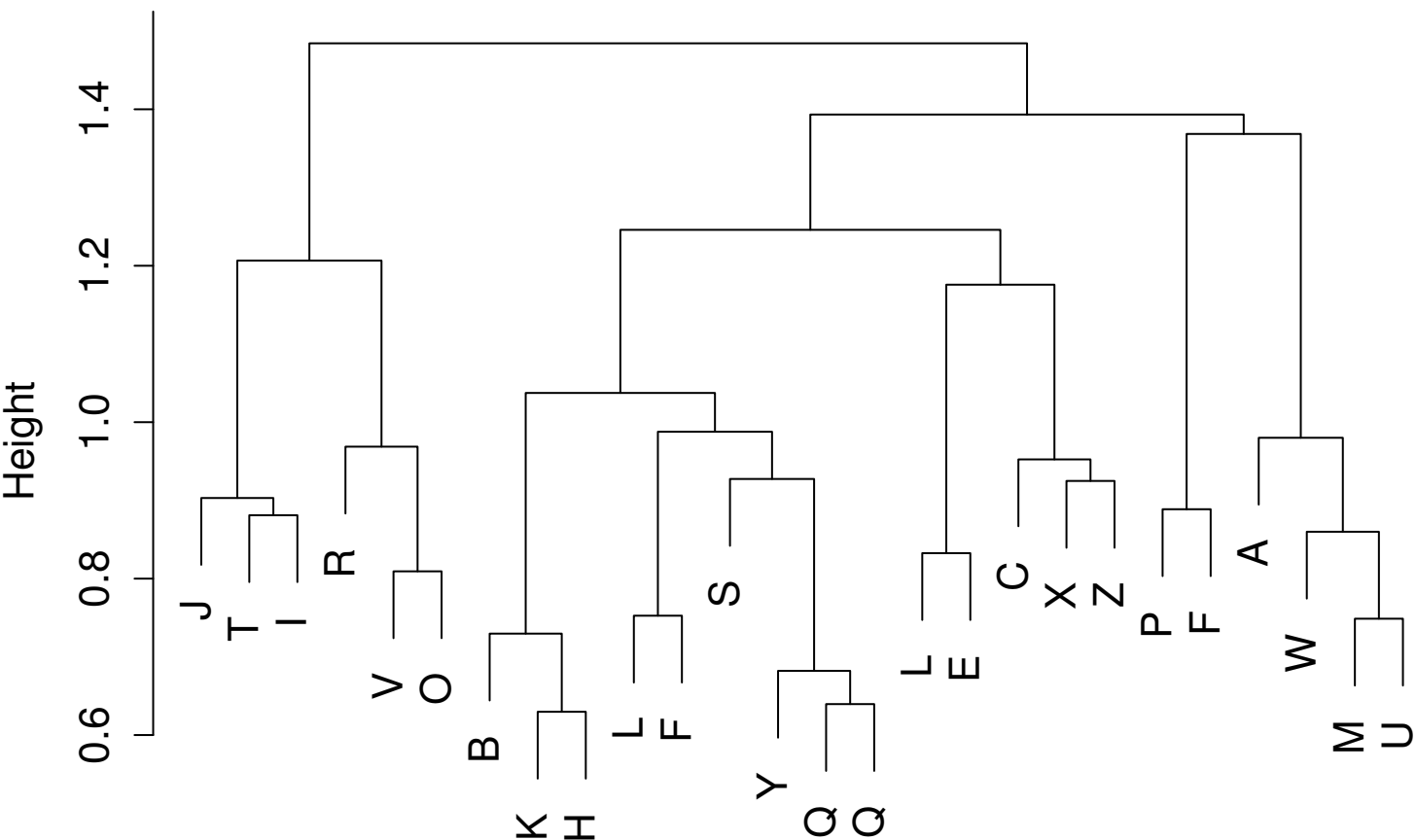


# Cluster Dendrogram



```
a <- dist(output$centers, method = "euclidean")  
hclust (*, "average")
```