

Title: The Data - Pre-processing and dissimilarities

Course: Machine Learning

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Date:

Master: Data Science and Business Analytics

Academic Year: 2022/2023

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# Data pre-processing

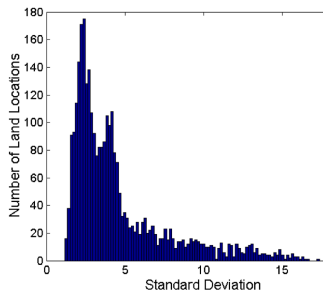
- Aggregation
- Sampling
- Dimensionality Reduction
- Feature subset selection
- Feature creation
- Discretization and Binarization Attribute Transformation

# Aggregation

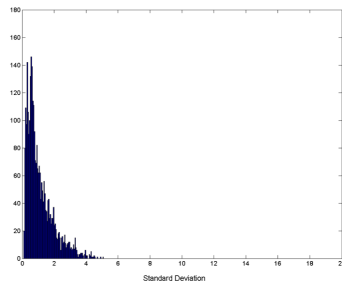
- Combining two or more attributes (or objects) into a single attribute (or object)
- Purpose
  - Data reduction
    - Reduce the number of attributes or objects
  - Change of scale
    - Cities aggregated into regions, states, countries, etc
  - *More stable* data
    - Aggregated data tends to have less variability

# Aggregation – Example

## Variation of precipitation in Australia



Standard Deviation of  
Average Monthly Precipitation



Standard Deviation of  
Average Yearly Precipitation

# Sampling I

- For both **preliminary** investigation and final data analysis
- Statistician perspective
  - **obtaining** the entire data set could be impossible or too expensive
- Data processing perspective
  - **processing** the entire data set could be too expensive or time consuming

# Sampling II

1. using a sample will work almost as well as using the entire data sets, *if the sample is representative*
2. A sample is representative if it has approximately the same property (of interest) as the original set of data

# Types of sampling

## 1. Simple random

- a single random choice of an object with given probability distribution

## 2. With replacement

- repetition of independent extractions of type 1

## 3. Without replacement

- repetition of extractions, extracted element is removed from the population

## 4. Stratified

- split data into several partitions according to some criteria, then draw the random samples from each partition
- used when the data set is split into subsets with homogeneous characteristics
- the representativity is guaranteed inside each subset



# Sample size

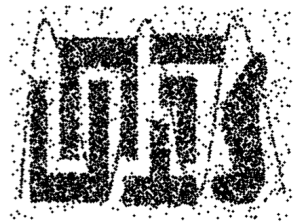
- Statistics provides techniques to assess
  - optimal sample size
  - sample significativity
- Tradeoff between data reduction and precision

# Sampling with/without replacement

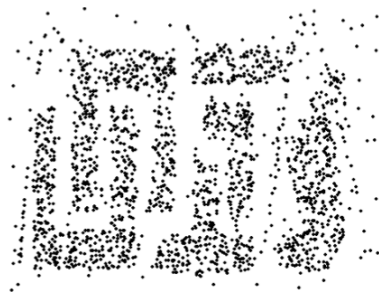
- they are nearly equivalent if sample size is a small fraction of data set size
- with replacement, in a small population a small subset could be underestimated
- sampling with replacement is
  - much easier to implement
  - much easier to be interpreted from a statistical point of view
    - extractions are statistically independent

# Sample size – Example

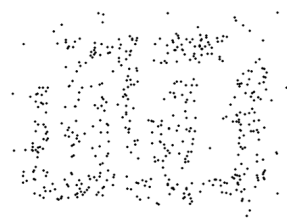
Loss of information



8000 points



2000 points



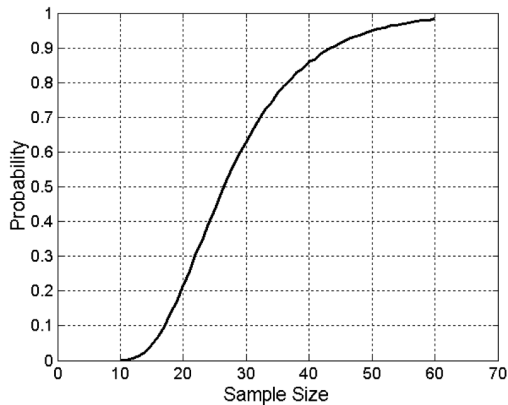
500 points

# Sample size – Missing class I<sup>1</sup>

- Probability of sampling at least one element for each class (with replacement)
  - it is independent from the size of the data set!

