Decision Trees and Random Forests

Reference: Leo Breiman, http://www.stat.berkeley.edu/~breiman/RandomForests

1. Decision trees

Example (Guerts, Fillet, et al., Bioinformatics 2005):

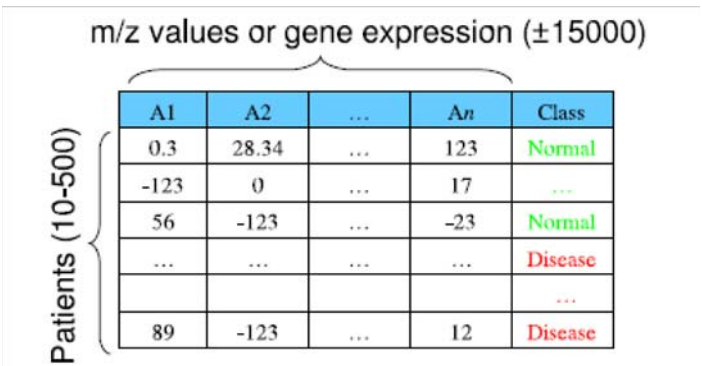
Patients to be classified: normal vs. diseased

Decision trees

Classification of biomarker data: large number of values (e.g., microarray or mass spectrometry analysis of biological sample)

Decision trees

Mass spectrometry parameters or
gene expression parameters (around 15k values)



A1	A2	…	A*n*	Class
0.3	28.34	…	123	Normal
-123	0	…	17	…
56	-123	…	-23	Normal
…	…	…	…	Disease
				…
89	-123	…	12	Disease

Given new patient with biomarker data, is s/he normal or ill?

Decision trees

Needed: selection of relevant variables from many

Number n of known examples in $D = \{(\mathbf{x}_i, y_i)\}_{i=1}^{n}$
is small
(characteristic of data mining problems)

Assume we have for each biological sample a feature vector **x**, and will classify it:

diseased: $y = 1$; normal: $y = -1$.

Goal: find function $f(\mathbf{x}) \approx y$ which predicts y from **x**.

Decision trees

How to estimate error of $f(\mathbf{x})$ and avoid over-fitting the small dataset D?

Use cross-validation to test predictor $f(\mathbf{x})$ in an unexamined part of the sample D.

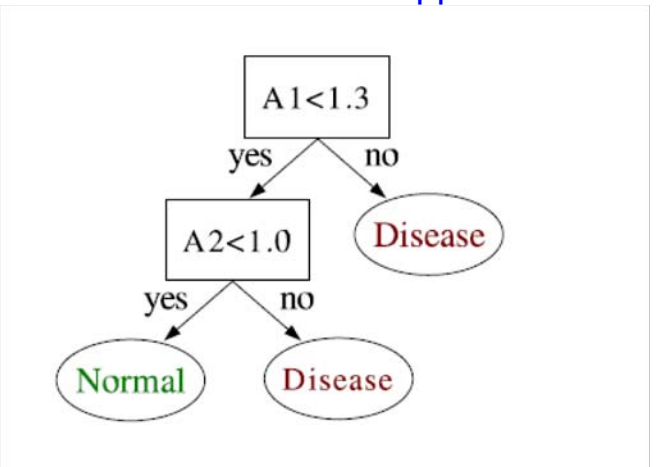
For biological sample, feature vector $\mathbf{x} = (x_1, \ldots, x_d)$ consists of *features* (or *biomarkers* or *attributes*) $x_i = A_i$ describing the biological sample from which **x** is obtained.

The decision tree approach

Decision tree approach to finding predictor $f(\mathbf{x}) = y$ based on data set D:

- $\oplus$ form a tree whose nodes are attributes $x_i = A_i$ in **x**
- $\oplus$ decide which attributes A_i to look at first in predicting y from **x** find those with highest information gain - place these at top of tree
- $\oplus$ then use recursion to form sub-trees based on attributes not used in the higher nodes:

The decision tree approach



Advantages: interpretable, easy to use, scalable, robust

Decision tree example

Example 1 (Moore): UCI data repository (http://www.ics.uci.edu/~mlearn/MLRepository.html)

MPG ratings of cars:

Goal: predict MPG rating of a car from a set of attributes A_i

Decision tree example

Examples (each row is attribute set for a sample car):

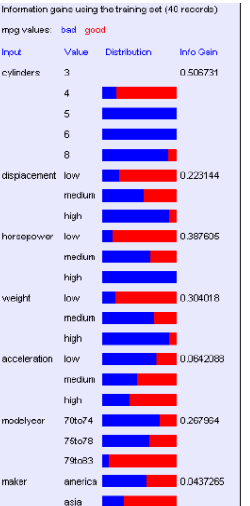
mpg	cylinders	displacement	horsepower	weight	acceleration	modelyear	maker
good	4	low	low	low	high	75to78	asia
bad	6	medium	medium	medium	medium	70to74	america
bad	4	medium	medium	medium	low	75to78	europe
bad	8	high	high	high	low	70to74	america
bad	6	medium	medium	medium	medium	70to74	america
bad	4	low	medium	low	medium	70to74	asia
bad	4	low	medium	low	low	70to74	asia
bad	8	high	high	high	low	75to78	america
:	:	:	:	:	:	:	:
:	:	:	:	:	:	:	:
:	:	:	:	:	:	:	:
bad	8	high	high	high	low	70to74	america
good	8	high	medium	high	high	79to83	america
bad	8	high	high	high	low	75to78	america
good	4	low	low	low	low	79to83	america
bad	6	medium	medium	medium	high	75to78	america
good	4	medium	low	low	low	79to83	america
good	4	low	low	medium	high	79to83	america
bad	8	high	high	high	low	70to74	america
good	4	low	medium	low	medium	75to78	europe
bad	5	medium	medium	medium	medium	75to78	europe

R. Quinlan

Decision tree example

Simple assessment of information gain: how much does a particular attribute A_i help to classify a car with respect to MPG?

