

Assignment #4

Sarah Kate Shore

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```
library(vegan)
```

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

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

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

```
data(dune) #community data
data(dune.env) #environmental data
?dune
```

```
#Indirect Ordination
```

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

```
## Run 0 stress 0.1192678
```

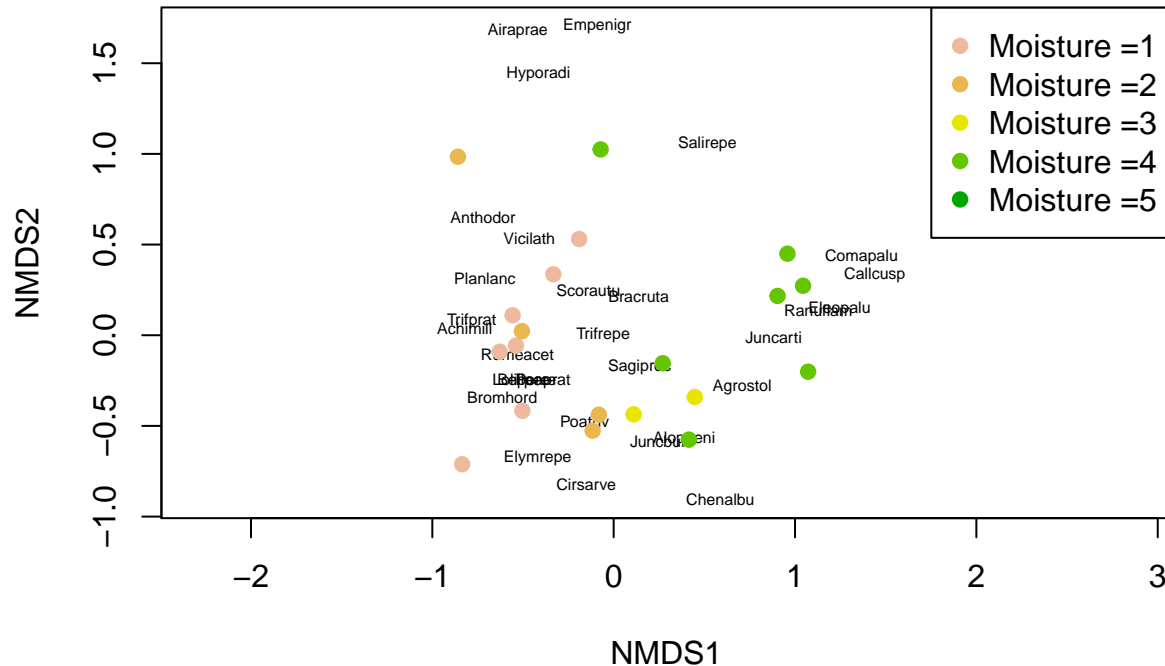
```
## Run 1 stress 0.1192683
```

