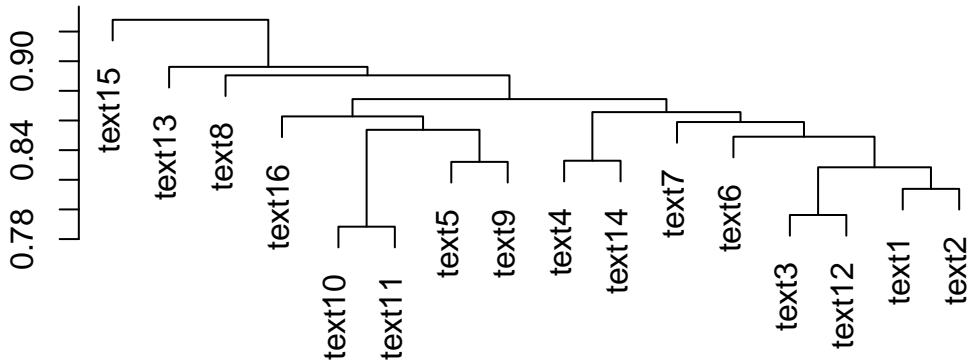


Cluster Dendrogram

Height



```
as.dist(1 - data.jac)  
hclust (*, "complete")
```