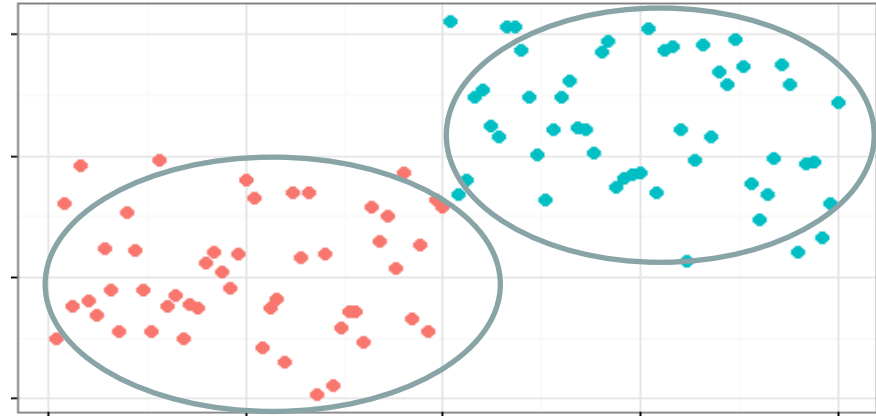
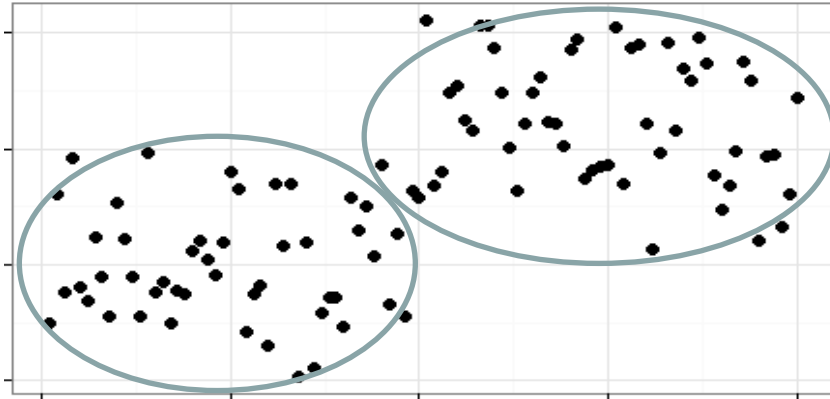




Inspire...Educate...Transform.

Clustering and Linear algebra

Dr. Kishore Reddy Konda
Mentor, INSOF



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
- It is not uncommon to have over 100,000 segments in insurance clustering
- Given a collection of text documents, organize them according to their content similarities,
 - E.g., Google news
- Blind signal separation (separating two speakers)



Algorithms

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



UNDERSTANDING DISTANCE

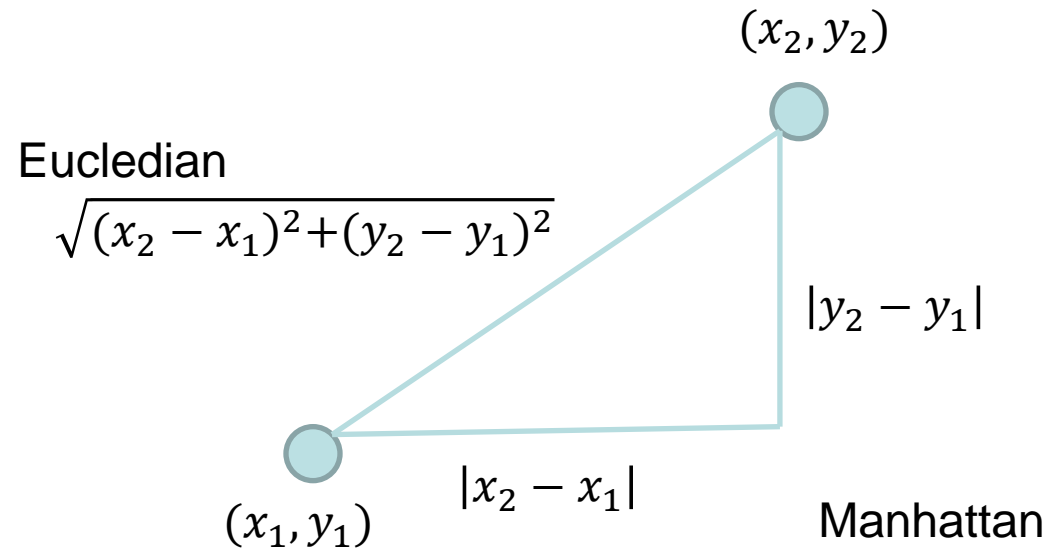


Desiderata for proximity

- If d_1 is near d_2 , then d_2 is near d_1 .
- If d_1 near d_2 , and d_2 near d_3 , then d_1 is not far from d_3 .
- No document is closer to d than d itself.



Numeric



Some Other Common Metrics

- Weighted distances
 - More important variables get higher weights
- Minkowski distance
 - $\sqrt[n]{(x_2 - x_1)^n + (y_2 - y_1)^n}$
- The maximum distance amongst all attributes
- Correlation between rows



Norms

The inner product generated norm $\|X\|_W = \sqrt{\langle X, \bar{X} \rangle_W}$

Euclidean or l_2 norm $\|X\|_2 = \sqrt{X \cdot \bar{X}}$

The l_1 norm $\|X\|_1 = |x_1| + |x_2| + |x_3| + \dots + |x_n|$

The l_∞ norm $\|X\|_\infty = \max(|x_1|, |x_2|, |x_3|, \dots, |x_n|)$

The l_p norm $\|X\|_p = (|x_1|^p + |x_2|^p + |x_3|^p + \dots + |x_n|^p)^{\frac{1}{p}}$

Frobenius norm of a matrix is Euclidean version

$$\|A\|_F = \sqrt{\sum \sum |a_{ij}|^2}$$



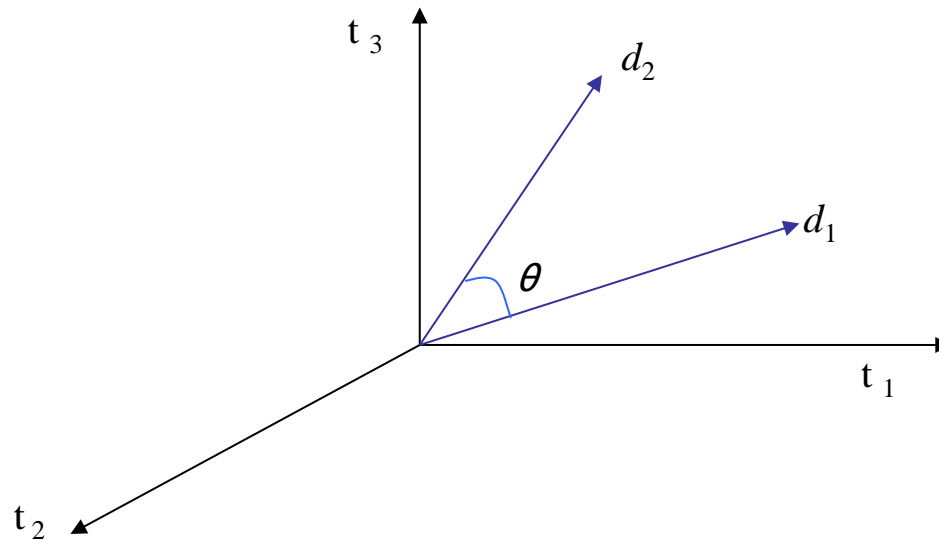
Similarity Measure for documents

- We now have vectors for all documents in the collection, a vector for the query, how to compute **similarity**?
- Using a similarity measure between the query and each document:
 - It is possible to rank the retrieved documents in the order of presumed relevance (query-dependent ranking).
 - It is possible to enforce a certain threshold so that the size of the retrieved set can be controlled.



Cosine similarity

- Distance between vectors d_1 and d_2 captured by the cosine of the angle θ between them.
- Note – this is actually *similarity*, not distance



Cosine similarity

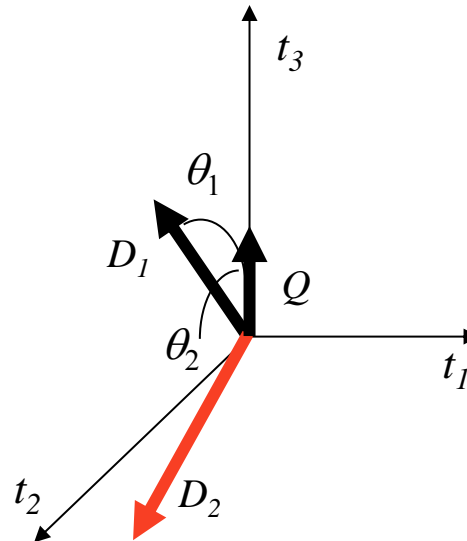
$$\text{sim}(d_j, d_k) = \frac{\vec{d}_j \cdot \vec{d}_k}{|\vec{d}_j| |\vec{d}_k|} = \frac{\sum_{i=1}^n w_{i,j} w_{i,k}}{\sqrt{\sum_{i=1}^n w_{i,j}^2} \sqrt{\sum_{i=1}^n w_{i,k}^2}}$$

- Cosine of angle between two vectors
- The denominator involves the lengths of the vectors
- The cosine measure is also known as the *normalized inner product*



Cosine Similarity vs. Inner Product

$$\begin{aligned} D_1 &= 2T_1 + 3T_2 + 5T_3 & \text{CosSim}(D_1, Q) &= 10 / \sqrt{(4+9+25)(0+0+4)} = 0.81 \\ D_2 &= 3T_1 + 7T_2 + 1T_3 & \text{CosSim}(D_2, Q) &= 2 / \sqrt{(9+49+1)(0+0+4)} = 0.13 \\ Q &= 0T_1 + 0T_2 + 2T_3 \end{aligned}$$



D_1 is 6 times better than D_2 using cosine similarity but only 5 times better using inner product.

Categorical Attributes in Unsupervised Settings

- Unsupervised setting
 - Approach 1: Create dummies and use the same metric you use for numeric attributes

Attribute
1
2
3



Attribute	a1	a2	a3
1	1	0	0
2	0	1	0
3	0	0	1

Categorical Attributes in Unsupervised Settings: II

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

$$\text{Hamming distance} = \frac{\text{\#of dissimilar attributes}}{\text{\#of dissimilar} + \text{\#of similar}} = \frac{b + c}{b + c + a + d}$$



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
 - We can have some variations, adding weights

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

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

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

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

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



Cat variables: Supervised learning

Cat Attribute	C1	C2	C3
L1	78	22	0
L2	90	7	3
L3	77	22	1
L4			
L5			
L6			

Use this information for clustering or distances

R1: L1, R2: L2, R3:L3

R1-R2 is farther than R1-R3:



Ordinal Variables

- Same as numeric
- Look up is better than computation



Look Up Matrix for Ordinal with 3 States

	1	2	3
1	0	1	4
2	1	0	1
3	4	1	0

BACK TO MODELS



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

	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

	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

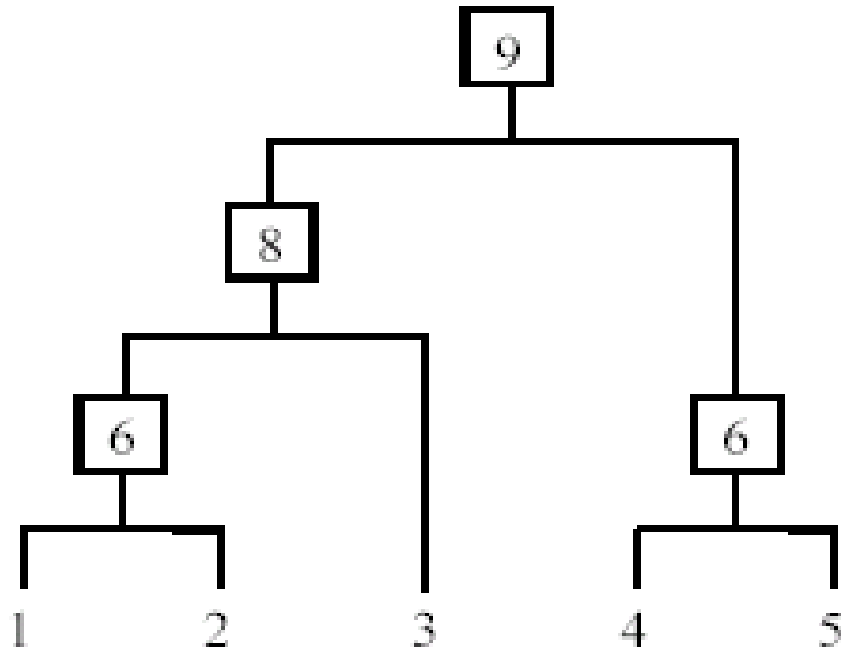
	BOS/NY/DC/ CHI	MIA	SEA	SF/LA	DEN
BOS/NY/DC/CHI	0	1075	2013	2054	996
MIA	1075	0	3273	2687	2037
SEA	2013	3273	0	808	1307
SF/LA	2054	2687	808	0	1059
DEN	996	2037	1307	1059	0

	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

Hierarchical Clustering



Decomposes data objects into several levels of nested partitioning (tree of clusters).

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

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 .



