Classification by Nearest Shrunken Centroids and Support Vector Machines

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Two roads to classification

1. model **class probabilities**
   $\longrightarrow$ QDA, LDA, ...

2. model **class boundaries** directly
   $\longrightarrow$ Optimal Separating Hyperplanes, SVM

What's the problem?

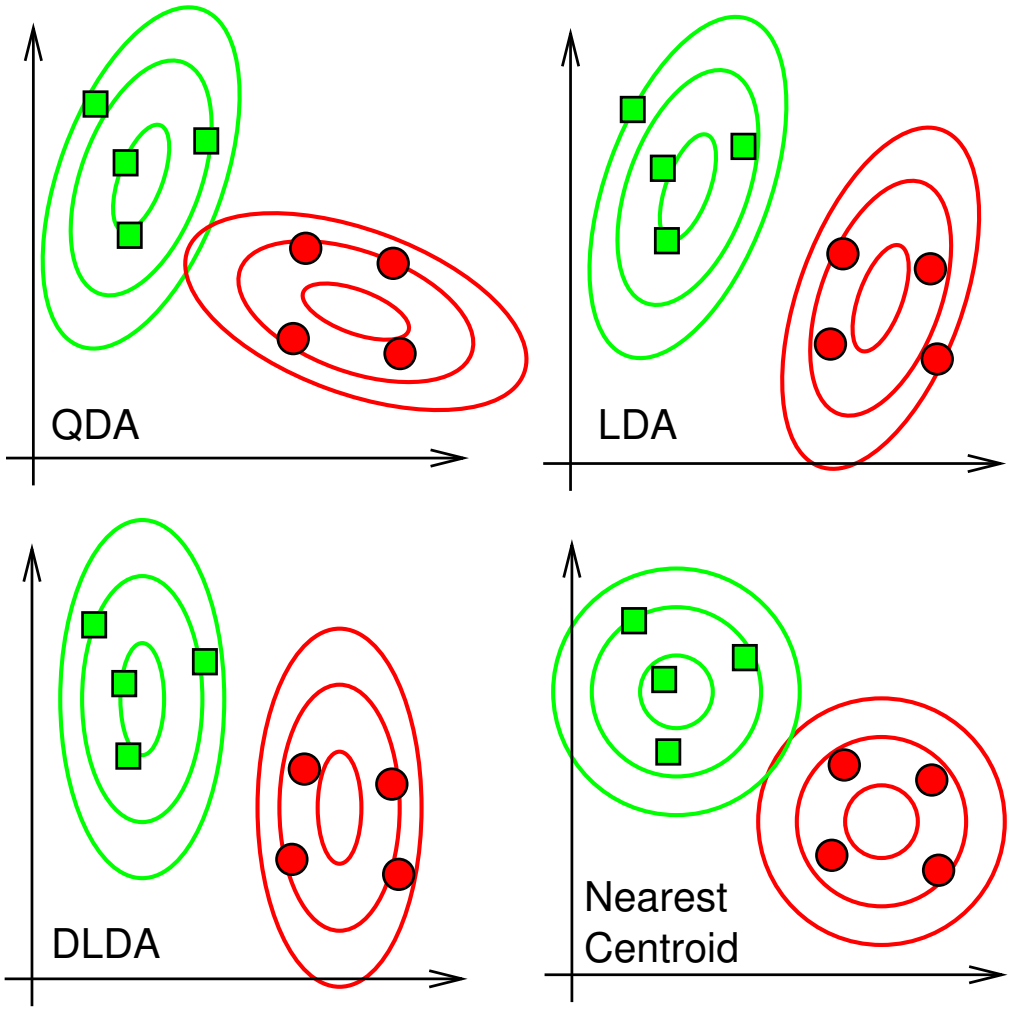
In classification you have to trade off **overfitting vs.underfitting** and **bias vs. variance**.

In 12'000 dimensions even linear methods are very complex $\longrightarrow$ high variance!

Simplify your models

Discriminant analysis and gene selection

Disriminant analysis in a nutshell



Characterize each class by **mean (centroid)** and **covariance structure**.

- **Quadratic D.A.**
different COVs
- **Linear D.A.**
requires same COVs.
- **Diagonal linear D.A.**
same diagonal COVs.
- **Nearest centroids**
forces COVs to $\sigma^2\mathbf{I}$.

Feature selection

Next simplification:

Base the classification only on a small number of genes.

Feature selection: Find the **most discriminative genes**.