A	B	C	D	E
F	G	H	I	J

Ten classes



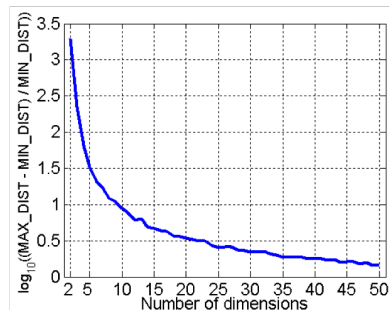
1 It is an instance of the [Coupon Collector's Problem](#)

# Sample size – Missing class - II

- This aspect becomes relevant, for example, in a supervised dataset with a high number of different values of the target
- If the number data elements is not big enough, it can be difficult to guarantee a stratified partitioning in train/test split or in cross-validation split
- Example:
  - $N = 1000$ ,  $C = 10$ , test-set-size = 300, cross-validation-folds = 10
  - the probability of folds without adequate representation of some classes becomes quite high
- When designing the training processes it is necessary to consider those aspects
  - in the example, one could use only 3 folds in cross-validation

# The curse of dimensionality

- When dimensionality is very high the occupation of the space becomes very sparse
- Discrimination on the basis of the distance becomes ineffective
- Experiment:
  - random generation of 500 points
  - plot the relative difference between the maximum and the minimum distance between pairs of points



# Dimensionality reduction

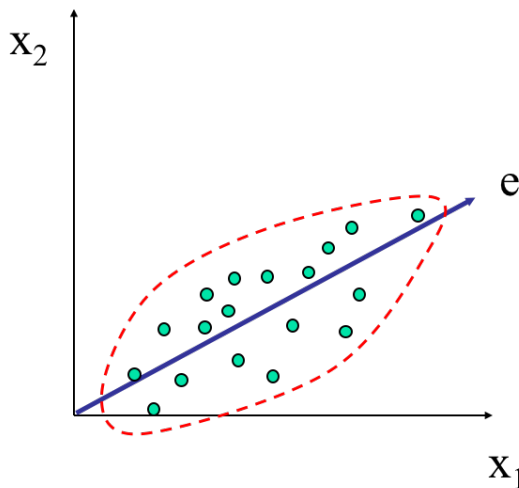
- Purposes:
  - avoid the *curse of dimensionality*
  - noise reduction
  - reduce time and memory complexity of the mining algorithms
  - visualization
- Techniques:
  - principal component analysis
  - singular values decomposition
  - supervised techniques
  - non-linear techniques

# PCA

Find projections that capture most of the data variation

- Find the eigenvector of the covariance matrix
- the eigenvectors define the new space

The new dataset will have *only the attributes* which capture most of the data variation





# Feature subset selection I

A *local* way to reduce dimensionality

- Redundant attributes
  - duplicate most of the information contained in other attributes
    - e.g. price and v.a.t. amount
- Irrelevant attributes
  - do not contain any information useful for analysis
    - e.g. SSN is not relevant to predict wealth

# Feature subset selection II

## 1. Brute force

- try all possible feature subsets as input to data mining algorithm and measure the effectiveness of the algorithm with the reduced dataset

## 2. Embedded approach

- Feature selection occurs naturally as part of the data mining algorithm
  - e.g. decision trees

