

Statistics 452: Statistical Learning and Prediction

Chapter 10, part 2: Cluster Analysis

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Clustering

- ▶ Clustering is a set of techniques for finding *subgroups*, or clusters, in a data set.
- ▶ A good set of clusters is a partition of the data such that observations are *similar* within clusters and *dissimilar* between clusters.
- ▶ Example: Suppose we have n observations of p features for cancer patients.
 - ▶ We can cluster to look for cancer sub-types.
 - ▶ However, these clusters will be highly dependent on how we measure similarity/dissimilarity.
 - ▶ Plus, we don't *know* that clusters correspond to cancer sub-types.

Clustering as Dimension Reduction

- ▶ We can view clustering as an exploratory method to understand possible structure in our data.
- ▶ Similar in spirit to PCA, but a different mechanism
 - ▶ PCA finds a low-dimensional representation of observations explaining a good proportion of the variance
 - ▶ Clustering looks to find homogeneous sub-groups.

Clustering Methods

- ▶ There are many.
- ▶ We focus on K -means/medoids and hierarchical clustering, and assume all features are quantitative.
- ▶ In K -means we partition into a pre-specified number of clusters.
- ▶ In hierarchical clustering we successively group observations.
 - ▶ Represent the nested partitions as a tree-like structure called a *dendrogram*.

K-means Clustering

- ▶ Choose the desired number of clusters, K . The K -means clustering algorithm will assign each observation to *exactly one* of the K clusters.
- ▶ Let C_k be the set of indices for observations assigned to cluster k , $k = 1, \dots, K$.
- ▶ K -means clustering chooses clusters to solve

$$\min_{C_1, \dots, C_K} \sum_{k=1}^K W(C_k),$$

where $W(C_k)$ is a measure of the amount by which observations within cluster C_k differ from one another.

K-means Clustering: Choice of $W(C_k)$

- ▶ For continuous variables, the standard choice for $W(C_k)$ is the squared Euclidean distance,

$$W(C_k) = \frac{1}{|C_k|} \sum_{i,i' \in C_k} \sum_{j=1}^p (x_{ij} - x_{i'j})^2$$

where $|C_k|$ denotes the number of observations in cluster k .

- ▶ It turns out that

$$\frac{1}{|C_k|} \sum_{i,i' \in C_k} \sum_{j=1}^p (x_{ij} - x_{i'j})^2 = 2 \sum_{i \in C_k} \sum_{j=1}^p (x_{ij} - \bar{x}_{kj})^2$$

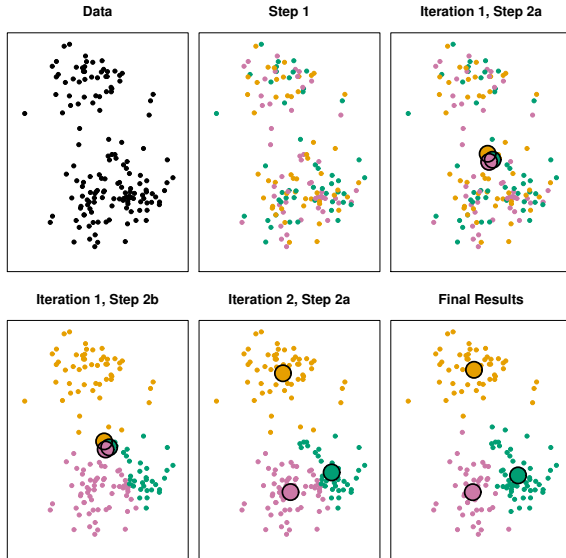
where the *cluster centroid* $\bar{x}_{kj} = \frac{1}{|C_k|} \sum_{i \in C_k} x_{ij}$.

- ▶ We can see where the name “K-means” comes from.

K-means Clustering Algorithm

1. Randomly assign a number, from $1, \dots, K$ to each of the observations. They serve as the initial cluster assignments for the observations.
2. Iterate the following steps until the cluster assignments stop changing:
 - 2.1 For each of the K clusters, compute the cluster centroid.
The k th cluster centroid is the vector of the p feature means for the observations in the k th cluster for continuous variables.
 - 2.2 Assign each observation to the cluster whose centroid is closest in terms of Euclidean distance.

