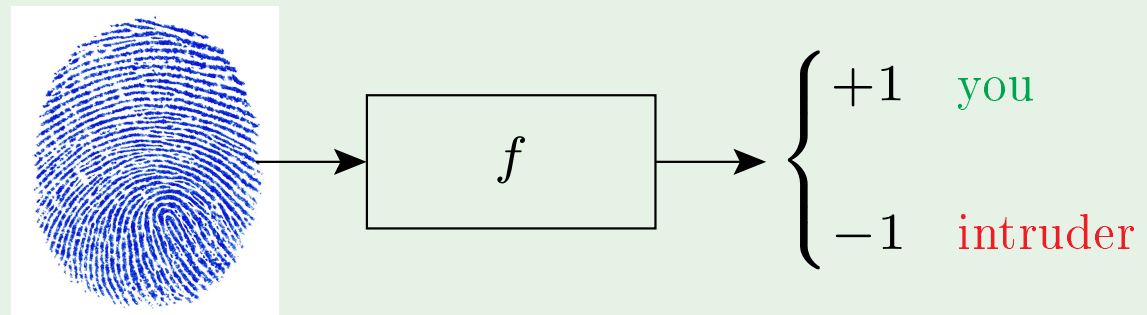


Review of Lecture 4

- Error measures

- User-specified $e(h(\mathbf{x}), f(\mathbf{x}))$



- In-sample:

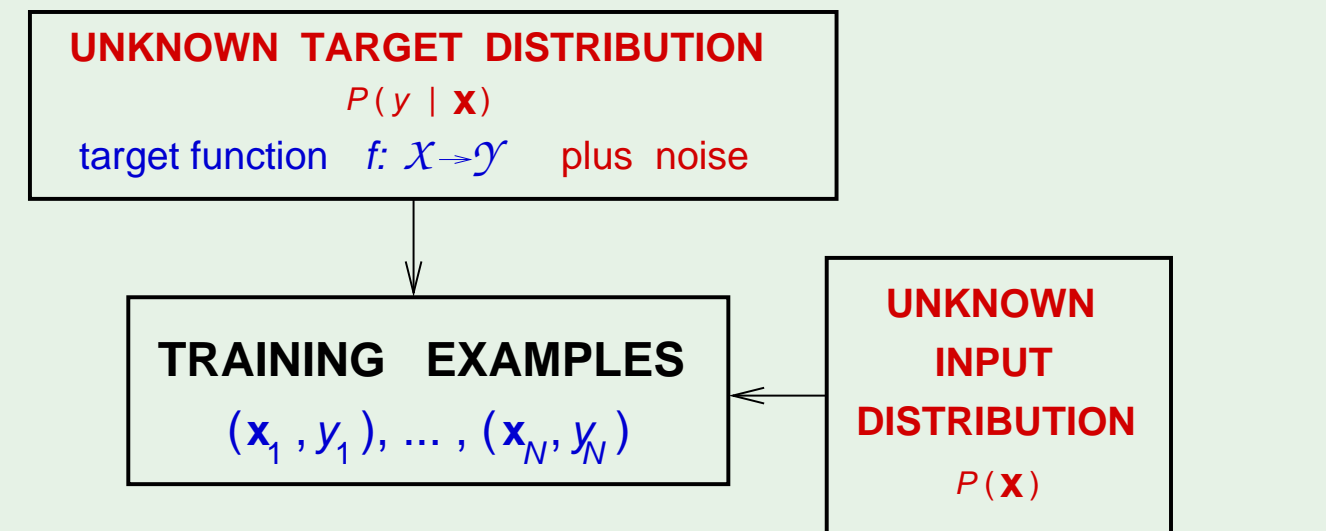
$$E_{\text{in}}(h) = \frac{1}{N} \sum_{n=1}^N e(h(\mathbf{x}_n), f(\mathbf{x}_n))$$

- Out-of-sample

$$E_{\text{out}}(h) = \mathbb{E}_{\mathbf{x}} [e(h(\mathbf{x}), f(\mathbf{x}))]$$

- Noisy targets

$$y = f(\mathbf{x}) \longrightarrow y \sim P(y | \mathbf{x})$$



- $(\mathbf{x}_1, y_1), \dots, (\mathbf{x}_N, y_N)$ generated by each independently

$$P(\mathbf{x}, y) = P(\mathbf{x})P(y|\mathbf{x})$$

- $E_{\text{out}}(h)$ is now $\mathbb{E}_{\mathbf{x}, y} [e(h(\mathbf{x}), y)]$

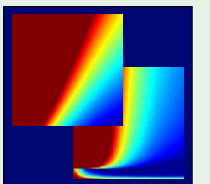
Learning From Data

Yaser S. Abu-Mostafa
California Institute of Technology

Lecture 5: Training versus Testing



Sponsored by Caltech's Provost Office, E&AS Division, and IST • Tuesday, April 17, 2012



