

Applied statistics and Machine learning in Python with subsurface applications

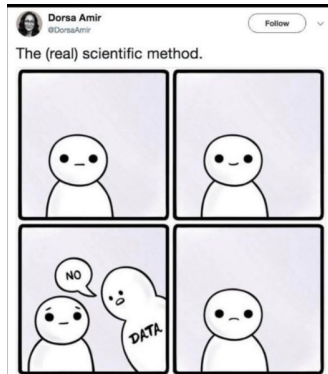
Enrico Riccardi, University of Stavanger

Feb 29, 2024



- 1 Data properties
- 2 Classification types
- 3 Agglomerative algorithms
- 4 k-means cluster analysis
- 5 Gaussian Mixture Model (GMM)
- 6 PCA

Data



A representation should **capture** the nature of the subject being studied.

Example: If you want to evaluate the 3D structure of a wind turbine, a set of descriptors can be:

- 1 Blade length
- 2 Turbine height
- 3 Geographical position
- 4 Output power
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which are two decimal numbers, a 2d tuple, a 1D time series and a 2D time series (or 3D even).

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- Are there such things as good data and bad data?

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- Data **DO NOT** *always* have value.

- TRASH in TRASH out

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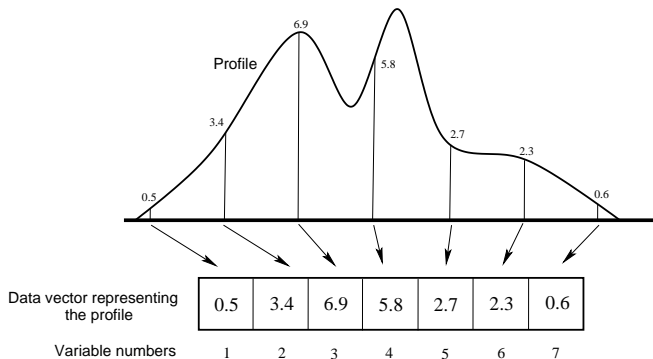
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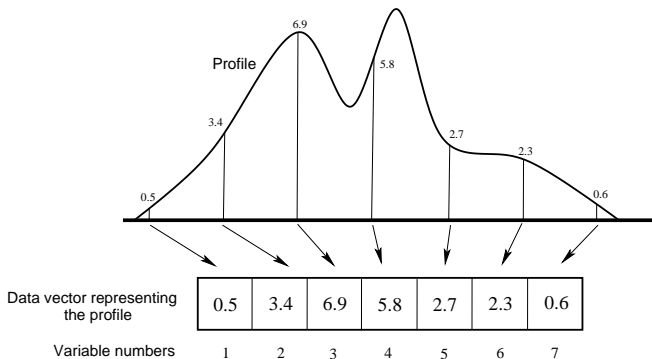
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- An intuitive way to represent curves and spectra is the **sampling point representation**.
- We sample at regular intervals where each sample point is represented by a variable



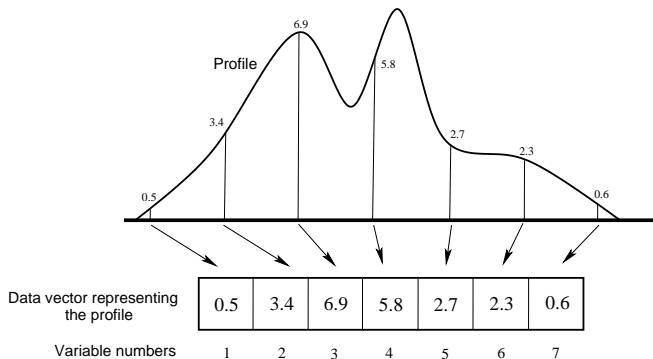
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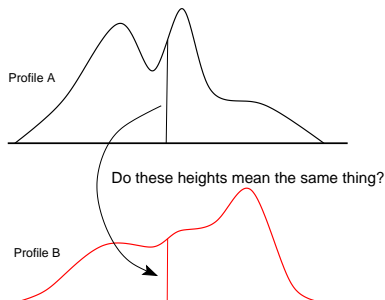
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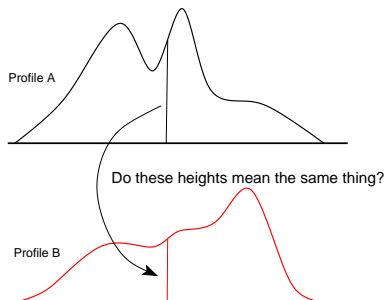
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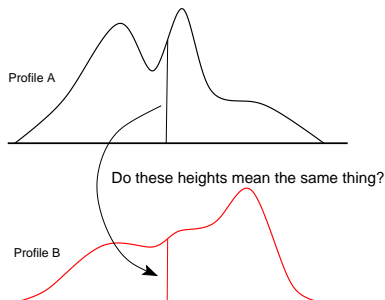
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Given a representation, it is then needed to decide on a suitable **data structure** for the problem.

