# Advanced statistical methods for data analysis – Lecture 4



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### Outline

Multivariate methods in particle physics

Some general considerations

Brief review of statistical formalism

Multivariate classifiers:

Linear discriminant function

Neural networks

Naive Bayes classifier

*k*-Nearest-Neighbour method

Decision trees

**Support Vector Machines** 

Lecture 4 start

#### Decision trees

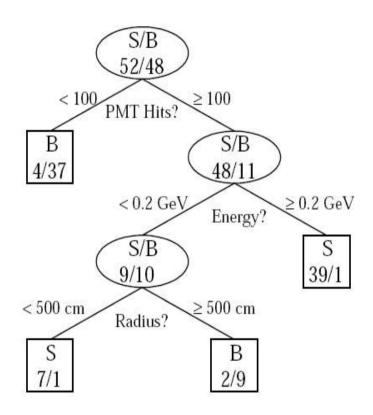
In a decision tree repeated cuts are made on a single variable until some stop criterion is reached.

The decision as to which variable is used is based on best achieved improvement in signal purity:

$$P = \frac{\sum_{\text{signal}} w_i}{\sum_{\text{signal}} w_i + \sum_{\text{background}} w_i}$$

where  $w_i$  is the weight of the *i*th event.

Iterate until stop criterion reached, based e.g. on purity and minimum number of events in a node.



Example by MiniBooNE experiment, B. Roe et al., NIM 543 (2005) 577

## Decision trees (2)

The terminal nodes (leaves) are classified as signal or background depending on majority vote (or e.g. signal fraction greater than a specified threshold).

This classifies every point in input-variable space as either signal or background, a decision tree classifier, with the discriminant function

$$f(x)=1$$
 if  $x \in \text{signal region}$ ,  $-1$  otherwise

The same variable may be used at several nodes; others may not be used at all.

In principle a decision tree classifier can have perfect separation between the event classes (will happen e.g. if the terminal nodes have a single event).

This would clearly be a very over-trained classifier.

## Decision tree size and stability

Usually one grows the tree first to a very large (e.g. maximum) size and then applies pruning.

For example one can recombine leaves based on some measure of generalization performance (e.g. using statistical error of purity estimates).

Decision trees tend to be very sensitive to statistical fluctuations in the training sample.

Methods such as boosting can be used to stabilize the tree.

## Boosting

Boosting is a general method of creating a set of classifiers which can be combined to achieve a new classifier that is more stable and has a smaller error than any individual one.

Often applied to decision trees but, can be applied to any classifier.

Suppose we have a training sample T consisting of N events with

 $x_1, ..., x_N$  event data vectors (each x multivariate)

 $y_1, \dots, y_N$  true class labels, +1 for signal, -1 for background

 $w_1, \dots, w_N$  event weights

Now define a rule to create from this an ensemble of training samples  $T_1, T_2, \dots$ , derive a classifier from each and average them.

Trick is to create modifications in the training sample that give classifiers with smaller error rates than those of the preceding ones.

A successful example is AdaBoost (Freund and Schapire, 1997).

#### AdaBoost

First initialize the training sample  $T_1$  using the original

$$x_1,...,x_N$$
 event data vectors  $y_1,...,y_N$  true class labels (+1 or -1)  $w_1^{(1)},...,w_N^{(1)}$  event weights

with the weights equal and normalized such that

$$\sum_{i=1}^{N} w_i^{(1)} = 1$$

Then train the classifier  $f_1(x)$  (e.g. a decision tree) with a method that incorporates the event weights. For an event with data  $x_i$ ,

$$f_k(\mathbf{x}_i) > 0$$
 classify as signal  $f_k(\mathbf{x}_i) < 0$  classify as background

## Updating the event weights

Define the training sample for step k+1 from that of k by updating the event weights according to

$$w_i^{(k+1)} = w_i^{(k)} \frac{e^{-\alpha_k f_k(\mathbf{x}_i) y_i/2}}{Z_k}$$

$$i = \text{event index} \qquad k = \text{training sample index}$$

where  $Z_k$  is a normalization factor defined such that the sum of the weights over all events is equal to one.

