

PRML

April 17, 2024

1. Introduction

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```
[1]: import math
import numpy as np
import matplotlib.pyplot as plt

from prml.datasets import generate_toy_data
from prml.preprocessing import PolynomialFeature
from prml.linear.linear_regression import LinearRegression
from prml.linear.ridge_regression import RidgeRegression
from prml.distribution import Gaussian, MultivariateGaussian

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'
```

1.1. Example: Polynomial Curve Fitting

For presentation purposes, consider a synthetically generated example dataset. The data were generated from the function $\sin(2\pi x)$ by adding random Gaussian noise having standard deviation $\sigma = 0.3$.

We generated $N = 10$ observations spaced uniformly in range $[0, 1]$. These observations comprise

the input data vector,

$$\mathbf{x} = (x_1, \dots, x_N)^T$$

For each generated observation x we obtained its corresponding value of the function $\sin(2\pi x)$ and then adding the random noise to capture the real-life situation of missing information.

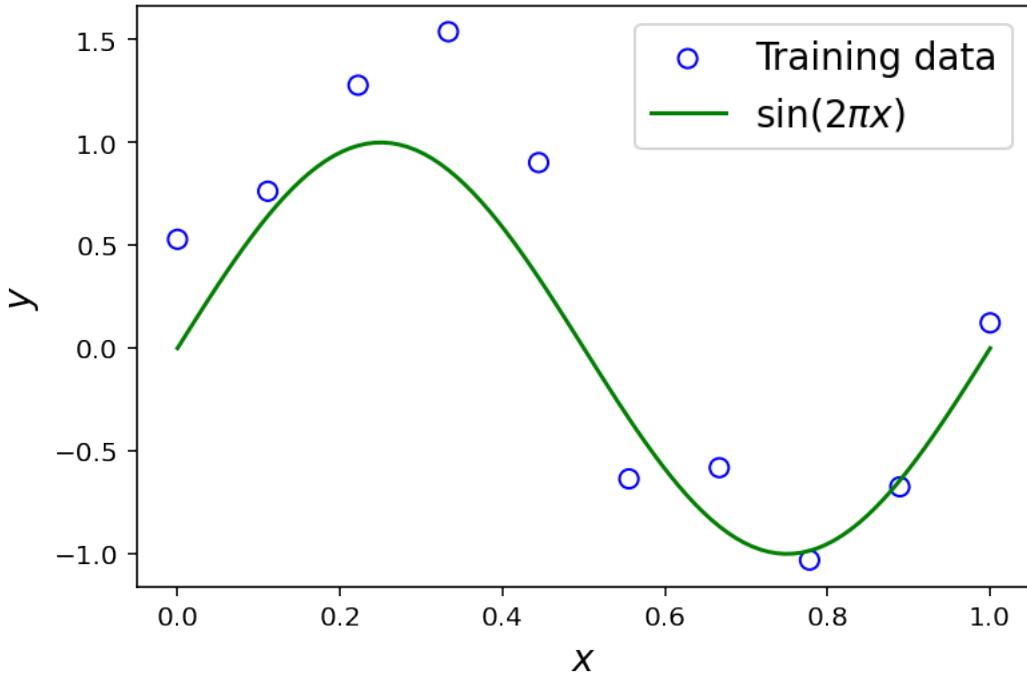
$$\mathbf{t} = (t_1, \dots, t_N)^T$$

```
[2]: # Sine function
def sin(x: np.ndarray) -> np.ndarray:
    return np.sin(2 * np.pi * x)

# Generate a train data set
x_train, y_train = generate_toy_data(sin, 10, 0.3)

# Generate a test data set
x_test = np.linspace(0, 1, 100)
y_test = sin(x_test)

plt.scatter(x_train, y_train, facecolor="none", edgecolor="b", s=50, ▾
            label="Training data")
plt.plot(x_test, y_test, color="g", label="$\sin(2\pi x)$")
plt.xlabel("$x$", fontsize=14)
plt.ylabel("$y$", fontsize=14)
plt.legend(fontsize=14)
plt.show()
```



The generated training dataset of $N = 10$ points is shown as blue circles, each comprising an observation of the input variable x along with the corresponding target variable t . The green curve shows the function $\sin(2\pi x)$ used to generate the data.

Polynomial Linear Model

Our goal is to predict the value of \hat{t} for some **new** value of \hat{x} , in the absence of any knowledge for the green curve. To that end, we consider a simple approach based on curve fitting. In particular, we shall try to fit the data using a polynomial function of the form

$$y(x, \mathbf{w}) = w_0 + w_1 x + w_2 x^2 + \cdots + w_M x^M = \sum_{j=0}^M w_j x^j$$

where M is the *order* of the polynomial. Functions, such as $y(x, \mathbf{w})$, that are linear functions of the unknown coefficients \mathbf{w} , are called *linear models*.

Error Function

Next, we need to determine the values of the coefficients \mathbf{w} by fitting the polynomial to the training data. This can be done by minimizing an *error function* that measures the misfit between the function $y(x, \mathbf{w})$, for a given value of \mathbf{w} , and the training data points.

One simple error function is the *sum of squares of the errors* between $y(x, \mathbf{w})$ and the corresponding target values t_n

$$E(\mathbf{w}) = \frac{1}{2} \sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2 \geq 0$$

where the function becomes zero if, and only if, the function $y(x, \mathbf{w})$ were to pass exactly through each training data point.

We can solve the curve fitting problem by choosing the value of \mathbf{w} for which $E(\mathbf{w})$ is as small as possible. Because the error function is quadratic, its derivatives are linear, and so the minimization of the function has a unique closed form solution, denoted by \mathbf{w}^* . To minimize the error function we should derive the gradient vector, set it equal to zero and solve for \mathbf{w}^* as follows,

$$\nabla E(\mathbf{w}^*) = \mathbf{0}$$

First, we have to substitute the polynomial into the error function

$$E(\mathbf{w}) = \frac{1}{2} \sum_{n=1}^N \left(\sum_{j=0}^M w_j x_n^j - t_n \right)^2$$

Note that each of the N data points from the generated training set has 1 dimension, that is $x \in \mathbb{R}$. However, the polynomial function populates M features for each input x , essentially transforming x into a M -dimensional vector. Thus, the training set \mathbf{x} can be written as a $N \times M$ matrix \mathbf{X} where \mathbf{X}_{nj} represents x_n^j , that is, the n th input value raised in the power of j .

To find the gradient vector, we take the partial derivative of E with respect to an arbitrary w_k . Differentiating the sum, term by term, we get

$$\begin{aligned} \nabla E(\mathbf{w}^*)_k &= \frac{\partial}{\partial w_k} (\mathbf{w}) \\ &= \frac{1}{2} \sum_{n=1}^N 2 \left(\sum_{j=0}^M w_j x_n^j - t_n \right) x_n^k = \sum_{n=1}^N \left(\sum_{j=0}^M w_j x_n^j - t_n \right) x_n^k \\ &= \sum_{n=1}^N (\mathbf{X}\mathbf{w} - \mathbf{t})_n \mathbf{X}_{nk} = \sum_{n=1}^N \mathbf{X}_{kn}^T (\mathbf{X}\mathbf{w} - \mathbf{t})_n \\ &= (\mathbf{X}^T (\mathbf{X}\mathbf{w} - \mathbf{t}))_k \end{aligned}$$

Using the partial derivative for one component, we compute the gradient vector by dropping the k subscript. Thus, the minimizer \mathbf{w}^* must satisfy

$$\nabla E(\mathbf{w}^*) = \mathbf{X}^T (\mathbf{X}\mathbf{w}^* - \mathbf{t}) = \mathbf{0}$$

Solving for \mathbf{w}^* gives the unique solution of the curve fitting problem

$$\mathbf{X}^T (\mathbf{X}\mathbf{w}^* - \mathbf{t}) = \mathbf{0} \Leftrightarrow \mathbf{X}^T \mathbf{X}\mathbf{w}^* = \mathbf{X}^T \mathbf{t} \Leftrightarrow \mathbf{w}^* = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{t}$$

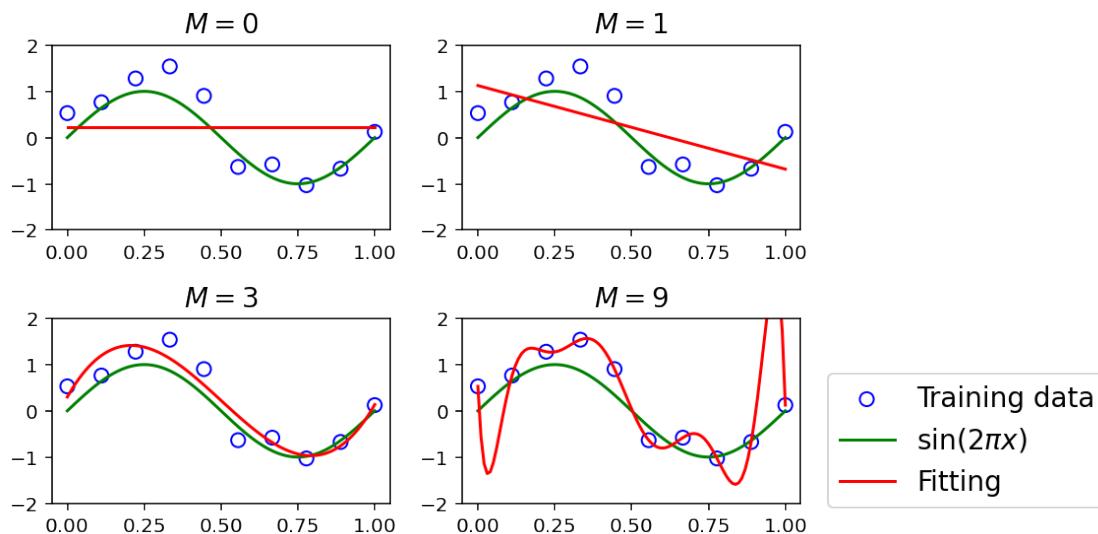
The resulting polynomial is given by the function $y(x, \mathbf{w}^*)$.

Model Selection

There remains the problem of choosing the order M of the polynomial, which is an example of the important concept called *model selection*.

In order to study the effect of different M values, we plot the result of fitting polynomials having orders $M = 0, 1, 3, 9$ to the data set.

```
[3]: for i, degree in enumerate([0, 1, 3, 9]):  
    plt.subplot(2, 2, i + 1)  
    plt.tight_layout()  
  
    feature = PolynomialFeature(degree)  
    x_train_features = feature.transform(x_train)  
    x_test_features = feature.transform(x_test)  
  
    model = LinearRegression()  
    model.fit(x_train_features, y_train)  
    y, _ = model.predict(x_test_features)  
  
    plt.scatter(x_train, y_train, facecolor="none", edgecolor="b", s=50, ▾  
    label="Training data")  
    plt.plot(x_test, y_test, color="g", label="$\sin(2\pi x)$")  
    plt.plot(x_test, y, color="r", label="Fitting")  
    plt.ylim(-2, 2)  
    plt.title("$M={}$".format(degree), fontsize=14)  
  
plt.legend(bbox_to_anchor=(1, 0.85), loc=2, borderaxespad=1, fontsize=14)  
plt.show()
```



Note that the constant ($M = 0$) and first order ($M = 1$) polynomials give rather poor fits to the data. The third order ($M = 3$) polynomial seems to give the best fit, while the higher order one ($M = 9$) achieves an excellent fit to the data, that is, $E(\mathbf{w}^*) = \mathbf{0}$. However, the fitted curve gives a poor representation of the underlying function $\sin(2\pi x)$. This phenomenon is known as *over-fitting*.

A more quantitative insight into the generalization performance on M can be obtained by using the *root-mean-square* (RMS) error defined as

$$E_{RMS} = \sqrt{2 \frac{E(\mathbf{w}^*)}{N}}$$

The RMS error on both training and test data points for each value of M is shown in the following figure:

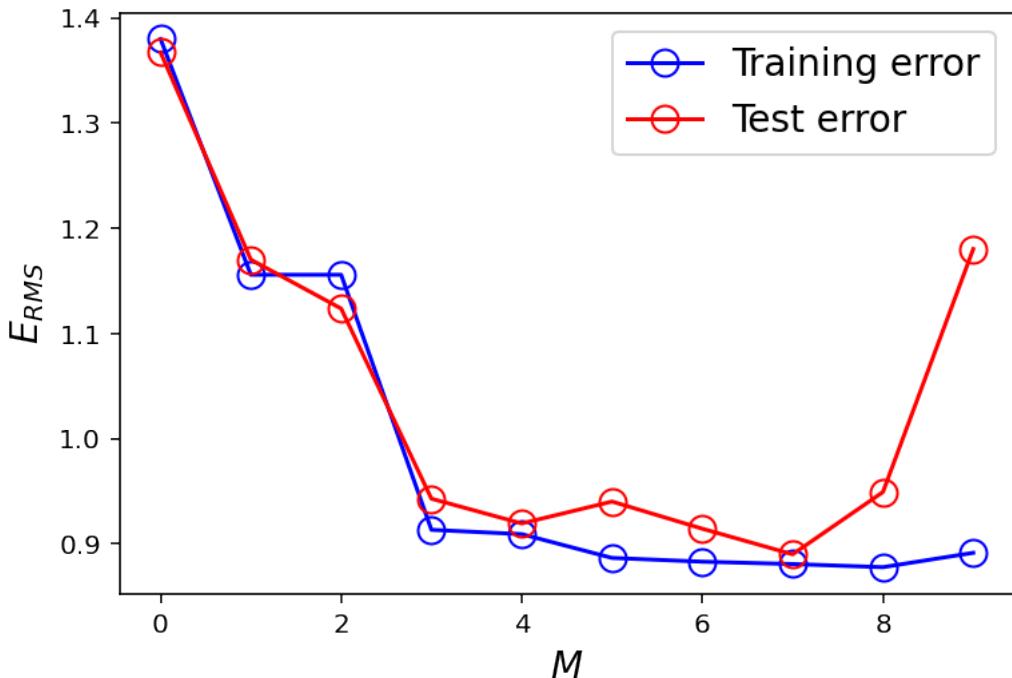
```
[4]: def rms_error(a, b):
    return np.sqrt(2 * np.mean(np.square(a - b)))

training_errors = []
test_errors = []

for i in range(10):
    feature = PolynomialFeature(i)
    x_train_features = feature.transform(x_train)
    x_test_features = feature.transform(x_test)

    model = LinearRegression()
    model.fit(x_train_features, y_train)
    y, _ = model.predict(x_test_features)
    training_errors.append(rms_error(model.predict(x_train_features), y_train))
    test_errors.append(
        rms_error(model.predict(x_test_features), y_test + np.random.
        ~normal(scale=0.3, size=len(y_test)))
    )

plt.plot(training_errors, "o-", mfc="none", mec="b", ms=10, c="b",_
         label="Training error")
plt.plot(test_errors, "o-", mfc="none", mec="r", ms=10, c="r", label="Test error")
plt.xlabel("$M$", fontsize=14)
plt.ylabel("$E_{RMS}$", fontsize=14)
plt.legend(fontsize=14)
plt.show()
```



The test set error is measuring how well we are doing in predicting the values of t for new data observations of x . For $M = 9$, the training set error goes to zero, because the polynomial contains 10 degrees of freedom and so it can be tuned exactly to the 10 data points in the training set.

It is also interesting to examine the behavior of the model as the size of the data increases. The following figure depicts the result of fitting the $M = 9$ polynomial for $N = 15$ and $N = 100$ data points.

```
[5]: for i, size in enumerate([15, 100]):
    plt.subplot(1, 2, i + 1)

    # Generate a train set
    x_train_100, y_train_100 = generate_toy_data(sin, size, 0.3)

    # Generate a test set
    x_test_100 = np.linspace(0, 1, 100)
    y_test_100 = sin(x_test)

    feature = PolynomialFeature(9)
    x_train_100_features = feature.transform(x_train_100)
    x_test_100_features = feature.transform(x_test_100)

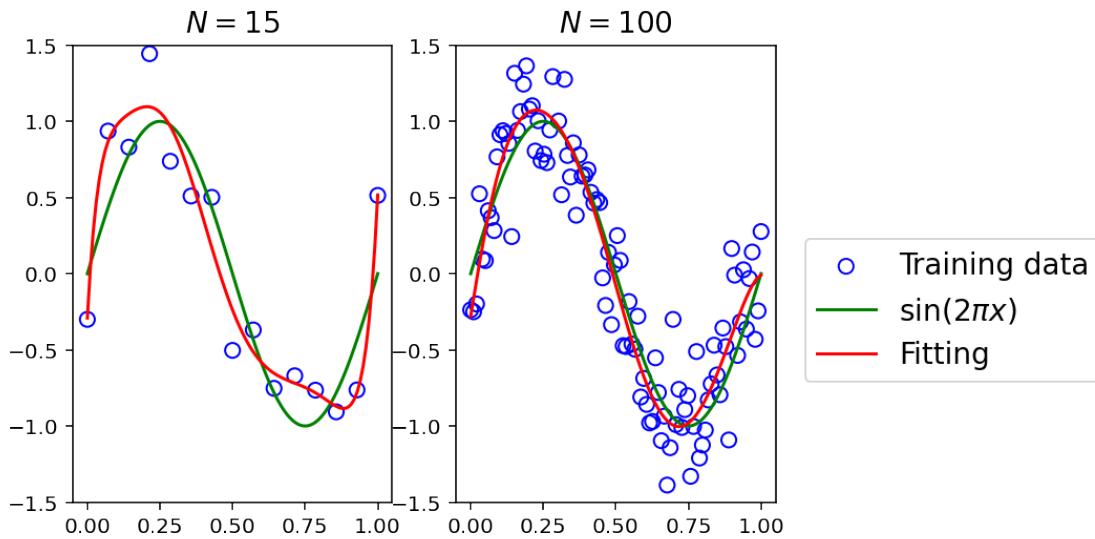
    model = LinearRegression()
    model.fit(x_train_100_features, y_train_100)
    y, _ = model.predict(x_test_100_features)
```

```

plt.scatter(x_train_100, y_train_100, facecolor="none", edgecolor="b", s=50, label="Training data")
plt.plot(x_test_100, y_test_100, color="g", label="$\sin(2\pi x)$")
plt.plot(x_test_100, y, color="r", label="Fitting")
plt.ylim(-1.5, 1.5)
plt.title("$N={}$".format(size), fontsize=14)

plt.legend(bbox_to_anchor=(1, 0.64), loc=2, borderaxespad=1, fontsize=14)
plt.show()

```



Note that the over-fitting problem becomes less severe as the size of the data set increases. In other words, the larger the data set, the more complex the model that we can afford to fit to the data.

Regularization

One technique that is often used to control the over-fitting phenomenon is that of *regularization*, which adds a penalty term to the error function in order to discourage the coefficients from reaching large values. The simplest such penalty term is the sum of squares of all of the coefficients, leading to a modified error function of the following form

$$\tilde{E}(\mathbf{w}) = \frac{1}{2} \sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2 + \lambda \|\mathbf{w}\|_2^2$$

Such techniques are known as *shrinkage* methods because they reduce the value of the coefficients. The particular case of the quadratic regularization is called *ridge regression*. In neural networks, this approach is also known as *weight decay*.

Similar to the previous case, the ridge error function can be minimized exactly in closed form as follows,

$$\begin{aligned}
\nabla E(\mathbf{w}^*)_k &= \frac{\partial}{\partial w_k}(\mathbf{w}) \\
&= \frac{1}{2} \sum_{n=1}^N 2 \left(\sum_{j=0}^M w_j x_n^j - t_n \right) x_n^k + \frac{1}{2} \lambda 2 w_k \\
&= \sum_{n=1}^N \left(\sum_{j=0}^M w_j x_n^j - t_n \right) x_n^k + \lambda w_k \\
&= \sum_{n=1}^N (\mathbf{X}\mathbf{w} - \mathbf{t})_n \mathbf{X}_{nk} + \lambda w_k = \sum_{n=1}^N \mathbf{X}_{kn}^T (\mathbf{X}\mathbf{w} - \mathbf{t})_n + \lambda w_k \\
&= (\mathbf{X}^T (\mathbf{X}\mathbf{w} - \mathbf{t}))_k + \lambda w_k
\end{aligned}$$

Using the partial derivative for one component, we compute the gradient vector by dropping the k subscript. Then, the minimizer \mathbf{w}^* must satisfy

$$\nabla E(\mathbf{w}^*) = \mathbf{X}^T (\mathbf{X}\mathbf{w}^* - \mathbf{t}) + \lambda \mathbf{w}^* \mathbf{I} = \mathbf{0}$$

Solving for \mathbf{w}^* gives the unique solution that minimizes the ridge error

$$\begin{aligned}
\mathbf{X}^T (\mathbf{X}\mathbf{w}^* - \mathbf{t}) + \lambda \mathbf{w}^* \mathbf{I} &= \mathbf{0} \Leftrightarrow \\
\mathbf{X}^T \mathbf{X}\mathbf{w}^* - \mathbf{X}^T \mathbf{t} + \lambda \mathbf{w}^* \mathbf{I} &= \mathbf{0} \Leftrightarrow \\
\mathbf{X}^T \mathbf{X}\mathbf{w}^* + \lambda \mathbf{w}^* \mathbf{I} &= \mathbf{X}^T \mathbf{t} \Leftrightarrow \\
\mathbf{w}^* (\mathbf{X}^T \mathbf{X} + \lambda \mathbf{I}) &= \mathbf{X}^T \mathbf{t} \Leftrightarrow \\
\mathbf{w}^* &= (\mathbf{X}^T \mathbf{X} + \lambda \mathbf{I})^{-1} \mathbf{X}^T \mathbf{t}
\end{aligned}$$

The following figures depict the results of fitting the polynomial of order $M = 9$ to the same data set as before but this time using the regularized error function. We see that, for a value of $\ln \lambda = -18$, the over-fitting has been suppressed and we obtain a much closer representation of the underlying function $\sin(2\pi x)$. If, however, we use too large a value for λ then we again obtain a poor fit.

```
[6]: feature = PolynomialFeature(9)
x_train_features = feature.transform(x_train)
x_test_features = feature.transform(x_test)

for i, ln_lambda in enumerate([float("-inf"), -18, 0]):
    plt.subplot(1, 3, i + 1)
    plt.tight_layout()

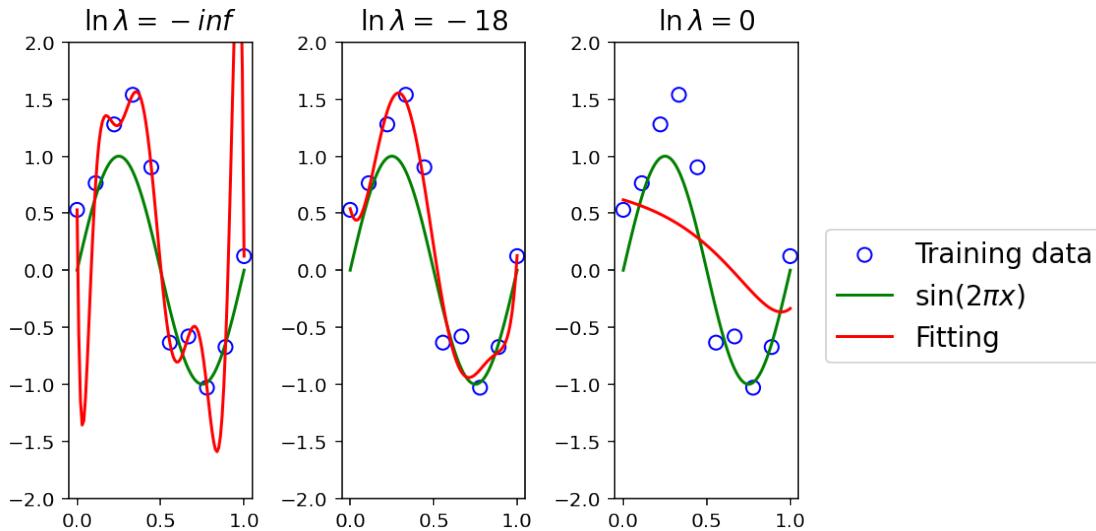
    model = RidgeRegression(alpha=math.exp(ln_lambda))
    model.fit(x_train_features, y_train)
    y, _ = model.predict(x_test_features)
```

```

plt.scatter(x_train, y_train, facecolor="none", edgecolor="b", s=50, u
label="Training data")
plt.plot(x_test, y_test, color="g", label="$\sin(2\pi x)$")
plt.plot(x_test, y, color="r", label="Fitting")
plt.ylim(-2, 2)
plt.title("$\ln\lambda={}$.format(ln_lambda), fontsize=14)

plt.legend(bbox_to_anchor=(1, 0.65), loc=2, borderaxespad=1, fontsize=14)
plt.show()

```



A sample of coefficients from the fitted polynomials is presented in the table below, showing that regularization has the desired effect of reducing the magnitude of the coefficients.

$\ln \lambda = -\infty$	$\ln \lambda = -18$	$\ln \lambda = 0$
0.39	0.38	0.36
-135.04	-2.14	-0.46
3206.76	81.88	-0.39
-29215.92	-390.51	-0.22
139594.34	578.12	-0.05
-388863.80	-31.48	0.07
652373.24	-49.12	0.17
-648124.69	-28.57	0.25
350721.94	540.17	0.31
-79556.29	-255.65	0.35

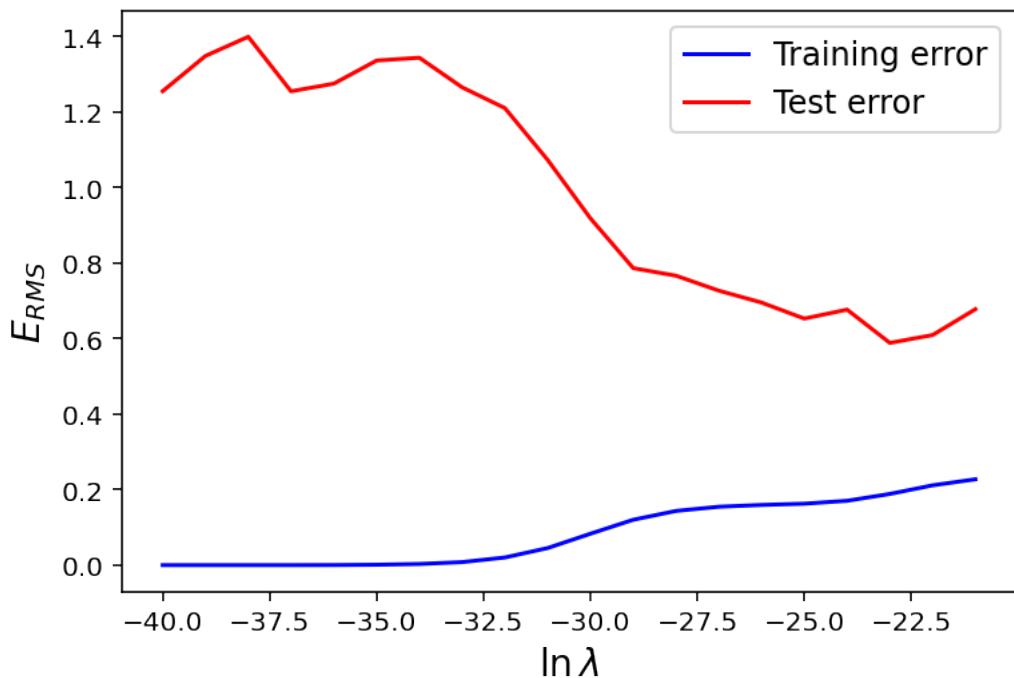
The impact of the regularization term on the generalization error can be seen by plotting the value of the RMS error for both training and test sets against $\ln \lambda$, as shown in the next figure. We see that λ controls the effective complexity of the model and hence determines the degree of over-fitting.

```
[7]: training_errors = []
test_errors = []

feature = PolynomialFeature(9)
x_train_features = feature.transform(x_train)
x_test_features = feature.transform(x_test)

ln_lambda_values = range(-40, -20, 1)
for ln_lambda in ln_lambda_values:
    model = RidgeRegression(alpha=math.exp(ln_lambda))
    model.fit(x_train_features, y_train)
    training_errors.append(rms_error(model.predict(x_train_features)[0], y_train))
    test_errors.append(
        rms_error(model.predict(x_test_features)[0], y_test + np.random.normal(scale=0.3, size=len(y_test)))
    )

plt.plot(ln_lambda_values, training_errors, mfc="none", mec="b", ms=10, c="b", label="Training error")
plt.plot(ln_lambda_values, test_errors, mfc="none", mec="r", ms=10, c="r", label="Test error")
plt.xlabel("$\ln\lambda$", fontsize=14)
plt.ylabel("$E_{RMS}$", fontsize=14)
plt.legend(fontsize=12)
plt.show()
```



1.2 Probability Theory

The probability $p(A)$ of an event A is always a non-negative number, i.e.,

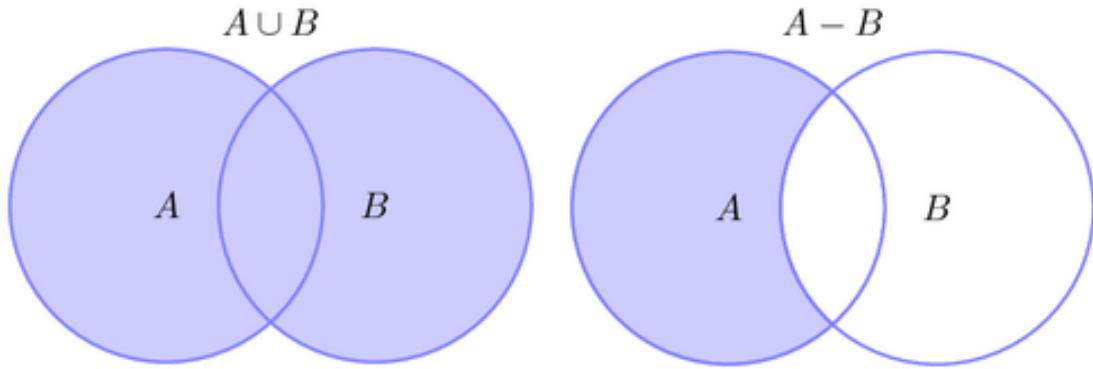
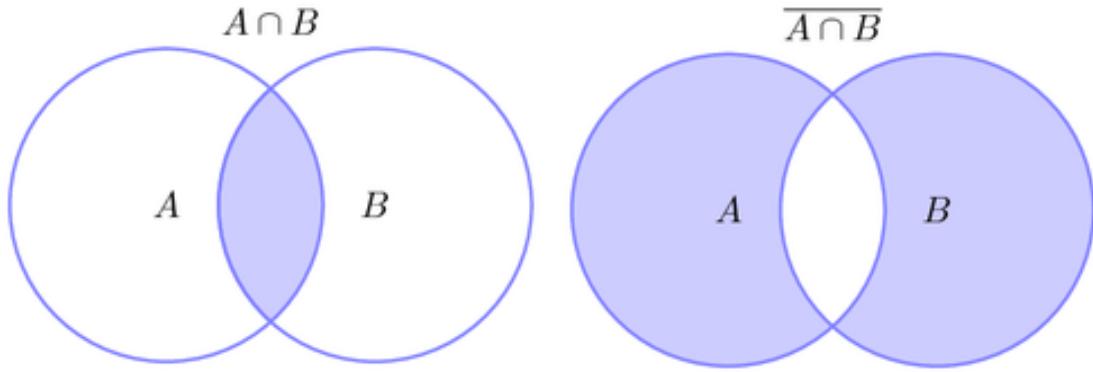
$$p(A) \geq 0$$

The probability $p(B)$ of an event B which is certain to occur is always equal to one, i.e.,

$$p(B) = 1$$

In case two events A and B are **mutually exclusive**, that is, they cannot occur simultaneously $p(A \cap B) = 0$, then the probability of occurrence of either A or B is denoted as $A \cup B$ and is given by

$$p(A \cup B) = p(A) + p(B) - 2p(A \cap B) = p(A) + p(B)$$



Rules of Probability

Consider the slightly more general example involving two random variables X and Y instead of just two events (which are essentially binary random variables). Suppose that X can take any of the values x_i , and Y can take the values y_j . Moreover, consider a total of N trials, and let the number of such trials in which $X = x_i$ and $Y = y_j$ be n_{ij} . Also, let the number of trials in which X takes the value x_i (irrespective of the value that Y takes) be denoted by c_i , and similarly let the number of trials in which Y takes the value y_j be denoted by r_j .

Then the **marginal**, **conditional** and **joint probabilities** are given by

$$p(X = x_i) = \frac{c_i}{N} \quad p(Y = y_j) = \frac{r_j}{N} \quad p(X = x_i, Y = y_j) = \frac{n_{ij}}{N} \quad p(Y = y_j | X = x_i) = \frac{r_j}{c_i}$$

Note that the joint probability $p(X = x_i, Y = y_j)$ is short notation for $p(X = x_i \cap Y = y_j)$.

Sum rule:

$$p(X) = \sum_Y p(X, Y) = \int_Y p(X, Y) dY$$

Applying the sum rule as above is called “marginalizing out Y ”.

Product rule:

$$p(X, Y) = p(Y|X)p(X)$$

Computing $p(Y|X)$ is called “conditioning on X ”. The product rule is generalized as follows

$$p(X_1, X_2, \dots, X_K) = p(X_K|X_{K-1}, \dots, X_1)p(X_{K-1}, \dots, X_1), \dots$$

Note that if the *joint distribution* of two random variables factorizes into the product of their marginals, so that $p(X, Y) = p(X)p(Y)$, then X and Y are said to be *statistically independent*. In such case, the product rule becomes $p(Y|X) = p(Y)$.

Bayes Theorem

From the *product rule*, we can immediately obtain the *Bayes’ theorem*, using the symmetry property $p(X, Y) = p(Y, X)$ as follows

$$\begin{aligned} p(X, Y) &= p(Y|X)p(X) \Leftrightarrow \\ p(Y|X) &= \frac{p(X, Y)}{p(X)} \Leftrightarrow \\ p(Y|X) &= \frac{p(Y, X)}{p(X)} \Leftrightarrow \\ p(Y|X) &= \frac{p(X|Y)p(Y)}{p(X)} \end{aligned}$$

Using the *sum* and *product rules*, the marginal probability $p(X)$ in the denominator can be expressed in terms of the quantities in the numerator

$$p(Y|X) = \frac{p(X|Y)p(Y)}{\sum_Y p(X, Y)} = \frac{p(X|Y)p(Y)}{\sum_Y p(X|Y)p(Y)}$$

An interpretation of the Bayes theorem is that if we had been asked which is the most probable value of Y , *before* we observe any value for X , then the most complete information we have available is provided by the *prior probability* $p(Y)$. *After* we observe the value of X , we can use the Bayes theorem to compute the the *posterior* probability $p(Y|X)$, which represents our updated knowledge after incorporating the evidence provided by the observed data.

Let \mathbf{w} be parameters and \mathcal{D} be data. Bayes theorem is given by

$$p(\mathbf{w}|\mathcal{D}) = \frac{p(\mathcal{D}|\mathbf{w})p(\mathbf{w})}{p(\mathcal{D})} \Leftrightarrow \text{posterior} = \frac{\text{likelihood} \times \text{prior}}{\text{evidence}}$$

The frequentist paradigm generally quantifies the properties of data driven quantities in the light of the fixed model parameters, while the Bayesian paradigm generally quantifies the properties of unknown model parameters in light of observed data.

1.2.1 Probability densities

If the probability of a real-valued variable x falling in the interval $(u, u + \delta)$ is given by $p_x(u)\delta$, then $p_x(x)$ is called the probability density function over x .

$$p(u \leq x \leq u + \delta) = \int_u^{u+\delta} p(x)dx = P_x(u + \delta) - P_x(u) = \frac{P_x(u + \delta) - P_x(u)}{\delta} \delta$$

Then we have that

$$\lim_{\delta \rightarrow 0} \frac{P_x(u + \delta) - P_x(u)}{\delta} \delta = \frac{dP_x(u)}{dx} \delta = p_x(u) \delta$$

Therefore, the probability that x will lie in an interval (a, b) is then given by

$$p(a \leq x \leq b) = \int_a^b p_x(x)dx$$

and it must satisfy the following two conditions

$$\begin{aligned} p_x(x) &\geq 0 \\ \int_{-\infty}^{\infty} p_x(x)dx &= 1 \end{aligned}$$

The probability that x lies in the interval $(-\infty, z)$ is given by the *cumulative distribution function* (CDF) given by

$$P_x(z) = \int_{-\infty}^z p_x(x)dx$$

where

$$p(x) = \frac{dP_x(x)}{dx}$$

If x is a discrete variable, then $p_x(x)$ is sometimes called a *probability mass function* (PMF) because it can be regarded as a set of *probability masses* concentrated at the allowed values of x .

1.2.2 Expectations and covariances

The average value of some function $f(x)$ under a probability distribution $p_x(x)$ is called the *expectation* of $f(x)$ and is denoted by $\mathbb{E}[f]$. The average is weighted by the relative probabilities of the different values of x as follows

$$\mathbb{E}[f] = \sum_x p_x(x)f(x) = \int p_x(x)f(x)dx$$

For a finite number of N points drawn from the probability distribution, then the expectation can be approximated as a finite sum over these points

$$\mathbb{E}[f] \approx \frac{1}{N} \sum_{n=1}^N f(x_n)$$

Note that the expectations of functions of several variables, may use a subscript to indicate which variable is being averaged, i.e., $\mathbb{E}_x[f(x, y)]$.

Whereas the expectation provides a measure of centrality, the variance of a random variable quantifies the spread of that random variable's distribution. Thus, the variance provides a measure of how much variability there is in $f(x)$ around its mean value $\mathbb{E}[f(x)]$ and is defined as follows

$$\begin{aligned}\text{var}[f] &= \mathbb{E}[(f(x) - \mathbb{E}[f(x)])^2] \\ &= \mathbb{E}[f(x)^2 - 2f(x)\mathbb{E}[f(x)] + \mathbb{E}[f(x)]^2] \\ &= \mathbb{E}[f(x)^2] - \mathbb{E}[2f(x)\mathbb{E}[f(x)]] + \mathbb{E}[\mathbb{E}[f(x)]^2] \\ &= \mathbb{E}[f(x)^2] - 2\mathbb{E}[f(x)]\mathbb{E}[f(x)] + \mathbb{E}[f(x)]^2 \\ &= \mathbb{E}[f(x)^2] - \mathbb{E}[f(x)]^2\end{aligned}$$

The covariance expresses the extent to which x and y vary together and is given by

$$\text{cov}[x, y] = \mathbb{E}_{x,y}[(x - \mathbb{E}[x])(y - \mathbb{E}[y])] = \mathbb{E}_{x,y}[xy] - \mathbb{E}[x]\mathbb{E}[y]$$

A covariance matrix has entries σ_{ij} corresponding to the covariance of variables i and j . If two variables are independent, then their covariance vanishes, e.g., $\text{cov}[x, y] = \mathbf{I}$.

1.2.4 The Gaussian distribution

The *Normal* or *Gaussian* distribution is one of the most important probability distributions for continuous variables. For the case of a single real-valued variable x , the distribution is defined as follows

$$\mathcal{N}(x|\mu, \sigma^2) = \frac{1}{(2\pi\sigma^2)^{1/2}} \exp\left\{-\frac{1}{2\sigma^2}(x-\mu)^2\right\}$$

and is governed by the parameters μ , called the *mean*, and σ^2 , called the *variance*. The square root of the variance σ is called *standard deviation*. An alternative way to represent a Gaussian distribution is by considering a *precision* term $\beta = \frac{1}{\sigma^2}$, denoted by

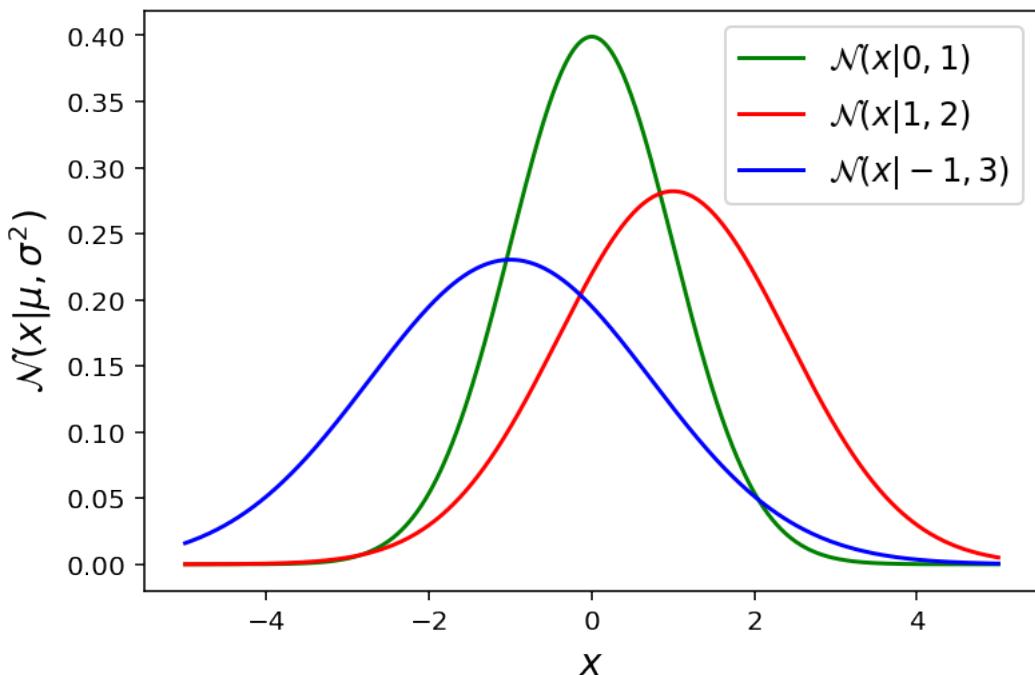
$$\mathcal{N}(x|\mu, \beta^{-1}) = \frac{\beta^{1/2}}{\sqrt{2\pi\sigma^2}} \exp \left\{ -\frac{\beta}{2}(x - \mu)^2 \right\}$$

```
[8]: x_space = np.linspace(-5, 5, 1000)

for mean, var, c in [(0, 1, "g"), (1, 2, "r"), (-1, 3, "b")]:
    N_distribution = Gaussian(mean, var)
    y = [N_distribution.pdf(x) for x in x_space]

    plt.plot(x_space, y, color=c, label="$\mathcal{N}(x|\mu, \sigma^2)$".
              format(mean, var))

plt.xlabel("$x$", fontsize=14)
plt.ylabel("$\mathcal{N}(x|\mu, \sigma^2)$", fontsize=14)
plt.legend(fontsize=12)
plt.show()
```



Note that the probability density function is *not an actual probability*, therefore it can take values $\mathcal{N}(x|\mu, \sigma^2) > 1$. We can see that the Gaussian distribution satisfies

$$\begin{aligned} \mathcal{N}(x|\mu, \sigma^2) &> 0 \\ \int \mathcal{N}(x|\mu, \sigma^2) dx &= 1 \end{aligned}$$

The Gaussian distribution can be also defined over a D -dimensional vector \mathbf{x} of continuous variables as follows:

$$\mathcal{N}(\mathbf{x} | \mu, \Sigma) = \frac{1}{(2\pi)^{D/2} |\Sigma|^{1/2}} \exp \left\{ -\frac{1}{2} (\mathbf{x} - \mu)^T \Sigma^{-1} (\mathbf{x} - \mu) \right\}$$

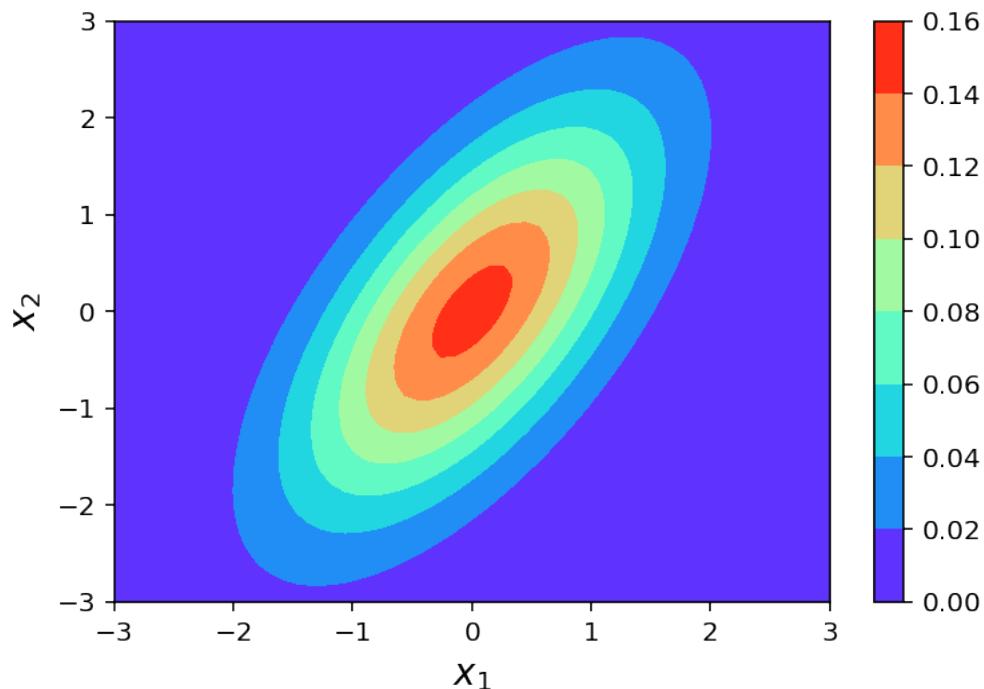
where the D -dimensional vector μ holds the mean of each dimension, while the $D \times D$ matrix Σ is the covariance.

```
[9]: mean = np.array([0, 0])
sigma = np.array([[1.0, 0.92], [0.92, 2.0]])

N_distribution = MultivariateGaussian(mean, sigma)

N = 100
x1, x2 = np.meshgrid(np.linspace(-5, 5, N), np.linspace(-5, 5, N))
p = np.zeros((N, N))
for i in range(N):
    for j in range(N):
        p[i, j] = N_distribution.pdf(np.array([x1[i, j], x2[i, j]]))

cp = plt.contourf(x1, x2, p, cmap="rainbow")
plt.colorbar(cp)
plt.xlabel("$x_1$", fontsize=14)
plt.ylabel("$x_2$", fontsize=14)
plt.axis([-3, 3, -3, 3])
plt.show()
```



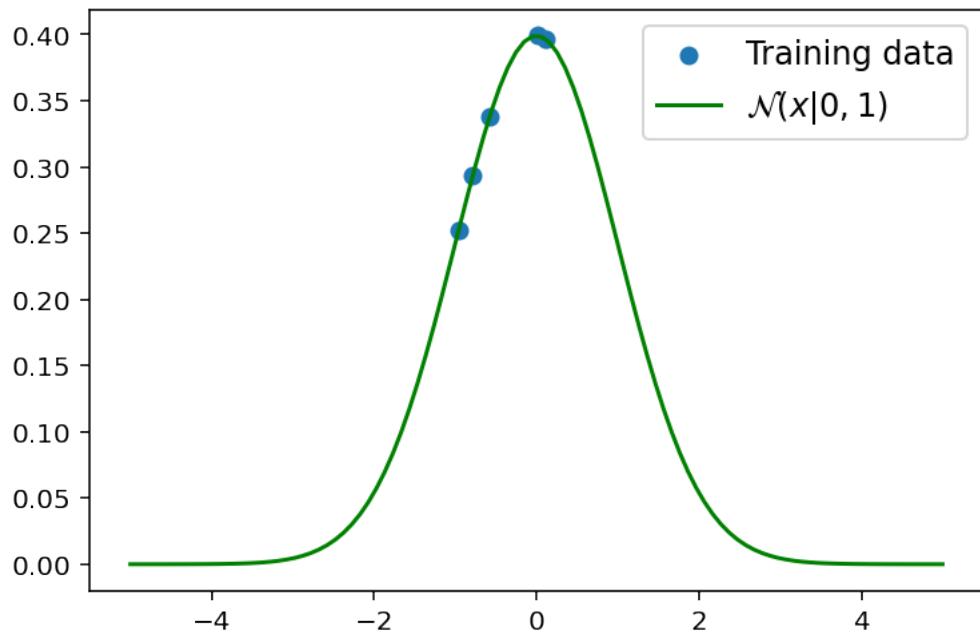
Maximum likelihood

Consider we have a data set of observations $\mathbf{x} = (x_1, \dots, x_N)^T$ drawn independently from a Gaussian distribution. Data points that are drawn independently from the same distribution are said to be *independent and identically distributed*.

```
[10]: N_distribution = Gaussian(0, 1)
x_sample_data = N_distribution.draw(5)
y_sample_data = [N_distribution.pdf(x) for x in x_sample_data]

x_space = np.linspace(-5, 5, 100)
y = [N_distribution.pdf(x) for x in x_space]

plt.scatter(x_sample_data, y_sample_data, label="Training data")
plt.plot(x_space, y, color="g", label="$\mathcal{N}(x|0, 1)$")
plt.legend(fontsize=12)
plt.show()
```



Because the data are independent, the likelihood function of the univariate Gaussian is as follows,

$$p(\mathbf{x}|\mu, \sigma^2) = \prod_{n=1}^N \mathcal{N}(x_n|\mu, \sigma^2)$$

which corresponds to the product of the blue points in the figure above. Therefore, in order to find the unknown parameters μ and σ^2 is to use the observed data set and find the parameter values that maximize the likelihood function.

The log likelihood function can be written as follows

$$\begin{aligned}
 \ln p(\mathbf{x}|\mu, \sigma^2) &= \ln \left[\prod_{n=1}^N \mathcal{N}(x_n|\mu, \sigma^2) \right] \\
 &= \sum_{n=1}^N \ln \mathcal{N}(x_n|\mu, \sigma^2) \\
 &\stackrel{(1.46)}{=} \sum_{n=1}^N \ln \left(\frac{1}{(2\pi\sigma^2)^{1/2}} \exp \left\{ -\frac{1}{2\sigma^2}(x_n - \mu)^2 \right\} \right) \\
 &= \sum_{n=1}^N \ln \left(\frac{1}{(2\pi\sigma^2)^{1/2}} \right) + \sum_{n=1}^N \ln \left(\exp \left\{ -\frac{1}{2\sigma^2}(x_n - \mu)^2 \right\} \right) \\
 &= N \ln \left(\frac{1}{(2\pi\sigma^2)^{1/2}} \right) - \sum_{n=1}^N \frac{1}{2\sigma^2}(x_n - \mu)^2 \\
 &= N \ln 1 - N \ln(2\pi\sigma^2)^{1/2} - \frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2 \\
 &\stackrel{\ln 1 = 0}{=} -N \ln(2\pi\sigma^2)^{1/2} - \frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2 \\
 &\stackrel{\ln x^y = y \ln x}{=} -\frac{N}{2} \ln 2\pi\sigma^2 - \frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2 \\
 &= -\frac{N}{2} \ln 2\pi - \frac{N}{2} \ln \sigma^2 - \frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2
 \end{aligned}$$

In the machine learning literature, the negative log of the likelihood function is called an error function. Since the negative logarithm is a monotonically decreasing function, maximizing the likelihood is equivalent to minimizing the error. The following figure depicts the likelihood of μ against σ^2 .

```
[11]: mu_space = np.linspace(-1, 1, 100)
var_space = np.linspace(0, 2, 100)
mu_mesh, var_mesh = np.meshgrid(mu_space, var_space)
ll = np.zeros((mu_space.size, var_space.size))

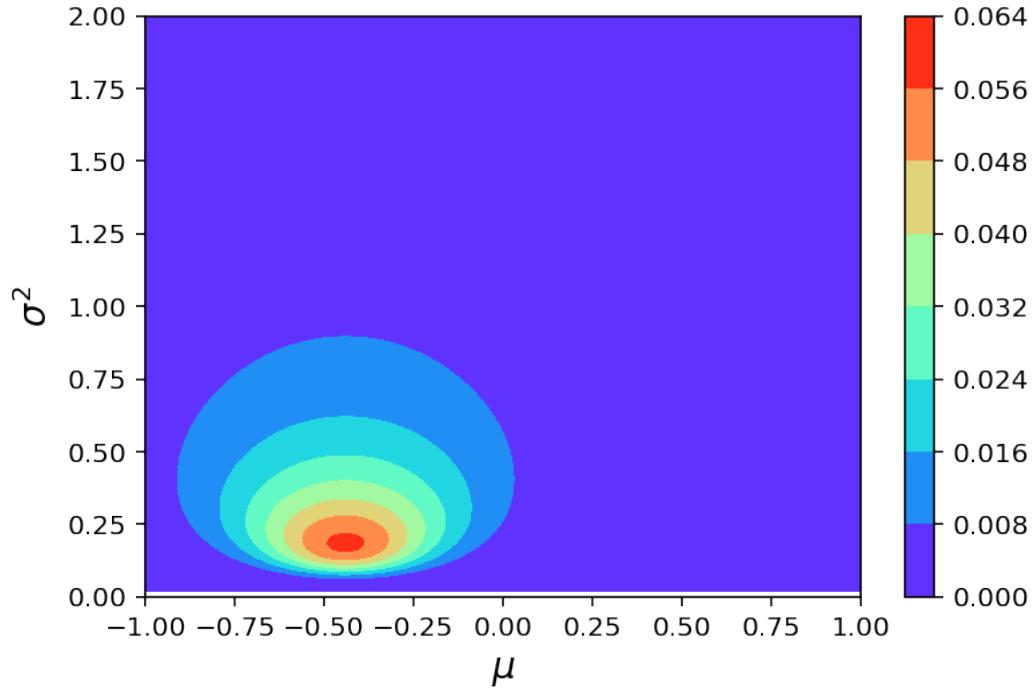
for i, mu in enumerate(mu_space):
    for j, var in enumerate(var_space):
        ll[i, j] = Gaussian(mu, var).likelihood_iid(x_sample_data)

cp = plt.contourf(mu_mesh, var_mesh, ll.T, cmap="rainbow")
plt.colorbar(cp)
plt.xlim(-1, 1)
```

```

plt.ylim(0, 2)
plt.xlabel("$\mu$", fontsize=14)
plt.ylabel("$\sigma^2$ ", fontsize=14)
plt.show()

```



Then by maximizing with respect to μ , we obtain the following solution

$$\begin{aligned}
\frac{\partial \ln p(\mathbf{x}|\mu, \sigma^2)}{\partial \mu} = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \mu} \left(\frac{N}{2} \ln 2\pi - \frac{N}{2} \ln \sigma^2 - \frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2 \right) = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \mu} \left(\frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2 \right) = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \mu} \sum_{n=1}^N (x_n - \mu)^2 = 0 &\Leftrightarrow \\
\sum_{n=1}^N (2\mu - 2x_n) = 0 &\Leftrightarrow 2 \sum_{n=1}^N (\mu - x_n) = 0 \Leftrightarrow \\
N\mu - \sum_{n=1}^N x_n = 0 &\Leftrightarrow N\mu = \sum_{n=1}^N x_n \Leftrightarrow \\
\mu_{ML} = \frac{1}{N} \sum_{n=1}^N x_n
\end{aligned}$$

which is the *sample mean* of the observed values \mathbf{x} . In a similar manner, maximizing with respect to σ^2 , we obtain the maximum likelihood solution for the variance as follows

$$\begin{aligned}
\frac{\partial \ln p(\mathbf{x}|\mu, \sigma^2)}{\partial \sigma^2} = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \sigma^2} \left(\frac{N}{2} \ln 2\pi - \frac{N}{2} \ln \sigma^2 - \frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2 \right) = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \sigma^2} \left(-\frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2 - \frac{N}{2} \ln \sigma^2 \right) = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \sigma^2} \left(-\frac{1}{2\sigma^2} \sum_{n=1}^N (x_n - \mu)^2 \right) + \frac{\partial}{\partial \sigma^2} \left(-\frac{N}{2} \ln \sigma^2 \right) = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \sigma^2} \left(-(2\sigma^2)^{-1} \sum_{n=1}^N (x_n - \mu)^2 \right) + -\frac{N}{2\sigma^2} = 0 &\Leftrightarrow \\
\frac{1}{4\sigma^4} \sum_{n=1}^N (x_n - \mu)^2 - \frac{N}{2\sigma^2} = 0 &\Leftrightarrow \\
\frac{1}{4\sigma^4} \sum_{n=1}^N (x_n - \mu)^2 = \frac{N}{2\sigma^2} &\Leftrightarrow \\
\sigma_{ML}^2 = \frac{1}{N} \sum_{n=1}^N (x_n - \mu_{ML})^2
\end{aligned}$$

which is the *sample variance* measured with respect to the sample mean μ_{ML} .

A problem that arises in the context of our solutions for the maximum likelihood approach is that it systematically underestimates the variance of the Gaussian distribution. This is an example of

a phenomenon called bias and is related to the problem of over-fitting encountered in the context of polynomial curve fitting. First note that the maximum likelihood solutions μ_{ML} and σ_{ML} are functions of the data set values x_n . Now, consider the expectations of these quantities with respect to the data set values, which themselves come from a Gaussian distribution with parameters μ and σ^2 , given by

$$\mathbb{E}[\mu_{ML}] = \mathbb{E}\left[\frac{1}{N} \sum_{n=1}^N x_n\right] = \frac{1}{N} \sum_{n=1}^N \mathbb{E}[x_n] = \frac{1}{N} N\mu = \mu$$

and

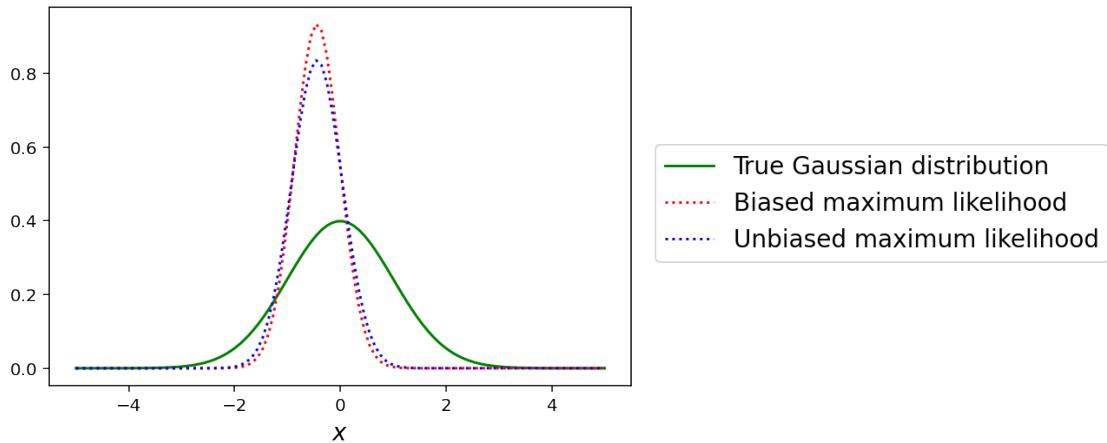
$$\begin{aligned} \mathbb{E}[\sigma_{ML}^2] &= \mathbb{E}\left[\frac{1}{N} \sum_{n=1}^N (x_n - \mu_{ML})^2\right] \\ &= \frac{1}{N} \mathbb{E}\left[\sum_{n=1}^N (x_n - \mu_{ML})^2\right] \\ &= \frac{1}{N} \mathbb{E}\left[\sum_{n=1}^N (x_n^2 - 2x_n\mu_{ML} + \mu_{ML}^2)\right] \\ &= \frac{1}{N} \left(\mathbb{E}\left[\sum_{n=1}^N x_n^2\right] - \mathbb{E}\left[\sum_{n=1}^N 2x_n\mu_{ML}\right] + \mathbb{E}\left[\sum_{n=1}^N \mu_{ML}^2\right] \right) \\ &\stackrel{(1.50)}{=} \mu^2 + \sigma^2 - \frac{1}{N} \left(\mathbb{E}\left[\sum_{n=1}^N 2x_n\mu_{ML}\right] + \mathbb{E}\left[\sum_{n=1}^N \mu_{ML}^2\right] \right) \\ &\stackrel{(1.55)}{=} \mu^2 + \sigma^2 - \frac{2}{N} \mathbb{E}\left[\sum_{n=1}^N x_n \left(\frac{1}{N} \sum_{n=1}^N x_n\right)\right] + \mathbb{E}\left[\left(\frac{1}{N} \sum_{n=1}^N x_n\right)^2\right] \\ &= \mu^2 + \sigma^2 - \frac{2}{N^2} \mathbb{E}\left[\sum_{n=1}^N x_n \left(\sum_{n=1}^N x_n\right)\right] + \frac{1}{N^2} \mathbb{E}\left[\left(\sum_{n=1}^N x_n\right)^2\right] \\ &= \mu^2 + \sigma^2 - \frac{2}{N^2} \mathbb{E}\left[\left(\sum_{n=1}^N x_n\right)^2\right] + \frac{1}{N^2} \mathbb{E}\left[\left(\sum_{n=1}^N x_n\right)^2\right] \\ &= \mu^2 + \sigma^2 - \frac{1}{N^2} \mathbb{E}\left[\left(\sum_{n=1}^N x_n\right)^2\right] \\ &= \mu^2 + \sigma^2 - \frac{1}{N^2} (N^2\mu^2 + N\sigma^2) \\ &= \mu^2 + \sigma^2 - \mu^2 + \frac{1}{N}\sigma^2 \\ &= \frac{N-1}{N}\sigma^2 \end{aligned}$$

Therefore, on average the maximum likelihood estimate obtains the correct mean but it underestimates the true variance by a factor $(N-1)/N$. The estimate for the unbiased variance parameter is given by

$$\tilde{\sigma}^2 = \frac{N}{N-1} \sigma_{ML}^2 = \frac{1}{N-1} \sum_{n=1}^N (x_n - \mu_{ML})^2$$

```
[12]: N_distribution.ml(x_sample_data, unbiased=False)
y_biased = [N_distribution.pdf(x) for x in x_space]
N_distribution.ml(x_sample_data, unbiased=True)
y_unbiased = [N_distribution.pdf(x) for x in x_space]

plt.plot(x_space, y, color="g", label="True Gaussian distribution")
plt.plot(x_space, y_biased, color="r", ls=":", label="Biased maximum likelihood")
plt.plot(x_space, y_unbiased, color="b", ls=":", label="Unbiased maximum likelihood")
plt.xlabel("$x$", fontsize=14)
plt.legend(bbox_to_anchor=(1, 0.7), loc=2, borderaxespad=1, fontsize=14)
plt.show()
```



1.2.5 Curve fitting re-visited

Now, let's return to the curve fitting example and examine it from a probabilistic perspective, thereby gaining some insights into error functions and regularization, as well as, taking us towards a full Bayesian treatment. We shall assume that, the target variable t has a Gaussian distribution having mean equal to $y(x, \mathbf{w})$ of the polynomial curve, given by

$$p(t|x, \mathbf{w}, \beta) = \mathcal{N}(t|y(x, \mathbf{w}), \beta^{-1})$$

where we have defined β to be the precision parameter, corresponding to the inverse variance.

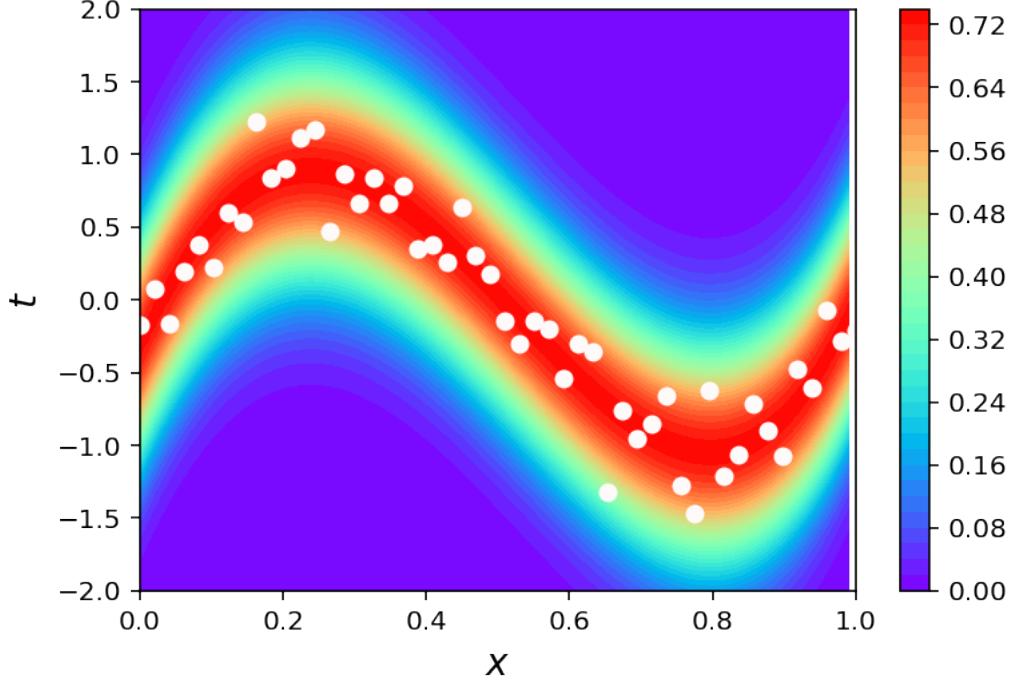
Each input point x defines a Gaussian distribution located into prediction of $y(x, \mathbf{w})$. We plot the Gaussian distribution heatmap of the values of x against t .

