Inspire...Educate...Transform.






Inspire…Educate…Transform.

# Unsupervised models

## Clustering

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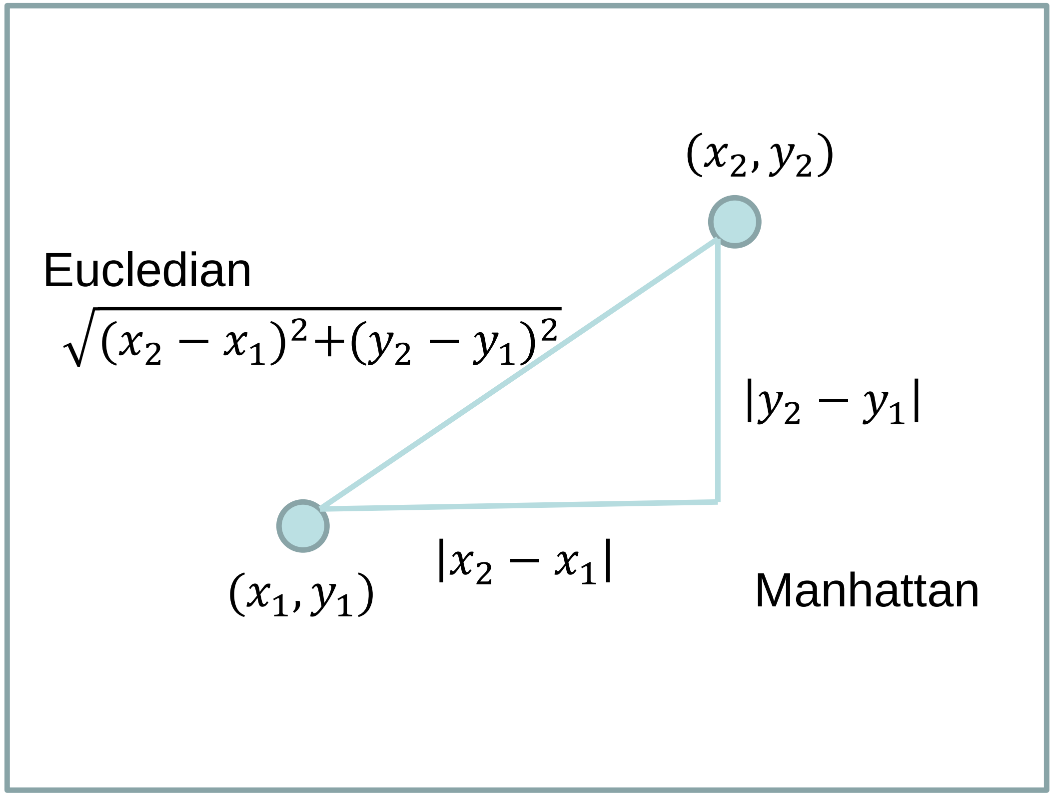
# UNDERSTANDING DISTANCE

# Numeric



# Distance between categorical attributes

- For each categorical variable
  - Distance is zero if two records have same value
  - 1 if different
  - Sum the total distance across all attributes

# Categorical attributes

| | |
|---|---|
| $x_i \rightarrow$ | 1 1 1 0 1 0 0 1 0 1 0 1 |
| $x_j \rightarrow$ | 1 1 0 1 1 0 1 1 0 0 1 1 |

| | | Data point $j$ | | |
|---|---|---|---|---|
| | | 1 | 0 | |
| Data point $i$ | 1 | $a$ | $b$ | $a+b$ |
| | 0 | $c$ | $d$ | $c+d$ |
| | | $a+c$ | $b+d$ | $a+b+c+d$ |

For example, in above two feature vectors:

a=5

$\boxed{\text{b=2}}$ (10)

$\boxed{\text{c=3}}$

d=2

$a$: the number of attributes with the value of 1 for both data points.

$b$: the number of attributes for which $x_{if} = 1$ and $x_{jf} = 0$, where $x_{if}$ ($x_{jf}$) is the value of the $f$th attribute of the data point $\mathbf{x}_i$ ($\mathbf{x}_j$).

$c$: the number of attributes for which $x_{if} = 0$ and $x_{jf} = 1$.

$d$: the number of attributes with the value of 0 for both data points.

# Symmetric binary attributes

- Hamming distance function: Simple Matching Coefficient, proportion of mismatches of their values

$$dist(\mathbf{x}_i, \mathbf{x}_j) = \frac{b+c}{a+b+c+d}$$

$$Dist = \frac{number\ of\ dissimiar\ attributes\ between\ the\ records}{number\ of\ dissimilar\ attributes + number\ of\ similar\ attributes}$$

# Asymmetric binary attributes

- Asymmetric: if one of the states is more important or more valuable than the other.
  - By convention, state 1 represents the more important state, which is typically the rare or infrequent state.
  - Jaccard coefficient is a popular measure

$$Dist = \frac{\text{number of dissimiar attributes between the records}}{\text{number of dissimilar attributes} + \text{number of similar attributes (excluding records with 0,0)}}$$

$$dist(\mathbf{x}_i, \mathbf{x}_j) = \frac{b+c}{a+b+c}$$

  - We can have some variations, adding weights

# Dissimilarity between Binary Variables

- Example

| Name | Gender | Fever | Cough | Test-1 | Test-2 | Test-3 | Test-4 |
|---|---|---|---|---|---|---|---|
| Jack | M | Y | N | P | N | N | N |
| Mary | F | Y | N | P | N | P | N |
| Jim | M | Y | P | N | N | N | N |

  - gender is a symmetric attribute
  - the remaining attributes are asymmetric binary
  - let the values Y and P be set to 1, and the value N be set to 0

$$d(jack, mary) = \frac{0+1}{2+0+1} = 0.33$$

$$d(jack, jim) = \frac{1+1}{1+1+1} = 0.67$$

$$d(jim, mary) = \frac{1+2}{1+1+2} = 0.75$$

# Another distance metric used in supervised learning

Value difference measure (VDM):$d_{ij}$

$$\sum_{h=1}^{All\ classes} |P(h|val_i) - P\left(h\middle|val_j\right)|$$

# Value Distance Measure

| ID | Age | Income | Family | CCAvg | Personal Loan |
|---|---|---|---|---|---|
| 1 | Young | Low | 4 | Low | 0 |
| 2 | Old | Low | 3 | Low | 0 |
| 3 | Middle | Low | 1 | Low | 0 |
| 4 | Middle | Medium | 1 | Low | 0 |
| 5 | Middle | Low | 4 | Low | 0 |
| 6 | Middle | Low | 4 | Low | 0 |
| 10 | Middle | High | 1 | High | 1 |
| 17 | Middle | Medium | 4 | Medium | 1 |
| 19 | Old | High | 2 | High | 1 |
| 30 | Middle | Medium | 1 | Medium | 1 |
| 39 | Old | Medium | 3 | Medium | 1 |
| 43 | Young | Medium | 4 | Low | 1 |
| 48 | Middle | High | 4 | Low | 1 |

$$VDM_{family1,family2}$$

$$|P(0|f_1) - P(0|f_2)| + |P(1|f_1) - P(1|f_2)|$$

$$|0.5 - 0| + |0.5 - 1|$$

$$= 1$$

$$VDM_{family1,family3} = |P(0|f_1) - P(0|f_3)| + |P(1|f_1) - P(1|f_3)| = |0.5 - 0.5| + |0.5 - 0.5| = 0$$

# Ordinal variables

- Same as numeric
- Look up is better than computation

# Look up matrix for ordinal with 3 states

$$
\begin{array}{cc}
 & \begin{matrix} 1 & 2 & 3 \end{matrix} \\
\begin{matrix} 1 \\ 2 \\ 3 \end{matrix} & \begin{bmatrix} 0 & 1 & 2 \\ 1 & 0 & 1 \\ 2 & 1 & 0 \end{bmatrix}
\end{array}
\qquad\qquad
\begin{array}{cc}
 & \begin{matrix} 1 & 2 & 3 \end{matrix} \\
\begin{matrix} 1 \\ 2 \\ 3 \end{matrix} & \begin{bmatrix} 0 & 1 & 3 \\ 1 & 0 & 2 \\ 3 & 2 & 0 \end{bmatrix}
\end{array}
$$

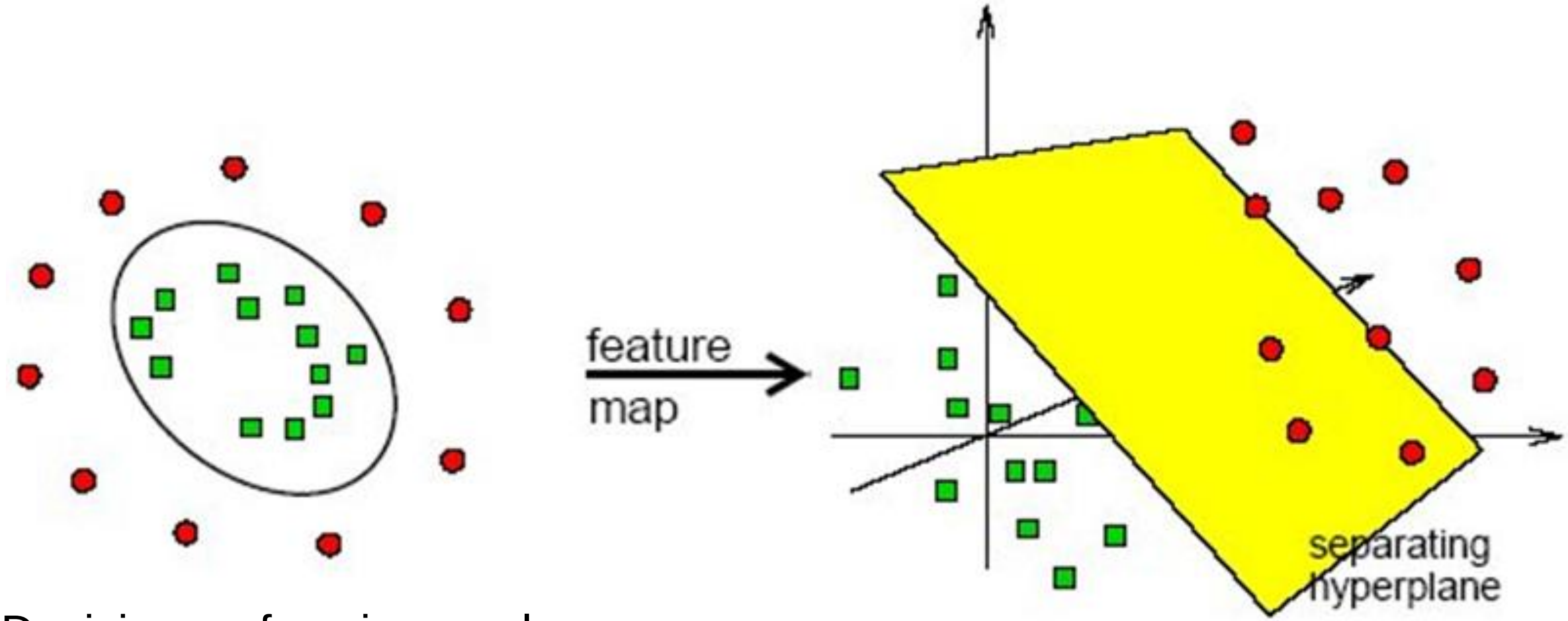
Distance between different ordinals may not be same !!! On the right, distance between state 1 and state 2 is much less than distance between state 1 and state 3.