Outline

- From training to testing
- Illustrative examples
- Key notion: break point
- Puzzle

The final exam

Testing:

fixed hypothesis, hence $M=1$

$$\mathbb{P} \left[|E_{\text{in}} - E_{\text{out}}| > \epsilon \right] \leq 2 e^{-2\epsilon^2 N}$$

Training:

trialling hypotheses

$$\mathbb{P} \left[|E_{\text{in}} - E_{\text{out}}| > \epsilon \right] \leq 2\textcolor{red}{M} e^{-2\epsilon^2 N}$$

Where did the M come from?

The *Bad* events \mathcal{B}_m are

$$“|E_{\text{in}}(h_m) - E_{\text{out}}(h_m)| > \epsilon”$$

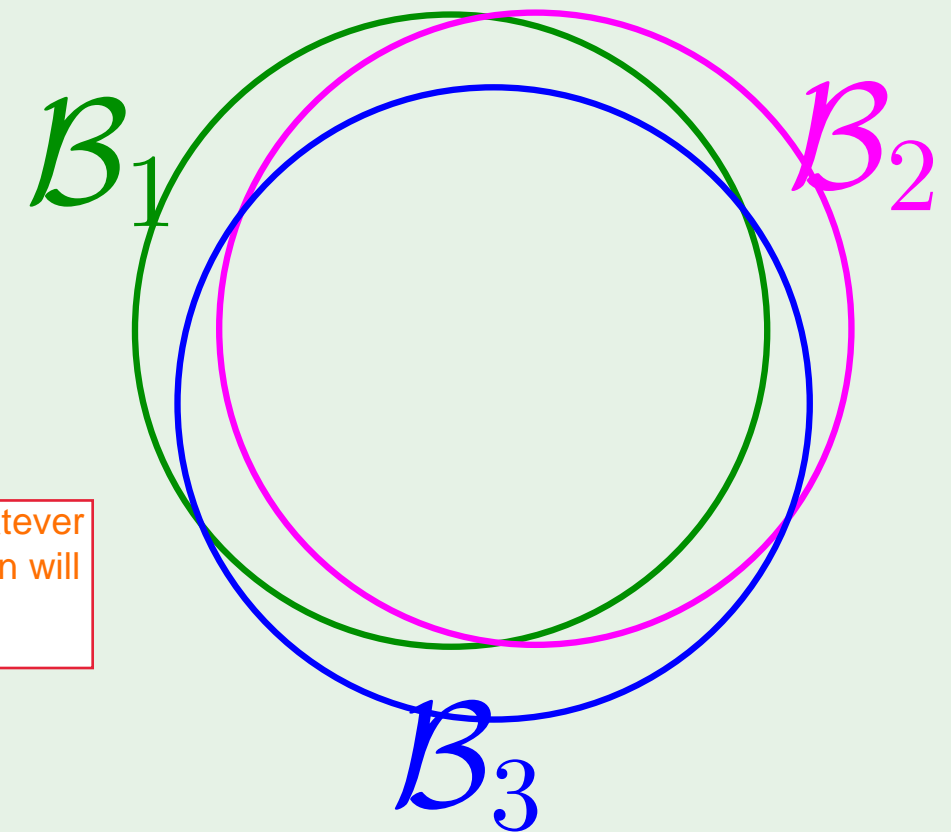
The union bound:

$$\mathbb{P}[\mathcal{B}_1 \text{ or } \mathcal{B}_2 \text{ or } \dots \text{ or } \mathcal{B}_M]$$

$$\leq \underbrace{\mathbb{P}[\mathcal{B}_1] + \mathbb{P}[\mathcal{B}_2] + \dots + \mathbb{P}[\mathcal{B}_M]}$$

no overlaps: M terms

We want $\mathbb{P}(\mathcal{B}_1 \text{ or } \mathcal{B}_2 \text{ or } \dots)$ to be small so that whatever final hypothesis the learning algorithm picks, its E_{in} will track E_{out} well (which is something we require).



Can we improve on M ?

