





"6 Supervised Learning"

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From previous lecture

- Evaluating clustering results
 - Dunn index
 - Rand index
 - Silhouette coefficient
 - Mutual information
- Clustering techniques
 - K-Means
 - Expectation Maximization
 - DBSCAN
 - Agglomerative Hierarchical Clustering
- Clustering for high-dimensional datasets
 - Dimensionality reduction
 - Superspace clustering



Agenda

- KNN
- K-D Tree
- Bayes Theorem
- Naive Bayes



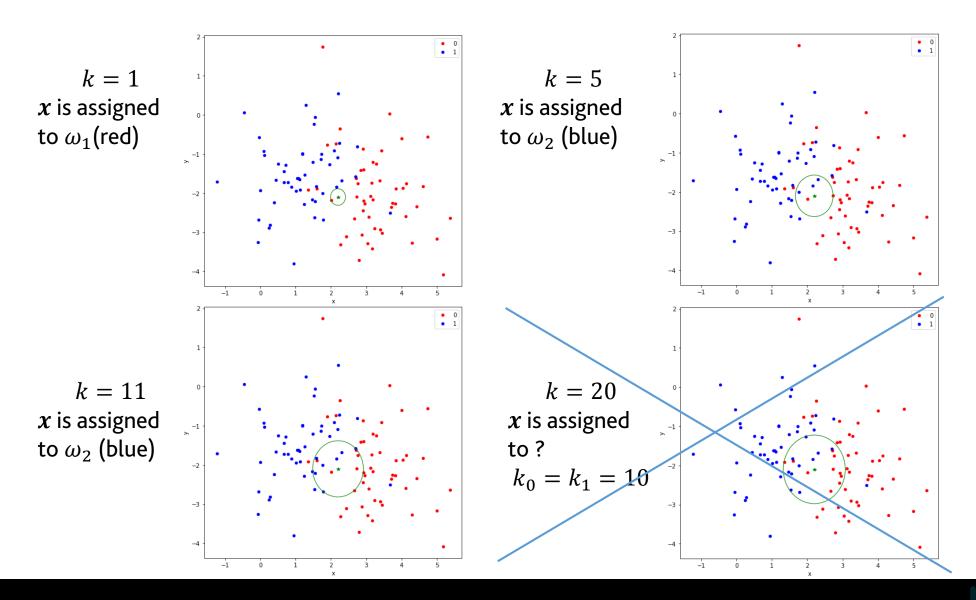


- Given:
 - A classification problem with two classes ω_1 and ω_2 ,
 - The training feature vectors x_i , $i=1,\ldots,N_1$ labelled as ω_1 and the training feature vectors x_j , $j=1,\ldots,N_2$ labelled as ω_2 , Note that $N=N_1+N_2$,
 - An unknown feature vector x,
 - A distance measure.
- To which class ω_1 or ω_2 , does x belong?



- To which class ω_1 or ω_2 , does x belong?
 - Out of x_i , i = 1, ..., N, k nearest neighbours (instances represented by their feature vectors) are identified.
 - Regardless of the class label.
 - Regardless of the number of classes $|\Omega|$.
 - k should be odd (when $|\Omega| = 2$).
 - Preferably, $k\%|\Omega| \neq 0$
 - Out of the k instances, k_u that belongs to ω_u , u=1,2, are identified.
 - Clearly, $\sum_{u} k_{u} = k$.
 - x is assigned to $\omega_{\widehat{u}}$, where $\widehat{u} = \underset{u}{\operatorname{argmax}} k_u$

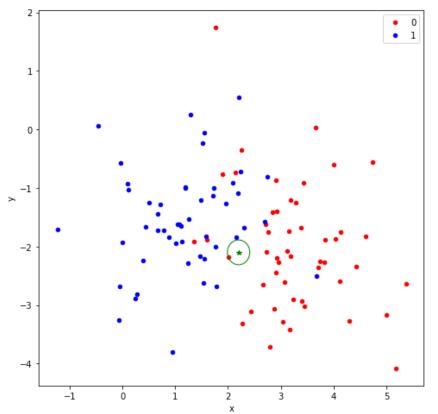






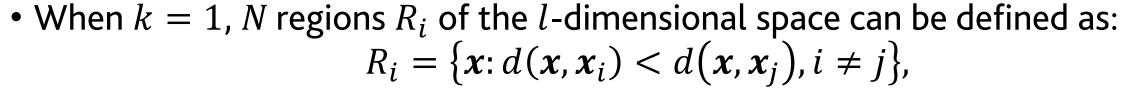
• The simplest version of kNN is for k=1. It is known as the *nearest neighbour* rule.

- In general, a small k means:
 - High sensitivity.
 - Little generalization.

