

# Probabilistic Methods in Bioinformatics

Pabitra Mitra  
[pabitra@cse.iitkgp.ernet.in](mailto:pabitra@cse.iitkgp.ernet.in)

# Probability in Bioinformatics

---

- ▶ **Classification**

- ▶ Categorize a new object into a known class
- ▶ Supervised learning/predictive analysis

- ▶ **Regression**

- ▶ Supervised prediction of continuous valued variables

- ▶ **Clustering**

- ▶ Extract homogenous groups in population
- ▶ Unsupervised learning/exploratory analysis

- ▶ **Sequence analysis**

- ▶ **Relation and graph structure analysis**



# Probabilistic Algorithms

---

- ▶ **Classification**

- ▶ Bayes classification, graphical models

- ▶ **Regression**

- ▶ Logistic regression

- ▶ **Clustering**

- ▶ Gaussian mixture models

- ▶ **Sequence analysis**

- ▶ Markov models, hidden markov models, conditional random fields

- ▶ **Relation analysis**

- ▶ Markov processes, graph structure analysis

*many many more.....*

---



# A Simple Species Classification Problem

---

- ▶ Measure the *length* of a fish, and decide its class
  - ▶ Hilsa or Tuna



# Collect Statistics ...

---



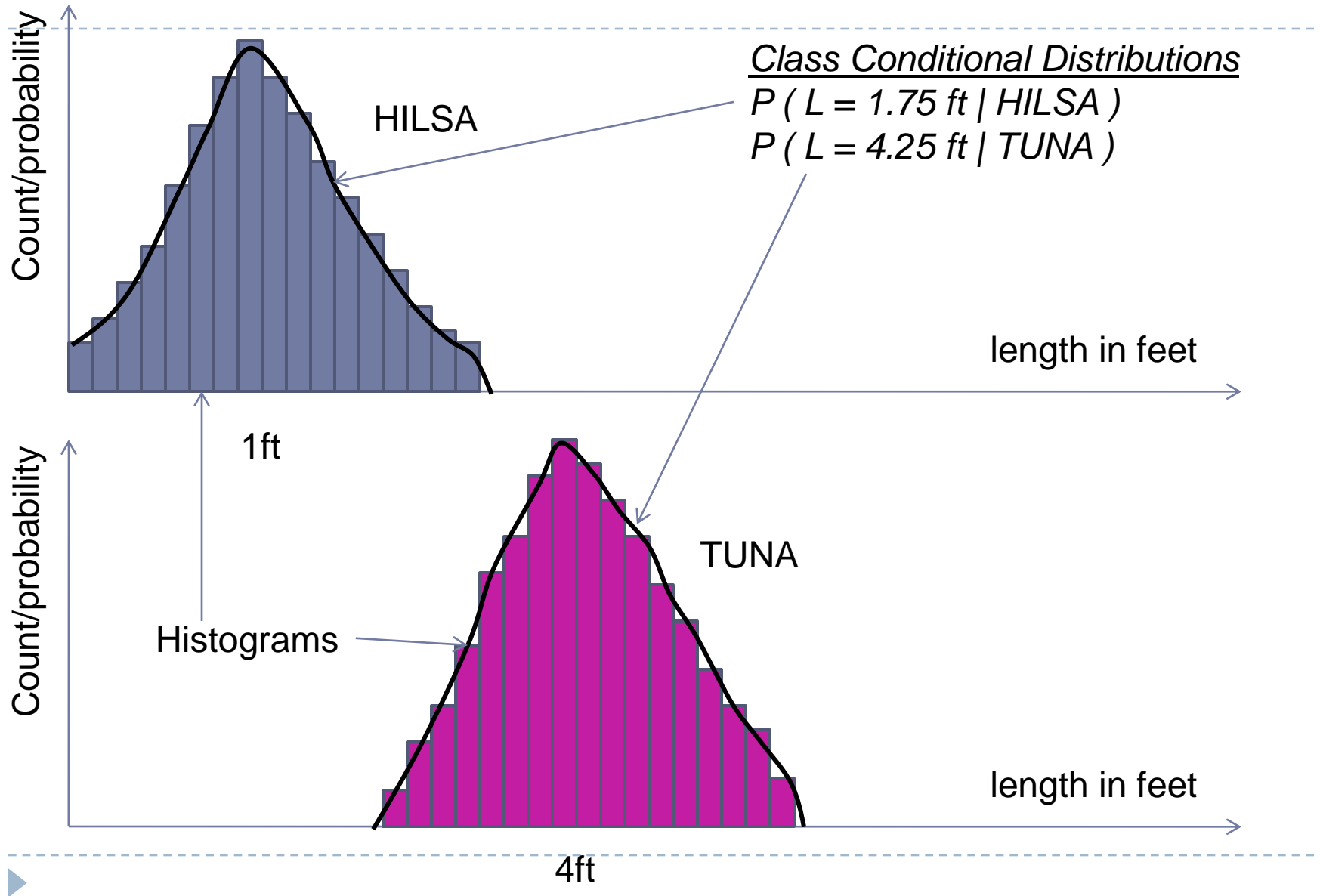
Population for Class Hilsa



Population for Class Tuna

---

# Distribution of “Fish Length”



# Decision Rule

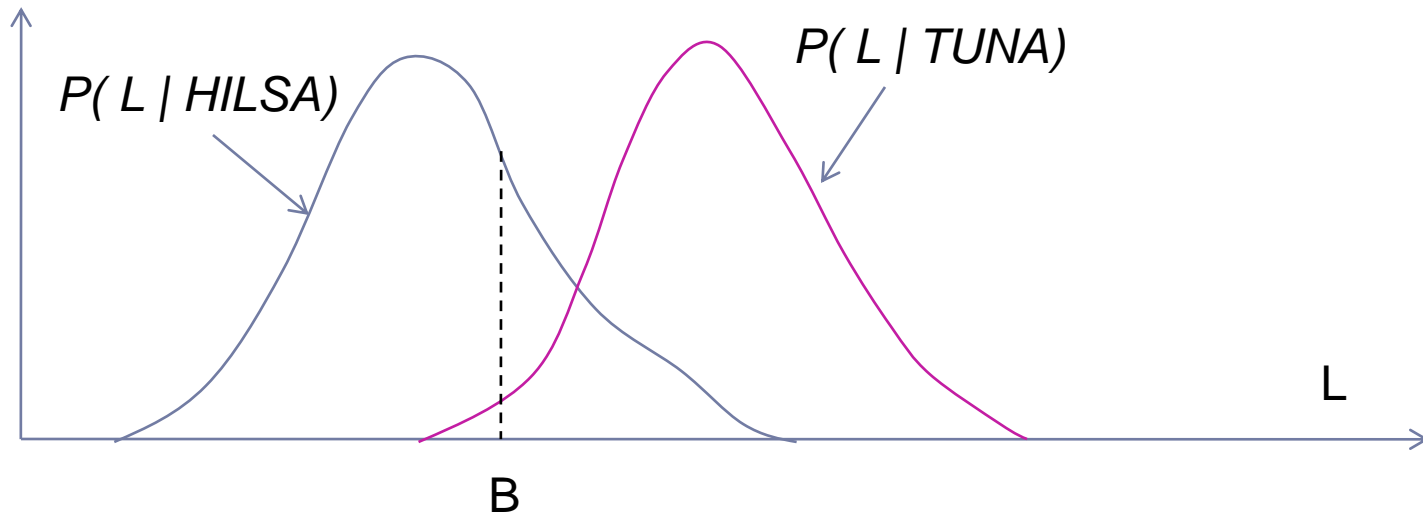
---

- ▶ If length  $L \leq B$ 
  - ▶ HILSA
- ▶ ELSE
  - ▶ TUNA
- ▶ What should be the value of B (“boundary” length) ?
  - ▶ Based on population statistics



# Error of Decision Rule

---



Errors: Type 1 + Type 2,

Type 1: Actually Tuna, Classified as Hilsa (area under pink curve to the left of a  $B$ )