```
[13]: x_sample, t_sample = generate_toy_data(sin, 50, 0.3)

feature = PolynomialFeature(4)
x_features = feature.transform(x_sample)
model = LinearRegression()
model.fit(x_features, t_sample)

x_space = np.arange(0, 1, 0.01)
t_space = np.arange(-2, 2, 0.01)
X, Y = np.meshgrid(x_space, t_space)
Z = np.zeros((x_space.size, t_space.size))
for i, x in enumerate(x_space):
    # create the Gaussian distribution for a given input value
    predicted_mu, _ = model.predict(feature.transform(x))
    g = Gaussian(predicted_mu[0], 0.3)
    for j, t in enumerate(t_space):
        # compute the value of the Gaussian for each target value
        Z[i, j] = g.pdf(t)

cp = plt.contourf(X, Y, Z.T.reshape(X.shape), cmap="rainbow", levels=40)
plt.scatter(x_sample, t_sample, color="snow")
plt.xlim(0, 1)
plt.ylim(-2, 2)
plt.xlabel("$x$", fontsize=14)
plt.ylabel("$t$", fontsize=14)
plt.colorbar(cp)
plt.show()
```



Then, we can use the training data \mathbf{x}, \mathbf{t} to determine the values of the unknown parameters \mathbf{w}, β by maximum likelihood. Assuming the data are i.i.d, the likelihood function is given by

$$p(\mathbf{t}|\mathbf{x}, \mathbf{w}, \beta) = \prod_{n=1}^N \mathcal{N}(t_n | y(x, \mathbf{w}), \beta^{-1})$$

Similar to the Gaussian distribution earlier, we maximize the logarithm of the likelihood function in the form

$$\ln p(\mathbf{t}|\mathbf{x}, \mathbf{w}, \beta) = -\frac{\beta}{2} \sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2 + \frac{N}{2} \ln \beta - \frac{N}{2} \ln 2\pi$$

For determining the maximum likelihood solution for the polynomial coefficients \mathbf{w}_{ML} , we can omit the terms that do not depend on \mathbf{w} . Since the β does not alter the location of the function it can be replaced by 1. Therefore, the maximization is equivalent to minimizing the *sum of squares error function*, as presented the polynomial curve fitting example. The sum of squares error function has arisen as a consequence of maximizing the likelihood under the assumption of a Gaussian noise distribution!

As a final step, we can also use maximum likelihood to determine the precision parameter β , as follows:

$$\begin{aligned}
\frac{\partial}{\partial \beta} \ln p(\mathbf{t}|\mathbf{x}, \mathbf{w}, \beta) = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \beta} \left[-\frac{\beta}{2} \sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2 + \frac{N}{2} \ln \beta - \frac{N}{2} \ln 2\pi \right] = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \beta} \left[-\frac{\beta}{2} \sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2 \right] + \frac{\partial}{\partial \beta} \left[\frac{N}{2} \ln \beta \right] = 0 &\Leftrightarrow \\
-\frac{1}{2} \sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2 + \frac{N}{2} \frac{1}{\beta} = 0 &\Leftrightarrow \\
\sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2 = \frac{N}{\beta} &\Leftrightarrow \\
\frac{1}{\beta_{ML}} = \frac{1}{N} \sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2
\end{aligned}$$

Since we have a probabilistic model, we can use the predictive distribution that gives the probability distribution over t , rather than a simple point estimate.

$$p(t|x, \mathbf{w}_{ML}, \beta_{ML}) = \mathcal{N}(t|y(x, \mathbf{w}_{ML}), \beta_{ML}^{-1})$$

We can further introduce a prior distribution over the polynomial coefficients \mathbf{w} , in order to take a step towards a more Bayesian approach. Consider for instance a Gaussian prior of the form

$$p(\mathbf{w}|\alpha) = \mathcal{N}(\mathbf{w}|\mathbf{0}, \alpha^{-1}\mathbf{I}) = \left(\frac{\alpha}{2\pi} \right)^{(M+1)/2} \exp \left\{ -\frac{\alpha}{2} \mathbf{w}^T \mathbf{w} \right\}$$

where α is the precision of the multivariate Gaussian, and M is the order of the polynomial, that is, the dimension of the parameter vector \mathbf{w} . Then from the Bayes theorem we have that

$$p(\mathbf{w}|\mathbf{x}, \mathbf{t}, \alpha, \beta) \propto p(\mathbf{t}|\mathbf{x}, \mathbf{w}, \beta)p(\mathbf{w}|\alpha)$$

Therefore, we can determine \mathbf{w} , by maximizing the posterior distribution. This technique is known as *maximum posterior* or MAP inference. The maximum of the posterior is given by the minimum of the negative logarithm, which it can be proved to be

$$\frac{\beta}{2} \sum_{n=1}^N (y(x, \mathbf{w}) - t_n)^2 + \frac{\alpha}{2} \mathbf{w}^T \mathbf{w}$$

Thus we see that maximizing the posterior distribution is equivalent to minimizing the regularized sum of squared error function encountered in Regularization, where $\lambda = \alpha/\beta$.

1.6 Information Theory

How much information is received when we observe a specific variable?

Consider for instance the event of seeing an alien spaceship appearing in the sky. We have never seen one and we would be extremely surprised if one day such an event occurred, since it is unexpected given our current knowledge. Therefore, the amount of information can be viewed as the *degree of surprise* on learning the value of x . The measure of information content is therefore depend on the probability distribution $p(x)$ and in particular is given by the logarithm of $p(x)$ as follows,

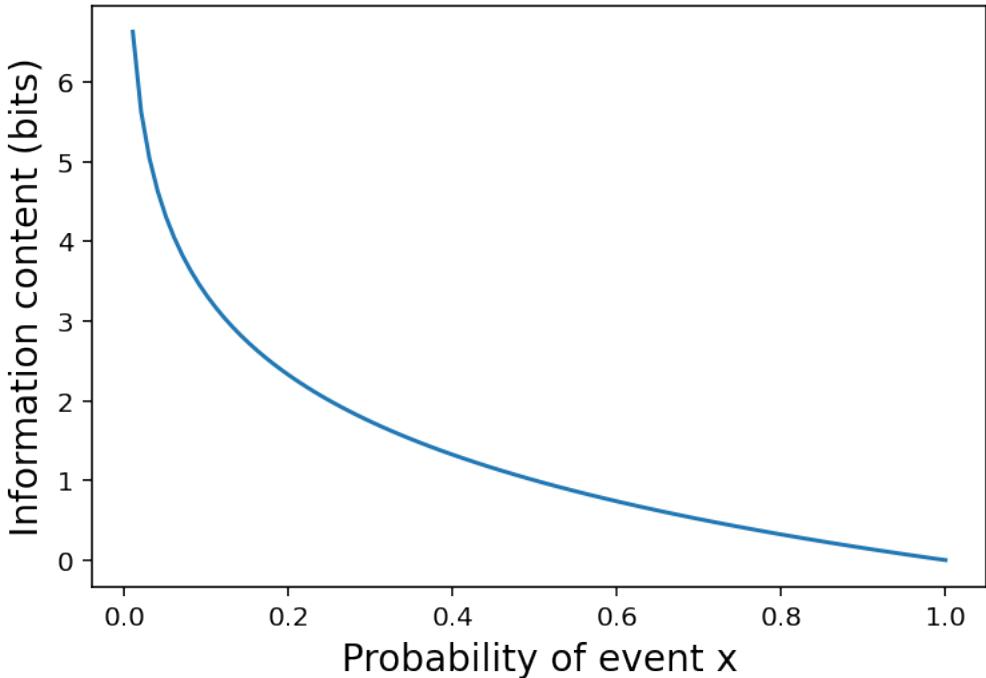
$$h(x) = -\log_2 p(x)$$

where the negative sign ensures that $h(x) \geq 0$. When the base of the logarithm is 2 the units of $h(x)$ are **bits**.

```
[14]: def h(prob: float) -> float:
    if not 0 <= prob <= 1:
        raise ValueError("Probability should be [0,1].")
    elif prob == 0:
        return float("-inf")
    else:
        return -math.log2(prob)

px_space = np.linspace(0, 1, 100)
y = [h(px) for px in px_space]

plt.plot(px_space, y)
plt.xlabel("Probability of event x", fontsize=14)
plt.ylabel("Information content (bits)", fontsize=14)
plt.show()
```



The average amount of information is obtained by taking the expectation over the information content, given by,

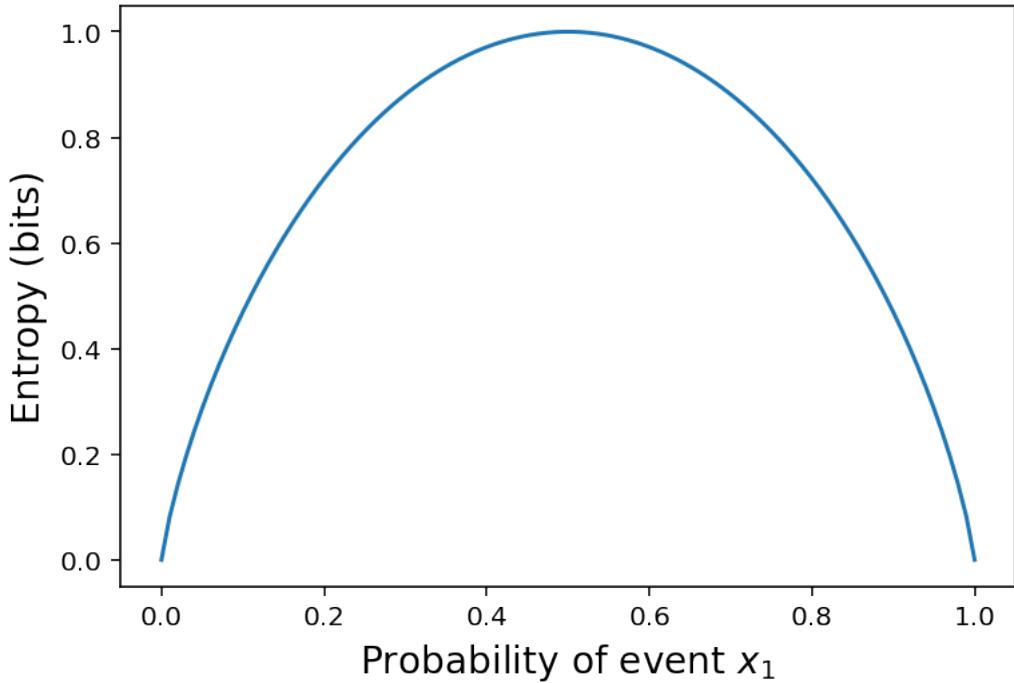
$$H[x] = - \sum_x p(x)h(x) = - \sum_x p(x) \log_2 p(x)$$

This important quantity is called *entropy* of the random variable X . Consider a discrete random variable X having two possible values x_1 and x_2 with probabilities p and $1 - p$.

```
[15]: def entropy(probs):
    if 0 in probs:
        return 0
    else:
        return sum([px * h(px) for px in probs])

px_space = np.linspace(0, 1, 100)
y = [entropy([px, 1 - px]) for px in px_space]

plt.plot(px_space, y)
plt.xlabel("Probability of event $x_1$", fontsize=14)
plt.ylabel("Entropy (bits)", fontsize=14)
plt.show()
```



Note that the entropy is maximized when the two events are equiprobable, that is, for uniform distributions. The entropy is also defined in a similar way for continuous random variables and is called *differential entropy*:

$$H[\mathbf{x}] = - \int p(\mathbf{x}) \ln p(\mathbf{x}) d\mathbf{x}$$

In the case of a joint distribution $p(\mathbf{x}, \mathbf{y})$, the average additional information needed to specify \mathbf{y} given that the value of \mathbf{x} is already known, is called *conditional entropy*, and is given by

$$H[\mathbf{y}|\mathbf{x}] = - \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{y}|\mathbf{x}) d\mathbf{x} d\mathbf{y}$$

Moreover it is easily seen, using the product rule, that the conditional entropy satisfies the relation,

$$\begin{aligned}
H[\mathbf{x}, \mathbf{y}] &= - \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{x}, \mathbf{y}) d\mathbf{x} d\mathbf{y} \\
&= - \int \int p(\mathbf{x}, \mathbf{y}) \ln (p(\mathbf{y}|\mathbf{x})p(\mathbf{x})) d\mathbf{x} d\mathbf{y} \\
&= - \int \int p(\mathbf{x}, \mathbf{y})(\ln p(\mathbf{y}|\mathbf{x}) + \ln p(\mathbf{x})) d\mathbf{x} d\mathbf{y} \\
&= - \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{y}|\mathbf{x}) d\mathbf{x} d\mathbf{y} - \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{x}) d\mathbf{x} d\mathbf{y} \\
&= - \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{y}|\mathbf{x}) d\mathbf{x} d\mathbf{y} - \int \int p(\mathbf{x}, \mathbf{y}) d\mathbf{y} \ln p(\mathbf{x}) d\mathbf{x} \\
&= - \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{y}|\mathbf{x}) d\mathbf{x} d\mathbf{y} - \int p(\mathbf{x}) \ln p(\mathbf{x}) d\mathbf{x} \\
&= H[\mathbf{y}|\mathbf{x}] + H[\mathbf{x}]
\end{aligned}$$

stating that the information needed to describe \mathbf{x} and \mathbf{y} is given by the information needed to describe \mathbf{x} alone plus the additional information to specify \mathbf{y} .

1.6.1 Relative entropy and mutual information

Consider some unknown distribution $p(\mathbf{x})$ that we have modelled using an approximate distribution $q(\mathbf{x})$. Then, the average *additional* information required to specify a value of \mathbf{x} as a result of using $q(\mathbf{x})$ instead of $p(\mathbf{x})$ is given by

$$KL(p||q) = - \int p(\mathbf{x}) \ln q(\mathbf{x}) d\mathbf{x} - \left(- \int p(\mathbf{x}) \ln q(\mathbf{x}) d\mathbf{x} \right) = - \int p(\mathbf{x})(\ln q(\mathbf{x}) - \ln p(\mathbf{x})) d\mathbf{x} = - \int p(\mathbf{x}) \ln \left(\frac{q(\mathbf{x})}{p(\mathbf{x})} \right) d\mathbf{x}.$$

This is known as the *relative entropy* or *Kullback-Leibler divergence* between distributions $p(\mathbf{x})$ and $q(\mathbf{x})$. Note that it is not a symmetrical quantity, that is to say $KL(p||q) \neq KL(q||p)$. Moreover the Kullback-Leibler divergence satisfies $KL(p||q) \geq 0$, where the equality holds if, and only if, $p(\mathbf{x}) = q(\mathbf{x})$. Thus, we can interpret the Kullback-Leibler divergence as a measure of dissimilarity of the two distributions.

Since the most efficient compression is achieved when we know the true distribution, otherwise additional information is required, there is an important relationship between data compression and density estimation.

Suppose we are trying to approximate the unknown distribution using some parametric distribution $q(\mathbf{x}| \theta)$, governed by a set of adjustable parameters θ , for instance a multivariate Gaussian distribution. One way to determine θ is to minimize the Kullback-Leibler divergence between $p(\mathbf{x})$ and $q(\mathbf{x}| \theta)$. This is impossible since we do not know $p(\mathbf{x})$. However, if we have observed a finite set of training points \mathbf{x}_n drawn from $p(\mathbf{x})$, then the expectation with respect to $p(\mathbf{x})$ can be approximated by a finite sum over these points, using (1.35), so that,

$$KL(p||q) \approx \frac{1}{N} \sum_{n=1}^N (-\ln q(\mathbf{x}_n | \theta) + \ln p(\mathbf{x}_n))$$

Since the second term is independent of θ , minimizing this **approximated** Kullback-Leibler divergence is equivalent to minimizing the log likelihood function of $q(\mathbf{x}_n | \theta)$ evaluated on the training set.

Mutual information

Consider the joint distribution $p(\mathbf{x}, \mathbf{y})$ between two sets of variables \mathbf{x} and \mathbf{y} . If the sets are independent, then $p(\mathbf{x}, \mathbf{y}) = p(\mathbf{x})(\mathbf{y})$. If the variables are not independent, we can measure whether they are *close* to being independent* by considering the Kullback-Leibler divergence between the joint distribution and the product of their marginals, given by

$$I[\mathbf{x}, \mathbf{y}] = \text{KL}(p(\mathbf{x}, \mathbf{y}) || p(\mathbf{x})p(\mathbf{y})) = - \int \int p(\mathbf{x}, \mathbf{y}) \ln \left(\frac{p(\mathbf{x})p(\mathbf{y})}{p(\mathbf{x}, \mathbf{y})} \right) d\mathbf{x}d\mathbf{y}$$

which is called the *mutual information* of variables \mathbf{x} and \mathbf{y} . The mutual information satisfies $I[\mathbf{x}, \mathbf{y}] \geq 0$ where the equality holds if, and only if, \mathbf{x} and \mathbf{y} are independent. Moreover, using the sum and product rules of probability, we can prove that the mutual information is related to the conditional entropy,

$$\begin{aligned} I[\mathbf{x}, \mathbf{y}] &= - \int \int p(\mathbf{x}, \mathbf{y}) \ln \left(\frac{p(\mathbf{x})p(\mathbf{y})}{p(\mathbf{x}, \mathbf{y})} \right) d\mathbf{x}d\mathbf{y} \\ &= - \int \int p(\mathbf{x}, \mathbf{y}) \ln \left(\frac{p(\mathbf{x})p(\mathbf{y})}{p(\mathbf{x}|\mathbf{y})p(\mathbf{y})} \right) d\mathbf{x}d\mathbf{y} \\ &= - \int \int p(\mathbf{x}, \mathbf{y}) \ln \left(\frac{p(\mathbf{x})}{p(\mathbf{x}|\mathbf{y})} \right) d\mathbf{x}d\mathbf{y} \\ &= - \int \int p(\mathbf{x}, \mathbf{y}) \left(\ln p(\mathbf{x}) - \ln p(\mathbf{x}|\mathbf{y}) \right) d\mathbf{x}d\mathbf{y} \\ &= - \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{x}) d\mathbf{x}d\mathbf{y} + \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{x}|\mathbf{y}) d\mathbf{x}d\mathbf{y} \\ &= - \int \int p(\mathbf{x}, \mathbf{y}) d\mathbf{y} \ln p(\mathbf{x}) d\mathbf{x} + \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{x}|\mathbf{y}) d\mathbf{x}d\mathbf{y} \\ &= - \int p(\mathbf{x}) \ln p(\mathbf{x}) d\mathbf{x} + \int \int p(\mathbf{x}, \mathbf{y}) \ln p(\mathbf{x}|\mathbf{y}) d\mathbf{x}d\mathbf{y} \\ &= H[\mathbf{x}] - H[\mathbf{x}|\mathbf{y}] = H[\mathbf{y}] - H[\mathbf{y}|\mathbf{x}] \end{aligned}$$

2. Probability Distributions

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- 2.3.7 Student’s t-distribution
- 2.3.9 Mixtures of Gaussians
- 2.5 Nonparametric Methods
 - 2.5.1 Kernel density estimators
 - 2.5.2 Nearest-neighbour methods

```
[1]: import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits import mplot3d
from sklearn.datasets import make_classification
from prml.datasets import load_old_faithful
from prml.distribution import (
    Bernoulli,
    Binomial,
    Beta,
    Categorical,
    Multinomial,
    Dirichlet,
    Gaussian,
    MultivariateGaussian,
    Gamma,
    StudentT,
)
from prml.neighbors import NearestNeighborsDensity, KNearestNeighborsClassifier

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'
```

2.1 Binary Variables

Consider a single binary random variable $x \in \{0, 1\}$, for instance x might be the outcome of flipping a coin. Then, the probability of heads ($x = 1$) can be denoted by a parameter μ so that,

$$p(x = 1|\mu) = \mu$$

where $0 \leq \mu \leq 1$. The *Bernoulli* probability distribution over x has therefore the form,

$$\text{Bern}(x|\mu) = \mu^x(1 - \mu)^{1-x}$$

It is easily verified that the Bernoulli distribution has mean given by,

$$\mathbb{E}[x] = \sum_{x \in \{0,1\}} x \text{Bern}(x|\mu) = \sum_{x \in \{0,1\}} x \mu^x (1-\mu)^{1-x} = \mu^1 (1-\mu)^0 = \mu$$

and variance given by,

$$\begin{aligned}\text{var}[x] &= \mathbb{E}[x]^2 - \mathbb{E}[x^2] \\ &= \mu^2 - \sum_{x \in \{0,1\}} x^2 \text{Bern}(x|\mu) \\ &= \mu^2 - \sum_{x \in \{0,1\}} x^2 \mu^x (1-\mu)^{1-x} \\ &= \mu^2 - \mu = \mu(\mu - 1)\end{aligned}$$

Now suppose we have given a data set $\mathcal{D} = \{x_1, \dots, x_N\}$ of observed values sampled from an **unknown** Bernoulli distribution (outcomes of coin tosses), that is, the μ parameter (probability of heads) is unknown.

```
[2]: # For demonstration purposes we shall create a data set from a fair coin (mu = 0.5)
# and another data set from a biased coin favoring tails (mu = 0.2).

# Number of coin tosses per data set
N = 100

# Fair coin
mu_fair = 0.5
true_distribution_fair = Bernoulli(mu_fair)
D_fair = true_distribution_fair.draw(N)

print("Fair coin -- ", "Heads:", sum(D_fair == 1), "Tails:", sum(D_fair == 0))

# Biased coin
mu_biased = 0.2
true_distribution_biased = Bernoulli(mu_biased)
D_biased = true_distribution_biased.draw(N)

print("Biased coin -- ", "Heads:", sum(D_biased == 1), "Tails:", sum(D_biased == 0))

plt.figure(figsize=(8, 4))
plt.subplot(1, 2, 1)
b = plt.bar([0, 1], [sum(D_fair == 0), sum(D_fair == 1)], color=["red", "blue"], width=0.5)
b[0].set_label("Tails")
b[1].set_label("Heads")
plt.ylabel("Number of observed outcomes", fontsize=14)
plt.xticks([0, 1])
```

```

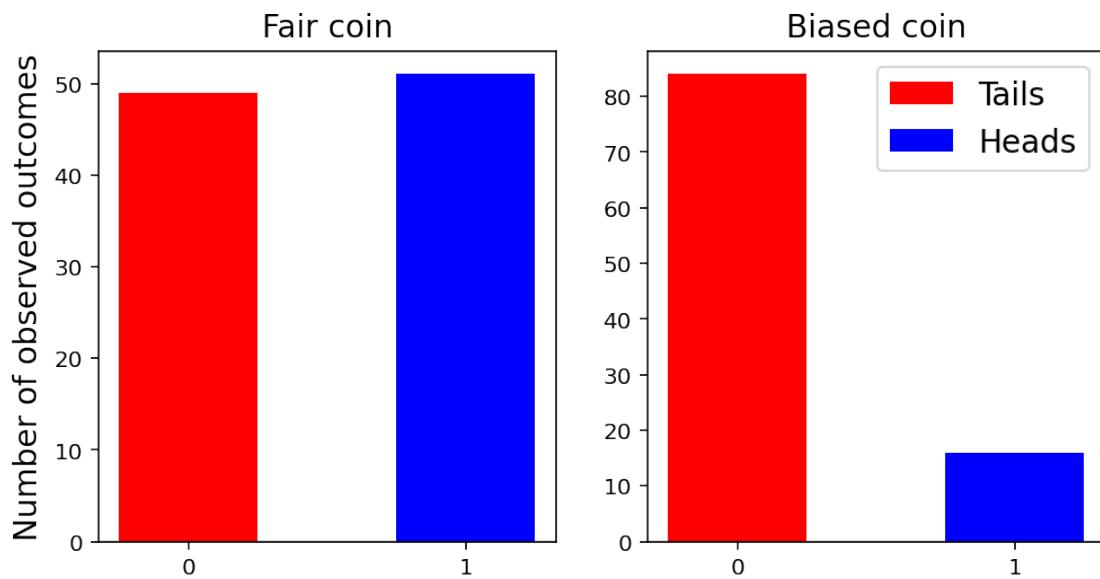
plt.title("Fair coin", fontsize=14)

plt.subplot(1, 2, 1)
b = plt.bar([0, 1], [sum(D_biased == 0), sum(D_biased == 1)], color=["red", "blue"], width=0.5)
b[0].set_label("Tails")
b[1].set_label("Heads")
plt.xticks([0, 1])
plt.title("Biased coin", fontsize=14)
plt.legend(fontsize=14)

plt.show()

```

Fair coin -- Heads: 51 Tails: 49
 Biased coin -- Heads: 16 Tails: 84



We can use the likelihood function on the assumption that the observations are drawn independently from $\text{Bern}(x|\mu)$, so that,

$$p(\mathcal{D}|\mu) = \prod_{n=1}^N \text{Bern}(x_n|\mu) = \prod_{n=1}^N \mu^{x_n} (1-\mu)^{1-x_n}$$

Then, following the frequentist approach, we can estimate the value of μ by maximizing the logarithm of the likelihood given by

$$\begin{aligned}
\ln p(\mathcal{D}|\mu) &= \ln \left(\prod_{n=1}^N \mu^{x_n} (1-\mu)^{1-x_n} \right) \\
&= \sum_{n=1}^N \ln (\mu^{x_n} (1-\mu)^{1-x_n}) \\
&= \sum_{n=1}^N \left(\ln(\mu^{x_n}) + \ln((1-\mu)^{1-x_n}) \right) \\
&= \sum_{n=1}^N \left(x_n \ln \mu + (1-x_n) \ln(1-\mu) \right)
\end{aligned}$$

Given an observed data set \mathcal{D} , we can plot the value of the log-likelihood against the values of $\mu \in [0, 1]$.

```
[3]: mu_space = np.arange(0.01, 1, 0.01)
ll = np.zeros(mu_space.shape)

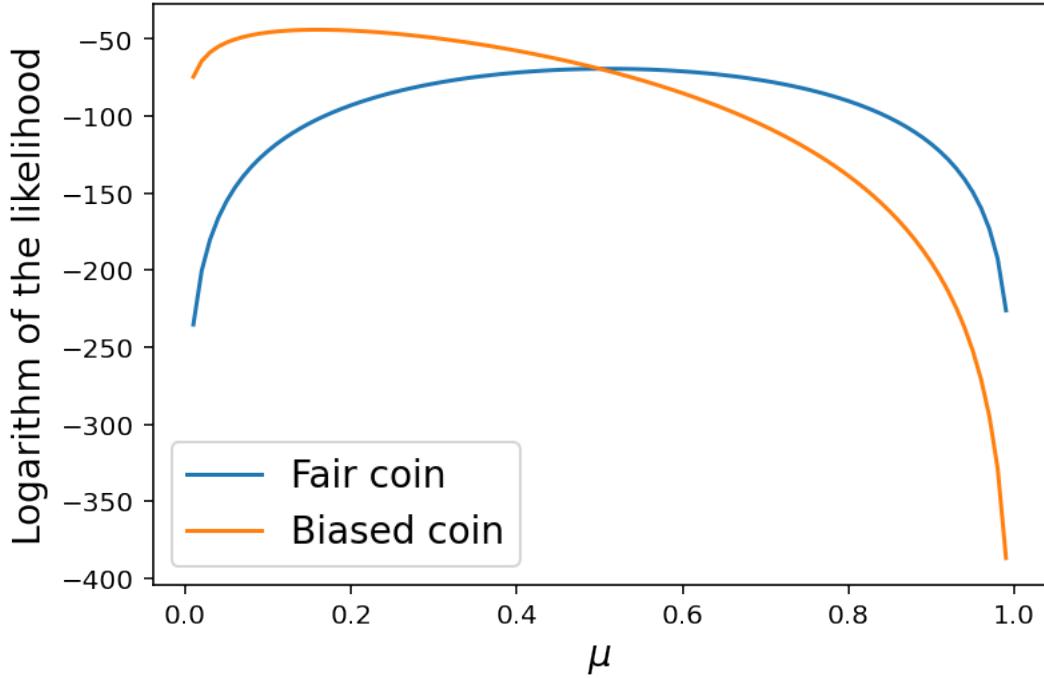
for i, mu_i in enumerate(mu_space):
    ll[i] = Bernoulli(mu_i).log_likelihood_iid(D_fair)

plt.plot(mu_space, ll, label="Fair coin")

for i, mu_i in enumerate(mu_space):
    ll[i] = Bernoulli(mu_i).log_likelihood_iid(D_biased)

plt.plot(mu_space, ll, label="Biased coin")

plt.xlabel("\u03bc", fontsize=14)
plt.ylabel("Logarithm of the likelihood", fontsize=14)
plt.legend(fontsize=14)
plt.show()
```



Note that the **maximum** of the likelihood is achieved around $\mu = 0.5$ for the fair coin and $\mu = 0.2$ for the biased coin. Therefore, using calculus, if we set the derivative of $\ln p(\mathcal{D}|\mu)$ with respect to μ equal to zero, we obtain

$$\begin{aligned}
\frac{\partial}{\partial \mu} \ln p(\mathcal{D}|\mu) = 0 &\Leftrightarrow \\
\frac{\partial}{\partial \mu} \sum_{n=1}^N \left(x_n \ln \mu + (1-x_n) \ln(1-\mu) \right) = 0 &\Leftrightarrow \\
\sum_{n=1}^N \frac{\partial}{\partial \mu} \left(x_n \ln \mu + (1-x_n) \ln(1-\mu) \right) = 0 &\Leftrightarrow \\
\sum_{n=1}^N \left(\frac{1}{\mu} x_n - \frac{1}{1-\mu} (1-x_n) \right) = 0 &\Leftrightarrow \\
\sum_{n=1}^N \left(\frac{1}{\mu} x_n - \frac{1}{1-\mu} + \frac{1}{1-\mu} x_n \right) = 0 &\Leftrightarrow \\
\sum_{n=1}^N \left(\frac{1}{\mu} x_n + \frac{1}{1-\mu} x_n \right) = \frac{N}{1-\mu} &\Leftrightarrow \\
\sum_{n=1}^N \left(\frac{1-\mu}{\mu} x_n + x_n \right) = N &\Leftrightarrow \\
\sum_{n=1}^N \frac{1}{\mu} x_n = N &\Leftrightarrow \\
\mu_{ML} = \frac{1}{N} \sum_{n=1}^N x_n
\end{aligned}$$

which is known as the *sample mean*. Thus, the probability of landing heads (μ), according to the maximum likelihood estimator, is given by the fraction of observations of heads in the data set \mathcal{D} . Indeed calculating the sample mean gives us a very accurate estimation of the true values for μ .

```
[4]: print("Maximum likelihood for the fair coin is", sum(D_fair == 1) / N)
print("Maximum likelihood for the biased coin is", sum(D_biased == 1) / N)
```

```
Maximum likelihood for the fair coin is 0.51
Maximum likelihood for the biased coin is 0.16
```

However, A problem that arises from this result is that for small data sets the estimation can be unreasonable. For instance, in the following plot, note that for small data sets $N < 100$, the estimated μ_{ML} can deviate significantly from the true μ leading to incorrect probabilities for the future observations.

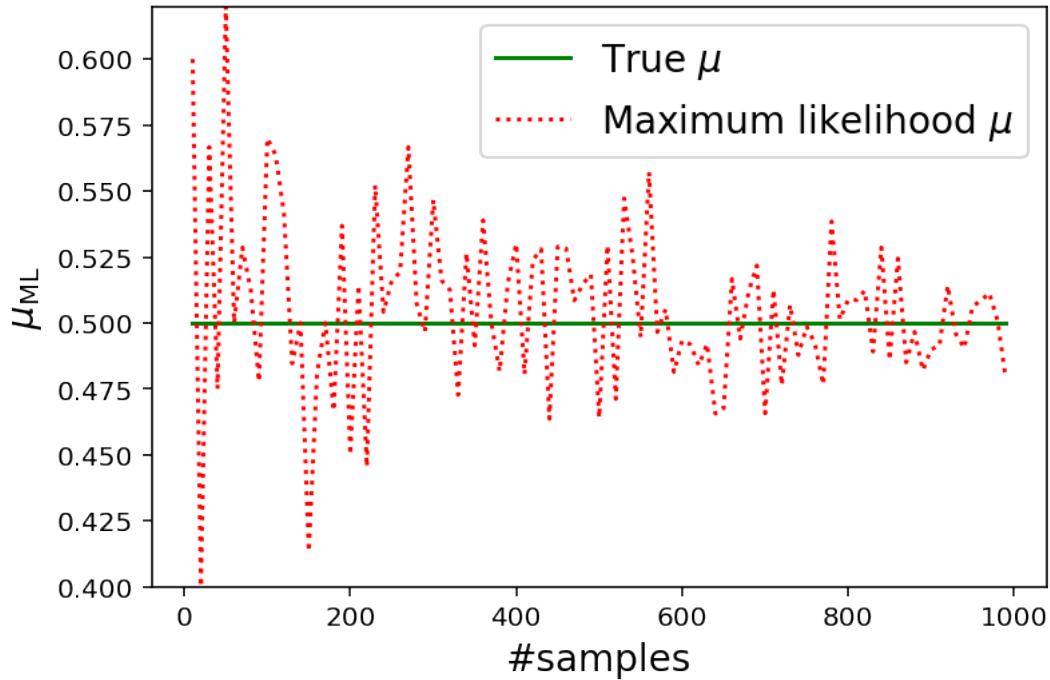
```
[5]: ml_model = Bernoulli()
samples = list(range(10, 1000, 10))
mu_estimations = []

for N in samples:
    D = true_distribution_fair.draw(N)
    ml_model.ml(D)
    mu_estimations.append(ml_model.mu)
```

```

plt.plot(samples, [mu_fair for N in samples], color="g", label="True $\mu$")
plt.plot(samples, mu_estimations, color="r", linestyle=":", label="Maximum likelihood $\mu$")
plt.xlabel("#samples", fontsize=14)
plt.ylabel("$\mu_{\text{ML}}$ \mathbf{\mu}_{\text{ML}}", fontsize=14)
plt.ylim([min(mu_estimations), max(mu_estimations)])
plt.legend(fontsize=14)
plt.show()

```



Now, if we toss a coin 5 times, then, the probability of getting 3 heads and then 2 tails is

$$p(x_1 = 1)p(x_2 = 1)p(x_3 = 1)p(x_4 = 0)p(x_5 = 0) = \mu \times \mu \times \mu \times (1 - \mu) \times (1 - \mu)$$

or more general for N times and m heads,

$$\mu^m(1 - \mu)^{N-m}$$

However, this is just one way to get m heads, there are many other sequences of N trials that would give us m heads. How many exactly?

The distribution describing the number of m observations of $x = 1$ in a sample dataset of size N is called the *Binomial distribution*, and is given by

$$\text{Bin}(m|N, \mu) = \binom{N}{m} \mu^m (1 - \mu)^{N-m}$$

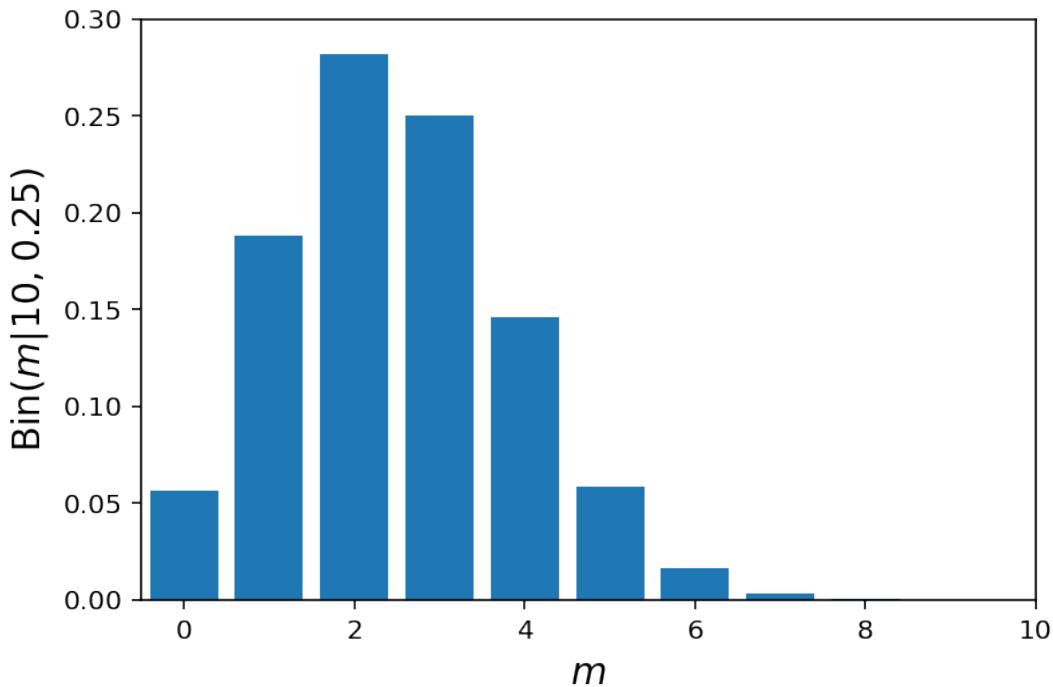
where

$$\binom{N}{m} = \frac{N!}{(N-m)!m!}$$

is the numbers of ways of choosing m objects out of a total of N identical objects, and is called the **binomial coefficient**.

```
[6]: model = Binomial(10, 0.25)
y = model.pdf(np.arange(0, 10))

plt.bar(np.arange(0, 10), y)
plt.xlim([-0.5, 10])
plt.ylim([0, 0.3])
plt.xlabel("$m$", fontsize=14)
plt.ylabel("$\text{Bin}(m|10, 0.25)$", fontsize=14)
plt.show()
```



2.1.1 The beta distribution

We have seen that the maximum likelihood estimator for the parameter μ in the Bernoulli and binomial distributions, is given by the fraction of the observations in the data having $x = 1$, which can lead to over-fitted results for small data sets. In order to arrive to more sensible results, we develop a **Bayesian treatment** for the problem by introducing a prior distribution $p(\mu)$ over the parameter μ .

Note that the likelihood function takes the form of the product of factors of the form $\mu^x(1-\mu)^{1-x}$. We would like to choose a prior proportional to powers of μ and $(1 - \mu)$ in order for the posterior to have the same functional form as the prior, since the posterior is proportional to the product of the prior and the likelihood. This important property is called **conjugacy**.

We therefore we choose a prior, called the **beta** distribution, given by

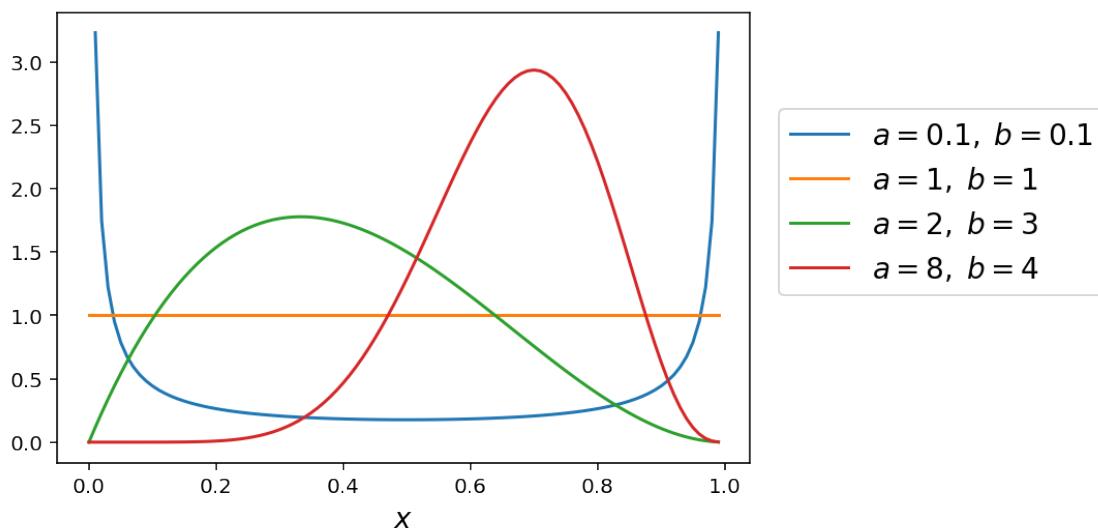
$$\text{Beta}(\mu|a, b) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)}\mu^{a-1}(1-\mu)^{b-1}$$

where a and b are often called hyperparameters because they control the distribution of the parameter μ . In order to give an intuition about the hyperparameters, we plot the beta distribution for various values of a and b .

```
[7]: x_space = np.arange(0, 1, 0.01)

for a, b in [(0.1, 0.1), (1, 1), (2, 3), (8, 4)]:
    model = Beta(a, b)
    plt.plot(x_space, model.pdf(x_space), label="$a={} ,\ b={} $".format(a, b))

plt.xlabel("$x$ ", fontsize=14)
plt.legend(bbox_to_anchor=(1, 0.85), loc=2, borderaxespad=1, fontsize=14)
plt.show()
```



The fraction of $\Gamma(x)$ functions ensures that the beta distribution is normalized, so that

$$\int_0^1 \text{Beta}(\mu|a, b) d\mu = 1$$

The mean is given by

$$\begin{aligned}\mathbb{E}[\mu] &= \int_0^1 \mu \text{Beta}(\mu|a, b) d\mu \\ &= \int_0^1 \mu \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \mu^{a-1} (1-\mu)^{b-1} d\mu \\ &= \int_0^1 \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \mu^a (1-\mu)^{b-1} d\mu \\ &= \int_0^1 \frac{a\Gamma(a+b+1)}{(a+b)\Gamma(a+1)\Gamma(b)} \mu^a (1-\mu)^{b-1} d\mu \\ &= \frac{a}{a+b} \int_0^1 \frac{\Gamma(a+b+1)}{\Gamma(a+1)\Gamma(b)} \mu^a (1-\mu)^{b-1} d\mu \\ &= \frac{a}{a+b} \int_0^1 \text{Beta}(\mu|a+1, b) d\mu \\ &= \frac{a}{a+b}\end{aligned}$$

where we have taken advantage of the property $\Gamma(x+1) = x\Gamma(x)$. The variance is given by

$$\text{var}[\mu] = \frac{ab}{(a+b)^2(a+b+1)}$$

The posterior distribution over μ can be obtained by multiplying the beta prior by the binomial likelihood function and **normalizing**,

$$p(\mu|m, l, a, b) = \frac{\Gamma(m+a+l+b)}{\Gamma(m+a)\Gamma(l+b)} \mu^{m+a-1} (1-\mu)^{l+b-1}$$

where $l = N - m$, and corresponds to the number of times $x = 0$.

Note that the effect of observing a data set of m observations of $x = 1$ and l observations of $x = 0$ is to increase the value of a by m , and the value of b by l , from the prior to the posterior distribution. Thus, the hyperparameters a and b in the prior represent the number of observations of $x = 1$ and $x = 0$, respectively. Furthermore, the posterior distribution can act as the prior if subsequent observations arrive. Imagine taking one observation at a time and after each observation updating the current posterior distribution by multiplying by the likelihood of the incoming observation. At each stage, the posterior is a beta distribution incorporating some number of (prior and actual) observed values for $x = 1$ and $x = 0$ given by the parameters a and b . Incorporating an additional observation of $x = 1$ corresponds to incrementing the value of a by 1, whereas for $x = 0$ increment b by 1.

We present a sequence of such Bayesian inference steps, where three observations of $x = 1$ arrive before a single observation of $x = 0$. Note how the prior revises the form of the **unnormalized** posterior on each update step according to the likelihood. Apart from the first step, where the prior is a Beta distribution having parameter $a = 2$ and $b = 2$, in each subsequent step the prior is the **unnormalized** posterior of the previous step.

```
[8]: # The Beta conjugate prior for the Binomial distribution (starting parameter
    ↪ a=2, b=2)
prior = Beta(a=2, b=2)
plt.plot(mu_space, prior.pdf(mu_space), color="red")
plt.xlabel("$\mu$", fontsize=14)
plt.ylabel("$\mathbf{\text{Beta}}(\mu|2,2)$", fontsize=14)
plt.title(prior.change_notation({"x": "mu"}).to_latex, fontsize=14)
plt.show()

# Apply a sequence of Bayesian inference steps, as more observations arrive in
    ↪ the form of a likelihood
plt.figure(figsize=(20, 5))

# Row 1
plt.subplot(2, 4, 1)
plt.tight_layout()
likelihood = Binomial(n=1).pdf(1)
plt.plot(mu_space, likelihood.pdf(mu=mu_space), color="blue")
plt.title(likelihood.to_latex, fontsize=18)

plt.subplot(2, 4, 2)
plt.tight_layout()
posterior = prior.change_notation({"x": "mu"}) * likelihood
plt.plot(mu_space, posterior.pdf(mu=mu_space), "g")
plt.title(posterior.to_latex, fontsize=18)

plt.subplot(2, 4, 3)
plt.tight_layout()
likelihood = Binomial(n=1).pdf(1)
plt.plot(mu_space, likelihood.pdf(mu=mu_space), color="blue")
plt.title(likelihood.to_latex, fontsize=18)

plt.subplot(2, 4, 4)
plt.tight_layout()
posterior = posterior * likelihood
plt.plot(mu_space, posterior.pdf(mu=mu_space), "g")
plt.title(posterior.to_latex, fontsize=18)

# Row 2
plt.subplot(2, 4, 5)
plt.tight_layout()
```

```

likelihood = Binomial(n=1).pdf(1)
plt.plot(mu_space, likelihood.pdf(mu=mu_space), color="blue")
plt.title(likelihood.to_latex, fontsize=18)

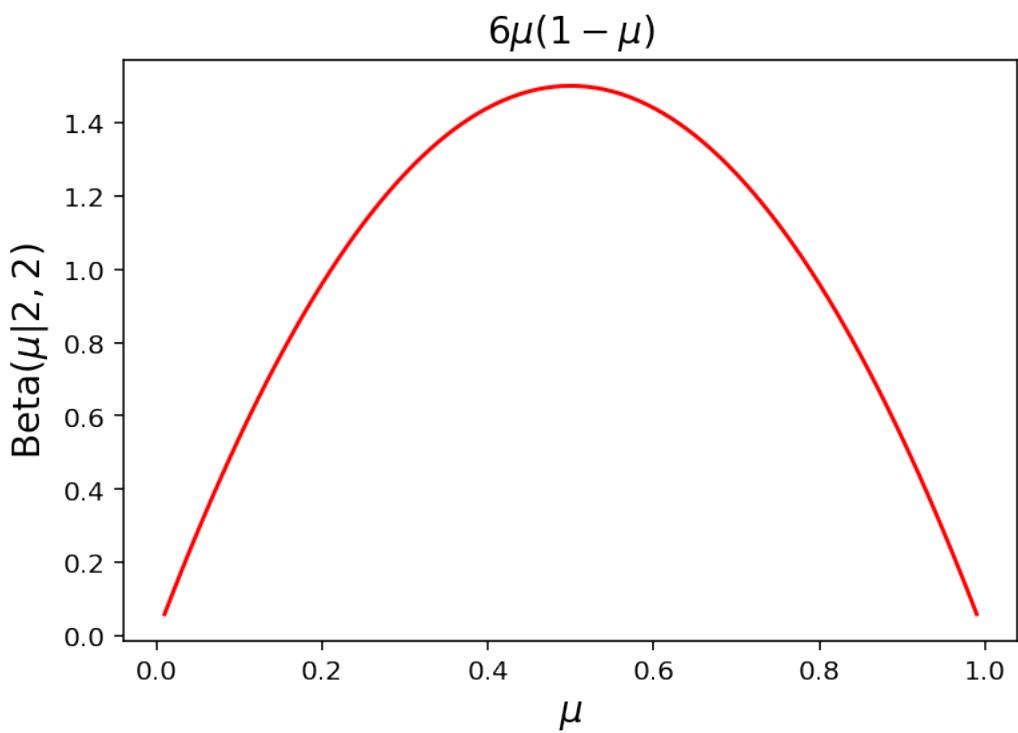
plt.subplot(2, 4, 6)
plt.tight_layout()
posterior = posterior * likelihood
plt.plot(mu_space, posterior.pdf(mu=mu_space), "g")
plt.title(posterior.to_latex, fontsize=18)

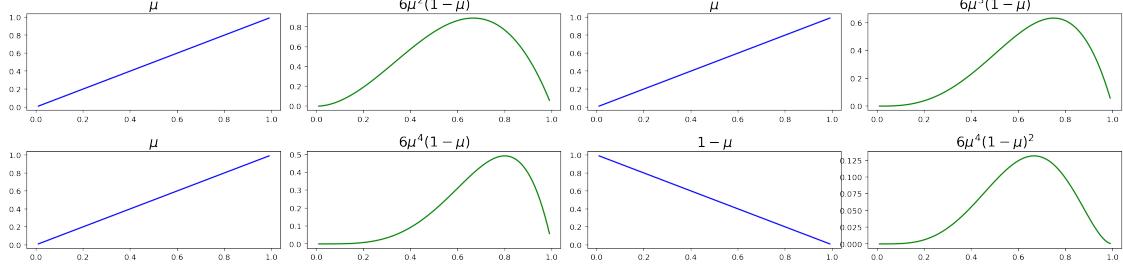
plt.subplot(2, 4, 7)
plt.tight_layout()
likelihood = Binomial(n=1).pdf(0)
plt.plot(mu_space, likelihood.pdf(mu=mu_space), color="blue")
plt.title(likelihood.to_latex, fontsize=18)

plt.subplot(2, 4, 8)
plt.tight_layout()
posterior = posterior * likelihood
plt.plot(mu_space, posterior.pdf(mu=mu_space), "g")
plt.title(posterior.to_latex, fontsize=18)

plt.show()

```





Thus, the **sequential** approach to learning arises naturally when we adopt a Bayesian viewpoint. It is **independent** of the choice of prior and of the likelihood function and **depends only** on the assumption of i.i.d. data. Sequential methods make use of observations one at a time, or in small batches, and then discard them before the next observations are used. They can be used, for example, in real-time learning scenarios where a steady stream of data is arriving, and predictions must be made before all of the data is seen. Maximum likelihood methods can also be cast into a sequential framework.

If our goal is to predict the outcome of the next trial, then we must evaluate the predictive distribution of x given the observed data \mathcal{D} given by,

$$p(x = 1|\mathcal{D}) = \frac{m + a}{m + a + l + b}$$

which essentially represents the fraction of observations (actual and prior) that corresponds to $x = 1$. Note that in the limit of an infinitely large data set $m, l \rightarrow \infty$, $p(x = 1|\mathcal{D})$ reduces to the maximum likelihood estimator $\frac{m}{N}$.

It is a very **general property** that the Bayesian and maximum likelihood results are identical in the limit of infinitely large data sets. For finite data set, the posterior mean for μ always lies between the prior mean and the maximum likelihood estimate for μ , corresponding to the sample mean.

2.2 Multinomial Variables

A binary variable is good for representing a coin toss, but generally we would like to have more states, such as the number rolled on a die. Such discrete random variables can take on one of K possible mutually exclusive states of the form

$$\mathbf{x} = (0, 0, 1, 0, 0, 0)^T$$

where each state k is represented by the k^{th} element being 1 and all other elements being 0. If we denote the probability of $x_k = 1$ by the parameter μ_k , then the distribution over \mathbf{x} can be regarded as a generalization of the Bernoulli distribution, called the *categorical distribution*, and is given by

$$p(\mathbf{x}|\mu) = \prod_{k=1}^K \mu_k^{x_k}$$

where the parameters $\mathbf{x} = (\mu_1, \dots, \mu_K)^T$ must satisfy $\mu_k \geq 0$ and $\sum_k \mu_k = 1$ because they represent probabilities. Note that $\mu_k^{x_k}$ becomes 1 for every element except the $x_k = 1$, and so the product picks the probability μ_k for the state represented by \mathbf{x} .

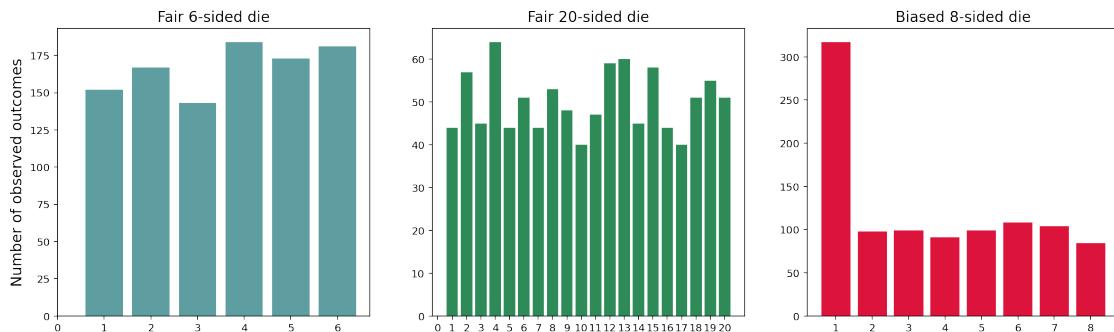
```
[9]: plt.figure(figsize=(18, 5))

# Lets roll 1000 fair 6-sided dice
plt.subplot(1, 3, 1)
fair_rolls_6 = Categorical(mu=np.ones(6) / 6).draw(1000)
plt.bar(np.arange(1, 7), sum(fair_rolls_6), color="cadetblue")
plt.ylabel("Number of observed outcomes", fontsize=14)
plt.xticks(np.arange(6 + 1))
plt.title("Fair 6-sided die", fontsize=14)

# then 1000 fair 20-sided dice
plt.subplot(1, 3, 2)
fair_rolls_20 = Categorical(mu=np.ones(20) / 20).draw(1000)
plt.bar(np.arange(1, 21), sum(fair_rolls_20), color="seagreen")
plt.xticks(np.arange(20 + 1))
plt.title("Fair 20-sided die", fontsize=14)

# finally 1000 biased 8-sided dice
plt.subplot(1, 3, 3)
biased_rolls_8 = Categorical(mu=np.array([3, 1, 1, 1, 1, 1, 1, 1], float) / 10).
    draw(1000)
plt.bar(np.arange(1, 9), sum(biased_rolls_8), color="crimson")
plt.title("Biased 8-sided die", fontsize=14)

plt.show()
```



It is easily seen that the distribution is normalized

$$\begin{aligned}
\sum_{\mathbf{x}} p(\mathbf{x}|\mu) &= \sum_{\mathbf{x}} \prod_{k=1}^K \mu_k^{x_k} \\
&= \prod_{k=1}^K \mu_k^{x_k^1} + \cdots + \prod_{k=1}^K \mu_k^{x_k^K} \\
&= \sum_{k=1}^K \mu_k = 1
\end{aligned}$$

and that

$$\begin{aligned}
\mathbb{E}[\mathbf{x}] &= \mathbb{E}[\mathbf{x}|\mu] \\
&= \sum_{\mathbf{x}} \mathbf{x} p(\mathbf{x}|\mu) \\
&= \sum_{\mathbf{x}} \mathbf{x} \prod_{k=1}^K \mu_k^{x_k} \\
&= \mathbf{x}^1 \prod_{k=1}^K \mu_k^{x_k^1} + \cdots + \mathbf{x}^K \prod_{k=1}^K \mu_k^{x_k^K} \\
&= (\mu_1, \dots, \mu_K)^T
\end{aligned}$$

Consider a data set \mathcal{D} of N independent observations $\mathbf{x}_1, \dots, \mathbf{x}_N$, the corresponding likelihood function is given by

$$\begin{aligned}
p(\mathcal{D}|\mu) &= \prod_{n=1}^N \prod_{k=1}^K \mu_k^{x_{nk}} \\
&= \prod_{k=1}^K \mu_k^{(\sum_{n=1}^N x_{nk})} \\
&= \prod_{k=1}^K \mu_k^{m_k}
\end{aligned}$$

Therefore, given some observed dice rolls, we can plot, for instance, how likely it is that the number one in the die that produced these observations is biased in a certain way

[10]: `N = 100`

```

def likelihood(mu_1, data):
    mus = (np.ones(6) * (1 - mu_1)) / 5
    mus[0] = mu_1
    return Categorical(mu=mus).log_likelihood_iid(data)

mu_space = np.linspace(0, 1, 100)

```

```

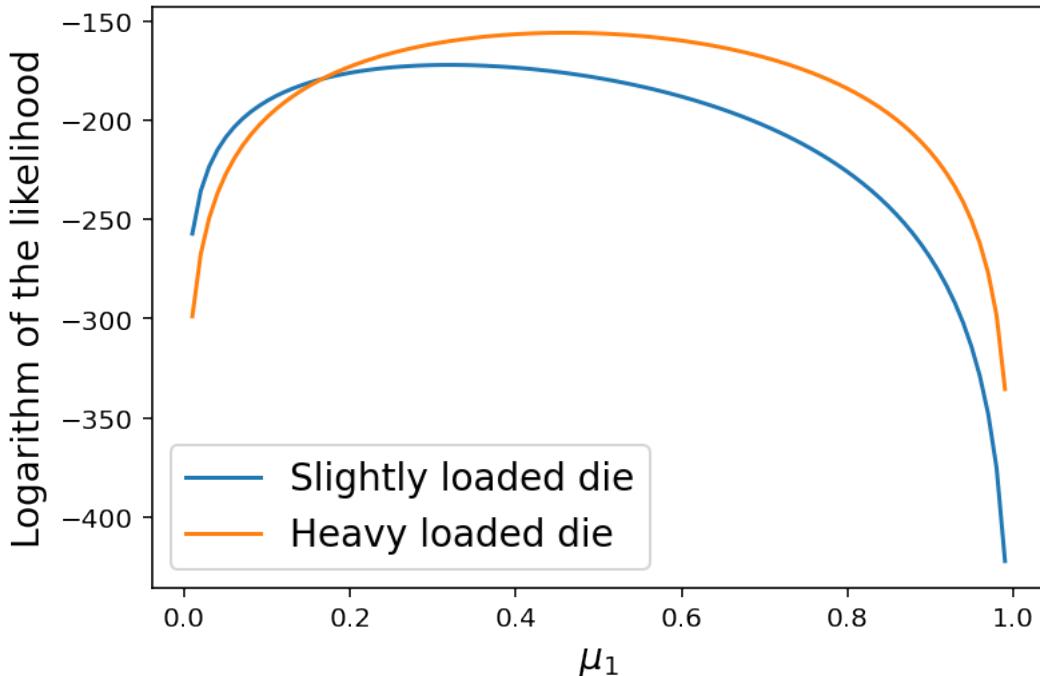
nums = np.array([2, 1, 1, 1, 1, 1], float)
print(nums / sum(nums))
slightly_loaded_data = Categorical(mu=nums / sum(nums)).draw(N)
plt.plot(mu_space, [likelihood(mu_1, slightly_loaded_data) for mu_1 in mu_space], label="Slightly loaded die")

nums = np.array([5, 1, 1, 1, 1, 1], float)
print(nums / sum(nums))
heavy_loaded_data = Categorical(mu=nums / sum(nums)).draw(N)
plt.plot(mu_space, [likelihood(mu_1, heavy_loaded_data) for mu_1 in mu_space], label="Heavy loaded die")

plt.xlabel("\mu_1", fontsize=14)
plt.ylabel("Logarithm of the likelihood", fontsize=14)
plt.legend(fontsize=14)
plt.show()

```

[0.28571429 0.14285714 0.14285714 0.14285714 0.14285714 0.14285714]
[0.5 0.1 0.1 0.1 0.1 0.1]



In order to maximize $\ln p(\mathcal{D}|\mu)$, taking account of the constraint $c(\mu) = \sum_k \mu_k - 1$, we use a Lagrange multiplier λ and maximizing

$$L(\mu, \lambda) = \ln p(\mathcal{D}|\mu) + \lambda c(\mu)$$

By setting the gradient to zero, we obtain the maximum likelihood solution in the form

$$\mu_k = \frac{m_k}{N}$$

which is the fraction of the N observations for which $x_k = 1$. Thus, the maximum likelihood solution, similar to the Bernoulli distribution, is the *sample mean* on each dimension.

```
[11]: print("Maximum likelihood of for the slightly loaded die is", np.
    ↪mean(slightly_loaded_data, axis=0))
print("Maximum likelihood of for the heavy loaded die is", np.
    ↪mean(heavy_loaded_data, axis=0))
```

```
Maximum likelihood of for the slightly loaded die is [0.32 0.13 0.14 0.12 0.13
0.16]
Maximum likelihood of for the heavy loaded die is [0.46 0.11 0.11 0.12 0.09
0.11]
```

The joint distribution of the quantities m_1, \dots, m_K , conditioned on the parameters μ and the total number N of observations, is known as the *multinomial* distribution. It would give us the number of 1, 2, 3, ... rolled in a sample dataset of size N , the same way the binomial distribution gave us the number of heads. The multinomial distribution is given by

$$\text{Mult}(m_1, \dots, m_K | \mu, N) = \binom{N}{m_1 m_2 \dots m_K} \prod_{k=1}^K \mu_k^{m_k}$$

where

$$\binom{N}{m_1 m_2 \dots m_K} = \frac{N!}{m_1! m_2! \dots m_K!}$$

is the number of ways to partition N objects into K groups of size m_1, \dots, m_K , and is called the *multinomial coefficient*.

We cannot really plot the multinomial distribution directly, because of the many dimensions of \mathbf{m} . However, we can show the distribution of the number of ones rolled (constraining the other numbers), using various weighted dice.

```
[12]: # Consider N tosses of a 6-sided die.
N = 35
m_space = np.arange(1, 15)

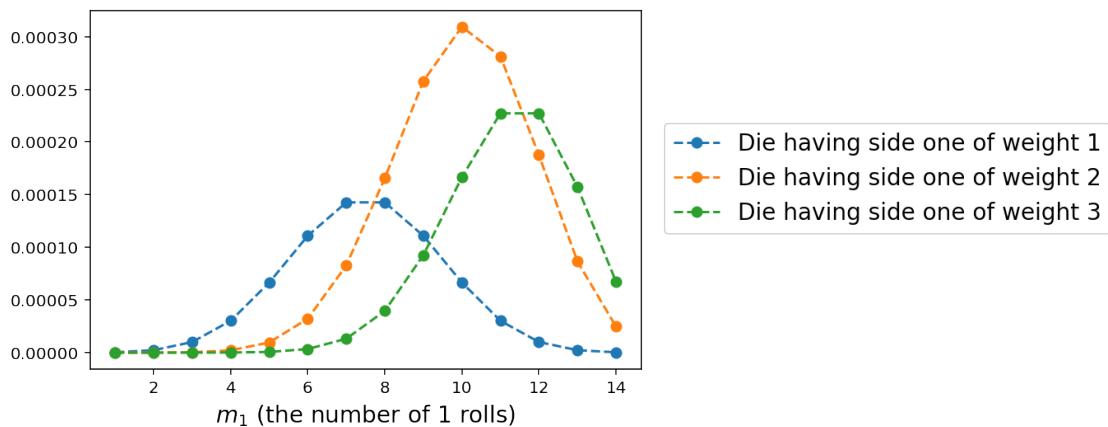
# The weight parameter determines how biased is side 1 of the die
for w in [1, 2, 3]:
    nums = np.array([w, 1, 1, 1, 1, 1])
    distribution = Multinomial(N, mu=nums / sum(nums))
    plt.plot(
        m_space,
```

```

    [distribution.pdf(np.array([m1, 5, 5, 5, 5, 5, 15 - m1]).T) for m1 in
     m_space,
     "o--",
     label="Die having side one of weight %s" % w,
     )

plt.xlabel("$m_1$ (the number of $1$ rolls)", fontsize=14)
plt.legend(bbox_to_anchor=(1, 0.75), loc=2, borderaxespad=1, fontsize=14)
plt.show()

```



And we can plot the distribution over a 3 sided die in using a colormap. Note that the plot only depicts two variables on the axes, since the third can be inferred as they sum to N.

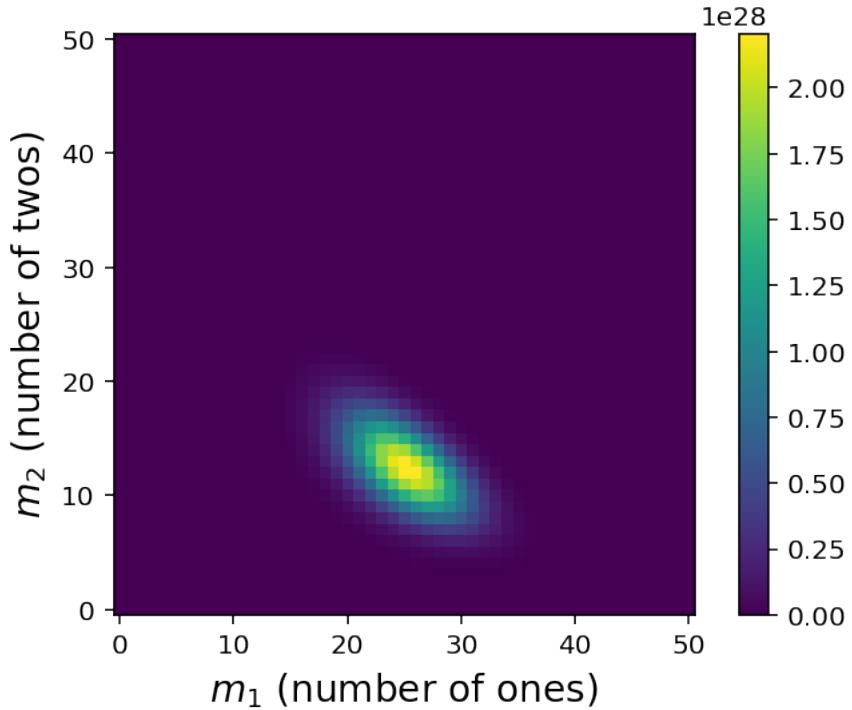
```

[13]: N = 50
m_space = np.arange(N + 1)
distribution = Multinomial(N, mu=np.array([2, 1, 1]).T)

o = np.ones((N + 1, N + 1))
for m1 in m_space:
    for m2 in np.arange((N - m1) + 1):
        m3 = N - m1 - m2
        o[m2, m1] = distribution.pdf(np.array([m1, m2, m3]).T)

plt.imshow(o, origin="lower")
plt.xlabel("$m_1$ (number of ones)", fontsize=14)
plt.ylabel("$m_2$ (number of twos)", fontsize=14)
plt.colorbar()
plt.show()

```



2.2.1 The Dirichlet distribution

Similar to the Beta distribution, consider a family of prior distributions for the parameters μ of the multinomial distribution, called the *Dirichlet* distribution

$$\text{Dir}(\mu|\alpha) = \frac{\Gamma(\alpha_0)}{\Gamma(\alpha_1)\cdots\Gamma(\alpha_K)} \prod_{k=1}^K \mu_k^{\alpha_k-1}$$

In order to give an intuition we plot the Dirichlet distribution over three variables. Two of them are shown in horizontal axes are coordinates in the plane of the simplex, while the vertical axis corresponds to the value of the density.

