

Neurocomputing

Learning theory

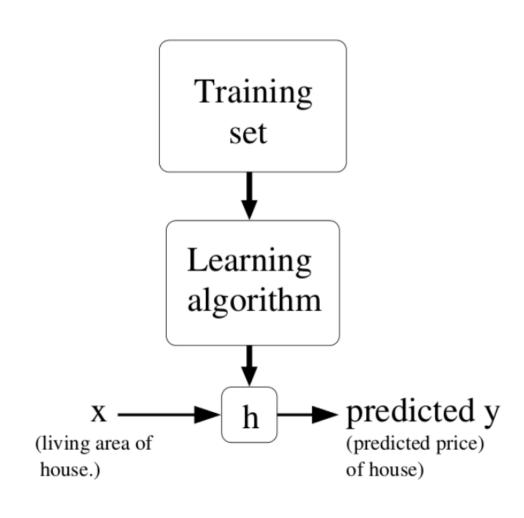
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https://tu-chemnitz.de/informatik/KI/edu/neurocomputing

1 - Error measurements

Training vs. Generalization error



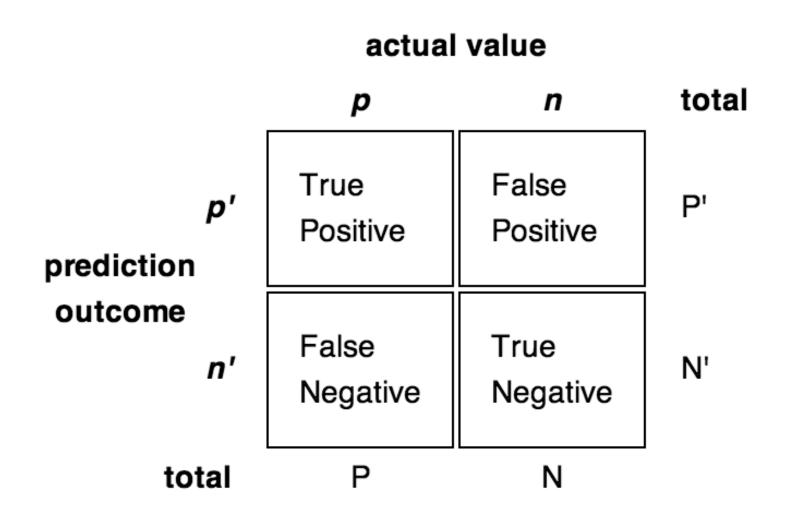
- The **training error** is the error made on the training set.
 - Easy to measure for classification: number of misclassified examples divided by the total number.

$$\epsilon_D = \frac{\text{\# misclassifications}}{\text{\# examples}}$$

- For regression, the mse is generally used.
- Totally irrelevant on usage: reading the training set has a training error of 0%.
- What matters is the **generalization error**, which is the error that will be made on new examples (not used during learning).
 - Much harder to measure (potentially infinite number of new examples, what is the correct answer?).
 - Often approximated by the empirical error: one keeps a number of training examples out of the learning phase and one tests the performance on them.

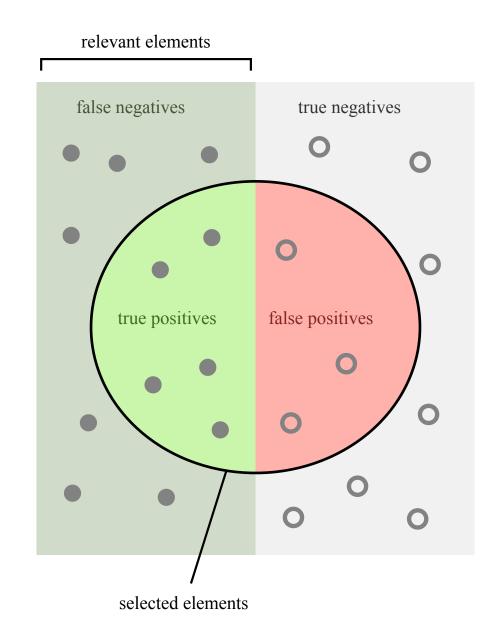
Classification errors

Confusion matrix



- Classification errors can also depend on the class:
 - False Positive errors (FP, false alarm, type I) is when the classifier predicts a positive class for a negative example.
 - False Negative errors (FN, miss, type II) is when the classifier predicts a negative class for a positive example.
- True Positive (TP) and True Negative (TN) are correctly classified examples.
- Is it better to fail to detect a cancer (FN) or to incorrectly predict one (FP)?

Classification errors



How many selected items are relevant?

How many relevant items are selected?

Recall =

Error

$$\epsilon = \frac{\text{FP} + \text{FN}}{\text{TP} + \text{FP} + \text{TN} + \text{FN}}$$

• Accuracy (1 - error)

$$acc = \frac{TP + TN}{TP + FP + TN + FN}$$

Recall (hit rate, sensitivity) and Precision (specificity)

$$R = \frac{\text{TP}}{\text{TP} + \text{FN}}$$
 $P = \frac{\text{TP}}{\text{TP} + \text{FP}}$

• F1 score = harmonic mean of precision and recall

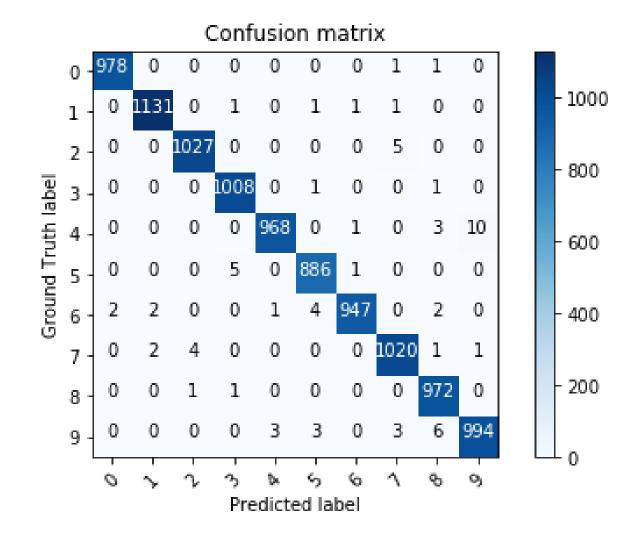
$$F1 = \frac{2PR}{P+R}$$

Source:

https://upload.wikimedia.org/wikipedia/commons/2/26/Precisionrecall.svg

Confusion matrix

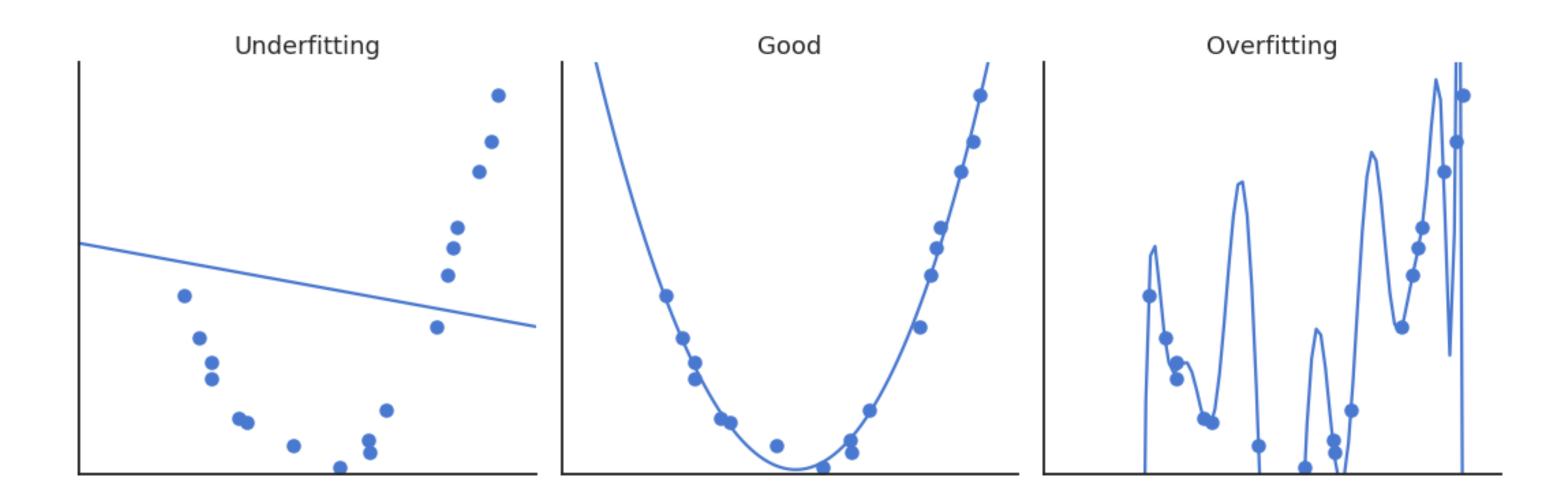
- For multiclass classification problems, the confusion matrix tells how many examples are correctly classified and where confusion happens.
- One axis is the predicted class, the other is the target class.
- Each element of the matrix tells how many examples are classified or misclassified.
- The matrix should be as diagonal as possible.



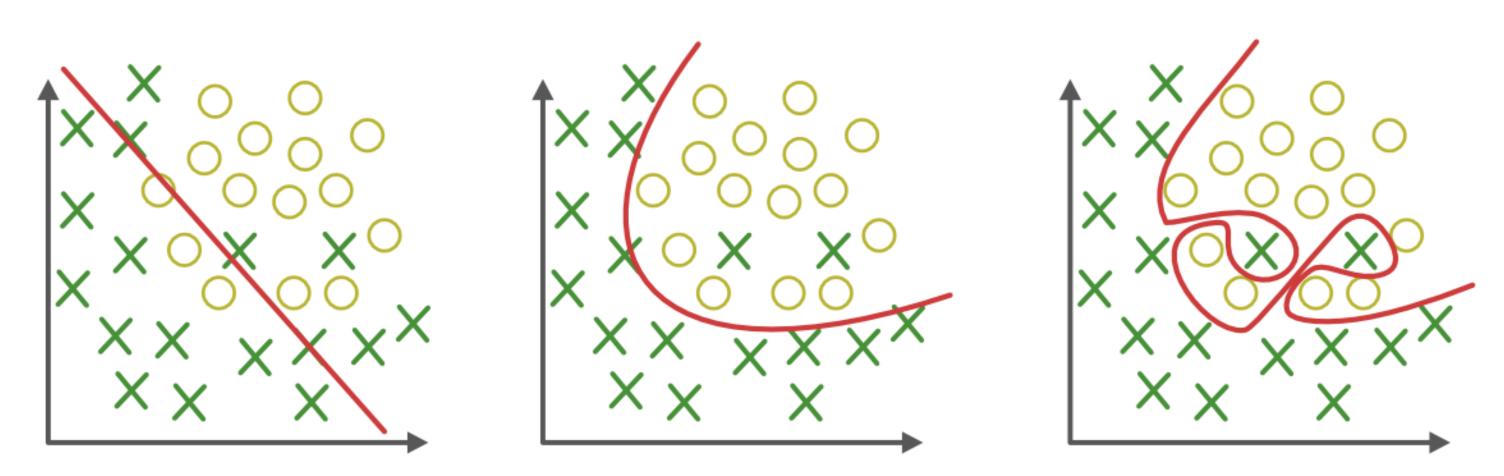
• Using scikit-learn:

```
1 from sklearn.metrics import confusion_matrix
2
3 m = confusion_matrix(t, y)
```

