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```
# import of data via clipboard

veg.data <- read.delim ('clipboard', row.names = 1)
env.data <- read.delim ('clipboard', row.names = 1)

# calculating distance matrix (square root transformation of data)
dis <- dist (sqrt (veg.data), 'euclidean')

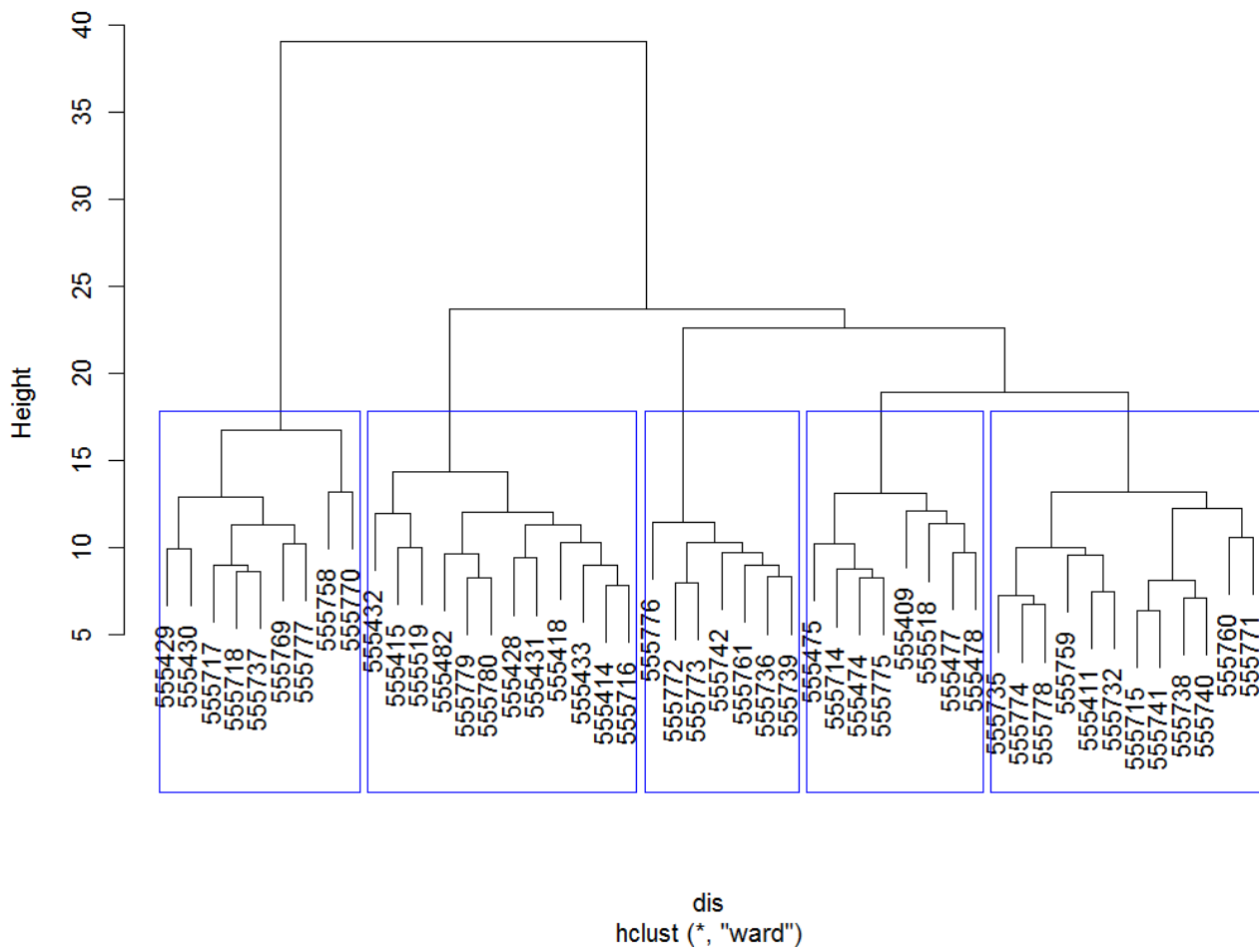
# classification using ward
cluster.ward <- hclust (dis, 'ward')

