# GRAU EN ENGINYERIA DE DADES **104365 Visualització de Dades**

## Teoria 6. Tractament de dades II

Departament de Matemàtiques





## Data processing for visualization

- Chapter 5 Data processing for visualization (I)
  - Uncertainty and error
  - Transformations and data massage (+ seminars & PRT1)
- > Chapter 6 (today) Data processing for visualization (II)
  - Dimensionality reduction
  - Computation and important metrics selection





## 6. Data processing for visualization (II). Contents:

## 1. Dimensionality reduction

- 1. Introduction
- 2. Correlograms
- 3. Feature projection PCA
- 4. Discriminant analysis (linear) LDA
- 5. T-Distributed stochastic neighbour embedding (t-SNE)
- 6. Tomography- Slice along a plane, 2D isosurfaces for a 3D field, isocontours

## 2. Computation and important metrics selection

1. Quality metrics: Noise reduction, clutter reduction, search outliers





Dimensionality reduction (DR) means: the process of transformation of data from high dimensional space to low dimensional space while maintaining most of the meaningful insights from the original data.

The goal is to preserve the meaningful structure of a dataset while using fewer attributes to represent the items.

For example: We have a dataset contains hundred columns (i.e features) or it could be an array of points that make up a large sphere in the 3D space. DR?

DR entails lowering the number of columns to a smaller number, such as 2D.





Dimensionality reduction (DR) has two primary use cases:

- data exploration
- machine learning.

DR is a strategy for managing complexity in visualization:

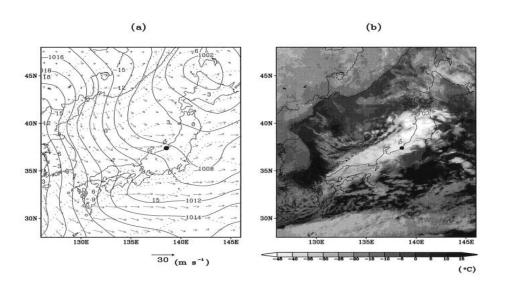
It is useful *for data exploration* because **dimensionality reduction to few dimensions** (e.g., 2D or 3D) **allows for visualizing the samples.** 

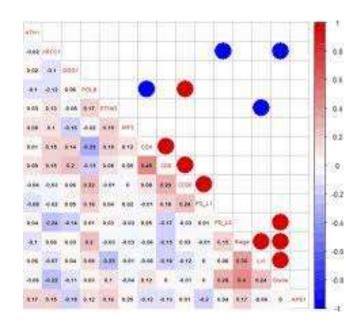
Such a visualization can then be used to obtain insights from the data (e.g., detect clusters and identify outliers).

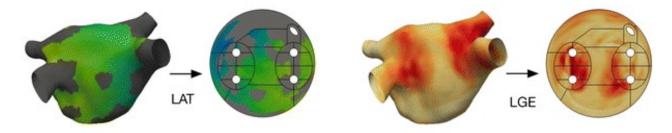




### Examples of dimension reduction:



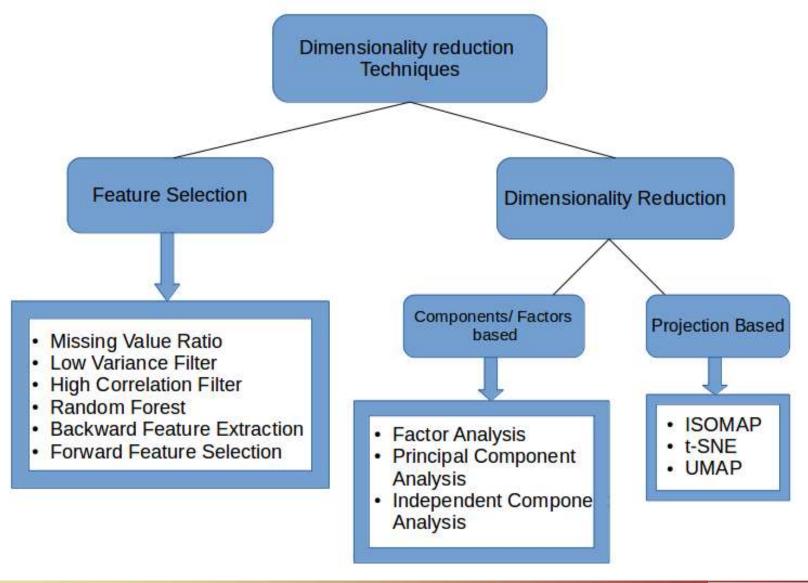




DOI: <u>10.1007/s10840-017-0281-3</u>





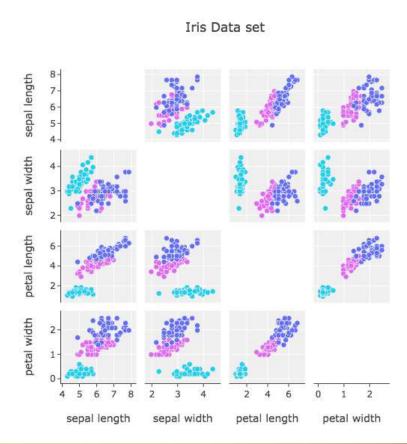






## 6.1.1. Remember: Scatterplot matrix limitation

We saw: **Scatterplot matrix (SPLOM)** uses multiple scatterplots to determine the correlation (if any) between a series of variables.



