

## Chapter 5

# Machine Learning Basics

Deep learning is a specific kind of machine learning. To understand it well, one must have a solid understanding of the basic principles. This chapter provides a brief course in the most important concepts that are applied throughout the rest of the book. Novice readers with a wider perspective are encouraged to consider machine learning from a more comprehensive coverage of the fundamentals, such as [M \(2006\)](#). If you are already familiar with machine learning, jump ahead to section [5.11](#). That section covers some perspectives on learning techniques that have strongly influenced the development of modern algorithms.

We begin with a definition of what a learning algorithm is. For example: the linear regression algorithm. We then proceed to discuss the

descent. We describe how to combine various algorithm an optimization algorithm, a cost function, a model, and machine learning algorithm. Finally, in section 5.11, we factors that have limited the ability of traditional machine These challenges have motivated the development of deep le overcome these obstacles.

## 5.1 Learning Algorithms

A machine learning algorithm is an algorithm that is ab But what do we mean by learning? Mitchell (1997) provide “A computer program is said to learn from experience  $E$  class of tasks  $T$  and performance measure  $P$ , if its perform measured by  $P$ , improves with experience  $E$ .” One can im experiences  $E$ , tasks  $T$ , and performance measures  $P$ , and this book to formally define what may be used for each of in the following sections, we provide intuitive description different kinds of tasks, performance measures, and experie to construct machine learning algorithms.

### 5.1.1 The Task, $T$

Machine learning enables us to tackle tasks that are too fixed programs written and designed by human beings. philosophical point of view, machine learning is interesting understanding of it entails developing our understanding underlie intelligence

Many kinds of tasks can be solved with machine learning. Common machine learning tasks include the following:

- **Classification:** In this type of task, the computer program must determine which of  $k$  categories some input belongs to. To solve this task, a learning algorithm is usually asked to produce a function  $f : \mathbb{R}^n \rightarrow \{1, \dots, k\}$ . Given an input  $\mathbf{x}$ , the model assigns an input described by  $\mathbf{x}$  to one of the  $k$  categories identified by numeric code  $y$ . There are other variations of classification tasks, for example, where  $f$  outputs a probability distribution over the  $k$  categories. An example of a classification task is object recognition. In a typical object recognition task, an image (usually described as a set of pixel brightness values) is input, and the output is a numeric code identifying the object in the image. For example, the Willow Garage PR2 robot is able to act as a waiter, identifying different kinds of drinks and deliver them to people (Fergus *et al.*, 2010). Modern object recognition is based on deep learning (Krizhevsky *et al.*, 2012; Ioffe and Szegedy, 2015). Face recognition is the same basic technology that enables social media sites to recognize faces (Taigman *et al.*, 2014), which can be used to automatically tag photos in photo collections and for computers to interact more naturally with users.
- **Classification with missing inputs:** Classification is challenging if the computer program is not guaranteed that its input vector will always be provided. To solve this task, a learning algorithm only has to define a *single* function that maps an input to a categorical output. When some of the input features are missing, rather than providing a single classification function, the model must learn a *set* of functions. Each function corresponds to a specific input vector.

- **Regression:** In this type of task, the computer program is asked to output a numerical value given some input. To solve this task, the program is asked to output a function  $f : \mathbb{R}^n \rightarrow \mathbb{R}$ . This type of task is similar to classification, except that the format of output is different. Examples of regression tasks include the prediction of the expected cost of an insured person will make (used to set insurance premiums) and the prediction of future prices of securities. These kinds of prediction tasks are often used in algorithmic trading.
- **Transcription:** In this type of task, the machine learning program is asked to observe a relatively unstructured representation of information and transcribe the information into discrete textual form. For example, in optical character recognition, the computer program is given an image containing an image of text and is asked to return the text. In speech recognition, a sequence of characters (e.g., in ASCII or Unicode format) is returned. Google View uses deep learning to process address numbers in a map (e.g., [et al., 2014d](#)). Another example is speech recognition where a program is provided an audio waveform and emits a sequence of word ID codes describing the words that were spoken. Deep learning is a crucial component of modern speech recognition systems used at major companies, including Microsoft, IBM, and Google ([et al., 2012b](#)).
- **Machine translation:** In a machine translation task, the program is given a sequence of symbols in some language, and is asked to convert this into a sequence of symbols in another language. This is commonly applied to natural languages, such as translating English to French. Deep learning has recently begun to have an impact on machine translation ([et al., 2014c](#)).

For example, deep learning can be used to annotate in aerial photographs (Mnih and Hinton, 2010). It does not mirror the structure of the input as closely as in other tasks. For example, in image captioning, the computer takes an image as input and outputs a natural language sentence describing the image (Sutskever et al., 2014a,b; Mao et al., 2015; Vinyals et al., 2015b; Karpathy and Li, 2015; Fang et al., 2015; Xu et al., 2015). These tasks are called *structured output tasks* because the program outputs values that are all tightly interrelated. For example, in an image captioning program must form a valid sentence.

- **Anomaly detection:** In this type of task, the computer looks through a set of events or objects and flags some of them as normal or atypical. An example of an anomaly detection task is credit card fraud detection. By modeling your purchasing habits, a credit card company can detect misuse of your cards. If a thief steals your credit card information, the thief's purchases will often come from a different geographical distribution over purchase types than your own. The company can prevent fraud by placing a hold on an account as soon as it has been used for an uncharacteristic purchase. See Chan et al. (2015) for a survey of anomaly detection methods.
- **Synthesis and sampling:** In this type of task, the computer algorithm is asked to generate new examples that are similar to the training data. Synthesis and sampling via machine learning are used for media applications when generating large volumes of data would be expensive, boring, or require too much time. For example, games can automatically generate textures for large

missing. The algorithm must provide a prediction of the missing entries.

- **Denoising:** In this type of task, the machine learning algorithm is given as input a *corrupted example*  $\tilde{\mathbf{x}} \in \mathbb{R}^n$  obtained by an unknown transformation from a *clean example*  $\mathbf{x} \in \mathbb{R}^n$ . The learner must predict  $\mathbf{x}$  from its corrupted version  $\tilde{\mathbf{x}}$ , or more generally predict the underlying probability distribution  $p(\mathbf{x} \mid \tilde{\mathbf{x}})$ .
- **Density estimation or probability mass function estimation:** In a density estimation problem, the machine learning algorithm is given a function  $p_{\text{model}} : \mathbb{R}^n \rightarrow \mathbb{R}$ , where  $p_{\text{model}}(\mathbf{x})$  can be interpreted as a density function (if  $\mathbf{x}$  is continuous) or a probability mass function (if  $\mathbf{x}$  is discrete) on the space that the examples were drawn from. If the algorithm performs well (we will specify exactly what that means when we discuss the evaluation measures  $P$ ), the algorithm needs to learn the structure of the underlying distribution. It must know where examples cluster tightly and where they are sparse. Most of the tasks described above require the algorithm to at least implicitly capture the structure of the underlying probability distribution. Density estimation enables us to explicitly capture that distribution. Once we have a model  $p(\mathbf{x})$ , we can then perform computations on that distribution for a variety of tasks as well. For example, if we have performed density estimation and learned a probability distribution  $p(\mathbf{x})$ , we can use that distribution to solve a missing value imputation task. If a value  $x_i$  is missing in an example  $\mathbf{x}$ , and the other values, denoted  $\mathbf{x}_{-i}$ , are given, then we know the distribution of  $x_i$  given  $\mathbf{x}_{-i}$  is  $p(x_i \mid \mathbf{x}_{-i})$ . In practice, density estimation does not solve all these related tasks, because in many cases the underlying distribution  $p(\mathbf{x})$  is computationally intractable.

proportion of examples for which the model produces the correct output. We can also obtain equivalent information by measuring the **error rate**, the proportion of examples for which the model produces an incorrect output. The error rate is the expected 0-1 loss. The 0-1 loss on a prediction is 0 if it is correctly classified and 1 if it is not. For tasks such as image classification, it does not make sense to measure accuracy, error rate, or loss. Instead, we must use a different performance metric that provides a continuous-valued score for each example. The most common metric is to report the average log-probability the model assigns to the correct class.

Usually we are interested in how well the machine learning system performs on data that it has not seen before, since this determines how well the system will be deployed in the real world. We therefore evaluate these performance metrics on a **test set** of data that is separate from the data used for training the learning system.

The choice of performance measure may seem straightforward, but it is often difficult to choose a performance measure that accurately reflects the desired behavior of the system.

In some cases, this is because it is difficult to decide what the system should do. For example, when performing a transcription task, should we evaluate the system based on whether it transcribes entire sequences correctly, or should we use a performance measure that gives partial credit for getting parts of the sequence correct? When performing a regression task, should we evaluate the system more if it frequently makes medium-sized mistakes, or if it makes a few very large mistakes? These kinds of design choices depend on the specific application.

In other cases, we know what quantity we would ideally like to maximize, but measuring it is impractical. For example, this arises frequently in the context of **density estimation**. Many of the best probabilistic models for

to experience an entire **dataset**. A dataset is a collection defined in section 5.1.1. Sometimes we call examples **data**

One of the oldest datasets studied by statisticians and searchers is the Iris dataset (Fisher, 1936). It is a collection of different parts of 150 iris plants. Each individual plant is an example. The features within each example are the measurements of the plant: the sepal length, sepal width, petal length. The dataset also records which species each plant belonged to. These species are represented in the dataset.

**Unsupervised learning algorithms** experience a dataset of features, then learn useful properties of the structure of this dataset. In the context of deep learning, we usually want to learn the entire probability distribution generated by a dataset, whether explicitly, as in density estimation tasks like synthesis or denoising. Some other unsupervised algorithms perform other roles, like clustering, which consists of dividing the dataset into clusters of similar examples.

**Supervised learning algorithms** experience a dataset where each example is also associated with a **label** or **target**. For example, the Iris dataset is annotated with the species of each iris plant. A supervised learning algorithm can study the Iris dataset and learn to classify different species based on their measurements.

Roughly speaking, unsupervised learning involves observing a random vector  $\mathbf{x}$  and attempting to implicitly or explicitly estimate the probability distribution  $p(\mathbf{x})$ , or some interesting properties of this distribution. Supervised learning involves observing several examples of  $\mathbf{x}$  and an associated value or vector  $\mathbf{y}$ , then learning to predict  $\mathbf{y}$  by estimating  $p(\mathbf{y} | \mathbf{x})$ . The term **supervised learning** originates from the analogy of a teacher supervising a student.



modeling  $p(\mathbf{x})$  by splitting it into  $n$  supervised learning problems. We can solve the supervised learning problem of learning  $p(y | \mathbf{x})$ . Unsupervised learning technologies to learn the joint distribution  $p(\mathbf{x}, y)$  are called joint distribution learning or joint distribution inferring.

$$p(y | \mathbf{x}) = \frac{p(\mathbf{x}, y)}{\sum_y p(\mathbf{x}, y')}.$$

Though unsupervised learning and supervised learning are two distinct concepts, they do help roughly categorize some of the machine learning algorithms. Traditionally, people refer to regression and structured output problems as supervised learning. Problems without support of other tasks is usually considered unsupervised learning.

Other variants of the learning paradigm are possible. In semi-supervised learning, some examples include a supervisor and some do not. In multi-instance learning, an entire collection of examples is either containing or not containing an example of a class, but the individual examples of the collection are not labeled. For a recent example of multi-instance learning with deep models, see [Kotzias \*et al.\* \(2015\)](#).

Some machine learning algorithms do not just experience a single example. For example, **reinforcement learning** algorithms interact with an environment where there is a feedback loop between the learning system and the environment. Algorithms are beyond the scope of this book. Please see [Sutton](#) or [Bertsekas and Tsitsiklis \(1996\)](#) for information about reinforcement learning and [Mnih \*et al.\* \(2013\)](#) for the deep learning approach to reinforcement learning.

Most machine learning algorithms simply experience a collection of examples that can be described in many ways. In all cases, a dataset is a collection of examples which are in turn collections of features.

length of vector. In Section 9.7 and chapter 10, we describe types of such heterogeneous data. In cases like these, rather than a dataset as a matrix with  $m$  rows, we describe it as a set of vectors  $\{\mathbf{x}^{(1)}, \mathbf{x}^{(2)}, \dots, \mathbf{x}^{(m)}\}$ . This notation does not imply that all  $\mathbf{x}^{(i)}$  and  $\mathbf{x}^{(j)}$  have the same size.

In the case of supervised learning, the example contains not only a collection of features, but also a label. For example, if we want to use a machine learning algorithm to perform object recognition from photographs, we need to know the label of each photo that appears in each of the photos. We might do this with a vector of labels  $\mathbf{y}$ , where  $y_i$  signifies a person, 1 signifying a car, 2 signifying a cat, and so on. When working with a dataset containing a design matrix of features  $\mathbf{X}$ , we also provide a vector of labels  $\mathbf{y}$ , with  $y_i$  providing the label for the  $i$ -th example.

Of course, sometimes the label may be more than just a single value. For example, if we want to train a speech recognition system to recognize sentences, then the label for each example sentence is a sequence of words.

Just as there is no formal definition of supervised and unsupervised learning, there is no rigid taxonomy of datasets or experiences. The standard definitions cover most cases, but it is always possible to design new ones for specific applications.