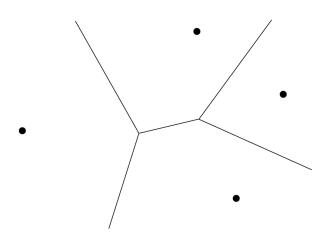




1-nearest neighbour: Voronoi tessellation



- Where d(.) is a distance metric.
- This partition is known as Voronoi tessellation.





- Make k larger.
 - Low sensitivity.
 - Higher generalization.
- But
 - High complexity in search of the nearest neighbours among the N available training samples = O(lN + kN).
 - The problem is severe in high-dimensional feature spaces.
 - The closer k to N, the more k-NN is approaching the prior classifier. We will see it later!



- In case of continuous prediction, k-NN can be identically used to predict a value \hat{y} for an unknown feature vector x.
- Given:
 - The training feature vectors x_i , i = 1, ..., N associated with real-valued targets y_i ,
 - An unknown feature vector x,
 - A distance measure.

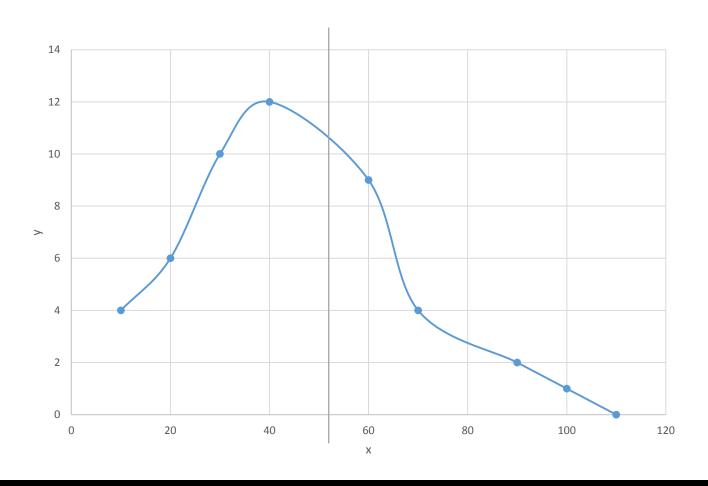


- What is the predicted value \hat{y} for x?
 - Out of x_i , i=1,...,N, k nearest neighbours (samples represented by their feature vectors) are identified.
 - Regardless of y_i .
 - \hat{y} is computed as the mean of y_u , $u=1,\ldots,k$:

$$\hat{y} = \frac{1}{k} \sum_{u=1}^{k} y_u$$

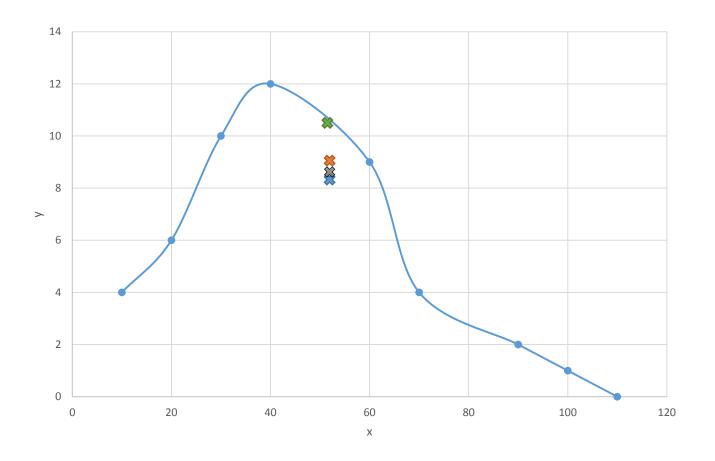


• Let's predict \hat{y} for x = 52





•
$$k = 1$$
, $k = 2$, $k = 3$, $k = 4$



Advantages

- It can achieve good results when the data set (N) is large.
- Easy to implement.

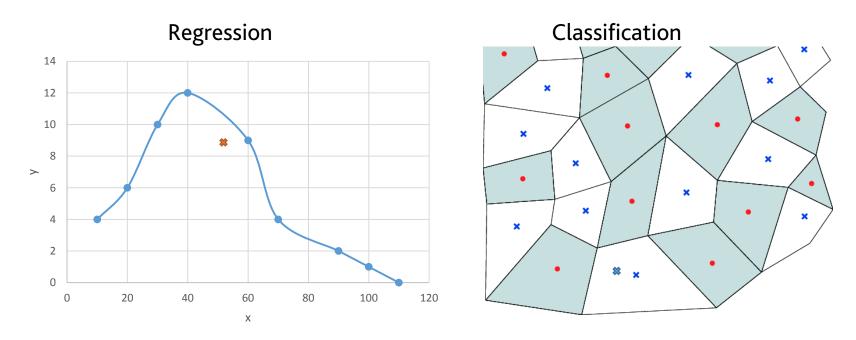
Disadvantages

- Its performance may degrade dramatically when the value of N is relatively small.
- High computational cost when the data is very large.
- Best *k* has to be found.
- data-adaptive distance metric that leads to an optimal performance has to be found (when the data set is small).

