

## Elaborated Nonmetric Multidimensional Scaling

Nonmetric Multidimensional Scaling is the ordination equivalent of a non-parametric procedure. There are no assumptions of specific distributions (normality) or linearity. Outliers have minimal influence on the final ordination as the technique does not try to maintain the distances, but rather the rank order of the distances – which would not distort the procedure to the same degree as other techniques. Screening of the data should be conducted, but evaluation of the assumptions is less involved.

### Setup

This dataset is part of an aquatic ecology dataset. The data represents the number of fish of different species that were caught at a number of different sites. We want to reduce the number of variables (species) that we need consider but capture as much of the variation in the original communities as we can.

### Set the working directory and load the dataset

```
setwd("C:\\Multi\\")  
  
DoubSp <- read.table("DoubSpe.txt", header=TRUE)
```

### Perform the NMDS

```
library(vegan)  
  
DoubSp.nmDS <- metaMDS(DoubSp, distance="bray")  
  
DoubSp.nmDS  
  
DoubSp.nmDS$stress  
  
windows(title="NMDS on fish species - Bray")  
  
plot(DoubSp.nmDS, type="t", main=paste("NMDS/Bray - Stress =",  
round(DoubSp.nmDS$stress,3)))
```

### Goodness of Fit Diagnostics

```
stressplot(DoubSp.nmDS, main="Shepard plot")
```

## Combining Ordination and Cluster result

### Perform cluster analysis

```
species.bray <- vegdist(DoubsSp, "bray")  
species.bray.complete <- hclust(species.bray, method="complete")  
plot(species.bray.complete)
```

### Extract 5 Clusters from the Dendrogram

```
species.bray.complete.groups <- cutree(species.bray.complete, k=5)  
group.level <- levels(factor(species.bray.complete.groups))
```

### Combine Clusters with Ordination Results

```
site.scores <- scores(DoubsSp.nmnds)  
windows(title="NMDS plot with cluster colors")  
p <- ordiplot(site.scores, type="n", main="NMDS/Bray + clusters  
Complete/Bray")  
for (i in 1:length(group.level)) {  
  points(site.scores[species.bray.complete.groups==i,], pch=(14+i), cex=2,  
    col=i+1)  
}  
text(site.scores, row.names(DoubsSp), pos=4, cex=0.7)
```

### Add Dendrogram to the Ordination

```
ordicluster(p, species.bray.complete, col="dark grey")  
legend(locator(1), paste("Group",c(1:length(group.level))),  
  pch=14+c(1:length(group.level)), col=1+c(1:length(group.level)),  
  pt.cex=2)
```