Depends on what the ordinals represent.

E.g.: If ordinals represent education: class 5, Class 10, Degree. Distance between class 5 and class 10 may be considered less than distance between class 10 and degree

# KERNEL TRICK

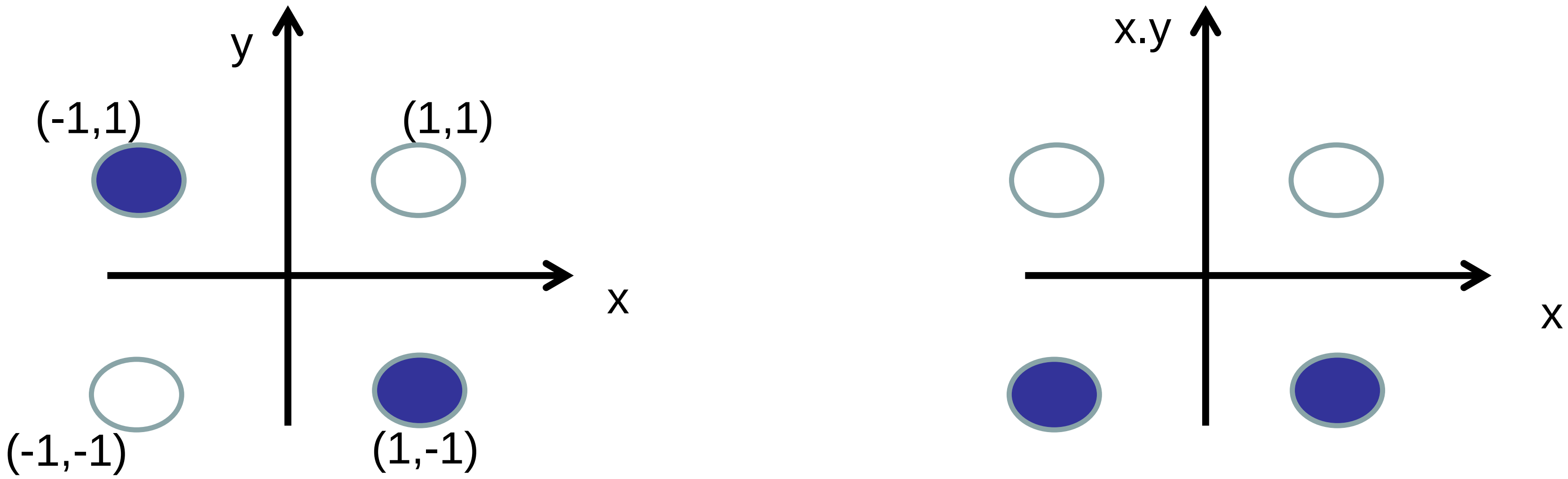
# Moving into higher dimensions




Decision surface is complex in lower dimension

Decision surface is simple in higher dimension

# Linear Separation of XOR




- XOR is not linearly separable in x,y space
- Linearly separable in x.y space
  - The kernel here is K(x,y) = x.y

Reference: http://www.doc.ic.ac.uk/~dfg/ProbabilisticInference/IDAPILecture18.pdf, Duda and Hart, chapter 3.

# Standard Kernels

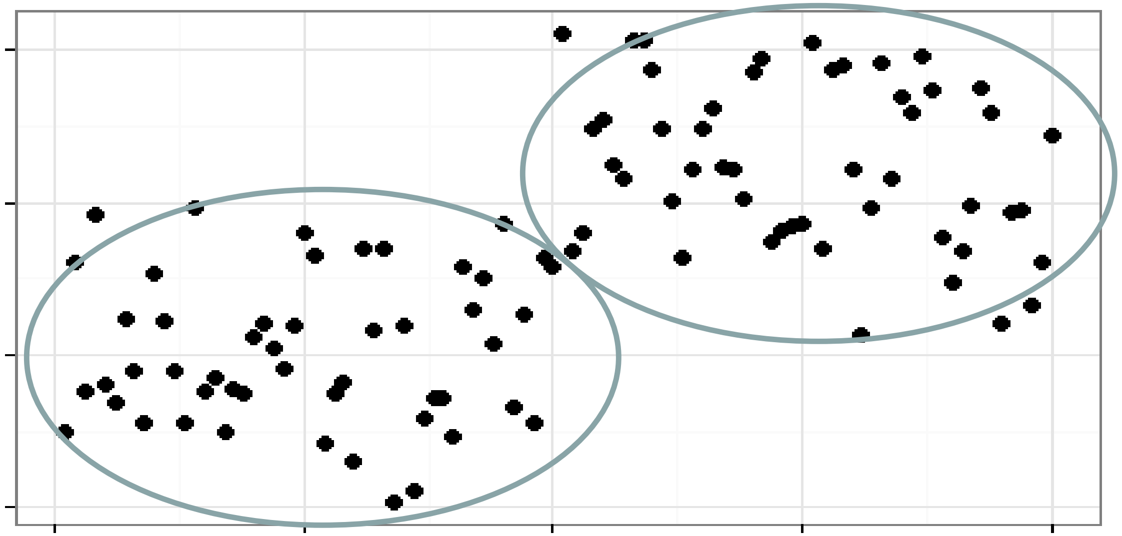
- Polynomial
  - $(\alpha x^T y + c)^d$
- Radial Basis
  - $\exp(-\gamma||x - y||^2)$

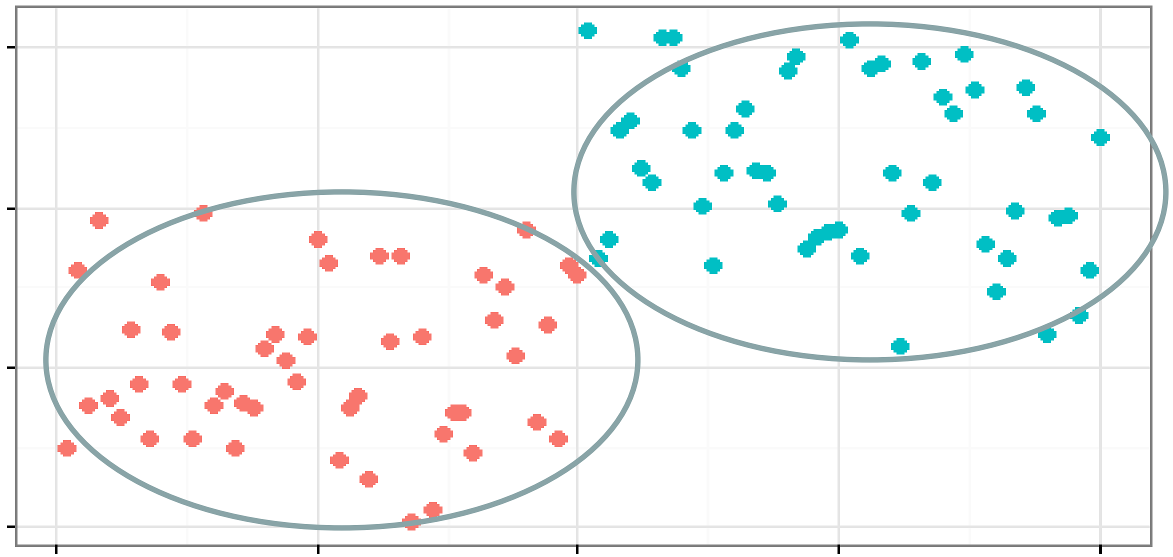
# Clustering

# Unsupervised learning

- Supervised: Data and target

- Unsupervised: Just data





# Clustering

- Finding similarity groups in data, called **clusters**. I.e.,
  - data instances that are similar to (near) each other are in the same cluster
  - data instances that are very different (far away) from each other fall in different clusters.

# A few clustering applications

- In marketing, segment customers according to their similarities
  - To do targeted marketing.
  - It is not uncommon to have over 100,000 segments in insurance clustering

# Google search

- Given a collection of text documents, organize them according to their content similarities,
  - E.g., Google news
- Blind signal separation (separating two speakers)

# Algorithms

- **<u>Hierarchical</u>** <u>approach</u>: Create a hierarchical decomposition of the set of data (or objects) using some criterion (Wald)
- **<u>Partitioning</u>** <u>approach</u>: Construct various partitions and then evaluate them by some criterion, e.g., minimizing the sum of square errors (K-means, Spectral clustering)
- **<u>Model-based</u>** <u>methods:</u> A model is hypothesized for each of the clusters and tries to find the best fit of that model to each other (Gaussian mixture model using EM)

# HIERARCHICAL (AGGLOMERATIVE) CLUSTERING

# Example of agglomerative clustering

| | BOS | NY | DC | MIA | CHI | SEA | SF | LA | DEN |
|---|---|---|---|---|---|---|---|---|---|
| BOS | 0 | 206 | 429 | 1504 | 963 | 2976 | 3095 | 2979 | 1949 |
| NY | 206 | 0 | 233 | 1308 | 802 | 2815 | 2934 | 2786 | 1771 |
| DC | 429 | 233 | 0 | 1075 | 671 | 2684 | 2799 | 2631 | 1616 |
| MIA | 1504 | 1308 | 1075 | 0 | 1329 | 3273 | 3053 | 2687 | 2037 |
| CHI | 963 | 802 | 671 | 1329 | 0 | 2013 | 2142 | 2054 | 996 |
| SEA | 2976 | 2815 | 2684 | 3273 | 2013 | 0 | 808 | 1131 | 1307 |
| SF | 3095 | 2934 | 2799 | 3053 | 2142 | 808 | 0 | 379 | 1235 |
| LA | 2979 | 2786 | 2631 | 2687 | 2054 | 1131 | 379 | 0 | 1059 |
| DEN | 1949 | 1771 | 1616 | 2037 | 996 | 1307 | 1235 | 1059 | 0 |

At each iteration, pick two data points that have least distance between them. Add the points into a cluster.

| | BOS/NY | DC | MIA | CHI | SEA | SF | LA | DEN |
|---|---|---|---|---|---|---|---|---|
| BOS/NY | 0 | 223 | 1308 | 802 | 2815 | 2934 | 2786 | 1771 |
| DC | 223 | 0 | 1075 | 671 | 2684 | 2799 | 2631 | 1616 |
| MIA | 1308 | 1075 | 0 | 1329 | 3273 | 3053 | 2687 | 2037 |
| CHI | 802 | 671 | 1329 | 0 | 2013 | 2142 | 2054 | 996 |
| SEA | 2815 | 2684 | 3273 | 2013 | 0 | 808 | 1131 | 1307 |
| SF | 2934 | 2799 | 3053 | 2142 | 808 | 0 | 379 | 1235 |
| LA | 2786 | 2631 | 2687 | 2054 | 1131 | 379 | 0 | 1059 |
| DEN | 1771 | 1616 | 2037 | 996 | 1307 | 1235 | 1059 | 0 |

Note how we update distances between other clusters. The lower distance is picked. Distance between BOS to DC was 429, now set to 233. Distance from BOS to MIA was 1504, now set to 1308.