!! When we have >3 or 4 quantitative variables — scatterplot matrices quickly become unwieldy





## 6.1.1. Correlation coefficients

We saw: **Scatterplot matrix (SPLOM)** uses multiple scatterplots to determine *the correlation (if any) between a series of variables.* 

!! When we have >3 or 4 quantitative variables — scatterplot matrices quickly become unwieldy

In this case, it is more useful to quantify the amount of association between pairs of variables and visualize these quantities rather than the raw data.

One common way to do this is to calculate **correlation coefficients**.





## 6.1.1. Correlation coefficient

- Having two sets of observations:  $x_i$  and  $y_i$
- And:  $\bar{x}$  and  $\bar{y}$  the corresponding sample means

The correlation coefficient is:

$$R = \frac{\sum_{i} (x_{i} - \bar{x})(yi - \bar{y})}{\sqrt{\sum_{i} (x_{i} - \bar{x})^{2}} \sqrt{\sum_{i} (y - \bar{y})^{2}}}$$

The correlation coefficient R is a number between -1 and 1 that measures to what extent two variables are correlated





## 6.1.1. Correlation coefficients

$$R = \frac{\sum_{i} (x_{i} - \bar{x})(y_{i} - \bar{y})}{\sqrt{\sum_{i} (x_{i} - \bar{x})^{2}} \sqrt{\sum_{i} (y_{i} - \bar{y})^{2}}}, -1 < R < 1$$

- R = 0 means there is **no association** whatsoever
- R = 1 or -1 indicates a perfect association

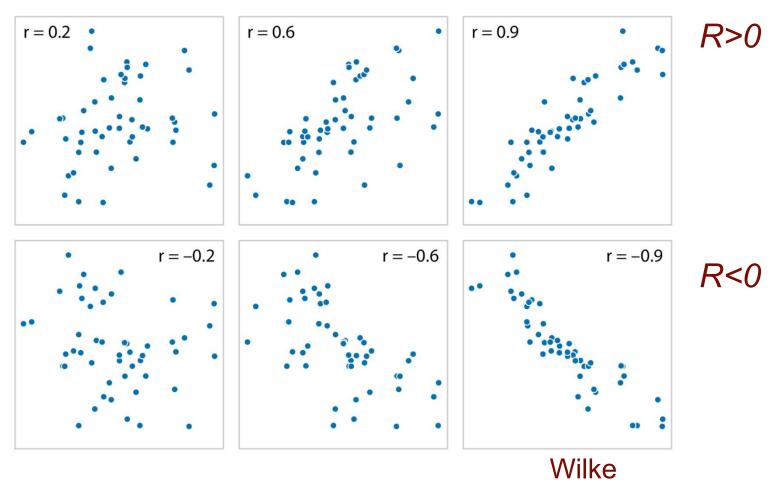
The sign of the correlation coefficient R indicates:

- *R* >0: variables are **correlated** (larger values in one variable coincide with larger values in the other)
- *R*<0: anticorrelated (larger values in one variable coincide with smaller values in the other)





## 6.1.1. Correlation coefficients

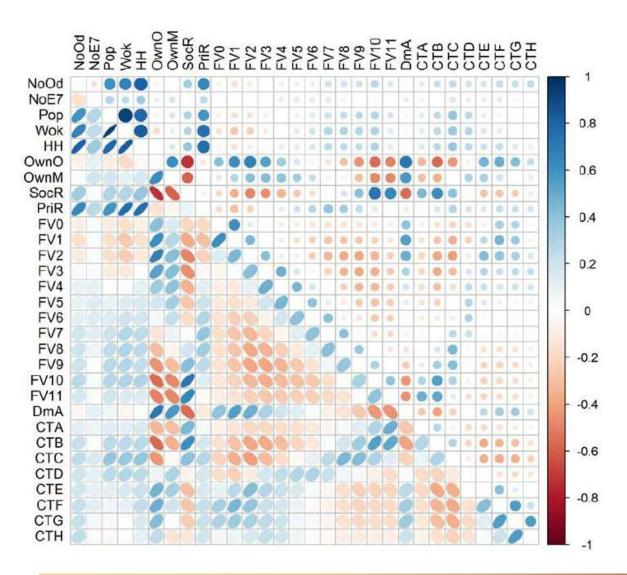


Examples of correlations of different magnitude and direction, with associated correlation coefficient R





