

Machine Learning for Bioinformatics & Systems Biology

2. Classification

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Some material courtesy of Robert Duin and David Tax

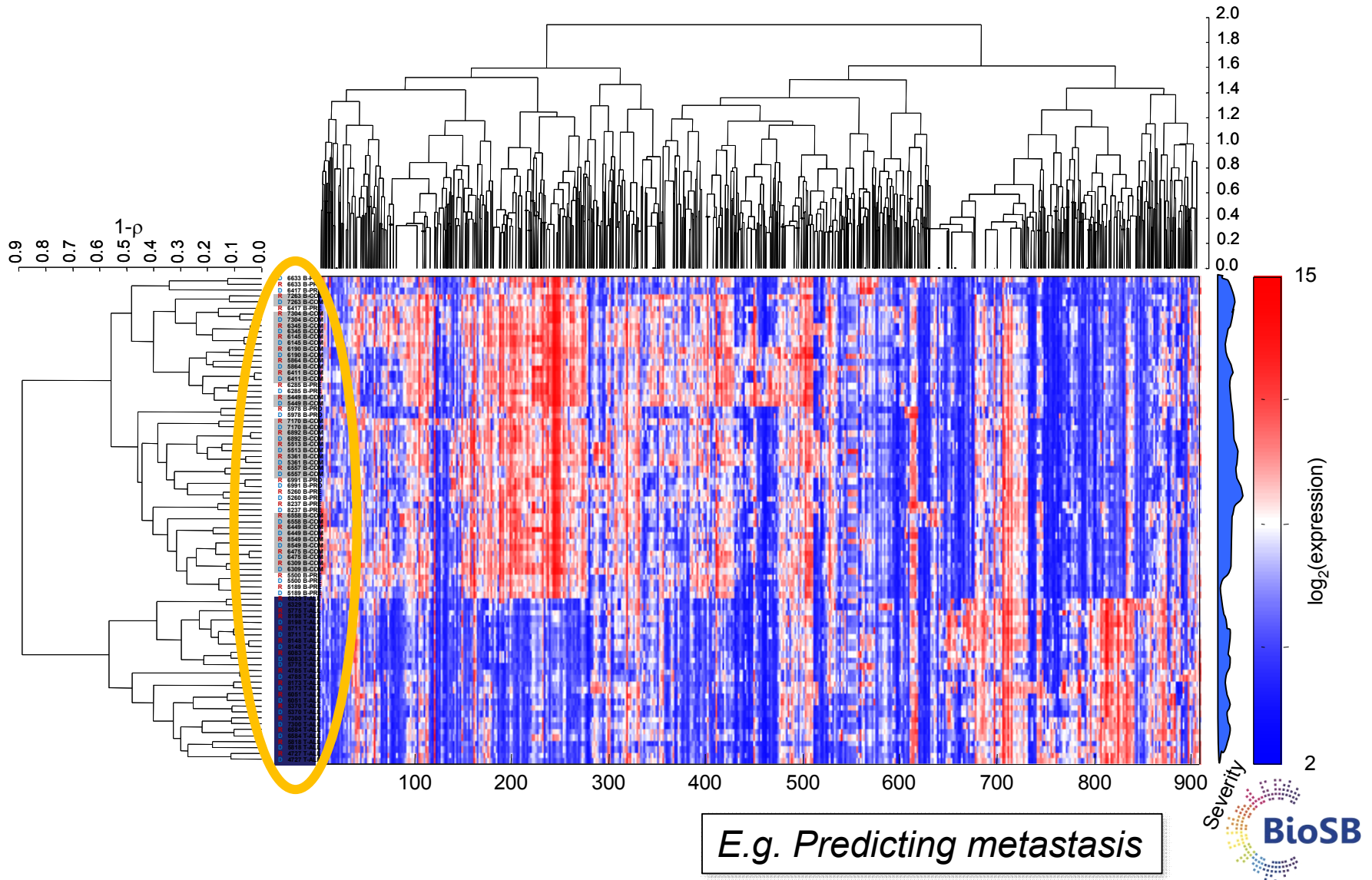
Classification



- How to distinguish between the apples and the pears?



Classification in bioinformatics



Classification in bioinformatics (2)

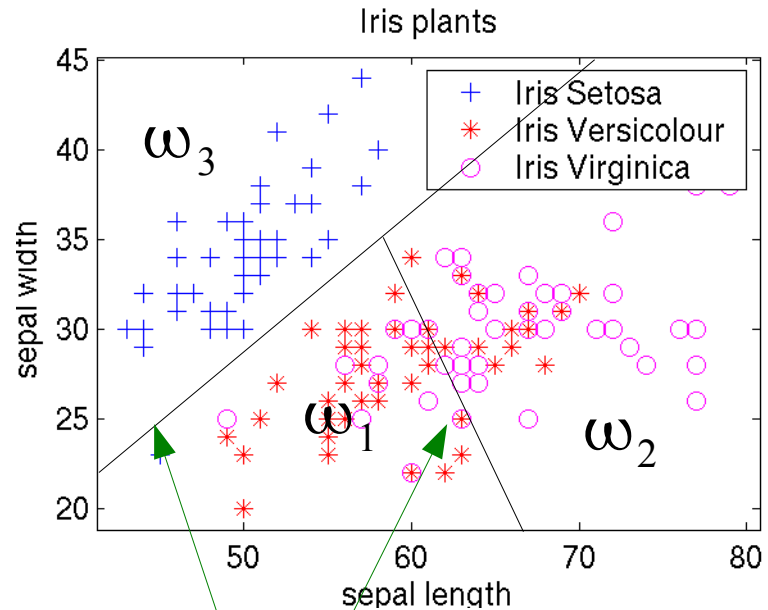
- Secondary structure prediction
amino acids of a protein sequence $\rightarrow \{H, E, -\} = \{\text{alpha helix, beta strand, turn}\}$
- Protein localization prediction
 $\{\text{sequence, ...}\} \rightarrow \{\text{cell organelle}\}$
- Genome annotation
 $\{\text{sequence, ...}\} \rightarrow \{\text{exon, intron, splice site, ...}\}$
- ...

Classification (2)

- Formulation of two-class problems
- Logistic classifier
- Plug-in Bayes classifiers
 - Density-based classification: Parzen, nearest neighbour, Gaussian
- Linear discriminant analysis
 - Fisher classifier
- Decision trees and random forests

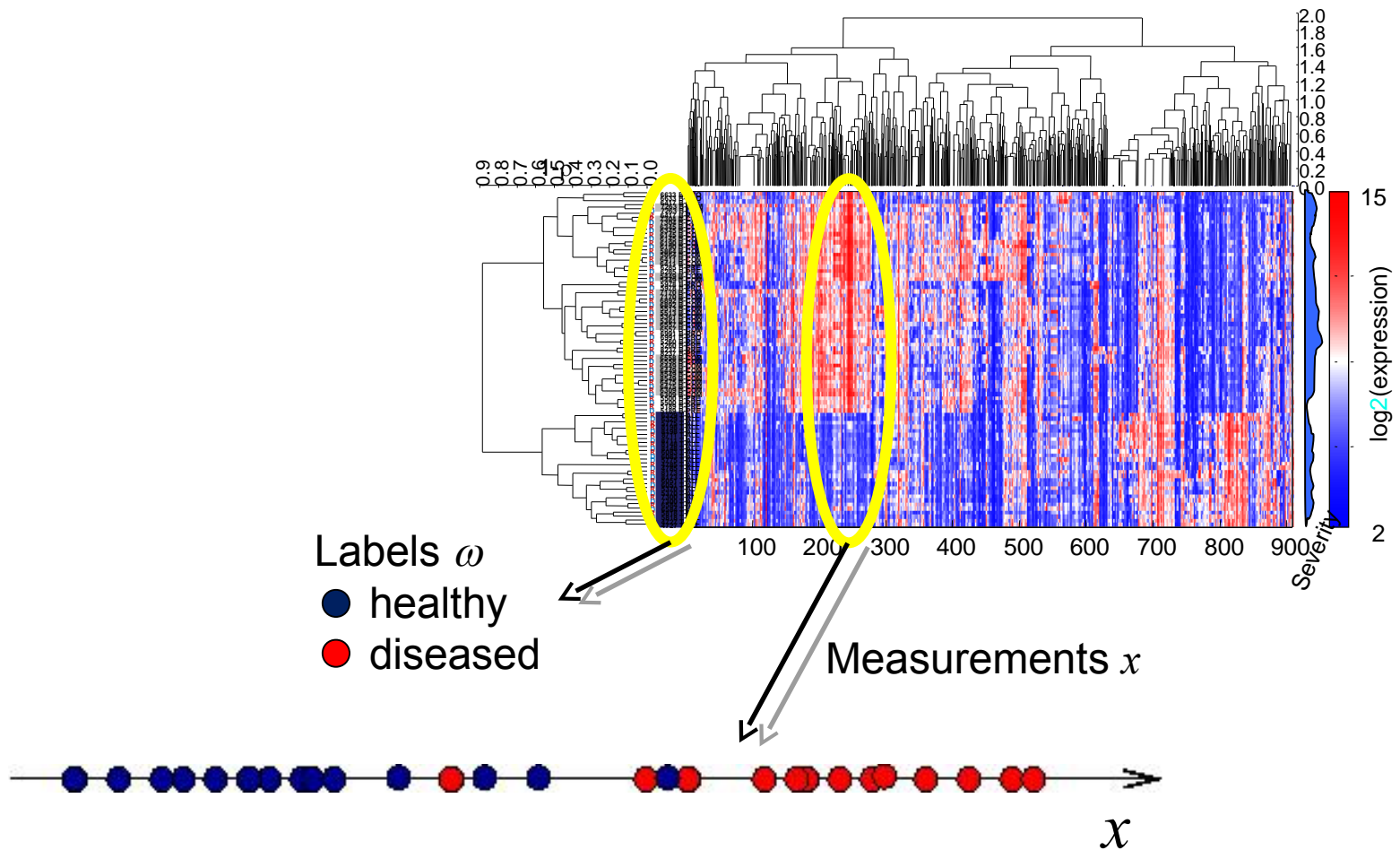
Classification (3)

- Given labeled data: \mathbf{x}
- Assign to each object a class label ω
- In effect splits the feature space in separate regions



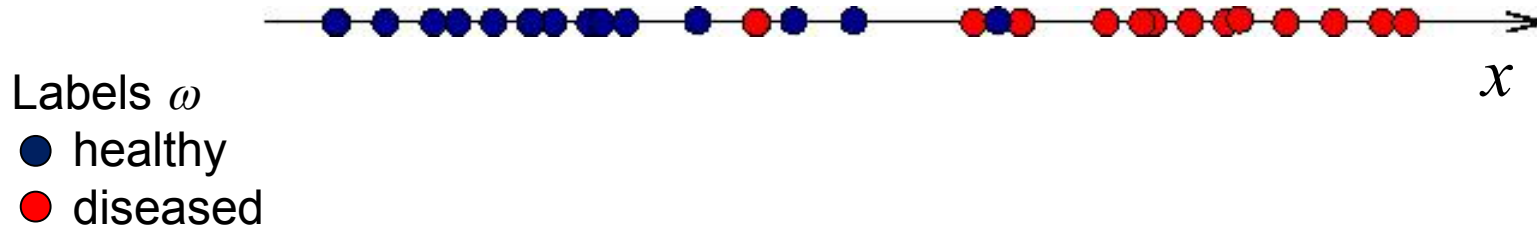
decision boundary

Classification (4)



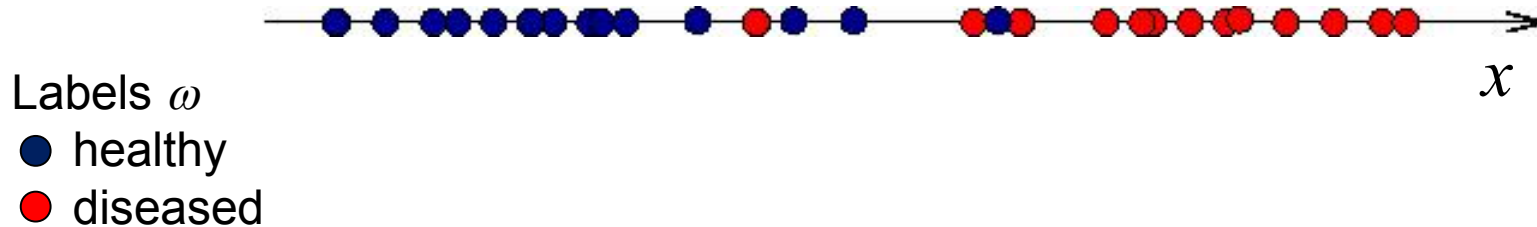
Class posterior probability

- For each object we have to estimate posterior $p(\omega=c|\mathbf{x})$



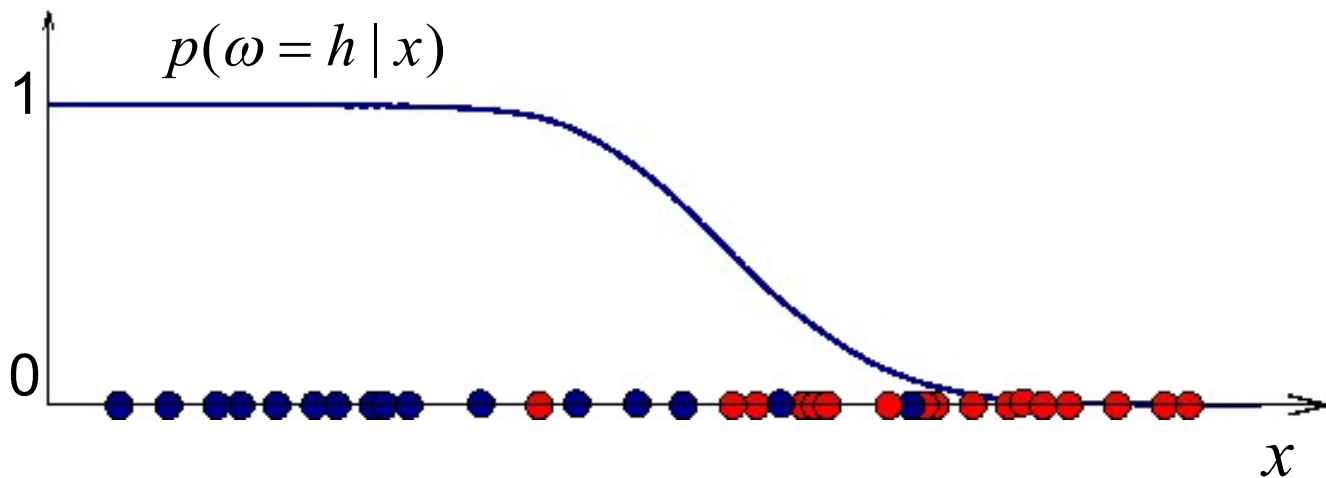
Class posterior probability

- For each object we have to estimate posterior $p(\omega=c|\mathbf{x})$



Class posterior probability (2)

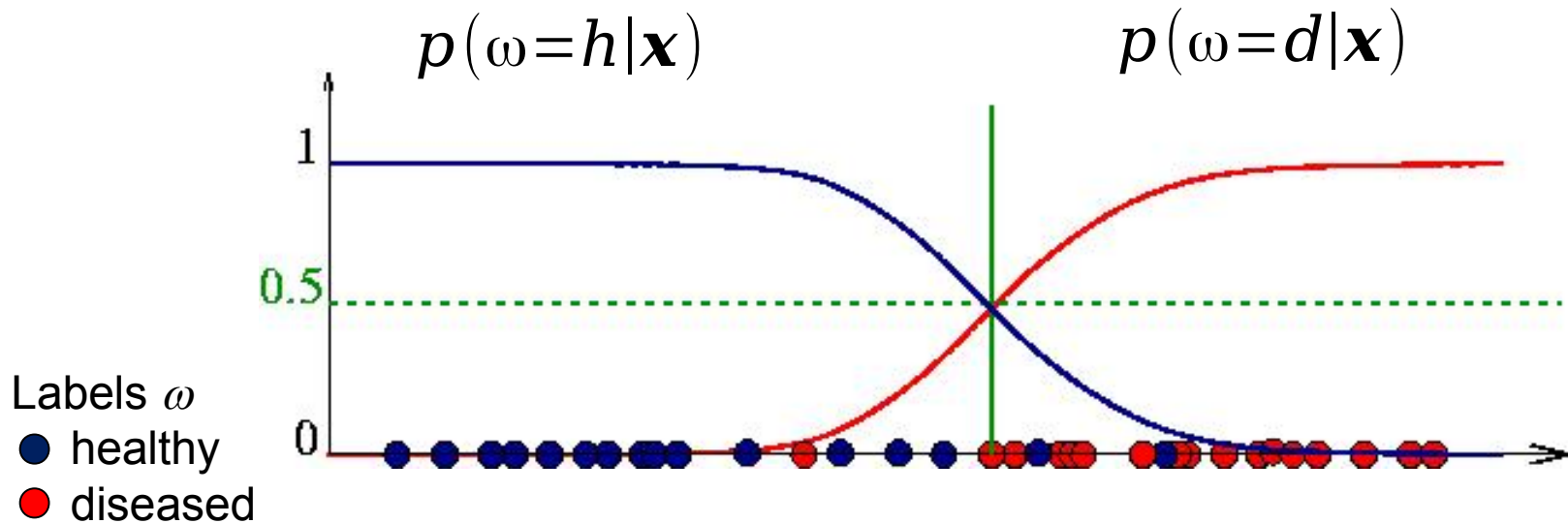
- For each object we have to estimate posterior $p(\omega=c|\mathbf{x})$



Labels ω
● healthy
● diseased

Class posterior probability (3)

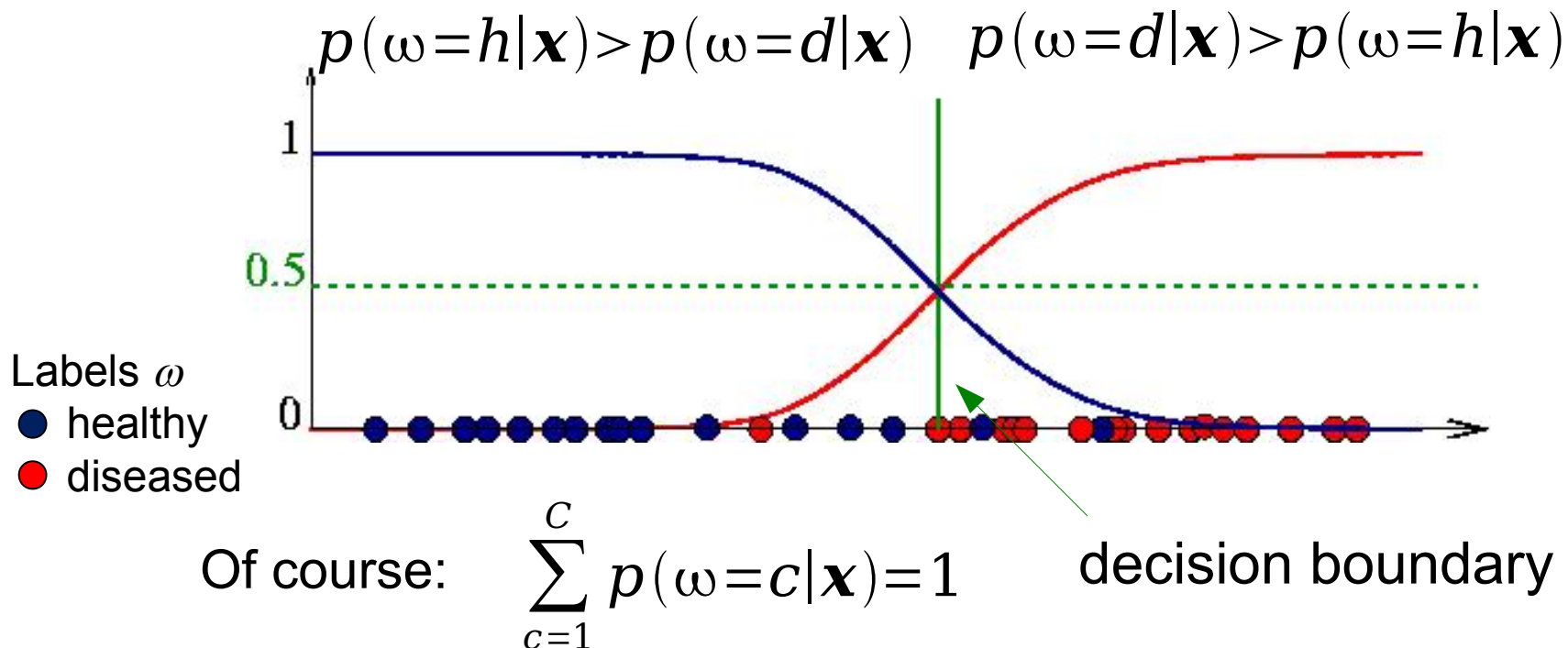
- For each object we have to estimate posterior $p(\omega=c|\mathbf{x})$



Of course:
$$\sum_{c=1}^C p(\omega=c|\mathbf{x})=1$$

Class posterior probability (4)

- For each object we have to estimate posterior $p(\omega=c|\mathbf{x})$



- Assign label of class with the largest posterior probability

Description of a classifier

There are several ways to describe the classifier:

- If $p(\omega=h|\mathbf{x}) > p(\omega=d|\mathbf{x})$ then assign to h otherwise to d
- If $p(\omega=h|\mathbf{x}) - p(\omega=d|\mathbf{x}) > 0$ then assign to h
- If $\frac{p(\omega=h|\mathbf{x})}{p(\omega=d|\mathbf{x})} > 1$ then assign to h
- If $\ln(p(\omega=h|\mathbf{x})) - \ln(p(\omega=d|\mathbf{x})) > 0$ then assign to h

A Bayesian classifier is a *threshold* on the difference between *posterior probabilities*

Logistic classifier

- We can rewrite:

$$\ln(p(\omega=h|\mathbf{x})) - \ln(p(\omega=d|\mathbf{x})) = \ln\left(\frac{p(\omega=h|\mathbf{x})}{p(\omega=d|\mathbf{x})}\right)$$

logit, log-odds

- Assume we can approximate:

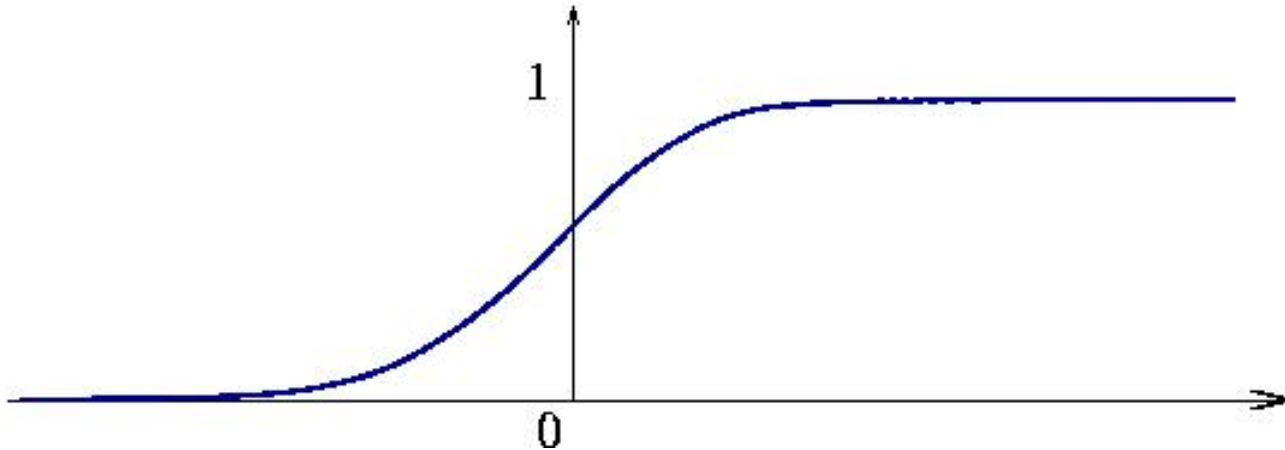
$$\ln\left(\frac{p(\omega=h|\mathbf{x})}{p(\omega=d|\mathbf{x})}\right) = w_0 + \mathbf{w}^T \mathbf{x}$$

- The classifier becomes (computer lab exercise):

$$p(\omega=d|\mathbf{x}) = \frac{1}{1 + \exp(\mathbf{w}^T \mathbf{x} + w_0)}$$

Logistic function

- The function looks like:

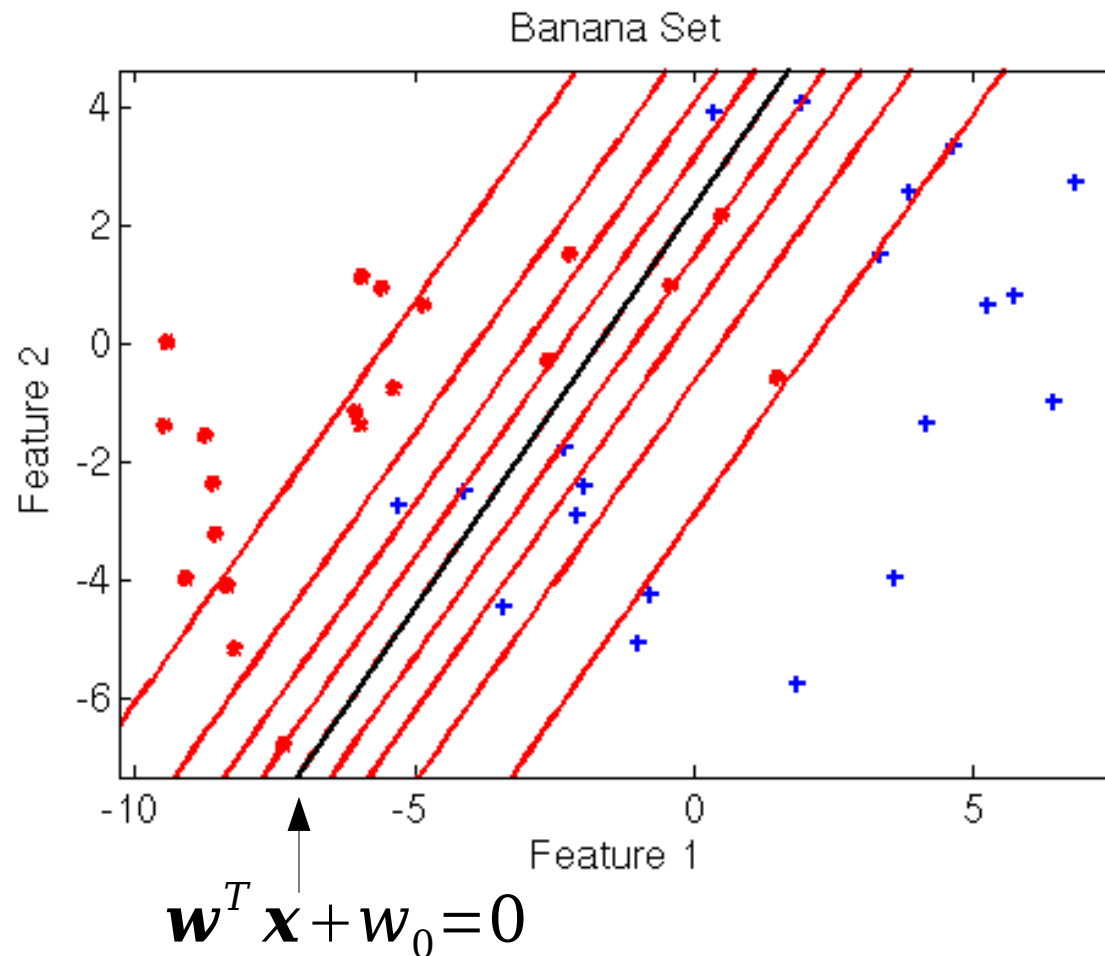


$$f(x) = \frac{1}{1 + \exp(-x)}$$

logistic (sigmoid) function

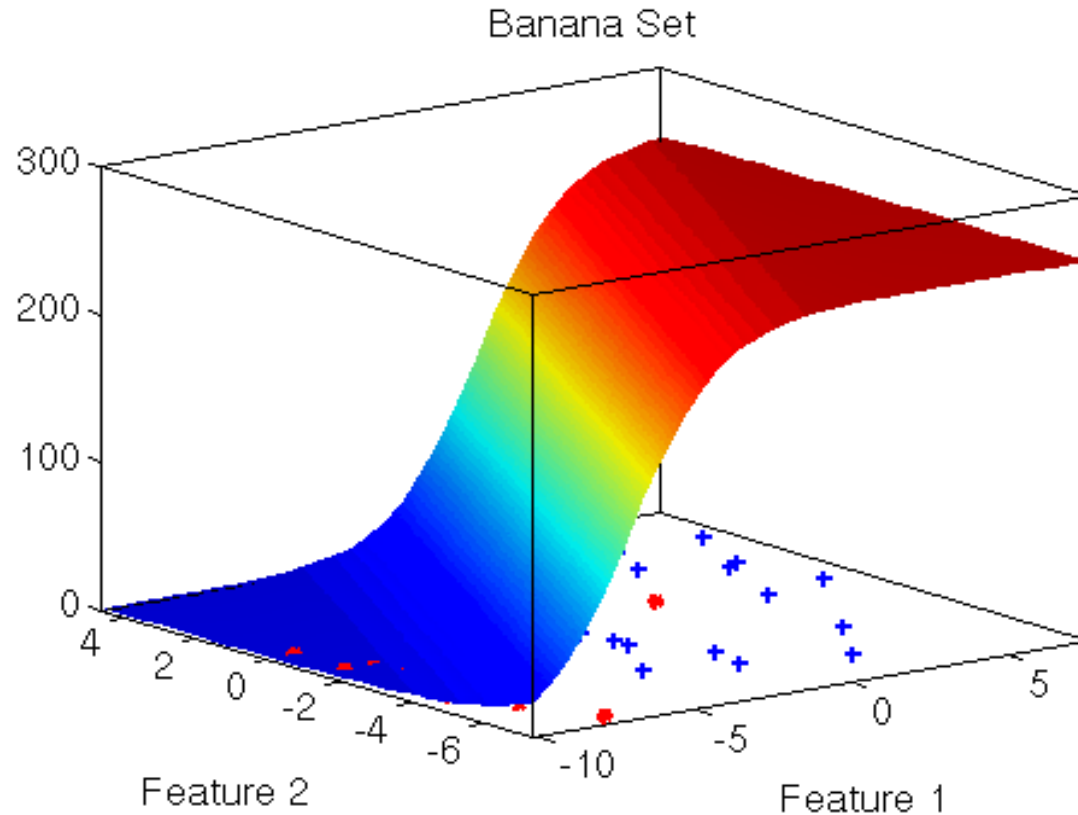
Logistic classifier (2)

- On a two-dimensional dataset it looks like:



Logistic classifier (3)

- On a two-dimensional dataset it looks like:



Optimizing the logistic classifier

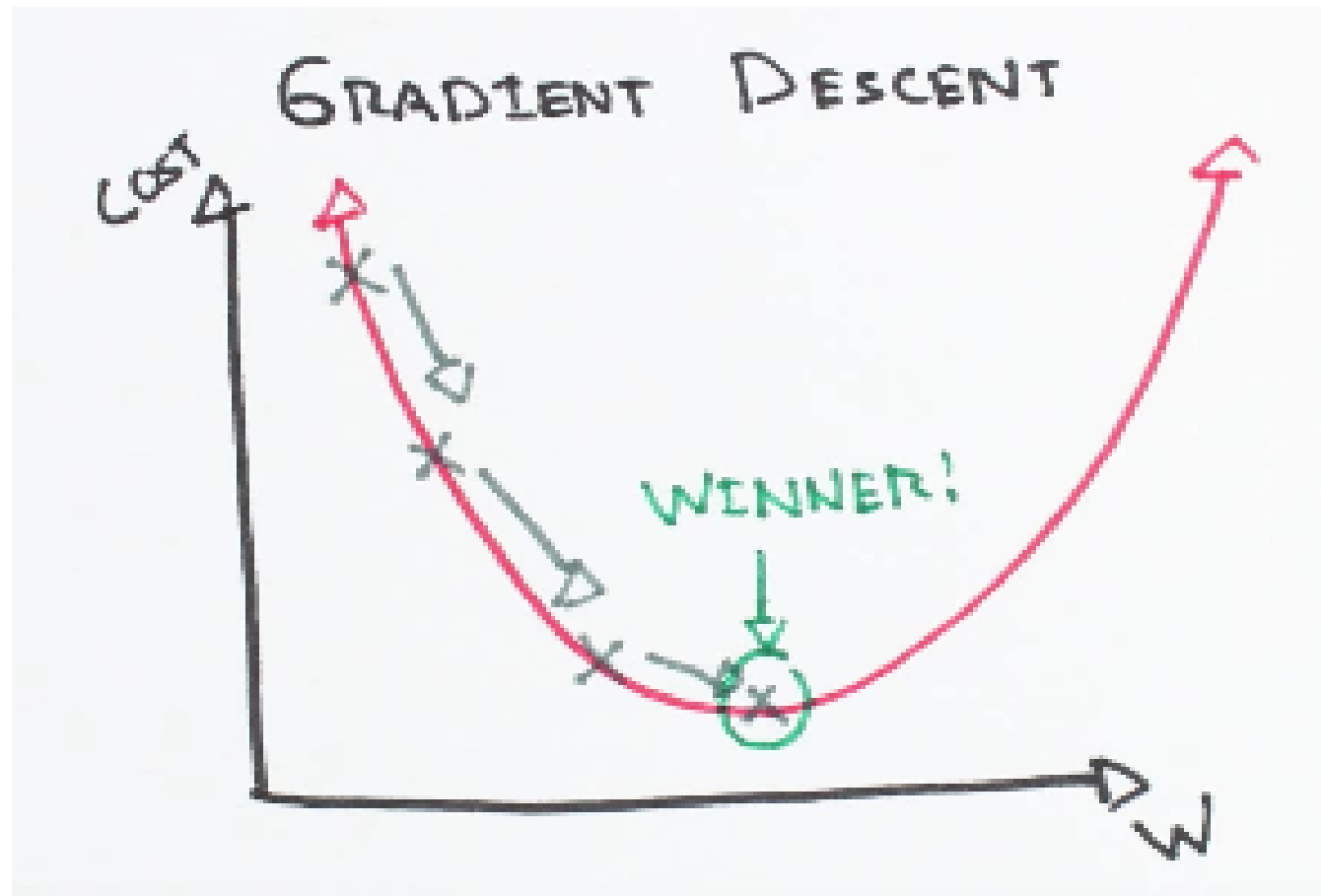
- To optimize the parameters on a training set, maximize the likelihood

$$L = \prod_{i=1}^{n_1} p(\mathbf{x}_i^{(1)} | \omega_1) \prod_{j=1}^{n_2} p(\mathbf{x}_j^{(2)} | \omega_2)$$

where $\mathbf{x}_i^{(j)}$ is the i -th object from class j

- Maximization using gradient ascent
- Appears to be easier to maximize $\log(L)$
- Weights are iteratively updated as:

$$\mathbf{w}_{new} = \mathbf{w}_{old} + \eta \frac{\partial \log(L)}{\partial \mathbf{w}}$$



Optimizing the logistic classifier (2)

- Function to maximize

$$L = \prod_{i=1}^{n_1} p(\mathbf{x}_i^{(1)} | \omega_1) \prod_{j=1}^{n_2} p(\mathbf{x}_j^{(2)} | \omega_2)$$

- Use $\log(L)$

$$\log(L) = \sum_{i=1}^{n_1} \log(p(\mathbf{x}_i^{(1)} | \omega_1)) + \sum_{j=1}^{n_2} \log(p(\mathbf{x}_j^{(2)} | \omega_2))$$

- Use Bayes' theorem

$$\log p(\mathbf{x}_i^{(1)} | \omega_1) = \log p(\omega_1 | \mathbf{x}_i^{(1)}) - \log p(\omega_1) + \log p(\mathbf{x}_i^{(1)})$$

- Therefore

$$\log(L) = \sum_{i=1}^{n_1} \log(p(\omega_1 | \mathbf{x}_i^{(1)})) + \sum_{j=1}^{n_2} \log(p(\omega_2 | \mathbf{x}_j^{(2)})) + C$$

constant

Optimizing the logistic classifier (3)

- Filling in that

$$p(\omega_2|\mathbf{x}) = \frac{1}{1 + \exp(\mathbf{w}^T \mathbf{x} + w_0)}$$

gives

$$\log(L) = \sum_{i=1}^{n_1} (w_0 + \mathbf{w}^T \mathbf{x}_i^{(1)}) - \sum_{j=1}^{n_1 + n_2} \log(1 + \exp(w_0 + \mathbf{w}^T \mathbf{x}_j))$$

Derivative of the log-likelihood

- The gradient of $\log(L)$ is

$$\frac{\partial \log(L)}{\partial w_0} = n_1 - \sum_{i=1}^{n_1+n_2} p(\omega_1 | \mathbf{x}_i)$$

$$\frac{\partial \log(L)}{\partial w_j} = \sum_{i=1}^{n_1} (\mathbf{x}_i^{(1)})_j - \sum_{i=1}^{n_1+n_2} p(\omega_1 | \mathbf{x}_i) (\mathbf{x}_i)_j, j=1, \dots, p$$

- Take initial values: $w_0=0, \mathbf{w}=\mathbf{0}$
- Keep iterating $\mathbf{w}_{new} = \mathbf{w}_{old} + \eta \frac{\partial \log(L)}{\partial \mathbf{w}}$

till convergence

Bayes' error

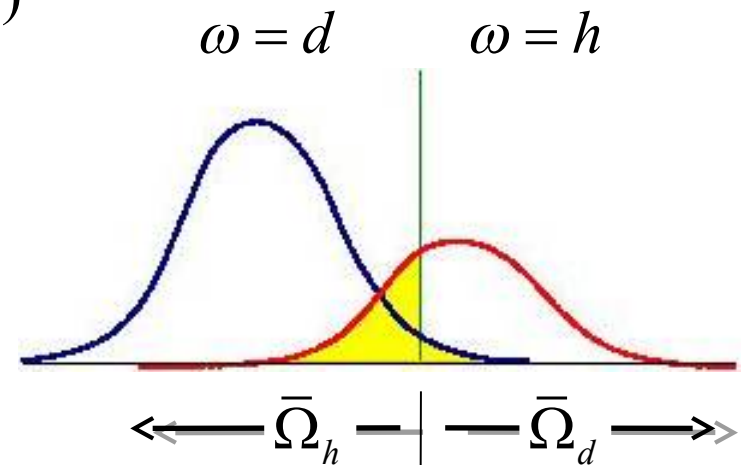
- The error we make can be described as

$$p(\text{error}) = \sum_{c=1}^C p(\text{error} \mid \omega = c) p(\omega = c)$$

- For a single class:

$$p(\text{error} \mid \omega = c) = \int_{\bar{\Omega}_c} p(x \mid \omega = c) dx$$

where $\bar{\Omega}_c$ is the complement of the region Ω_c in which objects are assigned to class c

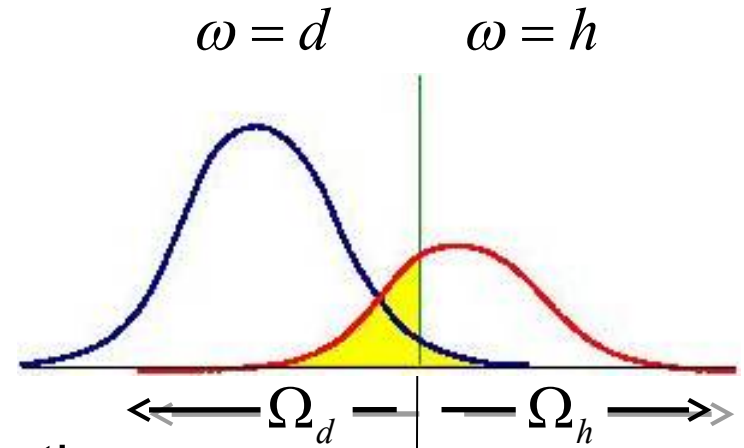


Bayes' error (2)

- Minimizing $p(\text{error})$ is equivalent to *maximizing*

$$\sum_{c=1}^C \int_{\Omega_c} p(x | \omega = c) p(\omega = c) dx$$

i.e. the probability of correct classification

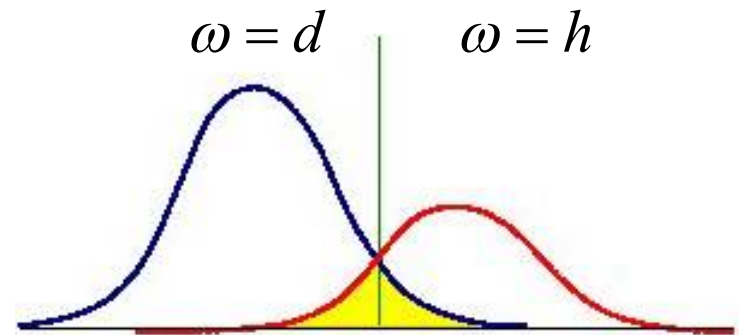


- At every x , pick class label ω s.t. the above integral is maximal:

$$c_{opt} = \arg \max_c p(x | \omega = c) p(\omega = c)$$

- Bayes' error:

$$e = 1 - \int \max_c p(x | \omega = c) p(\omega = c) dx$$



Misclassification error

- What is...
 - the maximum error for a problem with C classes?
 - the error of a rather dumb classifier, labeling all data to class c ?
 - the error of this classifier for a 10-class problem, with equal class priors?

Misclassification error

- What is...
 - the maximum error for a problem with C classes?
 - the error of a rather dumb classifier, labeling all data to class c ?
 - the error of this classifier for a 10-class problem, with equal class priors?

Bayes' risk

- Conditional risk of assigning object x to class c' :

$$r(\omega = c' | x) = \sum_{c=1}^C \Lambda(\omega = c', \omega = c) p(\omega = c | x)$$

- Average risk over class c' :

$$\begin{aligned} r(\omega = c') &= \int_{\Omega_{c'}} r(\omega = c' | x) p(x) dx \\ &= \int_{\Omega_{c'}} \sum_{c=1}^C \Lambda(\omega = c', \omega = c) p(\omega = c | x) p(x) dx \end{aligned}$$

- Overall expected risk (at every x):

$$R = \sum_{c'=1}^C r(\omega = c') = \sum_{c'=1}^C \int_{\Omega_{c'}} \sum_{c=1}^C \Lambda(\omega = c', \omega = c) p(\omega = c | x) p(x) dx$$

Bayes' risk (2)

- Overall expected risk is minimized if class label c' is chosen s.t.

$$c_{opt} = \arg \min_{c'} \sum_{c=1}^C \Lambda(\omega = c', \omega = c) p(\omega = c | x) p(x)$$

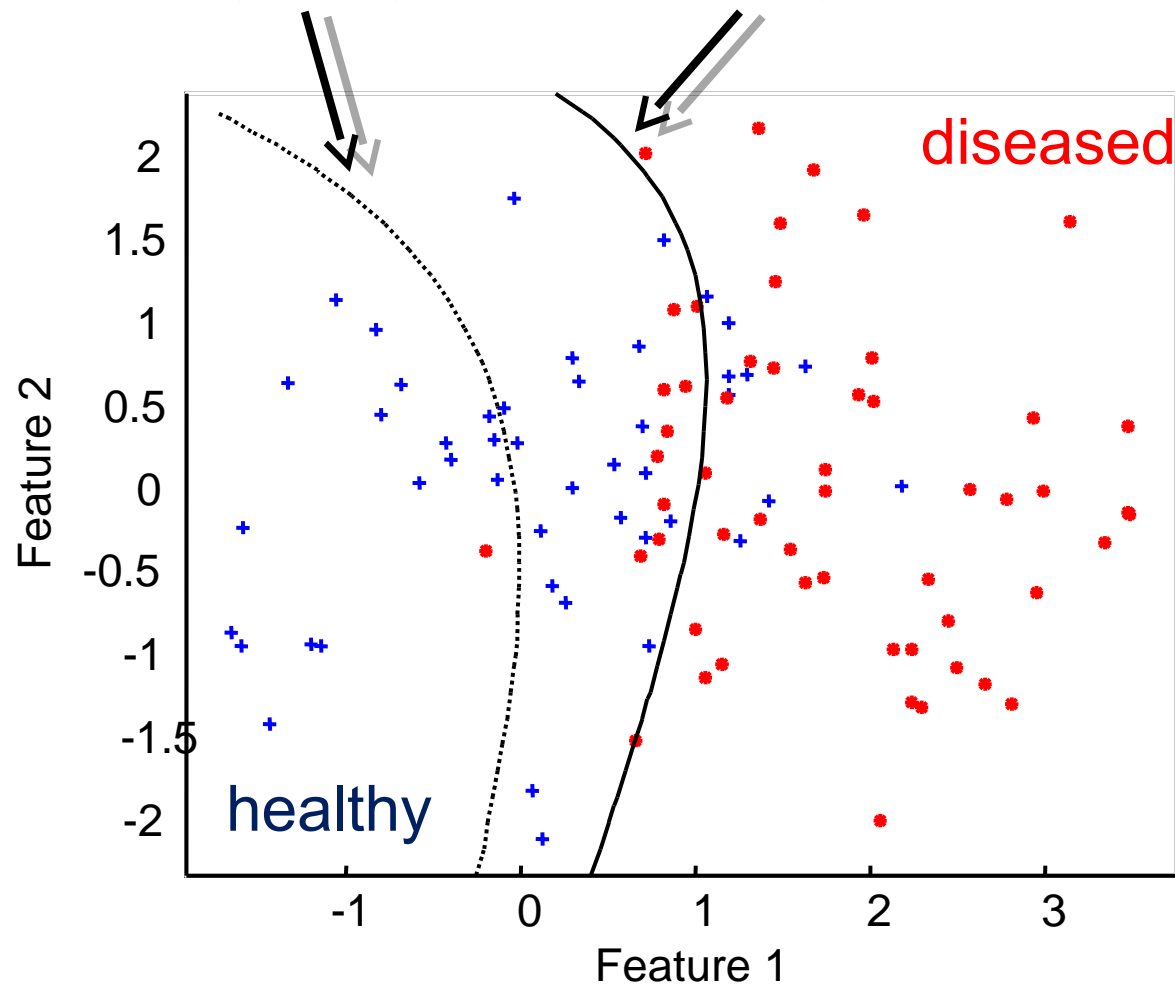
- For equal cost $\Lambda(.,.)$ this is identical to Bayes' rule for minimum error
- The minimum overall risk then is:

$$r^* = \int \min_{c'} \sum_{c=1}^C \Lambda(\omega = c', \omega = c) p(\omega = c | x) p(x) dx$$

Example

$$\Lambda = \begin{pmatrix} h & d \\ 0 & 10 \\ 1 & 0 \end{pmatrix}$$

$$\Lambda = \begin{pmatrix} h & d \\ 0 & 1 \\ 1 & 0 \end{pmatrix}$$



Reject option

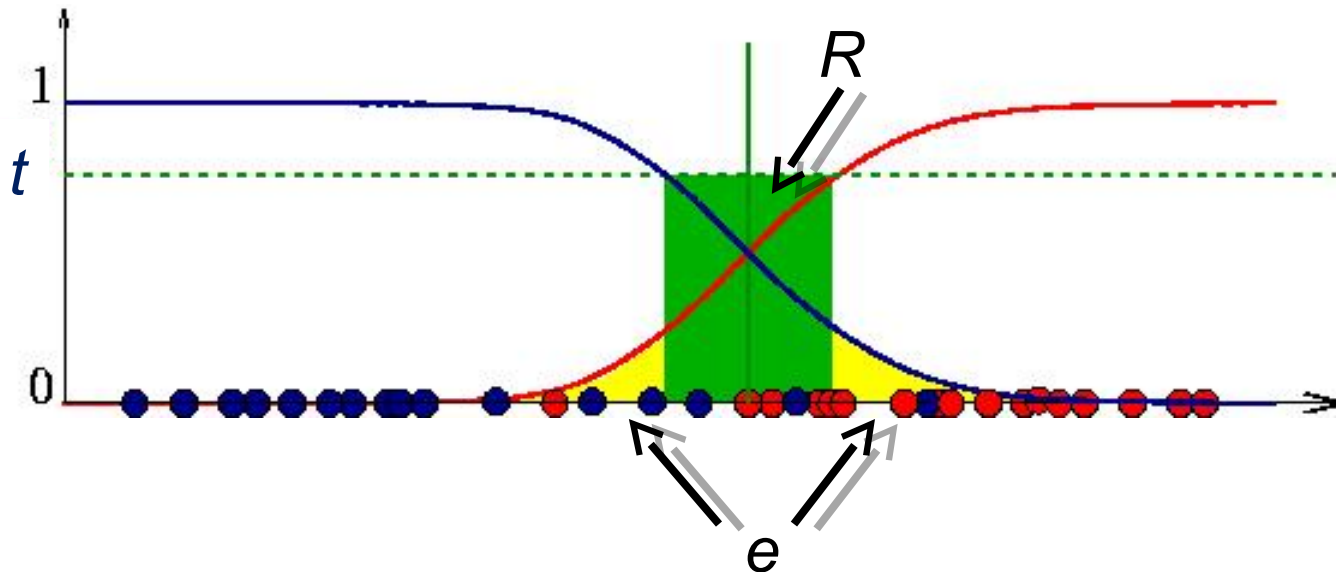
- Reject classification of objects with insufficient certainty (too low confidence in any class assignment)
- The reject area R can be written as:

$$R = \{x \mid \max_c p(\omega = c \mid x) < t\}$$

- Rejected objects should be classified by an expert, or by another classifier
- In Bayesian estimation, the reject option can be modeled as an additional class with certain (high) misclassification cost