### 5.1.4 Example: Linear Regression

Our definition of a machine learning algorithm as an algorithm that improves a computer program's performance at some task is somewhat abstract. To make this more concrete, we present a simple machine learning algorithm: **linear regression**. We will use this example repeatedly as we introduce more machine learning algorithms to help us understand the algorithm's behavior.

each feature affects the prediction. If a feature  $x_i$  receives a positive weight, then increasing the value of that feature increases the value of our prediction. If a feature receives a negative weight, then increasing the value of that feature decreases the value of our prediction. If a feature's weight is large, then it has a large effect on the prediction. If a feature's weight is small, then it has a small effect on the prediction.

We thus have a definition of our task  $T$ : to predict  $y$  given  $\hat{\mathbf{y}} = \mathbf{w}^\top \mathbf{x}$ . Next we need a definition of our performance measure.

Suppose that we have a design matrix of  $m$  examples  $\mathbf{X}$  and a vector of regression targets  $\mathbf{y}$  providing the correct values for the targets. We use  $\mathbf{X}$  for training, only for evaluating how well the model predicts on a new set of examples. Because this dataset will only be used for evaluation, we refer to the design matrix of inputs as  $\mathbf{X}^{(\text{test})}$  and the targets as  $\mathbf{y}^{(\text{test})}$ .

One way of measuring the performance of the model is the **squared error** of the model on the test set. If  $\hat{\mathbf{y}}^{(\text{test})}$  gives the predicted values of the model on the test set, then the mean squared error is given by

$$\text{MSE}_{\text{test}} = \frac{1}{m} \sum_i (\hat{\mathbf{y}}^{(\text{test})}_i - \mathbf{y}^{(\text{test})}_i)^2.$$

Intuitively, one can see that this error measure decreases to zero as the model's predictions get closer to the targets. We can also see that

$$\text{MSE}_{\text{test}} = \frac{1}{m} \|\hat{\mathbf{y}}^{(\text{test})} - \mathbf{y}^{(\text{test})}\|_2^2,$$

so the error increases whenever the Euclidean distance between the predicted values and the targets increases.

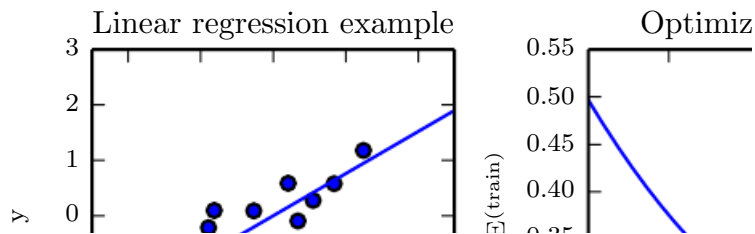
$$\begin{aligned}
&\Rightarrow \frac{1}{m} \nabla_{\mathbf{w}} \|\mathbf{X}^{(\text{train})} \mathbf{w} - \mathbf{y}^{(\text{train})}\|_2^2 = 0 \\
&\Rightarrow \nabla_{\mathbf{w}} \left( \mathbf{X}^{(\text{train})} \mathbf{w} - \mathbf{y}^{(\text{train})} \right)^\top \left( \mathbf{X}^{(\text{train})} \mathbf{w} - \mathbf{y}^{(\text{train})} \right) \\
&\Rightarrow \nabla_{\mathbf{w}} \left( \mathbf{w}^\top \mathbf{X}^{(\text{train})\top} \mathbf{X}^{(\text{train})} \mathbf{w} - 2 \mathbf{w}^\top \mathbf{X}^{(\text{train})\top} \mathbf{y}^{(\text{train})} + \right. \\
&\quad \left. \mathbf{y}^{(\text{train})\top} \mathbf{X}^{(\text{train})} \mathbf{X}^{(\text{train})\top} \mathbf{y}^{(\text{train})} \right) \\
&\Rightarrow 2 \mathbf{X}^{(\text{train})\top} \mathbf{X}^{(\text{train})} \mathbf{w} - 2 \mathbf{X}^{(\text{train})\top} \mathbf{y}^{(\text{train})} \\
&\Rightarrow \mathbf{w} = \left( \mathbf{X}^{(\text{train})\top} \mathbf{X}^{(\text{train})} \right)^{-1} \mathbf{X}^{(\text{train})\top} \mathbf{y}^{(\text{train})}
\end{aligned}$$

The system of equations whose solution is given by equation 5.12 is called the **normal equations**. Evaluating equation 5.12 constitutes the normal equations algorithm. For an example of the linear regression learner see figure 5.1.

It is worth noting that the term **linear regression** is a slightly more sophisticated model with one additional parameter  $b$ . In this model

$$\hat{y} = \mathbf{w}^\top \mathbf{x} + b,$$

so the mapping from parameters to predictions is still a linear mapping, the mapping from features to predictions is now an affine function.



affine functions means that the plot of the model's prediction line, but it need not pass through the origin. Instead of adding  $b$ , one can continue to use the model with only weights  $b$  as an extra entry that is always set to 1. The weight corresponding to this entry plays the role of the bias parameter. We frequently use this notation when referring to affine functions throughout this book.

The intercept term  $b$  is often called the **bias** parameter. This terminology derives from the point of view that the transformation is biased toward being  $b$  in the absence of data. This is different from the idea of a statistical bias, in which an algorithm's expected estimate of a quantity is not equal to the true value.

Linear regression is of course an extremely simple and limited model, but it provides an example of how a learning algorithm can be designed. In the sections we describe some of the basic principles underlying the design and demonstrate how these principles can be used to design more complex learning algorithms.

## 5.2 Capacity, Overfitting and Underfitting

The central challenge in machine learning is that our algorithm must perform well on *new, previously unseen* inputs—not just those on which it was trained. The ability to perform well on previously unseen inputs is called **generalization**.

Typically, when training a machine learning model, we have a set of training data; we can compute some error measure on the training set, called the **training error**; and we reduce this training error. So far, what we have

but we actually care about the test error,  $\frac{1}{m^{(\text{test})}} \|\mathbf{X}^{(\text{test})} \mathbf{w}\|$

How can we affect performance on the test set when we train on the training set? The field of **statistical learning theory** precisely studies how the training and the test set are collected arbitrarily, there are no assumptions. If we are allowed to make some assumptions about how the training and test set are collected, then we can make some progress.

The training and test data are generated by a probabilistic process called the **data-generating process**. We typically make assumptions known collectively as the **i.i.d. assumptions**, which state that the examples in each dataset are **independent** from each other and the training set and test set are **identically distributed**, meaning they follow the same probability distribution as each other. This assumption is often modeled by the data-generating process with a probability distribution  $p_{\text{data}}$ . The same distribution is then used to generate every training and test example. We call that shared underlying distribution the **data distribution**, denoted  $p_{\text{data}}$ . This probabilistic framework enables us to mathematically study the relationship between training and test error.

One immediate connection we can observe between training and test error is that the expected training error of a randomly selected model is equal to the expected test error of that model. Suppose we have a probability distribution  $p(\mathbf{x}, y)$  and we sample from it repeatedly to generate the training and test set. For some fixed value  $\mathbf{w}$ , the expected training set error is equal to the expected test set error, because both expectations are taken over the dataset sampling process. The only difference between the training and test error is the name we assign to the dataset we sample from.

Of course, when we use a machine learning algorithm to learn a model from the training set, we are not interested in the expected test error of that model. We are interested in the expected test error of the best model we can find from the training set. This is the **test error of the best model**, which is the expected test error of the best model we can find from the training set. This is the **test error of the best model**, which is the expected test error of the best model we can find from the training set.

obtain a sufficiently low error value on the training set. On the other hand, if the gap between the training error and test error is too large, the model is overfitting.

We can control whether a model is more likely to overfit by controlling its **capacity**. Informally, a model's capacity is its ability to represent a wide range of functions. Models with low capacity may struggle to fit the training data, while models with high capacity can overfit by memorizing properties of the training data that do not serve them well on the test set.

One way to control the capacity of a learning algorithm is by controlling its **hypothesis space**, the set of functions that the algorithm selects as being the solution. For example, the linear regression model selects the set of all linear functions of its input as its hypothesis space. To increase the capacity of linear regression, we can expand the hypothesis space to include polynomials, rather than just linear functions. Doing so increases the model's capacity.

A polynomial of degree 1 gives us the linear regression model, which is already familiar, with the prediction

$$\hat{y} = b + wx.$$

By introducing  $x^2$  as another feature provided to the linear model, we can learn a model that is quadratic as a function of  $x$ :

$$\hat{y} = b + w_1x + w_2x^2.$$

Though this model implements a quadratic function of  $x$ , it is still a linear function of the *parameters*, so we can still use the same methods to train the model in closed form. We can continue to add additional features, for example, to obtain a polynomial of

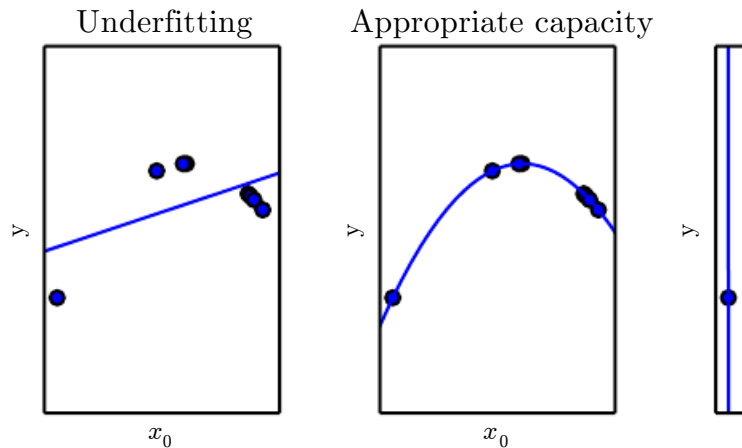


Figure 5.2: We fit three models to this example training set, generated synthetically, by randomly sampling  $x$  values and choosing by evaluating a quadratic function. *(Left)* A linear function fit underfitting—it cannot capture the curvature that is present in the quadratic function fit to the data. *(Middle)* A quadratic function fit to the data generalizes well to an unseen point  $x_0$ . *(Right)* A polynomial fit to the data suffers from overfitting. Here we used the Moore-Penrose pseudoinverse to solve the underdetermined normal equations. The solution passes through the training points exactly, but we have not been lucky enough for it to extract the underlying function. It now has a deep valley between two training points that does not exist in the underlying function. It also increases sharply on the left side of the plot and decreases sharply on the right side of the plot.

The true underlying function is quadratic. The linear function is unable to capture the true underlying problem, so it underfits. The degree-9 polynomial is a good representation of the correct function, but it is also capable of capturing noise in the training data.



function within this family is a difficult optimization problem. A learning algorithm does not actually find the best function in the family, so it may not significantly reduce the training error. These additional limitations, due to the imperfection of the optimization algorithm, mean that the **effective capacity** may be less than the representational capacity of the function family.

Our modern ideas about improving the generalization of machine learning models are refinements of thought dating back to philosopher William of Ockham. Many early scholars invoke a principle of parsimony, widely known as **Occam's razor** (c. 1287–1347). This principle states that among competing hypotheses that explain known observations, we should choose the “simplest” one. This idea was formalized and generalized in the twentieth century by the founders of statistical learning theory: [Chervonenkis, 1971](#); [Vapnik, 1982](#); [Blumer \*et al.\*, 1989](#); [Vapnik and Chervonenkis, 1991](#).

Statistical learning theory provides various means of quantifying model capacity. Among these, the most well known is the **Vapnik-Chervonenkis (VC) dimension**. The VC dimension measures the capacity of a model. The VC dimension is defined as being the largest possible number of points that exists a training set of  $m$  different  $\mathbf{x}$  points that the classifier can perfectly separate.

Quantifying the capacity of the model enables statisticians to make quantitative predictions. The most important results of statistical learning theory show that the discrepancy between training error and test error is bounded from above by a quantity that grows as the model capacity increases and shrinks as the number of training examples increases ([Vapnik and Chervonenkis, 1991](#); [Vapnik, 1982](#); [Blumer \*et al.\*, 1989](#); [Vapnik, 1995](#)). This provides an intellectual justification that machine learning algorithms are not overfitting, a concept rarely used in practice when working with deep learning.

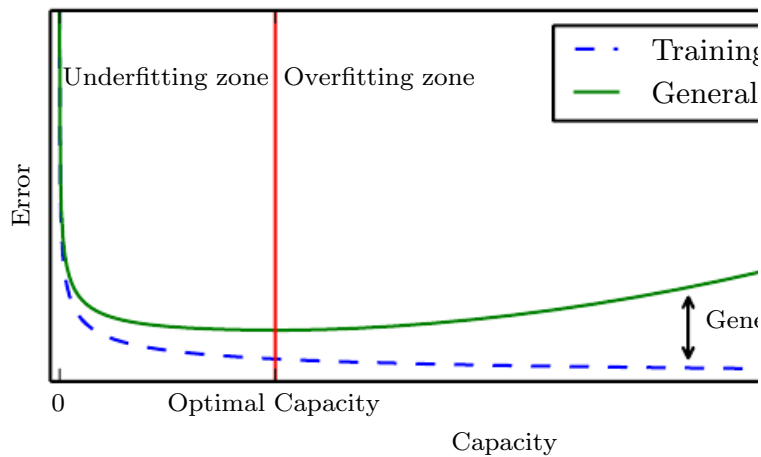


Figure 5.3: Typical relationship between capacity and error. Training and generalization errors behave differently. At the left end of the graph, training and generalization errors are both high. This is the **underfitting regime**. As we increase capacity, training error decreases, but the gap between training and generalization errors increases. At the right end, the size of this gap outweighs the decrease in training error, and the error increases. This is the **overfitting regime**, where capacity is too large, above the **optimal capacity**.

generalization error has a U-shaped curve as a function of capacity, as is illustrated in figure 5.3.