## 6.1.2. Correlogram



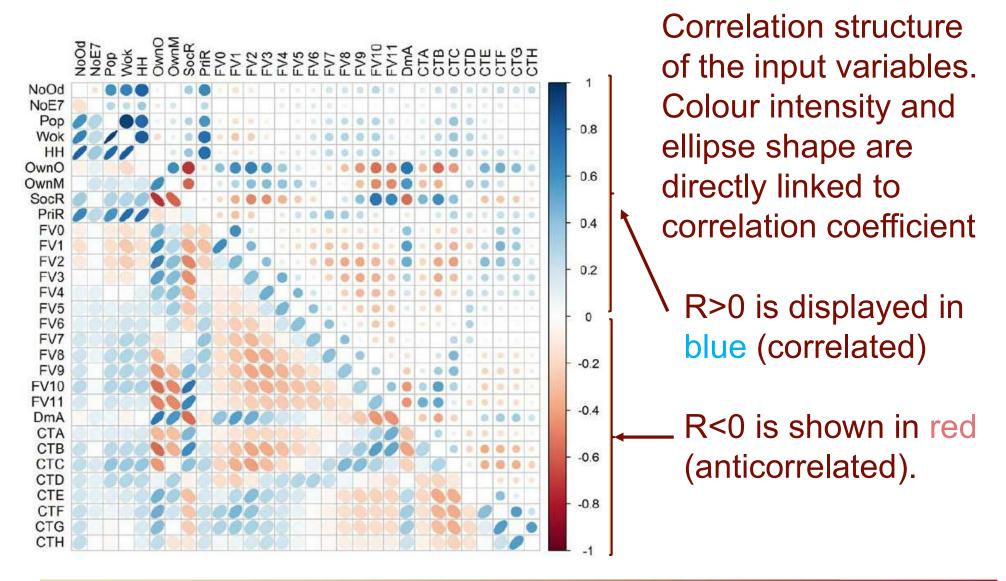
Correlation structure of the input variables. Colour intensity and ellipse shape are directly linked to correlation coefficient

DOI: <u>10.1016/j.proeng.2015.0</u> <u>8.1069</u>





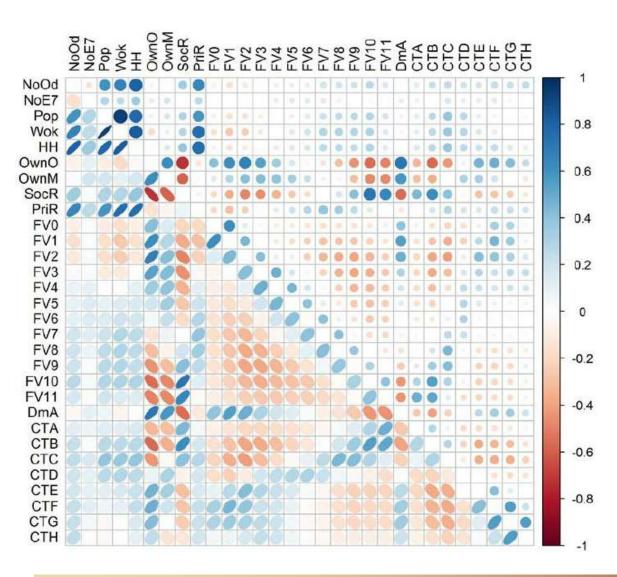
## 6.1.2. Correlogram







## 6.1.2 Correlogram



- there is a higher negative correlation coefficient between two variables.
- indicates a weak correlation for two factors
- : there is a higher positive correlation coefficient between two variables





## 6.1. Correlation & Dimensionality reduction

DR relies on the key insight that **most high-dimensional** datasets consist of multiple correlated variables that convey overlapping information

Such datasets can be reduced to a smaller number of key dimensions without loss of much critical information.

DR can be achieved by:

- Feature elimination we reduce the feature space by elimination feature
- Feature selection process of selecting required features from all the features available in data. Goal: to choose features that represent the dataset perfectly
- Feature Engineering process of transforming raw data into feature, which represent the dataset well





## 6.1. Correlation & Dimensionality reduction

DR relies on the key insight that most high-dimensional datasets consist of multiple correlated variables that convey overlapping information

Such datasets can be reduced to a smaller number of key dimensions without loss of much critical information.

There are many techniques for dimension reduction. We will see:

- Principal Components Analysis (PCA)
- Linear Discriminant Analysis (LDA)
- T-Distributed Stochastic Neighbour Embedding (t-SNE) (next day)





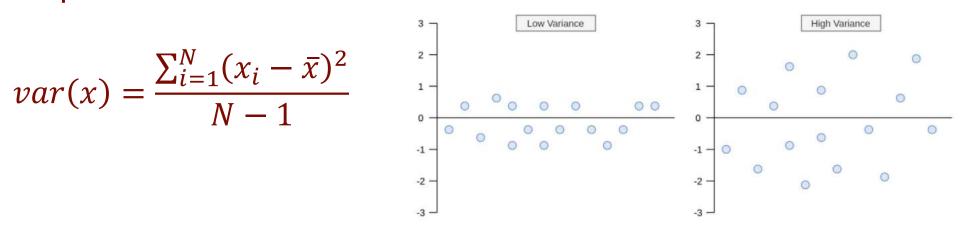
## **6.1.** Remember: Variance

Before going further, let's clarify some concepts:

 We know that variance represents the variation of values in a single variable. It depends on how the values far from each other.

Having a set of observations:  $x_i$  and  $\bar{x}$  the corresponding sample mean:

$$var(x) = \frac{\sum_{i=1}^{N} (x_i - \bar{x})^2}{N - 1}$$



Sergen Cansiz





## 6.1. Remember: Covariance

### Before going further, let's clarify some concepts:

- Unlike the variance, covariance is calculated between two different variables. Its purpose is to find the value that indicates how these two variables vary together.
- Having two sets of observations:  $x_i$  and  $y_i$
- And:  $\bar{x}$  and  $\bar{y}$  the corresponding sample means

$$cov(x,y) = \frac{\sum_{i=1}^{N} (x_i - \bar{x})(y_i - \bar{y})}{N-1}$$





## 6.1. Remember: Covariance vs correlation

### Before going further, let's clarify some concepts:

- Covariance vs correlation
- Having two sets of observations:  $x_i$  and  $y_i$
- And:  $\bar{x}$  and  $\bar{y}$  the corresponding sample means

$$cov(x,y) = \frac{\sum_{i=1}^{N} (x_i - \bar{x})(y_i - \bar{y})}{N-1}$$

$$var(x) = \frac{\sum_{i=1}^{N} (x_i - \bar{x})^2}{N - 1}$$

$$R(x,y) = \frac{\sum_{i} (x_{i} - \bar{x})(yi - \bar{y})}{\sqrt{\sum_{i} (x_{i} - \bar{x})^{2}} \sqrt{\sum_{i} (y - \bar{y})^{2}}}$$