Therefore event weight for event i is increased in the k+1 training sample if it was classified incorrectly in sample k.

Idea is that next time around the classifier should pay more attention to this event and try to get it right.

#### Error rate of the kth classifier

At each step the classifiers  $f_k(x)$  are defined so as to minimize the error rate  $\varepsilon_k$ ,

$$\varepsilon_{k} = \sum_{i=1}^{N} w_{i}^{(k)} I(y_{i} f_{k}(\boldsymbol{x}_{i}) \leq 0)$$

where I(X) = 1 if X is true and is zero otherwise.

## Assigning the classifier score

Assign a score to the kth classifier based on its error rate,

$$\alpha_k = \ln \frac{1 - \varepsilon_k}{\varepsilon_k}$$

If we define the final classifier as  $f(\mathbf{x}) = \sum_{k=1}^{K} \alpha_k f_k(\mathbf{x}, T_k)$ 

then one can show that its error rate on the training data satisfies the bound

$$\varepsilon \leq \prod_{k=1}^{K} 2\sqrt{\varepsilon_k (1 - \varepsilon_k)}$$

#### AdaBoost error rate

So providing each classifier in the ensemble has  $\varepsilon_k > \frac{1}{2}$ , i.e., better than random guessing, then the error rate for the final classifier on the training data (not on unseen data) drops to zero.

That is, for sufficiently large *K* the training data will be over fitted.

The error rate on a validation sample would reach some minimum after a certain number of steps and then could rise.

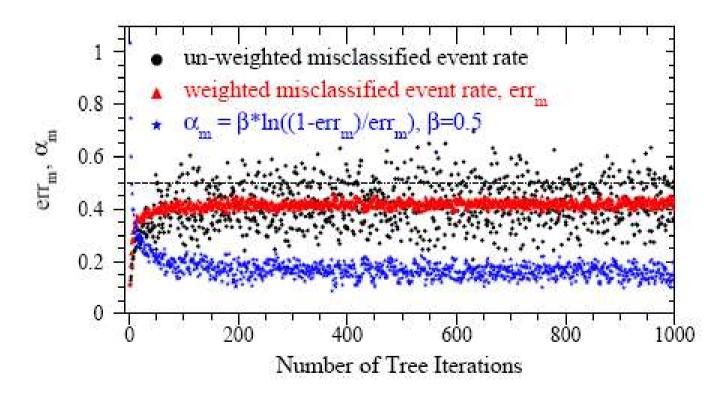
So the procedure is to monitor the error rate of the combined classifier at each step with a validation sample and to stop before it starts to rise.

Although in principle AdaBoost must overfit, in practice following this procedure overtraining is not a big problem.

## BDT example from MiniBooNE

~200 input variables for each event ( $\nu$  interaction producing e,  $\mu$  or  $\pi$ ).

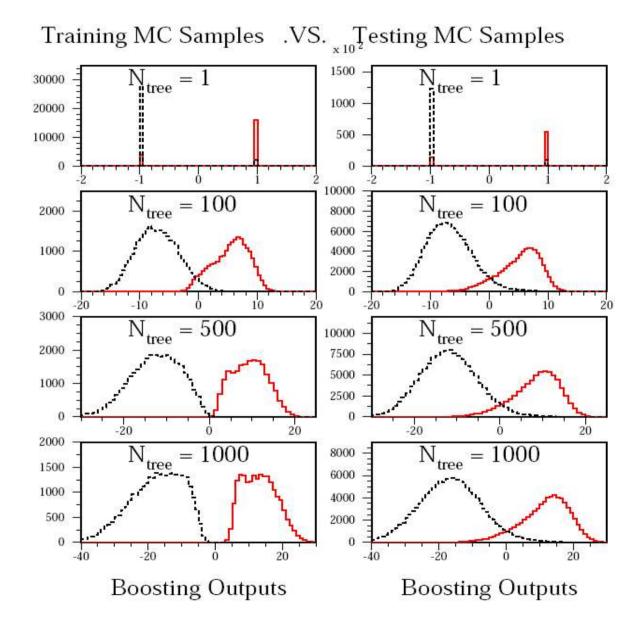
Each individual tree is relatively weak, with a misclassification error rate  $\sim 0.4 - 0.45$ 



B. Roe et al., NIM 543 (2005) 577

## Monitoring overtraining

From MiniBooNE example



## Boosted decision tree summary

Advantage of boosted decision tree is it can handle a large number of inputs. Those that provide little/no separation are rarely used as tree splitters are effectively ignored.

