

# 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 11.9 0.4  
          V10WBSW 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 0.6 1.9 0 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 0  
          V56FTC V57PINK V580BO V59YR V60LFB V61SPW V62RBTR V63DWS V64BELL  
Reedy Lake 0 0 0 0 2.9 0 0 0.4 0  
          V65LWB V66CBW V67GCC V68PIL V69SKF V70RSL V71PD0V V72CRP V73JW  
Reedy Lake 0 0 0 0 1.9 6.7 0 0 0  
          V74BCHE 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	9.1	0	0	0
Reedy Lake	V101LCOR	V102KING						

## 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”):

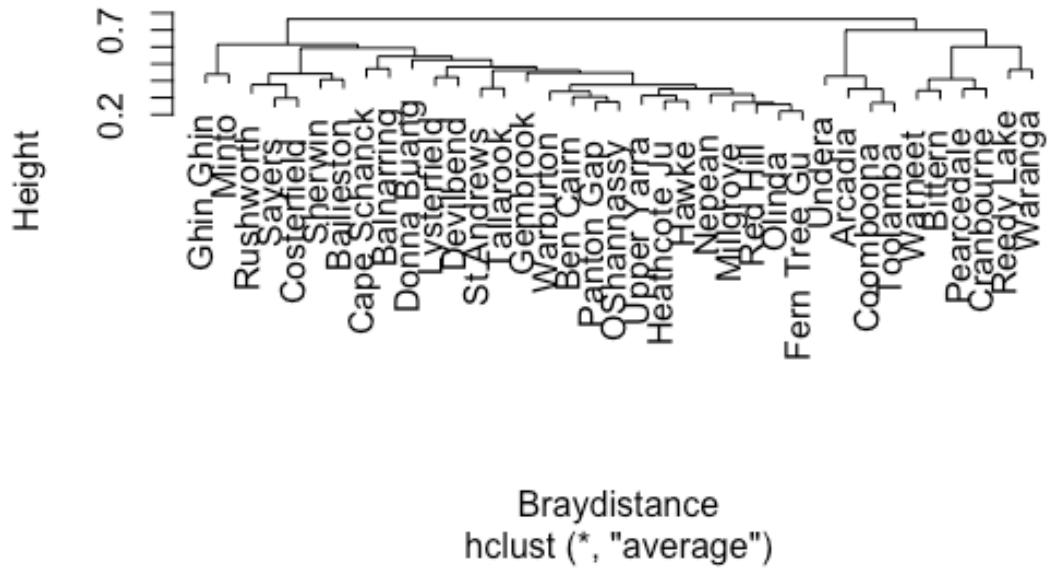
```
CODE
hc ← hclust(Braydistance, method = "average")
```

## Plot the Dendrogram

Plot the dendrogram:

```
CODE
plot(hc)
```

## Cluster Dendrogram

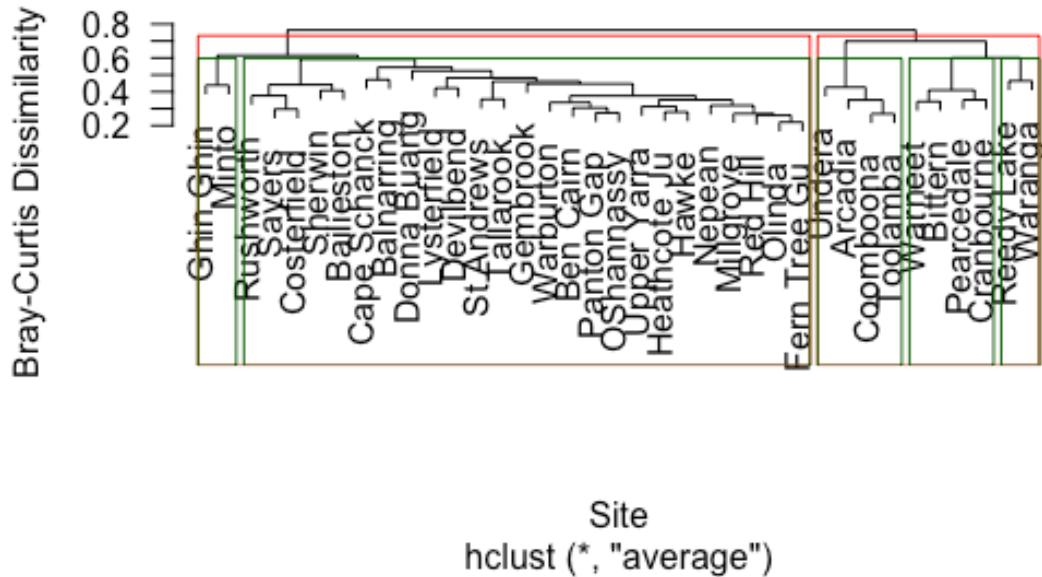


Braydistance  
hclust (\*, "average")

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.