To reach the most extreme case of arbitrarily high capacity, we introduce the concept of **nonparametric models**. So far, we have discussed parametric models, such as linear regression. Parametric models learn by a parameter vector whose size is finite and fixed before training. Nonparametric models have no such limitation.

Sometimes, nonparametric models are just theoretical

might be greater than zero, if two identical inputs are associated with different outputs) on any regression dataset.

Finally, we can also create a nonparametric learning algorithm by wrapping a parametric learning algorithm inside another algorithm that chooses the number of parameters as needed. For example, we could imagine an algorithm that changes the degree of the polynomial learned by linear regression based on the polynomial expansion of the input.

The ideal model is an oracle that simply knows the true function that generates the data. Even such a model will still incur errors, because there may still be some noise in the data. In the context of supervised learning, the mapping from  $\mathbf{x}$  to  $y$  may be noisy, or  $y$  may be a deterministic function that involves other variables not included in  $\mathbf{x}$ . The error incurred by an oracle making predictions on a distribution  $p(\mathbf{x}, y)$  is called the **Bayes error**.

Training and generalization error vary as the size of the training set increases. Expected generalization error can never increase as the number of training examples increases. For nonparametric models, more data yield better results, and the best possible error is achieved. Any fixed parametric model's optimal capacity will asymptote to an error value that exists. See figure 5.4 for an illustration. Note that it is possible to reach optimal capacity and yet still have a large gap between training and test errors. In this situation, we may be able to reduce this gap by adding more training examples.

### 5.2.1 The No Free Lunch Theorem

Learning theory claims that a machine learning algorithm cannot consistently outperform a random guess on any arbitrary set of

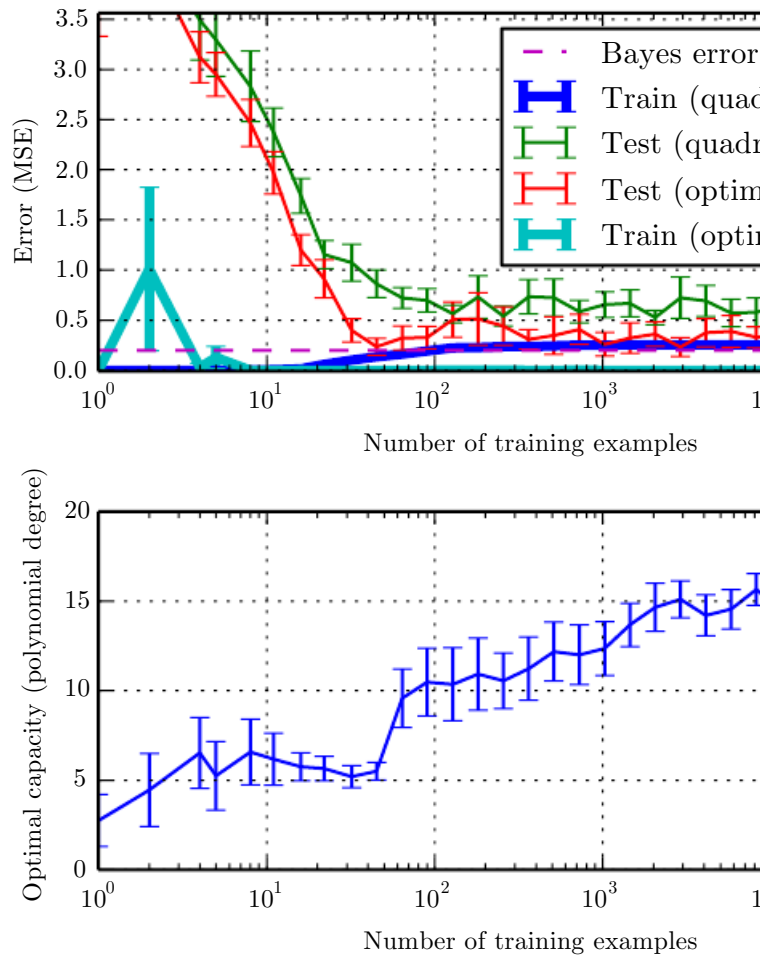


Figure 5.4: The effect of the training dataset size on the train and test error and on the optimal model capacity. We constructed a synthetic regression problem by adding a moderate amount of noise to a degree-5 polynomial, generated the data, and then generated several different sizes of training set. For each size, we generated 100 different training sets in order to plot error bars showing 95 percent confidence intervals.

same error rate when classifying previously unobserved  $p$  in some sense, no machine learning algorithm is universal other. The most sophisticated algorithm we can conceive of performance (over all possible tasks) as merely predicting  $t$  to the same class.

Fortunately, these results hold only when we average generating distributions. If we make assumptions about the distributions we encounter in real-world applications, then algorithms that perform well on these distributions.

This means that the goal of machine learning research is learning algorithm or the absolute best learning algorithm. understand what kinds of distributions are relevant to the ‘agent experiences, and what kinds of machine learning algorithms data drawn from the kinds of data-generating distributions.

### 5.2.2 Regularization

The no free lunch theorem implies that we must design algorithms to perform well on a specific task. We do so preferences into the learning algorithm. When these preferences the learning problems that we ask the algorithm to solve, it

So far, the only method of modifying a learning algorithm concretely is to increase or decrease the model’s representational or removing functions from the hypothesis space of solutions is able to choose from. We gave the specific example of increasing the degree of a polynomial for a regression problem. The version so far is oversimplified

in its hypothesis space. This means that both functions are preferred. The unpreferred solution will be chosen only if it is significantly better than the preferred solution.

For example, we can modify the training criterion for linear regression with **weight decay**. To perform linear regression with weight decay, the cost function comprises both the mean squared error on the training data and a term that expresses a preference for the weights to have smaller squared magnitudes:

$$J(\mathbf{w}) = \text{MSE}_{\text{train}} + \lambda \mathbf{w}^\top \mathbf{w},$$

where  $\lambda$  is a value chosen ahead of time that controls the strength of the preference for smaller weights. When  $\lambda = 0$ , we impose no preference, and the solution is the one that minimizes the training error. As  $\lambda$  increases, the weights are forced to become smaller. Minimizing  $J(\mathbf{w})$  results in a tradeoff between fitting the training data and keeping the weights small. We can make a tradeoff between fitting the training data and keeping the weights small by choosing different values of  $\lambda$ . See figure 5.5 for the results.

More generally, we can regularize a model that learns by adding a penalty called a **regularizer** to the cost function. In the case of weight decay, the regularizer is  $\Omega(\mathbf{w}) = \mathbf{w}^\top \mathbf{w}$ . In chapter 7, we will see other types of regularizers that are possible.

Expressing preferences for one function over another is a way of controlling a model's capacity. We can think of including or excluding a function from the hypothesis space. We can think of excluding a function from the hypothesis space as expressing an infinitely strong preference against that function.

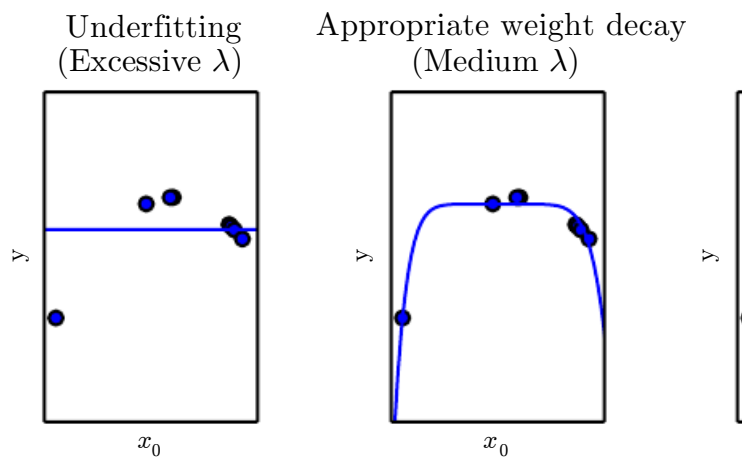
In our weight decay example, we expressed our preference for smaller weights by adding a term to the cost function.

people can do) may all be solved effectively using very general regularization.

## 5.3 Hyperparameters and Validation Set

Most machine learning algorithms have hyperparameters used to control the algorithm's behavior. The values of hyperparameters are often adapted by the learning algorithm itself (though we can describe a procedure in which one learning algorithm learns the best hyperparameters for another learning algorithm).

The polynomial regression example in figure 5.2 has a hyperparameter, the degree of the polynomial, which acts as a **capacity** hyperparameter. A  $\lambda$  value used to control the strength of weight decay is another hyperparameter.



Sometimes a setting is chosen to be a hyperparameter but the algorithm does not learn because the setting is difficult to optimize. The setting must be a hyperparameter because it is not applied to the training set. This applies to all hyperparameters that control model capacity. If learned on the training set, such as polynomial degree, we always choose the maximum possible model capacity, resulting in overfitting (see figure 5.3). For example, we can always fit the training data with a higher-degree polynomial and a weight decay setting of  $\lambda = 0$  than with a lower-degree polynomial and a positive weight decay setting.

To solve this problem, we need a **validation set** of examples that the learning algorithm does not observe.

Earlier we discussed how a held-out test set, composed of examples from the same distribution as the training set, can be used to estimate the error of a learner, after the learning process has completed. The test examples are not used in any way to make choices about the learner's hyperparameters. For this reason, no example from the training set is in the validation set. Therefore, we always construct the validation set from the *training* data. Specifically, we split the training data into two subsets. One of these subsets is used to learn the parameters. The other subset, the validation set, is used to estimate the generalization error during the learning process, allowing for the hyperparameters to be updated according to the validation error. The subset used to learn the parameters is still typically called the training set, but this may be confused with the larger pool of data used in the learning process. The subset of data used to guide the selection of hyperparameters is called the validation set. Typically, one uses about 80 percent of the training data for training and 20 percent for validation. Since the validation set is used to “train” the hyperparameters, the validation set error is



### 5.3.1 Cross-Validation

Dividing the dataset into a fixed training set and a fixed test set can be problematic if it results in the test set being small. A small test set implies high variance around the estimated average test error, making it difficult to compare algorithms.  $A$  works better than algorithm  $B$  on the given task.

When the dataset has hundreds of thousands of examples, this is not a serious issue. When the dataset is too small, there are alternative methods to use all the examples in the estimation of the mean test error without increased computational cost. These procedures are based on repeating the training and testing computation on different random splits of the original dataset. The most common of these is the *k*-fold cross-validation procedure, shown in algorithm 5.1, in which the dataset is split into  $k$  nonoverlapping subsets. The test error is estimated by taking the average test error across  $k$  trials. On trial  $i$ , subset  $i$  of the data is used as the test set, and the rest of the data is used as the training set. One problem is that no unbiased estimators of the variance of the test error exist (Bengio and Grandvalet, 2004), but approximations are used.

## 5.4 Estimators, Bias and Variance

The field of statistics gives us many tools to achieve the goal of solving a task not only on the training set but also to generalize to new data. Concepts such as parameter estimation, bias and variance help to characterize notions of generalization, underfitting and overfitting.

**Algorithm 5.1** The  $k$ -fold cross-validation algorithm. It estimates the generalization error of a learning algorithm  $A$  when the dataset is small for a simple train/test or train/valid split to yield a small generalization error, because the mean of a loss  $L$  on a small dataset has a high variance. The dataset  $\mathbb{D}$  contains as elements the absolute values of the  $i$ -th example), which could stand for an (input,target) pair in the case of supervised learning, or for just an input  $\mathbf{z}$  in the case of unsupervised learning. The algorithm returns the vector of the mean of the loss on each example in  $\mathbb{D}$ , whose mean is the estimated generalization error. Individual examples can be used to compute a confidence interval (equation 5.47). Though these confidence intervals are available after the use of cross-validation, it is still common practice to say that algorithm  $A$  is better than algorithm  $B$  only if the confidence interval of algorithm  $A$  lies below and does not intersect the confidence interval of algorithm  $B$ .

---

**Define**  $\text{KFoldXV}(\mathbb{D}, A, L, k)$ :

**Require:**  $\mathbb{D}$ , the given dataset, with elements  $\mathbf{z}^{(i)}$

**Require:**  $A$ , the learning algorithm, seen as a function that takes an input and outputs a learned function

**Require:**  $L$ , the loss function, seen as a function from a learned function and an example  $\mathbf{z}^{(i)} \in \mathbb{D}$  to a scalar  $\in \mathbb{R}$

**Require:**  $k$ , the number of folds

Split  $\mathbb{D}$  into  $k$  mutually exclusive subsets  $\mathbb{D}_i$ , whose union is  $\mathbb{D}$

**for**  $i$  from 1 to  $k$  **do**

$f_i = A(\mathbb{D} \setminus \mathbb{D}_i)$

**for**  $\mathbf{z}^{(j)}$  in  $\mathbb{D}_i$  **do**

$e_j = L(f_i, \mathbf{z}^{(j)})$

**end for**

a good estimator is a function whose output is close to the generated the training data.