Definition

A data structure is a way of storing and organising data in a computer so that it can be used effectively.

Typical data structures used in data analysis are:

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- Arrays (vectors, matrices, N-mode (way) arrays)
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Data has to be prepared with these steps in mind

- 1 Plan experiments: Use experimental design to set up experiments in a *systematic* way
- 2 Pre-processing: Is there systematic variation in the data which should be removed Can cross-checking/validation procedures be designed?
- 3 Examine the data: Look at data (tables and plots). Strange behaviours? Smooth behaviour? WARNING!
- 4 Define desired model outcomes (speed, accuracy, false positive/negatives rate)
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Statistics is collecting, organising, and interpreting data

Spatial and temporal statistics is a branch of applied statistics that emphasises:

- 1 the geo context of the data
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$$X = \begin{bmatrix} 95 & 89 & 82 \\ 23 & 76 & 44 \\ 61 & 46 & 62 \\ 49 & 2 & 79 \end{bmatrix}$$

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There are different conventions. Commonly we will construct data matrix such that:

- Rows are called instances, objects or samples.
- Columns are called features, variables.

One can think of each row to be an experiment, and the rows its properties. Each row (experiment, object, sample, ...) is thus a list of values, one for property.

Note

Mathematically speaking, this is just a notation. As long as one keeps track and is consistent, columns can be used as rows and vice versa.

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A quick example

Environmental measurements of rivers. The features (properties) can be:

- pH
- Temperature
- Concentration of pollutants
- Flow rate
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- Po
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Data into Machine Learning algorithms: normalisation

Different measurements can lead to different data distribution and numerical values.

When fed to numerical recipes, data is just a set of numbers.

For faster computations, data can be **normalized**: i.e. rescaled to the same numerical interval.

Normalisation

The procedure simplifies the numerical recipes work, but it also loses information

As it is not possible to complete sample any distribution, data might be disproportionately handled depending upon data collection (i.e. this can be an error source).

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Classification types

There are two main types of classification methods for analysis of a set of objects stored in matrix X :

Unsupervised classification

- Only the X data is used
- "Natural"
classes/clusters/groupings in X are discovered

Supervised classification

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- k-means cluster analysis
- Fuzzy c-means cluster analysis
- Self organising feature maps (SOFM)

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Limitations of unsupervised classification

- Do "natural" clusters in a data set exist and/or have any meaning?
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- Objects that are **close** have low dissimilarity and high similarity.

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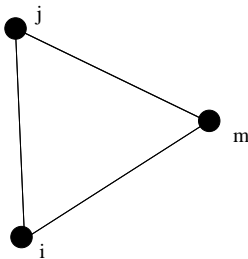
Proximity: Continuous variables

Triangle inequality

Considering a vectors in an N-dimensional space, to be a **distance** it must satisfy the **triangle inequality**:

$$d_{ij} + d_{im} \geq d_{jm}$$

If also $d_{jj} = 0$, if $i = j$ and $d_{jj} - d_{ii} = 0$, then we call it a *metric*.



