

# Lectures 5, 6: Unsupervised learning, cluster analysis

Data Science 2  
CS 109b, Stat 121b, AC 209b, E-109b

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Reading: James et al., chapter 10.

## Basics of unsupervised learning

- Want to discover subgroups among variables or observations, but not in how they relate to a response variable.
- Usually no precise goal of analysis. Often can be used as a descriptive tool.
- Often easier to obtain data without a response variable.

We will focus on cluster analysis.

## Example applications

- Collect breast cancer patients; want to find subgroups according to similar gene expressions.
- Obtain browser usage and purchasing history of online shoppers; want to find subgroups that relate to their browsing and purchasing patterns.
- Want to group movies according to ratings assigned by movie viewers.

## Difference in attitude between PCA and clustering

Both are multivariate techniques, but with slightly different goals.

- PCA (principal components analysis) attempts to find a low-dimensional representation of the observations that explains a large fraction of the variation. Often used for variable reduction (as you have seen in CS109a), but can also be helpful for visualization in seeing groupings of data.
- Clustering instead seeks homogeneous subgroups among the observations.

## Cluster analysis outline

- Inter-observation distances

- Partition-based clustering
- Hierarchical clustering
- Diagnostics, and optimizing the number of clusters
- Graphs, graphs and more graphs

## Clustering

- Cluster analysis consist of techniques for finding subgroups or clusters in a multivariate data set.
- Want to partition the data into distinct groups so that observations within each group are similar to each other.
- Need to define concretely what it means for observations to be similar or different. This is usually domain-specific.

## Notation

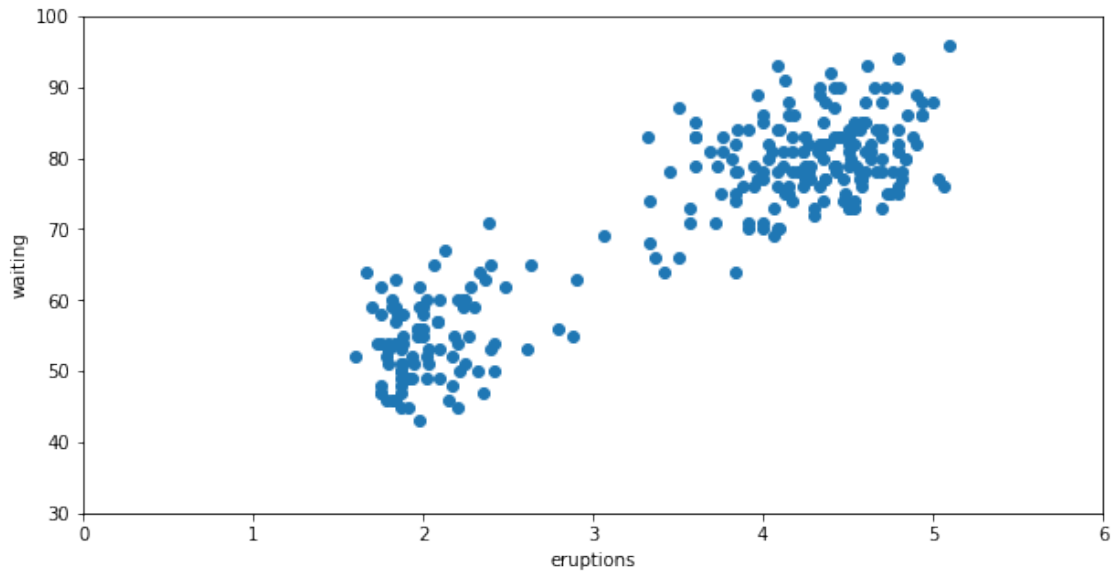
- Assume  $n$  observations are measured on  $p$  variables or features.
- Let  $X$  be an  $n \times p$  matrix of data. Let  $X_{ij}$ , for  $i = 1, \dots, n$  and  $j = 1, \dots, p$ , be the value of feature  $j$  on observation  $i$ .
- Interested in finding subsets of rows of  $X$  that are similar to each other, which will form a "cluster."

## Simple example: Eruptions of Old Faithful

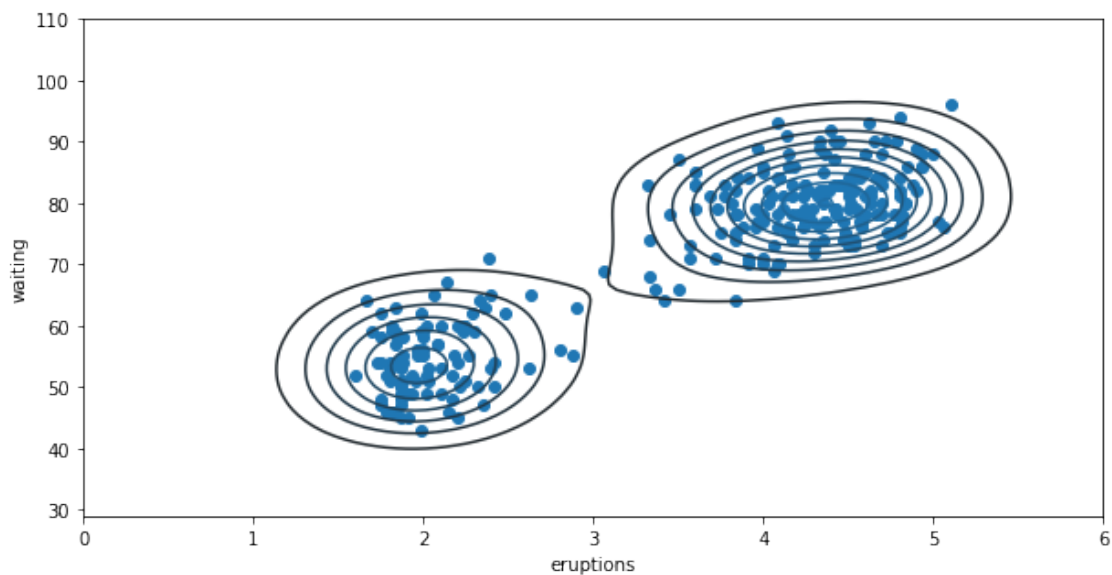
Data were collected on time between eruptions and the duration of eruptions for the Old Faithful geyser at Yellowstone National Park.

	eruptions	waiting
count	272.000000	272.000000
mean	3.487783	70.897059
std	1.141371	13.594974
min	1.600000	43.000000
25%	2.162750	58.000000
50%	4.000000	76.000000
75%	4.454250	82.000000
max	5.100000	96.000000

## Old Faithful geyser



Old Faithful geyser (with density contours)



## Two main types of approaches to clustering

- Partitioning clustering - specify the number of clusters in advance, and then invoke an algorithm to partition the data
- Hierarchical clustering - iteratively merge (or divide) the data typically one observation at a time, and then decide on partitions afterward

## Distances between observations: The building block of clustering

- The choice of distance measures is a critical step in clustering. The pairwise distance calculation can influence the shape of the clusters.

- Observations to be clustered can be non-standard (e.g., pictures, audio signals), so the process of computing distances first followed by clustering can be an effective approach.

Assume  $n$  observations are measured on  $p$  variables or features. Let  $X_{ij}$ , for  $i = 1, \dots, n$  and  $j = 1, \dots, p$ , be the value of feature  $j$  on observation  $i$ .

[Two common distance measures](#) For observations  $\mathbf{x}_i$  and  $\mathbf{x}_k$  (of length  $p$ )

$$d_{Euc}(\mathbf{x}_i, \mathbf{x}_k) = \sqrt{\sum_{j=1}^p (X_{ij} - X_{kj})^2} \quad \text{Euclidean distance } (L_2)$$

$$d_{Man}(\mathbf{x}_i, \mathbf{x}_k) = \sum_{j=1}^p |X_{ij} - X_{kj}| \quad \text{Manhattan distance } (L_1)$$

[Other distance measures: Correlation-based measures](#)

$$d_{Pearson}(\mathbf{x}_i, \mathbf{x}_k) = 1 - \frac{\sum_{j=1}^p (X_{ij} - \bar{x}_i)(X_{kj} - \bar{x}_k)}{\sqrt{\sum_{j=1}^p (X_{ij} - \bar{x}_i)^2 \sum_{j=1}^p (X_{kj} - \bar{x}_k)^2}}$$

$$d_{Spearman}(\mathbf{x}_i, \mathbf{x}_k) = 1 - \frac{\sum_{j=1}^p (W_{ij} - \bar{w}_i)(W_{kj} - \bar{w}_k)}{\sqrt{\sum_{j=1}^p (W_{ij} - \bar{w}_i)^2 \sum_{j=1}^p (W_{kj} - \bar{w}_k)^2}}$$

where  $W_{ij}$  are the ranks of  $X_{ij}$  for feature  $j$ , and  $\bar{w}_i$  is the average of the ranks for observation  $i$ .

Correlation distances are often used for micro-array analyses.

Spearman correlation is used when outliers might be a concern in the data.

### Distance and scaling

Consider a data set that looks like the following:

X1	X2	X3	X4
435201	0.04	0.21	0.35
839940	0.01	0.33	0.21
582048	0.23	0.19	0.25
390392	0.18	0.30	0.19
...	...	...	...
298989	0.15	0.23	0.27

The distance between any two observations is basically determined by feature 1. This is an undesired consequence of variables having different scales.

Usually want to ensure each variable has equal contribution to the clustering algorithm, and therefore the distance computation.