Pvclust: Stability Experiment

- A number of bootstrapped samples
- See how many times a cluster is formed at that level
- Declare a probability value for the cluster based on the count



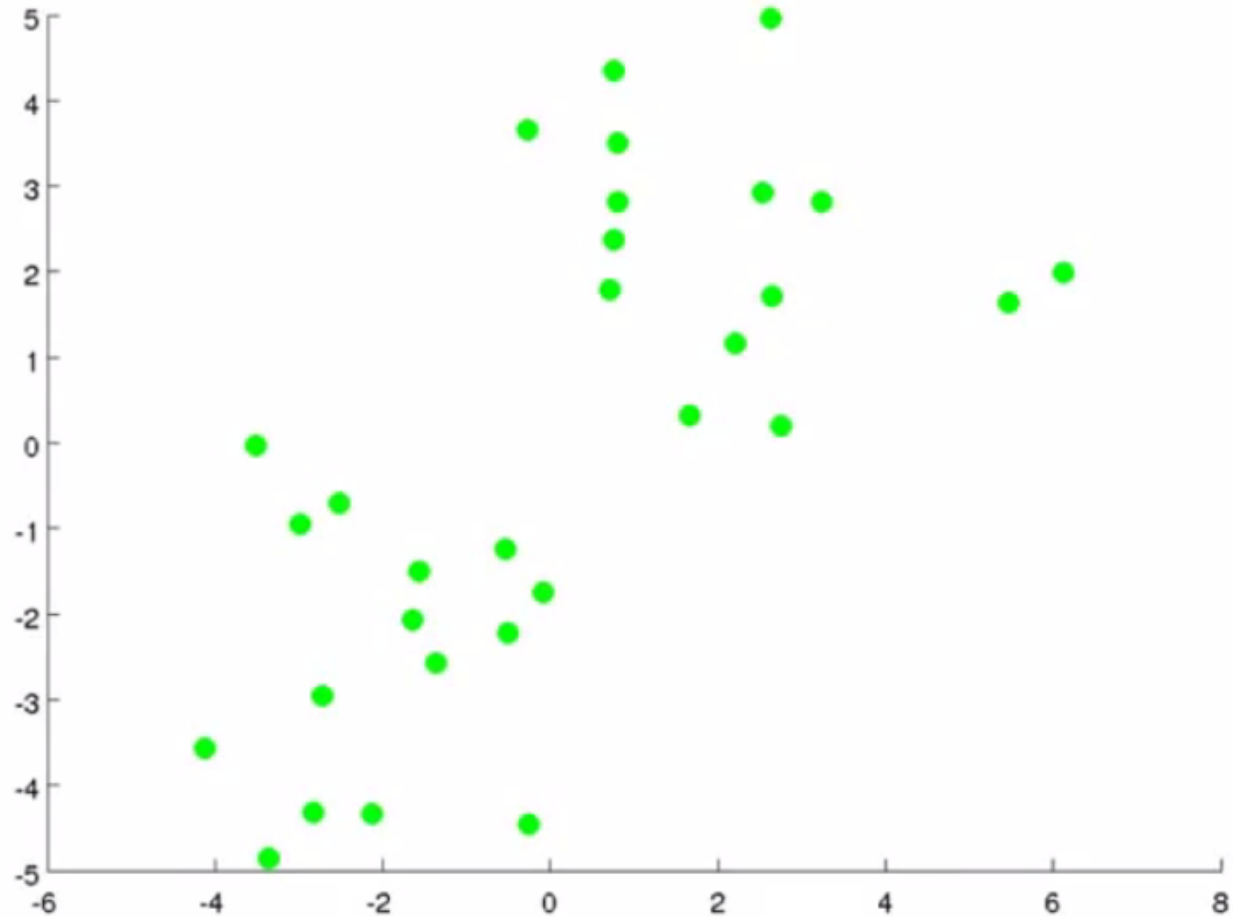
PARTITIONING ALGORITHMS: K-MEANS & K-MEDOIDS



K-Means Clustering

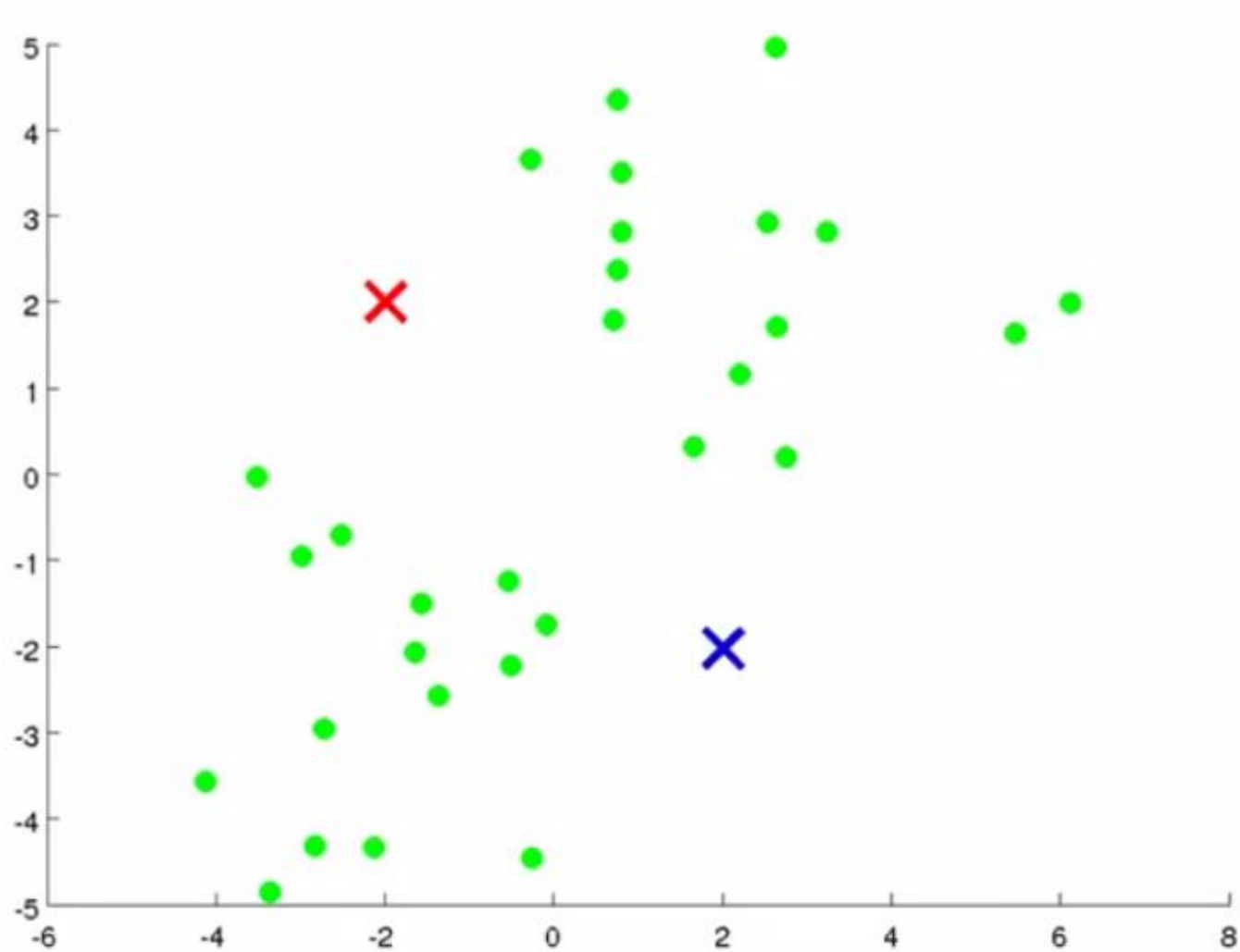
- K-means is a partitional clustering algorithm as it partitions the given data into k clusters.
 - Each cluster has a cluster **center**, called **centroid**.
 - k is specified by the user