Easy to deal with inputs of mixed types (real, integer, categorical...).

If a tree has only a few leaves it is easy to visualize (but rarely use only a single tree).

There are a number of boosting algorithms, which differ primarily in the rule for updating the weights (\varepsilon-Boost, LogitBoost,...)

Other ways of combining weaker classifiers: Bagging (Boostrap-Aggregating), generates the ensemble of classifiers by random sampling with replacement from the full training sample.

## Support Vector Machines

Support Vector Machines (SVMs) are an example of a kernel-based classifier, which exploits a nonlinear mapping of the input variables onto a higher dimensional feature space.

The SVM finds a linear decision boundary in the higher dimensional space.

But thanks to the "kernel trick" one does not every have to write down explicitly the feature space transformation.

Some references for kernel methods and SVMs:

The books mentioned on Monday

C. Burges, A Tutorial on Support Vector Machines for Pattern Recognition, research.microsoft.com/~cburges/papers/SVMTutorial.pdf

N. Cristianini and J.Shawe-Taylor. An Introduction to Support Vector Machines and other kernel-based learning methods. Cambridge University Press, 2000. The TMVA manual (!)

#### Linear SVMs

Consider a training data set consisting of

$$x_1, \dots, x_N$$
 event data vectors

$$y_1, \dots, y_N$$
 true class labels (+1 or -1)

Suppose the classes can be separated by a hyperplane defined by a normal vector w and scalar offset b (the "bias"). We have

$$x_i \cdot w + b \ge +1$$

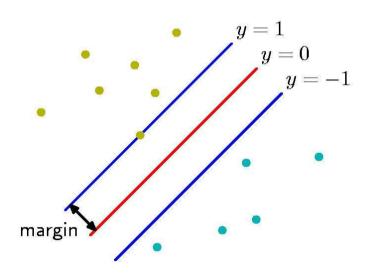
for all 
$$y_i = +1$$

$$x_i \cdot w + b \leq -1$$

for all 
$$y_i = -1$$

or equivalently

$$y_i(\mathbf{x}_i \cdot \mathbf{w} + b) - 1 \ge 0$$
 for all  $i$ 

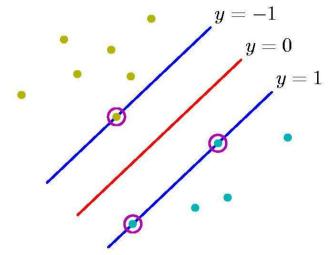


Bishop Ch. 7

## Margin and support vectors

The distance between the hyperplanes defined by y(x) = +1 and y(x) = -1 is called the margin, which is:

$$\text{margin} = \frac{2}{\|\boldsymbol{w}\|}$$



If the training data are perfectly separated then this means there are no points inside the margin.

Suppose there are points on the margin (this is equivalent to defining the scale of w). These points are called support vectors.

#### Linear SVM classifier

We can define the classifier using

$$y(\mathbf{x}) = \operatorname{sign}(\mathbf{x} \cdot \mathbf{w} + b)$$

which is +1 for points on one side of the hyperplane and -1 on the other.

The best classifier should have a large margin, so to maximize

$$margin = \frac{2}{\|\mathbf{w}\|}$$

we can minimize  $\|\mathbf{w}\|^2$  subject to the constraints

$$y_i(\mathbf{x}_i \cdot \mathbf{w} + b) - 1 \ge 0$$
 for all  $i$ 

## Lagrangian formulation

This constrained minimization problem can be reformulated using a Lagrangian

$$L = \frac{1}{2} ||\mathbf{w}||^2 - \sum_{i=1}^{N} \alpha_i (y_i (\mathbf{x}_i \cdot \mathbf{w} + b) - 1)$$

positive Lagrange multipliers α,

We need to minimize L with respect to w and b and maximize with respect to  $\alpha_i$ .

