0934841192 -0.049574095 0.1534216980 -0.198470510
## pH.KCl 0.0376335186 0.0038235203 0.031339544 -0.0352468546 0.015167519
## N.. 0.0656569007 -0.0448676996 -0.127389763 -0.0270326796 -0.161319818
## P.mg.kg -0.0009256143 -0.0005009939 0.007591486 -0.0013406729 0.008864201
## K.mg.kg -0.0017163995 -0.0001214159 -0.001985042 0.0005801034 0.001283194
## URTIdioi VEROffi VIOLcani VIOLepip VIOLrivi.
## (Intercept) -0.214974155 -0.0950206963 -0.09623928 0.1936459309 -0.2116686368
## pH.KCl 0.117541288 0.0332826284 0.06825439 -0.0374279665 0.0916172138
## N.. 0.549315982 -0.0306894404 -0.28715013 0.2775854902 -0.1830270715
## P.mg.kg -0.003515685 -0.0009528379 0.01089347 0.0007016396 0.0032572797
## K.mg.kg -0.002582387 0.0005087706 -0.00227935 -0.0015105274 -0.0003496213
##
## $coef.sites
## X001Vapramae X002Illl X003Vitipalu X004Konguta X005Vehendi
## (Intercept) 0.9342271445 0.2495334918 1.202750143 0.963867263 0.080121250
## pH.KCl -0.0785389296 0.1096002972 -0.126358875 -0.045350352 0.194848535
## N.. 0.0791571765 0.0035233790 0.207570800 -0.337912794 0.007061422
## P.mg.kg -0.0046965518 -0.0003174406 -0.008618990 -0.001672614 0.004602406
## K.mg.kg 0.0005484047 0.0010613351 0.001323062 0.001101107 -0.001275498

```