```
## ... procrustes: rmse 0.0003951249 max resid 0.001213539
```

```
## *** Solution reached
```

```
plot(dune_mds, type='n', main = "Moisture NMDS")
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)
```

Moisture NMDS



#This plot shows the relationship of different dune species to moisture levels in the environment. The different moisture levels correspond to certain species and it appears from brief visual inspection that there are more species in the lower two moisture classes.

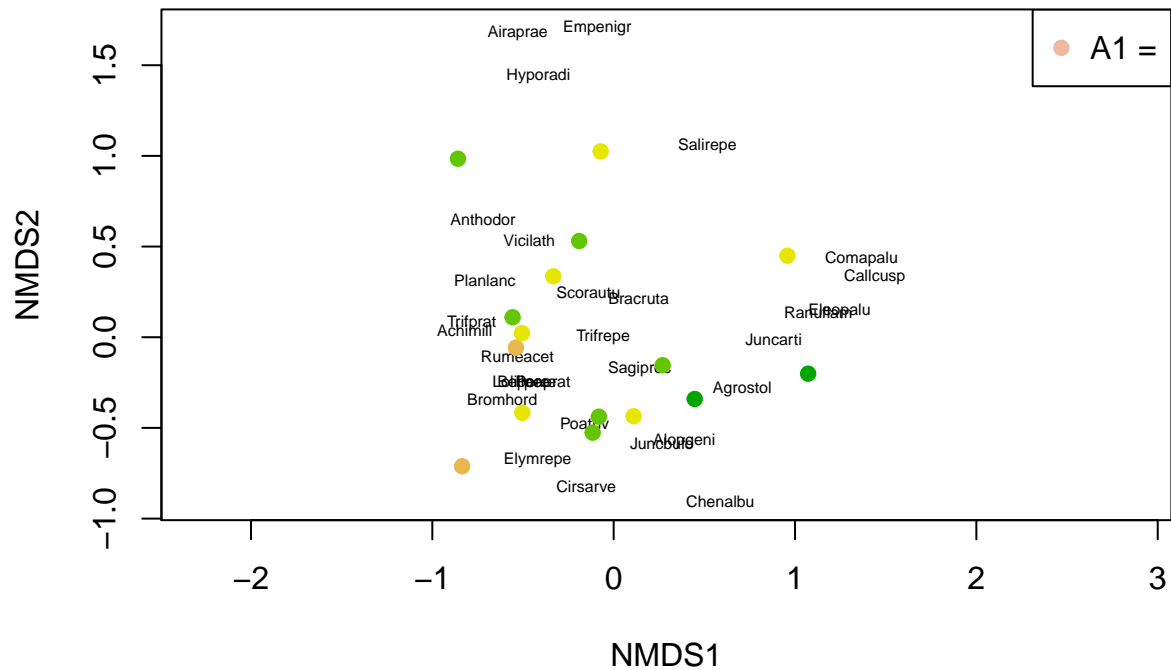
A1

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

```
## Run 0 stress 0.1192678
## Run 1 stress 0.119268
## ... procrustes: rmse 0.0002336713  max resid 0.0007319334
## *** Solution reached
```

```
plot(dune_mds, type='n', main = "A1 NMDS")
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$A1])
legend('topright', paste("A1 =", sep=''),
       col=color_vect, pch=19)
```

A1 NMDS

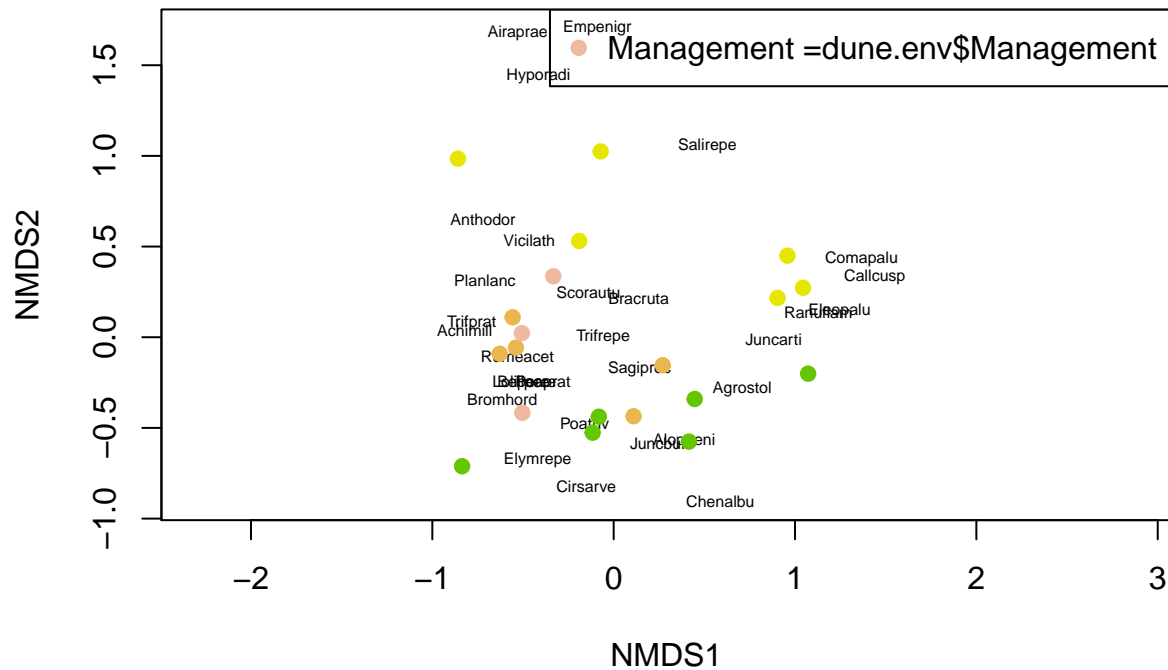