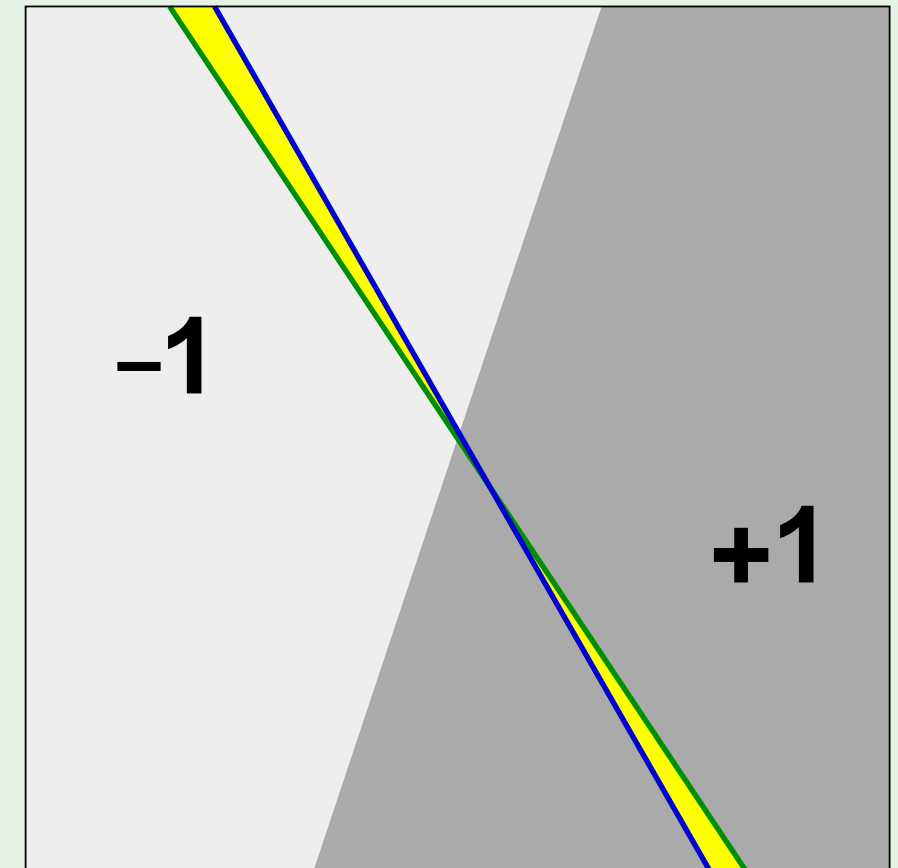
We want to extract a quantity from the hypothesis set to characterize the overlap and get us a good bound without having to go through the details of how the and events are correlated.

Yes, bad events are *very* overlapping!

ΔE_{out} : change in $+1$ and -1 areas

ΔE_{in} : change in labels of data points

$$|E_{\text{in}}(h_1) - E_{\text{out}}(h_1)| \approx |E_{\text{in}}(h_2) - E_{\text{out}}(h_2)|$$



We are interested in showing E_{in} tracks E_{out} for h_1 is approximately equal to how they track for h_2 , or that if the LHS exceeds epsilon then RHS also exceeds epsilon most of the time - so there is a lot of overlap in the bad events B .