```

##          X006.Erumae X007Porgumae X008Aardla X009Kurepalu
## (Intercept) 0.4968760568 1.6319595598 0.8661877602 0.0256923971
## pH.KCl      0.0545725708 -0.2089603076 -0.0312537828 0.2006142551
## N.         -0.0938961566 0.1248746094 -0.0052716260 -0.0279062274
## P.mg.kg     0.0010517872 0.0003586717 -0.0003522762 0.0047933146
## K.mg.kg     0.0008193536 -0.0017162835 0.0010334459 -0.0008419604
##          X010Sarakuste X011Kannu X012Vonnu X013Rookse X014Kammeri
## (Intercept) 1.1226532294 1.1768718738 1.006156869 1.269753485 0.5999093574
## pH.KCl      -0.1133820721 -0.1136101862 -0.046404629 -0.134456375 0.0079243715
## N.          0.1866030918 0.1191885257 0.117973017 0.186941286 0.0972577092
## P.mg.kg     -0.0029750237 -0.0038708229 -0.007078214 -0.004706770 -0.0019666087
## K.mg.kg     -0.0006574349 -0.0006674585 -0.000349342 -0.001340028 -0.0003761794
##          X015Kambja X016Reola X017Ignase X018Unikula
## (Intercept) 1.2970014713 0.8364778602 1.1223903296 1.067648e+00
## pH.KCl      -0.1411642166 -0.0469820987 -0.0867735000 -1.026232e-01
## N.          0.1400657636 -0.0415083406 0.1604193811 2.168173e-01
## P.mg.kg     -0.0036366926 -0.0037181484 -0.0065316137 -6.907894e-03
## K.mg.kg     -0.0008784383 0.0009517684 -0.0001335282 4.136024e-05
##          X019Haavametsa X020Kruusahaua X021Aravu X026Pedajamae
## (Intercept) -1.390989e-01 1.029772049 -0.035311937 1.0994446661
## pH.KCl      2.129575e-01 -0.092637725 0.204967893 -0.1076539302
## N.         -2.551768e-02 0.017339670 -0.038250503 0.1269071746
## P.mg.kg     3.658069e-03 -0.001679218 0.004638452 -0.0045158342
## K.mg.kg     2.477846e-05 0.001176559 -0.001152913 0.0001419637
##          X027Miti X028Puhaste X031Pimmelaan X032Logina X033Voorepalu
## (Intercept) -0.2066581395 0.085156055 1.059765e+00 0.625475686 3.525508e-01
## pH.KCl      0.2204654094 0.177104650 -9.361284e-02 0.032035360 7.067962e-02
## N.         -0.0120321774 -0.049507063 9.330757e-02 0.071433876 6.856848e-02
## P.mg.kg     0.0035428842 0.004661677 -4.011061e-03 -0.000851880 7.395259e-06
## K.mg.kg     0.0002485567 -0.001283576 4.664047e-05 -0.001111349 -5.265512e-04
##          X036Taevaskoja X044Savimae X073Pausakunnu
## (Intercept) -0.031627676 0.309932685 1.187701e+00
## pH.KCl      0.194864796 0.123643521 -1.080184e-01
## N.         -0.053663529 -0.068294775 -2.158916e-02
## P.mg.kg     0.004337565 0.001984238 -4.280075e-05
## K.mg.kg     -0.000685181 -0.001311756 -5.160028e-04
##
## $f.perms
##          [,1]      [,2]      [,3]      [,4]
## [1,] 1.1097100 0.7823936 0.5802194 0.6451478
## [2,] 0.8424794 0.6250877 0.8299106 0.7807209
## [3,] 1.5098961 1.3451517 0.8526403 0.4592869
## [4,] 0.6445894 0.8659630 2.3275830 0.7373308
## [5,] 1.2871370 1.3770136 2.4922227 2.2855710
## [6,] 0.7333667 0.6451492 0.7327674 0.8512084
## [7,] 0.3638300 1.0329459 1.0802246 0.2335364
## [8,] 0.7825265 1.4391468 0.6663216 1.0860438
## [9,] 0.6921459 0.9632808 0.8455652 1.2027623
## [10,] 0.8547637 1.1147385 1.5336607 0.6972813
## [11,] 1.0568346 1.7888618 0.3589306 0.5799374
## [12,] 0.9194157 0.4222210 1.1823450 0.5236207
## [13,] 0.8408528 0.7801575 1.2506638 1.0023886
## [14,] 0.6269419 1.3459332 0.9829328 0.7492888

```