There is an  $\alpha_i$  for every training point. Those that lie on the margin (the support vectors) have  $\alpha_i > 0$ , all others have  $\alpha_i = 0$ . The solution can be written

$$w = \sum_{i} \alpha_{i} y_{i} x_{i}$$
 (sum only contains support vectors)

#### Dual formulation

The classifier function is thus

$$y(\mathbf{x}) = \operatorname{sign}(\mathbf{x} \cdot \mathbf{w} + b) = \operatorname{sign}\left(\sum_{i} \alpha_{i} y_{i} \mathbf{x} \cdot \mathbf{x}_{i} + b\right)$$

It can be shown that one finds the same solution a by minimizing the dual Lagrangian

$$L_D = \sum_i \alpha_i - \frac{1}{2} \sum_{i,j} \alpha_i \alpha_j y_i y_j x_i \cdot x_j$$

So this means that both the classifier function and the Lagrangian only involve dot products of vectors in the input variable space.

## Nonseparable data

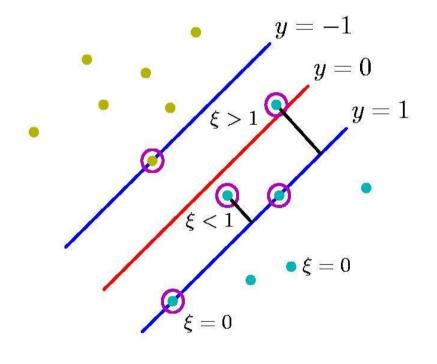
If the training data points cannot be separated by a hyperplane, one can redefine the constraints by adding slack variables  $\xi_i$ :

$$y_i(\mathbf{x}_i \cdot \mathbf{w} + b) + \xi_i - 1 \ge 0 \text{ with } \xi_i \ge 0 \text{ for all } i$$

Thus the training point  $x_i$  is allowed to be up to a distance  $\xi_i$  on the wrong side of the boundary, and  $\xi_i = 0$  at or on the right side of the boundary.

For an error to occur we have  $\xi_i > 1$ , so

$$\sum_{i} \xi_{i}$$



is an upper bound on the number of training errors.

## Cost function for nonseparable case

To limit the magnitudes of the  $\xi_i$  we can define the error function that we minimize to determine w to be

$$E(\mathbf{w}) = \frac{1}{2} ||\mathbf{w}||^2 + C \left(\sum_{i} \xi_{i}\right)^{k}$$

where C is a cost parameter we must choose that limits the amount of misclassification. It turns out that for k=1 or 2 this is a quadratic programming problem and furthermore for k=1 it corresponds to minimizing the same dual Lagrangian

$$L_D = \sum_i \alpha_i - \frac{1}{2} \sum_{i,j} \alpha_i \alpha_j y_i y_j x_i \cdot x_j$$

where the constraints on the  $\alpha_i$  become  $0 \le \alpha_i \le C$ .

#### Nonlinear SVM

So far we have only reformulated a way to determine a linear classifier, which we know is useful only in limited circumstances.

But the important extension to nonlinear classifiers comes from first transforming the input variables to feature space:

$$\vec{\boldsymbol{\varphi}}(\boldsymbol{x}) = (\boldsymbol{\varphi}_1(\boldsymbol{x}), \dots, \boldsymbol{\varphi}_m(\boldsymbol{x}))$$

These will behave just as our new "input variables". Everything about the mathematical formulation of the SVM will look the same as before except with  $\phi(x)$  appearing in the place of x.