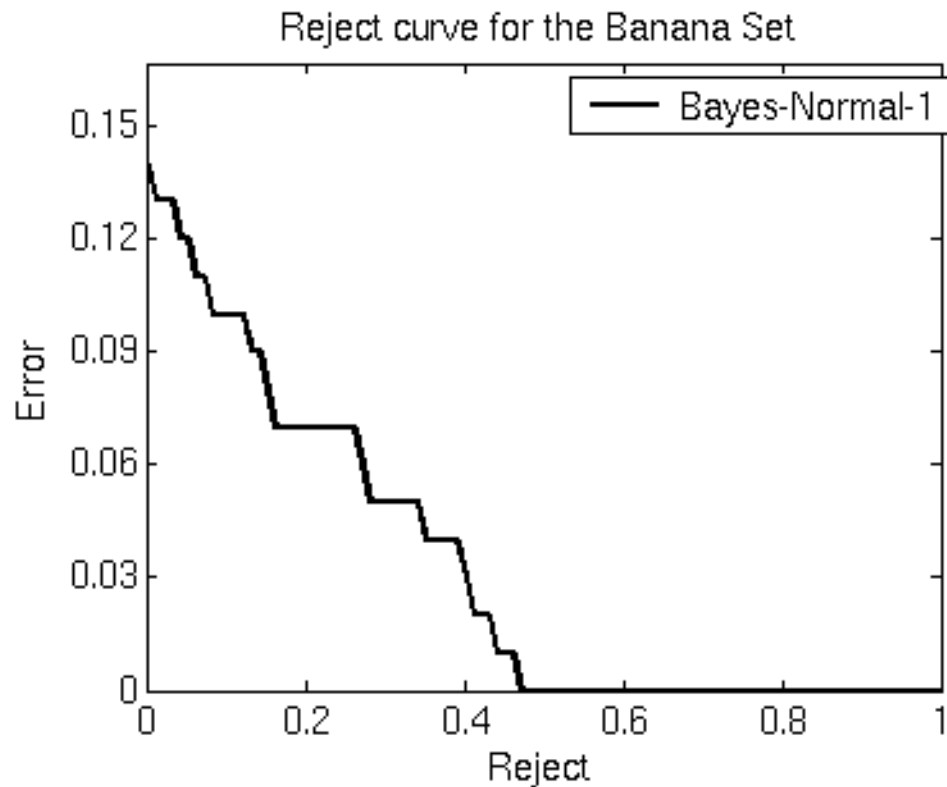
Reject option (2)

- Define the threshold t
- Reject all objects in the green area R
- Objects in the yellow area are still errors



Error-reject curve

- By changing the threshold t , the error decreases, but the percentage rejected increases



Recapitulation

- For classification we want the posterior $p(\omega|\mathbf{x})$
- We can approximate the posterior directly: logistic classifier
- Assigning an object to the class with maximum posterior probability gives the Bayes classifier
- Bayes classifier is the optimal classifier
- The Bayes' error is the smallest error attainable
- The Bayes' risk is the smallest risk attainable

10min break

Exercises 2.1-2.7

Discord

Lecture room:	Channel where lectures are given
Meeting room:	Channel where general meetings can take place
Chill room:	Channel to hang-out
TA-X-room:	Channel where assistants are online You can enter and start discussion/question Do see whether other people are already there
Chat-XX:	Chat room for a group
Room-XX:	Channel for a group

Plug-in Bayes classification

- In many cases the posterior is hard to estimate
- Often a functional form of the class distributions can be assumed
- Use Bayes' theorem to rewrite one into the other:

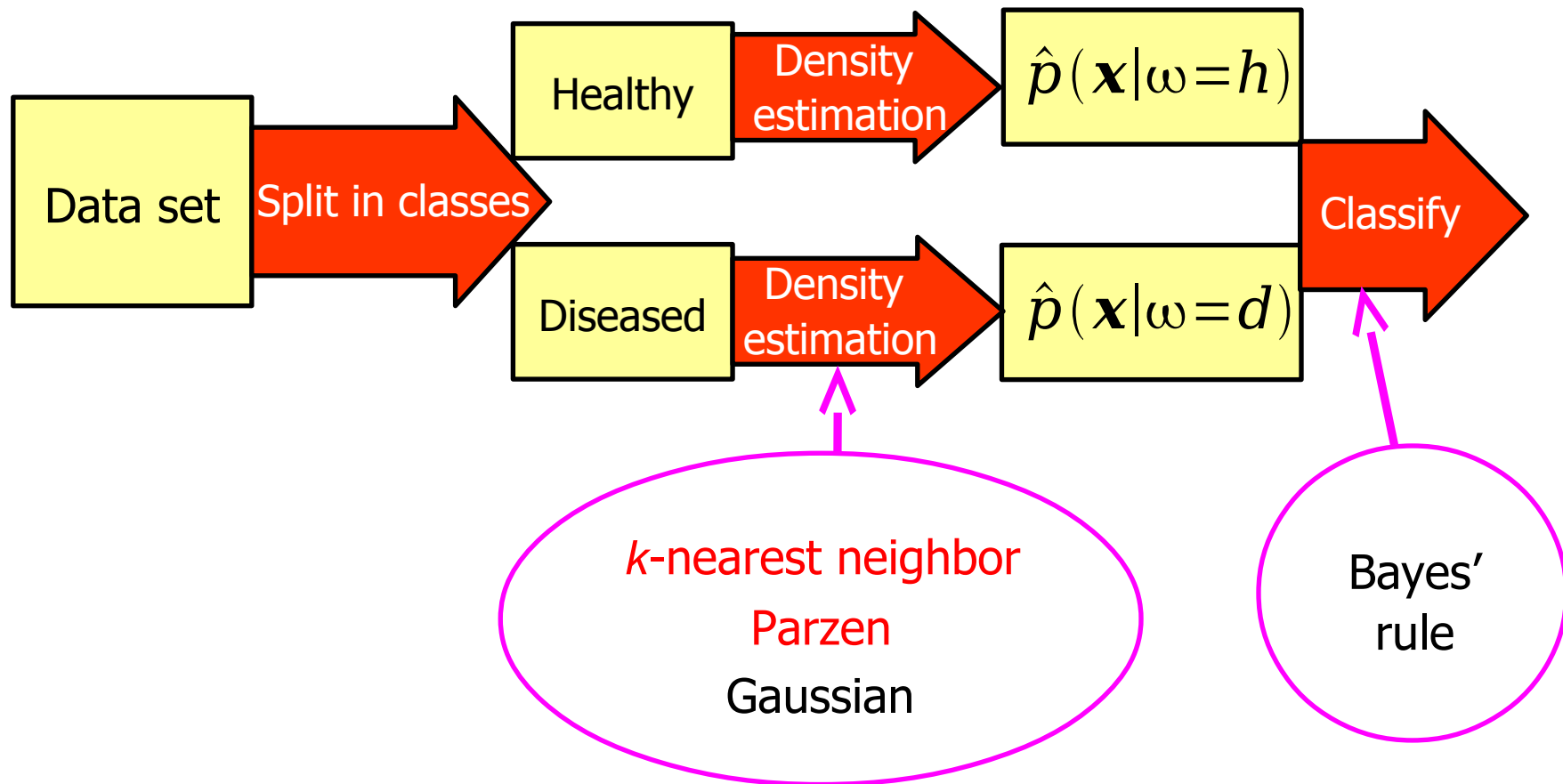
$$p(\omega|\mathbf{x}) = \frac{p(\mathbf{x}|\omega) p(\omega)}{p(\mathbf{x})}$$

class-conditional distribution: $p(\mathbf{x}|\omega)$

prior distribution: $p(\omega)$

data distribution: $p(\mathbf{x})$

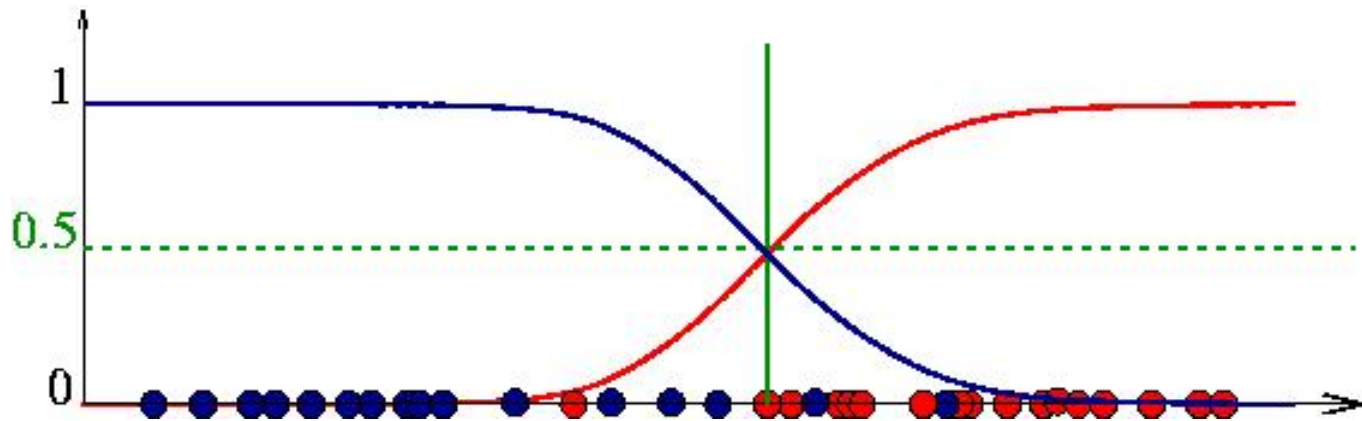
Plug-in Bayes classification (2)



Plug-in Bayes classification (3)

- For each object we estimate $p(\omega=c|\mathbf{x})$ using Bayes' rule

$$p(\mathbf{x}|\omega=h)p(\omega=h) > p(\mathbf{x}|\omega=d)p(\omega=d)$$

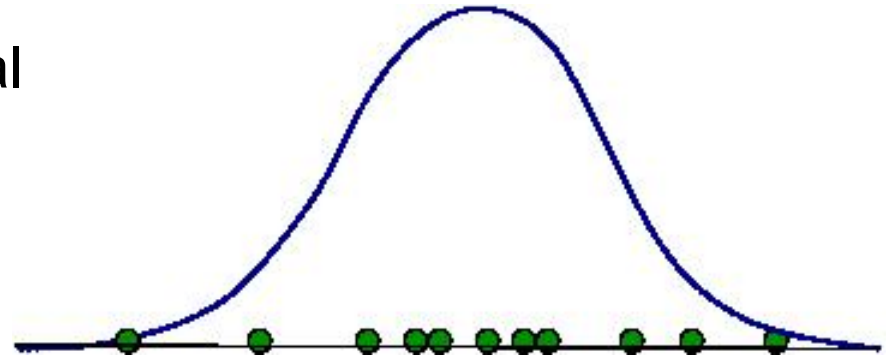


$$p(\mathbf{x}|\omega=d)p(\omega=d) > p(\mathbf{x}|\omega=h)p(\omega=h)$$

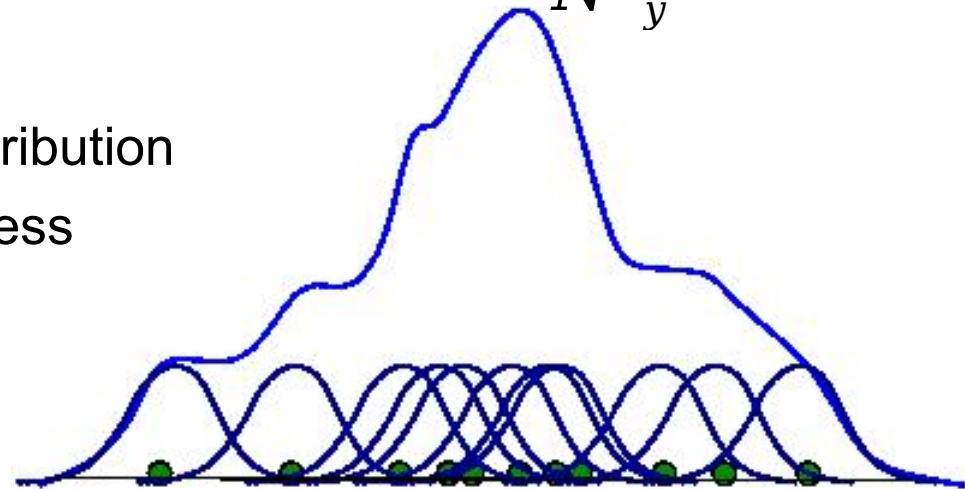
Bayes decision making

$$\hat{p}(\mathbf{x}|\omega_i) = N(\mathbf{x}; \mu, \sigma)$$

- Estimate the class-conditional density (Day 1) $\hat{p}(\mathbf{x}|\omega_i)$
- Parametric
 - Known distribution
 - Estimate parameters on training set
- Non-parametric
 - No knowledge on distribution
 - Manage the smoothness of the distribution



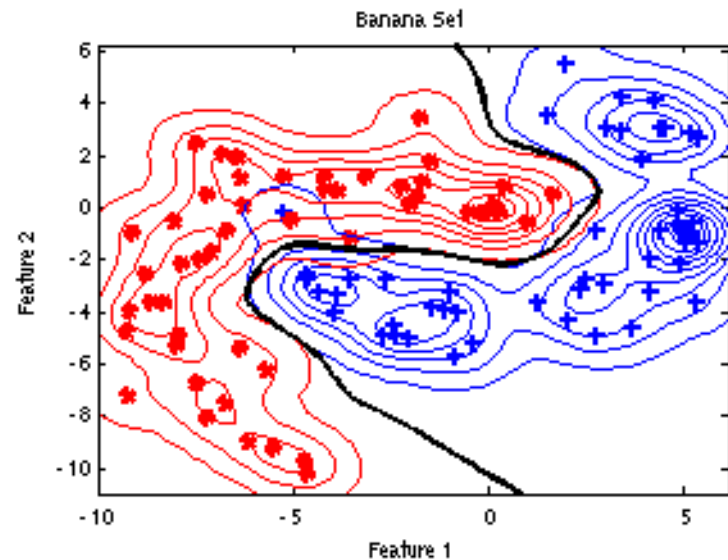
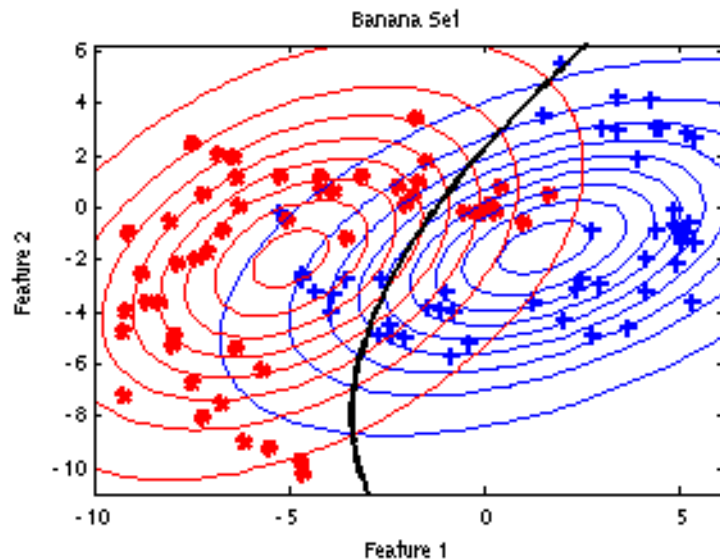
$$\hat{p}(\mathbf{x}|\omega_i) = \frac{1}{N} \sum_y K(\mathbf{x}, \mathbf{y})$$



Example plugin

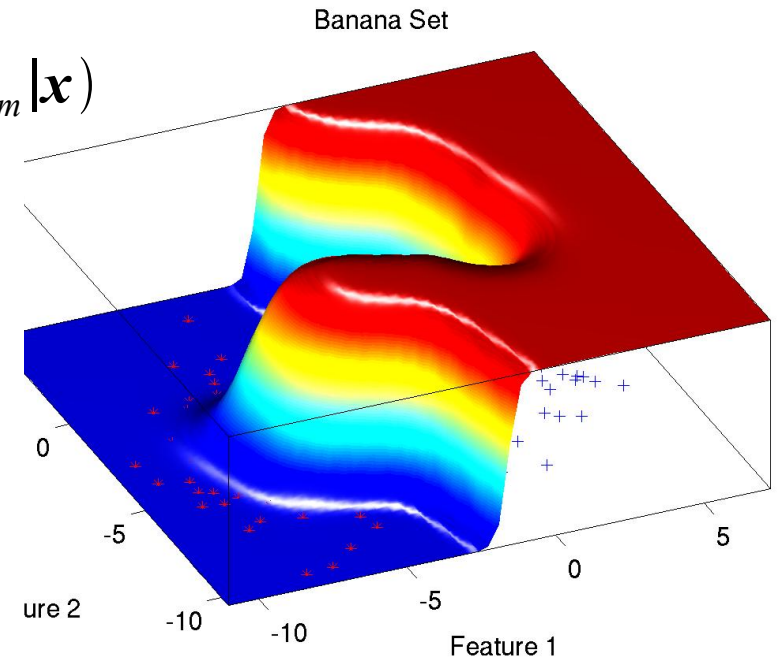
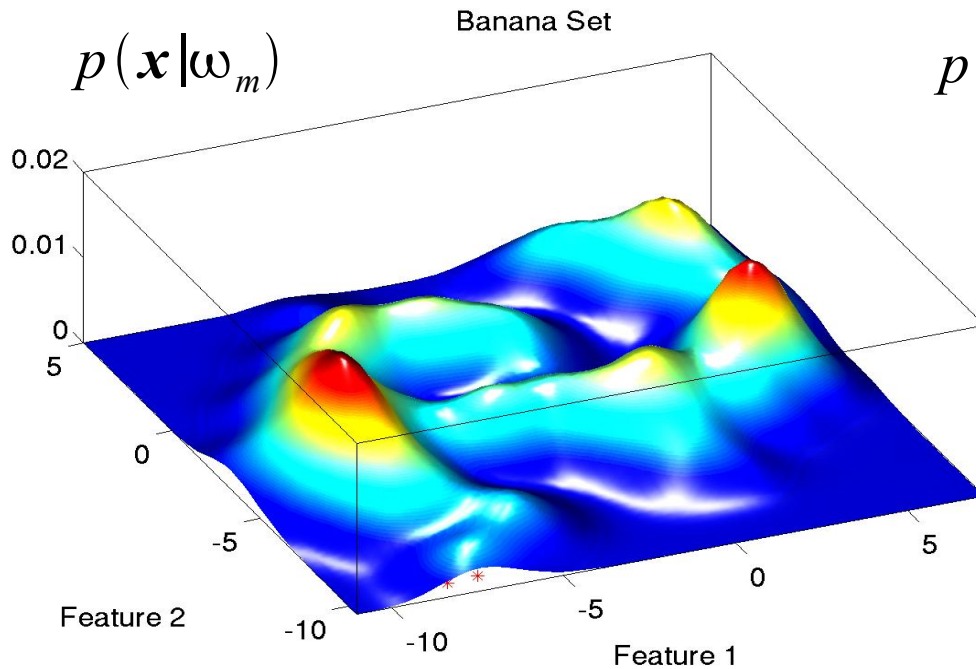
- Two examples

Normal density estimation Parzen density estimation



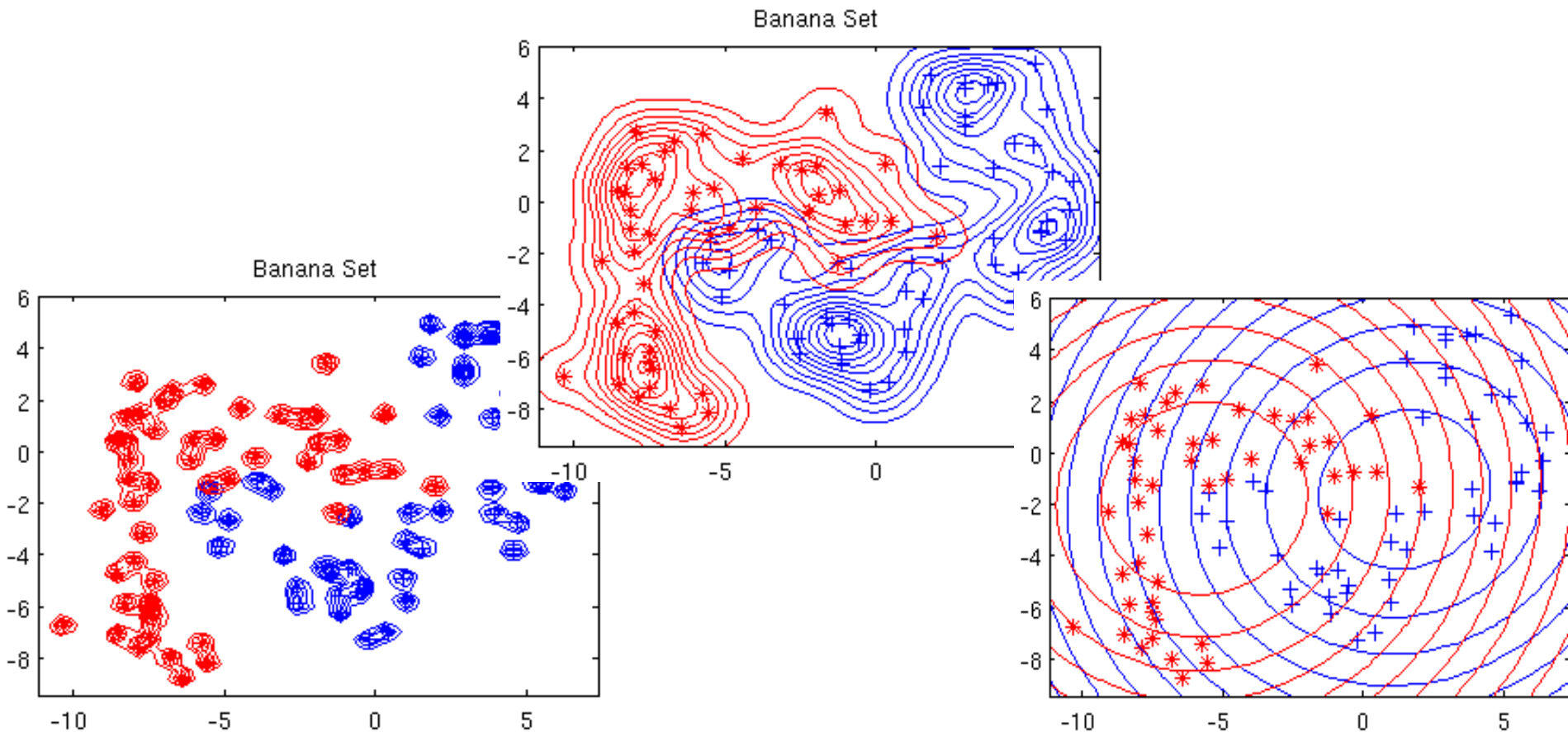
Parzen classifier

$$p(\mathbf{x}|\omega_m) = \frac{1}{N} \sum_{i=1}^{N_m} N(\mathbf{x}; \mathbf{x}_i, h\mathbf{I})$$



Parzen width parameter

- The width parameter h has a large influence



Optimization of h

- Use the average k -nearest neighbor distance ($k=10$ is suggested...)