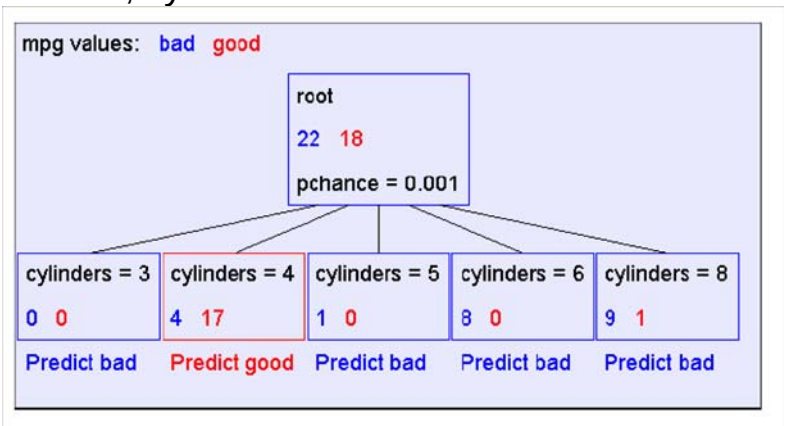
Decision tree example



Begin the decision tree: start with most informative

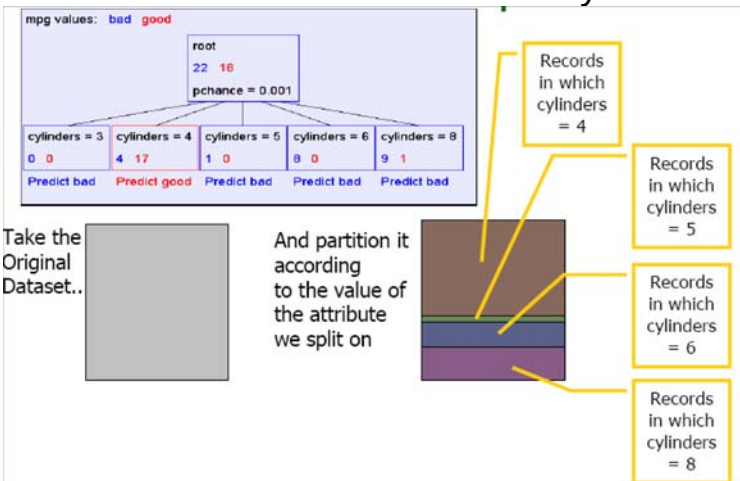
Decision tree example

criterion, cylinders:



Decision tree example

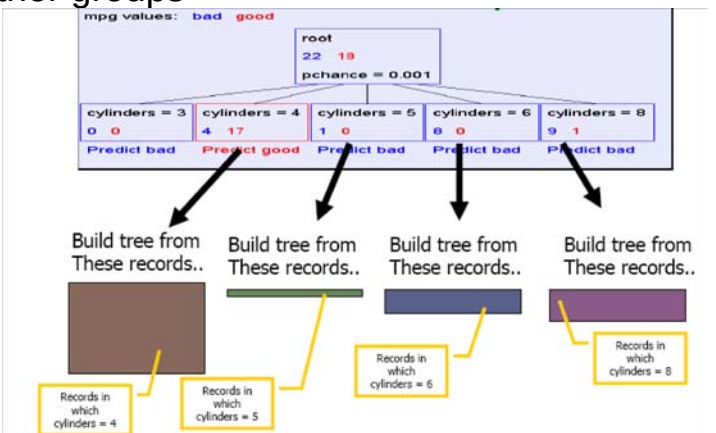
Recursion: build next level of tree. Initially have:



Now build sub-trees: split each set of cylinder numbers into

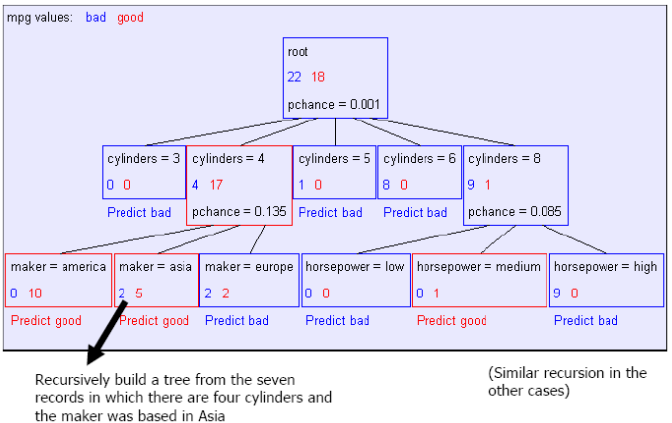
Decision tree example

further groups-



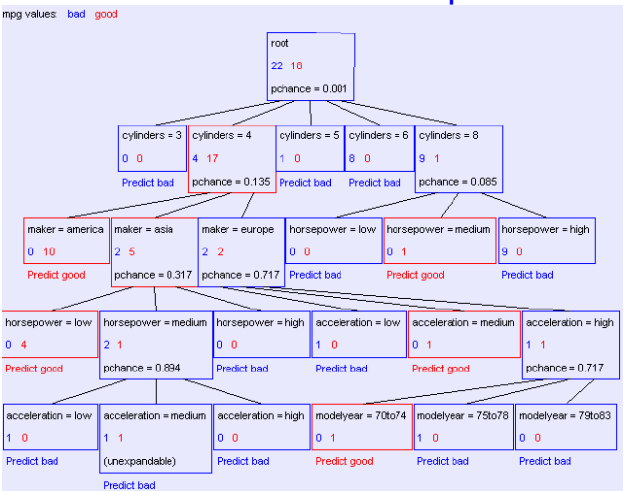
Resulting next level:

Decision tree example



Final tree:

Decision tree example



Decision tree example

Points:

- Don't split node if all records have same value (e.g. cylinders $= 6$)
- Don't split node if can't have more than 1 child (e.g. acceleration $=$ medium)