K-means Clustering Algorithm, Simulated Data Example



K-means Clustering and Local Minima

- ▶ The algorithm is guaranteed to decrease the value of $\sum_k W(C_k)$ until no further improvement is possible, resulting in a *local* minimum.
- ▶ However, the local min depends on the random initialization. Hence, in practice we re-run the algorithm several times and keep the solution that achieves the lowest overall criterion value.
- ▶ See the video demo at <http://www.youtube.com/watch?v=zaKjh2N8jN4>.

K-means Clustering with Different Initialization



Text, Fig 10.7. K -means clustering performed six times on the same data with $K = 3$ different random initializations. Above each plot is the value of the objective function. Three different local optimums were found. The overall minimum is 235.8.

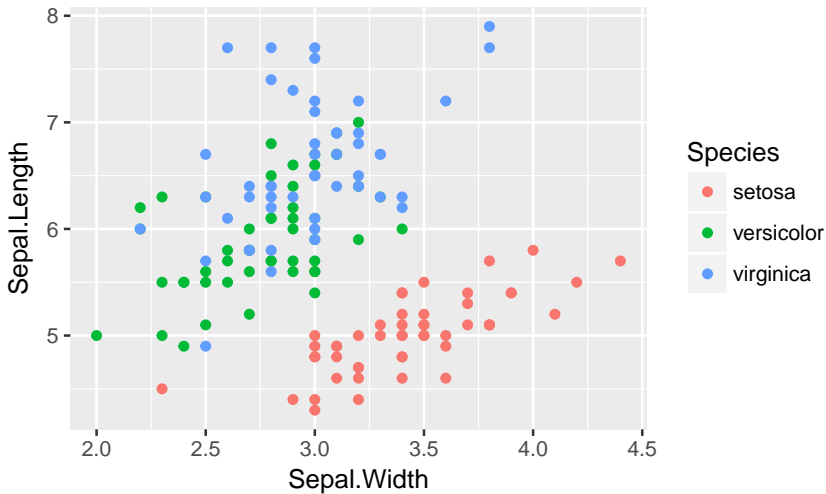
K Means Clustering of the Iris Data

- We know there are three species of iris. Ignore the species labels and do the clustering.

```
library(ggplot2)
data(iris) # help(iris)
head(iris) # plot sepal length vs width with labels
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3.0	1.4	0.2	setosa
## 3	4.7	3.2	1.3	0.2	setosa
## 4	4.6	3.1	1.5	0.2	setosa
## 5	5.0	3.6	1.4	0.2	setosa
## 6	5.4	3.9	1.7	0.4	setosa

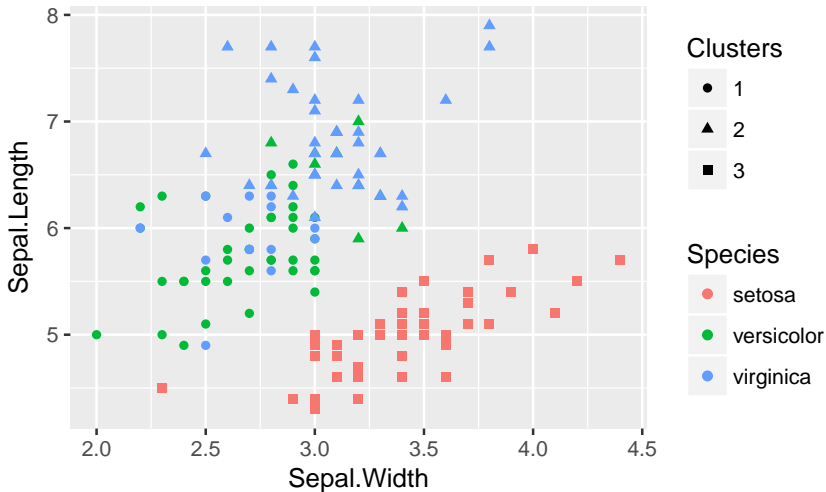
```
ggplot(iris,aes(x=Sepal.Width,y=Sepal.Length,color=Species)) +  
  geom_point()
```



