# Practice-module-08

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**Loading and scaling the Iris Dataset**

```
df <- iris #loading data
df <- scale(df [c(1:4)]) #scaling the data
library(cluster) #loading package
```

**Using agnes function and computing different linkage method**

```
hc_single <- agnes(df, method = "single")
hc_complete <- agnes(df, method = "complete")
hc_average <- agnes(df, method = "average")
```

**deciding which linkage method to use based on the values.**

```
print(hc_single$ac)
```

```
## [1] 0.8023794
```

```
## [1] 0.8023794
print(hc_complete$ac)
```

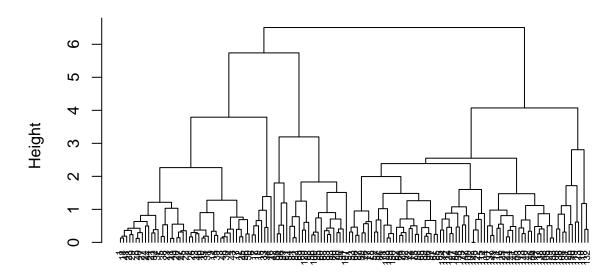```
## [1] 0.9438858
```

```
## [1] 0.9438858
print(hc_average$ac)
```

```
## [1] 0.9035705
```

```
## [1] 0.9035705
```

**as per the above computed value complete is the best linkage method**

**Ploting the dendrogram of the clustering results**

```
pltree(hc_complete, cex = 0.6, hang = -1, main = "Dendrogram of agnes")
```

## Dendrogram of agnes



df
agnes (*, "complete")