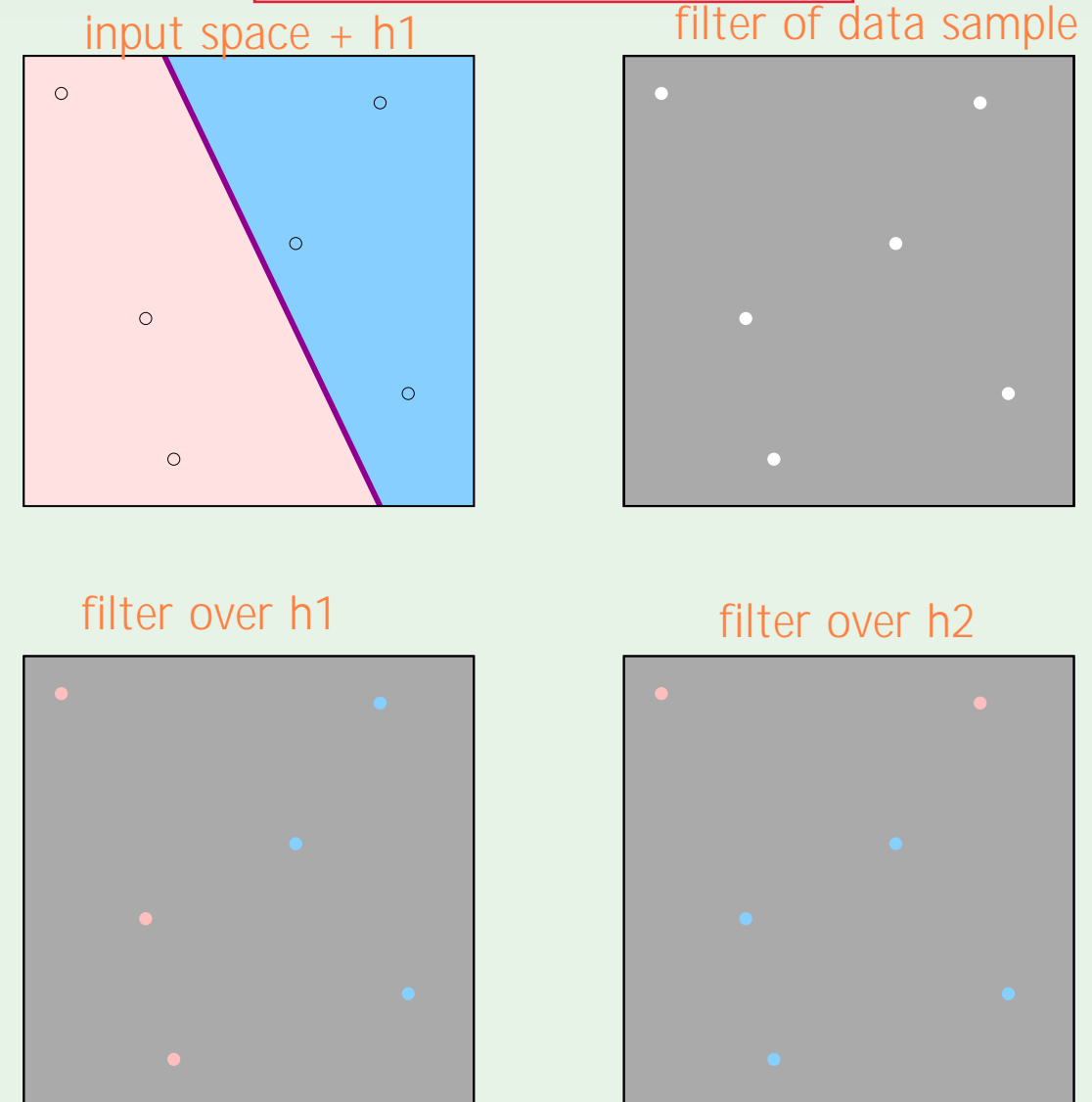
What can we replace M with?

Instead of the whole input space,
we consider a finite set of input points,

and count the number of *dichotomies*

i.e. how many patterns of red/blue points can we get - it characterizes the strength/power of the hypothesis set since if a hyp set can give all the combinations of red/blue points, it is a powerful set (and vice versa if it can only model a few combinations)
- we tried to characterise the power of a hypothesis set with M .

How we can consider dichotomies



We reduce the problem to looking at it through a sheet with N holes over the data sample (so not the whole input space). So can change the hypothesis without the boundary crossing a point and the filtered picture doesn't change. When we cross a point ($h1 \rightarrow h2$), we have another pattern.

Dichotomies: mini-hypotheses

A hypothesis $h : \mathcal{X} \rightarrow \{-1, +1\}$

A dichotomy $h : \{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N\} \rightarrow \{-1, +1\}$

Number of hypotheses $|\mathcal{H}|$ can be infinite

Number of dichotomies $|\mathcal{H}(\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N)|$ is at most 2^N

Candidate for replacing M

- where we apply each member h from the set H to all of the data points $\{x_1, x_2, \dots, x_N\}$ and create a dichotomy: a vector of length N of ± 1 . Many of the h applied to $\{x_i\}$ will return the exact same dichotomy since it is quite restricted and only returns ± 1 on each point, hence not infinite.

The growth function

The growth function counts the most dichotomies on any N points

$$m_{\mathcal{H}}(N) = \max_{\mathbf{x}_1, \dots, \mathbf{x}_N \in \mathcal{X}} |\mathcal{H}(\mathbf{x}_1, \dots, \mathbf{x}_N)|$$

cardinality of set of dichotomies

max w.r.t. any choice of N points from X

The growth function satisfies:

$$m_{\mathcal{H}}(N) \leq 2^N$$

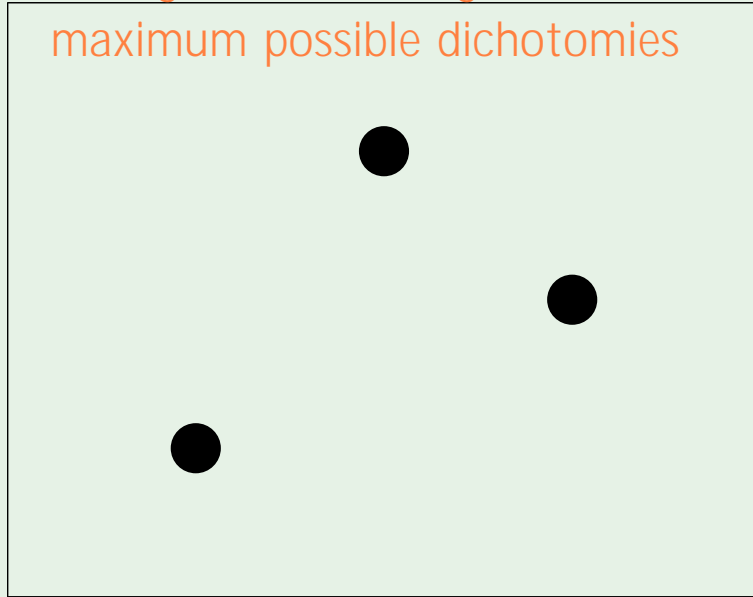
Let's apply the definition.

We may have an X and H where we can generate any pattern we want, so m can $= 2^N$. However in most cases, using h from H means we can miss out on some patterns, so $< 2^N$

- given N points, the growth function returns the most dichotomies possible (not N points from our data set, but it picks from the input space to give the max number of dichotomies). So we wisely pick N points from X with a view to maximizing the dichotomies such that the number we get is more than any number someones else can get with N points. It finds the most possible dichotomies - e.g. if all the points were on a line (colinear), it would have fewer dichotomies as fewer ways to separate, so this would likely not be the maximum value. m returns the most expressive facet of the hyp set on the N points.

Applying $m_{\mathcal{H}}(N)$ definition - perceptrons

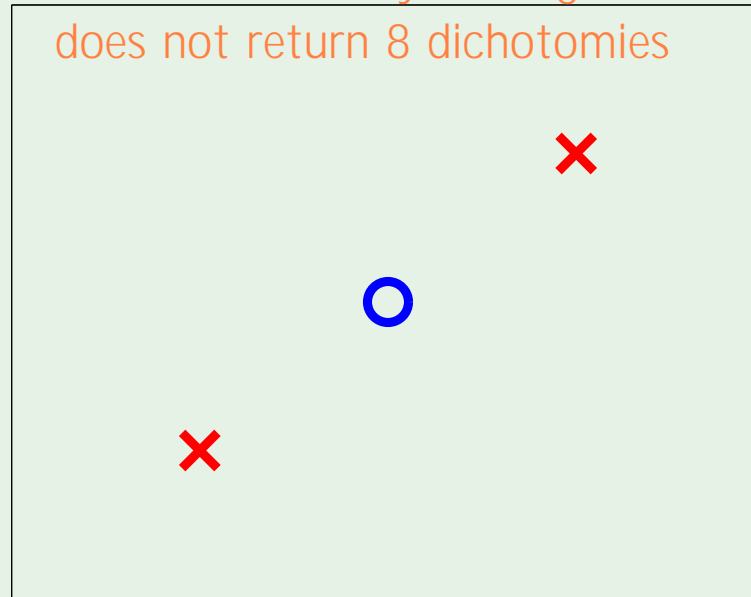
arrangement which gives the maximum possible dichotomies



$$N = 3$$

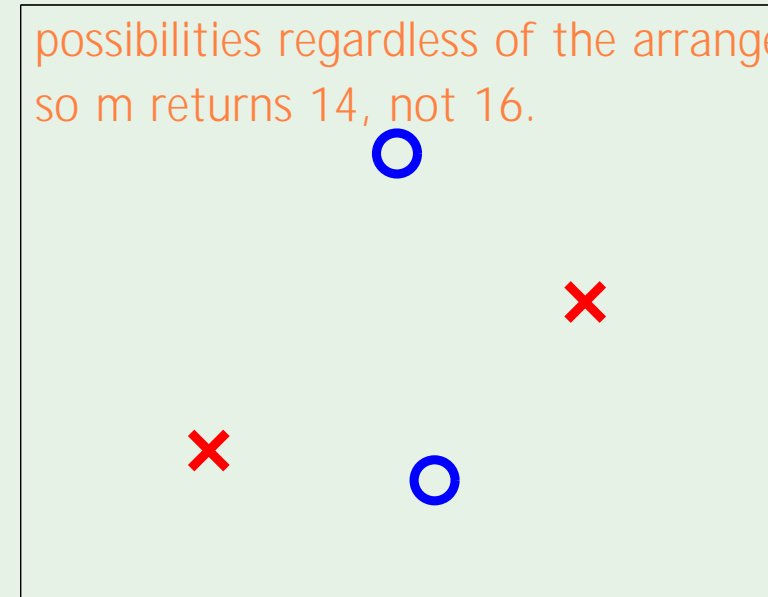
$$m_{\mathcal{H}}(3) = 8$$

due to collinearity, arrangement does not return 8 dichotomies



$$N = 3$$

Here with $N=4$ we miss two (or more) of the possibilities regardless of the arrangement, so m returns 14, not 16.