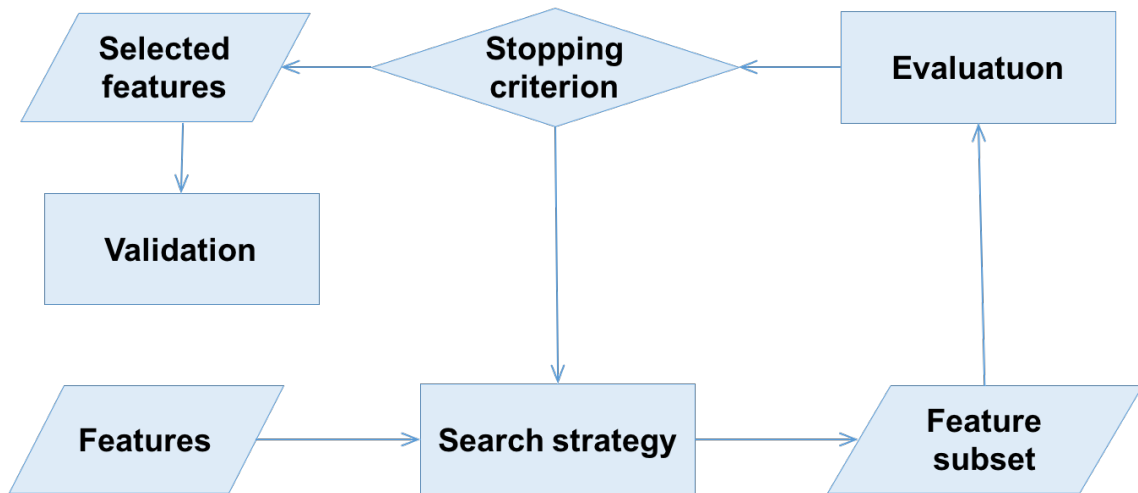
## 3. Filter approach

- Features are selected before data mining algorithm is run

## 4. Wrapper approaches

- A data mining algorithm can choose the best set of attributes
  - try as in 1, but without exhaustive search

# An Architecture for Feature Subset Selection

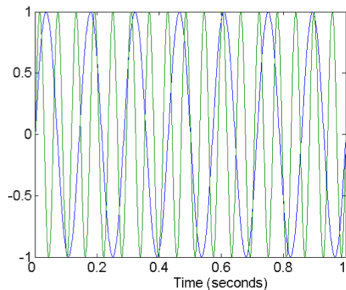


# Feature creation

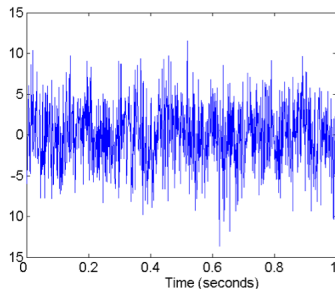
New features can capture more efficiently data characteristics

- Feature extraction
  - pixel picture with a face  $\Rightarrow$  eye distance, . . .
- Mapping to a new space
  - e.g. signal to frequencies with Fourier transform
- New features
  - e.g. volume and weight to density

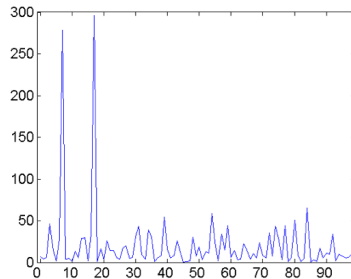
# Space transformation example



Two sinusoids



Two sinusoids with noise



Transformation in the domain of frequencies

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# Why do we need type conversion?

- Many algorithms require numeric features
  - categorical features must be transformed into numeric
  - ordinal features must be transformed into numeric, and the order must be preserved
- Classification requires a target with nominal values
  - a numerical target can be discretised
- Discovery of association rules require boolean features
  - a numerical feature can be discretised and transformed into a series of boolean features

# Binarization of discrete attributes

Attribute  $d$  allowing  $V$  values  $\Rightarrow V$  binary attributes.

<i>Quality</i>	<i>Quality-Awful</i>	<i>Quality-Poor</i>	<i>Quality-OK</i>	<i>Quality-Good</i>	<i>Quality-Great</i>
Awful	1	0	0	0	0
Poor	0	1	0	0	0
Ok	0	0	1	0	0
Good	0	0	0	1	0
Great	0	0	0	0	1



# Nominal to numeric

- One-Hot-Encoding

- a feature with  $V$  unique values is substituted by  $V$  binary features each one corresponding to one of the unique values
- if object  $x$  has value  $v$  in feature  $d$  then the binary feature corresponding to  $v$  has True for  $x$ , all the other binary features have value False
- True and False are represented as 1 and 0, therefore can be processed by also by procedures working only on numeric data, as is the case for the estimators available in scikit-learn

- `sklearn.preprocessing.OneHotEncoder`

[link to manual page](#)

# Ordinal to numeric

- The ordered sequence is transformed into consecutive integers
  - by default the lexicographic order is assumed
  - The user can specify the proper order of the sequence
- `sklearn.preprocessing.OrdinalEncoder`

[link to manual page](#)

# Numeric to binary with threshold

- Not greater than the threshold becomes zero
- Greater than the threshold becomes one
- `sklearn.preprocessing.Binarizer`

[link to manual page](#)