Pseudocode:

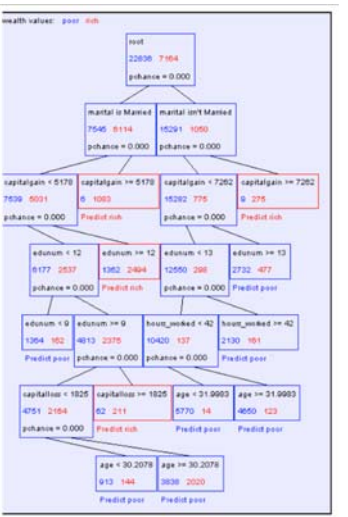
Program Tree(Input, Output)

If all output values are the same,
then return leaf (terminal) node which predicts the unique output
If input values are balanced in a leaf node (e.g. 1 good, 1 bad in acceleration)
then return leaf predicting majority of outputs on same level (e.g. bad in this case)
Else find attribute A_i with highest information gain

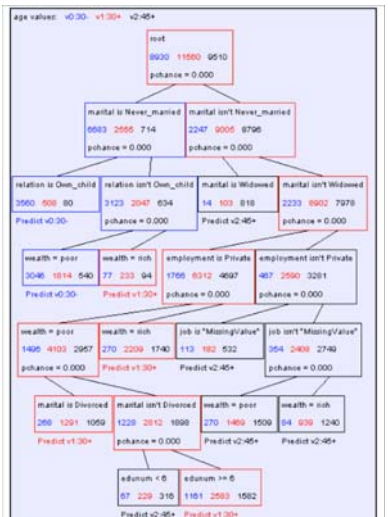
If attribute A_i at current node has m values

then Return internal (non-leaf) node with m children
Build child i by calling Tree(NewIn,
NewOut), where
NewIn $=$ values in
dataset consistent with value A_i and all
values above this node

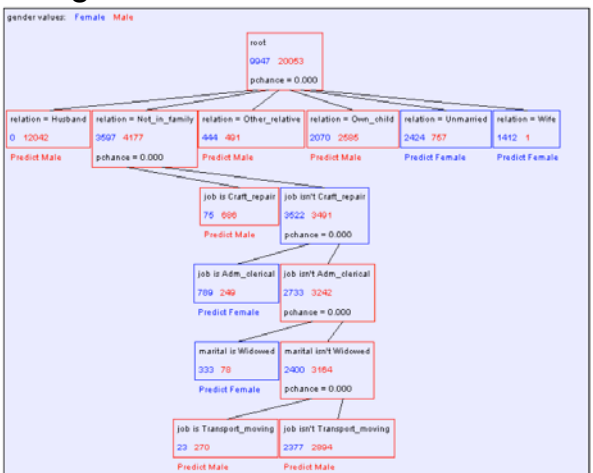
Another decision tree: prediction of wealth from census data (Moore):



Prediction of age from census:



Prediction of gender from census:



A. Moore

2. Important point: always cross-validate

It is important to test your model on *new* data (test data) which are different from the data used to train the model (training data).

This is *cross-validation.*

Cross-validation error – 2% is good; 40% is poor.

3. Background: mass spectroscopy

What does a mass spectrometer do?

1. It measures masses of molecules better than any other technique.

2. It can give information about chemical structures of molecules.

Mass spectroscopy

How does it work?

1. Takes unknown molecule M, adds i protons to it giving it charge $+i$ (forming MH_i^+)

2. Accelerates ion MH_i^+ in *known* electric field E.

3. Measures time of flight along a *known* distance D.

4. Time T of flight is inversely proportional to electric charge i and proportional to mass m of ion.

Mass spectroscopy

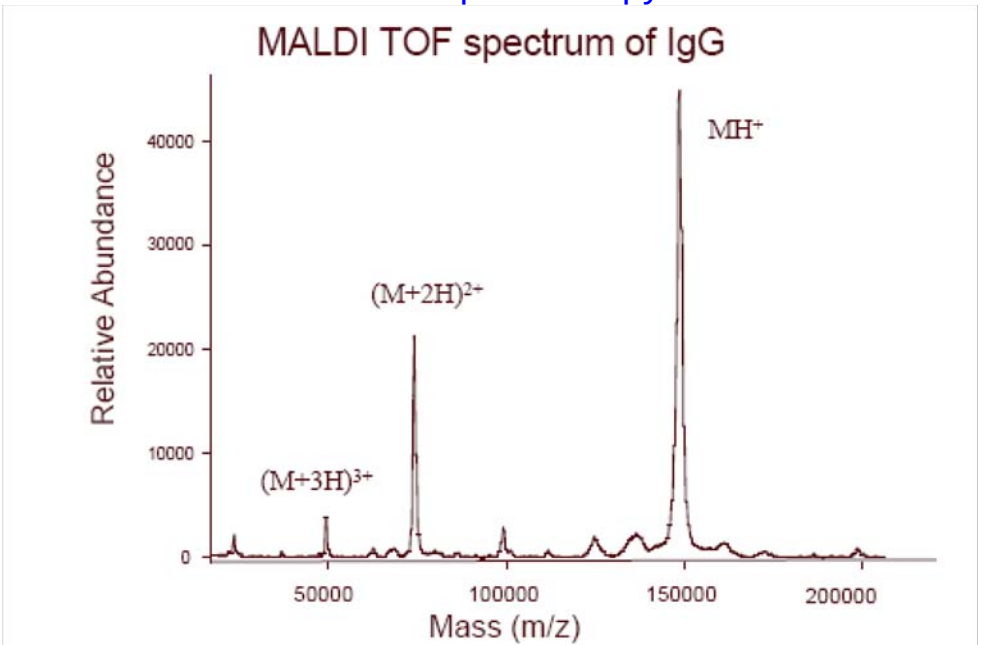
Thus

$$T \propto i/m$$

So mass spectrometer measures ratio of charge i (also known as z) and m, i.e., $i/m = z/m$.