[Solution](#) Standardize the variables prior to computing distances.

Standardizing usually just involves transforming each  $X_{ij}$  by

$$\frac{X_{ij} - \text{center}(\mathbf{x}_j)}{\text{scale}(\mathbf{x}_j)}$$

where  $\text{center}(\mathbf{x}_j)$  can be the sample mean or median of the  $j$ -th variable, and  $\text{scale}(\mathbf{x}_j)$  can be the sample standard deviation or **mean absolute deviation of the  $j$ -th variable**.

### [Main example: Violent crime rates by State](#)

This data set reports arrests per 100,000 residents for assault, murder, and rape in each of the 50 US states in 1973. Also given is the percent of the population living in urban areas.

### [Summary](#)

	Murder	Assault	UrbanPop	Rape
count	50.00000	50.000000	50.000000	50.000000
mean	7.78800	170.760000	65.540000	21.232000
std	4.35551	83.337661	14.474763	9.366385
min	0.80000	45.000000	32.000000	7.300000
25%	4.07500	109.000000	54.500000	15.075000
50%	7.25000	159.000000	66.000000	20.100000
75%	11.25000	249.000000	77.750000	26.175000
max	17.40000	337.000000	91.000000	46.000000

### [Biplot for PCA of crime rates](#)

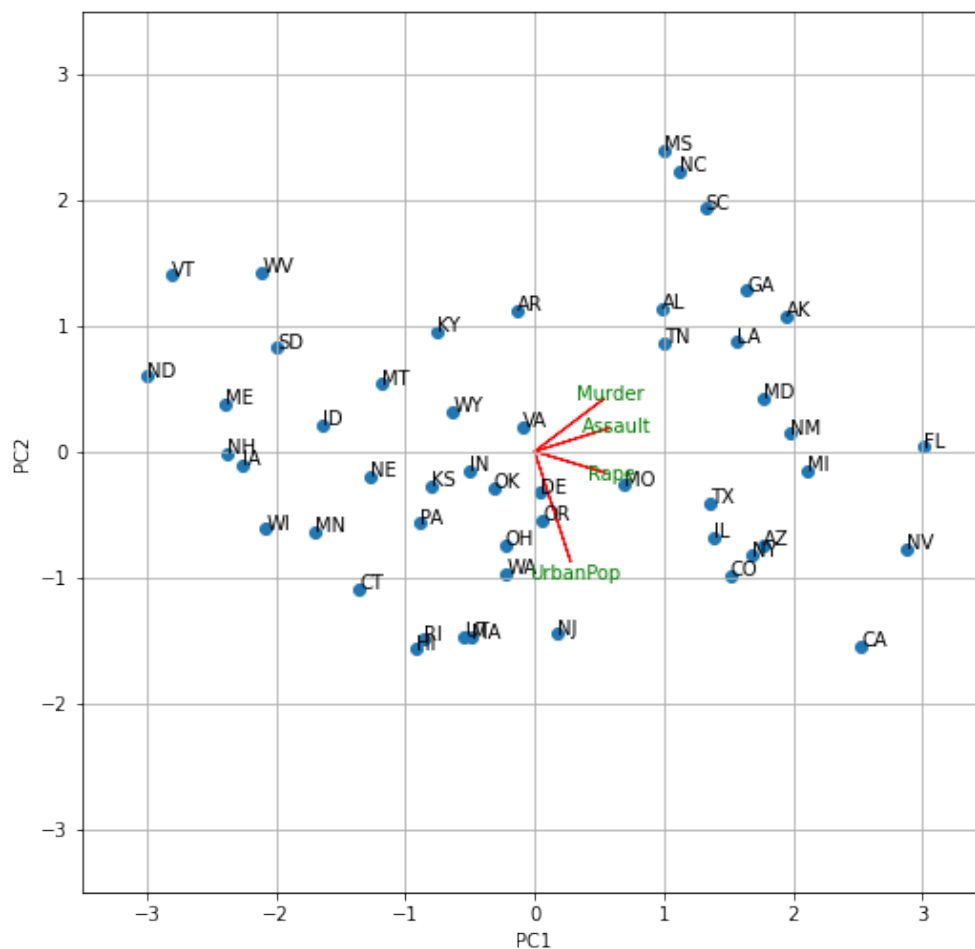


Figure contains a scatter plot of the first two principal components.

- Each state is plotted according to its first two principal components.
- The red arrows indicate the first two PC loading vectors. For example, the loading for Rape on the first PC is 0.543, and 0.167 on the second PC [the word Rape is centered at (0.543, 0.167)].
- This figure is known as a “biplot” as it displays both the PC scores and the PC loadings.

### Distances and violent crimes

First few randomly chosen observations

State	Murder	Assault	UrbanPop	Rape	StateAbbrev
Hawaii	5.3	46	83	20.2	HI
Indiana	7.2	113	65	21.0	IN
New Mexico	11.4	285	70	32.1	NM
Washington	4.0	145	73	26.2	WA
Maine	2.1	83	51	7.8	ME

Alabama	13.2	236	58	21.2	AL
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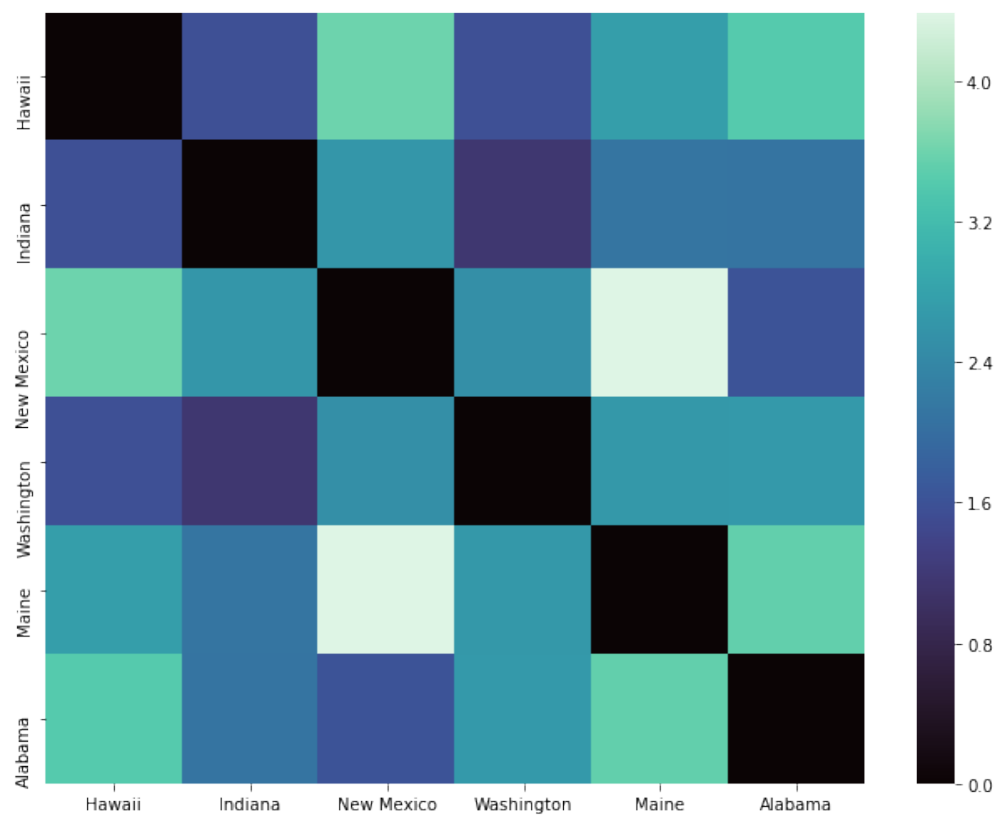
Now rescale the observations (subtract mean, divide by std dev)

State	Murder	Assault	UrbanPop	Rape
Hawaii	-0.58	-1.51	1.22	-0.11
Indiana	-0.14	-0.70	-0.04	-0.03
New Mexico	0.84	1.38	0.31	1.17
Washington	-0.88	-0.31	0.52	0.54
Maine	-1.32	-1.06	-1.01	-1.45
Alabama	1.26	0.79	-0.53	-0.00

