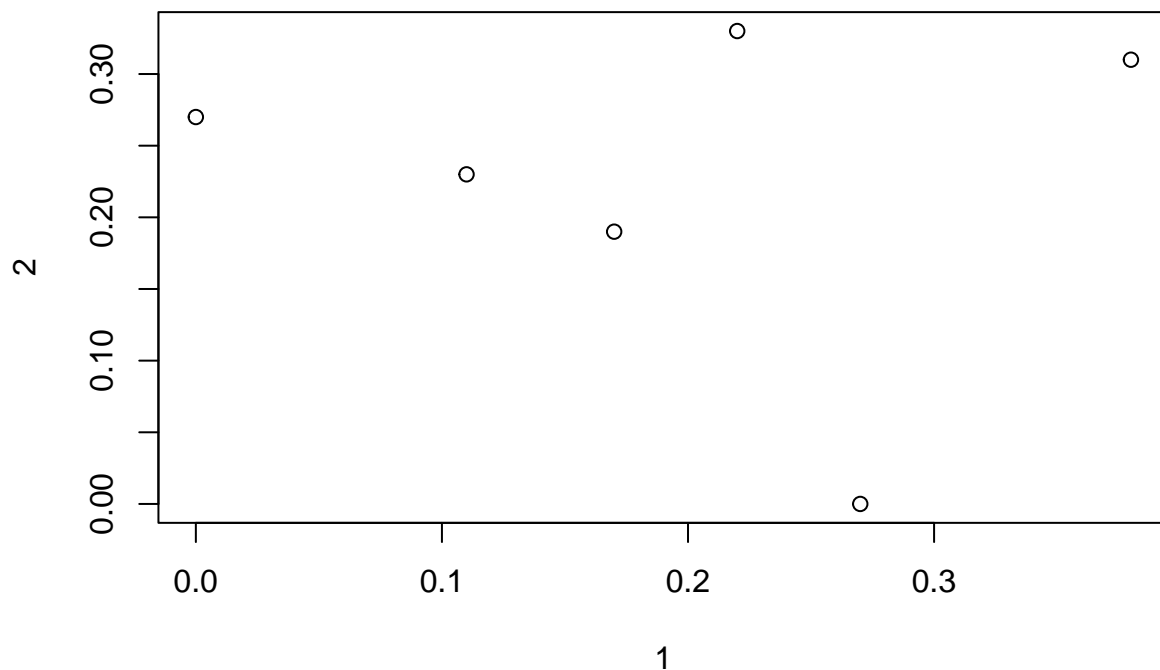


```

M = matrix(c(0, 0.27, 0.11,0.22, 0.38, 0.17, 0.27,
             0, 0.23, 0.33, 0.31,0.19, 0.11, 0.23,
             0, 0.37, 0.4, 0.25, 0.22, 0.33, 0.37,
             0, 0.29, 0.13, 0.38, 0.31, 0.4, 0.29,
             0,0.12, 0.17, 0.19, 0.25,0.13, 0.12, 0
             ), byrow = T, ncol = 6)
rownames(M) = c("1","2","3","4","5","6")
colnames(M) = c("1","2","3","4","5","6")

plot(M)

```



```

hc = hclust(dist(M), "complete")
hc$merge

```

```

##      [,1] [,2]
## [1,]  -1  -3
## [2,]  -4  -6
## [3,]  -2   1
## [4,]  -5   2
## [5,]   3   4