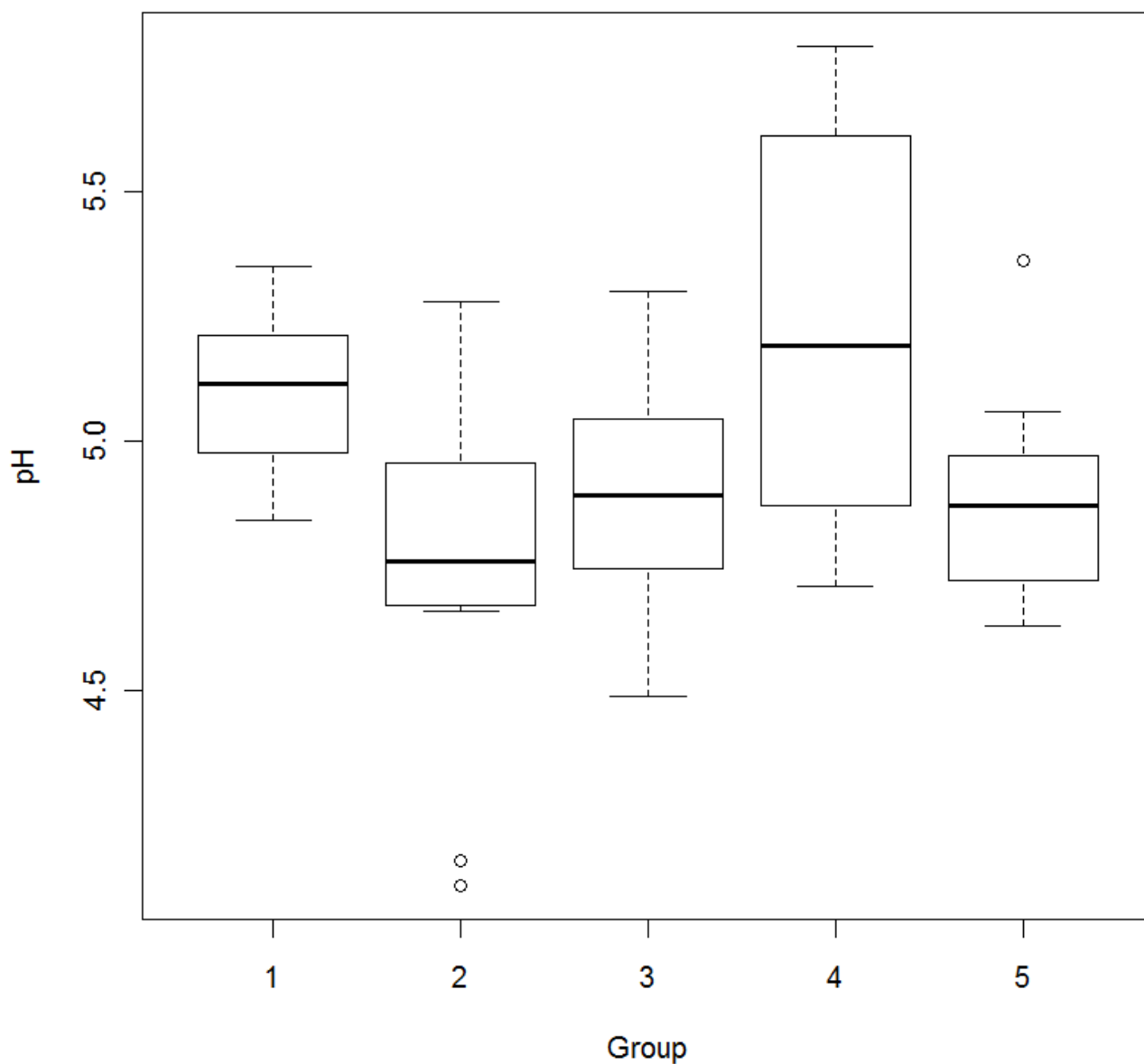
# plotting the dendrogram
plot (cluster.ward)

# plotting the boxes around
rect.hclust (cluster.ward, k = 5, border = 'blue')

# boxplot with differences in pH
cl <- cutree (cluster.ward, k = 5)
boxplot (env.data$pH.H ~ as.factor (cl), xlab = 'Group', ylab = 'pH')
```

Cluster Dendrogram





From:

<https://davidzeleny.net/anadat-r/> - **Analysis of community ecology data in R**

Permanent link:

https://davidzeleny.net/anadat-r/doku.php/cs:classification:solution_ex1

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