Common metrics:

- Euclidean.

$$d_{ij}^{(E)} = \left[\sum_{k=1}^N (x_{ik} - x_{jk})^2 \right]^{\frac{1}{2}}$$

- Manhattan

$$d_{ij}^{(M)} = \sum_{k=1}^N \|x_{ik} - x_{jk}\|$$

- Minkowski

$$d_{ij}^{(M(p))} = \left[\sum_{k=1}^N (x_{ik} - x_{jk})^p \right]^{\frac{1}{p}}$$

Proximity: Categorical variables

- Many applications consist of binary vectors, typical is "yes" and "no" answers to a lot of tests
- It is tempting to use distance between binary vectors to signify distance. However that is *by far* not optimal.

Lets look at an example:

- $\mathbf{v}_1 = [1 \ 1 \ 0 \ 0 \ 0 \ 0]$
- $\mathbf{v}_2 = [0 \ 0 \ 1 \ 1 \ 0 \ 0]$
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Proximity: Categorical variables: Binary matching

	<i>Object B</i> value 1	<i>Object B</i> value 0
<i>Object A</i> value 1	a	b
<i>Object A</i> value 0	c	d

Example

$$\mathbf{a} = [0 \ 0 \ 0 \ 1]$$

$$\mathbf{b} = [1 \ 1 \ 0 \ 1]$$

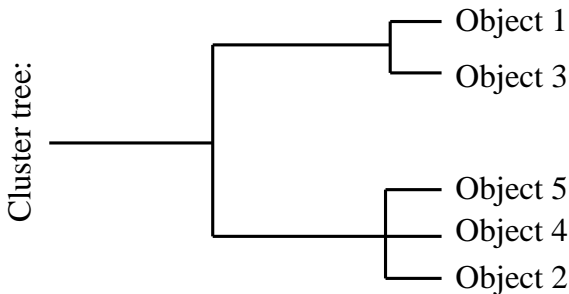
- $c = 2$: two places where A has 0 and B has 1.
- $d = 1$: one place where A and B are equal to 0.
- $a = 1$: one place where A and B are equal to 1.

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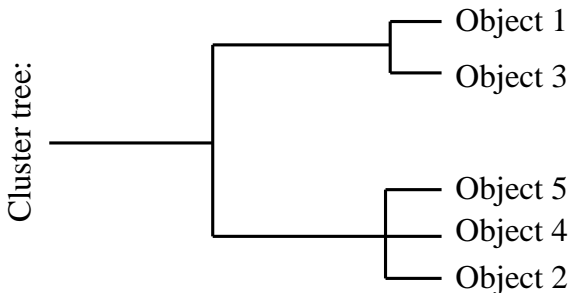
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Clumping objects

One of the simplest iterative approaches for unsupervised clustering is:

`n_clusters = n_datapoints`

- 1 WHILE no. clusters $>$ 1
- 2 Find smallest **distance** between clusters A and B
- 3 Merge clusters A and B
- 4 Define a new cluster (AB)
- 5 **Distance** matrix between all clusters
- 6 ENDWHILE

Unsupervised learning

Unsupervised learning, a term that resonates with the autonomy of machine intelligence, operates on the principle of identifying patterns and structures in datasets without labelled responses.

This branch of machine learning is distinguished by its lack of explicit guidance, where algorithms are tasked with uncovering hidden structures from unlabeled data.

The most common clustering strategies are :

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Still, it has been shown efficient for:

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Goals

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Relevant is not the same as causal.

Correlation is not causation.

As we do not have a 'truth', or a supervision, we can look for data-patterns by

- grouping strategy according to some properties analogy
- reducing variance within groups.

Note: these approaches will (almost) always converge or provide information. Which is a better outcome, strategy or model parameter can be, at the end, only evaluated with domain expertise.

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- reducing variance within groups.

Note: these approaches will (almost) always converge or provide information. Which is a better outcome, strategy or model parameter can be, at the end, only evaluated with domain expertise.

The number of unsupervised approach is tremendous, yet, the most common are the following:

- k-means (rigid clustering)
- Gaussian mixed model (soft clustering)
- Hierarchical clustering (grouping into trees/dendrograms)
- Principal component analysis (PCA) (Principal components identifications,)
- Auto-encoders (data compression)

We will discuss a few of them.