Averaging may also be used instead of taking distance to the closest point.

| | BOS/NY/DC | MIA | CHI | SEA | SF | LA | DEN |
|---|---|---|---|---|---|---|---|
| BOS/NY/DC | 0 | 1075 | 671 | 2684 | 2799 | 2631 | 1616 |
| MIA | 1075 | 0 | 1329 | 3273 | 3053 | 2687 | 2037 |
| CHI | 671 | 1329 | 0 | 2013 | 2142 | 2054 | 996 |
| SEA | 2684 | 3273 | 2013 | 0 | 808 | 1131 | 1307 |
| SF | 2799 | 3053 | 2142 | 808 | 0 | 379 | 1235 |
| LA | 2631 | 2687 | 2054 | 1131 | 379 | 0 | 1059 |
| DEN | 1616 | 2037 | 996 | 1307 | 1235 | 1059 | 0 |

| | BOS/ NY/DC | MIA | CHI | SEA | SF/LA | DEN |
|---|---|---|---|---|---|---|
| BOS/NY/DC | 0 | 1075 | 671 | 2684 | 2631 | 1616 |
| MIA | 1075 | 0 | 1329 | 3273 | 2687 | 2037 |
| CHI | 671 | 1329 | 0 | 2013 | 2054 | 996 |
| SEA | 2684 | 3273 | 2013 | 0 | 808 | 1307 |
| SF/LA | 2631 | 2687 | 2054 | 808 | 0 | 1059 |
| DEN | 1616 | 2037 | 996 | 1307 | 1059 | 0 |

Note how creation of SF/LA cluster has changed distances

| | BOS/NY/DC | MIA | CHI | SEA | SF | LA | DEN |
|---|---|---|---|---|---|---|---|
| BOS/NY/DC | 0 | 1075 | 671 | 2684 | 2799 | 2631 | 1616 |
| MIA | 1075 | 0 | 1329 | 3273 | 3053 | 2687 | 2037 |
| CHI | 671 | 1329 | 0 | 2013 | 2142 | 2054 | 996 |
| SEA | 2684 | 3273 | 2013 | 0 | 808 | 1131 | 1307 |
| SF | 2799 | 3053 | 2142 | 808 | 0 | 379 | 1235 |
| LA | 2631 | 2687 | 2054 | 1131 | 379 | 0 | 1059 |
| DEN | 1616 | 2037 | 996 | 1307 | 1235 | 1059 | 0 |

| | BOS/NY/DC/<br>CHI | MIA | SEA | SF/LA | DEN |
|---|---|---|---|---|---|
| BOS/NY/DC/CHI | 0 | 1075 | 2013 | 2054 | 996 |
| MIA | 1075 | 0 | 3273 | 2687 | 2037 |
| SEA | 2013 | 3273 | 0 | 808 | 1307 |
| SF/LA | 2054 | 2687 | 808 | 0 | 1059 |
| DEN | 996 | 2037 | 1307 | 1059 | 0 |

| | BOS/NY/DC/CHI | MIA | SF/LA/SEA | DEN |
|---|---|---|---|---|
| BOS/NY/DC/CHI | 0 | 1075 | 2013 | 996 |
| MIA | 1075 | 0 | 2687 | 2037 |
| SF/LA/SEA | 2054 | 2687 | 0 | 1059 |
| DEN | 996 | 2037 | 1059 | 0 |

| | BOS/NY /DC/CHI/DEN | MIA | SF/LA/SEA |
|---|---|---|---|
| BOS/NY/DC/CHI/DEN | 0 | 1075 | 1059 |
| MIA | 1075 | 0 | 2687 |
| SF/LA/SEA | 1059 | 2687 | 0 |

| | BOS/NY /DC/CHI /DEN/SF /LA/SEA | MIA |
|---|---|---|
| BOS/NY/DC/CHI/DEN/SF/LA/SEA | 0 | 1075 |
| MIA | 1075 | 0 |

# Agglomerative clustering (Hierarchical)

| |
|---|
| BOS |
| NY |
| DC |
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| |
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| BOS/NY |
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| DEN |

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| SF/LA/SEA |
| DEN |

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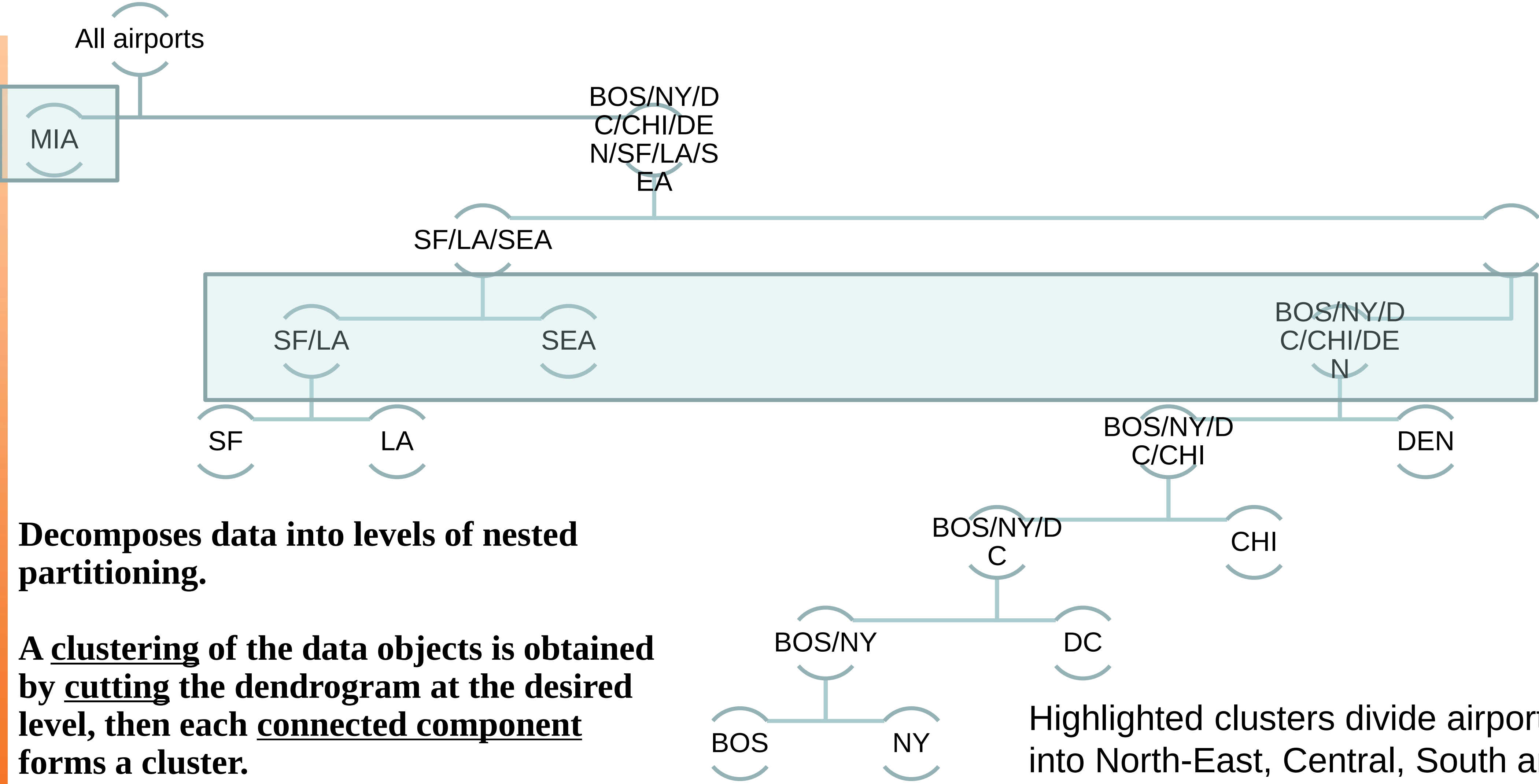
| BOS/NY/DC/CHI/DEN |
| MIA |
| SF/LA/SEA |

| |
|---|
| BOS/NY/DC/CHI/DEN/SF/LA/SEA |
| MIA |

Typically, a particular "level" of the hierarchy is selected to be your clustering result

Highlighted clusters divide airports into North-East, Central, South and Pacific areas

# Agglomerative clustering (Hierarchical)




**Decomposes data into levels of nested partitioning.**

**A <u>clustering</u> of the data objects is obtained by <u>cutting</u> the dendrogram at the desired level, then each <u>connected component</u> forms a cluster.**

Highlighted clusters divide airports into North-East, Central, South and Pacific areas

# Agglomerative clustering (Hierarchical)

- Assign each item to its own cluster, so that if you have N items, you now have N clusters, each containing just one item.
- Merge most similar clusters into a single cluster, so that now you have one less cluster.
- Compute distances (similarities) between the new cluster and each of the old clusters.
- Repeat steps 2 and 3 until all items are clustered into a single cluster of size N.

