W9. Unsupervised Learning - Clustering & PCA

Guang Cheng

University of California, Los Angeles guangcheng@ucla.edu

Week 9

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- That's where Principal Component Analysis (PCA) is used.

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 Principal component analysis, or PCA, is a statistical procedure that allows you to summarize the information content in large data tables by means of a smaller set of "summary indices" that can be more easily visualized and analyzed.

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- The underlying data can be measurements describing properties of production samples, chemical compounds or reactions, process time points of a continuous process, batches from a batch process, biological individuals or trials of a DOE-protocol, for example.

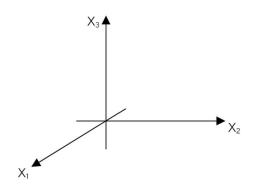
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- The underlying data can be measurements describing properties of production samples, chemical compounds or reactions, process time points of a continuous process, batches from a batch process, biological individuals or trials of a DOE-protocol, for example.
- PCA is often used in the preliminary data analytics, before running any machine learning tasks.

Consider a matrix X with N rows (aka "observations") and K columns (aka "variables").

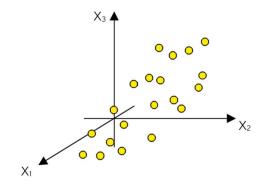
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- Each variable represents one coordinate axis. For each variable, the length has been standardized according to a scaling criterion, normally by scaling to unit variance.

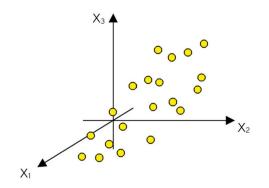


 A K-dimensional variable space. For simplicity, only three variables axes are displayed. The "length" of each coordinate axis has been standardized according to a specific criterion, usually unit variance scaling.

• In the next step, each observation (row) of the X-matrix is placed in the K-dimensional variable space. Consequently, the rows in the data table form a swarm of points in this space.

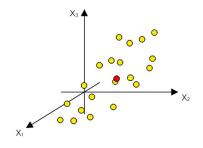


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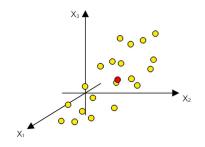


• The observations (rows) in the data matrix X can be understood as a swarm of points in the variable space (K-space).

• Next, mean-centering involves the subtraction of the variable averages from the data. The vector of averages corresponds to a point in the K-space.

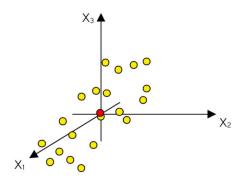


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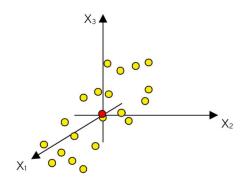


• In the mean-centering procedure, you first compute the variable averages. This vector of averages is interpretable as a point (here in red) in space. The point is situated in the middle of the point swarm (at the center of gravity).

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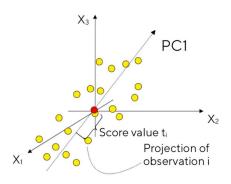


• The mean-centering procedure corresponds to moving the origin of the coordinate system to coincide with the average point (here in red).

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- Each observation (yellow dot) may now be projected onto this line in order to get a coordinate value along the PC-line. This new coordinate value is also known as the score.



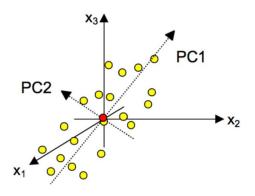
• The first principal component (PC1) is the line that best accounts for the shape of the point swarm. It represents the *maximum variance direction* in the data.

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- This line also passes through the average point.



 The second principal component (PC2) is oriented such that it reflects the second largest source of variation in the data while being orthogonal to the first PC. PC2 also passes through the average point.

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• Standardize the data: Ensure that each feature has a mean of 0 and a standard deviation of 1. This is important for PCA because it is sensitive to the scales of the variables.

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- Calculate the covariance matrix: The covariance matrix is a square matrix that captures the covariance between each pair of features in the dataset. The covariance matrix (with dimension $k \times k$) is

$$\widehat{\Sigma} = \frac{1}{n-1} X^T X,$$

where X is the standardized data matrix (dimnesion $n \times k$) with n observations and k features.

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 \bullet The eigen-decomposition of $\widehat{\Sigma}$ can be written as

$$\widehat{\Sigma} = V \Lambda V^T$$
,

where V is a matrix containing the eigen-vectors and Λ is a diagonal matrix with diagonal elements as eigenvalues.

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- Then PC1 and PC2 can be represented as

$$PC1 = v_1$$

$$PC2 = v_2$$

where v_1 and v_2 are the eigenvectors corresponding to the largest and second largest eigenvalues, respectively.