## Discretization/Reduction of the number of distinct values

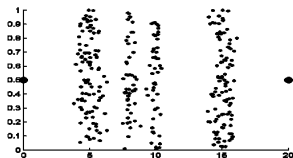
- Some algorithms work better with categorical data
- A small number of distinct values can let patterns emerge more clearly
- A small number of distinct values let the algorithms to be less influenced by noise and random effects

# Discretization

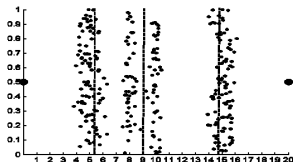
- Continuous  $\Rightarrow$  Discrete
  - thresholds
    - many options
    - binarization  $\Rightarrow$  single threshold
- Discrete with many values  $\Rightarrow$  Discrete with less values
  - guided by domain knowledge

# Continuous $\Rightarrow$ Discrete

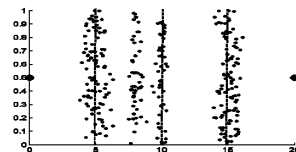
Boundaries on x axis – Unsupervised



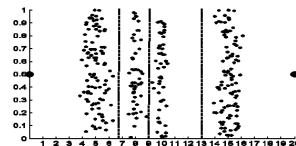
Data



Equal frequency



Equal width



K-means

# Numeric to $k$ values

- The numbers are discretised into a sequence of integers 0 to  $k - 1$
- Several strategies are available
  - {'uniform', 'quantile', 'means'}
- `sklearn.preprocessing.KBinsDiscretizer`

[link to manual page](#)

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# Similarity and dissimilarity

- Similarity

- Numerical measure of how alike two data objects are
- Is higher when objects are more alike
- Often falls in the range  $[0,1]$

- Dissimilarity

- Numerical measure of how different are two data objects
- Lower when objects are more alike
- Minimum dissimilarity is often 0
- Upper limit varies

- Proximity refers to a similarity or dissimilarity

# Similarity and Dissimilarity by Attribute type

$p$  and  $q$  are the values of an attribute for two data objects

Attribute type	Dissimilarity	Similarity
Nominal	$d = \begin{cases} 0 & \text{if } p = q \\ 1 & \text{if } p \neq q \end{cases}$	$s = \begin{cases} 1 & \text{if } p = q \\ 0 & \text{if } p \neq q \end{cases}$
Ordinal Values mapped to integers 0 to $V-1$	$d = \frac{ p-q }{V-1}$	$s = 1 - \frac{ p-q }{V-1}$
Interval or Ratio	$d =  p - q $	$s = \frac{1}{1+d} \quad \text{or} \quad s = 1 - \frac{d - \min(d)}{\max(d) - \min(d)}$

# Euclidean distance – $L_2$

$$\text{dist} = \sqrt{\sum_{d=1}^D (p_d - q_d)^2}$$

- Where  $D$  is the number of dimensions (attributes) and  $p_d$  and  $q_d$  are, respectively, the  $d$ -th attributes (components) of data objects  $p$  and  $q$
- Standardization/Rescaling is necessary if scales differ

# Minkowski distance – $L_r$

$$\text{dist} = \left( \sum_{d=1}^D |p_d - q_d|^r \right)^{\frac{1}{r}}$$

- Where  $D$  is the number of dimensions (attributes) and  $p_d$  and  $q_d$  are, respectively, the  $d$ -th attributes (components) of data objects  $p$  and  $q$
- Standardization/Rescaling is necessary if scales differ
- $r$  is a *parameter* which is chosen depending on the data set and the application

# Minkowski distance – Cases

$r = 1$  also named *city block*, *Manhattan*,  $L_1$  norm

- it is the best way to discriminate between zero distance and *near zero* distance
- a  $\epsilon$  change on any coordinate causes a  $\epsilon$  change in the distance
- works better than euclidean in very high dimensional spaces

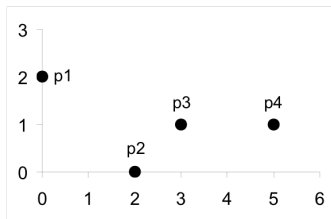
$r = 2$  euclidean,  $L_2$  norm

$r = \infty$  also named Chebyshev, *supremum*,  $L_{max}$  norm,  $L_\infty$  norm