## Only dot products

Recall the SVM problem was formulated entirely in terms of dot products of the input variables, e.g., the classifier is

$$y(\mathbf{x}) = \operatorname{sign}\left(\sum_{i} \alpha_{i} y_{i} \mathbf{x} \cdot \mathbf{x}_{i} + b\right)$$

so in the feature space this becomes

$$y(\mathbf{x}) = \operatorname{sign}\left(\sum_{i} \alpha_{i} y_{i} \vec{\boldsymbol{\varphi}}(\mathbf{x}) \cdot \vec{\boldsymbol{\varphi}}(\mathbf{x}_{i}) + b\right)$$

#### The Kernel trick

How do the dot products help? It turns on that a broad class of kernel functions can be written in the form:

$$K(\mathbf{x}, \mathbf{x}') = \vec{\boldsymbol{\varphi}}(\mathbf{x}) \cdot \vec{\boldsymbol{\varphi}}(\mathbf{x}')$$

Functions having this property must satisfy Mercer's condition

$$\int K(\mathbf{x}, \mathbf{x}') g(\mathbf{x}) g(\mathbf{x}') d\mathbf{x} d\mathbf{x}' \ge 0$$

for any function g where  $\int g^2(x) dx$  is finite.

So we don't even need to find explicitly the feature space transformation  $\phi(x)$ , we only need a kernel.

## Finding kernels

There are a number of techniques for finding kernels, e.g., constructing new ones from known ones according to certain rules (cf. Bishop Ch 6).

Frequently used kernels to construct classifiers are e.g.

$$K(\mathbf{x}, \mathbf{x}') = (\mathbf{x} \cdot \mathbf{x}' + \theta)^p$$

polynomial

$$K(\boldsymbol{x}, \boldsymbol{x}') = \exp\left(\frac{-\|\boldsymbol{x}-\boldsymbol{x}'\|^2}{2\sigma^2}\right)$$

Gaussian

$$K(\mathbf{x}, \mathbf{x}') = \tanh(\kappa(\mathbf{x} \cdot \mathbf{x}') + \theta)$$

sigmoidal

## Using an SVM

To use an SVM the user must as a minimum choose

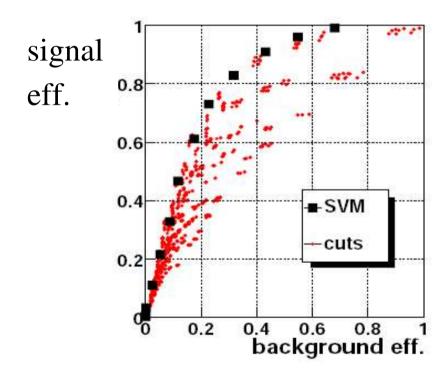
a kernel function (e.g. Gaussian) any free parameters in the kernel (e.g. the  $\sigma$  of the Gaussian) the cost parameter C (plays role of regularization parameter)

The training is relatively straightforward because, in contrast to neural networks, the function to be minimized has a single global minimum.

Furthermore evaluating the classifier only requires that one retain and sum over the support vectors, a relatively small number of points.

### SVM in HEP

SVMs are very popular in the Machine Learning community but have yet to find wide application in HEP. Here is an early example from a CDF top quark anlaysis (A. Vaiciulis, contribution to PHYSTAT02).



#### Multivariate analysis discussion

For all methods, need to check:

Sensitivity to statistically unimportant variables (best to drop those that don't provide discrimination);

Level of smoothness in decision boundary (sensitivity to over-training)

Given the test variable, next step is e.g., select n events and estimate a cross section of signal:  $\hat{\sigma}_s = (n-b)/\varepsilon_s L$ 

Now need to estimate systematic error...

If e.g. training (MC) data  $\neq$  Nature, test variable is not optimal, but not necessarily biased.

But our estimates of background b and efficiencies would then be biased if based on MC. (True also for 'simple cuts'.)

#### Multivariate analysis discussion (2)

But in a cut-based analysis it may be easier to avoid regions where untested features of MC are strongly influencing the decision boundary.