With a large number of molecules in a biosample, this gives a spectrum of z/m values, which allows identification of molecules in sample (here IgG $=$ immunoglobin G)

Mass spectroscopy



Mass spectroscopy

What are the measurements good for?

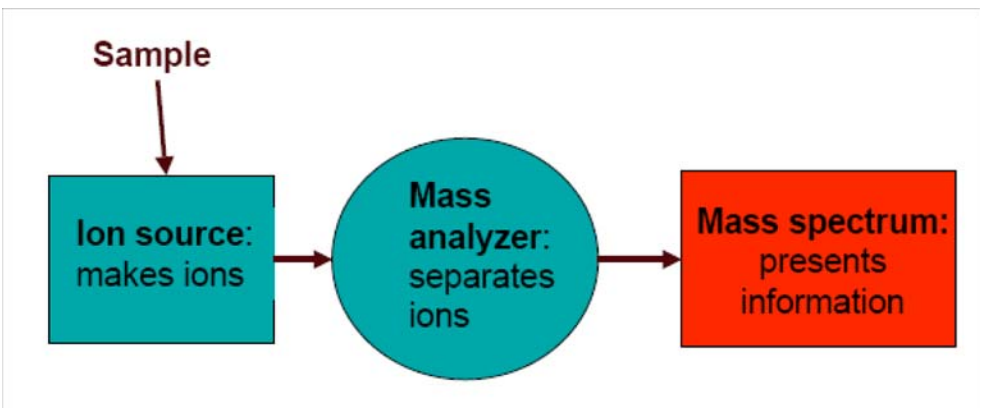
To identify, verify, and quantify: metabolites, proteins, oligonucleotides, drug candidates, peptides, synthetic organic chemicals, polymers

Applications of Mass Spectrometry

Biomolecule characterization
Pharmaceutical analysis
Proteins and peptides
Oligonucleotides

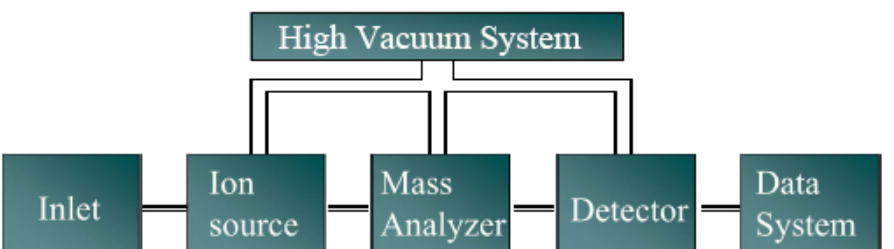
Mass spectroscopy

How does a mass spectrometer work?



Mass spectroscopy

Mass Spectrometer Block Diagram



[Source: Sandler Mass Spectroscopy]

Mass spectroscopy

Two types of ionization:

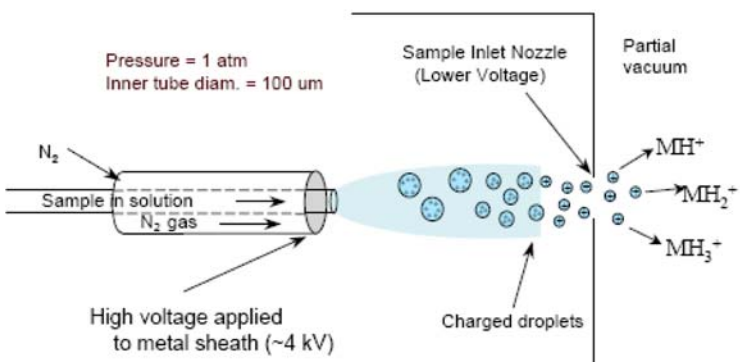
1. Electrospray ionization (ESI):

Mass spectroscopy

Ion Sources make ions from sample molecules

(Ions are easier to detect than neutral molecules.)

Electrospray ionization:



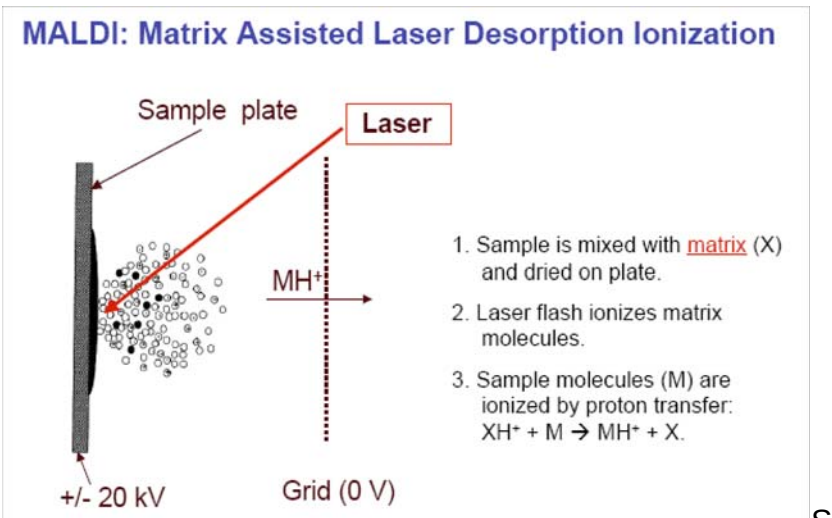
SMS

Mass spectroscopy

[above MH_i^+ denotes molecule with i protons (H^+) attached]

Mass spectroscopy

2. MALDI:



Mass spectroscopy

Mass analyzers separate ions based on their mass-to-charge ratio (m/z)

¤ Operate under high vacuum
¤ Measure mass-to-charge ratio of ions (m/z)