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- 2 Classification types
- 3 Agglomerative algorithms
- 4 k-means cluster analysis**
- 5 Gaussian Mixture Model (GMM)
- 6 PCA

k-means cluster analysis

With the raise of Machine Learning, one of the most popular approach is k-means.

The algorithm consists of:

- 1 Select the number of clusters $K \leq K_{max}$ to look for
- 2 Start by creating K random cluster centres \mathbf{m}_k
- 3 For each object \mathbf{x}_j assign it to the cluster center it is nearest to
- 4 Re-compute center points \mathbf{m}_k for the new clusters and re-iterate towards convergence

This procedure minimises the within-cluster variance

Optimal no of clusters

In k-means cluster analysis we assume a **true** number of clusters.

To estimate the optimal no. of clusters K^* from data we may do as follows:

- 1 Compute k means for $K \in [1, 2, \dots, K_{max}]$
- 2 Compute the mean **within cluster variance** W_K for each selection of $K \in [1, K_{max}]$
- 3 The variances $[W_1, W_2, \dots, W_{max}]$ generally decrease with increasing K . This will even be the case for an independent test set such that cross-validation cannot be used.

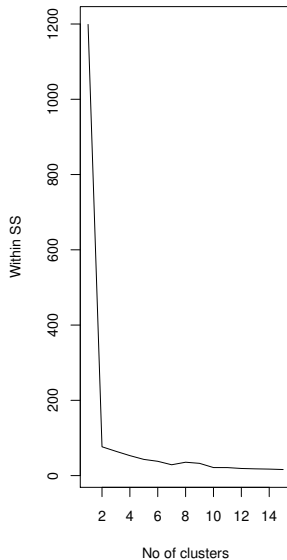
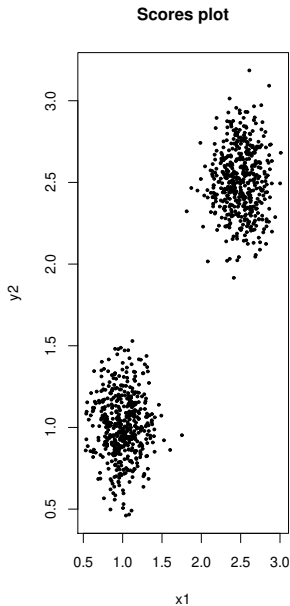
Optimal no of clusters

- 1 Intuitively, when $K < K^*$ we expect that an additional cluster will lower the within cluster variance: $W_{K+1} \ll W_K$.
- 2 When $K > K^*$ the decrease of the variance will be less evident.

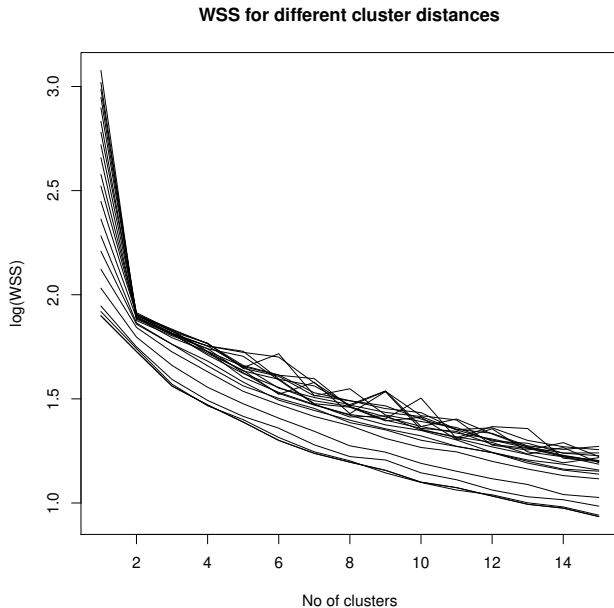
Optimal $n_clusters$

This means there will be flattening of the W_j curve. A sharp drop in the variance may be used to identify the optimal no. of clusters.

