# DENDOGRAM



Height

3.0

2.0
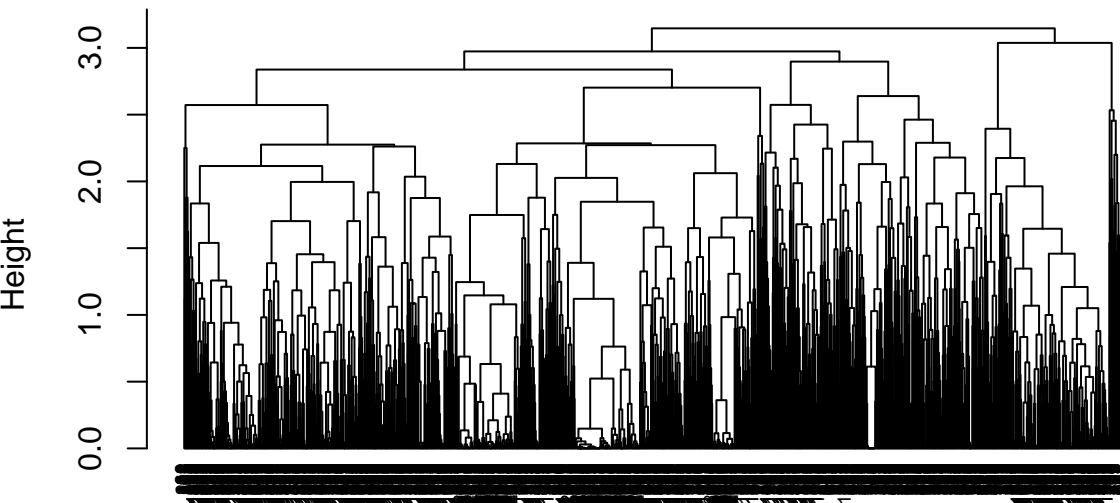
1.0

0.0

dist(obesity.cluster[, 1:15], method = "euclidean")
hclust (*, "complete")