Two principal components define a model plane

 When two principal components have been derived, they together define a place, a window into the K-dimensional variable space.

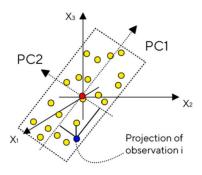
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- By projecting all the observations onto the low-dimensional sub-space and plotting the results, it is possible to visualize the structure of the investigated data set.
- The coordinate values of the observations on this plane are called scores, and hence the plotting of such a projected configuration is known as a score plot.

Two principal components define a model plane



 Two PCs form a plane. This plane is a window into the multidimensional space, which can be visualized graphically. Each observation may be projected onto this plane, giving a score for each.

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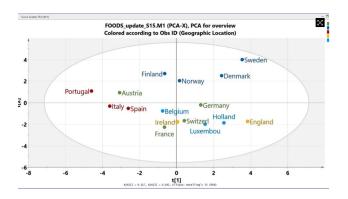
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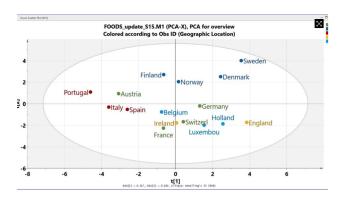
• Here, the first column of T contains the scores for the first principal component (PC1), the second column contains the scores for the second principal component (PC2), and so on.

 Now, let's consider what this looks like using a data set of foods commonly consumed in different European countries. The figure in the next page displays the score plot of the first two principal components. These scores are called t₁ and t₂.

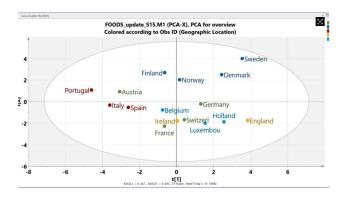
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- The score plot is a map of 16 countries. Countries close to each other have similar food consumption profiles, whereas those far from each other are dissimilar.



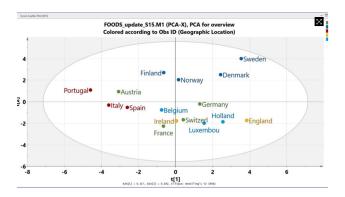
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- The first component explains 32% of the variation, and the second component 19%.



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- Belgium and Germany are close to the center (origin) of the plot, which indicates they have average properties.

	Χ	Υ
	1	2
•	3	4
	5	6

ullet Consider the following dataset with two variables X and Y

	Χ	Υ
	1	2
•	3	4
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• Centered data table

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- Find the eigenvalues and eigenvectors:
 - eigenvalues : 0,8
 - eigenvectors:

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$$\begin{bmatrix} 1/\sqrt{2} \ 1/\sqrt{2} \end{bmatrix}$$

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- Calculate the scores: Project the centered data onto the principal component: Scores = Centered data × Principal component =

$$\begin{bmatrix} -2\sqrt{2} & 2\sqrt{2} \\ 0 & 0 \\ 2\sqrt{2} & -2\sqrt{2} \end{bmatrix}$$

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- However, standard PCA is sensitive to outliers and noise, which can significantly affect the computed principal components.
- Need for Robust PCA: To address the limitations of standard PCA, Robust PCA was developed.
- Unlike standard PCA, Robust PCA is designed to separate the low-rank structure of the data (representing the true signal) from the sparse noise or outliers. This makes it more suitable for real-world datasets that are often corrupted by noise or contain anomalies.

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- The L-1 norm of a matrix A is defined as the sum of the absolute values of all its entries.

Clustering

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- Now, the bank can potentially have millions of customers. Does it make sense to look at the details of each customer separately and then make a decision?
- Certainly not! It is a manual process and will take a huge amount of time.
- So what can the bank do?

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- The bank can now make three different strategies or offers, one for each group, instead of creating different strategies for individual customers.
- Note that "high income," "average income," "low income" are not pre-specified lable, but the outcome of clustering. So, this is un-supervised learning.

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- Here, we are given feature vectors for each data point $x^{(i)} \in \mathbb{R}^n$ as usual; but no labels $y^{(i)}$ (making this an unsupervised learning problem).
- Our goal is to predict k centroids and a label " $c^{(i)}$ " (corresponding to different clusters) for each datapoint. The k-means clustering algorithm is as follows:

• K-Means is one of the most popular "clustering" algorithms.

