# Philosophical Fundamentals of Machine Learning

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Week 2

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- 2 Bayesian Statistical Decision Theory
- ROC Curves
- Empirical Risk Minimization
- Bias-Complexity Tradeoff
- Maive Bayes
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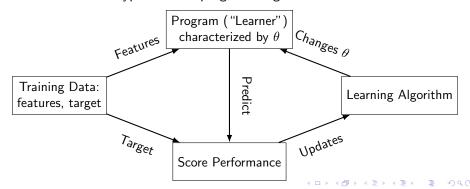
Question: How does Machine Learning (ML) work in supervised learning?

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**Question:** How does Machine Learning (ML) work in supervised learning? **Answer:** ML is a type of meta-programming.

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**Question:** How does Machine Learning (ML) work in supervised learning? **Answer:** ML is a type of meta-programming.



When building supervised learning models, the algorithm we follow is:

Evaluate data.

- Evaluate data.
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- Deploy and apply ML model.

So how do we evaluate ML models?

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- Internal: do we do as well as we can do by our own beliefs?
- External: do we do as well as we can do reliably?

The two methods we consider in this course are **Bayesian Statistical Decision Theory** and **Empirical Risk Minimization**.

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#### Example

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We can think of the QALYs as measuring the relative *utility* of our predictions. If we take our goal to minimize the relative lost utility compared to how well we could do, then we have what is called a *loss* or *cost* function. **Our goal is to minimize this loss**.

#### Recall

The expected value of a function g(x) with respect to a discrete random variable  $X \sim p(x)$  is given by:

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If we let our disutility be characterized by the loss function  $l:Y\to\mathbb{R}$ , then we say that *quality of our prediction* is given by the expected loss with respect to the target random variable Y from  $Y\sim p(y)$ , where the predictions of our model characterized by  $\hat{y}$ :

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Assuming we see features  $\mathbf{x}$ , our goal is to predict the targets, which is the posterior probability of the targets given the data  $p(y|\mathbf{x})$ .

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The goal then is to find the **optimal predictor** that minimizes the expected risk:

$$\pi^*(\mathbf{x}) = \operatorname*{arg\,min}_{\hat{y} \in \hat{Y}} R(\hat{y}|\mathbf{x})$$

#### Example

Returning to our drug example, if we have a posterior distribution given by:

Cancer	Drugs	l(cancer, prediction)	$p(\cdot \mathbf{x})$
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$$R(c,d) = p(c|\mathbf{x})l(c,d) + p(not c|\mathbf{x})l(not c,d)$$
  
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The better model is then the first model.

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#### Example

In the previous example, our assessment of the better model would change based on how prevalent we thought cancer was. For example, if we thought  $p(cancer|\mathbf{x}) = 0.1$  while  $p(not\ cancer|\mathbf{x}) = 0.9$ , then we would recommend the second ML model

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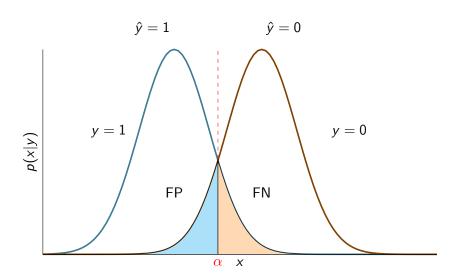
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probability	type	
$p(\hat{y}=1 y=0)$	false positive rate (FPR)	
$p(\hat{y}=1 y=1)$	true positive rate (TPR)	
$p(\hat{y}=0 y=1)$	false negative rate (FNR)	
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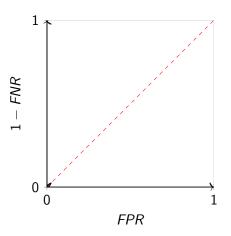
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These are defined such that the TPR is 1 - FPR and the TNR is 1 - FPR.



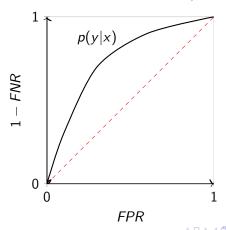
### Receiver Operator Characteristic

We can plot the trade off between FPR and FNR through a **Receiver Operator Characteristic** (ROC) plot. Here the dashed red-line indicates a random guessing decision procedure.