Euclidean distances on scaled observations

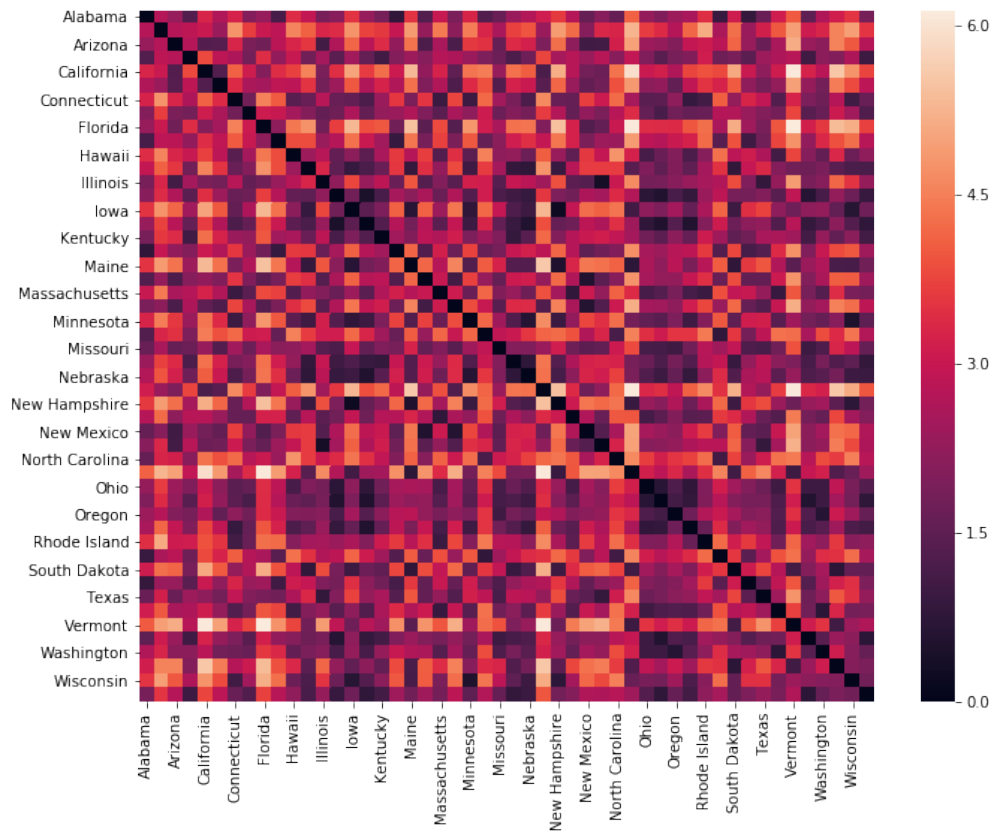
	Hawaii	Indiana	New Mexico	Washington	Maine	Alabama
<b>Hawaii</b>	0.000000	1.561769	3.586656	1.560979	2.743631	3.422932
<b>Indiana</b>	1.561769	0.000000	2.617305	1.152154	2.124266	2.097219
<b>New Mexico</b>	3.586656	2.617305	0.000000	2.504780	4.390177	1.615635
<b>Washington</b>	1.560979	1.152154	2.504780	0.000000	2.655948	2.675068
<b>Maine</b>	2.743631	2.124266	4.390177	2.655948	0.000000	3.520494
<b>Alabama</b>	3.422932	2.097219	1.615635	2.675068	3.520494	0.000000

Coarse heatmap on randomly selected states





### Full heatmap



### Clustering via partitioning methods

Basic idea - specify the number of clusters into which the data will be partitioned, and then perform computation to group data so that

1. observations within clusters are similar (low distances/dissimilarities), and
2. observations in different clusters are dissimilar (high distances/dissimilarities)

Separately can address the optimal number of clusters.

### K-means clustering

Let  $C_1, \dots, C_K$  denote sets containing the indices of observations within the  $K$  clusters such that

1.  $C_1 \cup C_2 \cup \dots \cup C_K = \{1, 2, \dots, n\}$ , and
2.  $C_k \cap C_\ell = \emptyset$  for  $k \neq \ell$ .

Let

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

be the within-cluster variation.

An interesting mathematical fact that we will use shortly is that

$$W(C_k) = 2 \sum_{i \in C_k} \sum_{j=1}^p (X_{ij} - \bar{x}_{jk})^2$$

where  $\bar{x}_{jk}$  is the sample mean of the  $X_{ij}$  for  $i \in C_k$ .

### Goal of $K$ -means clustering

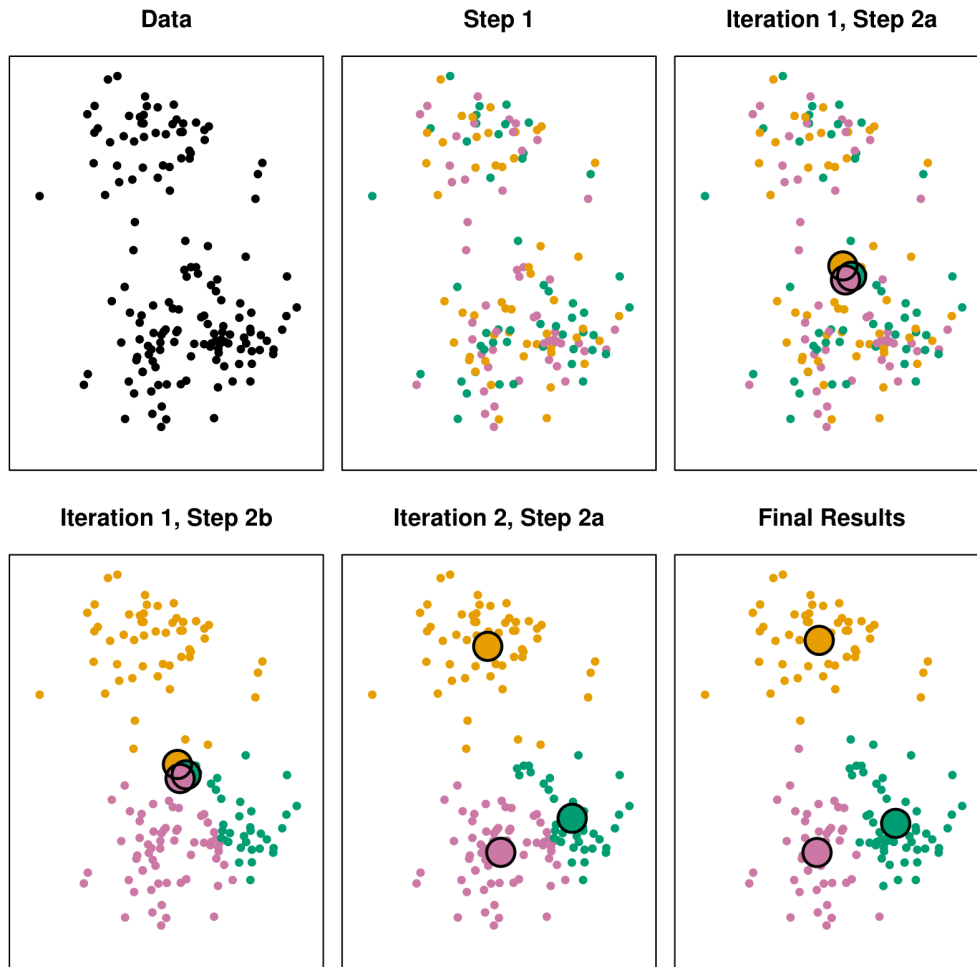
Determine  $C_1, \dots, C_K$  such that the expression

$$\sum_{k=1}^K W(C_k)$$

is minimized. This value is twice the within-cluster sums-of-squares, which is sometimes called the *inertia*.

### $K$ -means clustering algorithm

1. Randomly assign each observation to one of  $K$  clusters at random.
2. Repeat the following two steps until clusters do not change:
  - (a) For each cluster  $k$ , compute the cluster centroid  $\bar{x}_k$  (the variable-wise average of the observations in cluster  $k$ ).
  - (b) Given the  $K$  centroids, reassign all observations to clusters based on their closeness to the centroids.



### The bad and the good

- Requires analyst to select  $K$  in advance.
- **The algorithm is locally optimal, not globally optimal.** As a consequence this means you can get different clusterings depending on the starting cluster assignment.

### Potential solutions

- Can try various values of  $K$  and compare results. We will dig deeper into this approach shortly.
- Can try different initial cluster assignments in parallel, and then choose the solution with the best within-cluster sum of squared deviations.

### Six results from different initializations



### Application to violent crimes data

Choose 4 clusters for now.

	<b>Murder</b>	<b>Assault</b>	<b>UrbanPop</b>	<b>Rape</b>
<b>0</b>	-0.494407	-0.386484	0.581676	-0.264310
<b>1</b>	0.702127	1.049994	0.729974	1.289904
<b>2</b>	-0.971303	-1.117836	-0.939550	-0.976578
<b>3</b>	1.426224	0.883211	-0.822791	0.019467

### Cluster labels

	Murder	Assault	UrbanPop	Rape	Cluster
State					
Alabama	1.255179	0.790787	-0.526195	-0.003451	3
Alaska	0.513019	1.118060	-1.224067	2.509424	1
Arizona	0.072361	1.493817	1.009122	1.053466	1
Arkansas	0.234708	0.233212	-1.084492	-0.186794	3
California	0.281093	1.275635	1.776781	2.088814	1

Can compute the (unscaled) mean of each variable within cluster:

	Murder	Assault	UrbanPop	Rape
Cluster				
0	5.656250	138.875000	73.875000	18.781250
1	10.815385	257.384615	76.000000	33.192308
2	3.600000	78.538462	52.076923	12.176923
3	13.937500	243.625000	53.750000	21.412500

[Silhouette plot: A diagnostic for K-means \(and other\) clustering](#)

Once a clustering has been determined, let

- $a_i$  = average dissimilarity between observation  $i$  and the other points in the cluster to which  $i$  belongs
- $b_i$  = average dissimilarity between observation  $i$  and the other points in the next closest cluster to observation  $i$