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## [15,] 0.4254952 0.8516473 0.3830867 0.5999938
## [16,] 1.6388481 0.4997916 0.3104862 0.7969518
## [17,] 1.4658424 1.7320445 1.0480734 1.1001321
## [18,] 1.2713324 1.3359129 1.1567467 0.9050518
## [19,] 0.7689631 1.1964239 0.2262761 0.8766486
## [20,] 1.0657675 1.2665405 1.0887311 0.7976326
## [21,] 2.2600204 1.2928806 0.7885255 1.9662410
## [22,] 0.9759900 1.4801629 0.4649859 0.9430451
## [23,] 1.0524073 0.3589864 0.7834003 0.7171506
## [24,] 0.5832141 0.7762883 0.6630785 0.9022877
## [25,] 1.1915740 1.6848467 0.8859050 0.3742492
## [26,] 2.3598113 0.8606073 2.1221440 0.7408352
## [27,] 0.4683060 0.6894424 0.6046896 0.6379533
## [28,] 1.5476050 0.7851038 0.3836557 1.5692819
## [29,] 0.4940604 0.8052181 0.6049751 0.9079594
## [30,] 0.9225004 1.8818267 0.7814681 1.1983545
## [31,] 0.5708619 0.7406943 0.8706186 0.9292205
## [32,] 1.5624140 0.7431676 0.6968342 1.4875193
## [33,] 0.9573730 0.6349737 0.9395921 0.5362482
## [34,] 1.0535767 1.4050585 1.4085005 1.0976647
## [35,] 0.6335351 2.0124370 0.7437915 0.6449466
## [36,] 0.4464534 2.1596685 1.2262219 0.7914121
## [37,] 0.5999333 0.9709713 2.1175188 0.6223015
## [38,] 0.5186249 1.3813590 0.4213047 0.7895505
## [39,] 0.5818087 0.7847696 1.3837785 1.1686635
## [40,] 1.2221343 0.4489231 0.5795698 0.7085416
## [41,] 0.5551209 1.0498921 0.7436346 1.1381598
## [42,] 0.3266718 0.5598576 0.5818388 1.0127289
## [43,] 1.8300316 0.4010414 0.8937821 1.1761176
## [44,] 0.5560863 0.5751612 2.1100566 1.5987215
## [45,] 0.9041828 1.1394095 0.8630325 0.6758783
## [46,] 0.9501665 0.7436024 0.7983279 0.5963338
## [47,] 0.7570346 0.7617378 0.4310836 1.1829575
## [48,] 1.4318468 0.5014709 0.4252648 1.2950253
## [49,] 0.5425595 0.3238000 2.0349166 0.4210330
## [50,] 0.5263415 0.4100521 0.6133520 0.6570316
## [51,] 0.9107294 1.1852209 1.4265500 0.7919951
## [52,] 0.9924168 1.4189038 0.6529072 1.4232801
## [53,] 1.4729014 1.0476321 0.8426109 3.0599991
## [54,] 0.3496940 1.8545200 0.8428074 2.7867196
## [55,] 1.8657716 0.8577182 0.5020314 0.7412575
## [56,] 3.1862371 1.0346427 1.2124412 0.9116844
## [57,] 0.5036259 1.0676397 0.3720963 0.5810241
## [58,] 1.1229340 0.6626092 0.9279408 0.6488147
## [59,] 0.7951672 0.7943735 1.6793257 0.4521188
## [60,] 0.7913100 1.0610103 0.7275623 0.3840801
## [61,] 0.5697555 1.1136078 0.9744544 1.2350863
## [62,] 0.5949083 1.0639512 0.9032702 1.0977578
## [63,] 0.7701621 0.8700468 0.6365514 0.5900959
## [64,] 1.1091446 0.8922943 0.6795131 1.2138175
## [65,] 0.6567081 1.3123544 1.3490017 2.3389036
## [66,] 1.3010149 1.1457120 1.1906039 0.3604831
## [67,] 1.4664664 1.3561985 0.6474444 0.3846847