$$N = 4$$

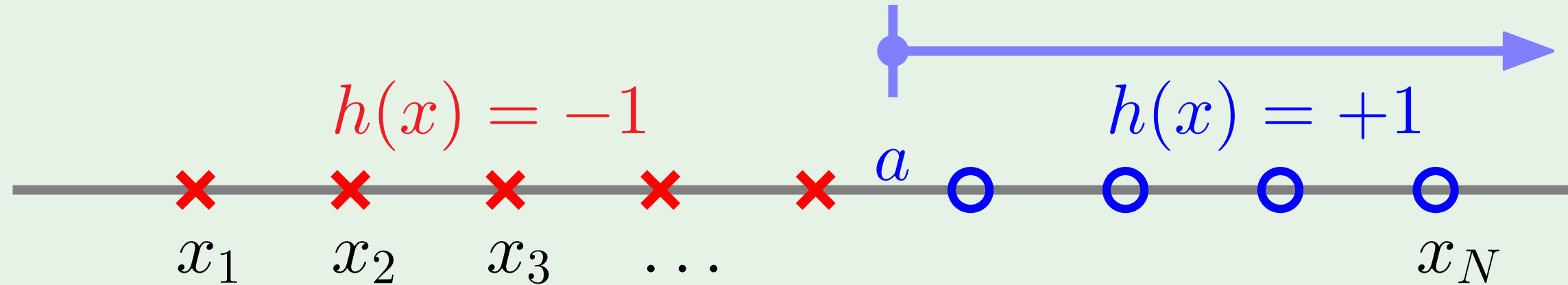
$$m_{\mathcal{H}}(4) = 14$$

So for $N=4$, perceptrons start to become limited and cannot create two of the dichotomies

Outline

- From training to testing
- Illustrative examples
- Key notion: break point
- Puzzle

Example 1: positive rays



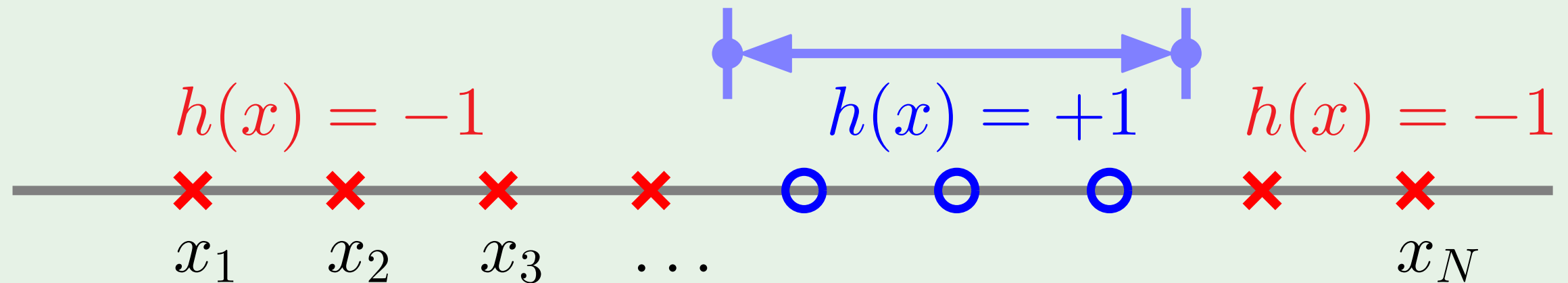
Must count number of possible choices of a which give us different dichotomies, so since there are $N-1$ sandwiched line segments, $+1$ if a is to left of x_1 , $+1$ if a is to right of x_N , so $N+1$ overall

\mathcal{H} is set of $h: \mathbb{R} \rightarrow \{-1, +1\}$

$$h(x) = \text{sign}(x - a)$$

$$m_{\mathcal{H}}(N) = N + 1$$

Example 2: positive intervals



\mathcal{H} is set of $h: \mathbb{R} \rightarrow \{-1, +1\}$

Place interval ends in two of $N + 1$ spots

$$m_{\mathcal{H}}(N) = \binom{N+1}{2} + 1 = \frac{1}{2}N^2 + \frac{1}{2}N + 1$$

+1 to account for all red - when the two intervals
are at the same point

Example 3: convex sets

$h(x) = +1$ if at x , it is a convex region. A convex region is a region where, if you pick any two points within the region, the entire line segment connecting them lies within the region.

