

NumberOfClusters

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```
pathTodata = "C:/Users/nz1413/Desktop/"
PathToReport = "C:/Users/nz1413/Desktop/AnalysisTag/DiseaseSubTypeDiscovery/Final/report/"

data <- t(read.table(paste(pathTodata, "/dataTAC/sputum_508genes.txt", sep = ""), header = TRUE))
dataScaled = scale(data)

library(factoextra)

## Loading required package: ggplot2

## Welcome! Related Books: `Practical Guide To Cluster Analysis in R` at https://goo.gl/13EFCZ

Methods= c("silhouette", "wss","gap_stat")
Clustering.method = c("kmeans", "hcut","pam")
pdf(paste(PathToReport , "numberOfClusters.pdf", sep=""))
set.seed(123)
for(emethod in Methods)
{
  # for average silhouette width
  fviz_nbclust(dataScaled, FUNcluster = kmeans, nstart=25, method = emethod, print.summary = TRUE)+
    geom_vline(xintercept = 4, linetype = 2)
}

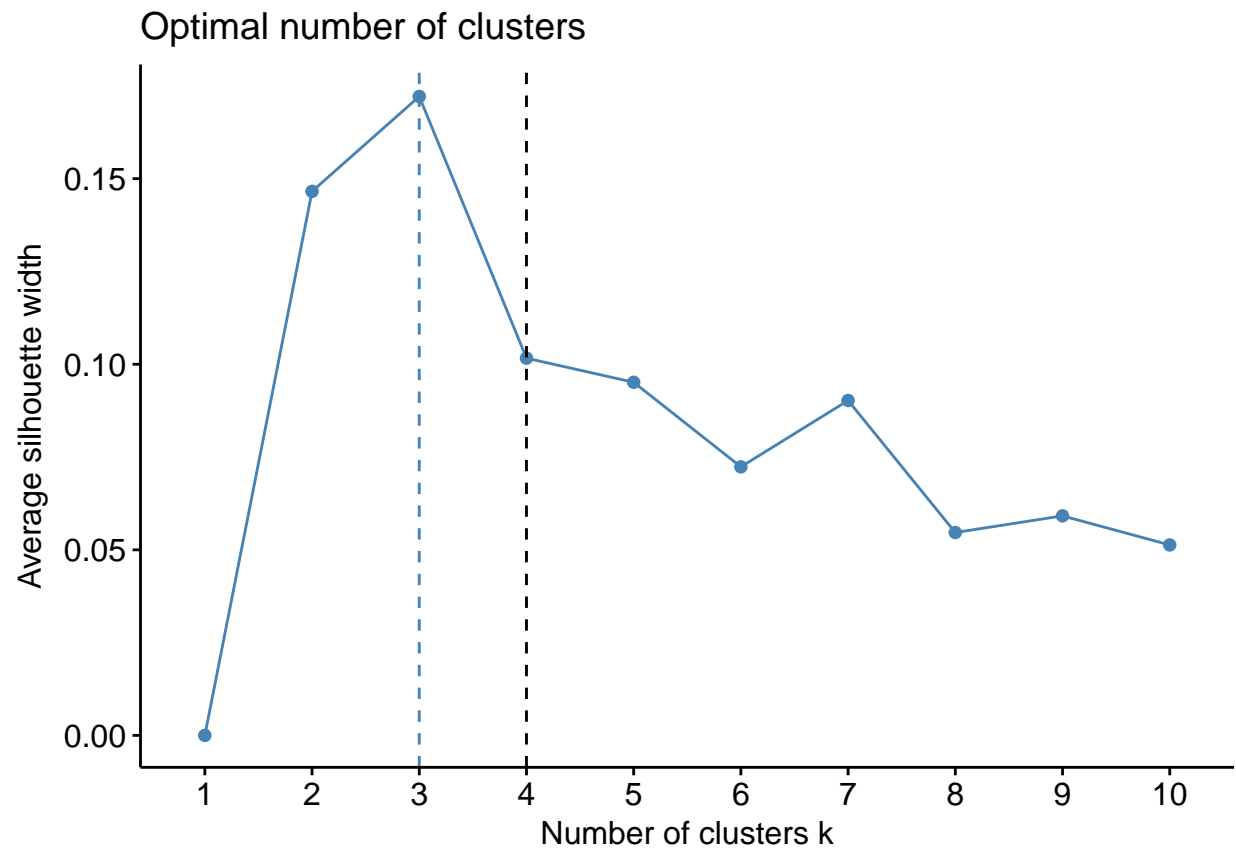
hc_method = "complete"