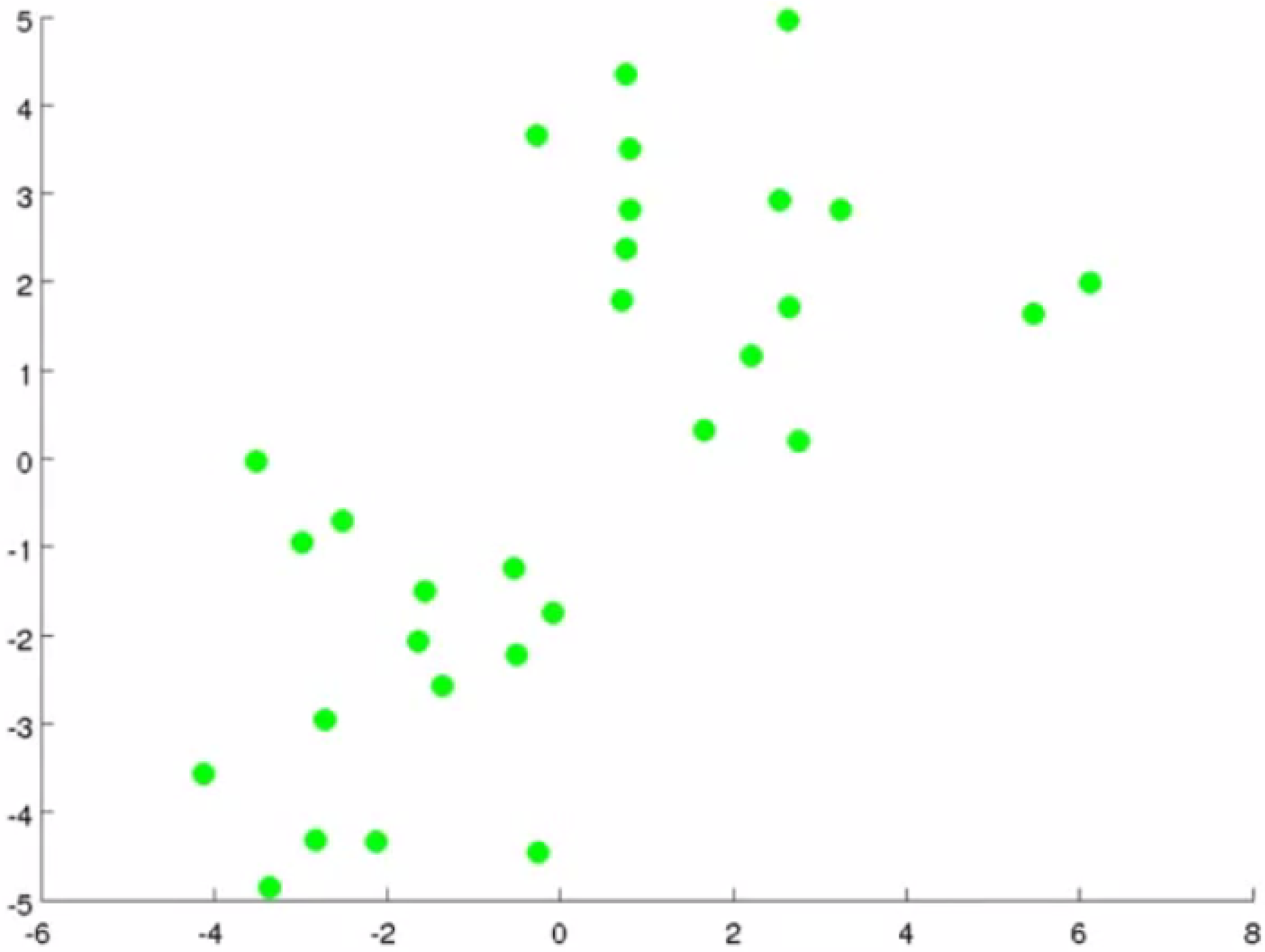
Partitioning algorithms

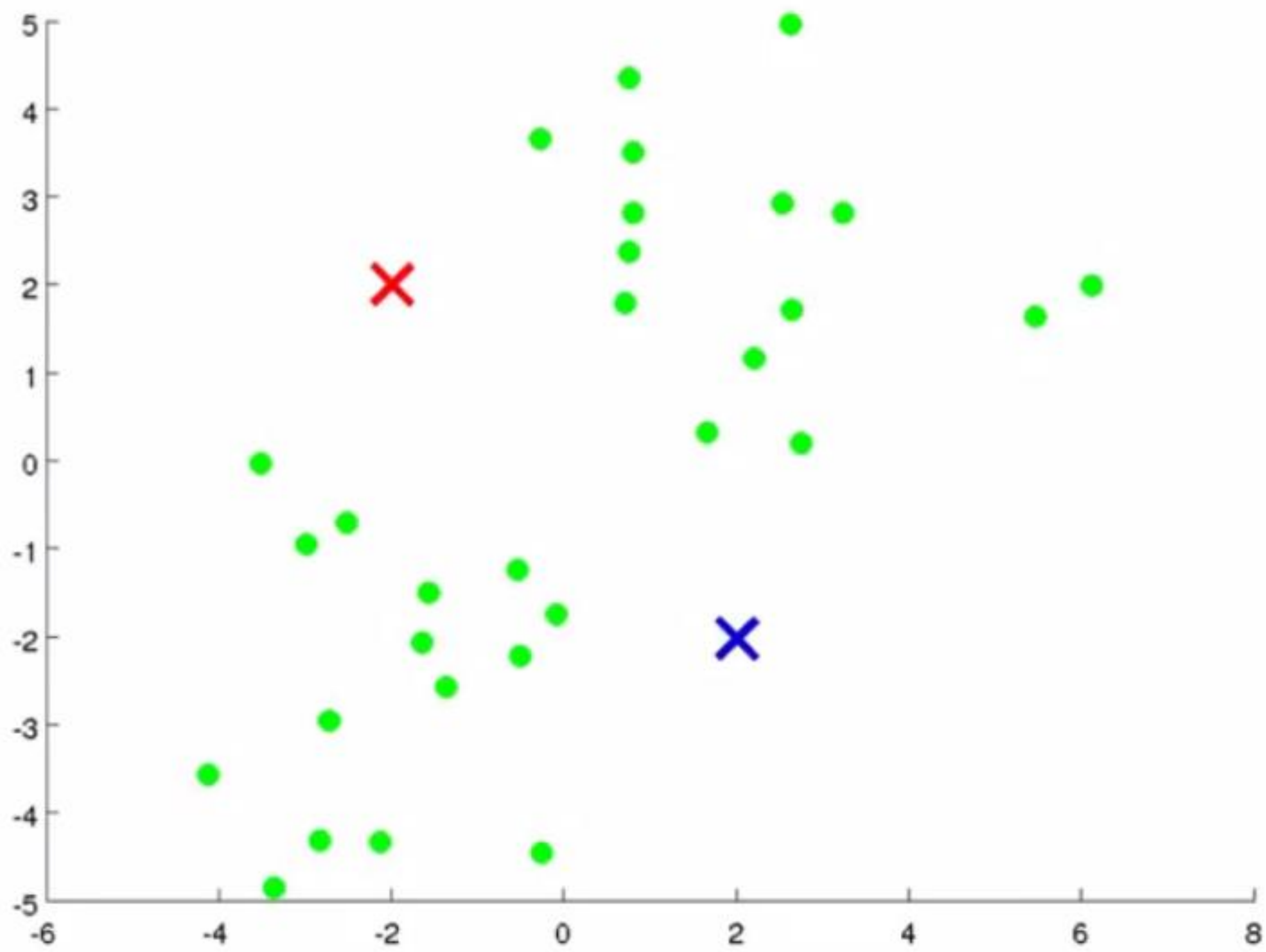
# K-MEANS AND K-MEDOIDS

# K-means clustering

- K-means is a partitional clustering algorithm as it partitions the given data into *k* clusters.
  - Each cluster has a cluster **center**, called **centroid**.
  - *k* is specified by the user

Pictures courtesy Andrew Ngs course on Coursera

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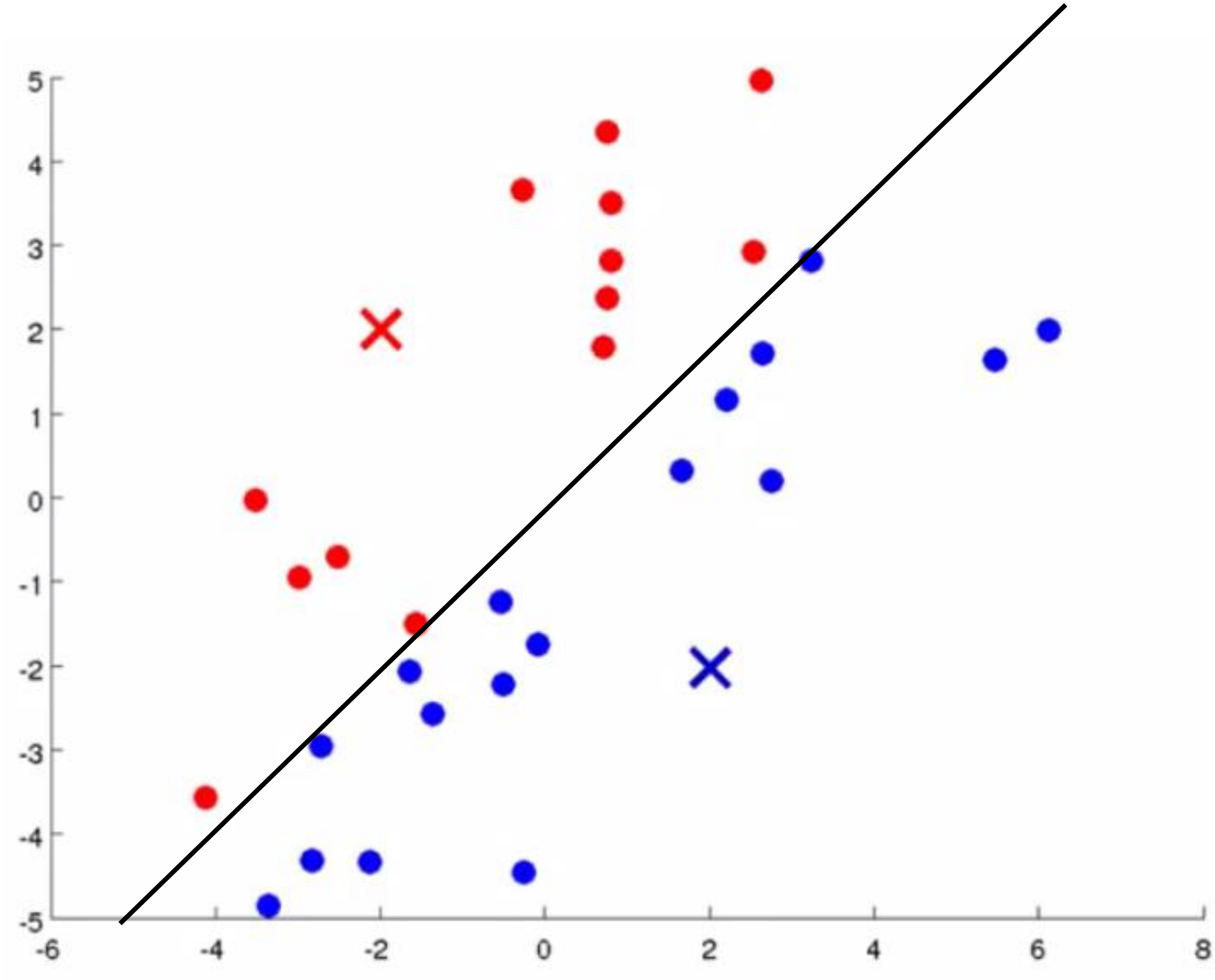
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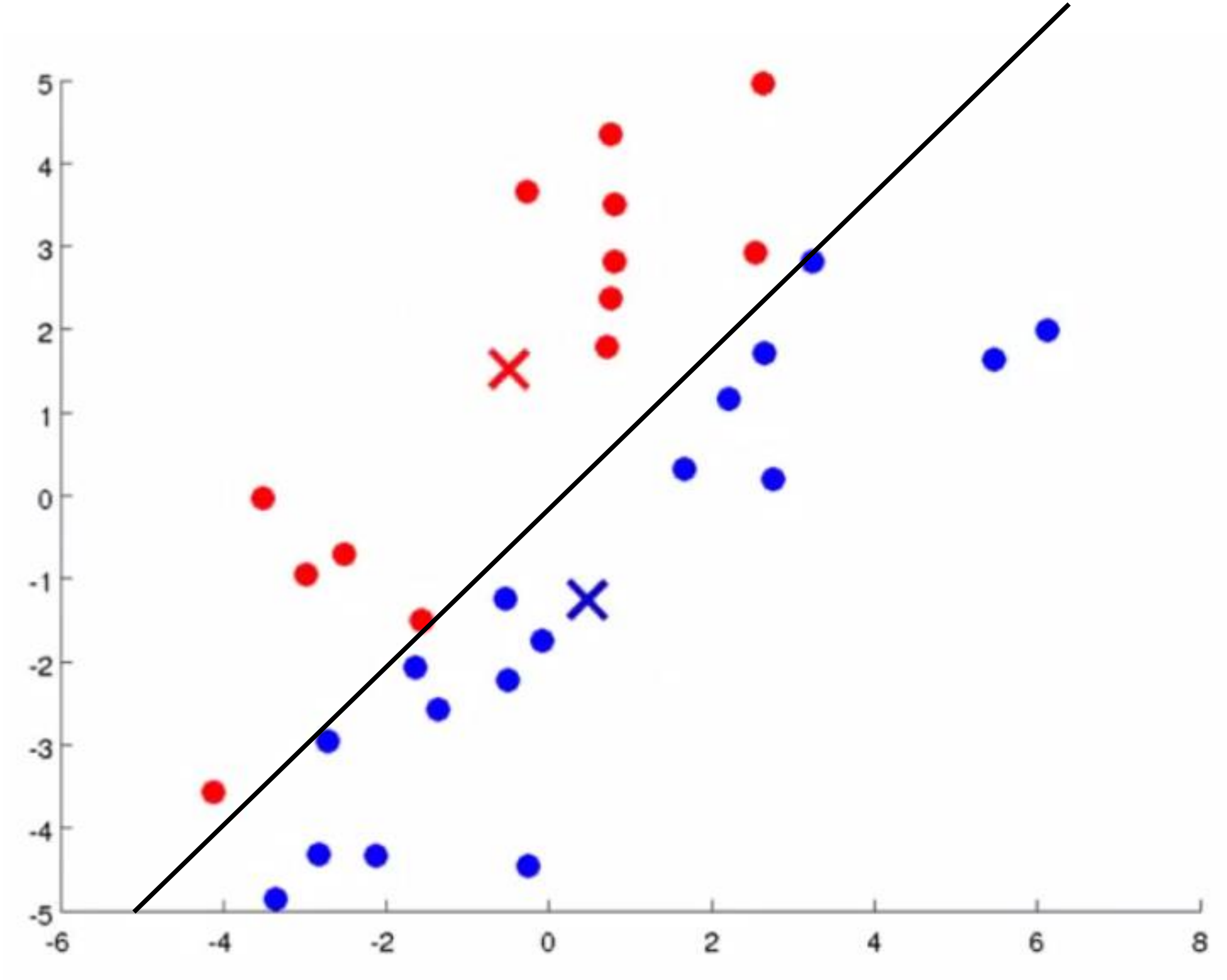