```
library(dplyr)
irisX <- iris %>% select(-Species) %>% scale()
kout3 <- kmeans(irisX,centers=3,nstart=10)
iris <- data.frame(iris,Clusters=factor(kout3$cluster))
with(iris,table(Species,Clusters))
```

```
##           Clusters
## Species      1  2  3
##  setosa       0  0 50
##  versicolor  39 11  0
##  virginica   14 36  0
```

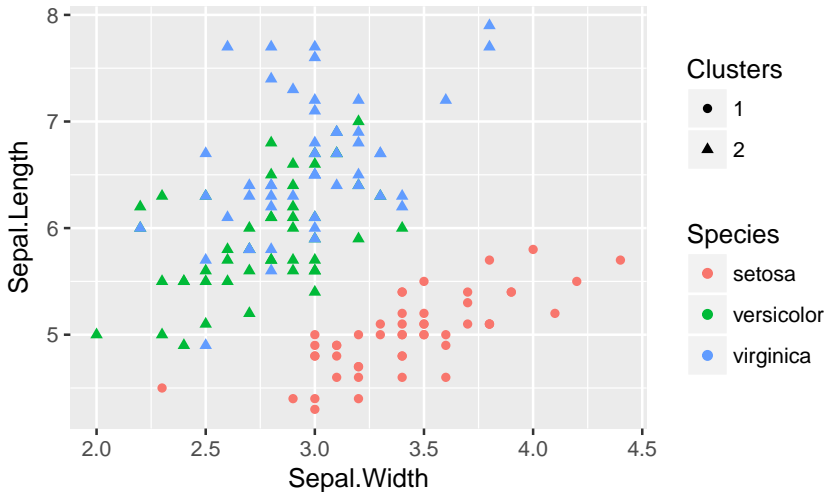
```
ggplot(iris,  
  aes(x=Sepal.Width,y=Sepal.Length,color=Species,shape=Clusters)) +  
  geom_point()
```



```
kout2 <- kmeans(irisX,centers=2,nstart=10)
iris$Clusters <- factor(kout2$cluster)
with(iris,table(Species,Clusters))
```

```
##           Clusters
## Species      1  2
##   setosa     50  0
##   versicolor  0 50
##   virginica   0 50
```

```
ggplot(iris,  
  aes(x=Sepal.Width,y=Sepal.Length,color=Species,shape=Clusters)) +  
  geom_point()
```



Scaling Variables

- ▶ Whether or not to scale variables depends on the context, but usually we will.

Choosing K

- ▶ Like PCA, there is no “best” method for choosing K .
- ▶ Cross-validation is not an option because there is no outcome.
- ▶ For small p , can visualize the clusters, but this becomes difficult as p grows.
- ▶ The silhouette plot is a graphical approach.
 - ▶ Discussed after the PAM algorithm below.

Sensitivity to Outliers

- ▶ Means and Euclidean distances are sensitive to outliers and K -means depends on both
 - ▶ Means are cluster centroids.
 - ▶ Criterion to minimize is a sum of squared Euclidean distances.

K-Medoids Clustering

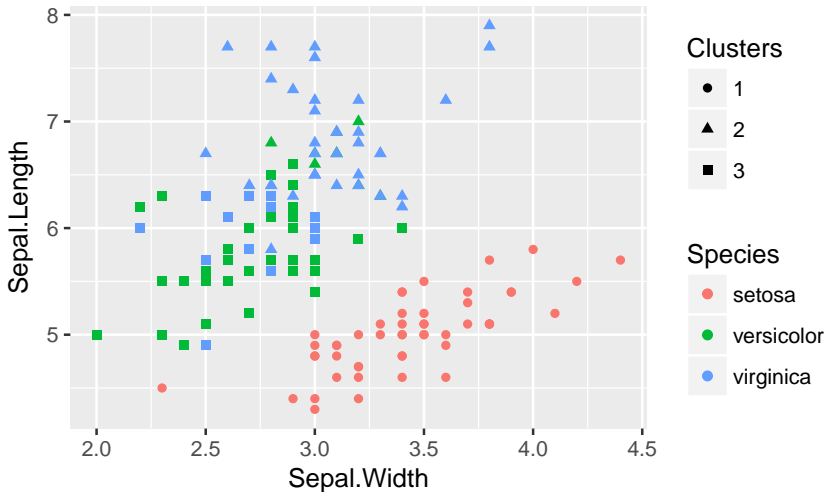
- ▶ An alternative to K -means is K -medoids clustering.
- ▶ Cluster centres are medoids, which are observations chosen to represent each cluster.
- ▶ There is flexibility in choosing the dissimilarity measure
 - ▶ Can choose a more robust measure, such as ℓ_1 (so-called Manhattan) distance.
- ▶ An implementation of K -medoids is the PAM (partitioning around medoids) algorithm.

PAM on the Iris Data