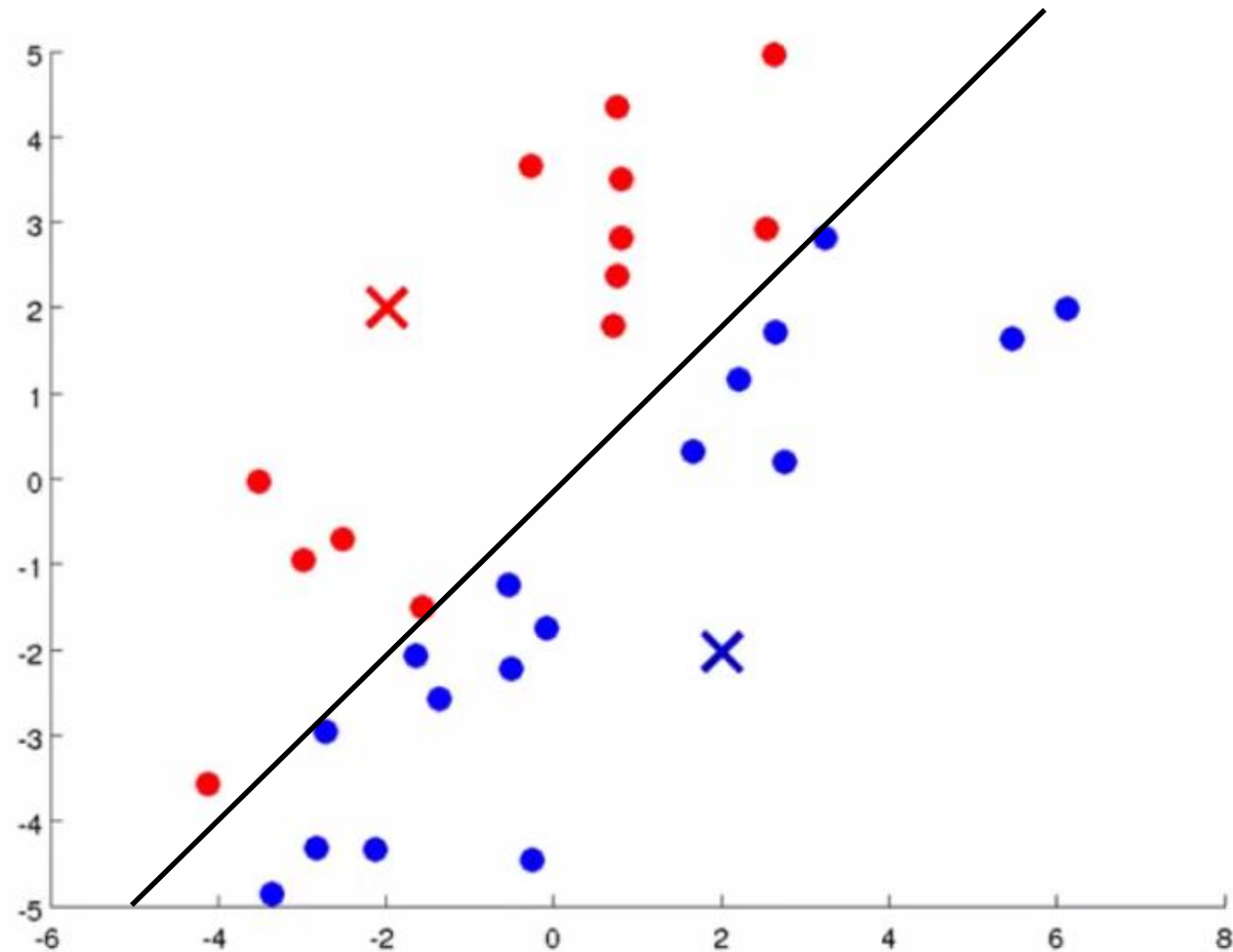


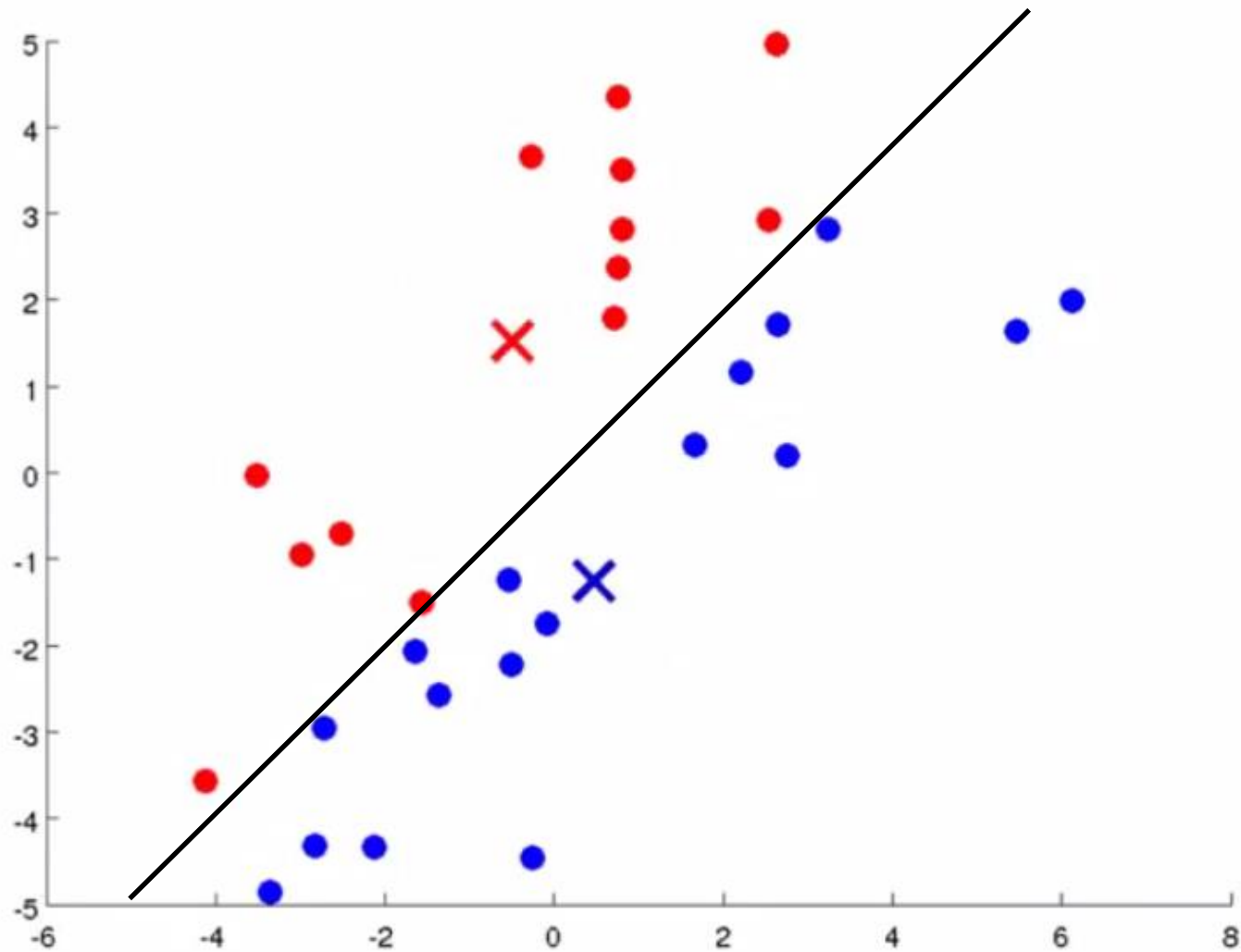


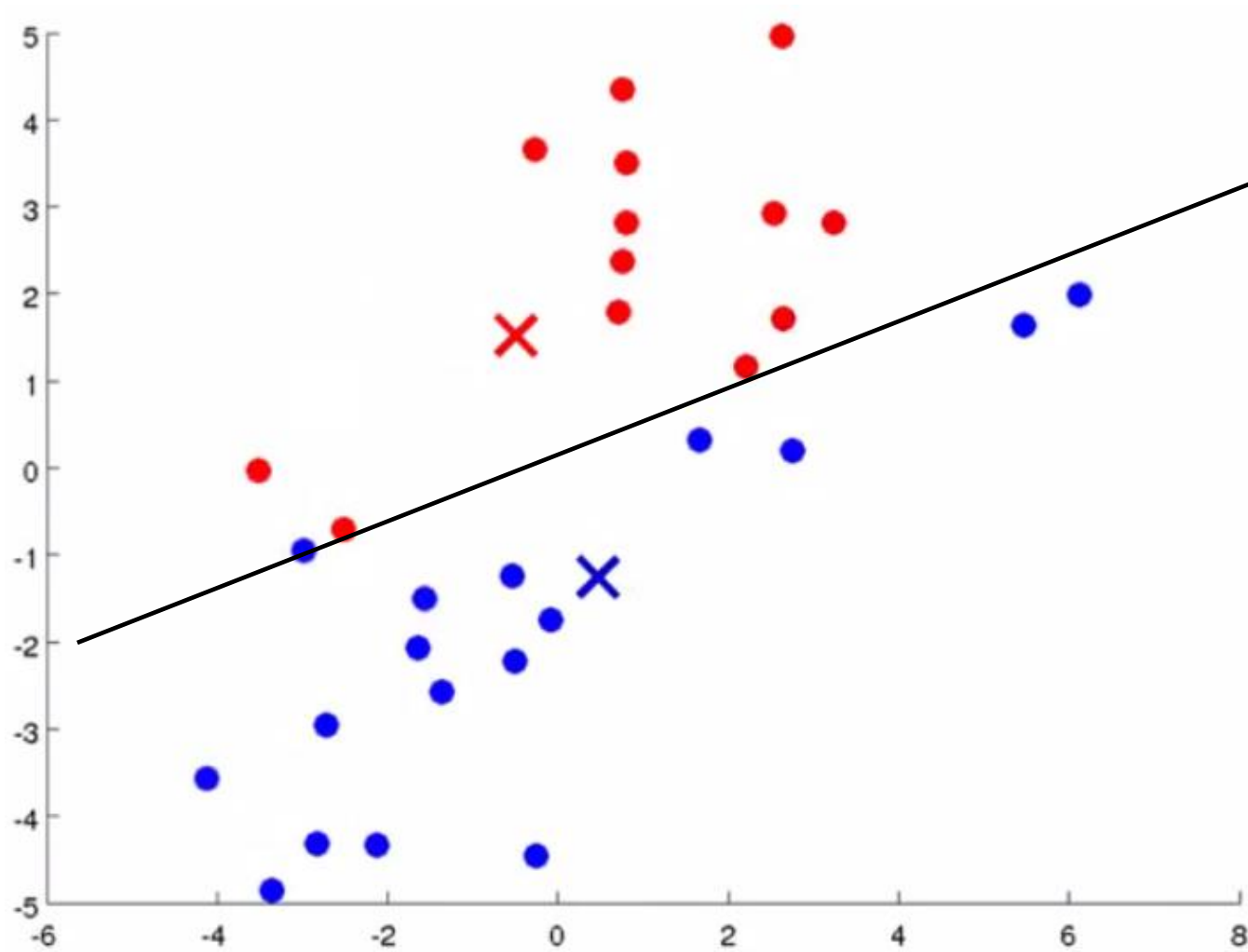
Pictures courtesy of Andrew Ng's course on Coursera.