```
[14]: fig = plt.figure(figsize=(20, 5))

for i, alpha in enumerate([0.1, 1, 10]):
    distribution = Dirichlet(np.array([alpha, alpha, alpha]))
    X1, X2 = np.meshgrid(np.arange(0, 1, 0.01), np.arange(0, 1, 0.01))
    X3 = 1 - (X1 + X2)

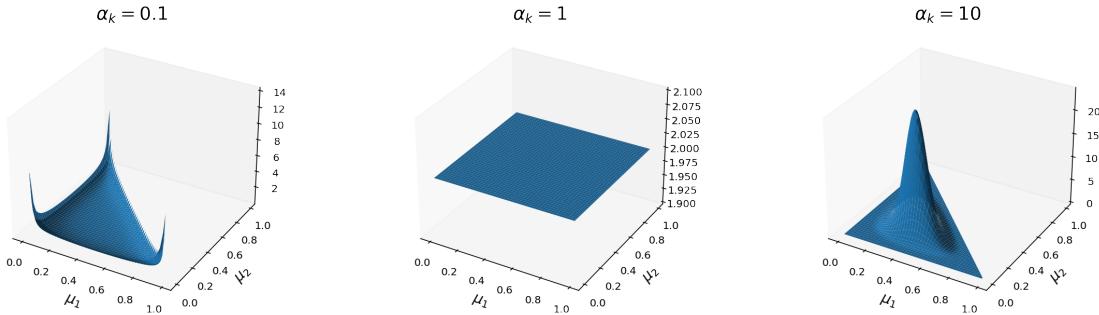
    X = np.array([np.ravel(X1), np.ravel(X2), [float("nan") if x < 0 else x for x in np.ravel(X3)]]).T
    Z = distribution.pdf(X).reshape(X1.shape)
```

```

ax = fig.add_subplot(1, 3, i + 1, projection="3d")
ax.grid(visible=None)
ax.plot_surface(X1, X2, Z)
ax.set_xlabel("$\mu_1$", fontsize=14)
ax.set_ylabel("$\mu_2$", fontsize=14)
ax.set_title("$\alpha_k={}$".format(str(alpha)), fontsize=18)

plt.show()

```



Multiplying the Dirichlet prior by the multinomial likelihood function and **normalizing**, we obtain the posterior distribution for the parameters μ in the form

$$p(\mu|\mathcal{D}, \alpha) = \text{Dir}(\mu|\alpha + \mathbf{m}) = \frac{\Gamma(\alpha_0 + N)}{\Gamma(\alpha_1 + m_1) \cdots \Gamma(\alpha_K + m_K)} \prod_{k=1}^K \mu_k^{\alpha_k + m_k - 1}$$

Note that the posterior distribution again takes the form of a Dirichlet distribution, confirming that the Dirichlet is indeed a **conjugate prior** for the multinomial distribution. As in the case of the binomial distribution and the beta prior, the parameters α_k of the Dirichlet prior can be interpreted as an *effective number of observations* of $x_k = 1$. Thus, the effect of observing a data set of \mathbf{m} observations for the K states of \mathbf{x} is to increase the values of α by \mathbf{m} from the prior to the posterior distribution.

To that end, we present a Bayesian inference step, where an observations of $\mathbf{x} = (1, 0, 0)^T$ arrives. Given a Dirichlet prior having parameters $\alpha = (2, 2, 2)^T$, note how the prior revises the form of the **unnormalized** posterior according to the likelihood.

```
[15]: # Apply a sequence of Bayesian inference steps, as more observations arrive in
      # the form of a likelihood
fig = plt.figure(figsize=(20, 5))

# The Dirichlet conjugate prior for the multinomial distribution (starting
# parameters a=[2, 2, 2])
prior = Dirichlet(alpha=np.array([2, 2, 2]).T)
Z = prior.pdf(X).reshape(X1.shape)
ax = fig.add_subplot(1, 3, 1, projection="3d")
```

```

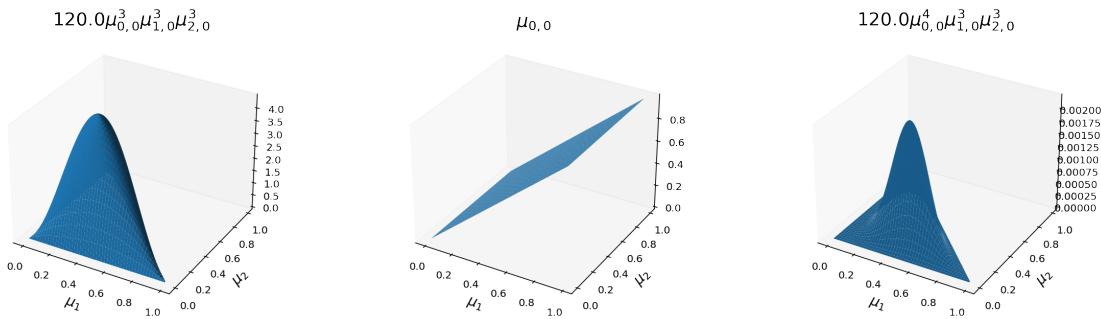
ax.grid(visible=None)
ax.plot_surface(X1, X2, Z)
ax.set_xlabel("$\mu_1$", fontsize=14)
ax.set_ylabel("$\mu_2$", fontsize=14)
ax.set_title(prior.change_notation({"x": "mu"}).to_latex, fontsize=18)

# The multinomial likelihood
ax = fig.add_subplot(1, 3, 2, projection="3d")
ax.grid(visible=None)
likelihood = Multinomial(n=1, dim=3).pdf(np.array([1, 0, 0]).T)
Z = likelihood.pdf(mu=X).reshape(X1.shape)
ax.plot_surface(X1, X2, Z)
ax.set_xlabel("$\mu_1$", fontsize=14)
ax.set_ylabel("$\mu_2$", fontsize=14)
ax.set_title(likelihood.to_latex, fontsize=18)

# The resulting posterior
ax = fig.add_subplot(1, 3, 3, projection="3d")
ax.grid(visible=None)
posterior = prior.change_notation({"x": "mu"}) * likelihood
Z = posterior.pdf(mu=X).reshape(X1.shape)
ax.plot_surface(X1, X2, Z)
ax.set_xlabel("$\mu_1$", fontsize=14)
ax.set_ylabel("$\mu_2$", fontsize=14)
ax.set_title(posterior.to_latex, fontsize=18)

plt.show()

```



2.3 Gaussian Distribution

The *Gaussian*, also known as the normal distribution, is a model for the distribution of continuous random variables. In the case of single variable x , the Gaussian distribution is given by

$$\mathcal{N}(x|\mu, \sigma^2) = \frac{1}{(2\pi\sigma^2)^{1/2}} \exp \left\{ -\frac{1}{2\sigma^2} (x - \mu)^2 \right\}$$

For a D -dimensional vector \mathbf{x} , the multivariate Gaussian distribution takes the form

$$\mathcal{N}(\mathbf{x}|\mu, \Sigma) = \frac{1}{(2\pi)^{D/2} |\Sigma|^{1/2}} \exp \left\{ -\frac{1}{2} (\mathbf{x} - \mu)^T \Sigma^{-1} (\mathbf{x} - \mu) \right\}$$

where μ is a D -dimensional mean vector, Σ is a $D \times D$ covariance matrix, while $|\cdot|$ denotes the determinant of Σ .

The Gaussian distribution can be motivated from a variety of perspectives. For instance, we have seen that for continuous variables, the distribution **maximizing the entropy** is a Gaussian distribution. Moreover, the *central limit theorem* tell us that the sum of a set of random variables, which is of course itself a random variable, has a distribution that becomes increasingly Gaussian as the number of terms increases.

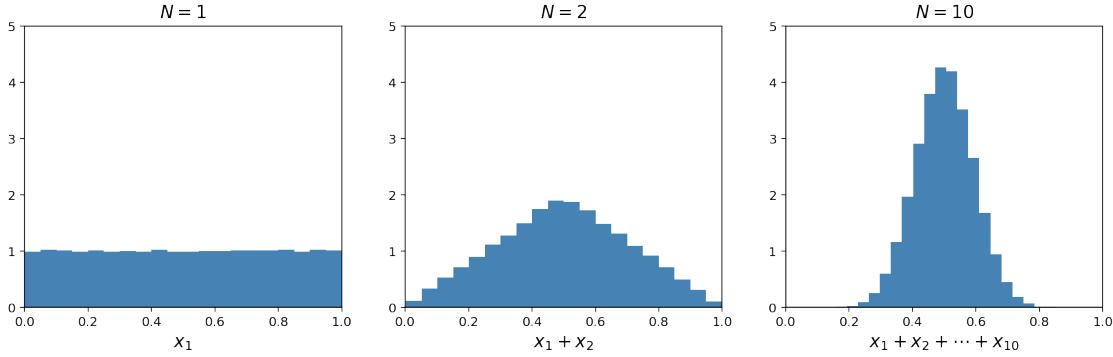
```
[16]: plt.figure(figsize=(15, 4))

plt.subplot(1, 3, 1)
sample = np.mean(np.random.uniform(0, 1, size=(1, 100000)), axis=0)
plt.hist(sample, bins=20, density=True, color="steelblue")
plt.xlabel("$x_1$", fontsize=14)
plt.xlim(0, 1)
plt.ylim(0, 5)
plt.title("$N=1$", fontsize=14)

plt.subplot(1, 3, 2)
sample = np.mean(np.random.uniform(0, 1, size=(2, 100000)), axis=0)
plt.hist(sample, bins=20, density=True, color="steelblue")
plt.xlabel("$x_1+x_2$", fontsize=14)
plt.xlim(0, 1)
plt.ylim(0, 5)
plt.title("$N=2$", fontsize=14)

plt.subplot(1, 3, 3)
sample = np.mean(np.random.uniform(0, 1, size=(10, 100000)), axis=0)
plt.hist(sample, bins=20, density=True, color="steelblue")
plt.xlabel("$x_1+x_2+\dots+x_{10}$", fontsize=14)
plt.xlim(0, 1)
plt.ylim(0, 5)
plt.title("$N=10$", fontsize=14)

plt.show()
```



Although the Gaussian distribution is widely used as a density model, it suffers from significant limitations:

1. Consider the number of free parameters in the distribution. A general symmetric covariance matrix has $D(D + 1)/2$ independent parameters, and there are another D independent parameters in μ , resulting in $D(D + 3)/2$ parameters in total. Since the total number of parameters grows quadratically with D , manipulation and inversion of large matrices becomes prohibitive.
2. One way of addressing these problems is by considering restricted forms of the covariance matrix, such as *diagonal*, $= \text{diag}(\sigma_i^2)$, or even *isotropic*, $= \sigma^2 \mathbf{I}$, covariance matrices. Unfortunately, whereas such approaches limit the number of degrees of freedom in the distribution, making the inversion of the covariance matrix faster, they also greatly restrict the form of the probability density and its ability to capture interesting correlations in the data.
3. The Gaussian distribution is intrinsically unimodal (i.e., has a single maximum), and so is unable to approximate multimodal distributions.

```
[17]: # Generate 100 points in the interval [-5, 5]
N = 100
X1, X2 = np.meshgrid(np.linspace(-5, 5, N), np.linspace(-5, 5, N))
X = np.array([np.ravel(X1), np.ravel(X2)])

plt.figure(figsize=(18, 5))

# General covariance matrix
generic_sigma = np.array([[1.5, 0.92], [0.92, 2.2]])
N_distribution = MultivariateGaussian(np.zeros((2, 1)), generic_sigma)
p = np.diag(N_distribution.pdf(X)).reshape(X1.shape)

plt.subplot(1, 3, 1)
plt.contourf(X1, X2, p, cmap="binary")
plt.xlabel("$x_1$", fontsize=14)
plt.ylabel("$x_2$", fontsize=14)
plt.axis([-3, 3, -3, 3])
```

```

# Diagonal covariance matrix
diagonal_sigma = np.array([[1.5, 0], [0, 2.2]])
N_distribution = MultivariateGaussian(np.zeros((2, 1)), diagonal_sigma)
p = np.diag(N_distribution.pdf(X)).reshape(X1.shape)

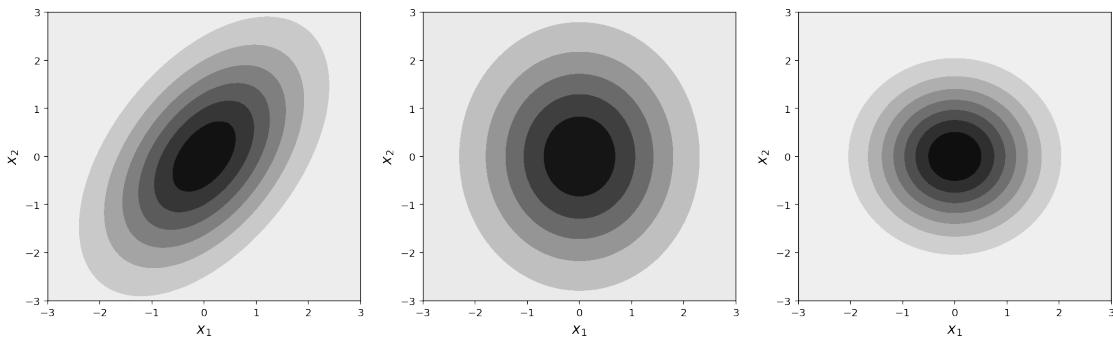
plt.subplot(1, 3, 1)
plt.contourf(X1, X2, p, cmap="binary")
plt.xlabel("$x_1$", fontsize=14)
plt.ylabel("$x_2$", fontsize=14)
plt.axis([-3, 3, -3, 3])

# Isotropic covariance matrix
isotropic_sigma = np.array([[1.0, 0], [0, 1.0]])
N_distribution = MultivariateGaussian(np.zeros((2, 1)), isotropic_sigma)
p = np.diag(N_distribution.pdf(X)).reshape(X1.shape)

plt.subplot(1, 3, 2)
plt.contourf(X1, X2, p, cmap="binary")
plt.xlabel("$x_1$", fontsize=14)
plt.ylabel("$x_2$", fontsize=14)
plt.axis([-3, 3, -3, 3])

plt.show()

```



2.3.4 Maximum likelihood for the Gaussian

Given a data set $\mathbf{X} = (\mathbf{x}_1, \dots, \mathbf{x}_N)^T$, in which the observations \mathbf{x}_n are assumed to be drawn independently from a multivariate Gaussian distribution, we can estimate the parameters of the distribution by maximum likelihood. The logarithm of the likelihood function is given by

$$\begin{aligned}
\ln p(\mathbf{X}|\mu, \Sigma) &= \ln \left(\prod_{n=1}^N \mathcal{N}(\mathbf{x}_n|\mu, \Sigma) \right) \\
&= \ln \left(\prod_{n=1}^N \frac{1}{(2\pi)^{D/2} |\Sigma|^{1/2}} \exp \left\{ -\frac{1}{2} (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \right\} \right) \\
&= \sum_{n=1}^N \ln \left(\frac{1}{(2\pi)^{D/2} |\Sigma|^{1/2}} \exp \left\{ -\frac{1}{2} (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \right\} \right) \\
&= \sum_{n=1}^N \ln \left(\frac{1}{(2\pi)^{D/2} |\Sigma|^{1/2}} \right) + \sum_{n=1}^N \ln \exp \left\{ -\frac{1}{2} (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \right\} \\
&= N \ln \left(\frac{1}{(2\pi)^{D/2} |\Sigma|^{1/2}} \right) - \frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \\
&= -N \ln ((2\pi)^{D/2} |\Sigma|^{1/2}) - \frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \\
&= -\frac{ND}{2} \ln(2\pi) - \frac{N}{2} \ln |\Sigma| - \frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu)
\end{aligned}$$

Taking the derivative of the log-likelihood over μ and set it equal to 0, we obtain the solution for the maximum likelihood estimate of the mean, given by

$$\begin{aligned}
\frac{\partial}{\partial \mu} \ln p(\mathbf{X}|\mu, \Sigma) = 0 &\Leftrightarrow \frac{\partial}{\partial \mu} \left(-\frac{ND}{2} \ln(2\pi) - \frac{N}{2} \ln |\Sigma| - \frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \right) = 0 \\
&\Leftrightarrow \frac{\partial}{\partial \mu} \left(-\frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \right) = 0 \\
&\Leftrightarrow -\frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) = 0 \\
&\Leftrightarrow \sum_{n=1}^N \mathbf{x}_n - N\mu = 0 \\
&\Leftrightarrow \mu_{ML} = \frac{1}{N} \sum_{n=1}^N \mathbf{x}_n
\end{aligned}$$

which is often called the *sample mean vector*. Calculating the derivative of the log-likelihood over Σ and set it equal to 0 is given by

$$\begin{aligned}
\frac{\partial}{\partial \Sigma} \ln p(\mathbf{X}|\mu, \Sigma) = 0 &\Leftrightarrow \frac{\partial}{\partial \Sigma} \left(-\frac{ND}{2} \ln(2\pi) - \frac{N}{2} \ln |\Sigma| - \frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \right) = 0 \\
&\Leftrightarrow \frac{\partial}{\partial \Sigma} \left(-\frac{N}{2} \ln |\Sigma| \right) - \frac{\partial}{\partial \Sigma} \left(\frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \right) = 0
\end{aligned}$$

By using (C.28) the first term can be reduced to

$$\frac{\partial}{\partial} \left(-\frac{N}{2} \ln |\Sigma| \right) = -\frac{N}{2} (\Sigma^{-1})^T = -\frac{N}{2} \Sigma^{-1}$$

where the last equality holds because Σ is symmetric. For the second term, we can derive that,

$$\frac{\partial}{\partial} \left(\frac{1}{2} \sum_{n=1}^N (\mathbf{x}_n - \mu)^T \Sigma^{-1} (\mathbf{x}_n - \mu) \right) = \frac{N}{2} \Sigma^{-1} \mathbf{S}$$

where

$$\mathbf{S} = \frac{1}{N} \sum_{n=1}^N (\mathbf{x}_n - \mu)(\mathbf{x}_n - \mu)^T$$

Thus, we obtain

$$\begin{aligned} -\frac{N}{2} \Sigma^{-1} + \frac{N}{2} \Sigma^{-1} \mathbf{S} &= 0 \Leftrightarrow \\ \frac{N}{2} \Sigma^{-1} \mathbf{S} &= \frac{N}{2} \Sigma^{-1} \Leftrightarrow \\ &= \mathbf{S} \Leftrightarrow \\ \mu_{ML} &= \frac{1}{N} \sum_{n=1}^N (\mathbf{x}_n - \mu_{ML})(\mathbf{x}_n - \mu_{ML})^T \end{aligned}$$

However, if we evaluate the expectations of the maximum likelihood solutions under the true distribution, we obtain the following results

$$\mathbb{E}[\mu_{ML}] = \frac{1}{N} \mathbb{E} \left[\sum_{n=1}^N \mathbf{x}_n \right] = \frac{1}{N} \sum_{n=1}^N \mathbb{E}[\mathbf{x}_n] = \frac{1}{N} N \mu = \mu$$

and

$$\mathbb{E}[\Sigma_{ML}] = \frac{N-1}{N}$$

Thus, similar to the univariate Gaussian distribution, the expectation of the maximum likelihood estimate for the mean is equal to the true mean, while for the covariance has an expectation that is less than the true value, and hence it is biased. We can correct the bias by defining a different estimator given by

$$\hat{\Sigma} = \frac{1}{N-1} \sum_{n=1}^N (\mathbf{x}_n - \mu_{ML})(\mathbf{x}_n - \mu_{ML})^T$$

```
[18]: X = np.random.multivariate_normal(mean=np.array([0, 0]), cov=1.5**2 * np.
    eye(2), size=5)
```

```

x, y = np.meshgrid(np.linspace(-5, 5, 100), np.linspace(-5, 5, 100))

plt.figure(figsize=(18, 5))

gaussian = MultivariateGaussian(mu=np.zeros((2, 1)), cov=1.5**2 * np.eye(2))
p = np.diag(gaussian.pdf(np.array([x, y]).reshape(2, -1))).reshape(100, 100)

plt.subplot(1, 3, 1)
plt.contour(x, y, p)
plt.scatter(X[:, 0], X[:, 1], facecolor="none", edgecolor="steelblue")
plt.xlabel("$x_1$", fontsize=14)
plt.ylabel("$x_2$", fontsize=14)
plt.title("True distribution")

gaussian = MultivariateGaussian(dim=2)
gaussian.ml(X, unbiased=False)
p = np.diag(gaussian.pdf(np.array([x, y]).reshape(2, -1))).reshape(100, 100)

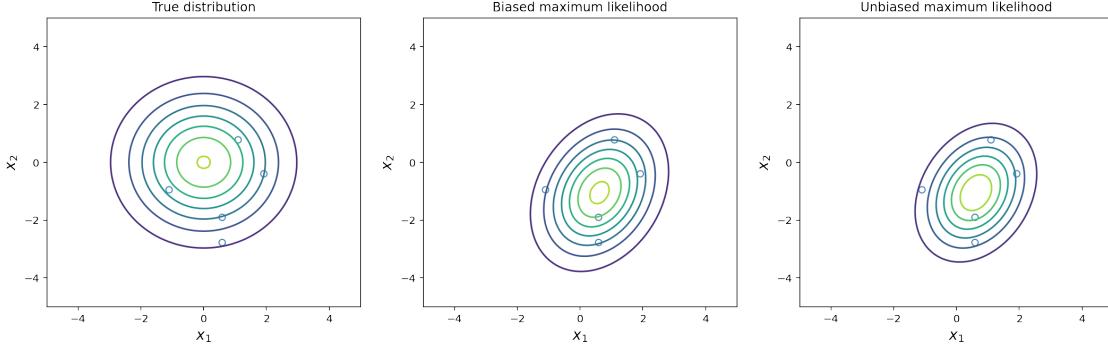
plt.subplot(1, 3, 2)
plt.contour(x, y, p)
plt.scatter(X[:, 0], X[:, 1], facecolor="none", edgecolor="steelblue")
plt.xlabel("$x_1$", fontsize=14)
plt.ylabel("$x_2$", fontsize=14)
plt.title("Biased maximum likelihood")

gaussian1 = MultivariateGaussian(dim=2)
gaussian1.ml(X, unbiased=True)
p1 = np.diag(gaussian1.pdf(np.array([x, y]).reshape(2, -1))).reshape(100, 100)

plt.subplot(1, 3, 3)
plt.contour(x, y, p1)
plt.scatter(X[:, 0], X[:, 1], facecolor="none", edgecolor="steelblue")
plt.xlabel("$x_1$", fontsize=14)
plt.ylabel("$x_2$", fontsize=14)
plt.title("Unbiased maximum likelihood")

plt.show()

```



2.3.5 Sequential estimation

Sequential or online methods allow data points to be processed one at a time and then discarded. They are important when large data sets are involved so that batch processing of all data at once is infeasible. Consider for instance, the maximum likelihood solution for the multivariate Gaussian distribution. Lets denote the solution based on N observations as $\mu_{ML}^{(N)}$. Then, by dissecting the contribution from the final data point \mathbf{x}_N we obtain

$$\begin{aligned}\mu_{ML}^{(N)} &= \frac{1}{N} \sum_{n=1}^N \mathbf{x}_n \\ &= \frac{1}{N} \mathbf{x}_N + \frac{1}{N} \sum_{n=1}^{N-1} \mathbf{x}_n \\ &= \frac{1}{N} \mathbf{x}_N + \frac{N-1}{N} \mu_{ML}^{(N-1)} \\ &= \mu_{ML}^{(N-1)} + \frac{1}{N} (\mathbf{x}_N - \mu_{ML}^{(N-1)})\end{aligned}$$

Therefore, observing the data point \mathbf{x}_N revises the estimate by moving the old estimate $\mu_{ML}^{(N-1)}$ a small amount proportional to $1/N$ in the direction of the *error signal* $(\mathbf{x}_N - \mu_{ML}^{(N-1)})$. Note that, as N increases, the contribution of successive data points gets smaller. Similarly, for $\Sigma_{ML}^{(N)}$, we obtain

$$\begin{aligned}\Sigma_{ML}^{(N)} &= \frac{1}{N} \sum_{n=1}^N (\mathbf{x}_n - \mu_{ML})(\mathbf{x}_n - \mu_{ML})^T \\ &= \frac{1}{N} \sum_{n=1}^{N-1} (\mathbf{x}_n - \mu_{ML})(\mathbf{x}_n - \mu_{ML})^T + (\mathbf{x}_N - \mu_{ML})(\mathbf{x}_N - \mu_{ML})^T \\ &= \frac{N-1}{N} \Sigma_{ML}^{(N-1)} + (\mathbf{x}_N - \mu_{ML})(\mathbf{x}_N - \mu_{ML})^T \\ &= \Sigma_{ML}^{(N-1)} + \frac{1}{N} ((\mathbf{x}_N - \mu_{ML})(\mathbf{x}_N - \mu_{ML})^T - \Sigma_{ML}^{(N-1)})\end{aligned}$$

Unfortunately, there is not always possible to derive a sequential algorithm by this route for any distribution. Therefore, we seek a more general formulation of sequential learning, which leads us

to the **Robbins-Monro** algorithm. Consider a pair of random variables θ and z governed by a joint distribution $p(\theta, z)$. The conditional expectation of z given θ is given by

$$\mathbb{E}[z|\theta] = \int z p(z|\theta) dz$$

The Robbins-Monro procedure defines a sequence of successive estimates of the root θ^* given by

$$\theta^{(N)} = \theta^{(N-1)} - a_{N-1} z(\theta^{(N-1)})$$

where $z(\theta^{(N-1)})$ is the observed value of z when θ takes the value $\theta^{(N-1)}$.

In the case of the maximum likelihood solution we know that

$$\frac{\partial}{\partial \theta} \left\{ -\frac{1}{N} \sum_{n=1}^N \ln p(x_n|\theta) \right\} = 0 \Leftrightarrow -\frac{1}{N} \sum_{n=1}^N \frac{\partial}{\partial \theta} \ln p(x_n|\theta) = 0$$

Taking the limit $N \rightarrow \infty$ we have

$$-\lim_{N \rightarrow \infty} \frac{1}{N} \sum_{n=1}^N \frac{\partial}{\partial \theta} \ln p(x_n|\theta) = \mathbb{E} \left[-\frac{\partial}{\partial \theta} \ln p(x_n|\theta) \right]$$

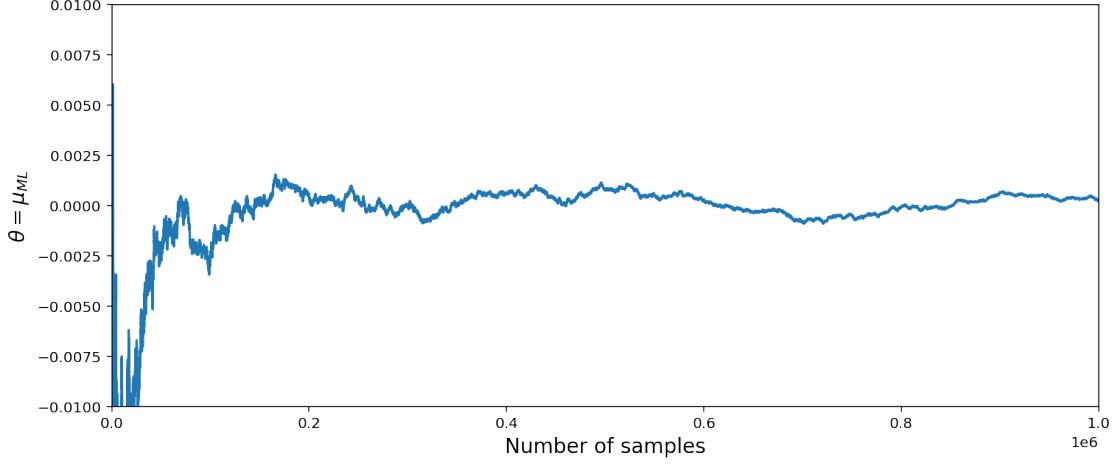
and so finding the maximum likelihood solution corresponds to finding the root of the regression function. Thus, Robbins-Monro procedure takes the form

$$\theta^{(N)} = \theta^{(N-1)} - a_{N-1} \frac{\partial}{\partial \theta^{(N-1)}} [-\ln p(x_n|\theta^{(N-1)})]$$

```
[19]: sample = np.random.randn(1000000)

sum_s = sample[0]
theta_n = sum_s / 1
history = [theta_n]
for N, s in enumerate(sample[1:], 2):
    theta_n = sum_s / N + 1 / N * (s - sum_s / N)
    sum_s += s
    history.append(theta_n)

plt.figure(figsize=(12, 5))
plt.plot(history)
plt.xlim(0, 1000000)
plt.ylim(-0.01, 0.01)
plt.xlabel("Number of samples", fontsize=14)
plt.ylabel("$\\theta = \\mu_{ML}$", fontsize=14)
plt.show()
```



2.3.6 Bayesian inference for the Gaussian

Now we develop a Bayesian treatment by introducing prior distributions over the parameters for the mean and variance. Consider a single Gaussian random variable x , for which we are given a set of N observations $\mathbf{x} = \{x_1, \dots, x_N\}$.

- 1. Suppose that the variance σ^2 is known and we consider the task of inferring the mean μ :**

The likelihood function is given by

$$p(\mathbf{x}|\mu) = \prod_{n=1}^N p(x_n|\mu) = \prod_{n=1}^N \frac{1}{(2\pi\sigma^2)^{1/2}} \exp\left\{-\frac{1}{2\sigma^2}(x_n-\mu)^2\right\} = \frac{1}{(2\pi\sigma^2)^{N/2}} \exp\left\{-\frac{1}{2\sigma^2} \sum_{n=1}^N (x_n-\mu)^2\right\}$$

NOTE: The likelihood function is **not** a probability distribution over μ and is not normalized.

A Gaussian prior $p(\mu)$ is a conjugate for the likelihood function, because the corresponding posterior is then given by the product of exponentials of quadratic functions of μ that results in a Gaussian. Thererfore, the prior has the form

$$p(\mu) = \mathcal{N}(\mu|\mu_0, \sigma_0^2)$$

and the posterior distribution can be proved to be given by

$$p(\mu|\mathbf{x}) = \mathcal{N}(\mu|\mu_N, \sigma_N^2)$$

where

$$\mu_N = \frac{\sigma^2}{N\sigma_0^2 + \sigma^2} \mu_0 + \frac{N\sigma_0^2}{N\sigma_0^2 + \sigma^2} \mu_{ML}^2$$

$$\sigma_N^2 = \sigma_0^2 + \frac{1}{N} \sigma^2$$

Note that the mean of the posterior is a compromise between the prior mean μ_0 and the maximum likelihood solution μ_{ML} . If the number of observed data points $N = 0$, then μ_N and σ_N^2 reduce to the prior mean μ_0 and variance σ_0^2 as expected. For $N \rightarrow \infty$, the posterior mean is given by the maximum likelihood solution μ_{ML} , while the variance goes to zero and the posterior distribution becomes infinitely peaked around the maximum likelihood solution.

```
[20]: x = np.linspace(-1, 1, 100)

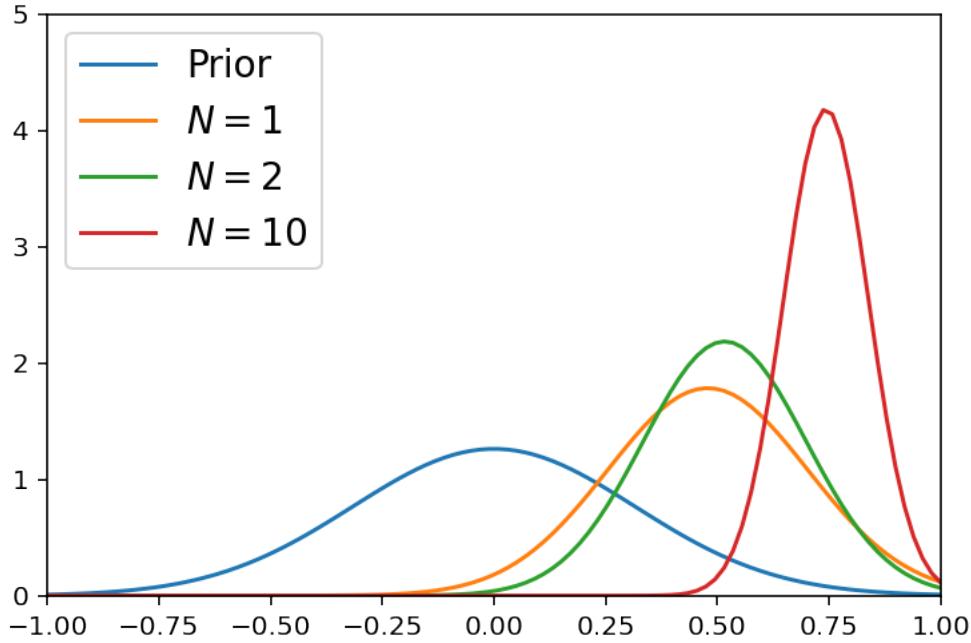
prior = Gaussian(0, 0.1)
plt.plot(x, prior.pdf(x), label="Prior")

N = 1
sample = Gaussian(mu=0.8, var=0.1**2).draw(N)
mN = (N * 0.1 * np.mean(sample)) / (N * 0.1 + 0.1)
varN = 1 / ((1 / 0.1) + (N / 0.1))
plt.plot(x, Gaussian(mN, varN).pdf(x), label="$N=1$")

N = 2
sample = Gaussian(mu=0.8, var=0.1**2).draw(N)
mN = (N * (0.1) * np.mean(sample)) / (N * 0.1 + 0.1)
varN = 1 / ((1 / 0.1) + (N / 0.1))
plt.plot(x, Gaussian(mN, varN).pdf(x), label="$N=2$")

N = 10
sample = Gaussian(mu=0.8, var=0.1**2).draw(N)
mN = (N * 0.1 * np.mean(sample)) / (N * 0.1 + 0.1)
varN = 1 / ((1 / 0.1) + (N / 0.1))
plt.plot(x, Gaussian(mN, varN).pdf(x), label="$N=10$")

plt.xlim(-1, 1)
plt.ylim(0, 5)
plt.legend(fontsize=14)
plt.show()
```



2. Suppose that the mean μ is known and we wish to infer the variance σ^2 :

The likelihood function is given by

$$p(\mathbf{x}|\lambda^{-1}) = \prod_{n=1}^N p(x_n|\lambda^{-1}) = \frac{\lambda^{N/2}}{\sqrt{2\pi\sigma^2}} \exp\left\{-\frac{\lambda}{2}\sum_{n=1}^N (x_n - \mu)^2\right\}$$

where we choose to use the precision $\lambda = 1/\sigma^2$ for convenience.

The corresponding conjugate prior should therefore be proportional to the product of a power of λ and the exponential of a linear function of λ , which corresponds to a *gamma* distribution

$$\text{Gam}(\lambda|a, b) = \frac{1}{\Gamma(a)} b^a \lambda^{a-1} \exp(-b\lambda)$$

In the case of variance, the conjugate prior is called the *inverse gamma* distribution. The mean of the gamma distribution is given by

$$\begin{aligned}
\mathbb{E}[\lambda] &= \int_0^\infty \lambda \frac{1}{\Gamma(a)} b^a \lambda^{a-1} \exp(-b\lambda) d\lambda \\
&= \frac{b^a}{\Gamma(a)} \int_0^\infty \lambda^a \exp(-b\lambda) d\lambda \\
&\stackrel{u=b\lambda}{=} \frac{b^a}{\Gamma(a)} \int_0^\infty \frac{u^a}{b^a} \exp(-u) \frac{1}{b} du \\
&= \frac{1}{b\Gamma(a)} \int_0^\infty u^a \exp(-u) du \\
&= \frac{1}{b\Gamma(a)} \int_0^\infty u^a \exp(-u) du \\
&= \frac{1}{b\Gamma(a)} \Gamma(a+1) = \frac{1}{b\Gamma(a)} a\Gamma(a) = \frac{a}{b}
\end{aligned}$$

where we have used the gamma function definition

$$\Gamma(x) = \int_0^\infty u^{x-1} e^{-u} du$$

The variance is given by

$$\begin{aligned}
\text{var}[\lambda] &= \mathbb{E}[\lambda^2] - \mathbb{E}[\lambda]^2 \\
&= \mathbb{E}[\lambda^2] - \frac{a^2}{b^2} \\
&= \int_0^\infty \lambda^2 \text{Gam}(\lambda|a, b) d\lambda - \frac{a^2}{b^2} \\
&= \int_0^\infty \lambda^2 \frac{1}{\Gamma(a)} b^a \lambda^{a-1} \exp(-b\lambda) d\lambda - \frac{a^2}{b^2} \\
&= \frac{b^a}{\Gamma(a)} \int_0^\infty \lambda^{a+1} \exp(-b\lambda) d\lambda - \frac{a^2}{b^2} \\
&\stackrel{u=b\lambda}{=} \frac{b^a}{\Gamma(a)} \int_0^\infty \frac{u^{a+1}}{b^{a+1}} \exp(-u) \frac{1}{b} du - \frac{a^2}{b^2} \\
&= \frac{1}{b^2 \Gamma(a)} \int_0^\infty u^{a+1} \exp(-u) du - \frac{a^2}{b^2} \\
&= \frac{1}{b^2 \Gamma(a)} \Gamma(a+2) - \frac{a^2}{b^2} \\
&= \frac{1}{b^2 \Gamma(a)} a(a+1)\Gamma(a) - \frac{a^2}{b^2} = \frac{a(a+1)}{b^2} - \frac{a^2}{b^2} = \frac{a}{b^2}
\end{aligned}$$

```
[21]: lambda_space = np.arange(0, 2, 0.01)

plt.figure(figsize=(18, 5))

plt.subplot(1, 3, 1)
```

```

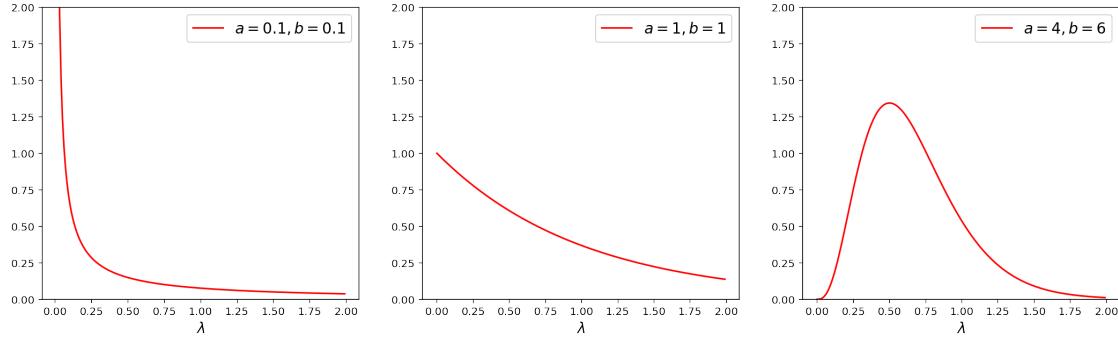
plt.plot(lambda_space, Gamma(a=0.1, b=0.1).pdf(lambda_space), color="red", u
        ↓label="$a=0.1, b=0.1$")
plt.ylim(0, 2)
plt.xlabel("$\lambda$", fontsize=14)
plt.legend(fontsize=14)

plt.subplot(1, 3, 2)
plt.plot(lambda_space, Gamma(a=1, b=1).pdf(lambda_space), color="red", u
        ↓label="$a=1, b=1$")
plt.ylim(0, 2)
plt.xlabel("$\lambda$", fontsize=14)
plt.legend(fontsize=14)

plt.subplot(1, 3, 3)
plt.plot(lambda_space, Gamma(a=4, b=6).pdf(lambda_space), color="red", u
        ↓label="$a=4, b=6$")
plt.ylim(0, 2)
plt.xlabel("$\lambda$", fontsize=14)
plt.legend(fontsize=14)

plt.show()

```



Considering a prior $\text{Gam}(\lambda|a_0, b_0)$ and multiplying by the likelihood function, we obtain an **un-normalized** posterior distribution of the form

$$p(\lambda|x) \propto \lambda^{a_0-1} \lambda^{N/2} \exp\left\{-b_0\lambda - \frac{\lambda}{2} \sum_{n=1}^N (x_n - \mu)^2\right\}$$

which is a gamma distribution $\text{Gam}(\lambda|a_N, b_N)$

$$\begin{aligned} a_N &= a_0 + \frac{N}{2} \\ b_N &= b_0 + \frac{1}{2} \sum_{n=1}^N (x_n - \mu)^2 = b_0 + \frac{N}{2} \sigma_{ML}^2 \end{aligned}$$

Thus, the effect of observing N data points is to increase the value of the coefficient a by $\frac{N}{2}$ and the value of coefficient b by $\frac{N}{2}\sigma_{ML}^2$.

3. Suppose that both the mean μ and the variance σ^2 are unknown:

TODO

2.3.7 Student's t-distribution

Consider a univariate Gaussian distribution $\mathcal{N}(x|\mu, \tau^{-1})$ and a gamma prior $\text{Gam}(\tau|a, b)$. If we integrate out the precision τ , we obtain the marginal distribution of x in the form

$$p(x|\mu, a, b) = \int_0^\infty \mathcal{N}(x|\mu, \tau^{-1}) \text{Gam}(\tau|a, b) d\tau = \frac{b^a}{\Gamma(a)} \left(\frac{1}{2\pi} \right)^{1/2} \left[b + \frac{(x-\mu)^2}{2} \right]^{-a-1/2} \Gamma(a+1/2)$$

where we have made the change of variable $z = \tau[b + (x - \mu)^2/2]$. By defining new parameters given by $\nu = 2a$ and $\lambda = a/b$, the distribution $p(x|\mu, a, b)$ takes the form

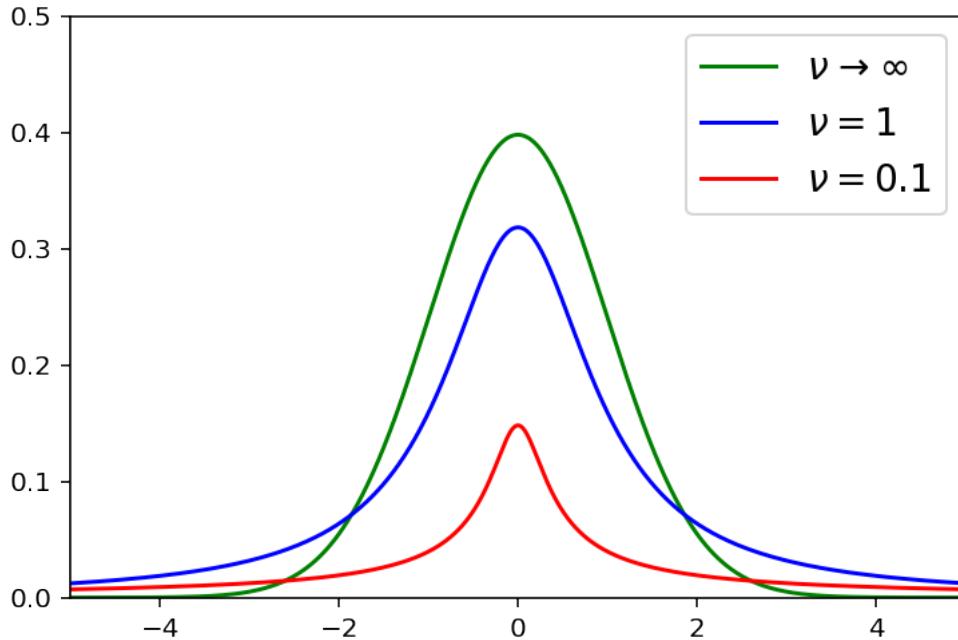
$$\text{St}(x|\mu, \lambda, \nu) = \frac{\Gamma(\nu/2 + 1/2)}{\Gamma(\nu/2)} \left(\frac{\lambda}{\pi\nu} \right)^{1/2} \left[1 + \frac{\lambda(x-\mu)^2}{\nu} \right]^{-\nu/2-1/2}$$

which is known as *Student's t-distribution*. The parameter λ is called the *precision* of the t-distribution, even though it is not equal to inverse of the variance, while the parameter ν is called the degrees of freedom.

```
[22]: x_space = np.arange(-5, 5, 0.01)

plt.plot(x_space, StudentT(nu=100).pdf(x_space), color="green", label="$\\nu\\$;  
$\leftrightarrow$\\to\\;\\infty$")
plt.plot(x_space, StudentT(nu=1).pdf(x_space), color="blue", label="$\\nu=1$")
plt.plot(x_space, StudentT(nu=0.1).pdf(x_space), color="red", label="$\\nu=0."  
$\leftrightarrow$1$")
plt.xlim(-5, 5)
plt.ylim(0, 0.5)
plt.legend(fontsize=14)

plt.show()
```



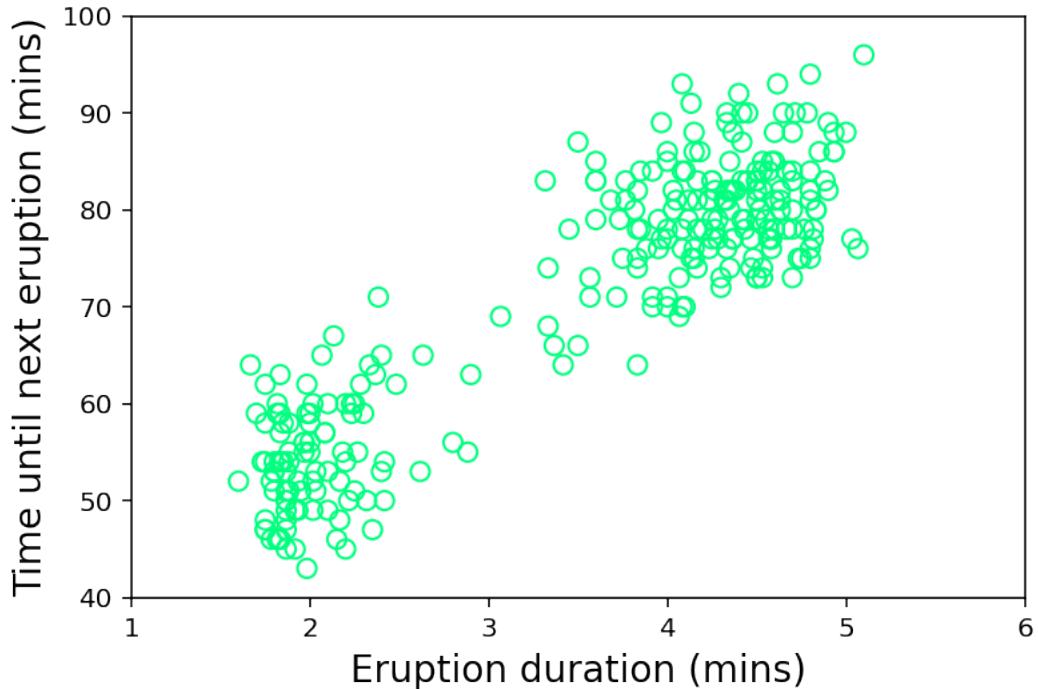
For $\nu = 1$ the t-distribution reduces to the *Cauchy* distribution, while for $\nu \rightarrow \infty$ the t-distribution becomes a Gaussian.

Note that the Student's t-distribution is obtained by adding up an infinite number of Gaussian distributions having the same mean, but different precisions. Thus, the t-distribution can be interpreted as a *mixture* of Gaussians. The result of this mixture is that the distribution has longer *tails*, which gives the t-distribution an important property called *robustness*. Essentially, it is much less sensitive, than the Gaussian, to the presence of few data points which are *outliers*.

2.3.9 Mixtures of Gaussians

Although the Gaussian distribution has important analytical properties, it also has significant limitations regarding to modelling real data sets. Consider for instance the *Old Faithful* dataset comprise 272 measurements of the eruption of the Old Faithful geyser at Yellowstone National Park in the USA.

```
[23]: old_faithful = load_old_faithful()
plt.scatter(old_faithful[:, :1], old_faithful[:, 1:2], color="springgreen", ▾
           facecolors="none", s=50)
plt.xlim(1, 6)
plt.ylim(40, 100)
plt.xlabel("Eruption duration (mins)", fontsize=14)
plt.ylabel("Time until next eruption (mins)", fontsize=14)
plt.show()
```

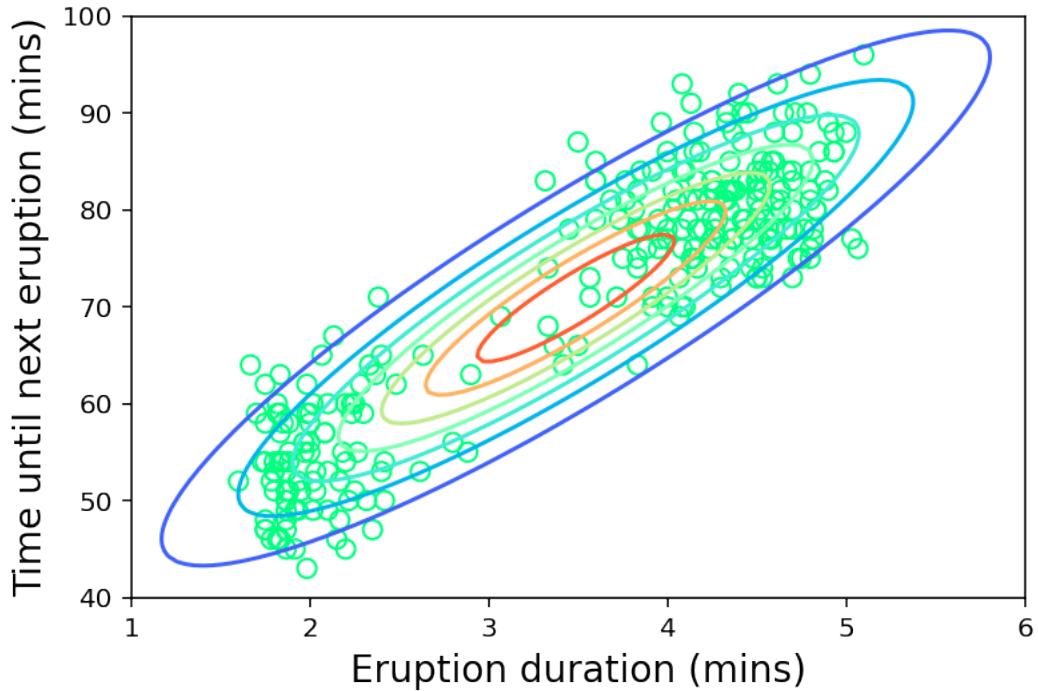


Each measurement comprises the duration of the eruption in minutes (x -axis) and the time in minutes to the next eruption (y -axis). Note that the data forms two dominant modes. Therefore, a simple Gaussian distribution **should be unable to capture this structure**.

```
[24]: x, y = np.meshgrid(np.linspace(1, 6, 100), np.linspace(40, 100, 100))

# Perform maximum likelihood over the dataset
model = MultivariateGaussian(dim=2)
model.ml(old_faithful)
p = np.diag(model.pdf(np.array([x, y]).reshape(2, -1))).reshape(100, 100)

plt.scatter(old_faithful[:, :1], old_faithful[:, 1:2], color="springgreen", ▾
           facecolors="none", s=50)
plt.contour(x, y, p, cmap="rainbow")
plt.xlim(1, 6)
plt.ylim(40, 100)
plt.xlabel("Eruption duration (mins)", fontsize=14)
plt.ylabel("Time until next eruption (mins)", fontsize=14)
plt.show()
```



On the other hand, a linear combination (superposition) of two Gaussians should give a better characterization of the data since it should be able to place one Gaussian on each mode of the data. Such superpositions, formed by taking linear combinations of more basic distributions such as Gaussians, can be formulated as probabilistic models known as *mixture distributions*. We therefore define a superposition of K Gaussian densities of the form

$$p(\mathbf{x}) = \sum_{k=1}^K \pi_k \mathcal{N}(\mathbf{x} | \mu_k, \Sigma_k)$$

which is called a *mixture of Gaussians*. Each Gaussian density is called a *component of the mixture* and the parameters π_k are called the *mixing coefficients*. By using a sufficient number of Gaussians, and by optimizing their means and covariances, as well as the coefficients π_k in the linear combination, almost any continuous density can be approximated to arbitrary accuracy.

By integrating both sides of (2.188) over \mathbf{x} , and noting that both $p(\mathbf{x})$ and the individual Gaussian components are normalized, we obtain

$$\begin{aligned} \int p(\mathbf{x}) d\mathbf{x} &= \int \sum_{k=1}^K \pi_k \mathcal{N}(\mathbf{x} | \mu_k, \Sigma_k) d\mathbf{x} \Leftrightarrow \\ \sum_{k=1}^K \pi_k \int \mathcal{N}(\mathbf{x} | \mu_k, \Sigma_k) d\mathbf{x} &= 1 \Leftrightarrow \\ \sum_{k=1}^K \pi_k &= 1 \end{aligned}$$

```
[25]: x_space = np.linspace(-3, 3, 100)

# Mixture component's parameters and coefficients
mu1, mu2, mu3 = -1.2, 1.2, 0.6
var1, var2, var3 = 0.4, 0.4, 1
pi1, pi2, pi3 = 0.4, 0.2, 0.3

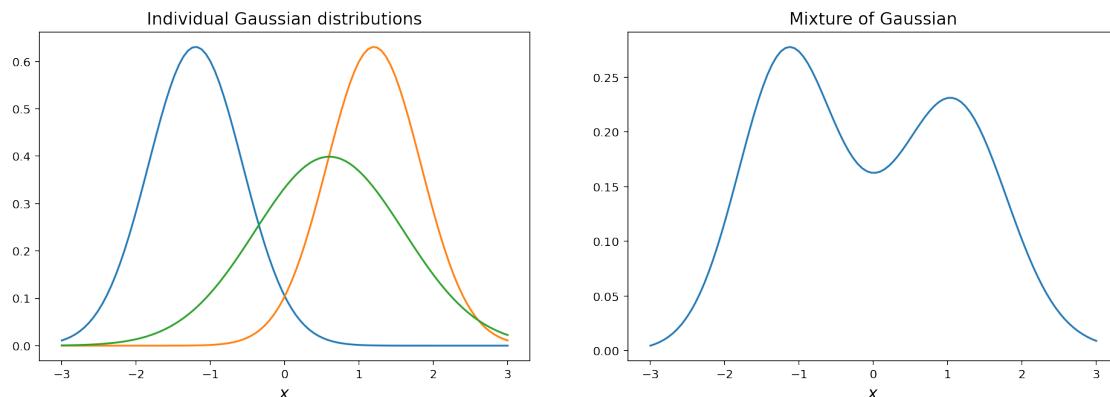
component1 = Gaussian(mu=mu1, var=var1).pdf(x_space)
component2 = Gaussian(mu=mu2, var=var2).pdf(x_space)
component3 = Gaussian(mu=mu3, var=var3).pdf(x_space)

plt.figure(figsize=(16, 5))

plt.subplot(1, 2, 1)
plt.plot(x_space, component1, label="component 1")
plt.plot(x_space, component2, label="component 1")
plt.plot(x_space, component3, label="component 1")
plt.xlabel("$x$", fontsize=14)
plt.title("Individual Gaussian distributions", fontsize=14)

plt.subplot(1, 2, 2)
plt.plot(x_space, pi1 * component1 + pi2 * component2 + pi3 * component3)
plt.xlabel("$x$", fontsize=14)
plt.title("Mixture of Gaussian", fontsize=14)

plt.show()
```



Given a dataset $\mathbf{X} = \{\mathbf{x}_1, \dots, \mathbf{x}_N\}$, one way of finding the values of the parameters is to use maximum likelihood

$$\ln p(\mathbf{X}|\pi, \mu, \sigma^2) = \ln \left(\prod_{n=1}^N \sum_{k=1}^K \pi_k \mathcal{N}(\mathbf{x}_n | \mu_k, \sigma_k^2) \right)$$

Due to the presence of the summation over k inside the logarithm, the derivation is much more complex than the case of a single Gaussian. As a result, the maximum likelihood solution for the parameters no longer has a closed-form analytical solution. One approach to maximizing the likelihood function is to use iterative numerical optimization techniques or employ a powerful framework called *Expectation-Maximization*.

2.5 Nonparametric Methods

The use of probability distributions of specific functional forms governed by a number of parameters whose values are to be determined from the data are called **parametric** approaches to density modelling. The main limitation of such approaches is that the assumed density might be a poor model of the true underlying distribution that generated the data in the first place. This leads to poor predictive performance, such as in the case of the *Old faithful* dataset and the simple unimodal Gaussian distribution.

Now we consider some **nonparametric** approaches to density estimation that make fewer assumptions about the form of the distribution. We focus mainly on simple frequentist methods, however, there are also nonparametric Bayesian methods.

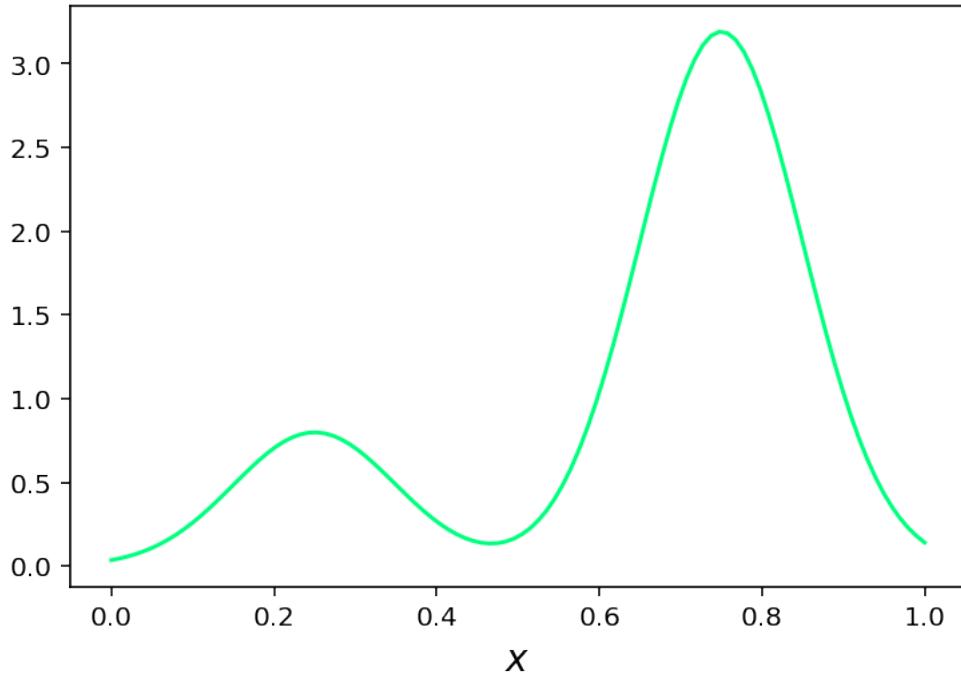
For presentation purposes, consider a single continuous variable x that follows a mixture of two Gaussian distributions.

```
[26]: means = [0.25, 0.75]
variances = [0.01, 0.01]
proportions = [0.2, 0.8]

component1 = Gaussian(mu=means[0], var=variances[0])
component2 = Gaussian(mu=means[1], var=variances[1])

x_space = np.linspace(0, 1, 100)
y_space = proportions[0] * component1.pdf(x_space) + proportions[1] * component2.pdf(x_space)

plt.plot(x_space, y_space, color="springgreen")
plt.xlabel("$x$", fontsize=14)
plt.show()
```



First, let's discuss the histogram methods for density estimation. Standard histograms simply partition x into distinct bins of width Δ_i and then count the number n_i of observations of x falling in bin i . In order to turn the counts into a normalized probability density, we divide by the total number N of observations and by the width Δ_i of the bins to obtain probability values for each bin given by

$$p_i = \frac{n_i}{N\Delta_i}$$

Given a sample dataset of $N = 50$ points, we plot three histogram density estimates corresponding to three choices for the bin width Δ . For very small Δ , the resulted density model is very spiky, while for very large Δ the result is too smooth and fails to capture the bimodal property of the curve. The best results are obtained by the intermediate value.

```
[27]: # Sample N points from the mixture
N = 50
N1 = int(N * proportions[0])
N2 = N - N1
sampled_points = component1.draw(N1)
sampled_points = np.append(sampled_points, component2.draw(N2))

plt.figure(figsize=(16, 5))

plt.subplot(1, 3, 1)
plt.plot(x_space, y_space, color="springgreen")
```

```

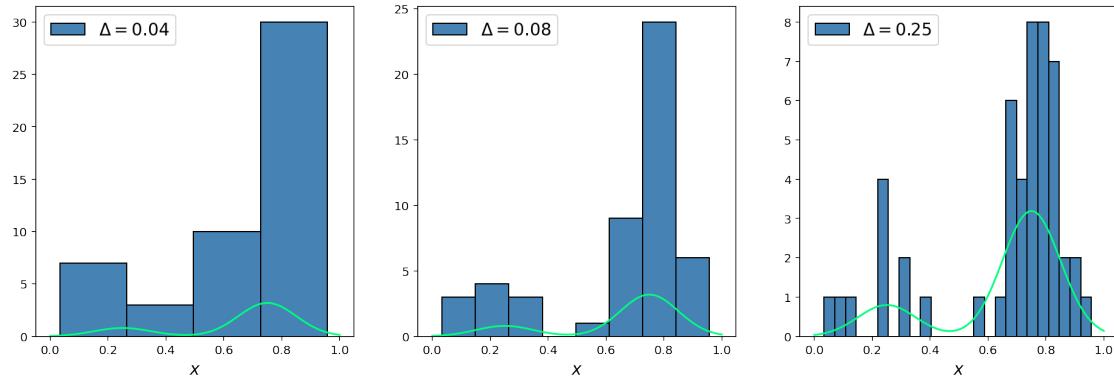
plt.hist(sampled_points, bins=4, edgecolor="black", color="steelblue", □
    ↪label="$\Delta=0.04$")
plt.xlabel("$x$", fontsize=14)
plt.legend(fontsize=14)

plt.subplot(1, 3, 2)
plt.plot(x_space, y_space, color="springgreen")
plt.hist(sampled_points, bins=8, edgecolor="black", color="steelblue", □
    ↪label="$\Delta=0.08$")
plt.xlabel("$x$", fontsize=14)
plt.legend(fontsize=14)

plt.subplot(1, 3, 3)
plt.plot(x_space, y_space, color="springgreen")
plt.hist(sampled_points, bins=25, edgecolor="black", color="steelblue", □
    ↪label="$\Delta=0.25$")
plt.xlabel("$x$", fontsize=14)
plt.legend(fontsize=14)

plt.show()

```



The histogram method has the desired property that, once the histogram has been computed, the data itself can be discarded. Moreover, the approach is easily applied to data points arriving sequentially. However, a major limitation is its scaling on high dimensional data. If we divide each variable in a D -dimensional space into M bins, then the total number of bins is M^D . Therefore, in a space of high dimensionality, the quantity of data needed to provide meaningful estimates of local probability density would be prohibitive.

The histogram approach to density estimation does, however, teach us two important lessons.

1. In order to estimate the probability density at a particular location, we should consider the data points that lie within some local neighbourhood of that location. For histograms, the neighbourhood property was defined by the bins.
2. The value of the smoothing parameter should be neither too large nor too small in order to

obtain good results.

2.5.1 Kernel density estimators

Now, suppose that observations are being drawn from an unknown probability density $p(\mathbf{x})$ in a D -dimensional Euclidean space. From our earlier insights about locality, let us consider a small region \mathcal{R} containing \mathbf{x} . Then, the probability mass of this region is given by

$$P_{\mathcal{R}} = \int_{\mathcal{R}} p(\mathbf{x}) d\mathbf{x}$$

Then, given a data set comprising N observations drawn from $p(\mathbf{x})$, each data point has a probability $P_{\mathcal{R}}$ of falling into the region \mathcal{R} . Thus, in general, the total number K of points out of N , that lie inside \mathcal{R} are distributed according to a binomial distribution

$$\text{Bin}(K|N, P_{\mathcal{R}}) = \frac{N!}{K!(N-K)!} P_{\mathcal{R}}^K (1 - P_{\mathcal{R}})^{1-K}$$

We can prove that the mean fraction of points falling inside the region \mathcal{R} is $\mathbb{E}[K/N] = \frac{1}{N}NP_{\mathcal{R}} = P_{\mathcal{R}}$, and the variance around the mean $\text{var}[K/N] = P_{\mathcal{R}}(1 - P_{\mathcal{R}})/N$. Therefore, assuming a large N , variance is going to shrink and the distribution is going to be sharply peaked around the mean, leading to a $P_{\mathcal{R}}$ proportion of the N points (K) to be located inside \mathcal{R}

$$K \approx NP_{\mathcal{R}}$$

Furthermore, assuming that the region \mathcal{R} is sufficiently small that the probability density $p(\mathbf{x})$ is roughly constant over the region, then we have

$$P_{\mathcal{R}} \approx p(\mathbf{x})V$$

where V is the volume of \mathcal{R} . Combining these two assumptions, we obtain a density estimate in the form

$$p(\mathbf{x}) = \frac{K}{NV}$$

Note that the validity of the density depends on two **contradictory assumptions**, namely that the region \mathcal{R} is sufficiently small that the density is approximately constant over the region and yet sufficiently large (in relation to the value of that density) that the number K of points falling inside the region is sufficient for the binomial distribution to be sharply peaked.

We can exploit the resulted density in two different ways:

1. Assume a K and determine the value of V from the data, giving rise to the k -nearest neighbour technique.
2. Assume a V and determine K from the data, giving rise to the kernel approach

It can be proved that both the k -nearest neighbour density estimator and the kernel density estimator converge to the true probability density in the limit $N \rightarrow \infty$ provided V shrinks suitably with N , and K grows with N .

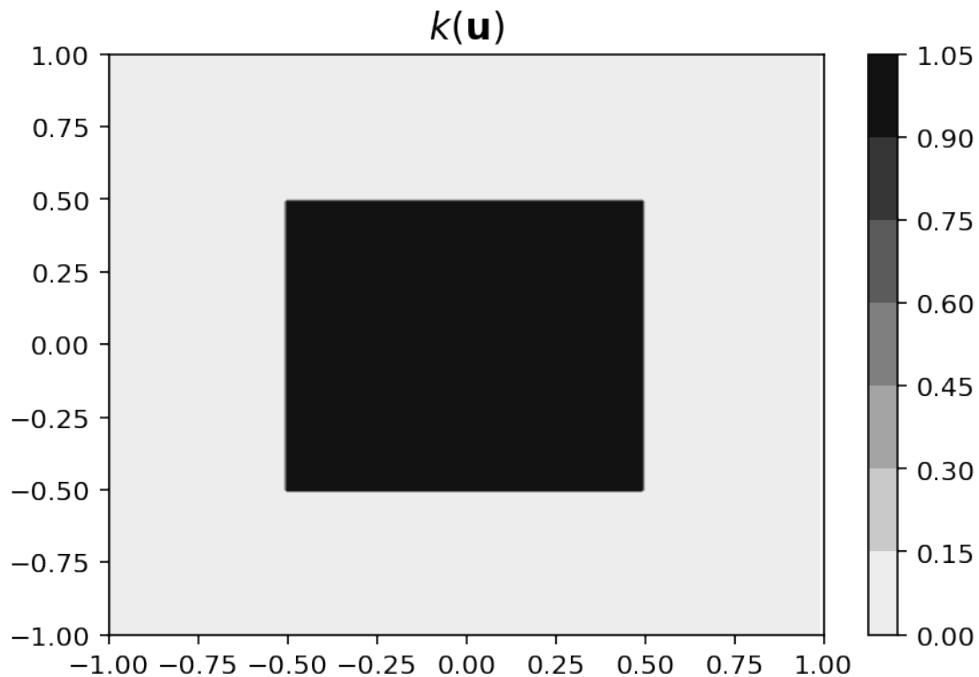
Consider the region \mathcal{R} to be a small hypercube centred on the point \mathbf{x} at which we wish to determine the probability density. In order to count the number K of points falling inside \mathcal{R} , it is convenient to define the function

$$k(\mathbf{u}) = \begin{cases} 1, & |u_i| \leq \frac{1}{2}, \quad \forall i \in \{1, \dots, D\} \\ 0, & \text{otherwise} \end{cases}$$

which represents a unit cube centred on the origin.

