

Clustering: Measuring Cluster Goodness

Lecture/Practical-20

20/09/2021

Measuring Cluster Goodness

- Clustering models need to be evaluated.
- There are two methods for measuring cluster goodness.
 - Silhouette Method
 - Psuedo-F statistic
- Sum of Squares Error (SSE) is also a good measure of cluster quality.

- Any measure of cluster goodness , or cluster quality should address the concept of **cluster separation as well as cluster cohesion**. Cluster separation represents how distant the clusters are from each other. Cluster cohesion refers to how tightly related the records within the individual clusters.
- Sum of Squares Error (SSE) is a good measure of cluster quality. However, by measuring the distance between each record and its cluster center, SSE accounts only for cluster cohesion and does not account for cluster separation.
- SSE will monotonically decrease as the number of clusters increases which is not a desired property of a valid measure of cluster goodness.

Silhouette Method

- Silhouette is a characteristic of each data value and is defined as follows.
- For each data value i ,

$$\text{Silhouette}_i = (b_i - a_i) / \max(b_i, a_i)$$

where a_i is the distance between the data value and its cluster center and b_i is the distance between the data value and the next closest cluster center

Silhouette Value

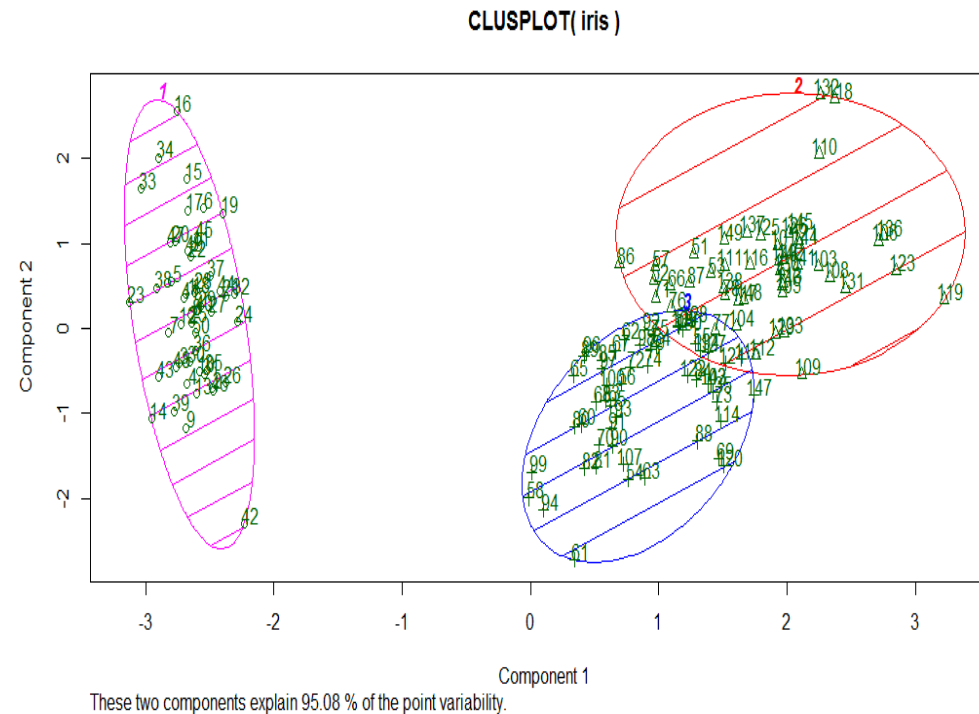
- It is used to assess how good the cluster assignment is for that particular point.
- A positive value indicates that the assignment is good with higher values being better than lower values.
- A value which is close to 0 is considered to be a weak assignment as the observation could have been assigned to the next closest cluster with limited consequence.
- A negative silhouette value is considered to be misclassified, as assignment to the next closest cluster would have been better.