```



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## [68,] 0.8535622 1.3891464 1.1199662 2.0610475
## [69,] 0.6541360 1.5645405 2.2193472 0.3943162
## [70,] 0.4680007 0.7603868 1.1942411 0.7817231
## [71,] 0.4404458 0.5879396 0.5367412 0.7239913
## [72,] 0.6579880 0.8795934 0.7962462 1.1999143
## [73,] 0.6904304 0.4476974 1.1065208 0.4932515
## [74,] 0.7576140 0.8076252 0.7824431 0.8042516
## [75,] 1.2771032 1.2273362 0.4837224 0.6008210
## [76,] 0.7112975 1.3074423 0.9516250 0.8587287
## [77,] 2.0645331 1.3786603 0.5981744 0.9305382
## [78,] 0.3890577 0.8271244 1.0687003 0.8016680
## [79,] 0.9118781 1.4318817 3.4411256 1.2025690
## [80,] 0.6693686 1.4121941 2.3804074 1.3067589
## [81,] 0.7546749 0.6237358 0.5989446 1.0741005
## [82,] 1.5011436 0.9275523 0.7482807 0.4757079
## [83,] 0.4431462 0.8350194 0.8003523 1.9663139
## [84,] 3.2867435 1.2063106 1.0993551 0.4745414
## [85,] 1.6424431 0.9356984 0.9268027 0.8834138
## [86,] 0.6853292 0.7559759 1.4151120 0.3971877
## [87,] 0.6332132 0.9185463 1.1811787 1.1014897
## [88,] 0.8757769 1.1729411 0.8226294 0.6529210
## [89,] 0.9978857 1.4564042 2.6450148 0.9687830
## [90,] 1.0135392 0.6046742 1.5370337 2.3742102
## [91,] 0.5712381 2.0507861 2.5788780 1.9443566
## [92,] 1.1074710 0.7389377 0.3074382 1.0802105
## [93,] 0.8000966 1.6927596 1.1634497 1.2361129
## [94,] 1.2685667 0.7208544 0.7060304 1.0352233
## [95,] 0.7602449 0.6372987 0.9808238 0.7111964
## [96,] 0.2229950 1.5119644 0.6290095 0.4529026
## [97,] 1.1439092 0.6861301 1.7939256 0.9853231
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## [985,] 0.6117056 0.5110993 1.0297286 0.5406957
## [986,] 0.9855289 0.7262838 1.2683635 0.5209976
## [987,] 2.0512587 0.7967755 0.8675036 0.4098856
## [988,] 1.1088719 1.4275717 2.2032894 1.7117208
## [989,] 0.6531139 0.6387234 1.0566323 0.9821535
## [990,] 1.7759323 0.1792676 0.8475075 0.7860997
## [991,] 0.6696699 0.7971362 0.5098499 0.6522430
## [992,] 0.6298624 0.9184068 2.5528431 0.7144617
## [993,] 0.4407775 0.7278796 0.8364736 0.5143896
## [994,] 0.6652730 0.6821184 1.3607206 1.0663583
## [995,] 0.7621848 0.6765777 1.0089493 0.6896284
## [996,] 0.9656537 0.8299540 1.2177612 4.3218559
## [997,] 0.6188808 1.8676075 0.9116077 1.7839781
## [998,] 0.6605170 1.0716436 1.2035893 0.4972733
## [999,] 0.8170743 1.2031119 1.2848284 0.6019083
##
## $model.matrix
##      (Intercept) pH.KCl      N..      P.mg.kg      K.mg.kg
## 1              1    3.72 0.4246261 31.571334 79.04454
## 2              1    3.65 0.1364021 22.264589 42.73691
## 3              1    4.25 0.2500752 58.047875 60.71264
## 4              1    4.40 2.3192906 63.004453 131.18302
## 5              1    2.62 0.3698321 25.623389 131.56542
## 6              1    3.28 0.2426881 16.215942 66.16427
## 7              1    5.77 0.2557405 8.214731 99.41711
## 8              1    4.01 0.2749614 13.283927 64.78593
## 9              1    2.51 0.3133842 15.479056 89.14338
## 10             1    4.04 0.2550077 18.696151 86.72334
## 11             1    3.45 0.3518922 13.284533 71.89113
## 12             1    3.13 0.7552086 65.774300 148.45346
## 13             1    3.87 0.3768197 51.118770 167.18983
## 14             1    2.82 0.2495660 12.757784 68.25374
## 15             1    3.94 0.2228461 11.421171 84.96703
## 16             1    2.92 0.4507300 29.924303 82.64504
## 17             1    3.40 0.2200201 37.057869 79.17404
## 18             1    3.85 0.1762699 50.911118 71.75413
## 19             1    2.69 0.1794443 8.860196 65.97427

```

```
## 20      1  4.39 0.2592368 10.073987 32.93117
## 21      1  2.75 0.4787677 24.440573 107.38674
## 22      1  4.39 0.2691432 12.495427 82.79072
## 23      1  2.98 0.1188524 16.727024 41.51526
## 24      1  3.38 0.3361435 16.531787 96.44632
## 25      1  4.72 0.1634929 25.261675 68.99408
## 26      1  3.44 0.5404526 25.979380 138.94642
## 27      1  4.01 0.2014326 12.415253 71.46143
## 28      1  2.96 0.2040349 16.122918 93.36687
## 29      1  2.85 0.7959958 41.964598 151.10819
## 30      1  3.60 0.2448960 9.110415 62.30611
##
## $terms
## vas.plants ~ pH.KCl + N.. + P.mg.kg + K.mg.kg
## attr("variables")
## list(vas.plants, pH.KCl, N.., P.mg.kg, K.mg.kg)
## attr("factors")
##           pH.KCl N.. P.mg.kg K.mg.kg
## vas.plants      0  0         0       0
## pH.KCl          1  0         0       0
## N..             0  1         0       0
## P.mg.kg         0  0         1       0
## K.mg.kg         0  0         0       1
## attr("term.labels")
## [1] "pH.KCl" "N.." "P.mg.kg" "K.mg.kg"
## attr("order")
## [1] 1 1 1 1
## attr("intercept")
## [1] 1
## attr("response")
## [1] 1
## attr(".Environment")
## <environment: R_GlobalEnv>
##
## attr("class")
## [1] "adonis"
```

## Species Distribution modelling (SDM)

Exploring if species presences/absences are related to some parameters. Can be used to predict changes in distribution if the environment changes (e.g. due to global change).