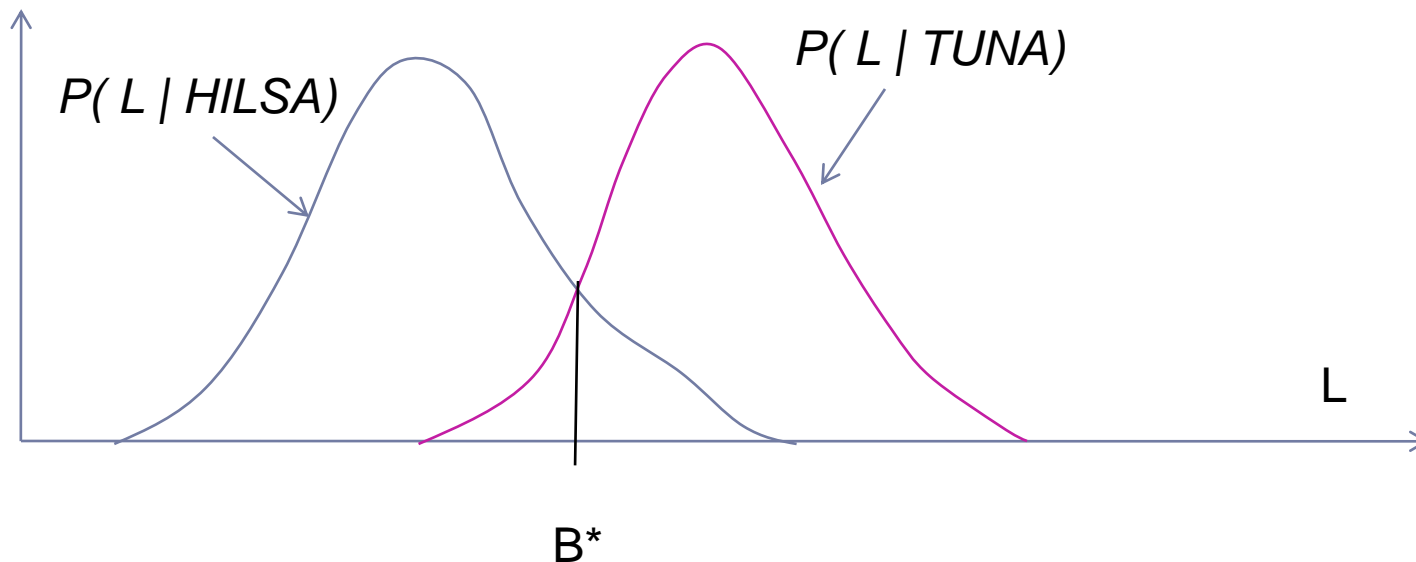
Type 2: Actually Hilsa, Classified as Tuna (area under blue curve to the right of a  $B$ )





# Optimal Decision Rule

---



$B^*$ : Optimal Value of  $B$ , (Optimal Decision Boundary)

Minimum Possible Error

$$P(B^* | HILSA) = P(B^* | TUNA)$$

If Type 1 and Type 2 errors have different costs : optimal boundary shifts

---

# Species Identification Problem

---

- ▶ Measure lengths of a (sizeable) population of Hilsa and Tuna fishes
- ▶ Estimate Class Conditional Distributions for Hilsa and Tuna classes respectively
- ▶ Find Optimal Decision Boundary  $B^*$  from the distributions
- ▶ Apply Decision Rule to classify a newly caught (and measured) fish as either Hilsa or Tuna
  - ▶ (with minimum error probability)



# Location/Time of Experiment

---

- ▶ Calcutta in Monsoon
  - ▶ More Hilsa few Tuna
- ▶ California in Winter
  - ▶ More Tuna less Hilsa
- ▶ Even a 2ft fish is likely to be Hilsa in Calcutta (2000 Rs/Kilo!),
- ▶ a 1.5ft fish may be Tuna in California



# Apriori Probability

---

- ▶ Without measuring length what can we guess about the class of a fish
  - ▶ Depends on location/time of experiment
    - ▶ Calcutta : Hilsa, California:Tuna
- ▶ Apriori probability:  $P(HILSA)$ ,  $P(TUNA)$ 
  - ▶ Property of the frequency of classes during experiment
    - ▶ Not a property of length of the fish
  - ▶ Calcutta:  $P(Hilsa) = 0.90$ ,  $P(Tuna) = 0.10$
  - ▶ California:  $P(Tuna) = 0.95$ ,  $P(Hilsa) = 0.05$
  - ▶ London:  $P(Tuna) = 0.50$ ,  $P(Hilsa) = 0.50$
- ▶ Also a determining factor in class decision along with class conditional probability