- Use a heuristic
$$h = \sigma \left(\frac{4}{p+2} \right)^{\frac{1}{p+4}} n^{\frac{-1}{p+4}}$$

$$\sigma^2 = \frac{1}{p} \sum_{i=1}^p s_{ii}$$

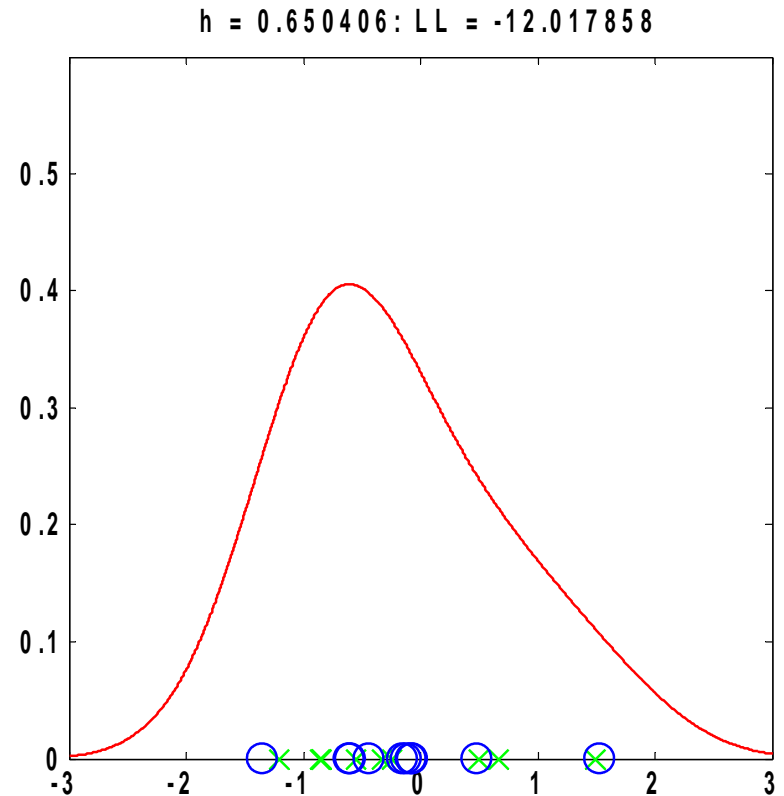
- Optimize the likelihood using cross-validation

$$\prod_{i=1}^n \hat{p}(\mathbf{x}_i)$$

- and more...

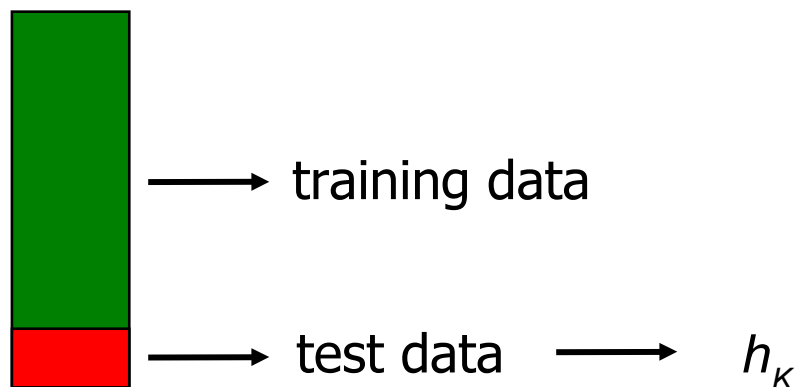
Cross-validation

- Scheme:
 - Split data into *training set* and *test set*
 - Optimise h w.r.t. likelihood of test set, given Parzen model trained on training set
- Problems:
 - Uses a lot of valuable data
 - Sensitive to split of data



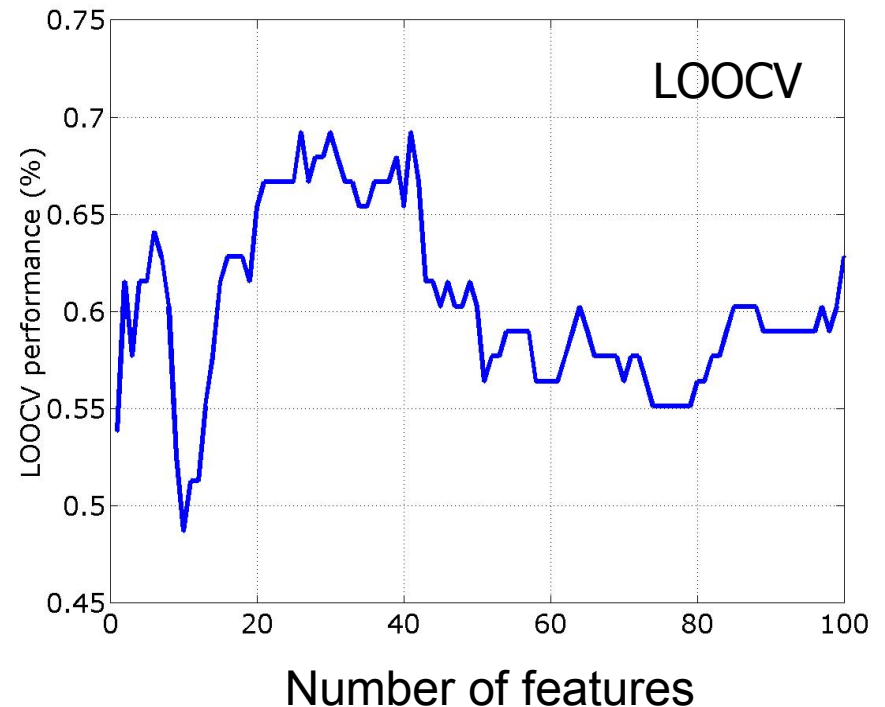
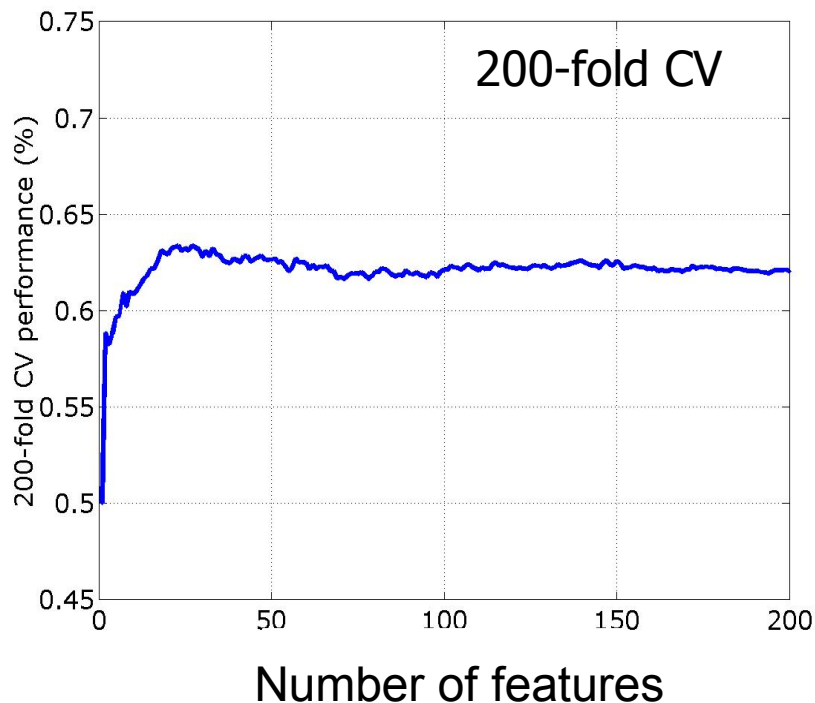
Cross-validation (2)

- Better solution: K -fold crossvalidation
 - Split data into K parts ($K = n$: leave-one-out)
 - Repeat K times:
 - Find h using $(K - 1)$ parts for training and 1 part for testing
 - Use average of h 's as kernel width



Cross-validation (3)

- Prefer K -fold cross-validation over leave-one-out
 - Smoother (less variance) and more biased (conservative)



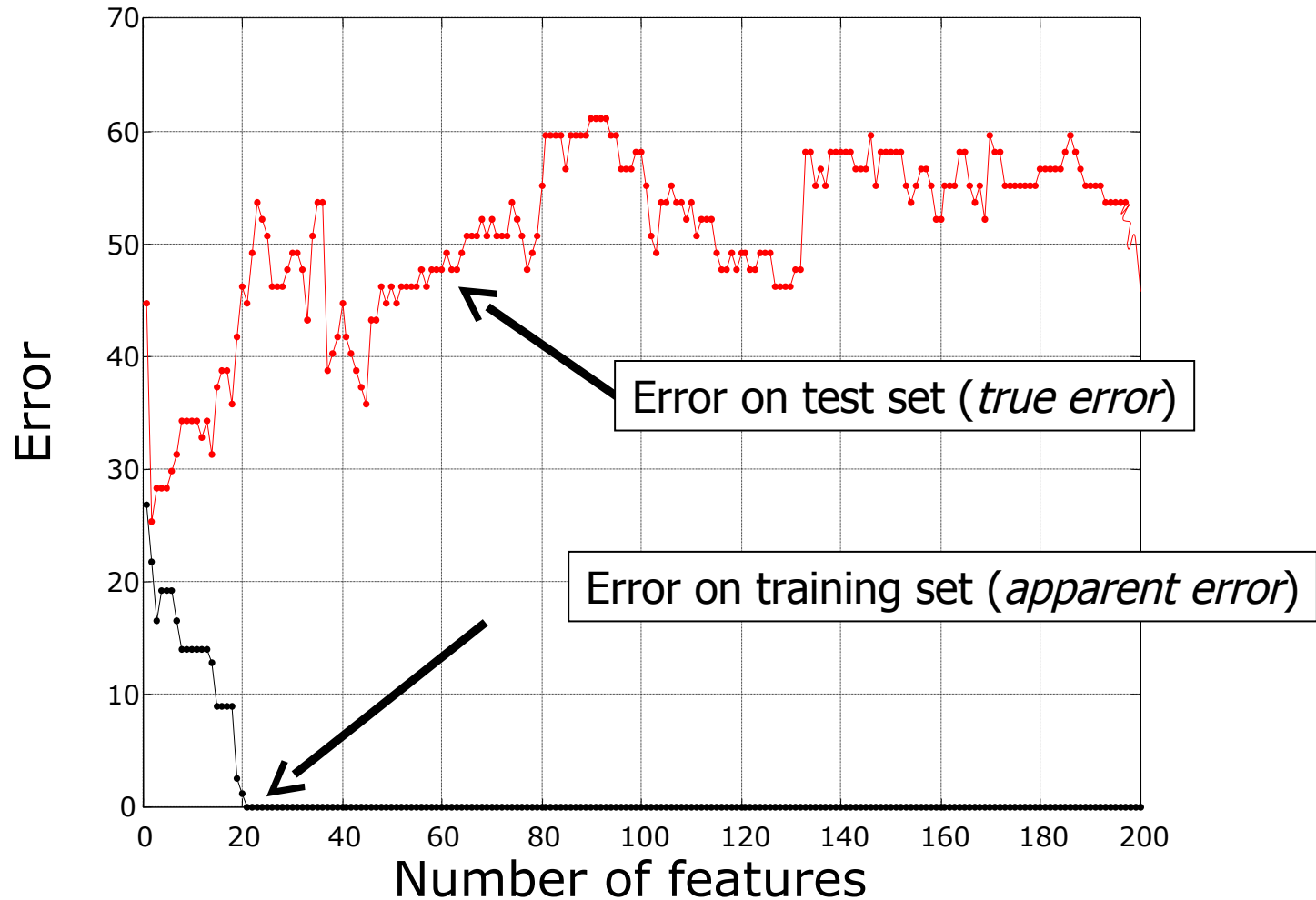
Bootstrap

- Alternative to cross-validation:
 - Repeat K times:
 - Draw n objects from the dataset, with replacement (some objects will be selected more than once)
 - Test using objects that were not selected
- Cross-validation and bootstrap estimates are *biased*
 - They are conservative (i.e. too pessimistic) because they do not use all data available

Training, validation and test sets

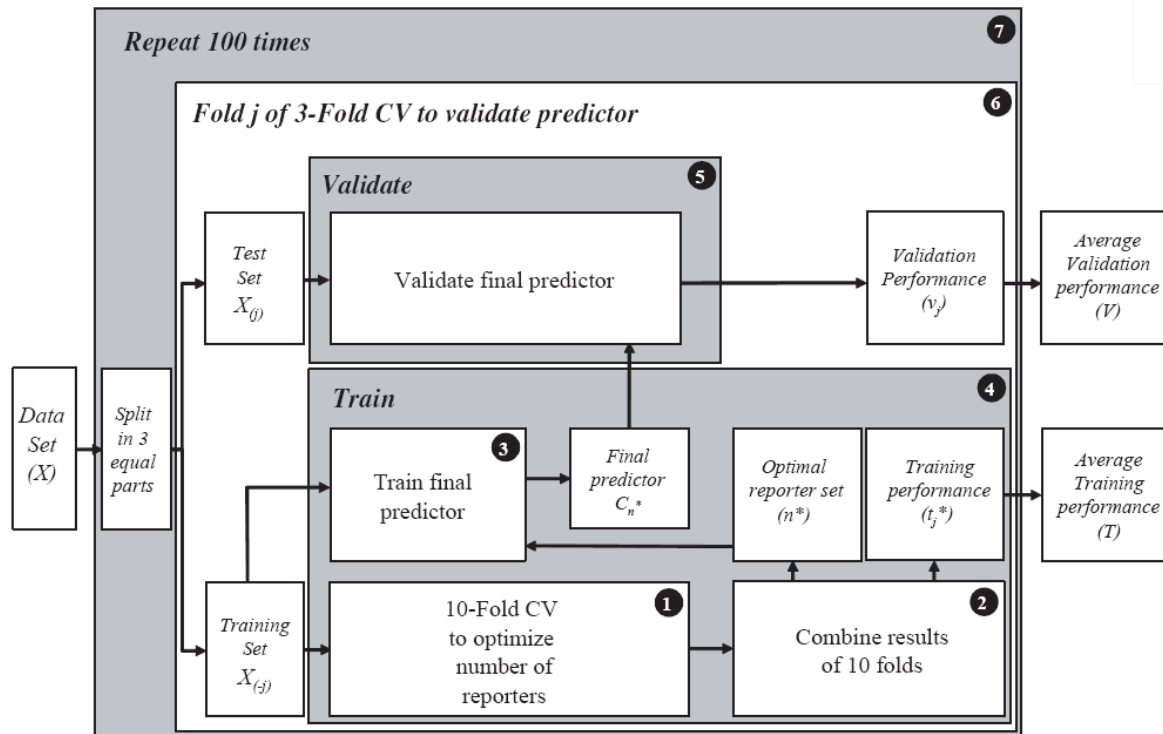
- Terminology:
 - A *training set* is used to estimate parameters
 - An optional *validation set* is used to optimise parameter settings, e.g. by calculating classifier error on this set
 - A *test set* is only used to judge performance of the entire classifier
- Error estimates:
 - On training set: *apparent error*
 - On test set: *true error*
- The test set should *never* be used to set any parameters!
This leads to biased estimates of performance -- in practice we may do much worse than we predict

Training, validation and test sets (2)

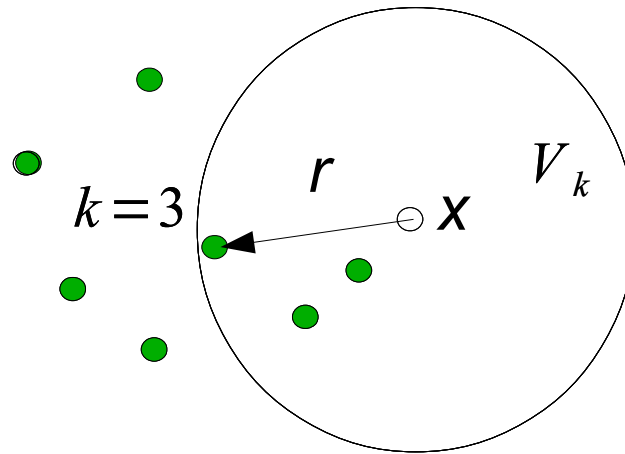


Training, validation and test sets (3)

- Can lead to complicated schemes for estimating parameters, e.g. double cross-validation loops



Nearest neighbor classification

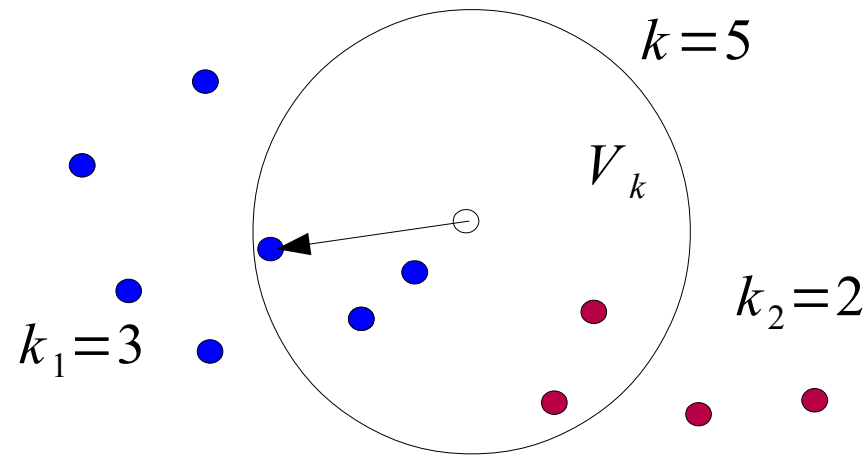


- For the k-nearest neighbor density we defined:

$$\hat{p}(\mathbf{x}) = \frac{k}{n V_k}$$

where V_k is the volume of the sphere centered at x , with radius r the distance to the k -th nearest neighbor

Nearest neighbor classification (2)



- When more classes are present, count how many objects of each of the classes are members of the k neighbors
- Class-conditional density:

$$\hat{p}(\mathbf{x}|\omega_m) = \frac{k_m}{n_m V_k}$$

Nearest neighbor classification (3)

- Using Bayes: $\hat{p}(\mathbf{x}|\omega_m) \hat{p}(\omega_m) \geq \hat{p}(\mathbf{x}|\omega_i) \hat{p}(\omega_i)$

- Estimate the prior probability by counting:

$$\hat{p}(\omega_m) = \frac{n_m}{n}$$

- Fill in:

$$\frac{k_m}{n_m} \frac{n_m}{V_k} \geq \frac{k_i}{n_i} \frac{n_i}{V_k} \quad \Rightarrow \quad k_m \geq k_i$$

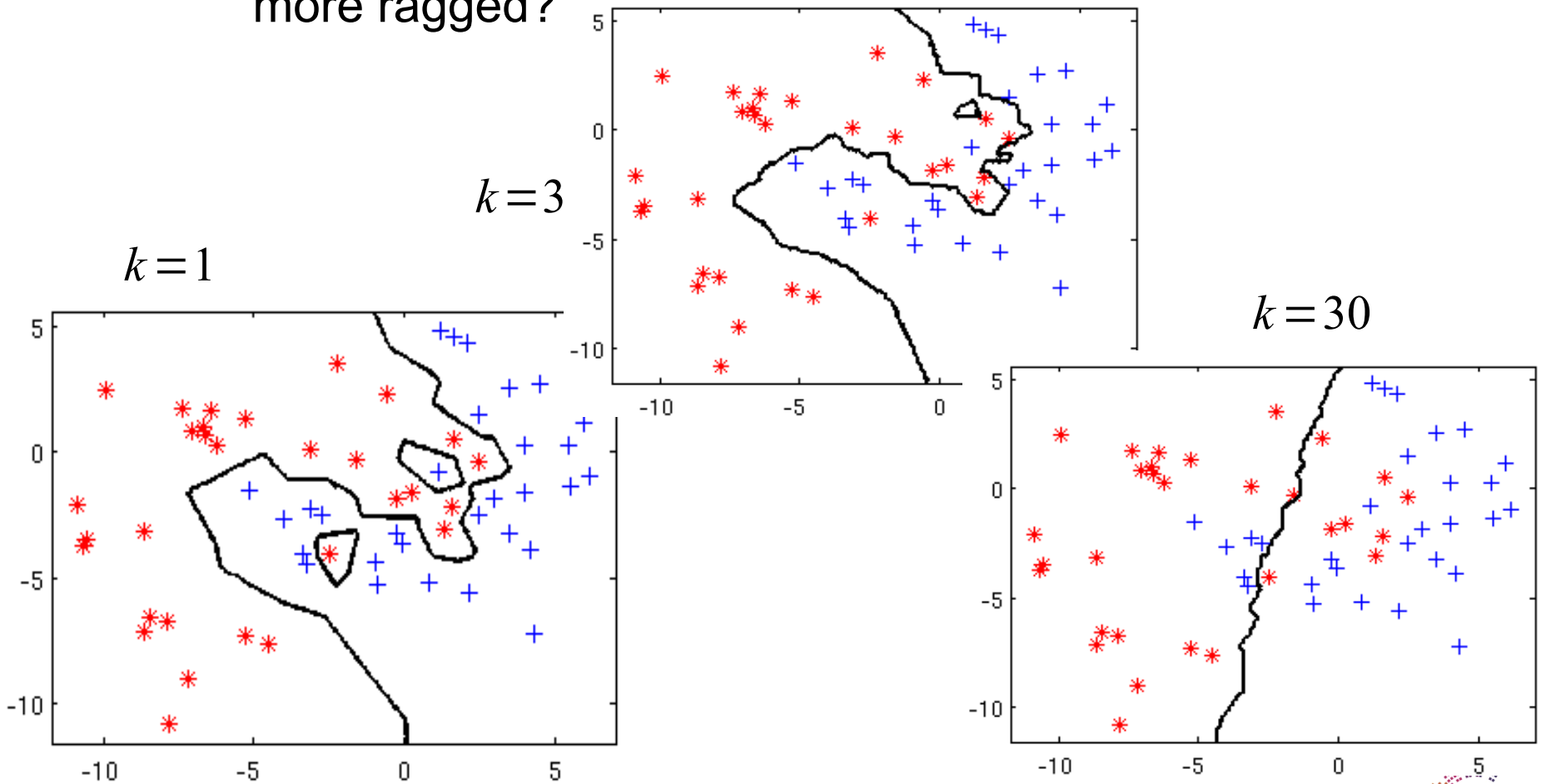
- No density estimation is needed!

The choice of k

- When does the classifier become more smooth? When more ragged?
- What happens for $k = 1$, and $k = n$?

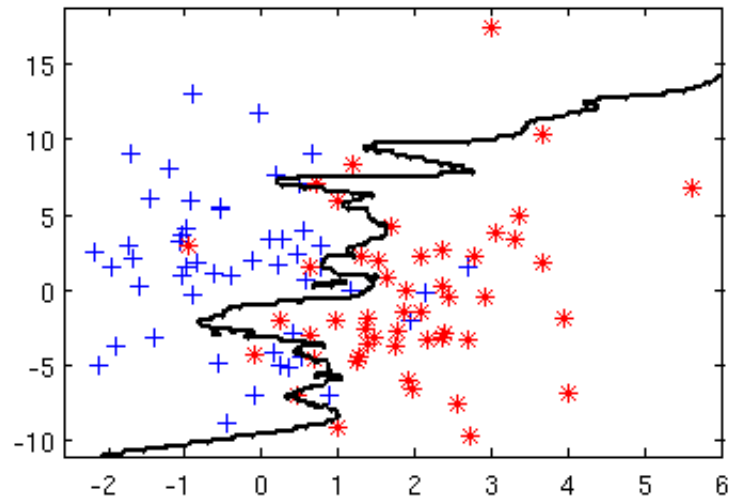
The choice of k (2)

- When does the classifier become more smooth? When more ragged?