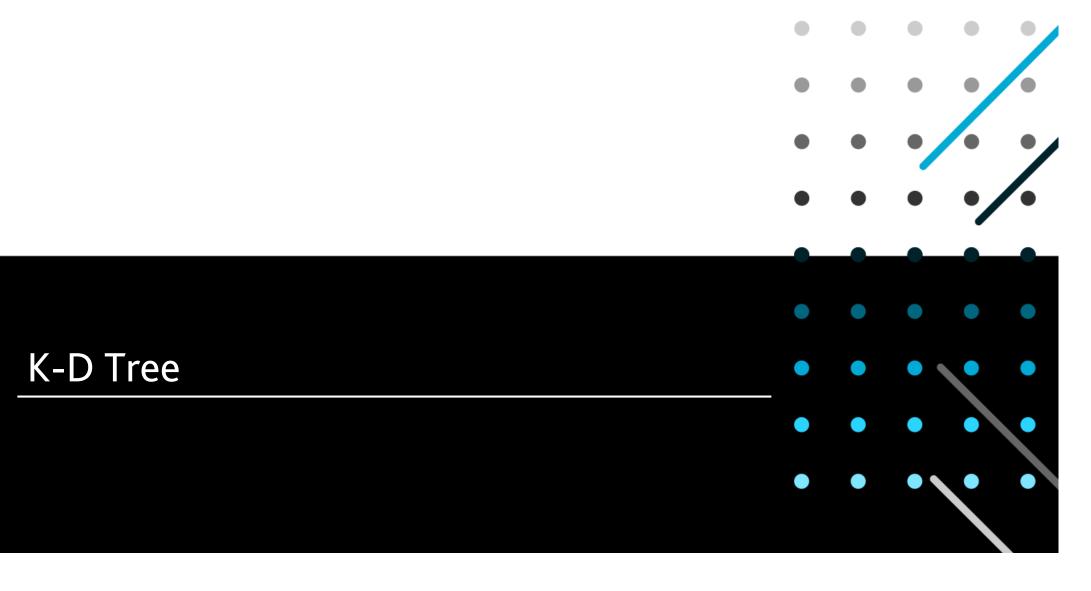


Overfitting

- When k is very small but > 1, the training samples are well modelled.
 - The error on the training set tends to be close to zero.
- When k=1, the training samples are perfectly modelled.
 - The error on the training set = 0.