### 6.1. Covariance vs correlation

### Before going further, let's clarify some concepts:

#### Covariance vs correlation

Covariance	Correlation		
Covariance is a <b>measure</b> to indicate the extent to which <b>two random variables change</b> <i>in</i> <b>tandem</b>	Correlation is a <b>measure</b> used to represent how strongly <b>two random variables are related</b> <i>to each other</i>		
Covariance indicates the direction of the linear relationship between variables			
Covariance can vary between $-\infty$ and $+\infty$	Correlation ranges between -1 and 1		





## 6.1. Covariance vs correlation

### Before going further, let's clarify some concepts:

#### Covariance vs correlation

Covariance	Correlation		
Covariance is affected by the change in scale. If all the values of one variable are multiplied by a constant and all the values of another variable are multiplied, by a similar or different constant, then the covariance is changed	-		
Covariance of two <i>dependent variables</i> measures <b>how much in real quantity</b> (i.e, e.g., cm, km, liters) <b>on average they</b> <i>covary.</i>	measures the proportion of how much		
Covariance is zero for independent variables	Completely independent variables have a zero correlation		





### Before going further, let's clarify some concepts:

#### Covariance matrix

Because covariance can only be calculated between two variables, covariance matrices stand for representing covariance values of each pair of variables in multivariate data. Also, the covariance between the same variables equals variance, so, the diagonal shows the variance of each variable

Symmetric matrix

$$\begin{bmatrix} \mathbf{var}(x) & \mathbf{cov}(x,y) \\ \mathbf{vov}(x,y) & \mathbf{var}(y) \end{bmatrix} \quad \mathbf{var}(x) \quad \begin{bmatrix} \mathbf{var}(x) & \mathbf{cov}(x,y) & \mathbf{cov}(x,z) \\ \mathbf{cov}(x,y) & \mathbf{var}(y) & \mathbf{cov}(y,z) \\ \mathbf{cov}(x,z) & \mathbf{cov}(y,z) & \mathbf{var}(z) \end{bmatrix}$$

2 and 3- dimensional covariance matrices





### Before going further, let's clarify some concepts:

#### Covariance matrix

These *values* in the covariance matrix **show the distribution magnitude** and **direction** of multivariate data in multidimensional space.

By controlling these values we can have information about how data spread among two dimensions.

Symmetric matrix

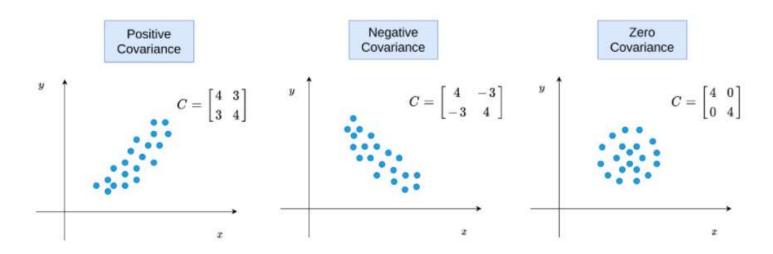
2 and 3- dimensional covariance matrices





### Before going further, let's clarify some concepts:

Covariance matrix

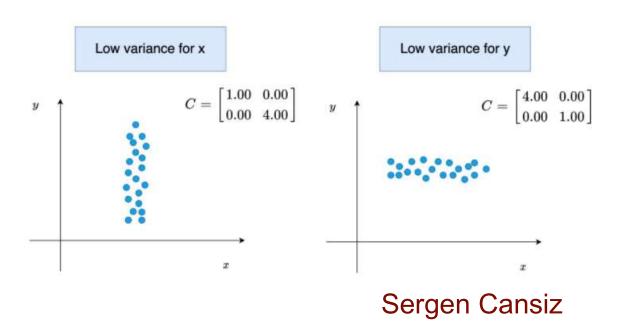


Sergen Cansiz



### Before going further, let's clarify some concepts:

Covariance matrix



Covariance near zero and different variances





When should I use PCA?

- 1. Do you want to reduce the number of variables, but **you** are not able to identify variables to completely remove from consideration?
- 2. Do you want **to ensure your variables are independent** of one another?
- 3. Are you comfortable making your independent variable less interpretable?





- PCA introduces a **new set of variables (smaller number of variables)**, called **principal components (PCs)**, by linear combination of the original variables in the data, standardized to zero mean and unit variance.
- The axes or new variables are the PCs and are ordered by variance:
  - The first component, *PC 1*, represents the *direction of the highest variance of the data*.
  - The direction of the *PC* 2, represents the *highest of the* remaining variance **orthogonal** to the *PC* 1.

This can be naturally extended to obtain the required number of components, which together span a component space covering the desired amount of variance.