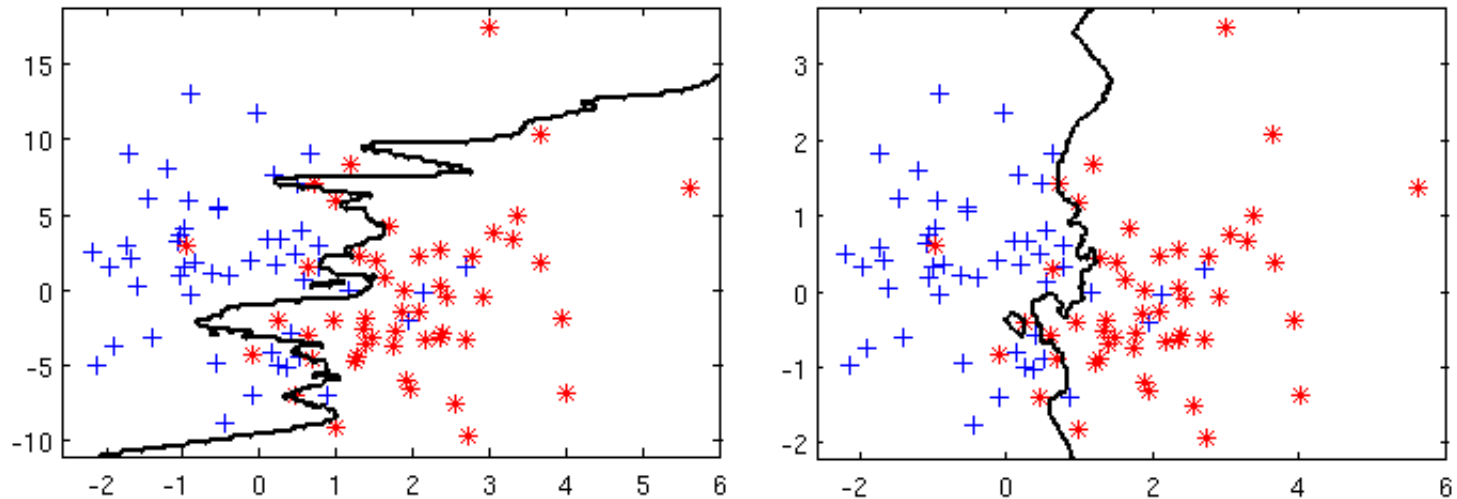
Sometimes strange results:

$$k=5$$



Sometimes strange results (2):

$k=5$

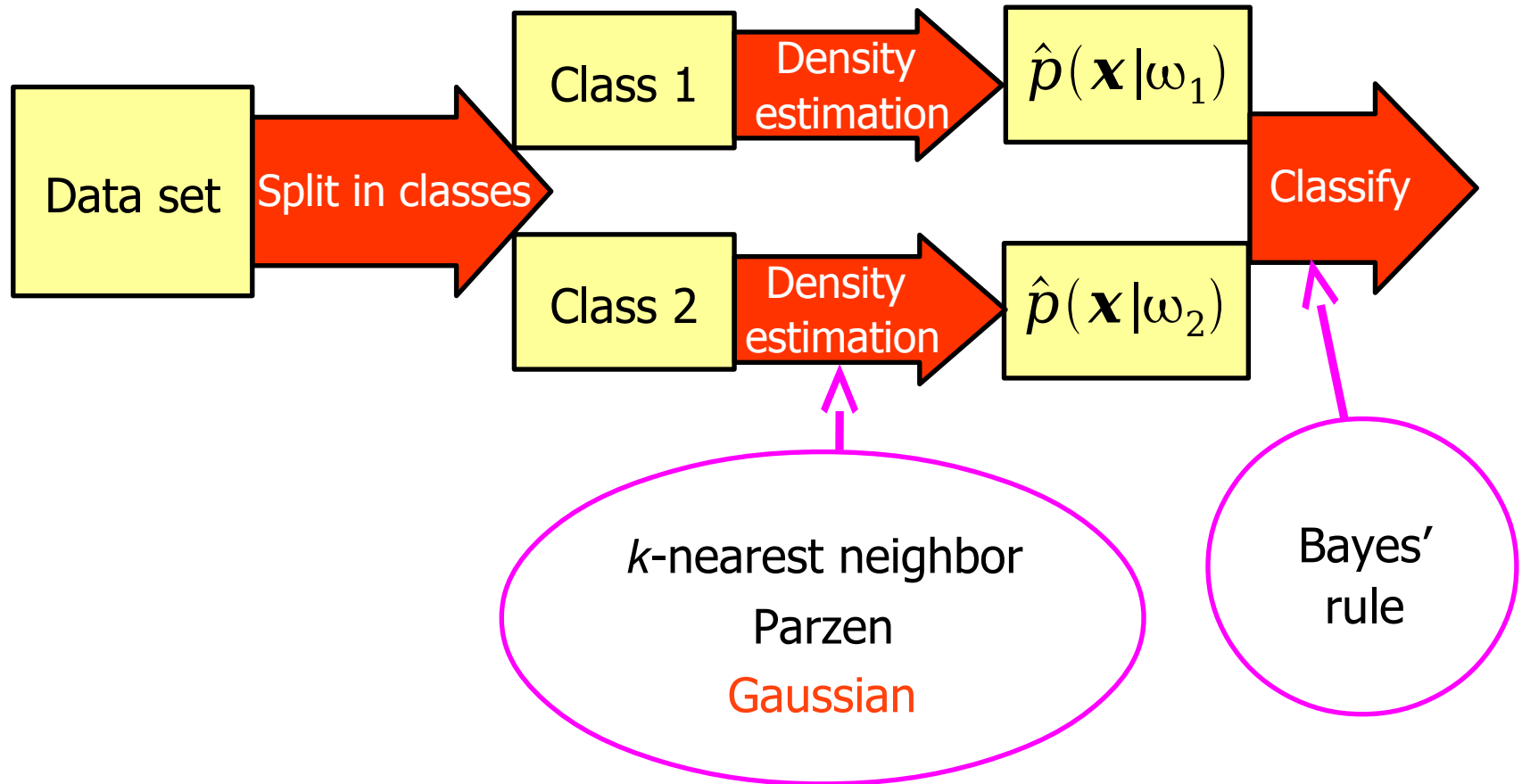


Rescaling the features has large influence!

Advantages/disadvantages

- simple and flexible classifier
- often a very good classification performance
- it is simple to adapt the complexity of the classifier
- you have to store the complete training set
- distances to all training objects have to be computed
- scaling of the features should be sensible
- you have to optimize k or h

Classifying with densities



Plug-in Gaussian distribution

- Now take the most obvious choice: the Gaussian distribution

$$\hat{p}(\mathbf{x}|\omega) = \frac{1}{\sqrt{2\pi^p \det(\hat{\Sigma}_\omega)}} \exp\left(-\frac{1}{2}(\mathbf{x} - \hat{\mu}_\omega)^T \hat{\Sigma}_\omega^{-1} (\mathbf{x} - \hat{\mu}_\omega)\right)$$

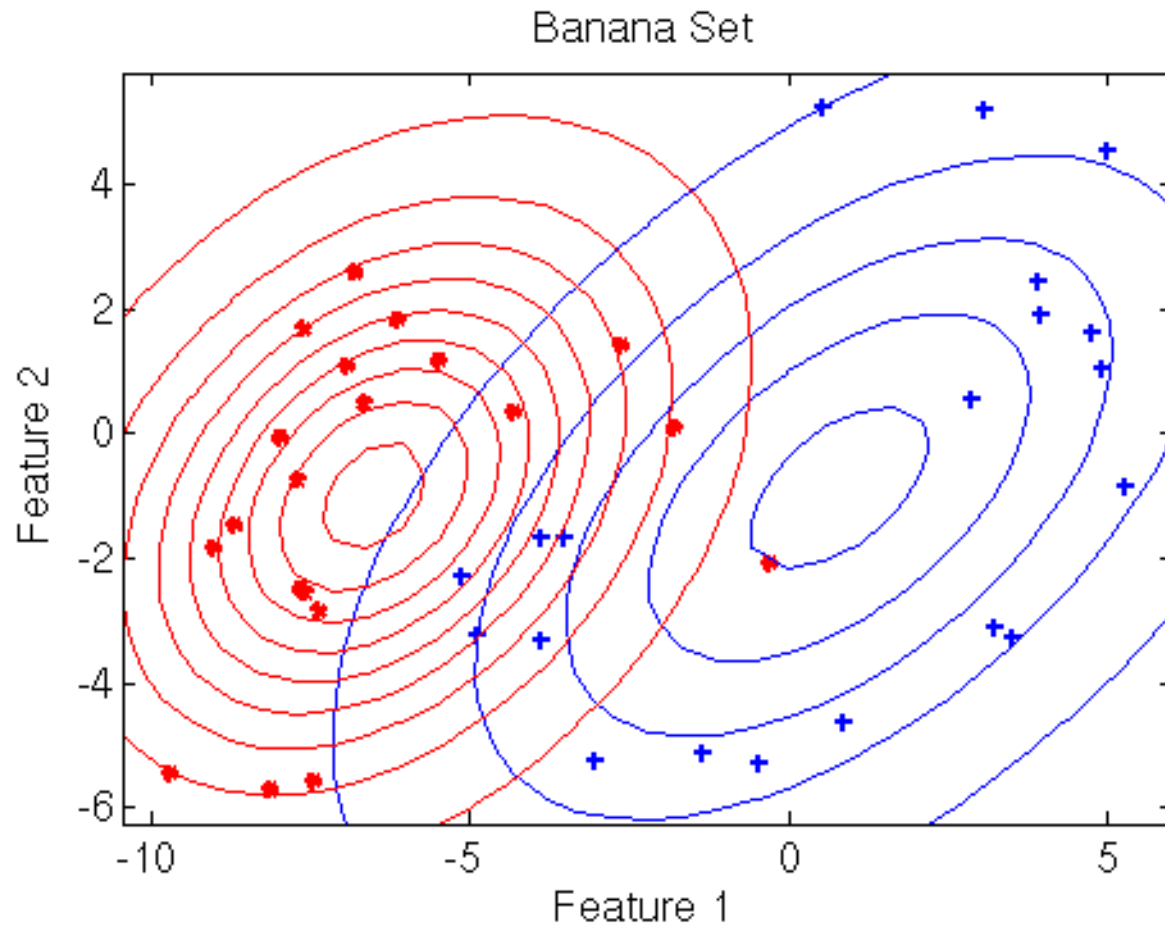
- So-called parametric density estimation
- We have to estimate the parameters via maximum likelihood:

$$\hat{\mu} = \frac{1}{n} \sum_{i=1}^n \mathbf{x}_i$$

$$\hat{\Sigma} = \frac{1}{n} \sum_{i=1}^n (\mathbf{x}_i - \hat{\mu})(\mathbf{x}_i - \hat{\mu})^T$$

Example on banana data

- A single Gaussian distribution on each class:



Class-conditional densities

- Combining

$$\hat{p}(\mathbf{x}|\omega_i) = \frac{1}{\sqrt{2\pi^p \det(\Sigma_i)}} \exp\left(-\frac{1}{2}(\mathbf{x} - \mu_i)^T \Sigma_i^{-1}(\mathbf{x} - \mu_i)\right)$$
$$p(\omega|\mathbf{x}) = \frac{p(\mathbf{x}|\omega)p(\omega)}{p(\mathbf{x})}$$

we can derive for $\log(p)$:

$$\log(\hat{p}(\omega_i|\mathbf{x})) = -\frac{p}{2}\log(2\pi) - \frac{1}{2}\log(\det \Sigma_i)$$
$$-\frac{1}{2}(\mathbf{x} - \mu_i)^T \Sigma_i^{-1}(\mathbf{x} - \mu_i) + \log(p(\omega_i)) - \log(p(\mathbf{x}))$$

Normal density-based classifier

- $p(\mathbf{x})$ is independent of the classes and can be dropped

$$g_i(\mathbf{x}) = -\frac{1}{2} \log(\det \Sigma_i) - \frac{1}{2} (\mathbf{x} - \mu_i)^T \Sigma_i^{-1} (\mathbf{x} - \mu_i) + \log(p(\omega_i))$$

- Classifier becomes:

assign x to class ω_i when for all $i \neq j$: $g_i(\mathbf{x}) > g_j(\mathbf{x})$

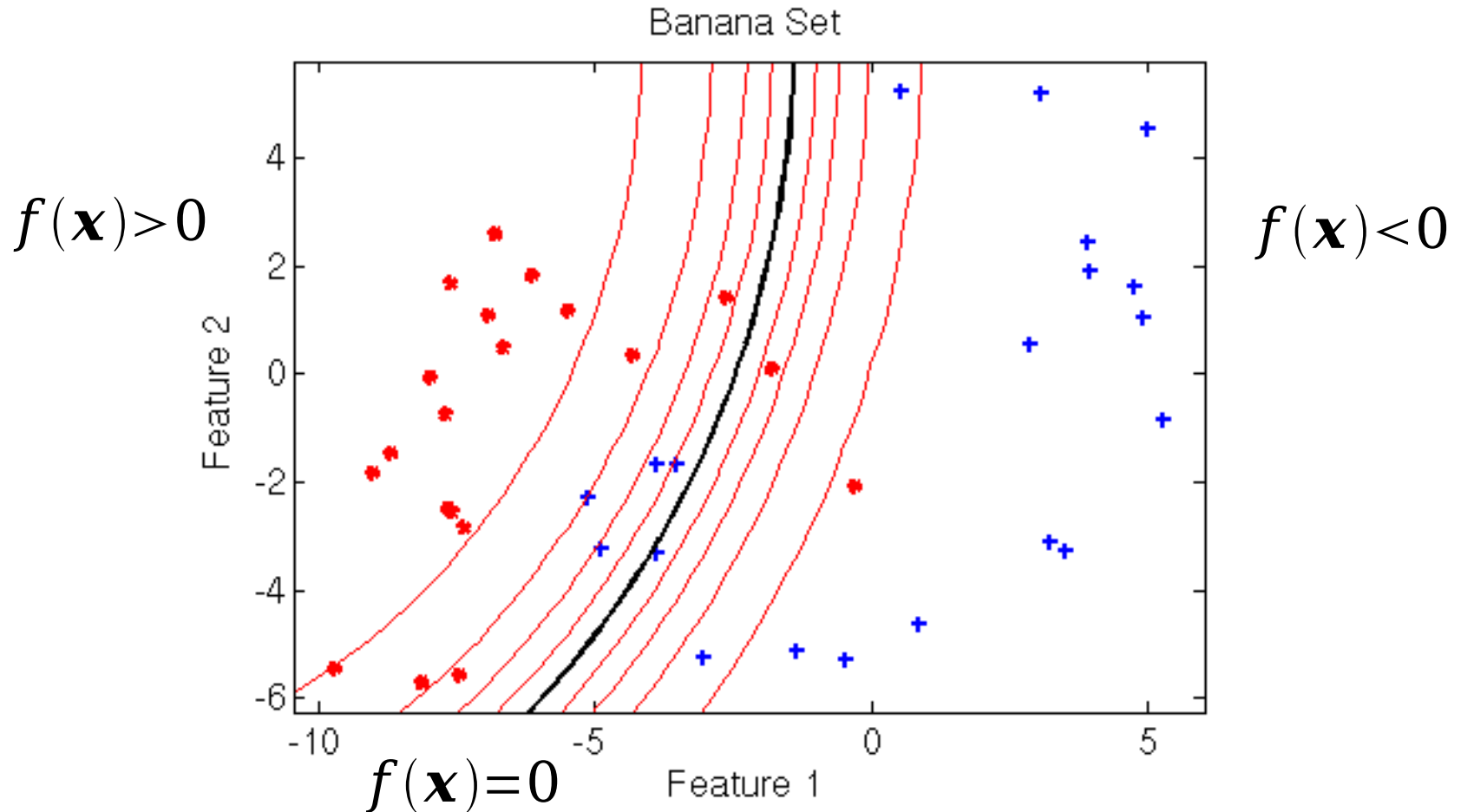
The two-class case

- Define the discriminant $f(\mathbf{x}) = p(\omega_1|\mathbf{x}) - p(\omega_2|\mathbf{x}) > 0$
- We get (laboratory exercise):

$$f(\mathbf{x}) = \mathbf{x}^T \mathbf{W} \mathbf{x} + \mathbf{w}^T \mathbf{x} + w_0$$

- This is a quadratic classifier because
the decision boundary is a quadratic function of x

Quadratic classifier on banana data



Estimating the covariance matrix

- For the quadratic classifier you need to estimate

$$\hat{\Sigma}_k = \frac{1}{n} \sum_{i=1}^n (\mathbf{x}_i - \hat{\mu}_k)(\mathbf{x}_i - \hat{\mu}_k)^T$$

for each of the classes!

- When you have insufficient data, this covariance matrix cannot be inverted
- Average over the covariance matrices of different classes:

$$\hat{\Sigma} = \frac{1}{C} \sum_{k=1}^C \hat{\Sigma}_k$$

Average covariance matrix

- When we use the averaged covariance matrix:

$$g_i(\mathbf{x}) = -\frac{1}{2} \log(\det \hat{\Sigma}) - \frac{1}{2} (\mathbf{x} - \hat{\mu}_i)^T \hat{\Sigma}^{-1} (\mathbf{x} - \hat{\mu}_i) + \log(p(\omega_i))$$

- First term and quadratic term are always the same for all classes
- We end up with:

$$g_i(\mathbf{x}) = -\frac{1}{2} \hat{\mu}_i^T \hat{\Sigma}^{-1} \hat{\mu}_i - \frac{1}{2} \hat{\mu}_i^T \hat{\Sigma}^{-1} \mathbf{x} + \log(p(\omega_i))$$

- This classifier is *linear*:
the linear normal density-based classifier.

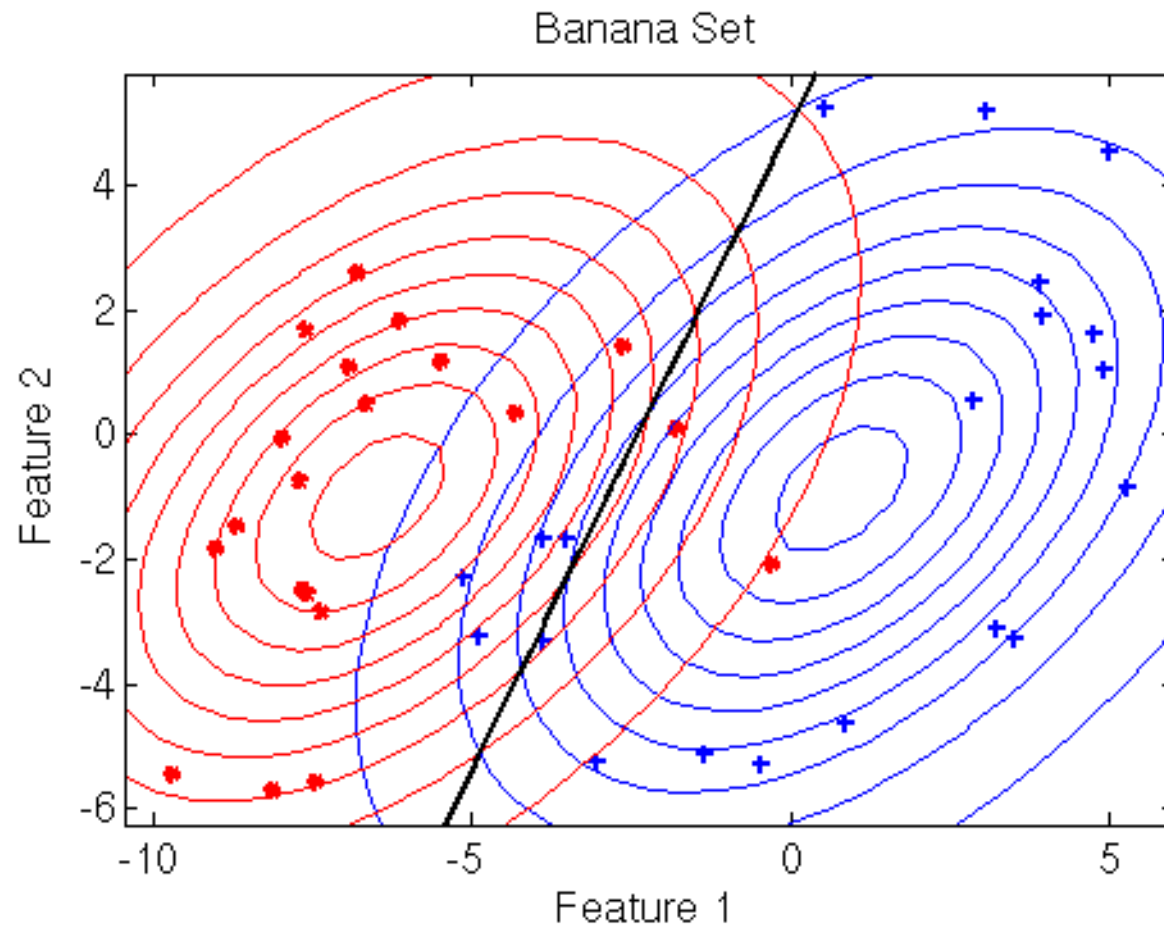
The two-class case (2)

- Define the discriminant $f(\mathbf{x}) = p(\omega_1|\mathbf{x}) - p(\omega_2|\mathbf{x}) > 0$
- We get $f(\mathbf{x}) = \mathbf{w}^T \mathbf{x} + w_0$

with $\mathbf{w} = \hat{\Sigma}^{-1}(\hat{\mu}_1 - \hat{\mu}_2)$

$$w_0 = \frac{1}{2} \hat{\mu}_2^T \hat{\Sigma}^{-1} \hat{\mu}_2 - \frac{1}{2} \hat{\mu}_1^T \hat{\Sigma}^{-1} \hat{\mu}_1 + \log \frac{p(\omega_1)}{p(\omega_2)}$$

Linear classifier on banana data



No estimated full covariance matrix

- In some cases even the averaged covariance matrix is too much to estimate
- Assume that all features have the same variance, and are uncorrelated:

$$\hat{\Sigma} = \sigma^2 I$$

- Then it becomes even simpler:

$$g_i(\mathbf{x}) = -\frac{1}{2\hat{\sigma}^2}(\hat{\mu}_i^T \hat{\mu}_i - \hat{\mu}_i^T \mathbf{x}) + \log(p(\omega_i))$$

Nearest mean classifier

- Define the discriminant: $f(\mathbf{x}) = p(\omega_1|\mathbf{x}) - p(\omega_2|\mathbf{x}) > 0$

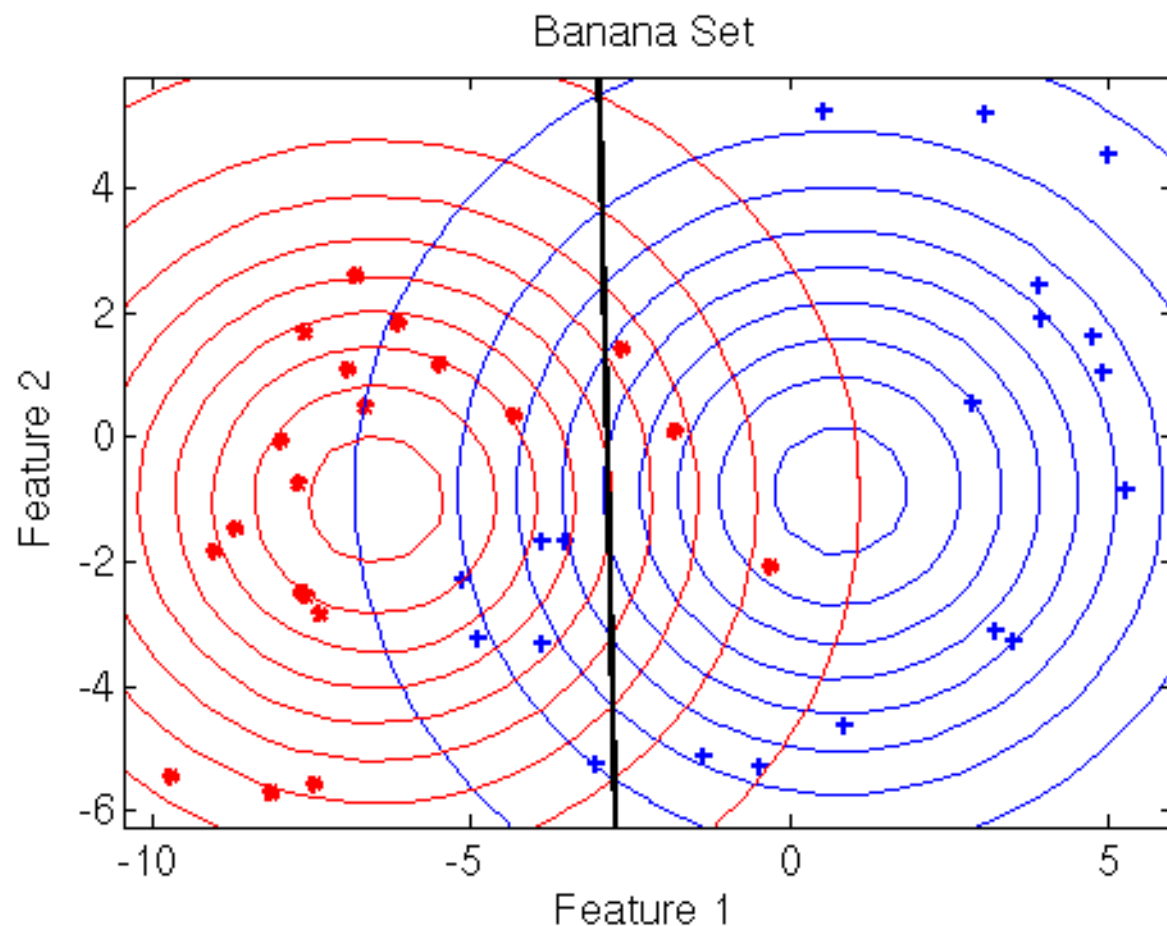
- We get
$$f(\mathbf{x}) = \mathbf{w}^T \mathbf{x} + w_0$$