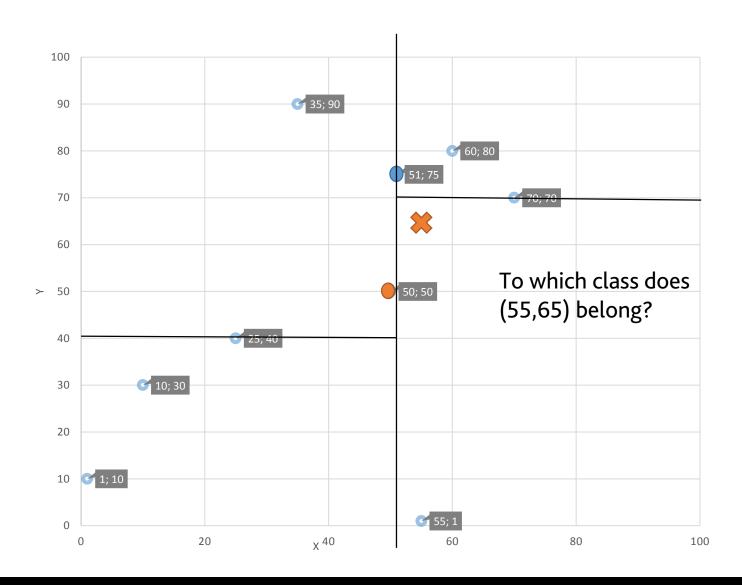


K-D Tree

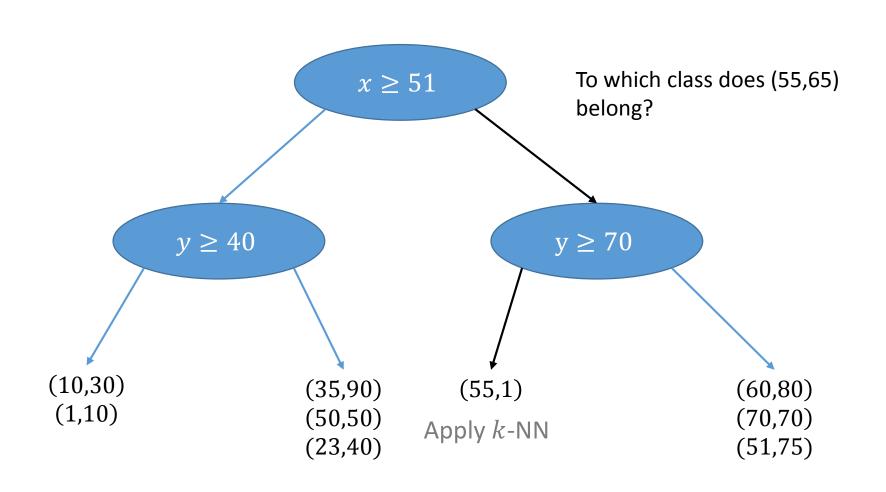
- When N is very large, it is not practical to compute the distance between the unseen sample and all training samples.
- K-D Tree is an improvement over KNN that builds a data structure such as the whole data is organized as a tree.
 - Repeat until reaching the threshold:
 - Picking a random dimension (attribute) from the *K* dimensions.
 - Finding the median.
 - Splitting the data "evenly" w.r.t median value.
 - The threshold is the predetermined number of instances in each branch.



K-D Tree









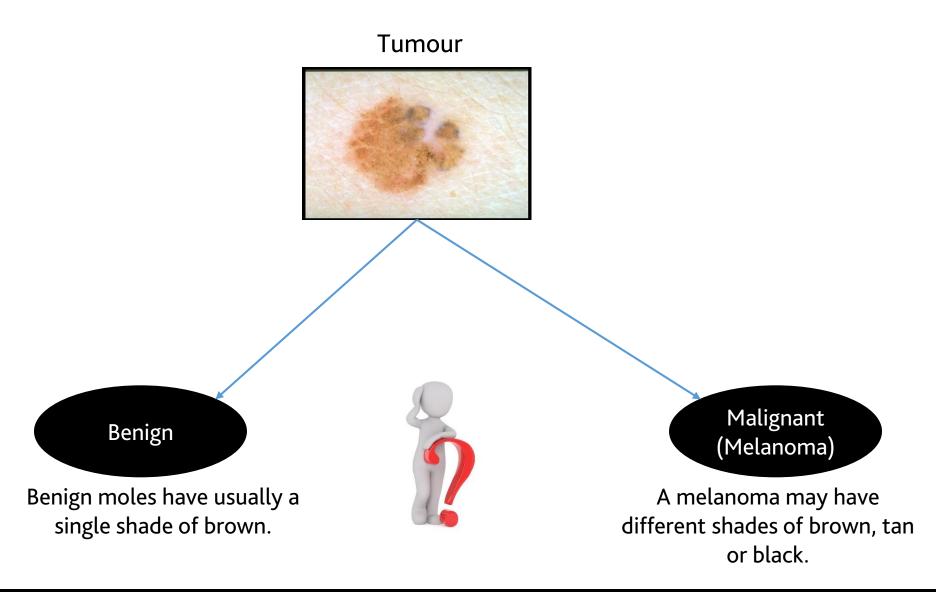
Recall



•
$$P(A|B) = \frac{P(A,B)}{P(B)}$$
.

- The conditional probability of B given A:
 - $P(B|A) = \frac{P(A,B)}{P(A)}$.
- Remember that:
 - $P(A|B) \neq P(B|A)$.
 - P(A) and P(B) are marginal probabilities.
- The joint probability of *A* and *B*:
 - $\bullet \ P(A,B) = P(A|B) * P(B).$
 - P(A,B) = P(B|A) * P(A).







- From previous experiences;
 - Out of 120 benign cases,
 - 60 have a single shade of brown.
 - 60 have different shades of different dark colours.
 - Out of 40 malignant cases,
 - 3 have a single shade of brown.
 - 37 have different shades of different colours.
- More benign cases with different shades than malignant cases.