- considers only the dimension where the difference is maximum
- provides a simplified evaluation, disregarding the dimensions with lower differences

$$\text{dist}_\infty = \lim_{r \rightarrow \infty} \left( \sum_{d=1}^D |p_d - q_d|^r \right)^{\frac{1}{r}} = \max_d |p_d - q_d|$$

# Minkowski distances – Example



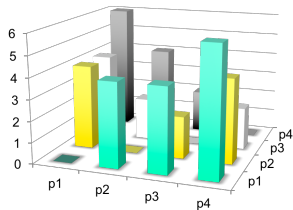
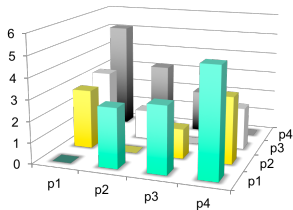
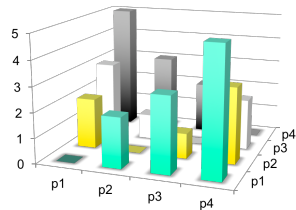
<i>point</i>	<i>x</i>	<i>y</i>
p1	0	2
p2	2	0
p3	3	1
p4	5	1

$L_1$	p1	p2	p3	p4
p1	0	4	4	6
p2	4	0	2	4
p3	4	2	0	2
p4	6	4	2	0

$L_2$	p1	p2	p3	p4
p1	0	2.828	3.162	5.099
p2	2.828	0	1.414	3.162
p3	3.162	1.414	0	2
p4	5.099	3.162	2	0

$L_\infty$	p1	p2	p3	p4
p1	0	2	3	5
p2	2	0	1	3
p3	3	1	0	2
p4	5	3	2	0

# Comparison


 $L_1$ 

 $L_2$ 

 $L_\infty$

# Mahalanobis Distance

OPTIONAL

- Considers **data distribution**
- The Mahalanobis distance between two points  $p$  and  $q$  decreases if, keeping the same euclidean distance, the segment connecting the points is stretched along a direction of greater variation of data
- The distribution is described by the **covariance matrix** of the data set

$$\Sigma_{ij} = \frac{1}{N-1} \sum_{k=1}^N (x_{ki} - \bar{x}_i)(x_{kj} - \bar{x}_j)$$

$$\text{dist}_m = \sqrt{(p - q)\Sigma^{-1}(p - q)^T}$$



# Mahalanobis Distance – Example

OPTIONAL

$$\Sigma = \begin{bmatrix} 0.3 & 0.2 \\ 0.2 & 0.3 \end{bmatrix}$$

$$A = (0.5, 0.5)$$

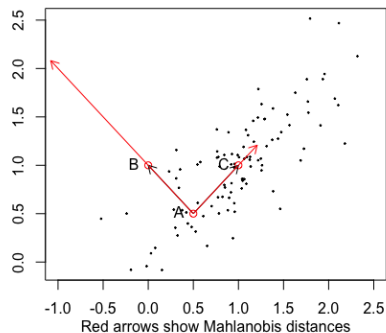
$$B = (0, 1)$$

$$C = (1, 1)$$

The euclidean distances AB and AC are the same

$$\text{dist}_m(A, B) = 2.236068$$

$$\text{dist}_m(A, C) = 1$$



# Covariance matrix

OPTIONAL

- Variation of pairs of random variables
- The summation is over all the observations
- The main diagonal contains the variances
- The values are positive if the two variables grow together
- If the matrix is diagonal the variables are non-correlated
- If the variables are standardised the diagonal contains “one”
- If the variables are standardised and non correlated, the matrix is the identity and the Mahalanobis distance is the same as the euclidean

# Common properties of a distance

1. **Positive definiteness:**  $\text{Dist}(p, q) \geq 0 \forall p, q$   
and  $\text{Dist}(p, q) = 0$  if and only if  $p = q$
2. **Symmetry:**  $\text{Dist}(p, q) = \text{Dist}(q, p)$
3. **Triangle inequality:**  $\text{Dist}(p, q) \leq \text{Dist}(p, r) + \text{Dist}(r, q) \forall p, q, r$

A distance function satisfying all the properties above is called a **metric**

# Common properties of a Similarity

1.  $\text{Sim}(p, q) = 1$  only if  $p = q$
2.  $\text{Sim}(p, q) = \text{Sim}(q, p)$