```
# Selecting a common taxa (SDM cannot work with very rare taxa)
pa=vas.plants[,"RUBUsaxa"]>0 # presence/absence
plot(pa~soil.data$pH.KCl)

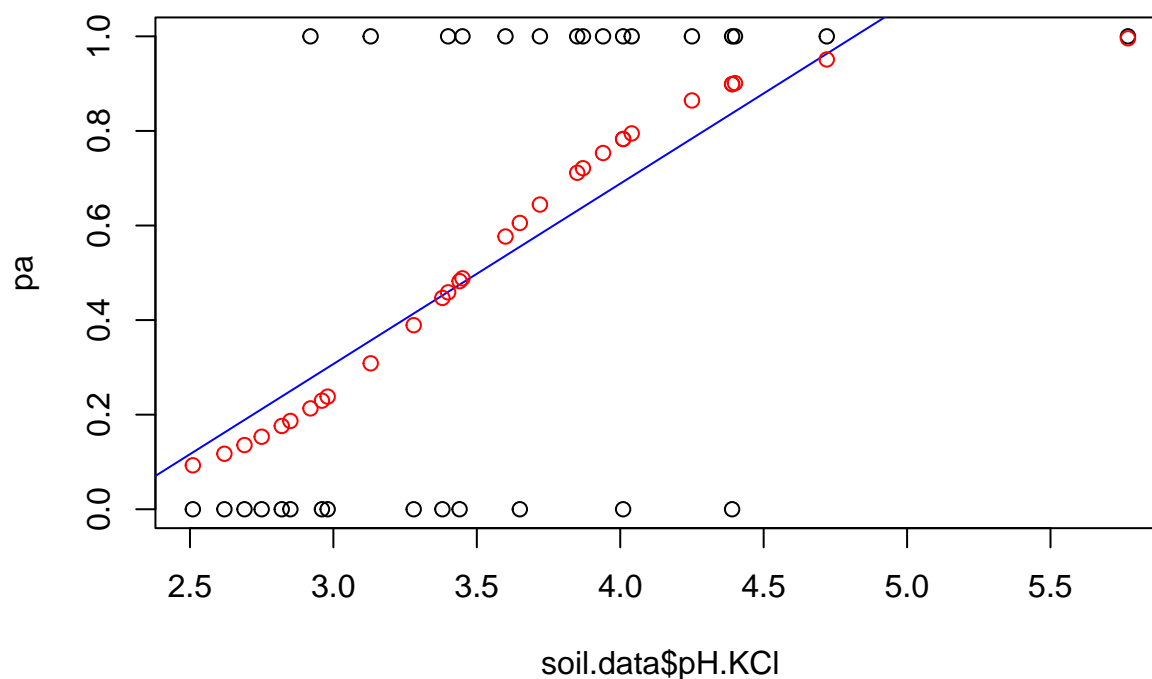
m=lm(pa~soil.data$pH.KCl) # linear model
summary(m)
##
## Call:
## lm(formula = pa ~ soil.data$pH.KCl)
##
```



```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.83734 -0.29760 -0.04173  0.35433  0.72338
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.8372     0.3987  -2.100  0.04489 *
## soil.data$pH.KCl  0.3814     0.1088   3.506  0.00155 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4305 on 28 degrees of freedom
## Multiple R-squared:  0.3051, Adjusted R-squared:  0.2803
## F-statistic: 12.29 on 1 and 28 DF,  p-value: 0.001552
abline(m,col="blue") # does not fit well, we need curvilinear model ...