## 6.1.3. Covariance matrix – relation with PCA

Before going further, let's clarify some concepts:

- Eigenvalues and eigenvectors of covariance matrix:
- The eigenvalues represent the magnitude of the spread in the direction of the principal components in PCA.
- The eigenvectors show the direction.

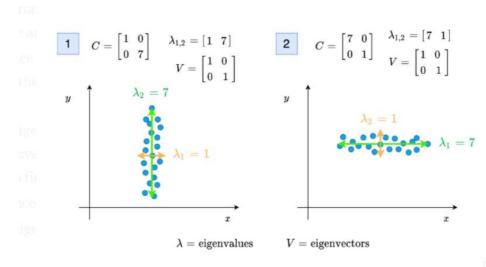




## 6.1.3 Covariance matrix – relation with PCA

## Before going further, let's clarify some concepts:

Eigenvalues and eigenvectors of covariance matrix

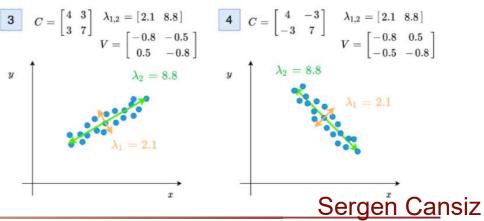


 The first and second plots show the distribution of points when the covariance is near zero (independent variables).

Note: when the covariance is zero the eigenvalues=variance values

- The third and fourth plots represent the distribution of points when the covariance is different from zero.

Note: here we need to calculate the eigenvalues and eigenvectors







PCA is maybe the most popular technique to examine high-dimensional data (unsupervised learning)

PCA computes a rotation matrix :  $W \in \mathbb{R}^{P \times P}$  from the matrix of features  $X \in \mathbb{R}^{N \times P}$ 

W can be understood as a mapping function that transforms the observations in X to a rotated space

The coordinates of observations in  $\boldsymbol{X}$  are transformed to their new form,  $\boldsymbol{Z}$ , via: Z = XW

The rotation matrix, *W*, is constructed through orthogonal linear transformations. Each of these transformations is performed in order to maximize the variance on the data



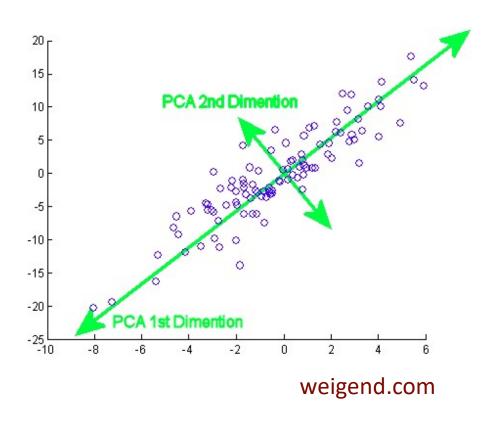


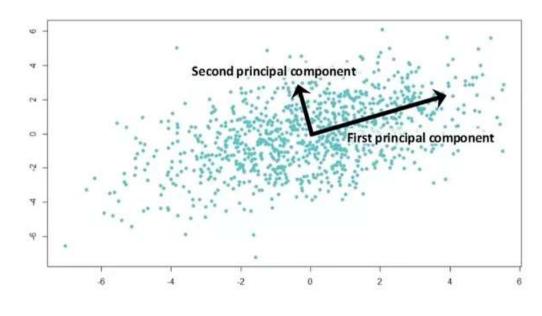
### Steps:

- 1. Take the matrix of features  $X \in \mathbb{R}^{N \times P}$ , N > P
- 2. Compute the **mean vector for each dimension**
- 3. Compute the **covariance matrix**
- 4. Compute the eigenvectors and corresponding eigenvalues for each dimension
- 5. Sort the eigenvectors by decreasing eigenvalues and choose P eigenvectors with the largest eigenvalues to form a new matrix  $W \in \mathbb{R}^{P \times P}$
- 6. Use this eigenvector matrix to transform the samples onto the new subspace: Z = XW







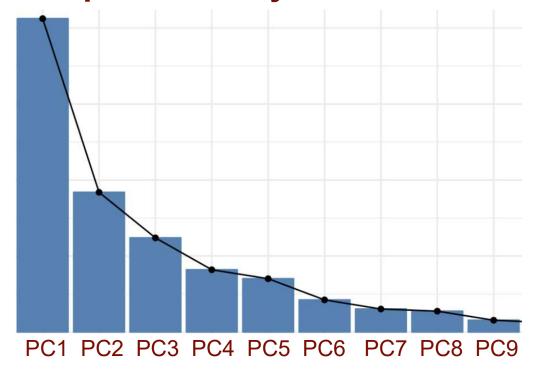


Wavy AI Research Foundation





- In highly dimensional datasets, the vast majority of the variance in the data is often captured by a small number of principal components.
- A plot of the distribution of the variance across principal components may look like this:







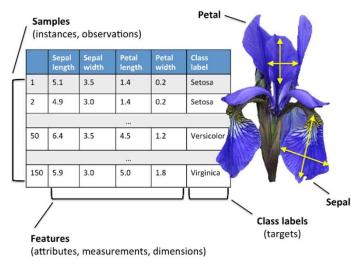




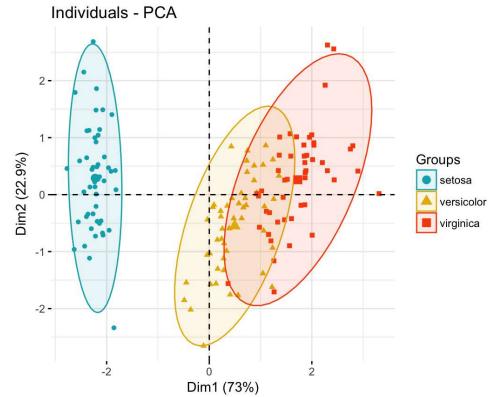


##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	4.7	3.2	1.3	0.2	setosa

# 3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width



PCA identifies the combination of attributes (PCs, or directions in the feature space) that account for the most variance in the data.



