```r
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 3.5.3
```

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

```
## Warning: package 'permute' was built under R version 3.5.3
```

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

```
## Warning: package 'lattice' was built under R version 3.5.3
```

```
## This is vegan 2.5-6
```

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

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

```
##  done
```

```r
dune_mds <- metaMDS(dune)
```

```
## Run 0 stress 0.1192678
## Run 1 stress 0.1889684
## Run 2 stress 0.1192678
## ... Procrustes: rmse 3.703024e-05  max resid 9.42907e-05
## ... Similar to previous best
## Run 3 stress 0.2075713
## Run 4 stress 0.1183186
## ... New best solution
## ... Procrustes: rmse 0.02026841  max resid 0.06494889
## Run 5 stress 0.1192679
## Run 6 stress 0.1192678
## Run 7 stress 0.1192679
## Run 8 stress 0.1183186
## ... Procrustes: rmse 1.499698e-05  max resid 4.09466e-05
## ... Similar to previous best
## Run 9 stress 0.1192682
## Run 10 stress 0.1183186
## ... Procrustes: rmse 4.935426e-05  max resid 0.000153607
## ... Similar to previous best
## Run 11 stress 0.1183186
## ... Procrustes: rmse 7.448297e-05  max resid 0.0002297646
## ... Similar to previous best
## Run 12 stress 0.1183186
## ... New best solution
## ... Procrustes: rmse 4.121012e-06  max resid 1.291327e-05
## ... Similar to previous best
## Run 13 stress 0.1183186
## ... Procrustes: rmse 1.961574e-05  max resid 4.332317e-05
## ... Similar to previous best
## Run 14 stress 0.1192678
## Run 15 stress 0.1183186
## ... Procrustes: rmse 3.132007e-05  max resid 0.0001102496
## ... Similar to previous best
## Run 16 stress 