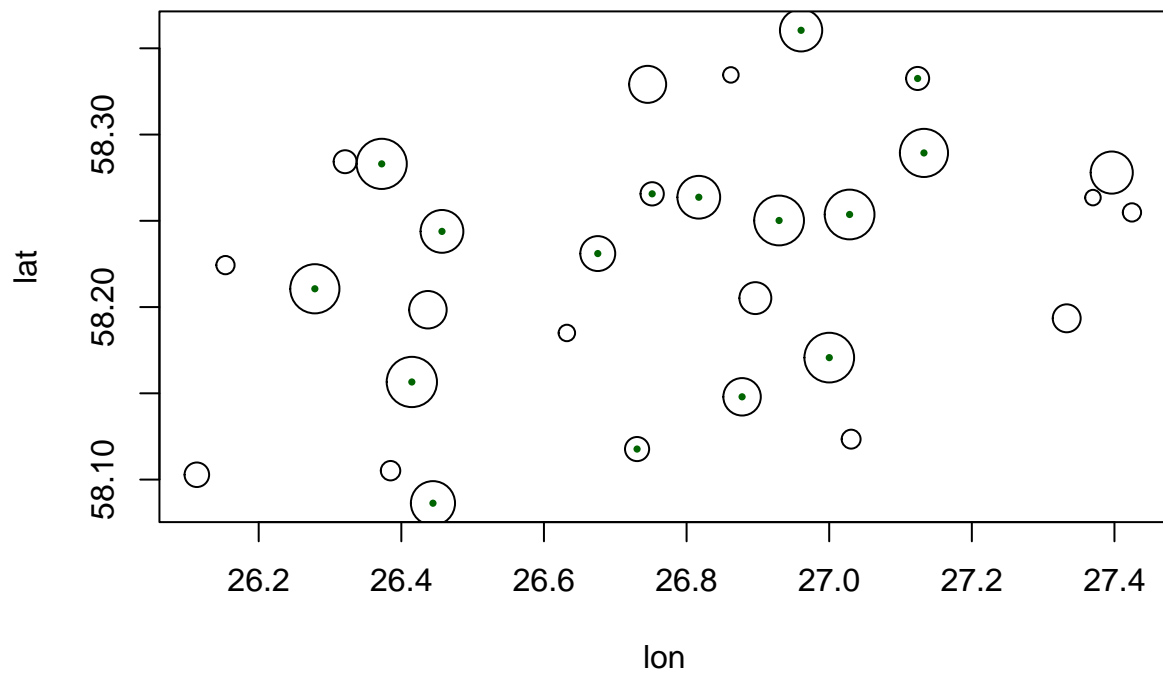
m=glm(pa~soil.data$pH.KCl,family=binomial)
summary(m)
##
## Call:
## glm(formula = pa ~ soil.data$pH.KCl, family = binomial)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -8.2388     3.1321  -2.630  0.00853 **
## soil.data$pH.KCl  2.3744     0.8891   2.671  0.00757 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 41.455  on 29  degrees of freedom
## Residual deviance: 30.007  on 28  degrees of freedom
## AIC: 34.007
##
## Number of Fisher Scoring iterations: 5
pr.glm=predict(m,type="response")