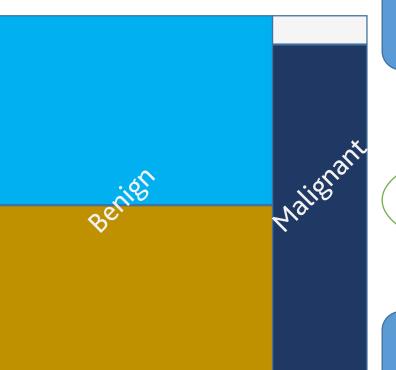


60 benign cases with a single shade (37,5%)

120 Benign cases (75%)

60 benign cases with different shades (37,5%)

63 cases with a single shade (39,375%)



97 cases with different shades (60,625%)

3 malignant cases with a single shade (1,875%)

40 Malignant cases (25%)

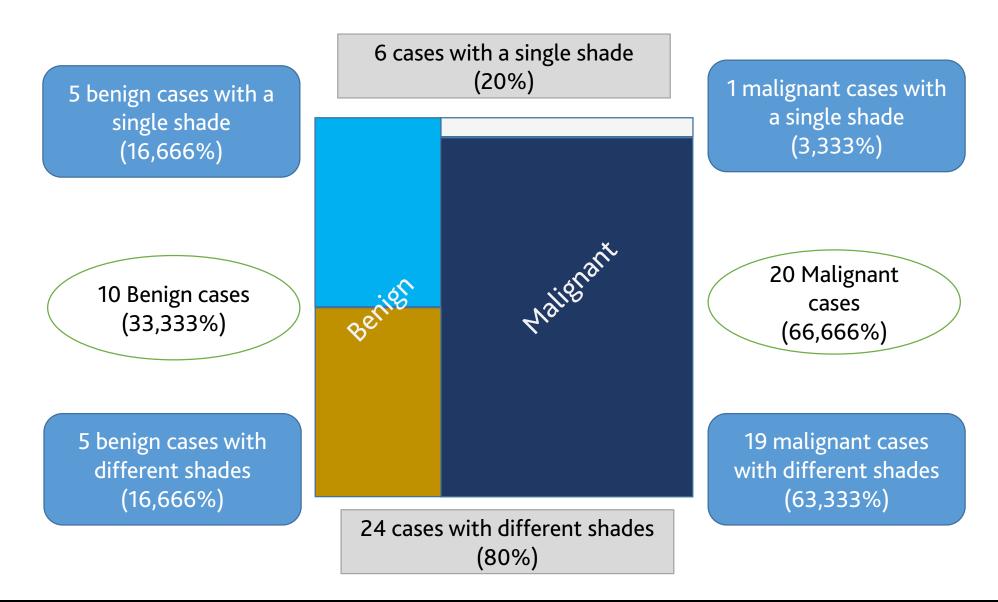
37 malignant cases with different shades (23,125%)



After obtaining the health history of the patient, it has been noticed that he/she got another malignant tumour in the past five years.

- From previous experiences with a second malignant tumour,
 - Out of 10 benign cases,
 - 5 have a single shade of brown.
 - 5 have different shades of different colours.
 - Out of 20 malignant cases,
 - 1 has a single shade of brown.
 - 19 have different shades of different colours.
- More malignant cases with different shades than benign cases.







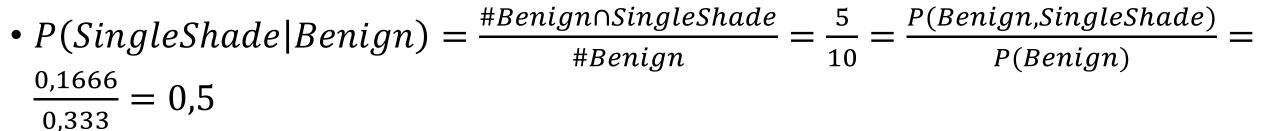
Joint probabilities

	Benign	Malignant	Total
Single Shade	0,1666	0,0333	0,2
Different Shades	0,1666	0,6333	0,8
Total	0,3333	0,6666	

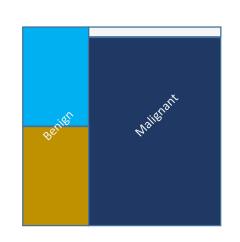
Marginal probabilities



- P(Benign) = 0.333
- P(Malignant) = 0,666
- P(SingleShade) = 0.2
- P(DifferentShades) = 0.8
- P(Benign, SingleShade) = 0,1666



•
$$P(Benign|SingleShade) = \frac{\#Benign\cap SingleShade}{\#SingleShade} = \frac{5}{6} = \frac{P(Benign,SingleShade)}{P(SingleShade)} = \frac{0,1666}{0,2} = \frac{P(Benign)*P(SingleShade|Benign)}{P(SingleShade)} = \frac{0,333*0,5}{0,2} = 0,8333$$





$$P(A|B) = \frac{P(B|A) * P(A)}{P(B)}$$



- Given:
 - A classification task of k classes; $\omega_1, ..., \omega_k$
 - An unknown instance represented by a feature vector x
- k conditional probabilities $p(\omega_j|\mathbf{x})$, $j=1,\ldots,k$ are formed.
- They are also referred to as a posteriori probabilities.