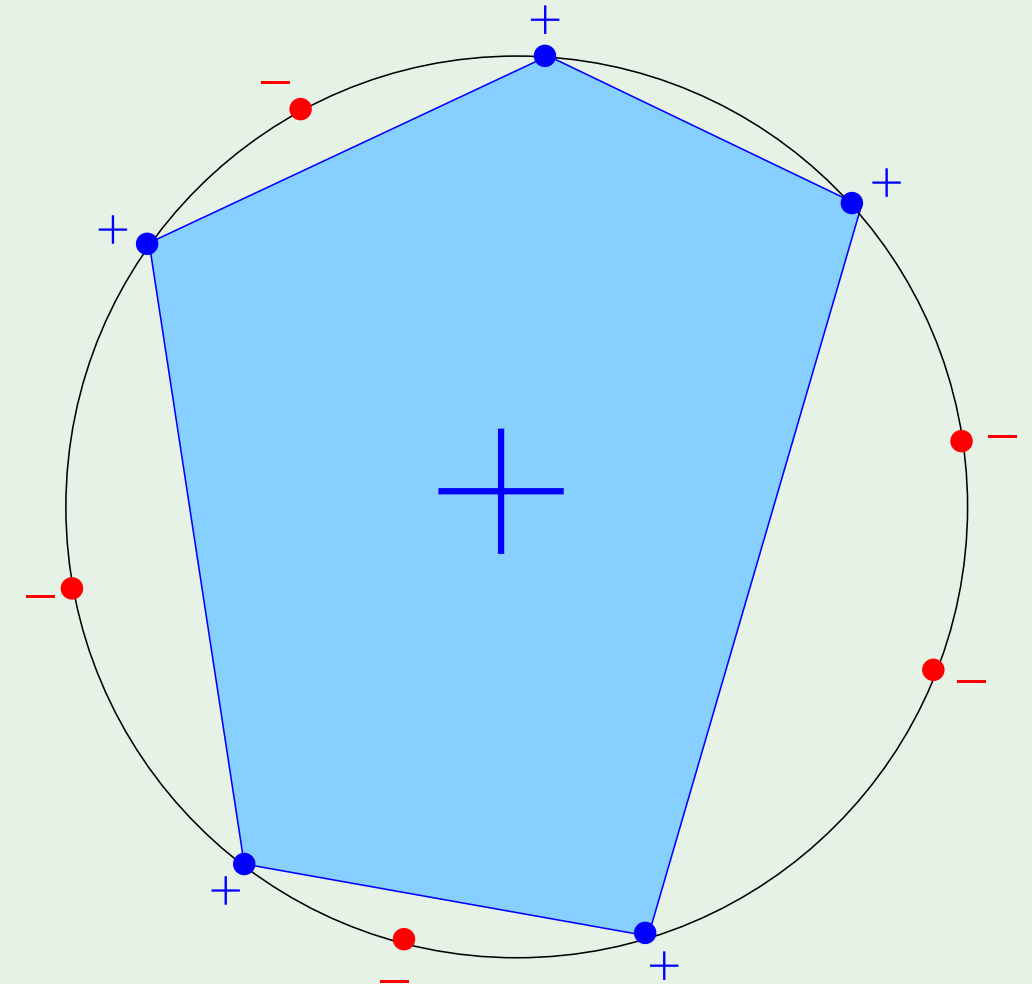
\mathcal{H} is set of $h: \mathbb{R}^2 \rightarrow \{-1, +1\}$

$h(\mathbf{x}) = +1$ is convex

$$m_{\mathcal{H}}(N) = 2^N$$

The N points are 'shattered' by convex sets

occurs when you get all possible dichotomies (2^N) from a hypothesis set



Putting the points on a circle gives the maximum possible dichotomies using convex regions since all the points that are convex (and therefore need to connect via a line segment) can connect if on the perimeter of a circle.

The 3 growth functions

- \mathcal{H} is positive rays:

$$m_{\mathcal{H}}(N) = N + 1$$

- \mathcal{H} is positive intervals:

$$m_{\mathcal{H}}(N) = \frac{1}{2}N^2 + \frac{1}{2}N + 1$$

- \mathcal{H} is convex sets:

$$m_{\mathcal{H}}(N) = 2^N$$

Back to the big picture

Remember this inequality?

$$\mathbb{P} [|E_{\text{in}} - E_{\text{out}}| > \epsilon] \leq 2M e^{-2\epsilon^2 N}$$

What happens if $m_{\mathcal{H}}(N)$ replaces M ?