Overfitting in regression

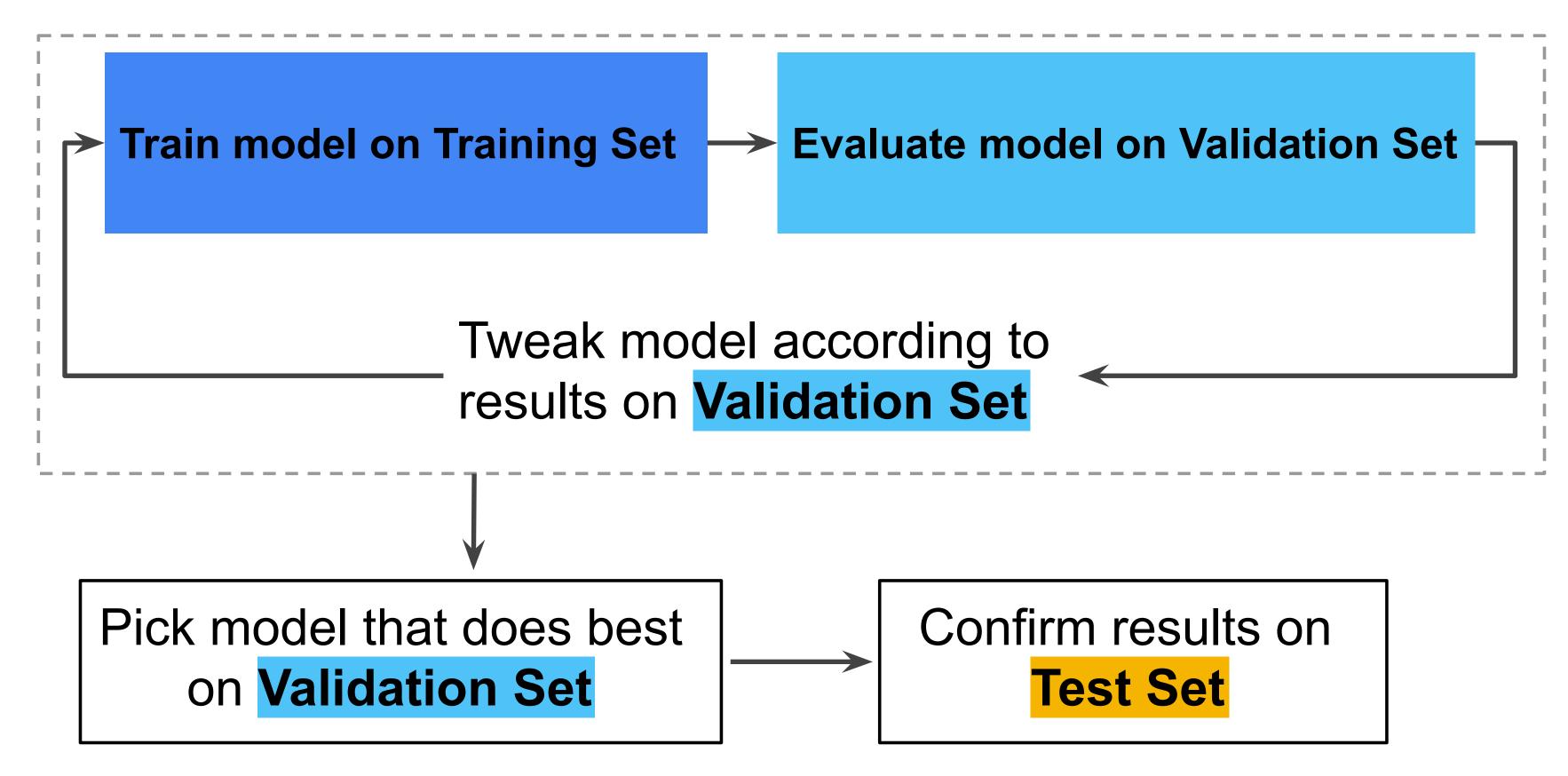


Overfitting in classification



Cross-validation

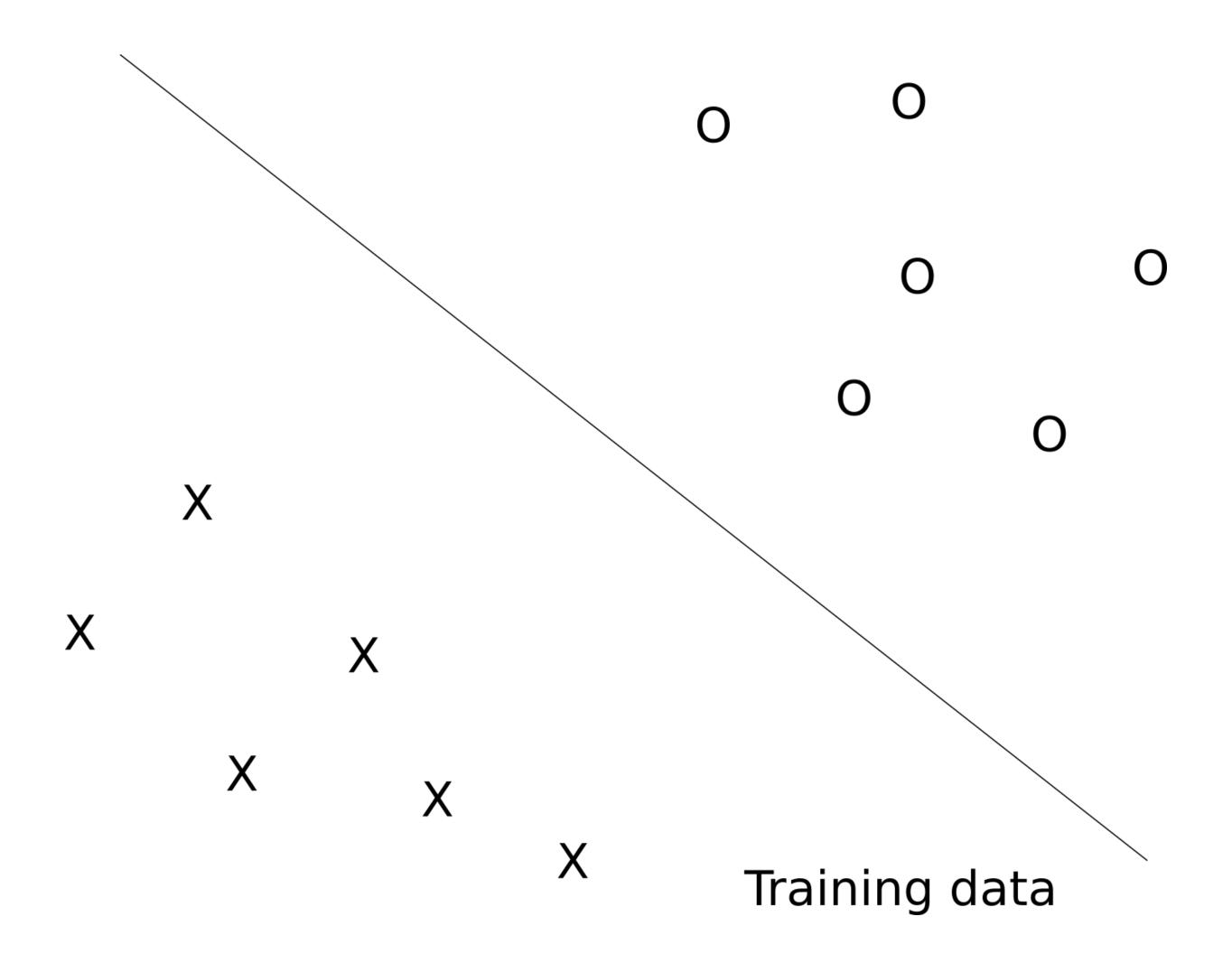
- In classification too, cross-validation has to be used to prevent overfitting.
- The classifier is trained on the **training set** and tested on the **test set**.
- Optionally, a third validation set can be used to track overfitting during training.



Source: https://developers.google.com/machine-learning/crash-course/validation/another-partition

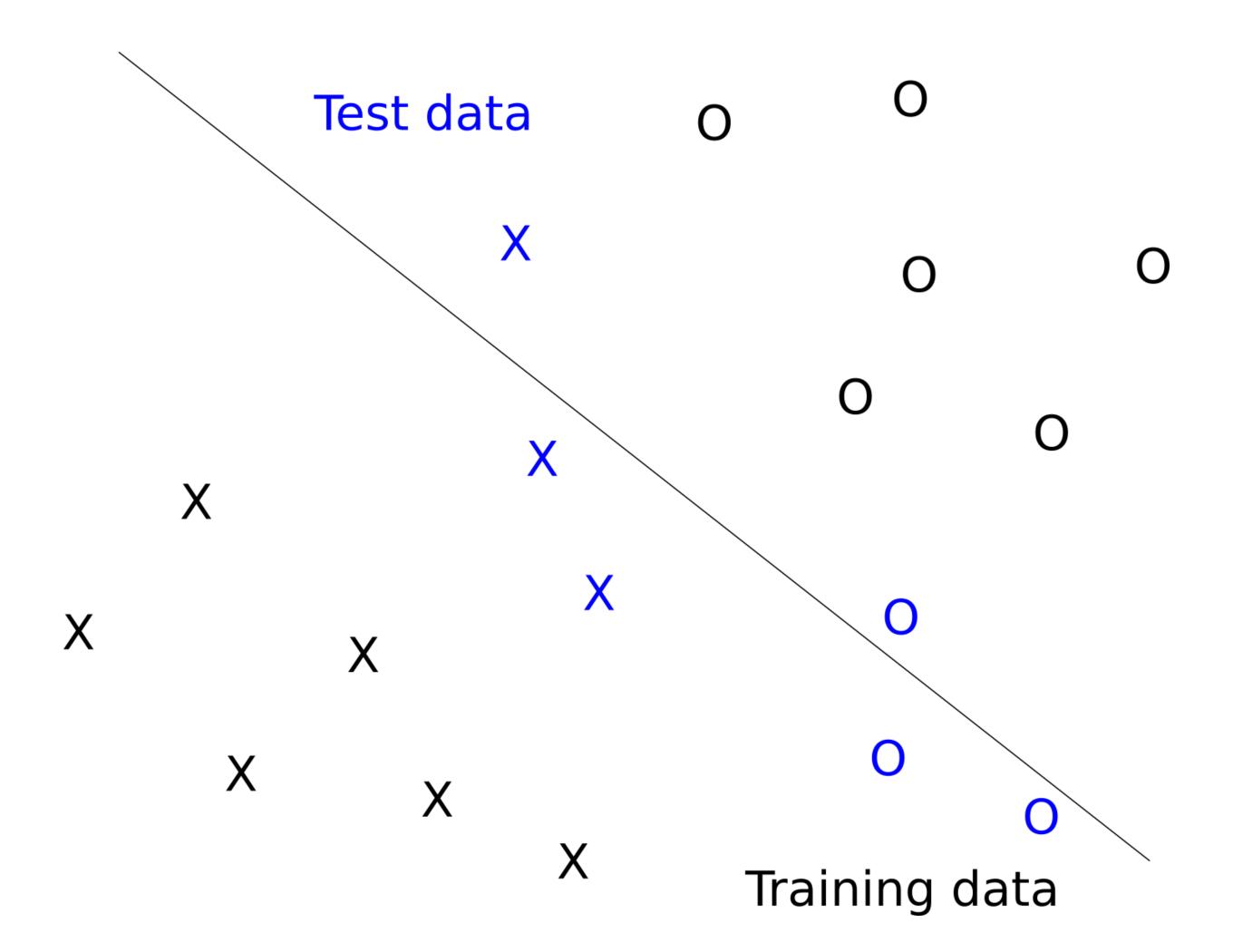
Training and test data distribution

• Beware: the test data must come from the same distribution as the training data, otherwise it makes no sense.