```
library(cluster)
pout3 <- pam(irisX,k=3)
iris$Clusters <- factor(pout3$cluster)
with(iris,table(Species,Clusters))
```

```
##           Clusters
## Species      1  2  3
##  setosa      50  0  0
##  versicolor  0  9 41
##  virginica   0 36 14
```

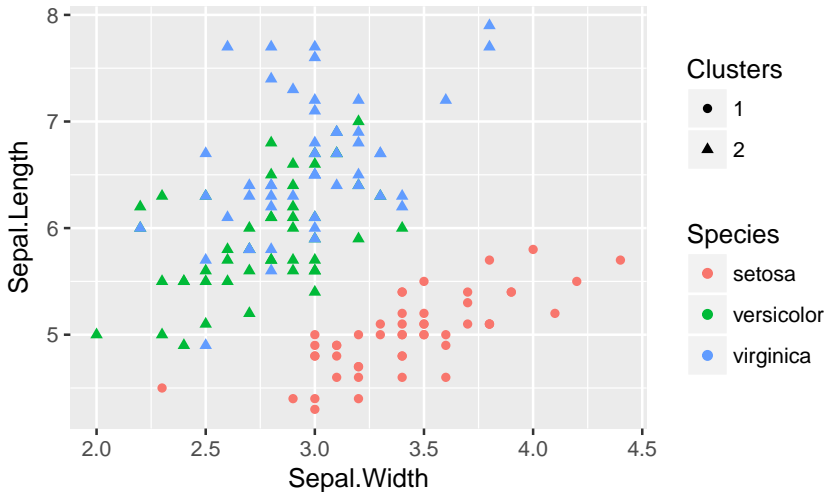
```
ggplot(iris,  
  aes(x=Sepal.Width,y=Sepal.Length,color=Species,shape=Clusters)) +  
  geom_point()
```



```
pout2 <- pam(irisX,k=2)
iris$Clusters <- factor(pout2$cluster)
with(iris,table(Species,Clusters))
```

```
##              Clusters
## Species        1  2
##   setosa       50  0
##   versicolor   0 50
##   virginica    0 50
```