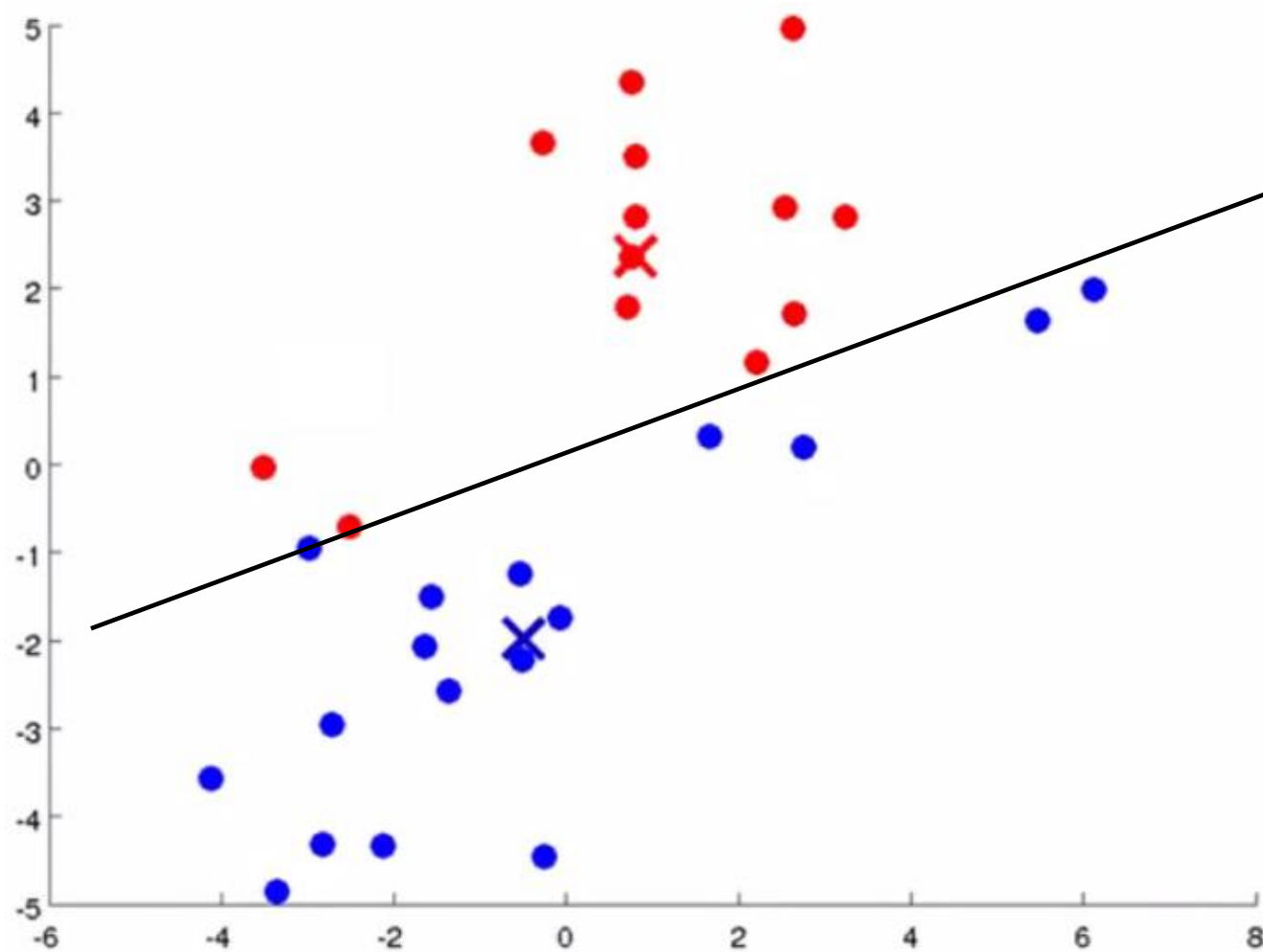


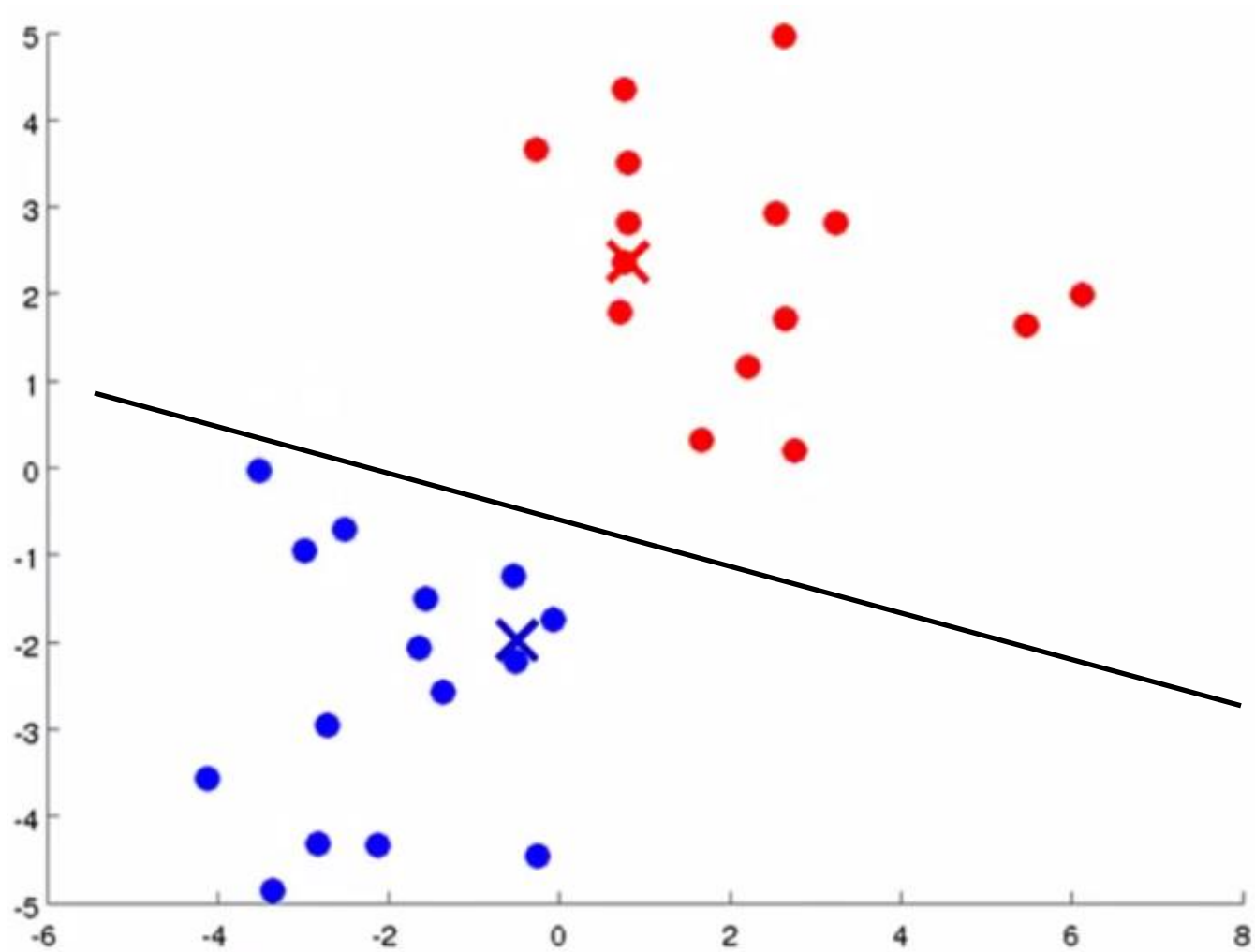


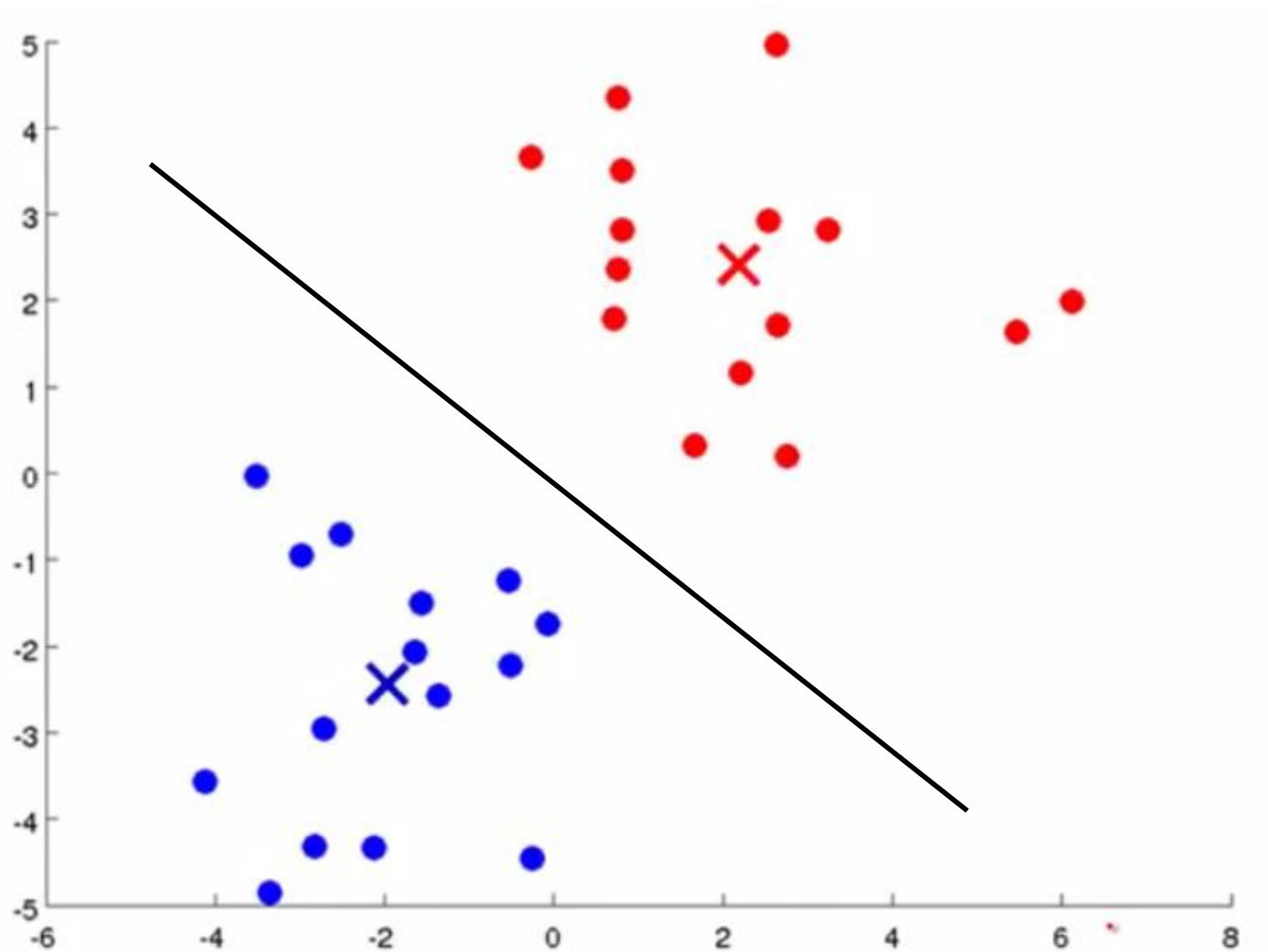












K-Means Algorithm

- 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, or **if some clusters don't get any points**, go to **2**.



Optimizing

$$\frac{1}{m} \sum_{i=1}^m ||x^{(i)} - \mu_{c(i)}||^2$$

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)**,

$$SSE = \sum_{j=1}^k \sum_{\mathbf{x} \in C_j} dist(\mathbf{x}, \mathbf{m}_j)^2 \quad (1)$$

- C_j is the j th cluster, \mathbf{m}_j is the centroid of cluster C_j (the mean vector of all the data points in C_j)



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



Centroid, Radius, and 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

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



ENGINEERING

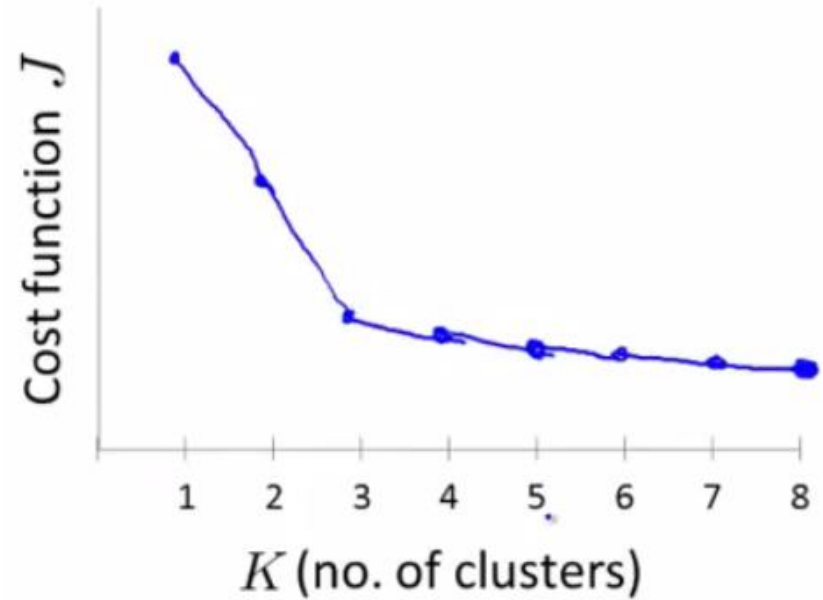
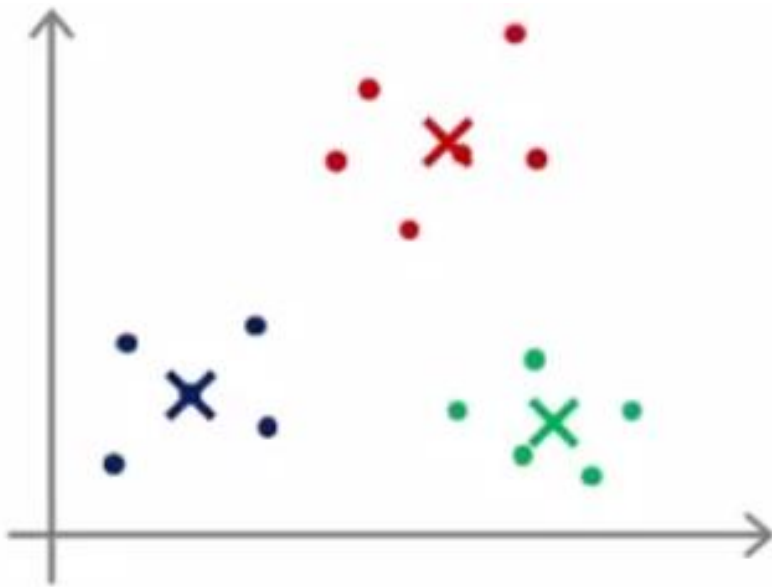


Stability Check of the Clusters

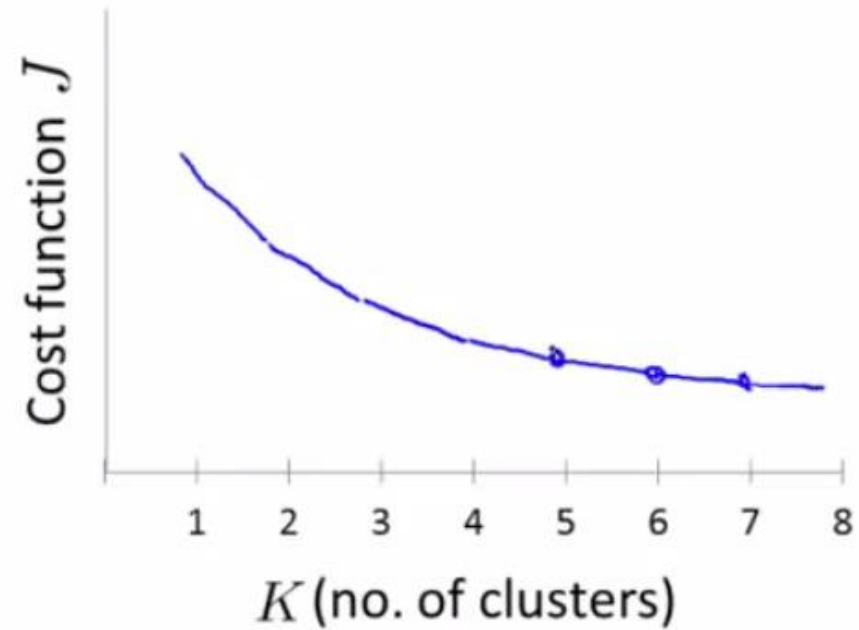
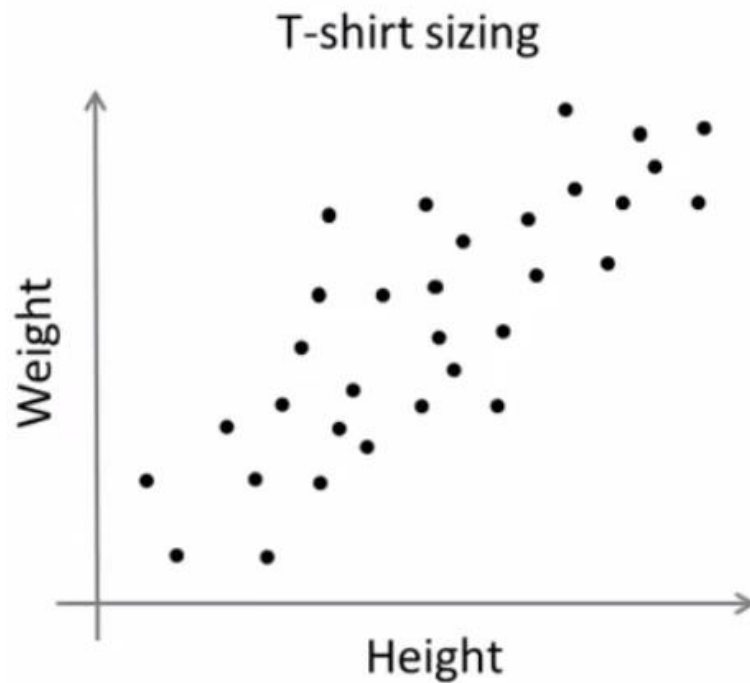
- To check the stability of the clusters take a random sample of 95% of records.
- Compute the clusters.
- If the clusters formed are very similar to the original, then the clusters are fine.

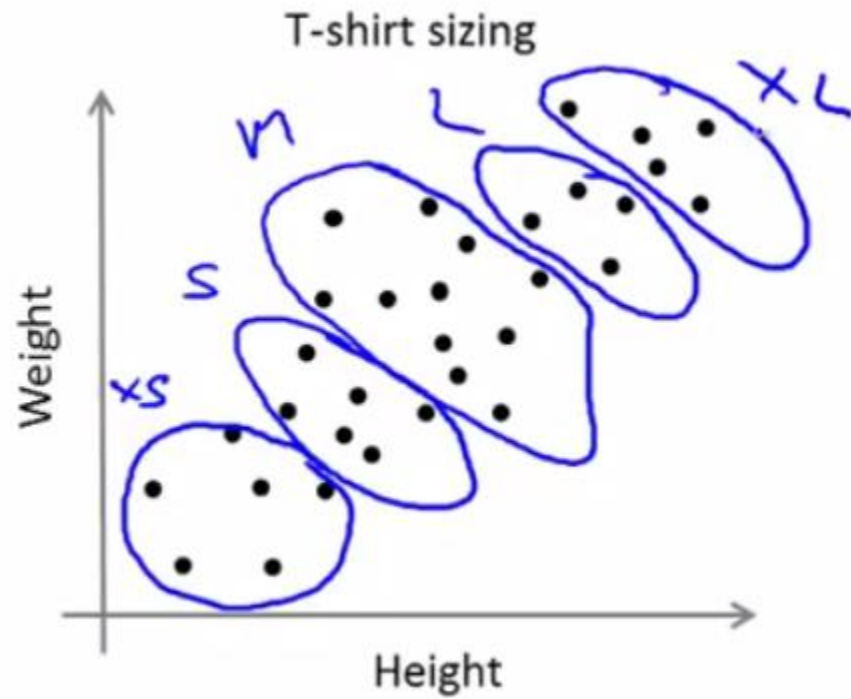
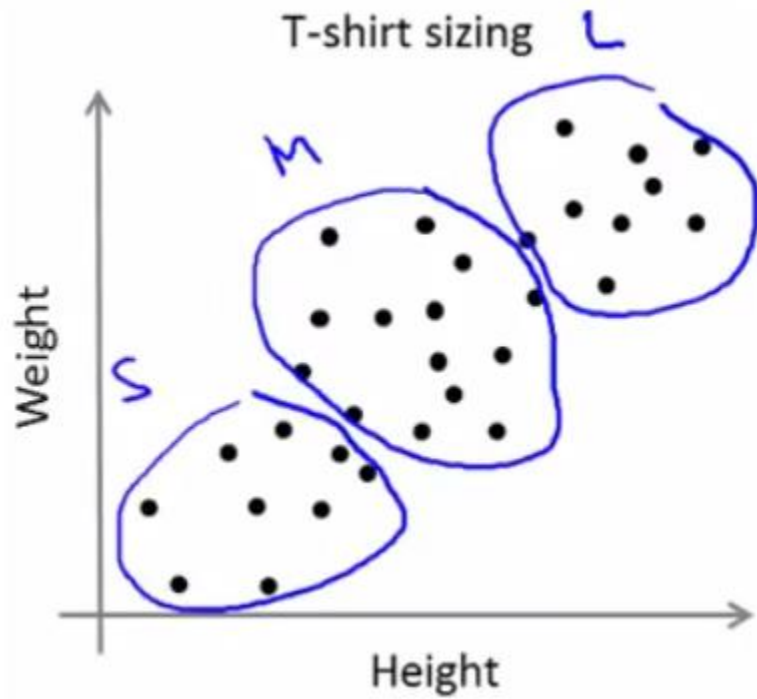