### Receiver Operator Characteristic

We can then plot the optimal Bayesian predictor in terms of our posterior probability. The area under curve (AUC) of this Bayesian predictor is as best we can do given our best beliefs. We then assess the quality of our ML algorithms by how close their AUC is to the optimal predictor:



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We turn to the second now with **Empirical Risk Minimization**.

### Definition (Population Risk)

Suppose we have some random variables of features X and targets Y sampled from some distribution  $X, Y \sim p^*(\mathbf{x}, y)$ .

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$$R(f, p^*) := \mathbb{E}_{X, Y \sim p^*(\mathbf{x}, y)}[l(y, f(\mathbf{x}))] = \sum_{\mathbf{x}, y \in X, Y} l(y, f(\mathbf{x}))p^*(\mathbf{x}, y)$$

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#### Remark

The population risk is very similar to the posterior risk in that it is a weighted average by some probability distribution and a loss function. However, they should not be confused because the population risk assumes to true, target distribution  $p^*$  that is "out in the world", and it weights the losses of our model by the *joint probability* of features and labels, instead of a posterior probability.

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1	1	0	10	0.1
1	0	1	2	0.15
1	0	0	0	0.15
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If we administer the drug when IBD is present, our population risk is then (0.1)(5) + (0.15)(2) + (0.05)(10) + (0.7)(0) = 1.3.

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If we administer the drug when IBD is present, our population risk is then (0.1)(5) + (0.15)(2) + (0.05)(10) + (0.7)(0) = 1.3. If we do the opposite, the population risk is (0.1)(10) + (0.15)(0) + (0.05)(5) + (0.7)(2) = 2.65.

# **Empirical Risk**

#### Remark

Our problem is that the population distribution  $p^*$  is *unknown*. So we have to approximate it using the empirical distribution from our collected data  $\mathcal{D} = \{(\mathbf{x}^{(i)}, y^{(i)})\}_{i=1,\dots,N}$  that has N samples.

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$$R(f,\mathcal{D}) := \mathbb{E}_{X,Y \sim p_{\mathcal{D}}(\mathbf{x},y)}[l(y,f(\mathbf{x}))] = \frac{1}{N} \sum_{i=1}^{N} l(y^{(i)},f(\mathbf{x}^{(i)}))$$

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IBD	Cancer	Drugs	$l(y, \hat{y})$	Counts	$p_{\mathcal{D}}(IBD, \mathit{Cancer})$
1	1	1	5	90	0.06
1	1	0	10	90	0.00
1	0	1	2	200	0.14
1	0	0	0	200	0.14
0	1	1	5	30	0.02
0	1	0	10	30	0.02
0	0	1	2	1100	0.78
0	0	0	0	1100	0.70

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1	0	0	0	200	0.14
0	1	1	5	30	0.02
0	1	0	10	30	0.02
0	0	1	2	1100	0.78
0	0	0	0	1100	0.70

If we administer the drug when IBD is present, our empirical risk is then (0.06)(5) + (0.14)(2) + (0.02)(10) + (0.78)(0) = 0.78.

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IBD	Cancer	Drugs	$l(y, \hat{y})$	Counts	$p_{\mathcal{D}}(IBD, \mathit{Cancer})$
1	1	1	5	90	0.06
1	1	0	10	90	0.00
1	0	1	2	200	0.14
1	0	0	0	200	0.14
0	1	1	5	30	0.02
0	1	0	10	30	0.02
0	0	1	2	1100	0.78
0	0	0	0	1100	0.70

If we administer the drug when IBD is present, our empirical risk is then (0.06)(5) + (0.14)(2) + (0.02)(10) + (0.78)(0) = 0.78. If we do the opposite the risk is (0.06)(10) + (0.14)(0) + (0.02)(5) + (0.78)(2) = 2.26.

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Of course, we don't know the population risk so we cannot calculate the generalization error directly.

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The  $\epsilon_H(N,\delta)$  is a risk bounding function parameterized by the complexity

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- **1** It is distribution agnostic. Namely, it does not depend on what the true, underlying population distribution  $p^*$  happens to be.
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- The less complex the class of models, the tighter the upper bound. We don't want models that are too complex less we worry about generalization.

In contrast to the internalist method of evaluation, this allows ERM to be largely about just the structure of the machine learning problem. It provides us a *reliability* assurance about how our models will perform.