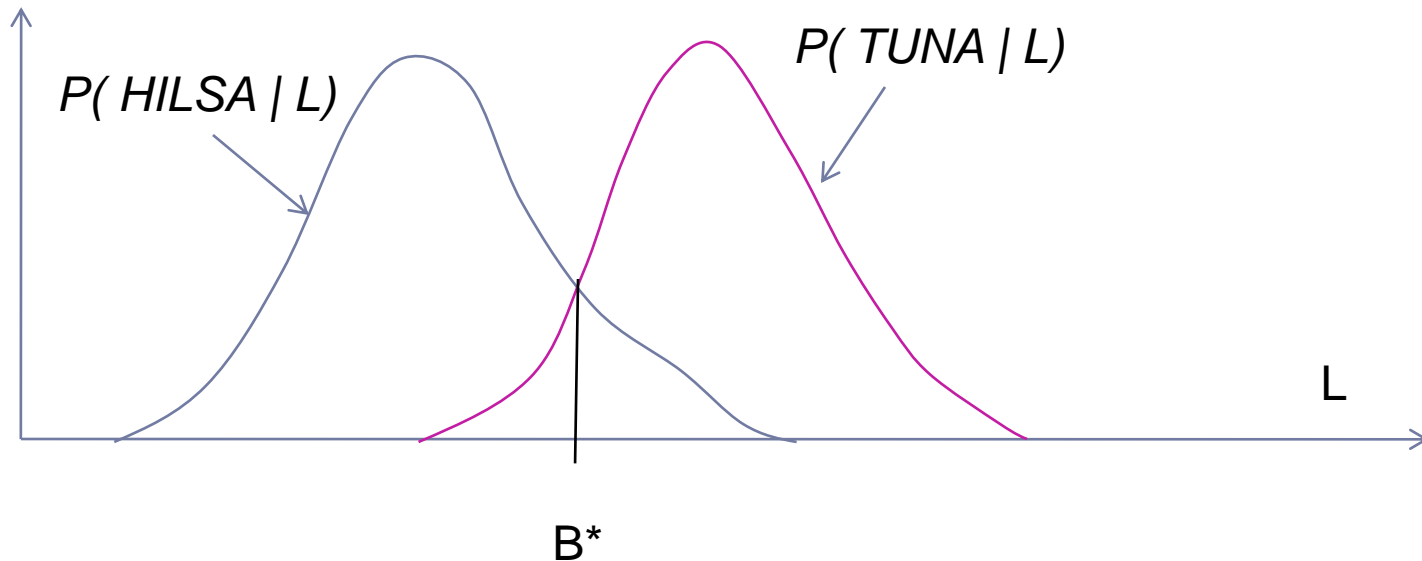
# Classification Decision

- ▶ We consider the product of *Apriori* and *Class conditional* probability factors
- ▶ *Posteriori probability (Bayes rule)*
  - ▶  $P(\text{HILSA} \mid L = 2\text{ft}) = P(\text{HILSA}) \times P(L=2\text{ft} \mid \text{HILSA}) / P(L=2\text{ft})$
  - ▶ *Posteriori  $\approx$  Apriori  $\times$  Class conditional*
  - ▶ *denominator is constant for all classes*
- ▶ *Apriori*: Without any measurement - based on just location/time – what can we guess about class membership (estimated from size of class populations)
- ▶ *Class conditional*: Given the fish belongs to a particular class what is the probability that its length is  $L=2\text{ft}$  (estimated from population)
- ▶ *Posteriori*: Given the measurement that the length of the fish is  $L=2\text{ft}$  what is the probability that the fish belongs to a particular class (obtained using Bayes rule from above two probabilities).
  - ▶ Useful in decision making using evidences/measurements.

# Bayes Classification Rule (Bayes Classifier)

---

Posteriori Distributions



$B^*$ : Optimal Value of  $B$ , (Bayes Decision Boundary)

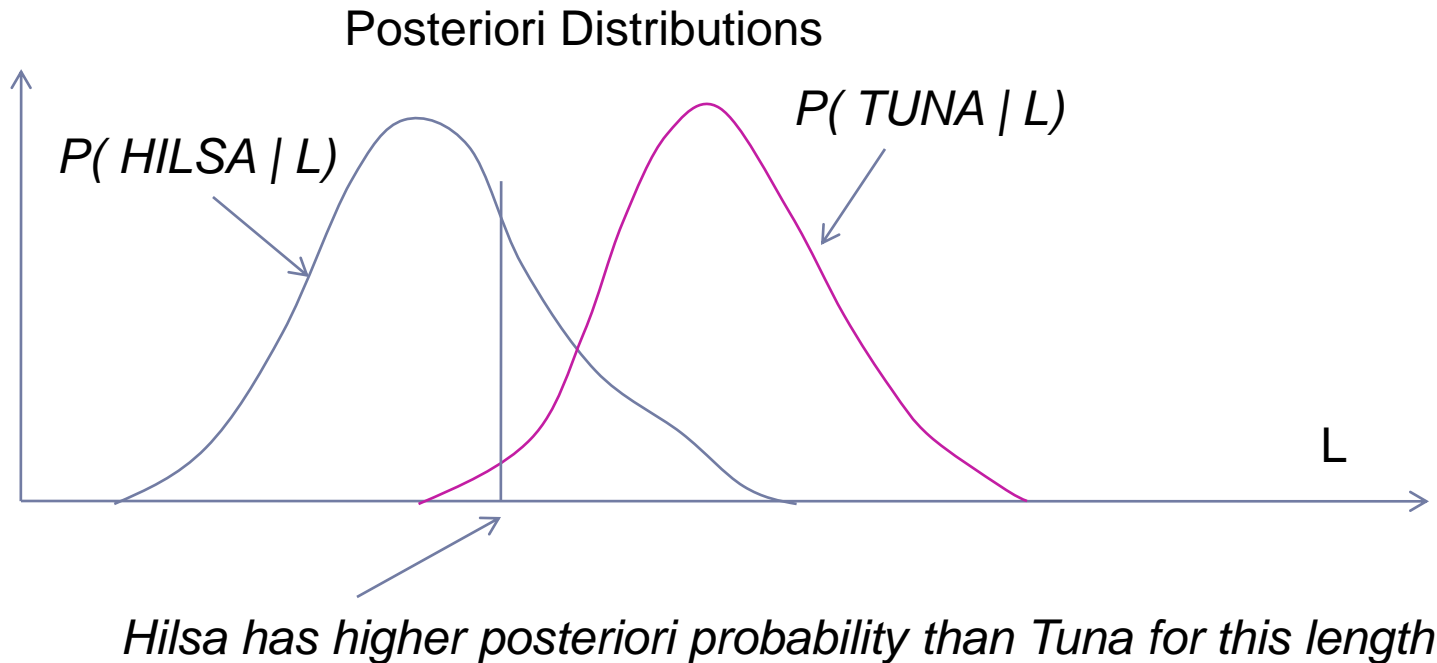
$$P(HILSA | L = B^*) = P(TUNA | L = B^*)$$