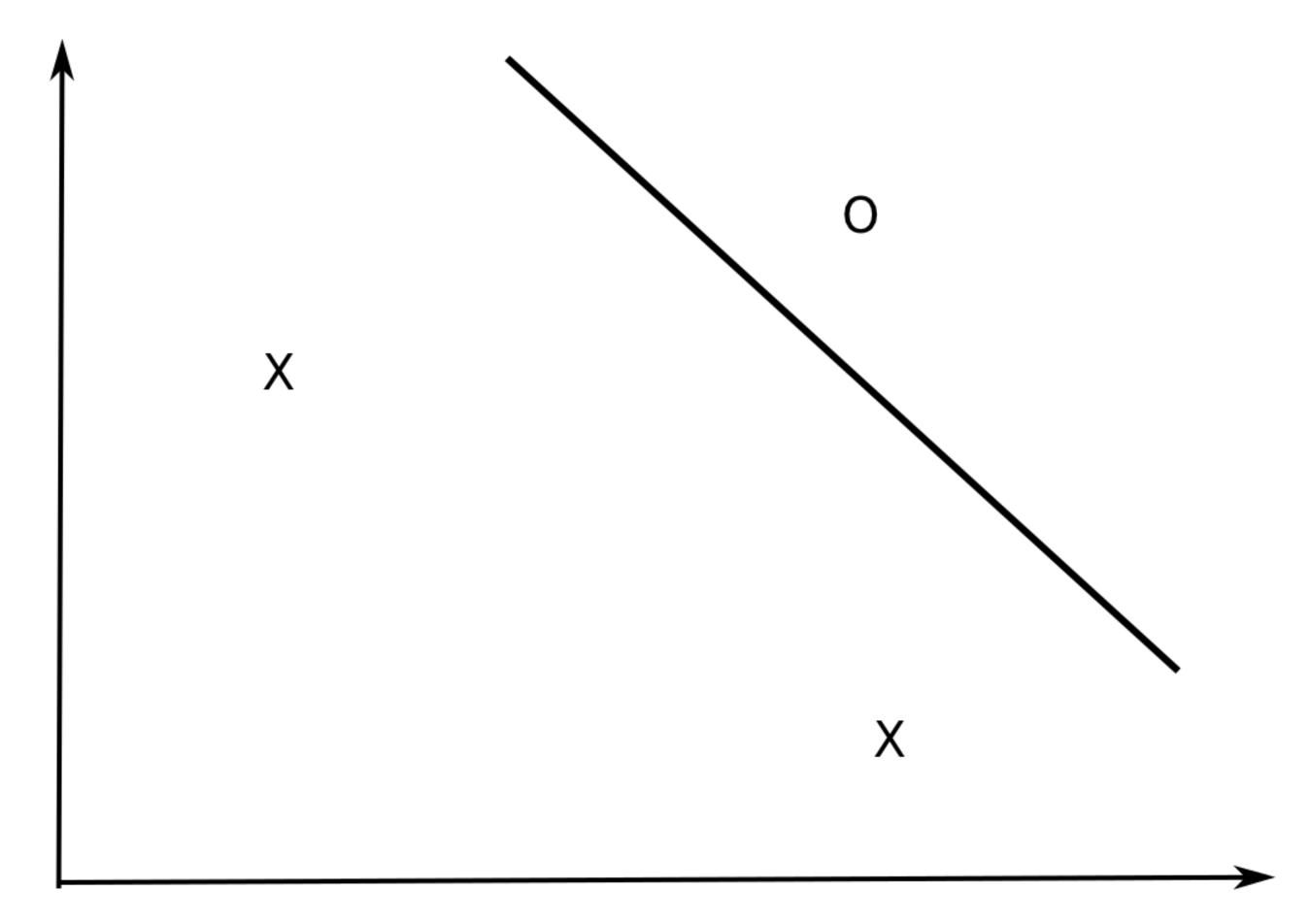
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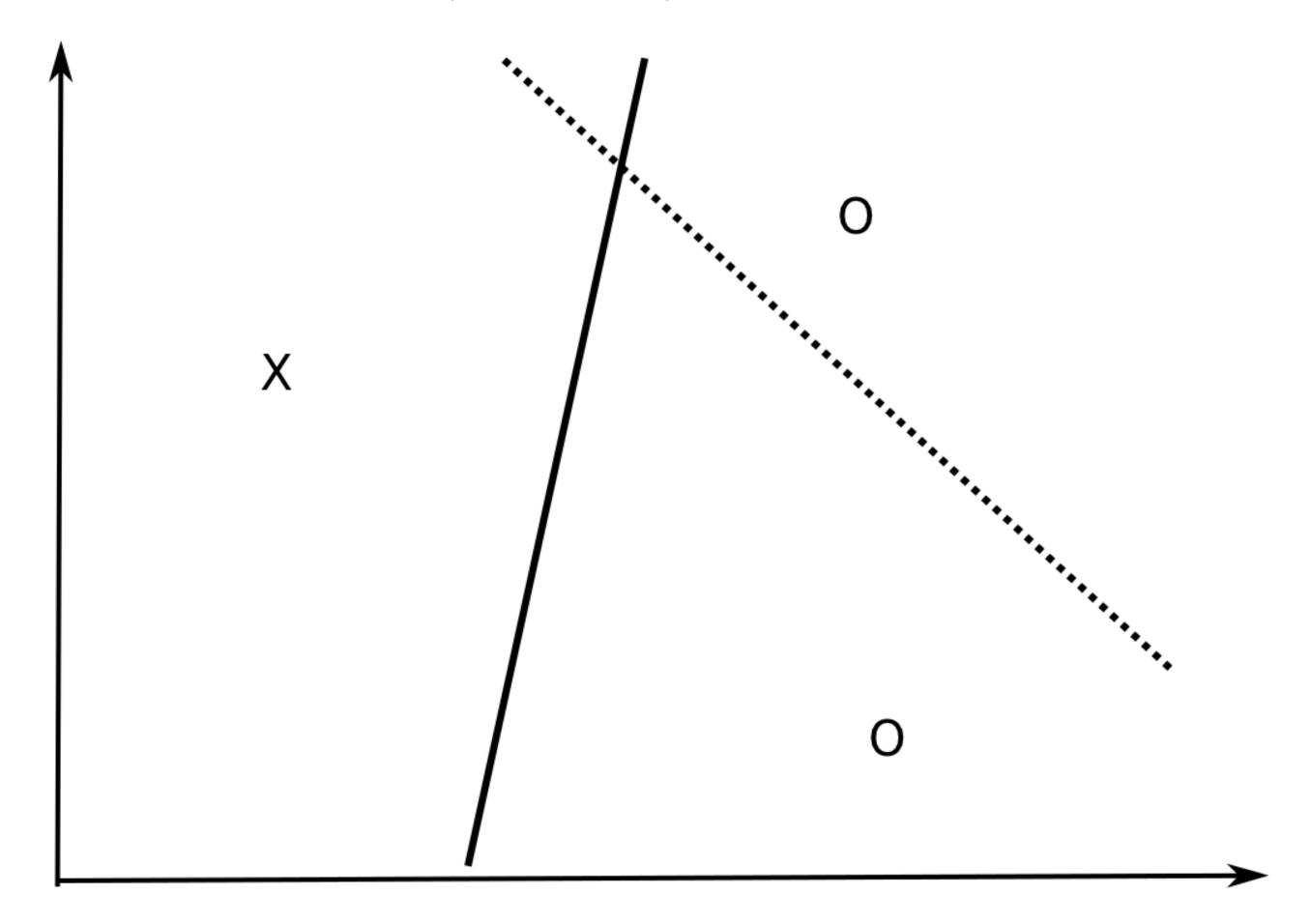


