assignment 4 mult models

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```r
library(vegan)
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.3-3
```

```r
data(dune)
data(dune.env)
?dune
```

```
## starting httpd help server ...
```

```
##   done
```

```r
head(dune)
```

```
##    Achimill Agrostol Airaprae Alopgeni Anthodor Bellpere Bromhord Chenalbu
## 1         1        0        0        0        0        0        0        0
## 2         3        0        0        2        0        3        4        0
## 3         0        4        0        7        0        2        0        0
## 4         0        8        0        2        0        2        3        0
## 5         2        0        0        0        4        2        2        0
## 6         2        0        0        0        3        0        0        0
##    Cirsarve Comapalu Eleopalu Elymrepe Empenigr Hyporadi Juncarti Juncbufo
## 1         0        0        0        4        0        0        0        0
## 2         0        0        0        4        0        0        0        0
## 3         0        0        0        4        0        0        0        0
## 4         2        0        0        4        0        0        0        0
## 5         0        0        0        4        0        0        0        0
## 6         0        0        0        0        0        0        0        0
##    Lolipere Planlanc Poaprat Poatriv Ranuflam Rumeacet Sagiproc Salirepe
## 1         7        0       4       2        0        0        0        0
## 2         5        0       4       7        0        0        0        0
## 3         6        0       5       6        0        0        0        0
## 4         5        0       4       5        0        0        5        0
## 5         2        5       2       6        0        5        0        0
## 6         6        5       3       4        0        6        0        0
##    Scorautu Trifprat Trifrepe Vicilath Bracruta Callcusp
## 1         0        0        0        0        0        0
## 2         5        0        5        0        0        0
## 3         2        0        2        0        2        0
## 4         2        0        1        0        2        0
```

```
## 5         3         2         2         0         2         0
## 6         3         5         5         0         6         0
```

```
dim(dune)
```

```
## [1] 20 30
```

1. NMDS of dune

```
dune_mds = metaMDS(dune)
```

```
## Run 0 stress 0.1192678
## Run 1 stress 0.1809578
## Run 2 stress 0.1183186
## ... New best solution
## ... procrustes: rmse 0.02026495  max resid 0.06493387
## Run 3 stress 0.1192679
## Run 4 stress 0.119268
## Run 5 stress 0.1183186
## ... procrustes: rmse 8.499781e-05  max resid 0.0002667488
## *** Solution reached
```

```
dune_mds
```

```
##
## Call:
## metaMDS(comm = dune)
##
## global Multidimensional Scaling using monoMDS
##
## Data:      dune
## Distance: bray
##
## Dimensions: 2
## Stress:     0.1183186
## Stress type 1, weak ties
## Two convergent solutions found after 5 tries
## Scaling: centring, PC rotation, halfchange scaling
## Species: expanded scores based on 'dune'
```

```
plot(dune_mds, type='n')
text(dune_mds, 'sp', cex=.5)
# generate vector of colors
color_vect = rev(terrain.colors(6))[-1]
points(dune_mds, 'sites', pch=19,
       col=color_vect[dune.env$Moisture])
legend('topright', paste("Moisture =", 1:5, sep=''),
       col=color_vect, pch=19)
```
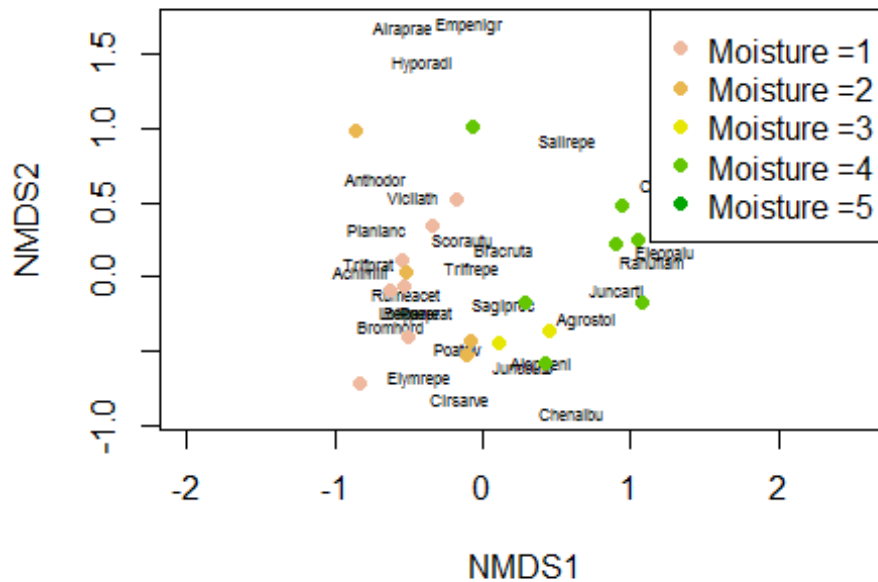
1. The NMDS plot shows that some of the species are associated with higher moisture and some are associated with lower moisture, but does not show any strong trends. A CCA might show how much moisture contributes to each axis.