Minimum error probability: Bayes error



# MAP Representation of Bayes Classifier

---



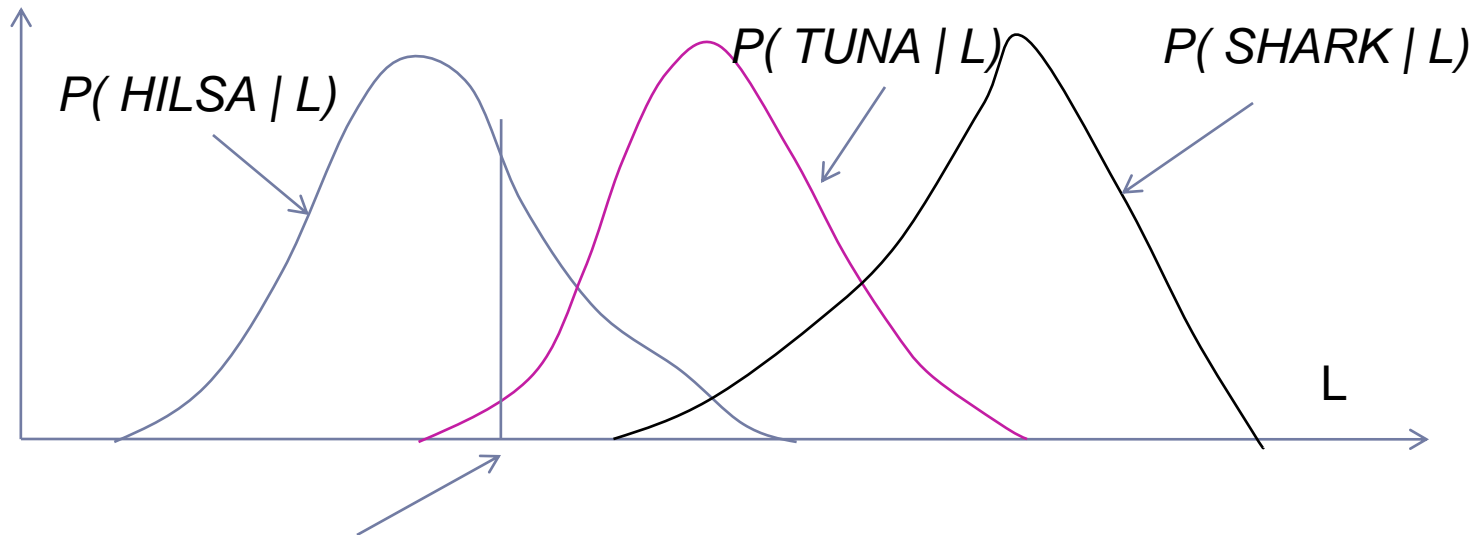
Instead of finding decision boundary  $B^*$ , state classification rule as:

*Classify an object in to the class for which it has the highest posteriori prob.*  
**(MAP: Maximum Aposteriori Probability)**

# MAP Multiclass Classifier

---

Posteriori Distributions



*Hilsa has highest posteriori probability among all classes for this length*

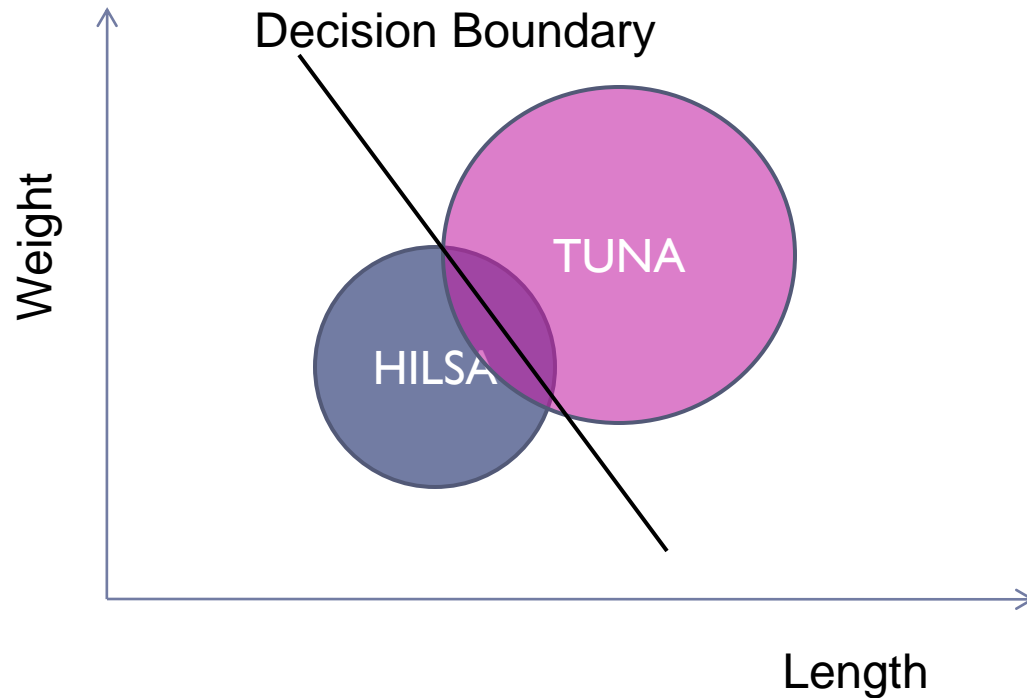
*Classify an object in to the class for which it has the highest posteriori prob.  
(MAP: Maximum Aposteriori Probability)*





# Multivariate Bayes Classifier

---



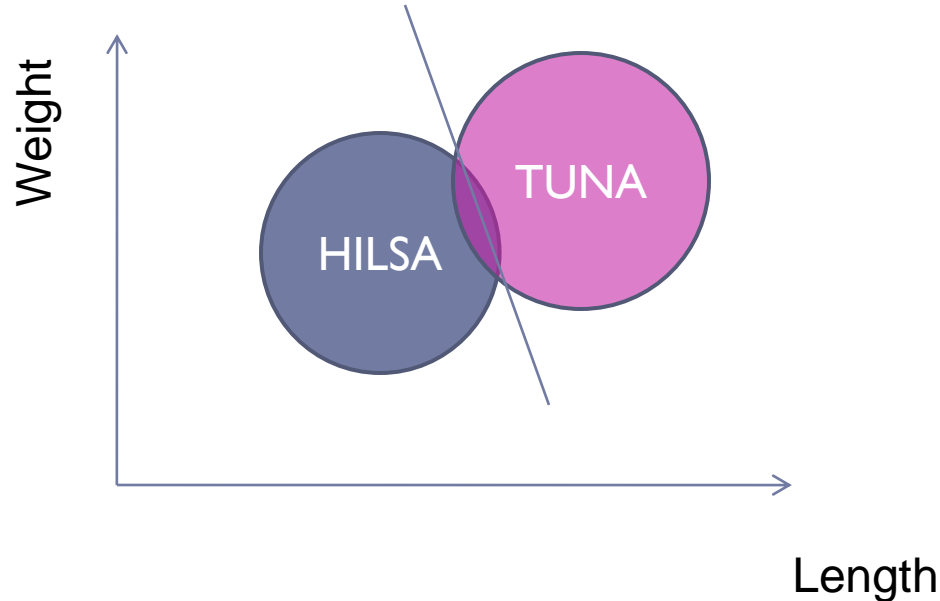
- Feature or Attribute Space
- Class Separability