with $\mathbf{w} = \hat{\mu}_1 - \hat{\mu}_2$

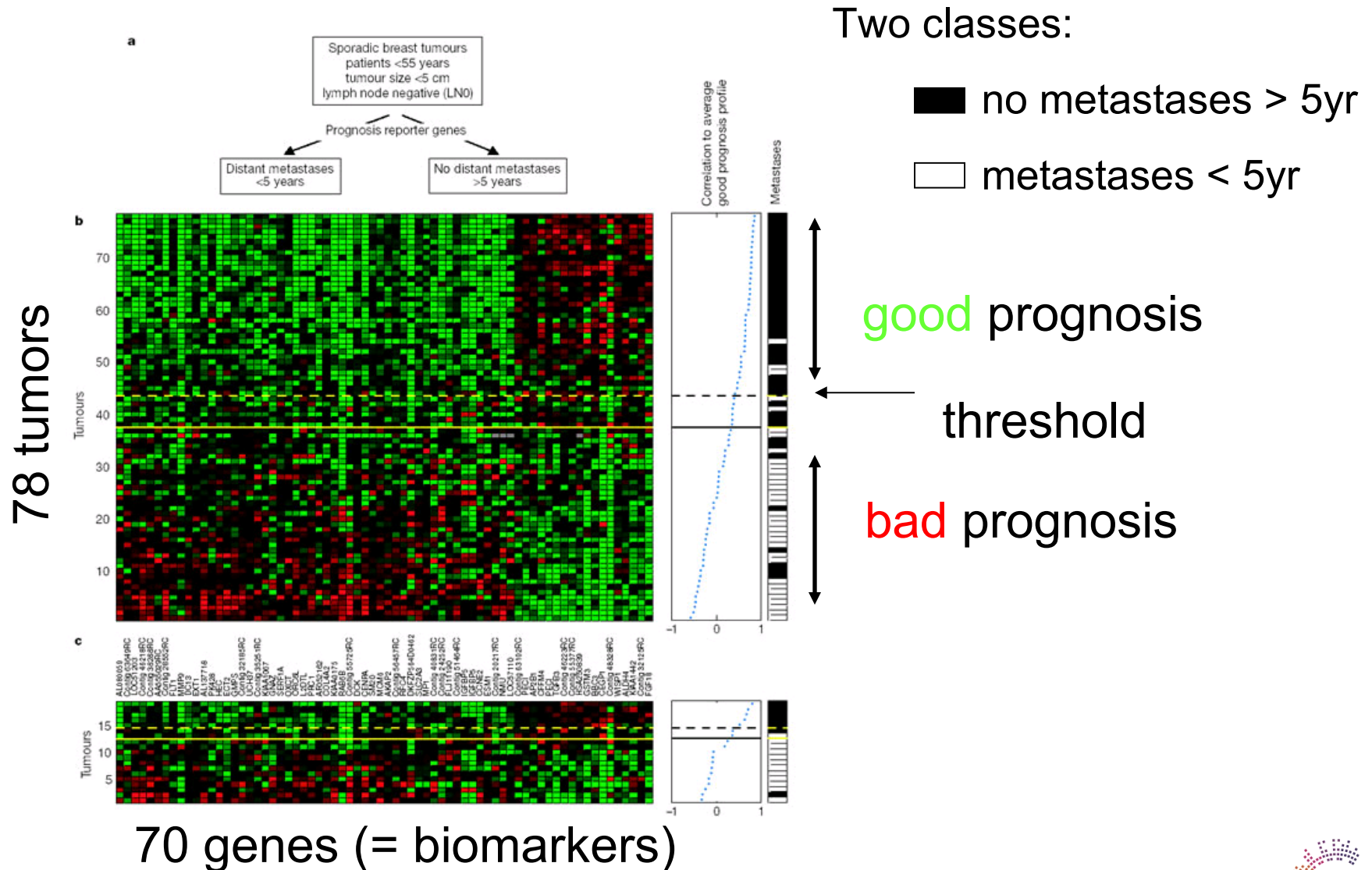
$$w_0 = \frac{1}{2} \hat{\mu}_2^T \hat{\mu}_2 - \frac{1}{2} \hat{\mu}_1^T \hat{\mu}_1 + \hat{\sigma}^2 \log \frac{p(\omega_1)}{p(\omega_2)}$$

- Again a linear classifier, but it only uses the distance to the mean of each of the classes: *nearest mean* classifier

Nearest mean on banana data



Nearest mean on gene expression data



ROC curve

- Recall minimum cost classification:

$$\begin{aligned}c_{opt} &= \arg \min_{c'} \sum_{c=1}^C \Lambda(\omega = c', \omega = c) p(\omega = c | x) p(x) \\&= \arg \min_{c'} \sum_{c=1}^C \Lambda(\omega = c', \omega = c) p(x | \omega = c) p(\omega = c)\end{aligned}$$

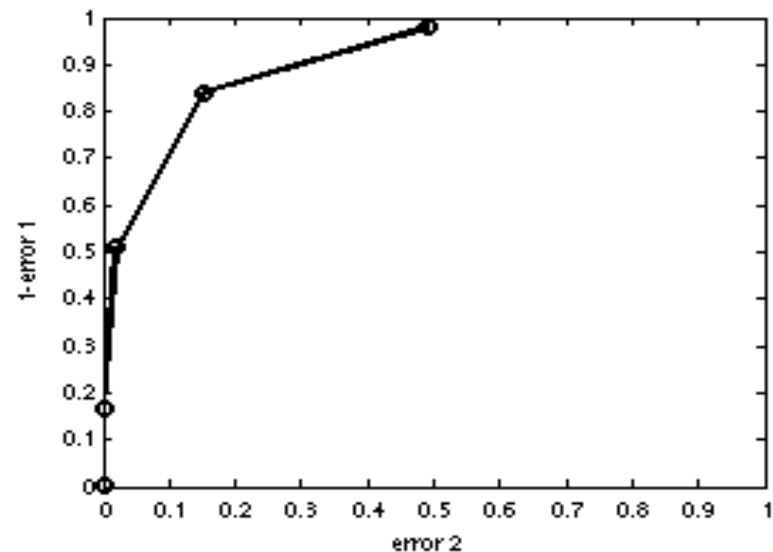
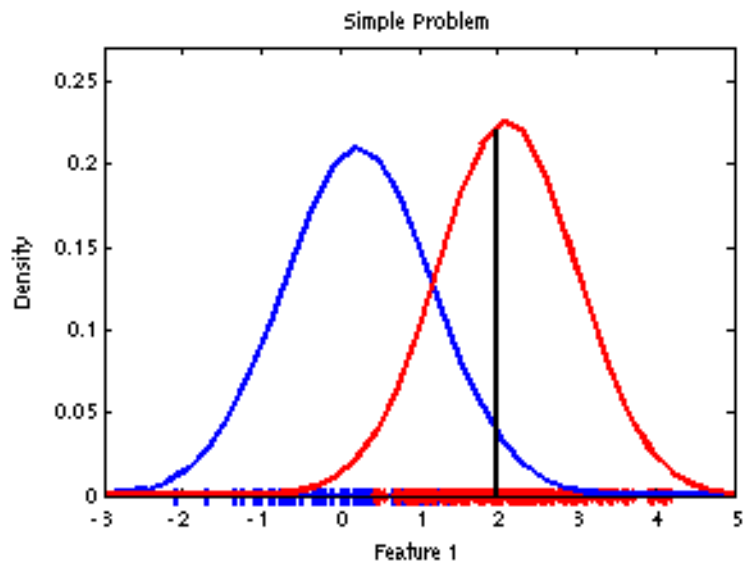
- In the two-class case, cost can be absorbed into prior:

$$c_{opt} = \arg \min_{c'} \sum_{c=1}^2 p(x | \omega = c) \tilde{p}(\omega = c)$$

i.e. changing the costs is like changing the class priors

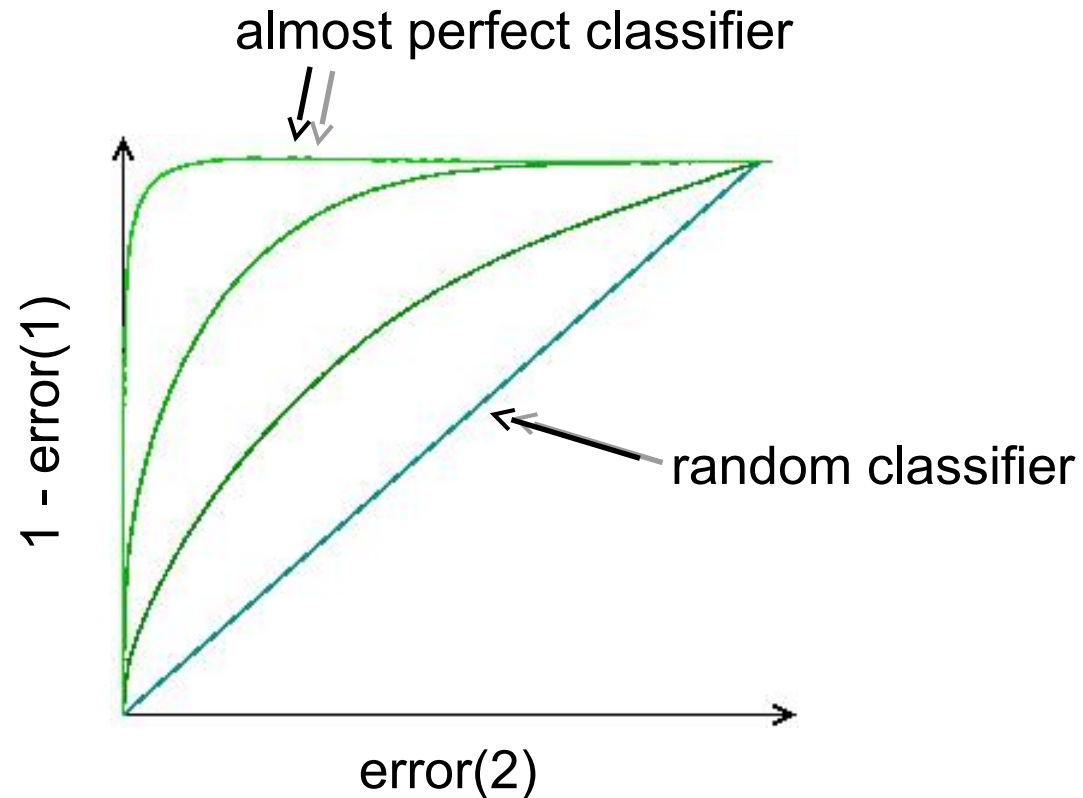
ROC curve (2)

- Error as a function of the threshold gives an overview of all possible cost/prior scenarios: *receiver-operator characteristic curve*
- Classifier: any x left of the threshold belongs to the blue class, any x to the right to the red class



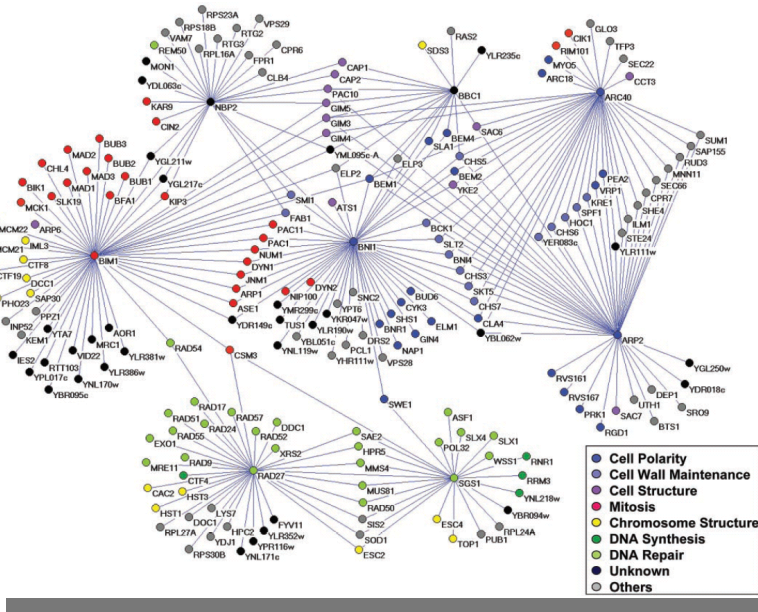
ROC curve (3)

- Different classifiers have different ROC curves

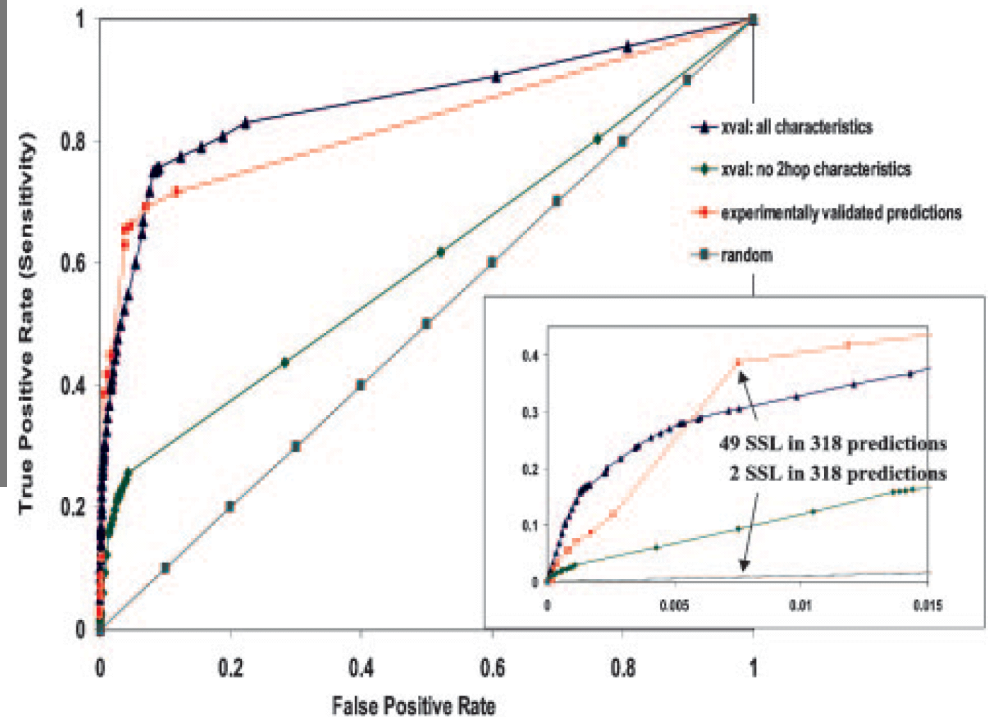


ROC curve (4)

- Example: prediction of synthetic genetic interactions (SGAs)



*Wong et al.,
PNAS 2004*



ROC for two-class problems: changing threshold

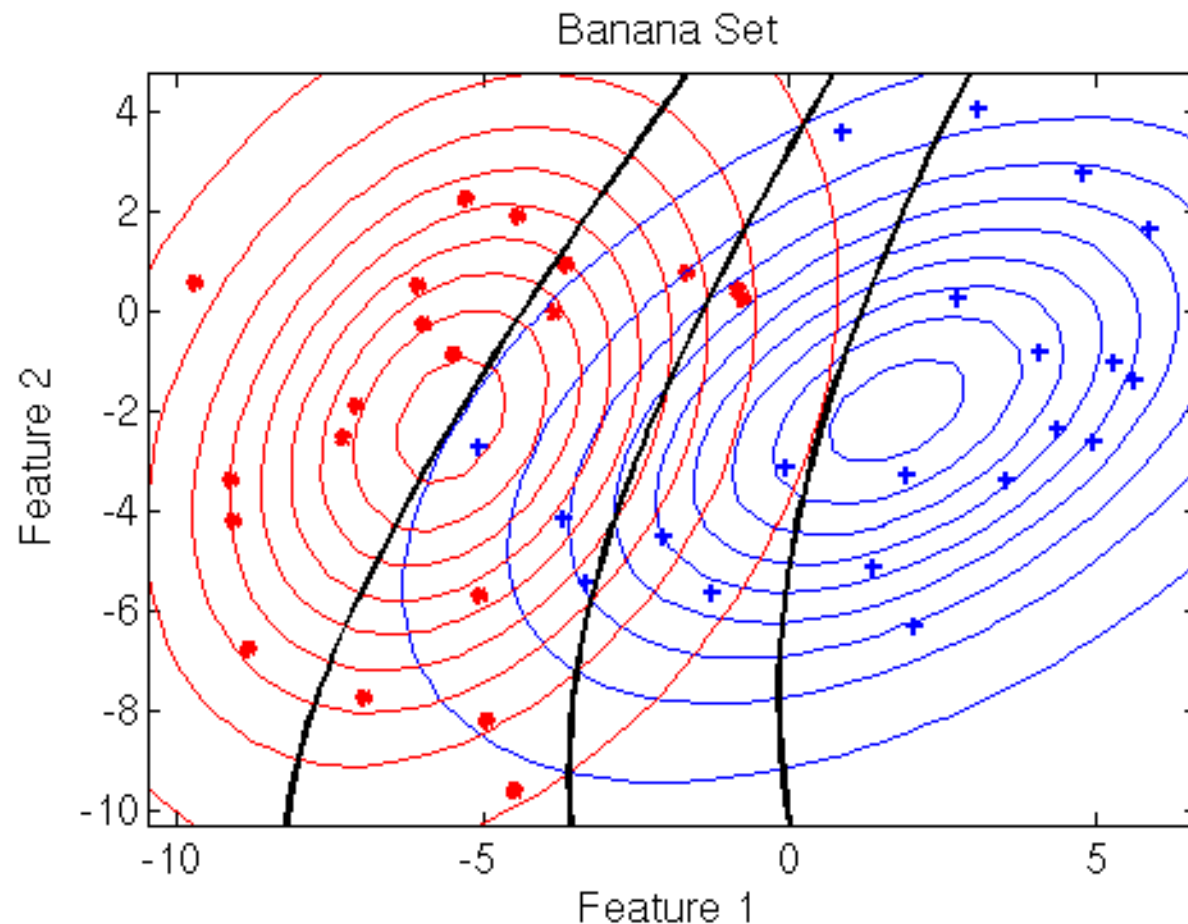
- Changing class costs = changing priors = moving the decision boundary = changing threshold
- Look at the general form of the normal-based classifiers:

$$g_i(\mathbf{x}) = -\frac{1}{2} \log(\det \Sigma_i) - \frac{1}{2} (\mathbf{x} - \mu_i)^T \Sigma_i^{-1} (\mathbf{x} - \mu_i) + \log(p(\omega_i))$$

- Changing the prior affects only the 'offset' (=threshold)
- It means only the thresholds have to be adapted:

$$f(\mathbf{x}) = \mathbf{w}^T \mathbf{x} + w_0$$
$$f(\mathbf{x}) = \mathbf{x}^T \mathbf{W} \mathbf{x} + \mathbf{w}^T \mathbf{x} + w_0$$

Changing threshold in banana data



Recapitulation

- Using the Parzen density and nearest neighbor density we can derive the Parzen classifier and nearest neighbor classifier
- Using the plug-in Bayes' rule with a normal distribution for each of the classes gives different classifiers
 - Separate mean and covariance matrix per class gives the quadratic classifier
 - Separate mean, equal covariance matrix per class gives the linear classifier (see Fisher classifier, for two classes)
 - Separate mean, identity covariance matrix per class gives the nearest mean classifier
- By changing the thresholds a ROC curve is obtained, showing the error on both classes.

10min break

Exercises 2.8-2.15

Discriminant analysis

- Different approach to classifiers: avoid estimating the (class conditional) probabilities altogether
 - Linear discriminant
 - Fisher classifier

Avoid density estimation

- From the k -nearest neighbor we saw already that we don't need to explicitly estimate a density
- Estimating densities is hard, in particular when we have a high number of features (high dimensional feature space, curse of dimensionality)
- Now, we start from the other end:
 - Assume we have a function to describe the decision boundary
 - Optimize the free parameters of this function directly
 - No Bayes' theorem, no density estimates

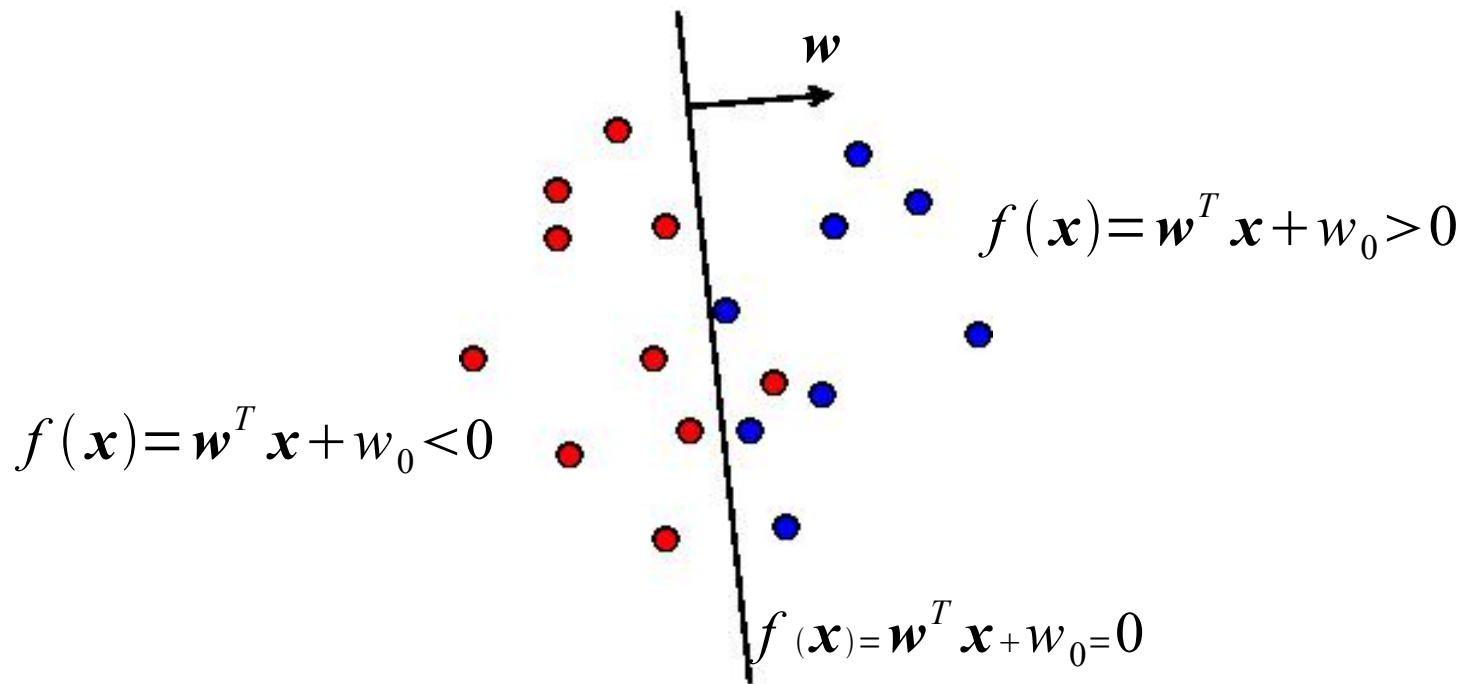
Linear discriminant

- Let us assume we can describe the discriminant by:

$$f(\mathbf{x}) = \mathbf{w}^T \mathbf{x} + w_0$$

- There are several ways to optimize \mathbf{w} and w_0
- This is generally called linear discriminant analysis

Linear discriminant (2)



- Classifier is a linear function of the features
- The classification depends on whether the weighted sum of the features is above or below 0

Fisher classifier

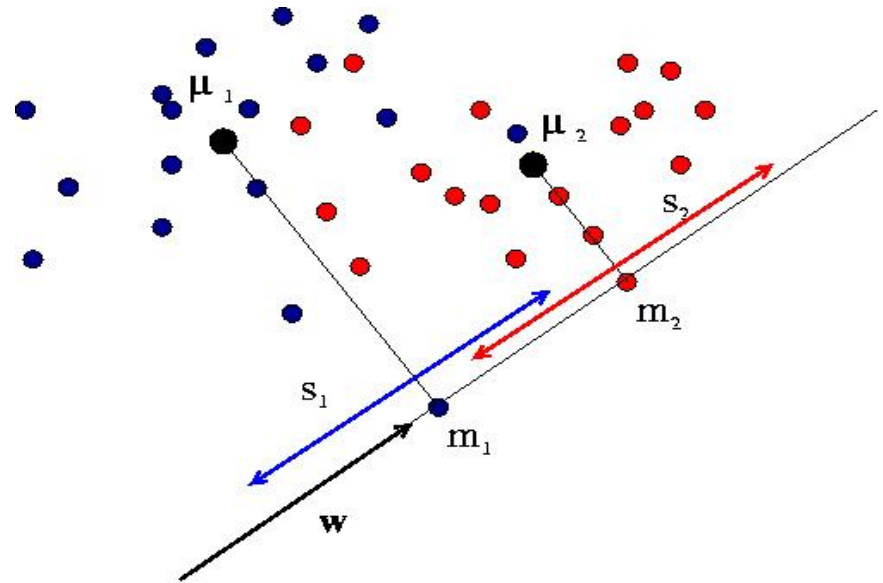
- Linear projection onto 1-D:

$$y = \mathbf{w}^T \mathbf{x}$$

- Maximize Fisher criterion:

$$J = \frac{|m_1 - m_2|^2}{(s_1^2 + s_2^2)}$$

- Maximizing J implies that after projection:
 - Means should be far apart
 - Variances should be small
- Find a projection direction \mathbf{w} for which J is optimized



Derivation Fisher classifier

- Map the means on w :

$$m_1 = \mathbf{w}^T \boldsymbol{\mu}_1, \quad m_2 = \mathbf{w}^T \boldsymbol{\mu}_2$$

- Map the differences in mean:

$$\begin{aligned} |m_1 - m_2|^2 &= (\mathbf{w}^T \boldsymbol{\mu}_1 - \mathbf{w}^T \boldsymbol{\mu}_2)^2 \\ &= \mathbf{w}^T (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)(\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)^T \mathbf{w} = \mathbf{w}^T \mathbf{S}_B \mathbf{w} \end{aligned}$$

- Compute the mapped variance:

$$\begin{aligned} s_i^2 &= \sum_j (\mathbf{w}^T \mathbf{x}_j^{(i)} - \mathbf{w}^T \boldsymbol{\mu}_i)^2 \\ &= \sum_j \mathbf{w}^T (\mathbf{x}_j^{(i)} - \boldsymbol{\mu}_i)(\mathbf{x}_j^{(i)} - \boldsymbol{\mu}_i)^T \mathbf{w} = \mathbf{w}^T \mathbf{S}_i \mathbf{w} \end{aligned}$$

Derivation Fisher discriminant

- Combine both results from the previous slide.