Average Silhouette Value

- Taking the average silhouette value over all records yields a useful measure of how well the cluster solution fits the data.
- Interpretation
 - 0.5 or better: Good evidence of reality of the clusters in the data.
 - 0.25-0.5: some evidence of reality of clusters in the data.
 - Less than 0.25: Scant evidence of cluster reality

Plotting cluster plot (k=3)

- `clusplot(iris, km$cluster, color=TRUE, shade=TRUE, labels=2, lines=0)`



Silhouette Plot with average values

Silhouette plot of (x = km\$cluster, dist = dist)

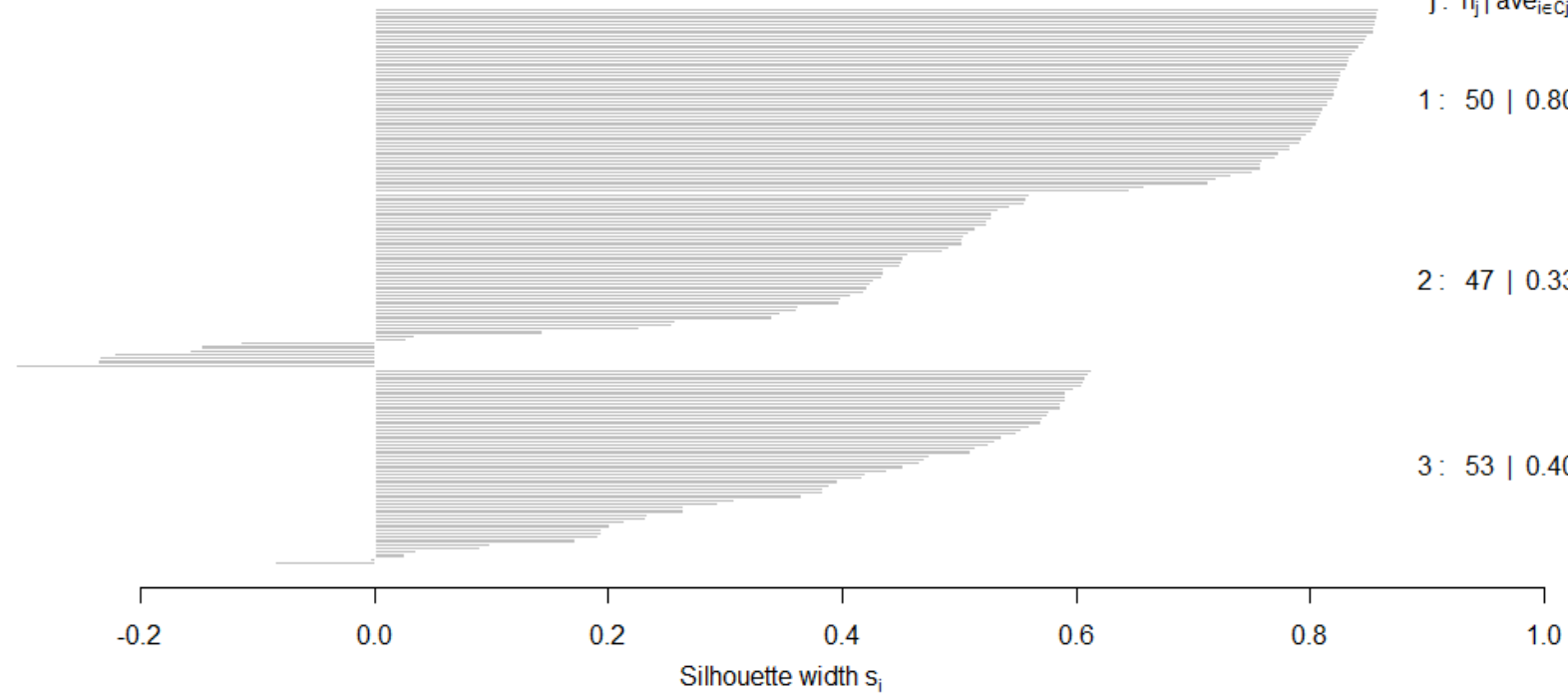
n = 150

3 clusters C_j
 $j : n_j \mid \text{ave}_{i \in C_j} s_i$

1: 50 | 0.80

2: 47 | 0.33

3: 53 | 0.40

