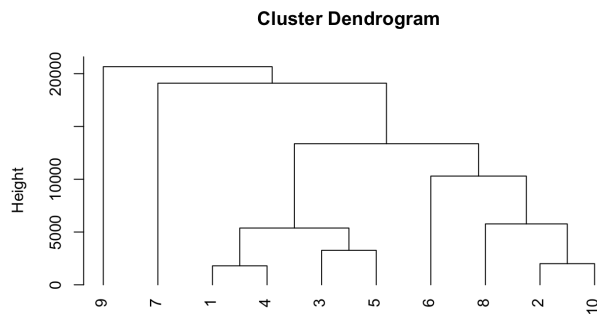


```

dim(DataTable)
d1 <- dist(DataTable[1:10,-1], method = "euclidean")
hc1 <- hclust(d1, method = "single")
hc1
plot(hc1, hang = -1, ann = TRUE)
memb1 <- cutree(hc1, k = 3)
memb1
centers1 <- aggregate(. ~ memb1, data = DataTable[1:10,-1], FUN = mean)
centers1

```



```

d1
hclust ("single")
DataTable <- sapply(DataTable[1:30,c(2:4, 7:10, 12:15)], scale)
dim(DataTable)
d.norm <- dist(DataTable, method = "euclidean")
hc2 <- hclust(d.norm, method = "single")
plot(hc2, hang = -1, ann = TRUE)
memb2 <- cutree(hc2, k = 4)
memb2
centers2 <- aggregate(. ~ memb2, data = data.frame(DataTable), FUN = mean)
centers2

```