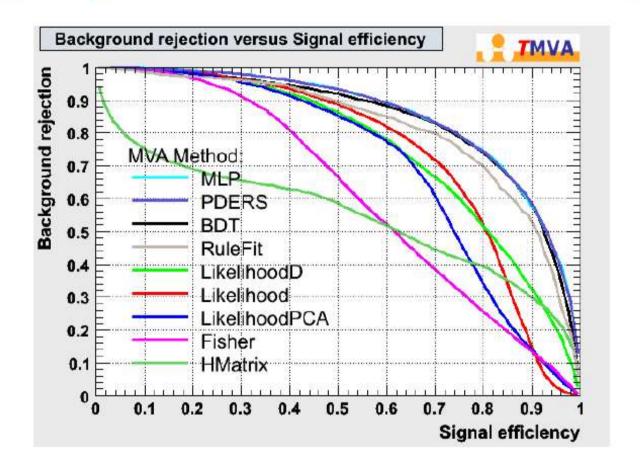
Look at control samples to test joint distributions of inputs.

Try to estimate backgrounds directly from the data (sidebands).

The purpose of the statistical test is often to select objects for further study and then measure their properties.

Need to avoid input variables that are correlated with the properties of the selected objects that you want to study. (Not always easy; correlations may be poorly known.)

#### Comparing multivariate methods (TMVA)



Choose the best one!

## Lecture 4 summary

Boosted Decision Trees and Support Vector Machines are two examples of relatively modern developments in Machine Learning that are only recently attracting attention in HEP.

There are now many multivariate methods on the market and it is difficult to make general statements about performance; this is often very specific to the problem.

Expect advanced multivariate methods to have a major impact in areas where one struggles for statistical significance, not in precision measurements.

Fortunately tools to investigate these methods are now widely available.

## Quotes I like

"Keep it simple.

As simple as possible.

Not any simpler."

- A. Einstein

"If you believe in something
you don't understand, you suffer,.."

- Stevie Wonder

## Extra slides

## Boosted decision tree example

First use of boosted decision trees in HEP was for particle identification for the MiniBoone neutrino oscillation experiment.

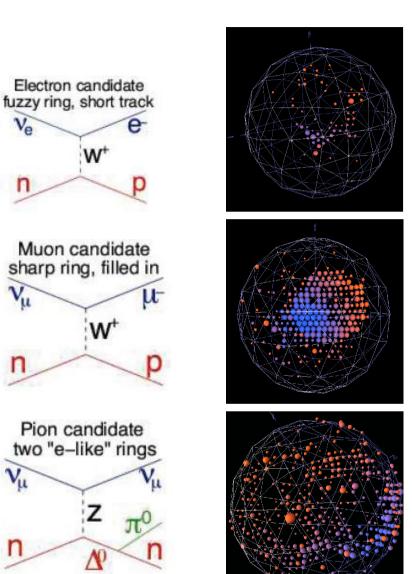
H.J.Yang, B.P. Roe, J. Zhu, "Studies of Boosted Decision Trees for MiniBooNE Particle Identification", Physics/0508045, Nucl. Instum. & Meth. A 555(2005) 370-385.

B.P. Roe, H.J. Yang, J. Zhu, Y. Liu, I. Stancu, G. McGregor, "Boosted decision trees as an alternative to artificial neural networks for particle identification", physics/0408124, NIMA 543 (2005) 577-584.

### Particle i.d. in MiniBooNE

Search for  $v_{\mu}$  to  $v_{e}$  oscillations required particle i.d. using information from Cherenkov detector.

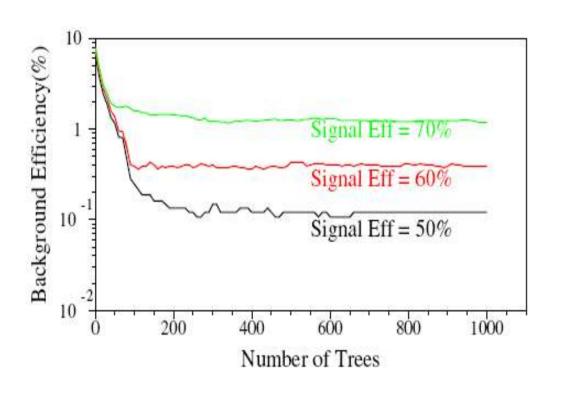
Large number (~200) input variables measured for each event.