Here we plot the different samples on the 2 first PCs.





#### In the theoretical class, we saw:



##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	4.7	3.2	1.3	0.2	setosa

3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width

### **How to do PCA Visualization using R:**

The following functions, from factoextra package can be used:

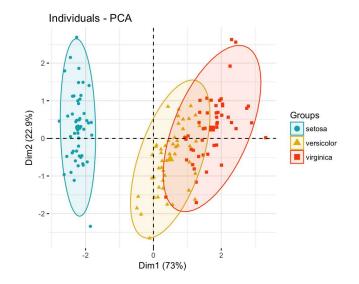
fviz\_pca\_ind(): Graph of individuals
fviz\_pca\_var(): Graph of variables

fviz\_pca\_biplot() (or fviz\_pca()): Biplot of

individuals and variables

PCA identifies the combination of attributes (PCs, or directions in the feature space) that account for the most variance in the data.

### In practice:







#### In the theoretical class, we saw:







##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	4.7	3.2	1.3	0.2	setosa

3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width

#### First, we need to install the packages and load the libraries:

- > install.packages("devtools")
- > library("devtools")
- > install.packages("factoextra")
- > library("factoextra")

#### Afterwards, we prepare the dataframe if needed:

The variable Species (index = 5) is removed (not numerical)

We use 'center=TRUE' to center the variables to 0 and we scale them to have variance 1 by using 'scale.

=TRUE'

> iris\_pca<-prcomp(iris[,-5], center=TRUE, scale.=TRUE)</pre>





### In the theoretical class, we saw:







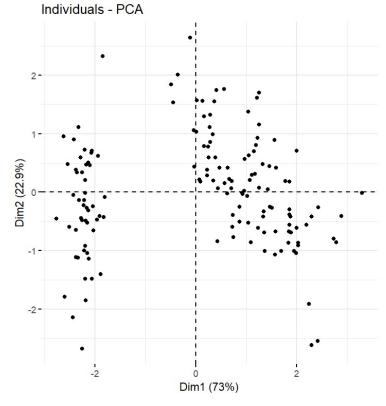
##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	4.7	3.2	1.3	0.2	setosa

3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width

## How to do PCA Visualization using R:

fviz\_pca\_ind(iris\_pca, geom="point")

# Graph of individuals using only points







### In the theoretical class, we saw:





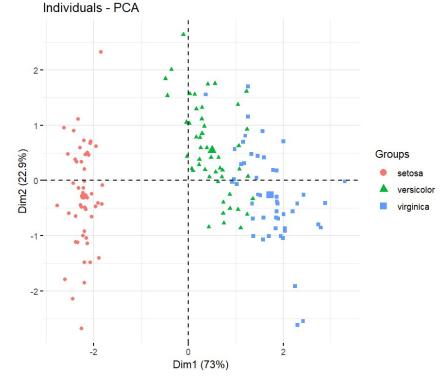


##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	4.7	3.2	1.3	0.2	setosa

3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width

### How to do PCA Visualization using R:

fviz\_pca\_ind(iris\_pca, geom="point")
# Graph of individuals using only points
fviz\_pca\_ind(iris\_pca, label="none",
habillage=iris\$Species)
# To Color individuals by groups







#### In the theoretical class, we saw:





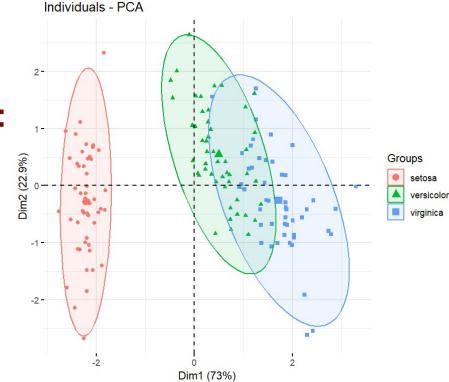


##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	4.7	3.2	1.3	0.2	setosa

3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width

### How to do PCA Visualization using R:

```
fviz_pca_ind(iris_pca, geom="point")
# Graph of individuals using only points
fviz_pca_ind(iris_pca, label="none",
habillage=iris$Species)
# To Color individuals by groups
fviz_pca_ind(iris_pca, label="none",
habillage=iris$Species,
addEllipses=TRUE, ellipse.level=0.95)
# To add ellipses
```







#### In the theoretical class, we saw:







##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	4.7	3.2	1.3	0.2	setosa

3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width

#### More options in:

http://www.sthda.com/english/wiki/fvizpca-quick-principal-componentanalysis-data-visualization-r-softwareand-data-mining