```
dune_mds = metaMDS(dune)
```

```
## Run 0 stress 0.1192678
## Run 1 stress 0.1808919
## Run 2 stress 0.1808915
## Run 3 stress 0.1192679
## ... procrustes: rmse 0.0001213039 max resid 0.0003706388
## *** Solution reached
```

```
plot(dune_mds, type='n', main = "Management NMDS")
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$Management])
legend('topright', paste("Management =", unique = "dune.env$Management", sep=''),
      col=color_vect, pch=19)
```

Management NMDS



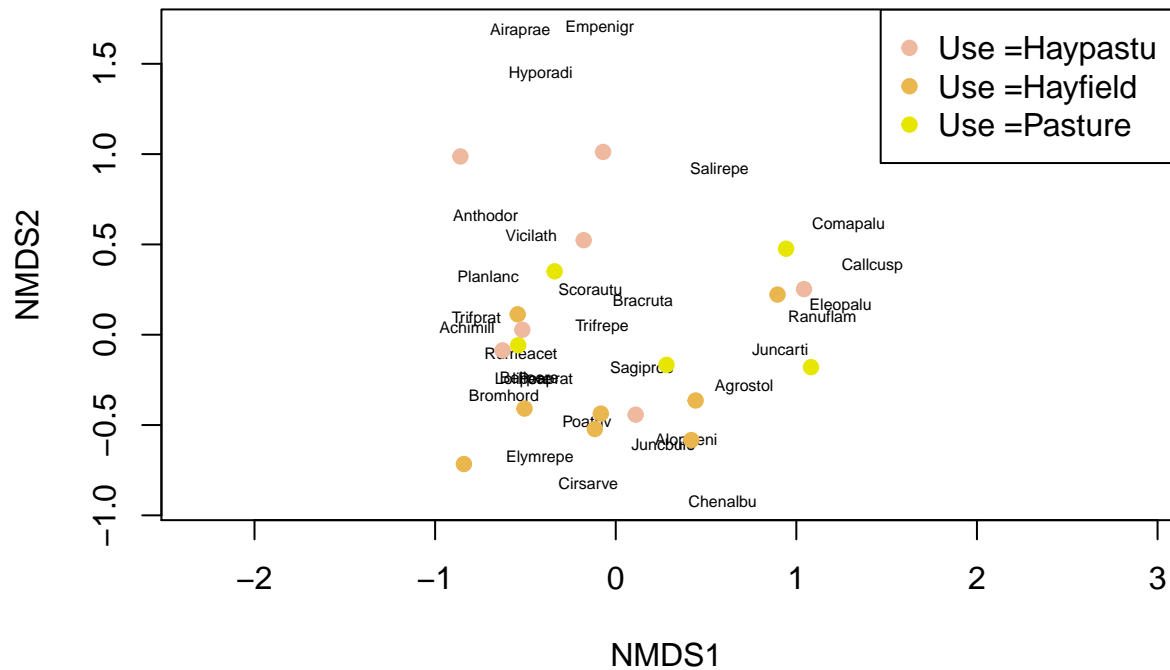
#Use

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