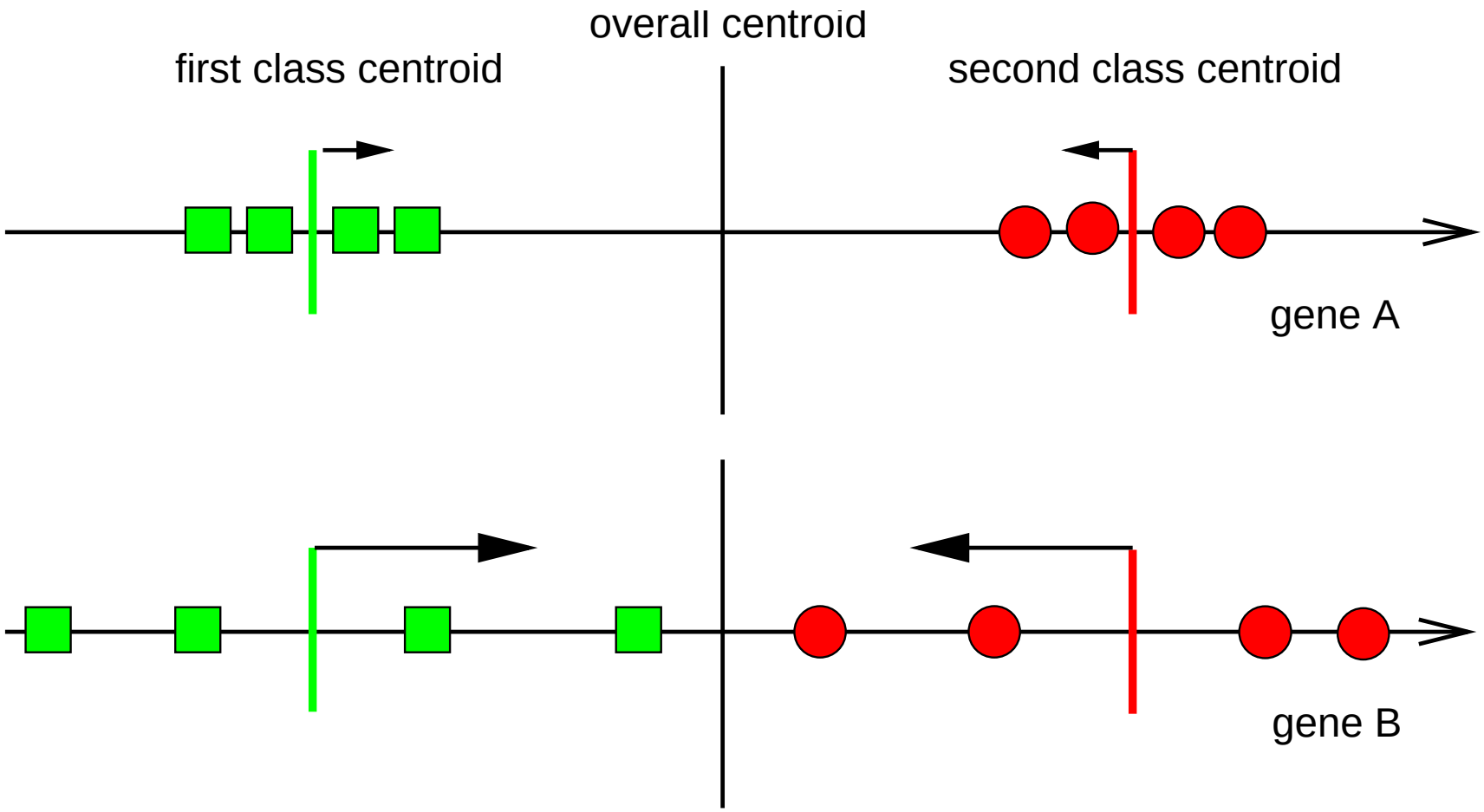
This task is different from testing for differential expression. Genes can be significantly differential expressed, but still useless for classification.

Feature selection

1. **Filter:**
   - Rank genes according to discriminative power by t-statistic, Wilcoxon, ...
   - Use only the first k for classification.
   - Discrete, hard thresholding.

2. **Shrinkage:**
   - Continously shrink genes until only a few have influence on classification.
   - Example: Nearest Shrunken Centroids.

Shrunken Centroids



Nearest Shrunken Centroids *cont'd*

The group centroid $\bar{x}_{gk}$ for gene g and class k is compared to the overall centroid $\bar{x}_g$ by

$$\bar{x}_{gk} \;=\; \bar{x}_g + m_k(s_g + s_0)\; d_{gk}\;,$$

where s_g is the pooled within-class standard deviation of gene g and s_0 is an offset to guard against genes with low expression levels.

Shrinkage: Each d_{gk} is reduced by Δ in absolute value, until it reaches zero. Genes with $d_{gk} = 0$ for all classes do not contribute to the classification.

(Tibshirani *et al.*, 2002)