# Decision Boundary: Normal Distribution

---

- ▶ Two spherical classes having different means, but same variance (diagonal covariance matrix with same variances)



Decision Boundary: Perpendicular bisector of the mean vectors

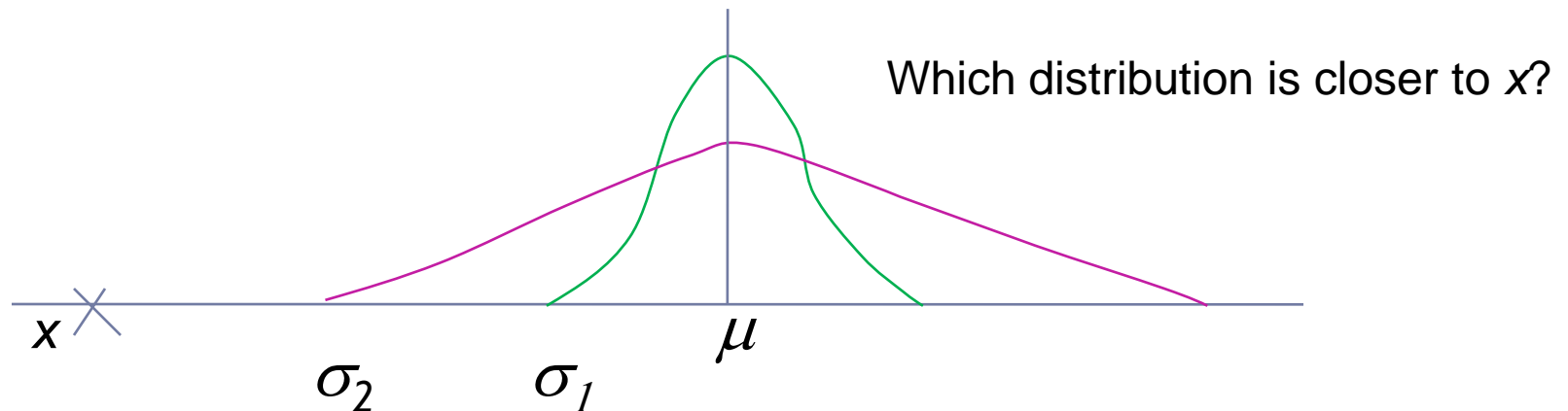
---



# Distances

---

- ▶ Two vectors: Euclidean, Minkowski etc
- ▶ A vector and a distribution: Mahalanobis, Bhattacharya



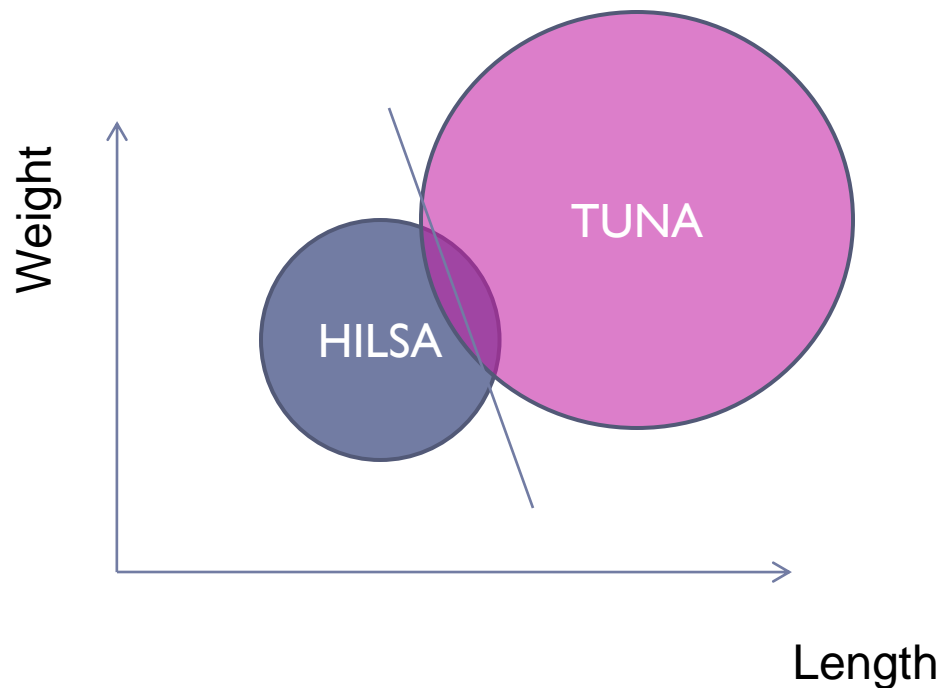
$$d_M = \frac{(x - \mu)^2}{\sigma}, d_M = (X - \mu)\Sigma^{-1}(X - \mu)^T$$

- ▶ Between two distributions: Kullback-Liebler Divergence
-

# Decision Boundary: Normal Distribution

---

- ▶ Two spherical classes having different means and variances (diagonal covariance matrix with different variances)