2 - VC dimension

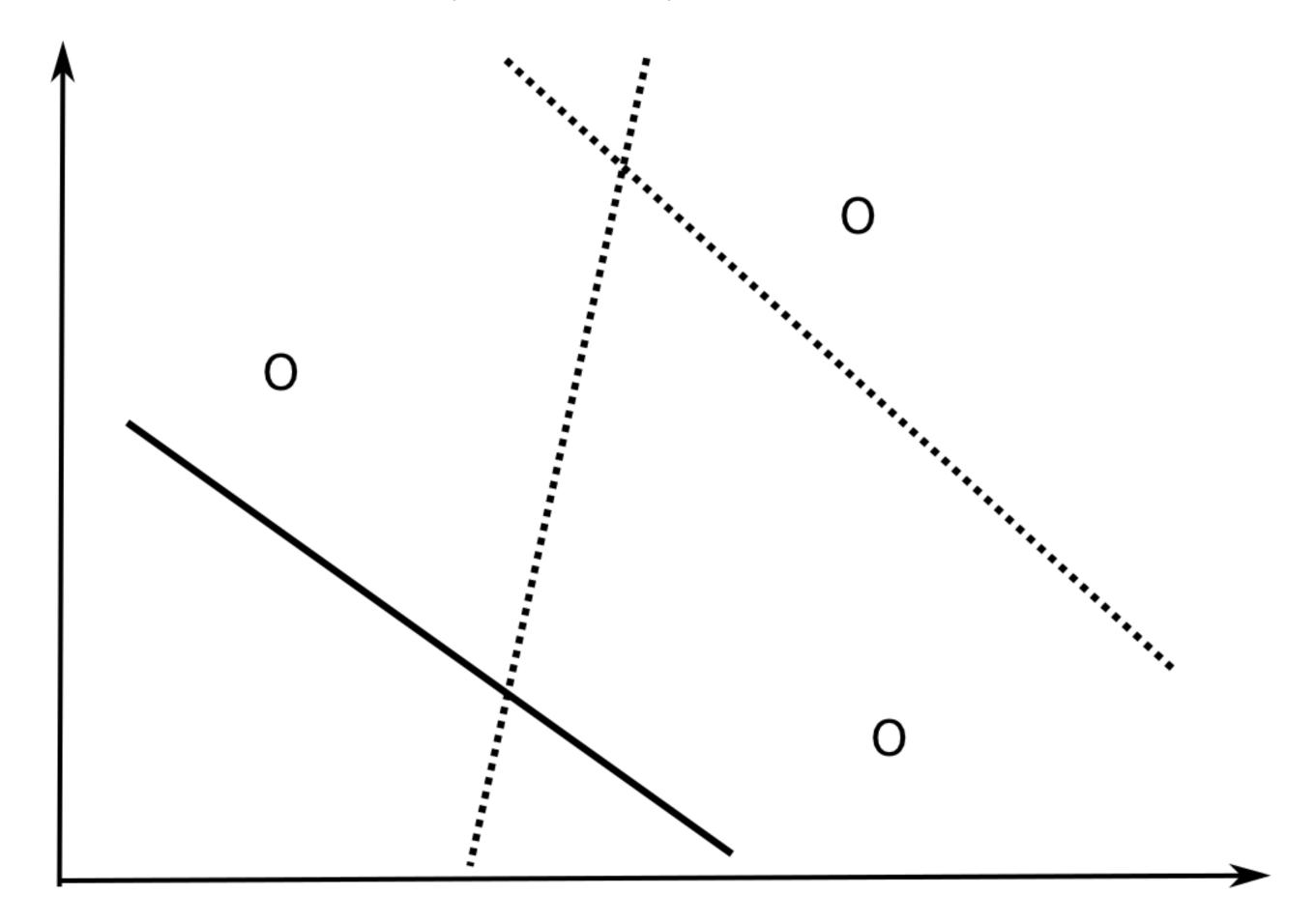
How many data examples can be correctly classified by a linear model in \Re^d ?



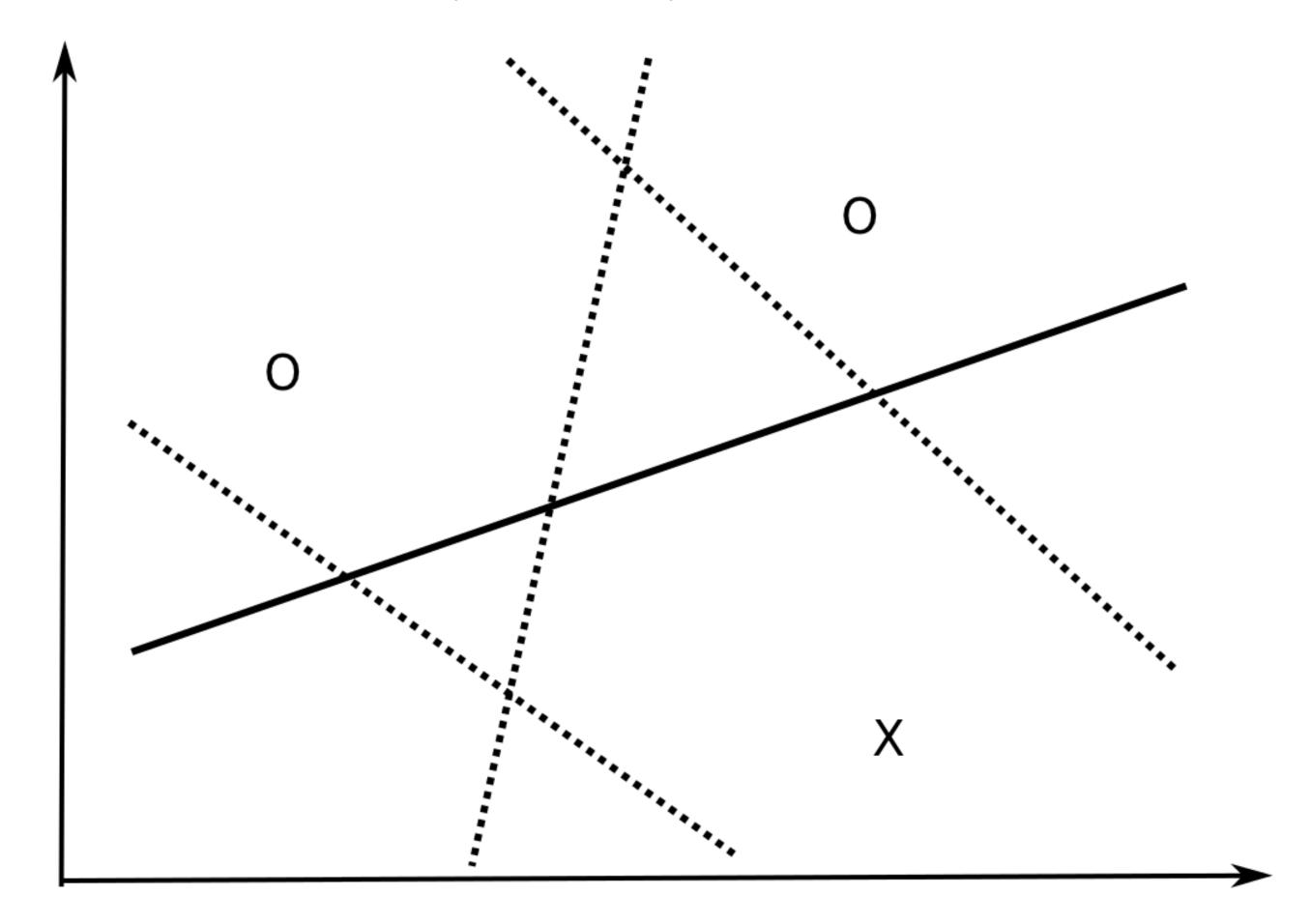
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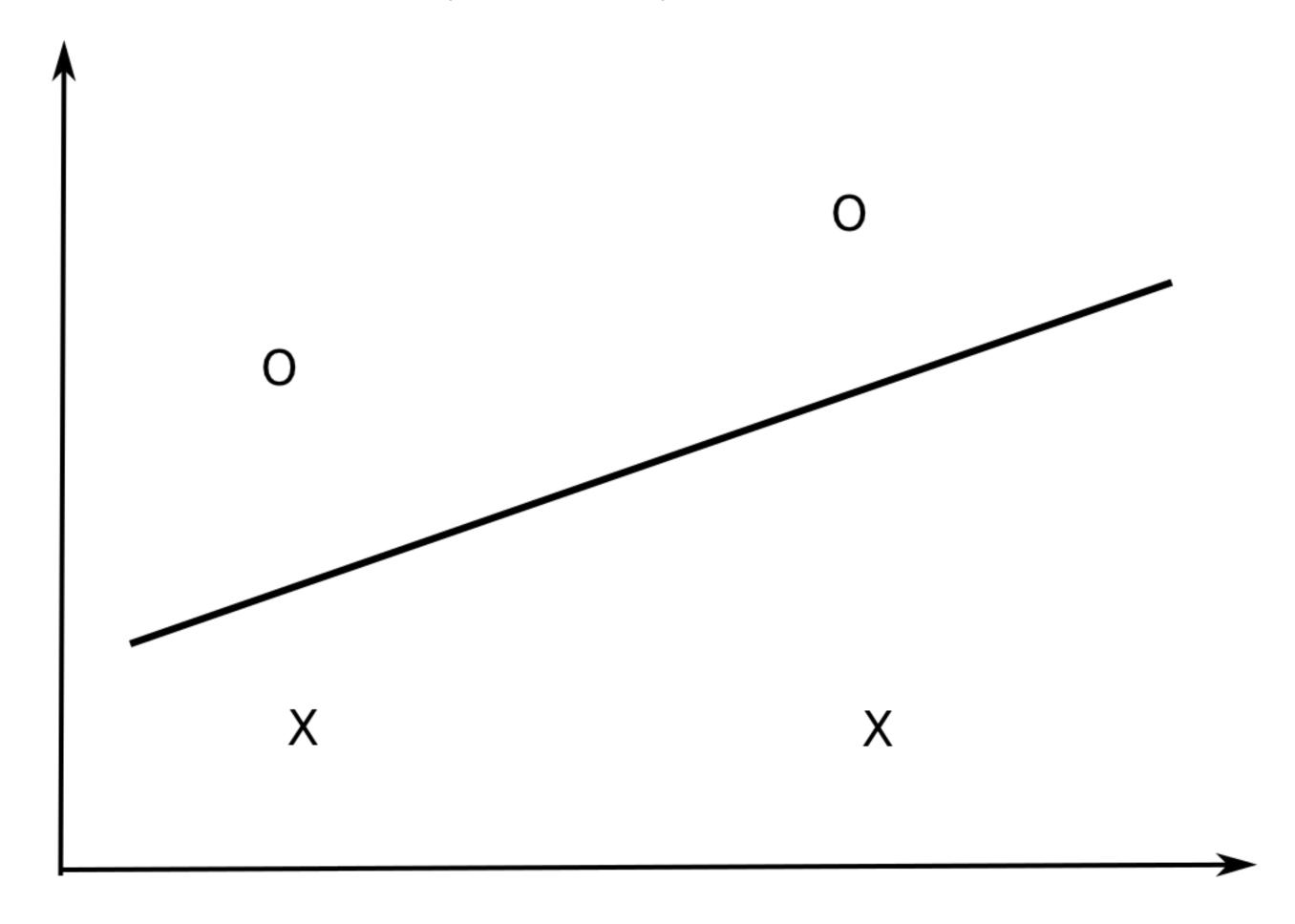
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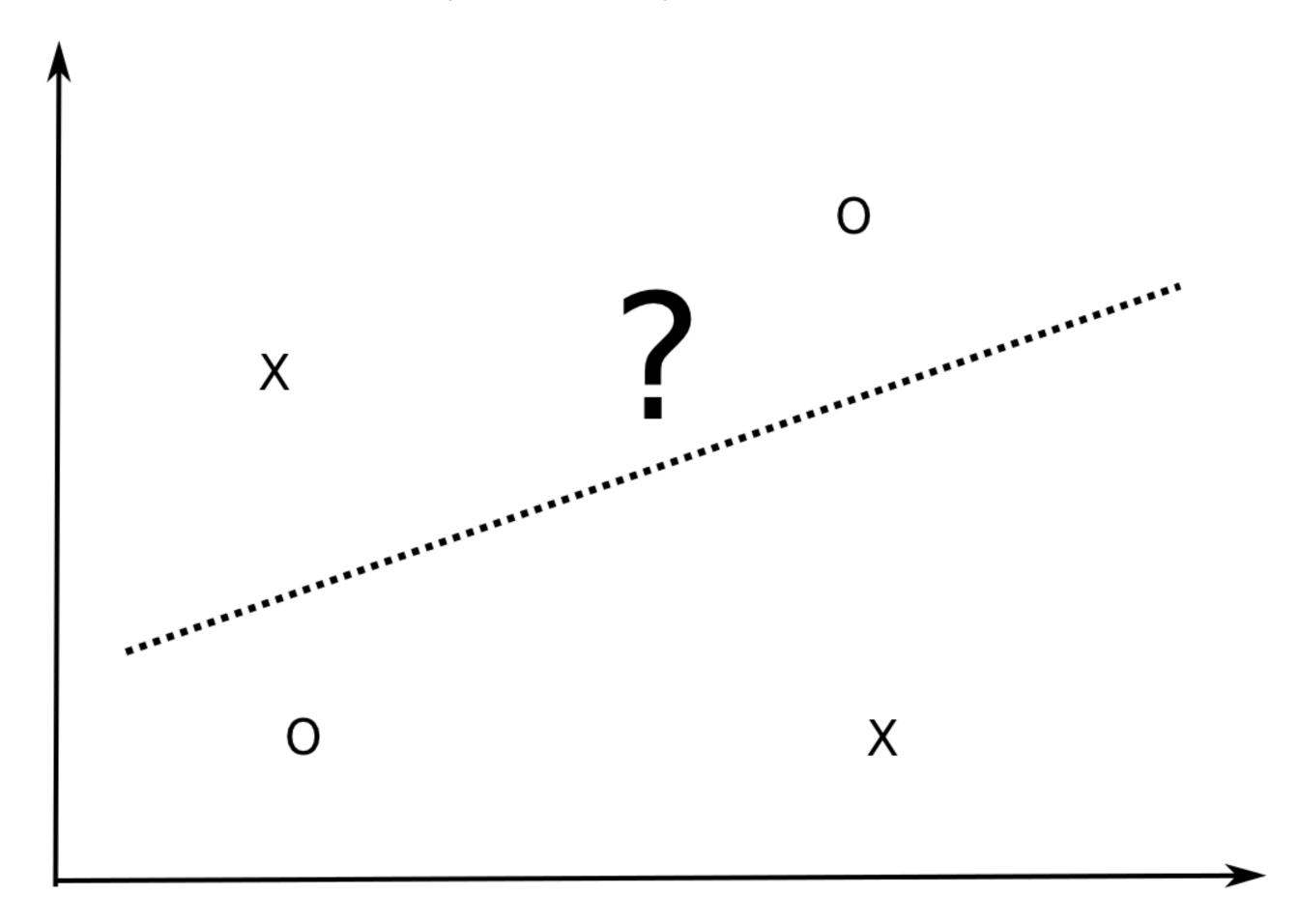