Linearly Clustered Data



Linearly Separable but Merged



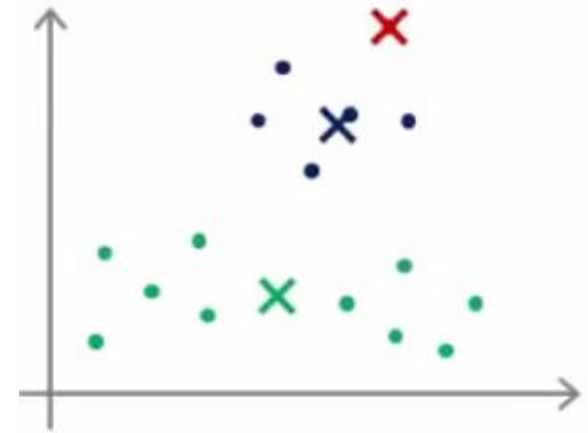
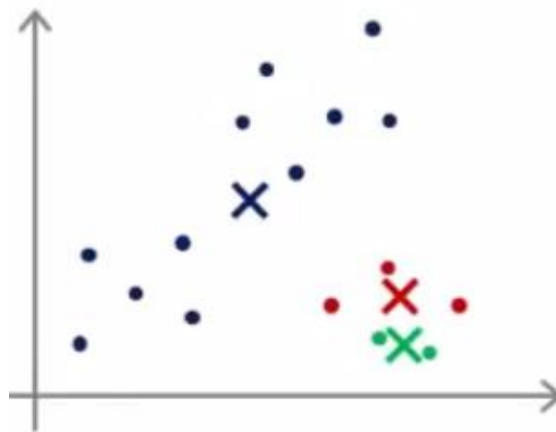
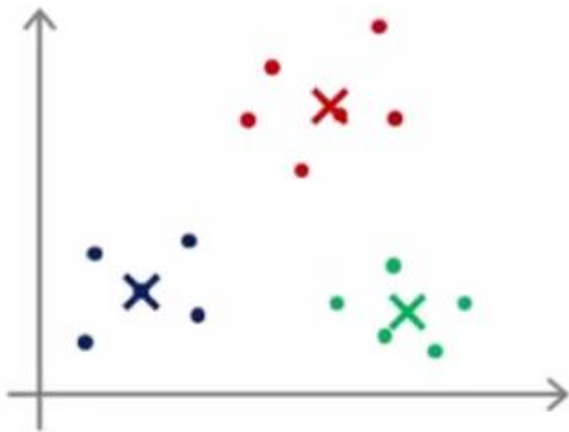
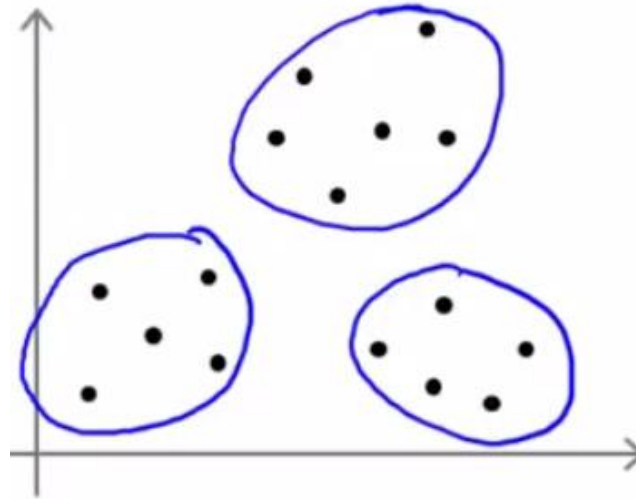


Linearly Separable

- 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 S



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.
 - $O(k(n-k)^2)$ for each iteration

where n is # of data, k is # of clusters



K-Means vs. Hierarchical

- Flat clustering produces a single partitioning
- Flat clustering needs the number of clusters to be specified
- Flat clustering is usually more efficient run-time wise
- Hierarchical Clustering can give different partitionings 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)





- <http://www.naftaliharris.com/blog/visualizing-dbscan-clustering/>
- http://scikit-learn.org/stable/auto_examples/cluster/plot_cluster_comparison.html

MATRICES AND PCA



Matrix is very flexible representation

- Several different physical quantities can be represented as matrices
 - Transformations
 - Data
 - States
 - Relationships & graphs



MATRIX AS TRANSFORMATIONS

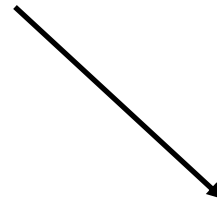


System of equations: Row view

$$a_{11}x_1 + a_{12}x_2 + a_{13}x_3 = b_1$$

$$a_{21}x_1 + a_{22}x_2 + a_{23}x_3 = b_2$$

$$a_{31}x_1 + a_{32}x_2 + a_{33}x_3 = b_3$$



Vectors

$$\begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{bmatrix} \begin{bmatrix} x_1 \\ x_2 \\ x_3 \end{bmatrix} = \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix}$$

MATRIX AS COORDINATE AXES



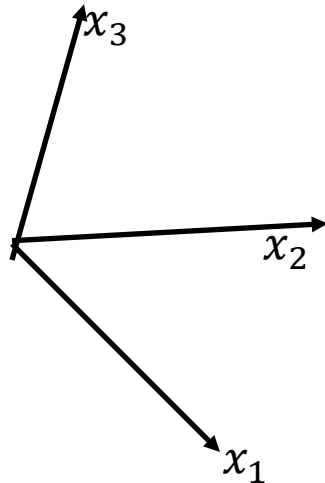
System of equations: Column view

$$a_{11}x_1 + a_{12}x_2 + a_{13}x_3 = b_1$$

$$a_{21}x_1 + a_{22}x_2 + a_{23}x_3 = b_2$$

$$a_{31}x_1 + a_{32}x_2 + a_{33}x_3 = b_3$$

Type equation here.



$$x_1 \begin{bmatrix} a_{11} \\ a_{21} \\ a_{31} \end{bmatrix} + x_2 \begin{bmatrix} a_{12} \\ a_{22} \\ a_{32} \end{bmatrix} + x_3 \begin{bmatrix} a_{13} \\ a_{23} \\ a_{33} \end{bmatrix} = \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix}$$

An alternate view

- Row view gives equations
- Column view gives coordinate axes



Inner products

- W is a nonsingular $n \times n$ matrix.
- The inner product of 2 n dimensional column vectors x and y

$$\langle X, Y \rangle_W = (WX) \cdot (\overline{WY})$$

When $W = I$

$$\langle X, Y \rangle = X \cdot \bar{Y}$$

Norms

The inner product generated norm $\|X\|_W = \sqrt{\langle X, \bar{X} \rangle_W}$

Eucledean or l_2 norm $\|X\|_2 = \sqrt{X \cdot \bar{X}}$

The l_1 norm $\|X\|_1 = |x_1| + |x_2| + |x_3| + \dots + |x_n|$

The l_∞ norm $\|X\|_\infty = \max(|x_1|, |x_2|, |x_3|, \dots, |x_n|)$

The l_p norm $\|X\|_p = (|x_1|^p + |x_2|^p + |x_3|^p + \dots + |x_n|^p)^{\frac{1}{p}}$

Frobenius norm of a matrix is Eucledean version

$$\|A\|_F = \sqrt{\sum \sum |a|_{ij}^2}$$



Orthogonal vectors

- Inner product is zero (so, w.r.t one matrix they may be orthogonal, w.r.t other they may not be)
- Gram Schmidt orthogonalization
 - Every finite set of linearly independent vectors can be combined to create same number of orthogonal vectors



Orthogonal matrices

- Formed by orthonormal vectors (unit orthogonal)

$$Q^T Q = Q Q^T = I$$

Transpose is the inverse



Vector spaces

- Vectors that are linearly independent of each other. In n dimensions, if we have n linearly independent vectors, we can span the entire space
- These vectors are called bases



4 Sub spaces of a matrix

- For $m \times n$ matrix
 - Column space: $C(A)$ in \mathbb{R}^n
 - Null Space: $N(A)$ in \mathbb{R}^n (Solution of $Ax=0$)
 - Row Space: $C(A^T)$ in \mathbb{R}^m
 - (left) Null Space of A^T : $N(A^T)$ in \mathbb{R}^m



Rank of a matrix

- Linear independence: How many attributes are dependent on others (can be expressed as linear combinations)
- The number of linearly independent rows/columns is the rank



Determinant of a matrix: Cross product of column vectors

X2 (0,1)



$$\begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$

Determinant is a single number representation of the matrix.

Geometrically, it is area in 2 dimensions

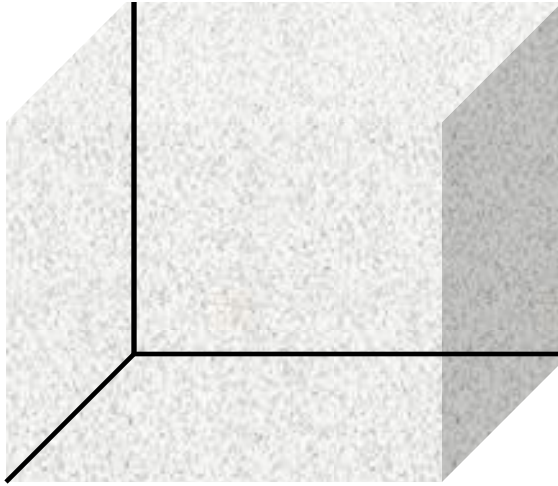
X1 (1,0)

It is signed. If we consider $\begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}$, *the area is -1*

Determinant changes sign if rows or columns are interchanged



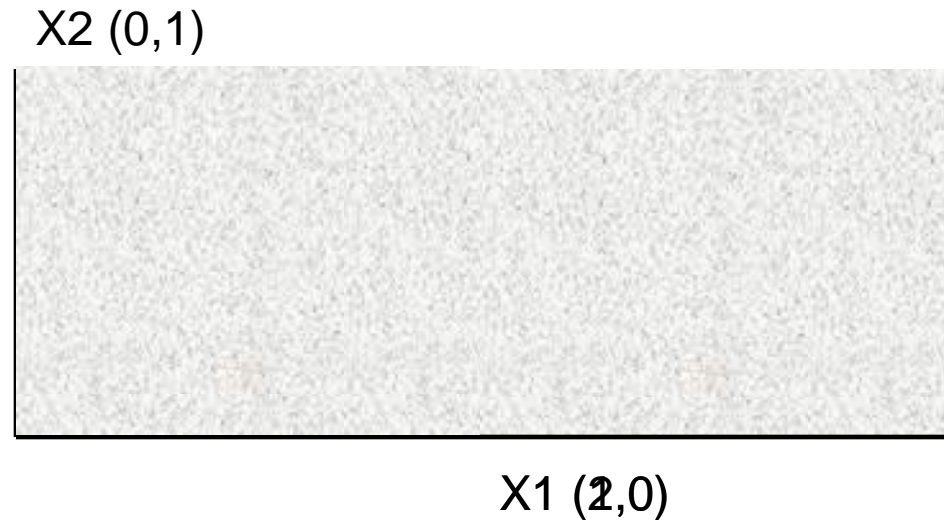
In higher dimensions



determinant is the
Signed volume of vectors comprised

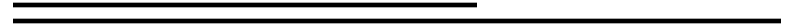
Naturally

- If you multiply a column or row by a number
- determinant gets multiplied by the same



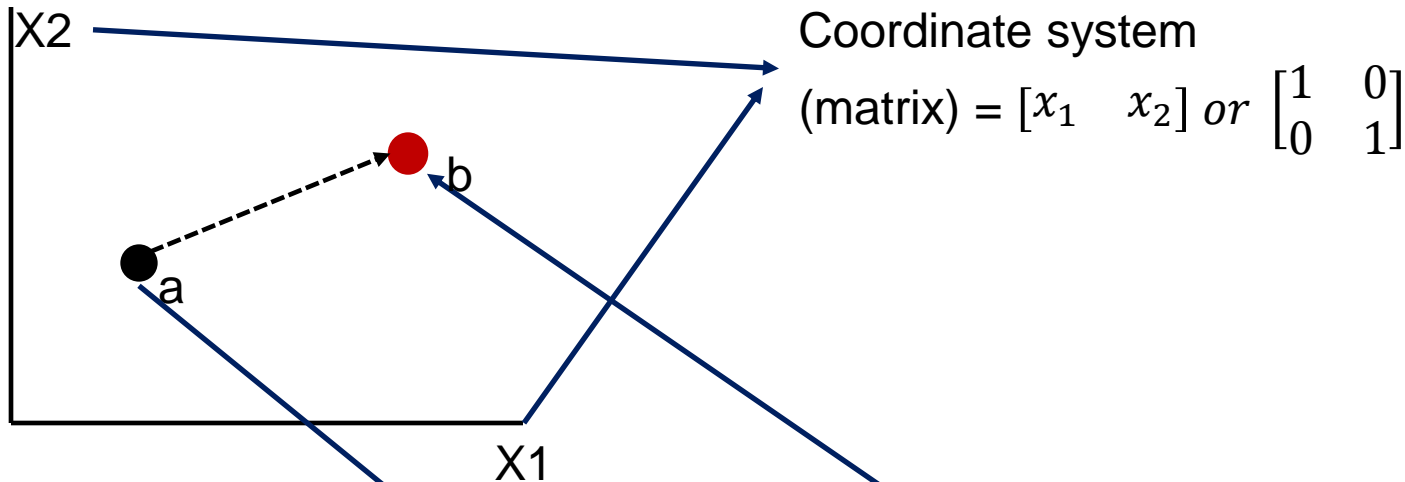
Naturally

- If both axes are linearly dependent ($X_2=k.X_1$), then the determinant is zero