Shortcomings of filter and shrinkage methods

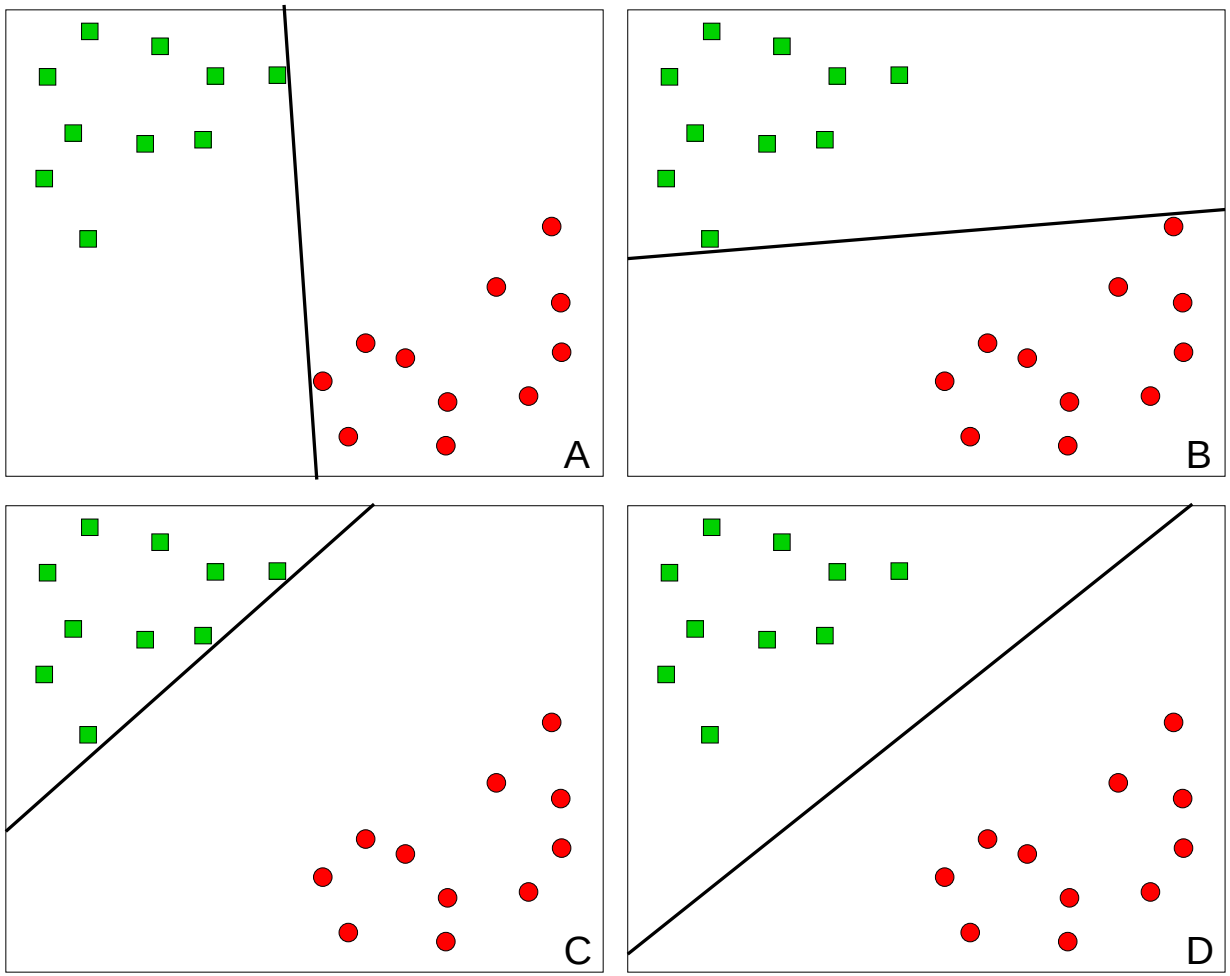
1. High correlated genes get similar score but offer no new information.
   But see (Jaeger *et al.*, 2003) for a cure.

2. Filter and Shrinkage work only on single genes.
   They don't find interactions between groups of genes.

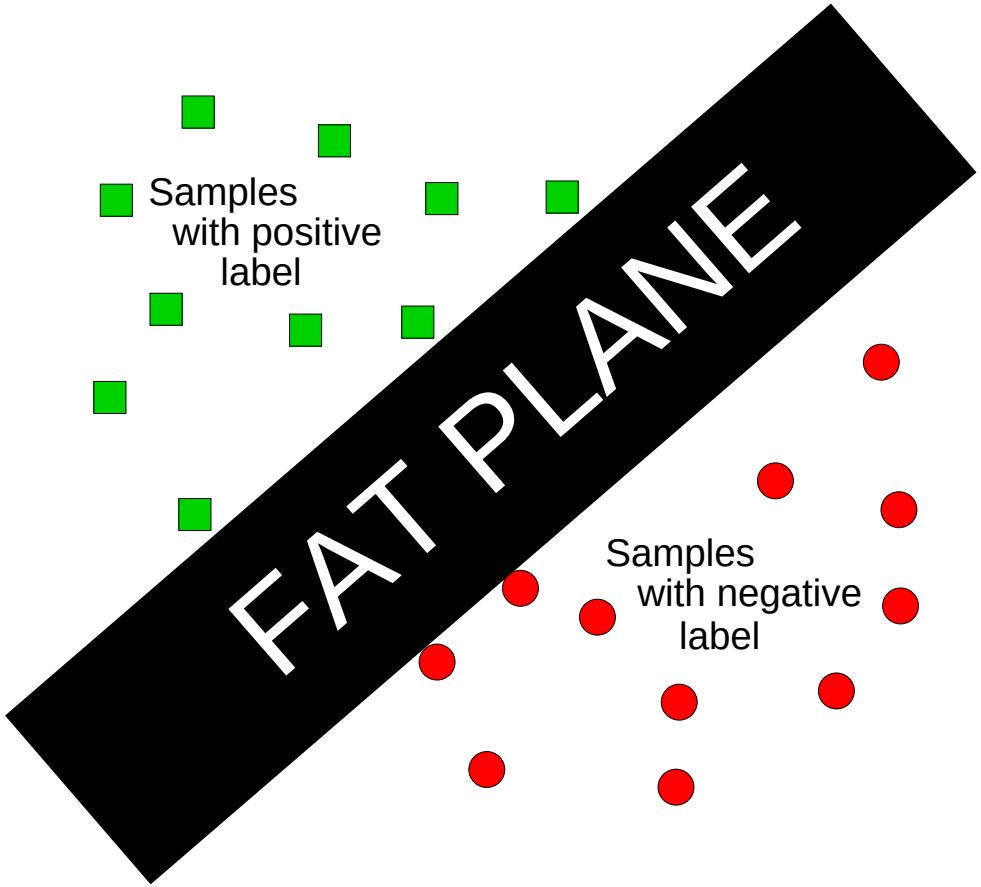
3. Filter and Shrinkage methods are only heuristics.
   Search for *best subset* is infeasible for more than 30 genes.