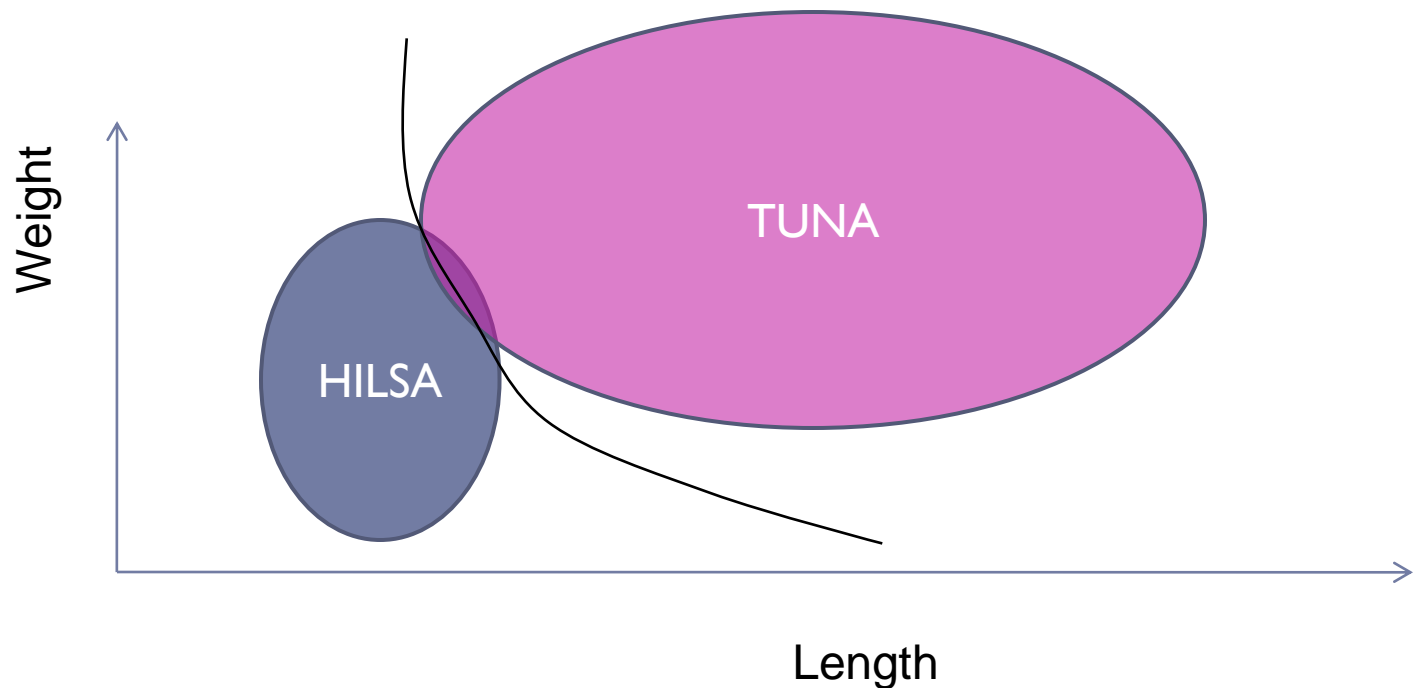
Boundary: Locus of equi-Mahalanobis distance points from the class distributions.  
(still a straight line)

---

# Decision Boundary: Normal Distribution

---

- ▶ Two elliptical classes having different means and variances (general covariance matrix with different variances)



Class Boundary: Parabolic



# Bayesian Classifiers

---

- ▶ Approach:

- ▶ compute the posterior probability  $P(C | A_1, A_2, \dots, A_n)$  for all values of  $C$  using the Bayes theorem

$$P(C | A_1 A_2 \dots A_n) = \frac{P(A_1 A_2 \dots A_n | C) P(C)}{P(A_1 A_2 \dots A_n)}$$

- ▶ Choose value of  $C$  that maximizes

$$P(C | A_1, A_2, \dots, A_n)$$

- ▶ Equivalent to choosing value of  $C$  that maximizes

$$P(A_1, A_2, \dots, A_n | C) P(C)$$

- ▶ How to estimate  $P(A_1, A_2, \dots, A_n | C)$ ?
- 



# Estimating Multivariate Class Distributions

---

## ▶ Sample size requirement

- ▶ In a small sample: difficult to find a Hilsa fish whose length is 1.5ft and weight is 2 kilos, as compared to that of just finding a fish whose length is 1.5ft
- ▶  $P(L=1.5, W=2 \mid \text{Hilsa}), P(L=1.5 \mid \text{Hilsa})$
- ▶ Curse of dimensionality

## ▶ Independence Assumption

- ▶ Assume length and weight are independent
  - ▶  $P(L=1.5, W=2 \mid \text{Hilsa}) = P(L=1.5 \mid \text{Hilsa}) \times P(W=2 \mid \text{Hilsa})$
  - ▶ Joint distribution = product of marginal distributions
  - ▶ Marginals are easier to estimate from a small sample
- 



# Naïve Bayes Classifier

---

- ▶ Assume independence among attributes  $A_i$  when class is given:
  - ▶  $P(A_1, A_2, \dots, A_n | C) = P(A_1 | C_j) P(A_2 | C_j) \dots P(A_n | C_j)$
  - ▶ Can estimate  $P(A_i | C_j)$  for all  $A_i$  and  $C_j$ .
  - ▶ New point is classified to  $C_j$  if  $P(C_j) \prod P(A_i | C_j)$  is maximal.





# Example of Naïve Bayes Classifier

Name	Give Birth	Can Fly	Live in Water	Have Legs	Class
human	yes	no	no	yes	mammals
python	no	no	no	no	non-mammals
salmon	no	no	yes	no	non-mammals
whale	yes	no	yes	no	mammals
frog	no	no	sometimes	yes	non-mammals
komodo	no	no	no	yes	non-mammals
bat	yes	yes	no	yes	mammals
pigeon	no	yes	no	yes	non-mammals
cat	yes	no	no	yes	mammals
leopard shark	yes	no	yes	no	non-mammals
turtle	no	no	sometimes	yes	non-mammals
penguin	no	no	sometimes	yes	non-mammals
porcupine	yes	no	no	yes	mammals
eel	no	no	yes	no	non-mammals
salamander	no	no	sometimes	yes	non-mammals
gila monster	no	no	no	yes	non-mammals
platypus	no	no	no	yes	mammals
owl	no	yes	no	yes	non-mammals
dolphin	yes	no	yes	no	mammals
eagle	no	yes	no	yes	non-mammals

A: attributes

M: mammals

N: non-mammals

$$P(A | M) = \frac{6}{7} \times \frac{6}{7} \times \frac{2}{7} \times \frac{2}{7} = 0.06$$

$$P(A | N) = \frac{1}{13} \times \frac{10}{13} \times \frac{3}{13} \times \frac{4}{13} = 0.0042$$

$$P(A | M)P(M) = 0.06 \times \frac{7}{20} = 0.021$$

$$P(A | N)P(N) = 0.004 \times \frac{13}{20} = 0.0027$$

Give Birth	Can Fly	Live in Water	Have Legs	Class
yes	no	yes	no	?

$$P(A|M)P(M) > P(A|N)P(N)$$

=> Mammals

# How to Estimate Probabilities from Data?

---

- ▶ For continuous attributes:

- ▶ **Discretize** the range into bins

- ▶ one ordinal attribute per bin
    - ▶ violates independence assumption

- ▶ **Two-way split:**  $(A < v)$  or  $(A > v)$

- ▶ choose only one of the two splits as new attribute

- ▶ **Probability density estimation:**

- ▶ Assume attribute follows a normal distribution
    - ▶ Use data to estimate parameters of distribution (e.g., mean and standard deviation)
    - ▶ Once probability distribution is known, can use it to estimate the conditional probability  $P(A_i|c)$

k



# Naïve Bayes Classifier

---

- ▶ If one of the conditional probability is zero, then the entire expression becomes zero
- ▶ Probability estimation:

$$\text{Original : } P(A_i | C) = \frac{N_{ic}}{N_c}$$

$$\text{Laplace : } P(A_i | C) = \frac{N_{ic} + 1}{N_c + c}$$

$$\text{m - estimate : } P(A_i | C) = \frac{N_{ic} + mp}{N_c + m}$$

c: number of classes

p: prior probability

m: parameter



# Bayes Classifier (Summary)

---

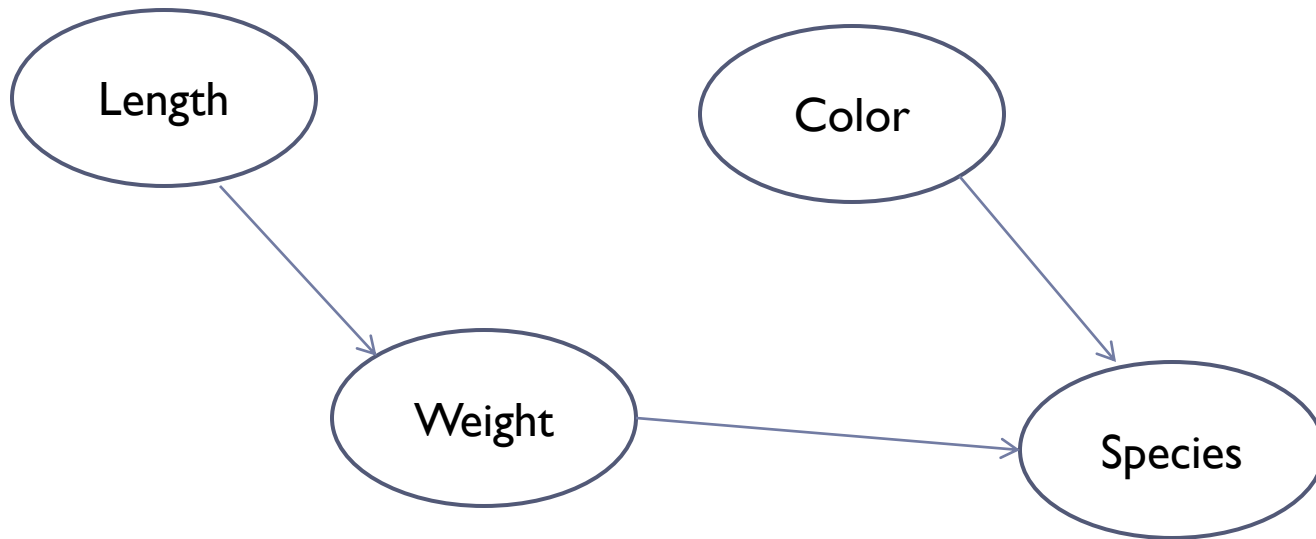
- ▶ Robust to isolated noise points
- ▶ Handle missing values by ignoring the instance during probability estimate calculations
- ▶ Robust to irrelevant attributes
- ▶ Independence assumption may not hold for some attributes
  - ▶ Length and weight of a fish are not independent



# Bayesian Belief Network

---

- ▶ A directed acyclic probabilistic graphical model that captures dependence among the attributes



Nodes: Variable/Attributes/Class  
Directed edges: Causality  
Absence of edge: independence

Network structure: domain knowledge  
Joint probabilities: from data

---



# Nonparametric Statistics

---

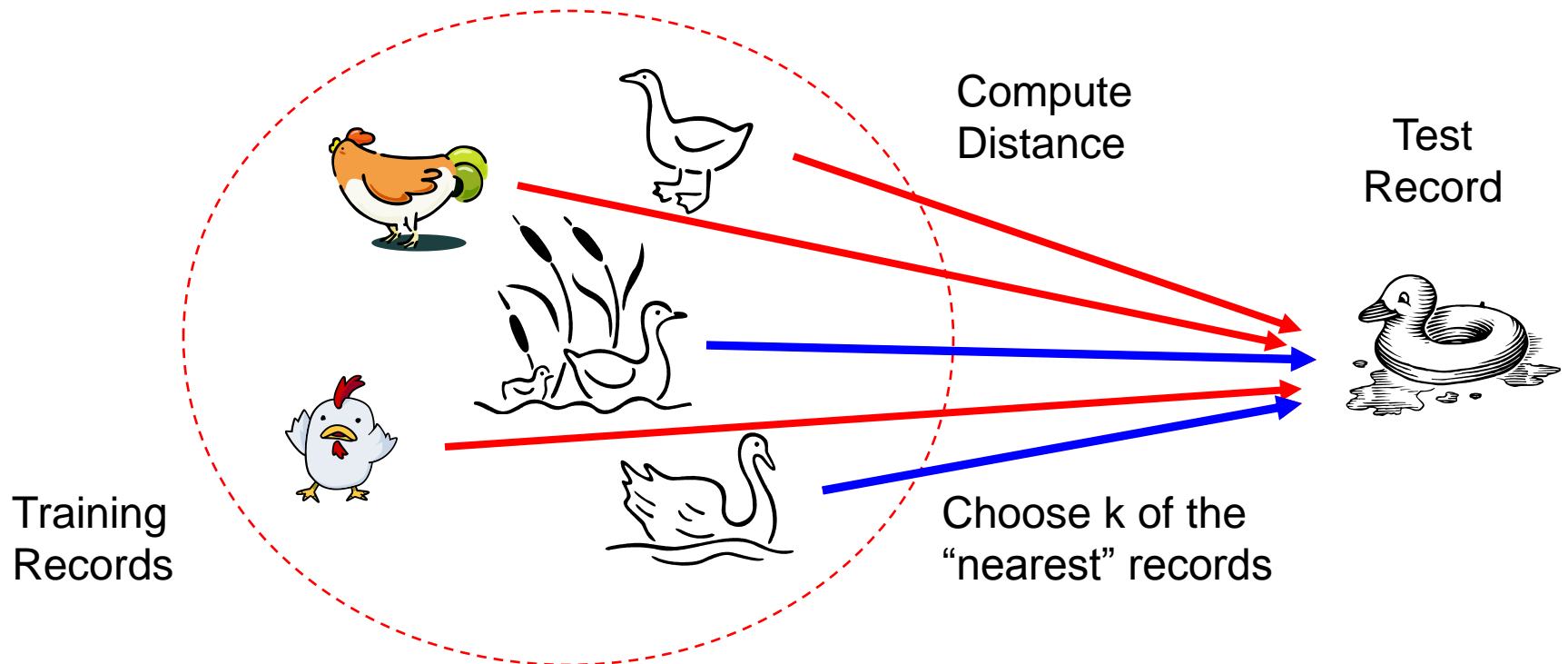
- ▶ Do not assume parametric data distribution/model
- ▶ Take decisions based on given sample
- ▶ Bayesian statistics vs frequentist statistics