Optimal no of clusters, example



Optimal no of clusters, example



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Gaussian Mixture Model (GMM)

Gaussian Mixture is a probabilistic model that tries to split the data into clusters.

Each cluster is represented by a center (its mean) and a Gaussian distribution around it with different variance for the different dimensions.

To each datapoint, a belonging probability to each cluster is assigned.

Assumption

Data points are generated from a mixture of a finite number of Gaussian distributions with unknown parameters.

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The method is rather powerful, but it has quite significant drawbacks:

- The method can be rather unstable and not converge for 'poor' data.
- Iterative procedure is usually needed and convergence dependend on initial guest.
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GMM usage example

GMM is used in a large span of fields:

- Clustering: GMMs can identify clusters with different shapes and sizes due to their probabilistic nature, making them suitable for more complex datasets.
- Density Estimation: GMMs can model the probability distribution of a dataset
- Anomaly Detection: By modeling the normal behavior of data through its distribution, GMMs can be used to detect outliers or anomalous events.
- Image Segmentation: In computer vision, GMMs can be used for image segmentation, where the goal is to partition an image into segments based on the colors or textures.
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$$p(x) = \sum_{k=1}^K w_k f_k(x, \theta_k)$$

where

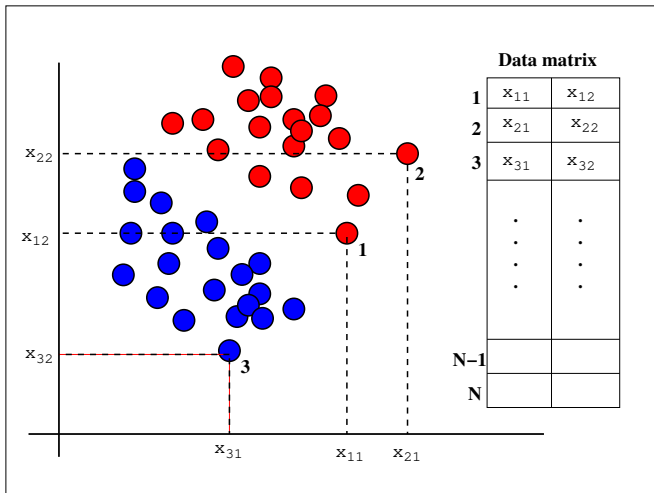
- $p(x)$ is the overall density or mass function of the mixture model.
- K is the number of distributions to be considered
- $g_k(x, \theta_k)$ is the density mass function of the k -th component
- θ_k are the parameters for the $g_k()$ distribution

and where a Gaussian is:

$$g(x) = \frac{1}{\sigma \sqrt{2\pi}} \exp\left(-\frac{1}{2} \frac{(x - \mu)^2}{\sigma^2}\right)$$

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Central in any data analysis is the use of a *data matrix*



Question:

How can we understand the information contained in such a data matrix?

- The geometry of the "object cloud" in N dimensions is used to understand relations

Geometrical insights

Plotting provides **geometrical insights** and observation of **hidden data structures** and **patterns**

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Correlated variables

Problem

How can we use plotting if we have more than 3 variables?

Solution

- 1 Seek for **correlated variables** in the data matrix
- 2 Seek for latent variable
- 3 Give up (use AI)

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Correlated variables

- Correlated variables contain approximately the same information.
- Several correlated variables suggests:
 - the same **phenomenon** is manifested in different way
 - an **underlying phenomenon** more fundamental exists

Let's assume the latter:

Linear combinations

Assuming the latent variables to be a linear combinations of the original variables, i.e.:

$$LV = a_1x_1 + a_2x_2 + \cdots + a_nx_n$$

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A new coordinate system

- 1 Latent variables are based on creating a new coordinate system based on linear combination of the original variables
- 2 Objects are projected from a higher dimensional data space onto this new (lower dimensional) coordinate system
- 1 The new coordinate system improves interpretation and prediction.

