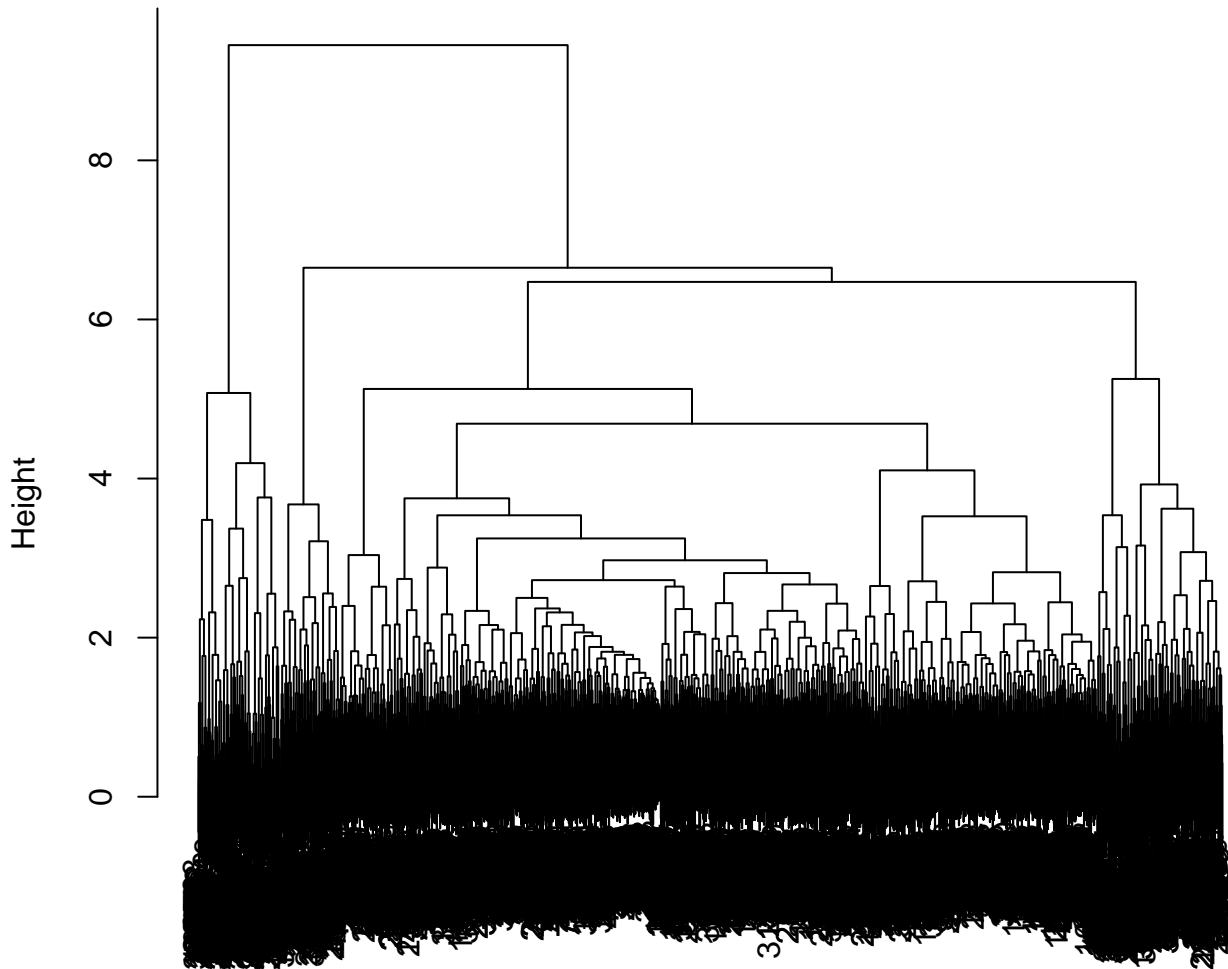


# Cluster Dendrogram



as.dist(1 - modelo\$proximity)  
hclust (\*, "ward.D2")