points(pr.glm~soil.data$pH.KCl,col="red")
```



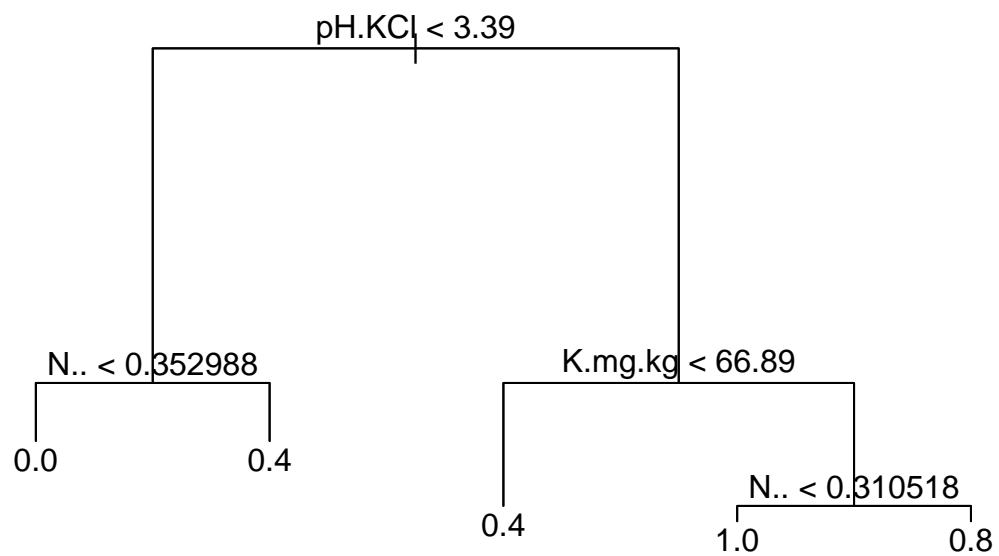
```
# Now all soil data
m=glm(pa~.,soil.data[,-5],family=binomial) #~. means that all parameters from data are included
summary(m)
##
## Call:
## glm(formula = pa ~ ., family = binomial, data = soil.data[, -5])
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -11.721287   4.923054  -2.381   0.0173 *
## pH.KCl       2.796036   1.124265   2.487   0.0129 *
## N..          -1.649511   3.110033  -0.530   0.5958
## P.mg.kg       0.099349   0.062678   1.585   0.1130
## K.mg.kg       0.002568   0.023451   0.110   0.9128
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 41.455  on 29  degrees of freedom
## Residual deviance: 24.174  on 25  degrees of freedom
## AIC: 34.174
##
## Number of Fisher Scoring iterations: 6
pr.glm=predict(m,type="response")
```

```
#Predicted distribution map
plot(xy[, -3], cex=pr.glm*2.5+1)
points(xy[pa>0, -3], pch=16, cex=0.5, col="darkgreen") # Actual presence-absence
```

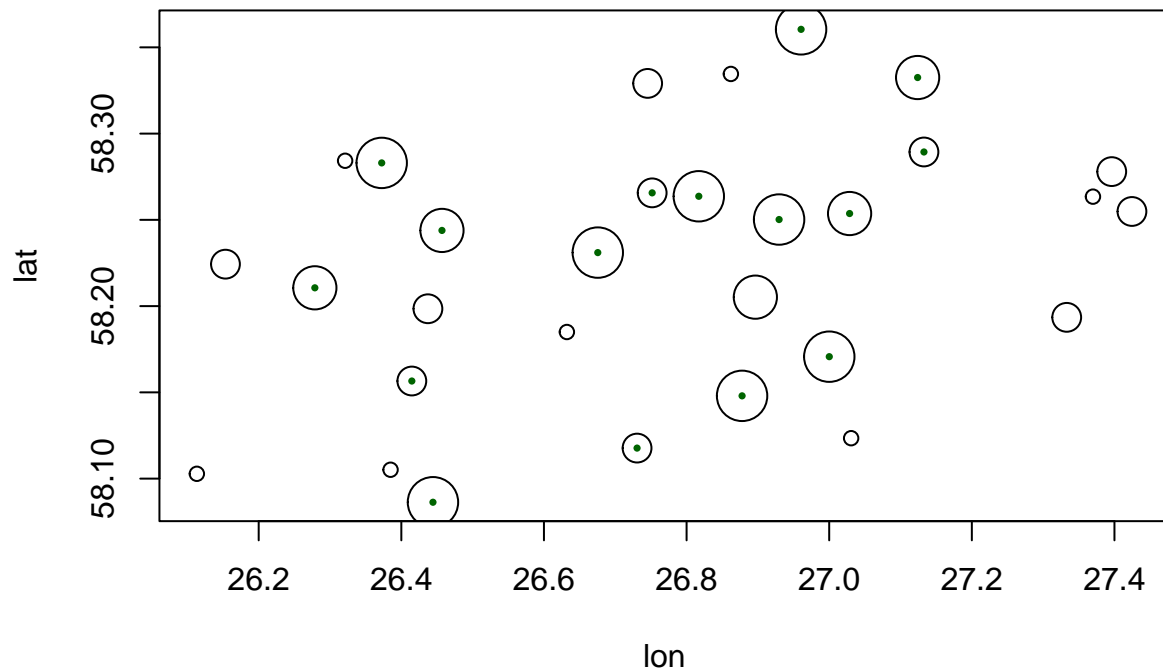