$m_{\mathcal{H}}(N)$ polynomial \implies Good!

Just prove that $m_{\mathcal{H}}(N)$ is polynomial?

if polynomial learning is feasible given that, due to the exponential factor (with epsilon generally very small), the exponential will eventually (depending on the patience of the customer or size of the dataset) kill any polynomial it is multiplied by. Note that m will always either be polynomial or 2^N .

Outline

- From training to testing
- Illustrative examples
- Key notion: **break point**
- Puzzle

Break point of \mathcal{H}

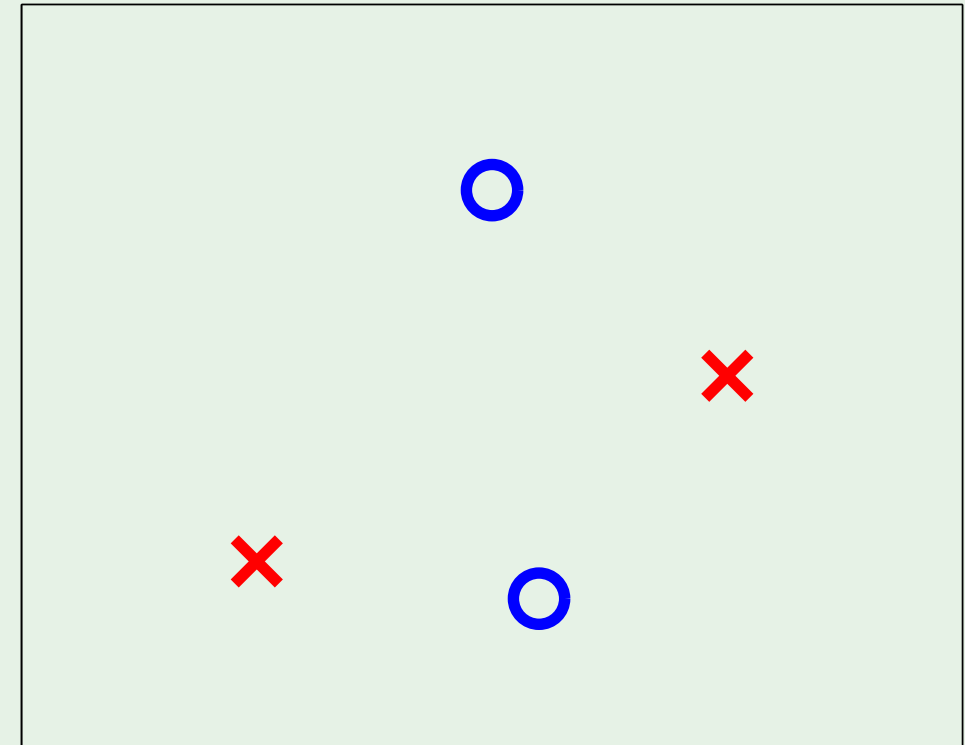
Definition:

If no data set of size k can be shattered by \mathcal{H} , then k is a break point for \mathcal{H}

$$m_{\mathcal{H}}(k) < 2^k$$

For 2D perceptrons, $k = 4$

A bigger data set cannot be shattered either



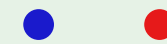
It is the data size at which there is no constellation choice such that the hypothesis set can produce all possible dichotomies - e.g. $k=4$ for 2D perceptrons because at $N=4$, we could only get 14, not $2^4=16$ dichotomies.

Break point - the 3 examples

i.e. for what N does m , the growth function, stop giving 2^N ?

- Positive rays $m_{\mathcal{H}}(N) = N + 1$

break point $k = 2$



- Positive intervals $m_{\mathcal{H}}(N) = \frac{1}{2}N^2 + \frac{1}{2}N + 1$

break point $k = 3$



- Convex sets $m_{\mathcal{H}}(N) = 2^N$

break point $k = \infty$

Main result

No break point $\implies m_{\mathcal{H}}(N) = 2^N$

Any break point $\implies m_{\mathcal{H}}(N)$ is **polynomial** in N

In principle, the existence of a break point indicates that learning is feasible with the hypothesis set. Meanwhile the value of the break point tells us the resources needed (size of training data) for a certain performance.

Puzzle

\mathbf{X}_1	\mathbf{X}_2	\mathbf{X}_3
<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>
<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>