Support Vector Machines
— SVM —

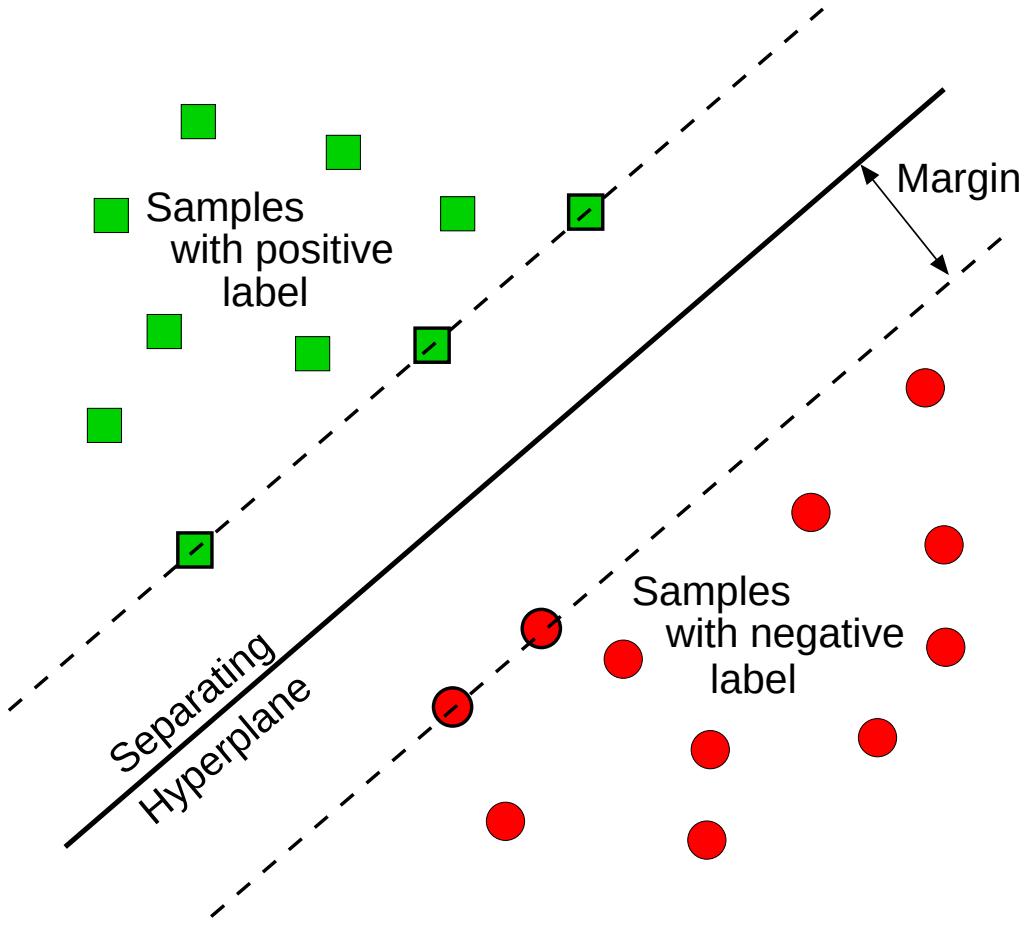
Which hyperplane is the best?



No sharp knife, but a fat plane



Separate the training set with maximal margin

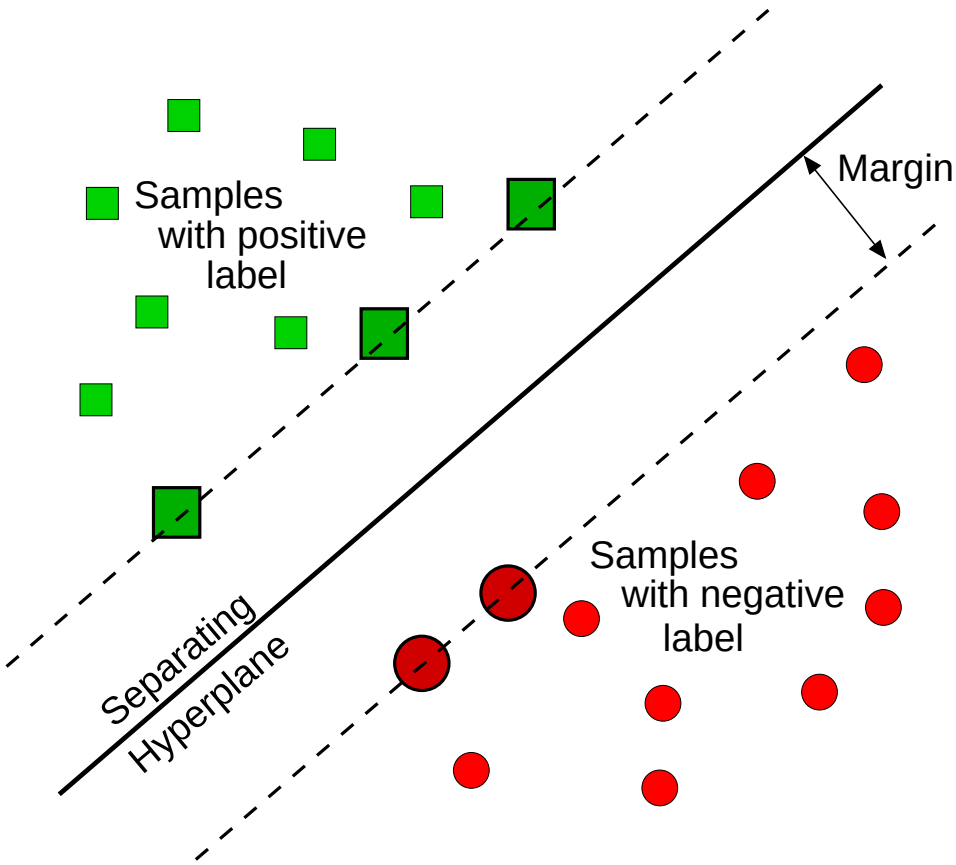


What are Support Vectors?