# Similarity between binary vectors

- Consider the counts below

$M_{00}$  the number of attributes where  $p$  is 0 and  $q$  is 0

$M_{01}$  the number of attributes where  $p$  is 0 and  $q$  is 1

$M_{10}$  the number of attributes where  $p$  is 1 and  $q$  is 0

$M_{11}$  the number of attributes where  $p$  is 1 and  $q$  is 1

- Simple Matching Coefficient

$$\text{SMC} = \frac{\text{number of matches}}{\text{number of attributes}} = \frac{M_{00} + M_{11}}{M_{00} + M_{01} + M_{10} + M_{11}}$$

- Jaccard Coefficient

$$\text{JC} = \frac{\text{number of 11 matches}}{\text{number of non-both-zero attributes}} = \frac{M_{11}}{M_{01} + M_{10} + M_{11}}$$

# Cosine similarity

- It is the cosine of the angle between two vectors

$$\cos(p, q) = \frac{p \cdot q}{\|p\| \|q\|}$$

- Example

$$p = 3 \ 2 \ 0 \ 5 \ 0 \ 0 \ 0 \ 2 \ 0 \ 0$$

$$q = 1 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 1 \ 0 \ 2$$

$$p \cdot q = 3 * 1 + 2 * 0 + 0 * 0 + 5 * 0 + 0 * 0 + 0 * 0 + 0 * 0 + 2 * 1 + 0 * 0 + 0 * 2 = 5$$

$$\|p\| = \sqrt{3 * 3 + 2 * 2 + 0 * 0 + 5 * 5 + 0 * 0 + 0 * 0 + 0 * 0 + 2 * 2 + 0 * 0 + 0 * 0} = 6.481$$

$$\|q\| = \sqrt{1 * 1 + 0 * 0 + 0 * 0 + 0 * 0 + 0 * 0 + 0 * 0 + 0 * 0 + 1 * 1 + 0 * 0 + 2 * 2} = 2.245$$

$$\cos(p, q) = .3150$$

# Extended Jaccard Coefficient (Tanimoto)

OPTIONAL

- Variation of Jaccard for continuous or count attributes
  - reduces to Jaccard for binary attributes

$$T(p, q) = \frac{p \cdot q}{\|p\|^2 + \|q\|^2 - p \cdot q}$$

# Choose the right proximity measure

It depends on data

- Dense, continuous
  - a **metric** measure, such as the euclidean distance
- Sparse, asymmetric data
  - cosine, jaccard, extended jaccard



# Correlation of quantitative data (Pearson's) OPTIONAL

Measure of the linear relationship between a pair of attributes

- Standardize the values
- For two given attributes  $p$  and  $q$ , consider as vectors the ordered lists of the values over all the data records
- Compute the dot product of the vectors

$$\mathbf{p} = [p_1, \dots, p_N] \xrightarrow{\text{standardize}} \mathbf{p}'$$

$$\mathbf{q} = [q_1, \dots, q_N] \xrightarrow{\text{standardize}} \mathbf{q}'$$

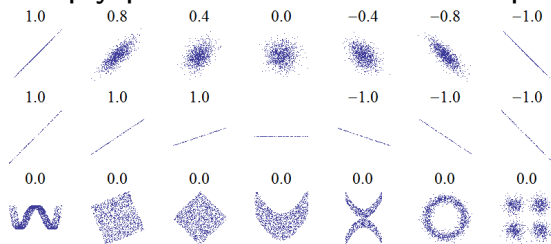
$$\text{corr}(p, q) = \mathbf{p}' \bullet \mathbf{q}'$$

There is an alternative definition based on covariance and variances

# Correlation – Discussion

OPTIONAL

- Independent variables  $\Rightarrow$  correlation is zero
  - the inverse is not valid *in general*
- Correlation zero  $\Rightarrow$  absence of *linear relationship* between the variables
- Positive values imply positive linear relationship



From “Correlation and Dependence” on Wikipedia

# Correlation between nominal attributes

OPTIONAL

Symmetric Uncertainty [Witten et al.(2011)Witten, Frank, and Hall]

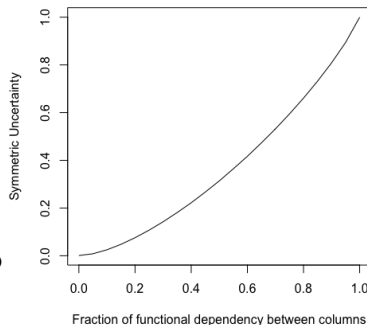
$$U(p, q) = 2 \frac{H(p) + H(q) - H(p, q)}{H(p) + H(q)}$$