```
[28]: def k(u):
    return np.all(np.abs(u) <= 0.5)

U1, U2 = np.meshgrid(np.arange(-1, 1, 0.01), np.arange(-1, 1, 0.01))
plt.contourf(U1, U2, np.apply_along_axis(k, 0, np.array([U1, U2])), cmaps.cmap="binary")
plt.title("$k(\\mathbf{u})$".format(), fontsize=14)
plt.xlim(-1, 1)
plt.ylim(-1, 1)
plt.colorbar()
plt.show()
```



The function $k(\mathbf{u})$ is an example of a *kernel function*, also called a **Parzen window**. The quantity $k\left(\frac{\mathbf{x}-\mathbf{x}_n}{h}\right)$ is 1 if the data point \mathbf{x}_n lies inside a cube of side h centred on \mathbf{x} , and zero otherwise. The total number of data points lying inside this cube is therefore given by

$$K = \sum_{n=1}^N k\left(\frac{\mathbf{x}-\mathbf{x}_n}{h}\right)$$

By substituting the expression for K into the formula of $p(\mathbf{x})$ derived above, we obtain the estimated density at \mathbf{x} using a Parzen window

$$p(\mathbf{x}) = \frac{1}{N} \sum_{n=1}^N \frac{1}{h^D} k\left(\frac{\mathbf{x}-\mathbf{x}_n}{h}\right)$$

where $h^D = V$ for the volume of a hypercube of side h in D dimensions.

We can also interpret the above equation, not as a single cube centred on \mathbf{x} but instead as the sum over N cubes centred on the N data points \mathbf{x}_n .

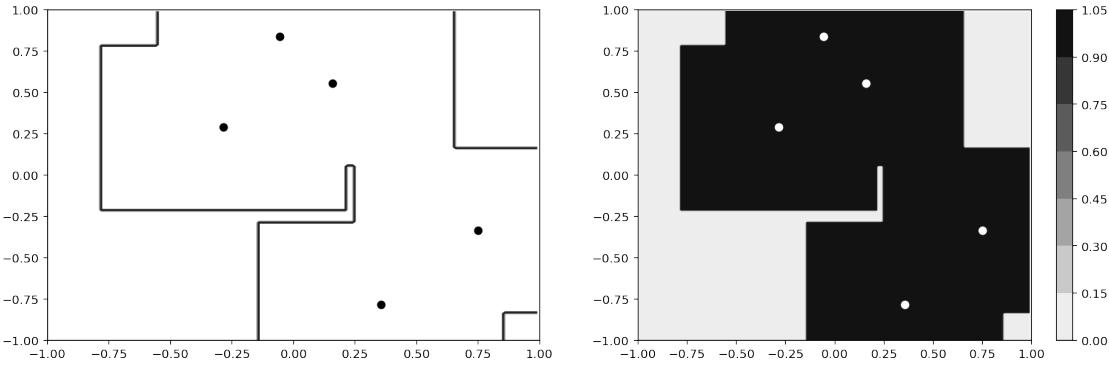
```
[29]: N = 5
h = 1
data = np.random.uniform(-1, 1, size=(N, 2))
U1, U2 = np.meshgrid(np.arange(-1, 1, 0.01), np.arange(-1, 1, 0.01))

K = np.zeros(U1.shape)
for x in data:
    k = lambda u: np.all(np.abs(x - u) <= h / 2)
    K += np.apply_along_axis(k, 0, np.array([U1, U2]))

plt.figure(figsize=(16, 5))

plt.subplot(1, 2, 1)
plt.contour(U1, U2, K > 0, cmap="binary")
plt.scatter(data[:, 0], data[:, 1], color="black")
plt.xlim(-1, 1)
plt.ylim(-1, 1)

plt.subplot(1, 2, 2)
c = plt.contourf(U1, U2, K > 0, cmap="binary")
plt.scatter(data[:, 0], data[:, 1], color="w")
plt.xlim(-1, 1)
plt.ylim(-1, 1)
plt.colorbar(c)
plt.show()
```



The kernel density estimator suffers from one of the same problems that the histogram method suffered from, namely the presence of artificial discontinuities, in this case at the boundaries of the cubes. We can obtain a smoother density model if we choose a smoother kernel function, and a common choice is the Gaussian, that gives rise to the following kernel density model

$$p(\mathbf{x}) = \frac{1}{N} \sum_{n=1}^N \frac{1}{(2\pi h^2)^{1/2}} \exp \left\{ -\frac{\|\mathbf{x} - \mathbf{x}_n\|^2}{2h^2} \right\}$$

where h represents the standard deviation of the Gaussian components. Thus, the density model is obtained by placing a Gaussian over each data point, adding up the contributions over the whole data set, and then dividing by N so that the density is correctly normalized.

```
[30]: N = 5
h = 1
data = np.random.uniform(-1, 1, size=(N, 2))
U1, U2 = np.meshgrid(np.arange(-1, 1, 0.01), np.arange(-1, 1, 0.01))

K = np.zeros(U1.shape)
for x in data:
    k = lambda u: np.exp(-np.linalg.norm(x - u) ** 2 / (2 * h**2)) / np.sqrt(2 * np.pi * h**2)
    K += np.apply_along_axis(k, 0, np.array([U1, U2]))

plt.figure(figsize=(16, 5))

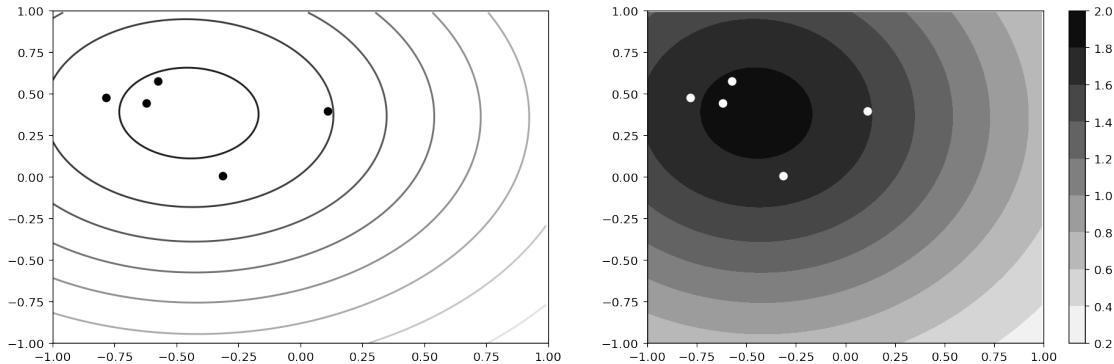
plt.subplot(1, 2, 1)
plt.contour(U1, U2, K, cmap="binary")
plt.scatter(data[:, 0], data[:, 1], color="black")
plt.xlim(-1, 1)
plt.ylim(-1, 1)

plt.subplot(1, 2, 2)
c = plt.contourf(U1, U2, K, cmap="binary")
```

```

plt.scatter(data[:, 0], data[:, 1], color="w")
plt.xlim(-1, 1)
plt.ylim(-1, 1)
plt.colorbar(c)
plt.show()

```



Applying the Gaussian kernel to the data set used earlier to demonstrate the histogram technique, we see that, as expected, the parameter h plays the role of a smoothing parameter, and there is a trade-off between sensitivity to noise at small h and over-smoothing at large h . Again, the optimization of h is a problem in model complexity, analogous to the choice of bin width in histogram density estimation, or the degree of the polynomial used in curve fitting.

```

[31]: def gaussian_kernel_density(h, data, x):
    K = 0
    for xn in data:
        k = lambda x: np.exp(
            -np.linalg.norm(
                x - xn,
            )
            ** 2
            / (2 * h**2)
        ) / np.sqrt(2 * np.pi * h**2)
        K += k(x)
    return K / len(data)

def kdeg(x, X, h):
    """
    KDE under a gaussian kernel
    """
    N, D = X.shape
    nden, _ = x.shape # number of density points
    Xhat = X.reshape(D, 1, N)
    xhat = x.reshape(D, nden, 1)

```

```

px = np.exp(-np.linalg.norm(xhat - Xhat, axis=0) ** 2 / (2 * h**2)).
    sum(axis=1) / (
        N * np.sqrt(2 * np.pi * h**2)
    )
return px

plt.figure(figsize=(16, 5))

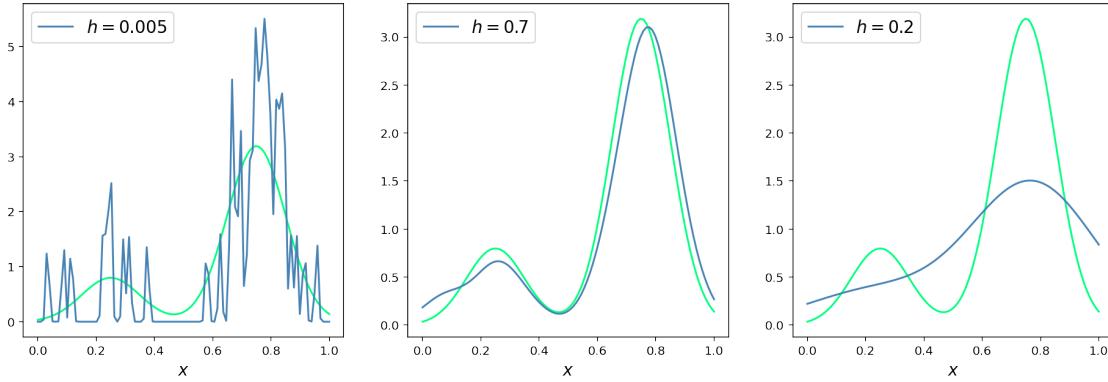
plt.subplot(1, 3, 1)
plt.plot(x_space, y_space, color="springgreen")
plt.plot(
    x_space, kdeg(x_space.reshape(-1, 1), sampled_points.reshape(-1, 1), 0.
    ↪005), color="steelblue", label="$h=0.005$"
)
plt.xlabel("$x$", fontsize=14)
plt.legend(fontsize=14)

plt.subplot(1, 3, 2)
plt.plot(x_space, y_space, color="springgreen")
plt.plot(
    x_space, [gaussian_kernel_density(0.07, sampled_points, x) for x in
    ↪x_space], color="steelblue", label="$h=0.7$"
)
plt.xlabel("$x$", fontsize=14)
plt.legend(fontsize=14)

plt.subplot(1, 3, 3)
plt.plot(x_space, y_space, color="springgreen")
plt.plot(
    x_space, [gaussian_kernel_density(0.2, sampled_points, x) for x in
    ↪x_space], color="steelblue", label="$h=0.2$"
)
plt.xlabel("$x$", fontsize=14)
plt.legend(fontsize=14)

plt.show()

```



The class of density models given by the Parzen estimators have the advantage that there is no computation involved during the *training* phase. They simply store the training set. However, this is also their great weakness, since the cost of evaluating the density grows linearly with the size of the data.

2.5.2 Nearest-neighbour methods

This issue is addressed by nearest-neighbour methods for density estimation.

We therefore return to our general result (2.246) for local density estimation, and assume a value for K and use the data to find an appropriate value for V . To that end, we consider a small sphere centred on the point \mathbf{x} at which we wish to estimate the density $p(\mathbf{x})$. Then, we allow the radius of the sphere to grow until it contains precisely K data points. The estimate of the density is then given by

$$p(\mathbf{x}) = \frac{K}{V_{\text{sphere}} N}$$

where V_{sphere} is volume of the resulting sphere. This technique is known as K nearest neighbours.

The n-dimensional volume of a Euclidean ball of radius R in n-dimensional Euclidean space is

$$V_{\text{sphere}} = \frac{\pi^{D/2} r^D}{\Gamma(\frac{D}{2} + 1)}$$

and is illustrated in Figure 2.26, for various choices of the parameter K , using the same data set as used in Figure 2.24 and Figure 2.25. We see that the value of K now governs the degree of smoothing and that again there is an optimum choice for K that is neither too large nor too small. Note that the model produced by K nearest neighbours is not a true density model because the integral over all space diverges.

```
[32]: plt.figure(figsize=(16, 5))

plt.subplot(1, 3, 1)
plt.plot(x_space, y_space, color="springgreen")
```

```

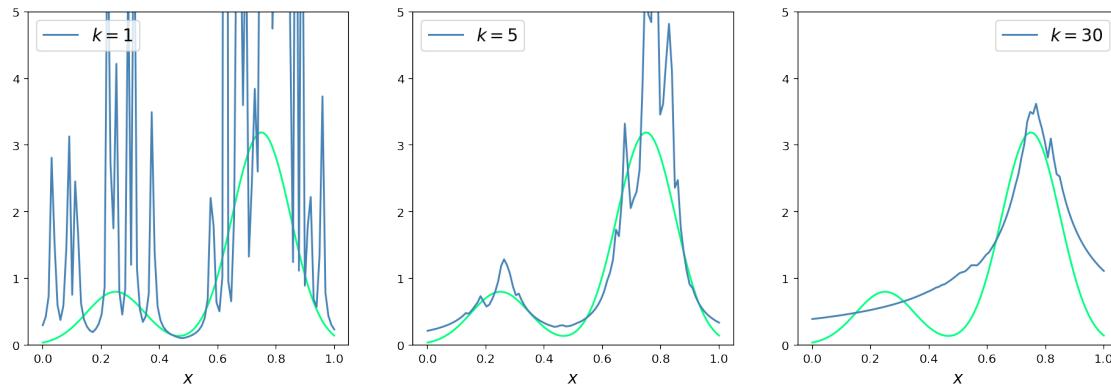
model = NearestNeighborsDensity(k=1, data=sampled_points)
plt.plot(x_space, model.predict(x_space), color="steelblue", label="$k=1$")
plt.xlabel("$x$", fontsize=14)
plt.ylim(0, 5)
plt.legend(fontsize=14)

plt.subplot(1, 3, 2)
plt.plot(x_space, y_space, color="springgreen")
model = NearestNeighborsDensity(k=5, data=sampled_points)
plt.plot(x_space, model.predict(x_space), color="steelblue", label="$k=5$")
plt.xlabel("$x$", fontsize=14)
plt.ylim(0, 5)
plt.legend(fontsize=14)

plt.subplot(1, 3, 3)
plt.plot(x_space, y_space, color="springgreen")
model = NearestNeighborsDensity(k=30, data=sampled_points)
plt.plot(x_space, model.predict(x_space), color="steelblue", label="$k=30$")
plt.xlabel("$x$", fontsize=14)
plt.ylim(0, 5)
plt.legend(fontsize=14)

plt.show()

```



The K -nearest-neighbour technique for density estimation can also be used for classification. To do so, we apply the K -nearest-neighbour density estimation technique to each class separately and then use the Bayes' theorem. Consider a data set comprising N_k points in class \mathcal{C}_k and N points in total, so that $\sum_k N_k = N$. A sphere of volume V containing K_k points from class \mathcal{C}_k defines the density of each class, given by

$$p(\mathbf{x}|\mathcal{C}_k) = \frac{K_k}{N_k V}$$

while, the unconditional density is given by

$$p(\mathbf{x}) = \frac{K}{NV}$$

and the class prior is given by

$$p(\mathcal{C}_k) = \frac{N_k}{N}$$

Using Bayes' theorem, we obtain the posterior probability of class membership

$$p(\mathcal{C}_k|\mathbf{x}) = \frac{p(\mathbf{x}|\mathcal{C}_k)p(\mathcal{C}_k)}{p(\mathbf{x})} = \frac{K_k}{K}$$

Thus, to classify a new point, we identify the K -nearest points from the training data set and then assign the new point to the class having the largest number of representatives amongst this set. Ties can be broken at random. The particular case of $K = 1$ is called the *nearest-neighbour rule*, because a test point is simply assigned to the same class as the nearest point from the training set.

An interesting property of the nearest-neighbour rule classifier is that, in the limit $N \rightarrow \infty$, the error rate is never more than double the minimum achievable error rate of an optimal classifier, i.e., one that uses the true class distributions.

```
[33]: N = 50
D = 2

x, t = make_classification(n_features=D, n_informative=D, n_redundant=0, n_classes=2, n_samples=N)

x_space = np.arange(-5, 5, 0.02)
x1, x2 = np.meshgrid(x_space, x_space)
x_hat = np.vstack((x1.ravel(), x2.ravel())).T

class_colors = ["coral" if t[i] == 1 else "snow" for i in range(t.shape[0])]

plt.figure(figsize=(16, 5))

plt.subplot(1, 3, 1)
model = KNearestNeighborsClassifier(1, x, t)
Z = model.predict(x_hat).reshape(-1, 1)
plt.contourf(
    x_space, x_space, Z[:, 0].reshape(x1.shape), cmap="winter", levels=np.arange(-0.1, 1.1, 0.05), antialiased=True
)
plt.scatter(x[:, 0], x[:, 1], color=class_colors)
plt.title("$K=1$", fontsize=14)

plt.subplot(1, 3, 2)
```

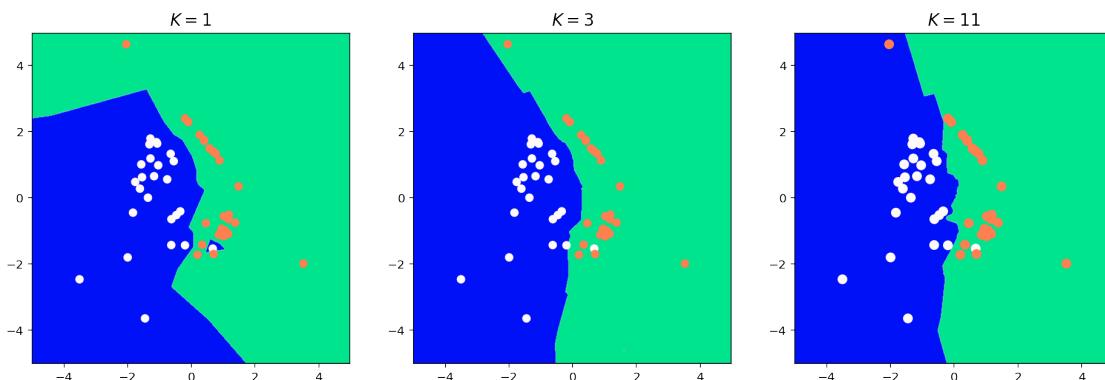
```

model = KNearestNeighborsClassifier(3, x, t)
Z = model.predict(x_hat).reshape(-1, 1)
plt.contourf(
    x_space, x_space, Z[:, 0].reshape(x1.shape), cmap="winter", levels=np.
    arange(-0.1, 1.1, 0.05), antialiased=True
)
plt.scatter(x[:, 0], x[:, 1], color=class_colors)
plt.title("$K=3$", fontsize=14)

plt.subplot(1, 3, 3)
model = KNearestNeighborsClassifier(11, x, t)
Z = model.predict(x_hat).reshape(-1, 1)
plt.contourf(
    x_space, x_space, Z[:, 0].reshape(x1.shape), cmap="winter", levels=np.
    arange(-0.1, 1.1, 0.05), antialiased=True
)
plt.scatter(x[:, 0], x[:, 1], color=class_colors, s=50)
plt.title("$K=11$", fontsize=14)

plt.show()

```



[34]:

```

N = 50
D = 2

x, t = make_classification(n_features=D, n_informative=D, n_redundant=0,
                           n_classes=2, n_samples=N)

x_space = np.arange(-5, 5, 0.02)
x1, x2 = np.meshgrid(x_space, x_space)
x_hat = np.vstack((x1.ravel(), x2.ravel())).T

class_colors = ["coral" if t[i] == 1 else "snow" for i in range(t.shape[0])]

```

```

plt.figure(figsize=(16, 5))

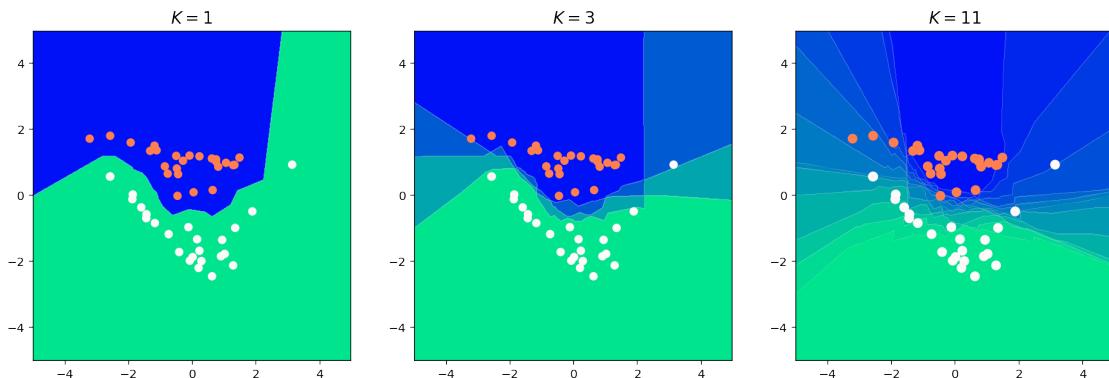
plt.subplot(1, 3, 1)
model = KNearestNeighborsClassifier(1, x, t)
Z = model.predict_proba(x_hat)
plt.contourf(
    x_space, x_space, Z[:, 0].reshape(x1.shape), cmap="winter", levels=np.
    arange(-0.1, 1.1, 0.05), antialiased=True
)
plt.scatter(x[:, 0], x[:, 1], color=class_colors)
plt.title("$K=1$", fontsize=14)

plt.subplot(1, 3, 2)
model = KNearestNeighborsClassifier(3, x, t)
Z = model.predict_proba(x_hat)
plt.contourf(
    x_space, x_space, Z[:, 0].reshape(x1.shape), cmap="winter", levels=np.
    arange(-0.1, 1.1, 0.05), antialiased=True
)
plt.scatter(x[:, 0], x[:, 1], color=class_colors)
plt.title("$K=3$", fontsize=14)

plt.subplot(1, 3, 3)
model = KNearestNeighborsClassifier(11, x, t)
Z = model.predict_proba(x_hat)
plt.contourf(
    x_space, x_space, Z[:, 0].reshape(x1.shape), cmap="winter", levels=np.
    arange(-0.1, 1.1, 0.05), antialiased=True
)
plt.scatter(x[:, 0], x[:, 1], color=class_colors, s=50)
plt.title("$K=11$", fontsize=14)

plt.show()

```



3. Linear Models for Regression

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 - 3.3.1 Parameter distribution
 - 3.3.2 Predictive distribution
 - 3.3.3 Equivalent kernel
- 3.5 The Evidence Approximation
 - 3.5.1 Evaluation of the evidence function
 - 3.5.2 Maximizing the evidence function

```
[1]: import math
import numpy as np
import matplotlib.pyplot as plt
from prml.datasets import generate_toy_data
from prml.distribution import Gaussian, MultivariateGaussian
from prml.preprocessing import PolynomialFeature, GaussianFeature, ↵
    SigmoidFeature
from prml.linear import LinearRegression, RidgeRegression, BayesianRegression, ↵
    EvidenceApproximation

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'
```

The goal of regression is to predict the value of one or more **continuous** target variables t given the value of a D -dimensional vector \mathbf{x} of input variables. The polynomial curve that we used in [Chapter 1](#) belongs to a broader class of functions called linear regression models, that are linear functions of the adjustable parameters. The simplest form of linear regression models are also linear functions of the input variables \mathbf{x} . However, a much more useful class of functions is the linear combinations of a fixed set of nonlinear functions of the input variables, known as *basis functions*.

3.1 Linear Basis Function Models

The simplest linear model for regression is one that involves a linear combination of the input variables

$$y(\mathbf{x}, \mathbf{w}) = w_0 + w_1 x_1 + \cdots + w_D x_D$$

which is simply known as *linear regression*. This model is a linear function of the parameters and a linear function of the input variables, and this imposes significant limitations on the model. We therefore extend the class of models by considering linear combinations of fixed nonlinear functions of the input variables, of the form

$$y(\mathbf{x}, \mathbf{w}) = w_0 + \sum_{j=1}^{M-1} w_j \phi_j(\mathbf{x}) = \sum_{j=0}^{M-1} w_j \phi_j(\mathbf{x}) = \mathbf{w}^T \phi(\mathbf{x})$$

where $\phi_j(\mathbf{x})$ are known as *basis functions*.

The polynomial regression considered in [Chapter 1](#) is an example of this model in which there is a single input variable x , and the basis functions take the form of powers of x so that $\phi_j(x) = x^j$. There is a plethora of possible choices for the basis functions, for instance

$$\phi_j(x) = \exp \left\{ -\frac{(x - \mu_j)^2}{2s^2} \right\}$$

are referred to as *Gaussian* basis functions, where μ_j govern the locations of the functions in input space, and s governs their spatial scale. Another possibility is the sigmoidal basis function of the form

$$\phi_j(x) = \sigma \left(\frac{x - \mu_j}{s} \right)$$

where $\sigma(a)$ is the logistic sigmoid function defined by

$$\sigma(a) = \frac{1}{1 + \exp(-a)}$$

We present examples of these three families of basis functions using different parameters.

```
[2]: x_space = np.linspace(-1, 1, 100)

# Create 10 degree polynomial basis functions
x_polynomial = PolynomialFeature(degree=12).transform(x_space)

# Create 10 Gaussian basis functions
x_gaussian = GaussianFeature(mean=np.linspace(-1, 1, 12), sigma=0.1).
    transform(x_space)

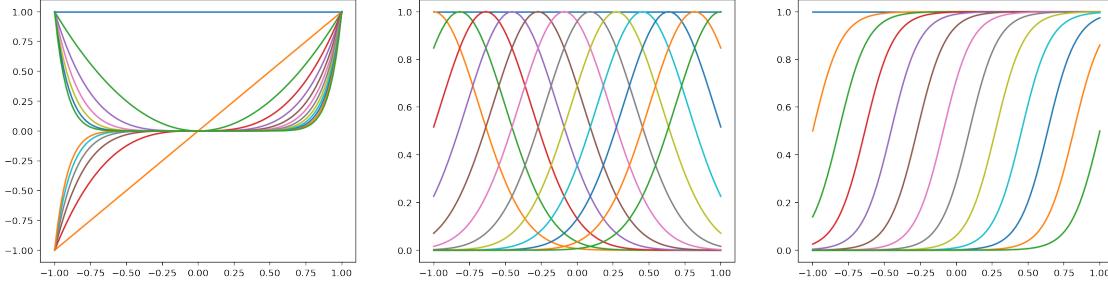
# Create 10 sigmoid basis functions
x_sigmoid = SigmoidFeature(mean=np.linspace(-1, 1, 12), sigma=0.1).
    transform(x_space)

plt.figure(figsize=(20, 5))
```

```

for i, x in enumerate([x_polynomial, x_gaussian, x_sigmoid]):
    plt.subplot(1, 3, i + 1)
    for j in range(x.shape[1]):
        plt.plot(x_space, x[:, j])

```



3.1.1 Maximum likelihood and least squares

In Chapter 1, we fitted polynomial functions to data sets by minimizing a sum-of-squares error function. We also showed that this error function could be motivated as the maximum likelihood solution under an assumed Gaussian noise model. Let us return to the discussion of Chapter 1 and consider the least squares approach, and its relation to maximum likelihood, in more detail.

As before, we assume that the target variable t is given by a deterministic function $y(\mathbf{x}, \mathbf{w})$ having additive Gaussian noise so that

$$t = y(\mathbf{x}, \mathbf{w}) + \epsilon$$

where ϵ is a zero mean Gaussian random variable with precision (inverse variance) β . Thus we can write

$$p(t|\mathbf{x}, \mathbf{w}, \beta) = \mathcal{N}(t|y(\mathbf{x}, \mathbf{w}), \beta^{-1})$$

Note that the Gaussian noise assumption implies that the conditional distribution of t given \mathbf{x} is unimodal, which may be inappropriate for some applications.

Now consider a data set of inputs $\mathbf{X} = \{\mathbf{x}_1, \dots, \mathbf{x}_N\}$ along corresponding target values $\mathbf{t} = (t_1, \dots, t_N)^T$. Assuming that the data points are i.i.d, we obtain the likelihood function (function of the adjustable parameters \mathbf{w} and β), in the form

$$p(\mathbf{t}|\mathbf{X}, \mathbf{w}, \beta) = \prod_{n=1}^N \mathcal{N}(t_n|y(\mathbf{x}_n, \mathbf{w}), \beta^{-1}) = \prod_{n=1}^N \mathcal{N}(t_n|\mathbf{w}^T \phi(\mathbf{x}_n), \beta^{-1})$$

NOTE: In many textbooks, the input variables \mathbf{x} are dropped from the set of conditioning variables, since, we do not seek to model the distribution of \mathbf{x} .

Taking the logarithm of the likelihood function, we have,

$$\begin{aligned}
\ln p(\mathbf{t}|\mathbf{X}, \mathbf{w}, \beta) &= \sum_{n=1}^N \ln \mathcal{N}(t_n | \mathbf{w}^T \phi(\mathbf{x}_n), \beta^{-1}) \\
&= \frac{N}{2} \ln \beta - \frac{N}{2} \ln 2\pi - \frac{\beta}{2} \sum_{n=1}^N (t_n - \mathbf{w}^T \phi(\mathbf{x}_n))^2 \\
&= \frac{N}{2} \ln \beta - \frac{N}{2} \ln 2\pi - \beta E_D(\mathbf{w})
\end{aligned}$$

By maximizing likelihood we can determine the parameters \mathbf{w} and β . As already observed in [Chapter 1](#) the maximization under a conditional Gaussian noise distribution is equivalent to minimizing the sum-of-squares error function given by $E_D(\mathbf{w})$. The gradient of the log likelihood function takes the form

$$\nabla p(\mathbf{t}|\mathbf{X}, \mathbf{w}, \beta) = \sum_{n=1}^N (t_n - \mathbf{w}^T \phi(\mathbf{x}_n)) \phi(\mathbf{x}_n)^T$$

Setting this gradient to zero and solving for \mathbf{w} gives

$$\mathbf{w}_{ML} = (\mathbf{X}^T)^{-1} \mathbf{X}^T \mathbf{t}$$

which are known as the *normal equations* for the least squares problem. Here \mathbf{X} is an $N \times M$ matrix, called the *design matrix*, whose elements are given by $\Phi_{nj} = \phi_j(\mathbf{x}_n)$, so that

$$= \begin{pmatrix} \phi_0(\mathbf{x}_1) & \phi_1(\mathbf{x}_1) & \cdots & \phi_{M-1}(\mathbf{x}_1) \\ \phi_0(\mathbf{x}_2) & \phi_1(\mathbf{x}_2) & \cdots & \phi_{M-1}(\mathbf{x}_2) \\ \vdots & \vdots & \ddots & \vdots \\ \phi_0(\mathbf{x}_N) & \phi_1(\mathbf{x}_N) & \cdots & \phi_{M-1}(\mathbf{x}_N) \end{pmatrix}$$

By maximizing the log likelihood function over the noise precision parameter β , we obtain

$$\beta_{ML} = \frac{1}{N} \sum_{n=1}^N (t_n - \mathbf{w}^T \phi(\mathbf{x}_n))^2$$

```
[3]: # Create polynomial, gaussian and sigmoid basis functions
polynomial_basis = PolynomialFeature(degree=10)
gaussian_basis = GaussianFeature(mean=np.arange(-9, 9, 0.5), sigma=1)
sigmoid_basis = SigmoidFeature(mean=np.arange(-9, 9, 0.5), sigma=1)

# Lets train a linear regression model on a couple of datasets
model = LinearRegression()

plt.figure(figsize=(20, 5))

X = np.arange(-10, 10, 0.5).reshape((-1, 1))
y = np.sin(X) + np.random.randn(X.shape[0], X.shape[1]) * 0.3
```

```

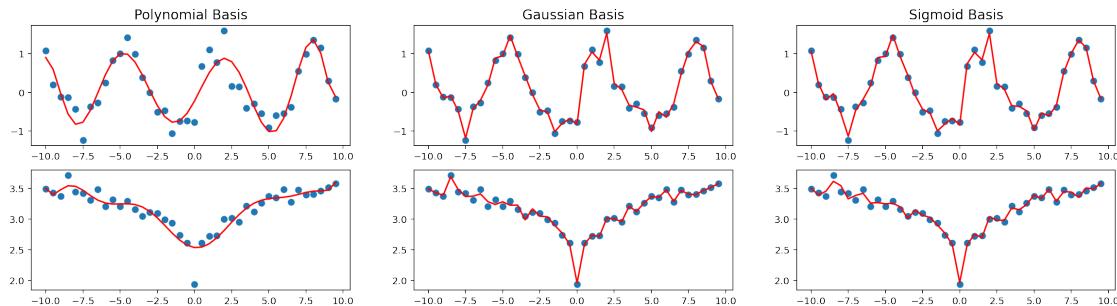
for i, basis in enumerate([polynomial_basis, gaussian_basis, sigmoid_basis]):
    plt.subplot(2, 3, i + 1)
    plt.scatter(X, y)
    x_train_features = basis.transform(X)
    model.fit(x_train_features, y)
    plt.plot(X, model.predict(x_train_features)[0], color="red")
    plt.title(["Polynomial Basis", "Gaussian Basis", "Sigmoid Basis"][i], u
    ↪fontsize=14)

X = np.arange(-10, 10, 0.5)
y = 0.8 * abs(X) ** 0.3 + 2 + np.random.randn(X.shape[0]) * 0.1

for i, basis in enumerate([polynomial_basis, gaussian_basis, sigmoid_basis]):
    plt.subplot(2, 3, i + 4)
    plt.scatter(X, y)
    x_train_features = basis.transform(X)
    model.fit(x_train_features, y)
    plt.plot(X, model.predict(x_train_features)[0], color="red")

plt.show()

```



3.1.3 Sequential learning

Batch learning, such as the maximum likelihood solution, requires processing of the entire training set at once. However, this can be computationally costly for large datasets. Sequential learning or *online* learning algorithms consider data points one at a time and update the model parameters after processing each point. We can obtain a sequential learning algorithm by applying a technique called *stochastic gradient descent* also known as *sequential gradient descent*.

If an error function comprises a sum over data points, then for a data point n , the stochastic gradient descent updates the parameter vector \mathbf{w} as follows,

$$\mathbf{w}^{(\tau+1)} = \mathbf{w}^{(\tau)} - \eta \nabla E_n$$

where τ is the iteration number and η is a learning rate parameter. The value of $\mathbf{w}^{(0)}$ can be

initialized to some random vector. For the case of the sum-of-squares error function, this gives

$$\mathbf{w}^{(\tau+1)} = \mathbf{w}^{(\tau)} - \eta(\mathbf{w}^{(\tau)T}\phi_n - t_n)\phi_n$$

This is also known as the *least-mean-squares* (LMS) algorithm or more commonly as gradient descent.

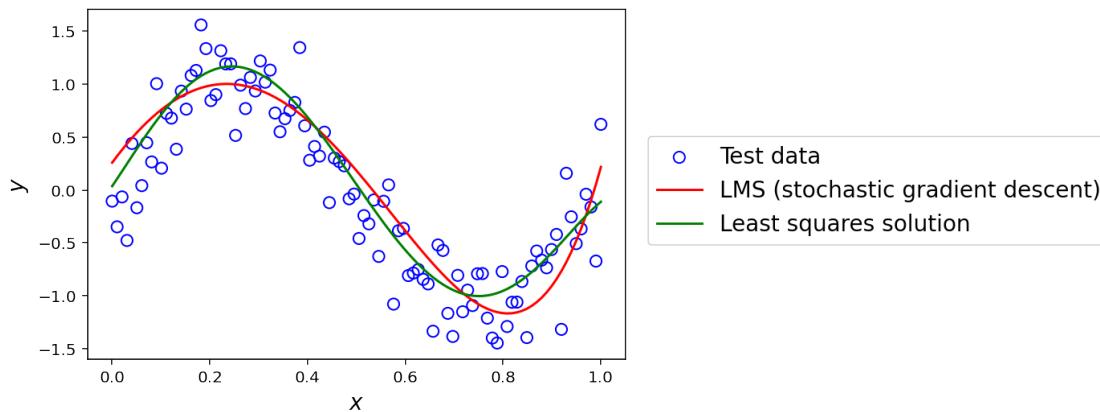
```
[4]: # Generate an example dataset
sin = lambda x: np.sin(2 * np.pi * x)
x_train, y_train = generate_toy_data(sin, sample_size=100, std=0.3)
x_test, y_test = generate_toy_data(sin, sample_size=100, std=0.3)

# Create polynomial features
polynomial = PolynomialFeature(degree=5)
x_train_features = polynomial.transform(x_train)
x_test_features = polynomial.transform(x_test)

# Fit linear regression using both gradient descent and least squares
model = LinearRegression()
model.fit_lms(x_train_features, y_train, eta=0.1)
y_pred_lms, _ = model.predict(x_test_features)

model.fit(x_train_features, y_train)
y_pred_ls, _ = model.predict(x_test_features)

plt.scatter(x_test, y_test, facecolor="none", edgecolor="b", s=50, label="Test data")
plt.plot(x_test, y_pred_lms, color="r", label="LMS (stochastic gradient descent)")
plt.plot(x_test, y_pred_ls, color="g", label="Least squares solution")
plt.xlabel("$x$", fontsize=14)
plt.ylabel("$y$", fontsize=14)
plt.legend(bbox_to_anchor=(1, 0.7), loc=2, borderaxespad=1, fontsize=14)
plt.show()
```



3.1.4 Regularized least squares

In Chapter 1, we introduced the idea of adding a regularization term to the error function in order to control over-fitting. To that end, the total error function to be minimized takes the form,

$$E_D(\mathbf{w}) + \lambda E_W(\mathbf{w})$$

where λ is the regularization coefficient that controls the balance between the *data-dependent error* $E_D(\mathbf{w})$ and the regularization term over the parameters $E_W(\mathbf{w})$. One of the simplest regularizers we can employ is given by the sum-of-squares of the weight vector

$$E_W(\mathbf{w}) = \frac{1}{2} \mathbf{w}^T \mathbf{w}$$

Combining the sum-of-squares error function for the data and the quadratic regularizer leads to the following total error function

$$\frac{1}{2} \sum_{n=1}^N \{t_n - \mathbf{w}^T \phi(\mathbf{x}_n)\}^2 + \frac{\lambda}{2} \mathbf{w}^T \mathbf{w}$$

This particular regularizer is also known as *weight decay* since it encourages weight values to decay towards zero, unless supported by data. In statistics, it provides an example of a *parameter shrinkage* method. Moreover, it has the advantage that the error function remains quadratic over \mathbf{w} , thus, it can be minimized in closed form using calculus.

A more general formulation for the regularized error is given by

$$E_W(\mathbf{w}) = \frac{\lambda}{2} \sum_{j=1}^M |w_j|^q$$

where $q = 2$ recovers the quadratic regularizer. The case of $q = 1$ is known as the *lasso* in the literature. It has the property that if λ is sufficiently large, some of the parameters w_j are driven to zero, leading to sparse models in which the corresponding basis function plays no role.

Regularization allows complex models (having a large number of parameters) to be trained on data sets of limited size, avoiding over-fitting. Unfortunately, the problem of determining the optimal model is then shifted from finding the appropriate number of basis functions to determining a suitable value for the regularization coefficient λ .

3.2 Bias-Variance Decomposition

The introduction of regularization terms can control over-fitting for models having many parameters. However, the question of how to determine a suitable value for the regularization coefficient λ remains. Seeking the solution that minimizes the regularized error function with respect to both

the weight vector and the regularization coefficient λ is not the right approach since it leads to the unregularized solution $\lambda = 0$.

The optimal prediction for the squared loss function is given by the conditional expectation

$$h(\mathbf{x}) = \mathbb{E}[t|\mathbf{x}] = \int tp(t|\mathbf{x})dt$$

Moreover, the expected squared loss is given by

$$\mathbb{E}[L] = \int \{y(\mathbf{x}) - h(\mathbf{x})\}^2 p(\mathbf{x})d\mathbf{x} + \int \int \{h(\mathbf{x}) - t\}^2 p(\mathbf{x}, t)d\mathbf{x}dt$$

The second term is independent of $y(\mathbf{x})$ and arises from the intrinsic noise on the data. Assuming we can find a function $y(\mathbf{x}) = h(\mathbf{x})$, the second term represents the minimum achievable value of the expected loss. Thus, our goal is indeed to find a function $y(\mathbf{x})$ that makes the first term a minimum, ideally zero, since the loss function is always non-negative.

A frequentist treatment of the problem involves making an estimate of \mathbf{w} based on a data set \mathcal{D} . In order to interpret the uncertainty of this estimate consider the following thought experiment. Suppose we had a large number of data sets each of size N , drawn independently from $p(t, \mathbf{x})$. Then, considering each dataset in turn, we can obtain a prediction function $y(\mathbf{x}; \mathcal{D})$. As expected, each dataset should give a different functions and consequently different values for the squared loss. The performance of a particular learning algorithm can then be assessed by taking the average over this ensemble of data sets.

Now consider the integrand of the first term, given a particular dataset,

$$\{y(\mathbf{x}; \mathcal{D}) - h(\mathbf{x})\}^2$$

If we add and subtract the average of $y(\mathbf{x}; \mathcal{D})$ over the ensemble of data sets, expressed as $\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]$, we obtain

$$\begin{aligned} & \{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] + \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\}^2 \\ &= \{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}^2 + \{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\}^2 - 2\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}\{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\} \end{aligned}$$

By taking the expectation over all data sets \mathcal{D} on both sides of the equation, we obtain

$$\begin{aligned}
& \mathbb{E}_{\mathcal{D}} \left[\{y(\mathbf{x}; \mathcal{D}) - h(\mathbf{x})\}^2 \right] \\
&= \mathbb{E}_{\mathcal{D}} \left[\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}^2 + \{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\}^2 - 2\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}\{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\} \right] \\
&= \mathbb{E}_{\mathcal{D}} \left[\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}^2 \right] + \mathbb{E}_{\mathcal{D}} \left[\{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\}^2 \right] - \mathbb{E}_{\mathcal{D}} \left[2\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}\{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\} \right] \\
&= \mathbb{E}_{\mathcal{D}} \left[\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}^2 \right] + \mathbb{E}_{\mathcal{D}} \left[\{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\}^2 \right] \\
&\quad - \mathbb{E}_{\mathcal{D}} \left[2\{y(\mathbf{x}; \mathcal{D})\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - y(\mathbf{x}; \mathcal{D})h(\mathbf{x}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]^2 + \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]h(\mathbf{x})\} \right] \\
&= \mathbb{E}_{\mathcal{D}} \left[\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}^2 \right] + \mathbb{E}_{\mathcal{D}} \left[\{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\}^2 \right] \\
&\quad - 2\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]^2 + 2\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]h(\mathbf{x}) + 2\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]^2 - 2\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]h(\mathbf{x}) \\
&= \mathbb{E}_{\mathcal{D}} \left[\{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\}^2 \right] + \mathbb{E}_{\mathcal{D}} \left[\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}^2 \right] \\
&= \{\mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})] - h(\mathbf{x})\}^2 + \mathbb{E}_{\mathcal{D}} \left[\{y(\mathbf{x}; \mathcal{D}) - \mathbb{E}_{\mathcal{D}}[y(\mathbf{x}; \mathcal{D})]\}^2 \right]
\end{aligned}$$

Note that the last term vanished giving a sum of two terms for the expected squared loss. The first term, called the **squared bias**, represents the extend to which the average prediction over all data sets differs from the optimal loss function $h(\mathbf{x})$. The second term, called **variance**, measures the extend to which the solutions for each data set vary around their average, in other words, it measures how sensitive is function $y(\mathbf{x}; \mathcal{D})$ to the particular choice of data set.

By substituting this decomposition of the squared loss back into the expected squared loss, we note that

$$\text{expected loss} = (\text{bias})^2 + \text{variance} + \text{noise}$$

Our goal is to minimize the expected loss, thus, minimizing both the bias and the variance. However, there is a trade-off between bias and variance. Very flexible models have low bias and high variance, while relatively rigid models have high bias and low variance. The best model is the one that balances these two quantities.

Consider $L = 100$ data sets, each containing $N = 25$ data points, independently from the sinusoidal curve $h(x) = \sin(2\pi x)$. For each data set $\mathcal{D}^{(l)}$, a model using 24 Gaussian basis functions is trained, by minimizing the regularized error function to give a prediction function $y^{(l)}$.

```
[5]: L = 100 # number of datasets
N = 25 # number of points per dataset

# the optimal regression function is the sinusoidal
def h(x):
    return np.sin(2 * np.pi * x)

gaussian_basis = GaussianFeature(np.linspace(0, 1, 24), 0.1)
```

```

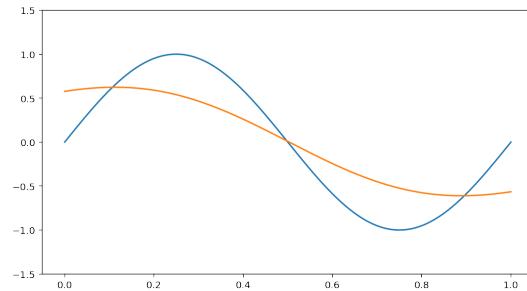
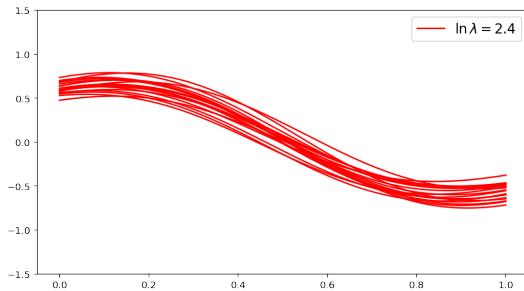
# create a test set
x_test = np.linspace(0, 1, 1000)
x_test_features = gaussian_basis.transform(x_test)
y_test = h(x_test)

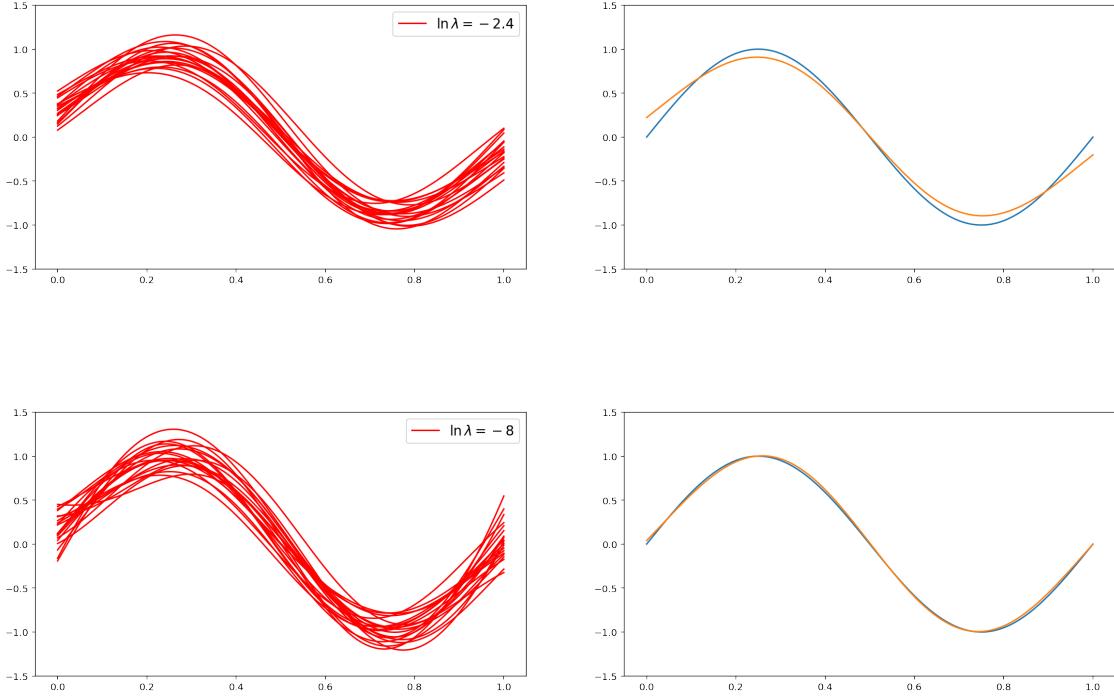
# create L datasets
datasets = []
for i in range(L):
    x_train, y_train = generate_toy_data(h, N, 0.3)
    x_train_features = gaussian_basis.transform(x_train)
    datasets.append((x_train_features, y_train))

# apply ridge regression on the L datasets
for ln_lambda in [2.4, -2.4, -8]:
    predictions = []
    plt.figure(figsize=(20, 5))
    plt.subplot(1, 2, 1)
    for i, (x_train, y_train) in enumerate(datasets):
        model = RidgeRegression(alpha=math.exp(ln_lambda))
        model.fit(x_train, y_train)
        y, _ = model.predict(x_test_features)
        predictions.append(y)
    if i == 0:
        plt.plot(x_test, y, color="red", label=f"$\ln\lambda={ln_lambda}$")
        plt.ylim(-1.5, 1.5)
    elif i < 20:
        plt.plot(x_test, y, color="red")
    plt.legend(fontsize=14)

    plt.subplot(1, 2, 2)
    plt.plot(x_test, y_test)
    plt.plot(x_test, np.asarray(predictions).mean(axis=0))
    plt.ylim(-1.5, 1.5)
    plt.show()

```





The top row corresponds to a larger value for the regularization coefficient λ and results in low variance but high bias. The bottom row for which λ is small, there is a large variance but low bias.

Note that the result of averaging many solutions for a complex model ($M = 25$) is very good, suggesting that averaging may be a beneficial procedure. Indeed, the weighted average of multiple solutions lies at the core of a Bayesian approach, although the averaging is done respect to the posterior distribution of the parameters, not to multiple datasets.

3.3 Bayesian Linear Regression

In order to tackle the over-fitting of maximum likelihood, we turn to the Bayesian treatment of linear regression that leads to automatic methods for determining model complexity using the training data alone.

3.3.1 Parameter distribution

We begin our discussion of the Bayesian treatment of linear regression by introducing a prior probability distribution over the model parameters \mathbf{w} . Assume for the moment, that the noise precision parameter β is a known constant. Note that the likelihood function $p(\mathbf{t}|\mathbf{X}, \mathbf{w})$ is the exponential of a quadratic function of \mathbf{w} . Thus, the corresponding conjugate prior is given by a Gaussian distribution of the form

$$p(\mathbf{w}) = \mathcal{N}(\mathbf{w}|\mathbf{m}_0, \mathbf{S}_0)$$

The posterior distribution is proportional to the product of the likelihood and the prior. Due to the choice of a conjugate Gaussian prior distribution, the posterior is also Gaussian. Thus, to derive

the form of the posterior, we focus on the exponential term

$$\begin{aligned}
\text{exponential term} &= -\frac{\beta}{2} \sum_{n=1}^N \{t_n - \mathbf{w}^T \phi(\mathbf{x}_n)\}^2 - \frac{1}{2} (\mathbf{w} - \mathbf{m}_0)^T \mathbf{S}_0^{-1} (\mathbf{w} - \mathbf{m}_0) \\
&= -\frac{\beta}{2} \sum_{n=1}^N \{t_n^2 - 2t_n \mathbf{w}^T \phi(\mathbf{x}_n) - \mathbf{w}^T \phi(\mathbf{x}_n) \phi(\mathbf{x}_n)^T \mathbf{w}\} - \frac{1}{2} (\mathbf{w}^T \mathbf{S}_0^{-1} \mathbf{w} - 2\mathbf{m}_0^T \mathbf{S}_0^{-1} \mathbf{w} + \mathbf{m}_0^T \mathbf{S}_0^{-1} \mathbf{m}_0) \\
&= -\frac{1}{2} \mathbf{w}^T \left(\sum_{n=1}^N \beta \phi(\mathbf{x}_n) \phi(\mathbf{x}_n)^T + \mathbf{S}_0^{-1} \right) \mathbf{w} - \frac{1}{2} \mathbf{w}^T \left(-2\mathbf{S}_0^{-1} \mathbf{m}_0 - \sum_{n=1}^N 2\beta t_n \phi(\mathbf{x}_n) \right) - \frac{1}{2} \left(\sum_{n=1}^N \beta t_n^2 + \mathbf{m}_0^T \mathbf{S}_0^{-1} \mathbf{m}_0 \right) \\
&= -\frac{1}{2} \mathbf{w}^T \left(\sum_{n=1}^N \beta \phi(\mathbf{x}_n) \phi(\mathbf{x}_n)^T + \mathbf{S}_0^{-1} \right) \mathbf{w} + \mathbf{w}^T \left(\mathbf{S}_0^{-1} \mathbf{m}_0 + \sum_{n=1}^N \beta t_n \phi(\mathbf{x}_n) \right) - \frac{1}{2} \left(\sum_{n=1}^N \beta t_n^2 + \mathbf{m}_0^T \mathbf{S}_0^{-1} \mathbf{m}_0 \right)
\end{aligned}$$

Completing the square is a common operation for Gaussian distributions, where given a quadratic form defining the exponent terms in a Gaussian distribution, and we seek to determine the corresponding mean and covariance. Such problems can be solved easily by noting that the exponent in a general Gaussian distribution $\mathcal{N}(\mathbf{x}|\mu, \Sigma)$ can be formulated as

$$-\frac{1}{2}(\mathbf{x} - \mu)^T \Sigma^{-1} (\mathbf{x} - \mu) = -\frac{1}{2} \mathbf{x}^T \Sigma^{-1} \mathbf{x} + \mathbf{x}^T \Sigma^{-1} \mu - \frac{1}{2} \mu^T \Sigma^{-1} \mu$$

then, we can equate the matrix of coefficients in the second order term to the inverse covariance matrix Σ^{-1} and the coefficient of the linear term to $\Sigma^{-1} \mu$, in order to obtain μ .

Hence, by comparing the quadratic term to the standard Gaussian Distribution we obtain

$$\mathbf{S}_N^{-1} = \mathbf{S}_0^{-1} + \sum_{n=1}^N \beta \phi(\mathbf{x}_n) \phi(\mathbf{x}_n)^T = \mathbf{S}_0^{-1} + \beta \Phi^T \Phi$$

Then, by comparing the linear term we obtain

$$\begin{aligned}
\mathbf{S}_N^{-1} \mathbf{m}_N &= \mathbf{S}_0^{-1} \mathbf{m}_0 + \sum_{n=1}^N \beta t_n \phi(\mathbf{x}_n) = \mathbf{S}_0^{-1} \mathbf{m}_0 + \beta \Phi^T \mathbf{t} \Leftrightarrow \\
\mathbf{m}_N &= \mathbf{S}_N (\mathbf{S}_0^{-1} \mathbf{m}_0 + \beta \Phi^T \mathbf{t})
\end{aligned}$$

Therefore, the posterior distribution is given by

$$p(\mathbf{w}|\mathbf{X}, \mathbf{t}) = \mathcal{N}(\mathbf{w}|\mathbf{m}_N, \mathbf{S}_N)$$

where

$$\begin{aligned}
\mathbf{m}_N &= \mathbf{S}_N (\mathbf{S}_0^{-1} \mathbf{m}_0 + \beta \Phi^T \mathbf{t}) \\
\mathbf{S}_N^{-1} &= \mathbf{S}_0^{-1} + \beta \Phi^T \Phi
\end{aligned}$$

Consider now, for the sake of simplicity, a zero-mean isotropic Gaussian prior governed by a single parameter α so that,

$$p(\mathbf{w}|\alpha) = \mathcal{N}(\mathbf{w}|\mathbf{0}, \alpha^{-1}\mathbf{I})$$

Then, the corresponding posterior distribution over \mathbf{w} becomes

$$\begin{aligned}\mathbf{m}_N &= \beta \mathbf{S}_N \Phi^T \mathbf{t} \\ \mathbf{S}_N^{-1} &= \alpha \mathbf{I} + \beta \Phi^T \Phi\end{aligned}$$

For this particular choice of prior, the maximization of the log of the posterior is equivalent to the minimization of the regularized sum-of-squares error function.

```
[6]: alpha = 2.0
beta = 25.0
N = 20
f = lambda x: 0.5 * x - 0.3

x_train, y_train = generate_toy_data(f, N, 0.2, (-1, 1))
x_train_linear = PolynomialFeature(degree=1).transform(x_train)

w0, w1 = np.meshgrid(np.linspace(-1, 1, 100), np.linspace(-1, 1, 100))
w = np.array([np.ravel(w0), np.ravel(w1)])

# Prior for the parameters (assuming zero-mean isotropic Gaussian)
prior_posterior = MultivariateGaussian(mu=np.zeros((2, 1)), cov=(1 / alpha) * np.eye(2))

for i, x in enumerate(x_train_linear):
    # compute the posterior according to (3.50) and (3.51)
    if i > 0:
        prev_precision = np.linalg.inv(prior_posterior.cov)
        cur_precision = prev_precision + beta * x_train_linear.T @ x_train_linear
        cur_cov = np.linalg.inv(cur_precision)
        cur_mean = cur_cov @ ((prev_precision @ prior_posterior.mu).T + beta * x_train_linear.T @ y_train).reshape(-1, 1)
    )
    prior_posterior = MultivariateGaussian(mu=cur_mean, cov=cur_cov)

# create figures only for the three starting iterations and the last one
if i < 3 or i == N - 1:
    plt.figure(figsize=(20, 5))
```

```

# likelihood
plt.subplot(1, 3, 1)
if i == 0:
    plt.title("Likelihood", fontsize=14)
else:
    likelihood = Gaussian(var=1 / beta).pdf(y_train[i])
    z = likelihood.pdf(mu=w.T @ x).reshape(w0.shape)
    plt.contourf(w0, w1, z, cmap="rainbow")
    plt.scatter(-0.3, 0.5, s=200, marker="x", color="white") # optimal ↴
    ↵parameter vector

plt.xlabel("$w_0$", fontsize=14)
plt.ylabel("$w_1$", fontsize=14)

# prior/posterior
plt.subplot(1, 3, 2)
plt.title("Prior/Posterior", fontsize=14)
z = np.diag(prior_posterior.pdf(w)).reshape(w0.shape)
plt.contourf(w0, w1, z, cmap="rainbow")
plt.scatter(-0.3, 0.5, s=200, marker="x", color="white") # optimal ↴
    ↵parameter vector

plt.xlabel("$w_0$", fontsize=14)
plt.ylabel("$w_1$", fontsize=14)

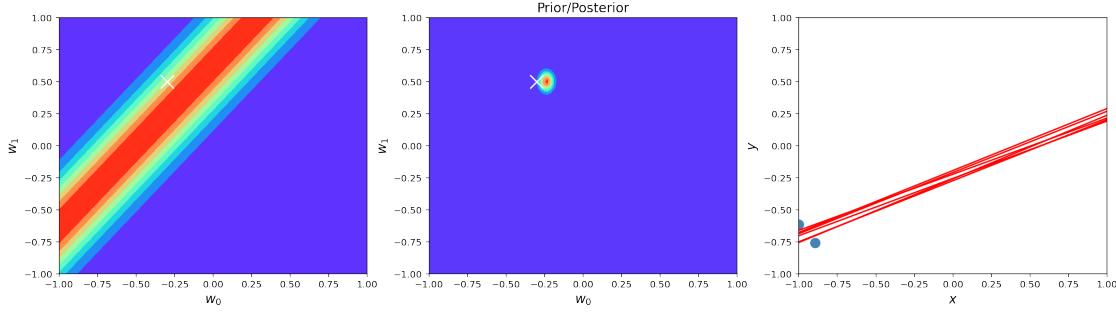
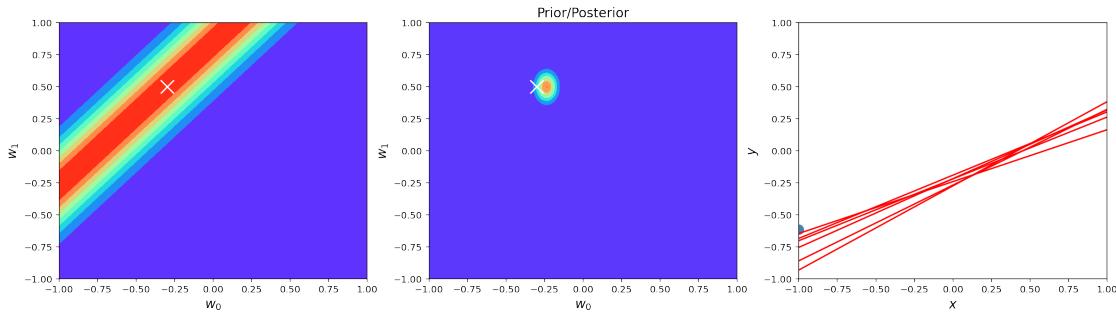
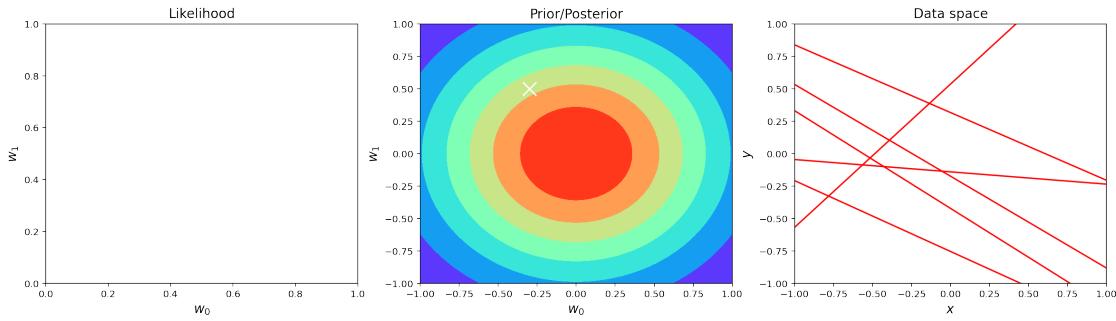
# data space
plt.subplot(1, 3, 3)
if i == 0:
    plt.title("Data space", fontsize=14)
else:
    plt.scatter(x_train[:i], y_train[:i], s=100, color="steelblue")

w_sample = prior_posterior.draw(6)
y_sample = x_train_linear @ w_sample.T
plt.plot(x_train, y_sample, color="red")

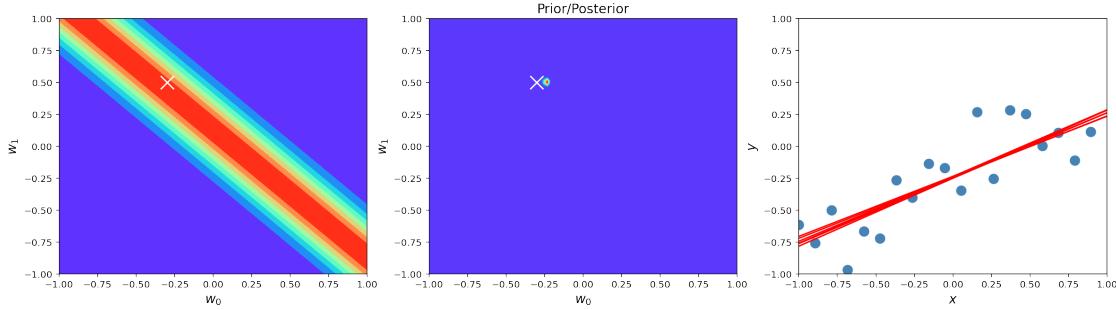
plt.xlim(-1, 1)
plt.ylim(-1, 1)
plt.xlabel("$x$", fontsize=14)
plt.ylabel("$y$", fontsize=14)

plt.show()

```



```
/Users/vagmcs/Work/dev/personal/prml/prml/distribution/multivariate_gaussian.py:
98: RuntimeWarning: overflow encountered in exp
 * np.exp(-0.5 * (np.linalg.solve(self.cov, d).T.dot(d)))
/Users/vagmcs/Work/dev/personal/prml/prml/distribution/multivariate_gaussian.py:
96: RuntimeWarning: overflow encountered in multiply
1
```



3.3.2 Predictive distribution

In practice however, our goal is make predictions of t for unseen values of $\mathbf{x}_{\text{unseen}}$, and thus, we are not actually interested in the value of \mathbf{w} itself. To that end, we evaluate the *predictive distribution* given by

$$p(t|\mathbf{x}_{\text{unseen}}, \mathbf{t}, \mathbf{X}, \alpha, \beta) = \int p(t|\mathbf{x}_{\text{unseen}}, \mathbf{w}, \beta)p(\mathbf{w}|\mathbf{t}, \mathbf{X}, \alpha, \beta)d\mathbf{w}$$

Note that the predictive distribution involves the convolution of the conditional Gaussian distribution of the target variable and the posterior weight Gaussian distribution.

$$\begin{aligned} p(t|\mathbf{x}, \mathbf{w}, \beta) &= \mathcal{N}(t|y(\mathbf{x}, \mathbf{w}), \beta^{-1}) = \mathcal{N}(t|\phi(\mathbf{x})^T \mathbf{w}, \beta^{-1}) \\ p(\mathbf{w}|\mathbf{t}, \mathbf{X}, \alpha, \beta) &= \mathcal{N}(\mathbf{w}|\mathbf{m}_N, \mathbf{S}_N) \end{aligned}$$

Taking advantage of (2.113), (2.114) and (2.115), we can obtain

$$p(t|\mathbf{x}_{\text{unseen}}, \mathbf{t}, \mathbf{X}, \alpha, \beta) = \mathcal{N}(t|\mathbf{m}_N^T \phi(\mathbf{x}_{\text{unseen}}), \sigma_N^2(\mathbf{x}_{\text{unseen}}))$$

where the variance $\sigma_N^2(\mathbf{x})$ of the predictive distribution is given by

$$\sigma_N^2(\mathbf{x}) = \frac{1}{\beta} + \phi(\mathbf{x})^T \mathbf{S}_N \phi(\mathbf{x})$$

The first term represents the noise on the data whereas the second term reflects the uncertainty associated with the parameters \mathbf{w} .