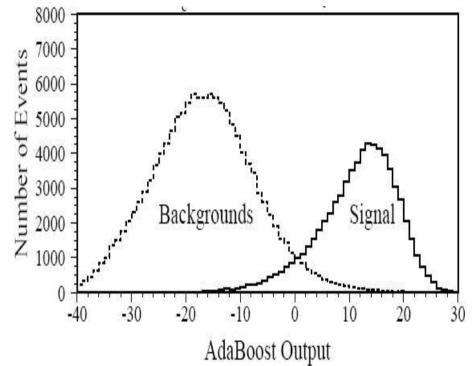


H.J. Yang, MiniBooNE PID, DNP06

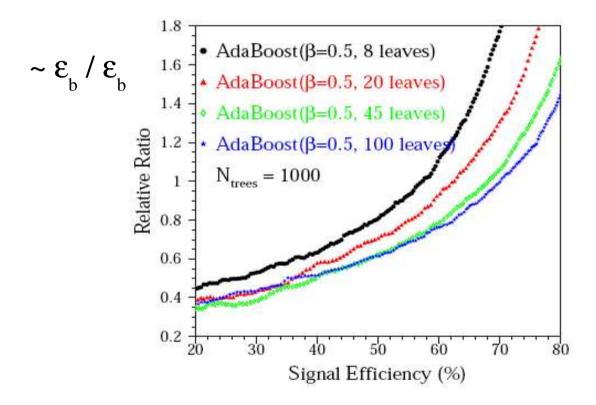
#### MiniBoone boosted decision tree

#### Here performance stable after a few hundred trees



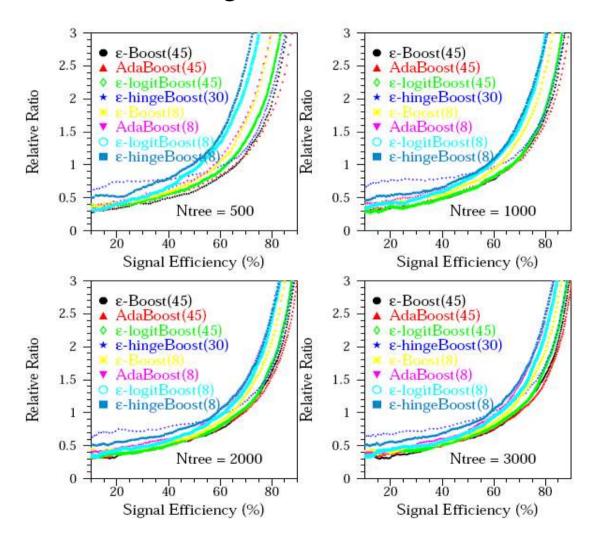


## MiniBooNE Decision tree performance



## Comparison of boosting algorithms

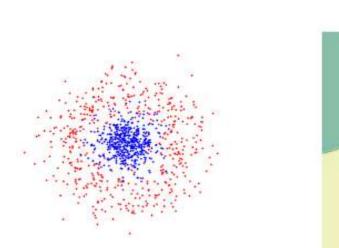
A number of boosting algorithms on the market; differ in the update rule for the tree weight.

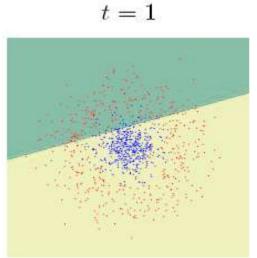


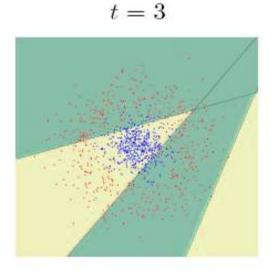
## AdaBoost study with linear classifier

J. Sochman, J. Matas, cmp.felk.cvut.cz

Start with a problem for which a linear classifier is weak:

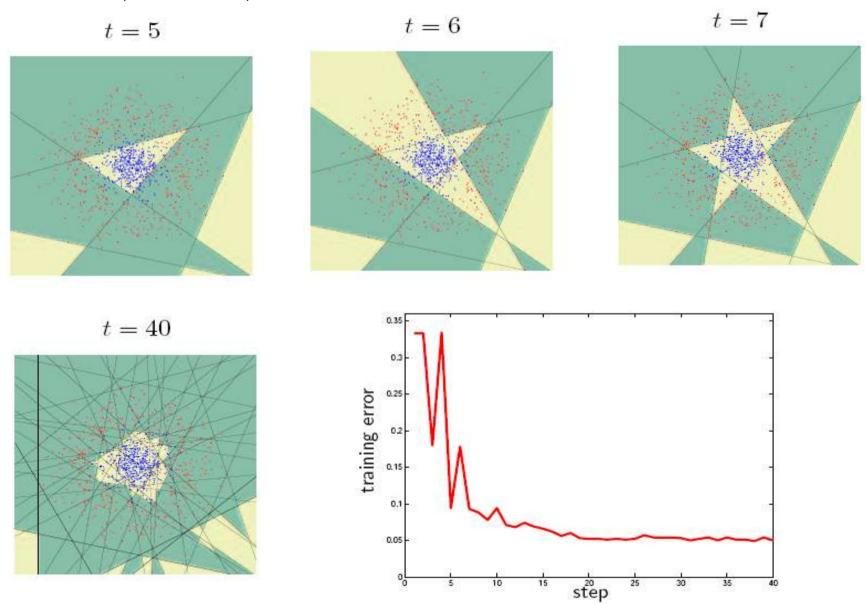






## AdaBoost study with linear classifier

J. Sochman, J. Matas, cmp.felk.cvut.cz



## Imperfect pdf estimation

What if the approximation we use (e.g., parametric form, assumption of variable independence, etc.) to estimate p(x) is wrong?

If we use poor estimates to construct the test variable

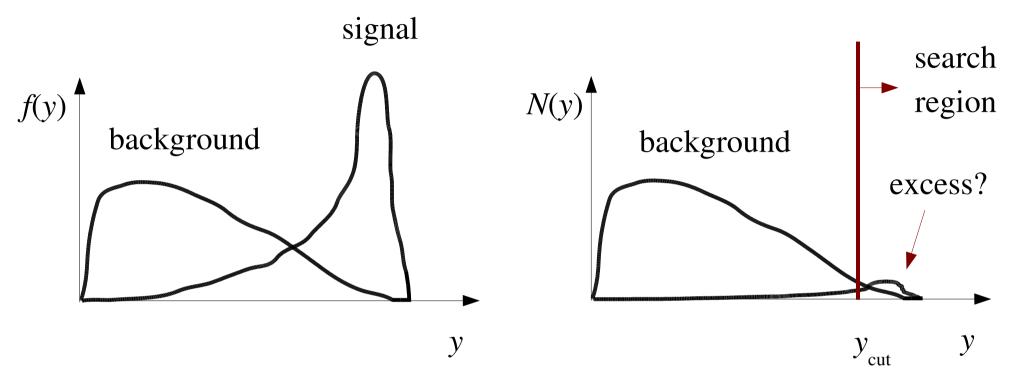
$$y(\vec{x}) = \frac{\hat{p}(\vec{x}|H_0)}{\hat{p}(\vec{x}|H_1)}$$

then the discrimination between the event classes will not be optimal.

But can this cause us e.g. to make a false discovery?

Even if the estimate of p(x) used in the discriminating variable are imperfect, this will not affect the accuracy of the distributions  $f(y|H_0)$ ,  $f(y|H_1)$ ; this only depends on the reliability of the training data.

## Using the classifier output for discovery



Normalized to unity

Normalized to expected number of events

Discovery = number of events found in search region incompatible with background-only hypothesis. Maximize the probability of this happening by setting  $y_{\text{cut}}$  for maximum  $s/\sqrt{b}$  (roughly true).

## Controlling false discovery

So for a reliable discovery what we depend on is an accurate estimate of the expected number of background events, and this accuracy only depends on the quality of the training data; works for any function y(x).

But we do not blindly rely on the MC model for the training data for background; we need to test it by comparing to real data in control samples where no signal is expected.

The ability to perform these tests will depend on on the complexity of the analysis methods.