```
## Run 0 stress 0.1192678
## Run 1 stress 0.3680169
## Run 2 stress 0.1183186
## ... New best solution
## ... procrustes: rmse 0.02026662 max resid 0.06494082
## Run 3 stress 0.1183186
## ... New best solution
## ... procrustes: rmse 2.040372e-05 max resid 4.932414e-05
## *** Solution reached
```

```
plot(dune_mds, type='n', main = 'Use NMDS')
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$Use])
legend('topright', paste("Use =", unique(dune.env$Use), sep=''),
      col=color_vect, pch=19)
```

Use NMDS



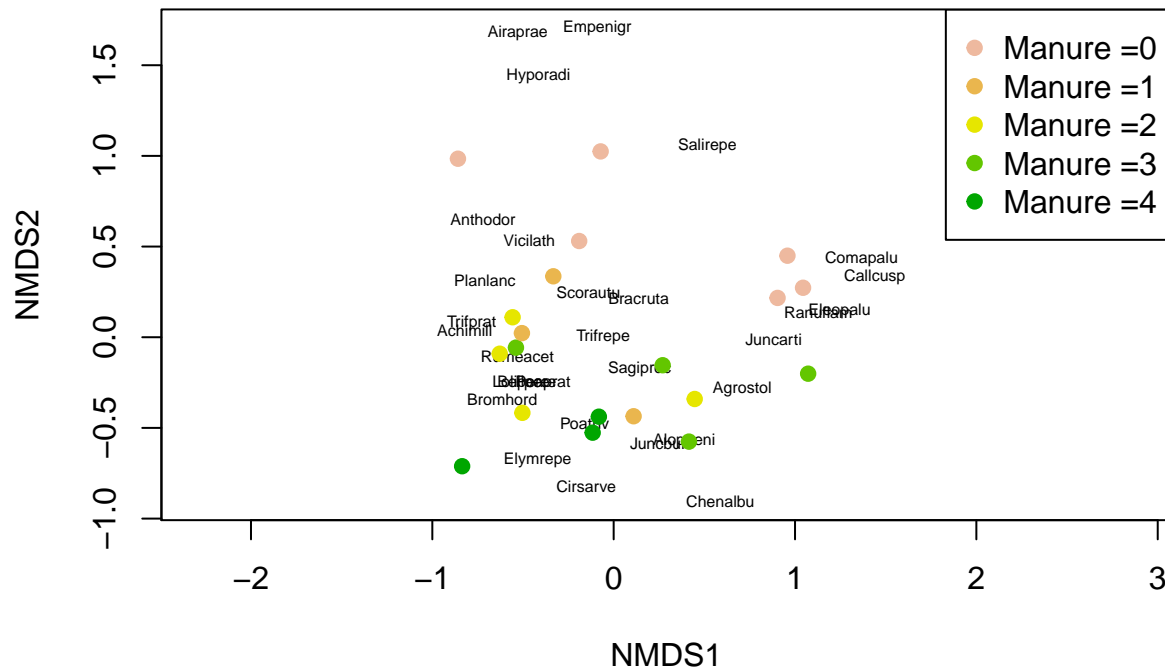
#Manure

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

```
## Run 0 stress 0.1192678
## Run 1 stress 0.1192679
## ... procrustes: rmse 0.000174903 max resid 0.0005375961
## *** Solution reached
```