For now, we take the frequentist perspective on statistics that the true parameter value  $\theta$  is fixed but unknown, while  $\hat{\theta}$  is a function of the data. Since the data is drawn from a function of the data is random. Therefore  $\hat{\theta}$  is a random variable.

Point estimation can also refer to the estimation of the input and target variables. We refer to these types of point estimators.

**Function Estimation** Sometimes we are interested in estimation (or function approximation). Here, we are trying to estimate  $y$  given an input vector  $x$ . We assume that there is a function that describes the approximate relationship between  $y$  and  $x$ . For example, we assume that  $y = f(x) + \epsilon$ , where  $\epsilon$  stands for the part of  $y$  that is not explained by  $x$ . In function estimation, we are interested in approximating the function  $f$ . Function estimation is really just the same as parameter estimation; the function estimator  $\hat{f}$  is simply a point estimator in the linear regression example (discussed in section 5.1.4) and the function estimation example (discussed in section 5.2) both illustrate scenarios that can be viewed as either estimating a parameter  $w$  or estimating a function  $f$  to  $y$ .

We now review the most commonly studied properties of estimators and discuss what they tell us about these estimators.

### 5.4.2 Bias

bution with mean  $\theta$ :

$$P(x^{(i)}; \theta) = \theta^{x^{(i)}}(1 - \theta)^{(1-x^{(i)})}.$$

A common estimator for the  $\theta$  parameter of this distributed training samples:

$$\hat{\theta}_m = \frac{1}{m} \sum_{i=1}^m x^{(i)}.$$

To determine whether this estimator is biased, we can substitute into equation 5.20:

$$\begin{aligned} \text{bias}(\hat{\theta}_m) &= \mathbb{E}[\hat{\theta}_m] - \theta \\ &= \mathbb{E}\left[\frac{1}{m} \sum_{i=1}^m x^{(i)}\right] - \theta \\ &= \frac{1}{m} \sum_{i=1}^m \mathbb{E}[x^{(i)}] - \theta \\ &= \frac{1}{m} \sum_{i=1}^m \sum_{x^{(i)}=0}^1 \left(x^{(i)} \theta^{x^{(i)}}(1 - \theta)^{(1-x^{(i)})}\right) - \theta \\ &= \frac{1}{m} \sum_{i=1}^m (\theta) - \theta \\ &= \theta - \theta = 0 \end{aligned}$$

Since  $\text{bias}(\hat{\theta}) = 0$ , we say that our estimator  $\hat{\theta}$  is unbiased.

**Example: Gaussian Distribution Estimator of the 1**

To determine the bias of the sample mean, we are again in its expectation:

$$\begin{aligned}\text{bias}(\hat{\mu}_m) &= \mathbb{E}[\hat{\mu}_m] - \mu \\ &= \mathbb{E}\left[\frac{1}{m} \sum_{i=1}^m x^{(i)}\right] - \mu \\ &= \left(\frac{1}{m} \sum_{i=1}^m \mathbb{E}[x^{(i)}]\right) - \mu \\ &= \left(\frac{1}{m} \sum_{i=1}^m \mu\right) - \mu \\ &= \mu - \mu = 0\end{aligned}$$

Thus we find that the sample mean is an unbiased estimate parameter.

**Example: Estimators of the Variance of a Gaussian**

In this example, we compare two different estimators of the variance of a Gaussian distribution. We are interested in knowing if either is unbiased.

The first estimator of  $\sigma^2$  we consider is known as the sample variance:

$$\hat{\sigma}_m^2 = \frac{1}{m} \sum_{i=1}^m \left(x^{(i)} - \hat{\mu}_m\right)^2,$$

where  $\hat{\mu}_m$  is the sample mean. More formally, we are interested in whether

The **unbiased sample variance** estimator

$$\tilde{\sigma}_m^2 = \frac{1}{m-1} \sum_{i=1}^m \left( x^{(i)} - \hat{\mu}_m \right)^2$$

provides an alternative approach. As the name suggests this estimator provides an unbiased estimate of the variance. That is, we find that  $\mathbb{E}[\tilde{\sigma}_m^2] = \sigma^2$ :

$$\begin{aligned} \mathbb{E}[\tilde{\sigma}_m^2] &= \mathbb{E} \left[ \frac{1}{m-1} \sum_{i=1}^m \left( x^{(i)} - \hat{\mu}_m \right)^2 \right] \\ &= \frac{m}{m-1} \mathbb{E}[\hat{\sigma}_m^2] \\ &= \frac{m}{m-1} \left( \frac{m-1}{m} \sigma^2 \right) \\ &= \sigma^2. \end{aligned}$$

We have two estimators: one is biased, and the other is unbiased. If both estimators are clearly desirable, they are not always the “best”. In this section, we will see we often use biased estimators that possess other desirable properties.

### 5.4.3 Variance and Standard Error

Another property of the estimator that we might want to consider is how much we expect it to vary as a function of the data sample. Just as we can take the expectation of the estimator to determine its bias, we can take the expectation of the squared deviation of the estimator from its expectation to determine its variance. The **variance** of an estimator is simply the variance of the estimator.

$$\text{var}(\hat{\theta}) = \mathbb{E}[(\hat{\theta} - \mathbb{E}[\hat{\theta}])^2]$$

been different. The expected degree of variation in any error that we want to quantify.

The standard error of the mean is given by

$$\text{SE}(\hat{\mu}_m) = \sqrt{\text{Var}\left[\frac{1}{m} \sum_{i=1}^m x^{(i)}\right]} = \frac{\sigma}{\sqrt{m}}$$

where  $\sigma^2$  is the true variance of the samples  $x^i$ . The standard error is estimated by using an estimate of  $\sigma$ . Unfortunately, neither the sample variance nor the square root of the unbiased estimate provide an unbiased estimate of the standard deviation. The sample standard deviation tends to underestimate the true standard deviation but is still a consistent estimator. The square root of the unbiased estimator of the variance is less biased. For large  $m$ , the approximation is quite reasonable.

The standard error of the mean is very useful in machine learning. We often estimate the generalization error by computing the error on the test set. The number of examples in the test set affects the accuracy of this estimate. Taking advantage of the central limit theorem tells us that the mean will be approximately distributed with a normal distribution. We can use the standard error to compute the probability that the error falls in any chosen interval. For example, the 95 percent confidence interval on the mean  $\hat{\mu}_m$  is

$$(\hat{\mu}_m - 1.96\text{SE}(\hat{\mu}_m), \hat{\mu}_m + 1.96\text{SE}(\hat{\mu}_m))$$

under the normal distribution with mean  $\hat{\mu}_m$  and variance  $\text{SE}(\hat{\mu}_m)^2$ . In machine learning experiments, it is common to say that algorithm  $A$  is

$$\begin{aligned} &= \frac{1}{m^2} \sum_{i=1}^m \text{Var} \left( x^{(i)} \right) \\ &= \frac{1}{m^2} \sum_{i=1}^m \theta(1 - \theta) \\ &= \frac{1}{m^2} m\theta(1 - \theta) \\ &= \frac{1}{m} \theta(1 - \theta) \end{aligned}$$

The variance of the estimator decreases as a function of  $m$ , the size of the dataset. This is a common property of popular estimators. We will return to when we discuss consistency (see section 5.4.5).

#### 5.4.4 Trading off Bias and Variance to Minimize Error

Bias and variance measure two different sources of error. Bias measures the expected deviation from the true value of the parameter. Variance on the other hand, provides a measure of the deviation of the estimator value that any particular sampling of the data is likely to have.

What happens when we are given a choice between two models, one with more bias and one with more variance? How do we choose? For example, imagine that we are interested in approximating the function in figure 5.2 and we are only offered the choice between a model that is biased but has low variance and a model that is unbiased but suffers from large variance. How do we choose between the two?

The most common way to negotiate this trade-off is to use cross-validation. Empirically, cross-validation is highly successful on many regression and classification problems.



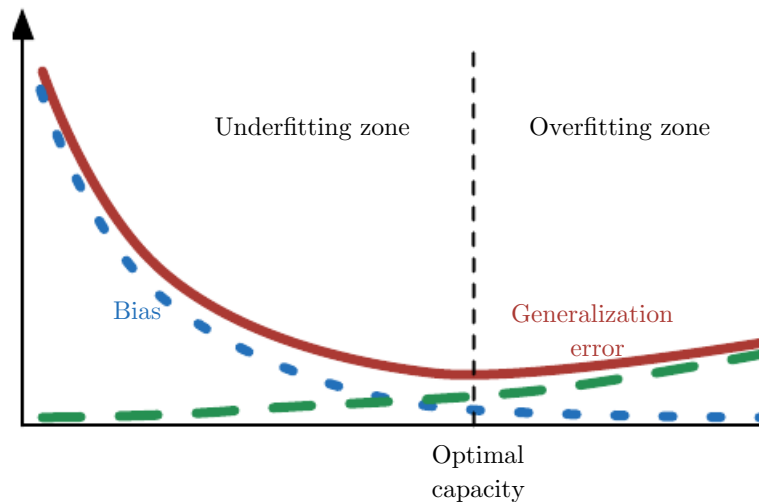


Figure 5.6: As capacity increases ( $x$ -axis), bias (dotted) tends to decrease, variance (dashed) tends to increase, yielding another U-shaped curve for generalization error (solid red curve). If we vary capacity along one axis, there is an optimal capacity when the capacity is below this optimum and underfitting when it is above. This is similar to the relationship between capacity, underfitting, and overfitting, and section 5.2 and figure 5.3.

Generalization error is measured by the MSE (where bias and variance are components of generalization error), increasing capacity tends to increase variance and decrease bias. This is illustrated in figure 5.6, where we see again generalization error as a function of capacity.

#### 5.4.5 Consistency

So far we have discussed the properties of various estimators and how they relate to the true function. In this section, we will discuss the concept of consistency, which is a property of an estimator that ensures that as the sample size increases, the estimator converges to the true function.

**sure convergence** of a sequence of random variables  $\mathbf{x}^{(1)}$  occurs when  $p(\lim_{m \rightarrow \infty} \mathbf{x}^{(m)} = \mathbf{x}) = 1$ .

Consistency ensures that the bias induced by the estimation number of data examples grows. However, the reverse is unbiasedness does not imply consistency. For example, consider the mean parameter  $\mu$  of a normal distribution  $\mathcal{N}(x; \mu, \sigma^2)$ , with  $m$  samples:  $\{x^{(1)}, \dots, x^{(m)}\}$ . We could use the first sample as an unbiased estimator:  $\hat{\theta} = x^{(1)}$ . In that case,  $\mathbb{E}(\hat{\theta}_m)$  is unbiased no matter how many data points are seen. That is, the estimate is asymptotically unbiased. However, that is not the case that  $\hat{\theta}_m \rightarrow \theta$  as  $m \rightarrow \infty$ .

## 5.5 Maximum Likelihood Estimation

We have seen some definitions of common estimators and an example. But where did these estimators come from? Rather than a function might make a good estimator and then analyzing it, we would like to have some principle from which we can deduce that are good estimators for different models.

The most common such principle is the maximum likelihood

Consider a set of  $m$  examples  $\mathbb{X} = \{\mathbf{x}^{(1)}, \dots, \mathbf{x}^{(m)}\}$  drawn from the true but unknown data-generating distribution  $p_{\text{data}}(\mathbf{x})$ .

Let  $p_{\text{model}}(\mathbf{x}; \boldsymbol{\theta})$  be a parametric family of probability distributions over the same space indexed by  $\boldsymbol{\theta}$ . In other words,  $p_{\text{model}}(\mathbf{x}; \boldsymbol{\theta})$  maps to a real number estimating the true probability  $p_{\text{data}}(\mathbf{x})$ .

