

Tutorial 11: Clustering

ENVX2001 – Applied Statistical Methods

Semester 1

Dissimilarity Matrices and Clustering

We are going to analyse the bird assemblage data from the lecture.

Setup

Load the vegan package:

```
CODE  
library(vegan)
```

Load the data

Read the data:

```
CODE  
macnally <- read.csv("data/macnally.csv", row.names = 1)  
head(macnally, 1)
```

```
OUTPUT  
      HABITAT V1GST V2EYR V3GF V4BTH V5GWH V6WTTR V7WEHE V8WNHE V9SFW  
Reedy Lake Mixed 3.4    0    0    0    0    0    0    11.9 0.4  
      V10BSW V11CR V12LK V13RWB V14AUR V15STTH V16LR V17WPHE V18YTH V19ER  
Reedy Lake    0    1.1 3.8    9.7    0    0    4.8 27.3    0 5.1  
      V20PCU V21ESP V22SCR V23RBFT V24BFCS V25WAG V26WWCH V27NHHE V28VS  
Reedy Lake    0    0    0    0    0    0.6 1.9    0    0    0  
      V29CST V30BTR V31AMAG V32SCC V33RWH V34WSW V35STP V36YFHE V37WHIP  
Reedy Lake 1.7 12.5    8.6 12.5    0.6    0    4.8    0    0  
      V38GAL V39FHE V40BRTH V41SPP V42SIL V43GCU V44MUSK V45MGLK V46BHHE  
Reedy Lake 4.8 26.2    0    0    0    0    13.1 1.7    1.1  
      V47RFC V48YTBC V49LYRE V50CHE V510WH V52TRM V53MB V54STHR V55LHE  
Reedy Lake    0    0    0    0    0    15    0    0    0  
      V56FTC V57PINK V580B0 V59YR V60LFB V61SPW V62RBTR V63DWS V64BELL  
Reedy Lake    0    0    0    0    2.9    0    0    0.4    0  
      V65LWB V66CBW V67GGC V68PIL V69SKF V70RSL V71PD0V V72CRP V73JW  
Reedy Lake    0    0    0    0    1.9 6.7    0    0    0  
      V74BCH V75RCR V76GBB V77RRP V78LLOR V79YTHE V80RF V81SHBC V82AZKF  
Reedy Lake    0    0    0    4.8    0    0    0    0    0  
      V83SFC V84YRTH V85ROSE V86BC00 V87LFC V88WG V89PC00 V90WTG V91NMIN  
Reedy Lake    0    0    0    0    0    0    1.9    0    0.2  
      V92NFB V93DB V94RBEE V95HBC V96DF V97PCL V98FLAME V99WWT V100WBWS
```

Reedy Lake	0	0	0	0	0	9.1	0	0	0
	V101LCOR	V102KING							
Reedy Lake	0	0							

Calculate Bray-Curtis Dissimilarity

Calculate the Bray-Curtis dissimilarity:

```
CODE
Braydistance <- vegdist(macnally[, 3:102])
```