```
plot(dune_mds, type='n', main = 'Manure NMDS')
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$Manure])
legend('topright', paste("Manure =", 0:4, sep=''),
       col=color_vect, pch=19)
```

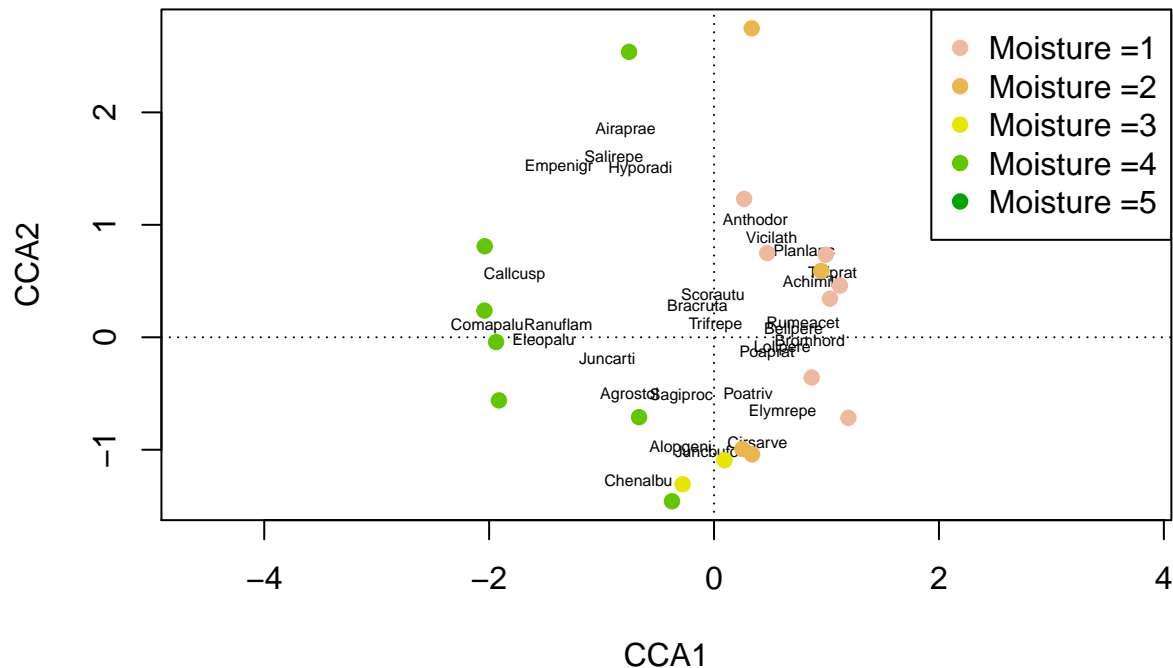
Manure NMDS



#Direct Ordination