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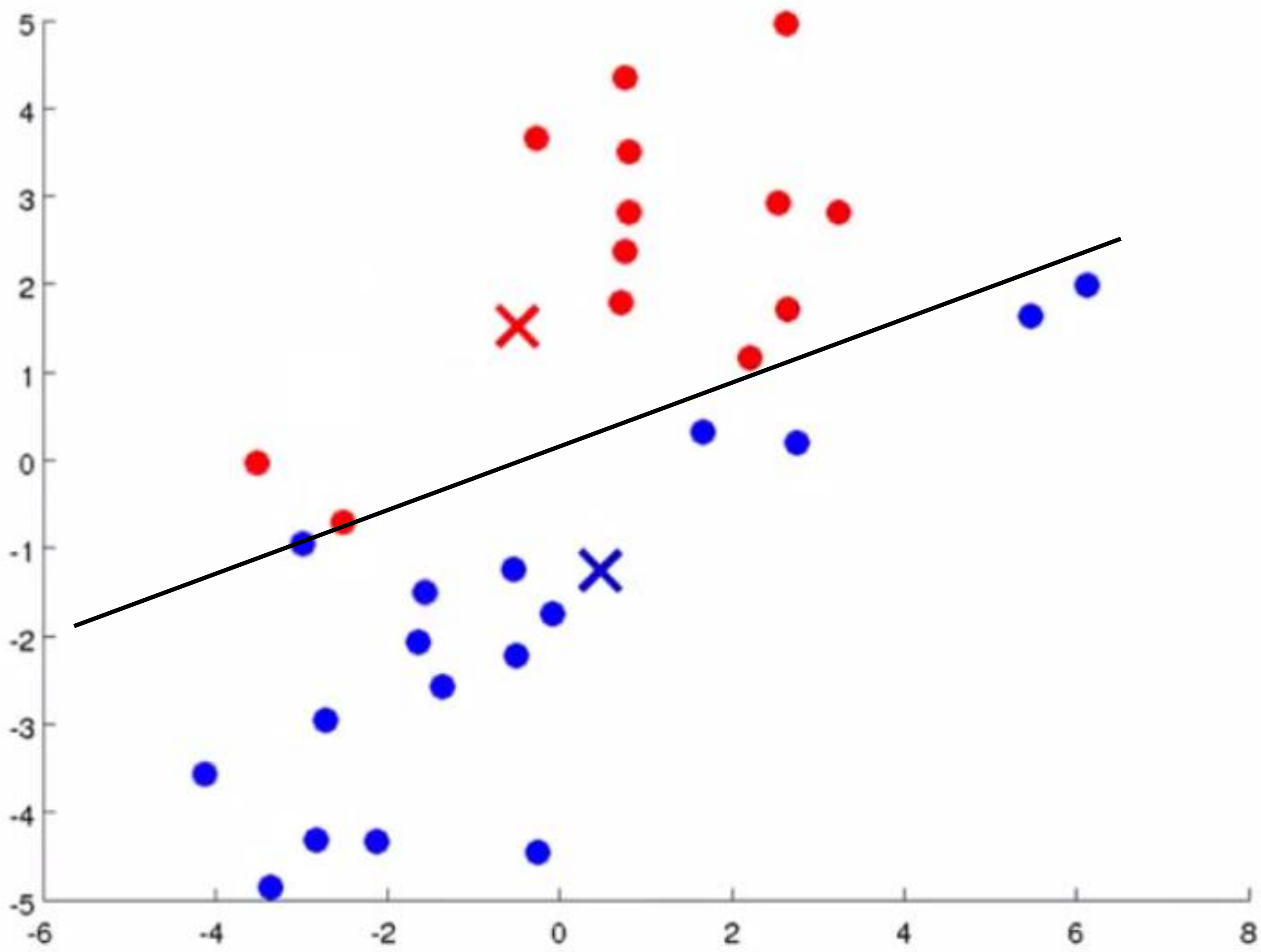
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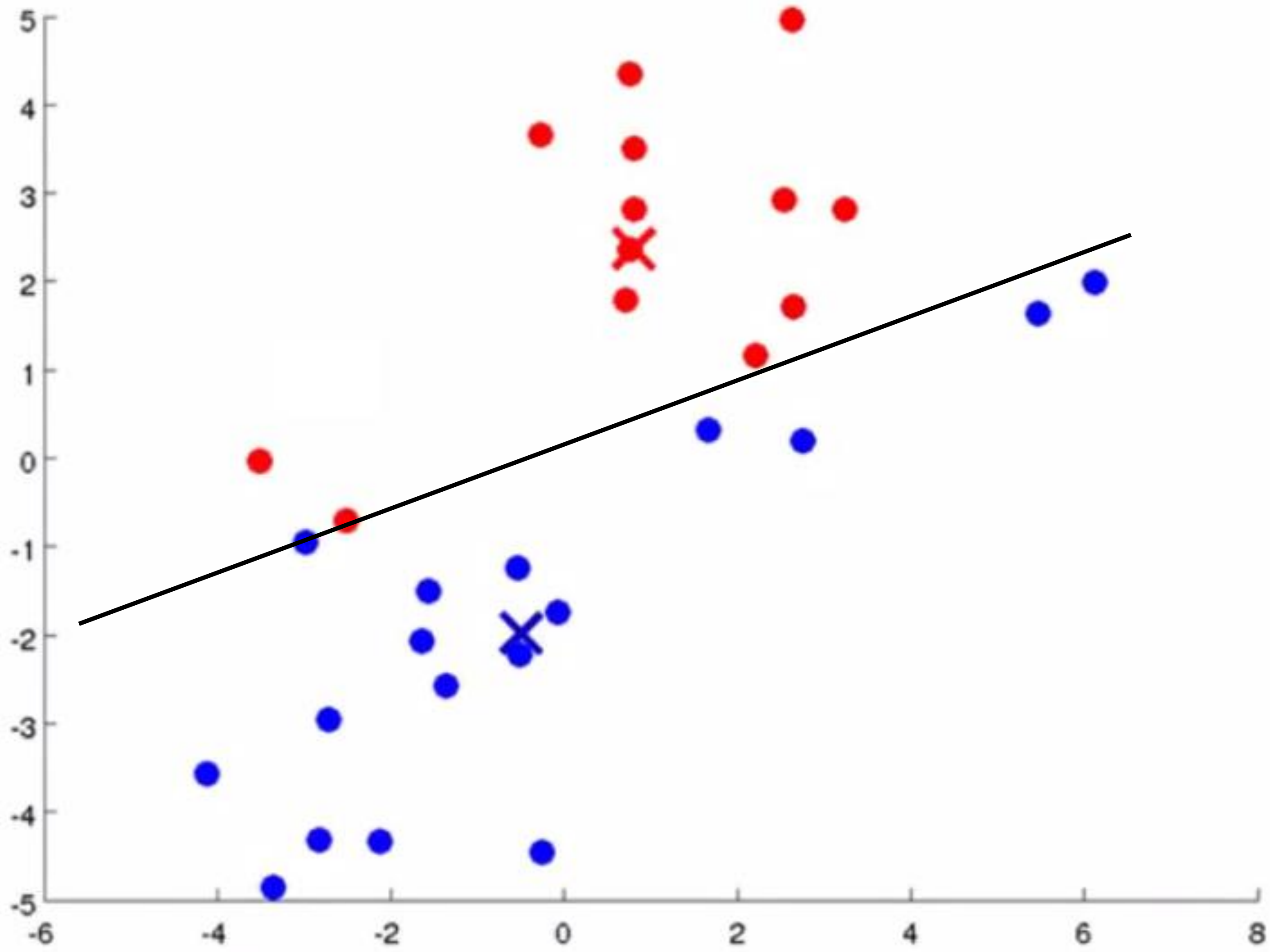
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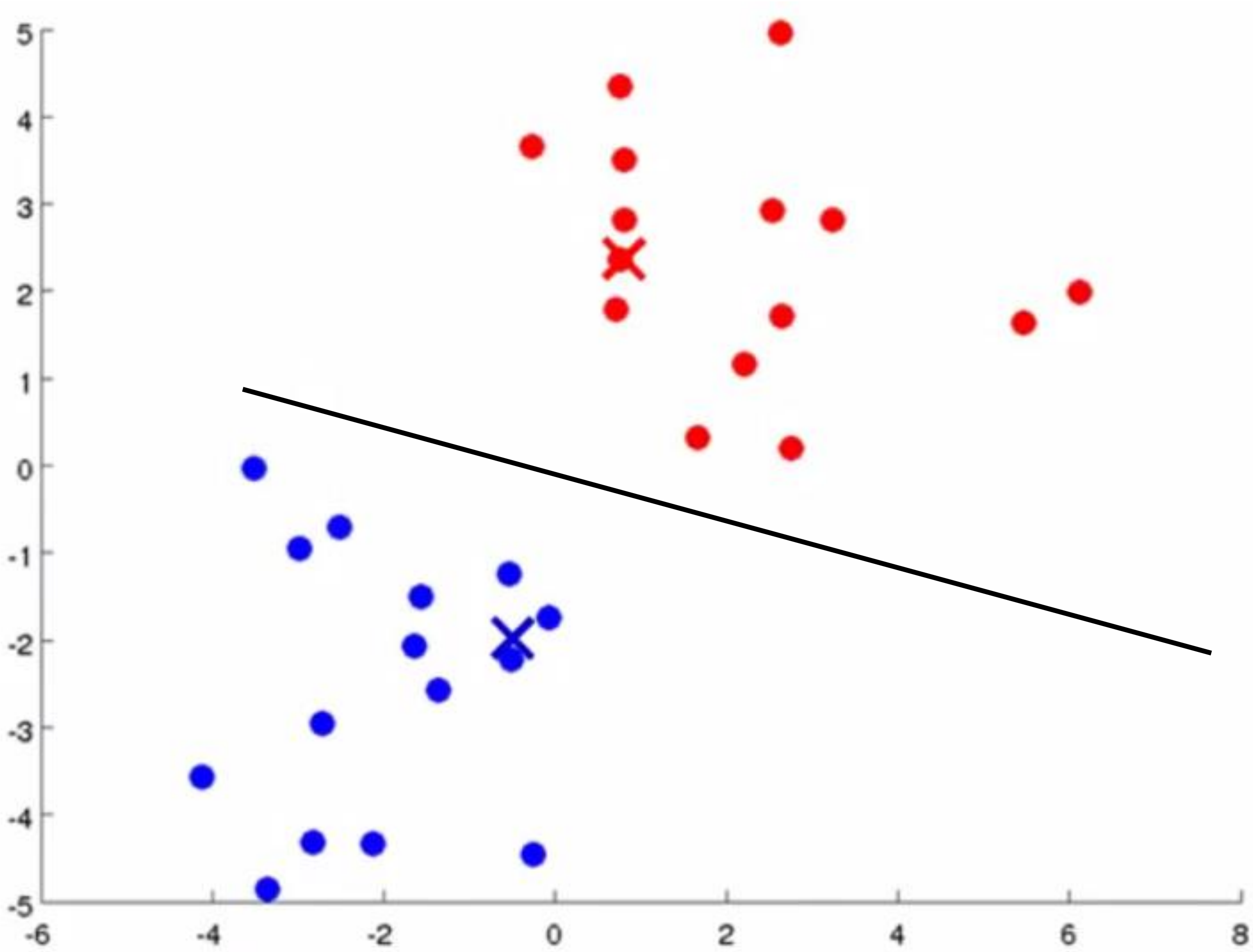
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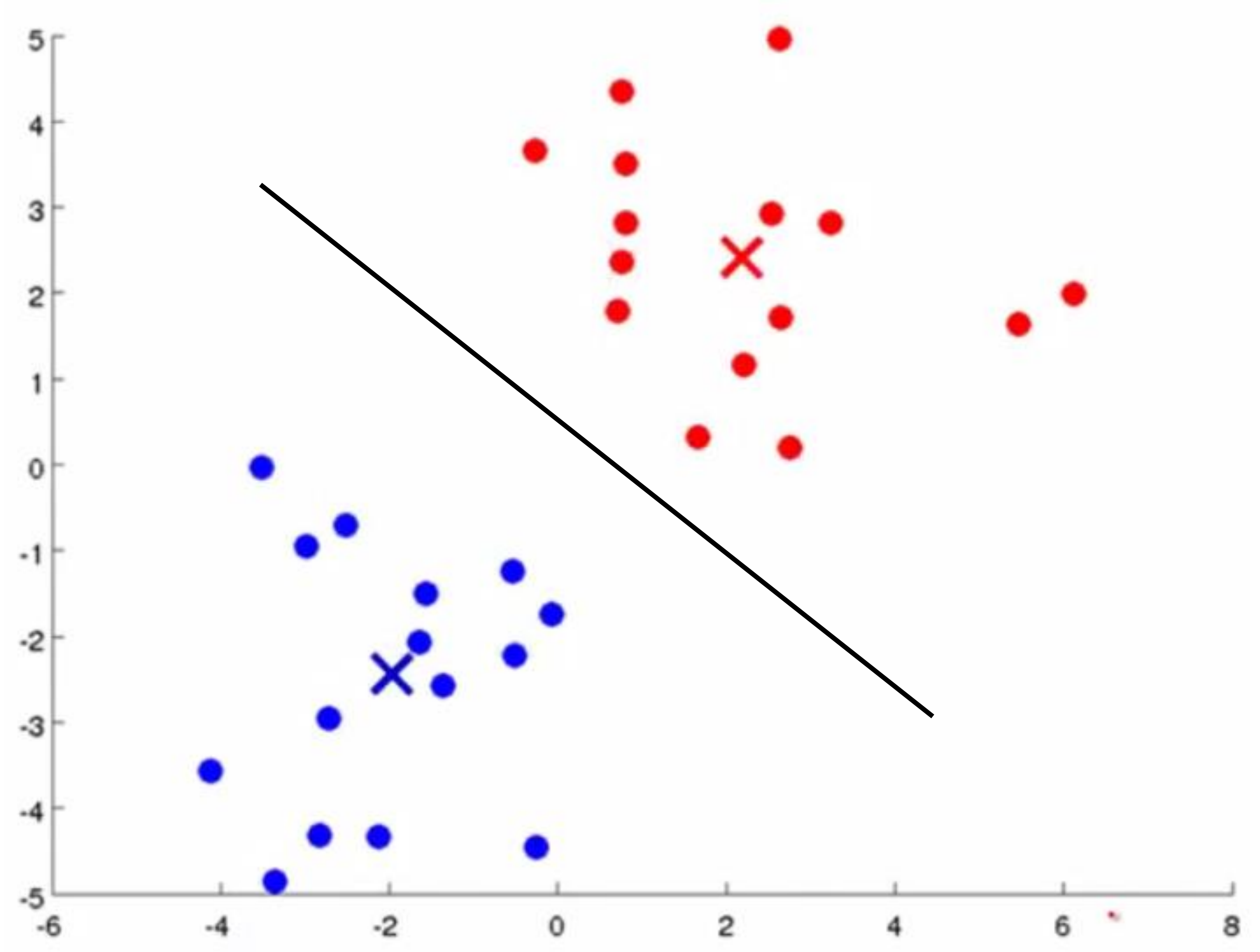