The points nearest to the separating hyperplane are called Support Vectors.

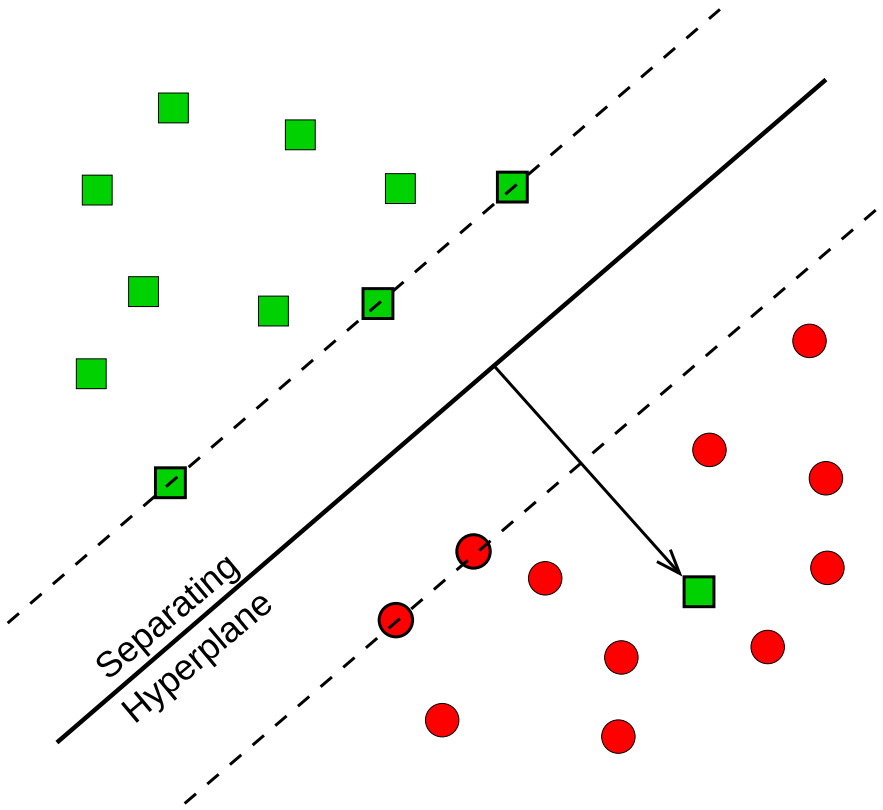
Only they determine the position of the hyperplane. **All other points have no influence!**

Mathematically: the weighted sum of the Support Vectors is the normal vector of the hyperplane.



Non-separable training sets

Use linear separation, but admit training errors.



Penalty of error: distance to hyperplane multiplied by *error cost* C.

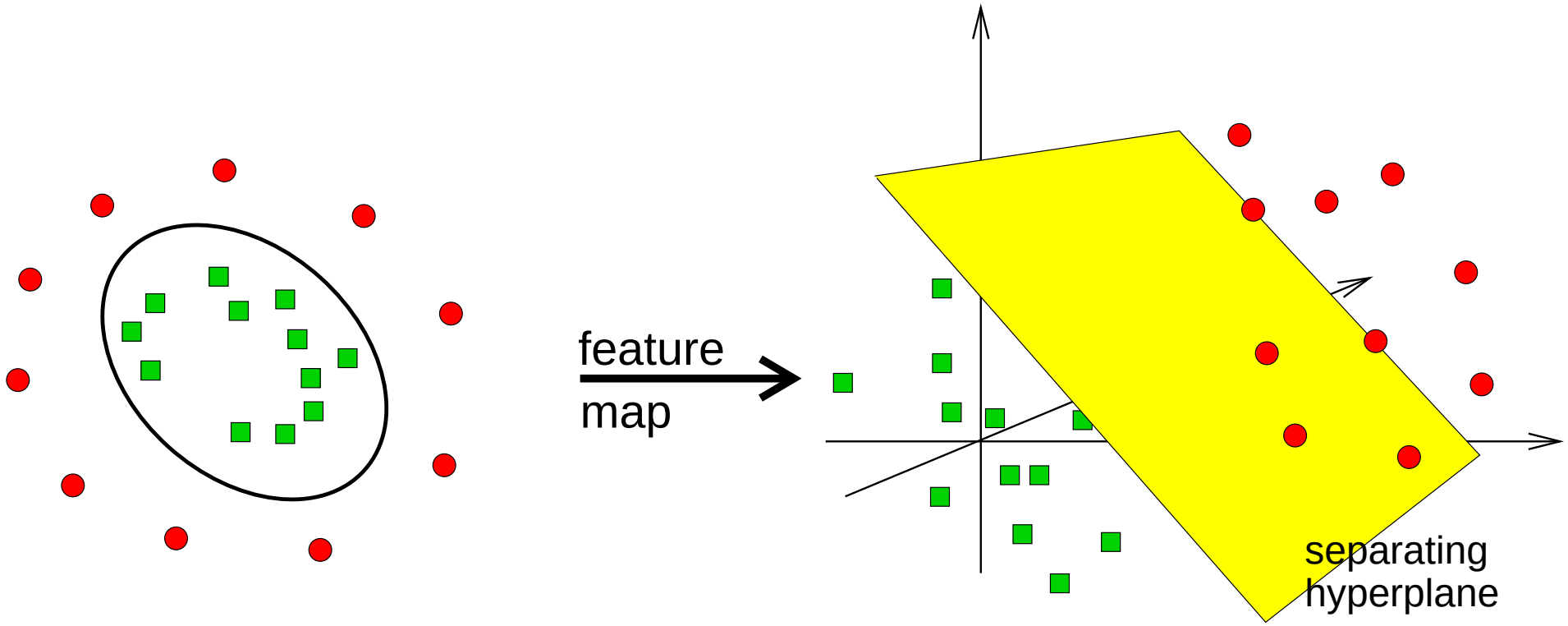
The end?