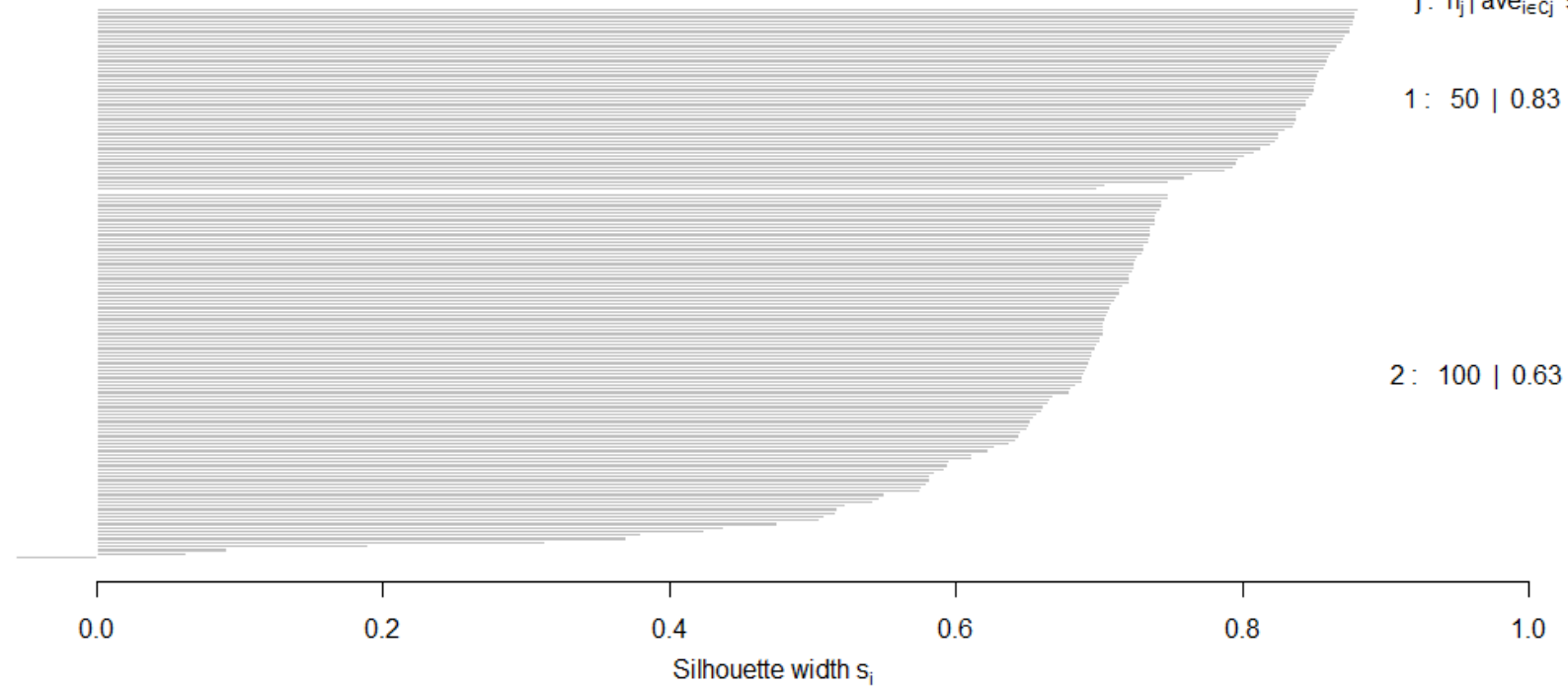


Average silhouette width : 0.51

Silhouette Analysis(k=2)

Silhouette plot of (x = km\$cluster, dist = dist)

n = 150



Pseudo-F statistic

- Pseudo-F statistic can be considered as one of the main method for determining the number of clusters.
- It compares the between-cluster to the within-cluster sum-of-squares.

- $$Pseudo - F = \frac{\left[\text{between-cluster-sum-of-squares} / (k-1) \right]}{\left[\text{within-cluster-sum-of-squares} / (n-k) \right]}$$

- where k the number of clusters and n the number of observations.
- Large Pseudo-F statistic indicates distinct clusters or peaks in the pseudo F statistic are indicators of greater cluster separation.