0.1192682
## Run 17 stress 0.1183186
## ... Procrustes: rmse 1.575368e-05  max resid 5.105237e-05
## ... Similar to previous best
## Run 18 stress 0.1192681
## Run 19 stress 0.1183186
## ... Procrustes: rmse 1.917776e-05  max resid 6.108187e-05
## ... Similar to previous best
## Run 20 stress 0.1192681
## *** Solution reached
```

```
plot(dune_mds, type='n')
text(dune_mds, 'sp', cex=.5)
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)
```
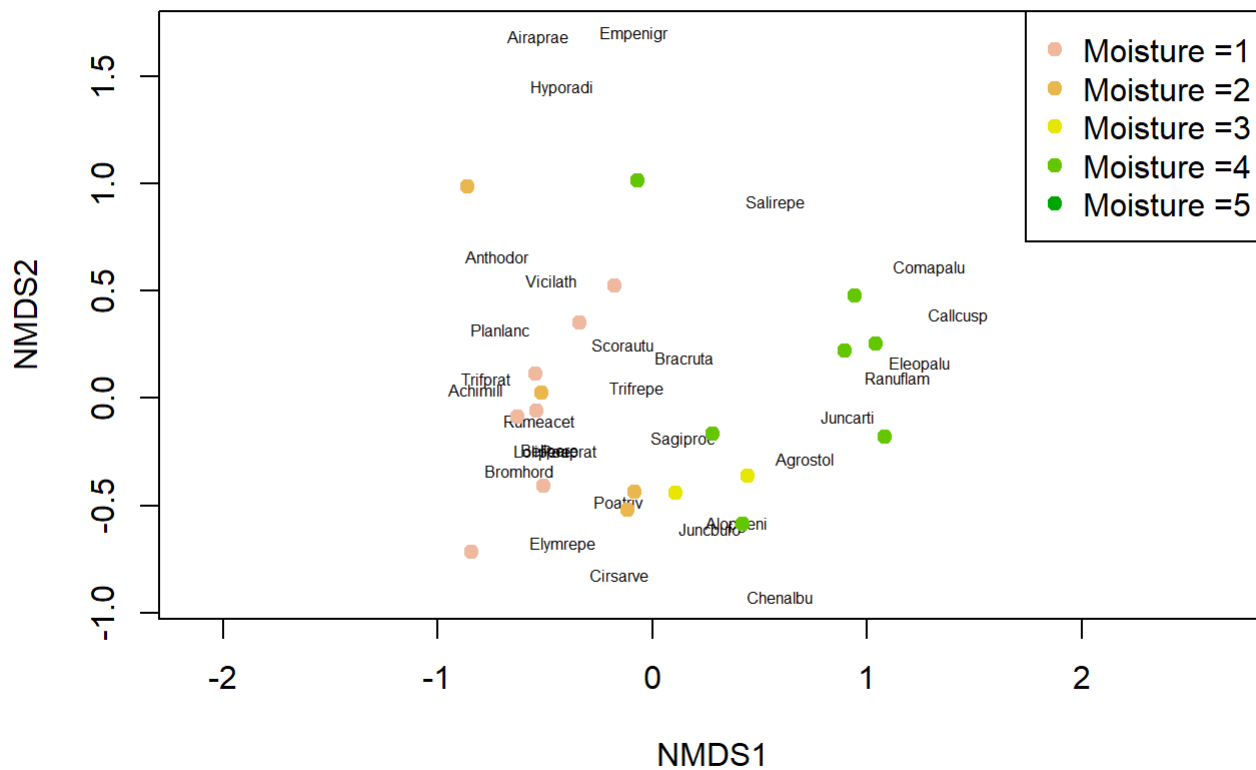
1. It looks like moisture is impacting the species, especially moisture 4 and 5. They are clustered farther away from the other points and moisture 1 and 2 are clustered on the other side of the plot. It would appear that moisture does have some sort of impact on the species.

```
dune.env$Moisture = factor(dune.env$Moisture, levels = 1:5, ordered = FALSE)
cca_dune <- cca(dune ~ ., data=dune.env)
cca_dune1 <- cca(dune ~ dune.env$Moisture + dune.env$A1 + dune.env$Management)
cca_dune2 <- cca(dune ~ dune.env$Moisture + dune.env$A1 + dune.env$Manure)
cca_dune3 <- cca(dune ~ dune.env$Moisture + dune.env$A1 + dune.env$Management + dune.env$Manure)
RsquareAdj(cca_dune, 100)
```

```
## $r.squared
## [1] 0.7106267
##
## $adj.r.squared
## [1] 0.220827
```

```
RsquareAdj(cca_dune1, 100)
```

```
## $r.squared
## [1] 0.5385459
##
## $adj.r.squared
## [1] 0.272208
```

```
RsquareAdj(cca_dune2, 100)
```

```
## $r.squared
## [1] 0.5770783
##
## $adj.r.squared
## [1] 0.2557728
```

```
RsquareAdj(cca_dune3, 100)
```

```
## $r.squared
## [1] 0.6491209
##
## $adj.r.squared
## [1] 0.2597712
```

```
anova(cca_dune, permutations = 999)
```

```