How many data examples can be correctly classified by a linear model in \Re^d ?



However, there exists sets of four examples in \Re^2 which can NOT be correctly classified by a linear model, i.e. they are not linearly separable.

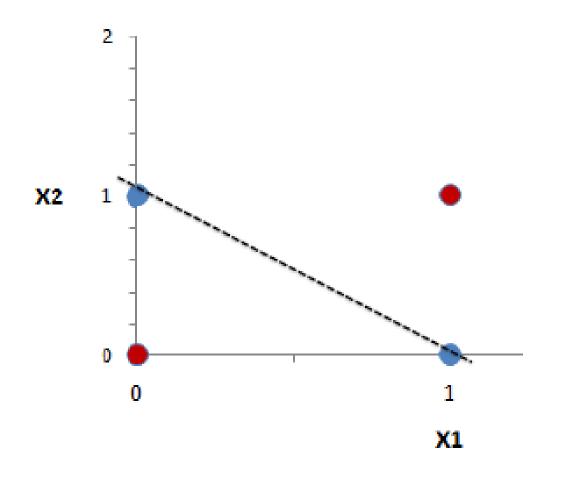
How many data examples can be correctly classified by a linear model in \Re^d ?



However, there exists sets of four examples in \Re^2 which can NOT be correctly classified by a linear model, i.e. they are not linearly separable.

Non-linearly separable data

• The XOR function in \Re^2 is for example not linearly separable, i.e. the Perceptron algorithm can not converge.



x_1	x_2	y
0	0	0
0	1	1
1	0	1
1	1	0

- The probability that a set of 3 (non-aligned) points in \Re^2 is linearly separable is 1, but the probability that a set of four points is linearly separable is smaller than 1 (but not zero).
- When a class of hypotheses \mathcal{H} can correctly classify all points of a training set \mathcal{D} , we say that \mathcal{H} shatters \mathcal{D} .

- The Vapnik-Chervonenkis dimension $VC_{dim}(\mathcal{H})$ of an hypothesis class \mathcal{H} is defined as the maximal number of training examples that \mathcal{H} can shatter.
- We saw that in \Re^2 , this dimension is 3:

$$VC_{dim}(Linear(\Re^2)) = 3$$

• This can be generalized to linear classifiers in \Re^d :

$$VC_{dim}(Linear(\Re^d)) = d + 1$$

- This corresponds to the number of **free parameters** of the linear classifier:
 - d parameters for the weight vector, 1 for the bias.
- Given any set of (d+1) examples in \Re^d , there exists a linear classifier able to classify them perfectly.
- For other types of (non-linear) hypotheses, the VC dimension is generally proportional to the number of free parameters.
- But regularization reduces the VC dimension of the classifier.

Vapnik-Chervonenkis theorem

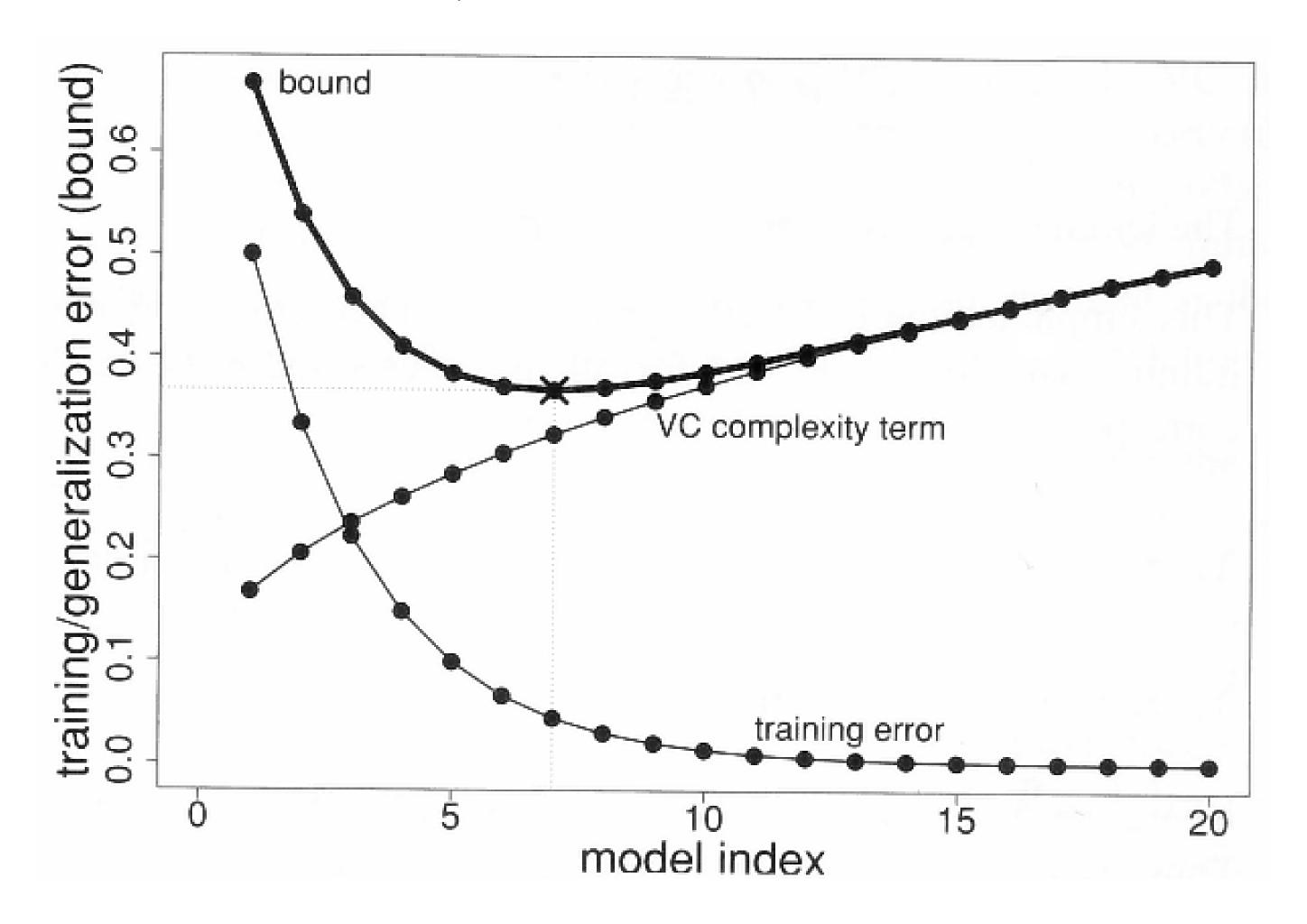
• The generalization error e(h) of an hypothesis h taken from a class \mathcal{H} of finite VC dimension and trained on N samples of S is bounded by the sum of the training error $\hat{e}_{S}(h)$ and the VC complexity term:

$$\epsilon(h) \leq \hat{\epsilon}_{S}(h) + \sqrt{\frac{\text{VC}_{\text{dim}}(\mathcal{H}) \cdot (1 + \log(\frac{2 \cdot N}{\text{VC}_{\text{dim}}(\mathcal{H})})) - \log(\frac{\delta}{4})}{N}}$$

with probability $1 - \delta$, if $VC_{dim}(\mathcal{H}) << N$.

Structural risk minimization

$$\epsilon(h) \le \hat{\epsilon}_{S(h)} + \sqrt{\frac{\text{VC}_{\text{dim}}(\mathcal{H}) \cdot (1 + \log(\frac{2 \cdot N}{\text{VC}_{\text{dim}}(\mathcal{H})})) - \log(\frac{\delta}{4})}{N}}$$



Structural risk minimization

$$\epsilon(h) \leq \hat{\epsilon}_{S(h)} + \sqrt{\frac{\text{VC}_{\text{dim}}(\mathcal{H}) \cdot (1 + \log(\frac{2 \cdot N}{\text{VC}_{\text{dim}}(\mathcal{H})})) - \log(\frac{\delta}{4})}{N}}$$

- The generalization error increases with the VC dimension, while the training error decreases.
- Structural risk minimization is an alternative method to cross-validation.
- The VC dimensions of various classes of hypothesis are already known (~ number of free parameters).
- This bounds tells how many training samples are needed by a given hypothesis class in order to obtain a satisfying generalization error.
 - The more complex the model, the more training data you will need to get a good generalization error!

$$\epsilon(h) \approx \frac{\text{VC}_{\text{dim}}(\mathcal{H})}{N}$$

- A learning algorithm should only try to minimize the training error, as the VC complexity term only depends on the model.
- This term is only an upper bound: most of the time, the real bound is usually 100 times smaller.