Let

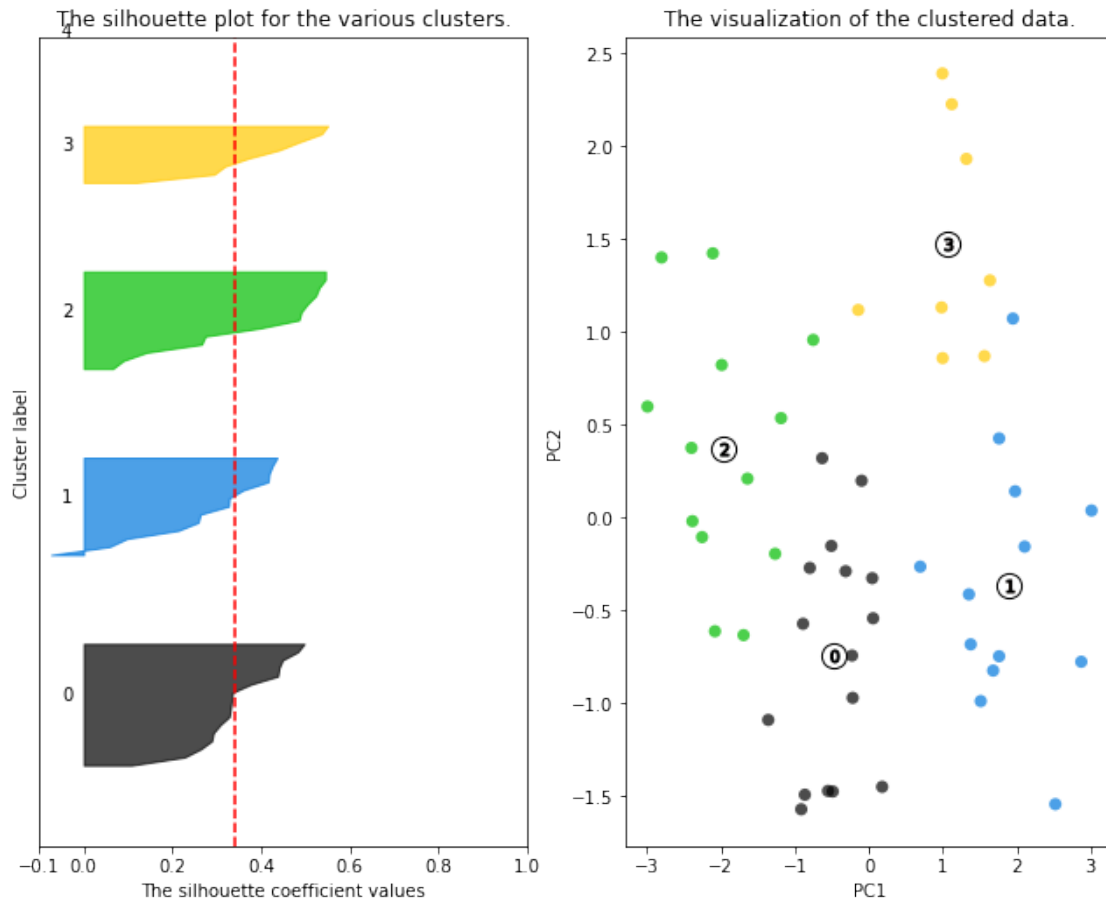
$$s_i = \frac{b_i - a_i}{\max(a_i, b_i)}$$

be the silhouette for observation  $i$ .

## Interpretation

- Observations with  $s_i \approx 1$  are well-clustered
- Observations with  $s_i \approx 0$  lie between two clusters
- Observations with  $s_i < 0$  are probably in the wrong cluster.

### **Silhouette analysis for KMeans clustering on sample data with n\_clusters = 4**



An observation may be in the wrong cluster!

	State	Murder	Assault	UrbanPop	Rape	StateAbbrev
24	Missouri	9.0	178	70	28.2	MO

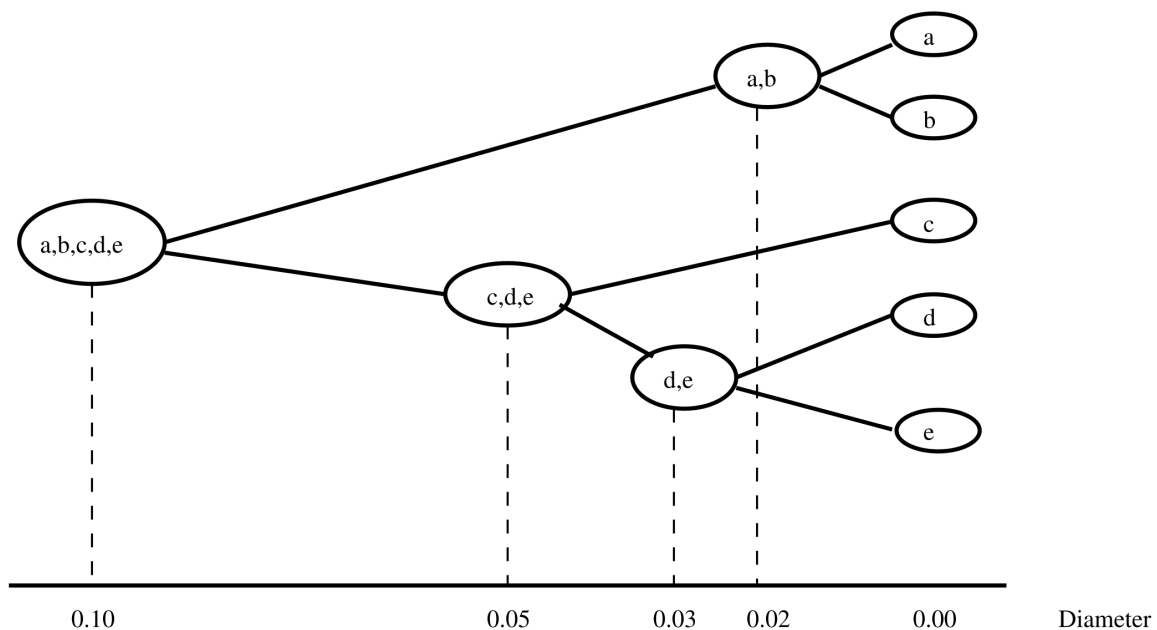
## Hierarchical clustering

- $K$ -means clustering requires pre-specifying the number of clusters  $K$ .

(though we will come back to address this point)

- Hierarchical clustering does not require committing to a particular number of clusters,  $K$ .
- Two types of hierarchical clustering:
  - Agglomerative clustering (bottom-up approach).
  - Divisive clustering (top-down approach).

Can summarize hierarchical clustering in a dendrogram



### Agglomerative clustering

The basic algorithm:

- Each observation starts as its own cluster.
- At each step of the algorithm, two clusters that are most “similar” (to be described shortly) are combined into a new larger cluster.
- This process of combining clusters is repeated until all observations are members of one single large cluster.

Particularly well-suited at identifying small clusters.

Agglomerative clustering (cont'd) How do we measure the dissimilarity between two clusters?

A few common approaches:

- Complete (or maximum) linkage clustering: For two clusters, determine the maximum dissimilarity between any observation in the first cluster and any observation in the second cluster.
- Single linkage clustering: For two clusters, determine the minimum dissimilarity between any observation in the first cluster and any observation in the second cluster.
- Average linkage clustering: Compute all pairwise dissimilarities between observations in the first and second cluster, and calculate the average.

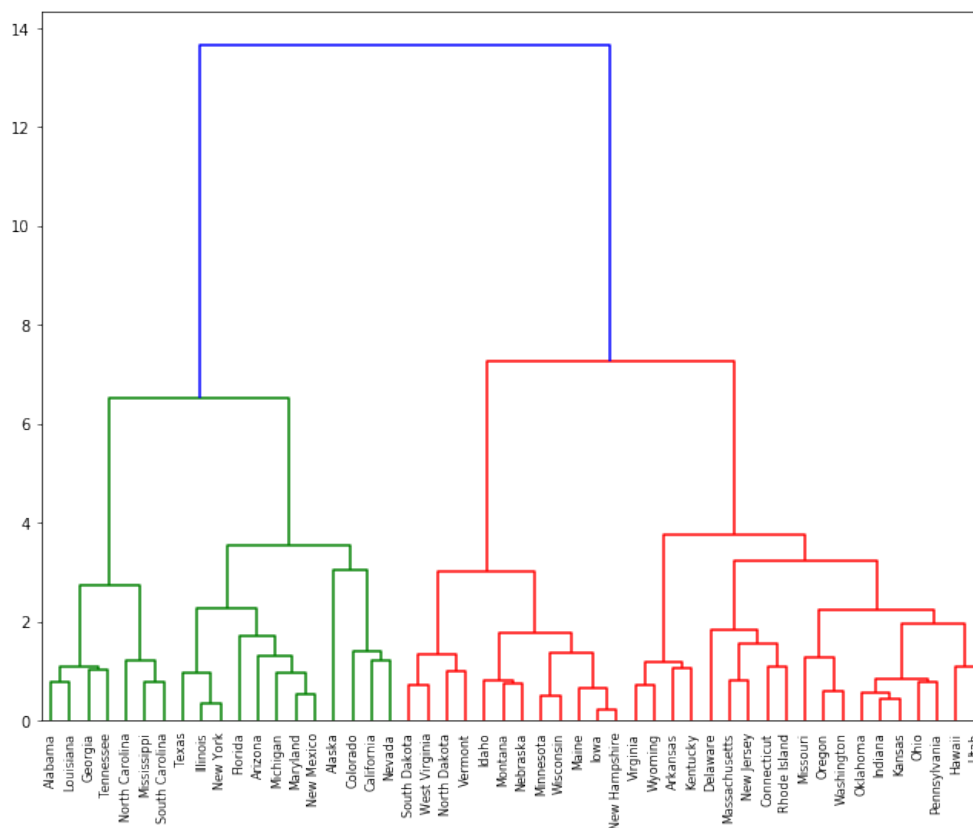
Another popular approach is Ward's method.

- Instead of joining two clusters based on their distances, use information about the variance of observations within clusters.
- Specifically, at each step, join two clusters whose merged cluster has the smallest within-cluster sum of squared distances.