```
[7]: N = 25
sinusoidal = lambda x: np.sin(2 * np.pi * x)

x_train, y_train = generate_toy_data(sinusoidal, N, 0.25)
x_test = np.linspace(0, 1, 100)
y_test = sinusoidal(x_test)

feature = GaussianFeature(np.linspace(0, 1, 9), 0.1)
```

```

X_train = feature.transform(x_train)
X_test = feature.transform(x_test)

fig_idx = 1
plt.figure(figsize=(20, 6))
for i, x in enumerate(X_train):
    if i < 4 or i == 7 or i == N - 1:
        model = BayesianRegression(alpha=1e-3, beta=2.0)
        model.fit(X_train[: i + 1], y_train[: i + 1])
        y, y_std = model.predict(X_test)

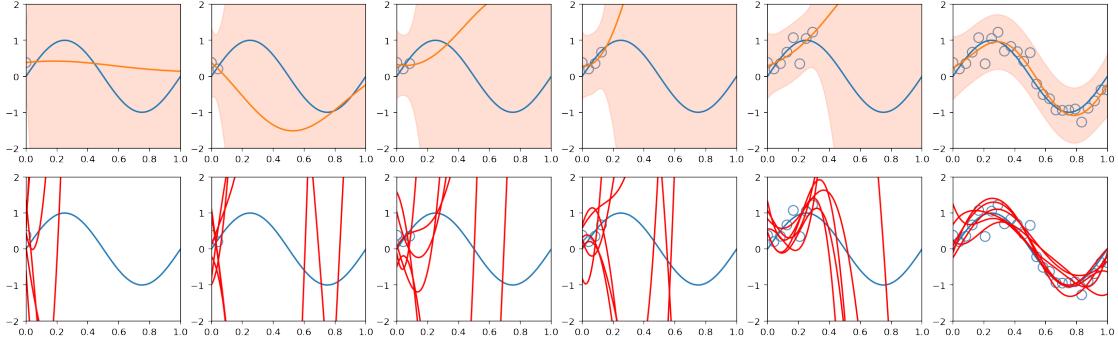
        plt.subplot(2, 6, fig_idx)
        fig_idx += 1
        plt.scatter(x_train[: i + 1], y_train[: i + 1], s=100, color="red",
                    facecolor="none", edgecolor="steelblue")
        plt.plot(x_test, y_test)
        plt.plot(x_test, y)
        plt.fill_between(x_test, y - y_std, y + y_std, color="coral", alpha=0.25)
        plt.xlim(0, 1)
        plt.ylim(-2, 2)

for i, x in enumerate(X_train):
    if i < 4 or i == 7 or i == N - 1:
        model = BayesianRegression(alpha=1e-3, beta=2.0)
        model.fit(X_train[: i + 1], y_train[: i + 1])
        w_samples = model.draw(6)

        plt.subplot(2, 6, fig_idx)
        fig_idx += 1
        plt.scatter(x_train[: i + 1], y_train[: i + 1], s=100, color="red",
                    facecolor="none", edgecolor="steelblue")
        plt.plot(x_test, y_test)
        plt.plot(x_test, X_test @ w_samples.T, color="red")
        plt.xlim(0, 1)
        plt.ylim(-2, 2)

plt.show()

```



3.3.3 Equivalent kernel

The posterior mean solution for the linear basis function model has an interesting interpretation. If we substitute the posterior mean solution \mathbf{m}_N , given by (3.53), into the expression (3.3), we note that the predictive mean can be expressed in the form

$$y(\mathbf{x}, \mathbf{m}_N) = \mathbf{m}_N^T \phi(\mathbf{x}) = \beta \phi(\mathbf{x})^T \mathbf{S}_N \Phi^T \mathbf{t} = \sum_{n=1}^N \beta \phi(\mathbf{x})^T \mathbf{S}_N \phi(\mathbf{x}_n) t_n$$

Thus the mean of the predictive distribution at point \mathbf{x} is given by a linear combination of the training data set target variables t_n .

$$y(\mathbf{x}, \mathbf{m}_N) = \sum_{n=1}^N k(\mathbf{x}, \mathbf{x}_n) t_n$$

where the function

$$k(\mathbf{x}, \mathbf{x}') = \beta \phi(\mathbf{x})^T \mathbf{S}_N \phi(\mathbf{x}')$$

is known as the *smoother matrix* or the *equivalent kernel*. Regression functions that make predictions by taking linear combinations of the training set target values are known as *linear smoothers*.

Further insight into the equivalent kernel can be obtained by considering the covariance between $y(\mathbf{x})$ and $y(\mathbf{x}')$,

$$\text{cov}[y(\mathbf{x}), y(\mathbf{x}')] = \text{cov}[\phi(\mathbf{x})^T \mathbf{w}, \mathbf{w}^T \phi(\mathbf{x}')] = \phi(\mathbf{x})^T \mathbf{S}_N \phi(\mathbf{x}') = \beta^{-1} k(\mathbf{x}, \mathbf{x}')$$

Therefore, the predictive mean at nearby points is highly correlated, whereas for more distant pairs of points the correlation is smaller.

!!! This formulation of linear regression suggests an alternative approach to regression as follows. Instead of introducing a set of basis functions ϕ_j to derive an equivalent kernel, we may instead define the kernel $k(\mathbf{x}, \mathbf{x}')$ directly and use it to make predictions, given an observed training set. This leads to a practical framework called *Gaussian processes*.

3.5 The Evidence Approximation

In a fully Bayesian treatment of the linear basis function model one can introduce prior distributions over the hyperparameters α and β and make predictions by marginalizing over these hyperparameters in addition to the model parameters \mathbf{w} . However, the complete marginalization over these variables is analytically intractable. A useful approximation is to set the hyperparameters to specific values by maximizing the marginal likelihood obtained by integrating over the model parameters \mathbf{w} . This framework is known in statistics as *empirical bayes* or *type 2 maximum likelihood* or *generalized maximum likelihood*. In machine learning is also called *evidence approximation*.

The predictive distribution is obtained by marginalizing over \mathbf{w} , α and β so that

$$p(t|\tilde{\mathbf{x}}, \mathbf{t}, \mathbf{X}) = \int \int \int p(t|\mathbf{w}, \tilde{\mathbf{x}}, \beta) p(\mathbf{w}|\mathbf{t}, \mathbf{X}, \alpha, \beta) p(\alpha, \beta|\mathbf{t}, \mathbf{X}) d\mathbf{w} d\alpha d\beta$$

Assuming that the posterior distribution $p(\alpha, \beta|\mathbf{t}, \mathbf{X})$ is sharply peaked around some values $\hat{\alpha}$ and $\hat{\beta}$, then the predictive distribution is obtained by fixing α and β to these values and marginalizing over \mathbf{w}

$$p(t|\tilde{\mathbf{x}}, \mathbf{t}, \mathbf{X}) \approx p(t|\tilde{\mathbf{x}}, \mathbf{t}, \mathbf{X}, \hat{\alpha}, \hat{\beta}) = \int p(t|\tilde{\mathbf{x}}, \mathbf{w}, \hat{\beta}) p(\mathbf{w}|\mathbf{t}, \mathbf{X}, \hat{\alpha}, \hat{\beta}) d\mathbf{w}$$

in which case we arrive at the simpler predictive distribution defined by (3.57).

The posterior distribution for α and β is given by

$$p(\alpha, \beta|\mathbf{t}, \mathbf{X}) \propto p(\mathbf{t}|\mathbf{X}, \alpha, \beta) p(\alpha, \beta)$$

Further assuming that the prior is relatively flat, that is, our prior belief is that different values of α and β are somewhat equiprobable. Then, the sharply peaked area assumed for the posterior ($\hat{\alpha}$ and $\hat{\beta}$) should be found by maximizing the marginal likelihood function $p(\mathbf{t}|\mathbf{X}, \alpha, \beta)$.

3.5.1 Evaluation of the evidence function

The marginal likelihood function $p(\mathbf{t}|\mathbf{X}, \alpha, \beta)$ is obtained by integrating over the model parameters \mathbf{w} , so that,

$$p(\mathbf{t}|\mathbf{X}, \alpha, \beta) = \int p(\mathbf{t}|\mathbf{X}, \mathbf{w}, \beta) p(\mathbf{w}|\alpha) d\mathbf{w}$$

From (3.10) we have that

$$\begin{aligned}
p(\mathbf{t}|\mathbf{X}, \mathbf{w}, \beta) &= \prod_{n=1}^N \mathcal{N}(t_n | \mathbf{w}^T \phi(\mathbf{x}_n), \beta^{-1}) \\
&= \prod_{n=1}^N \frac{1}{(2\pi\beta^{-1})^{1/2}} \exp \left\{ -\frac{1}{2\beta^{-1}} (t_n - \mathbf{w}^T \phi(\mathbf{x}_n))^2 \right\} \\
&= N \left(\frac{\beta}{2\pi} \right)^{1/2} \exp \left\{ \sum_{n=1}^N -\frac{1}{2\beta^{-1}} (t_n - \mathbf{w}^T \phi(\mathbf{x}_n))^2 \right\} \\
&= \left(\frac{\beta}{2\pi} \right)^{N/2} \exp \left\{ -\frac{\beta}{2} \|\mathbf{t} - \Phi\mathbf{w}\|^2 \right\}
\end{aligned}$$

From (3.52) we have that

$$p(\mathbf{w}|\alpha) = \mathcal{N}(\mathbf{w}|\mathbf{0}, \alpha^{-1}\mathbf{I}) = \frac{\alpha^{M/2}}{(2\pi)^{M/2}} \exp \left\{ -\frac{\alpha}{2} \|\mathbf{w}\|^2 \right\}$$

Substituting both these quantities back into the integral of the marginal likelihood, we have

$$p(\mathbf{t}|\mathbf{X}, \alpha, \beta) = \left(\frac{\beta}{2\pi} \right)^{N/2} \left(\frac{\alpha}{2\pi} \right)^{M/2} \int \exp \left\{ -\frac{\beta}{2} \|\mathbf{t} - \Phi\mathbf{w}\|^2 - \frac{\alpha}{2} \|\mathbf{w}\|^2 \right\} d\mathbf{w}$$

Using (3.25) and (3.26) we obtain

$$p(\mathbf{t}|\mathbf{X}, \alpha, \beta) = \left(\frac{\beta}{2\pi} \right)^{N/2} \left(\frac{\alpha}{2\pi} \right)^{M/2} \int \exp \{-E(\mathbf{w})\} d\mathbf{w}$$

where

$$E(\mathbf{w}) = \beta E_D(\mathbf{w}) + \alpha E_W(\mathbf{w})$$

Completing the square over \mathbf{w} , we obtain

$$\begin{aligned}
E(\mathbf{w}) &= \frac{\beta}{2} \|\mathbf{t} - \Phi\mathbf{w}\|^2 + \frac{\alpha}{2} \|\mathbf{w}\|^2 \\
&= \frac{\beta}{2} (\mathbf{t}^T \mathbf{t} - 2\mathbf{t}^T \Phi \mathbf{w} + \mathbf{w}^T \Phi^T \Phi \mathbf{w}) + \frac{\alpha}{2} \mathbf{w}^T \mathbf{w} \\
&= \frac{1}{2} (\mathbf{w}^T (\alpha \mathbf{I} + \beta \Phi^T \Phi) \mathbf{w} - 2\beta \mathbf{t}^T \Phi \mathbf{w} + \beta \mathbf{t}^T \mathbf{t})
\end{aligned}$$

where

$$\begin{aligned}
\mathbf{A} &= \mathbf{S}_N^{-1} = \alpha \mathbf{I} + \beta \Phi^T \Phi \\
\mathbf{m}_N^T \mathbf{S}_N^{-1} &= \beta \mathbf{t}^T \Phi \Leftrightarrow \\
\mathbf{m}_N^T &= \beta \mathbf{S}_N \mathbf{t}^T \Phi \Leftrightarrow \\
\mathbf{m}_N &= \beta \mathbf{S}_N \Phi^T \mathbf{t} = \beta \mathbf{A}^{-1} \Phi^T \mathbf{t}
\end{aligned}$$

By exploiting the fact $\mathbf{A}^{-1}\mathbf{A} = \mathbf{I}$ and adding $\mathbf{0} = \mathbf{m}_N^T \mathbf{A} \mathbf{m}_N - \mathbf{m}_N^T \mathbf{A} \mathbf{m}_N$, we can further derive that

$$\begin{aligned} E(\mathbf{w}) &= \frac{1}{2}(\mathbf{w}^T(\alpha\mathbf{I} + \beta\Phi^T\Phi)\mathbf{w} - 2\beta\mathbf{t}^T\Phi\mathbf{w} + \beta\mathbf{t}^T\mathbf{t}) \\ &= \frac{1}{2}(\mathbf{w}^T\mathbf{A}\mathbf{w} - 2\beta\mathbf{t}^T\Phi\mathbf{A}^{-1}\mathbf{A}\mathbf{w} + \beta\mathbf{t}^T\mathbf{t}) \\ &= \frac{1}{2}(\mathbf{w}^T\mathbf{A}\mathbf{w} - 2\mathbf{m}_N^T\mathbf{A}\mathbf{w} + \beta\mathbf{t}^T\mathbf{t} + \mathbf{m}_N^T\mathbf{A}\mathbf{m}_N - \mathbf{m}_N^T\mathbf{A}\mathbf{m}_N) \\ &= \frac{1}{2}(\beta\mathbf{t}^T\mathbf{t} - \mathbf{m}_N^T\mathbf{A}\mathbf{m}_N) + \frac{1}{2}(\mathbf{w} - \mathbf{m}_N)^T\mathbf{A}(\mathbf{w} - \mathbf{m}_N) \end{aligned}$$

At this point note that the first term is independent of the model parameters \mathbf{w} and the second term is an exponent of a Gaussian distribution over the model parameters. Therefore the integral over \mathbf{w} of $p(\mathbf{t}|\mathbf{X}, \alpha, \beta)$ is given by

$$p(\mathbf{t}|\mathbf{X}, \alpha, \beta) = \left(\frac{\beta}{2\pi}\right)^{N/2} \left(\frac{\alpha}{2\pi}\right)^{M/2} \exp\left\{-\frac{1}{2}(\beta\mathbf{t}^T\mathbf{t} - \mathbf{m}_N^T\mathbf{A}\mathbf{m}_N)\right\} \int \exp\left\{-\frac{1}{2}(\mathbf{w} - \mathbf{m}_N)^T\mathbf{A}(\mathbf{w} - \mathbf{m}_N)\right\} d\mathbf{w}$$

However, based on the standard form of a multivariate normal distribution, we know that

$$\begin{aligned} \int \frac{1}{(2\pi)^{M/2}} \frac{1}{|\mathbf{A}|^{1/2}} \exp\left\{-\frac{1}{2}(\mathbf{w} - \mathbf{m}_N)^T\mathbf{A}(\mathbf{w} - \mathbf{m}_N)\right\} d\mathbf{w} &= 1 \Leftrightarrow \\ \int \exp\left\{-\frac{1}{2}(\mathbf{w} - \mathbf{m}_N)^T\mathbf{A}(\mathbf{w} - \mathbf{m}_N)\right\} d\mathbf{w} &= (2\pi)^{M/2} |\mathbf{A}|^{-1/2} \end{aligned}$$

Thus,

$$p(\mathbf{t}|\mathbf{X}, \alpha, \beta) = \left(\frac{\beta}{2\pi}\right)^{N/2} \left(\frac{\alpha}{2\pi}\right)^{M/2} \exp\left\{-\frac{1}{2}(\beta\mathbf{t}^T\mathbf{t} - \mathbf{m}_N^T\mathbf{A}\mathbf{m}_N)\right\} (2\pi)^{M/2} |\mathbf{A}|^{-1/2}$$

Thus, the log of the marginal likelihood is given by

$$\begin{aligned} \log p(\mathbf{t}|\mathbf{X}, \alpha, \beta) &= \frac{N}{2} \log\left(\frac{\beta}{2\pi}\right) + \frac{M}{2} \log\left(\frac{\alpha}{2\pi}\right) - \frac{1}{2}(\beta\mathbf{t}^T\mathbf{t} - \mathbf{m}_N^T\mathbf{A}\mathbf{m}_N) + \frac{M}{2} \log(2\pi) - \frac{1}{2}|\mathbf{A}| \\ &= \frac{M}{2} \log \alpha + \frac{N}{2} \log \beta - \frac{1}{2}(\beta\mathbf{t}^T\mathbf{t} - \mathbf{m}_N^T\mathbf{A}\mathbf{m}_N) - \frac{1}{2}|\mathbf{A}| - \frac{N}{2} \log(2\pi) \end{aligned}$$

As a final step we are about to show that $\frac{1}{2}(\beta\mathbf{t}^T\mathbf{t} - \mathbf{m}_N^T\mathbf{A}\mathbf{m}_N) = E(\mathbf{w})$

$$\begin{aligned}
\frac{1}{2}(\beta \mathbf{t}^T \mathbf{t} - \mathbf{m}_N^T \mathbf{A} \mathbf{m}_N) &= \frac{1}{2}(\beta \mathbf{t}^T \mathbf{t} - 2\mathbf{m}_N^T \mathbf{A} \mathbf{m}_N + \mathbf{m}_N^T \mathbf{A} \mathbf{m}_N) \\
&\stackrel{(3.81)}{=} \frac{1}{2}(\beta \mathbf{t}^T \mathbf{t} - 2\mathbf{m}_N^T \mathbf{A} \mathbf{m}_N - \mathbf{m}_N^T (\alpha \mathbf{I} + \beta^T) \mathbf{m}_N) \\
&\stackrel{(3.84)}{=} \frac{1}{2}(\beta \mathbf{t}^T \mathbf{t} - 2\beta \mathbf{t}^T \mathbf{A}^{-1} \mathbf{A} \mathbf{m}_N - \mathbf{m}_N^T (\alpha \mathbf{I} + \beta^T) \mathbf{m}_N) \\
&= \frac{1}{2}(\beta \mathbf{t}^T \mathbf{t} - 2\beta \mathbf{t}^T \mathbf{m}_N - \mathbf{m}_N^T (\beta^T) \mathbf{m}_N) + \frac{\alpha}{2} \mathbf{m}_N^T \mathbf{m}_N \\
&= \frac{1}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 + \frac{\alpha}{2} \mathbf{m}_N^T \mathbf{m}_N = E(\mathbf{w})
\end{aligned}$$

3.5.2 Maximizing the evidence function

Lets consider the maximization of $p(\mathbf{t}|\mathbf{X}, \alpha, \beta)$ over α ,

$$\begin{aligned}
\frac{d}{d\alpha} p(\mathbf{t}|\mathbf{X}, \alpha, \beta) &= \frac{d}{d\alpha} \frac{M}{2} \log \alpha - \frac{d}{d\alpha} E(\mathbf{w}) - \frac{d}{d\alpha} \frac{1}{2} \log |\mathbf{A}| \\
&= \frac{M}{2\alpha} - \frac{1}{2} \mathbf{m}_N^T \mathbf{m}_N - \frac{1}{2} \frac{d}{d\alpha} \ln |\mathbf{A}|
\end{aligned}$$

In order to find the derivative of $\ln |\mathbf{A}|$, we use the eigenvector equation of (C.29)

$$\begin{aligned}
(\beta^T) \mathbf{u}_i = \lambda_i \mathbf{u}_i &\stackrel{(C.30)}{\Leftrightarrow} |\beta^T - \lambda_i \mathbf{I}| = \mathbf{0} \\
&\stackrel{(3.81)}{\Leftrightarrow} |\mathbf{A} - \alpha \mathbf{I} - \lambda_i \mathbf{I}| = \mathbf{0} \\
&\Leftrightarrow |\mathbf{A} - (\lambda_i + \alpha) \mathbf{I}| = \mathbf{0}
\end{aligned}$$

Therefore, we can derive that \mathbf{A} has eigenvalues $\lambda_i + \alpha$. In conclusion, the derivative of the term involving $\ln |\mathbf{A}|$ is given by

$$\frac{d}{d\alpha} \ln |\mathbf{A}| \stackrel{(C.47)}{=} \frac{d}{d\alpha} \ln \prod_{i=1}^M (\lambda_i + \alpha) = \frac{d}{d\alpha} \sum_{i=1}^M \ln(\lambda_i + \alpha) = \sum_{i=1}^M \frac{1}{\lambda_i + \alpha}$$

Thus, the resulting solution for α , as presented in eq. (3.92), is given by

$$\begin{aligned}
0 &= \frac{M}{2\alpha} - \frac{1}{2} \mathbf{m}_N^T \mathbf{m}_N - \frac{1}{2} \sum_{i=1}^M \frac{1}{\lambda_i + \alpha} \Leftrightarrow \\
\frac{1}{2} \mathbf{m}_N^T \mathbf{m}_N &= \frac{M}{2\alpha} - \frac{1}{2} \sum_{i=1}^M \frac{1}{\lambda_i + \alpha} \stackrel{\times 2\alpha}{\Leftrightarrow} \\
\alpha \mathbf{m}_N^T \mathbf{m}_N &= M - \alpha \sum_{i=1}^M \frac{1}{\lambda_i + \alpha} \Leftrightarrow \\
\alpha \mathbf{m}_N^T \mathbf{m}_N &= M \frac{\lambda_i + \alpha}{\lambda_i + \alpha} - \sum_{i=1}^M \frac{\alpha}{\lambda_i + \alpha} \Leftrightarrow \\
\alpha \mathbf{m}_N^T \mathbf{m}_N &= \sum_{i=1}^M \frac{\lambda_i}{\lambda_i + \alpha} = \gamma \Leftrightarrow \\
\alpha &= \frac{\gamma}{\mathbf{m}_N^T \mathbf{m}_N}
\end{aligned}$$

Note that this is an implicit solution for α , since both γ and \mathbf{m}_N depend on α . Thus, we have to use an iterative procedure to estimate α by making an starting choice for the value of α , computing \mathbf{m}_N , evaluating γ (3.91) and re-estimating α (3.92), until convergence. It should be *emphasized* that the value of α can be determined purely by looking at the training data. No independent dataset is required in order to optimize model complexity.

The maximization of $p(\mathbf{t}|\mathbf{X}, \alpha, \beta)$ over β is given by

$$\begin{aligned}
\frac{d}{d\beta} p(\mathbf{t}|\mathbf{X}, \alpha, \beta) &= \frac{d}{d\beta} \frac{N}{2} \log \beta - \frac{d}{d\beta} E(\mathbf{w}) - \frac{d}{d\beta} \frac{1}{2} \log |\mathbf{A}| \\
&= \frac{N}{2\beta} - \frac{d}{d\beta} E(\mathbf{w}) - \frac{1}{2} \frac{d}{d\beta} \ln |\mathbf{A}|
\end{aligned}$$

Lets take a closer look to the second term,

$$\begin{aligned}
\frac{d}{d\beta} E(\mathbf{w}) &= \frac{d}{d\beta} \frac{\beta}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 + \frac{d}{d\beta} \frac{\alpha}{2} \mathbf{m}_N^T \mathbf{m}_N \\
&\stackrel{\text{product rule}}{=} \frac{1}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 + \frac{\beta}{2} \frac{d}{d\beta} \|\mathbf{t} - \mathbf{m}_N\|^2 + \frac{d}{d\beta} \frac{\alpha}{2} \mathbf{m}_N^T \mathbf{m}_N \\
&\stackrel{\times d\mathbf{m}_N/d\beta}{=} \frac{1}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 + \left(\frac{\beta}{2} \frac{d}{d\mathbf{m}_N} \|\mathbf{t} - \mathbf{m}_N\|^2 + \frac{d}{d\mathbf{m}_N} \frac{\alpha}{2} \mathbf{m}_N^T \mathbf{m}_N \right) \frac{d\mathbf{m}_N}{d\beta} \\
&= \frac{1}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 + \left(\frac{\beta}{2} (-2^T(\mathbf{t} - \mathbf{m}_N)) + \frac{\alpha}{2} 2\mathbf{m}_N \right) \frac{d\mathbf{m}_N}{d\beta} \\
&= \frac{1}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 + \left(-\beta^T(\mathbf{t} - \mathbf{m}_N) + \alpha\mathbf{m}_N \right) \frac{d\mathbf{m}_N}{d\beta} \\
&= \frac{1}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 + \left(-\beta^T\mathbf{t} - (\alpha\mathbf{I} + \beta^T)\mathbf{m}_N \right) \frac{d\mathbf{m}_N}{d\beta} \\
&\stackrel{(3.81)}{=} \frac{1}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 + (-\beta^T\mathbf{t} - \mathbf{A}\mathbf{m}_N) \frac{d\mathbf{m}_N}{d\beta} \\
&\stackrel{(3.84)}{=} \frac{1}{2} \|\mathbf{t} - \mathbf{m}_N\|^2 = \frac{1}{2} \sum_{n=1}^N \{t_n - \mathbf{m}_N^T(\mathbf{x}_n)\}^2
\end{aligned}$$

The last term involving the derivative of $\ln |\mathbf{A}|$ becomes

$$\frac{d}{d\beta} \ln |\mathbf{A}| = \frac{d}{d\beta} \sum_{i=1}^M \ln(\lambda_i + \alpha) = \sum_{i=1}^M \frac{1}{\lambda_i + \alpha} \frac{d}{d\beta} \lambda_i = \frac{1}{\beta} \sum_{i=1}^M \frac{\lambda_i}{\lambda_i + \alpha} = \frac{\gamma}{\beta}$$

Finally, if we combine all these expressions together, we obtain

$$\begin{aligned}
0 &= \frac{N}{2\beta} - \frac{1}{2} \sum_{n=1}^N \{t_n - \mathbf{m}_N^T \phi(\mathbf{x}_n)\}^2 - \frac{\gamma}{2\beta} \Leftrightarrow \\
\frac{1}{\beta} &= \frac{1}{N - \gamma} \sum_{n=1}^N \{t_n - \mathbf{m}_N^T \phi(\mathbf{x}_n)\}^2
\end{aligned}$$

As expected, the solution for β is also implicit. If both α and β are to be determined, then their values can be re-estimated together after each update of γ .

```
[8]: cubic = lambda x: x * (x - 5) * (x + 5)
x_train, y_train = generate_toy_data(cubic, 30, 10, [-5, 5])
x_test = np.linspace(-5, 5, 100)

models = []
evidences = []
for i in range(8):
    feature = PolynomialFeature(degree=i)
    X_train = feature.transform(x_train)
    model = EvidenceApproximation(alpha=100.0, beta=100.0)
    model.fit(X_train, y_train, n_iter=100)
    evidences.append(model.log_evidence(X_train, y_train))
```

```

models.append(model)

# select the best performing degree (the one having the highest evidence)
degree = np.nanargmax(evidences)
regression = models[degree]

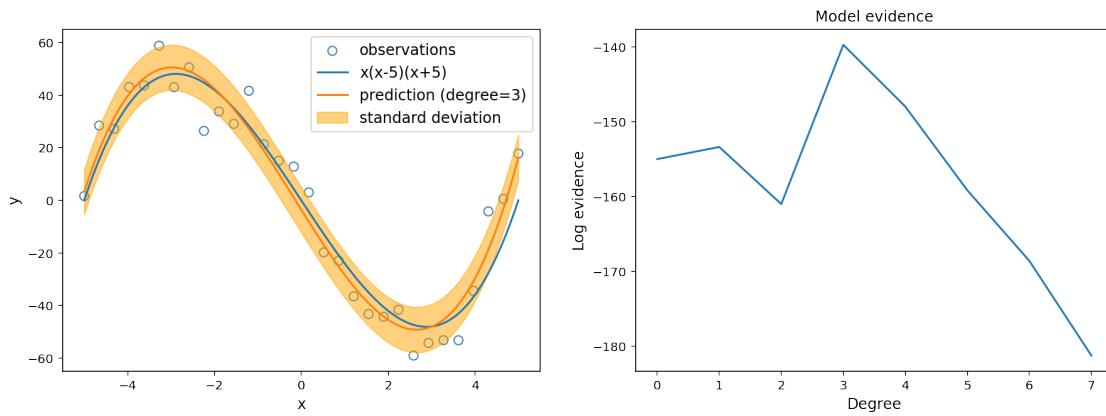
X_test = PolynomialFeature(degree=int(degree)).transform(x_test)
y, y_std = regression.predict(X_test)

plt.figure(figsize=(15, 5))

plt.subplot(1, 2, 1)
plt.scatter(x_train, y_train, s=50, facecolor="none", edgecolor="steelblue", label="observations")
plt.plot(x_test, cubic(x_test), label="x(x-5)(x+5)")
plt.plot(x_test, y, label=f"prediction (degree={degree})")
plt.fill_between(x_test, y - y_std, y + y_std, alpha=0.5, label="standard deviation", color="orange")
plt.xlabel("x", fontsize=12)
plt.ylabel("y", fontsize=12)
plt.legend(fontsize=12)

plt.subplot(1, 2, 2)
plt.plot(evidences)
plt.title("Model evidence", fontsize=12)
plt.xlabel("Degree", fontsize=12)
plt.ylabel("Log evidence", fontsize=12)
plt.show()

```



The left figure presents the fitted function estimated by evidence approximation for degree 3. The figure in the right depicts the log evidence of each polynomial feature degree. Note that the highest evidence is achieved for polynomial feature of degree 3.

4. Linear Models for Classification

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```
[1]: import math
import numpy as np
import matplotlib.pyplot as plt

from sklearn.datasets import make_classification
from prml.preprocessing import LinearFeature
from prml.linear import LeastSquaresClassifier
from prml.linear import FisherLinearDiscriminant
from prml.linear import Perceptron
from prml.linear import GenerativeClassifier
from prml.linear import LogisticRegression
from prml.linear import SoftmaxRegression
from prml.linear import BayesianLogisticRegression
from prml.distribution import Gaussian

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'

# Enable autoreload all modules before executing code
%load_ext autoreload
%autoreload 2
```

The goal in classification is to take an input vector \mathbf{x} and assign it to one of K discrete classes \mathcal{C}_k , where $k = 1 \dots, K$. The input space is thereby divided into *decision regions* whose boundaries are called *decision boundaries* or *decision surfaces*. Linear models define decision surfaces as linear functions of the input vector \mathbf{x} and hence are defined by $(D-1)$ -dimensional hyperplanes inside the D -dimensional space. Datasets whose classes can be separated exactly by linear decision surfaces are called *linearly separable*.

There are three distinct approaches to the classification problem:

1. Discriminant functions that directly assign each input vector \mathbf{x} to a class.
2. Models that directly learn the conditional probability $p(\mathcal{C}_k|\mathbf{x})$ using parametric modelling.
3. Generative approaches that model the class conditional density $p(\mathbf{x}|\mathcal{C}_k)$, and the prior probabilities $p(\mathcal{C}_k)$ for the classes. Then they derive the posterior using the Bayes theorem.

In the linear regression models, the model prediction $y(\mathbf{x}, \mathbf{w})$ was given by a linear function of the parameters \mathbf{w} . For classification problems, however, we wish to predict discrete class labels. To that end, we consider a generalization of the above model in which we transform the linear function using a nonlinear function $f(\cdot)$ so that

$$y(\mathbf{x}) = f(\mathbf{w}^T \mathbf{x} + w_0)$$

In machine learning, the function f is known as an *activation function*.

4.1 Discriminant Functions

A discriminant is a function that assigns one of K classes to an input vector \mathbf{x} . *Linear discriminants* define decision surfaces that are hyperplanes.

4.1.1 Two Classes

The simplest linear discriminant function is obtained by taking a linear function of the input vector so that,

$$y(\mathbf{x}) = \mathbf{w}^T \mathbf{x} + w_0$$

where \mathbf{w} is a *weight vector* and w_0 is a *bias* (the negative of the bias is also called *threshold*). Then, an input \mathbf{x} is assigned to a class \mathcal{C}_1 if $y(\mathbf{x}) \geq 0$ and to class \mathcal{C}_2 otherwise. Thus, the decision boundary is defined by $y(\mathbf{x}) = 0$.

Consider two points \mathbf{x}_A and \mathbf{x}_B onto the decision surface. Then, $y(\mathbf{x}_A) = y(\mathbf{x}_B) = 0 \Leftrightarrow \mathbf{w}^T(\mathbf{x}_A - \mathbf{x}_B) = 0$, which implies that the vector \mathbf{w} is orthogonal to every vector lying in the decision surface as depicted below:

Note that for more than two classes ($K > 2$), a *one-vs-the-rest* classifier can be used in order to avoid regions of input space that are ambiguously classified. The linear function of each class takes the form $y_k(\mathbf{x}) = \mathbf{w}_k^T \mathbf{x} + w_{k0}$, and assigns a point \mathbf{x} to class \mathcal{C}_k if $y_k(\mathbf{x}) > y_j(\mathbf{x}) \forall j \neq k$.

In the following section*'s we explore three approaches to learning the parameters of linear discriminant functions:

1. Least squares
2. Fisher's linear discriminant
3. Perceptron algorithm

4.1.3 Least squares for classification

In Chapter 3, we minimized the sum-of-squared error function led to a closed-form solution for the parameter values. Can we apply the same principle to classification problems?

Consider a general classification problem having K classes, using a 1-of- K binary coding scheme or *one-hot* encoding for the target vector. Each class \mathcal{C}_k is described by its own linear model y_k . We can group these models together using vector notation so that

$$y(\mathbf{x}) = \tilde{\mathbf{W}}^T \tilde{\mathbf{x}}$$

where $\tilde{\mathbf{W}}$ is a matrix whose k^{th} column comprises the $D + 1$ -dimensional vector $\tilde{\mathbf{w}}_k = (w_{k0}, \mathbf{w}_k^T)^T$ and $\tilde{\mathbf{x}}$ is the augmented vector $(1, \mathbf{x}^T)^T$. The parameter matrix $\tilde{\mathbf{W}}$ is determined by minimizing the sum-of-squares error function, as presented in Chapter 3. Thus, the solution for $\tilde{\mathbf{W}}$ is obtained from

$$\tilde{\mathbf{W}} = (\tilde{\mathbf{X}}^T \tilde{\mathbf{X}})^{-1} \tilde{\mathbf{X}}^T \mathbf{T}$$

```
[2]: # number of training points
N = 100

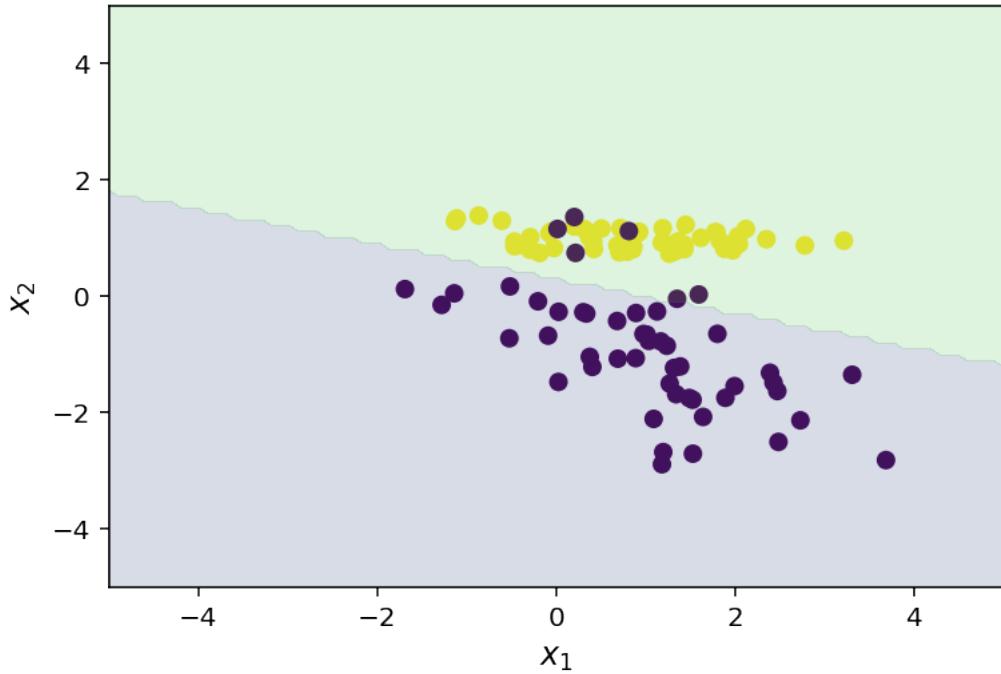
x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2,
    n_clusters_per_class=1, n_samples=N
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, 100), np.linspace(-5, 5, 100))
x_test = np.array([x1, x2]).reshape(2, -1).T

feature = LinearFeature()
x_train_linear = feature.transform(x_train)
x_test_linear = feature.transform(x_test)

model = LeastSquaresClassifier()
model.fit(x_train_linear, t)
predicted = model.predict(x_test_linear)

plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(100, 100), alpha=0.2, levels=np.
    linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)
plt.show()
```



The least-squares approach gives an exact closed-form solution for the discriminant function parameters. However, even as a discriminant function (making decisions directly) it suffers from some problems. We already know that least-squares solutions lack robustness to outliers, and this applies equally to classification, as depicted in the following figure. Note that the additional outlier data points produce a change in the location of the decision boundary, even though these point would be correctly classified by the original decision boundary. The sum-of-squares error function penalizes predictions that are *too correct* in that they lie a long way on the correct side of the decision boundary.

```
[3]: # number of training points
N = 100

# number of outlier points
n_outliers = 5

x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2,
    n_clusters_per_class=1, n_samples=N, random_state=12
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, 100), np.linspace(-5, 5, 100))
x_test = np.array([x1, x2]).reshape(2, -1).T

outliers = np.random.randint(0, 2, (n_outliers, 2)) + 3
x_train_outliers = np.vstack((x_train, outliers))
```

```

t_outliers = np.hstack((t, np.ones(n_outliers, dtype=int)))

feature = LinearFeature()
x_train_linear = feature.transform(x_train)
x_train_linear_outliers = feature.transform(x_train_outliers)
x_test_linear = feature.transform(x_test)

model = LeastSquaresClassifier()
model.fit(x_train_linear, t)
predicted = model.predict(x_test_linear)

plt.figure(figsize=(15, 5))

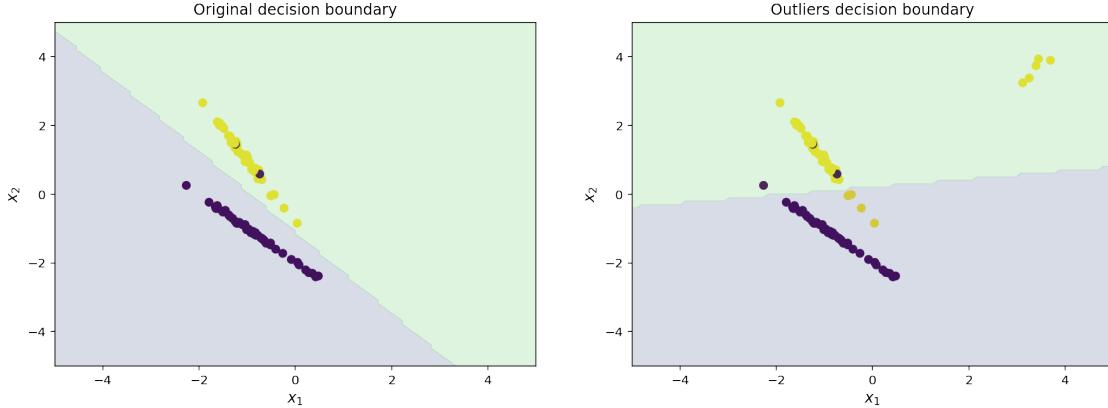
plt.subplot(1, 2, 1)
plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(100, 100), alpha=0.2, levels=np.
    ↪linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)
plt.title("Original decision boundary")

model.fit(x_train_linear_outliers, t_outliers)
predicted_outliers = model.predict(x_test_linear)

plt.subplot(1, 2, 2)
plt.scatter(x_train_outliers[:, 0], x_train_outliers[:, 1], c=t_outliers)
plt.contourf(x1, x2, predicted_outliers.reshape(100, 100), alpha=0.2, levels=np.
    ↪linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)
plt.title("Outliers decision boundary")

plt.show()

```



The failure of least squares should not surprise us since it corresponds to maximum likelihood under the assumption of a Gaussian conditional distribution, whereas binary target vectors clearly do not have a Gaussian distribution.

4.1.4 Fisher's linear discriminant

Consider a two-class problem in which there are N_1 points of class \mathcal{C}_1 and N_2 points from class \mathcal{C}_2 , so that the mean vectors of the two classes are given by

$$\mathbf{m}_1 = \frac{1}{N_1} \sum_{n \in \mathcal{C}_1} \mathbf{x}_n, \quad \mathbf{m}_2 = \frac{1}{N_2} \sum_{n \in \mathcal{C}_2} \mathbf{x}_n$$

Then, the simplest measure of separation of the classes, when projected onto \mathbf{w} , is the separation of the projected class means. This suggests that we might choose \mathbf{w} so as to maximize

$$m_2 - m_1 = \mathbf{w}^T (\mathbf{m}_2 - \mathbf{m}_1)$$

where

$$m_k = \mathbf{w}^T \mathbf{m}_k$$

is the mean of the projected data from class \mathcal{C}_k .

The idea proposed by Fisher is to maximize the function that gives a large separation between the projected class means while also giving a small variance within each class, thereby minimizing the class overlap. The within-class variance of the projected data from class \mathcal{C}_k is given by,

$$s_k^2 = \sum_{n \in \mathcal{C}_k} (y_n - m_k)^2$$

where $y_n = \mathbf{w}^T \mathbf{x}_n$ is the projected data point in the one-dimensional space. We can further define the total within-class variance for the whole data set to be simply $s_1^2 + s_2^2$. Then, the Fisher criterion is defined as the ratio of the *between-class* variance to the *within-class* variance as follows,

$$J(\mathbf{w}) = \frac{(m_2 - m_1)^2}{s_1^2 + s_2^2}$$

In order to explicitly show the dependence on \mathbf{w} , we may rewrite $J(\mathbf{w})$, using (4.20), (4.23), and (4.24), as follows,

$$\begin{aligned} J(\mathbf{w}) &= \frac{(m_2 - m_1)^2}{s_1^2 + s_2^2} \\ &= \frac{(\mathbf{w}^T \mathbf{m}_2 - \mathbf{w}^T \mathbf{m}_1)^2}{\sum_{n \in \mathcal{C}_k} (y_n - m_1)^2 + \sum_{n \in \mathcal{C}_k} (y_n - m_2)^2} \\ &= \frac{(\mathbf{w}^T (\mathbf{m}_2 - \mathbf{m}_1))^2}{\sum_{n \in \mathcal{C}_k} (\mathbf{w}^T (\mathbf{x}_n - \mathbf{m}_1))^2 + \sum_{n \in \mathcal{C}_k} (\mathbf{w}^T (\mathbf{x}_n - \mathbf{m}_2))^2} \\ &= \frac{\mathbf{w}^T (\mathbf{m}_2 - \mathbf{m}_1)^2 \mathbf{w}}{\mathbf{w}^T (\sum_{n \in \mathcal{C}_k} (\mathbf{x}_n - \mathbf{m}_1)^2 + \sum_{n \in \mathcal{C}_k} (\mathbf{x}_n - \mathbf{m}_2)^2) \mathbf{w}} \\ &= \frac{\mathbf{w}^T \mathbf{S}_B \mathbf{w}}{\mathbf{w}^T \mathbf{S}_W \mathbf{w}} \end{aligned}$$

Then, by computing the derivative with respect to \mathbf{w} , we find that $J(\mathbf{w})$ is maximized when,

$$(\mathbf{w}^T \mathbf{S}_B \mathbf{w}) \mathbf{S}_W \mathbf{w} = (\mathbf{w}^T \mathbf{S}_W \mathbf{w}) \mathbf{S}_B \mathbf{w} \Leftrightarrow \mathbf{w} \propto \mathbf{S}_W^{-1} (\mathbf{m}_2 - \mathbf{m}_1)$$

This result is known as the *Fisher's linear discriminant*. To that end, the projected data are compared against a threshold y_0 and classified as belonging to class \mathcal{C}_1 if $y(\mathbf{x}) \geq y_0$, and to class \mathcal{C}_2 otherwise.

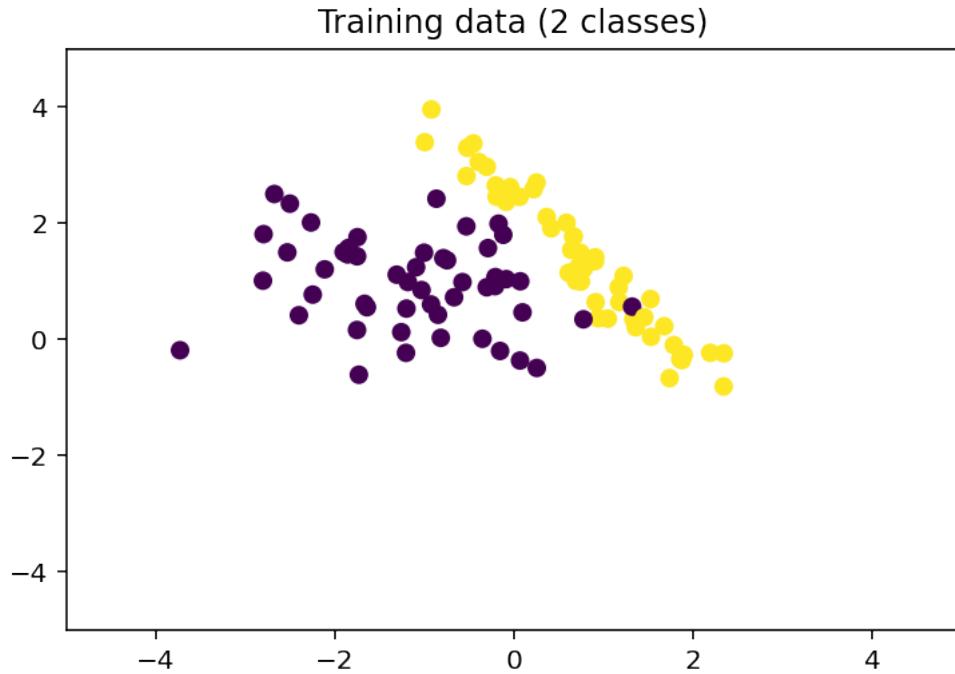
```
[4]: # number of training points
N = 100

x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2, n_clusters_per_class=1, n_samples=N, random_state=15
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, N), np.linspace(-5, 5, N))
x_test = np.array([x1, x2]).reshape(2, -1).T

plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.title("Training data (2 classes)")

plt.show()
```



One way of choosing the threshold y_0 is to model the class-conditional densities (one per class) $p(y|\mathcal{C}_k)$ as Gaussian distributions, then estimate their parameters using maximum likelihood, and finally, estimate the optimal threshold using decision theory. In the case of binary classification, we can equate the Gaussian functions and solve for x . The result is a quadratic equation having coefficients relating to the gaussian means and variances.

```
[5]: # split data points according to the classes
x_0 = x_train[t == 0]
x_1 = x_train[t == 1]

model = FisherLinearDiscriminant()
model.fit(x_train, t)

# create a Gaussian distribution per class
g0 = Gaussian()
g0.ml(x_0 @ model._w)
g1 = Gaussian()
g1.ml(x_1 @ model._w)

root = np.roots(
    [
        g1.var - g0.var,
        2 * (g0.var * g1.mu - g1.var * g0.mu),
        g1.var * g0.mu**2 - g0.var * g1.mu**2 - g1.var * g0.var * np.log(g1.var / g0.var),
    ]
)
```

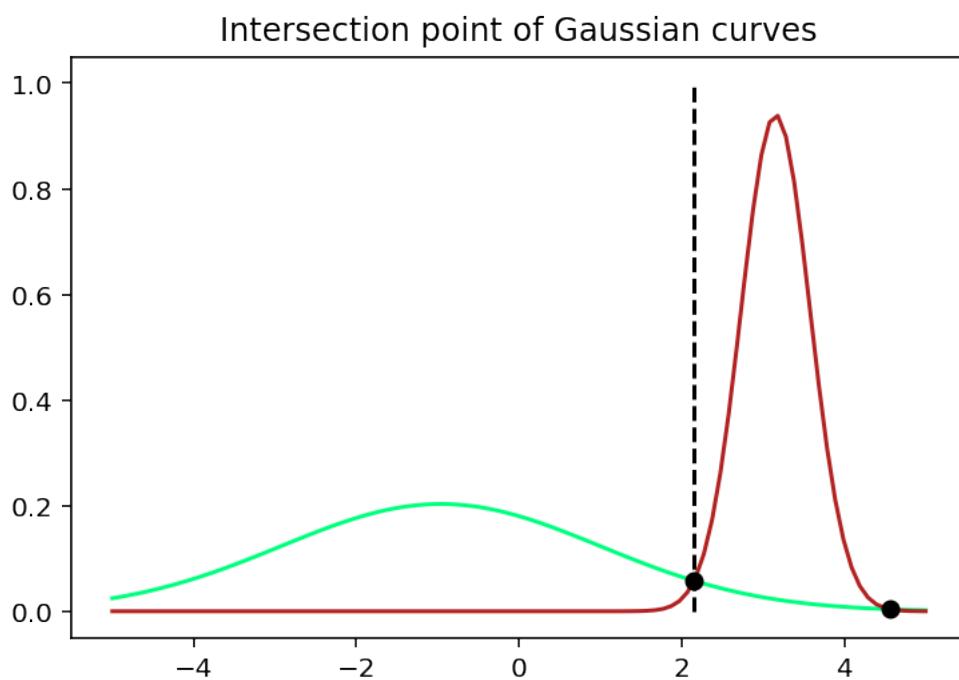
```

        ]
    )

x = np.linspace(-5, 5, N)
plt.plot(x, g0.pdf(x), "springgreen")
plt.plot(x, g1.pdf(x), "firebrick")
plt.plot(root[0], g0.pdf(root[0]), "ko")
plt.plot(root[1], g0.pdf(root[1]), "ko")
plt.plot(np.zeros(x.size) + root[1], np.linspace(0, 1, N), "k--")
plt.title("Intersection* point of Gaussian curves")

plt.show()

```



The figures below compares the optimal threshold against the naive zero threshold. Note that the selection of the decision threshold is crucial for an effective model.

```

[6]: model = FisherLinearDiscriminant()
model.fit(x_train, t)
optimal_threshold = model._threshold

plt.figure(figsize=(15, 5))

# predict classes using the optimal threshold
predicted = model.predict(x_test)

```

```

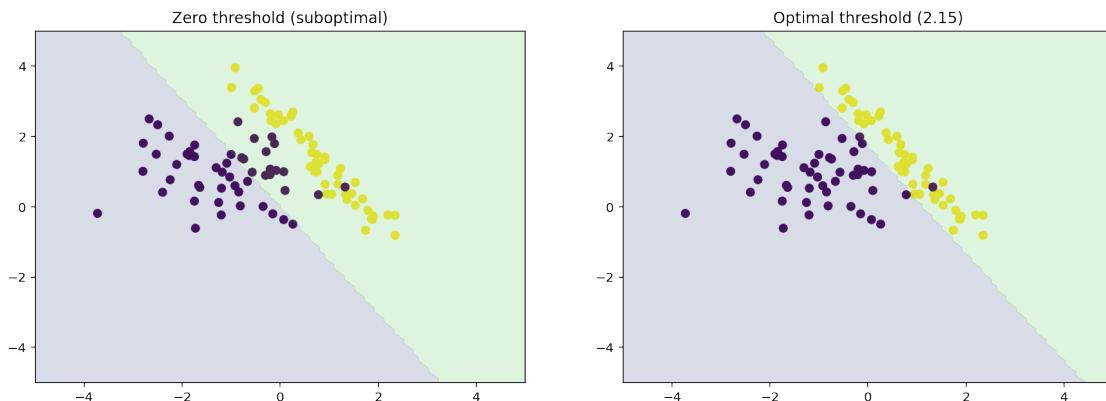
plt.subplot(1, 2, 2)
plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(N, N), alpha=0.2, levels=np.linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.title(f"Optimal threshold ({round(optimal_threshold, 2)})")

# set threshold to zero and make predictions
model._threshold = 0
predicted = model.predict(x_test)

plt.subplot(1, 2, 1)
plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(N, N), alpha=0.2, levels=np.linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.title("Zero threshold (suboptimal)")

plt.show()

```



4.1.7 The perceptron algorithm

Another linear discriminant model is the perceptron. It corresponds to a two-class model in which the input vector \mathbf{x} is first transformed using a nonlinear transformation to give a feature vector $\phi(\mathbf{x})$, and then use it to construct a generalized linear model of the form

$$y(\mathbf{x}) = f(\mathbf{w}^T \phi(\mathbf{x}))$$

We assume that the vector $\phi(\mathbf{x})$ typically includes the bias component ϕ_0 . The nonlinear activation function $f(\cdot)$ is given by a step function of the form

$$f(\alpha) = \begin{cases} +1, & \alpha \geq 0 \\ -1, & \alpha < 0 \end{cases}$$

That is because for the perceptron it is more convenient to use target values $t = +1$ for class \mathcal{C}_1 and $t = -1$ for class \mathcal{C}_2 , instead of $t \in \{0, 1\}$. We consider an error function called the *perceptron criterion*. Note that we are seeking a weight vector \mathbf{w} , such that the inputs \mathbf{x}_n , belonging in class \mathcal{C}_1 , have $\mathbf{w}^T \phi(\mathbf{x}_n) > 0$, whereas the ones belonging in class \mathcal{C}_2 , have $\mathbf{w}^T \phi(\mathbf{x}_n) < 0$. Given the coding scheme $t \in \{-1, +1\}$, it follows that all inputs must satisfy $\mathbf{w}^T \phi(\mathbf{x}_n) t_n > 0$. Thus, the perceptron criterion tries to minimize the quantity $-\mathbf{w}^T \phi(\mathbf{x}_n) t_n$, for all misclassified inputs. More formally,

$$E_P(\mathbf{w}) = - \sum_{n \in \mathcal{M}} \mathbf{w}^T \phi(\mathbf{x}_n) t_n$$

where \mathcal{M} denotes the set of misclassified patterns.

We apply the stochastic gradient descent algorithm to the error function. Thus, the change in the weight vector, according to gradient descent, is given by,

$$\mathbf{w}^{(\tau+1)} = \mathbf{w}^{(\tau)} - \eta \nabla E_P(\mathbf{w}) = \mathbf{w}^{(\tau)} + \eta \phi_n t_n$$

The *perceptron convergence theorem* states that if there exists an exact solution (the data are linearly separable), the the perceptron algorithm is guaranteed to find the solution in a finite number of steps. On the other hand, if the data are not linearly separable the perceptron never converges. Moreover, note that the perceptron **does not provide probabilistic outputs, nor does it generalize to $K > 2$ classes**.

Another important limitation arises from the fact that it is based on linear combinations of fixed basis functions.

```
[11]: # number of training points
N = 100

x1, x2 = np.meshgrid(np.linspace(-5, 5, N), np.linspace(-5, 5, N))
x_test = np.array([x1, x2]).reshape(2, -1).T

model = Perceptron()

plt.figure(figsize=(15, 5))

x_train, t = make_classification(
    n_features=2,
    n_informative=2,
    n_redundant=0,
    n_classes=2,
    n_clusters_per_class=1,
    n_samples=N,
```

```

    random_state=10,
    class_sep=2,
)

model.fit(x_train, np.where(t == 0, -1, 1))
predicted = model.predict(x_test)

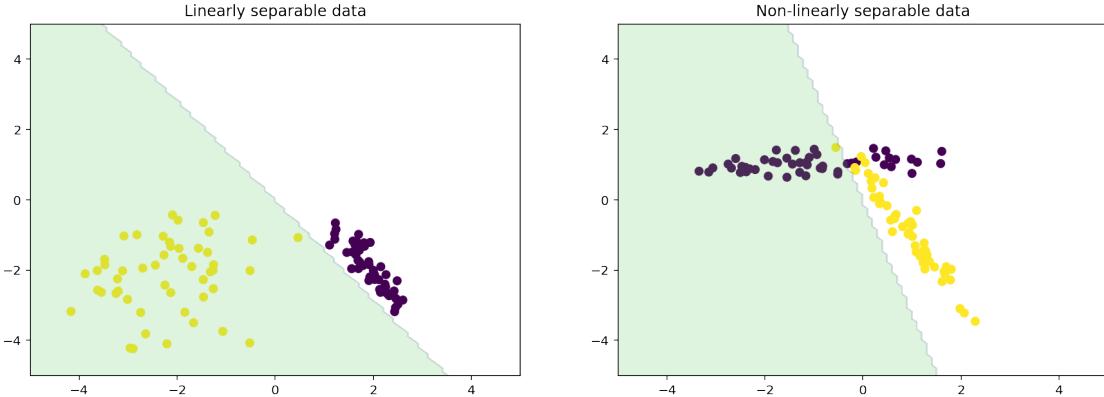
plt.subplot(1, 2, 1)
plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(N, N), alpha=0.2, levels=np.linspace(0, ④
    ↪1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.title("Linearly separable data")

x_train, t = make_classification(
    n_features=2,
    n_informative=2,
    n_redundant=0,
    n_classes=2,
    n_clusters_per_class=1,
    n_samples=N,
    random_state=14,
)
model.fit(x_train, np.where(t == 0, -1, 1))
predicted = model.predict(x_test)

plt.subplot(1, 2, 2)
plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(N, N), alpha=0.2, levels=np.linspace(0, ④
    ↪1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.title("Non-linearly separable data")

plt.show()

```



4.2 Probabilistic Generative Models

Models having linear decision boundaries arise from simple assumptions about the distribution of the data. A generative approach models the class-conditional densities $p(\mathbf{x}|\mathcal{C}_k)$, as well as the class priors $p(\mathcal{C}_k)$, and use them to compute the posterior probability $p(\mathcal{C}_k|\mathbf{x})$ through Bayes theorem. To that end, the posterior probability for class \mathcal{C}_1 , in a binary classification problem, is as follows,

$$\begin{aligned} p(\mathcal{C}_1|\mathbf{x}) &= \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x})} \\ &= \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1) + p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)} \\ &= \frac{1}{1 + \exp(-\alpha)} = \sigma(\alpha) \end{aligned}$$

where,

$$\alpha = \ln \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}$$

Proof

$$\begin{aligned}
\sigma(\alpha) &= \frac{1}{1 + \exp(-\alpha)} \\
&= \frac{1}{1 + \frac{1}{\exp(\alpha)}} = \frac{\exp(\alpha)}{1 + \exp(\alpha)} \\
&= \frac{\exp\left(\ln \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}\right)}{1 + \exp\left(\ln \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}\right)} \\
&= \frac{\frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}}{1 + \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}} = \frac{\frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}}{\frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1) + p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}} \\
&= \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)(p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1) + p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2))} \\
&= \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1) + p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)}
\end{aligned}$$

The function $\sigma(\alpha)$ is the **logistic sigmoid** briefly presented in [Chapter 3](#).

For $K > 2$ classes, the posterior for class \mathcal{C}_k is as follows,

$$\begin{aligned}
p(\mathcal{C}_k|\mathbf{x}) &= \frac{p(\mathbf{x}|\mathcal{C}_k)p(\mathcal{C}_k)}{p(\mathbf{x})} \\
&= \frac{p(\mathbf{x}|\mathcal{C}_k)p(\mathcal{C}_k)}{\sum_i p(\mathbf{x}|\mathcal{C}_i)} \\
&= \frac{\exp(\alpha_k)}{\sum_i \exp(\alpha_i)}
\end{aligned}$$

which is known as the *normalized exponential* and can be regarded as a multiclass generalization of the logistic sigmoid function. The quantities α_k are defined as follows,

$$\alpha_k = \ln(p(\mathbf{x}|\mathcal{C}_k)p(\mathcal{C}_k))$$

The normalized exponential is also known as the *softmax function*, since it represents a smoothed version of the max function, because if $\alpha_k \gg \alpha_i \forall i \neq k$, then $p(\mathcal{C}_k|\mathbf{x}) \approx 1$ and $p(\mathcal{C}_i|\mathbf{x}) \approx 0$.

4.2.1 Continuous inputs

Given the formulation above, the next step is to assume the form of the class-conditional densities. The Gaussian distributions may be used for modelling continuous variables. Assuming that all classes share the same covariance matrix, the density for class \mathcal{C}_k is given by

$$p(\mathbf{x}|\mathcal{C}_k) = \mathcal{N}(\mathbf{x}|\mu_k, \Sigma)$$

Thus, from (4.58), we have,

$$\begin{aligned}
\alpha &= \ln \frac{p(\mathbf{x}|\mathcal{C}_1)p(\mathcal{C}_1)}{p(\mathbf{x}|\mathcal{C}_2)p(\mathcal{C}_2)} = \ln \frac{\mathcal{N}(\mathbf{x}|\mu_1, \Sigma)p(\mathcal{C}_1)}{\mathcal{N}(\mathbf{x}|\mu_2, \Sigma)p(\mathcal{C}_2)} \\
&= \ln \frac{\mathcal{N}(\mathbf{x}|\mu_1, \Sigma)}{\mathcal{N}(\mathbf{x}|\mu_2, \Sigma)} + \ln \frac{p(\mathcal{C}_1)}{p(\mathcal{C}_2)} \\
&= \ln \frac{\exp \left\{ -\frac{1}{2}(\mathbf{x} - \mu_1)^T \Sigma^{-1} (\mathbf{x} - \mu_1) \right\}}{\exp \left\{ -\frac{1}{2}(\mathbf{x} - \mu_2)^T \Sigma^{-1} (\mathbf{x} - \mu_2) \right\}} + \ln \frac{p(\mathcal{C}_1)}{p(\mathcal{C}_2)} \\
&= -\frac{1}{2}(\mathbf{x} - \mu_1)^T \Sigma^{-1} (\mathbf{x} - \mu_1) + \frac{1}{2}(\mathbf{x} - \mu_2)^T \Sigma^{-1} (\mathbf{x} - \mu_2) + \ln \frac{p(\mathcal{C}_1)}{p(\mathcal{C}_2)} \\
&= -\frac{1}{2}\mathbf{x}^T \Sigma^{-1} \mathbf{x} + \mu_1^T \Sigma^{-1} \mathbf{x} - \frac{1}{2}\mu_1^T \Sigma^{-1} \mu_1 + \frac{1}{2}\mathbf{x}^T \Sigma^{-1} \mathbf{x} - \mu_2^T \Sigma^{-1} \mathbf{x} + \frac{1}{2}\mu_2^T \Sigma^{-1} \mu_2 + \ln \frac{p(\mathcal{C}_1)}{p(\mathcal{C}_2)} \\
&= \mu_1^T \Sigma^{-1} \mathbf{x} - \mu_2^T \Sigma^{-1} \mathbf{x} - \frac{1}{2}\mu_1^T \Sigma^{-1} \mu_1 + \frac{1}{2}\mu_2^T \Sigma^{-1} \mu_2 + \ln \frac{p(\mathcal{C}_1)}{p(\mathcal{C}_2)} \\
&= (\mu_1 - \mu_2)^T \Sigma^{-1} \mathbf{x} - \frac{1}{2}\mu_1^T \Sigma^{-1} \mu_1 + \frac{1}{2}\mu_2^T \Sigma^{-1} \mu_2 + \ln \frac{p(\mathcal{C}_1)}{p(\mathcal{C}_2)}
\end{aligned}$$

To that end, using (4.57), we derive that,

$$p(\mathcal{C}_1|\mathbf{x}) = \sigma(\mathbf{w}^T \mathbf{x} + w_0)$$

where,

$$\begin{aligned}
\mathbf{w} &= \Sigma^{-1}(\mu_1 - \mu_2) \\
w_0 &= -\frac{1}{2}\mu_1^T \Sigma^{-1} \mu_1 + \frac{1}{2}\mu_2^T \Sigma^{-1} \mu_2 + \ln \frac{p(\mathcal{C}_1)}{p(\mathcal{C}_2)}
\end{aligned}$$

Note that the prior probabilities $p(\mathcal{C}_k)$ enter through the bias parameter w_0 , thus making parallel shifts of the decision boundary.

For the general case of K classes, from (4.63), we have,

$$\begin{aligned}
\alpha_k &= \ln \left(\frac{1}{(2\pi)^{D/2}} \right) + \ln \left(\frac{1}{|\Sigma|^{1/2}} \right) - \frac{1}{2}(\mathbf{x} - \mu_k)^T \Sigma^{-1} (\mathbf{x} - \mu_k) + \ln p(\mathcal{C}_k) \\
&= \ln \left(\frac{1}{(2\pi)^{D/2}} \right) + \ln \left(\frac{1}{|\Sigma|^{1/2}} \right) - \frac{1}{2}\mathbf{x}^T \Sigma^{-1} \mathbf{x} + \mu_k^T \Sigma^{-1} \mathbf{x} - \frac{1}{2}\mu_k^T \Sigma^{-1} \mu_k + \ln p(\mathcal{C}_k) \\
&= \ln A + \ln B + Q + \mathbf{w}_k^T \mathbf{x} + w_{k0}
\end{aligned}$$

where,

$$\begin{aligned}
A &= \ln \left(\frac{1}{(2\pi)^{D/2}} \right) \\
B &= \ln \left(\frac{1}{|\Sigma|^{1/2}} \right) \\
Q &= -\frac{1}{2} \mathbf{x}^T \Sigma^{-1} \mathbf{x} \\
\mathbf{w}_k &= \Sigma^{-1} \mu_k \\
\mathbf{w}_{k0} &= -\frac{1}{2} \mu_k^T \Sigma^{-1} \mu_k + \ln p(\mathcal{C}_k)
\end{aligned}$$

Then using (4.62), we derive,

$$\begin{aligned}
p(\mathcal{C}_k | \mathbf{x}) &= \frac{\exp(\alpha_k)}{\sum_j \exp(\alpha_j)} \\
&= \frac{\exp(A + B + Q) \exp(\mathbf{w}_k^T \mathbf{x} + w_{k0})}{\exp(A + B + Q) \sum_j \exp(\mathbf{w}_j^T \mathbf{x} + w_{j0})}
\end{aligned}$$

and re-define α_k as follows,

$$a_k(\mathbf{x}) = \mathbf{w}_k^T \mathbf{x} + w_{k0}$$

Therefore, we see that for $K > 2$ classes, α_k are linear functions of \mathbf{x} since quadratic terms cancel each other due to the shared covariances. By relaxing the assumption of the shared covariance matrix among the classes, allowing each class to have its own covariance matrix Σ_k , then we obtain quadratic functions of \mathbf{x} , giving rise to *quadratic discriminant*.

4.2.2 Maximum likelihood solution

Given a set of data, comprising observations \mathbf{x} and corresponding class labels, we can determine the parameters of the class-conditional densities and class prior probabilities, using maximum likelihood. Suppose that we are given a dataset $\{\mathbf{x}, t_n\}$, where $t_n = 1$ denotes class \mathcal{C}_1 and $t_n = 0$ denotes \mathcal{C}_2 . Then, for a data point \mathbf{x}_n belonging to class \mathcal{C}_1 ($t_n = 1$), we have,

$$p(\mathbf{x}_n, \mathcal{C}_1) = p(\mathcal{C}_1)p(\mathbf{x}_n | \mathcal{C}_1) = \pi \mathcal{N}(\mathbf{x}_n | \mu_1, \Sigma)$$

Similarly, for class \mathcal{C}_2 ($t_n = 0$),

$$p(\mathbf{x}_n, \mathcal{C}_2) = p(\mathcal{C}_2)p(\mathbf{x}_n | \mathcal{C}_2) = (1 - \pi) \mathcal{N}(\mathbf{x}_n | \mu_2, \Sigma)$$

where $p(\mathcal{C}_1) = \pi$ and complementary $p(\mathcal{C}_2) = 1 - \pi$.