for(emethod in Methods)
{
  # for average silhouette width
  fviz_nbclust(dataScaled, FUNcluster = hcut, nstart=25, method = emethod, print.summary = TRUE)+
    geom_vline(xintercept = 4, linetype = 2)
}

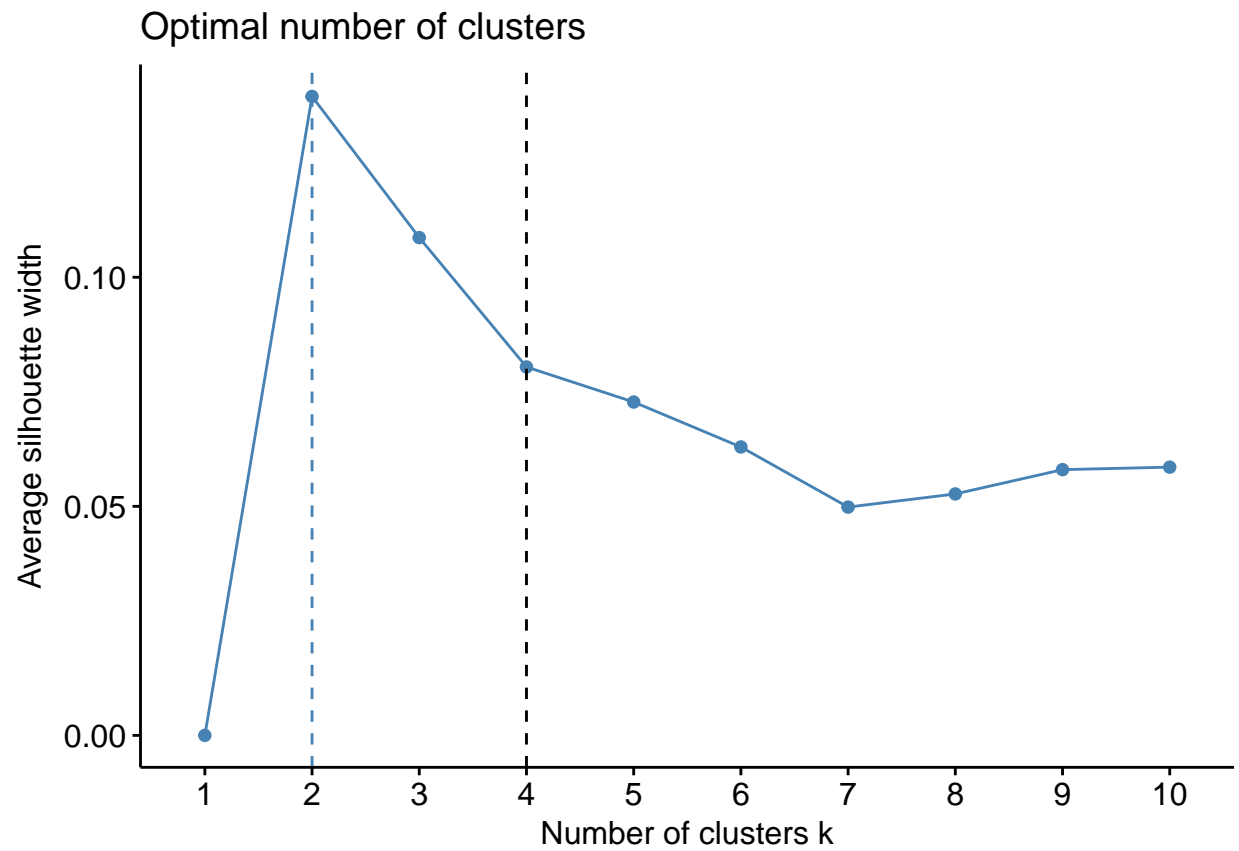
for(emethod in Methods)
{
  # for average silhouette width
  fviz_nbclust(dataScaled, FUNcluster = cluster::pam, method = emethod, print.summary = TRUE)
}
dev.off()