```
# Regression trees, can handle more complex relationships. Belongs to the machine learning method!
library(tree)

o.tree=tree(pa~., data=soil.data[, -5])
plot(o.tree)
text(o.tree)
```



```
pr.tree=predict(o.tree) # using the tree to predict
plot(xy[, -3], cex=pr.tree*2.5+1)
points(xy[pa>0, -3], pch=16, cex=0.5, col="darkgreen")
```

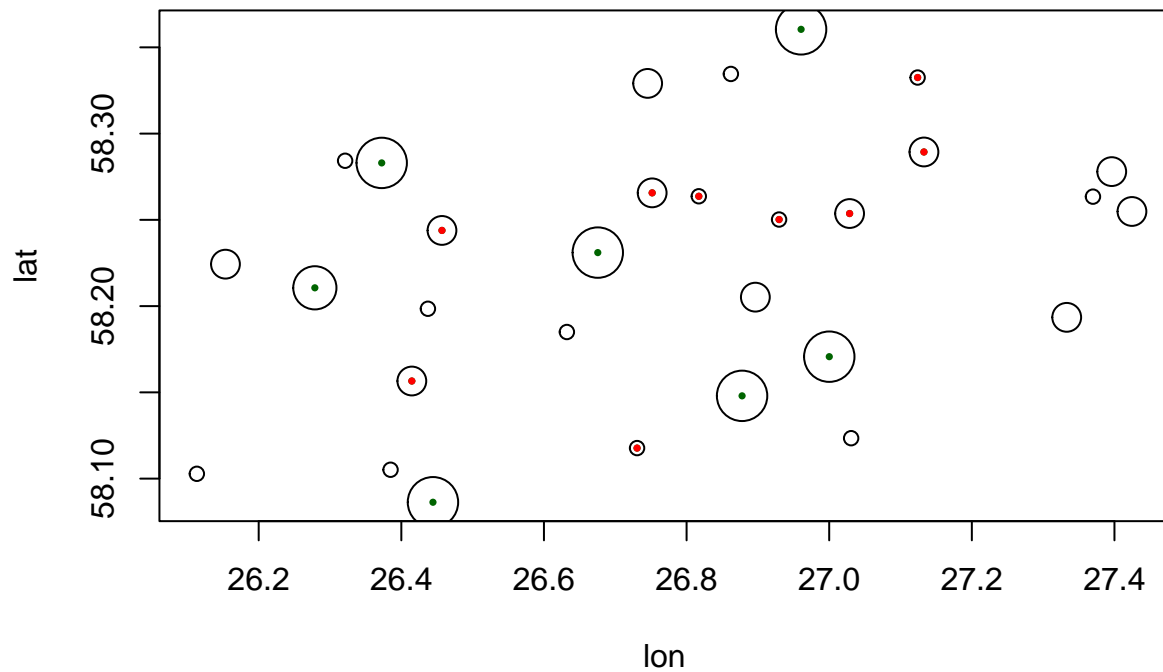


```
## Scenarios for future changes

## drop of pH 0.5 units

new.soil=soil.data[,-5]
new.soil[,1]=new.soil[,1]-0.5
pr.tree.1=predict(o.tree,new.soil)
plot(xy[,-3],cex=pr.tree.1*2.5+1)
points(xy[pa>0,-3],pch=16,cex=0.5,col="darkgreen")

points(xy[pa>0 & pr.tree.1 < 0.5,-3],pch=16,cex=0.5,col="red")
```



*# Red points show sites where the species will be probability < 0.5 after environmental change (likely)*

Try a scenario when soil pH is rising 0.5 points.

Answer

```
new.soil=soil.data[,-5]
new.soil[,1]=new.soil[,1]+0.5
pr.tree.1=predict(o.tree,new.soil)
plot(xy[,-3],cex=pr.tree.1*2.5+1)
points(xy[pa>0,-3],pch=16,cex=0.5,col="darkgreen")

points(xy[pa>0 & pr.tree.1 < 0.5,-3],pch=16,cex=0.5,col="red")
```