Implication for non-linear classifiers

• The VC dimension of linear classifiers in \Re^d is:

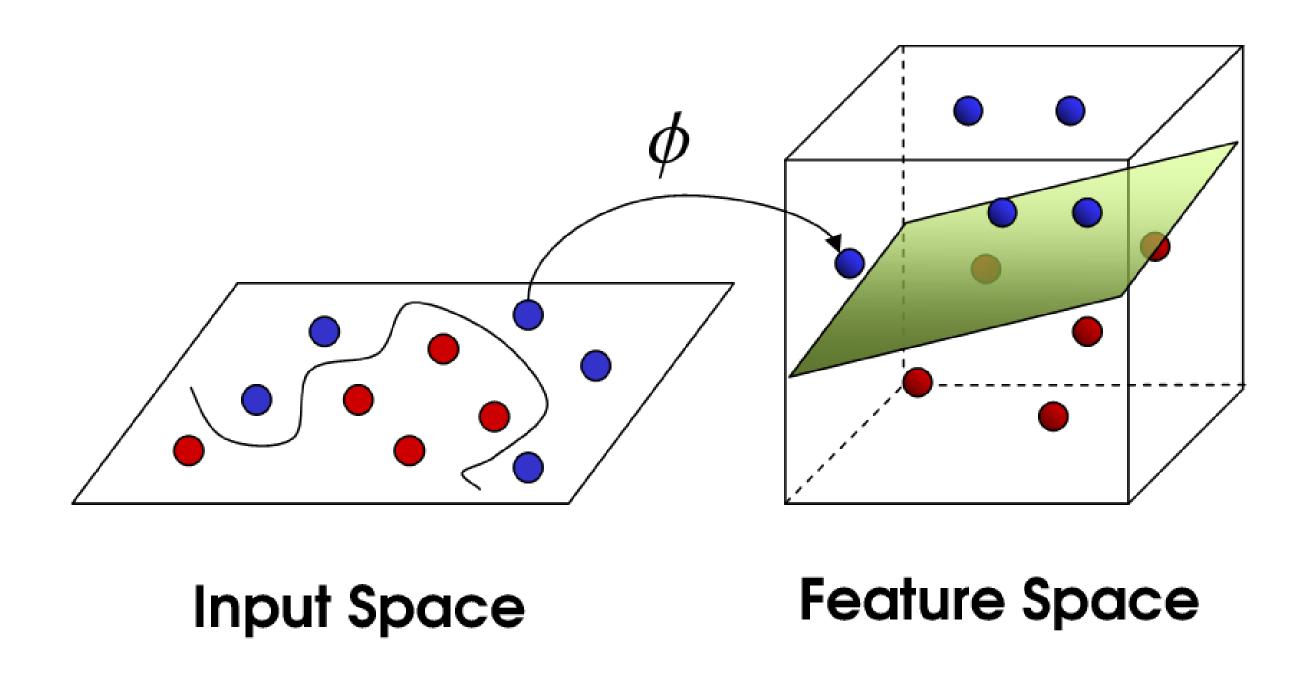
$$VC_{dim}(Linear(\Re^d)) = d + 1$$

- Given any set of (d+1) examples in \Re^d , there exists a linear classifier able to classify them perfectly.
- For N >> d the probability of having training errors becomes huge (the data is generally not linearly separable).
 - If we project the input data onto a space with sufficiently high dimensions, it becomes then possible to find a linear classifier on this projection space that is able to classify the data!
- However, if the space has too many dimensions, the VC dimension will increase and the generalization error will increase.
- Basic principle of all non-linear methods: multi-layer perceptron, radial-basis-function networks, support-vector machines...

3 - Feature space

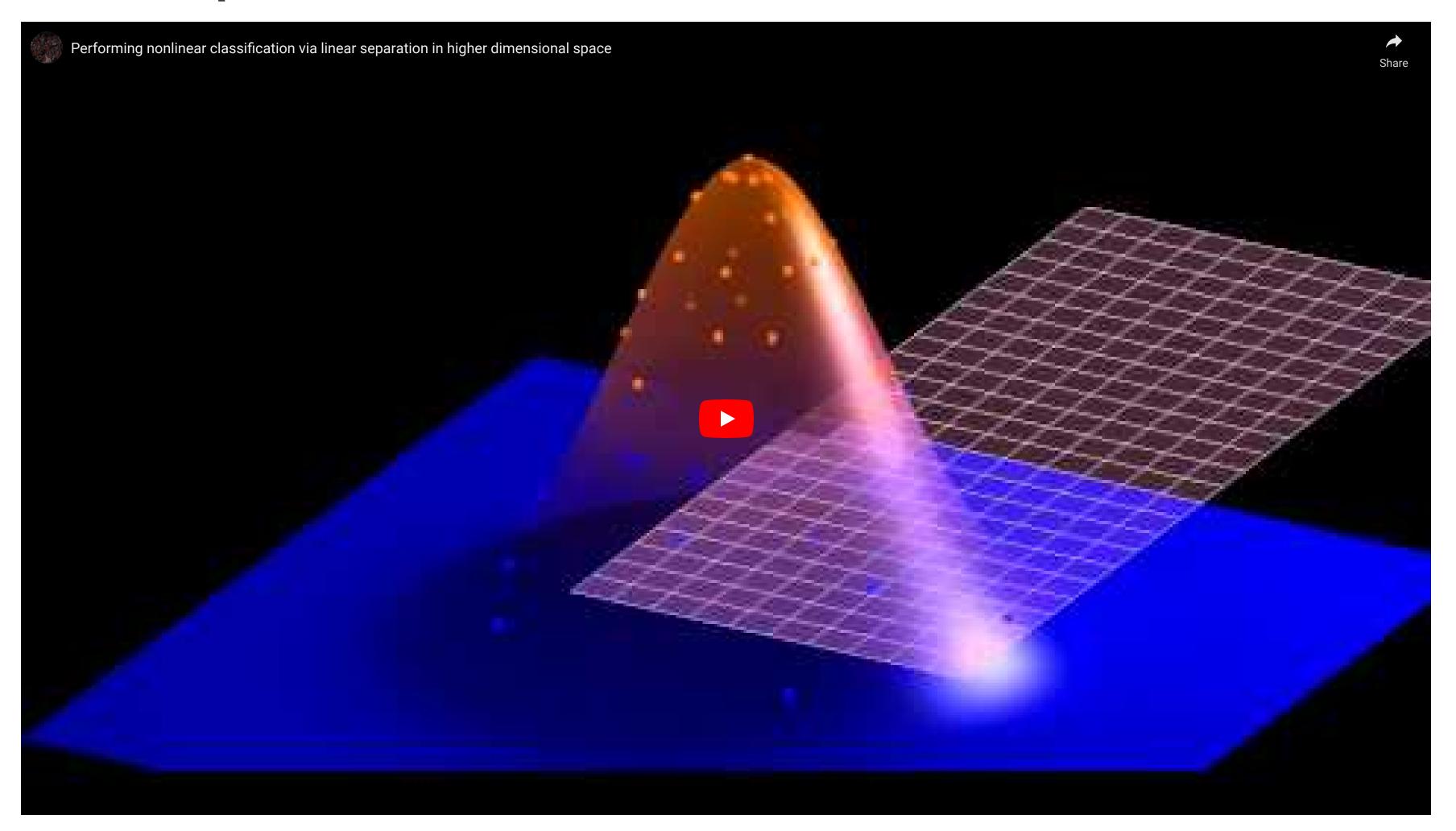
Cover's theorem on the separability of patterns (1965)

A complex pattern-classification problem, cast in a high dimensional space non-linearly, is more likely to be linearly separable than in a low-dimensional space, provided that the space is not densely populated.



- The highly dimensional space where the input data is projected is called the **feature space**.
- When the number of dimensions of the feature space increases:
 - the training error decreases (the pattern is more likely linearly separable);
 - the generalization error increases (the VC dimension increases).

Feature space

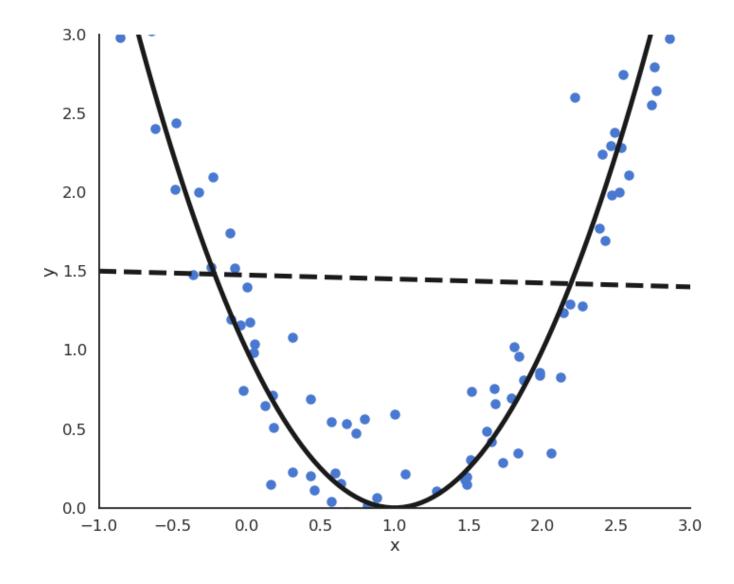


Polynomial features

For the polynomial regression of order p:

$$y = f_{\mathbf{w},b}(x) = w_1 x + w_2 x^2 + \dots + w_p x^p + b$$

the vector
$$\mathbf{x} = \begin{bmatrix} x \\ x^2 \\ \dots \\ x^p \end{bmatrix}$$
 defines a feature space for the input x .