- The Fisher criterion
$$J = \frac{|m_1 - m_2|^2}{(s_1^2 + s_2^2)}$$

can be written in terms of the weights

$$J(\mathbf{w}) = \frac{\mathbf{w}^T \mathbf{S}_B \mathbf{w}}{\mathbf{w}^T \mathbf{S}_W \mathbf{w}}$$

where $\mathbf{S}_W = \sum_i \frac{n_i}{n} \mathbf{S}_i$ is the 'within scatter matrix'

and $\mathbf{S}_B = (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)(\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)^T$ the 'between scatter matrix'.

Derivation Fisher discriminant (2)

- To optimize J , we set the derivative to 0:

$$(\mathbf{w}^T \mathbf{S}_B \mathbf{w}) \mathbf{S}_W \mathbf{w} = (\mathbf{w}^T \mathbf{S}_W \mathbf{w}) \mathbf{S}_B \mathbf{w}$$

- Because $\mathbf{S}_B = (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)(\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)^T$

$\mathbf{S}_B \mathbf{w}$ will always be in the direction $(\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)$

- We get: $(\mathbf{w}^T (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)) \mathbf{S}_W \mathbf{w} = (\mathbf{w}^T \mathbf{S}_W \mathbf{w}) (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)$

Derivation Fisher discriminant (3)

- Ignoring scalar factors, we get:

$$(\cancel{\mathbf{w}^T (\mu_1 - \mu_2)}) \mathbf{S}_W \mathbf{w} = (\cancel{\mathbf{w}^T \mathbf{S}_W \mathbf{w}}) (\mu_1 - \mu_2)$$

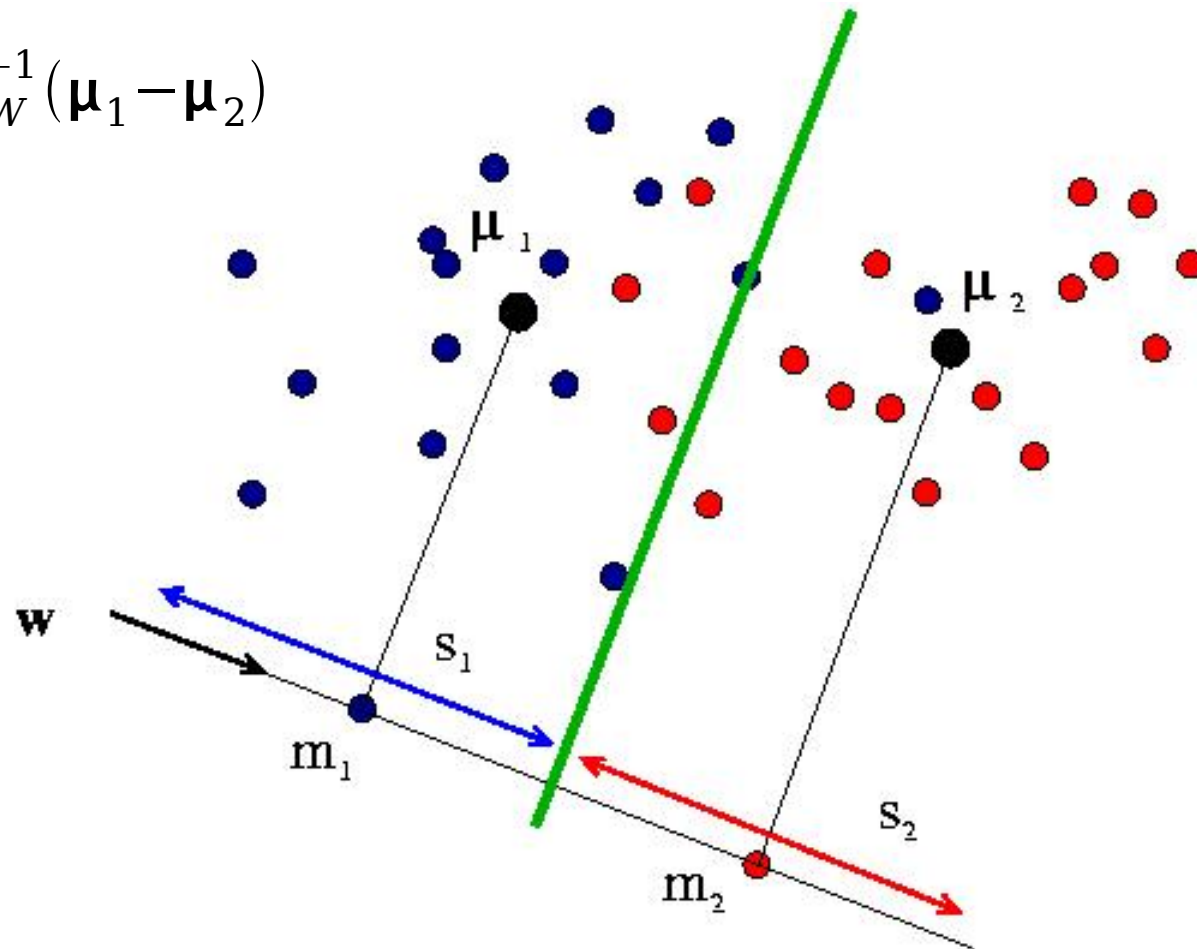
$$\mathbf{S}_W \mathbf{w} = C \cdot (\mu_1 - \mu_2)$$

$$\mathbf{w} \sim \mathbf{S}_W^{-1} (\mu_1 - \mu_2)$$

- Strictly speaking, we don't have a classifier yet, only a direction on which to project our data
- In practice, take the decision boundary in the middle

The result

$$\mathbf{w} \sim \mathbf{S}_W^{-1}(\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)$$



This is familiar...

- The expression for the Fisher discriminant

$$\mathbf{w} \sim \mathbf{S}_W^{-1} (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)$$

looks like the linear normal-based classifier:

$$f(\mathbf{x}) = \mathbf{w}^T \mathbf{x} + w_0$$

$$\mathbf{w} = \hat{\Sigma}^{-1} (\hat{\boldsymbol{\mu}}_1 - \hat{\boldsymbol{\mu}}_2)$$

$$w_0 = \frac{1}{2} \hat{\boldsymbol{\mu}}_2^T \hat{\Sigma}^{-1} \hat{\boldsymbol{\mu}}_2 - \frac{1}{2} \hat{\boldsymbol{\mu}}_1^T \hat{\Sigma}^{-1} \hat{\boldsymbol{\mu}}_1 + \log \frac{p(\omega_1)}{p(\omega_2)}$$

- For a two-class problem, both classifiers are identical

Comparison Fisher and Gauss

- The normal-based linear classifier assumes a density per class
- Fisher classifier just tries to optimise the Fisher criterion
 - For the Fisher classifier the bias term is (in principle) still free to optimise
- Both classifiers rely on the inverse of \mathbf{S}_W , so it can therefore become undefined when insufficient data is available

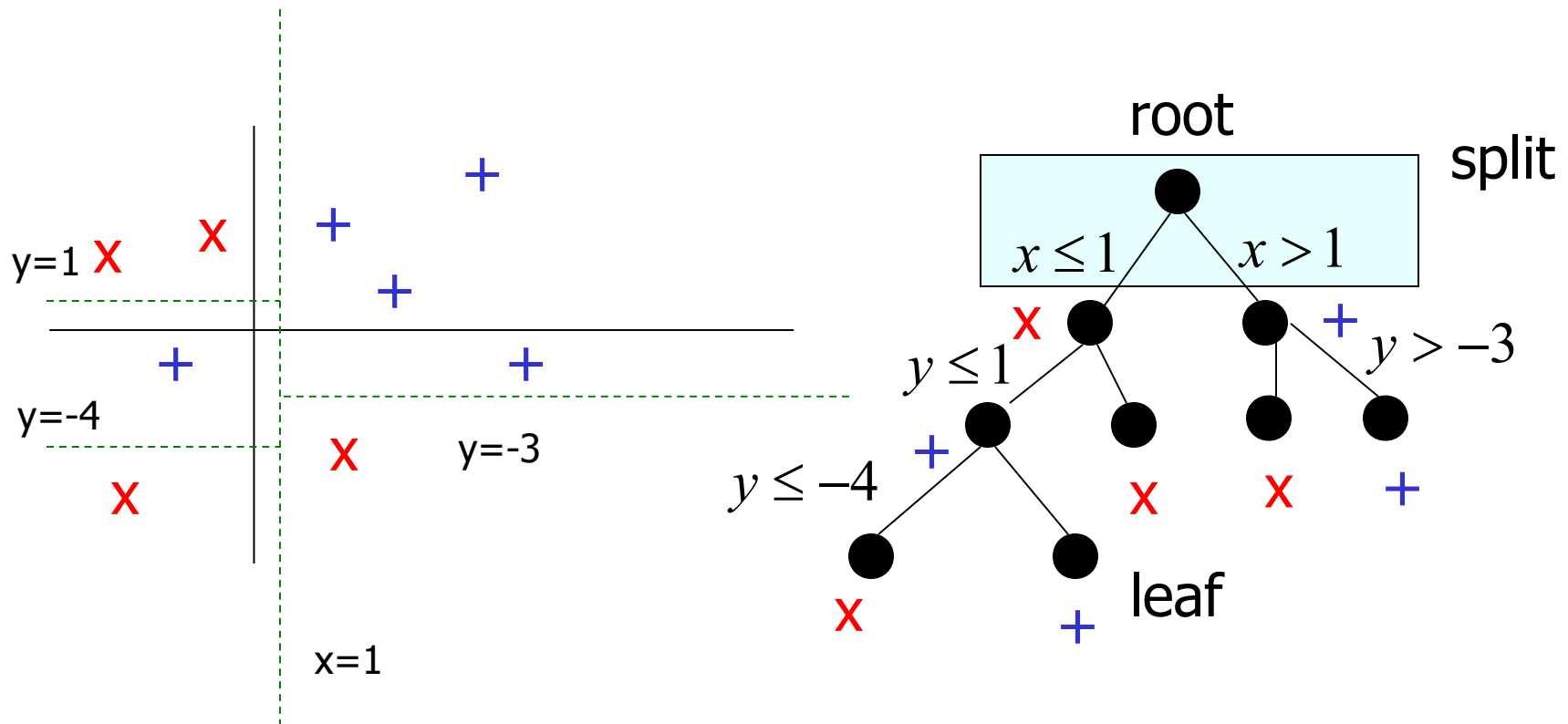
5min break

Exercises 2.16-2.18

Tree-based models

- Until now: mainly linear and quadratic decision surfaces, often real data is more complex
- Classification trees
 - Feature selection
- Random forests
 - Ensemble of trees
 - Randomization
 - Bootstrapping
- More on Day 5: neural networks, support vector machines

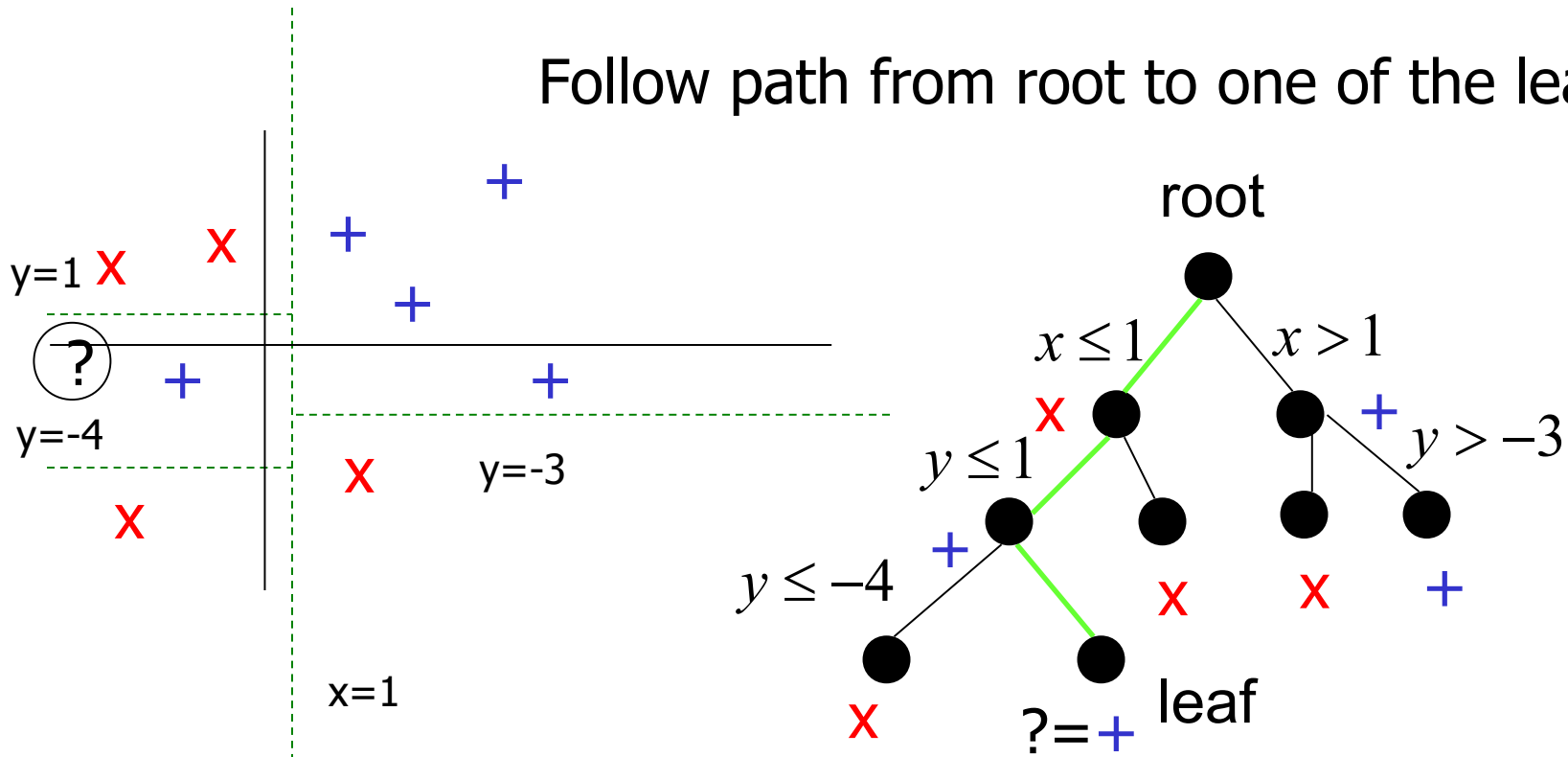
Classification trees



Build a tree of (binary) splits parallel to the axes in a greedy (=one by one) way.

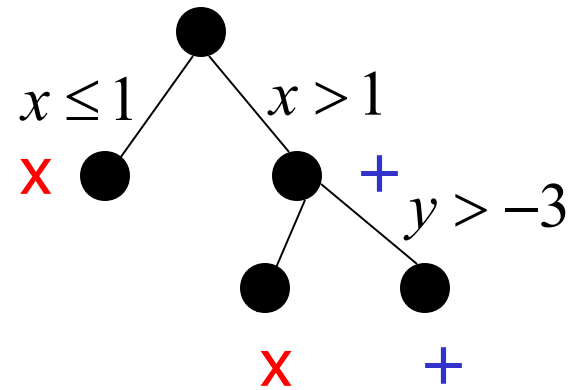
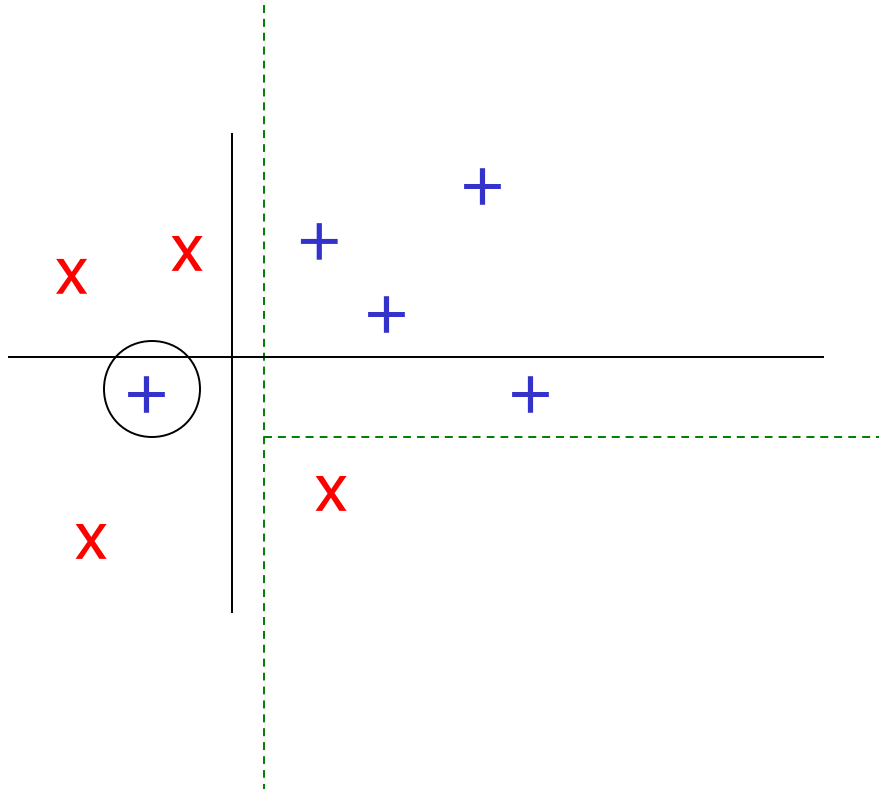
Classification trees: new data

Follow path from root to one of the leaves



Can perfectly fit the data: **overfitting**

Classification trees: pruning



Allow errors on training data in order to reduce overfitting

Tree ingredients

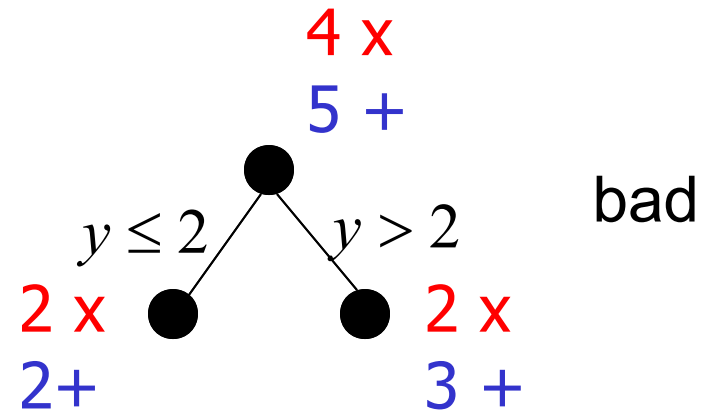
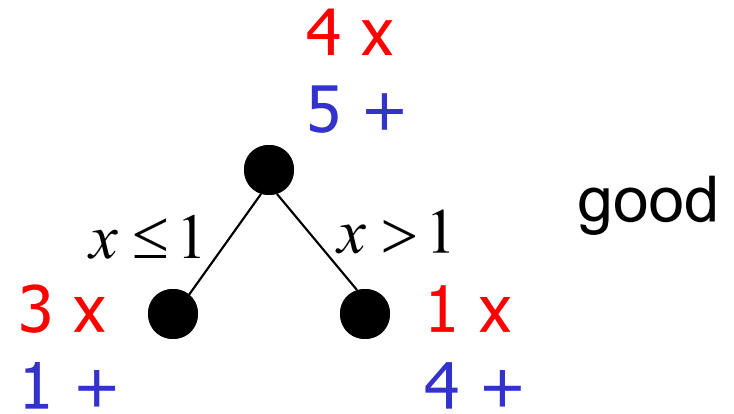
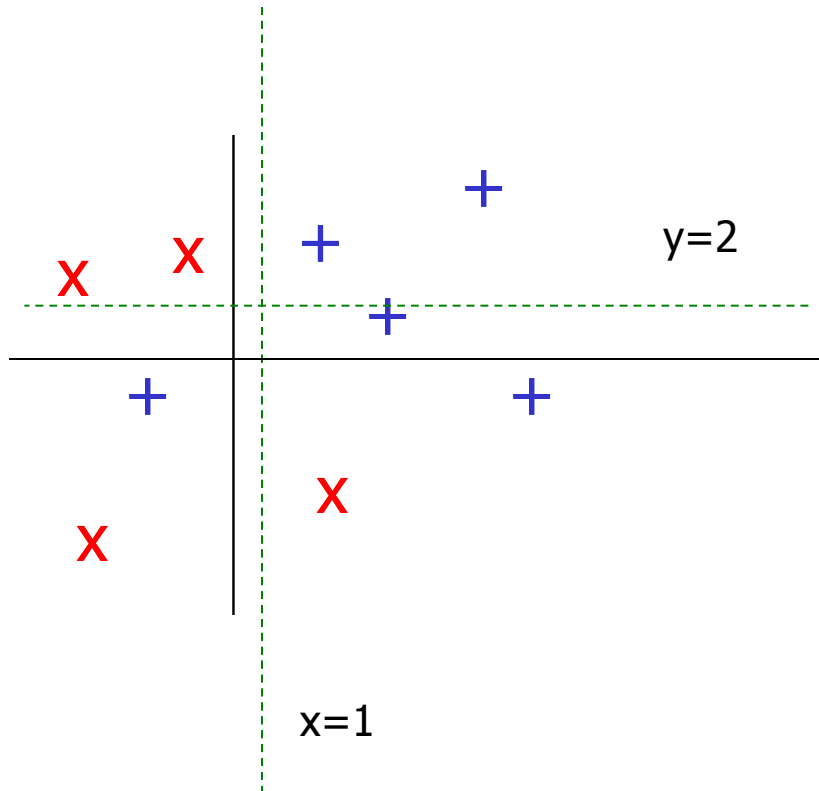
Trees are constructed in a **greedy** way:
starting with an empty tree and adding splits one by one
(and never coming back on a decision taken)

Main questions:

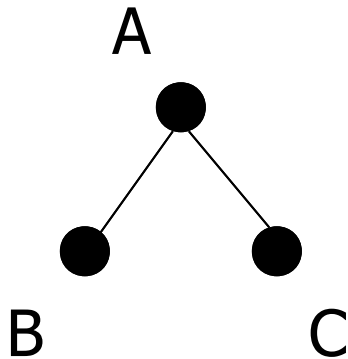
- How to choose a split
- How to choose a final tree?
 - Amount of pruning

Rest: details (but might be important ...)

How to choose a split?