Other aggregation approaches are possible.

Agglomerative clustering - Ward's method





### Choosing the optimal number of clusters

No single compelling way to choose clusters, but we will explore two types of methods.

- Direct methods that involve optimizing a particular criterion (elbow and silhouette methods)
- Testing methods that evaluate evidence against a null hypothesis (gap statistic)

### Elbow method: A little squishy, but useful

As previously, let  $W(C_k)$  be the within-cluster sum of squared distances between all pairs for cluster  $k$  for a particular clustering, and let

$$T_K = \sum_{k=1}^K W(C_k)$$

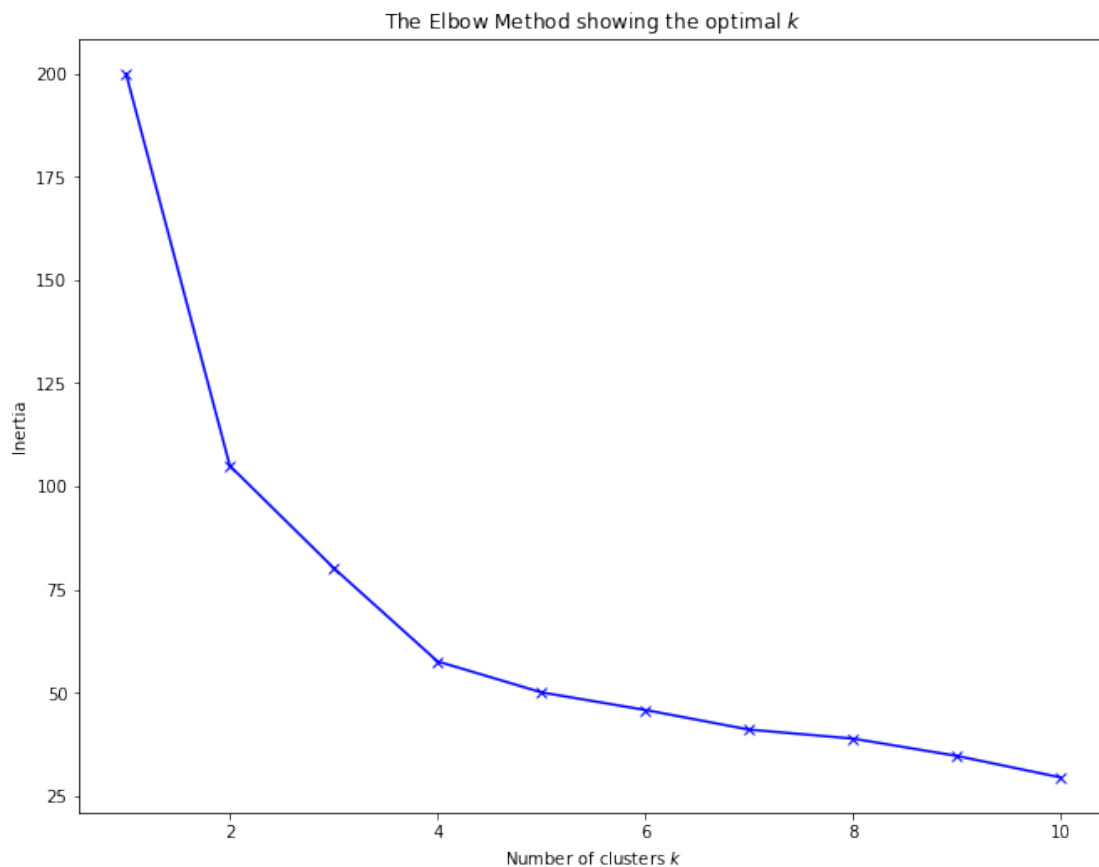
be the total within-cluster variation for the clustering with  $K$  clusters.

The method:

1. For the particular clustering method, let  $K$  vary over a range of values (say 1 to 10).
2. Compute  $T_K$  for each  $K$ .

3. Plot  $T_K$  against  $K$ , and look for a clear bend (“knee”) in the graph.

The value of  $K$  where the bend occurs is considered the appropriate number of clusters.



Average silhouette method Similar construction to the elbow method

1. Compute clustering algorithm for different numbers of clusters  $K$ , varying  $K$  from (say) 1 to 10.
2. For each  $K$ , calculate the average silhouette

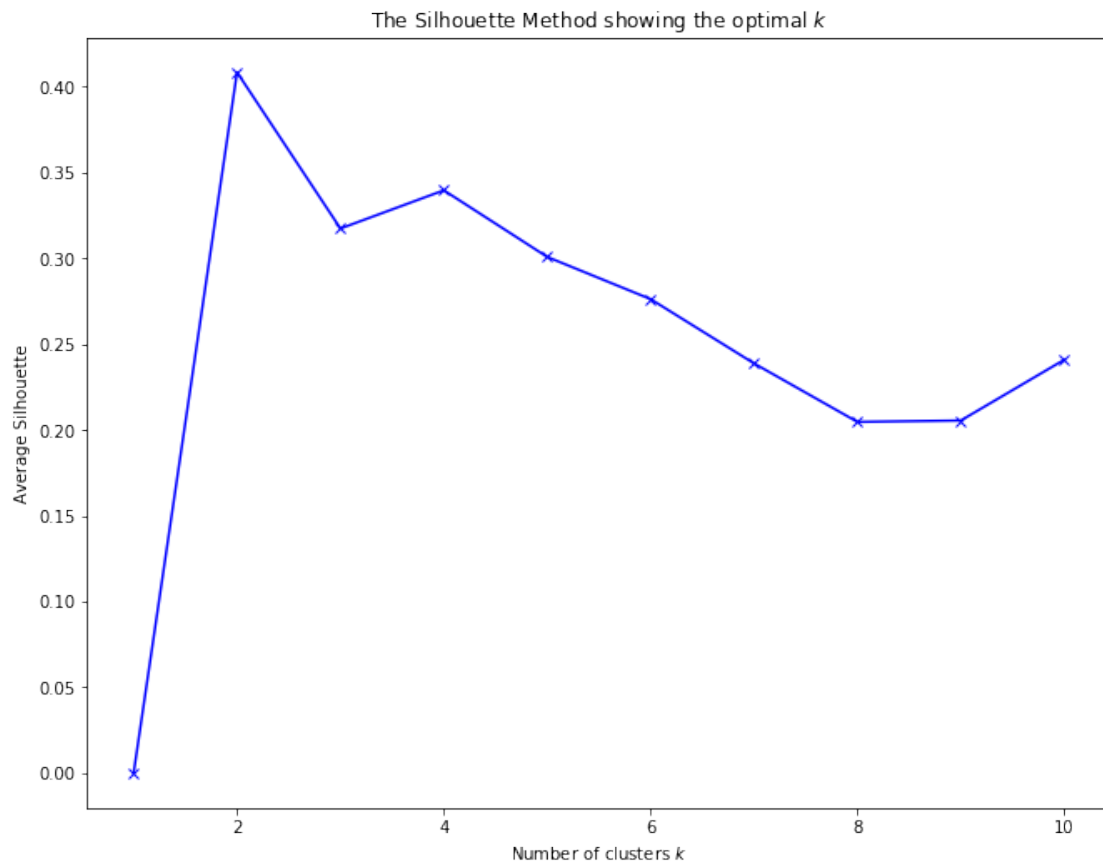
$$S_K = \frac{1}{n} \sum_{i=1}^n s_i$$

across all observations.

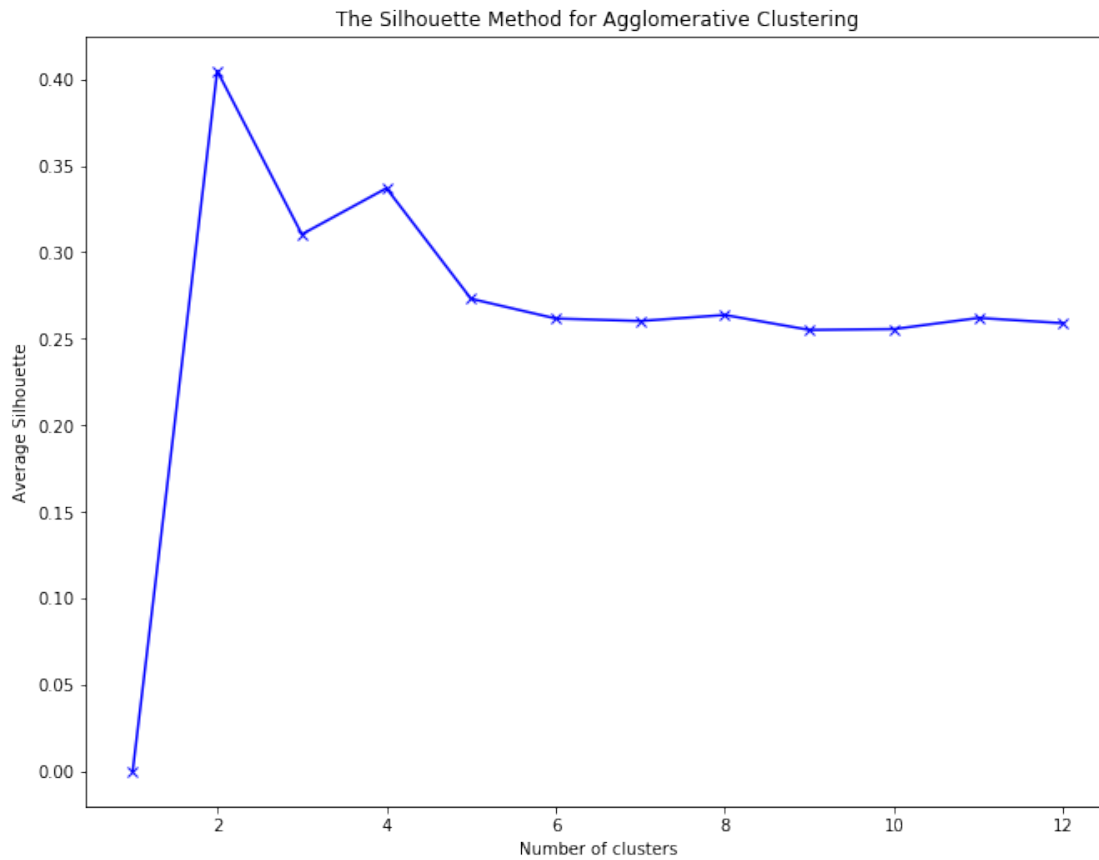
3. Plot  $S_K$  against  $K$ .