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# K-means algorithm

- Given *k*, the *k-means* algorithm works as follows:

1. Randomly choose *k* data points (seeds) to be the initial centroids, cluster centers
2. Assign each data point to the closest centroid
3. Re-compute the centroids using the current cluster memberships.
4. If a convergence criterion is not met, go to 2.

# Stopping/convergence criterion

1. no (or minimum) re-assignments of data points to different clusters,
2. no (or minimum) change of centroids, or
3. minimum decrease in the **sum of squared error** (SSE),

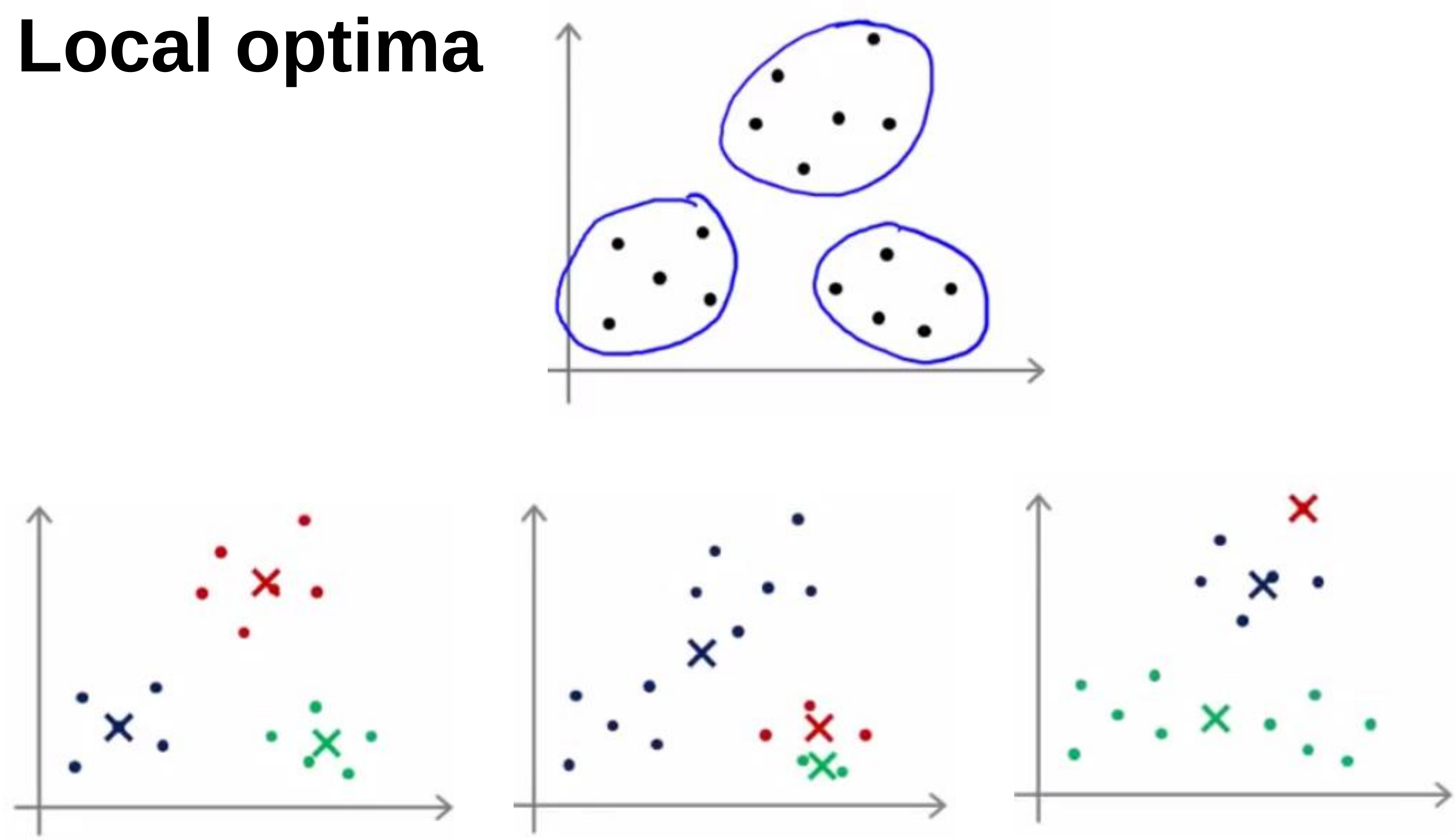
$$SSE = \sum_{j=1\ldots k} \sum_{x \in C_j} dist(x, m_j)^2 \qquad (1)$$

– $C_j$ is the $j$th cluster, $\mathbf{m}_j$ is the centroid (mean) of cluster $C_j$

Check SCREE plots.

http://stackoverflow.com/questions/15376075/cluster-analysis-in-r-determine-the-optimal-number-of-clusters

# Local optima



# What Is the Problem with K-Means?

- The k-means algorithm is sensitive to outliers !
- K-Medoids: Instead of taking the **mean** value of the object in a cluster as a reference point, **medoids** can be used, which is the **most centrally located** object in a cluster.