### **How to do PCA Visualization using R:**

summary(iris\_pca) # Give us the importance of the
components





## 6.1.3 Principal Components Analysis (PCA)

### Summarizing:

- PCA is a very interpretable method.
- Each PC is well-defined as we know that it is orthogonal to the other dimensions.
- We can obtain the variance that is explained by each PC to select an appropriate number of dimensions

#### Weakness of PCA:

It tends to be highly affected by outliers in the data

To overcome this issue many robust versions of PCA has been developed: RandomizedPCA, sparsePCA, etc

PCA works best only with continuous data





## 6.1.3 Principal Components Analysis (PCA)

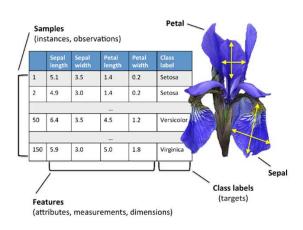


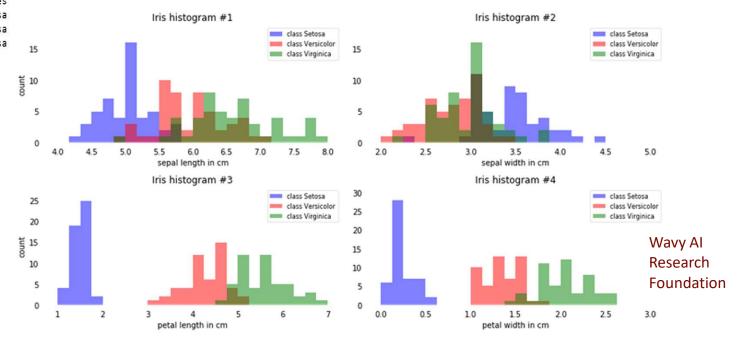




En numèriques

3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width





! Remark: For low-dimensional datasets like Iris, those histograms would already be very informative.





## 6.1.4 Linear Discriminant Analysis (LDA)

LDA seeks to best **separate** (or discriminate) **the samples** in the training dataset **by their class value**.

The fundamental idea of linear combinations goes back as far as the 1960s

√ The idea behind LDA: to find a new feature space to project the data in order to maximize classes separability

In 1988, the statiscian Ronald Fisher proposed:

- Maximize the function that represents the difference between the means, normalized by a measure of the within-class variability





## 6.1.4 Linear Discriminant Analysis (LDA)

The Fisher's model seeks to find a linear combination of input variables that:

- achieves the maximum separation for samples between classes (class centroids or means),
- and the minimum separation of samples within each class.

The LDA takes the mean value for each class and considers variants to make predictions assuming a Gaussian distribution

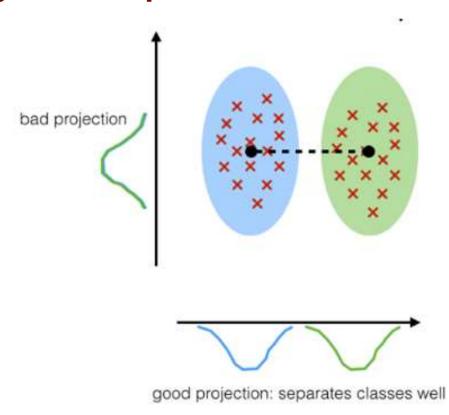




## 6.1.4 Linear Discriminant Analysis (LDA)

LDA seeks to best **separate** (or discriminate) **the samples** in the training dataset **by their class value**.

Maximizing the component axes for class-separation:



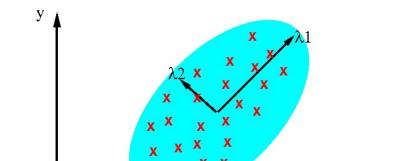
Wavy Al Research Foundation



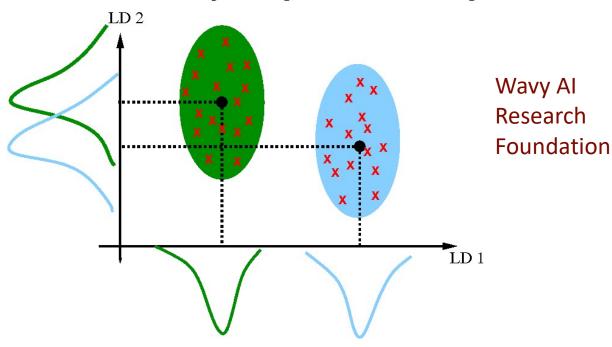


## 6.1.4 PCA versus LDA

PCA: component axes that maximize the variance



LDA: maximizing the component axes for class-separation



 Both, LDA and PCA are linear transformation techniques that are commonly used for dimensionality reduction (both are techniques for the data Matrix Factorization)