The value of  $K$  where  $S_K$  is maximized is considered the appropriate number of clusters.

Average silhouette for  $K$ -means



Average silhouette for agglomerative clustering



### Comments

- Elbow method suggests four clusters for  $K$ -means; average silhouette method suggests two clusters for both  $K$ -means and agglomerative clustering.
- Computation for each method are different enough that inconsistent results are not uncommon.
- Both approaches measure global clustering characteristics only, and are informal (and somewhat ad hoc) approaches.

### Gap statistic

Due to Tibshirani et al., (JRSS-B, 2001).

Idea For a particular choice of  $K$  clusters, compare the total within cluster variation to the expected within-cluster variation under the assumption that the data have no obvious clustering (i.e., randomly distributed).

The gap statistic in essence detects whether the data clustered into  $K$  groups is significantly better than if they were generated at random.

### Algorithm for computing Gap statistic

1. Cluster the data at varying number of total clusters  $K$ , say from 1 to 10. Let  $T_K$  be the total within-cluster sum of squared distances.
2. Generate  $B$  reference data sets of size  $n$ , with the simulated values of variable  $j$  uniformly generated over the range of the observed variable  $x_j$ . Typically  $B = 500$ .
3. For each generated data set  $b = 1, \dots, B$ , perform the clustering for each  $K$  (from 1 to 10, say). Compute the total within-cluster sum of squared distances  $T_K^{(b)}$ .
4. Compute the Gap statistic

$$\text{Gap}(K) = \left( \frac{1}{B} \sum_{b=1}^B \log(T_K^{(b)}) \right) - \log(T_K).$$

If it is computationally straightforward to evaluate  $\text{Gap}(K)$  for all possible values of  $K$ , then choose  $K$  that maximizes the Gap statistic.

Otherwise,

5. Let  $\bar{w} = \frac{1}{B} \sum_{b=1}^B \log(T_K^{(b)})$ . Compute the standard deviation

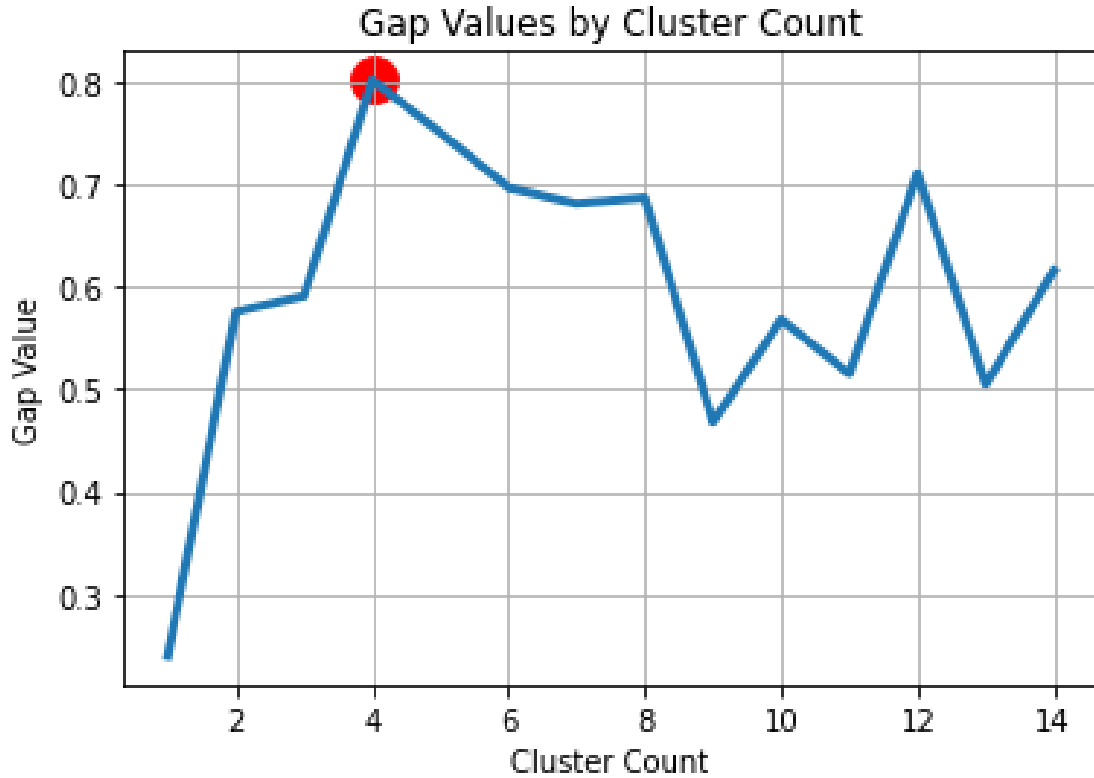
$$\text{sd}(K) = \sqrt{\frac{1}{B} \sum_{b=1}^B \left( \log(T_K^{(b)}) - \bar{w} \right)^2}.$$

Define  $s_K = \text{sd}(K) \sqrt{1 + 1/B}$ .

6. Finally, choose the number of clusters as the smallest  $K$  such that

$$\text{Gap}(K) \geq \text{Gap}(K + 1) - s_{K+1}.$$

Python results



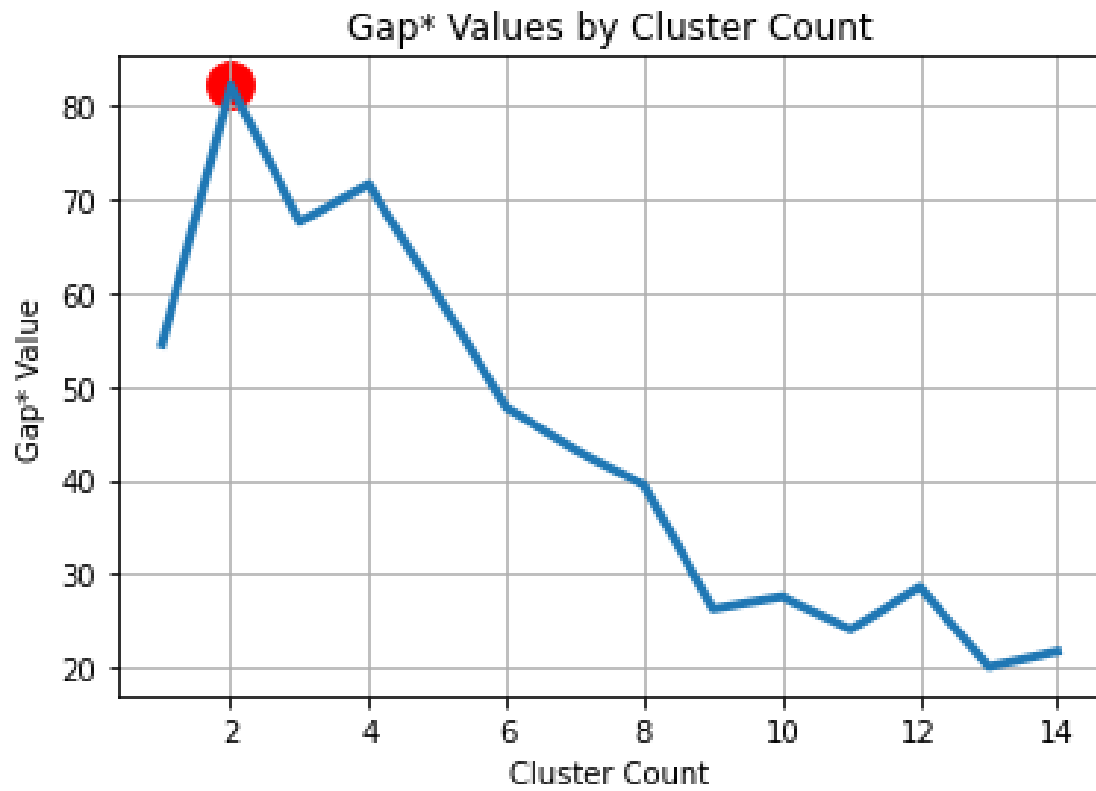
### Comments

- $K$ -means clustering is optimized for  $K = 4$  based on the Gap statistic. This value can (and does) change when rerunning the procedure.
- This is a more principled approach to choosing cluster sizes, though clearly different conclusions can be reached based on different clustering approaches.
- Generally understood to be conservative - tends to err on the side of picking a smaller number of clusters.