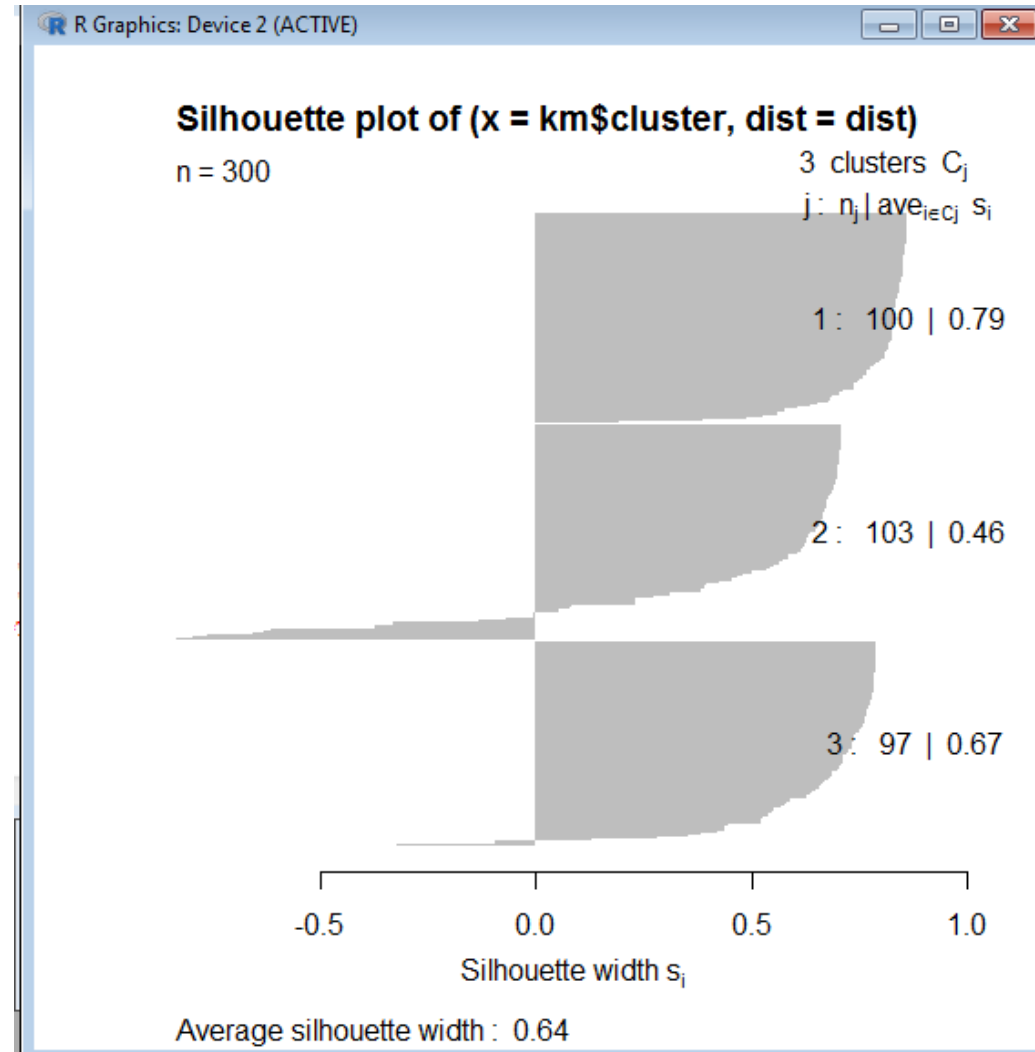
Using pseudo-F to select optimal number of clusters

- Use a clustering algorithm to develop a clustering solution for a variety of values of k
- Calculate the pseudo-F statistic and p-value for each candidate, and select the candidate with smallest p-value as the best clustering solution.
- Note : It has been written that the best clustering model is the one with largest value of pseudo-F. This is Not always correct. One must account for different d.f. $(k-1)$ and $(n-k)$ for each model.

Silhouette values and plot: R zone(income data)

- `dist<- dist(income, method ="euclidean")`
- `sil<-silhouette(km$cluster, dist)`
- `plot(sil)`

Silhouette values and plot



R zone: pseudo-F and p-value(income data)

- `library(clusterSim)`
- `n<-dim(income)[1]`
- `psF1<-index.G1(income,cl=km$cluster)`
- `psF1`
- `#The hypothesis being tested are the following`
- `#H0:There are no clusters in the data`
- `#H1:There are k clusters in the data.`
- `pf(psF1,3,n-3)`
- `#p value is not rejecting the Null Hypothesis`
- `psF2<-index.G1(income,cl=km1$cluster)`
- `psF2`
- `pf(psF2,2,n-2)`