Thus, the likelihood function is given by,

$$p(\mathbf{t}, \mathbf{X} | \pi, \mu_1, \mu_2, \Sigma) = \prod_{n=1}^N [\pi \mathcal{N}(\mathbf{x}_n | \mu_1, \Sigma)]^{t_n} [(1 - \pi) \mathcal{N}(\mathbf{x}_n | \mu_2, \Sigma)]^{1-t_n}$$

and the log-likelihood is as follows,

$$\ln p(\mathbf{t}, \mathbf{X} | \pi, \mu_1, \mu_2, \Sigma) = \sum_{n=1}^N t_n (\ln \pi + \ln \mathcal{N}(\mathbf{x}_n | \mu_1, \Sigma)) + (1 - t_n) (\ln(1 - \pi) + \ln \mathcal{N}(\mathbf{x}_n | \mu_2, \Sigma))$$

1. Setting the derivative for π equal to zero, we obtain,

$$\begin{aligned} \frac{d}{d\pi} \ln p(\mathbf{t}, \mathbf{X} | \pi, \mu_1, \mu_2, \Sigma) = 0 &\Leftrightarrow \\ \frac{d}{d\pi} \sum_{n=1}^N \{t_n \ln \pi + (1 - t_n) \ln(1 - \pi)\} = 0 &\Leftrightarrow \\ \frac{1}{\pi} \sum_{n=1}^N t_n - \frac{1}{1 - \pi} \sum_{n=1}^N (1 - t_n) = 0 &\Leftrightarrow \\ \frac{1}{\pi} \sum_{n=1}^N t_n - \frac{1}{1 - \pi} (N - \sum_{n=1}^N t_n) = 0 &\Leftrightarrow \\ \frac{1}{\pi} \sum_{n=1}^N t_n = \frac{1}{1 - \pi} (N - \sum_{n=1}^N t_n) &\Leftrightarrow \\ \frac{1 - \pi}{\pi} \sum_{n=1}^N t_n = N - \sum_{n=1}^N t_n &\Leftrightarrow \\ \frac{1}{\pi} \sum_{n=1}^N t_n - \sum_{n=1}^N t_n = N - \sum_{n=1}^N t_n &\Leftrightarrow \\ \pi = \frac{1}{N} \sum_{n=1}^N t_n & \end{aligned}$$

As expected, the maximum likelihood estimate for π , is simply the fraction of points in class \mathcal{C}_1 .

2. Setting the derivative for μ_1 equal to zero, we obtain,

$$\begin{aligned}
\frac{d}{d\mu_1} \ln p(\mathbf{t}, \mathbf{X} | \pi, \mu_1, \mu_2, \Sigma) = 0 &\Leftrightarrow \\
\frac{d}{d\mu_1} \sum_{n=1}^N t_n \ln \mathcal{N}(\mathbf{x}_n | \mu_1, \Sigma) = 0 &\Leftrightarrow \\
\frac{d}{d\mu_1} \left[-\frac{1}{2} \sum_{n=1}^N t_n (\mathbf{x}_n - \mu_1)^T \Sigma^{-1} (\mathbf{x}_n - \mu_1) \right] = 0 &\Leftrightarrow \\
-\frac{1}{2} \sum_{n=1}^N -2t_n \Sigma^{-1} (\mathbf{x}_n - \mu_1) = 0 &\Leftrightarrow \\
\sum_{n=1}^N t_n (\mathbf{x}_n - \mu_1) = 0 &\stackrel{\sum_{n=1}^N t_n = N_1}{\Leftrightarrow} \\
\sum_{n=1}^N t_n \mathbf{x}_n = N_1 \mu_1 &\Leftrightarrow \\
\mu_1 = \frac{1}{N_1} \sum_{n=1}^N t_n \mathbf{x}_n
\end{aligned}$$

3. Similarly, the corresponding result for μ_2 is given by,

$$\mu_2 = \frac{1}{N_2} \sum_{n=1}^N (t_n - 1) \mathbf{x}_n$$

4. Finally, the solution for the shared covariance matrix Σ is similar to the one derived for the multivariate Gaussian distribution in [Chapter 2](#), where the matrix Σ is defined in (4.78), (4.79), and (4.80).

Note: Fitting Gaussian distributions to the classes is not robust to outliers, because the maximum likelihood estimation of a Gaussian is not robust itself.

4.2.3 Discrete features

Consider the case of discrete binary feature values $x_i \in \{0, 1\}$. When there are D inputs, then a general distribution would correspond to $2^D - 1$ independent variables. Assuming a *naive Bayes* approach, we have the following class-conditional mass functions,

$$p(\mathbf{x} | \mathcal{C}_k) = \prod_{i=1}^D \mu_{ki}^{x_i} (1 - \mu_{ki})^{1-x_i}$$

For K classes, substituting into (4.63), gives,

$$\alpha_k(\mathbf{x}) = \sum_{i=1}^D (x_i \ln \mu_{ki} + (1 - x_i) \ln (1 - \mu_{ki})) + \ln p(\mathcal{C}_k)$$

In the more general case, where discrete variables can take $M > 2$ states, the class-conditional mass functions are defined as follows,

$$p(\mathbf{x}|\mathcal{C}_k) = \prod_{i=1}^D \prod_{m=1}^M \mu_{kim}^{\phi(x_i)_m}$$

where $\phi(x_i)$ produces a 1-of- M binary coding scheme, where only one of the value among $\phi(x_i)_1, \dots, \phi(x_i)_M$ is 1, and the others are all 0. Thus, by substituting the expression above into (4.63), gives,

$$\alpha_k(\mathbf{x}) = \sum_{i=1}^D \sum_{m=1}^M (\phi(x_i)_m \ln \mu_{kim}) + \ln p(\mathcal{C}_k)$$

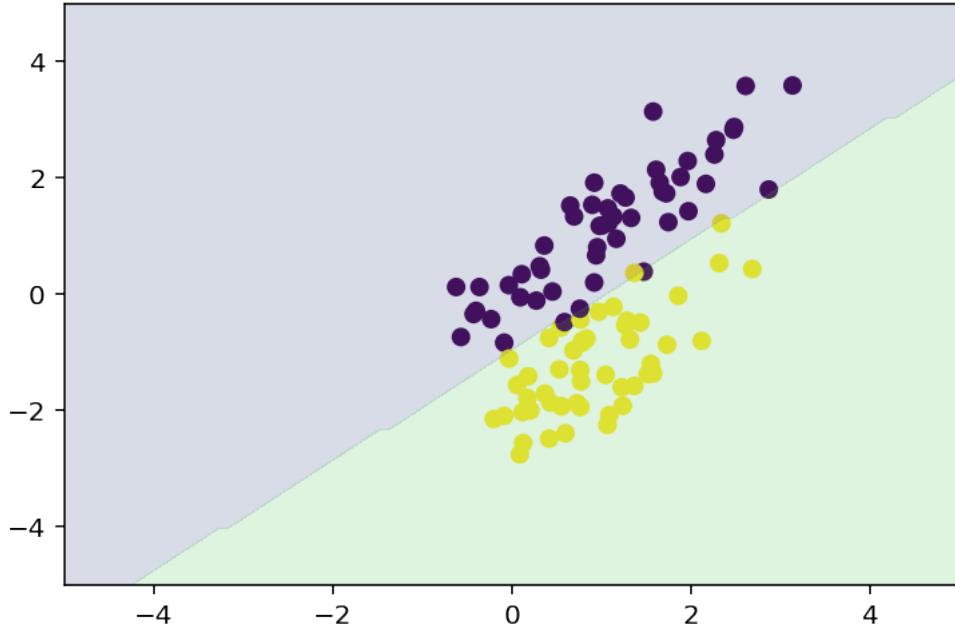
```
[3]: # number of training points
N = 100

x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2, n_clusters_per_class=1, n_samples=N, random_state=21
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, N), np.linspace(-5, 5, N))
x_test = np.array([x1, x2]).reshape(2, -1).T

model = GenerativeClassifier()
model.fit(x_train, t)
predicted = model.predict(np.array([np.ravel(x1), np.ravel(x2)]))

plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(N, N), alpha=0.2, levels=np.linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.show()
```



4.3 Probabilistic Discriminative Models

An alternative approach, called *discriminative training*, is to directly maximize the likelihood function defined through the conditional distribution $p(\mathcal{C}_k|\mathbf{x})$.

4.3.2 Logistic Regression

Consider the binary classification problem. In the analysis of generative approaches we saw that under rather general assumptions, the posterior probability of class \mathcal{C}_1 can be expressed as a logistic sigmoid acting on a linear function of the input vectors \mathbf{x} or the feature vector ϕ (see 4.65) so that,

$$p(\mathcal{C}_1|\phi) = y(\phi) = \sigma(\mathbf{w}^T \phi)$$

In the terminology of statistics, this model is known as *logistic regression*, although its a classification model.

One advantage of the discriminative approach is that there are typically fewer adaptive parameters to be determined. For an M -dimensional feature space, this model has M adjustable parameters. By contrast, the generative model using Gaussian class conditional densities, would have used $2M$ parameters for the means and $M(M + 1)/2$ parameters for the (shared) covariance matrix.

We can use maximum likelihood to determine the parameters of the logistic regression model. Given a data set $\{\phi_n, t_n\}$, where $t_n \in \{0, 1\}$, the likelihood function is given by,

$$p(\mathbf{t}|\Phi, \mathbf{w}) = \prod_{n=1}^N p(\mathcal{C}_1|\phi_n)^{t_n} (1 - p(\mathcal{C}_1|\phi_n))^{1-t_n} = \prod_{n=1}^N y_n^{t_n} (1 - y_n)^{1-t_n}$$

The maximum likelihood is equivalent to the minimum of the negative of the logarithm of the likelihood, which gives the *cross-entropy error function*,

$$E(\mathbf{w}) = -\ln p(\mathbf{t}|\Phi, \mathbf{w}) = -\sum_{n=1}^N t_n \ln y_n + (1-t_n) \ln(1-y_n)$$

Why is the error function called cross-entropy?

The cross-entropy for discrete probability distributions p and q is defined as $H(p, q) = \sum_x p(x) \log q(x)$. Since we assume that the target variables t_n are probabilities taking only extreme values 0 or 1, and y_n is a probability distribution, then $E(\mathbf{w})$ can be interpreted as the cross entropy of the target variables and the posterior probability distribution.

Then, taking the gradient of the error function over \mathbf{w} , we obtain,

$$\begin{aligned} \nabla E(\mathbf{w}) &= -\nabla \ln p(\mathbf{t}|\Phi, \mathbf{w}) \\ &= -\nabla \sum_{n=1}^N t_n \ln y_n + (1-t_n) \ln(1-y_n) \\ &= -\sum_{n=1}^N \frac{d}{dy_n} t_n \ln y_n + \frac{d}{dy_n} (1-t_n) \ln(1-y_n) \\ &\stackrel{\frac{d}{dx} \ln f(x) = \frac{f'(x)}{f(x)}}{=} -\sum_{n=1}^N \frac{d}{dy_n} t_n \ln y_n + \frac{d}{dy_n} (1-t_n) \ln(1-y_n) \\ &= -\sum_{n=1}^N \frac{t_n}{y_n} \frac{d}{da_n} y_n \frac{d}{d\mathbf{w}} a_n - \frac{1-t_n}{1-y_n} \frac{d}{da_n} y_n \frac{d}{d\mathbf{w}} a_n \\ &= -\sum_{n=1}^N \left(\frac{t_n}{y_n} - \frac{1-t_n}{1-y_n} \right) \frac{d}{da_n} y_n \frac{d}{d\mathbf{w}} a_n \\ &= -\sum_{n=1}^N \left(\frac{t_n}{y_n} - \frac{1-t_n}{1-y_n} \right) y_n (1-y_n) \phi_n \\ &\stackrel{(4.88)}{=} -\sum_{n=1}^N \frac{t_n - y_n}{y_n(1-t_n)} y_n (1-y_n) \phi_n \\ &= \sum_{n=1}^N (y_n - t_n) \phi_n \end{aligned}$$

Note that the gradient takes the same form as the gradient of the sum-of-squares error function, however, y_n involves a non-linear function. At this point we can make use of (4.91) and (3.22) to obtain a sequential algorithm (gradient descent) for optimizing the parameters.

[6]: # number of training points

N = 100

number of outlier points

n_outliers = 5

```

x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2, n_clusters_per_class=1, n_samples=N, random_state=12
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, 100), np.linspace(-5, 5, 100))
x_test = np.array([x1, x2]).reshape(2, -1).T

outliers = np.random.random_sample((n_outliers, 2)) + 3
x_train_outliers = np.vstack((x_train, outliers))
t_outliers = np.hstack((t, np.ones(n_outliers, dtype=int)))

feature = LinearFeature()
x_train_linear = feature.transform(x_train)
x_train_linear_outliers = feature.transform(x_train_outliers)
x_test_linear = feature.transform(x_test)

model = LogisticRegression()
model.fit_lms(x_train_linear, t, 0.01)
predicted = model.predict(x_test_linear)

plt.figure(figsize=(15, 5))

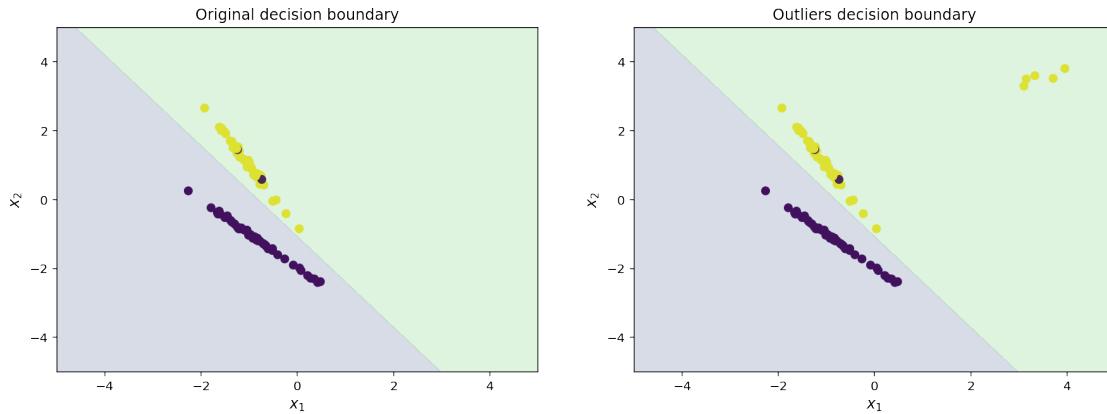
plt.subplot(1, 2, 1)
plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(100, 100), alpha=0.2, levels=np.linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)
plt.title("Original decision boundary")

model.fit_lms(x_train_linear_outliers, t_outliers, 0.01)
predicted_outliers = model.predict(x_test_linear)

plt.subplot(1, 2, 2)
plt.scatter(x_train_outliers[:, 0], x_train_outliers[:, 1], c=t_outliers)
plt.contourf(x1, x2, predicted_outliers.reshape(100, 100), alpha=0.2, levels=np.linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)
plt.title("Outliers decision boundary")

```

```
plt.show()
```



Note that logistic regression is robust to outliers in contrast to linear discriminants presented in section* 4.1.

4.3.3 Iterative reweighted least squares

In linear regression models, the maximum likelihood solution, on the assumption of Gaussian noise model, leads to a closed-form solution. For logistic regression, there is no longer a closed-form solution, due to the nonlinearity of the logistic sigmoid function. However, the error function is still convex and can be minimized by an efficient iterative technique based on *Newton-Raphson* iterative optimization scheme. This algorithm uses a local quadratic approximation to the log-likelihood, and takes the form

$$\mathbf{w}^{new} = \mathbf{w}^{old} - \mathbf{H}^{-1} \nabla E(\mathbf{w})$$

where \mathbf{H} is the Hessian matrix whose elements comprise the second derivatives of $E(\mathbf{w})$ over \mathbf{w} .

Note that, if we apply the *Newton-Raphson* algorithm to the linear regression model, we derive the standard least squares solution (see 4.94 and 4.95).

Applying the *Newton-Raphson* update to the cross-entropy error function for the logistic regression model, we obtain,

$$\nabla E(\mathbf{w}) = \sum_{n=1}^N (y_n - t_n) \phi_n = \Phi^T (\mathbf{y} - \mathbf{t})$$

and

$$\begin{aligned}
\mathbf{H} &= \nabla \nabla E(\mathbf{w}) \\
&= \nabla \sum_{n=1}^N (y_n - t_n) \phi_n \\
&= \nabla \sum_{n=1}^N y_n \phi_n \\
&\stackrel{(4.88)}{=} \sum_{n=1}^N y_n (1 - y_n) \phi_n \frac{d}{d\mathbf{w}} \mathbf{w}^T \phi_n \\
&= \sum_{n=1}^N y_n (1 - y_n) \phi_n \phi_n^T \\
&= {}^T \mathbf{R}
\end{aligned}$$

where \mathbf{R} is a diagonal matrix whose elements are $R_{nn} = y_n(1 - y_n)$. Then, the update formula becomes,

$$\mathbf{w}^{new} = \mathbf{w}^{old} - ({}^T \mathbf{R})^{-1} \Phi^T (\mathbf{y} - \mathbf{t})$$

Note that Hessian depends on \mathbf{w} through the weighting matrix \mathbf{R} , corresponding to the fact that the error function is no longer quadratic. Thus, we must apply the update formula iteratively, each time using the new weight vector \mathbf{w} to compute the revised weighting matrix \mathbf{R} . To that end, the algorithm is known as *iterative reweighted least squares* or *IRLS*.

The elements of \mathbf{R} can be interpreted as variances, given by,

$$\mathbb{E}[t] = \sum_{t \in \{0,1\}} tp(t|\mathbf{x}) = \sigma(x)$$

and

$$\text{var}[t] = \mathbb{E}[t^2] - \mathbb{E}[t]^2 \stackrel{t^2=t}{=} \mathbb{E}[t] - \mathbb{E}[t]^2 = \sigma(x) - \sigma(x)^2 = y(1 - y)$$

```
[11]: # number of training points
N = 100

# number of outlier points
n_outliers = 5

x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2, n_clusters_per_class=1, n_samples=N, random_state=12
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, 100), np.linspace(-5, 5, 100))
x_test = np.array([x1, x2]).reshape(2, -1).T
```

```

outliers = np.random.random_sample((n_outliers, 2)) + 3
x_train_outliers = np.vstack((x_train, outliers))
t_outliers = np.hstack((t, np.ones(n_outliers, dtype=int)))

feature = LinearFeature()
x_train_linear = feature.transform(x_train)
x_train_linear_outliers = feature.transform(x_train_outliers)
x_test_linear = feature.transform(x_test)

model = LogisticRegression()
model.fit(x_train_linear, t)
predicted = model.predict(x_test_linear)

plt.figure(figsize=(15, 5))

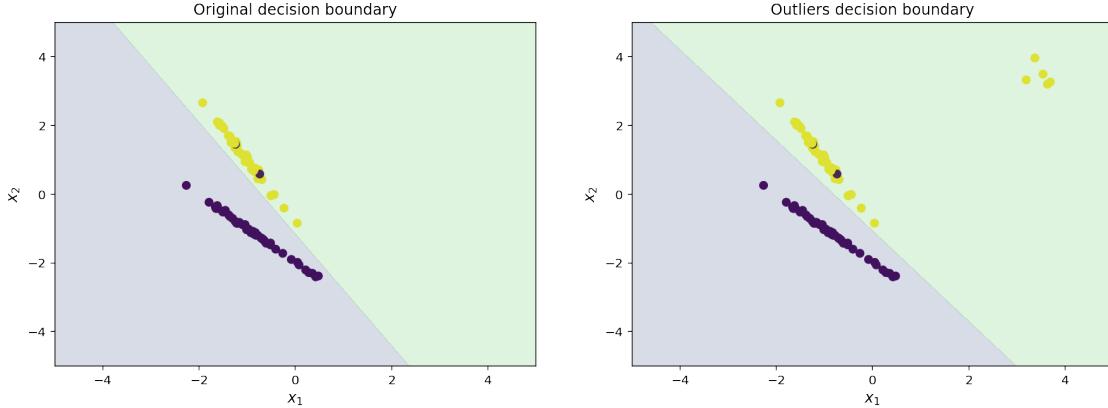
plt.subplot(1, 2, 1)
plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(100, 100), alpha=0.2, levels=np.
    ↪linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)
plt.title("Original decision boundary")

model.fit_lms(x_train_linear_outliers, t_outliers, 0.01)
predicted_outliers = model.predict(x_test_linear)

plt.subplot(1, 2, 2)
plt.scatter(x_train_outliers[:, 0], x_train_outliers[:, 1], c=t_outliers)
plt.contourf(x1, x2, predicted_outliers.reshape(100, 100), alpha=0.2, levels=np.
    ↪linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)
plt.title("Outliers decision boundary")

plt.show()

```



Gradient Descent vs Newton-Raphson

Newton-Raphson method requires to compute the Hessian (through solving a set of linear equations) and thus, the computational cost for each iteration is higher than that of gradient descent. However, it usually converges faster than gradient descent in the sense that the number of iterations required is much smaller.

4.3.4 Multiclass logistic regression

We have seen that for $K > 2$ classes, the posterior probabilities are given by a softmax transformation of linear functions of feature variables. Here, we consider the maximum likelihood to determine the parameters \mathbf{w}_k of the model directly. To that end, we need to calculate the derivatives of y_k (see 4.104) over the activation functions α_j (see 4.68 and 4.105).

In order to find the derivatives, we need to consider $k \neq j$ and $k = j$.

1. $k \neq j$

$$\begin{aligned}
\frac{\partial y_k}{\partial \alpha_k} &= \frac{\partial}{\partial \alpha_k} \frac{\exp(\alpha_k)}{\sum_j \exp(\alpha_j)} \\
&= \frac{-\exp(\alpha_k) \exp(\alpha_j)}{(\sum_j \exp(\alpha_j))^2} \\
&= -\frac{\exp(\alpha_k)}{\sum_j \exp(\alpha_j)} \frac{\exp(\alpha_j)}{\sum_j \exp(\alpha_j)} \\
&\stackrel{4.104}{=} -y_k y_j
\end{aligned}$$

2. $k = j$

$$\begin{aligned}
\frac{\partial y_k}{\partial \alpha_k} &= \frac{\partial}{\partial \alpha_k} \frac{\exp(\alpha_k)}{\sum_j \exp(\alpha_j)} \\
&= \frac{\exp(\alpha_k) \sum_j \exp(\alpha_j) - \exp(\alpha_k)^2}{(\sum_j \exp(\alpha_j))^2} \\
&= \frac{\exp(\alpha_k) \sum_j \exp(\alpha_j)}{(\sum_j \exp(\alpha_j))^2} - \frac{\exp(\alpha_k)^2}{(\sum_j \exp(\alpha_j))^2} \\
&= \frac{\exp(\alpha_k)}{\sum_j \exp(\alpha_j)} - \left(\frac{\exp(\alpha_k)}{\sum_j \exp(\alpha_j)} \right)^2 \\
&= y_k - y_k^2 \\
&= y_k(1 - y_k)
\end{aligned}$$

where we have used the quotient rule $(\frac{f}{g})' = \frac{f'g - fg'}{g^2}$.

Combining (1) and (2), we obtain,

$$\frac{\partial y_k}{\partial \alpha_k} = y_k(I_{kj} - y_j)$$

where I_{kj} are the elements of the identity matrix.

Assuming a 1-of- K coding scheme in which the target vector \mathbf{t}_k is a binary vector having all elements zero except for element k , which equals to one, then ,the likelihood function is then given by,

$$p(\mathbf{T}|\mathbf{w}_1, \dots, \mathbf{w}_k) = \prod_{n=1}^N \prod_{k=1}^K p(\mathbf{C}_k|\phi_n)^{t_{nk}} = \prod_{n=1}^N \prod_{k=1}^K y_k(\phi_n)^{t_{nk}}$$

where \mathbf{T} is a $N \times K$ matrix of target variables with elements t_{nk} . Taking the negative logarithm the gives,

$$E(\mathbf{w}_1, \dots, \mathbf{w}_k) = -\ln p(\mathbf{T}|\mathbf{w}_1, \dots, \mathbf{w}_k) = -\sum_{n=1}^N \sum_{k=1}^K t_{nk} \ln y_k(\phi_n)$$

which is the *cross-entropy* error function for the multiclass problem.

Taking the gradient of the error function over the parameter vector \mathbf{w}_j , we obtain

$$\begin{aligned}
\nabla_{\mathbf{w}_j} E(\mathbf{w}_1, \dots, \mathbf{w}_K) &= -\nabla_{\mathbf{w}_j} \sum_{n=1}^N \sum_{k=1}^K t_{nk} \ln y_k(\phi_n) \\
&= -\sum_{n=1}^N \sum_{k=1}^K t_{nk} \frac{1}{y_{nk}} y_{nk} (I_{kj} - y_{nj}) \phi_n \\
&= -\sum_{n=1}^N \sum_{k=1}^K t_{nk} (I_{kj} - y_{nj}) \phi_n \\
&= \sum_{n=1}^N \sum_{k=1}^K t_{nk} y_{nj} \phi_n - \sum_{n=1}^N \sum_{k=1}^K t_{nk} I_{kj} \phi_n \\
&= \sum_{n=1}^N \sum_{k=1}^K t_{nk} y_{nj} \phi_n - \sum_{n=1}^N t_{nj} \phi_n \\
&\stackrel{\sum_k t_{nk}=1}{=} \sum_{n=1}^N y_{nj} \phi_n - \sum_{n=1}^N t_{nj} \phi_n \\
&= \sum_{n=1}^N (y_{nj} - t_{nj}) \phi_n
\end{aligned}$$

The Newton-Raphson update formula, requires the evaluation of the Hessian matrix, given by

$$\begin{aligned}
\nabla_{\mathbf{w}_k} \nabla_{\mathbf{w}_j} E(\mathbf{w}_1, \dots, \mathbf{w}_K) &= -\nabla_{\mathbf{w}_k} \nabla_{\mathbf{w}_j} \ln p(\mathbf{T} | \mathbf{w}_1, \dots, \mathbf{w}_k) \\
&= -\nabla_{\mathbf{w}_k} \sum_{n=1}^N (y_{nj} - t_{nj}) \phi_n \\
&= -\nabla_{\mathbf{w}_k} \sum_{n=1}^N y_{nj} \phi_n \\
&= \sum_{n=1}^N \frac{\partial}{\partial \mathbf{w}_k} y_{nj} \phi_n \\
&= \sum_{n=1}^N y_{nk} (I_{kj} - y_{nj}) \phi_n \phi_n^T
\end{aligned}$$

Below we present a softmax regression example trained using gradient descent.

```
[13]: # number of training points
N = 100

x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=3,
    n_clusters_per_class=1, n_samples=N, random_state=21
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, 100), np.linspace(-5, 5, 100))
x_test = np.array([x1, x2]).reshape(2, -1).T
```

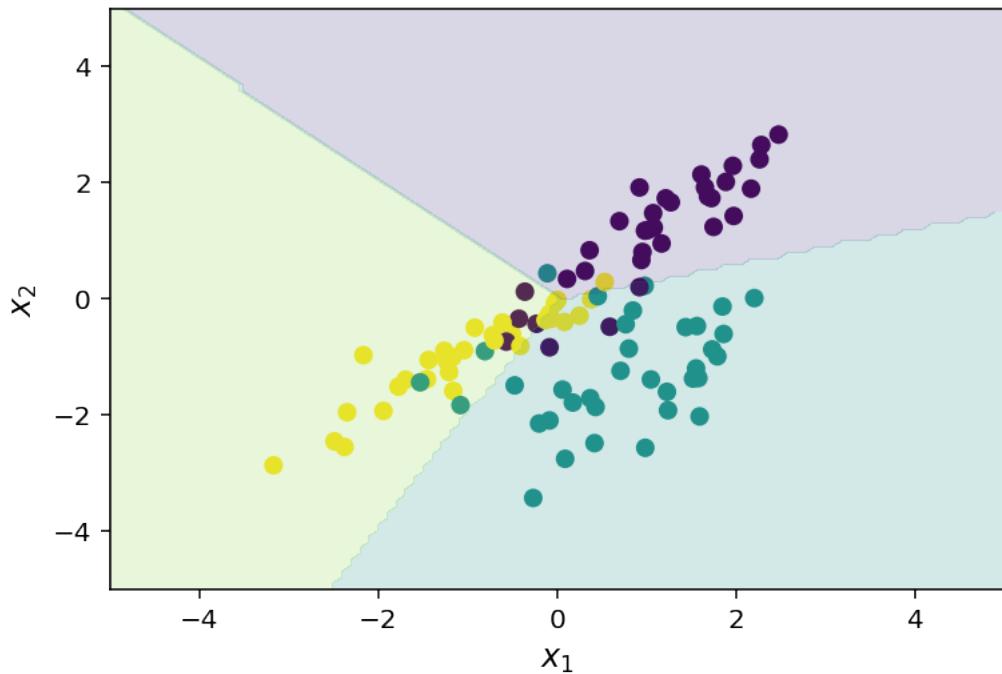
```

model = SoftmaxRegression()
model.fit(x_train, t)
predicted = model.predict(x_test)

plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(100, 100), alpha=0.2, levels=np.
    linspace(0, 2, 4))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)

plt.show()

```



4.4 Laplace Approximation

In contrast to the [Bayesian treatment of linear regression](#), in the Bayesian treatment of logistic regression, we cannot integrate exactly over the parameter vector \mathbf{w} since the posterior distribution is no longer Gaussian. To that end, we may use a widely used framework called the Laplace approximation, that aims to find a Gaussian approximation to a probability density defined over a set of continuous variables. Consider a single continuous variable z , having a distribution $p(z)$ defined by

$$p(z) = \frac{1}{Z} f(z)$$

where $Z = \int f(z)dz$ is the normalization coefficient. The goal is to find a Gaussian approximation $q(z)$ centered on a mode of the distribution $p(z)$. The first step is to find a mode of $p(z)$, that is, a point z_0 such that $p'(z_0) = 0$ or equivalently

$$\frac{df(z)}{dz} \Big|_{z=z_0} = 0$$

Then, we use a second-order Taylor expansion to approximate $g(z) = \ln f(z)$ (because the logarithm of any Gaussian distribution is a quadratic function of the variables), centered on the mode z_0 so that,

$$g(z) = \ln f(z) \approx \sum_{n=0}^2 \frac{g^{(n)}(z_0)}{n!} (z - z_0)^n = g(z_0) - \frac{1}{2} g''(z_0)(z - z_0)^2$$

Note that the first-order term is omitted since z_0 is a local maximum of the distribution and thus the derivative is zero. Then, taking the exponential on both sides of the expansion, we obtain

$$f(z) \approx f(z_0) \exp \left\{ -\frac{A}{2}(z - z_0)^2 \right\}$$

where $A = -\frac{d^2 f(z)}{dz^2}$ on z_0 . Therefore, using the standard result for the normalization of a Gaussian, the final normalized distribution $q(z)$ has the form,

$$q(z) = \left(\frac{A}{2\pi} \right)^{1/2} \exp \left\{ -\frac{A}{2}(z - z_0)^2 \right\} = \mathcal{N}(z|z_0, A)$$

Note that the Gaussian approximation is well defined only when its precision $A > 0$, which implies that z_0 must be a local maximum, not a minimum! In practice a mode may be found by running some form of numerical optimization. The Laplace approximation is depicted in the next Figure,

The same approximation can be applied to an M -dimensional space \mathbf{z} .

4.5 Bayesian Logistic Regression

Exact Bayesian inference for logistic regression, as well as, the evaluation of the predictive distribution are intractable. Thus, here, we consider the application of Laplace approximation for the problem of Bayesian logistic regression.

4.5.1 Laplace approximation

Similar to the Bayesian linear regression, we seek a Gaussian representation for the posterior distribution of the parameters, thus, we use a Gaussian (conjugate) prior in the general form,

$$p(\mathbf{w}) = \mathcal{N}(\mathbf{w}|\mathbf{m}_0, \mathbf{S}_0)$$

where $\mathbf{m}_0, \mathbf{S}_0$ are fixed hyperparameters. Then, the posterior over \mathbf{w} is given by

$$p(\mathbf{w}|\mathbf{t}) \propto p(\mathbf{t}|\mathbf{w})p(\mathbf{w})$$

Taking the natural logarithm on both sides, and substituting for the prior and the likelihood, we obtain

$$\ln p(\mathbf{w}|\mathbf{t}) = \ln \left(\prod_{n=1}^N y_n^{t_n} \{1-y_n\}^{1-t_n} \right) \ln \mathcal{N}(\mathbf{w}|\mathbf{m}_0, \mathbf{S}_0) = \sum_{n=1}^N \{t_n \ln y_n + (1-t_n) \ln(1-y_n)\} + \frac{1}{(2\pi)^{D/2} |\mathbf{S}_0|^{1/2}} - \frac{1}{2} (\mathbf{w} - \mathbf{m}_0)^T \mathbf{S}_0^{-1} (\mathbf{w} - \mathbf{m}_0)$$

Then, to obtain the Gaussian approximation of the posterior, first, we maximize the posterior to give the MAP solution \mathbf{w}_{MAP} , which corresponds to the mean of the approximated Gaussian. The covariance matrix is then given by the Hessian matrix of the negative log-likelihood,

$$\mathbf{S}_N^{-1} = -\nabla \nabla \ln p(\mathbf{w}|\mathbf{t}) = \mathbf{S}_0^{-1} + \sum_{n=1}^N y_n(1-y_n) \phi_n \phi_n^T$$

where we make use of (4.97). Thus, the Gaussian approximation of the posterior takes the form,

$$q(\mathbf{w}) = \mathcal{N}(\mathbf{w}|\mathbf{w}_{MAP}, \mathbf{S}_N)$$

4.5.2 Predictive distribution

The predictive distribution for class \mathcal{C}_1 , given a new feature vector ϕ_{unseen} , is obtained by marginalizing over the posterior distribution $p(\mathbf{w}|\mathbf{t})$, which is approximated by $q(\mathbf{w})$, so that,

$$p(\mathcal{C}_1|\phi_{unseen}, \mathbf{t}, \Phi) = \int p(\mathcal{C}_1|\phi_{unseen}, \mathbf{w}) p(\mathbf{w}|\mathbf{t}, \Phi) d\mathbf{w} \approx \int \sigma(\mathbf{w}^T \phi) q(\mathbf{w}) d\mathbf{w}$$

The evalution of the above integral is fairly complex and involves a significant number of steps. For more details see the corresponding section* in the book. The final approximate predictive distribution has the form,

$$p(\mathcal{C}_1|\phi_{unseen}, \mathbf{t}) = \sigma(\kappa(\sigma_\alpha^2) \mu_\alpha)$$

where $\kappa(\sigma_\alpha^2) = (1 + \pi\sigma_\alpha^2/8)^{-1/2}$, $\mu_\alpha = \mathbf{w}_{MAP}^T \phi_{unseen}$, and $\sigma_\alpha = \phi_{unseen}^T \mathbf{S}_N \phi_{unseen}$.

[18]: # number of training points

$N = 100$

```
x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2, n_clusters_per_class=1, n_samples=N, random_state=21
)
```

```
x1, x2 = np.meshgrid(np.linspace(-5, 5, N), np.linspace(-5, 5, N))
```

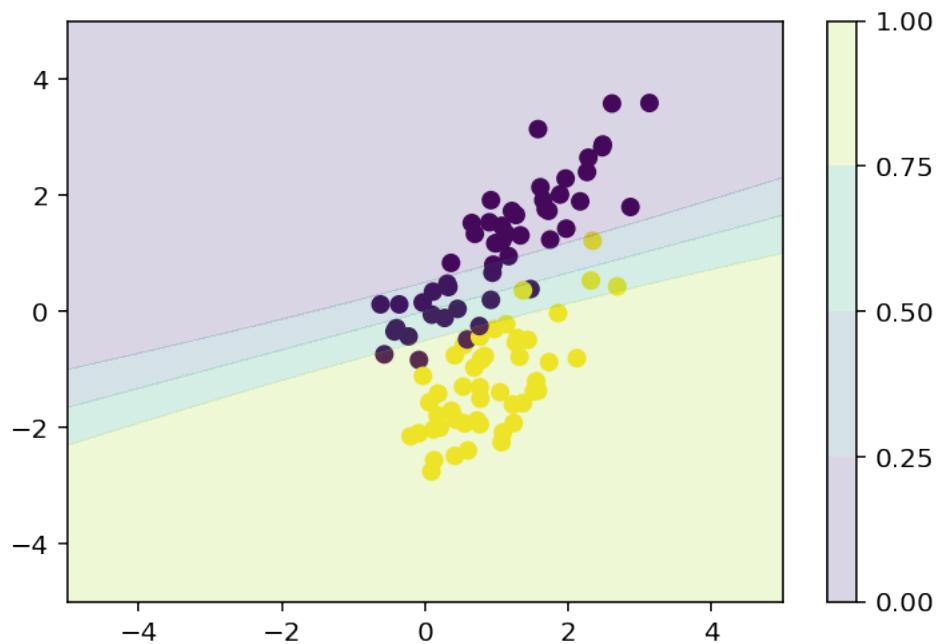
```

x_test = np.array([x1, x2]).reshape(2, -1).T

model = BayesianLogisticRegression()
model.fit(x_train, t)
predicted = model.predict(x_test)

plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(N, N), alpha=0.2, levels=np.linspace(0, 1, 5))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.colorbar()
plt.show()

```



5. Neural Networks

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- 5.5 Regularization in Neural Networks

- 5.5.2 Early Stopping
- 5.5.3 Invariances
- 5.5.6 Convolutional networks
- 5.6 Mixture Density Networks

```
[15]: import random
import numpy as np
import matplotlib.pyplot as plt
from prml import nn
from prml.linear import Perceptron, LogisticRegression
from prml.preprocessing import OneHotEncoder
from prml.datasets import generate_toy_data, load_planar_dataset, u
    ↪plot_2d_decision_boundary, load_mnist_dataset
from sklearn.datasets import make_classification
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'

# Enable autoreload all modules before executing code
%reload_ext autoreload
%autoreload 2
```

5.1 Feed-forward Network Functions

The linear models discussed in previous chapters are based on linear combinations of fixed (non)linear basis functions $\phi_j(\mathbf{x})$ and take the form,

$$y(\mathbf{x}, \mathbf{w}) = f\left(\sum_{j=1}^M w_j \phi_j(\mathbf{x})\right)$$

where $f(\cdot)$ is a nonlinear activation function in the case of classification and the identity in the case of regression. Although such models have useful analytical properties, they are limited by the curse of dimensionality, and they need to adapt the basis functions to the data for large-scale problems. An alternative is to use a predefined number of basis functions but allow them to be adaptive during training. Thus, an extension of the model above is making the basis functions $\phi_j(\mathbf{x})$ depend on parameters and then adjust them along the coefficients $\{w_j\}$, during training.

Neural networks use basis functions that follow the same form, that is, each basis function is itself a nonlinear function of a linear combination of the inputs, where the coefficients are adaptive

parameters. Thus, the basic neural network model is described as a series of functional transformations.

- Given the input variables x_1, \dots, x_D , we construct M linear combinations in the form:

$$a_j = \sum_{i=1}^D w_{ji}^{(1)} x_i + w_{j0}^{(1)}$$

where $j = 1, \dots, M$, and the superscript (1) indicates the corresponding parameters of the *first* layer of the network. The input layer often uses the superscript (0). The quantities a_j are known as activations and each of them is transformed using a *differentiable* nonlinear activation function $h(\cdot)$ to give

$$z_j = h(a_j)$$

these correspond to the outputs of the basis functions, and in the context of neural networks are called *hidden units*. The following figure presents the two step computation of a single unit or neuron.

- Following the same procedure, these output values from the *first* layer, are linearly combined again to give,

$$a_k = \sum_{j=1}^M w_{ki}^{(2)} z_j + w_{k0}^{(2)}$$

where $k = 1, \dots, K$. This transformation corresponds to the *second* layer of the network. These output activations are transformed again using an appropriate activation function h to give a set of outputs y_k . The following figure depicts the entire process for a 2-layer network.

It is called a 2-layer neural network because there are two layers of adaptive weights.

The output unit activation function is determined by the nature of the data and the assumed distribution of target variables. Thus, for regression problems, the activation function can be the **identity**, so that $y_k = \alpha_k$, and for classification, the output uses a **sigmoid**, or **softmax** function, so that $y_k = \sigma(\alpha_k)$.

We may combine these stages to obtain the overall network function (using a sigmoid output unit), as follows,

$$y_k(\mathbf{x}, \mathbf{w}) = \sigma \left(\sum_{j=1}^M w_{kj}^{(2)} h \left(\sum_{i=1}^D w_{ji}^{(1)} x_i + w_{j0}^{(1)} \right) + w_{k0}^{(2)} \right)$$

where biases on each layer can be absorbed into the set of weight parameters by defining an additional input variable $x_0 = 1$.

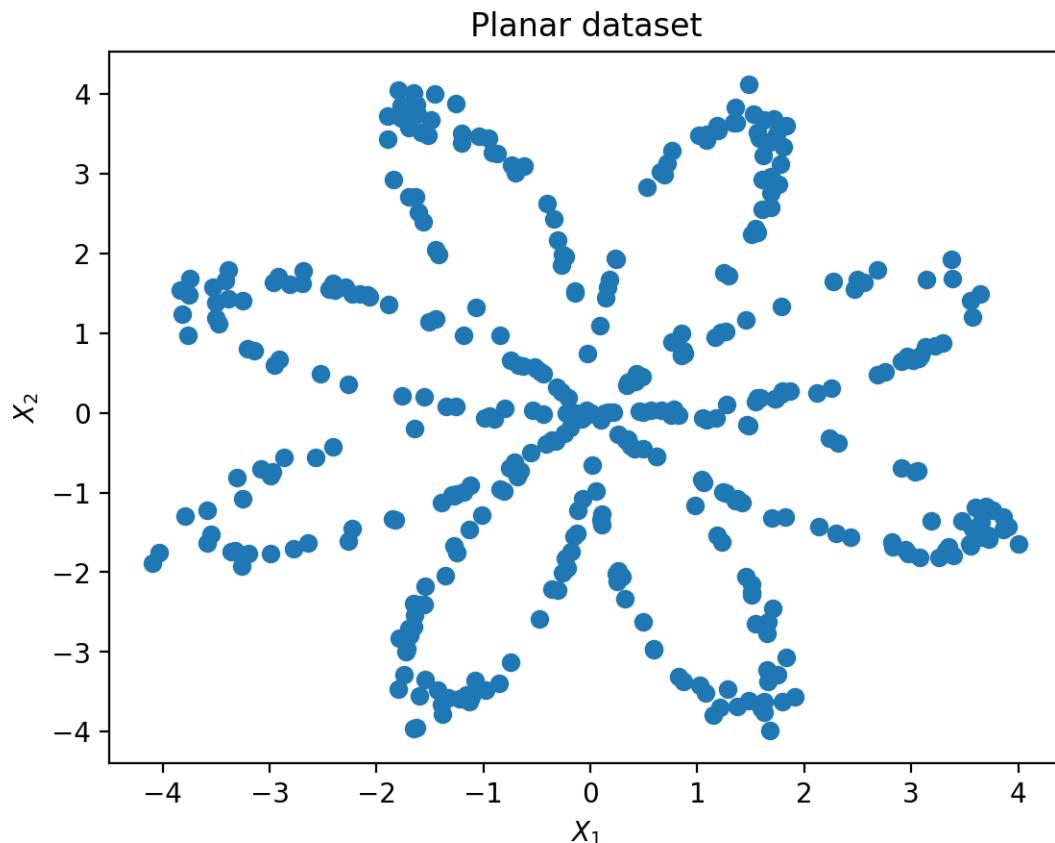
Important Notes:

- The **key difference** compared to the perceptron is that the neural network uses continuous sigmoidal non-linear hidden units, whereas the perceptron uses step-function non-linearities. This means that the neural network function is differentiable which plays a central role in network training.
- If the activation functions of all hidden units are taken to be linear, then any such network can be replaced by a network without the hidden units. This follows from the fact that the composition of successive linear transformations is itself a linear transformation.

In order to study these claims, let's consider a dataset, in which, the classes are separated by a non-linear decision boundary. Therefore, a simple linear model, without performing any sophisticated feature engineering, cannot capture.

```
[5]: x, y = load_planar_dataset()
plt.scatter(x[:, 0], x[:, 1])
plt.title("Planar dataset")
plt.xlabel("$X_1$")
plt.ylabel("$X_2$")
plt.show()

print(f"The shape of X is: {str(x.shape)}")
print(f"The shape of Y is: {str(y.shape)}")
print(f"We have {x.shape[1]} training examples!")
```

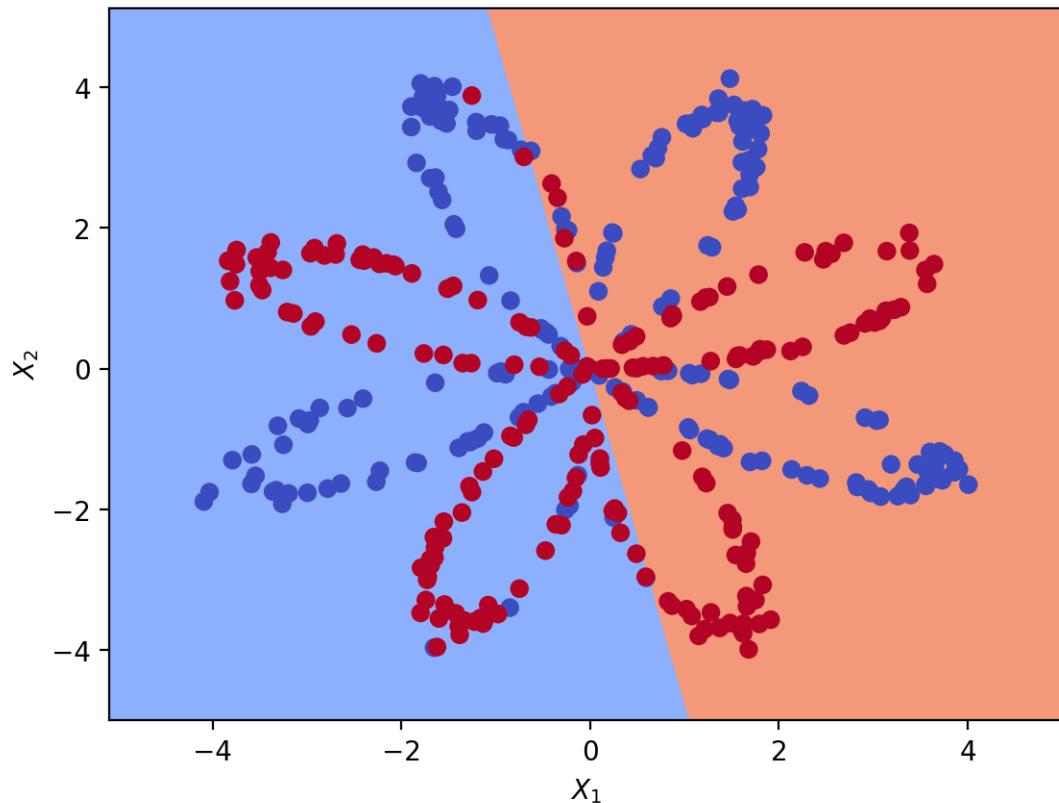


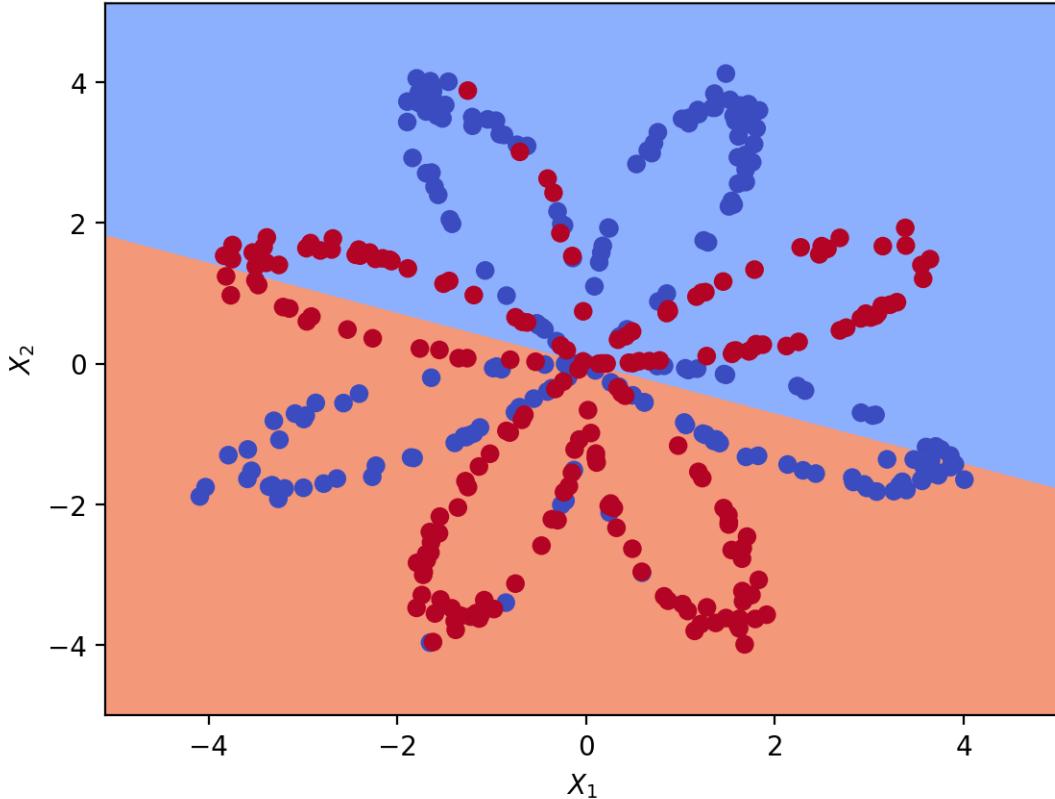
```
The shape of X is: (400, 2)
The shape of Y is: (400, 1)
We have 2 training examples!
```

Training either a simple perceptron or a logistic regression classifier, similar to the ones presented in [Chapter 4](#), only manages to learn an insufficient linear decision boundary that cannot capture the underlying data distribution.

```
[6]: classifier = Perceptron()
classifier.fit(x, np.squeeze(y))
plot_2d_decision_boundary(lambda x: classifier.predict(x) > 0.5, x, y)

classifier = LogisticRegression()
classifier.fit(x, np.squeeze(y))
plot_2d_decision_boundary(lambda x: classifier.predict(x) > 0.5, x, y)
```





Linear Algebra Notation

For efficiency reasons, in an actual implementation, it's more convenient to represent the activations in some ℓ -layer as an M -dimensional vector,

$$\mathbf{a}^{(\ell)} = \begin{bmatrix} a_1^{(\ell)} \\ a_2^{(\ell)} \\ \vdots \\ a_M^{(\ell)} \end{bmatrix} = \begin{bmatrix} \mathbf{w}_1^{(\ell)T} \mathbf{z}^{(\ell-1)} + w_{10}^{(\ell)} \\ \mathbf{w}_2^{(\ell)T} \mathbf{z}^{(\ell-1)} + w_{20}^{(\ell)} \\ \vdots \\ \mathbf{w}_M^{(\ell)T} \mathbf{z}^{(\ell-1)} + w_{M0}^{(\ell)} \end{bmatrix} = \begin{bmatrix} \mathbf{w}_1^{(\ell)T} \\ \mathbf{w}_2^{(\ell)T} \\ \vdots \\ \mathbf{w}_M^{(\ell)T} \end{bmatrix} \mathbf{z}^{(\ell-1)} + \mathbf{w}_0^{(\ell)} = \mathbf{W}^{(\ell)} \mathbf{z}^{(\ell-1)} + \mathbf{w}_0^{(\ell)}$$

In terms of matrix dimensions, we have $(M \times D)(D \times 1) + (M \times 1)$. Then, the activation function $h(\cdot)$ is applied on $\mathbf{a}^{(\ell)}$ to obtain,

$$\mathbf{z}^{(\ell)} = h^{(\ell)}(\mathbf{a}^{(\ell)})$$

This can also be generalized across N training examples \mathbf{x}_i , by stacking them in columns, creating a matrix \mathbf{X} of dimensions $(D \times N)$. Then, we obtain,

$$\mathbf{W}^{(\ell)} \mathbf{Z}^{(\ell-1)} + \mathbf{w}_0^{(\ell)}$$

and

$$\mathbf{Z}^{(\ell)} = h^{(\ell)}(\mathbf{A}^{(\ell)})$$

where $\mathbf{Z}^{(0)} = \mathbf{X}$.

Activation Functions

In the general case, we can use as an activation function any non-linear $h(\mathbf{z})$. Some popular choices are the following non-linear functions.

1. The sigmoid function or $\sigma(z) = \frac{1}{1+e^{-z}}$. Mostly used in the output layer for representing class probability. In the case of multi-class problems, the softmax activation function is used instead of the sigmoid.
2. The hyperbolic tangent or $\tanh(z) = \frac{e^z - e^{-z}}{e^z + e^{-z}}$. Note that the hyperbolic tangent is a shifted version of the sigmoid function, that crosses zero point and rescales so that it ranges from -1 to 1 . That means that it has the effect of centering the data around zero which is a desired property for learning algorithms.

However, a downside of both the sigmoid and the hyperbolic tangent is that as z gets very large or very small the slope of the function gets close to zero thus slowing down gradient descent.

3. The rectified linear unit or $\text{relu}(z) = \max(0, z)$. Thus, the derivative is 1 as long as $z > 0$ and 0 when $z \leq 0$.
4. The leaky rectified linear unit or $\text{leakyrelu}(z) = \max(0.01z, z)$, attempts to improves upon the dying ReLU problem, which is that all negative input values become zero immediately. Another variation is the parametric ReLU, which simply makes 0.01 a parameter, i.e., $\max(\alpha z, z)$.

Rectified linear unit activation functions, overcome the problem of vanishing gradients, and thus, they enable much faster training of neural networks.

5. The exponential linear unit (ELU) or $\text{elu}(z) = \begin{cases} z & z \geq 0 \\ \alpha(e^z - 1) & z < 0 \end{cases}$ uses a log curve to define the negative values unlike the parametric ReLU functions that use a straight line.
6. The self-gated activation function (Swish) or $\text{swish}(z) = z\sigma(z)$ is a smooth function that does not abruptly change direction $x = 0$. Rather, it smoothly bends from 0 towards values < 0 and then upwards again. It consistently matches or outperforms the ReLU activation functions.

```
[7]: import numpy as np
```

```
def sigmoid(z: np.ndarray) -> float:  
    return 1 / (1 + np.exp(-z))  
  
z = np.linspace(-5, 5)
```

```

plt.figure(figsize=(10, 4))

plt.subplot(2, 3, 1)
plt.tight_layout()
plt.plot(z, sigmoid(z))
plt.plot(z, sigmoid(z) * (1 - sigmoid(z)), "k", linestyle="dotted")
plt.xlabel("z")
plt.ylabel("$\sigma(z)$")
plt.legend(["sigmoid", "derivative"])

plt.subplot(2, 3, 2)
plt.tight_layout()
plt.plot(z, np.tanh(z), "r")
plt.plot(z, 1 - np.tanh(z) * np.tanh(z), "k", linestyle="dotted")
plt.xlabel("z")
plt.ylabel("$\tanh(z)$")
plt.legend(["tanh", "derivative"])

plt.subplot(2, 3, 3)
plt.tight_layout()
plt.plot(z, np.maximum(0, z), "g")
plt.plot(z, np.where(z > 0, 1, 0), "k", linestyle="dotted")
plt.xlabel("z")
plt.ylabel("$\text{ReLU}(z)$")
plt.legend(["ReLU", "derivative"])

plt.subplot(2, 3, 4)
plt.tight_layout()
plt.plot(z, np.maximum(0.01 * z, z), "b")
plt.plot(z, np.where(z > 0, 1, 0.01), "k", linestyle="dotted")
plt.xlabel("z")
plt.ylabel("$\text{Leaky ReLU}(z)$")
plt.legend(["Leaky ReLU", "derivative"])

plt.subplot(2, 3, 5)
plt.tight_layout()
plt.plot(z, np.where(z > 0, z, np.exp(z) - 1), "y")
plt.plot(z, np.where(z > 0, 1, np.where(z > 0, z, np.exp(z) - 1) + 1), "k", ↴
    linestyle="dotted")
plt.xlabel("z")
plt.ylabel("$\text{ELU (a=1)}(z)$")
plt.legend(["ELU (a=1)", "derivative"])

plt.subplot(2, 3, 6)
plt.tight_layout()
plt.plot(z, z * sigmoid(z), "m")

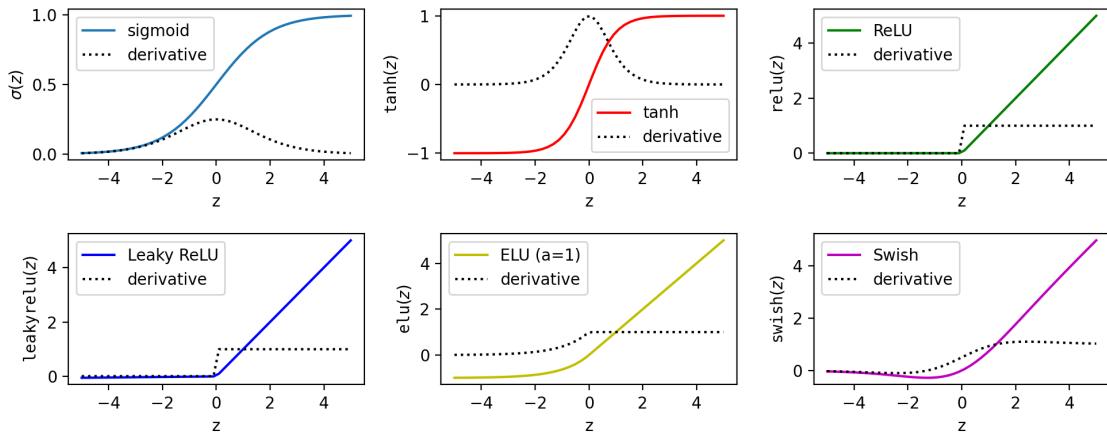
```

```

plt.plot(z, sigmoid(z) + z * sigmoid(z) * (1 - sigmoid(z)), "k", □
    ↵ linestyle="dotted")
plt.xlabel("z")
plt.ylabel("$\mathbf{swish}(z)$")
plt.legend(["Swish", "derivative"])

plt.show()

```



5.2 Network Training

Regression A simple approach to the problem of determining the network parameters is to revisit the discussion of polynomial curve fitting, and attempt to minimize a sum-of-squares error function. Thus, given a training set comprising a set of input vectors $\{\mathbf{x}_n\}$, where $n = 1, \dots, N$, and a corresponding set of target vectors $\{\mathbf{t}_n\}$, we minimize the error function,

$$E_n(\mathbf{w}) = \frac{1}{2} \sum_{n=1}^N \|\mathbf{y}(\mathbf{x}_n, \mathbf{w}) - \mathbf{t}_n\|^2$$

Consider regression problems, and for the moment, a single target variable t that may take any real value. Similar to Section 3.1, we assume that t follows a Gaussian distribution having an \mathbf{x} -dependent mean, which is given by the output of the neural network,

$$p(t|\mathbf{x}, \mathbf{w}) = \mathcal{N}(t|\mathbf{y}(\mathbf{x}, \mathbf{w}), \beta^{-1})$$

For the above conditional distribution, it is sufficient to take the output unit activation function to be the identity, because such a network can approximate any continuous function from \mathbf{x} to y . Given a data set of N independent, identically distributed observations \mathbf{X} , and the corresponding target values \mathbf{t} , the likelihood function is as follows,

$$p(\mathbf{t}|\mathbf{X}, \mathbf{w}, \beta) = \prod_{n=1}^N p(t_n|\mathbf{x}_n, \mathbf{w}, \beta) = \prod_{n=1}^N \mathcal{N}(t_n|\mathbf{y}(\mathbf{x}_n, \mathbf{w}), \beta^{-1})$$

Then, by taking the negative logarithm, we obtain the same error function derived in (3.11). By minimizing the error function, we obtain the maximum likelihood solution \mathbf{w}_{ML} . Having found \mathbf{w}_{ML} , the value of β can be found using (3.21), derived by minimizing the negative log likelihood.

IMPORTANT: Keep in mind, however, that the nonlinearity of the network function $y(\mathbf{x}_n, \mathbf{w})$ causes the error to be nonconvex, and so a local maxima of the likelihood may be found, corresponding to local minima of the error function.

Classification In binary classification a single target variable t such that $t = 1$ for class \mathcal{C}_1 and $t = 0$ for class \mathcal{C}_2 . We consider a network having a single output whose activation function is a logistic sigmoid,

$$y = \sigma(\alpha) = \frac{1}{1 + \exp(-\alpha)}$$

so that $0 \leq y(\mathbf{x}, \mathbf{w}) \leq 1$, is interpreted as the conditional probability $p(\mathcal{C}_k | \mathbf{x})$ given by $1 - y(\mathbf{x}, \mathbf{w})$. The conditional distribution of targets given inputs is then a Bernoulli distribution of the form,

$$p(t | \mathbf{x}, \mathbf{w}) = y(\mathbf{x}, \mathbf{w})^t \{1 - y(\mathbf{x}, \mathbf{w})\}^{1-t}$$

Given a training set of independent observations, the the error function by the negative log-likelihood, if the *cross-entropy* error function of the form,

$$E(\mathbf{w}) = - \sum_{n=1}^N \{t_n \ln y_n + (1 - t_n) \ln(1 - y_n)\}$$

NOTE: There is no analogue of the noise precision β because the target values are assumed to be correctly labelled.

IMPORTANT: There is a natural choice of both output unit activation function and matching error function, according to the type of problem being solved. For regression we rely on linear outputs and sum-of-squares error, and for binary logistic sigmoid (binary) or softmax (multiclass) outputs and cross-entropy error function.

5.2.1 Parameter optimization

The goal is to find a vector such that $E(\mathbf{w})$ is minimized. However, the error function has a highly nonlinear dependence on the weights, and so there are many points in the weight space at which the gradient vanishes. Since there is no hope of finding an analytical solution to the equation $\nabla E(\mathbf{w}) = 0$ we resort to iterative numerical procedures. Most of these techniques involve choosing an initial value $\mathbf{w}^{(0)}$ for the weight vector and then moving through weight space in a succession of steps of the form,

$$\mathbf{w}^{(\tau+1)} = \mathbf{w}^{(\tau)} + \Delta \mathbf{w}^{(\tau)}$$

Such algorithms involve different choices for the weight vector update $\Delta \mathbf{w}^{(\tau)}$. Usually, they make use of gradient information and therefore require that, after each update, the value of $\nabla E(\mathbf{w})$ is evaluated at the updated weight vector $\mathbf{w}^{(\tau+1)}$. In order to understand the importance of gradient

information, it is useful to consider a local approximation to the error function based on a Taylor expansion.

5.2.2 Local quadratic approximation

Consider the second-order Taylor expansion of $E(\mathbf{w})$ around some point $\hat{\mathbf{w}}$,

$$E(\mathbf{w}) \approx E(\hat{\mathbf{w}}) + (\mathbf{w} - \hat{\mathbf{w}})^T \mathbf{b} + \frac{1}{2}(\mathbf{w} - \hat{\mathbf{w}})^T \mathbf{H}(\mathbf{w} - \hat{\mathbf{w}})$$

where $\mathbf{b} = \nabla E|_{\mathbf{w}=\hat{\mathbf{w}}}$ and $\mathbf{H} = \nabla \nabla E$ is the Hessian matrix of second derivatives. Thus, the local approximation to the gradient is given by,

$$\nabla E(\mathbf{w}) \approx \mathbf{b} + \mathbf{H}(\mathbf{w} - \hat{\mathbf{w}})$$

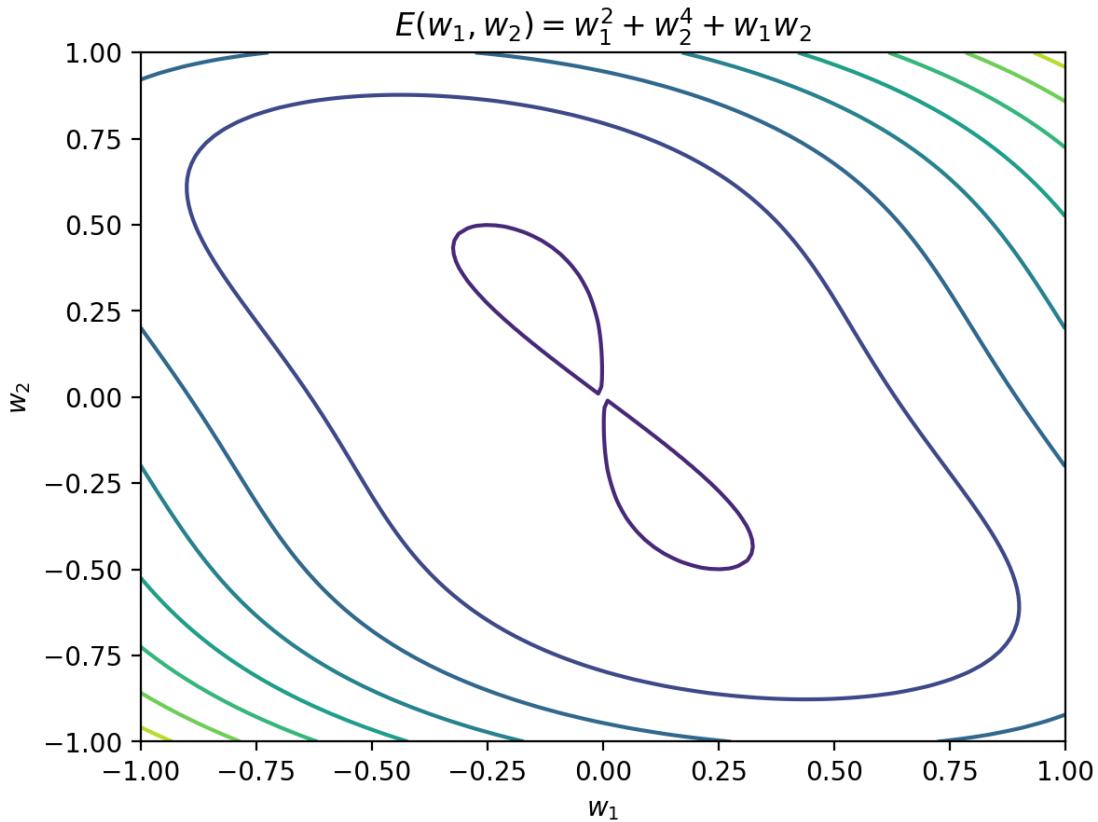
for points \mathbf{w} that are sufficiently close to $\hat{\mathbf{w}}$, these expressions give reasonable approximations for the error and its gradient.