- Let's consider the two classes ω_1 and ω_2 , to which all the training instances belong.
- The a priori probabilities $p(\omega_1)$ and $p(\omega_2)$ are assumed to be known.
 - They can be estimated as:
 - $p(\omega_u) \approx \frac{N_u}{N}$, u = 1,2.
- The class-conditional probability density functions $p(x|\omega_u)$, u=1,2, are assumed to be known.
 - They are also referred to as the likelihood function of ω_u w.r.t x.



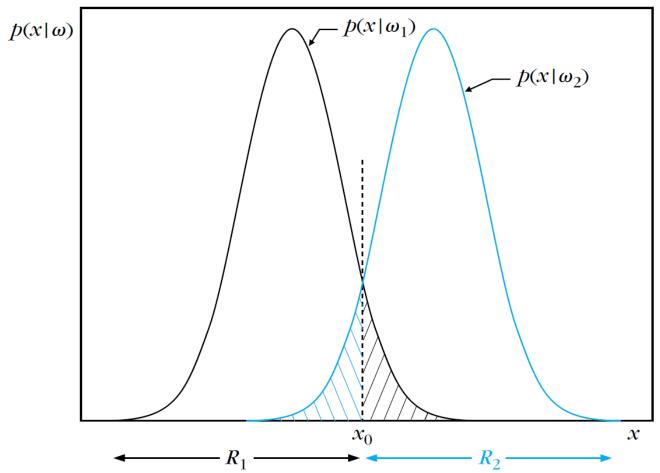
Following the Bayes theorem:

$$P(\omega_u|\mathbf{x}) = \frac{p(\mathbf{x}|\omega_u) * P(\omega_u)}{p(\mathbf{x})}$$

Where $p(\mathbf{x}) = \sum_{u=1}^{k} p(\mathbf{x}|\omega_u) P(\omega_u)$.

- The Bayes classification rule can now be stated as:
 - If $P(\omega_1|x) > P(\omega_2|x)$, x is classified to ω_1 .
 - If $P(\omega_2|x) > P(\omega_1|x)$, x is classified to ω_2 .
- Important to note:
 - Since p(x) is equal for all classes, it is not taken into consideration.
 - If the a priori probabilities $p(\omega_1)$ and $p(\omega_2)$ are equal, $P(\omega_u|\mathbf{x}) \propto p(\mathbf{x}|\omega_u)$





Source: Theodoridis, S., & Koutroumbas, K. "Pattern recognition." Fourth Edition, 9781597492720, 2008



Maximum Likelihood Estimation (MLE)

- What is the best $p(x|\omega_u; \theta)$ that explains well the data distribution in ω_u ?
 - We assume that N_u samples that belong to ω_i are drawn from a PDF, what are the parameters θ of this PDF?
 - We know $X = \{x_1, ..., x_{N_n}\}.$
- Let the PDF from which the N_u sample are drawn be: $p(x; \theta)$.
- Assuming that the samples are *statistically independent*, the joint pdf can be written as:

$$p(X;\boldsymbol{\theta}) = \prod_{i=1}^{N} p(\boldsymbol{x}_i;\boldsymbol{\theta}).$$



Maximum Likelihood Estimation (MLE)

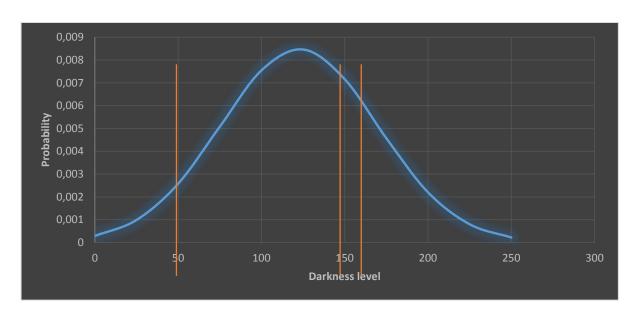
• The maximum likelihood estimation (MLE) estimates θ so that the likelihood function $p(X; \theta)$ is maximized, that is:

$$\widehat{\boldsymbol{\theta}} = \arg \max_{\boldsymbol{\theta}} \prod_{i=1}^{N} p(\boldsymbol{x}_i; \boldsymbol{\theta}).$$

Maximum Likelihood Estimation (MLE)

- Let's consider the darkness level of the mole as a feature for the melanoma classification problem.
 - The scale is from 0 (black) to 255 (white).
- Considering three samples: $x_1 = 151$, $x_2 = 165$ and $x_3 = 52$ belonging to the benign class.