- The elements of the feature space are called **polynomial features**.
- We can define polynomial features of more than one variable, e.g. $x^2 y$, $x^3 y^4$, etc.
- We then apply multiple **linear** regression (MLR) on the polynomial feature space to find the parameters:

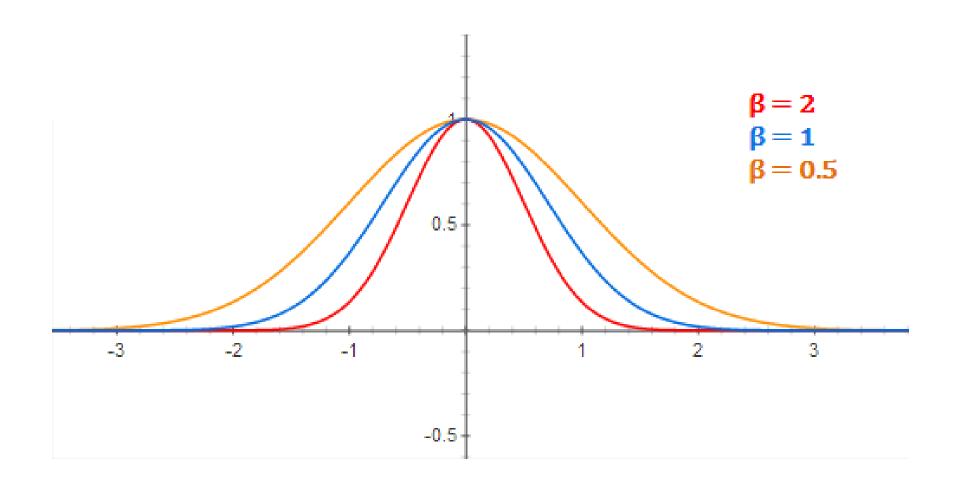
$$\Delta \mathbf{w} = \eta \left(t - \mathbf{y} \right) \mathbf{x}$$

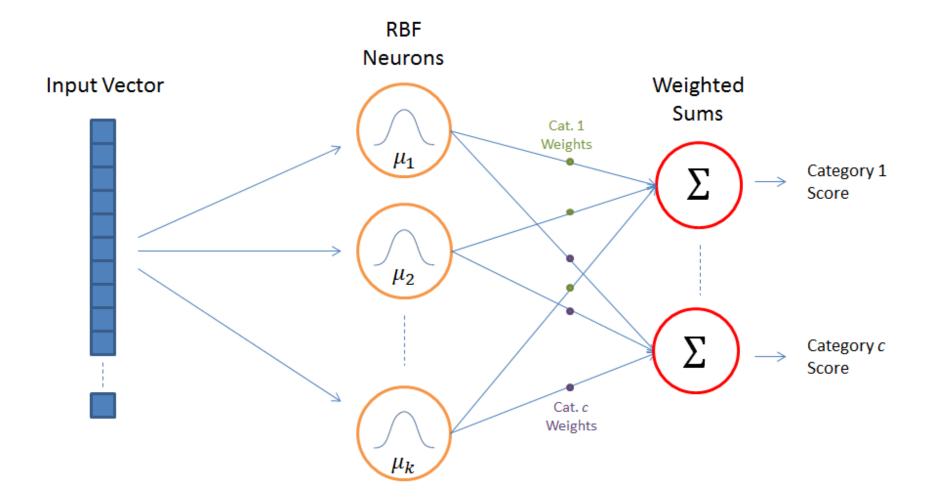
Radial-basis function networks

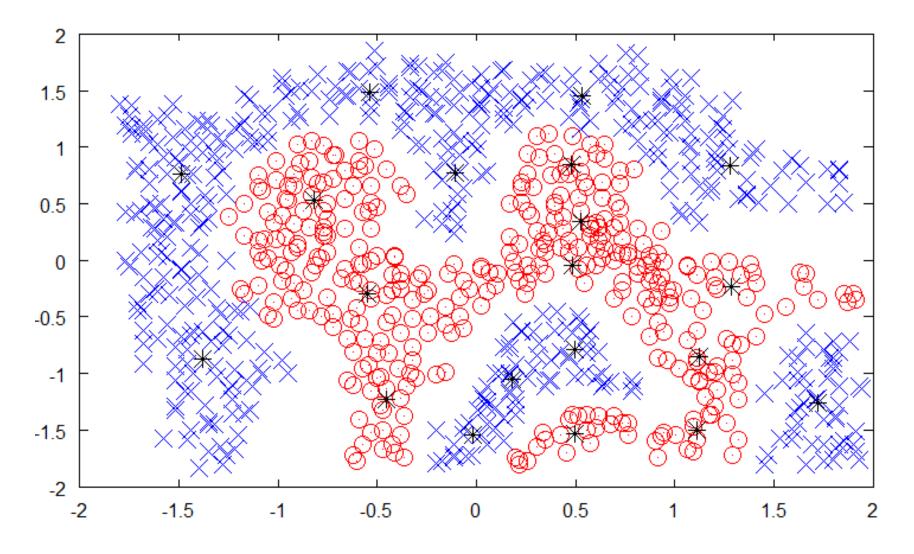
• Radial-basis function (**RBF**) networks samples a subset of *K* training examples and form the feature space using a **gaussian kernel**:

$$\phi(\mathbf{x}) = \begin{bmatrix} \varphi(\mathbf{x} - \mathbf{x}_1) \\ \varphi(\mathbf{x} - \mathbf{x}_2) \\ \dots \\ \varphi(\mathbf{x} - \mathbf{x}_K) \end{bmatrix}$$

with $\varphi(\mathbf{x} - \mathbf{x}_i) = \exp{-\beta ||\mathbf{x} - \mathbf{x}_i||^2}$ decreasing with the distance between the vectors.







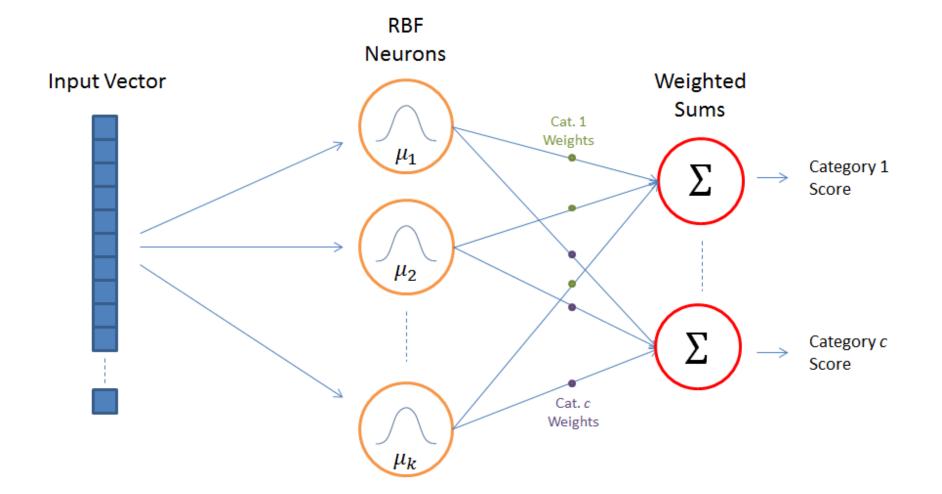
Radial-basis function networks

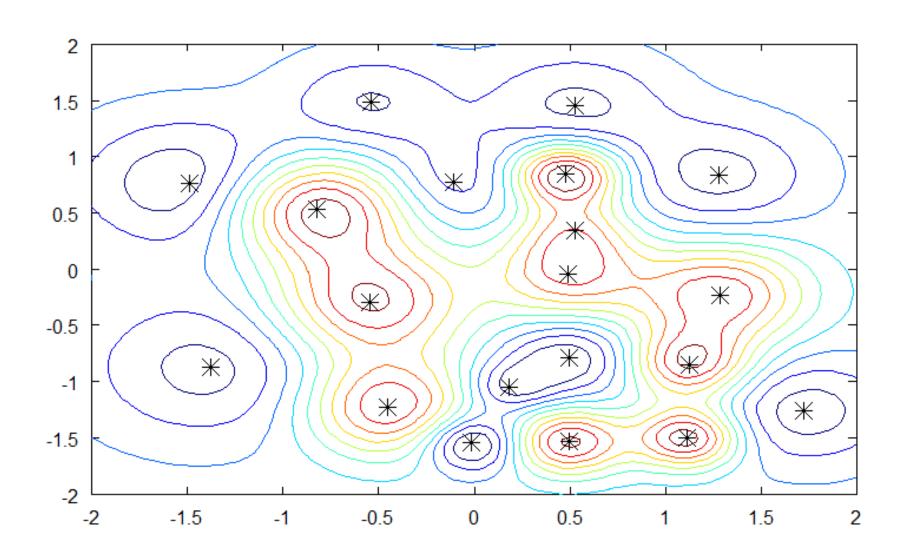
 By applying a linear classification algorithm on the RBF feature space:

$$\mathbf{y} = f(W \times \phi(\mathbf{x}) + \mathbf{b})$$

we obtain a smooth **non-linear** partition of the input space.

• The width of the gaussian kernel allows distancebased **generalization**.

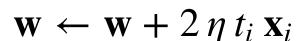




- What happens during online Perceptron learning?
- If an example \mathbf{x}_i is correctly classified $(y_i = t_i)$, the weight vector does not change.

$$\mathbf{w} \leftarrow \mathbf{w}$$

• If an example \mathbf{x}_i is miscorrectly classified $(y_i \neq t_i)$, the weight vector is increased from $t_i \mathbf{x}_i$.





Primal form of the online Perceptron algorithm

- for *M* epochs:
 - **for** each sample (\mathbf{x}_i, t_i) :

$$\circ \ y_i = \operatorname{sign}(\langle \mathbf{w} \cdot \mathbf{x}_i \rangle + b)$$

$$\circ \ \Delta \mathbf{w} = \eta \left(t_i - y_i \right) \mathbf{x}_i$$

$$\circ \ \Delta b = \eta \left(t_i - y_i \right)$$

• If you initialize the weight vector to 0, its final value will therefore be a **linear combination** of the input samples:

$$\mathbf{w} = \sum_{i=1}^{N} \alpha_i \, t_i \, \mathbf{x}_i$$

• The coefficients α_i represent the **embedding strength** of each example, i.e. how often they were misclassified.

• With $\mathbf{w} = \sum_{i=1}^{N} \alpha_i t_i \mathbf{x}_i$, the prediction for an input \mathbf{x} only depends on the training samples and their α_i value:

$$y = \operatorname{sign}(\sum_{i=1}^{N} \alpha_i t_i \langle \mathbf{x}_i \cdot \mathbf{x} \rangle)$$

- To make a prediction y, we need the dot product between the input x and all training examples x_i .
- We ignore the bias here, but it can be added back.