Consider, for instance, a simple 2-dimensional error function of the form $E(w_1, w_2) = w_1^2 + w_2^4 + w_1 w_2$.

```
[8]: w = np.linspace(-1, 1, 100)
w1, w2 = np.meshgrid(w, w)

def E(w1: float, w2: float) -> float:
    return w1**2 + w2**4 + w1 * w2

plt.contour(w1, w2, w1**2 + w2**4 + w1 * w2)
plt.xlabel("$w_1$")
plt.ylabel("$w_2$")
plt.title("$E(w_1, w_2) = w_1^2 + w_2^4 + w_1 w_2$")
plt.show()
```



The gradient of $E(w_1, w_2)$ is defined as follows,

$$\nabla E = \begin{bmatrix} \frac{\partial E}{w_1} \\ \frac{\partial E}{w_2} \end{bmatrix} = \begin{bmatrix} 2w_1 + w_2 \\ 4w_2 + w_1 \end{bmatrix}$$

and the Hessian matrix \mathbf{H} equals,

$$\mathbf{H} = \nabla \nabla E = \begin{bmatrix} \frac{\partial^2 E}{w_1^2} & \frac{\partial^2 E}{w_1 w_2} \\ \frac{\partial^2 E}{w_2 w_1} & \frac{\partial^2 E}{w_2^2} \end{bmatrix} = \begin{bmatrix} 2 & 1 \\ 1 & 4 \end{bmatrix}$$

```
[9]: def gradient(w1, w2):
    return np.array([2 * w1 + w2, 4 * w2 + w1])

H = np.array([[2, 1], [1, 4]])
```

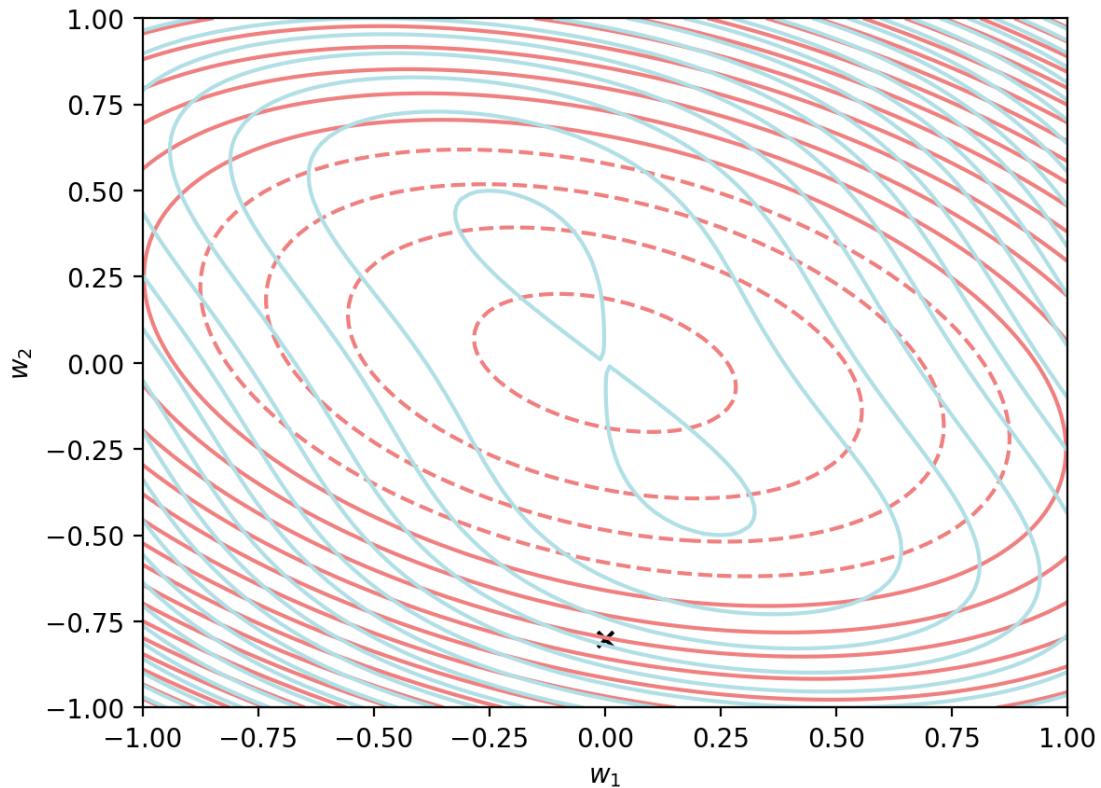
Then, given some point $\hat{\mathbf{w}} = [\hat{w}_1, \hat{w}_2]$, $E(w_1, w_2)$ can be approximated by,

$$E(w_1, w_2) \approx E(\hat{w}_1, \hat{w}_2) + [w_1 - \hat{w}_1, w_2 - \hat{w}_2] \begin{bmatrix} 2\hat{w}_1 + \hat{w}_2 \\ 4\hat{w}_2 + \hat{w}_1 \end{bmatrix} + \frac{1}{2} [w_1 - \hat{w}_1, w_2 - \hat{w}_2]^T \begin{bmatrix} 2 & 1 \\ 1 & 4 \end{bmatrix} [w_1 - \hat{w}_1, w_2 - \hat{w}_2]$$

```
[10]: w_hat = np.array([0, -0.8])
```

```
@np.vectorize
def E_approx(w1, w2):
    w = np.array([w1, w2])
    return E(*w_hat) + np.dot((w - w_hat), gradient(*w_hat)).T + 0.5 * np.dot(w - w_hat, np.dot(H, w - w_hat))

plt.contour(w1, w2, E_approx(w1, w2), 20, colors="lightcoral")
plt.contour(w1, w2, E(w1, w2), 20, colors="powderblue")
plt.scatter(*w_hat, color="black", marker="x")
plt.xlabel("$w_1$")
plt.ylabel("$w_2$")
plt.show()
```



5.2.4 Gradient descent optimization

The simplest approach to using gradient information is to choose the weight update to be a small step in the direction of the negative gradient, so that,

$$\mathbf{w}^{(\tau+1)} = \mathbf{w}^{(\tau)} - \eta \nabla E(\mathbf{w}^{(\tau)})$$

where the parameter $\eta > 0$ is known as *learning rate*. At each step the weight vector is moved in the direction of the greatest rate of decrease of the error function, and so the approach is known as *gradient descent* or *steepest descent*. Note that the error function is defined with respect to a training set, and thus, each step requires that the entire training set be processed in order to evaluate ∇E . Techniques that use the whole data set at once are called *batch* methods. Although such an approach might intuitively seem reasonable, in fact it turns out to be a poor algorithm.

For *batch optimization*, there are more efficient methods, such as conjugate gradients and quasi-Newton methods, which are much more robust and much faster than simple gradient descent. Unlike gradient descent, these algorithms have the property that the error function always decreases at each iteration unless the weight vector has arrived at a local or global minimum.

There is, however, an on-line version of gradient descent, known as *sequential gradient descent* or *stochastic gradient descent*, that has proved useful in practice for training neural networks on large data sets. Error functions based on maximum likelihood for a set of independent observations comprise a sum of terms, one for each data point,

$$E(\mathbf{w}) = \sum_{n=1}^N E_n(\mathbf{w})$$

Stochastic gradient descent makes an update to the weight vector based on **one data point** at a time, so that

$$\mathbf{w}^{(\tau+1)} = \mathbf{w}^{(\tau)} - \eta \nabla E_n(\mathbf{w}^{(\tau)})$$

The update is repeated by cycling through the data either in sequence or by selecting points at random with replacement. There are of course intermediate scenarios in which the updates are based on batches of data points. One advantage of on-line methods compared to batch methods is that the former handle redundancy in the data much more efficiently. To see, this consider an extreme example in which we take a data set and double its size by duplicating every data point. Note that this simply multiplies the error function by a factor of 2 and so is equivalent to using the original error function. Batch methods will require double the computational effort to evaluate the batch error function gradient, whereas online methods will be unaffected. Another property of on-line gradient descent is the possibility of escaping from local minima, since a stationary point with respect to the error function for the whole data set will generally not be a stationary point for each data point individually.

5.3 Error Backpropagation

Error backpropagation, or simply backprop, is an efficient technique for evaluating the gradient of an error function $E(\mathbf{w})$ for a feed-forward neural net. This can be achieved using a local

message passing scheme in which information is sent alternately forwards and backwards through the network.

Most training algorithms involve an iterative procedure for minimization of an error function. At each such step, we can distinguish between two stages:

1. The derivatives of the error function must be evaluated. The important contribution of the backpropagation technique is in providing a computationally efficient method for evaluating such derivatives. Since the errors are propagated backwards through the network, we use the term backpropagation to describe the evaluation of derivatives.
2. The derivatives are then used to compute the adjustments to be made to the weights, e.g., gradient descent.

It is important to recognize that these stages are distinct. Thus, the first stage, namely the propagation of errors backwards through the network in order to evaluate derivatives, can be applied to many other kinds of networks and not just the multilayer perceptron. It can also be applied to error functions other than the simple sum-of-squares, and to the evaluation of other derivatives, such as, the Jacobian and Hessian matrices.

5.3.1 Evaluation of error-function derivatives

The backpropagation algorithm can be applied to a general network of arbitrary topology, non-linear activation functions, and a broad class of error function. Many error functions of practical interest comprise a sum of terms, one of each data point, so that,

$$E(\mathbf{w}) = \sum_{n=1}^N E_n(\mathbf{w})$$

For simplicity, consider the evalution of a single term $\nabla E_n(\mathbf{w})$. Consider the first linear model, where the outputs are linear combinations of the input variables.

$$y_{nk} = y_k(\mathbf{x}_n, \mathbf{w}) = \sum_i w_{ki} x_i$$

thus, the error function for input example n , takes the form,

$$E_n = \frac{1}{2} \sum_k (y_{nk} - t_{nk})^2$$

and its gradient with respect to w_{ji} , is given by,

$$\frac{\partial E_n}{\partial w_{ji}} = (y_{nj} - t_{nj}) x_{ni}$$

In a general feed-forward network, each unit j (in any layer ℓ) computes a weighted sum of its inputs, as follows,

$$a_j = \sum_i w_{ji} z_i$$

where z_i is the activation of a unit in the previous layer ($\ell - 1$), that sends a connection to unit j , and w_{ji} is the weight associated with the connection. Then, the sum a_j is transformed by a non-linear activation function $h(\cdot)$ to give z_j in the form,

$$z_j = h(a_j)$$

In turn, z_j may be sent as a connection to a subsequent unit in order to participate in another activation. Note that using the vectorized notation introduced in the beginning of this chapter, we can compute the transformed activations of any layer ℓ as follows,

$$\begin{aligned}\mathbf{a}^\ell &= \mathbf{W}^\ell \mathbf{z}^{\ell-1} \\ \mathbf{z}^\ell &= h(\mathbf{a}^\ell)\end{aligned}$$

In order to apply backprop, we assume that we have computed the activations of all hidden and output units in the network, a process called *forward propagation* because it may be regarded as the forward flow of information through the network. Consider again the evaluation of the derivative E_n . Given an arbitrary unit j , E_n depends on the weight w_{ji} only via the input a_j . Therefore, according to the chain rule for partial derivatives, we obtain,

$$\frac{\partial E_n}{\partial w_{ji}} = \frac{\partial E_n}{\partial a_j} \frac{\partial a_j}{\partial w_{ji}} \stackrel{(5.48)}{=} \frac{\partial E_n}{\partial a_j} z_i$$

Since z_i is computed during forward propagation, we only need to compute $\frac{\partial E_n}{\partial a_j}$. For simplicity, let's define $\delta_j = \frac{\partial E_n}{\partial a_j}$.

1. For the output units, we have that $\delta_k = \frac{\partial E_n}{\partial y_k} \stackrel{(5.46)}{=} y_k - t_k$.
2. For hidden units, we apply again the chain rule,

$$\begin{aligned}\delta_j &= \frac{\partial E_n}{\partial a_j} = \sum_k \frac{\partial E_n}{\partial a_k} \frac{\partial a_k}{\partial a_j} \\ &= \sum_k \delta_k \frac{\partial a_k}{\partial a_j} \stackrel{(5.48)}{=} \sum_k \delta_k \left(\frac{\partial}{\partial a_j} \sum_j w_{kj} z_j \right) \stackrel{(5.49)}{=} \sum_k \delta_k \left(\frac{\partial}{\partial a_j} \sum_j w_{kj} h(a_j) \right) \\ &= h'(a_j) \sum_k w_{kj} \delta_k\end{aligned}$$

where the sum runs over all k units to which j sends connections. Thus, for a particular hidden unit, δ is obtained by propagating the δ backwards from units higher up in the network.

Since, we know the δ for the output units, we can recursively evaluate the δ for all the hidden units in a feed-forward neural net, regardless of the topology.

Error Backpropagation algorithm

1. Forward propagate any input vector \mathbf{x}_n using (5.48) and (5.49).
2. Evaluate δ_k for output units using (5.54).
3. Backpropagate δ using (5.56) to obtain δ_j for each hidden unit.
4. Evaluate the required derivatives using (5.53).

For batch methods, the derivative of the total error E is obtained by repeating the above steps for each example n and then summing over all examples.

Implementation notes

When implementing neural networks it is much more performant to perform forward and backward propagation using the matrix notation introduced in the beginning of this chapter. Therefore, here we present both propagations in matrix notation across multiple training examples.

Forward Propagation

1. $\mathbf{Z}^{(0)} = \mathbf{X}$
2. Repeat for each layer ℓ :
 - $\mathbf{A}^{(\ell)} = \mathbf{W}^{(\ell)}\mathbf{Z}^{(\ell-1)} + \mathbf{w}_0^{(\ell)}$
 - and $\mathbf{Z}^{(\ell)} = h^{(\ell)}(\mathbf{A}^{(\ell)})$

Backward Propagation

1. For the output layer evaluate $\delta^L = \mathbf{y} - \mathbf{t}$
2. Backpropagate $\delta^{\ell+1}$ to obtain $\delta^\ell = h'(\mathbf{a}^\ell) \odot (\mathbf{W}^{(\ell+1)T}\delta^{\ell+1})$
3. Evaluate derivatives $\nabla E_n(\mathbf{W}^\ell) = \delta^\ell \mathbf{z}^{\ell-1}$

Let's train a shallow 2-layer neural network for classification, on the planar dataset, using one hidden layer of hyperbolic tangent activation functions and one sigmoid output layer. In order to train the network for classification, we use a cross-entropy loss function, similar to logistic regression. The weights of the neural network are initialized at random, while biases are initialized to zero values.

```
[18]: x, y = load_planar_dataset()

net = nn.NeuralNetwork(
    nn.LinearLayer(2, 4),
    nn.Tanh(),
    nn.LinearLayer(4, 1),
    nn.Sigmoid(),
)

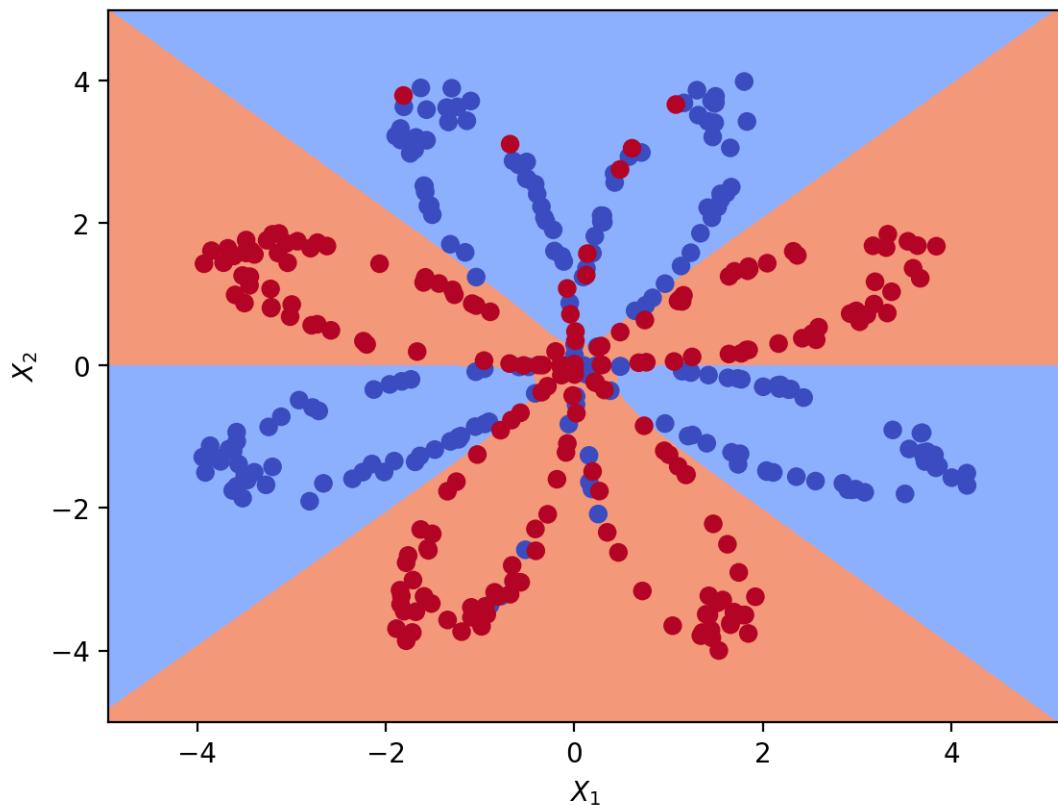
L = nn.BinaryCrossEntropyLoss()
net.fit(x, y, loss=L)
plot_2d_decision_boundary(lambda x: net.predict(x) > 0.5, x, y)
```

```
-- Epoch 1 ---
Cost: 0.7080379029345033
-- Epoch 101 ---
```

```

Cost: 0.5332581467045885
-- Epoch 201 ---
Cost: 0.4320979117595954
-- Epoch 301 ---
Cost: 0.37866149726575815
-- Epoch 401 ---
Cost: 0.3473329935455369
-- Epoch 501 ---
Cost: 0.32698746950287444
-- Epoch 601 ---
Cost: 0.31283296402612243
-- Epoch 701 ---
Cost: 0.30246073314522465
-- Epoch 801 ---
Cost: 0.294544357721986
-- Epoch 901 ---
Cost: 0.28830257594631986

```



Weight initialization helps, among others, avoiding vanishing/exloding gradients. A common choice is *Xavier initilization*, defined as follows,

$$w = \mathcal{N}(0, \sqrt{\frac{1}{N^{(\ell-1)}}})$$

Xavier initialization works better for networks using tangent activation functions. A popular choice for ReLU activation functions is

$$w = \mathcal{N}(0, \sqrt{\frac{2}{N^{(\ell-1)}}})$$

Another popular alternative is

$$w = \mathcal{N}(0, \sqrt{\frac{2}{N^{(\ell-1)} + N^\ell}})$$

What happens if all weights and biases are initialized to the same value? Then all hidden units are symmetric (completely identical), thus computing the same function, which is undesirable. Therefore, weights must be initialized randomly. Biases can still be zero since they represent a single dimension in the weight vectors of the hidden units which already differ due to the random initialization. As a proof of concept, lets re-train the same exact network but initialize weights and bias to a constant value.

```
[19]: net = nn.NeuralNetwork(
    nn.LinearLayer(2, 4, random_initialization=False),
    nn.Tanh(),
    nn.LinearLayer(4, 1, random_initialization=False),
    nn.Sigmoid(),
)

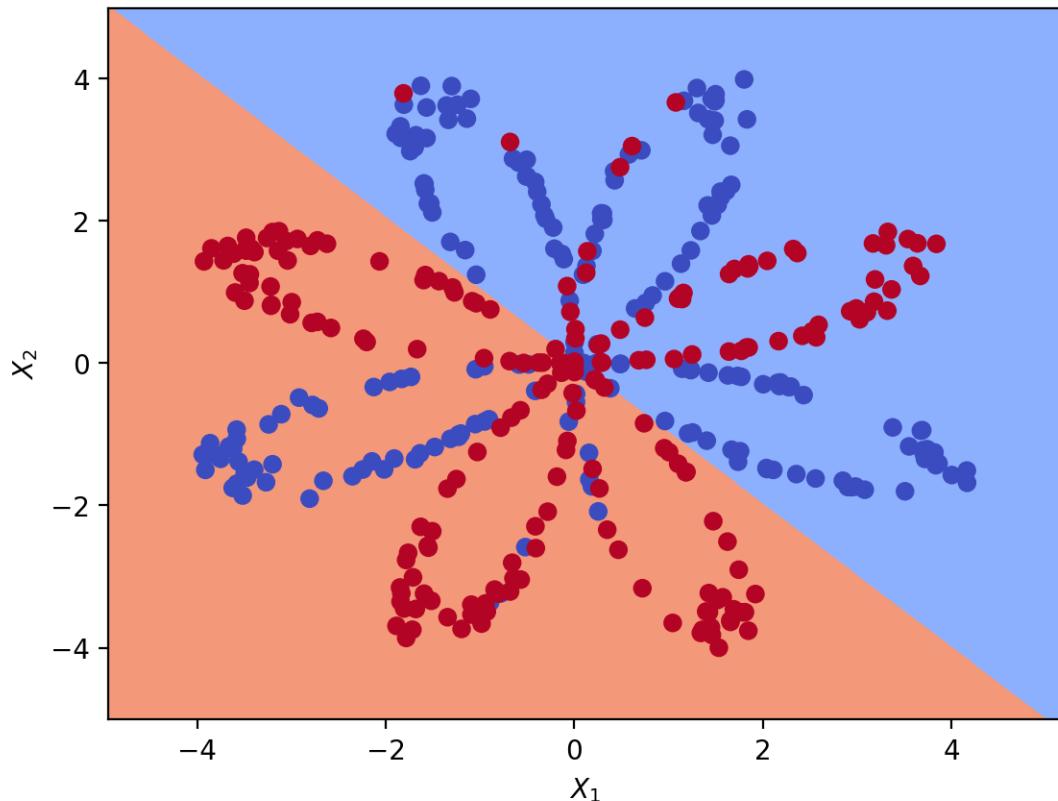
L = nn.BinaryCrossEntropyLoss()
net.fit(x, y, loss=L)
plot_2d_decision_boundary(lambda x: net.predict(x) > 0.5, x, y)
```

```
-- Epoch 1 ---
Cost: 0.6932673944222819
-- Epoch 101 ---
Cost: 0.6930829250688935
-- Epoch 201 ---
Cost: 0.6884763177838701
-- Epoch 301 ---
Cost: 0.6706060650349758
-- Epoch 401 ---
Cost: 0.668686022681725
-- Epoch 501 ---
Cost: 0.6683657053643131
-- Epoch 601 ---
Cost: 0.6676242897407316
-- Epoch 701 ---
```

```

Cost: 0.6658298361918764
-- Epoch 801 ---
Cost: 0.6627349400852941
-- Epoch 901 ---
Cost: 0.659059060995905

```



Note that the behavior of the trained network is identical to logistic regression and the perceptron models we used in the beginning of the chapter.

In case of multiclass classification the sigmoid activation in the final layer of the network should be replaced by a softmax activation, similar to softmax regression. For instance, consider a synthetic dataset comprise 100 training examples, each having 2 input features and belonging to one of 3 classes.

```
[22]: # number of training points
N = 100

x_train, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=3,
    n_clusters_per_class=1, n_samples=N, random_state=21
)
```

```

encoder = OneHotEncoder()
t_one_hot = encoder.encode(t)

model = nn.NeuralNetwork(nn.LinearLayer(2, 4), nn.ReLU(), nn.LinearLayer(4, 3),
                        nn.Softmax())

model.fit(
    x_train,
    t_one_hot,
    epochs=10000,
    loss=nn.CrossEntropyLoss(),
    optimizer=nn.GradientDescent(learning_rate=0.01),
    verbose=True,
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, 100), np.linspace(-5, 5, 100))
x_test = np.array([x1, x2]).reshape(2, -1).T

predicted = np.argmax(model.predict(x_test), axis=1)

print("Training Error:")
print(classification_report(t, np.argmax(model.predict(x_train), axis=-1)))

plt.scatter(x_train[:, 0], x_train[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(100, 100), alpha=0.2, levels=np.
              linspace(0, 2, 4))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.xlabel("$x_1$", fontsize=12)
plt.ylabel("$x_2$", fontsize=12)

plt.show()

```

```

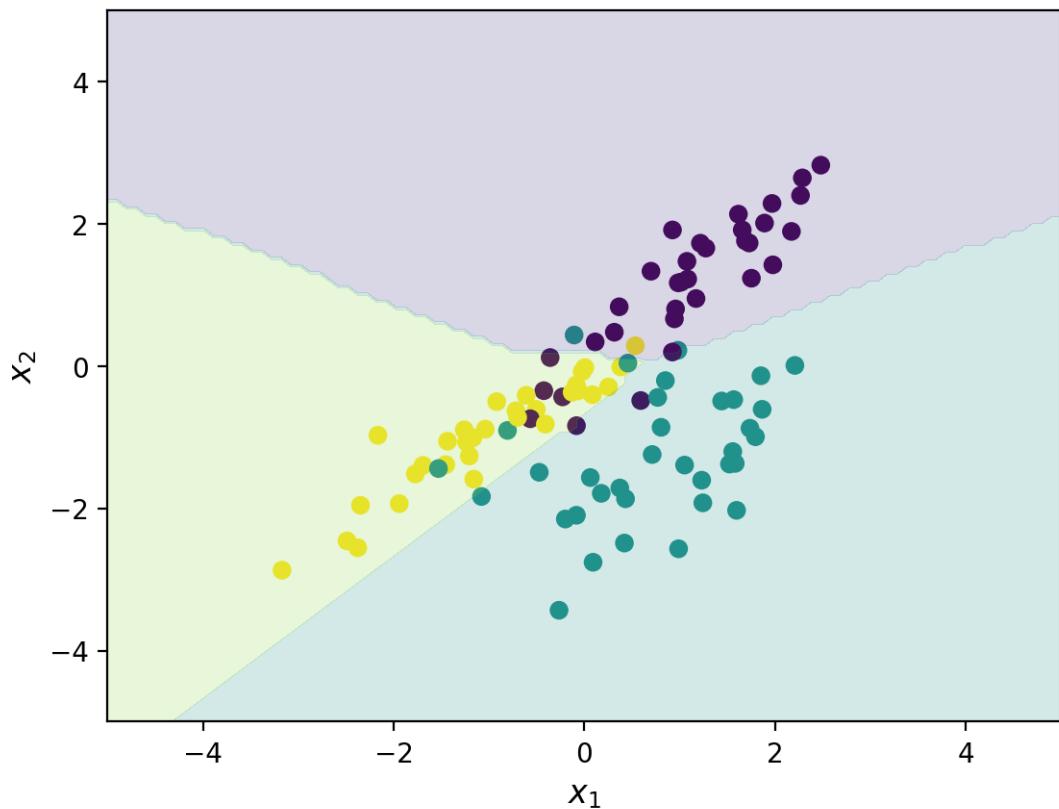
-- Epoch 1 ---
Cost: 1.10166804109341
-- Epoch 1001 ---
Cost: 0.4274539415136976
-- Epoch 2001 ---
Cost: 0.38231954420096187
-- Epoch 3001 ---
Cost: 0.3679944991104277
-- Epoch 4001 ---
Cost: 0.3585322733626179
-- Epoch 5001 ---
Cost: 0.34823524562803826
-- Epoch 6001 ---
Cost: 0.3399993027070345

```

```
-- Epoch 7001 ---  
Cost: 0.33318353101161735  
-- Epoch 8001 ---  
Cost: 0.3284922056777914  
-- Epoch 9001 ---  
Cost: 0.3244782822114613
```

Training Error:

	precision	recall	f1-score	support
0	0.90	0.82	0.86	33
1	0.94	0.86	0.90	35
2	0.82	0.97	0.89	32
accuracy			0.88	100
macro avg	0.88	0.88	0.88	100
weighted avg	0.89	0.88	0.88	100



5.3.3 Efficiency of backpropagation

Notes on the numerical approximation of the gradient Let a cost function $f(\theta)$, then by choosing a very small ϵ value, we can numerically approximate the gradient in any given point of the function by taking symmetrical central differences around that point, as depicted below,

Numerical differentiation is very important in practice, because a comparison of the derivatives calculated by backpropagation with those obtained using central differences provides a very accurate check on the correctness of any implementation of the backpropagation algorithm. When training networks in practice, derivatives should be evaluated using backpropagation, because this gives the greatest accuracy and numerical efficiency. However, the results should be compared with numerical differentiation in order to check the correctness of the implementation.

Basic recipe for training neural networks

1. In the presence of high bias, increasing the number of hidden units may increase performance.
2. If bias is reasonable, then variance may be high. In the presence of high variance, using more data or adding some form of regularization may increase performance.

Note that by using these steps, for many problems, you can achieve significant reduction in both bias and variance, in contrast to simpler models, where the bias-variance tradeoff is more hard or even impossible to overcome. The main drawback here is that larger networks require have higher computation cost to train, and more data are not always easy to find.

3. Normalizing inputs. When input features have very different scales, the cost function may be elongated, which, in turn, leads to slower learning, since gradient descent need small learning rate to converge. On the other hand, normalized inputs have spherical contours and, even for larger learning rates, gradient descent goes straight to the minimum.

5.5 Regularization in Neural Networks

The number M of hidden units is a free parameter, in contrast to input and output units, and can be adjusted to obtain the best predictive performance. Note that M indirectly controls the number of parameters (weights and biases) in the network, and therefore, we expect that by using maximum likelihood, we should find an optimal value for M that yields the best generalization performance, corresponding to the optimal balance between an under-fit and over-fit.

The generalization error, however, is not a simple function of M due to the presence of local minima in the error function. One approach of choosing M is to plot a graph of M against validation set performance and then choose the solution having the smallest validation set error, similar to model selection on [Chapter 1](#).

Another approach of course is to choose a relatively large value for M and add a regularization term to the error function in order to control the model complexity. The simplest regularizer is the quadratic, also known as *weight decay* in the context of neural networks,

$$\tilde{E}(\mathbf{w}) = E(\mathbf{w}) + \frac{\lambda}{2} \mathbf{w}^T \mathbf{w}$$

However, for the full neural network, the error function is obtained by,

$$\tilde{E} = E + \frac{\lambda}{2} \sum_{\ell=1}^L \|\mathbf{W}^\ell\|_F^2$$

where $\|\mathbf{W}^\ell\|_F^2$ is the Forbenius norm, defined as,

$$\|\mathbf{W}^\ell\|_F^2 = \sum_{i=1}^{M^\ell} \sum_{j=1}^{M^{(\ell-1)}} w_{ij}^2$$

The effective model complexity is then determined by the choice of λ . As discussed in [Chapter 1](#), the quadratic regularizer can be interpreted as the negative logarithm of a zero-mean Gaussian prior over the weight vector \mathbf{w} . Then, adding a quadratic regularization term, the error function for input example n , takes the form,

$$\tilde{E}_n = \frac{1}{2} \sum_k (y_{nk} - t_{nk})^2 + \frac{\lambda}{2} \sum_{k=1} w_k^2$$

where λ is called the *regularization parameter*, and the gradient is obtained as follows,

$$\frac{\partial \tilde{E}_n}{w_{ji}} = (y_{nj} - t_{nj})x_{ni} + \lambda w_j = \frac{\partial E_n}{w_{ji}} + \lambda w_j$$

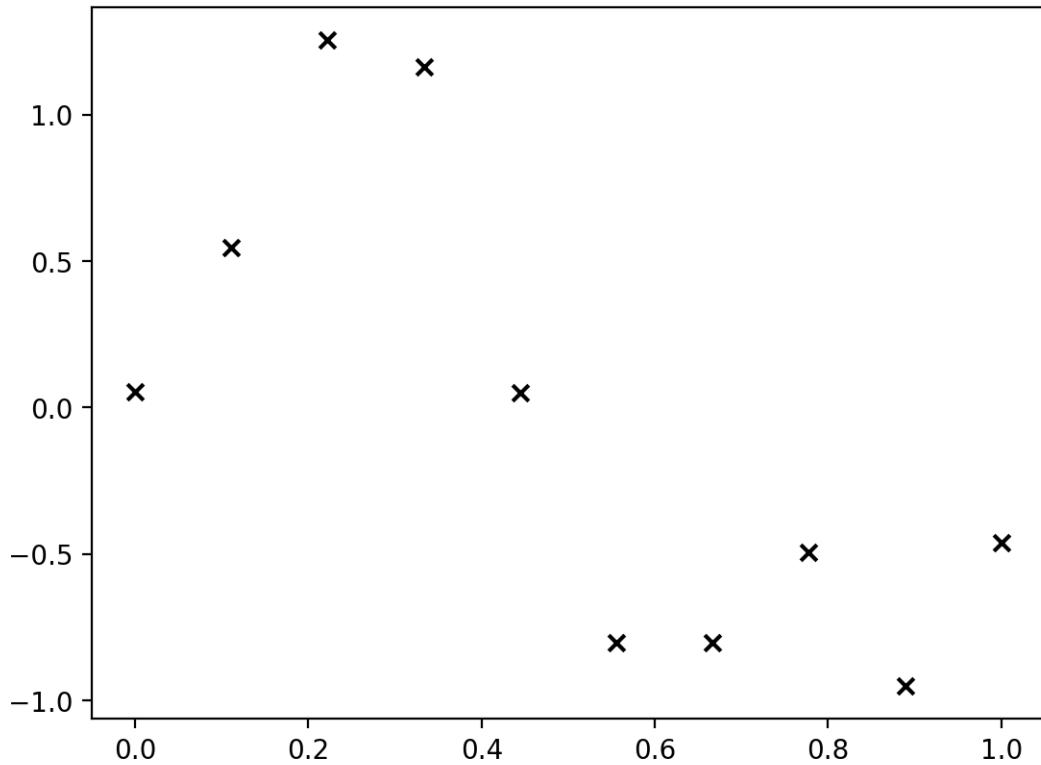
or

$$\nabla \tilde{E}_n = (\mathbf{y}_n - \mathbf{t}_n)\mathbf{x}_n + \lambda \mathbf{w} = \nabla E_n + \lambda \mathbf{w}$$

Then, by replacing back into (5.43), the stochastic gradient descent update becomes:

$$\mathbf{w}^{(\tau+1)} = \mathbf{w}^{(\tau)} - \eta \left(\nabla E_n(\mathbf{w}^{(\tau)}) + \lambda \mathbf{w}^{(\tau)} \right) = \mathbf{w}^{(\tau)} - \eta \nabla E_n(\mathbf{w}^{(\tau)}) - \eta \lambda \mathbf{w}^{(\tau)} = (1 - \eta \lambda) \mathbf{w}^{(\tau)} - \eta \nabla E_n(\mathbf{w}^{(\tau)})$$

```
[23]: x_train, y_train = generate_toy_data(lambda x: np.sin(2 * np.pi * x), sample_size=10, std=0.25)
plt.scatter(x_train, y_train, marker="x", color="k")
plt.show()
```



```
[24]: x_space = np.linspace(0, 1, 100)[:, None]

def create_network(m: int) -> nn.NeuralNetwork:
    return nn.NeuralNetwork(
        nn.LinearLayer(1, m),
        nn.Tanh(),
        nn.LinearLayer(m, 1),
        nn.Linear(),
    )

plt.figure(figsize=(20, 5))

for i, m in enumerate([1, 10]):
    model = create_network(m)
    model.fit(
        x_train[:, None],
        y_train[:, None],
        epochs=100000,
        loss=nn.SSELoss(),
        optimizer=nn.GradientDescent(learning_rate=0.01),
```

```

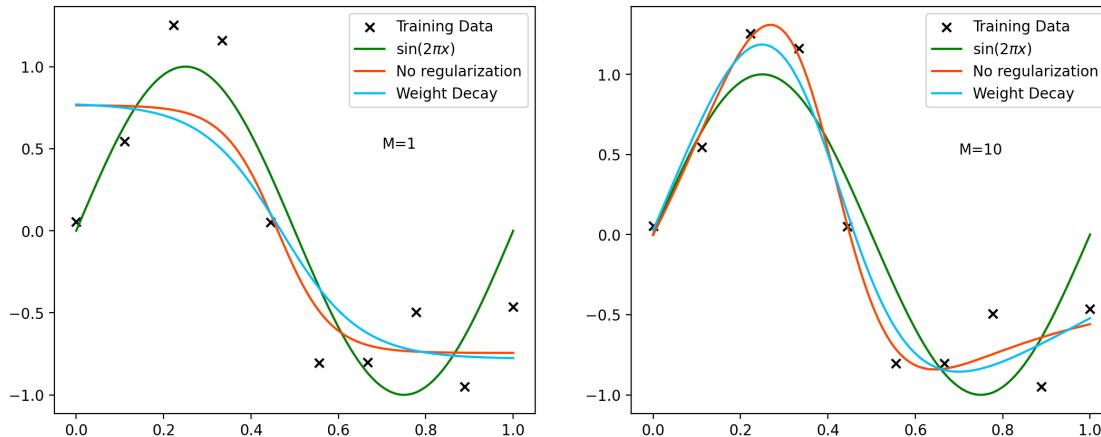
        verbose=False,
    )
y = model(x_space)

regularized_model = create_network(m)
regularized_model.fit(
    x_train[:, None],
    y_train[:, None],
    epochs=100000,
    loss=nn.SSELoss(),
    optimizer=nn.GradientDescent(learning_rate=0.01, weight_decay=1e-3),
    verbose=False,
)
y_regularized = regularized_model(x_space)

plt.subplot(1, 3, i + 1)
plt.scatter(x_train.ravel(), y_train.ravel(), marker="x", color="black")
plt.plot(x_space, np.sin(2 * np.pi * x_space), color="green")
plt.plot(x_space.ravel(), y.ravel(), color="orangered")
plt.plot(x_space.ravel(), y_regularized.ravel(), color="deepskyblue")
plt.annotate(f"M={m}", (0.7, 0.5))
plt.legend(["Training Data", "\sin(2\pi x)", "No regularization", "Weight Decay"])

plt.show()

```

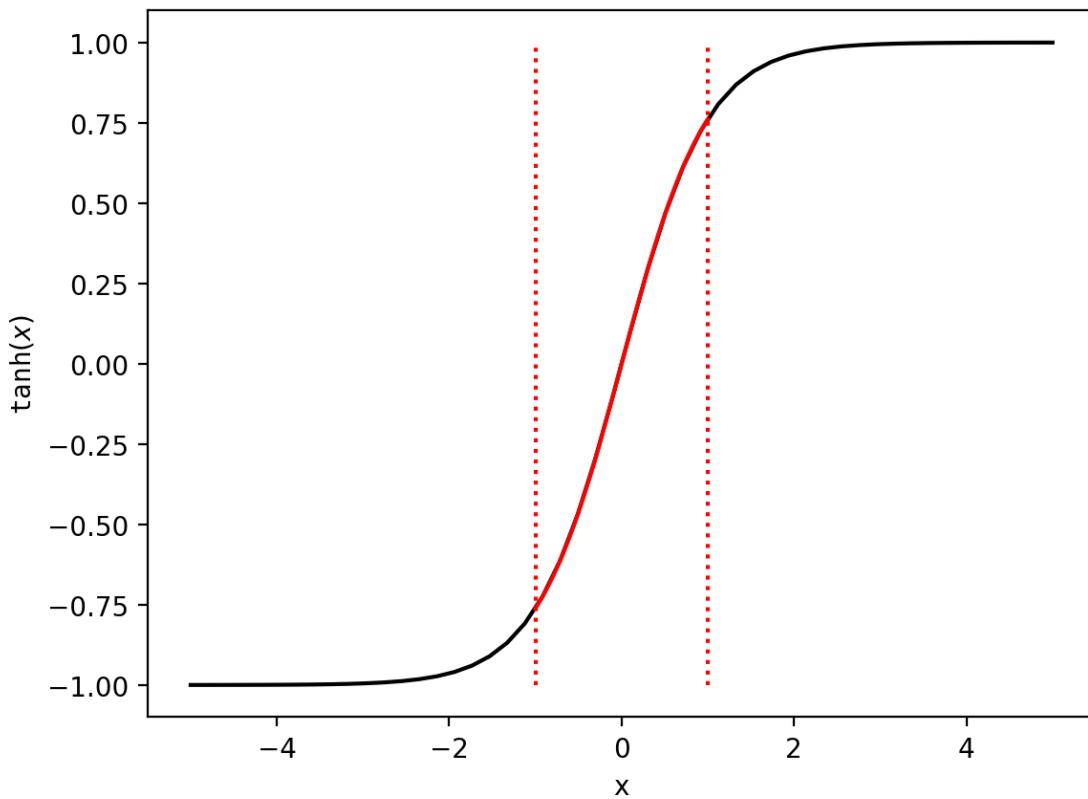


How does regularization reduces the over-fit? In the three figures above, the unregularized neural network (red line), has high bias on the left ($M = 1$) and high variance on the right ($M = 10$). Regularization helps combat high variance by making the network simpler by enforcing the deactivation of some hidden units (by penalizing weight parameters). Let's see an intuitive example. Assume that a neural network uses $\tanh(x)$ activation functions for the hidden units.

The $\tanh(x)$ activation has a roughly linear form for values close to zero, as shown in the following figure.

```
[25]: x = np.linspace(-5, 5)
narrow_x = np.linspace(-1, 1)

plt.plot(x, np.tanh(x), "k")
plt.plot(narrow_x, np.tanh(narrow_x), "r")
plt.vlines([-1, 1], -1, 1, colors="r", linestyles="dotted")
plt.xlabel("x")
plt.ylabel("$\tanh(x)$")
plt.show()
```



As the λ parameter gets larger, the effect of the regularization term penalizes the weight parameters to have smaller values (closer to zero). Note that hidden unit outputs (before activation) are a linear combination of the layer ℓ weights and the outputs of the previous layer, $\mathbf{A}^{(\ell)} = \mathbf{W}^{(\ell)} \mathbf{Z}^{(\ell-1)} + \mathbf{w}_0^{(\ell)}$, thus, in turn, the resulting $\mathbf{A}^{(\ell)}$ would be also smaller since $\mathbf{Z}^{(\ell-1)}$ are multiplied by smaller values. Therefore, when passed through the activation functions $\tanh(z)$ would respond more linearly. Increasing regularization (larger λ) enforces roughly linear activations and leads to simpler models which helps combat high variance.

Dropout Regularization

Dropout is another form of regularization that eliminates a percentage of the hidden units in the network by chance. For instance, you may toss a fair coin and have 50% chance of keeping each hidden unit in some layer ℓ . Then, by removing these units from the parameters \mathbf{W}^ℓ of the ℓ layer, the resulting network is much smaller. Dropout defines an indicator vector (mask) of zeros and ones, per hidden unit in the layer ℓ , which is used for *dropping* or deactivating a percentage of hidden units. More formally, assuming the layer ℓ has M hidden units,

$$\mathbf{d}^\ell \propto \text{Bin}(M, p)$$

where p is the probability of keeping a hidden unit, and

$$\mathbf{z}^\ell = \frac{\mathbf{d}^\ell \odot \mathbf{z}^\ell}{p}$$

where the division by p is called inverted dropout and ensures that the expected value of z remains the same after dropping a percentage of hidden units. For each training example a new \mathbf{d}^ℓ vector should be randomly chosen. Therefore given N training examples stacked in a matrix notation, the dropout mask is defined as,

$$\mathbf{D}^\ell = \begin{bmatrix} \text{Bin}_1(M, p) \\ \dots \\ \text{Bin}_N(M, p) \end{bmatrix}$$

and

$$\mathbf{Z}^\ell = \frac{\mathbf{D}^\ell \odot \mathbf{Z}^\ell}{p}$$

Note that on prediction (test) time, **dropout should not be used**, that is, the network should not activate hidden units at random, but instead should use all hidden units. Moreover, due to randomization, the error function is ill-defined and therefore it may not decrease in every iteration of gradient descent as expected.

```
[26]: x_space = np.linspace(0, 1, 100)[:, None]

def create_network(m: int, dropout: float = 0) -> nn.NeuralNetwork:
    return (
        nn.NeuralNetwork(
            nn.LinearLayer(1, m),
            nn.Dropout(dropout),
            nn.TanH(),
            nn.LinearLayer(m, 1),
            nn.Linear(),
        )
        if dropout > 0
    )
```

```

        else nn.NeuralNetwork(
            nn.LinearLayer(1, m),
            nn.TanH(),
            nn.LinearLayer(m, 1),
            nn.Linear(),
        )
    )

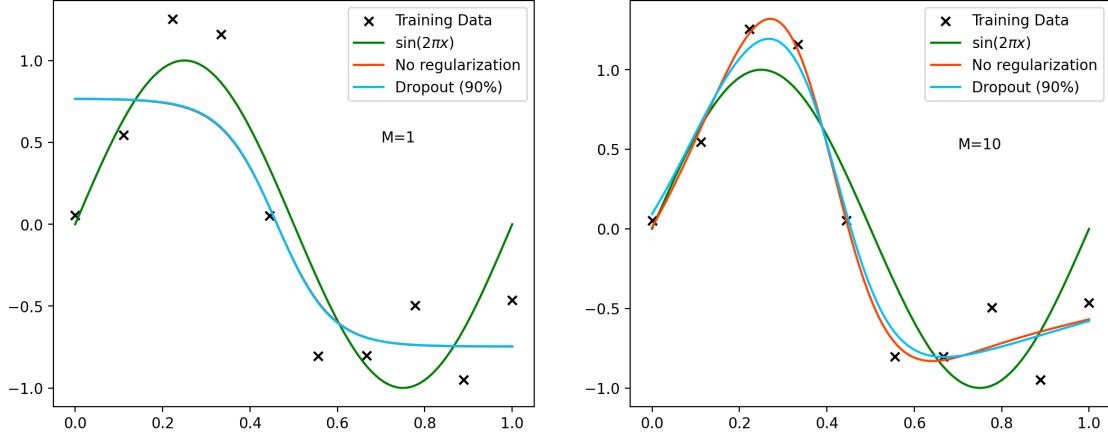
plt.figure(figsize=(20, 5))

for i, m in enumerate([1, 10]):
    model = create_network(m)
    model.fit(
        x_train[:, None],
        y_train[:, None],
        epochs=100000,
        loss=nn.SSELoss(),
        optimizer=nn.GradientDescent(learning_rate=0.01),
        verbose=False,
    )
    y = model(x_space)

    regularized_model = create_network(m, dropout=0.99)
    regularized_model.fit(
        x_train[:, None],
        y_train[:, None],
        epochs=100000,
        loss=nn.SSELoss(),
        optimizer=nn.GradientDescent(learning_rate=0.01),
        verbose=False,
    )
    y_regularized = regularized_model(x_space)

    plt.subplot(1, 3, i + 1)
    plt.scatter(x_train.ravel(), y_train.ravel(), marker="x", color="black")
    plt.plot(x_space, np.sin(2 * np.pi * x_space), color="green")
    plt.plot(x_space.ravel(), y.ravel(), color="orangered")
    plt.plot(x_space.ravel(), y_regularized.ravel(), color="deepskyblue")
    plt.annotate(f"M={m}", (0.7, 0.5))
    plt.legend(["Training Data", "$\\sin(2\\pi x)$", "No regularization", "Dropout (90%)"])

```



Why does dropout work? Since dropout randomly deactivates, in any given layer, a portion of the inputs, that means, intuitively, that the learning algorithm cannot rely on any feature, and so, it is forced to spread out the weights. To that end, it shrinks the squared norm of the weights. Note that dropout can be shown to be an adaptive form of ℓ_2 -regularization.

Batch Normalization

As discussed earlier, to facilitate learning, weights are initialized to have zero mean and small variance. As training progresses and the parameters are updated to different extents, the initial normalization is lost, which, in turn, slows down training and amplifies changes as the network becomes deeper. *Batch normalization* reestablishes these normalizations for every mini-batch of N training examples, on every layer ℓ . By making batch normalization part of the model architecture, we are able to use higher learning rates and pay less attention to the initialization parameters. Batch normalization additionally acts as a regularizer, reducing (and sometimes even eliminating) the need for Dropout. Batch normalization is usually applied on top of the activations $\alpha^{(\ell)}$ as follows:

$$\begin{aligned}\mu^{(\ell)} &= \frac{1}{N} \sum_{i=1}^N \alpha_i^{(\ell)} \\ \sigma^{(\ell)2} &= \frac{1}{m} \sum_{i=1}^N (\alpha_i^{(\ell)} - \mu^{(\ell)})^2 \\ \alpha_{i,norm}^{(\ell)} &= \frac{\alpha_i^{(\ell)} - \mu^{(\ell)}}{\sqrt{\sigma^{(\ell)2}} + \epsilon} \\ \hat{\alpha}_i^{(\ell)} &= \gamma^{(\ell)} \alpha_{i,norm}^{(\ell)} + \beta^{(\ell)}\end{aligned}$$

where $\gamma^{(\ell)}$ and $\beta^{(\ell)}$ are learnable parameters, thus allowing each layer to have a different distribution. In other words, during forward propagation, each neuron or hidden unit includes a batch normalization operator between the activations $\alpha^{(\ell)}$ and the nonlinear activation functions $h(\cdot)$.

However, the addition of the batch normalization operator, changes the derivation of backprop. During backward propagation, $\delta^{(\ell)} = \frac{\partial E_n}{\partial \alpha_i^{(\ell)}}$ should be derived using the chain rule as follows,

$$\frac{\partial E_n}{\partial \alpha_i^{(\ell)}} = \frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} \frac{\partial \alpha_{i,norm}^{(\ell)}}{\partial \alpha_i^{(\ell)}} + \frac{\partial E_n}{\partial \mu} \frac{\partial \mu}{\partial \alpha_i^{(\ell)}} + \frac{\partial E_n}{\partial \sigma^{(\ell)}} \frac{\partial \sigma^{(\ell)}}{\partial \alpha_i^{(\ell)}}$$

The chain rule results in a summation having three components. Let's start from the simpler terms, which are the second terms in the product of each component,

$$\frac{\partial \alpha_{i,norm}^{(\ell)}}{\partial \alpha_i^{(\ell)}} = \frac{1}{\sqrt{\sigma^{(\ell)2} + \epsilon}}, \quad \frac{\partial \mu^{(\ell)}}{\partial \alpha_i^{(\ell)}} = \frac{1}{m}, \quad \frac{\partial \sigma^{(\ell)2}}{\partial \alpha_i^{(\ell)}} = \frac{2(\alpha_i^{(\ell)} - \mu^{(\ell)})}{m}$$

then, let's move on to the first terms of the components,

$$\begin{aligned} \frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} &= \frac{\partial E_n}{\partial \hat{\alpha}_i^{(\ell)}} \frac{\partial \hat{\alpha}_i^{(\ell)}}{\partial \alpha_{i,norm}^{(\ell)}} = \frac{\partial E_n}{\partial \hat{\alpha}_i^{(\ell)}} \gamma^{(\ell)} \\ \frac{\partial E_n}{\partial \mu^{(\ell)}} &= \frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} \frac{\partial \alpha_{i,norm}^{(\ell)}}{\partial \mu^{(\ell)}} + \frac{\partial E_n}{\partial \sigma^{(\ell)2}} \frac{\partial \sigma^{(\ell)2}}{\partial \mu^{(\ell)}} \\ \frac{\partial \alpha_{i,norm}^{(\ell)}}{\partial \mu^{(\ell)}} &= \frac{-1}{\sqrt{\sigma^{(\ell)2} + \epsilon}} \\ \frac{\partial E_n}{\partial \sigma^{(\ell)2}} &= \frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} \frac{\partial \alpha_{i,norm}^{(\ell)}}{\partial \sigma^{(\ell)2}} = -\frac{1}{2} \sum_{i=1}^N (\alpha_i^{(\ell)} - \mu^{(\ell)}) (\sigma^{(\ell)2} + \epsilon)^{-1.5} \frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} \\ \frac{\partial \sigma^{(\ell)2}}{\partial \mu^{(\ell)}} &= -\frac{2}{m} \sum_{i=1}^N (\alpha_i^{(\ell)} - \mu^{(\ell)}) = -2 \left(\frac{1}{m} \sum_{i=1}^N \alpha_i^{(\ell)} - \frac{1}{m} \sum_{i=1}^N \mu^{(\ell)} \right) = -2 \left(\mu^{(\ell)} - \frac{m\mu^{(\ell)}}{m} \right) = 0 \end{aligned}$$

therefore,

$$\frac{\partial E_n}{\partial \mu^{(\ell)}} = \sum_{i=1}^N \frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} \frac{-1}{\sqrt{\sigma^{(\ell)2} + \epsilon}}$$

Finally, $\delta^{(\ell)}$ is obtained as follows,

$$\begin{aligned}
\delta^{(\ell)} &= \left(\frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} \frac{1}{\sqrt{\sigma^{(\ell)2} + \epsilon}} \right) + \left(\frac{1}{m} \sum_{j=1}^N \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} \frac{-1}{\sqrt{\sigma^{(\ell)2} + \epsilon}} \right) + \left(-\frac{1}{2} \sum_{j=1}^N (\alpha_j^{(\ell)} - \mu)(\sigma^{(\ell)2} + \epsilon)^{-1.5} \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} \frac{2(\alpha_i^{(\ell)} - \mu^{(\ell)})}{m} \right) \\
&= \left(\frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} \frac{1}{\sqrt{\sigma^{(\ell)2} + \epsilon}} \right) - \left(\sum_{j=1}^N \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} \frac{1}{m \sqrt{\sigma^{(\ell)2} + \epsilon}} \right) - \left(\sum_{j=1}^N (\alpha_j^{(\ell)} - \mu^{(\ell)}) (\sigma^{(\ell)2} + \epsilon)^{-1.5} \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} \frac{(\alpha_i^{(\ell)} - \mu^{(\ell)})}{m} \right) \\
&= \left(\frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} \frac{1}{\sqrt{\sigma^{(\ell)2} + \epsilon}} \right) - \left(\sum_{j=1}^N \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} \frac{1}{m \sqrt{\sigma^{(\ell)2} + \epsilon}} \right) - \left(\sum_{j=1}^N \frac{(\alpha_j^{(\ell)} - \mu^{(\ell)}) (\alpha_i^{(\ell)} - \mu^{(\ell)})}{m \sqrt{\sigma^{(\ell)2} + \epsilon}} \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} \right) \\
&= \frac{1}{m \sqrt{\sigma^{(\ell)2} + \epsilon}} \left(m \frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} - \sum_{j=1}^N \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} - \sum_{j=1}^N \frac{(\alpha_i^{(\ell)} - \mu^{(\ell)}) (\alpha_j^{(\ell)} - \mu^{(\ell)})}{\sqrt{\sigma^{(\ell)2} + \epsilon}} \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} \right) \\
&= \frac{1}{m \sqrt{\sigma^{(\ell)2} + \epsilon}} \left(m \frac{\partial E_n}{\partial \alpha_{i,norm}^{(\ell)}} - \sum_{j=1}^N \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} - \alpha_{i,norm}^{(\ell)} \sum_{j=1}^N \alpha_{j,norm}^{(\ell)} \frac{\partial E_n}{\partial \alpha_{j,norm}^{(\ell)}} \right)
\end{aligned}$$

The gradients for $\gamma^{(\ell)}$ and $\beta^{(\ell)}$ are obtained similarly,

$$\frac{\partial E_n}{\partial \gamma^{(\ell)}} = \sum_{i=1}^N \frac{\partial E_n}{\partial \hat{\alpha}_i^{(\ell)}} \frac{\partial \hat{\alpha}_i^{(\ell)}}{\partial \gamma^{(\ell)}} = \sum_{i=1}^N \frac{\partial E_n}{\partial \hat{\alpha}_i^{(\ell)}} \alpha_{i,norm}^{(\ell)}$$

and

$$\frac{\partial E_n}{\partial \beta^{(\ell)}} = \sum_{i=1}^N \frac{\partial E_n}{\partial \hat{\alpha}_i^{(\ell)}} \frac{\partial \hat{\alpha}_i^{(\ell)}}{\partial \beta^{(\ell)}} = \sum_{i=1}^N \frac{\partial E_n}{\partial \hat{\alpha}_i^{(\ell)}}$$

```
[28]: x_space = np.linspace(0, 1, 100)[:, None]

model = nn.NeuralNetwork(
    nn.LinearLayer(1, 10),
    nn.BatchNorm(),
    nn.Tanh(),
    nn.LinearLayer(10, 1),
    nn.Linear(),
)

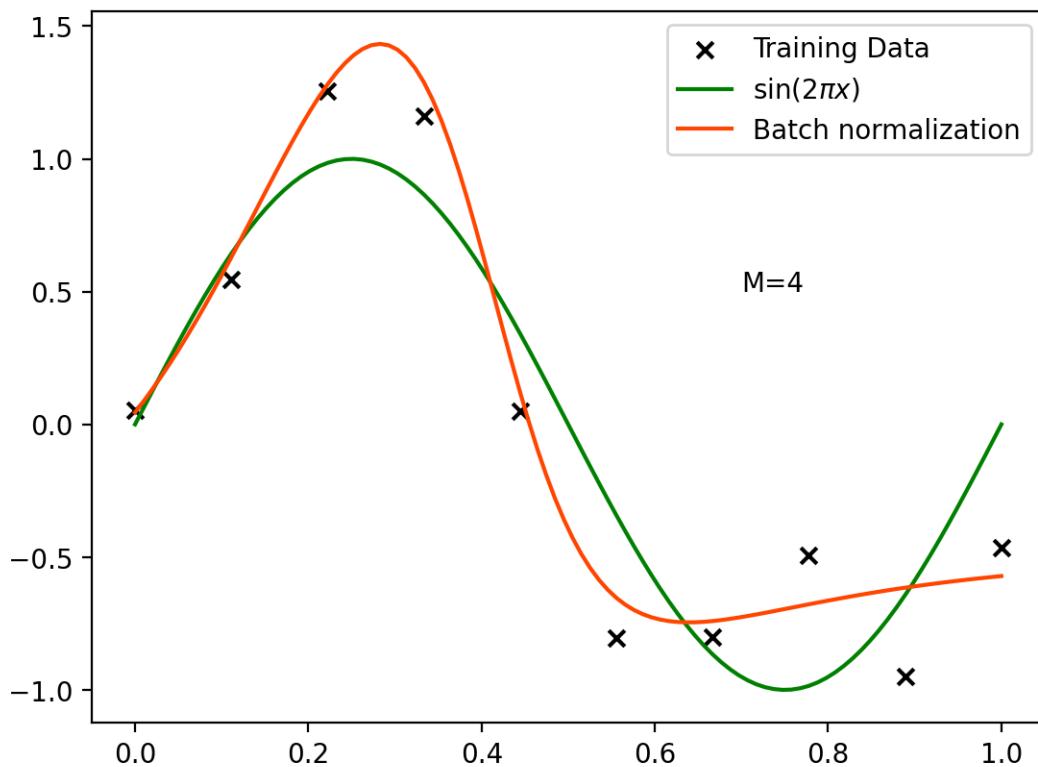
model.fit(
    x_train[:, None],
    y_train[:, None],
    epochs=10000,
    loss=nn.SSELoss(),
    optimizer=nn.GradientDescent(learning_rate=0.01),
    verbose=False,
)
```

```

y = model(x_space)

plt.scatter(x_train.ravel(), y_train.ravel(), marker="x", color="black")
plt.plot(x_space, np.sin(2 * np.pi * x_space), color="green")
plt.plot(x_space.ravel(), y.ravel(), color="orangered")
plt.annotate(f"M={4}", (0.7, 0.5))
plt.legend(["Training Data", "$\sin(2\pi x)$", "Batch normalization"])
plt.show()

```



5.5.1 Consistent Gaussian priors

Simple weight decay is affected by certain scaling properties of network mappings. A regularizer that is invariant to re-scaling of the weights and to shifts to biases, given a 2-layer neural network is defined as,

$$\frac{\lambda_1}{2} \sum_{w \in \mathcal{W}_1} w^2 + \frac{\lambda_2}{2} \sum_{w \in \mathcal{W}_2} w^2$$

where \mathcal{W}_1 denotes the weights of the first layer and \mathcal{W}_2 denotes the set of weights of the second layer and biases are excluded from the summations. The corresponding Gaussian prior for this regularizer takes the form

$$p(\mathbf{w}|\alpha_1, \alpha_2) \propto \left(-\frac{\alpha_1}{2} \sum_{w \in \mathcal{W}_1} w^2 - \frac{\alpha_2}{2} \sum_{w \in \mathcal{W}_2} w^2 \right)$$

Note that priors of this form are *improper*, that means they cannot be normalized, because bias parameters are unconstrained. Since improper priors lead to zero evidence in the Bayesian framework, it is common practice to include separate priors for the biases.

In the general case, weights can be divided into any number of groups \mathcal{W}_k , thus obtaining priors of the form,

$$p(\mathbf{w}|\alpha) \propto \left(-\frac{1}{2} \sum_k \alpha_k \|\mathbf{w}\|_k^2 \right)$$

where $\alpha = (\alpha_1, \dots, \alpha_k)$ and $\|\mathbf{w}\|_k^2 = \sum_{j \in \mathcal{W}_k} w_j^2$.

5.5.2 Early stopping

An alternative to regularization is the procedure of *early stopping*. For many algorithms used for network training, such as conjugate gradients, the error is a non-increasing function of the iteration index. However, the error measured on a validation set (independent data), often shows a decrease at first, followed by an increase as the network starts to over-fit. Training can thus be stopped at this point of smallest error with respect to the validation set in order to obtain good generalization performance.

Improving neural network performance guidelines

In order to achieve or surpass human-level performance, which can be considered as a proxy to optimal Bayes error, the model should minimize the error in the training set to be as close as possible to the error achieved by humans (avoidable bias). However, at the same time, the model should retain low variance, that is, low error on the validation or development set. In the first case, where the error in the training set is off by a large percentage compared to the error measured in humans, one should consider training a deeper model, using a better optimization algorithm or even alternative neural network architectures. On the other hand, when variance is high, the model may have overfitted, which can be dealt using regularization techniques, more training data or data augmentation to include invariances.

5.5.3 Invariances

Ideally, predictions should be unchanged or *invariant* under one or more transformations of the input variables. For example, in image classification tasks, such as digit recognition, the particular object should be assigned the same label irrespective of its position in the image (translation invariance) or of its size (scale invariance). Similar, in speech recognition, small levels of nonlinear warping along the time axis (assuming temporal ordering is preserved) should not change the interpretation of the signal.

Given a sufficiently large number of examples, an adaptive model can learn the invariance, even approximately. However, if the number of examples is limited, or there are several invariants, there is a number of alternative approaches for encouraging a model to exhibit the invariances:

1. Training set can be augmented to include replicas of training examples, transformed according to the desired invariances.
2. A regularization term can be added to the error function to penalize changes in the model output when the input is transformed, a technique called *tangent propagation*.
3. Extracting invariant features, thus building regression or classification systems that necessarily respect the invariances.
4. Build the invariance properties into the structure of the neural network, using local receptive fields and shared weights, such as convolutional neural networks.

5.5.6 Convolutional networks

Convolutional neural networks build invariance properties into the structure of the network and have been widely applied to image data. In general, image recognition may be performed using a fully connected neural network similar to the ones presented so far. Given sufficiently large training data, such a network could in principle yield a good solution and learn the appropriate invariances. However, typical neural networks ignore a key property of images, which is that nearby pixels are more strongly correlated than distance ones.

On the other hand, modern approaches to computer vision exploit this property by extracting local features that depend only on small subregions of the image. Information from such features are then merged in later stages of processing in order to detect higher-order features. Moreover, local features that are useful in one region of the image are likely to be useful in other regions of the image, for instance if the object of interest is translated.

These notions are incorporated into convolutional neural networks through three mechanisms:

1. Local receptive fields
2. Weight sharing
3. Subsampling

The convolution operation is one of the fundamental building blocks of the convolutional neural networks. As a motivating example, let's perform edge detection on an image in order to get a grasp of the convolution operation. Consider an input grayscale image of Dr. Freeman (the silent protagonist of Half-Life).