The maximum likelihood estimator for  $\boldsymbol{\theta}$  is then defined

into a sum:

$$\boldsymbol{\theta}_{\text{ML}} = \arg \max_{\boldsymbol{\theta}} \sum_{i=1}^m \log p_{\text{model}}(\mathbf{x}^{(i)}; \boldsymbol{\theta})$$

Because the  $\arg \max$  does not change when we rescale the divide by  $m$  to obtain a version of the criterion that is expressed with respect to the empirical distribution  $\hat{p}_{\text{data}}$  defined by

$$\boldsymbol{\theta}_{\text{ML}} = \arg \max_{\boldsymbol{\theta}} \mathbb{E}_{\mathbf{x} \sim \hat{p}_{\text{data}}} \log p_{\text{model}}(\mathbf{x}; \boldsymbol{\theta})$$

One way to interpret maximum likelihood estimation is to the dissimilarity between the empirical distribution  $\hat{p}_{\text{data}}$ , a set and the model distribution, with the degree of dissimilarity measured by the KL divergence. The KL divergence is given

$$D_{\text{KL}}(\hat{p}_{\text{data}} \| p_{\text{model}}) = \mathbb{E}_{\mathbf{x} \sim \hat{p}_{\text{data}}} [\log \hat{p}_{\text{data}}(\mathbf{x}) - \log p_{\text{model}}(\mathbf{x})]$$

The term on the left is a function only of the data-generating model. This means when we train the model to minimize we need only minimize

$$- \mathbb{E}_{\mathbf{x} \sim \hat{p}_{\text{data}}} [\log p_{\text{model}}(\mathbf{x})],$$

which is of course the same as the maximization in equation

Minimizing this KL divergence corresponds exactly to the cross-entropy between the distributions. Many authors use the term negative log-likelihood to identify specifically the negative log-likelihood of a Bernoulli distribution, but that is a misnomer. Any loss consisting of a negative log-likelihood is a cross-entropy between the empirical distribution defined by the data and the probability distribution defined by model. For example, the cross-entropy between the empirical distribution and a Gaussian distribution is

### 5.5.1 Conditional Log-Likelihood and Mean Squared Error

The maximum likelihood estimator can readily be generalized to predict a conditional probability  $P(\mathbf{y} \mid \mathbf{x}; \boldsymbol{\theta})$  in order to predict  $\mathbf{y}$  given  $\mathbf{x}$ . This is the most common situation because it forms the basis for most supervised learning algorithms.  $\mathbf{X}$  represents all our inputs and  $\mathbf{Y}$  all our observed target values. The maximum likelihood estimator is

$$\boldsymbol{\theta}_{\text{ML}} = \arg \max_{\boldsymbol{\theta}} P(\mathbf{Y} \mid \mathbf{X}; \boldsymbol{\theta}).$$

If the examples are assumed to be i.i.d., then this can be converted to

$$\boldsymbol{\theta}_{\text{ML}} = \arg \max_{\boldsymbol{\theta}} \sum_{i=1}^m \log P(\mathbf{y}^{(i)} \mid \mathbf{x}^{(i)}; \boldsymbol{\theta})$$

**Example: Linear Regression as Maximum Likelihood Estimation** The linear regression introduced in section 5.1.4, may be justified as a maximum likelihood estimation. Previously, we motivated linear regression as an algorithm that takes an input  $\mathbf{x}$  and produce an output value  $\hat{y}$ . The mapping from input to output was to minimize mean squared error, a criterion that we introduced in section 5.1.3. We now revisit linear regression from the point of view of maximum likelihood estimation. Instead of producing a single prediction  $\hat{y}$ , we think of it as producing a conditional distribution  $p(y \mid \mathbf{x})$ . We can think of the training set as an infinitely large training set, we might see several training examples with the same input value  $\mathbf{x}$  but different values of  $y$ . The goal of the learning algorithm is to fit the distribution  $p(y \mid \mathbf{x})$  to all those different  $y$  values for each  $\mathbf{x}$ . To derive the same linear regression algorithm we can assume that the data is generated by a linear model with Gaussian noise.

where  $\hat{y}^{(i)}$  is the output of the linear regression on the  $i$ -th number of the training examples. Comparing the log-likelihood squared error,

$$\text{MSE}_{\text{train}} = \frac{1}{m} \sum_{i=1}^m \|\hat{y}^{(i)} - y^{(i)}\|^2,$$

we immediately see that maximizing the log-likelihood with the same estimate of the parameters  $\mathbf{w}$  as does minimizing the MSE. The two criteria have different values but the same location. This justifies the use of the MSE as a maximum likelihood estimator. As we will see, the maximum likelihood estimator has several desirable properties.

### 5.5.2 Properties of Maximum Likelihood

The main appeal of the maximum likelihood estimator is that it is the best estimator asymptotically, as the number of examples  $m$  increases.

Under appropriate conditions, the maximum likelihood estimator has the property of consistency (see section 5.4.5), meaning that as the number of examples approaches infinity, the maximum likelihood estimator converges to the true value of the parameter. These conditions are:

- The true distribution  $p_{\text{data}}$  must lie within the model. Otherwise, no estimator can recover  $p_{\text{data}}$ .
- The true distribution  $p_{\text{data}}$  must correspond to exactly one parameter. Otherwise, maximum likelihood can recover the correct  $p_{\text{data}}$  but cannot determine which value of  $\theta$  was used by the data-generating process.

values, where the expectation is over  $m$  training samples from the distribution. That parametric mean squared error decreases for  $m$  large, the Cramér-Rao lower bound (Rao, 1945; Cra) no consistent estimator has a lower MSE than the maximum likelihood estimator.

For these reasons (consistency and efficiency), maximum likelihood is considered the preferred estimator to use for machine learning. If the number of examples is small enough to yield overfitting behavior, regularization, such as weight decay may be used to obtain a biased version of the estimator that has less variance when training data is limited.

## 5.6 Bayesian Statistics

So far we have discussed **frequentist statistics** and approximating a single value of  $\theta$ , then making all predictions therefrom. Another approach is to consider all possible values of  $\theta$  for prediction. The latter is the domain of **Bayesian statistics**.

As discussed in section 5.4.1, the frequentist perspective is that the parameter value  $\theta$  is fixed but unknown, while the point estimate is variable on account of it being a function of the dataset (which is random).

The Bayesian perspective on statistics is quite different. It treats the parameter probability to reflect degrees of certainty in states of knowledge. The parameter is directly observed and so is not random. On the other hand, the data is unknown or uncertain and thus is represented as a random variable.

Before observing the data, we represent our knowledge of the parameter as a **probability distribution**,  $p(\theta)$  (sometimes referred to as the **prior**). Generally, the machine learning practitioner selects a prior distribution that is conjugate to the likelihood function.

In the scenarios where Bayesian estimation is typically used, a relatively uniform or Gaussian distribution with high entropy of the data usually causes the posterior to lose entropy and a few highly likely values of the parameters.

Relative to maximum likelihood estimation, Bayesian has important differences. First, unlike the maximum likelihood predictions using a point estimate of  $\theta$ , the Bayesian approach uses a full distribution over  $\theta$ . For example, after observing  $x^{(1)}, \dots, x^{(m)}$ , the predicted distribution over the next data sample,  $x^{(m+1)}$ , is

$$p(x^{(m+1)} | x^{(1)}, \dots, x^{(m)}) = \int p(x^{(m+1)} | \theta) p(\theta | x^{(1)}, \dots, x^{(m)}) d\theta$$

Here each value of  $\theta$  with positive probability density contributes to the next example, with the contribution weighted by the probability of that value. After having observed  $\{x^{(1)}, \dots, x^{(m)}\}$ , if we are still quite uncertain about the value of  $\theta$ , then this uncertainty is incorporated directly into the prediction for  $x^{(m+1)}$ .

In section 5.4, we discussed how the frequentist approach to uncertainty in a given point estimate of  $\theta$  by evaluating its variance. The estimator is an assessment of how the estimate might change with different samplings of the observed data. The Bayesian answer to the question of uncertainty in the estimator is to simply integrate over the uncertainty. This integral is of course more computationally expensive than the frequentist machinery for constructing an estimator is based on. The Bayesian decision to summarize all knowledge contained in the data into a single estimate.

**Example: Bayesian Linear Regression** Here we consider a maximum a posteriori (MAP) approach to learning the linear regression parameters. We learn a linear mapping from an input vector  $\mathbf{x} \in \mathbb{R}^n$  to a scalar  $y \in \mathbb{R}$ . The prediction is parametrized by the vector

$$\hat{y} = \mathbf{w}^\top \mathbf{x}.$$

Given a set of  $m$  training samples  $(\mathbf{X}^{(\text{train})}, \mathbf{y}^{(\text{train})})$ , we can write the likelihood of  $\mathbf{y}$  over the entire training set as

$$\mathbf{y}^{(\text{train})} = \mathbf{X}^{(\text{train})} \mathbf{w}.$$

Expressed as a Gaussian conditional distribution on  $\mathbf{y}^{(\text{train})}$  given  $\mathbf{X}^{(\text{train})}$  and  $\mathbf{w}$ ,

$$\begin{aligned} p(\mathbf{y}^{(\text{train})} | \mathbf{X}^{(\text{train})}, \mathbf{w}) &= \mathcal{N}(\mathbf{y}^{(\text{train})}; \mathbf{X}^{(\text{train})} \mathbf{w}, \mathbf{I}) \\ &\propto \exp \left( -\frac{1}{2} (\mathbf{y}^{(\text{train})} - \mathbf{X}^{(\text{train})} \mathbf{w})^\top (\mathbf{y}^{(\text{train})} - \mathbf{X}^{(\text{train})} \mathbf{w}) \right) \end{aligned}$$

where we follow the standard MSE formulation in assuming a constant variance on  $y$  is one. In what follows, to reduce the notation, we will write  $(\mathbf{X}^{(\text{train})}, \mathbf{y}^{(\text{train})})$  as simply  $(\mathbf{X}, \mathbf{y})$ .

To determine the posterior distribution over the model parameters  $\mathbf{w}$ , we first need to specify a prior distribution. The prior should express our beliefs about the value of these parameters. While it is sometimes convenient to express our prior beliefs in terms of the parameters of the model, we typically assume a fairly broad distribution, expressing a high degree of uncertainty about  $\boldsymbol{\theta}$ . For real-valued parameters it is common to use a Gaussian prior.



$$\begin{aligned} &\propto \exp\left(-\frac{1}{2}(\mathbf{y} - \mathbf{X}\mathbf{w})^\top (\mathbf{y} - \mathbf{X}\mathbf{w})\right) \exp\left(-\frac{1}{2}(\mathbf{w} - \boldsymbol{\mu}_0)^\top \boldsymbol{\Lambda}_0^{-1}(\mathbf{w} - \boldsymbol{\mu}_0)\right) \\ &\propto \exp\left(-\frac{1}{2}\left(-2\mathbf{y}^\top \mathbf{X}\mathbf{w} + \mathbf{w}^\top \mathbf{X}^\top \mathbf{X}\mathbf{w} + \mathbf{w}^\top \boldsymbol{\Lambda}_0^{-1}\mathbf{w} - 2\boldsymbol{\mu}_0^\top \mathbf{X}\mathbf{w} + \boldsymbol{\mu}_0^\top \mathbf{X}\mathbf{X}^\top \boldsymbol{\mu}_0 + \boldsymbol{\mu}_0^\top \boldsymbol{\Lambda}_0^{-1}\boldsymbol{\mu}_0\right)\right) \end{aligned}$$

We now define  $\boldsymbol{\Lambda}_m = (\mathbf{X}^\top \mathbf{X} + \boldsymbol{\Lambda}_0^{-1})^{-1}$  and  $\boldsymbol{\mu}_m = \boldsymbol{\Lambda}_m$ . Using these new variables, we find that the posterior may be re-written as a Gaussian distribution:

$$\begin{aligned} p(\mathbf{w} \mid \mathbf{X}, \mathbf{y}) &\propto \exp\left(-\frac{1}{2}(\mathbf{w} - \boldsymbol{\mu}_m)^\top \boldsymbol{\Lambda}_m^{-1}(\mathbf{w} - \boldsymbol{\mu}_m) + \frac{1}{2}\mathbf{y}^\top \mathbf{y}\right) \\ &\propto \exp\left(-\frac{1}{2}(\mathbf{w} - \boldsymbol{\mu}_m)^\top \boldsymbol{\Lambda}_m^{-1}(\mathbf{w} - \boldsymbol{\mu}_m)\right). \end{aligned}$$

All terms that do not include the parameter vector  $\mathbf{w}$  have been dropped. These terms are implied by the fact that the distribution must be normalized. Equation 3.23 shows how to normalize a multivariate Gaussian distribution.

Examining this posterior distribution enables us to gain insight into the effect of Bayesian inference. In most situations, we set  $\boldsymbol{\mu}_0 = \mathbf{0}$  and  $\boldsymbol{\Lambda}_0 = \alpha \mathbf{I}$ . Then  $\boldsymbol{\mu}_m$  gives the same estimate of  $\mathbf{w}$  as does frequentist least squares. The weight decay penalty of  $\alpha \mathbf{w}^\top \mathbf{w}$ . One difference is that the frequentist estimate is undefined if  $\alpha$  is set to zero—we are not allowed to begin the least squares process with an infinitely wide prior on  $\mathbf{w}$ . The more important difference is that the Bayesian estimate provides a covariance matrix, showing how different values of  $\mathbf{w}$  are, rather than providing only the estimate.

maximal posterior probability (or maximal probability density case of continuous  $\boldsymbol{\theta}$ ):

$$\boldsymbol{\theta}_{\text{MAP}} = \arg \max_{\boldsymbol{\theta}} p(\boldsymbol{\theta} \mid \mathbf{x}) = \arg \max_{\boldsymbol{\theta}} \log p(\mathbf{x} \mid \boldsymbol{\theta}) + \log p(\boldsymbol{\theta})$$

We recognize, on the righthand side,  $\log p(\mathbf{x} \mid \boldsymbol{\theta})$ , the likelihood term, and  $\log p(\boldsymbol{\theta})$ , corresponding to the prior distribution.

As an example, consider a linear regression model with the weights  $\mathbf{w}$ . If this prior is given by  $\mathcal{N}(\mathbf{w}; \mathbf{0}, \frac{1}{\lambda} \mathbf{I}^2)$ , then equation 5.79 is proportional to the familiar  $\lambda \mathbf{w}^\top \mathbf{w}$  weight term that does not depend on  $\mathbf{w}$  and does not affect the likelihood. Bayesian inference with a Gaussian prior on the weights thus introduces weight decay.