- where  $H()$  is the entropy of a single attribute while  $H(, )$  is the joint entropy, computed from the joint probabilities
- is always between 0 and 1

## Correlation between nominal attributes – Experiment

OPTIONAL

- Behavior of SU for two independent uniformly distributed discrete attributes, say  $p$  and  $q$ 
  - in a variable fraction of records the value of  $p$  is copied to  $q$
- from complete independence (left) to complete biunivocal correspondence (right)
- when there is independence, the joint entropy is the sum of the individual entropies, and SU is zero
- when there is complete correspondence, the individual entropies and the joint entropy are equal and SU is one



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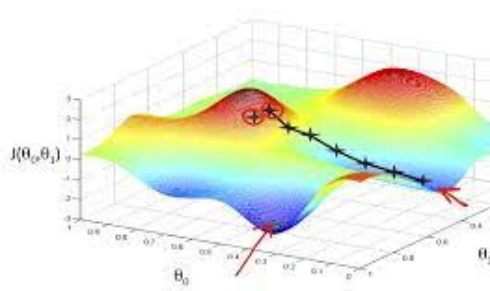
# *Why Data Transformation*

- the features may have different scales
  - this can alterate the results of many learning techniques
  - some machine learning algorithms are sensitive to feature scaling while others are virtually invariant to it
- there can be outliers

# Gradient descent

Machine learning algorithms that use *gradient descent* as an optimization technique require data to be scaled

- e.g. linear regression, logistic regression, neural network, etc.
- The presence of feature value  $X$  in the formula will affect the step size of the gradient descent
- The difference in ranges of features will cause different step sizes for each feature.
- Similar ranges of the various features ensure that the gradient descent moves smoothly towards the minima and that the steps for gradient descent are updated at the same rate for all the features



# Attribute transformation

- Map the entire set of values to a new set according to a function
  - $x^k, \log(x), e^x, |x|$
  - in general they change the *distribution of values*
- Standardization:  $x \rightarrow \frac{x-\mu}{\sigma}$ 
  - if the original values have a *gaussian* distribution, the transformed values will have a *standard* gaussian distribution ( $\mu = 0, \sigma = 1$ )
  - translation and shrinking/stretching, no change in distribution
- MinMax scaling (a.k.a. Rescaling): the domains are mapped to standard ranges

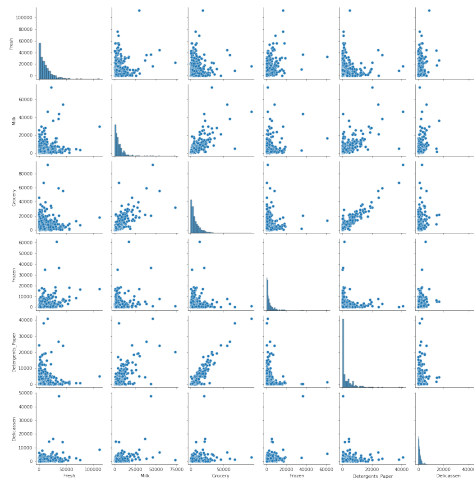
$$x \rightarrow \frac{x - x_{min}}{x_{max} - x_{min}} \quad (0 \text{ to } 1) \qquad x \rightarrow \frac{x - \frac{x_{max} + x_{min}}{2}}{\frac{x_{max} - x_{min}}{2}} \quad (-1 \text{ to } 1)$$

- translation and shrinking/stretching, no change in distribution



# Attribute transformation – Example I

Data with skewed distribution

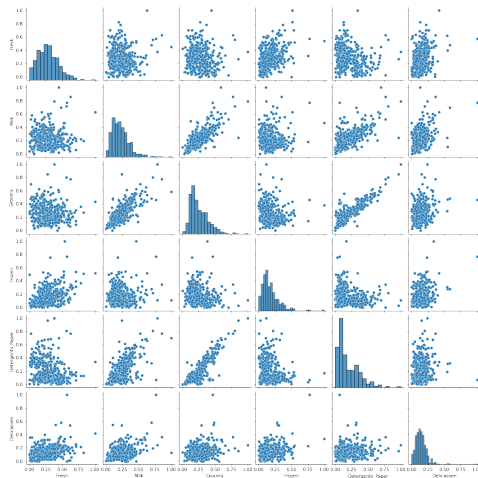


# Attribute transformation – Example II

Python code

```
from sklearn.preprocessing
    import PowerTransformer
pt = PowerTransformer(method='box-cox')
X = pd.DataFrame(pt.fit_transform(X0)
                 , columns = X0.columns)
```