MATRIX AS TRANSFORMATION ENGINE

Matrix as a transformation on a vector



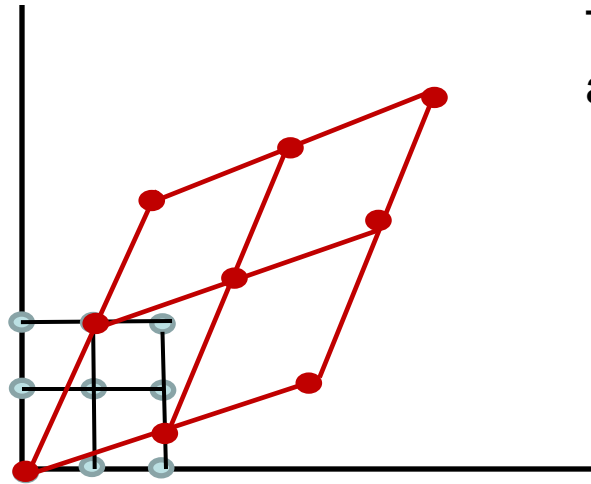
$$\begin{bmatrix} x_{11} & x_{21} \\ x_{21} & x_{22} \end{bmatrix}_{[2 \times 2]} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix}_{[2 \times 1]} = \begin{bmatrix} b_1 \\ b_2 \end{bmatrix}_{[2 \times 1]}$$

Transformation matrix

**A MATRIX OPERATES ON A
VECTOR AND TRANSFORMS
IT TO ANOTHER VECTOR**

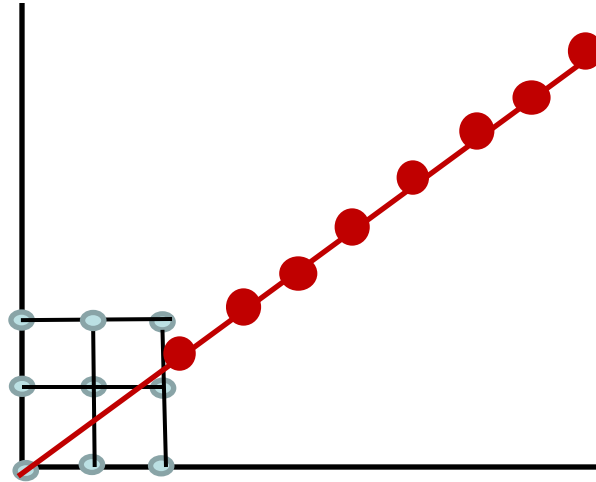


Matrix transformation on spaces



This matrix is stretching, rotating and skewing the space

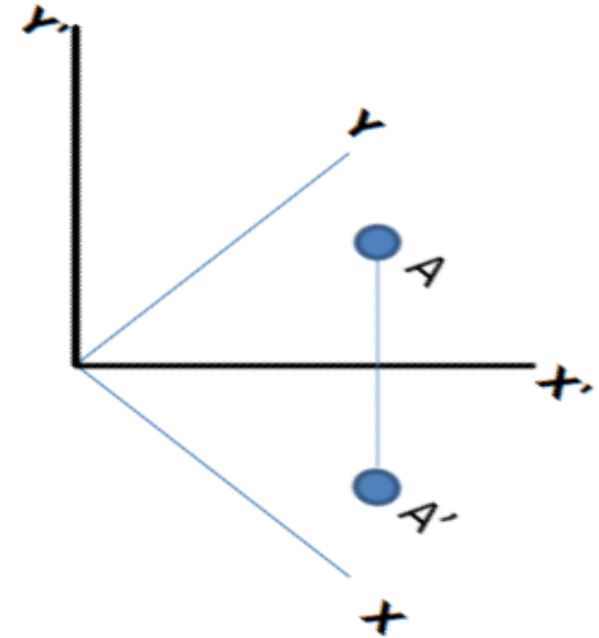
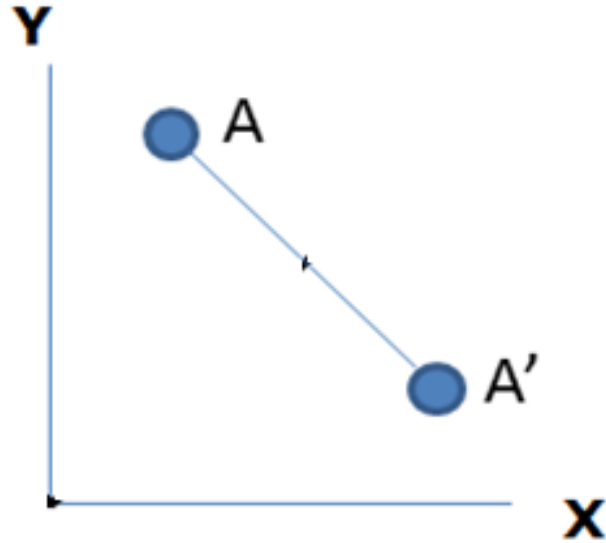
If determinant is zero for a transformation matrix, (they are singular)



Similarly, a low ranked transformation matrix takes the grid to a low dimensional space



Transformation operation is dependent on the basis!!!

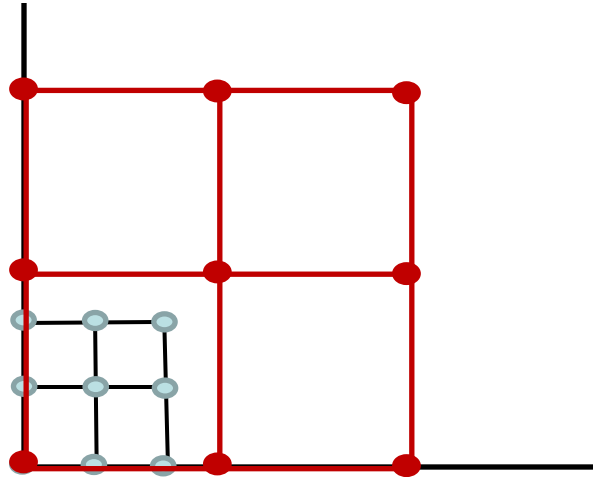


$$A = \frac{1}{\|\vec{l}\|^2} \begin{bmatrix} l_x^2 - l_y^2 & 2l_x l_y \\ 2l_x l_y & l_y^2 - l_x^2 \end{bmatrix}$$

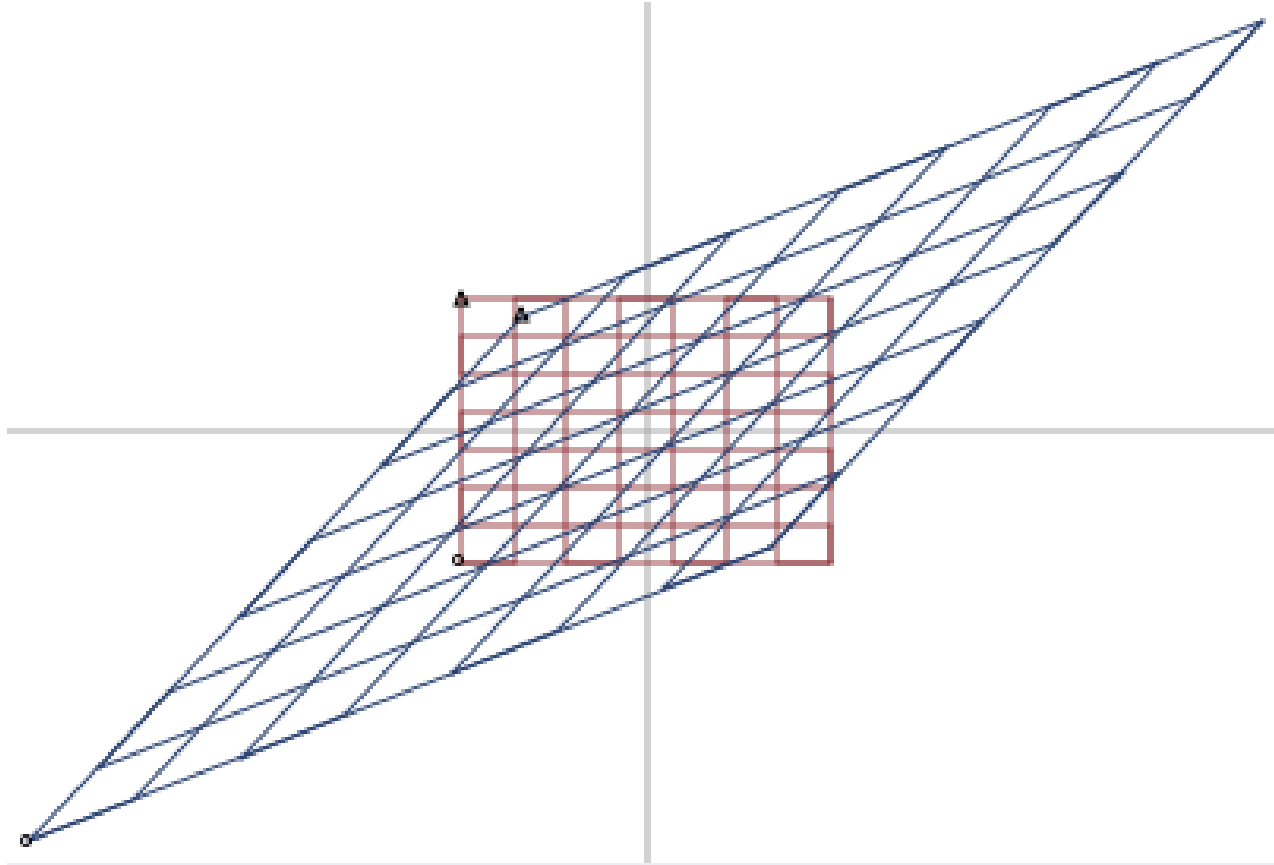
$$\begin{bmatrix} 1 & 0 \\ 0 & -1 \end{bmatrix}$$

**AHA! BY CHANGING THE
AXES, WE CAN MAKE A
COMPLEX
TRANSFORMATION SIMPLE**

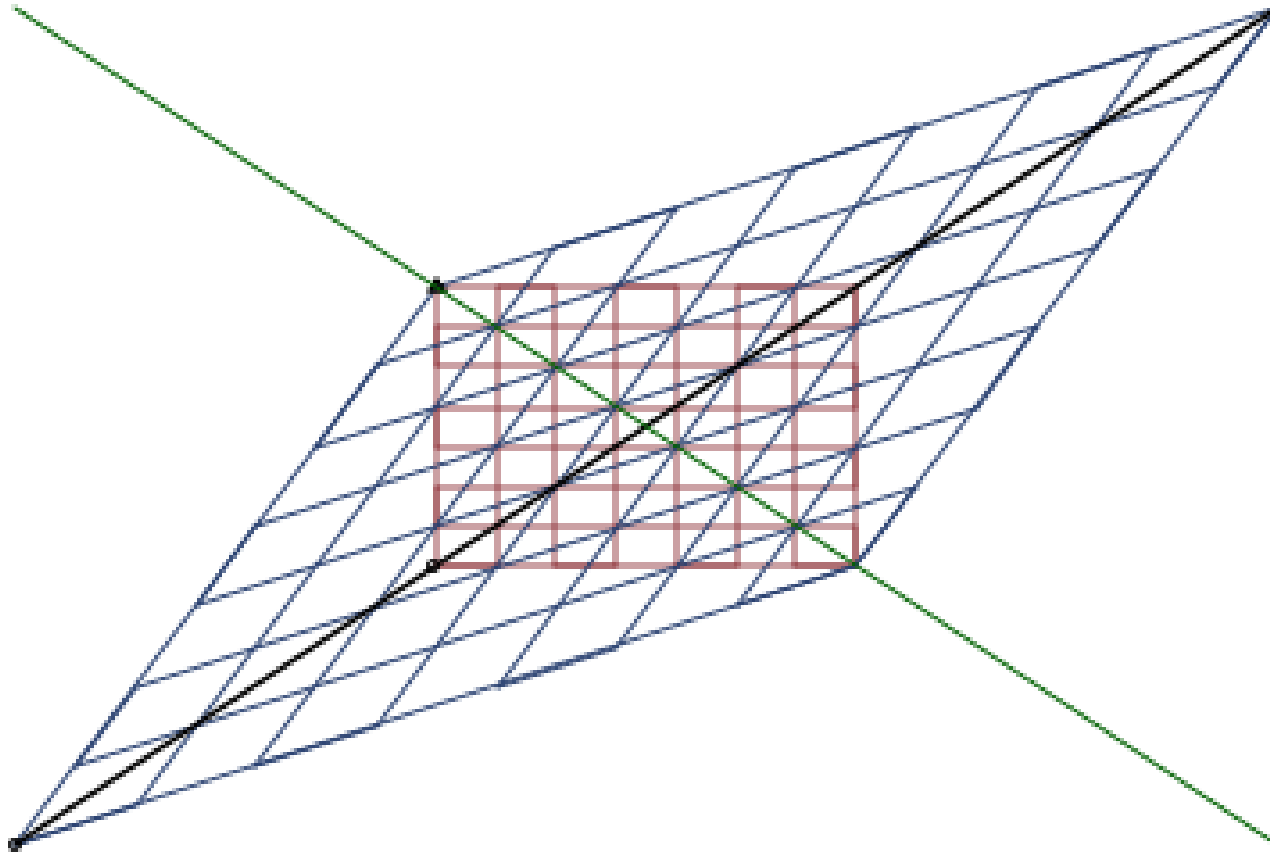
Can we find a basis where a transformation is changed to a purely stretch