As with full Bayesian inference, MAP Bayesian inference leverages information that is brought by the prior and the training data. This additional information helps to reduce the variance of the MAP point estimate (in comparison to the ML estimate). However, it also introduces a bias, which is the price of increased bias.

Many regularized estimation strategies, such as maximum a posteriori estimation, can be interpreted as making connections to Bayesian inference. This view applies when the regularization is achieved by adding an extra term to the objective function that corresponds to the prior. In this case, all regularization penalties correspond to MAP Bayesian inference. However, some regularizer terms may not be the logarithm of a probability density. Other regularization terms depend on the data, which of course is not allowed to do.

“supervisor,” but the term still applies even when the data is collected automatically.

### 5.7.1 Probabilistic Supervised Learning

Most supervised learning algorithms in this book are based on a probability distribution  $p(y \mid \mathbf{x})$ . We can do this simple maximum likelihood estimation to find the best parameter vector  $\boldsymbol{\theta}$  for a family of distributions  $p(y \mid \mathbf{x}; \boldsymbol{\theta})$ .

We have already seen that linear regression corresponds to the normal distribution.

$$p(y \mid \mathbf{x}; \boldsymbol{\theta}) = \mathcal{N}(y; \boldsymbol{\theta}^\top \mathbf{x}, I).$$

We can generalize linear regression to the classification problem by using a different family of probability distributions. If we have two classes, class 1, then we need only specify the probability of one class. The probability of class 1 determines the probability of class 0, because the probabilities must add up to 1.

The normal distribution over real-valued numbers that we used for linear regression is parametrized in terms of a mean. Any real number is valid. A distribution over a binary variable is slightly more complicated because its mean must always be between 0 and 1. One way to solve this is to use the logistic sigmoid function to squash the output of the linear model into the interval (0, 1) and interpret that value as a probability:

$$p(y = 1 \mid \mathbf{x}; \boldsymbol{\theta}) = \sigma(\boldsymbol{\theta}^\top \mathbf{x}).$$

This approach is known as **logistic regression** (a somewhat

### 5.7.2 Support Vector Machines

One of the most influential approaches to supervised learning machine (Boser *et al.*, 1992; Cortes and Vapnik, 1995). Unlike logistic regression in that it is driven by a linear function  $\mathbf{w}^\top \mathbf{x}$ , in support vector machine, the support vector machine does not provide a probability output, it only outputs a class identity. The SVM predicts that the positive class if  $\mathbf{w}^\top \mathbf{x} + b$  is positive. Likewise, it predicts that the negative class if  $\mathbf{w}^\top \mathbf{x} + b$  is negative.

One key innovation associated with support vector machine is the **kernel trick**. The kernel trick consists of observing that many machine learning algorithms can be written exclusively in terms of dot products between vectors. In fact, it can be shown that the linear function used by the support vector machine can be re-written as

$$\mathbf{w}^\top \mathbf{x} + b = b + \sum_{i=1}^m \alpha_i \mathbf{x}^\top \mathbf{x}^{(i)},$$

where  $\mathbf{x}^{(i)}$  is a training example, and  $\boldsymbol{\alpha}$  is a vector of coefficients. In support vector machine learning algorithm this way enables us to replace  $\mathbf{x}$  with the output of a feature map function  $\phi(\mathbf{x})$  and the dot product with a function  $k(\mathbf{x}, \mathbf{x}^{(i)})$ , where  $k$  is a **kernel**. The  $\cdot$  operator represents an inner product analog. For some feature spaces, we may not use literally the vector representation. For some infinite dimensional spaces, we need to use other kinds of inner products, for example, inner products based on integration rather than summation. The development of these kinds of inner products is beyond the scope of this book.

After replacing dot products with kernel evaluations, we can write the decision function using the function

$$f(\mathbf{x}) = b + \sum_{i=1}^m \alpha_i k(\mathbf{x}, \mathbf{x}^{(i)})$$

admits an implementation that is significantly more computationally efficient than naively constructing two  $\phi(\mathbf{x})$  vectors and explicitly taking their dot product.

In some cases,  $\phi(\mathbf{x})$  can even be infinite dimensional, incurring an infinite computational cost for the naive, explicit approach. However,  $k(\mathbf{x}, \mathbf{x}')$  is a nonlinear, tractable function of  $\mathbf{x}$  even when  $\phi(\mathbf{x})$  is infinite dimensional. For example, consider an infinite-dimensional feature space with basis functions  $\phi_i(x) = x^i$ . We can construct a feature mapping  $\phi(x)$  over the nonnegative integers. This mapping returns a vector containing  $x$  ones followed by zeros. We can write a kernel function  $k(x, x^{(i)}) = \min(x, x^{(i)})$  that corresponds to the corresponding infinite-dimensional dot product.

The most commonly used kernel is the **Gaussian kernel**:

$$k(\mathbf{u}, \mathbf{v}) = \mathcal{N}(\mathbf{u} - \mathbf{v}; 0, \sigma^2 \mathbf{I}),$$

where  $\mathcal{N}(\mathbf{x}; \boldsymbol{\mu}, \boldsymbol{\Sigma})$  is the standard normal density. This is also known as the **radial basis function** (RBF) kernel, because its value at  $\mathbf{v}$  is like a wave in  $\mathbf{v}$  space radiating outward from  $\mathbf{u}$ . The Gaussian kernel is computationally efficient in an infinite-dimensional space, but the derivation is more straightforward than in our example of the min kernel over the nonnegative integers.

We can think of the Gaussian kernel as performing a kind of **local averaging**. A training example  $\mathbf{x}$  associated with training label  $y$  for class  $y$ . When a test point  $\mathbf{x}'$  is near  $\mathbf{x}$  according to the Gaussian kernel has a large response, indicating that  $\mathbf{x}'$  is similar to the template. The model then puts a large weight on the associated training label  $y$ . Overall, the prediction will combine many such training labels, weighted by the similarity of the corresponding training examples.

Support vector machines are not the only algorithm that can be implemented using the kernel trick. Many other linear models can be implemented using the kernel trick.

generic kernels struggle to generalize well. We explain why the modern incarnation of deep learning was designed to overcome kernel machines. The current deep learning renaissance began in 2006, when LeCun et al. (2006) demonstrated that a neural network could outperform linear models on the MNIST benchmark.

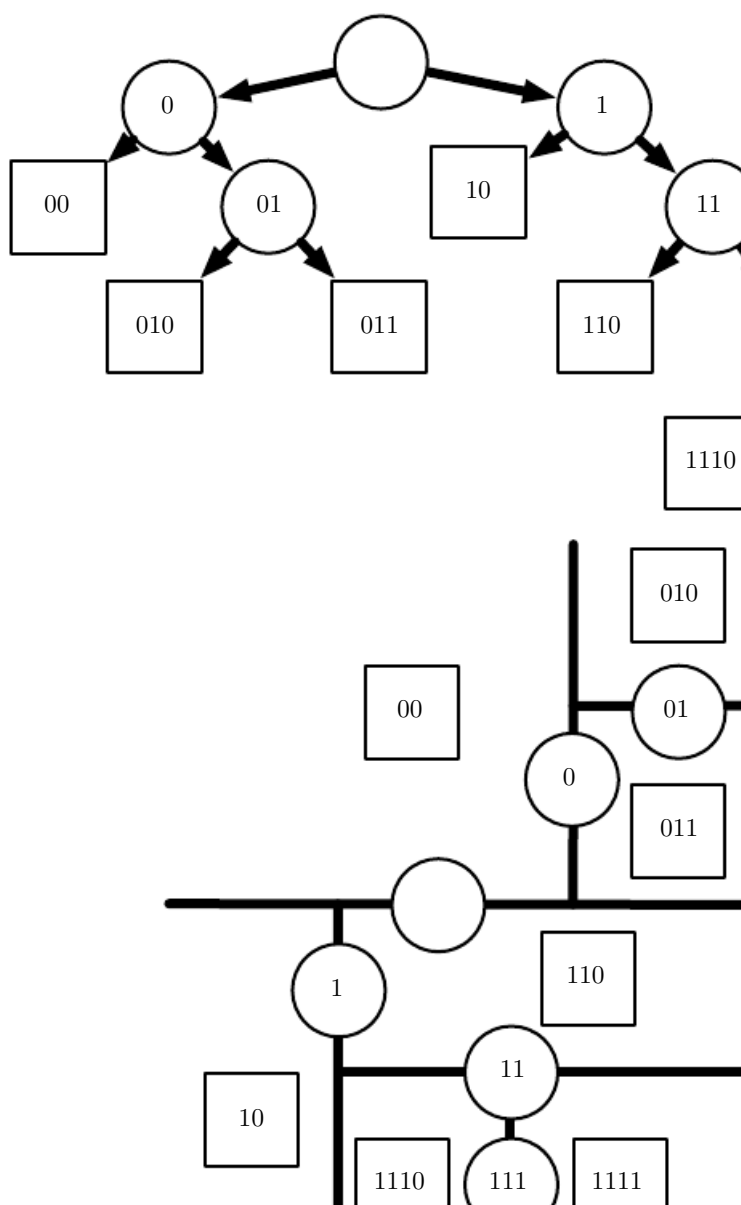
### 5.7.3 Other Simple Supervised Learning Algorithms

We have already briefly encountered another nonprobabilistic algorithm, nearest neighbor regression. More generally,  $k$ -nearest neighbor is a family of techniques that can be used for classification and regression.  $k$ -nearest neighbor is a nonparametric learning algorithm,  $k$ -nearest neighbors is a number of parameters. We usually think of the  $k$ -nearest neighbor as not having any parameters but rather implementing a search over the training data. In fact, there is not even really a training stage. Instead, at test time, when we want to produce an output  $y$  for a new input  $x$ , we find the  $k$ -nearest neighbors to  $x$  in the training data and take the average of the corresponding  $y$  values in the training set. This is true for any kind of supervised learning where we can define an average. In the case of classification, we can average over one-hot codes. Let  $c_i$  be the average of the  $i$ -th component of the one-hot codes of the  $k$ -nearest neighbors, and  $c_i = 0$  for all other values of  $i$ . We can then interpret the  $c_i$  as giving a probability distribution over classes. In the case of regression,  $k$ -nearest neighbor can achieve very high accuracy. Suppose we have a multiclass classification task and measure error by the squared loss. In this setting, 1-nearest neighbor converges to double the error of the best single neighbor as the number of training examples approaches infinity. The error of 1-nearest neighbor results from choosing a single neighbor by breaking ties randomly. When there is infinite training data, the error of 1-nearest neighbor is double the error of the best single neighbor.

The nearest neighbor of most points  $\mathbf{x}$  will be determined by features  $x_2$  through  $x_{100}$ , not by the lone feature  $x_1$ . Thus training sets will essentially be random.

Another type of learning algorithm that also breaks the i and has separate parameters for each region is the **decision tree** (Breiman 1984) and its many variants. As shown in figure 5.7, each node of a tree is associated with a region in the input space, and internal nodes split a region into one subregion for each child of the node (typically by axis-aligned cut). Space is thus subdivided into nonoverlapping regions, with a one-to-one correspondence between leaf nodes and input regions. Each leaf node maps every point in its input region to the same output. Decision trees are trained with specialized algorithms that are beyond the scope of this book. A learning algorithm can be considered nonparametric if it is not of arbitrary size, though decision trees are usually regularized to prevent overfitting that turn them into parametric models in practice. Decision trees are typically used, with axis-aligned splits and constant outputs, to solve some problems that are easy even for  $k$ -nearest neighbors. For example, if we have a two-class problem, and the positive class is defined by  $x_2 > x_1$ , the decision boundary is not axis aligned. The nearest neighbor algorithm needs to approximate the decision boundary with many nodes, and the function that constantly walks back and forth across the space with axis-aligned steps.

As we have seen, nearest neighbor predictors and decision trees have their limitations. Nonetheless, they are useful learning algorithms, and their resources are constrained. We can also build intuition for more sophisticated learning algorithms by thinking about the similarities and differences between  $k$ -nearest neighbors or decision trees and other algorithms.





examples. The term is usually associated with density estimation, drawing samples from a distribution, learning to denoise data, finding a manifold that the data lies near, or clustering the related examples.

A classic unsupervised learning task is to find the “best” data. By “best” we can mean different things, but generally seek for a representation that preserves as much information about  $x$  as possible while obeying some penalty or constraint aimed at keeping the representation more accessible than  $x$  itself.

There are multiple ways of defining a simpler representation. The most common include lower-dimensional representations, sparse representations, and independent representations. Low-dimensional representations compress as much information about  $x$  as possible in a smaller space. Sparse representations (Barlow, 1989; Olshausen and Field, 1996; Ghahramani, 1997) embed the dataset into a representation where most elements are mostly zeros for most inputs. The use of sparse representations, by increasing the dimensionality of the representation, so that only a few elements are non-zero, does not discard too much information. Sparse representations preserve the overall structure of the representation that tends to distribute the information across the representation space. Independent representations seek to identify the sources of variation underlying the data distribution such that the elements of the representation are statistically independent.