$$\mu = 122,666$$
 $\sigma = 47,1111$





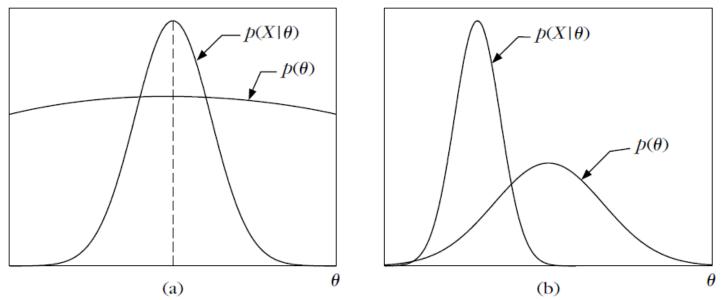
Maximum a Posteriori Probability Estimation (MAP)

- MLE is very sensitive to random variations and thus overfits the data.
- MAP regularizes this process by considering $oldsymbol{ heta}$ as a random vector.
- Given N_u samples represented by $X = \{x_1, ..., x_{N_u}\}$:

$$p(\boldsymbol{\theta}|X) = \frac{p(\boldsymbol{\theta}) * p(X|\boldsymbol{\theta})}{p(X)}$$



- MLE and MAP will be approximately similar is (a) as the prior $p(\theta)$ does not significantly affect the likelihood distribution $p(X|\theta)$
- In contrast, MLE and MAP will be different in (b).



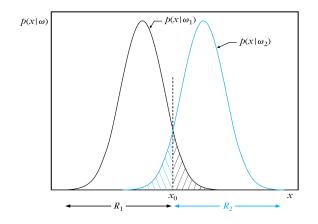
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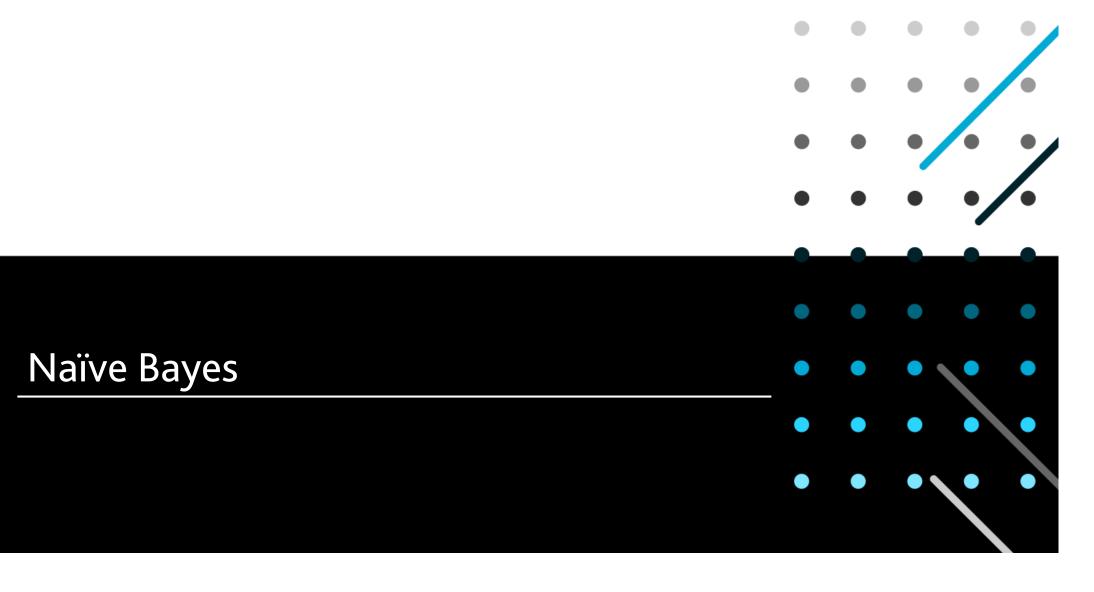
Classification error probability

- From the figure, there is a possibility that a sample lying in R_2 but belongs to ω_1 and vice-versa.
 - The decision errors are unavoidable.
- The maximum total probability of committing an error is:

$$P_e = P(\omega_2) \int_{-\infty}^{x_0} p(\mathbf{x}|\omega_2) d\mathbf{x} + P(\omega_1) \int_{x_0}^{+\infty} p(\mathbf{x}|\omega_1) d\mathbf{x}$$









Naïve bayes

- For good estimates of the PDFs, the number of training samples N must be large enough.
- If N could be regarded as a sufficient number of samples to obtain satisfactory estimates of a pdf in a one-dimensional (l=1) space,
 - N^l would be required for an l-dimensional space.
- ✓ It is assumed that individual features x_j , j = 1, ..., l are statistically independent.