Hierarchical Clustering

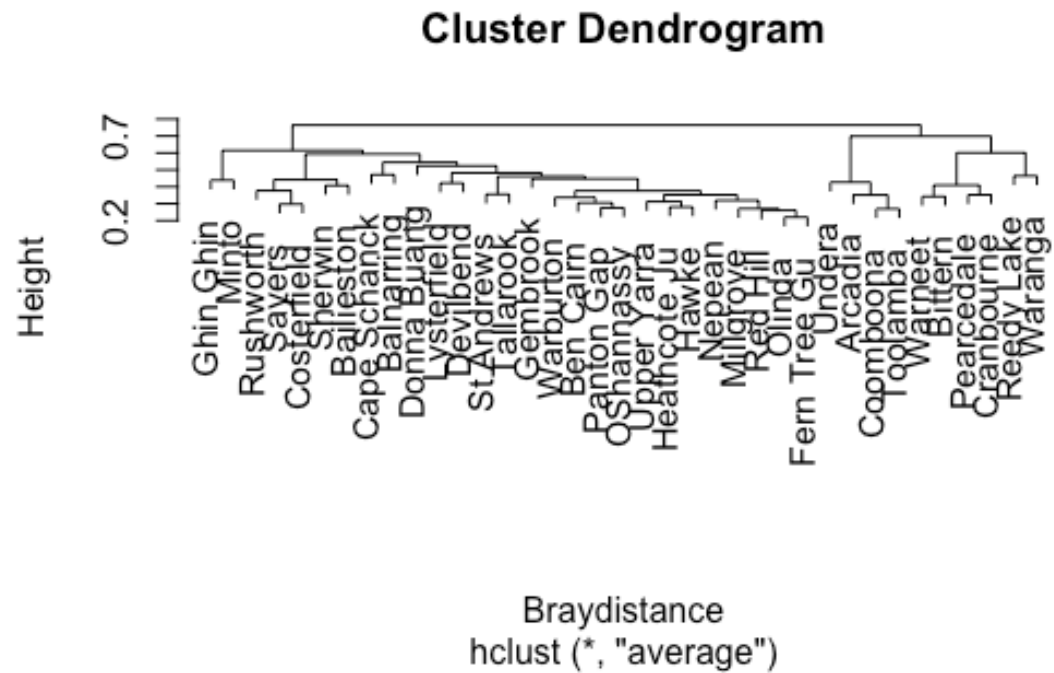
Apply hierarchical clustering using the UPGMA method (“average”):

```
CODE
hc <- hclust(Braydistance, method = "average")
```

Plot the Dendrogram

Plot the dendrogram:

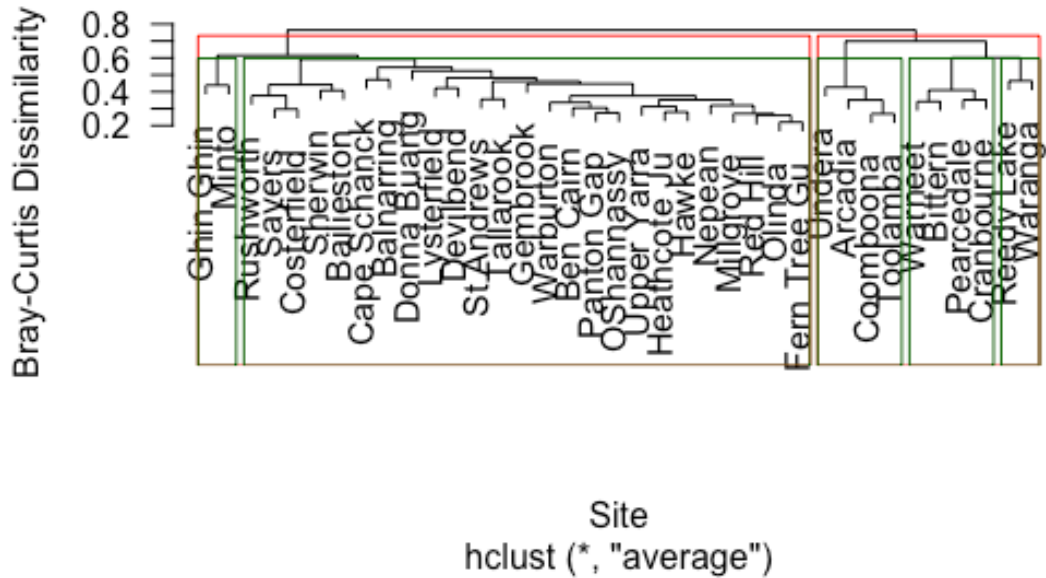
```
CODE
plot(hc)
```



Let's add some labels, and look at the potential number of clusters:

```
CODE
plot(hc, las = 1,
     main = "Cluster diagram of Bird Assemblages",
     xlab = "Site",
     ylab = "Bray-Curtis Dissimilarity")
rect.hclust(hc, 2, border = "red")
rect.hclust(hc, 5, border = "darkgreen")
```

Cluster diagram of Bird Assemblages



The rectangles show potential groupings at different levels of the dendrogram:

- **Red rectangles:** 2 clusters
- **Green rectangles:** 5 clusters

The choice of how many clusters to use depends on your research question and the level of dissimilarity that is meaningful for your study.