```
dune_cca = cca(dune ~ dune.env$A1 + dune.env$Moisture + dune.env$Management + dune.env$Use + dune.env$M
plot(dune_cca, type='n', main = "Moisture CCA")
text(dune_cca, 'sp', cex=.5)
# generate vector of colors
color_vect = rev(terrain.colors(6))[-1]
points(dune_cca, 'sites', pch=19,
       col=color_vect[dune.env$Moisture])
legend('topright', paste("Moisture =", 1:5, sep=''),
       col=color_vect, pch=19)
```

Moisture CCA



#This direct ordination shows a trend of greater species concentration around the lower moisture classes, similar to the NMDS but with greater species clustering.

Permutation test

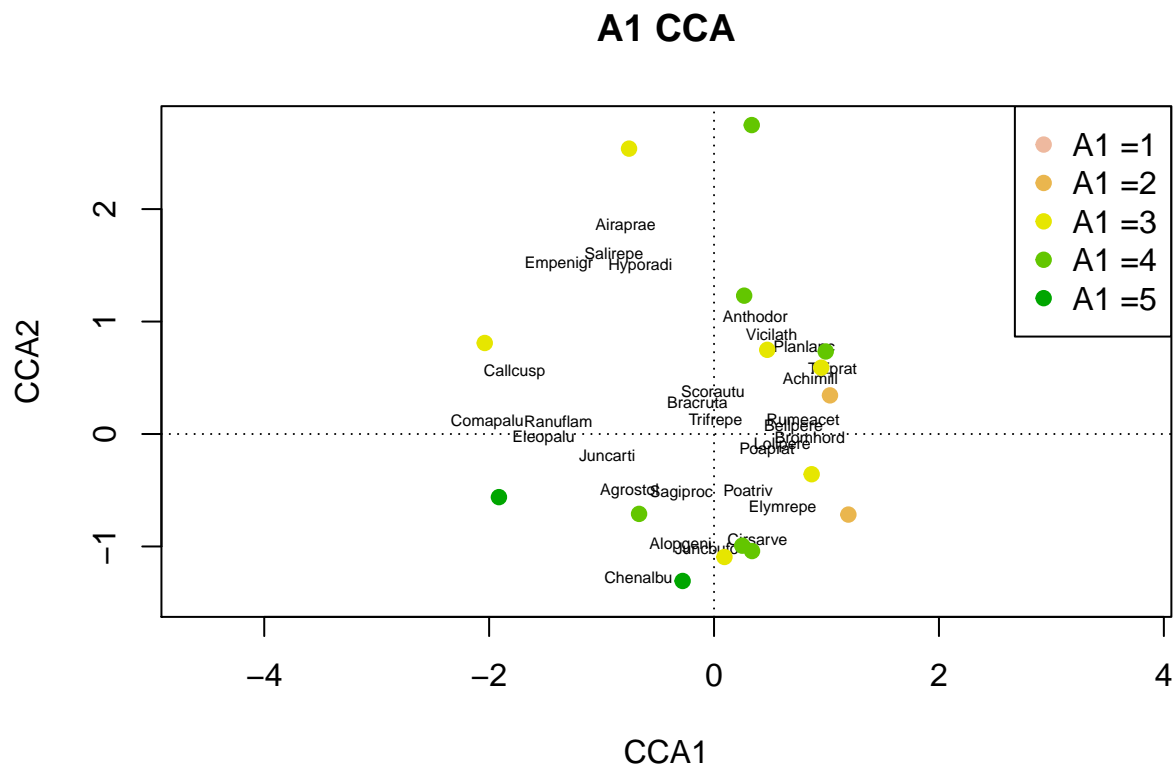
```
anova(dune_cca, by = 'margin', permutations = 10)
```

```
## Permutation test for cca under reduced model
## Marginal effects of terms
## Permutation: free
## Number of permutations: 10
##
## Model: cca(formula = dune ~ dune.env$A1 + dune.env$Moisture + dune.env$Management + dune.env$Use + dune.env$Manure, data = dune, method = "ml")
##              Df ChiSquare      F Pr(>F)
## dune.env$A1      1   0.11070 1.2660 0.36364
## dune.env$Moisture 3   0.31587 1.2041 0.09091 .
## dune.env$Management 2   0.15882 0.9081 0.63636
## dune.env$Use      2   0.13010 0.7439 0.63636
## dune.env$Manure    3   0.25490 0.9717 0.72727
## Residual          7   0.61210
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

It appears that the F values, which signify explained variance over unexplained variance, are greater than one for A1 and Moisture variables, but not for any others, indicating that A1 and Moisture are probably the strongest explanatory axes.

A1 CCA

```
dune_cca = cca(dune ~ dune.env$A1 + dune.env$Moisture + dune.env$Management + dune.env$Use + dune.env$M
plot(dune_cca, type='n', main = "A1 CCA")
text(dune_cca, 'sp', cex=.5)
# generate vector of colors
color_vect = rev(terrain.colors(6))[-1]
points(dune_cca, 'sites', pch=19,
       col=color_vect[dune.env$A1])
legend('topright', paste("A1 =", 1:5, sep=''),
      col=color_vect, pch=19)
```



#This seems to be more scattered in terms of sites (A1 values), perhaps the A1 legend should not be divided into classes. However, the species are still clustered similar to the Moisture CCA plot.

To compare the NDMS indirect or unconstrained ordination with the CCA direct or constrained ordination, the CCA plot seems to bring together the species similarities in a more tightly explained way, although the two methods are quite similar.