## 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  0.033 *
## Residual   7    0.6121
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(cca_dune, by = 'margin', permutations = 999)
```

```
## Permutation test for cca under reduced model
## Marginal effects of terms
## Permutation: free
## Number of permutations: 999
##
## Model: cca(formula = dune ~ A1 + Moisture + Management + Use + Manure, data = dune.env)
##            Df ChiSquare      F Pr(>F)
## A1          1   0.11070 1.2660  0.219
## Moisture    3   0.31587 1.2041  0.221
## Management  2   0.15882 0.9081  0.586
## Use         2   0.13010 0.7439  0.766
## Manure      3   0.25490 0.9717  0.504
## Residual    7   0.61210
```

```
plot(cca_dune, type='n', scaling=1)
orditorp(cca_dune, display='sp', cex=0.5, scaling=1, col='blue')
#text(cca_dune, display='bp', col='red')
orditorp(cca_dune, display='cn', col='red')
```
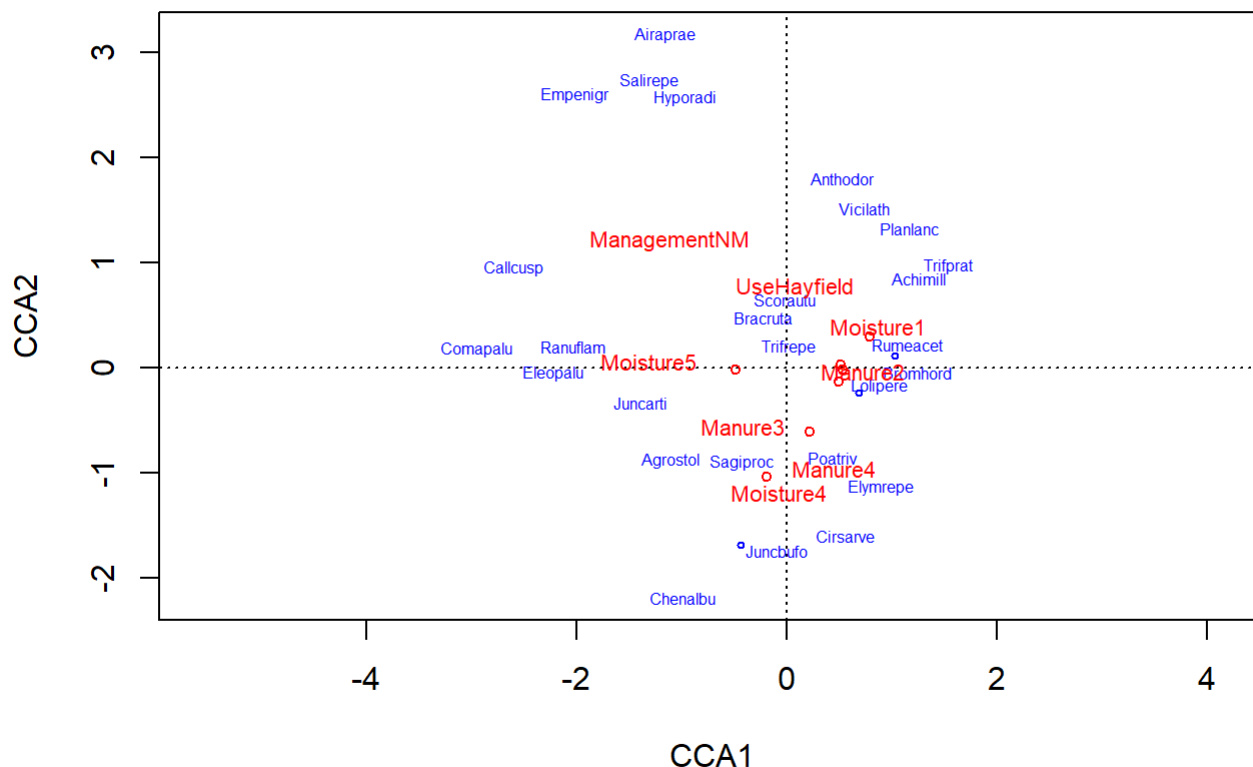

3. From this plot and analysis it complements the mds plot. Moisture is still an important variable. Moisture 5, 1, 3 have clearly distinct clusters. However the cca showed that management and manure also might be an important variable. We didn't see those in the mds, because we only plotted it for moisture. I think the cca analysis is more useful, but the mds plots look nicer and are easier to understand/make, but both are useful analyses.

```
dune.fit <- envfit(dune_mds, dune.env)
plot(dune_mds, type = 'n')
text(dune_mds, 'sp', cex = .5)
mois_lvs <- sort(unique(dune.env$Moisture))
color_vect <- rev(terrain.colors(length(mois_lvs) + 1))[-1]
points(dune_mds, 'sites', pch=19,
       col = color_vect[dune.env$Moisture])
plot(dune.fit, p.max = 0.01, cex = .75)
legend('topright', paste("Moisture =", mois_lvs, sep = ''),
       col =color_vect, pch=19)
```