Of course these three criteria are certainly not mutually exclusive. Lower-dimensional representations often yield elements that have more dependencies than the original high-dimensional data. This reduction in the size of a representation is to find and remove redundancy. Reducing and removing more redundancy enables the dimensionality

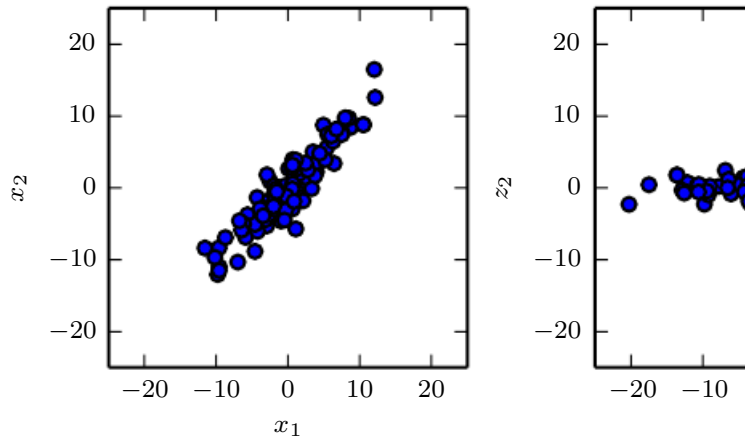


Figure 5.8: PCA learns a linear projection that aligns the direction the axes of the new space. (*Left*) The original data consist of sample variance might occur along directions that are not axis aligned. data  $\mathbf{z} = \mathbf{x}^\top \mathbf{W}$  now varies most along the axis  $z_1$ . The direction is now along  $z_2$ .

### 5.8.1 Principal Components Analysis

In section 2.12, we saw that the principal components analysis is a means of compressing data. We can also view PCA as an algorithm that learns a representation of data. This representation satisfies two of the criteria for a simple representation described in section 2.12: a representation that has lower dimensionality than the original data and a representation whose elements have no linear correlation. This is a first step toward the criterion of learning a representation that is statistically independent. To achieve full independence, a representation must also be uncorrelated with the original data.

a mean of zero,  $\mathbb{E}[\mathbf{x}] = \mathbf{0}$ . If this is not the case, the data is centered by subtracting the mean from all examples in a preprocess.

The unbiased sample covariance matrix associated with

$$\text{Var}[\mathbf{x}] = \frac{1}{m-1} \mathbf{X}^\top \mathbf{X}.$$

PCA finds a representation (through linear transformation) such that  $\text{Var}[\mathbf{z}]$  is diagonal.

In section 2.12, we saw that the principal components are given by the eigenvectors of  $\mathbf{X}^\top \mathbf{X}$ . From this view,

$$\mathbf{X}^\top \mathbf{X} = \mathbf{W} \mathbf{\Lambda} \mathbf{W}^\top.$$

In this section, we exploit an alternative derivation of the principal components. The principal components may also be obtained via singular value decomposition (SVD). Specifically, they are the right singular vectors of  $\mathbf{X}$ . In the SVD,  $\mathbf{X}$  is decomposed into the product of three matrices:  $\mathbf{X} = \mathbf{U} \mathbf{\Sigma} \mathbf{V}^\top$ , where  $\mathbf{U}$  and  $\mathbf{V}$  are orthogonal matrices, and  $\mathbf{\Sigma}$  is a diagonal matrix of singular values. The right singular vectors are the columns of  $\mathbf{V}$ . In the original eigenvector equation with  $\mathbf{W}$  as the eigenvectors,

$$\mathbf{X}^\top \mathbf{X} = (\mathbf{U} \mathbf{\Sigma} \mathbf{V}^\top)^\top \mathbf{U} \mathbf{\Sigma} \mathbf{V}^\top = \mathbf{V} \mathbf{\Sigma}^2 \mathbf{V}^\top$$

The SVD is helpful to show that PCA results in a diagonal covariance matrix. If we have the SVD of  $\mathbf{X}$ , we can express the variance of  $\mathbf{X}$  as:

$$\begin{aligned} \text{Var}[\mathbf{x}] &= \frac{1}{m-1} \mathbf{X}^\top \mathbf{X} \\ &= \frac{1}{m-1} (\mathbf{U} \mathbf{\Sigma} \mathbf{V}^\top)^\top \mathbf{U} \mathbf{\Sigma} \mathbf{V}^\top \end{aligned}$$

$$\begin{aligned} &= \frac{1}{m-1} \mathbf{W}^\top \mathbf{W} \mathbf{\Sigma}^2 \mathbf{W}^\top \mathbf{W} \\ &= \frac{1}{m-1} \mathbf{\Sigma}^2, \end{aligned}$$

where this time we use the fact that  $\mathbf{W}^\top \mathbf{W} = \mathbf{I}$ , again from SVD.

The above analysis shows that when we project the data transformation  $\mathbf{W}$ , the resulting representation has a diagonal covariance matrix (as given by  $\mathbf{\Sigma}^2$ ), which immediately implies that the individual features are mutually uncorrelated.

This ability of PCA to transform data into a representation where the features are mutually uncorrelated is a very important property. It provides an example of a representation that attempts to *disentangle the variation* underlying the data. In the case of PCA, this is done in the form of finding a rotation of the input space (described by the principal axes of variance) with the basis of the new representation  $\mathbf{z}$ .

While correlation is an important category of dependence in the data, we are also interested in learning representations that capture more complicated forms of feature dependencies. For this, we will see that more can be done with a simple linear transformation.

### 5.8.2 $k$ -means Clustering

Another example of a simple representation learning algorithm is  $k$ -means clustering. The  $k$ -means clustering algorithm divides the training set into  $k$  clusters, where each cluster is represented by a centroid. The algorithm iteratively updates the centroids to the mean of the data points in each cluster until the centroids no longer move.

may be captured by a single integer.

The  $k$ -means algorithm works by initializing  $k$  different centroids to different values, then alternating between two different steps. In one step, each training example is assigned to cluster  $i$ , the nearest centroid  $\mu^{(i)}$ . In the other step, each centroid is updated to the mean of all training examples  $\mathbf{x}^{(j)}$  assigned to cluster  $i$ .

One difficulty pertaining to clustering is that the clustering problem is ill posed, in the sense that there is no single criterion that guarantees that the clustering of the data corresponds to the real world. We can evaluate the quality of the clustering, such as the average Euclidean distance from each example to the members of the cluster. This enables us to tell how well the clustering reconstructs the training data from the cluster assignments. However, even if the cluster assignments correspond to properties of the real world, there may be many different clusterings that all correspond to the real world. We may hope to find a clustering that reliably captures the real world, but we can obtain a different, equally valid clustering that is not reliable. For example, suppose that we run two clustering algorithms on a dataset of images of red trucks, images of red cars, images of gray trucks, and images of gray cars. If we ask each clustering algorithm to find two clusters, the first algorithm finds a cluster of cars and a cluster of trucks, while the second algorithm finds a cluster of red vehicles and a cluster of gray vehicles. Suppose we also run a third clustering algorithm, which is allowed to determine the number of clusters. We set the number of clusters to four, and the algorithm finds four clusters: red cars, red trucks, gray cars, and gray trucks. This new clustering now at least captures information about both color and vehicle type, but it has lost information about similarity. Red cars are in a different cluster from gray cars, just as they are in a different cluster from gray trucks. A clustering algorithm that does not tell us that red cars are more similar to gray cars than to gray trucks is not capturing the real world.

attributes instead of just testing whether one attribute ma

## 5.9 Stochastic Gradient Descent

Nearly all of deep learning is powered by one very important **gradient descent** (SGD). Stochastic gradient descent is a variant of the gradient descent algorithm introduced in section 4.3.

A recurring problem in machine learning is that large training sets are good for generalization, but large training sets are also expensive.

The cost function used by a machine learning algorithm is the sum over training examples of some per-example loss function. For example, the negative conditional log-likelihood of the training data can

$$J(\boldsymbol{\theta}) = \mathbb{E}_{\mathbf{x}, y \sim \hat{p}_{\text{data}}} L(\mathbf{x}, y, \boldsymbol{\theta}) = \frac{1}{m} \sum_{i=1}^m L(\mathbf{x}^{(i)}, y^{(i)}, \boldsymbol{\theta}),$$

where  $L$  is the per-example loss  $L(\mathbf{x}, y, \boldsymbol{\theta}) = -\log p(y | \mathbf{x}; \boldsymbol{\theta})$ .

For these additive cost functions, gradient descent requires

$$\nabla_{\boldsymbol{\theta}} J(\boldsymbol{\theta}) = \frac{1}{m} \sum_{i=1}^m \nabla_{\boldsymbol{\theta}} L(\mathbf{x}^{(i)}, y^{(i)}, \boldsymbol{\theta}).$$

The computational cost of this operation is  $O(m)$ . As the training sets grow to billions of examples, the time to take a single gradient step becomes prohibitively long.

Stochastic gradient descent (SGD) is a method for minimizing the cost function

using examples from the minibatch  $\mathbb{B}$ . The stochastic gradient then follows the estimated gradient downhill:

$$\boldsymbol{\theta} \leftarrow \boldsymbol{\theta} - \epsilon \mathbf{g},$$

where  $\epsilon$  is the learning rate.

Gradient descent in general has often been regarded as the past, the application of gradient descent to nonconvex was regarded as foolhardy or unprincipled. Today, we know that learning models described in part II work very well when using gradient descent. The optimization algorithm may not be guaranteed to find a local minimum in a reasonable amount of time, but it often finds one of the cost function quickly enough to be useful.

Stochastic gradient descent has many important uses in deep learning. It is the main way to train large linear models on large datasets. For a fixed model size, the cost per SGD update is  $O(1/m)$  where  $m$  is the training set size. In practice, we often use a larger model size as the training set size increases, but we are not forced to do so. The number of updates to reach convergence usually increases with training set size. However, as  $m$  goes to infinity, the model will eventually converge to its best possible model. SGD has sampled every example in the training set. Increasing  $m$  extends the amount of training time needed to reach the minimum error. From this point of view, one can argue that the asymptotic complexity of a model with SGD is  $O(1)$  as a function of  $m$ .

Prior to the advent of deep learning, the main way to learn a linear model was to use the kernel trick in combination with a linear model. Kernel algorithms require constructing an  $m \times m$  matrix  $G_{i,j} = k(\mathbf{x}_i, \mathbf{x}_j)$ .

## 5.10 Building a Machine Learning Algorithm

Nearly all deep learning algorithms can be described as following a fairly simple recipe: combine a specification of a dataset, an optimization procedure and a model.

For example, the linear regression algorithm combines a dataset  $\mathbf{X}$  and  $\mathbf{y}$ , the cost function

$$J(\mathbf{w}, b) = -\mathbb{E}_{\mathbf{x}, y \sim \hat{p}_{\text{data}}} \log p_{\text{model}}(y \mid \mathbf{x}),$$

the model specification  $p_{\text{model}}(y \mid \mathbf{x}) = \mathcal{N}(y; \mathbf{x}^\top \mathbf{w} + b, 1)$ , and an optimization algorithm defined by solving for where the gradient is zero using the normal equations.

By realizing that we can replace any of these components with others, we can obtain a wide range of algorithms.

The cost function typically includes at least one term that penalizes the model for overfitting to the training process to perform statistical estimation. The most common choice is the negative log-likelihood, so that minimizing the cost function is equivalent to maximum likelihood estimation.

The cost function may also include additional terms, such as weight decay. For example, we can add weight decay to the linear regression cost function to obtain

$$J(\mathbf{w}, b) = \lambda \|\mathbf{w}\|_2^2 - \mathbb{E}_{\mathbf{x}, y \sim \hat{p}_{\text{data}}} \log p_{\text{model}}(y \mid \mathbf{x}),$$

This still allows closed form optimization.

If we change the model to be nonlinear, then most cost functions cannot be optimized in closed form. This requires us to choose an optimization procedure.



In some cases, the cost function may be a function that is difficult to evaluate, for computational reasons. In these cases, we can minimize it using iterative numerical optimization, as long as we are approximating its gradients.

Most machine learning algorithms make use of this recipe, and it is immediately obvious. If a machine learning algorithm seems hand designed, it can usually be understood as using a special set of models, such as decision trees and  $k$ -means, require special care. Their cost functions have flat regions that make them inappropriate for gradient-based optimizers. Recognizing that most machine learning can be described using this recipe helps to see the different taxonomy of methods for doing related tasks that work for different problems than as a long list of algorithms that each have separate justifications.

## 5.11 Challenges Motivating Deep Learning

The simple machine learning algorithms described in this chapter work on a wide variety of important problems. They have not succeeded on the central problems in AI, such as recognizing speech or recognizing objects in images.

The development of deep learning was motivated in part by the failure of traditional algorithms to generalize well on such AI tasks.

This section is about how the challenge of generalizing to new data is exponentially more difficult when working with high-dimensional data. The mechanisms used to achieve generalization in traditional machine learning are insufficient to learn complicated functions in high-dimensional spaces also often impose high computational costs. Deep learning addresses these challenges.