An alternative is the Gap statistic (Mohajer, M., Englmeier, K. H., & Schmid, V. J., 2011) which replaces  $\log(T_K)$  and  $\log(T_K^{(b)})$  in the formulas with

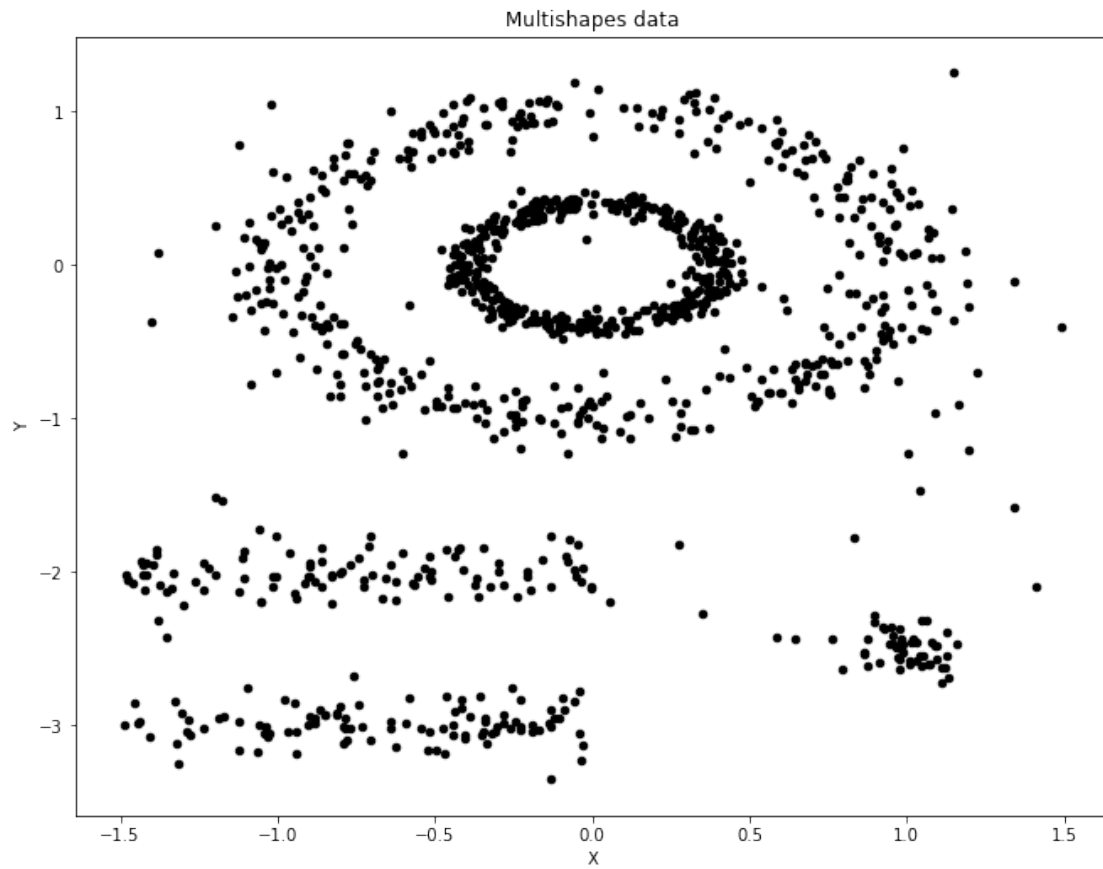
$$\text{Gap}^*(K) = \left( \frac{1}{B} \sum_{b=1}^B T_K^{(b)} \right) - T_K.$$

According to Mohajer et al., the Gap statistic turns out to result in more conservative clusterings (fewer clusters), but does not perform as reliably when the clusters overlap.



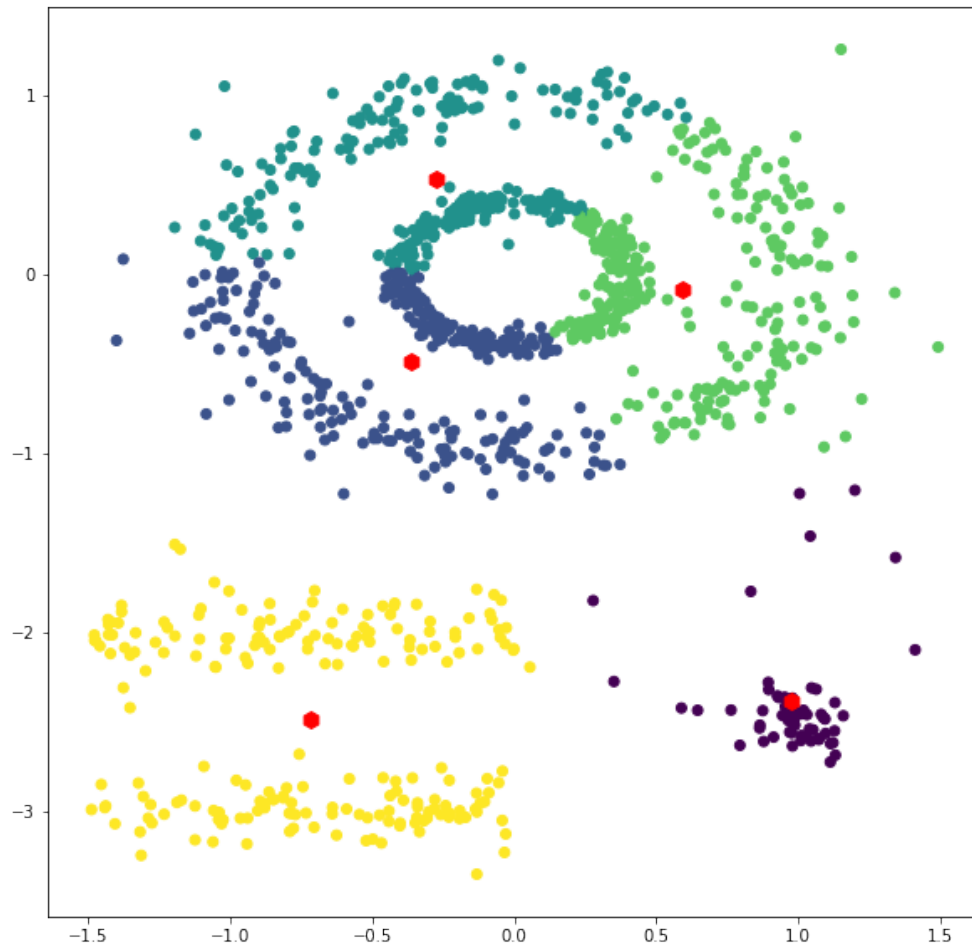
One final clustering algorithm

Imagine trying to cluster the following set of observations.



What happens if we try  $K$ -means?





DBSCAN: Density-based clustering algorithm (Ester et al., 1996, KDD-96)

Unlike previous clustering algorithms, DBSCAN

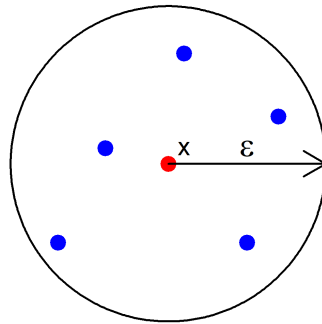
- can find any shape of clusters
- identifies observations that do not belong to clusters as outliers
- does not require specifying the number of clusters (like hierarchical clustering)
- can be used for predicting cluster membership for new data

DBSCAN algorithm: Identify dense regions of observations

Need to specify two parameters of the algorithm

1.  $\epsilon$ : the radius of a neighborhood around an observation
2.  $\text{MinPts}$ : the minimum number of points within an  $\epsilon$  radius of an observation to be considered a “core” point

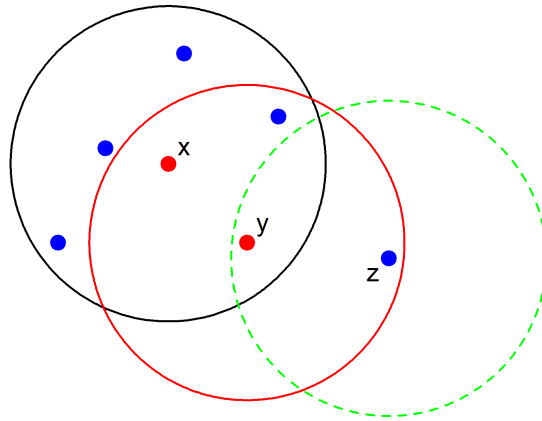
Example of core observation with  $\text{MinPts}=6$ .



### Three types of points

- Core points - observations with  $\text{MinPts}$  total observations within an  $\epsilon$  radius
- Border points - observations that are not core points, but are within  $\epsilon$  of a core point
- Noise points - everything else

In the following,  $x$  is a core point,  $y$  is a border point, and  $z$  is a noise point.



Two terms:

- Density-reachable: Point  $A$  is density-reachable from point  $B$  if there is a set of core points leading from  $B$  to  $A$ .
- Density-connected: Two points  $A$  and  $B$  are density-connected if there is a core point  $C$  such that both  $A$  and  $B$  are density-reachable from  $C$ .

A density-based cluster is defined as a group of density-connected points.

### Choosing MinPts

- MinPts must be at least 3 to produce non-trivial clustering.
- Rule of thumb: Choose MinPts to be twice the number of variables in the data being clustered.
- Larger values may be better for large data sets, for noisy data, or for data that contain repeats.