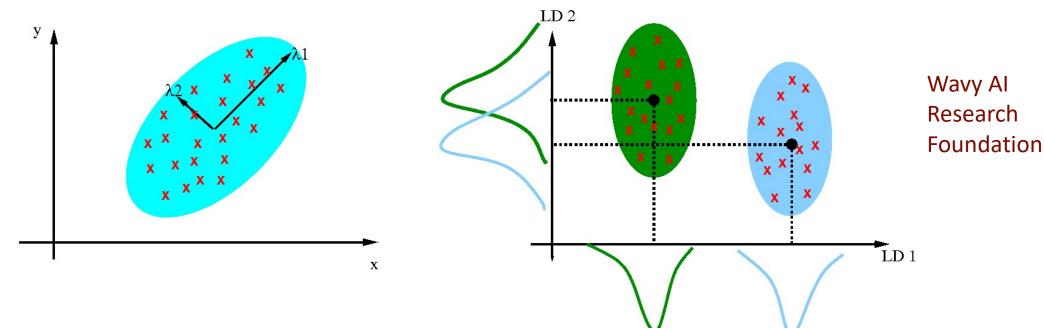




## 6.1.4 PCA versus LDA

PCA: component axes that maximize the variance

LDA: maximizing the component axes for class-separation

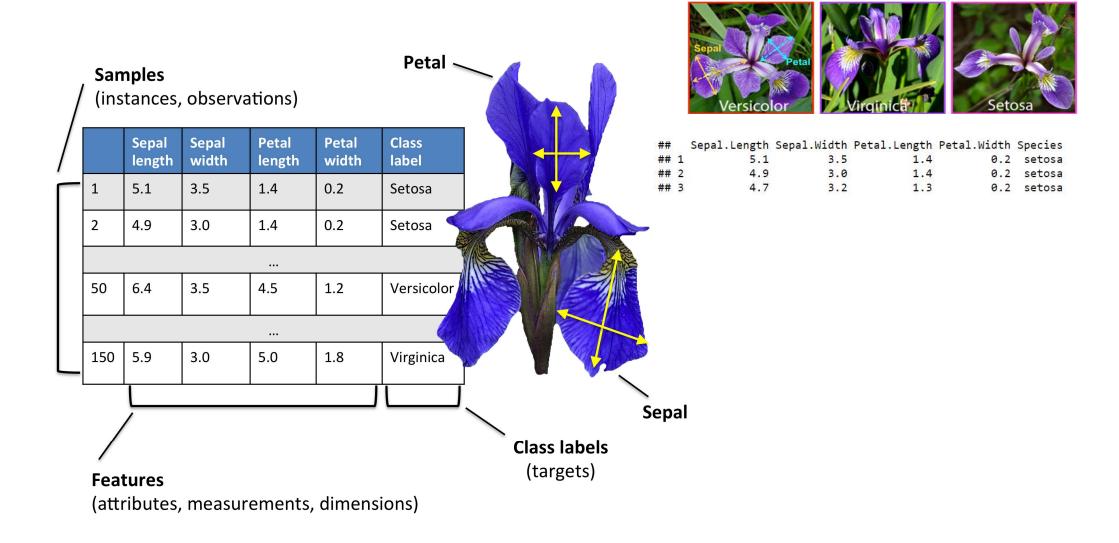


- PCA is unsupervised algorithm that attempts to find the orthogonal component axes of maximum variance in a dataset
- while the goal of LDA as supervised algorithm is to find the feature subspace that optimizes class separability.





## 6.1.4. PCA versus LDA







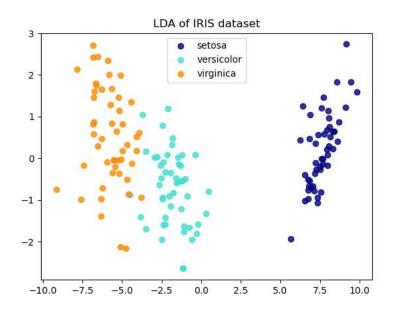
## 6.1.4. PCA versus LDA



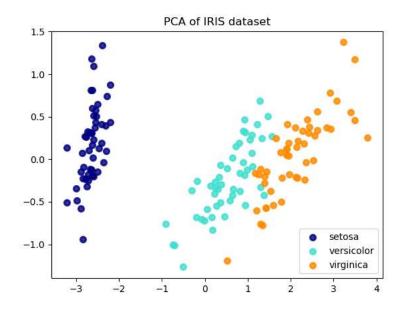




3 kind of Iris flowers with 4 attributes: sepal length, sepal width, petal length and petal width



PCA identifies the combination of attributes (PCs, or directions in the feature space) that account for the most variance in the data.



LDA: tries to identify attributes that account for the most variance between classes





## 6.1.4. Linear Discriminant Analysis (LDA)

Steps: (see this link for an example with iris dataframe)

- 1. Compute the **d-dimensional mean vector for the different** classes from the dataset. (in PCA was for each direction)
- 2. Compute the Scatter matrix (in between class and within the class scatter matrix)
- 3. Sort the Eigen Vector by decreasing Eigen Value order and choose *k* eigenvector with the largest eigenvalue to from a *dxk* dimensional matrix W (where every column represent an eigenvector)
- 4. Used *dxk* eigenvector matrix to transform the sample onto the new subspace. This can be summarised by the matrix multiplication:

$$Y = XW$$

where *X* is a *nxd* dimension matrix representing the *n* samples and you are transformed *nxk* dimensional samples in the new subspace.





## 6.1.4. Linear Discriminant Analysis (LDA)

LDA can be useful in areas like image recognition and predictive analysis in marketing

Weakness of LDA:

- LDA does not work well if the design is not balanced (i.e. the number of objects in various classes are (highly) different)
- If the distribution of your data is significantly non-Gaussian, the LDA might not perform very well.
- It is sensitive to overfit
- LDA is not applicable (inferior) for non-linear problems





# Thanks for your attention!

**Judit Chamorro Servent** 

Departament de Matemàtiques judit.chamorro@uab.cat