A transformation matrix that stretches, rotates and skews



Eigen vectors



Eigen vectors mathematics

- The eigenvectors and eigenvalues of matrix \mathbf{A} are defined to be the nonzero \mathbf{x} and λ values that solve
- $\mathbf{Ax} = \lambda\mathbf{x}$ (\mathbf{A} is just stretching)



Characteristic equations

The characteristic equation of a $n \times n$ matrix A is
The n th degree polynomial equation

$$\det(A - \lambda I) = 0$$



So

- Eigen vectors of a transformation is that basis where transformation is only a stretch
- Eigen values are the magnitude of stretch



Factorization

- Not much can be said about 1728
- But, a lot can be said about

$$2^6 \times 3^3$$



A matrix can be factorized too

- The idea of factorization is to split a non-special matrices into special constituents
- $A = LU$ (decomposition into lower and upper triangular matrices)
- Solving equations becomes easy (forward, backward substitutions)



Eigen decomposition (A factorization)

$$AQ = A[x_1 \ x_2 \ \dots x_n] = [\Lambda_1 x_1 \ \Lambda_2 x_2 \ \dots \Lambda_n x_n]$$

$$= [x_1 \ x_2 \ \dots x_n] \begin{bmatrix} \Lambda_1 & 0 & 0 \\ 0 & \Lambda_2 & 0 \\ 0 & 0 & \Lambda_n \end{bmatrix} = Q\Lambda$$

$$A = Q\Lambda Q^{-1}$$

A is an $n \times n$ square matrix with linearly independent eigen vectors

Q is the eigen vector matrix where each vector corresponds to one eigen value

Λ is a diagonal matrix formed by eigen values

An $n \times n$ matrix A is diagonalizable over the field F if it has n distinct eigenvalues in F , i.e. if its characteristic polynomial has n distinct roots in F ; however, the converse may be false. (unit matrix)



Powers

$$A = Q\Lambda Q^{-1}$$

$$A^2 = Q\Lambda Q^{-1}Q\Lambda Q^{-1} = Q\Lambda Q^{-1}$$

or

$$Ax = \Lambda x; A^2x = A\Lambda x = \Lambda Ax = \Lambda^2x$$

$$A^k = Q\Lambda^k Q^{-1}$$

- Any two matrices connected with the above relation are called similar matrices.
- So, diagonal matrix is a similar matrix in diagonal form.
- Similar matrices have same eigen values



Properties of Eigen values

- The sum of eigen values is equal to trace (sum of the main diagonal elements)
- A matrix and its transpose have same eigen values
- Eigen values of L and U are elements of its main diagonals



Hermitian matrices

- Hermitian transpose is a complex conjugate of a matrix.
- A normal matrix is where

$$AA^H = A^H A$$

A normal matrix has orthonormal eigen vectors and can be diagonalized



Hermitian matrices

- A matrix is Hermitian if it equals its Hermitian transpose

$$A = A^H$$

All real symmetric matrices are Hermitian and hence are normal



Variance-covariance matrix

$$\begin{bmatrix} \sigma_a^2 & \rho_{ab} & \rho_{ac} \\ \rho_{ba} & \sigma_b^2 & \rho_{bc} \\ \rho_{ca} & \rho_{cb} & \sigma_c^2 \end{bmatrix}$$

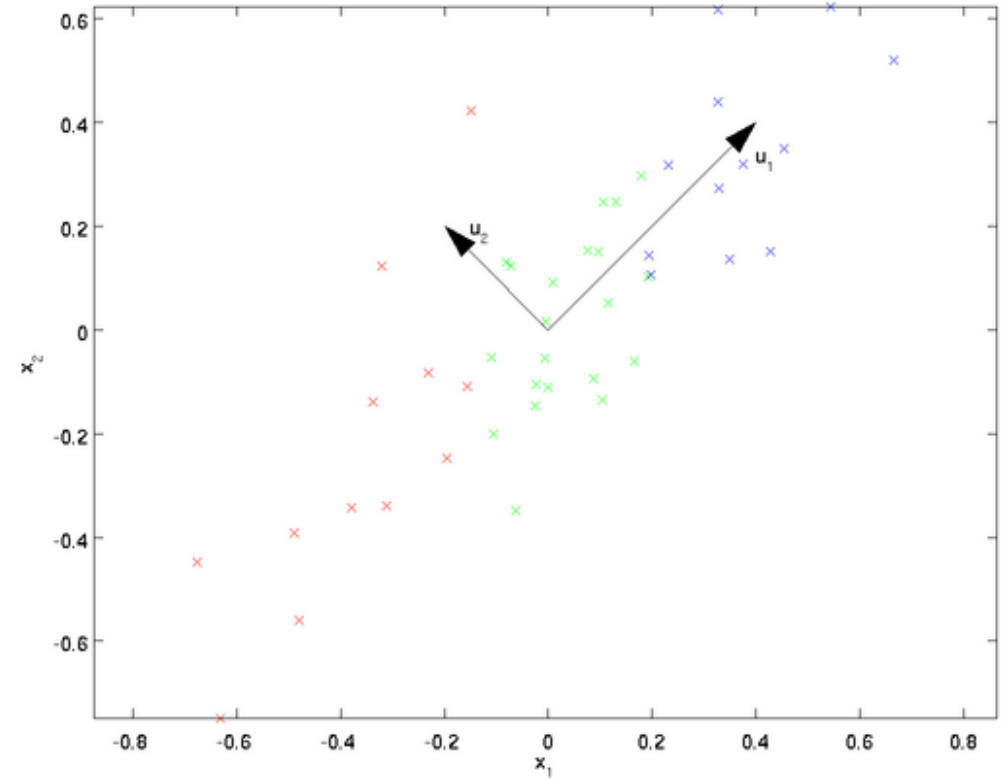
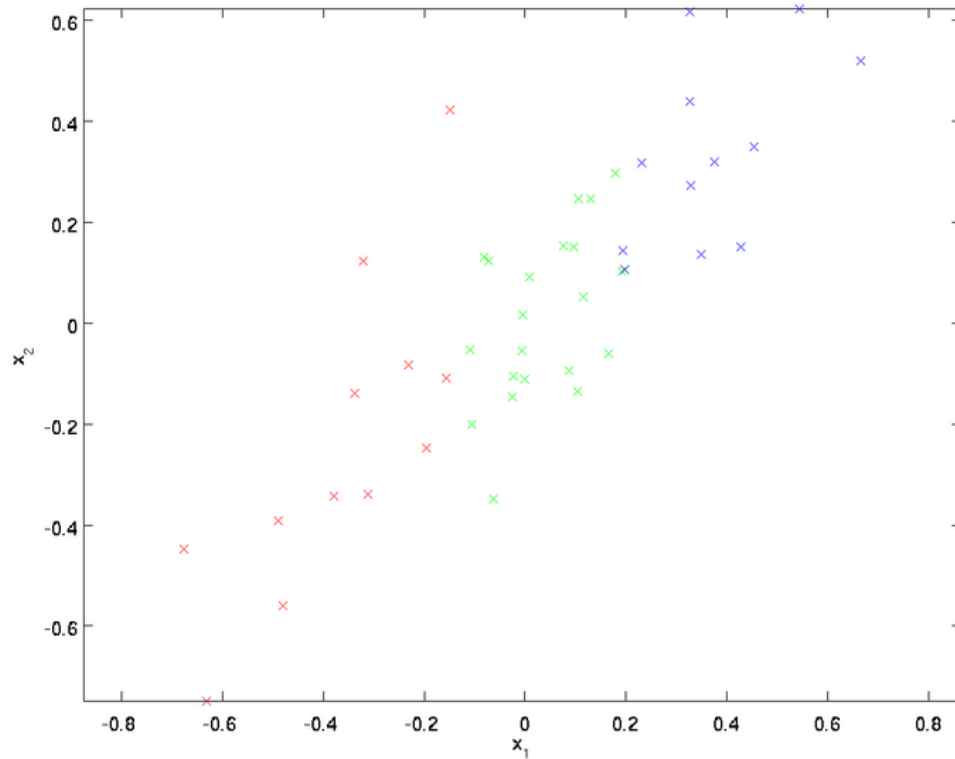
This is how data is spread in each axis

It is Hermitian and Normal and hence Diagonalizable with Orthonormal eigen vectors

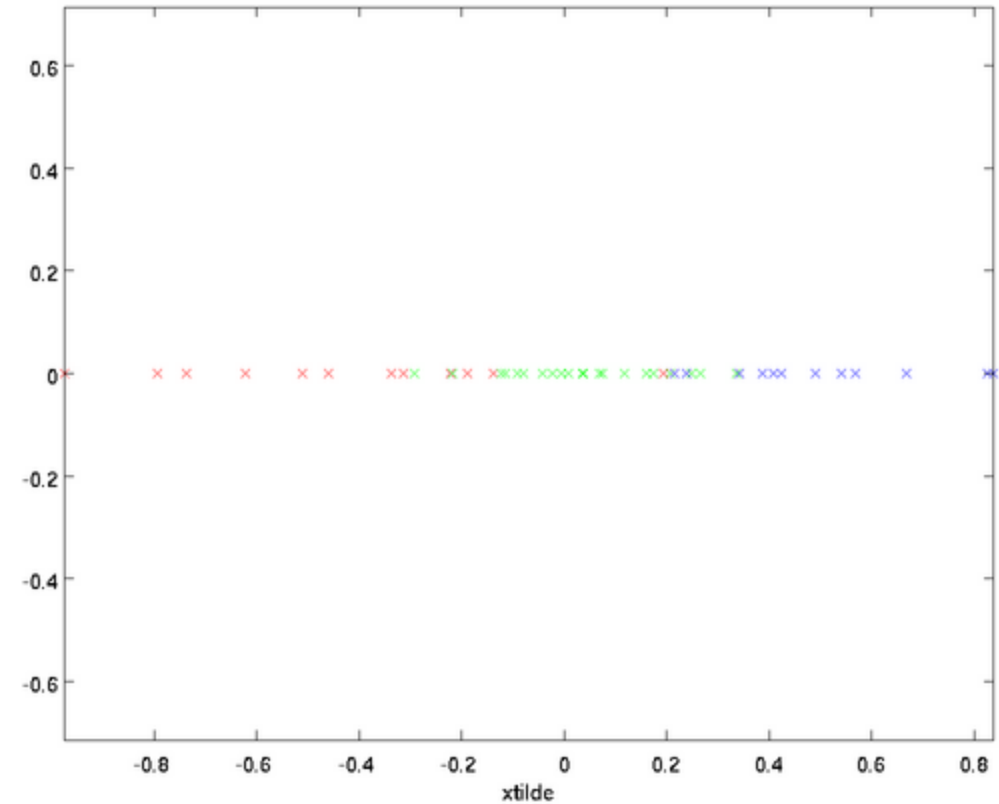
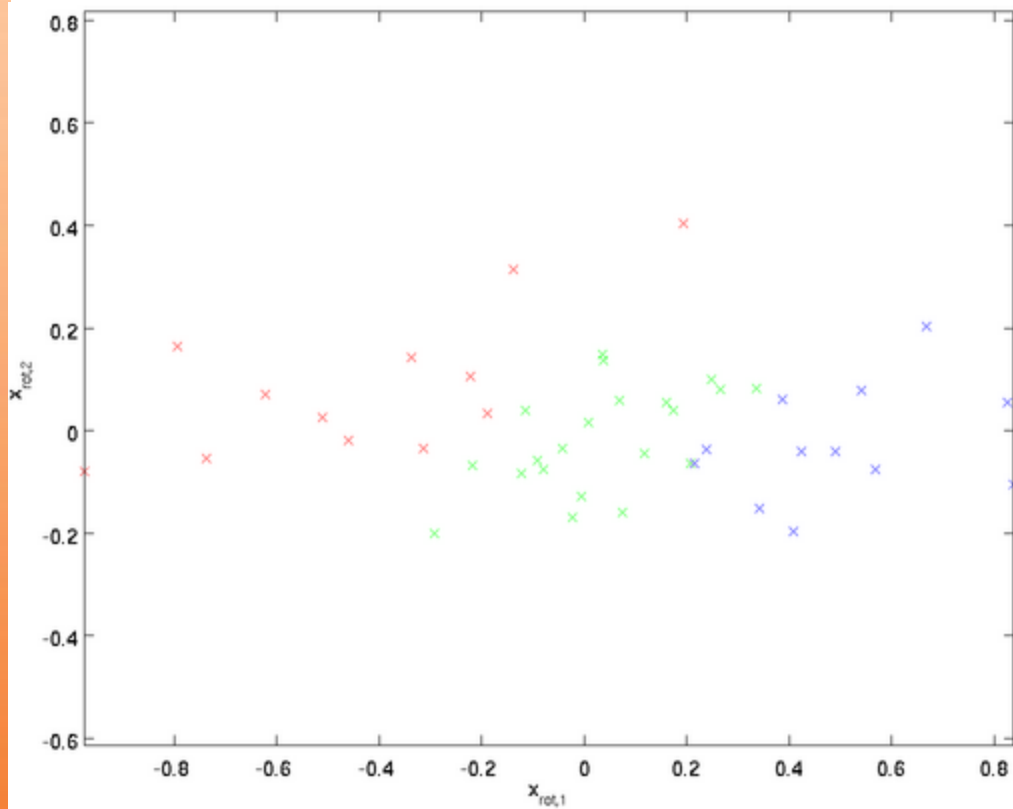
Now find the basis where it is just a stretch

$$\begin{bmatrix} \lambda_1 & 0 & 0 \\ 0 & \lambda_2 & 0 \\ 0 & 0 & \lambda_3 \end{bmatrix}$$