# What Is the Problem with Medoids?

- More robust than k-means in the presence of noise and outliers because a medoid is less influenced by outliers or other extreme values than a mean
- Works efficiently for small data sets but does not **scale well** for large data sets.
  - In regular K-Means, the new mean is merely average of values O(nkt)
  - In K-Medoid, if a particular cluster has $n_c$ data points, you will need $(n_c)^2$ computations to determine the medoid for that cluster
    - While the cost of the configuration decreases:
      - For each medoid *m*, for each non-medoid data point *o*:
        - » Swap *m* and *o*, recompute the cost (sum of distances of points to their medoid)
        - » If the total cost of the configuration increased in the previous step, undo the swap
  - $O(k(n-k)^2)$ for each iteration, where n is # of data, k is # of clusters, t: # of iterations

# K-means versus Hierarchical

- K-means produces a single partitioning
- K-means needs the number of clusters to be specified
- K-means is usually more efficient run-time wise

- Hierarchical Clustering can give different partitions depending on the level-of-resolution we are looking at
- Hierarchical clustering doesn’t need the number of clusters to be specified
- Hierarchical clustering can be slow (has to make several merge/Split decisions)

# HOW DO WE EMPLOY DISTANCE IN A CLUSTER

# What do we mean by distance *between* Clusters

- Single link: smallest distance between an element in one cluster and an element in the other, i.e., $dis(K_i, K_j) = min(t_{ip}, t_{jq})$
- Complete link: largest distance between an element in one cluster and an element in the other, i.e., $dis(K_i, K_j) = max(t_{ip}, t_{jq})$
- Average: average distance between an element in one cluster and an element in the other, i.e., $dis(K_i, K_j) = avg(t_{ip}, t_{jq})$
- **Centroid: distance between the centroids of two clusters, i.e., $dis(K_i, K_j) = dis(C_i, C_j)$**
- Medoid: distance between the medoids of two clusters, i.e., $dis(K_i, K_j) = dis(M_i, M_j)$
  - Medoid: one chosen, centrally located object in the cluster

# Centroid, Radius & Diameter of a Cluster (for numerical data sets)

- Centroid: the "middle" of a cluster

$$C_m = \frac{\sum_{i=1}^{N}(t_{ip})}{N}$$

- Radius: square root of average distance from any point of the cluster to its centroid

$$R_m = \sqrt{\frac{\sum_{i=1}^{N}(t_{ip} - c_m)^2}{N}}$$

- Diameter: square root of average mean squared distance between all pairs of points in the cluster

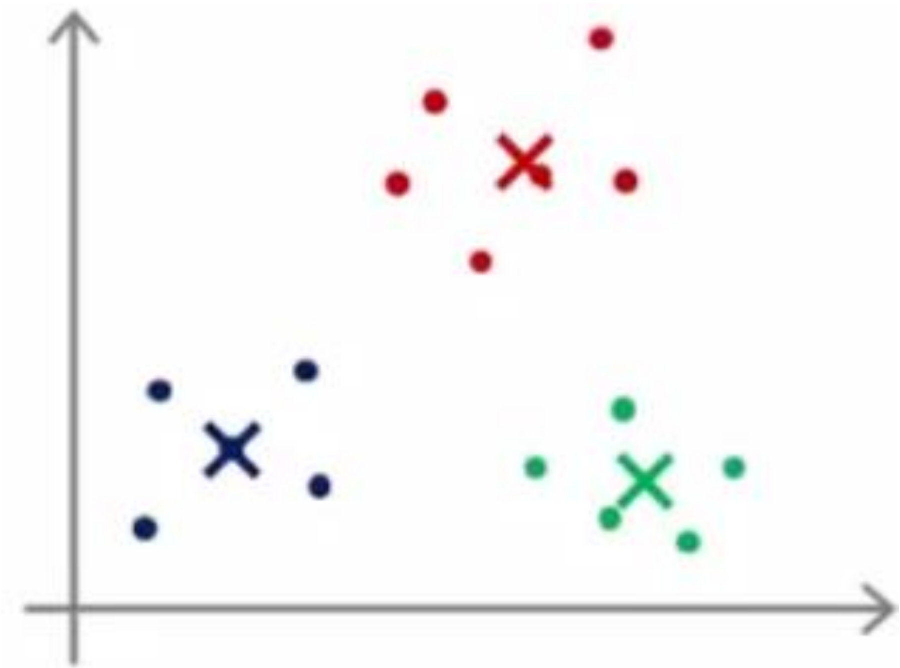
$$D_m = \sqrt{\frac{\sum_{i=1}^{N}\sum_{i=1}^{N}(t_{ip} - t_{iq})^2}{N(N-1)}}$$

# ENGINEERING

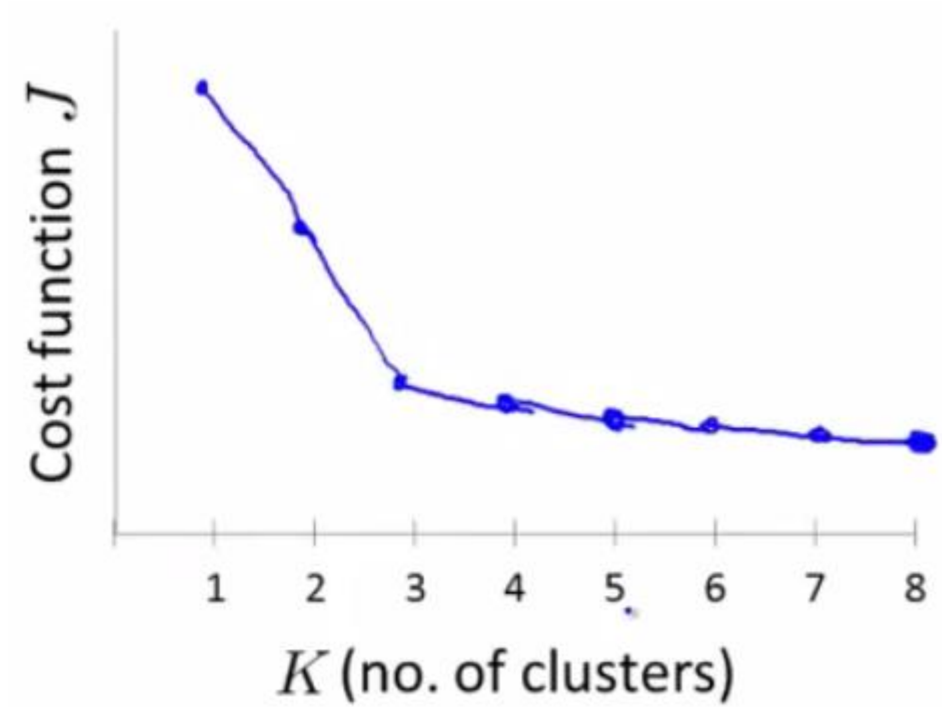
# Stability Check of the Clusters

- To check the stability of the clusters take a random sample of 95% of records. Compute the clusters. If the clusters formed are very similar to the original, then the clusters are fine.