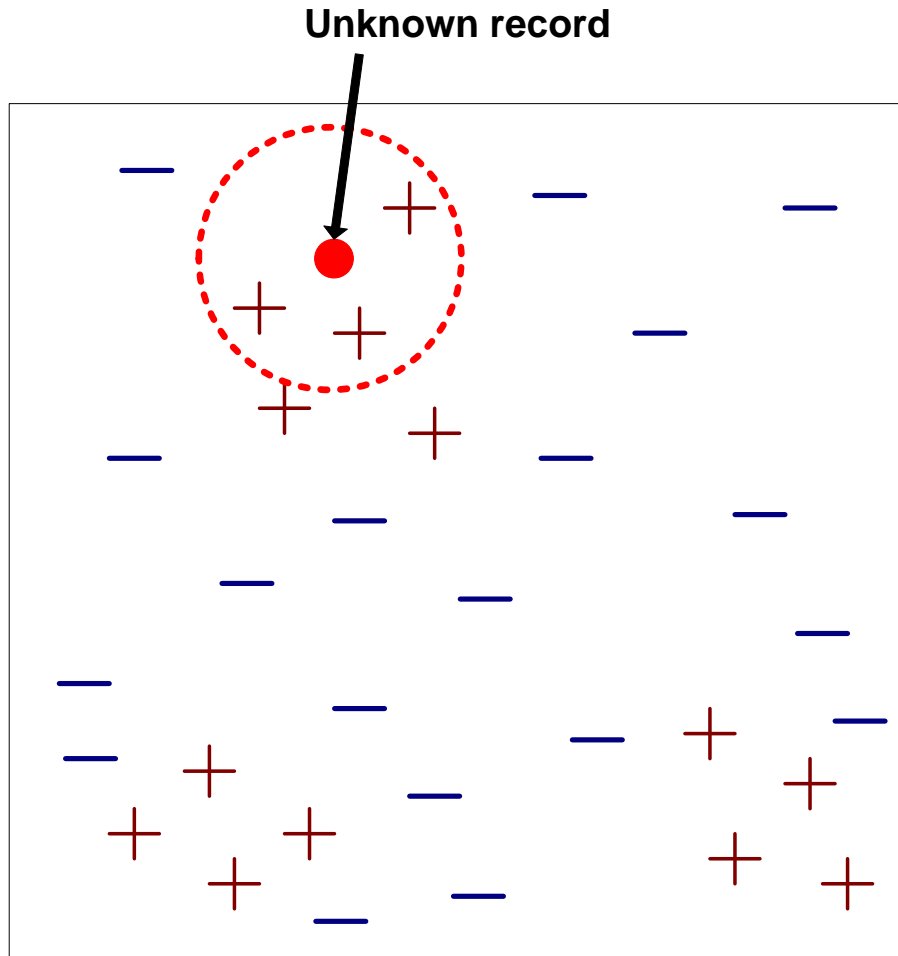
# Nearest Neighbor Classifiers

- ▶ **Basic idea:**

- ▶ If it walks like a duck, quacks like a duck, then it's probably a duck



# Nearest-Neighbor Classifiers



- Requires three things
  - The set of stored records
  - Distance Metric to compute distance between records
  - The value of  $k$ , the number of nearest neighbors to retrieve
- To classify an unknown record:
  - Compute distance to other training records
  - Identify  $k$  nearest neighbors
  - Use class labels of nearest neighbors to determine the class label of unknown record (e.g., by taking majority vote)



# Nearest Neighbor Classification

---

- ▶ Compute distance between two points:

- ▶ Euclidean distance

$$d(p, q) = \sqrt{\sum_i (p_i - q_i)^2}$$

- ▶ Determine the class from nearest neighbor list

- ▶ take the majority vote of class labels among the k-nearest neighbors

- ▶ Weigh the vote according to distance

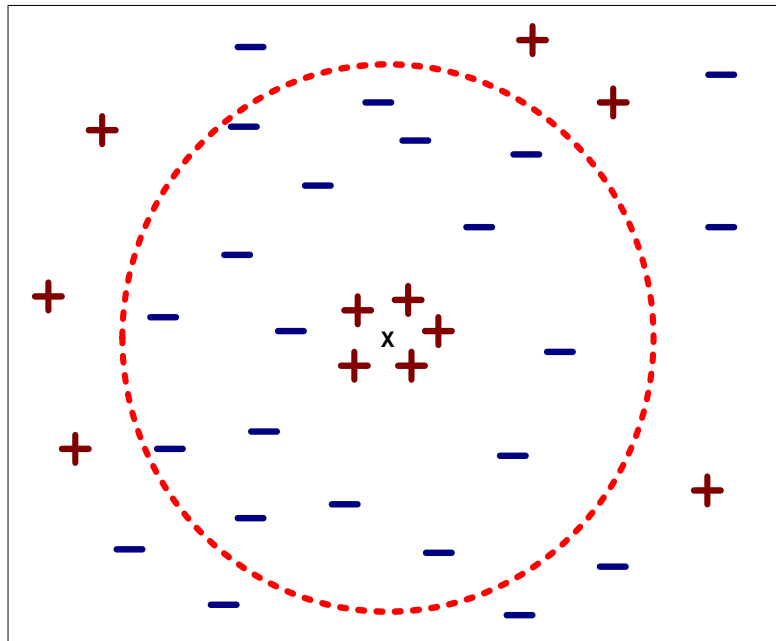
- ▶ weight factor,  $w = 1/d^2$



# Nearest Neighbor Classification...

---

- ▶ Choosing the value of  $k$ :
  - ▶ If  $k$  is too small, sensitive to noise points
  - ▶ If  $k$  is too large, neighborhood may include points from other classes



# Nearest neighbor Classification...

---

- ▶ **k-NN classifiers are lazy learners**
  - ▶ It does not build models explicitly
  - ▶ Unlike eager learners such as decision tree induction and rule-based systems
  - ▶ Classifying unknown records are relatively expensive



# DNA Coding Segment Identification

---

- ▶ Classes: Coding – noncoding segment
- ▶ Attributes/features: sequence information
- ▶ Complex interdependence among attributes



# Microarray Data Analysis

---

- ▶ **Classes: Disease classes**
- ▶ **Attributes/features: gene expression levels**
- ▶ **Large number attributes, fewer samples**



# Protein Secondary Structure Prediction

---

- ▶ Classes:  $\alpha$ -helix, coil etc
- ▶ Attributes/features: length, amino acid sequence, hydrophobicity, shape, ions
- ▶ Complex class distributions



# Protein Interaction Prediction

---

- ▶ **Classes: Binary**
- ▶ **Attributes/features: protein properties**
- ▶ **Presence of domain knowledge**



# References

---

- ▶ Pattern Classification, Duda, Hart and Stork, Wiley, 2010
- ▶ Slides on data mining by Vipin Kumar





# Questions!

---