```
#CCA of dune ~ dune.env
dune_cca = cca(dune ~ ., data=dune.env)
plot(dune_cca)
```
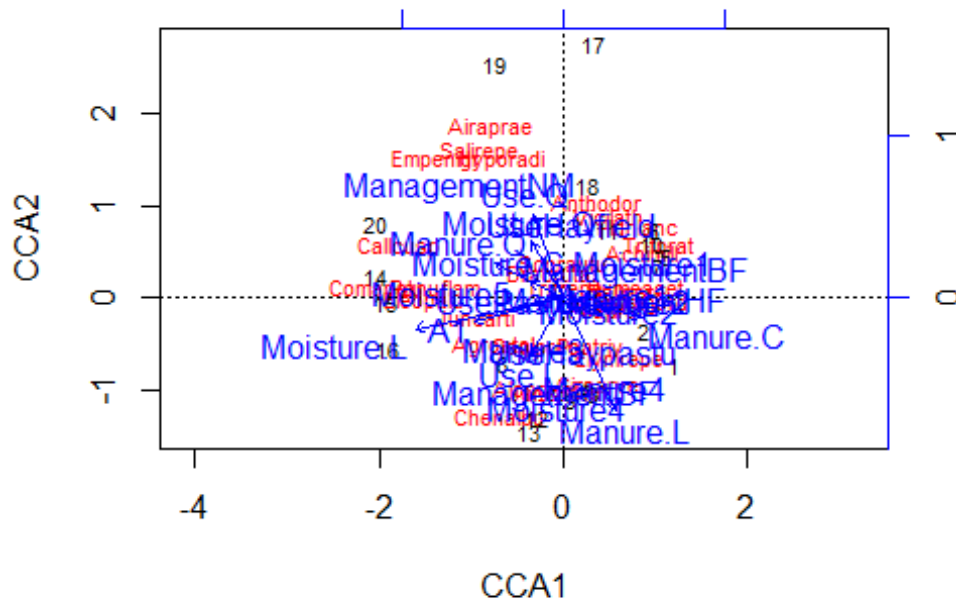
```
anova(dune_cca)

## Permutation test for cca under reduced model
## Permutation: free
## Number of permutations: 999
##
## Model: cca(formula = dune ~ A1 + Moisture + Management + Use + Manure,
data = dune.env)
##           Df ChiSquare      F Pr(>F)
## Model     12    1.5032 1.4325  0.024 *
## Residual  7    0.6121
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2. An anova of the CCA for the whole model showed that the model as a whole significantly explained the variance in the data. However, none of the variables, moisture included, showed significant contribution by themselves. A1 soil depth and moisture were the top contributing variables, but did not have a significant P-value.

3. The models seem to support each other. The NDMS model showed a slight trend that some species might be associated with moisture, but nothing obvious. The CCA model showed that the variables taken as a whole contributed significantly to the explanation of variance, but none of them individually contributed significantly. This suggests that the variance in species location may be an interactive effect between all the variables, or possibly that an unmeasured variable is causing the distribution.