The story of how to simplify your models is finished.

But for the sake of completeness:
How do we get from the simple linear Optimal Separating Hyperplane to a full-grown Support Vector Machine?

It's a trick, a **kernel trick**.

Separation may be easier in higher dimensions



complex in low dimensions

simple in higher dimensions

The kernel trick

Maximal margin hyperplanes in feature space

If classification is easier in a high-dimenisonal feature space, we would like to build a maximal margin hyperplane there.

The construction depends on inner products $\Rightarrow$ we will have to evaluate inner products in the feature space.

This can be computationally intractable, if the dimensions become too large!

Loophole Use a kernel function that lives in low dimensions, but behaves like an inner product in high dimensions.

Kernel functions

Expression profiles $p = (p_1, p_2, \ldots, p_g) \in \mathbb{R}^g$
and $q = (q_1, q_2, \ldots, q_g) \in \mathbb{R}^g$.

Similarity in gene space: INNER PRODUCT

$$\langle p, q \rangle = p_1 q_1 + p_2 q_2 + \ldots + p_g q_g$$

Similarity in feature space: KERNEL FUNCTION

$$\mathcal{K}(p, q) = \text{polynomial, radial basis, ...}$$

Examples of Kernels

linear $\mathcal{K}(p,q) = \langle p,q\rangle$

polynomial $\mathcal{K}(p,q) = (\gamma\langle p,q\rangle + c_0)^d$

radial basis function $\mathcal{K}(p,q) = \exp\left(-\gamma\|p-q\|^2\right)$

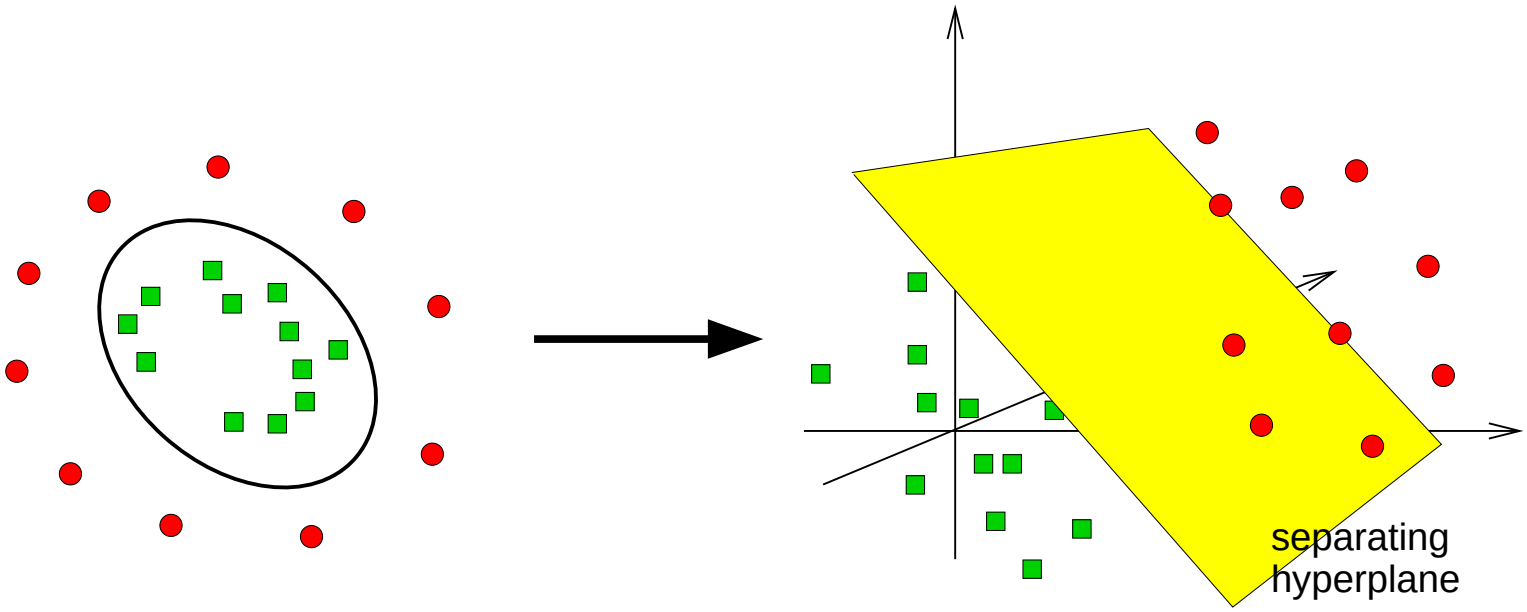
Why is it a trick?