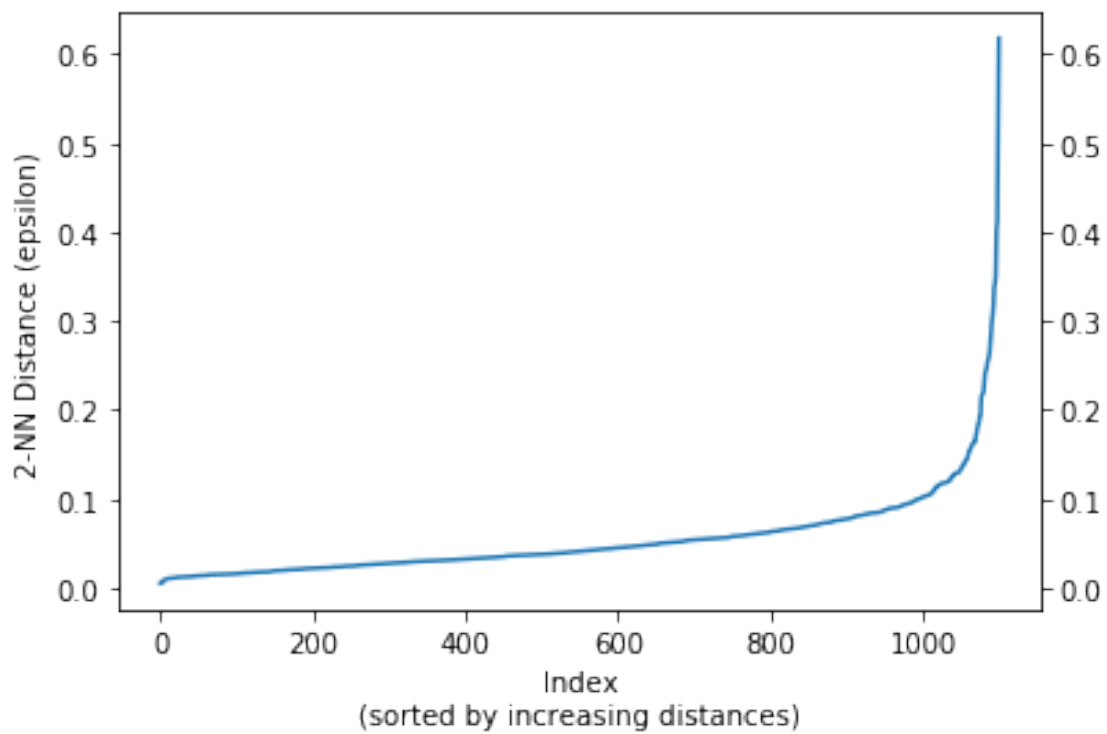
### Choosing $\epsilon$

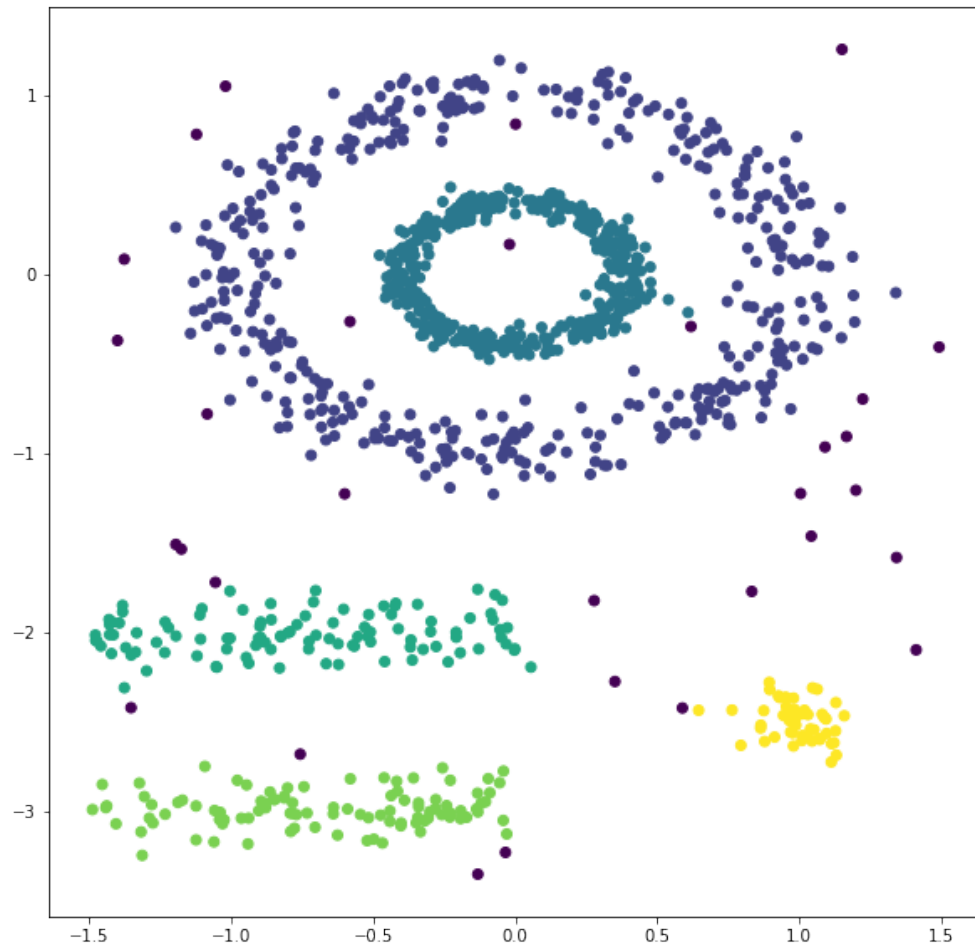
- Compute the  $k$ -th ( $k = \text{MinPts}$ ) nearest neighbor distance for each point.

- Plot the distances in sorted order.
- Look for a bend (the “knee”) in the plot, and use the distance at the knee as the choice of  $\epsilon$ .

Refer to Ester et al. for the algorithm details, as well as the optimizing the choice of  $\epsilon$ .

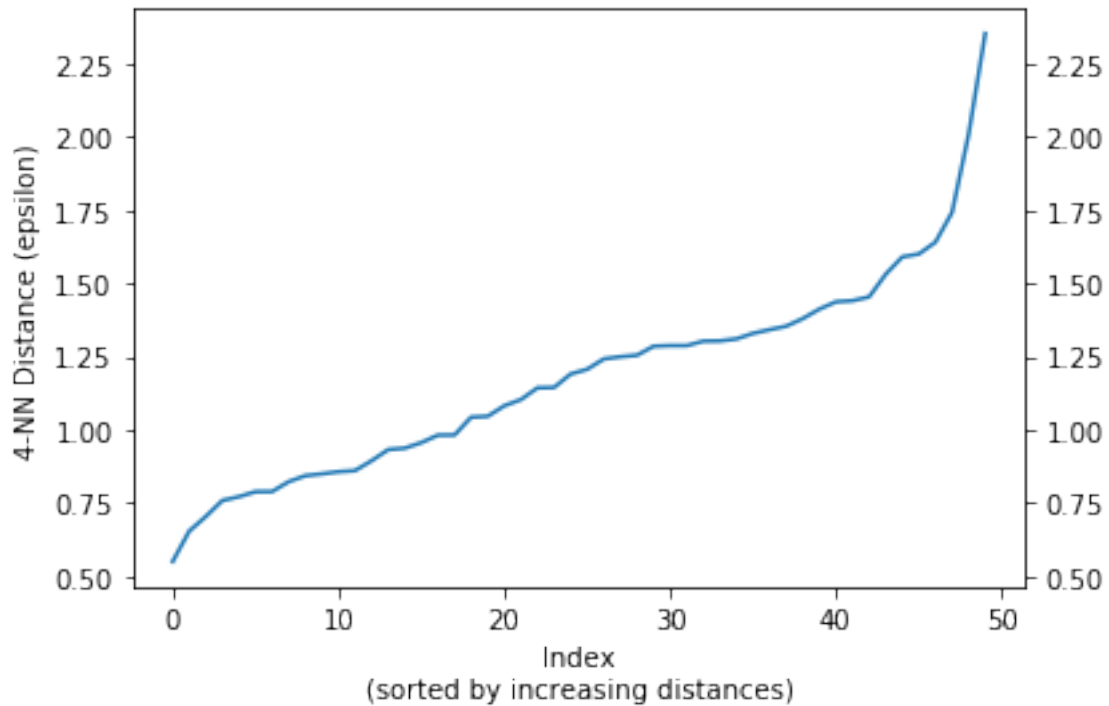
### Knee plot





#### Application to violent crime data

- Chose  $\epsilon = 1.4$  on standardized data based on knee plot, and `MinPts= 5` (default value – results fairly robust to other choices).
- Resulted in 1 density-based cluster, and 1 outlier.



### Now for something really different: Chernoff faces

An unusual graphical method to cluster data:

- Each observation is a face
- Each variable is a facial feature
- Invented mostly as a joke!

### Car data: Data on model year 1993 cars

Variables include:

Weight, MPG (city), MPG (highway), horsepower, engine size, minimum price, price, maximum price, RPM, revs per mile, fuel tank capacity, passenger capacity, length, wheel base.

### Example Chernoff faces: Car data

- Width of face – vehicle weight
- Height of face split – City MPG
- Length of face – Highway MPG
- Width of top half of face – Horsepower
- Width of bottom half of face – Engine size

Other facial features Length of nose, curvature of mouth, size of eyes, angle of eyebrows, etc.