- **for** *M* epochs:
 - for each sample (\mathbf{x}_i, t_i) :

$$\circ y_i = \operatorname{sign}(\sum_{j=1}^N \alpha_j t_j \langle \mathbf{x}_j \cdot \mathbf{x}_i \rangle)$$

$$\circ$$
 if $y_i \neq t_i$:

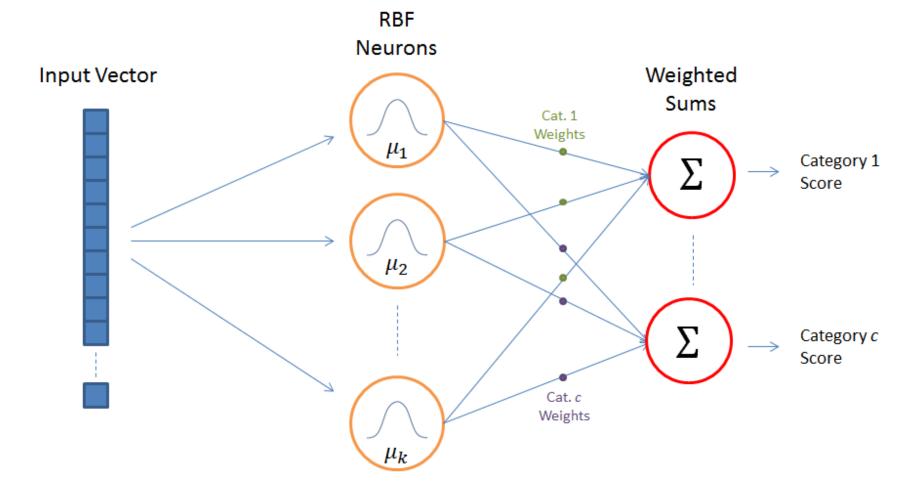
$$\circ \ \alpha_i \leftarrow \alpha_i + 1$$

- This dual form of the Perceptron algorithm is strictly equivalent to its primal form.
- It needs one parameter α_i per training example instead of a weight vector (N >> d), but relies on dot products between vectors.

 Why is it interesting to have an algorithm relying on dot products?

$$y = \operatorname{sign}(\sum_{i=1}^{N} \alpha_i t_i \langle \mathbf{x}_i \cdot \mathbf{x} \rangle)$$

• You can project the inputs ${\bf x}$ to a **feature space** $\phi({\bf x})$ and apply the same algorithm:



$$y = \operatorname{sign}(\sum_{i=1}^{N} \alpha_i t_i \langle \phi(\mathbf{x}_i) \cdot \phi(\mathbf{x}) \rangle)$$

But you do not need to compute the dot product in the feature space, all you need to know is its result.

$$K(\mathbf{x}_i, \mathbf{x}) = \langle \phi(\mathbf{x}_i) \cdot \phi(\mathbf{x}) \rangle$$

• **Kernel trick:** A kernel $K(\mathbf{x}, \mathbf{z})$ allows to compute the dot product between the feature space representation of two vectors without ever computing these representations!

Example of the polynomial kernel

• Let's consider the quadratic kernel in \Re^3 :

$$\forall (\mathbf{x}, \mathbf{z}) \in \Re^{3} \times \Re^{3}$$

$$K(\mathbf{x}, \mathbf{z}) = (\langle \mathbf{x} \cdot \mathbf{z} \rangle)^{2}$$

$$= (\sum_{i=1}^{3} x_{i} \cdot z_{i}) \cdot (\sum_{j=1}^{3} x_{j} \cdot z_{j})$$

$$= \sum_{i=1}^{3} \sum_{j=1}^{3} (x_{i} \cdot x_{j}) \cdot (z_{i} \cdot z_{j})$$

$$= \langle \phi(\mathbf{x}) \cdot \phi(\mathbf{z}) \rangle$$
with:
$$\phi(\mathbf{x}) = \begin{cases} x_{1} \cdot x_{2} \\ x_{1} \cdot x_{3} \\ x_{2} \cdot x_{1} \\ x_{2} \cdot x_{2} \\ x_{2} \cdot x_{3} \\ x_{3} \cdot x_{1} \\ x_{3} \cdot x_{2} \\ x_{3} \cdot x_{3} \end{bmatrix}$$

$$= \langle \phi(\mathbf{x}) \cdot \phi(\mathbf{z}) \rangle$$

• The quadratic kernel implicitely transforms an input space with three dimensions into a feature space of 9 dimensions.

Example of the polynomial kernel

• More generally, the polynomial kernel in \Re^d of degree p:

$$\forall (\mathbf{x}, \mathbf{z}) \in \Re^d \times \Re^d \qquad K(\mathbf{x}, \mathbf{z}) = (\langle \mathbf{x} \cdot \mathbf{z} \rangle)^p$$
$$= \langle \phi(\mathbf{x}) \cdot \phi(\mathbf{z}) \rangle$$

transforms the input from a space with d dimensions into a feature space of d^p dimensions.

- While the inner product in the feature space would require $O(d^p)$ operations, the calculation of the kernel directly in the input space only requires O(d) operations.
- This is called the **kernel trick**: when a linear algorithm only relies on the dot product between input vectors, it can be safely projected into a higher dimensional feature space through a kernel function, without increasing too much its computational complexity, and without ever computing the values in the feature space.

• The **kernel perceptron** is the dual form of the Perceptron algorithm using a kernel.



Kernel Perceptron

- **for** *M* epochs:
 - **for** each sample (\mathbf{x}_i, t_i) :

$$\circ y_i = \operatorname{sign}(\sum_{j=1}^N \alpha_j t_j K(\mathbf{x}_j, \mathbf{x}_i))$$

 \circ if $y_i \neq t_i$:

$$\circ \ \alpha_i \leftarrow \alpha_i + 1$$

• Depending on the kernel, the implicit dimensionality of the feature space can even be infinite!

• **Linear kernel**: dimension of the feature space = *d*.

$$K(\mathbf{x}, \mathbf{z}) = \langle \mathbf{x} \cdot \mathbf{z} \rangle$$

• **Polynomial kernel**: dimension of the feature space = d^p .

$$K(\mathbf{x}, \mathbf{z}) = (\langle \mathbf{x} \cdot \mathbf{z} \rangle)^p$$

• Gaussian kernel (or RBF kernel): dimension of the feature space= ∞ .

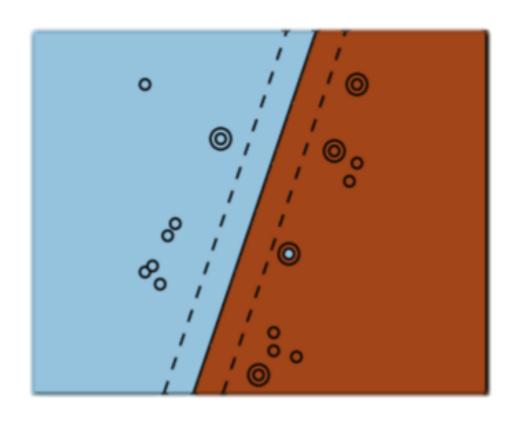
$$K(\mathbf{x}, \mathbf{z}) = \exp(-\frac{\|\mathbf{x} - \mathbf{z}\|^2}{2\sigma^2})$$

 Hyperbolic tangent kernel: dimension of the feature space = ∞

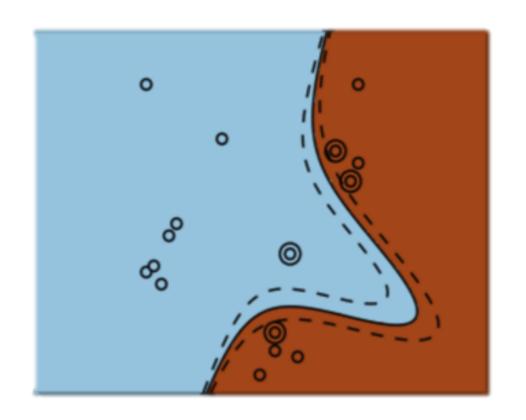
$$k(\mathbf{x}, \mathbf{z}) = \tanh(\langle \kappa \mathbf{x} \cdot \mathbf{z} \rangle + c)$$

Examples of kernels

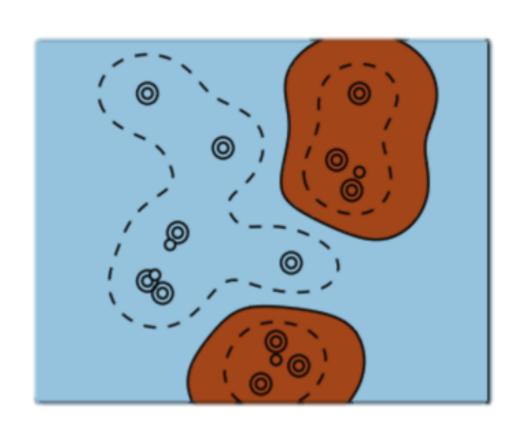
Linear Kernel



Polynomial Kernel



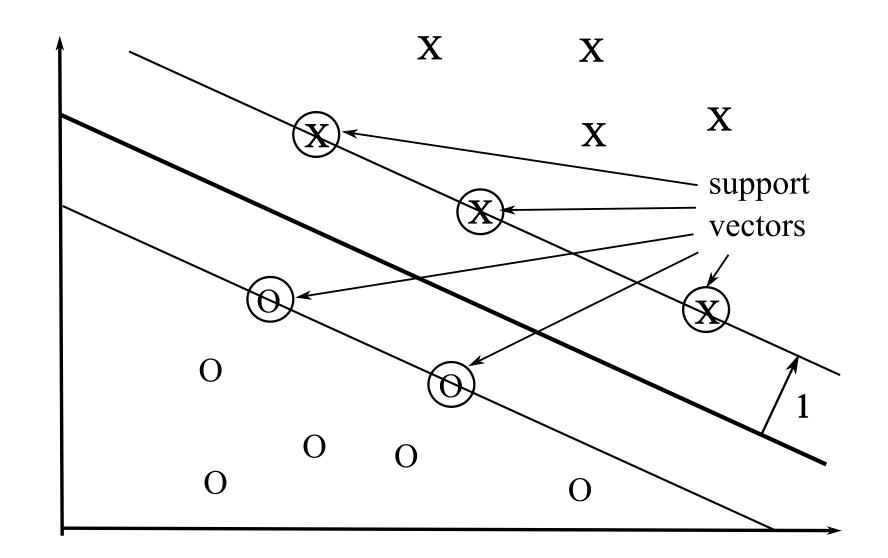
RBF Kernel



- In practice, the choice of the kernel family depends more on the nature of data (text, image...) and its distribution than on the complexity of the learning problem.
- RBF kernels tend to "group" positive examples together.
- Polynomial kernels are more like "distorted" hyperplanes.
- Kernels have parameters $(p, \sigma...)$ which have to found using cross-validation.

Support vector machines

- Support vector machines (SVM) extend the idea of a kernel perceptron using a different linear learning algorithm, the maximum margin classifier.
- Using Lagrange optimization and regularization, the maximal margin classifer tries to maximize the "safety zone" (geometric margin) between the classifier and the training examples.
- It also tries to reduce the number of non-zero α_i coefficients to keep the complexity of the classifier bounded, thereby improving the generalization:



$$\mathbf{y} = \operatorname{sign}(\sum_{i=1}^{N_{SV}} \alpha_i t_i K(\mathbf{x}_i, \mathbf{x}) + b)$$

- Coupled with a good kernel, a SVM can efficiently solve non-linear classification problems without overfitting.
- SVMs were the weapon of choice before the deep learning era, which deals better with huge datasets.