We do not need to know,
how the feature space really looks like,
we just need the kernel function as a measure of similarity.

This is kind of black magic: we do not know what happens inside the kernel, we just get the output.

Still, we have the geometric interpretation of the maximal margin hyperplane, so SVMs are more transparent than e. g. Artificial Neural Networks.

The kernel trick: summary



Non-linear separation
between vectors
in gene space
using kernel functions

=

Linear separation
between vectors
in feature space
using inner product

Support Vector Machines

A Support Vector Machine is

a maximal margin hyperplane in feature space

built by using a kernel function in gene space.

Parameters of SVM

Kernel Parameters	γ:	width of rbf coeff. in polynomial ($= 1$)
	d:	degree of polynomial
	c_0	additive constant in polynomial ($= 0$)
Error weight	C:	influence of training errors

SVM@work: low complexity

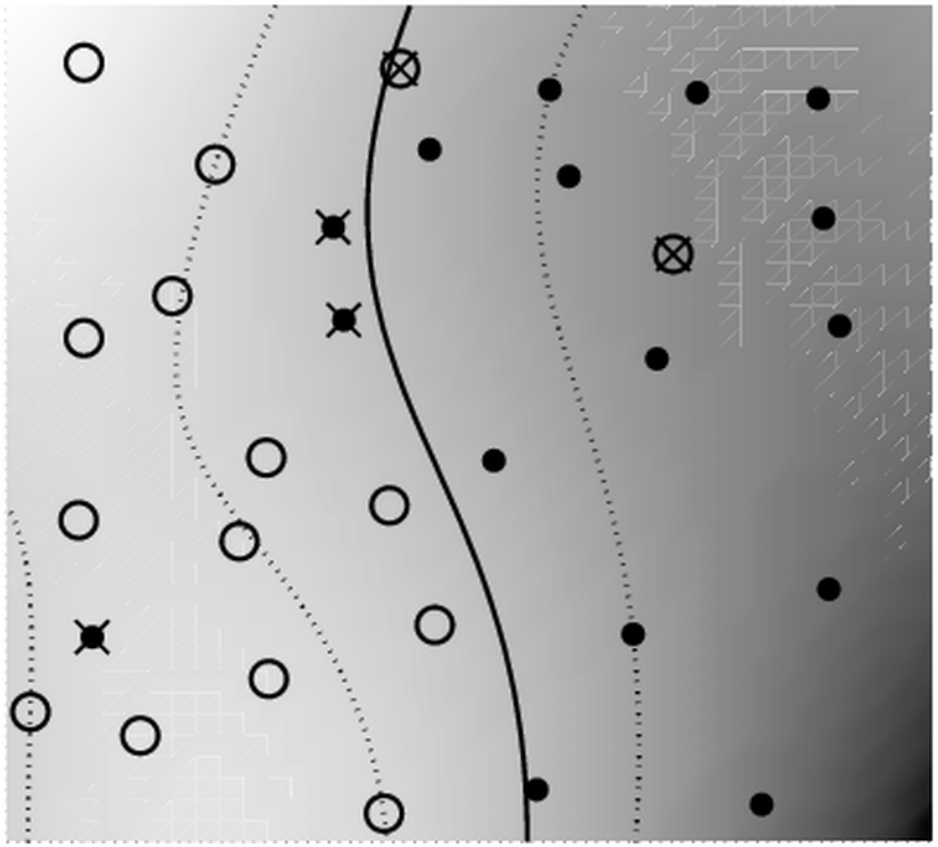


Figure taken from SCHÖLKOPF and SMOLA, *Learning with Kernels*, MIT Press 2002, p217