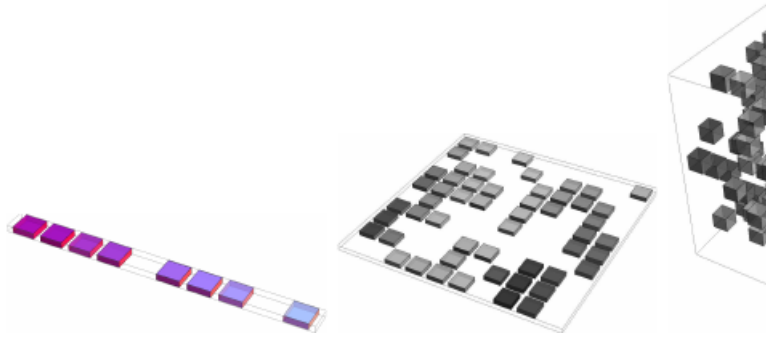


Figure 5.9: As the number of relevant dimensions of the data (right), the number of configurations of interest may grow exponentially. (Left) In a one-dimensional example, we have one variable for which we can define regions of interest. With enough examples falling within each of these regions (each corresponds to a cell in the illustration), learning algorithms can easily generalize. A straightforward way to generalize is to estimate the value of the target variable in each region (and possibly interpolate between neighboring regions). (Middle) With two dimensions, it is more difficult to distinguish 10 different values of the target variable. We need to keep track of up to  $10 \times 10 = 100$  regions, and we need at least 100 examples to cover all those regions. (Right) With three dimensions, this grows to  $10 \times 10 \times 10 = 1000$  regions, and we need at least that many examples. For  $d$  dimensions and  $v$  values per axis, we seem to need  $O(v^d)$  regions and examples. This is the curse of dimensionality. Figure graciously provided by Nicolas Chapados.

One challenge posed by the curse of dimensionality is the exponential growth of the number of possible configurations of  $\mathbf{x}$ . As illustrated in figure 5.9, a statistical challenge arises because the number of possible configurations of  $\mathbf{x}$  is much larger than the number of examples. To understand the issue, let us consider that the input space is a 10-dimensional space, as in the figure. We can describe low-dimensional space by a 10x10x10 grid of cells that are mostly occupied by the data. When gen-

algorithms simply assume that the output at a new point is the same as the output at the nearest training point.

### 5.11.2 Local Constancy and Smoothness Regularization

To generalize well, machine learning algorithms need to be able to learn about what kind of function they should learn. We have seen that we can encode these beliefs as explicit beliefs in the form of probability distributions over the model. More informally, we may also discuss prior beliefs about the *function* itself and influencing the parameters only indirectly through the relationship between the parameters and the function. Another way to discuss prior beliefs is as being expressed implicitly by choices that are biased toward choosing some class of functions over others. These biases may not be expressed (or even be possible to express) as a probability distribution representing our degree of belief in the space of functions.

Among the most widely used of these implicit “priors” are the **smoothness prior**, or **local constancy prior**. This prior states that the function should not change very much within a small region.

Many simpler algorithms rely exclusively on this prior. As a result, they fail to scale to the statistical challenges of high-dimensional tasks. Throughout this book, we describe how to use additional (explicit and implicit) priors in order to reduce error on sophisticated tasks. Here, we explain why the smoothness prior is insufficient for these tasks.

There are many different ways to implicitly or explicitly encode the belief that the learned function should be smooth or locally constant. Many methods are designed to encourage the learning process to learn a smooth function.

the training set. For  $k = 1$ , the number of distinguishable regions is less than the number of training examples.

While the  $k$ -nearest neighbors algorithm copies the output of the training examples, most kernel machines interpolate between training examples with nearby training examples. An important class of kernel machines are **kernels**, where  $k(\mathbf{u}, \mathbf{v})$  is large when  $\mathbf{u} = \mathbf{v}$  and decreases as  $\mathbf{u}$  and  $\mathbf{v}$  move apart from each other. A local kernel can be thought of as a model that performs template matching, by measuring how closely the input  $\mathbf{x}$  resembles each training example  $\mathbf{x}^{(i)}$ . Much of the modern machine learning is derived from studying the limitations of local models and how deep models are able to succeed in cases where local models fail (Bengio *et al.*, 2006b).

Decision trees also suffer from the limitations of exclusive learning, because they break the input space into as many regions as leaves and use a separate parameter (or sometimes many parameters) of decision trees) in each region. If the target function requires at least  $n$  leaves to be represented accurately, then at least  $n$  nodes are required to fit the tree. A multiple of  $n$  is needed to achieve high confidence in the predicted output.

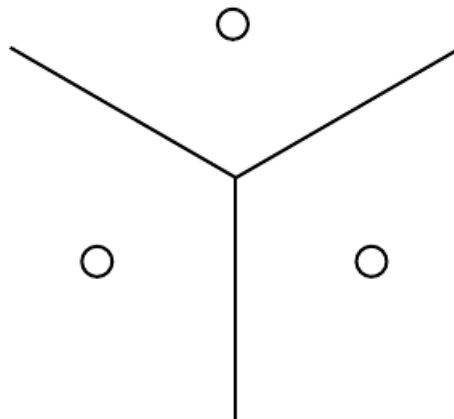
In general, to distinguish  $O(k)$  regions in input space, at least  $O(k)$  examples are needed. Typically there are  $O(k)$  parameters, each associated with each of the  $O(k)$  regions. The nearest neighbor model where each training example can be used to define at most one region is shown in figure 5.10.

Is there a way to represent a complex function that has more regions than the number of training examples? (The smoothness of the underlying function will not allow a local model to do this.)

least one example.

The smoothness assumption and the associated nonparametric algorithms work extremely well as long as there are enough examples to observe high points on most peaks and low points on most valleys of the true underlying function to be learned. This is generally true if the function to be learned is smooth enough and varies in frequency slowly enough. In high dimensions, even a very smooth function can change in a very different way along each dimension. If the function varies in a different way in various regions, it can become extremely complicated to learn from a small number of training examples. If the function is complicated (we want to learn a function with a large number of regions compared to the number of examples) can it still generalize well?

The answer to both of these questions—whether it is possible to learn a complicated function efficiently, and whether it is possible to learn a function to generalize well to new inputs—is yes. The key insight is that the number of regions, such as  $O(2^k)$ , can be defined with  $O(k)$  parameters.



introduce some dependencies between the regions through a model about the underlying data-generating distribution. In this way, we generalize nonlocally (Bengio and Monperrus, 2005; Bengio et al., 2007). Different deep learning algorithms provide implicit or explicit regularization, which is reasonable for a broad range of AI tasks in order to capture the underlying structure.

Other approaches to machine learning often make strong assumptions. For example, we could easily solve the checkerboard problem by making the assumption that the target function is periodic. Usually, we make strong, task-specific assumptions in neural networks so that they can be applied to a much wider variety of structures. AI tasks have structures that are too complex to be limited to simple, manually specified properties. So we want learning algorithms that embody more general assumptions. The core idea in deep learning is that we assume that the target function is a *composition of factors*, or features, potentially at multiple scales. Many other similarly generic assumptions can further guide the design of learning algorithms. These apparently mild assumptions allow an exponential relationship between the number of examples and the number of parameters to be distinguished. We describe these exponential gains more fully in 6.4.1, 15.4 and 15.5. The exponential advantages conferred by distributed representations counter the exponential challenge of dimensionality.

### 5.11.3 Manifold Learning

An important concept underlying many ideas in machine learning is the manifold.

A **manifold** is a connected region. Mathematically,

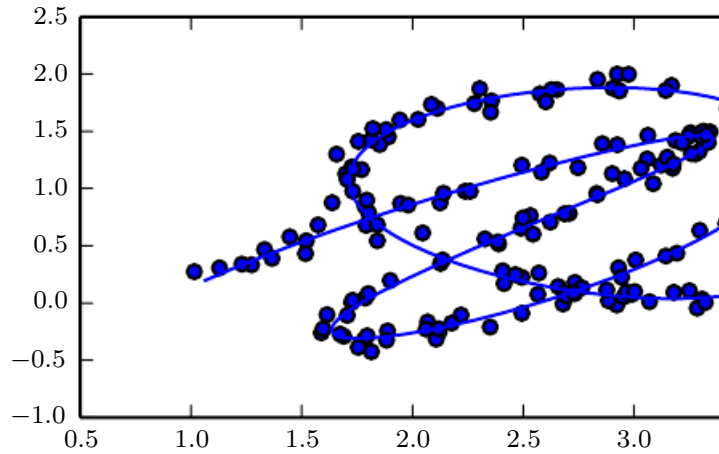
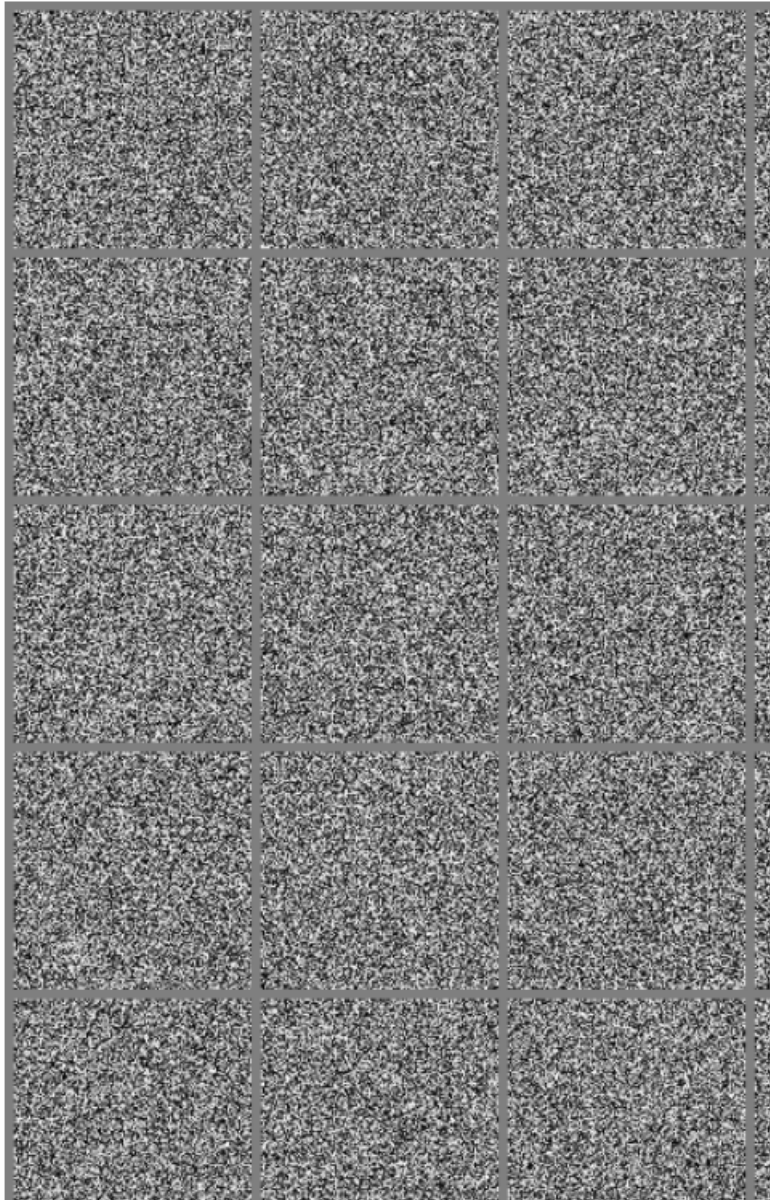


Figure 5.11: Data sampled from a distribution in a two-dimensional space concentrated near a one-dimensional manifold, like a twisted string. The goal is to infer the underlying manifold that the learner should infer.

degrees of freedom, or dimensions, embedded in a higher-dimensional space. A local direction of variation in a high-dimensional space corresponds to a local direction of variation in a lower-dimensional space. An example of training data lying near a one-dimensional manifold in a high-dimensional space. In the context of machine learning, we are interested in the manifold to vary from one point to another. This manifold intersects itself. For example, a figure eight is a manifold that is one-dimensional in most places but two-dimensional at the intersection.

Many machine learning problems seem hopeless if we have a learning algorithm to learn functions with interesting variations. **Manifold learning** algorithms surmount this obstacle by assuming that the set of valid inputs of  $\mathbb{R}^n$  consists of invalid inputs, and that interesting inputs





bility distribution over images, text strings, and sounds is highly concentrated. Uniform noise essentially never resembles these domains. Figure 5.12 shows how, instead, uniform noise looks like the patterns of static that appear on analog television when no signal is available. Similarly, if you generate a document by picking words at random, what is the probability that you will get a meaningful text? Almost zero, again, because most of the long sequences of words correspond to a natural language sequence: the distribution of natural language sequences occupies a very little volume in the total space of possible sequences.

Of course, concentrated probability distributions are not unique to data. The data lies on a reasonably small number of manifolds. Manifolds are spaces in which the examples we encounter are connected to each other. A manifold is a space in which each example is surrounded by other highly similar examples. We can traverse the manifold by applying transformations to the examples. The main idea in favor of the manifold hypothesis is that we can imagine such transformations, at least informally. In the case of images, there are many possible transformations that allow us to traverse the space: we can gradually dim or brighten the lights, gradually move objects in the image, gradually alter the colors on the surface, and so forth. Multiple manifolds are likely involved in most applications. For example, the manifold of human face images may not be connected to the manifold of human face images with different backgrounds.

These thought experiments convey some intuitive reasons for the manifold hypothesis. More rigorous experiments (Cayton, 2005; 2010; Schölkopf *et al.*, 1998; Roweis and Saul, 2000; Tenenbaum, 2003; Belkin and Niyogi, 2003; Donoho and Grimes, 2003; 2004) clearly support the hypothesis for a large class of data.

This concludes part I, which has provided the basic concepts and machine learning that are employed throughout the rest of the book. You are now prepared to embark on your study of deep