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The bias-complexity tradeoff—not to be confused with the bias-variance tradeoff!

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Importantly, this error is a function of how many models we consider: if we consider more possible models, then the approximation error will go down. Letting the number of models be a measure of complexity, then **the more complex a machine learning model**, **the lower the approximation error**.

#### Theorem

Suppose we want to ensure that our generalization error is less than or equal to  $\epsilon'$  for all models in class  $\mathcal H$  with probability  $1-\delta$  as we draw data  $\mathcal D$  i.i.d. from the population distribution  $p^*$ . Then the size of our data set, N, we would need is bounded by the size  $|\mathcal H|$ :

$$N \leq \frac{2\log(2|\mathcal{H}|/\delta)}{\epsilon'^2}$$

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#### Remark

The number of candidate models in our set  $\mathcal{H}$  is a measure of complexity of our machine learning models. This means that because we can bound our generalization error  $\epsilon$  by  $\epsilon'$  and supposing we ensure our dataset is the right size, then our generalization error is a function of how complex our model happens to be. The more complex our machine learning model, the higher the generalization error.

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- Our training data.

# Bias-Complexity Tradeoff

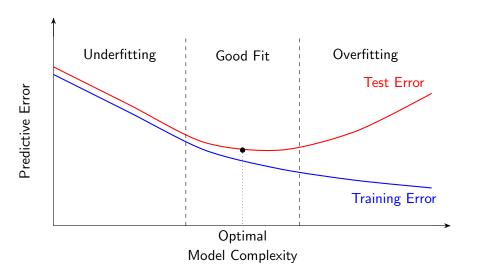
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So when using ERM, our "what you see is what you get" guarantee forces us to choose between:

- Complex models good at solving the problem at hand.
- Our How well we generalize from our training data.

This is sometimes called the tradeoff between overfitting and underfitting.

# **Underfitting-Overfitting**



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We use ERM to construct and select models during training. We check our generalization error and the degree to which we overfit or underfit the data by a **hold-out test set**. We then use AUC to measure how well we do to the optimal Bayes predictor.

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#### Recall

Let  $A, B, C \in \Sigma$  for the probability space  $(\Omega, \Sigma, \Pr)$ . A and B are conditionally independent given C if  $\Pr(A|B,C) = \Pr(A|C)$ . Alternatively, we can define it as  $\Pr(A,B|C) = \Pr(A|C) \Pr(B|C)$ .

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#### Naive Bayes

Consider the classification problem where we suspect that features  $X = \mathbf{x}$ , where  $x_i$  for i = 1, ..., n are independent of one another conditional on the class target Y, where  $y_k$  for k = 1, ..., m. That is:

$$\Pr(X = [x_1, \dots, x_n] | Y = y_k) = \prod_{i=1}^n \Pr(x_i | Y = y_k)$$

We can then use this simplifying assumption to directly learn  $Pr(y|\mathbf{x})$ , by using Bayes rule.

#### Naive Bayes continued

The Naive Bayes classifier for target  $Y = y_j$ :

$$\Pr(Y = y_j | X = [x_1, ..., x_n]) = \frac{\prod_{i=1}^{n} \Pr(x_i | Y = y_j) \Pr(Y = y_j)}{\sum_{k=1}^{m} \prod_{i=1}^{n} \Pr(x_i | Y = y_k) \Pr(Y = y_k)}$$

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#### Example

A common deployment of naive Bayes is as a span classifier in email: we treat the frequencies of certain words occurring, like "Nigerian Prince", as independent of one another conditional on whether the email is spam.

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### k-Nearest Neighbors

Suppose we have the classification problem with features  $X = \mathbf{x}$  and class targets Y. We have some distance metric  $d(\mathbf{x}, \mathbf{x}')$  between our samples, which we use to compute the K closest neighbors in our dataset  $\mathcal{D}$  to a sample  $\mathbf{x}$ ,  $N_K(\mathbf{x}, \mathcal{D})$ . Then our posterior predictive probability given the data is:

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#### Remark

When K = 1, we say our target is the same as that of the closest sample.

### Definition (Euclidean Distance)

A common distance metric is Euclidean Distance:

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#### Remark

We can think about K as controlling the complexity of our decision boundary between classes. Unintuitively, the lower K, the *more complex* the decision boundary while the higher the K, the *less complex* the decision boundary.