After the transformation the data are  
*less skewed*



# Distance-based algorithms

- KNN, K-Means, SVM, ...
- distances between points are used to determine their similarity

## Example

Original data		
Student	CGPA	Salary
A	3	60
B	3	40
C	4	40
D	4.5	50
E	4.2	52

Scaled data		
Student	CGPA	Salary
A	-1.18431	1.520013
B	-1.18431	-1.100699
C	0.41612	-1.100699
D	1.21635	0.209657
E	0.736212	0.471728

# Distances before and after scaling

$$\text{distance}(A, B) = \sqrt{(40 - 60)^2 + (3 - 3)^2} = 20$$

$$\text{distance}(B, C) = \sqrt{(40 - 40)^2 + (4 - 3)^2} = 1$$

$$\text{distance}(A_s, B_s) = \sqrt{(1.1 + 1.5)^2 + (1.18 - 1.18)^2} = 2.6$$

$$\text{distance}(B_s, C_s) = \sqrt{(1.1 - 1.1)^2 + (0.41 + 1.18)^2} = 1.59$$

Before the scaling the two distances seemed to be very different, due to the a big numeric difference in the Salary attribute, now they are comparable

# Range-based scaling and standardization

operate on single features

- **Range-based scaling** stretches/shrinks and translates the range, according to the **range** of the feature (there are some variants)
  - good when we know that the data are not gaussian, or we do not make any assumption on the distribution
  - the base variant, the MinMax scaler, remaps to 0, 1
- **Standardization** subtracts the mean and divides by the standard deviation
  - the resulting distribution has mean *zero* and *unitary* standard deviation
  - good when the distribution is gaussian
  - StandardScaler

# Range-based scalers in Scikit-Learn

**affine transformations:** linear transformation plus translation

- `MinMaxScaler` – remaps the feature to  $[0, 1]$
- `RobustScaler` – centering and scaling statistics is based on percentiles
  - not influenced by a few number of very large marginal outliers
  - the resulting range of the transformed feature values is larger than the one given by `MinMaxScaler` and `StandardScaler`

# Normalization

- **Normalization** is mentioned sometimes with different meanings
  - frequently it refers to MinMaxScaler
- in Scikit-learn the Normalizer normalizes each data row to **unit norm**

# Workflow

1. transform the features as required both for the train and test data
2. fit and optimize the model(s)
3. test
4. possibly, use the original data to plot relevant views (e.g. to plot cluster assignments)



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# Imbalanced data in classification

- The performance minority class (classes) has little impact on standard performance measures
- The optimised model could be less effective on minority class (classes)
- Some estimators allow to **weight** classes
- Some performance measures allow to take into account the contribution of minority class (classes)

# Cost Sensitive learning

Already introduced in *Machine-Learning-03-classification*

- several classifiers have the parameter `class_weight`
- it changes the **cost function** to take into account the imbalancing of classes
- in practice it is equivalent to **oversampling** the minority class, (repeating random examples) in order to produce a **balanced training set**

# Undersampling

- Obtains a balanced training set by randomly reducing the number of examples of the majority class
- Obviously part of the knowledge embedded in the training set is dropped out

# Oversampling with SMOTE

Synthetic Minority Oversampling Technique – a type of data augmentation

let the minority class be  $c_{min}$ , synthesise new examples of class  $c_{min}$

- choose from the *training set* random example  $x_r$  of class  $c_{min}$
- find in the training set the  $k$  nearest neighbours of  $x_r$  whose class is  $c_{min}$
- choose randomly one of the neighbours, say  $x_{rn}$  found above and *create* a new data element chosen randomly from the segment connecting  $x_r$   $x_{rn}$  in the feature space  $m = r * (x_r + x_{rn})/2$

Theory developed in [SMOTE: Synthetic Minority Over-sampling Technique](#)[Bowyer et al.(2011)Bowyer, Chawla, Hall, and Kegelmeyer]

# Workflow for *undersampling/oversampling*

- resample the training set
- fit and optimise the estimator
- test the fitted estimator on the test set (untouched)

# Bibliography I

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