Eigen vectors are the basis

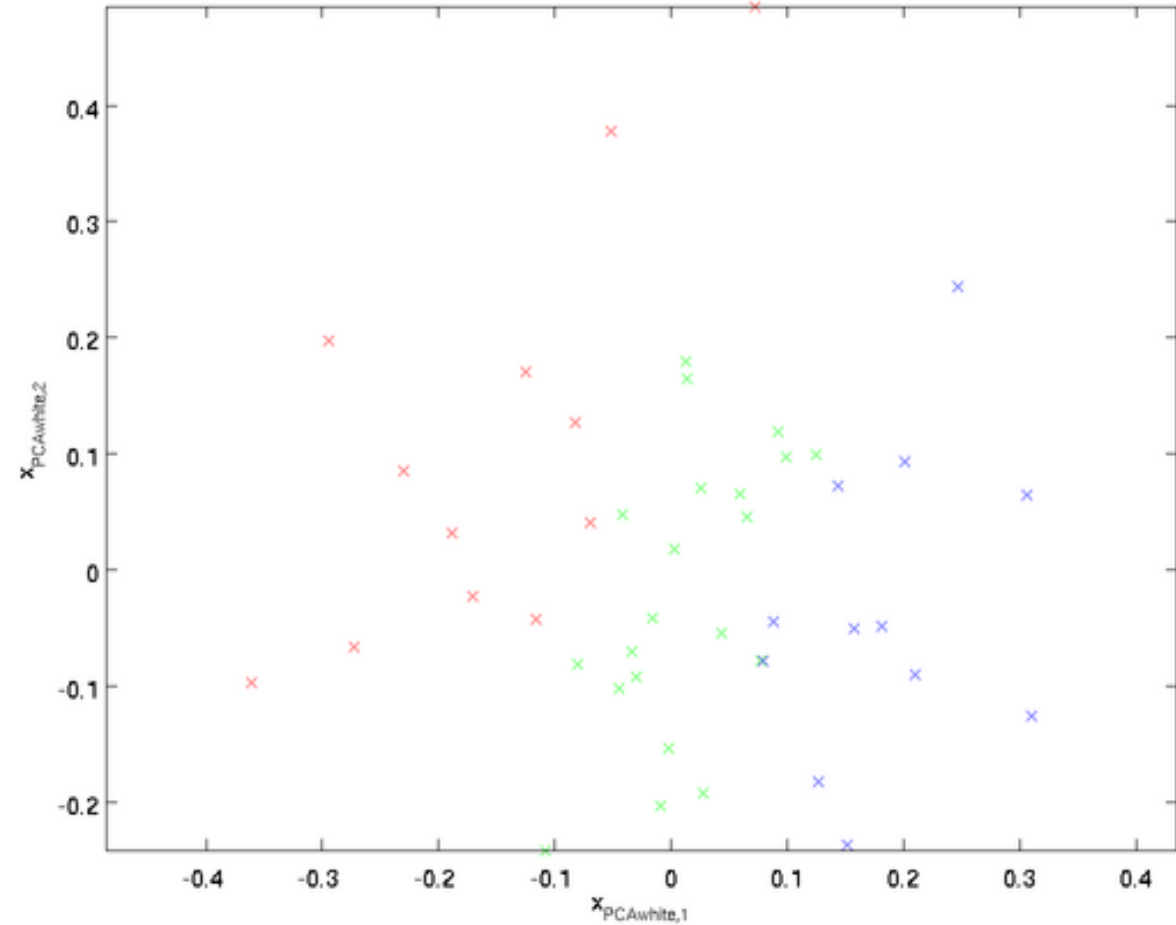


In the new space (and reduced dimensionality)



Whitening

$$x_{\text{PCAwhite},i} = \frac{x_{\text{rot},i}}{\sqrt{\lambda_i}}$$



Dimensionality reduction

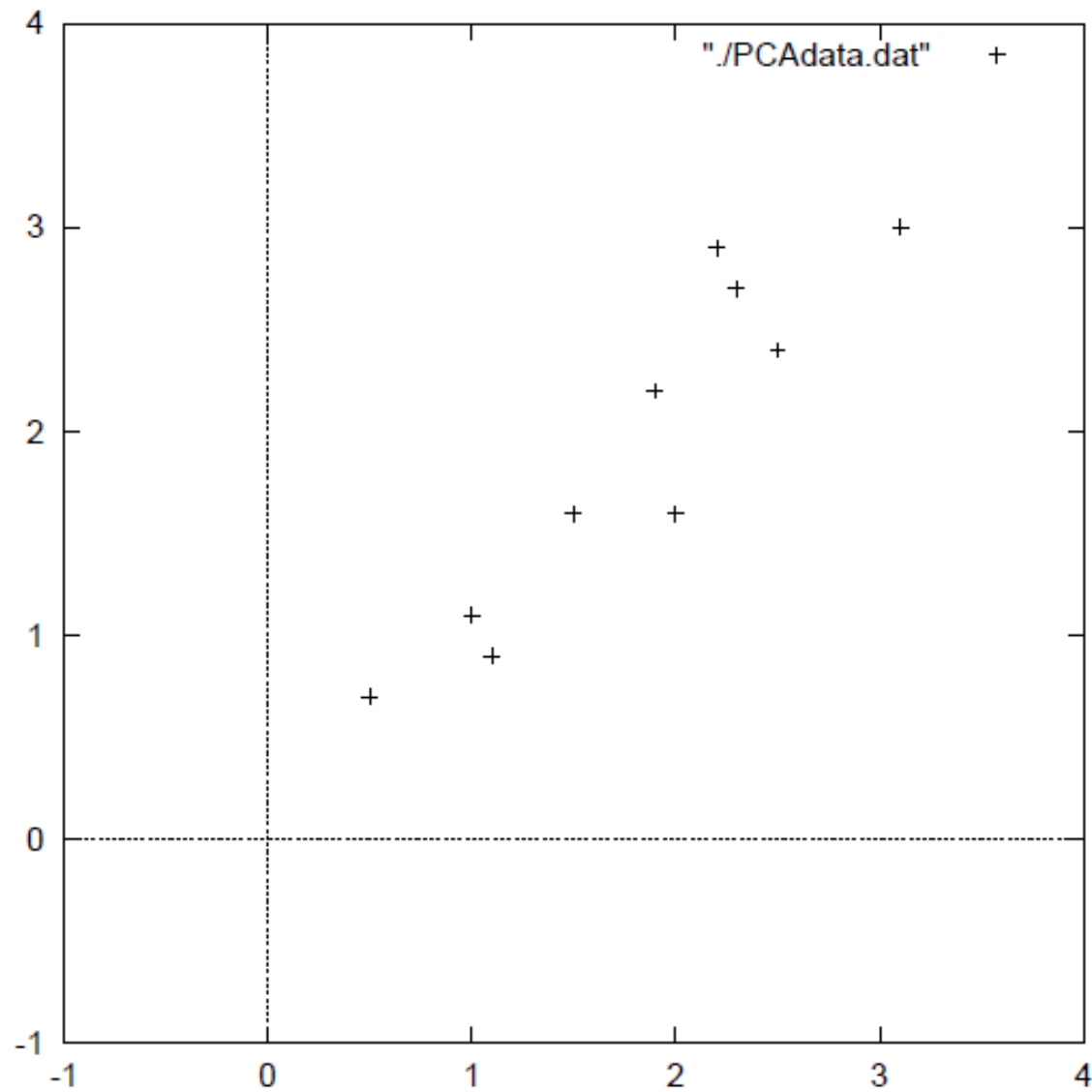
- Drop dimensions where eigen values are small because the variance (or stretch) in those axes is small



Process

	x	y
Data =	2.5	2.4
	0.5	0.7
	2.2	2.9
	1.9	2.2
	3.1	3.0
	2.3	2.7
	2	1.6
	1	1.1
	1.5	1.6
	1.1	0.9

	x	y
DataAdjust =	.69	.49
	-1.31	-1.21
	.39	.99
	.09	.29
	1.29	1.09
	.49	.79
	.19	-.31
	-.81	-.81
	-.31	-.31
	-.71	-1.01

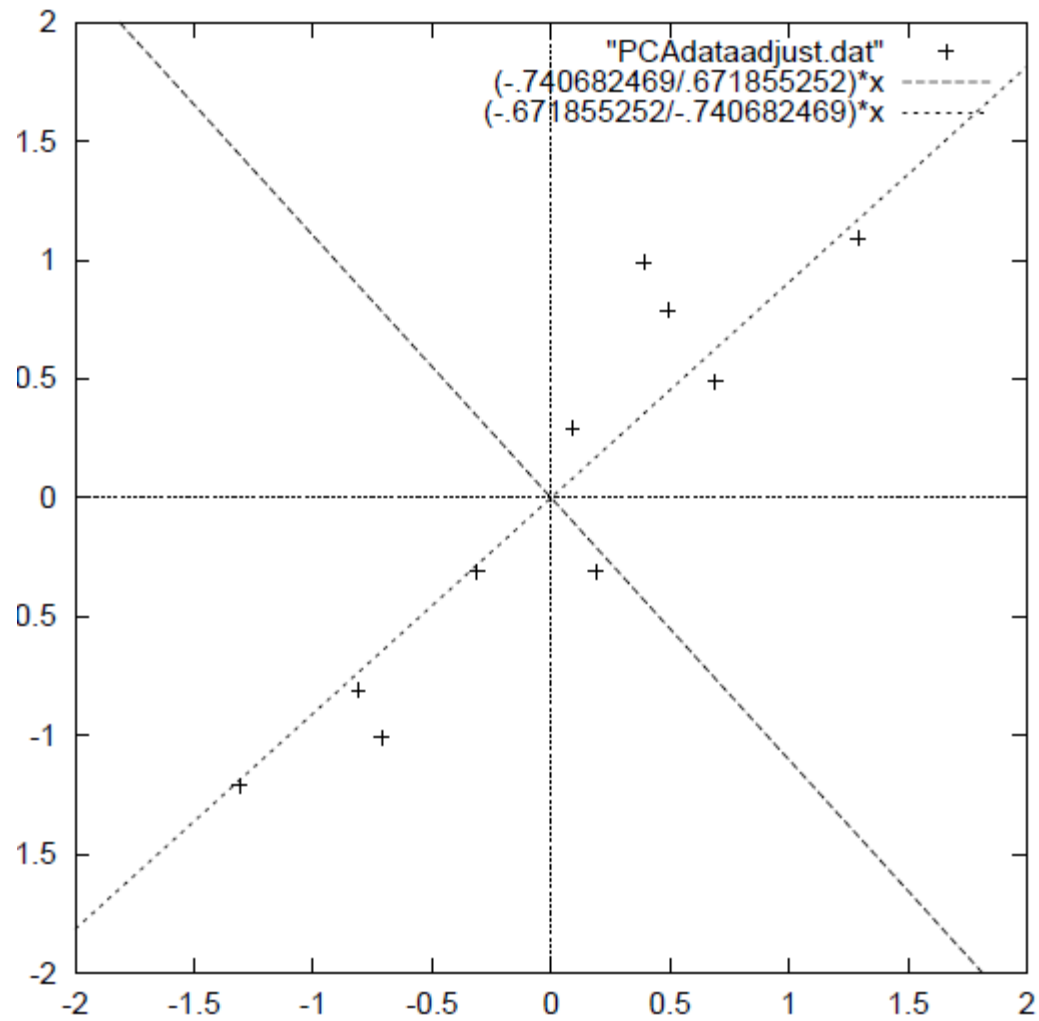


$$cov = \begin{pmatrix} .616555556 & .615444444 \\ .615444444 & .716555556 \end{pmatrix}$$

$$eigenvalues = \begin{pmatrix} .0490833989 \\ 1.28402771 \end{pmatrix}$$

$$eigenvectors = \begin{pmatrix} -.735178656 & -.677873399 \\ .677873399 & -.735178656 \end{pmatrix}$$





R implementation of PCA





HYDERABAD

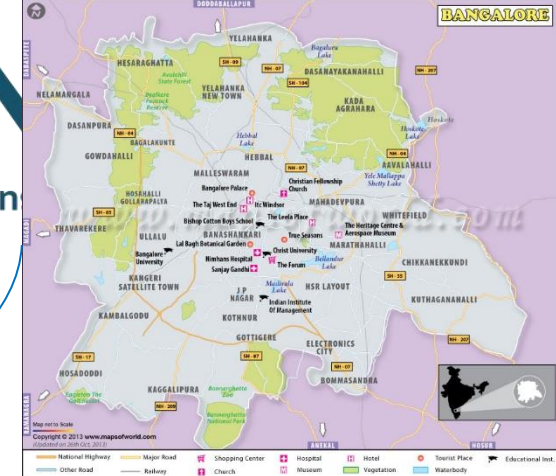
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