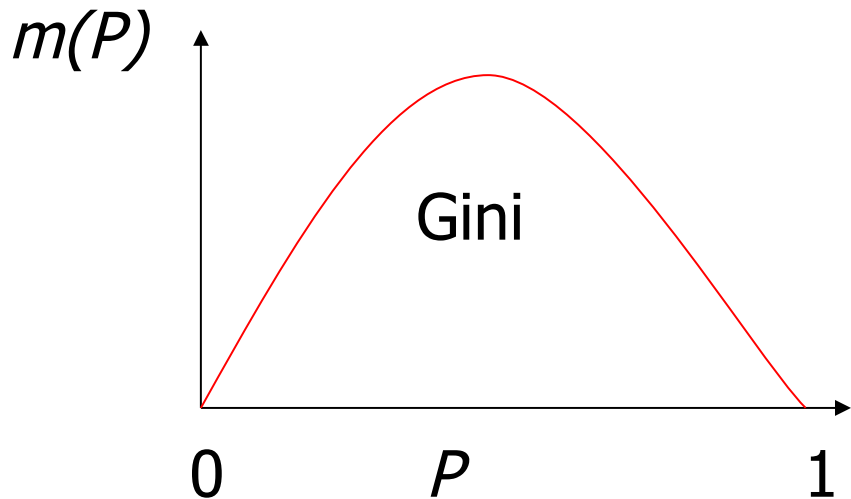
How to choose a split? (2)



Good split at A:

- few **x** & many **+** in B, C
- many **x** & few **+** in B, C

Find some measure m that captures goodness



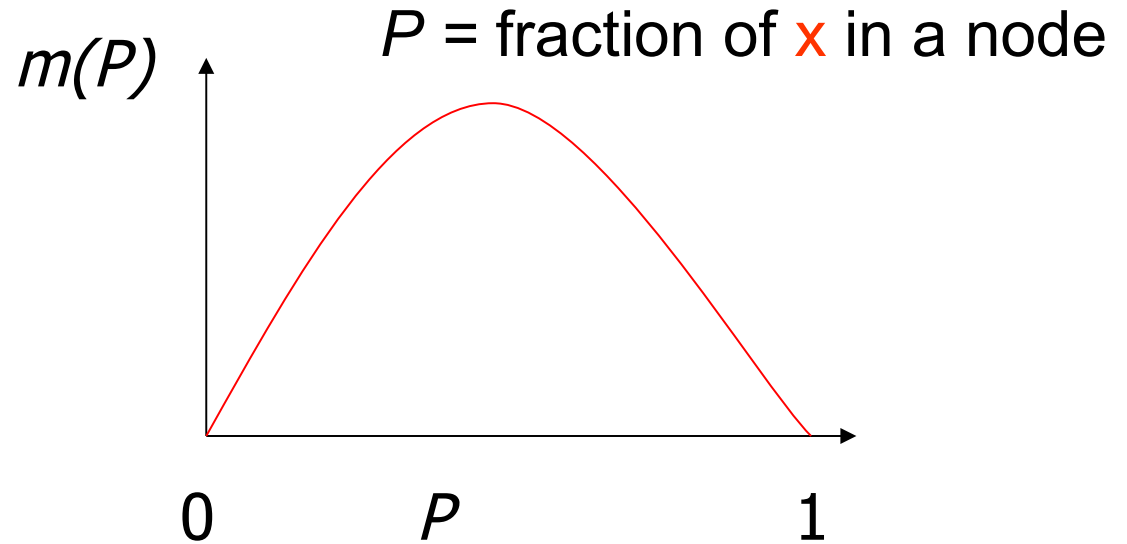
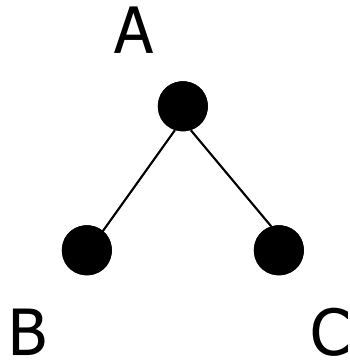
$$m(0)=0$$

$$m(1)=0$$

$$m(P)=P(1-P)$$

P = fraction of **x** in a node

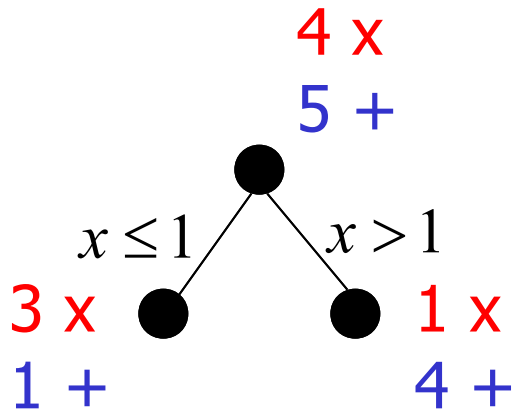
How to choose a split? (3)



$$\text{maximize } m(P_A) - P(B)m(P_B) - P(C)m(P_C)$$

$P(X)$: determined by number of \mathbf{x} and $\mathbf{+}$ at node X

How to choose a split? (4)



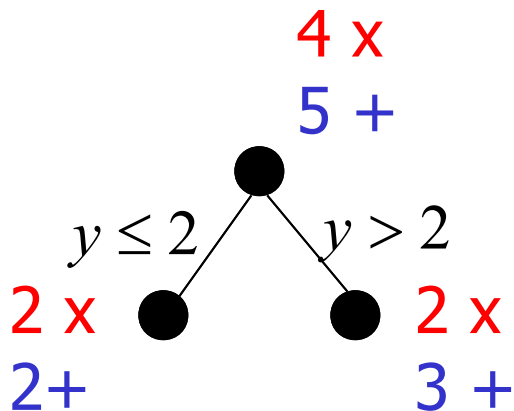
good

$$m(P_A) - P(B)m(P_B) - P(C)m(P_C)$$

$$\frac{4}{9} \frac{5}{9} - \frac{4}{9} \frac{3}{4} \frac{1}{4} - \frac{5}{9} \frac{1}{5} \frac{4}{5} =$$

0.075

maximum

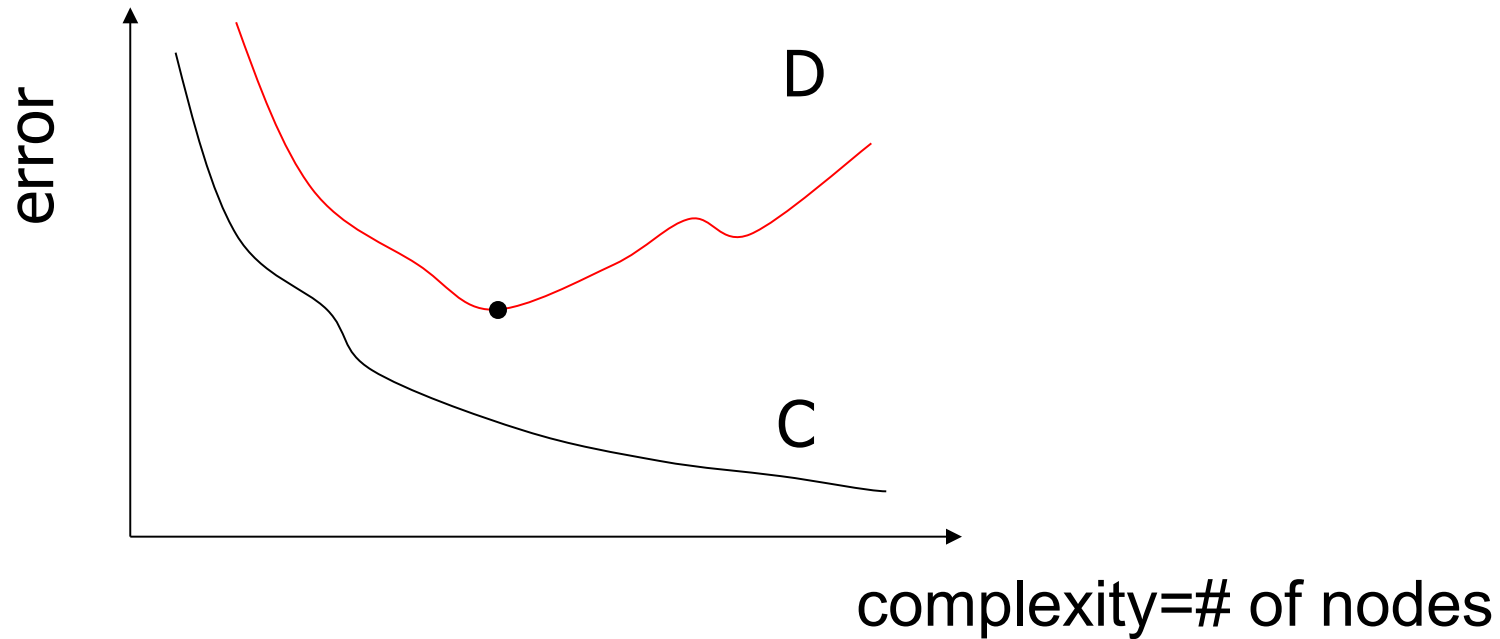


bad

$$\frac{4}{9} \frac{5}{9} - \frac{4}{9} \frac{2}{4} \frac{2}{4} - \frac{5}{9} \frac{2}{5} \frac{3}{5} =$$

0.0025

Pruning: one step back



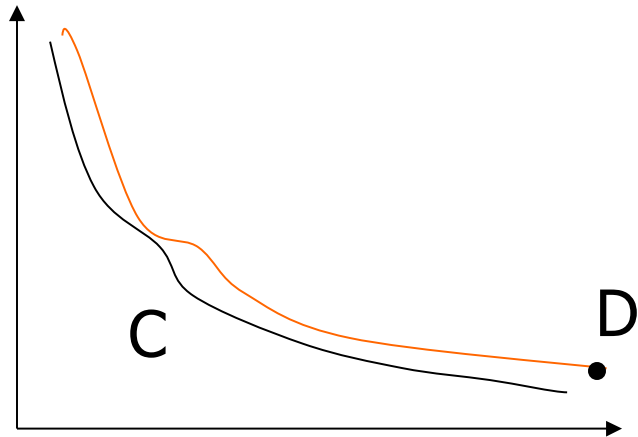
minimize: $D = C + k(\text{\# of leaf nodes in the tree})$

$0 \leq k$

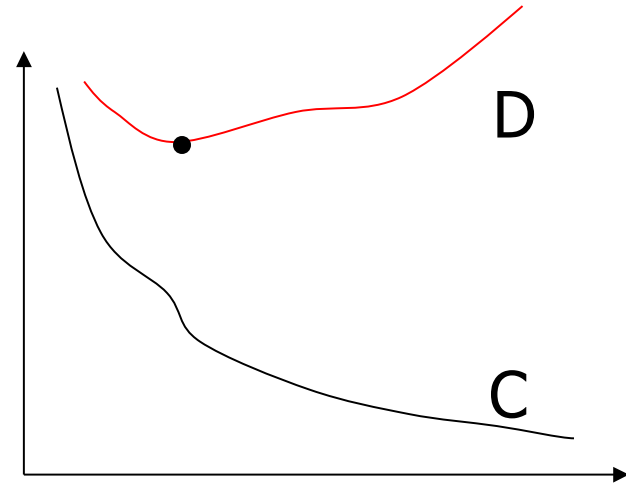
k : complexity parameter

k penalizes big trees

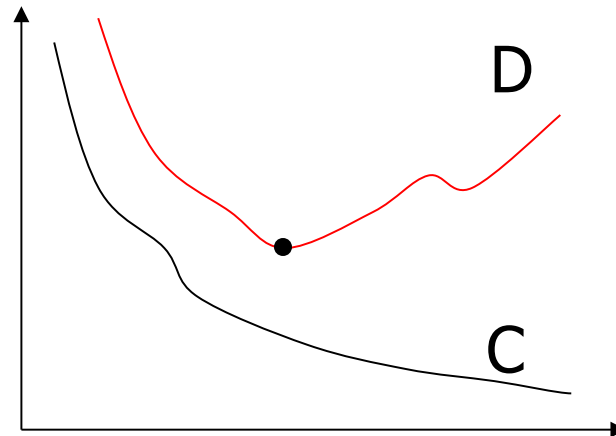
Pruning: one step back (2)



small k : big tree



large k : small tree



medium k : medium tree

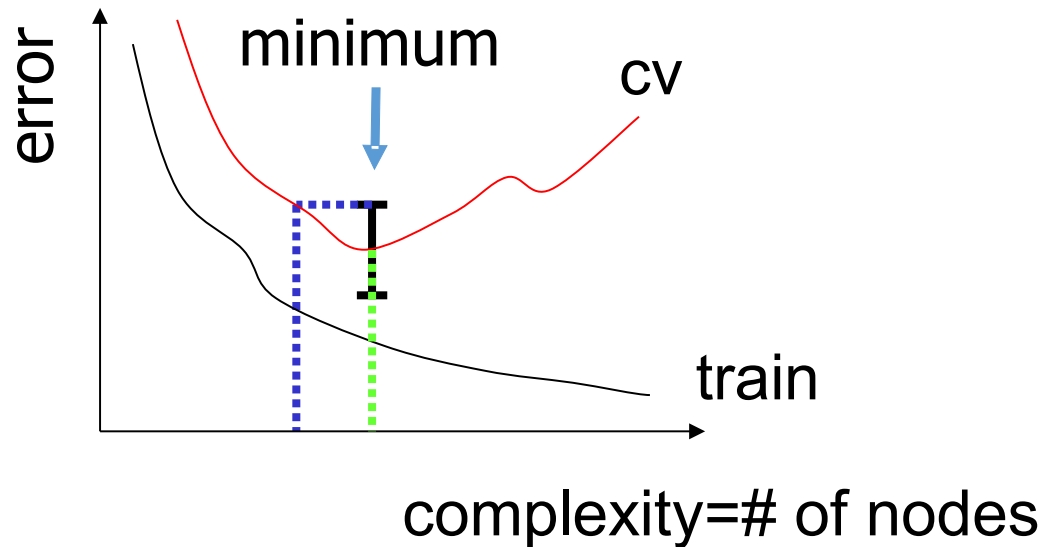
Pruning: CART

- Build a complete tree T
- With each subtree of T corresponds a choice of k

Cannot make choice of k on training set: **overfitting**

Optimal choice of k is made by cross-validation

Pruning: model selection



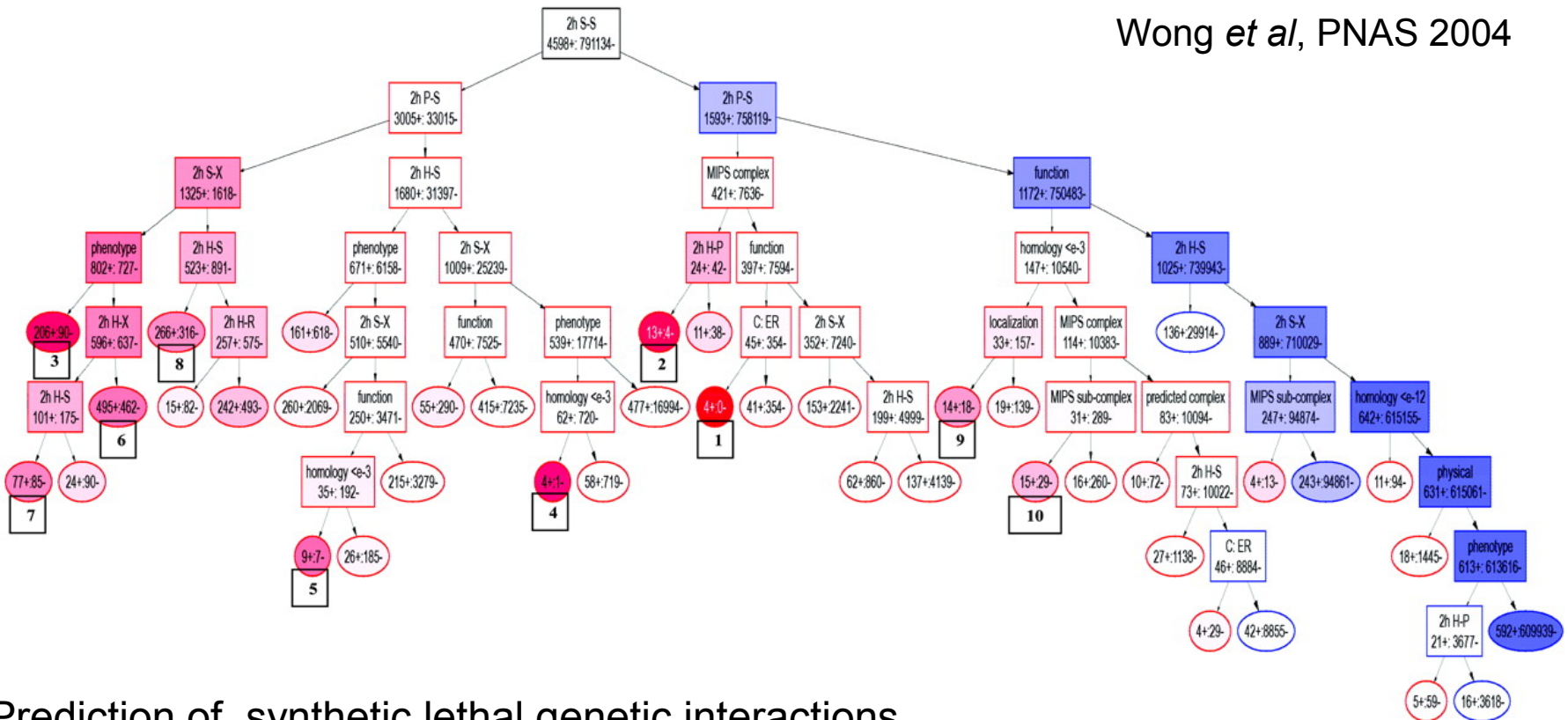
minimum

standard error (1-se)

10-fold cross-validation: mean +/- std. error

Decision tree: application

Wong *et al*, PNAS 2004



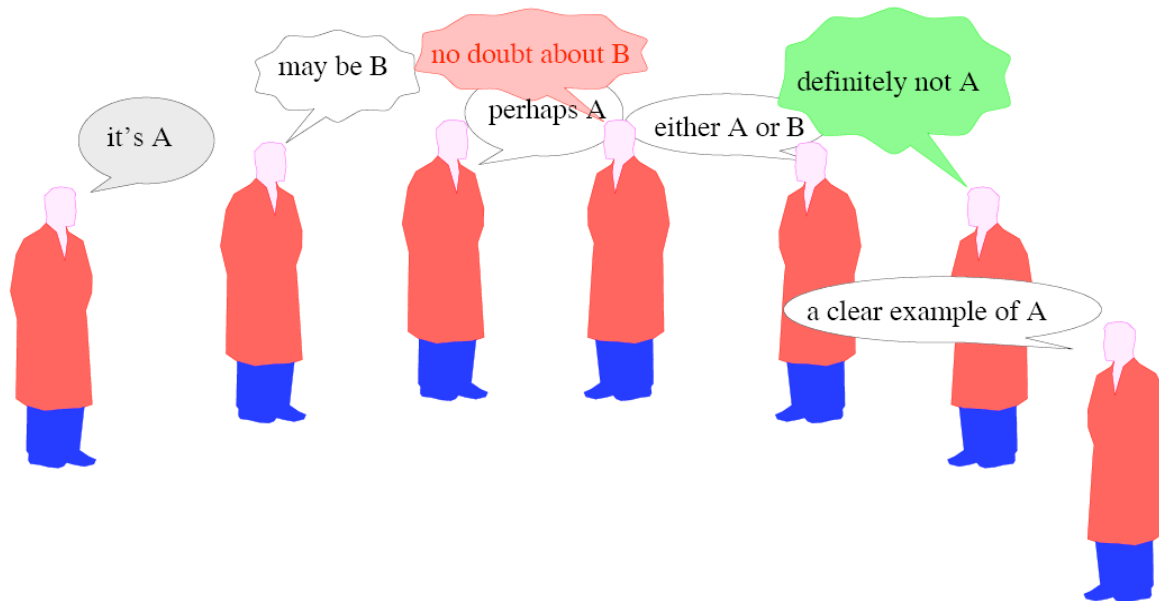
- Prediction of synthetic lethal genetic interactions
- Integrate multiple types of data: localization, mRNA expression, physical interaction, protein function, and characteristics of network topology

Advantages/disadvantages

- simple and flexible classifier
- combination of discrete and continuous features
- feature selection (Day 3)
- interpretability
- hard splits
- splits are axis-aligned
- sensitive to small variations in data (high variance, Day 5)

Classifier combination

- Idea: combine different classifiers and have them vote
- Design choices:
 - Identical or different?
 - Base classifiers, feature spaces, training sets, initialisations, etc.
 - Combination by a fixed rule or by another classifier?



Example: random forests

- General overview: Day 5
- Specific example: random forest – an ensemble of decision trees
- Choices to be made:
 - Base classifiers: identical – decision trees
 - Feature spaces: for each node in each tree sample randomly m features
 - $m \ll$ total number of features
 - Training sets: sampling with replacement (bootstrapping)
 - About two-third of the cases are used for training each tree
- Combination: majority vote

Characteristics

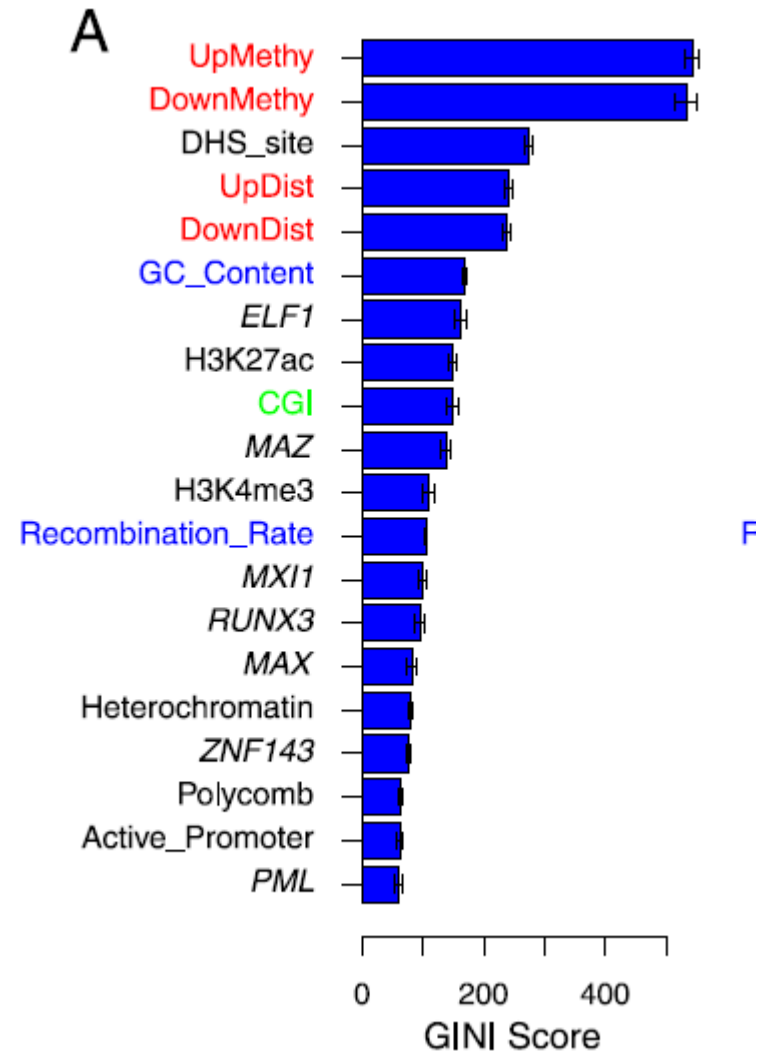
- Out-of-bag error (oob) estimate:
 - Each tree can be tested on about one-third of the cases – the out-of-bag samples
- Variable importance:
 - For each tree: predict the class for oob cases and count the number of votes cast for the correct class
 - For each tree: randomly permute the values of variable n in the oob cases and count the number of votes cast for the correct class
 - Importance: rank (from high to low) based on average difference of these two scores

Some intuition

- Breiman *et al.*, Machine Learning (2001) paper
- Accuracy depends on two factors:
 - Correlation between any two trees in the forest. Decreasing correlation increases the forest accuracy: **diversity**
 - Accuracy of each individual tree (strength) in the forest. Increasing strength of individual trees increases the forest accuracy
- Trade-off:
 - Reducing m reduces correlation and strength
 - Increasing m increases correlation and strength
- Solution: somewhere in between is an *optimal* range of m - usually quite wide. Using the oob error rate a value of m in the range can be found

Random forests: example

- Prediction of genome-wide DNA methylation
- Features:
 - Neighbors
 - Genomic position
 - DNA sequence properties
 - Cis-regulatory elements
- Random forest: feature selection



Recapitulation

- Decision trees: simple and flexible classifier
 - Incorporates feature selection
 - Interpretable
 - Hard, axis-aligned splits
 - Pruning is essential to avoid overfitting
- Random forest: example of ensemble method
 - Ensemble of decision trees
 - Variation between members introduced via randomness
 - When number of features is large and percentage of truly informative features is small (gene expression-based diagnostics): performance tends to decline significantly



Exercises 2.19-2.20