Mass spectroscopy

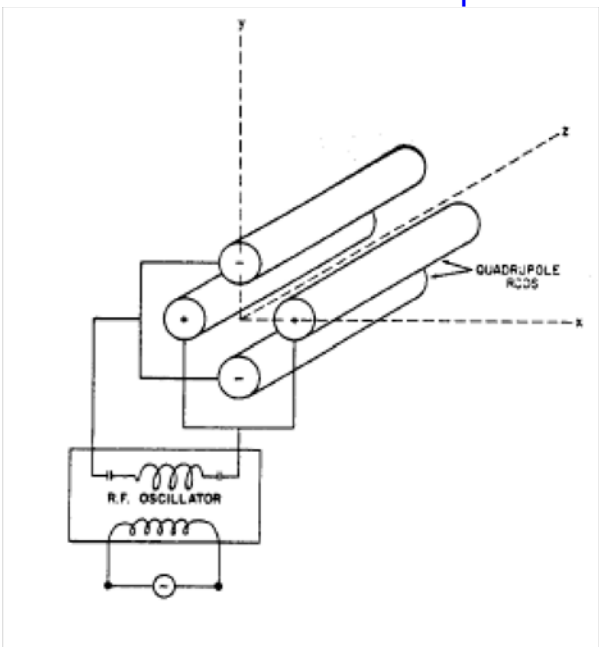
Components:

1. Quadrupole Mass Analyzer (filter)

Uses a combination of RF and DC voltages to operate as a mass filter before masses are accelerated.

- Has four parallel metal rods.
- Lets one mass pass through at a time.
- Can scan through all masses or only allow one fixed mass.

Mass spectroscopy

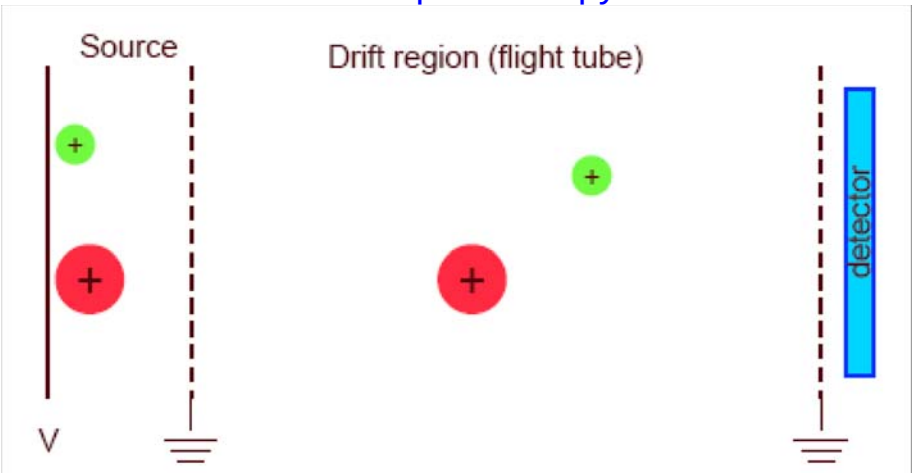


Mass spectroscopy

2. Time-of-flight (TOF) Mass Analyzer

Accelerates ions with electric field, detects them, analyzes flight time.

Mass spectroscopy



Mass spectroscopy

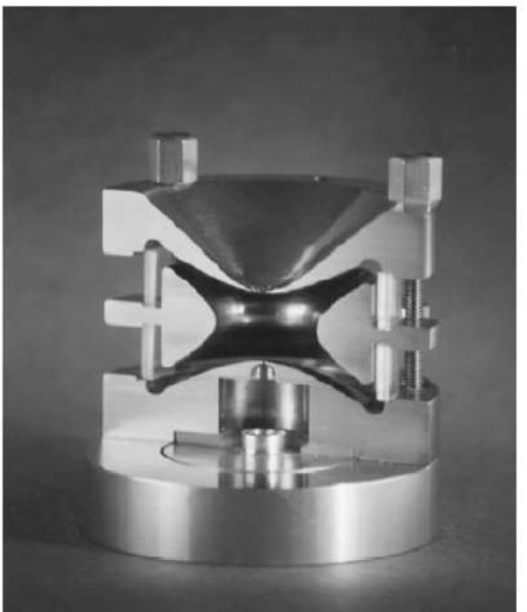
- Ions are formed in pulses.
- The drift region is field free.
- Measures the time for ions to reach the detector.
- Small ions reach the detector before large ones.

Ion trap mass analyzer:

Mass spectroscopy

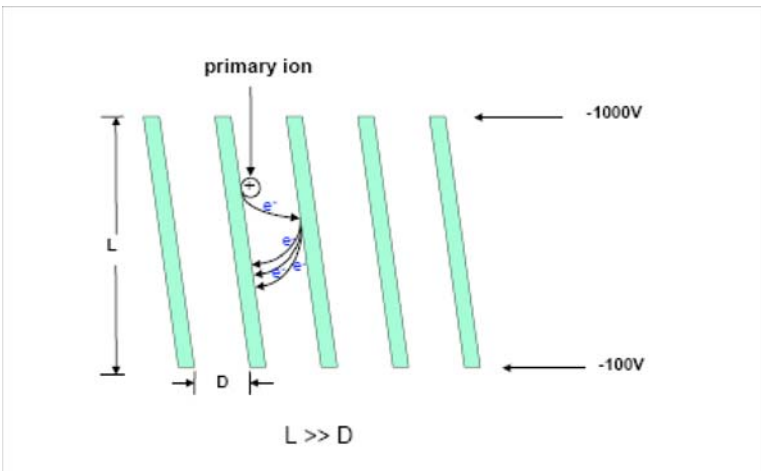
Top View

Cut away side view



Mass spectroscopy

3. Detector: Ions are detected with a microchannel plate:

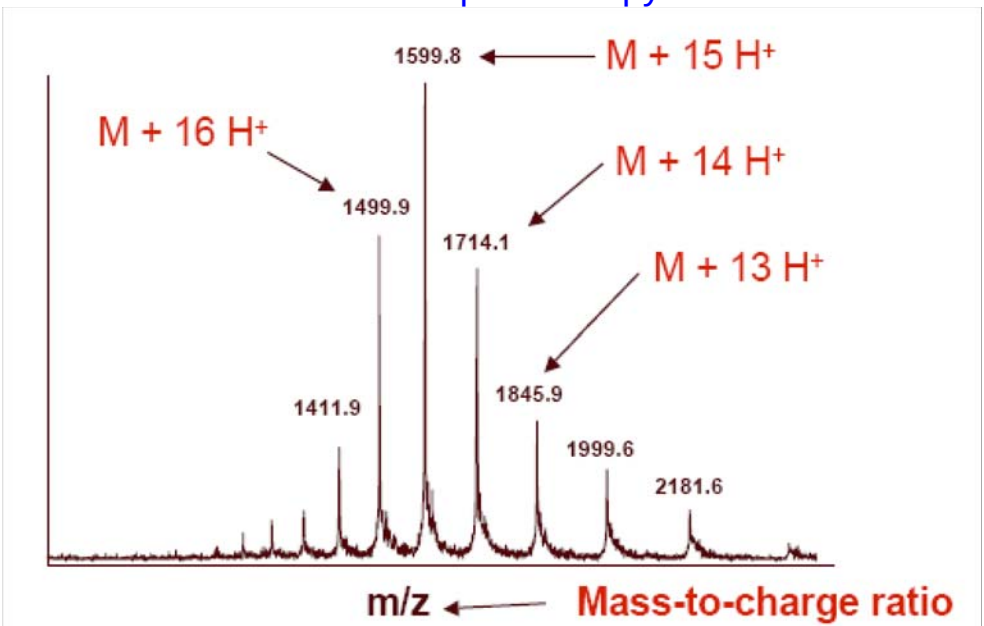


Mass spectroscopy

Mass spectrum shows the results:

ESI Spectrum of Trypsinogen (MW 23983)

Mass spectroscopy

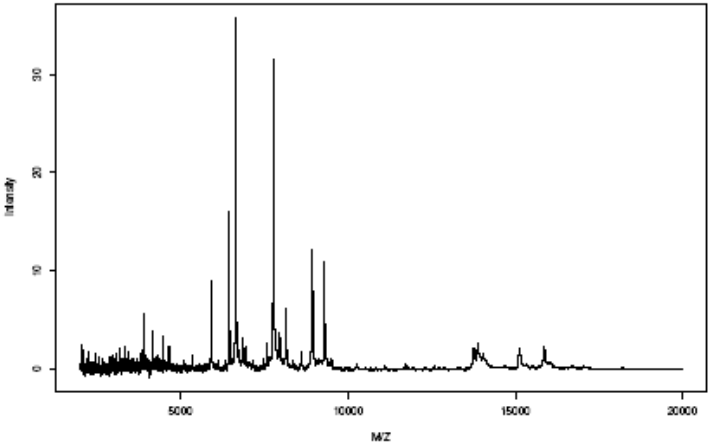


Mass spectroscopy

4. Dimensional reduction (G. Izmirlian):

Sometimes we perform a *dimension reduction* by reducing mass spectrum information of human subject i to store only peaks:

Mass spectroscopy



Mass spectroscopy

Then have (compressed) peak information in feature vector

$$\mathbf{x} = (x_1, \ldots, x_d),$$

with $x_k =$ location of k^{th} mass spectrum peak (above a fixed threshold).

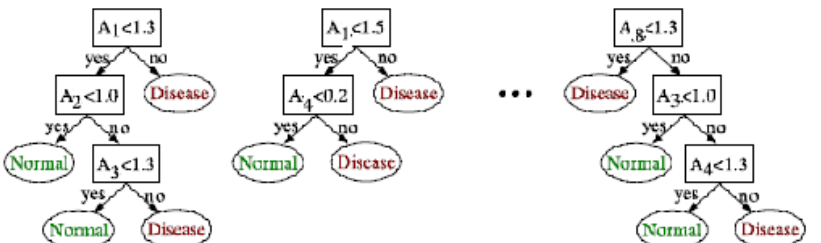
Compressed or not, outcome value to feature vector $\mathbf{x}_i$ for subject i is $y_i = \pm 1$.

5. Random forest example

Example (Guerts, et al.):

Normal/sick dichotomy for RA and for IBD (above - Geurts, et al.): we now build a forest of decision trees based on differing attributes in the nodes:

Random forest application

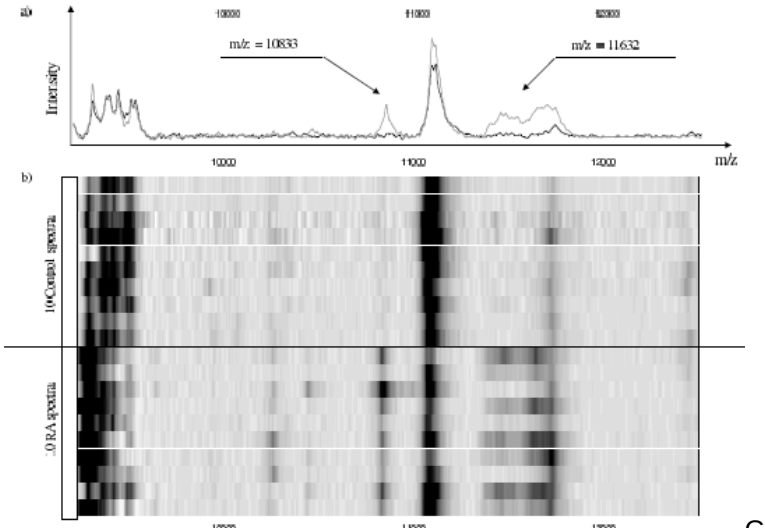


For example: Could use mass spectroscopy data to determine disease state

Random forest application

Mass Spec segregates protein and other molecules through spectrum of m/z ratios ($m =$ mass; $z =$ charge).

Random forest application



Geurts, et al.