```
ggplot(iris,  
  aes(x=Sepal.Width,y=Sepal.Length,color=Species,shape=Clusters)) +  
  geom_point()
```



The Silhouette Plot

- ▶ For each observation we compute a measure of cluster certainty, called the silhouette width, that takes values in $[-1, 1]$.
 - ▶ Values near 1 indicate certainty that the observation is in the right cluster and
 - ▶ Values near -1 indicate that the observation is in the wrong cluster.
- ▶ Formula for silhouette width is given in on the next slide.
- ▶ If the silhouette values in a cluster are, say, below average, this suggests the cluster can be merged with another.

Silhouette Widths

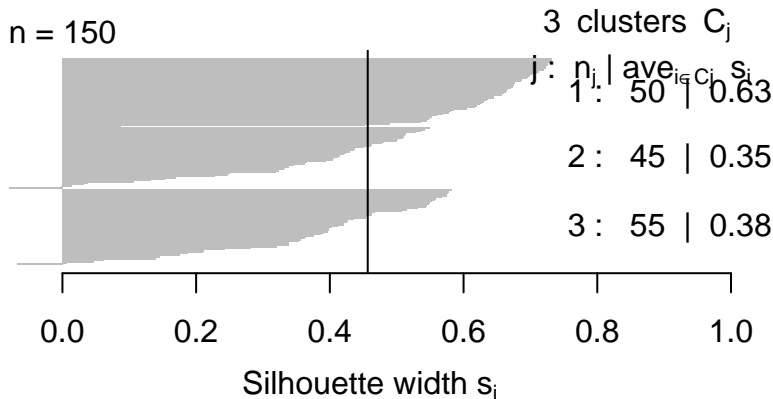
- ▶ For observation i in cluster k , the silhouette width $s(i)$ is defined as follows.
- ▶ Let $a(i)$ be the average dissimilarity between i and all other observations in cluster k .
- ▶ Let $d(i, C)$ be the average dissimilarity between i and all observations in cluster C .
- ▶ Let $b(i) = \min_C d(i, C)$.
- ▶ Then

$$s(i) = \frac{b(i) - a(i)}{\max(a(i), b(i))}$$

- ▶ Note: $a(i)$ is a *dissimilarity* measure, and should be $\ll b(i)$ if i confidently in cluster k .

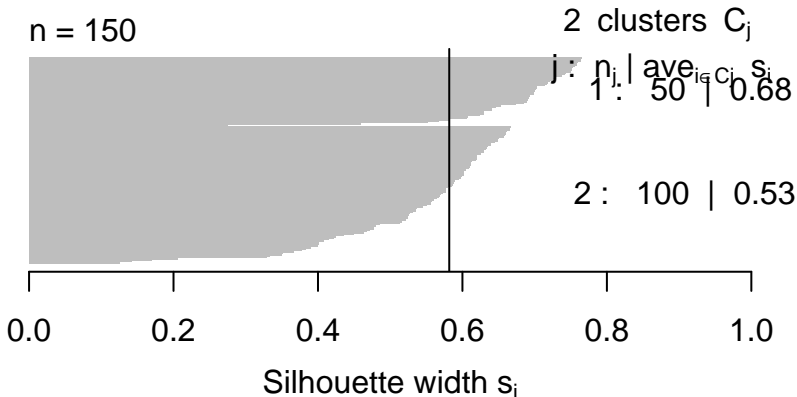
Silhouette Plots for the Iris Data

```
sil3 <- silhouette(pout3)
plot(sil3, main=""); abline(v=mean(sil3[, "sil_width"]))
```



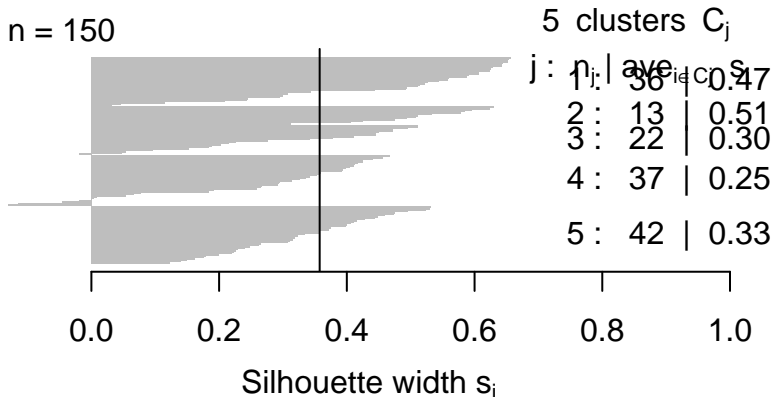
Average silhouette width : 0.46

```
sil2 <- silhouette(pout2)
plot(sil2,main=""); abline(v=mean(sil2[, "sil_width"]))
```



Average silhouette width : 0.58

```
sil5 <- silhouette(pam(irisX,k=5))
plot(sil5,main=""); abline(v=mean(sil5[, "sil_width"]))
```



Average silhouette width : 0.36