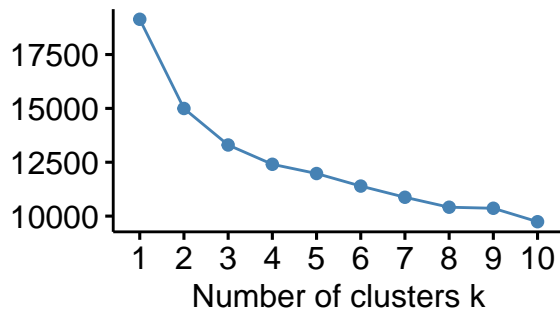


Optimal number of clusters
for kmeans (25% of genes)

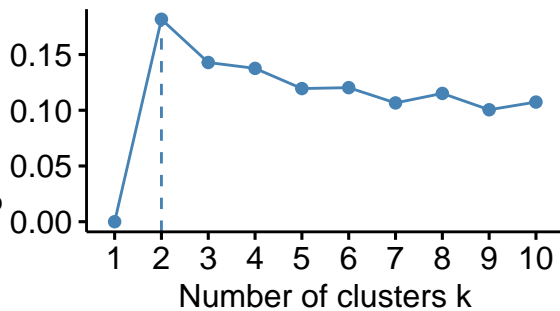
Total Within Sum of Square

Wss



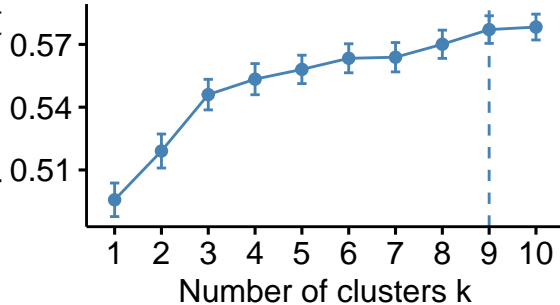
Average silhouette width

Silhouette



Gap statistic (k)

Gap



NbClust