## pdf
## 2

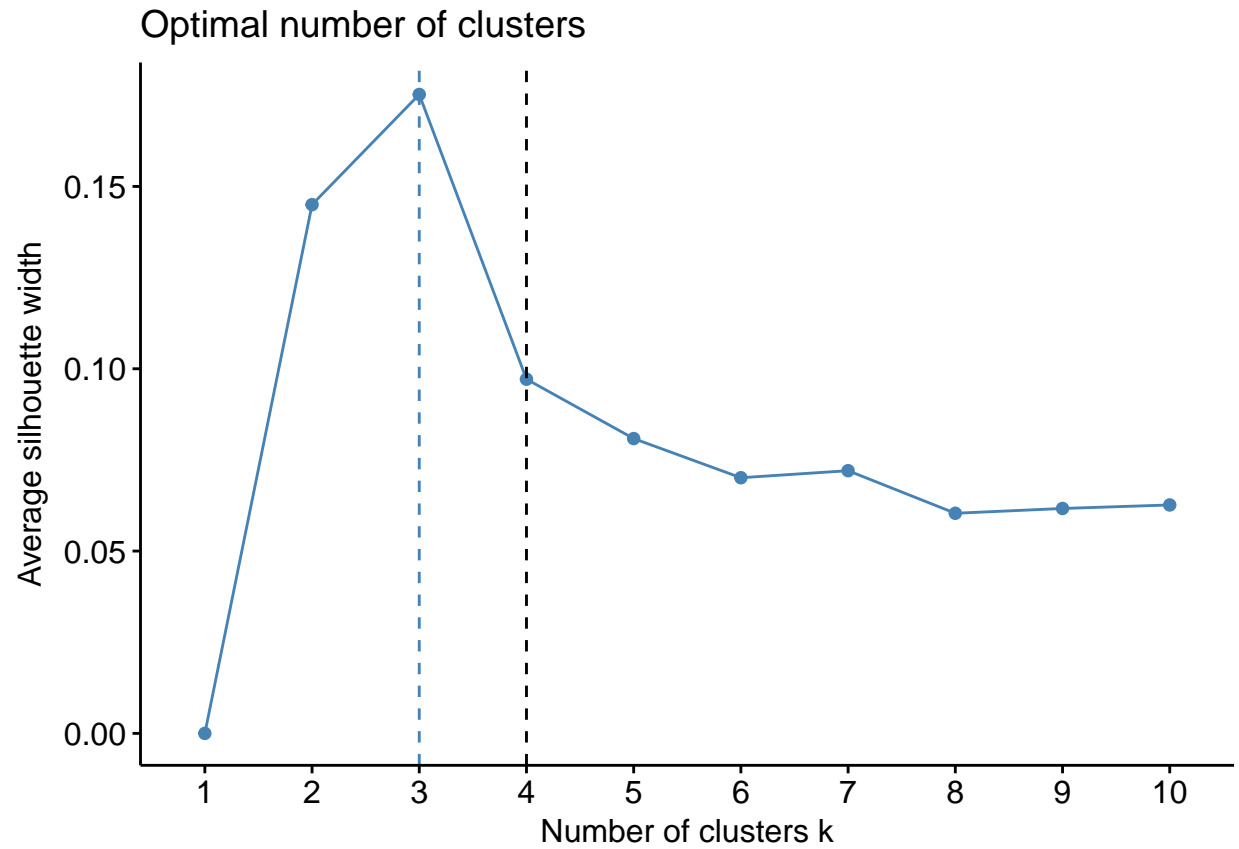
# for average silhouette width
fviz_nbclust(dataScaled, kmeans, nstart=25, method = "silhouette")+
  geom_vline(xintercept = 4, linetype = 2)
```



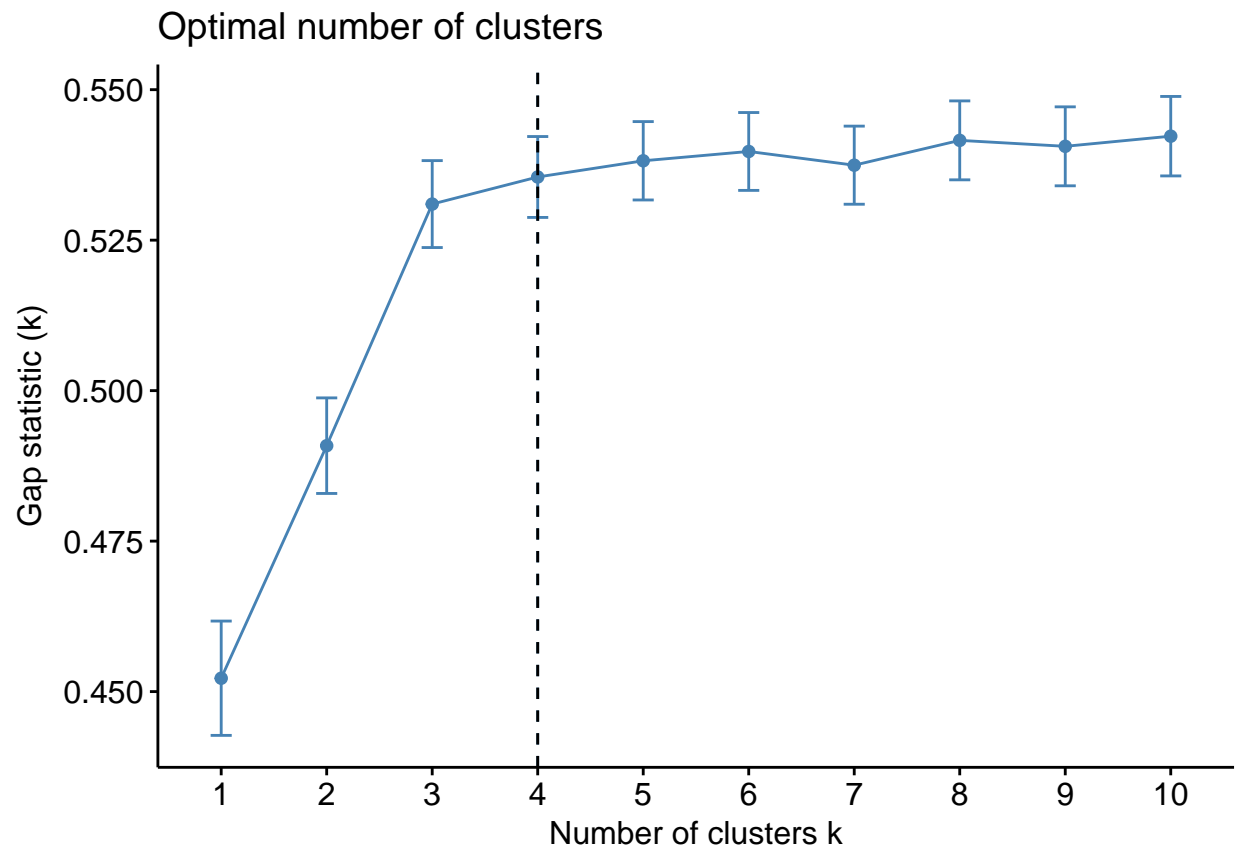
```
fviz_nbclust(dataScaled, cluster::pam, method = "silhouette")+  