Random Forests:

Advantages: accurate, easy to use (Breiman software), fast, robust

Disadvantages: difficult to interpret

More generally: How to combine results of different predictors (e.g. decision trees)?

Random forests are examples of *ensemble methods*, which combine predictions of weak classifiers $p_i(\mathbf{x})$.

Ensemble methods: observations

1. Boosting: As seen earlier, take linear combination of predictions $p_i(\mathbf{x})$ by classifiers i (assume these are decision trees)

$$f(\mathbf{x}) = \sum_i a_i p_i(\mathbf{x}), \tag{1}$$

where $p_i(\mathbf{x}) = \begin{cases} 1 & \text{if } i^{th} \text{ tree predicts illness} \\ -1 & \text{otherwise} \end{cases}$,

and predict $y = 1$ if $f(\mathbf{x}) \geq 0$ and $y = -1$ if $f(\mathbf{x}) < 0$.

Ensemble methods: observations

2. **Bagging:** Take a vote: majority rules (equivalent in this case to setting $a_i = 1$ for all i in (1) above).

Example of a **Bagging** algorithm is *random forest*, where a forest of decision trees takes a vote.

General features of a random forest:

If original feature vector **x** $\in \mathbb{R}^d$ has d features $A_1, \ldots, A_d$,

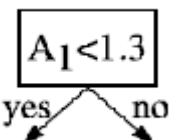
- Each tree uses a random selection of $m \approx \sqrt{d}$ features $\{A_{i_j}\}_{j=1}^{m}$ chosen from *all* features $A_1, A_2, \ldots, A_d$; the associated feature space is different for each tree and denoted by F_k, $1 \leq k \leq K = \#\,\text{trees}$.

  (Often $K = \#\,\text{trees}$ is large; e.g., $K = 500$).

- For each split in a tree node based on a given variable choose the variable A_i from information content.

Information content in a node

To compute information content of a node:



Assume input set to node is S: then information content of node N is

Information content in a node

$$I(N) = |S|\ H(S) - |S_L|\ H(S_L) - |S_R|\ H(S_R),$$

where

$|S| =$ input sample size; $|S_{L,R}| =$ size of left, right subclasses of S

$$H(S) = \text{Shannon entropy of } S = -\sum_{i=\pm 1} p_i \log_2 p_i$$

with

$$p_i = \widehat{P}(C_i|S) = \text{proportion of class } C_i \text{ in sample } S.$$

Information content in a node

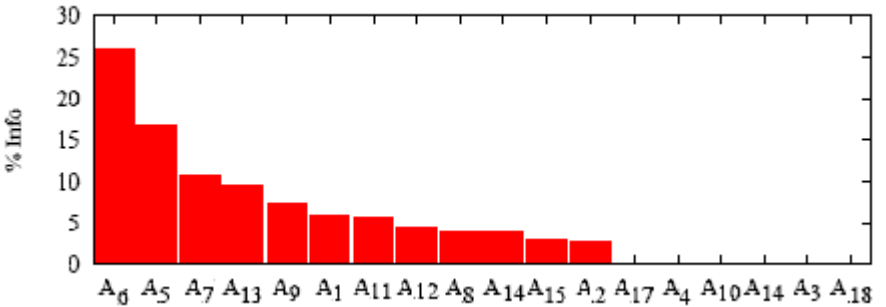
[later we will use *Gini index*, another criterion]

Thus $H(S) =$ "variablity" or "lack of full information" in the probabilities p_i forming sample S input into current node N.

$$I(N) = \text{"information from node } N\text{"}.$$

For each variable A_i, average over all nodes N in all trees involving this variable to find average information content $H_{\text{av}}(A_i)$ of A_i.

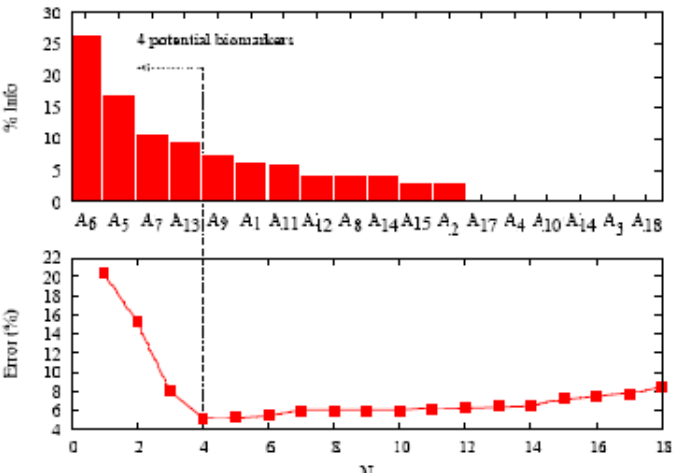
Information content in a node



(a) Rank all variables A_i according to information content

(b) For each fixed $n_1 < n$ use only the first n_1 variables. Select n_1 which minimizes prediction error.

Information content in a node



Geurts, et al.

Random forests: application

Application to:

- early diagnosis of Rehumatoid arthritis
- rapid diagnosis of inflammatory bowel diseases (IBD)

3 patient groups (University Hospital of Liege):

Random forests: application

	RA	IBD
Disease patients	34	60
Negative controls	29	30
Inflammatory controls	40	30
Total	103	120

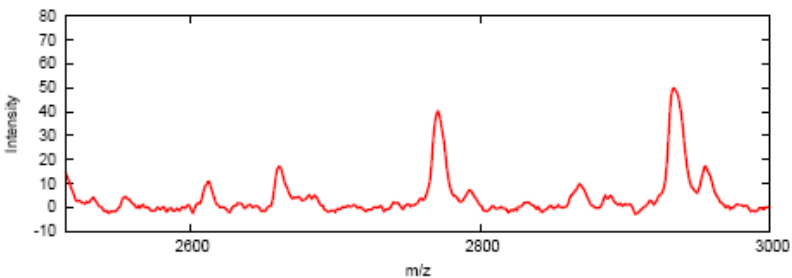
Mass spectra obtained by SELDI-TOF mass spectrometry on chip arrays:

Random forests: application

- Hydrophobic (H4)
- weak cation-exchange (CM10)
- strong cation-exchange (Q10)

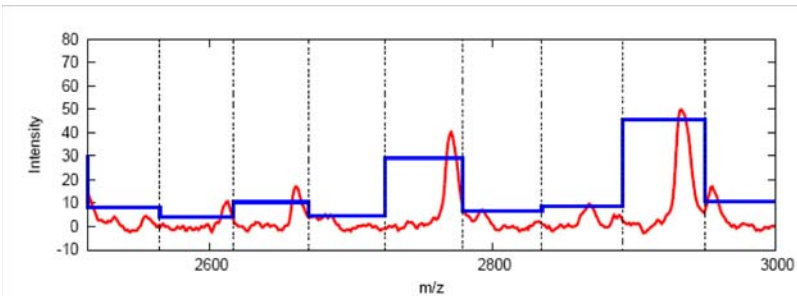
Random forests: application

Feature vectors: $\mathbf{x} \in F$ consists of about 15,000 values in each case.



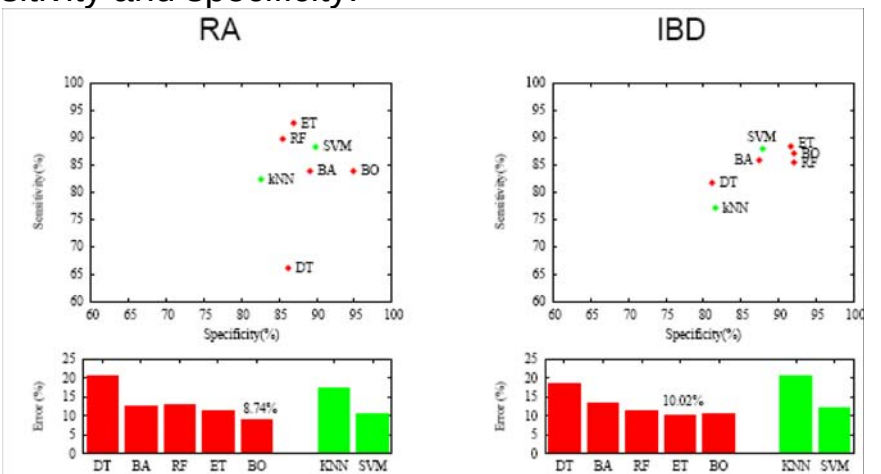
Effective dimension reduction method: Discretize horizontally and vertically to go from 15,000 to 300 variables

Random forests: application



Random forests: application

Sensitivity and specificity:



Random forests: application

Accuracy measures: DT=Decision tree;
RF=random forest; kNN = k-nearest neighbors;

Note on sensitivity and specificity: use confusion matrix

Test outcome

	Actual Condition: True	Actual Condition: False
Positive	TP	FP
Negative	FN	TN

Random forests: application

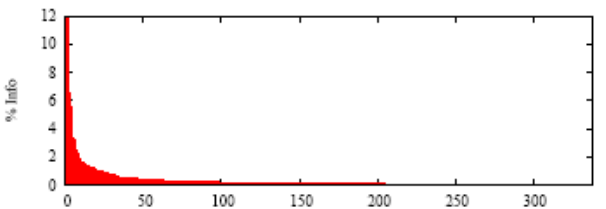
$$\text{Sensitivity} = \frac{TP}{TP + FN} = \frac{TP}{\text{Total positives}}$$

$$\text{Specificity} = \frac{TN}{TN + FP} = \frac{TN}{\text{Total negatives}}$$

$$\text{Positive predictive value} = \frac{TP}{TP+FP} = \frac{TP}{\text{Total predicted positives}}$$

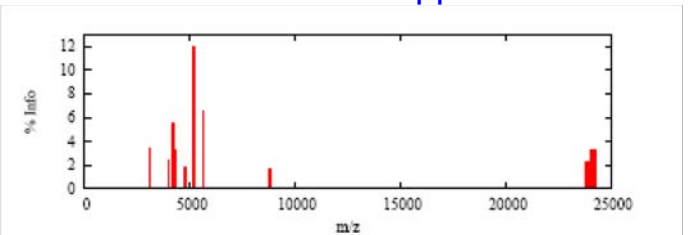
Random forests: application

Variable ranking on the IBD dataset:



10 most important variables in spectrum:

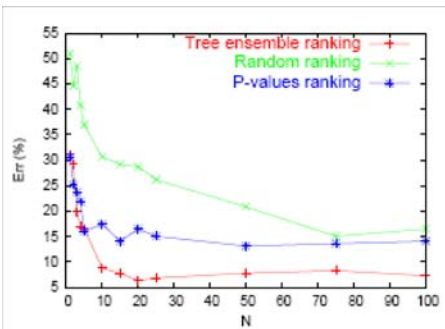
Random forests: application



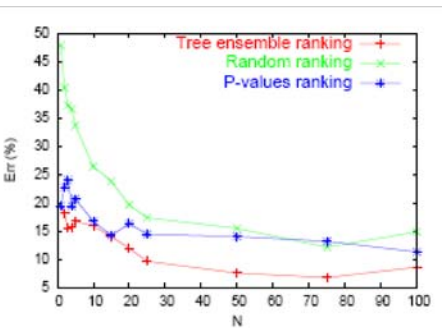
RF-based (tree ensemble) - based variable ranking
vs. variable ranking by individual variable p values:

Random forests: application

RA



IBD



6. RF software:

Spider:
http://www.kyb.tuebingen.mpg.de/bs/people/spider/whatisit.html

Leo Breiman:
http://www.stat.berkeley.edu/~breiman/RandomForests/cc_software.htm

WEKA machine learning software
http://www.cs.waikato.ac.nz/ml/weka/
http://en.wikipedia.org/wiki/Weka_(machine_learning)