Naïve Bayes

• Under this assumption,
$$p(\pmb{x}|\omega_u)$$
 becomes:
$$p(\pmb{x}|\omega_u) = \prod_{j=1}^l p(x_j|\omega_u), \qquad u=1,\dots k$$

- Remember that $p(x_j|\omega_u) = \frac{p(x,\omega_u)}{p(\omega_u)}$
- Now l * N samples (instead of N^l) would be enough in order to obtain good estimates.
- Naïve Bayes classifier assigns a sample represented by the feature vector x = $[x_1, x_2, ..., x_l]^T \in \mathbb{R}^l$ to the class:

$$\gamma(\mathbf{x}) = \underset{\omega_u}{\operatorname{arg\,max}} P(\omega_u) * \prod_{j=1}^l p(x_j | \omega_u), \qquad i = 1, ..., k$$



Naïve Bayes

- Assuming the attributes are categorical, what if, for example, $p(x_2|\omega_u)=0$, $u=1,\ldots,k$?
 - $P(\omega_u) * \prod_{j=1}^l p(x_j | \omega_u) = 0$
- Remember that for categorical features:
 - $p(x_j|\omega_u) = \frac{p(x,\omega_u)}{p(\omega_u)} = \frac{|x_j \cap \omega_u|}{|\omega_u|}$, where $|\omega_u|$ is the cardinality of the set of training samples belonging to ω_i .
- Use Laplace smoothing:
 - $p(x_j|\omega_u) = \frac{|x_j \cap \omega_u|+1}{|\omega_u|+|l_j|}$, where $|l_j|$ is the number of values the jth attribute can take.
- Or Generalized additive smoothing (Lidstone):
 - $p(x_j|\omega_u) = \frac{|x_j \cap \omega_u| + \lambda}{|\omega_u| + |l_j| * \lambda}$, where λ is a hyperparameter.

Smoothing is applied only on categorical attributes

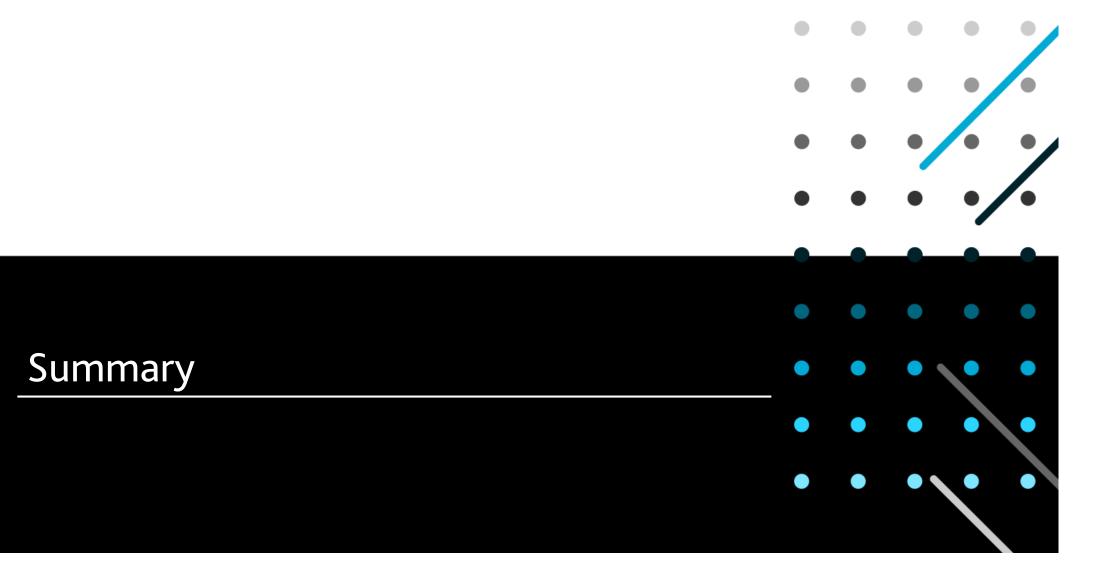


Naïve Bayes

$$p(\omega_u|\mathbf{x}) \propto P(\omega_u) * \prod_{j=1}^l p(x_j|\omega_u), \qquad u = 1, ..., k$$

- Multiplying many small values < 1
- ✓ It is more convenient to work with an equivalent function $g_i(.)$, for example:
 - $g_i(\mathbf{x}) \equiv \log(P(\omega_u|\mathbf{x})) \propto \log(P(\omega_u)) * \sum_{j=1}^l \log(p(x_j|\omega_u))$.







Summary

- KNN
- K-D Tree
- Bayes Theorem
- Naive Bayes

Thank you!



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