SVM@work: medium complexity

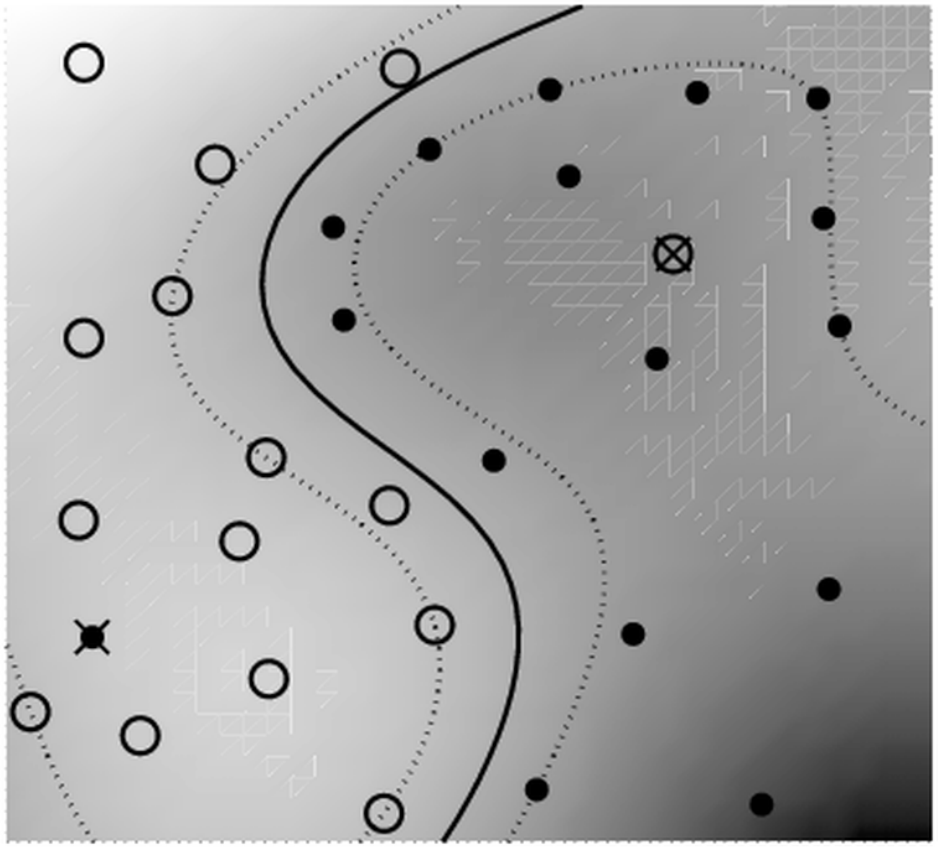


Figure taken from SCHÖLKOPF and SMOLA, *Learning with Kernels*, MIT Press 2002, p217

SVM@work: high complexity

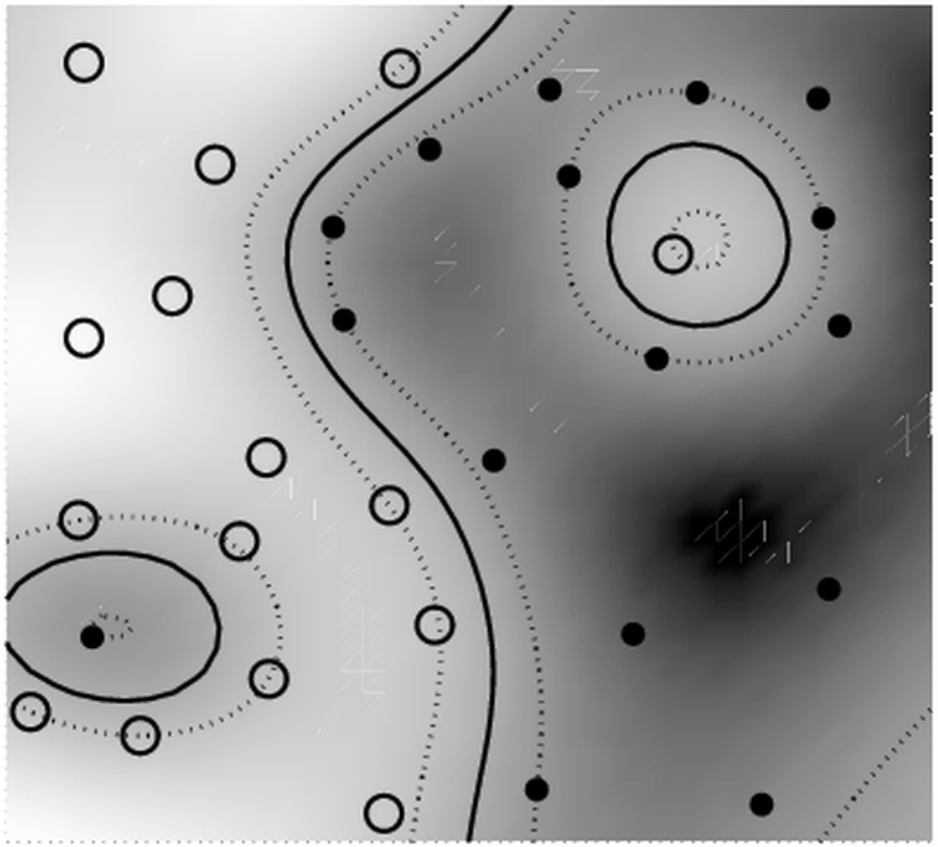


Figure taken from SCHÖLKOPF and SMOLA, *Learning with Kernels*, MIT Press 2002, p217

References

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   The Elements of Statistical Learning. Springer 2001.

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   Learning with Kernels. MIT Press, Cambridge, MA, 2002.

3. Robert Tibshirani, Trevor Hastie, Balasubramanian Narasimhan, Gilbert Chu
   Diagnosis of multiple cancer types by shrunken centroids of gene expression, PNAS, 99(10), 6567–6572, 2002.

4. Jochen Jäger, R. Sengupta and W.L. Ruzzo
   Improved Gene Selection for Classification of Microarrays, Proc. PSB 2003

Intro into practical session

Computational Diagnosis

TASK:

For 3 new patients in your hospital, decide whether they have a chromosomal translocation resulting in a BCR/ABL fusion gene or not.

IDEA:

Learn the difference between the cancer types from an archive of 76 expression profiles, which were analyzed and classified by an expert.

Training ... tuning ... testing

TRAINING:

```
model      <- svm(data       = "76 profiles",
                  labels     = "by an expert",
                  kernel     = "..",
                  parameters = "..")
```

TUNING:

```
svm.doctor <- tune.svm( data, labels,
                        different.parameter.values )
```

TESTING:

```
diagnosis <- predict(svm.doctor, new.patients)
```

Training ... tuning ... testing

TRAINING:

```
model       <- pamr.train( data , labels )
```

TUNING:

```
pamr.cv( data, labels )
```

TESTING:

```
diagnosis <- pamr.predic(new.patients, best.treshold)
```