Principal component analysis (PCA) can automatically create useful latent variables

Originally invented in 1901 by Karl Pearson and re-invented several times. The PCA method is also referred to as:

- 1 Singular value decomposition (numerical analysis)
- 2 Karhunen-Loeve expansion (electric engineering)
- 3 Eigenvector analysis (physical sciences)
- 4 Hotelling transform (image analysis/statistics)
- 5 Correspondence analysis (double scaled version of PCA)



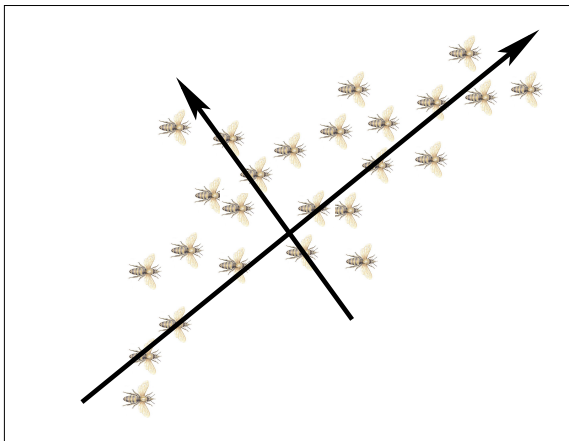
Karl Pearson

Goals of PCA:

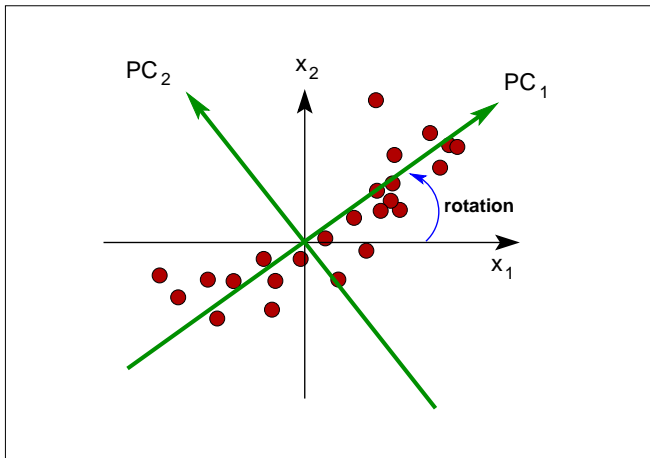
- ➊ Simplification.
- ➋ Data reduction and data compression
- ➌ Modeling
- ➍ Outlier detection
- ➎ Variable selection
- ➏ Classification
- ➐ Prediction
- ➑ ... world peace ...

Rotation of the coordinate system

In PCA the original coordinate system is rotated such that the new latent variable axes point in the direction of **max variance**

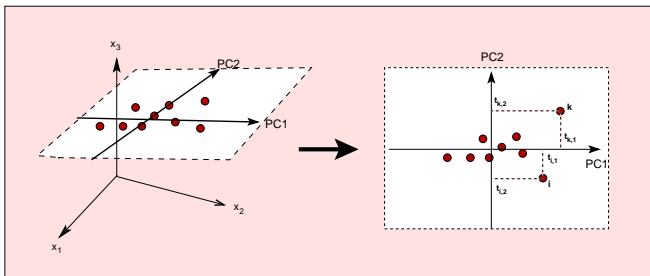


Rotation of the coordinate system



Scores are new coordinates

Scores are the coordinates of objects in the **new** coordinate system



Data = Model + Noise

Data
matrix

=

Model
matrix

+

Residual
matrix

PCA Model

$$X = M_1 + M_2 + \dots + M_{Aopt} + E$$

$$X = \begin{matrix} \text{---} \\ | \\ \text{---} \end{matrix} \begin{matrix} \text{---} \\ | \\ \text{---} \end{matrix} \begin{matrix} \text{---} \\ | \\ \text{---} \end{matrix} + \dots + \begin{matrix} \text{---} \\ | \\ \text{---} \end{matrix} + E$$

The diagram shows the decomposition of matrix X into a sum of principal components and an error term E . Each principal component is represented by a vertical rectangle labeled t_i and a horizontal rectangle labeled p_i , connected by a right-angle symbol. The components are $t_1, p_1, t_2, p_2, \dots, t_{Aopt}, p_{Aopt}$.

Residual variance plot