```

```

plot(hc, hang = -1)
b = cutree(hc, k = 2)
table(b)

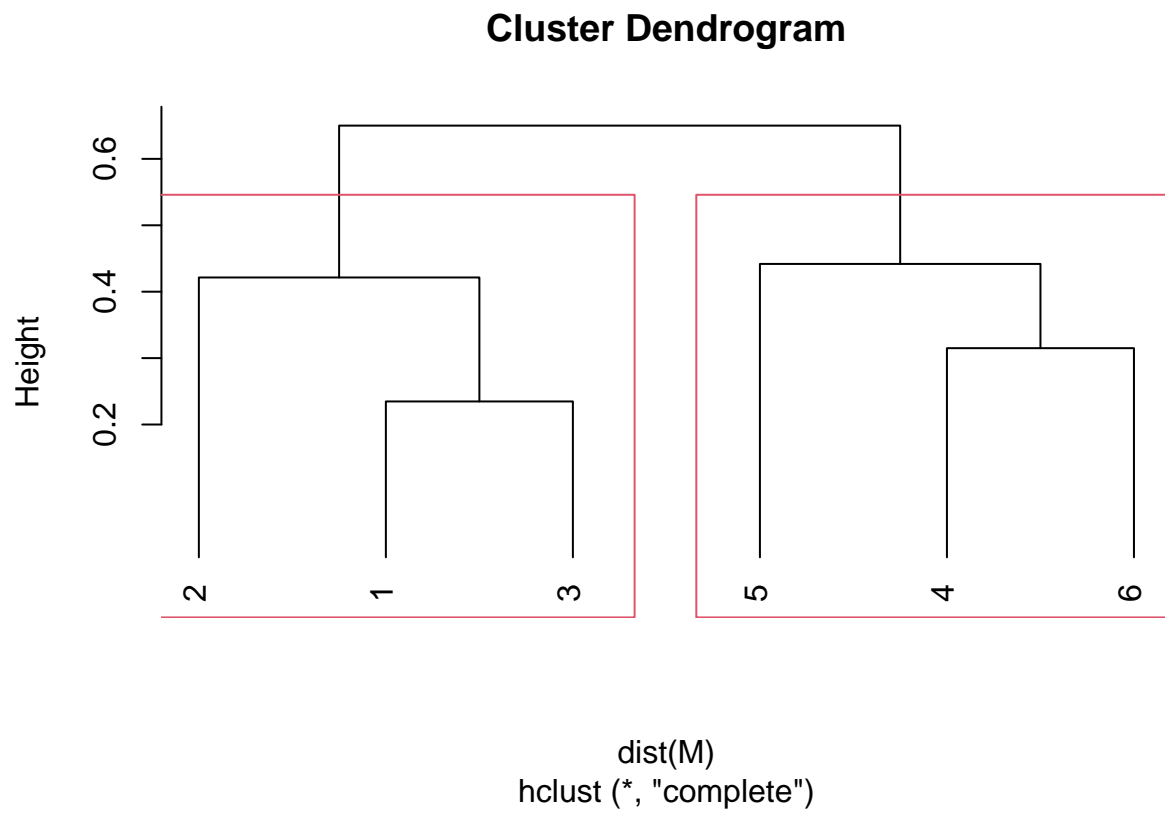
```

```
## b
## 1 2
## 3 3
```

```
(1:5)[b == 1]
```

```
## [1] 1 2 3
```

```
rect.hclust(hc, 2)
```



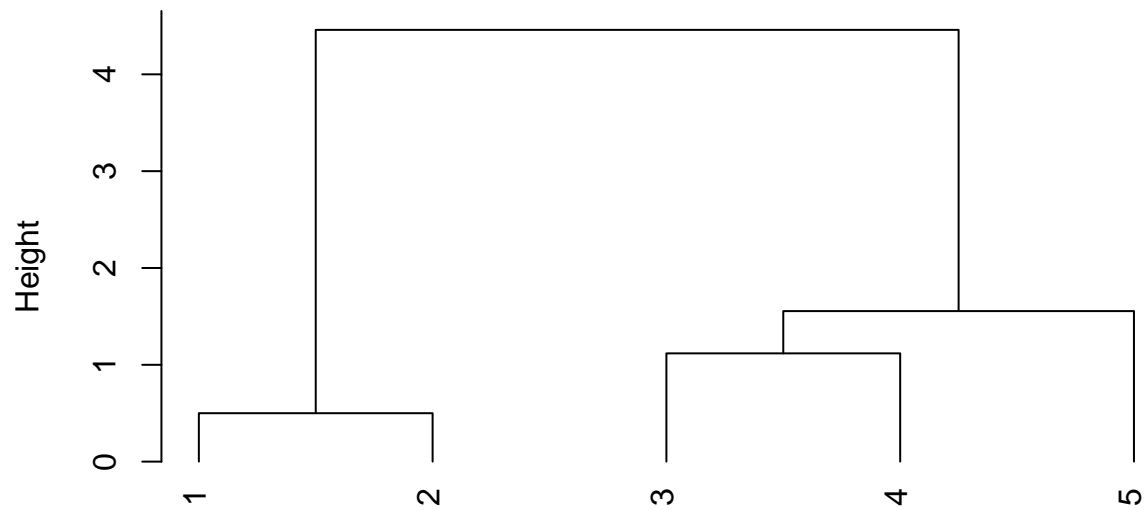
```
x = c(1, 1, 3, 4, 4, 2, 2.5, 1, 0.5, 2)
m = matrix(x, ncol = 2, nrow = 5)

m
```

```
##      [,1] [,2]
## [1,]    1  2.0
## [2,]    1  2.5
## [3,]    3  1.0
## [4,]    4  0.5
## [5,]    4  2.0
```

```
library(cluster)
ag = agnes(m, method = "ward")
pltree(ag, hang = -1)
```

**Dendrogram of `agnes(x = m, method = "ward")`**



m  
agnes (\*, "ward")