Cluster Dendrogram

Height
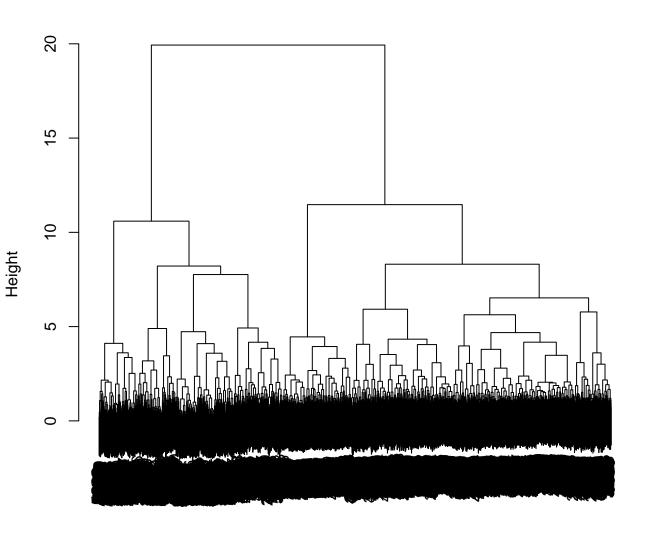
as.dist(1 − modelo$proximity)
hclust (*, "ward.D2")