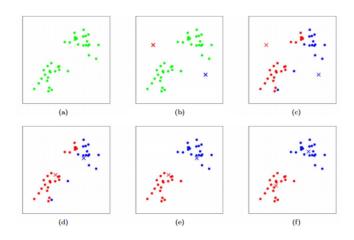
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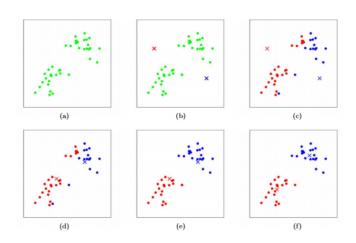
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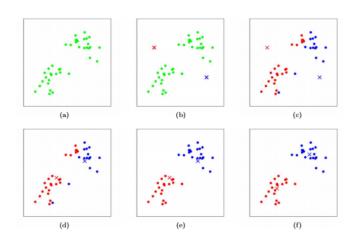
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- The value of *K* is often pre-specififed.



 Training examples are shown as dots, and cluster centroids are shown as crosses.

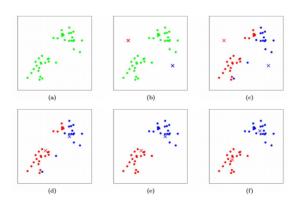


• (a) Original dataset.

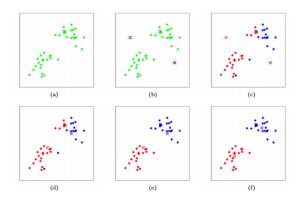


• (b) Random initial cluster centroids.

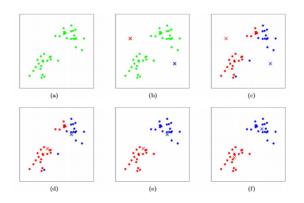
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• (c-f) Illustration of running two iterations of k-means.



 In each iteration, we assign each training example to the closest cluster centroid (shown by "painting" the training examples the same color as the cluster centroid to which is assigned);



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- Then we move each cluster centroid to the mean of the points assigned to it.

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 - For each j, set $\mu_j = \frac{\sum\limits_{i=1}^m 1\{c^{(i)}=j\}x^{(i)}}{\sum\limits_{i=1}^m 1\{c^{(i)}=j\}}$

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 - (4) Repeat Steps 2 and 3 until the centroids do not change.

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• Fuzzy C-Means (FCM) is a clustering algorithm that allows one piece of data to belong to two or more clusters.

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- This method is frequently used in pattern recognition and is an extension of the traditional k-means clustering algorithm.
- Unlike k-means, where each data point belongs to exactly one cluster, FCM introduces the concept of membership levels, allowing data points to have varying degrees of belonging to multiple clusters.

• Given a dataset $X = \{x_1, x_2, \dots, x_n\}$ consisting of n data points, the the goal of FCM is to partition the data into c fuzzy clusters, where c is a predefined number of clusters.

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- Each data point x_i has a degree of membership u_{ij} in each cluster j, where u_{ij} is a number between 0 and 1 representing the degree to which x_i belongs to cluster j.

• The FCM algorithm aims to minimize the following objective function:

$$J(U, V) = \sum_{i=1}^{n} \sum_{j=1}^{c} u_{ij}^{m} ||x_{i} - v_{j}||^{2}$$

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- $V = \{v_1, v_2, \dots, v_C\}$ is the set of cluster centers
- m is the fuzziness parameter which controls the level of cluster fuzziness
- $||x_i v_j||$ is the Euclidean distance between the data point x_i and the cluster center v_j .

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- Membership update:

$$u_{ij} = \frac{1}{\sum_{k=1}^{c} \left(\frac{\|x_i - v_j\|}{\|x_i - v_k\|}\right)^{\frac{2}{m-1}}}$$

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• The algorithm stops when the changes in the membership matrix between consecutive iterations are below a specified threshold.

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- Suppose we have a dataset with four points: A, B, C, and D. We want to cluster these points into two clusters using Fuzzy C-means.
 After running the algorithm, we might get the following membership values for each point in each cluster:

Point	Cluster 1	Cluster 2
Α	0.8	0.2
В	0.3	0.7
C	0.6	0.4
D	0.1	0.9

 Point A has a high membership value (0.8) in Cluster 1 and a low membership value (0.2) in Cluster 2. This means that Point A is strongly associated with Cluster 1 but has a slight association with Cluster 2.

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- Point C has a membership value of 0.6 in Cluster 1 and 0.4 in Cluster 2, suggesting that it belongs more to Cluster 1 but still has some association with Cluster 2.
- Point D has a very low membership value (0.1) in Cluster 1 and a high value (0.9) in Cluster 2, showing that it is strongly associated with Cluster 2.

Advantages

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- 1) Gives best result for overlapped data set and comparatively better then k-means algorithm.
- 2) Unlike k-means where data point must exclusively belong to one cluster center, here data point is assigned membership to each cluster center as a result of which data point may belong to more then one cluster center.

Disadvantages

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 - 1) Apriori specification of the number of clusters.

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 - 2) Euclidean distance measures can unequally weight underlying factors.