  geom_vline(xintercept = 4, linetype = 2)
```



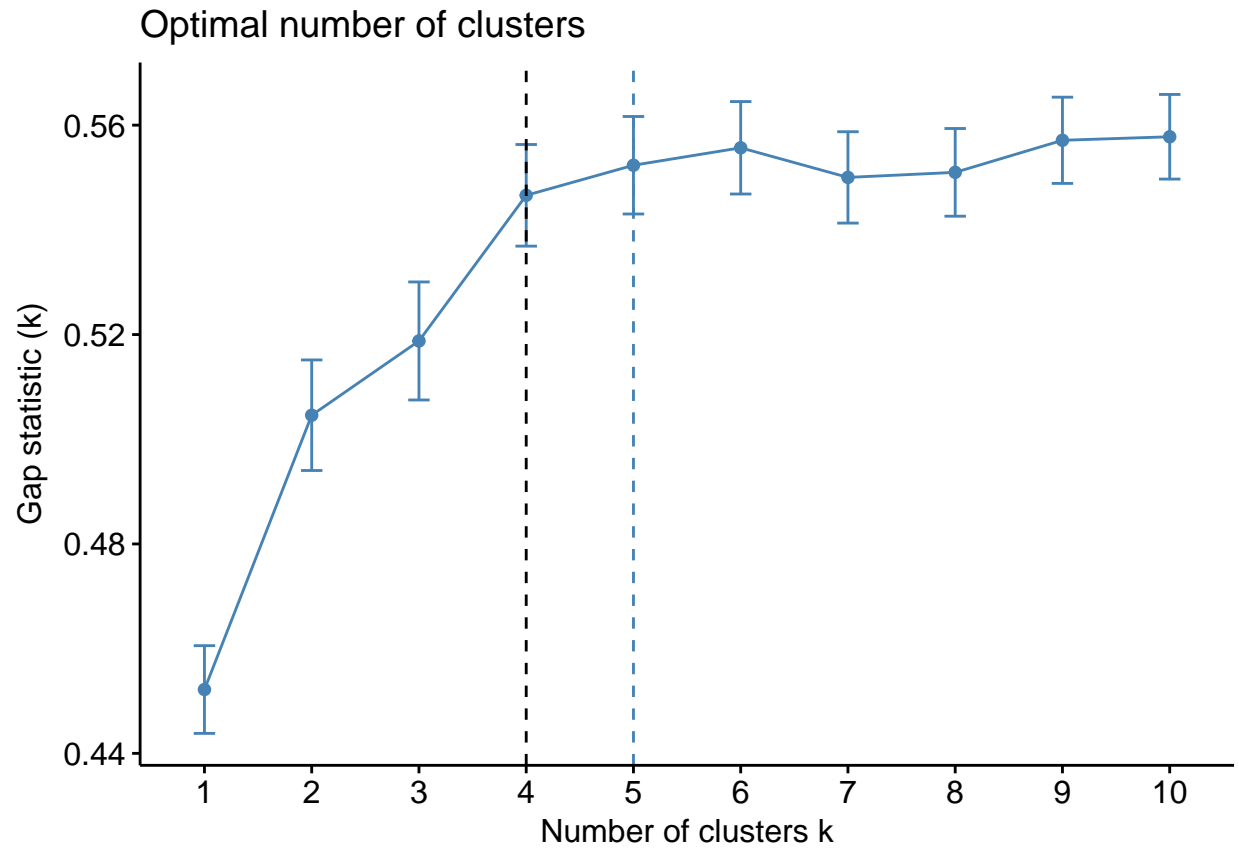
```
fviz_nbclust(dataScaled, hcut, method = "silhouette")+  
  geom_vline(xintercept = 4, linetype = 2)
```



```
# for gap statistics  
fviz_nbclust(dataScaled, kmeans, nstart=25, method = "gap_stat")+  
  geom_vline(xintercept = 4, linetype = 2)
```



```
fviz_nbclust(dataScaled, cluster::pam, method = "gap_stat")+  
  geom_vline(xintercept = 4, linetype = 2)
```



```
fviz_nbclust(dataScaled, hcut, method = "gap_stat")+  
  geom_vline(xintercept = 4, linetype = 2)
```