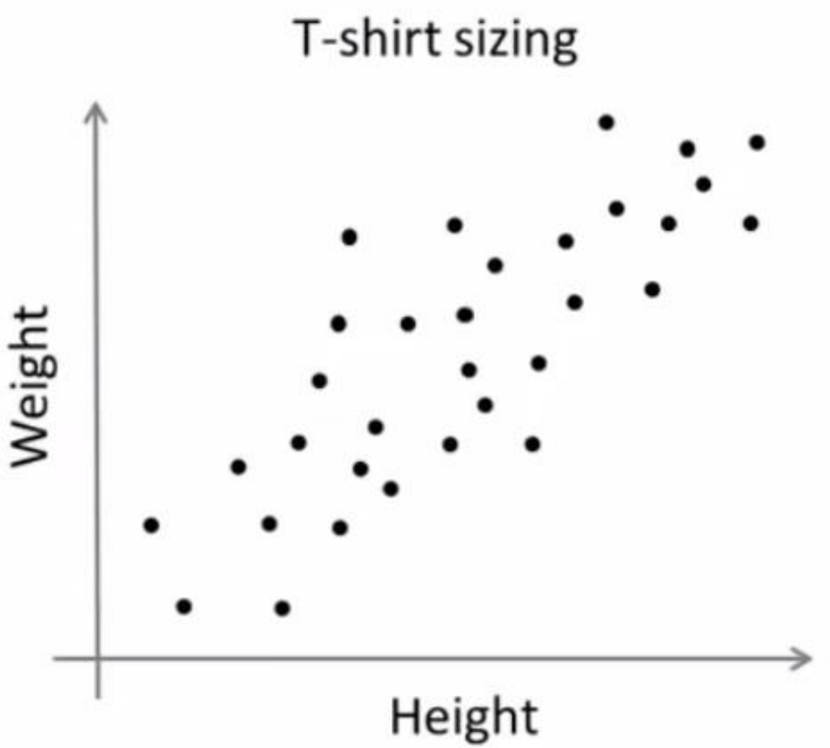
# Linearly clustered data

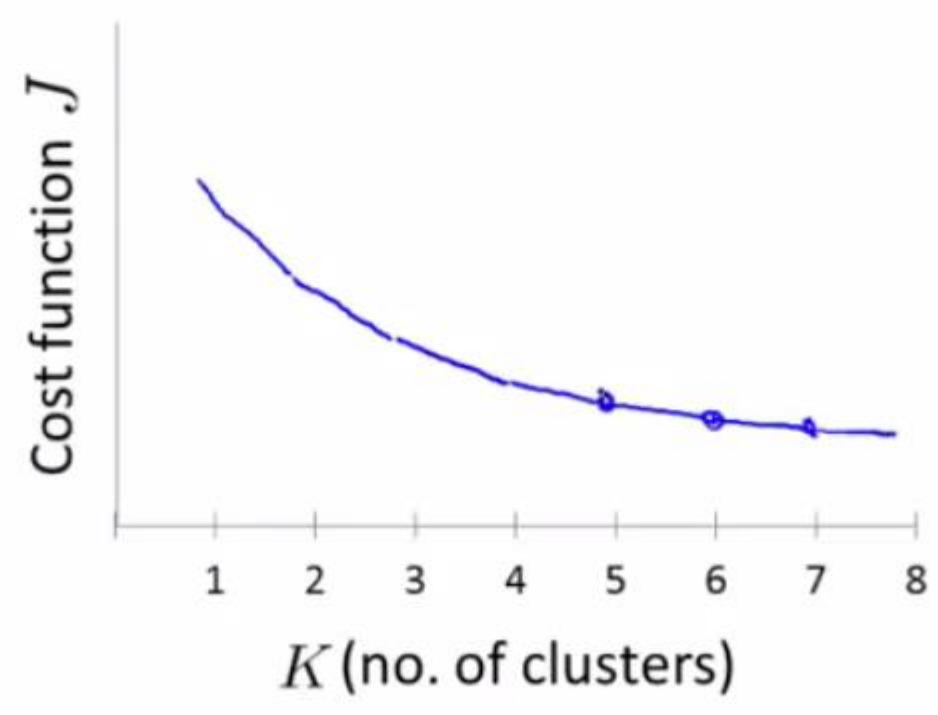


Nice



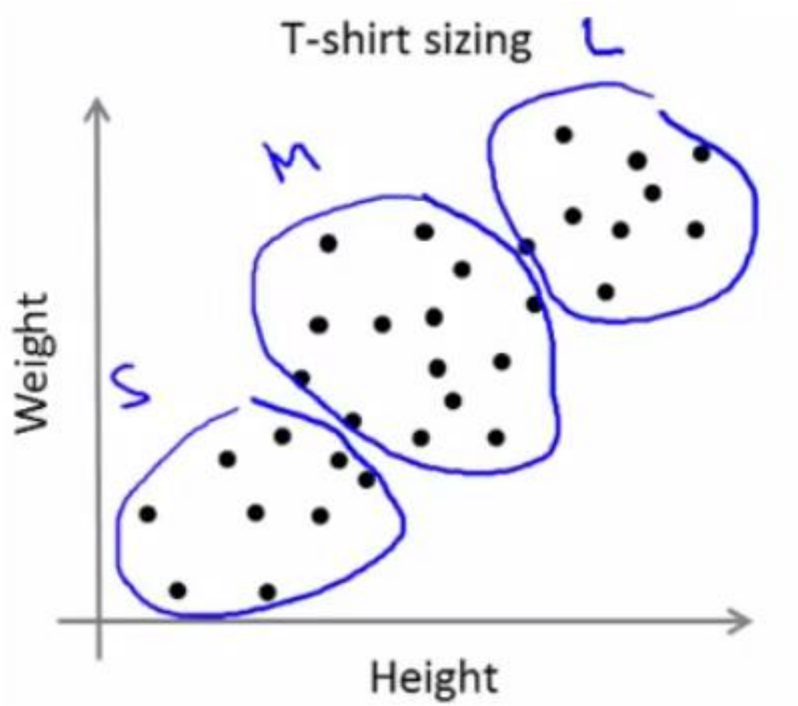
# Linearly separable but merged

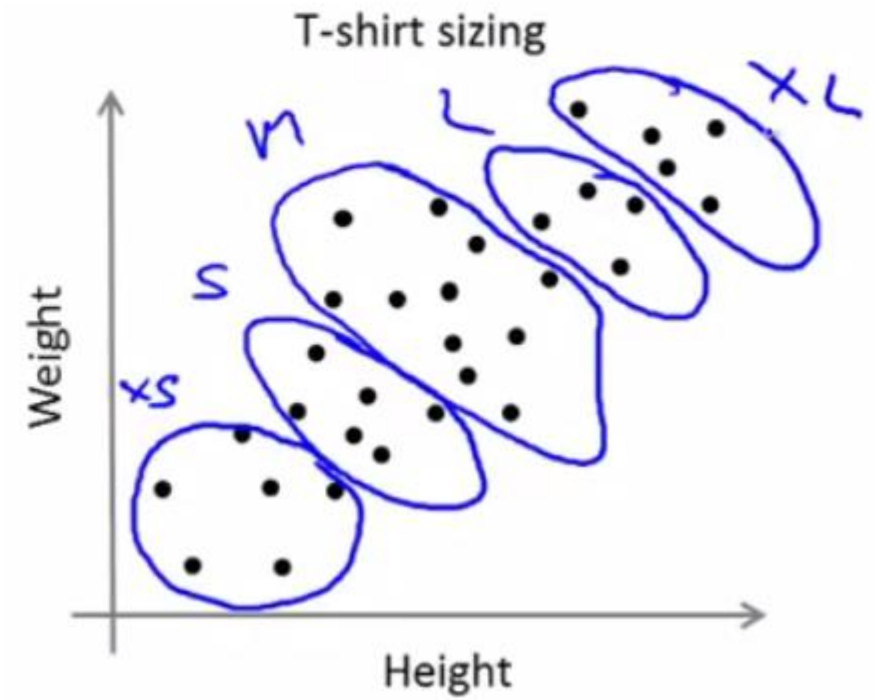



Data points of individuals of a particular height and weight

# Linearly separable but merged



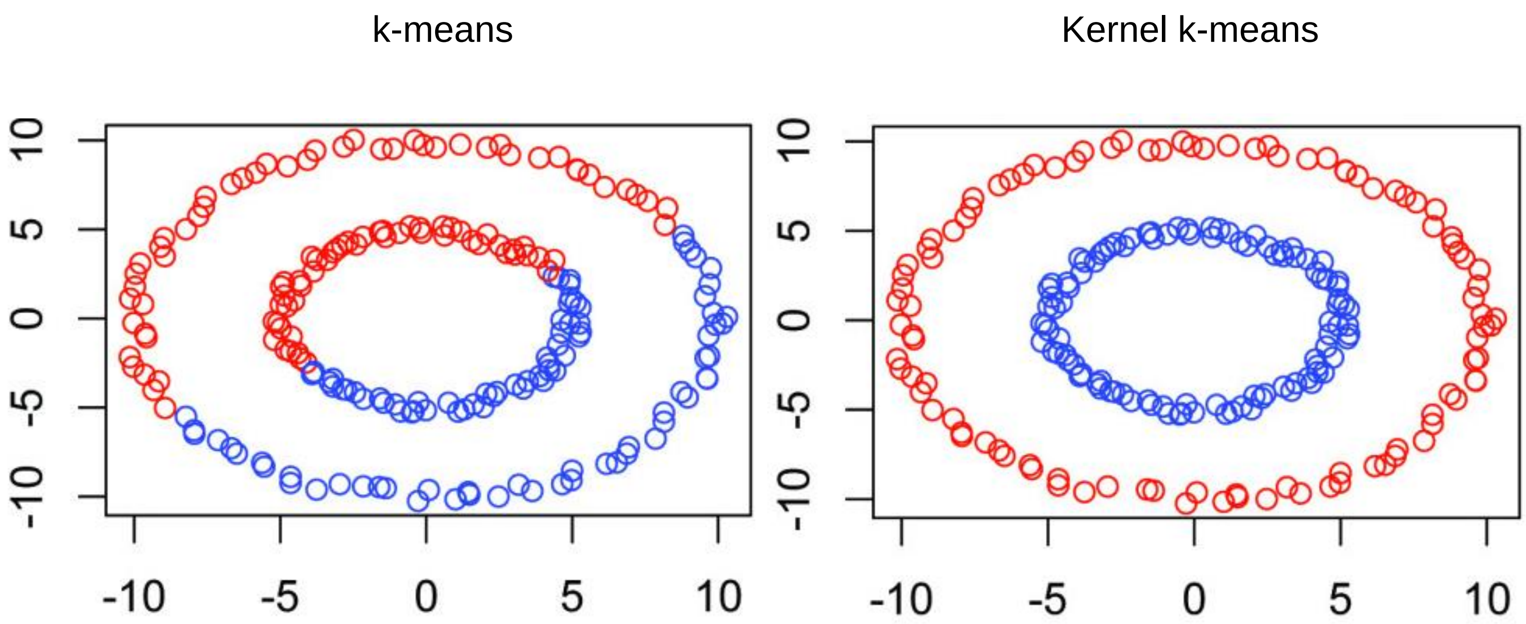




Clustering the data points into T-shirt sizes. Top: Three sizes, Right: Five sizes

# Linearly separable

- Run 50-500 simulations for small k (2-10). For large k (100 or so), we can do 1-5 simulations
- Pick the one that gives the best SSE

# k-means Vs. Kernel k-means



# Performance of Kernel K-means

Clustering accuracy (%) achieved by each clustering algorithm for 10 data sets

| Data set | Conventional *k*-means | Kernel *k*-means |
|---|---|---|
| BENSAID | 79.59 | 83.67 |
| DUNN | 70.00 | 71.11 |
| IRIS | 89.33 | 96.00 |
| ECOLI | 42.86 | 68.75 |
| CIRCLE | 50.76 | 100.0 |
| BLE-3 | 65.67 | 76.33 |
| BLE-2 | 88.50 | 100.0 |
| UE-4 | 77.25 | 100.0 |
| UE-3 | 95.83 | 98.83 |
| ULE-4 | 76.25 | 98.00 |
| Avg. (%) | 73.60 | 89.27 |

*Evaluation of the performance of clustering algorithms in kernel-induced feature space, Pattern Recognition, 2005*

# Kernel Trick

- The original way is to transform each data point into a high dimensional space and then do computation
  - This can be computationally complex
- Note that we need to compute distances in Euclidian space, or sometimes scalar product

# Kernel Trick

- Take two points: $X_1 = (x_{11}, x_{12})$ $X_2 = (x_{21}, x_{22})$
  - $Euclidian\ distance: d(X_1, X_2) = \sqrt{(x_{11} - x_{21})^2 + (x_{12} - x_{22})^2}$
  - $Dot\ product: X_1.X_2 = (x_{11}.x_{21}) + (x_{12}.x_{22})$
- Take to a higher dimensional space

$$\check{X}_1 = \left(x_{11}, x_{12}, {x_{11}}^2, {x_{12}}^2, \sqrt{2}x_{11}x_{12}\right)$$

$$\check{X}_2 = \left(x_{21}, x_{22}, {x_{21}}^2, {x_{22}}^2, \sqrt{2}x_{21}x_{22}\right)$$

$$\Phi(\mathbf{a}) \bullet \Phi(\mathbf{b}) = \begin{pmatrix} 1 \\ \sqrt{2}a_1 \\ \sqrt{2}a_2 \\ \vdots \\ \sqrt{2}a_m \\ a_1^2 \\ a_2^2 \\ \vdots \\ a_m^2 \\ \sqrt{2}a_1a_2 \\ \sqrt{2}a_1a_3 \\ \vdots \\ \sqrt{2}a_1a_m \\ \sqrt{2}a_2a_3 \\ \vdots \\ \sqrt{2}a_1a_m \\ \vdots \\ \sqrt{2}a_{m-1}a_m \end{pmatrix} \bullet \begin{pmatrix} 1 \\ \sqrt{2}b_1 \\ \sqrt{2}b_2 \\ \vdots \\ \sqrt{2}b_m \\ b_1^2 \\ b_2^2 \\ \vdots \\ b_m^2 \\ \sqrt{2}b_1b_2 \\ \sqrt{2}b_1b_3 \\ \vdots \\ \sqrt{2}b_1b_m \\ \sqrt{2}b_2b_3 \\ \vdots \\ \sqrt{2}b_1b_m \\ \vdots \\ \sqrt{2}b_{m-1}b_m \end{pmatrix}$$

$$1 + \sum_{i=1}^{m} 2a_ib_i + \sum_{i=1}^{m} a_i^2b_i^2 + \sum_{i=1}^{m}\sum_{j=i+1}^{m} 2a_ia_jb_ib_j$$

Define K(**a**,**b**) = $(\mathbf{a}.\mathbf{b}+1)^2$

$$= (\mathbf{a}.\mathbf{b})^2 + 2\mathbf{a}.\mathbf{b} + 1$$

$$= \left(\sum_{i=1}^{m} a_ib_i\right)^2 + 2\sum_{i=1}^{m} a_ib_i + 1$$

$$= \sum_{i=1}^{m}\sum_{j=1}^{m} a_ib_ia_jb_j + 2\sum_{i=1}^{m} a_ib_i + 1$$

$$= \sum_{i=1}^{m} (a_ib_i)^2 + 2\sum_{i=1}^{m}\sum_{j=i+1}^{m} a_ib_ia_jb_j + 2\sum_{i=1}^{m} a_ib_i + 1$$

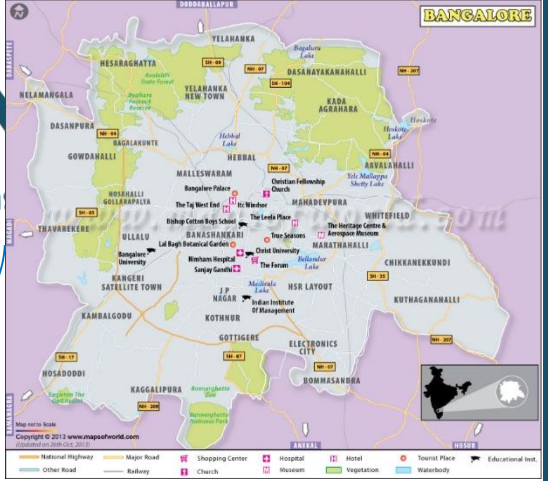
Both are same!

And K(a,b) is only O(m) to compute!

# Other Topics

- Clustering large datasets
  - Select a small % of data, run K-means or K-medoids
  - CLARA and CLARANS (Ng and Han 1994, 2002)
- Parallel and Efficient implementations of K-means / K-medoids

http://www.math.unipd.it/~dulli/corso04/ng94efficient.pdf
https://anuradhasrinivas.files.wordpress.com/2013/04/lesson8-clustering.pdf
http://www.vlfeat.org/overview/kmeans.html
http://repository.cmu.edu/cgi/viewcontent.cgi?article=2397&context=compsci
http://www.cs.ucsb.edu/~veronika/MAE/Global_Kernel_K-Means.pdf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