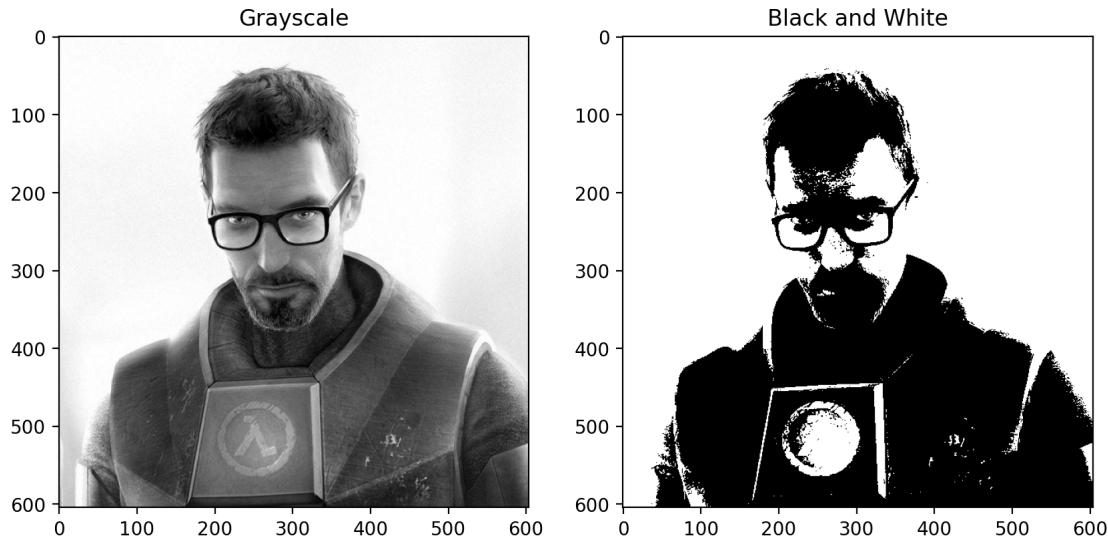
```
[29]: from PIL import Image

im = Image.open("../images/gordon_freeman.jpg").convert("L")
im_array = np.asarray(im)

THRESHOLD = 125
im_array = np.where(im_array > THRESHOLD, 255, np.where(im_array <= THRESHOLD, 0, im_array))

plt.figure(figsize=(10, 10))
plt.subplot(1, 2, 1)
plt.imshow(im, cmap="gray")
plt.title("Grayscale")
plt.subplot(1, 2, 2)
plt.imshow(im_array, cmap="gray")
```

```
plt.title("Black and White")
plt.show()
```



Each grayscale image comprises a set of pixel intensity values represented as a 2-dimensional array of integers in $[0, 255]$, where 0 represents completely black and 255 completely white. In order to make subsequent edge detection more apparent, we further transform the input image to black and white using thresholding on intensity value 125. To that end, the image of Dr. Freeman is represented by the following matrix:

[30]: im_array

```
[30]: array([[255, 255, 255, ..., 255, 255, 255],
   [255, 255, 255, ..., 255, 255, 255],
   [255, 255, 255, ..., 255, 255, 255],
   ...,
   [255, 255, 255, ..., 0, 0, 0],
   [255, 255, 255, ..., 0, 0, 0],
   [255, 255, 255, ..., 0, 0, 0]], dtype=uint8)
```

Then, in order to detect edges, we may construct a small matrix (called a filter or a kernel in computer vision literature) and convolve it with the image of Dr. Freeman. If we wish to detect vertical edges, then the filter may have the following form,

$$\begin{bmatrix} 1 & 0 & -1 \\ 1 & 0 & -1 \\ 1 & 0 & -1 \end{bmatrix}$$

or, in case of horizontal edges, it may take the form,

$$\begin{bmatrix} 1 & 1 & 1 \\ 0 & 0 & 0 \\ -1 & -1 & -1 \end{bmatrix}$$

The convolution of the image and the filter may be implemented as follows:

```
[31]: def convolve2D(image: np.ndarray, filter: np.ndarray, padding: int = 0, strides:
    ↪ int = 1) -> np.ndarray:
    assert padding >= 0, "Padding cannot be negative"
    assert strides > 0, "Stride cannot be zero or negative"

    n, m = image.shape
    f, k = filter.shape

    # shape of output convolution
    output_n = int(((n - f + 2 * padding) / strides) + 1)
    output_m = int(((m - k + 2 * padding) / strides) + 1)
    output = np.zeros((output_n, output_m), dtype=np.uint8)

    # apply padding
    if padding > 0:
        padded_image = np.zeros((n + padding * 2, m + padding * 2))
        padded_image[padding:-padding, padding:-padding] = image
    else:
        padded_image = image

    for i in range(output_n):
        for j in range(output_m):
            output[i, j] = (filter * padded_image[i * strides : i * strides + ↪
                ↪ f, j * strides : j * strides + f]).sum()

    return output
```

The following figure depicts the original black and white image along the horizontal and vertical edges detected by the filters.

```
[32]: horizontal_filter = np.array(
    [
        [1, 1, 1],
        [0, 0, 0],
        [-1, -1, -1],
    ]
)

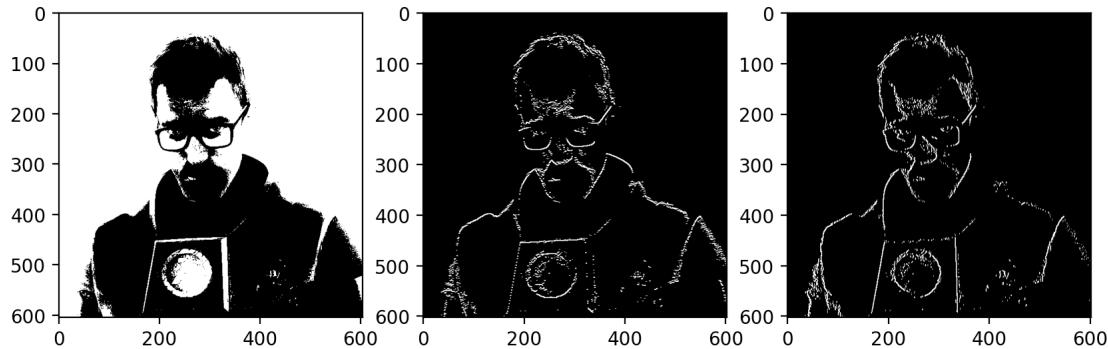
vertical_filter = np.array(
    [
        [1, 0, -1],
```

```

        [1, 0, -1],
        [1, 0, -1],
    ]
)

plt.figure(figsize=(10, 10))
plt.subplot(1, 3, 1)
plt.imshow(im_array, cmap="gray")
plt.subplot(1, 3, 2)
plt.imshow(convolve2D(im_array, horizontal_filter), cmap="gray")
plt.subplot(1, 3, 3)
plt.imshow(convolve2D(im_array, vertical_filter), cmap="gray")
plt.show()

```



Moreover, padding may be used on the original image before convolution in order for the output size to be the same as the input size.

```
[33]: print(
    f"Original size: {im_array.shape}, Output size (no padding): {convolve2D(im_array, horizontal_filter).shape}, Output size (padding): {convolve2D(im_array, horizontal_filter, 1).shape}"
)
```

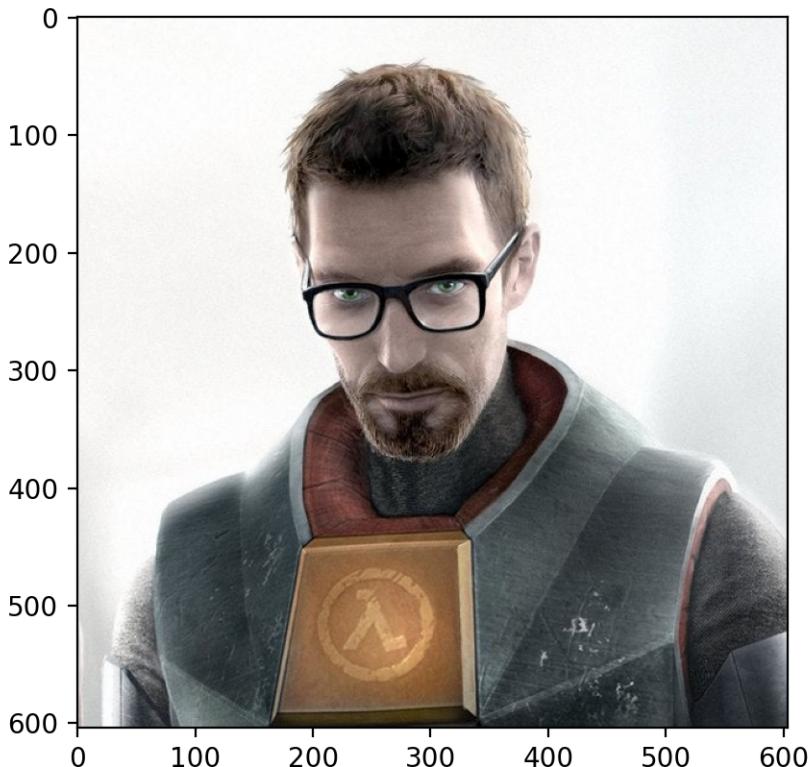
Original size: (604, 604), Output size (no padding): (602, 602), Output size (padding): (604, 604)

These filters detect or emphasize edges having horizontal or vertical orientation. On the other hand, there are numerous filters developed in the image processing literature. To that end, the idea behind convolutional neural networks is to learn such filters that detect useful local features (e.g. edges) over the input images. Thus, the filters in a convolutional layer are represented using the following parametric form:

$$\begin{bmatrix} w_1 & w_2 & w_3 \\ w_4 & w_5 & w_6 \\ w_7 & w_8 & w_9 \end{bmatrix}$$

In the convolutional layer the units are organized into planes, each of which is called a feature map. Units in a feature map take inputs only from a small subregion of the image, and all of the units in a feature map are constrained to share the same weight values. The convolutional layers can also learn filters or feature maps over multiple color channels. For instance, consider the RGB version of Dr. Freeman picture:

```
[34]: from PIL import Image  
  
im = Image.open("../images/gordon_freeman.jpg")  
im_array = np.asarray(im)  
  
plt.imshow(im, cmap="gray")  
plt.show()
```



Note that the image matrix has three channels in the third dimension.

```
[35]: im_array.shape
```

```
[35]: (604, 604, 3)
```

The convolution over multiple color channels is similar to the grayscale one:

```
[37]: def convolve3D(image: np.ndarray, filter: np.ndarray, padding: int = 0, strides: int = 1) -> np.ndarray:
    assert padding >= 0, "Padding cannot be negative"
    assert strides > 0, "Stride cannot be zero or negative"
    assert image.shape[2] == filter.shape[2], "Image and filter should have the same number of channels"

    n, m, nc = image.shape
    f, k, nc = filter.shape

    # shape of output convolution
    output_n = int(((n - f + 2 * padding) / strides) + 1)
    output_m = int(((m - k + 2 * padding) / strides) + 1)
    output = np.zeros((output_n, output_m), dtype=np.uint8)

    # apply padding
    if padding > 0:
        padded_image = np.zeros((n + padding * 2, m + padding * 2, nc))
        padded_image[padding:-padding, padding:-padding, :] = image
    else:
        padded_image = image

    for i in range(output_n):
        for j in range(output_m):
            output[i, j] = (
                filter * padded_image[i * strides : i * strides + f, j * strides : j * strides + f, :]
            ).sum()

    return output
```

The following figure depicts the original RGB image along with the horizontal and vertical edges detected by the 3-channel filters.

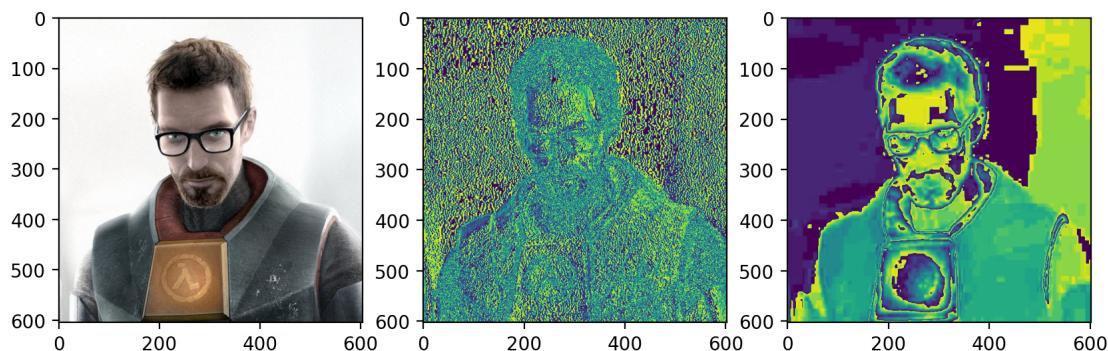
```
[38]: horizontal_filter = np.array(
    [
        [
            [1, 1, 1],
            [0, 0, 0],
            [-1, -1, -1],
        ],
        [
            [1, 1, 1],
            [0, 0, 0],
            [-1, -1, -1],
        ],
        [
    ]
```

```

        [1, 1, 1],
        [0, 0, 0],
        [-1, -1, -1],
    ],
]
)

vertical_filter = np.array(
[
[
    [
        [1, 0, -1],
        [1, 0, -1],
        [1, 0, -1],
    ],
[
        [
            [1, 0, -1],
            [1, 0, -1],
            [1, 0, -1],
        ],
[
            [
                [1, 0, -1],
                [1, 0, -1],
                [1, 0, -1],
            ],
        ],
    ],
]
)
plt.figure(figsize=(10, 10))
plt.subplot(1, 3, 1)
plt.imshow(im_array)
plt.subplot(1, 3, 2)
plt.imshow(convolve3D(im_array, horizontal_filter))
plt.subplot(1, 3, 3)
plt.imshow(convolve3D(im_array, vertical_filter))
plt.show()

```



For RGB images the respective convolutional layers learn filters having multiple channels (usually three), by representing them as tensors.

Convolutional Layer A single convolutional layer may take as input an RGB image and convolve it with a number of filters as depicted in the following figure:

Summary of the notation:

Symbol	Description
$n_h^{[l-1]}$	input height
$n_h^{[l]}$	output height
$n_w^{[l-1]}$	input width
$n_w^{[l]}$	output width
$f^{[l]}$	filter size
$p^{[l]}$	padding
$s^{[l]}$	stride
$n_c^{[l]}$	number of filters

Each filter convolution inside the layer yields an output matrix of dimension $\left(\frac{n_h^{[0]} - f^{[0]} + 2*p^{[0]}}{s^{[0]}} + 1\right) \times \left(\frac{n_w^{[0]} - f^{[0]} + 2*p^{[0]}}{s^{[0]}} + 1\right)$. Then the bias parameter is added to the resulting matrix and the result is passed through the activation function g . The final matrices across all $n_c^{[0]}$ filters of the layer are stacked together to yield a tensor of dimension $\left(\frac{n_h^{[0]} - f^{[0]} + 2*p^{[0]}}{s^{[0]}} + 1\right) \times \left(\frac{n_w^{[0]} - f^{[0]} + 2*p^{[0]}}{s^{[0]}} + 1\right) \times n_c^{[0]}$ (represented by the 3-dimensional rectangle). The parameter matrix $\mathbf{W}^{[l]}$ of the convolutional layer has dimension $f^{[l]} \times f^{[l]} \times n_c^{[l-1]} \times n_c^{[l]}$.

Why Convolutions?

Parameter Sharing: A feature detector that is useful in one part of the image is probably useful in another part of the image. Therefore filter parameters derived during a learning process are used to detect features or edges over many parts of the image.

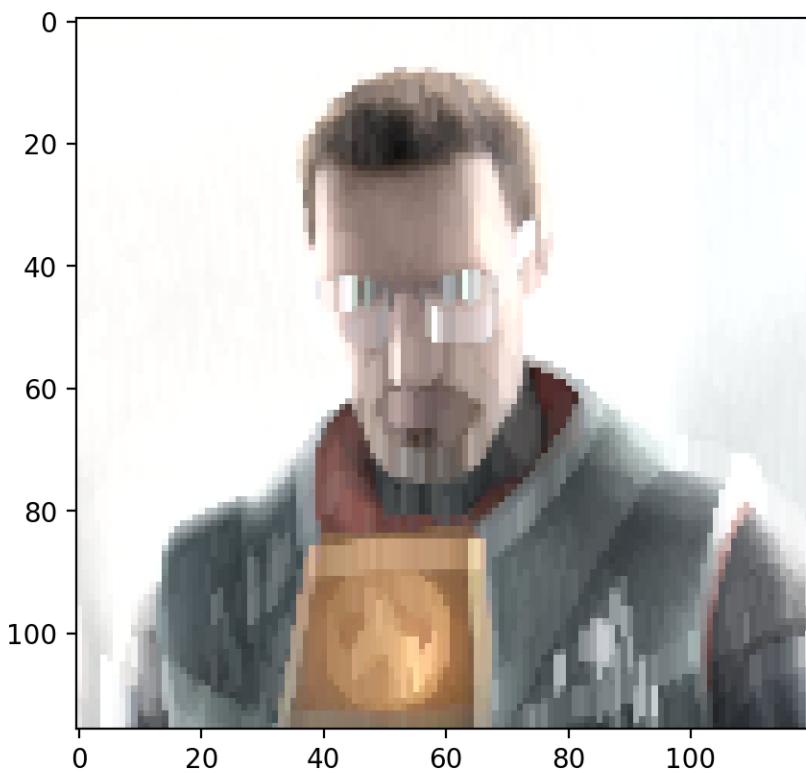
Sparsity of connections: In each layer, each output value depends only on a small number of inputs, that is, adjacent pixel values.

Both of these properties allows us to construct neural networks that have a lot fewer parameters than fully connected architectures. Moreover, fewer parameters can be learned using smaller training sets in contrast to the corresponding fully connected neural networks. Moreover, convolutional layers are effective at capturing translation invariance, which means that an image shifted by a few pixels should result in pretty similar features and to that end, classified in a similar way.

Pooling Layers Pooling layers perform a mathematical operation, usually an aggregation, over sub-regions of an image. For instance, max pooling computes the maximum pixel intensity of each sub-region of the input image. Thus, given a 4×4 image a max pooling layer of size 2 and stride 2, should yield the following:

Pooling layers are applied on each channel independently, thus computing an output tensor the same dimension. In the context of edge detection, a max pooling layer may intuitively keep stronger or more apparent edges. However, in practice, pooling is used because it is shown experimentally that works well and not because we have a concrete proof about its importance. There are other kinds of pooling, except max pooling, like average pooling which averages the pixel intensities of each region instead of computing the maximum. Note that pooling have no learnable parameters only a couple of hyperparameters.

```
[39]: pooled = nn.MaxPooling(pool_size=(25, 5), stride=5).forward(im_array[None, :])  
plt.imshow(pooled[0].astype(int))  
plt.show()
```



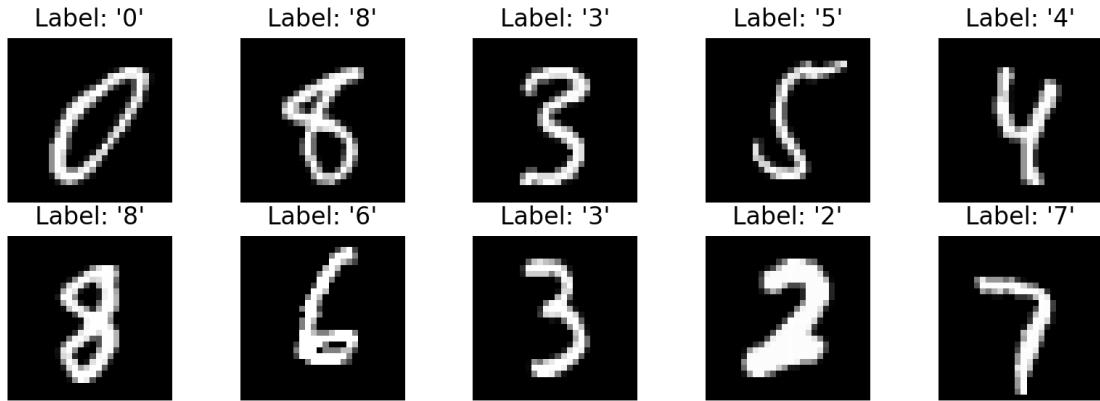
LeNet-5 MNIST

```
[46]: images, labels = load_mnist_dataset(500)  
  
random_indices = [random.randint(0, images.shape[0]) for _ in range(10)]  
  
plt.figure(figsize=(10, 5))  
  
for i, index in enumerate(random_indices):  
    image = images[index]
```

```

plt.subplot(int(len(random_indices) / 5) + 1, 5, i + 1)
plt.imshow(image, cmap=plt.cm.gray)
plt.title(f"Label: '{labels[index]}'")
plt.axis("off")

```



[47]:

```

images = (images - images.mean(axis=(1, 2), keepdims=True)) / images.
    std(axis=(1, 2), keepdims=True)

```

[48]:

```

encoder = OneHotEncoder()
one_hot_labels = encoder.encode(labels)

images_train, images_test, one_hot_labels_train, one_hot_labels_test =
    train_test_split(
        images, one_hot_labels, test_size=0.2, stratify=one_hot_labels
    )

```

[49]:

```
images[0].shape
```

[49]:

```
(28, 28)
```

[58]:

```

model = nn.NeuralNetwork(
    nn.ConvLayer(1, 6, kernel_size=(5, 5), padding=2),
    nn.ReLU(),
    nn.MaxPooling(pool_size=(2, 2), stride=2),
    nn.ConvLayer(6, 16, kernel_size=(5, 5)),
    nn.ReLU(),
    nn.MaxPooling(pool_size=(2, 2), stride=2),
    nn.Flatten(),
    nn.LinearLayer(400, 120),
    nn.ReLU(),
    nn.LinearLayer(120, 84),
    nn.ReLU(),

```

```
        nn.LinearLayer(84, 10),  
        nn.Softmax(),  
)
```

```
[60]: model.fit(  
    images_train[:, :, :, None],  
    one_hot_labels_train,  
    epochs=50,  
    batch_size=10,  
    loss=nn.CrossEntropyLoss(),  
    optimizer=nn.AdamW(learning_rate=0.00001, weight_decay=1e-2),  
)
```

```
-- Epoch 1 ---  
Cost: 1.598538332796852  
-- Epoch 3 ---  
Cost: 1.3129573812941102  
-- Epoch 5 ---  
Cost: 1.3086841008174646  
-- Epoch 7 ---  
Cost: 0.5296930303635164  
-- Epoch 9 ---  
Cost: 0.24401742821367545  
-- Epoch 11 ---  
Cost: 1.2518014840898435  
-- Epoch 13 ---  
Cost: 0.1519895430574175  
-- Epoch 15 ---  
Cost: 0.10023537642811078  
-- Epoch 17 ---  
Cost: 0.5512170802002273  
-- Epoch 19 ---  
Cost: 0.4524269162805252
```

```
[61]: train_predictions = np.argmax(model(images_train[:, :, :, None]), axis=1)  
print(classification_report(encoder.decode(one_hot_labels_train),  
                           train_predictions, zero_division=0))
```

	precision	recall	f1-score	support
0	0.95	0.97	0.96	39
1	0.94	0.96	0.95	46
2	0.97	0.88	0.93	42
3	0.90	0.93	0.91	40
4	1.00	0.72	0.84	39
5	0.88	0.81	0.84	36
6	0.83	1.00	0.90	38
7	0.82	0.88	0.85	41

8	0.84	0.82	0.83	39
9	0.76	0.85	0.80	40
accuracy			0.88	400
macro avg	0.89	0.88	0.88	400
weighted avg	0.89	0.88	0.88	400

```
[62]: test_predictions = np.argmax(model(images_test[:, :, :, None]), axis=1)
print(classification_report(encoder.decode(one_hot_labels_test), test_predictions, zero_division=0))
```

	precision	recall	f1-score	support
0	0.82	0.90	0.86	10
1	1.00	1.00	1.00	11
2	1.00	0.50	0.67	10
3	0.60	0.60	0.60	10
4	0.88	0.70	0.78	10
5	0.62	0.89	0.73	9
6	1.00	1.00	1.00	10
7	0.89	0.80	0.84	10
8	0.70	0.70	0.70	10
9	0.69	0.90	0.78	10
accuracy			0.80	100
macro avg	0.82	0.80	0.80	100
weighted avg	0.82	0.80	0.80	100

5.6 Mixture Density Networks

Consider a dataset generated by sampling a variable x uniformly over the interval $[0, 1]$ and the corresponding target values t by computing the function $f(x) = x + 0.3 \sin(2\pi x)$ and adding uniform noise over the interval $[-0.1, 0.1]$. The inverse dataset is obtained by exchanging the roles of x and t . Then, by training a 2-layer neural network having 6 hidden units and a single linear output unit, we can see that it leads to a very poor model for the highly non-Gaussian inverse problem. That is because least squares corresponds to maximum likelihood under a Gaussian assumption.

```
[66]: x, y = generate_toy_data(lambda x: x + 0.3 * np.sin(2 * np.pi * x),
                             sample_size=300, std=0.1, uniform=True)

model_xy = create_network(6)

model_xy.fit(x[:, None], y[:, None], epochs=100000, loss=nn.SSELoss(),
             verbose=False)

model_yx = create_network(6)
```

```

model_yx.fit(
    y[:, None],
    x[:, None],
    epochs=100000,
    optimizer=nn.GradientDescent(learning_rate=0.5),
    loss=nn.SSELoss(),
    verbose=False,
)

```

```

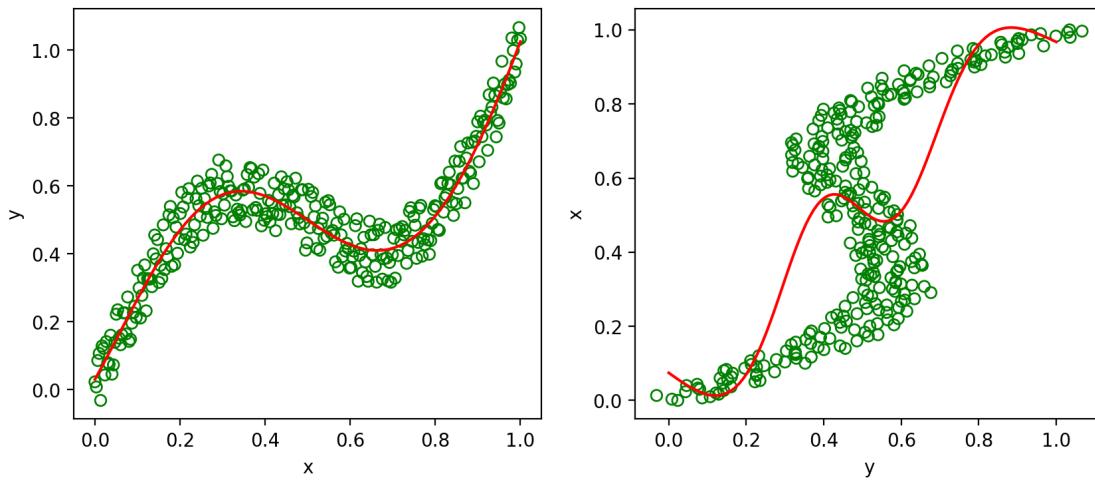
[67]: x_space = np.linspace(0, 1, 100)[:, None]
y_space = np.linspace(0, 1, 100)[:, None]

plt.figure(figsize=(10, 4))

plt.subplot(1, 2, 1)
plt.scatter(x, y, facecolors="none", edgecolors="green")
plt.plot(x_space, model_xy.predict(x_space), color="red")
plt.xlabel("x")
plt.ylabel("y")

plt.subplot(1, 2, 2)
plt.scatter(y, x, facecolors="none", edgecolors="green")
plt.plot(y_space, model_yx.predict(y_space), color="red")
plt.xlabel("y")
plt.ylabel("x")
plt.show()

```



We therefore seek a general framework for modelling conditional probability distributions. This can be achieved by using a mixture model for $p(\mathbf{t}|\mathbf{x})$ in which both the mixing coefficients as well as the component densities are parametric functions of the input \mathbf{x} , giving rise to the *mixture density*

network.

Any mixture of distributions may be used for the components, such as Bernoulli if the target variables are binary, however, we shall develop the model explicitly for Gaussian components, so that,

$$p(\mathbf{t}|\mathbf{x}) = \sum_{k=1}^K \pi_k(\mathbf{x}) \mathcal{N}(\mathbf{t}|\mu_k(\mathbf{x}), \sigma_k^2(\mathbf{x})\mathbf{I})$$

which is an example of a *heteroscedastic* model specialized to the case of isotropic covariances for the components.

The partial derivatives with respect to the mixing coefficients are obtained by

$$\begin{aligned} \frac{\partial E_n}{\partial a_j^\pi} &= -\frac{\partial}{\partial a_j^\pi} \ln \left\{ \sum_{k=1}^K \pi_k \mathcal{N}_{nk} \right\} \\ &= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \sum_{k=1}^K \frac{\partial \pi_k}{\partial a_j^\pi} \mathcal{N}_{nk} \\ &= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \sum_{k=1}^K \pi_j (I_{kj} - \pi_k) \mathcal{N}_{nk} \\ &= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \left(\pi_j \mathcal{N}_{jk} - \pi_j \sum_{k=1}^K \pi_k \mathcal{N}_{nk} \right) \\ &= \pi_j - \frac{\pi_j \mathcal{N}_{jk}}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \\ &= \pi_j - \gamma_{nj} \end{aligned}$$

Note that we use a_j^π instead of a_k^π for the subscript denoting the j component in order to avoid confusion with the summation subscript k . Thus, by changing the subscript back to k after the proof, we arrive at the same result presented in (5.154), that is, $\frac{\partial E_n}{\partial a_k^\pi} = \pi_k - \gamma_{nk}$.

The partial derivatives with respect to the component means are obtained by

$$\begin{aligned}
\frac{\partial E_n}{\partial \mathbf{a}_k^\mu} &\stackrel{(5.152)}{=} \frac{\partial E_n}{\partial \mu_k} \\
&= -\frac{\partial}{\partial \mu_k} \ln \left\{ \sum_{k=1}^K \pi_k \mathcal{N}_{nk} \right\} \\
&= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \frac{\partial}{\partial \mu_k} \pi_k \mathcal{N}_{nk} \\
&= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \frac{\partial}{\partial \mu_k} \left\{ -\frac{1}{2} (\mathbf{t}_n - \mu_k)^T (\sigma_k^2 \mathbf{I})^{-1} (\mathbf{t}_n - \mu_k) \right\} \\
&= -\frac{\pi_k \mathcal{N}_{nk}}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \left(-\frac{1}{2} \right) \left(-2 \frac{1}{\sigma_k^2} \mathbf{I} (\mathbf{t}_n - \mu_k) \right) \\
&= \frac{\pi_k \mathcal{N}_{nk}}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \frac{\mu_k - \mathbf{t}_n}{\sigma_k^2} \mathbf{I} \\
&\stackrel{(5.154)}{=} \gamma_{nk} \frac{\mu_k - \mathbf{t}_n}{\sigma_k^2} \mathbf{I}
\end{aligned}$$

Thus, for a particular dimension l , the final derivative would be,

$$\frac{\partial E_n}{\partial a_{kl}^\mu} = \gamma_{nk} \frac{\mu_{kl} - t_{nl}}{\sigma_k^2}$$

The partial derivatives with respect to the component of variances are obtained by

$$\begin{aligned}
\frac{\partial E_n}{\partial a_k^\sigma} &= -\frac{\partial}{\partial a_k^\sigma} \ln \left\{ \sum_{k=1}^K \pi_k \mathcal{N}_{nk} \right\} \\
&= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \frac{\partial}{\partial a_k^\sigma} \pi_k \mathcal{N}_{nk} \\
&= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \pi_k \frac{\partial}{\partial a_k^\sigma} \frac{1}{(2\pi)^{D/2} |\sigma_k \mathbf{I}|^{1/2}} \exp \left\{ -\frac{1}{2} (\mathbf{t}_n - \mu_k)^\top (\sigma_k \mathbf{I})^{-1} (\mathbf{t}_n - \mu_k) \right\} \\
&\stackrel{|\sigma_k \mathbf{I}| = \sigma_k^D}{=} -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \pi_k \frac{\partial}{\partial a_k^\sigma} \frac{1}{(2\pi)^{D/2} \sigma_k^{D/2}} \exp \left\{ -\frac{1}{2} (\mathbf{t}_n - \mu_k)^\top (\sigma_k \mathbf{I})^{-1} (\mathbf{t}_n - \mu_k) \right\} \\
&= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \pi_k \left[\frac{1}{(2\pi)^{D/2}} \frac{\partial}{\partial a_k^\sigma} \frac{1}{\sigma_k^{D/2}} \exp \left\{ -\frac{1}{2} (\mathbf{t}_n - \mu_k)^\top (\sigma_k \mathbf{I})^{-1} (\mathbf{t}_n - \mu_k) \right\} + \frac{1}{(2\pi)^{D/2} \sigma_k^{D/2}} \exp \left\{ -\frac{1}{2} (\mathbf{t}_n - \mu_k)^\top (\sigma_k \mathbf{I})^{-1} (\mathbf{t}_n - \mu_k) \right\} \right] \\
&= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \pi_k \left[\frac{-D}{2\sigma_k} \mathcal{N}_{nk} + \mathcal{N}_{nk} \frac{\partial}{\partial a_k^\sigma} \left(-\frac{1}{2} (\mathbf{t}_n - \mu_k)^\top (\sigma_k \mathbf{I})^{-1} (\mathbf{t}_n - \mu_k) \right) \right] \\
&= -\frac{1}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \pi_k \mathcal{N}_{nk} \left[-\frac{D}{2\sigma_k} + \frac{\partial}{\partial a_k^\sigma} \left(-\frac{1}{2} (\mathbf{t}_n - \mu_k)^\top (\sigma_k \mathbf{I})^{-1} (\mathbf{t}_n - \mu_k) \right) \right] \\
&= -\frac{\pi_k \mathcal{N}_{nk}}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \left[-\frac{D}{2\sigma_k} + \frac{\partial}{\partial a_k^\sigma} \left(-\frac{1}{2} \frac{\|\mathbf{t}_n - \mu_k\|^2}{\sigma_k} \mathbf{I} \right) \right] \\
&= -\frac{\pi_k \mathcal{N}_{nk}}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \left[-\frac{D}{2\sigma_k} + \frac{1}{2} \frac{\|\mathbf{t}_n - \mu_k\|^2}{\sigma_k^2} \mathbf{I} \right] \\
&= \frac{\pi_k \mathcal{N}_{nk}}{\sum_{k=1}^K \pi_k \mathcal{N}_{nk}} \left[\frac{D}{2\sigma_k} - \frac{1}{2} \frac{\|\mathbf{t}_n - \mu_k\|^2}{\sigma_k^2} \mathbf{I} \right] \\
&= \gamma_{nk} \left[\frac{D}{\sigma_k} - \frac{\|\mathbf{t}_n - \mu_k\|^2}{\sigma_k^2} \mathbf{I} \right]
\end{aligned}$$

```
[103]: model = nn.NeuralNetwork(
    nn.LinearLayer(1, 5), nn.Tanh(), nn.LinearLayer(5, 9), nn.Concat([nn.
    ↪Softmax(), nn.Linear(), nn.Exp()]))
)

model.fit(
    y[:, None],
    x[:, None],
    epochs=10000,
    batch_size=50,
    loss=nn.GaussianNLLoss(n_components=3),
    optimizer=nn.AdamW(learning_rate=0.0001, weight_decay=1e-2),
)
```

-- Epoch 1 --
Cost: 56.13401004150711

```
-- Epoch 1001 ---
Cost: -12.960075807796274
-- Epoch 2001 ---
Cost: -17.888693038278074
-- Epoch 3001 ---
Cost: -25.77117031181849
-- Epoch 4001 ---
Cost: -42.193536667020155
-- Epoch 5001 ---
Cost: -42.774433858274755
-- Epoch 6001 ---
Cost: -44.47439846519983
-- Epoch 7001 ---
Cost: -55.262623240038444
-- Epoch 8001 ---
Cost: -46.64232798438148
-- Epoch 9001 ---
Cost: -46.8022878753674
```

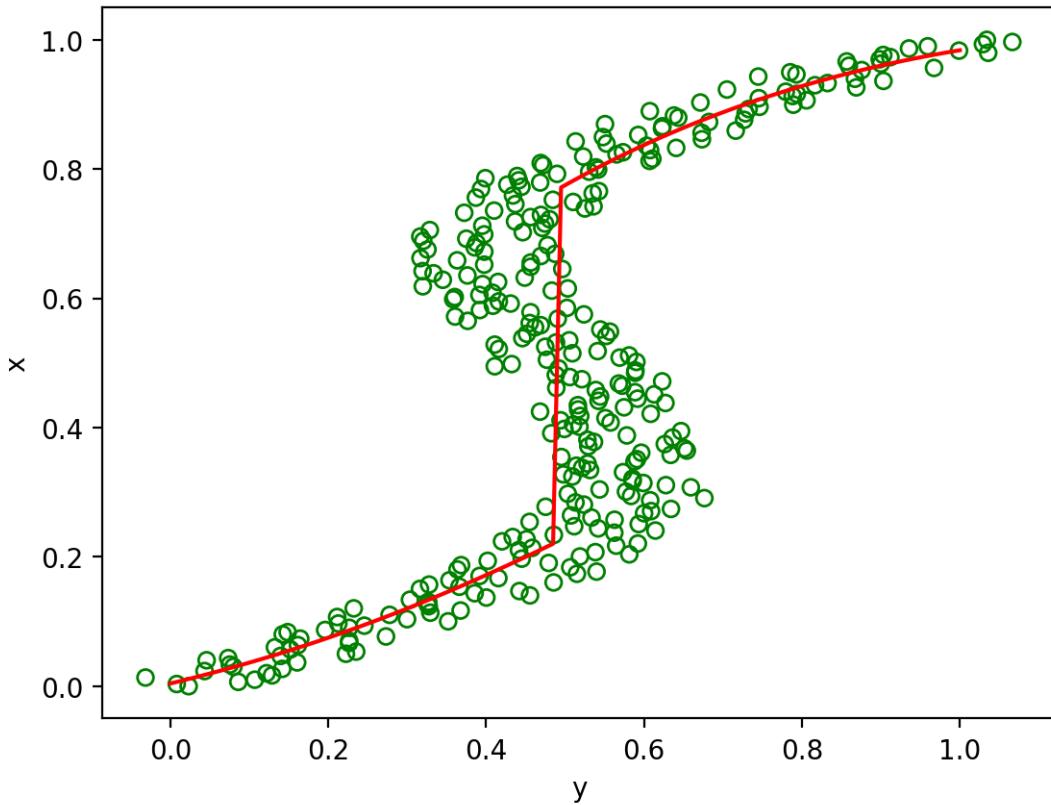
Once the mixture density network has been trained, it can predict the conditional density function of the target data for any given value of the input vector. For many problems we might be interested instead in finding one specific value for the output vector. The most *likely* value for the output vector, for a given input vector \mathbf{x} is given by the maximum of the conditional density $p(\mathbf{t}|\mathbf{x})$. Since this density is represented by a mixture model, the location of its global maximum is a problem of non-linear optimization. For applications where speed is important, a good approximation is to take the mean $\mu_i(\mathbf{x})$ for the largest central value,

$$\max_i \left\{ \frac{\pi_i(\mathbf{x})}{\sigma_i(\mathbf{x})^c} \right\}$$

```
[108]: densities = model.predict(y_space)
pi, mu, sigma = np.array_split(densities, 3, axis=1)

predictions = np.take_along_axis(mu, (pi / sigma).argmax(axis=1)[:, None], axis=1)

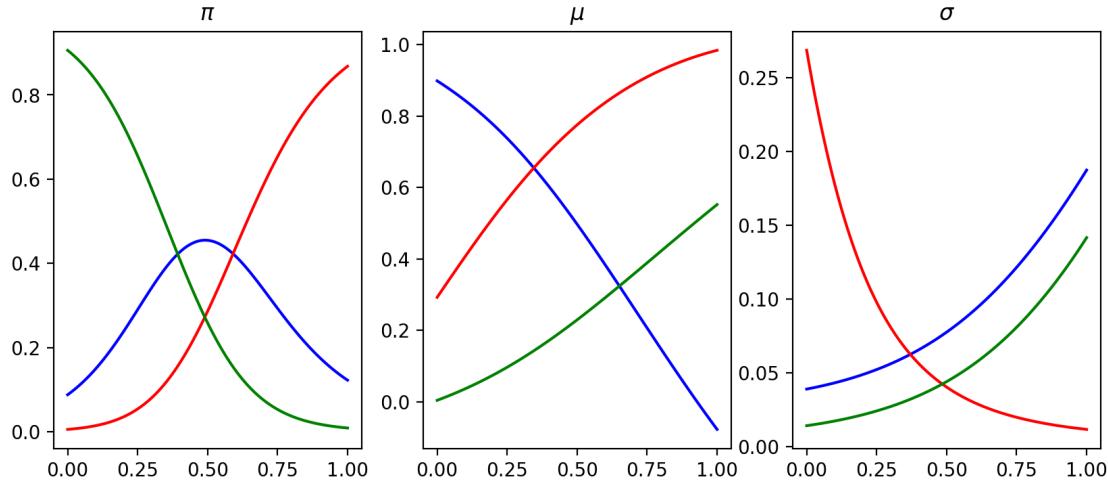
plt.scatter(y, x, facecolors="none", edgecolors="green")
plt.plot(y_space, predictions, color="red")
plt.xlabel("y")
plt.ylabel("x")
plt.show()
```



```
[105]: plt.figure(figsize=(10, 4))
plt.subplot(1, 3, 1)
plt.plot(y_space, pi[:, 0], color="blue")
plt.plot(y_space, pi[:, 1], color="red")
plt.plot(y_space, pi[:, 2], color="green")
plt.title("$\pi$")

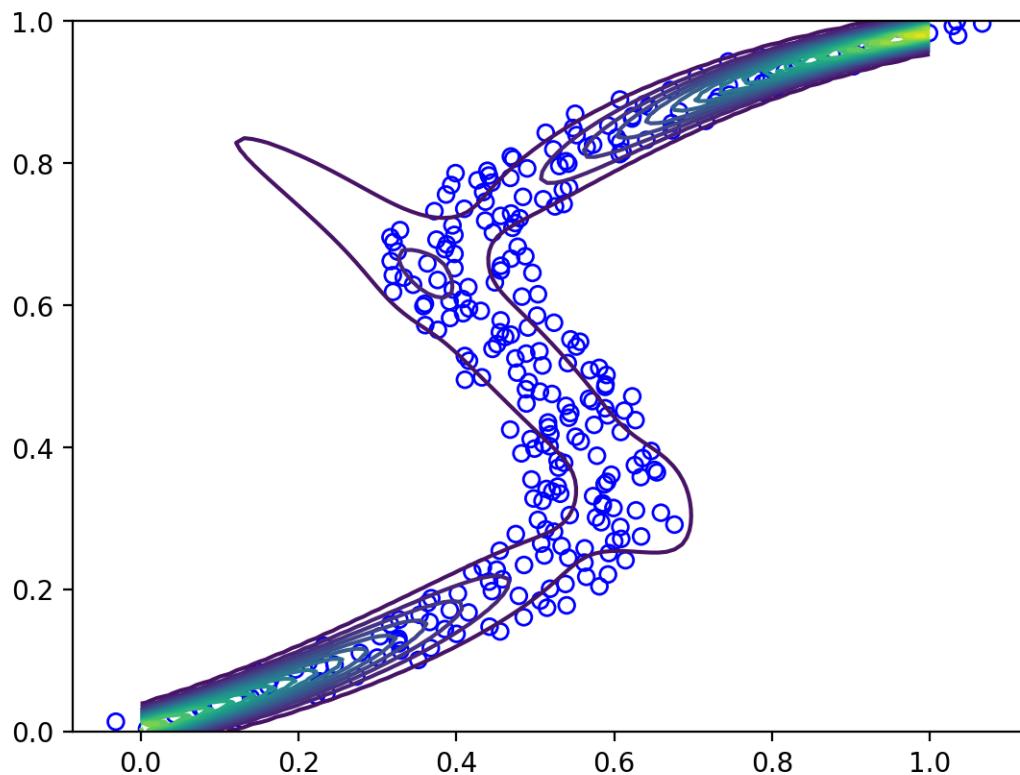
plt.subplot(1, 3, 2)
plt.plot(y_space, mu[:, 0], color="blue")
plt.plot(y_space, mu[:, 1], color="red")
plt.plot(y_space, mu[:, 2], color="green")
plt.title("$\mu$")

plt.subplot(1, 3, 3)
plt.plot(y_space, sigma[:, 0], color="blue")
plt.plot(y_space, sigma[:, 1], color="red")
plt.plot(y_space, sigma[:, 2], color="green")
plt.title("$\sigma$")
plt.show()
```



```
[110]: xx, yy = np.meshgrid(x_space.ravel(), y_space.ravel())
prob = pi * np.exp(-0.5 * ((y_space[:, None] - mu) ** 2) / sigma**2) / np.
    ↪sqrt(2 * np.pi * sigma**2)

plt.contour(xx, yy, prob.sum(axis=-1), levels=25)
plt.scatter(y, x, facecolor="none", edgecolor="b")
plt.show()
```



[]:

An overview of gradient descent algorithms

Gradient descent is the standard for optimizing many machine learning algorithms. Here, we explore some of the most popular gradient-based optimization algorithms, such as stochastic gradient descent, Adagrad and Adam. These notes are based on [An overview of gradient descent optimization algorithms](#) by Sebastian Ruder and [An updated overview of recent gradient descent algorithms](#) by John Chen.

```
[7]: import numpy as np
import matplotlib.pyplot as plt

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'

# Enable autoreload all modules before executing code
%load_ext autoreload
%autoreload 2
```

Gradient Descent

Gradient descent is one of the most popular algorithms to perform optimization and by far the most common way to optimize neural networks. More formally, gradient descent is a way to minimize an objective function $E(\mathbf{w})$ parameterized by a model's parameters $\mathbf{w} \in \mathbb{R}^D$ by updating the parameters in the opposite direction of the gradient of the objective function $\nabla E(\mathbf{w})$ w.r.t. to the parameters. The learning rate η determines the size of the steps towards reaching the (local) minimum. In other words, it follows the direction of the slope of the surface created by the objective function downhill until it reaches a valley.

The following section*'s introduce the most popular and interesting variants of gradient descent, provides intuitions towards their behaviour, and presents their motivation to resolve important optimization challenges and how this leads to the derivation of their update rules.

Batch vs Mini-batch gradient descent Vanilla gradient descent or **batch** gradient descent, computes the gradient of the cost function w.r.t. to the parameters for the entire training dataset $\mathbf{X} = [\mathbf{x}_1, \dots, \mathbf{x}_N]^T$, and thus it can be very slow or even intractable for very large datasets that do not fit in memory. Moreover, batch gradient descent does not allow us to update models online, as data stream-in. In contrast, stochastic gradient descent (SGD), usually refers to the

paradigm where parameter updates are performed for each single training example \mathbf{x}_i . Thus, SGD performs frequent updates having a high variance that cause the objective function to fluctuate heavily. These fluctuations enables SGD to jump to potentially better local minima, but, it also complicates convergence to the exact minimum, since SGD is keep overshooting. However, it has been shown that when we slowly decrease the learning rate, SGD shows the same convergence behaviour as batch gradient descent.

Mini-batch gradient descent takes the best of both worlds and performs an update for every mini-batch of n training examples,

$$\mathbf{w} = \mathbf{w} - \eta \nabla E(\mathbf{w}; \mathbf{X}_{i:i+n}; \mathbf{y}_{i:i+n})$$

This way, it a) reduces the variance of the parameter updates, which leads to more stable convergence; and b) can make use of highly optimized matrix optimizations common to state-of-the-art deep learning libraries that make computing the gradient w.r.t. a mini-batch very efficient. Usually mini-batch sizes vary between 32 and 512, but can vary for different applications, depending on the number of features and the size of the network. Mini-batch gradient descent is typically the algorithm of choice when training a neural network and the term SGD is also employed when mini-batches are used.

In order to understand the effect batch size, consider the function $f(x_1, x_2) = x_1 + x_2 + \sin(x_2)$. Lets assume that a random sample have been drawn from f as a training set \mathbf{X}, \mathbf{y} . Then, using the sum of squared error as an objective function, the figures below depict the contours of f and the parameter space defined by the error function.

```
[4]: x = np.linspace(-10, 10, 100)
x1, x2 = np.meshgrid(x, x)

f = lambda x1, x2: x1 + x2 + np.sin(x2)

x_sample = np.random.uniform(-10, 10, (10, 2))
y_sample = f(x_sample[:, 0], x_sample[:, 1])

plt.figure(figsize=(15, 5))

plt.subplot(1, 2, 1)
plt.contourf(x1, x2, f(x1, x2))
plt.colorbar()
plt.scatter(x_sample[:, 0], x_sample[:, 1], np.abs(y_sample * 10), c="black", marker="x")
plt.xlabel("$x_1$")
plt.ylabel("$x_2$")
plt.title("$f(x_1, x_2) = x_1 + x_2 + \sin(x_2)$")

w_init = np.array([-8, 8])
w = np.linspace(-10, 10, 100)
w1, w2 = np.meshgrid(w, w)
```

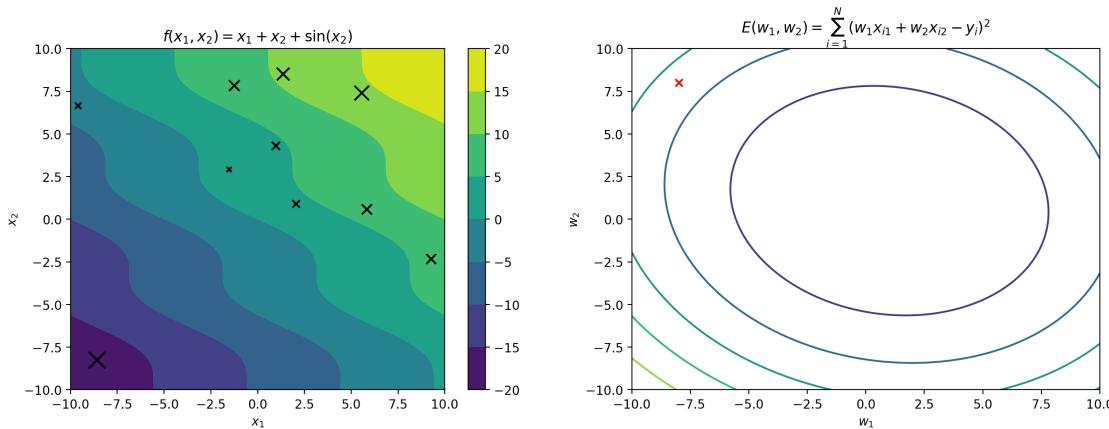
```

error = np.sum(
    (w1.reshape(-1, 1) * x_sample[:, 0] + w2.reshape(-1, 1) * x_sample[:, 1] - y_sample) ** 2, axis=1
).reshape(100, 100)

plt.subplot(1, 2, 2)
plt.contour(w1, w2, error)
plt.scatter(*w_init, color="red", marker="x")
plt.xlabel("$w_1$")
plt.ylabel("$w_2$")
plt.title("$E(w_1, w_2) = \sum_{i=1}^N (w_1 x_{i1} + w_2 x_{i2} - y_i)^2$")

plt.show()

```



Then, given a starting point in the error function (depicted by the red cross), gradient descent incrementally moves towards the optimal solution, since the error function is convex. However, keep in mind, that in a neural network the error function is **non-convex** and thus, there are multiple local optima. The following figures present the path followed by the batch gradient descent, SDG and mini-batch SDG to arrive to the optima of the sum of squared error function.

Batch gradient descent seems to move directly towards the optimal solution without fluctuations. However, since it requires the entire dataset to be loaded in memory it may become slow as the training dataset size increases. In a toy dataset, there is no such issue of course, but in real-world problems the issue is very common. On the other hand, SGD processes one example in every iteration, making training efficient in terms of memory, but there are fluctuations across iterations. Mini-batch gradient descent lies in-between. It does not fluctuate a lot across iterations, and it operates in a online fashion using a batch of data per iteration instead, thus avoiding memory problems. Moreover, mini-batch gradient descent is also much more efficient than SDG because it gains significant speedups from vectorization operations.

```
[5]: def error_gradient(w1, w2, x, y):
    if x.ndim == 1:
```

```

        return np.array([(w1 * x[0] + w2 * x[1] - y) * x[0], (w1 * x[0] + w2 * x[1] - y) * x[1]]).T
    else:
        return np.array(
            [(w1 * x[:, 0] + w2 * x[:, 1] - y) * x[:, 0], (w1 * x[:, 0] + w2 * x[:, 1] - y) * x[:, 1]]
        ).T.sum(axis=0)

n_epochs = 1000
learning_rate = 0.001
batch_gd_path, sgd_path, mini_batch_gd = [w_init], [w_init + 1], [w_init - 1]

# batch gradient descent
w_optimal = batch_gd_path[0]
for _ in range(n_epochs):
    w_optimal = w_optimal - learning_rate * error_gradient(w_optimal[0], w_optimal[1], x_sample, y_sample)
    batch_gd_path.append(w_optimal)

# stochastic gradient descent
w_optimal = sgd_path[0]
for _ in range(n_epochs):
    for i in range(x_sample.shape[0]):
        w_optimal = w_optimal - learning_rate * error_gradient(w_optimal[0], w_optimal[1], x_sample[i, :], y_sample[i])
    sgd_path.append(w_optimal)

# mini-batch gradient descent
w_optimal = mini_batch_gd[0]
mini_batches_x = np.split(x_sample, 2)
mini_batches_y = np.split(y_sample, 2)
for _ in range(n_epochs):
    for i in range(len(mini_batches_x)):
        w_optimal = w_optimal - learning_rate * error_gradient(
            w_optimal[0], w_optimal[1], mini_batches_x[i], mini_batches_y[i]
        )
    mini_batch_gd.append(w_optimal)

batch_gd_path = np.array(batch_gd_path)
sgd_path = np.array(sgd_path)
mini_batch_gd = np.array(mini_batch_gd)

plt.figure(figsize=(15, 5))

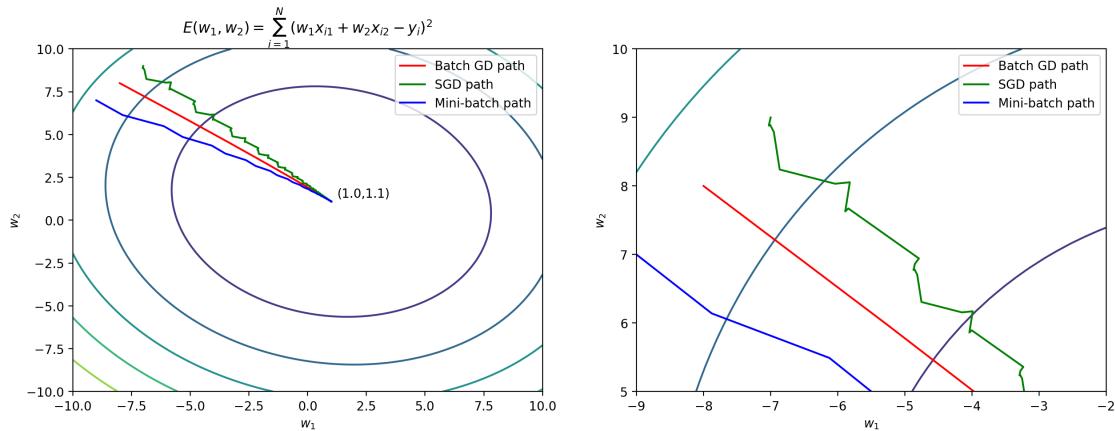
plt.subplot(1, 2, 1)
plt.contour(w1, w2, error)

```

```

plt.plot(batch_gd_path[:, 0], batch_gd_path[:, 1], color="r", markersize=3)
plt.plot(sgd_path[:, 0], sgd_path[:, 1], color="g")
plt.plot(mini_batch_gd[:, 0], mini_batch_gd[:, 1], color="b")
plt.xlabel("$w_1$")
plt.ylabel("$w_2$")
plt.title("$E(w_1, w_2) = \sum_{i=1}^N (w_1x_{i1} + w_2x_{i2} - y_i)^2$")
plt.legend(["Batch GD path", "SGD path", "Mini-batch path"])
plt.annotate(
    text=f"({round(batch_gd_path[-1][0], 1)},{round(batch_gd_path[-1][1], 1)})",
    xy=batch_gd_path[-1],
    xytext=batch_gd_path[-1] + 0.25,
)
plt.show()

```



Challenges

1. Choosing a proper learning rate can be cumbersome. A learning rate that is too small leads slow convergence, while a learning rate that is too large can hinder convergence and cause the loss function to fluctuate around the minimum or even to diverge.
2. Learning rate schedules try to adjust the learning rate during training by e.g., annealing,

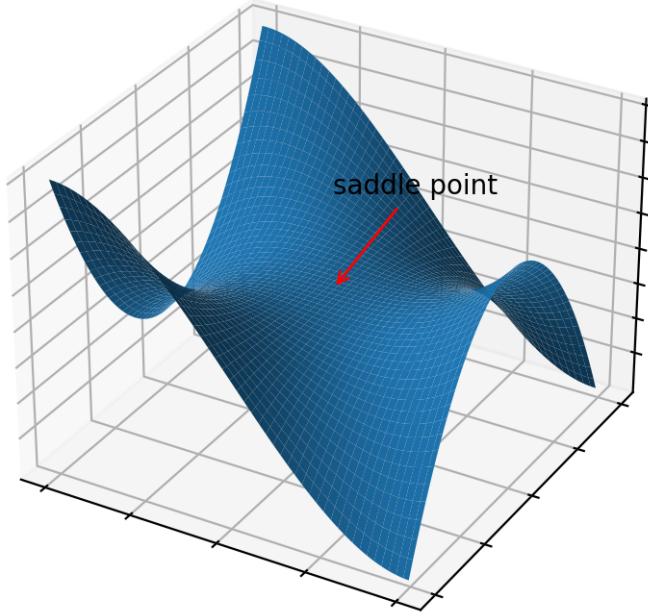
that is, reducing the learning rate according to a pre-defined schedule or when the change in objective between epochs falls below a threshold. These schedules and thresholds, however, have to be determined in advance and are unable to adapt to dataset's characteristics.

3. Learning rate applies horizontally to all parameter updates. If the data is sparse and the features have very different frequencies, we might not want to update all of them to the same extent, but instead, perform larger updates for rarely occurring features.
4. Another key challenge of minimizing highly non-convex error functions, which is common for neural networks, is avoiding getting trapped in their numerous suboptimal local minima. This difficulty arises from saddle points, i.e., points where one dimension slopes up and another slopes down (see the following figure). These saddle points are usually surrounded by a plateau of the same error, which makes it notoriously hard for SGD to escape, as the gradient is close to zero in all dimensions.

```
[6]: X1, X2 = np.meshgrid(np.arange(-1, 1, 0.01), np.arange(-1, 1, 0.01))
Z = X1**3 - 3 * X1 * X2**2

fig = plt.figure()
fig, ax = plt.subplots(subplot_kw={"projection": "3d"})
ax.plot_surface(X1, X2, Z)
ax.annotate("saddle point", (0, 0), (0, 0.025), arrowprops=dict(arrowstyle="->", color="red"))
ax.set_yticklabels([])
ax.set_xticklabels([])
ax.set_zticklabels([])
plt.show()
```

<Figure size 640x480 with 0 Axes>



Exponential Moving Average Before diving into momentum, let's take a moment to examine exponential moving average. The general equations for exponential moving average are as follows,

$$u_0 = 0 \\ u_t = \beta u_{t-1} + (1 - \beta) \theta_t$$

where parameter β controls the smoothing effect, that is, as the value of β increases, the resulting average curve becomes smoother. Intuitively, u_t is approximately the average over $\frac{1}{1-\beta}$ days. For instance, if $\beta = 0.9$ then the average is an approximation over 10 days. By recursively applying the u_t formula to itself, u_t results in a summation of weighted θ terms, as follows,

$$\begin{aligned} u_t &= \beta u_{t-1} + (1 - \beta) \theta_t \Leftrightarrow \\ u_t &= \beta(\beta u_{t-2} + (1 - \beta) \theta_{t-1}) + (1 - \beta) \theta_t \Leftrightarrow \\ u_t &= \beta^2 u_{t-2} + (1 - \beta)\beta \theta_{t-1} + (1 - \beta) \theta_t \Leftrightarrow \\ u_t &= \beta^3 u_{t-3} + (1 - \beta)\beta^2 \theta_{t-2} + (1 - \beta)\beta \theta_{t-1} + (1 - \beta) \theta_t \Leftrightarrow \\ &\dots \\ u_t &= \beta^{t+1} u_0 + (1 - \beta)\beta^t \theta_1 + \dots + (1 - \beta)\beta^2 \theta_{t-2} + (1 - \beta)\beta \theta_{t-1} + (1 - \beta) \theta_t \end{aligned}$$

Thus, u_t is a summation over past values, weighted by exponential versions of β . Since $\beta < 1$, as t increases, past values contribute increasingly less to the summation, leading to a form of exponential averaging. Given a dataset of observations across time (time-series), exponential moving average

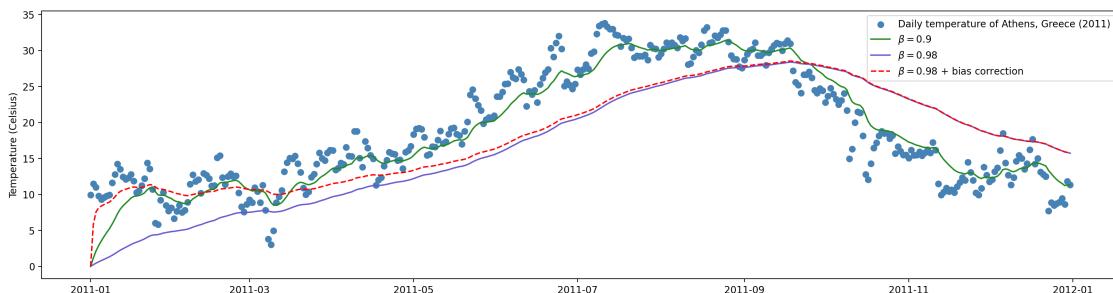
helps smooth the trajectory of these observations and reduce noise. For instance consider the following scatter of daily temperature readings from year 2011 in the city of Athens, Greece. Note that the exponential moving average (using $\beta = 0.9$) of the readings gives a smoother form.

```
[7]: import pandas as pd

df = pd.read_csv("../datasets/athens_temperature.csv", parse_dates=[0], ↴
    ↪dayfirst=True)
df = df[df["date"].dt.year == 2011]

def exponential_smoothing(x, beta: float, bias_correction: bool = False):
    y = [0]
    for i in range(1, len(x)):
        y.append(beta * y[i - 1] + (1 - beta) * x.iloc[i])
    return [yi / (1 - beta ** (i + 1)) for i, yi in enumerate(y)] if ↪
        ↪bias_correction else y


plt.figure(figsize=(20, 5))
plt.scatter(df["date"], df["avg_temperature"], color="steelblue")
plt.plot(df["date"], exponential_smoothing(df["avg_temperature"], 0.9), ↪
    ↪color="forestgreen")
plt.plot(df["date"], exponential_smoothing(df["avg_temperature"], 0.98), ↪
    ↪color="slateblue")
plt.plot(df["date"], exponential_smoothing(df["avg_temperature"], 0.98, True), ↪
    ↪color="red", linestyle="--")
plt.legend([
    "Daily temperature of Athens, Greece (2011)", "\beta=0.9", "\beta=0.98",
    "\beta=0.98 + bias correction"]
)
plt.ylabel("Temperature (Celsius)")
plt.show()
```



Finally, as depicted in the figure above, to account for bias introduced by the starting value u_0 , divide v_t by $1 - \beta^t$. Otherwise, exponential smoothing requires some time to warm up, analogous

to the choice of β .

Momentum SGD has trouble navigating areas where the surface curves much more steeply in one dimension than in another, which are common around local optima and saddle points. In these scenarios, SGD oscillates across the slopes of the area while only making hesitant progress along the bottom towards the local optimum. *Momentum* is a method that helps accelerate SGD in the relevant direction and dampens oscillations. Essentially, it uses exponential moving average over the gradient path by adding a fraction β of the update vector of the past update step to the current update vector as follows,

$$\begin{aligned}\mathbf{u}_\tau &= \beta \mathbf{u}_{\tau-1} + (1 - \beta) \nabla E(\mathbf{w}; \mathbf{X}_{i:i+n}; \mathbf{y}_{i:i+n}) \\ \mathbf{w} &= \mathbf{w} - \eta \mathbf{u}_\tau\end{aligned}$$

where the momentum term β is usually set to 0.9 or a similar value. Intuitively, when using momentum, we push a ball down the hill. The ball accumulates momentum as it rolls downhill, becoming faster and faster on the way. The parameter $\beta < 1$ plays the role of air resistance. The same thing happens to our parameter updates. The momentum term increases for dimensions whose gradients point in the same directions and reduces updates for dimensions whose gradients change directions. As a result, we gain faster convergence and reduced oscillation.

This can be seen by applying momentum to stochastic gradient descent (SGD), as depicted in the next figure. Momentum aids SGD to attain similar behavior to batch gradient descent. Moreover, note that it oscillates less than the mini-batch version. However, the combination of mini-batch gradient descent and momentum achieves similar results and is more on large datasets, due to vectorization.

```
[26]: beta = 0.9
momentum_gd_path = [w_init]
momentum_mini_batch_gd = [w_init]

# momentum stochastic gradient descent
u = 0
w_optimal = momentum_gd_path[0]
mini_batches_x = np.split(x_sample, 2)
mini_batches_y = np.split(y_sample, 2)
for _ in range(n_epochs):
    for i in range(x_sample.shape[0]):
        u = beta * u + (1 - beta) * error_gradient(w_optimal[0], w_optimal[1], x_sample[i, :], y_sample[i])
        w_optimal = w_optimal - learning_rate * u
        momentum_gd_path.append(w_optimal)

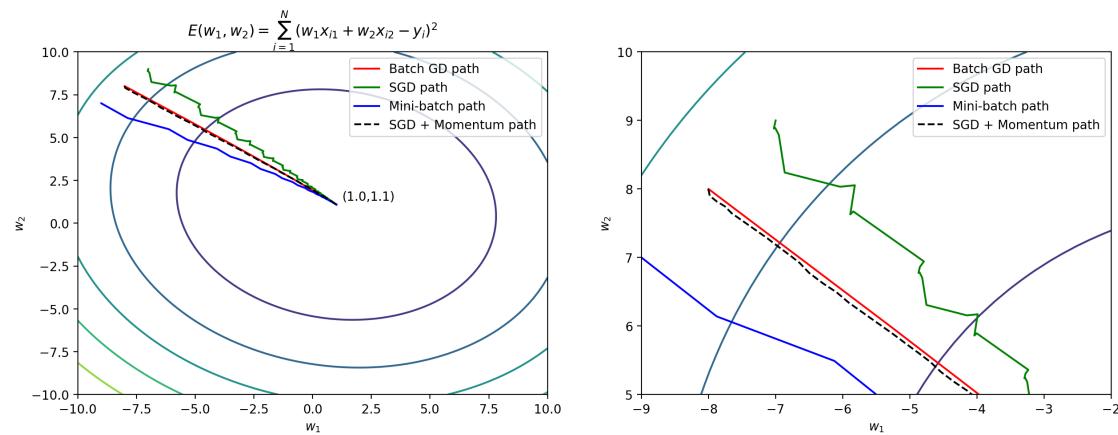
momentum_gd_path = np.array(momentum_gd_path)

plt.figure(figsize=(15, 5))
plt.subplot(1, 2, 1)
plt.contour(w1, w2, error)
```

```

plt.plot(batch_gd_path[:, 0], batch_gd_path[:, 1], color="r")
plt.plot(sgd_path[:, 0], sgd_path[:, 1], color="g")
plt.plot(mini_batch_gd[:, 0], mini_batch_gd[:, 1], color="b")
plt.plot(momentum_gd_path[:, 0], momentum_gd_path[:, 1], color="k", 
         linestyle="--")
plt.xlabel("$w_1$")
plt.ylabel("$w_2$")
plt.title("$E(w_1, w_2) = \sum_{i=1}^N (w_1x_{i1} + w_2x_{i2} - y_i)^2$")
plt.legend(["Batch GD path", "SGD path", "Mini-batch path", "SGD + Momentum path"])
plt.annotate(
    text=f"({round(batch_gd_path[-1][0], 1)},{round(batch_gd_path[-1][1], 1)})",
    xy=batch_gd_path[-1],
    xytext=batch_gd_path[-1] + 0.25,
)
plt.show()

```



Adaptive Learning Rates

Apart from adapting the updates to the slope of the error function in order to speed up SGD, in turn, it is also valuable to adapt SDG updates to each individual parameter and perform larger or smaller updates depending on their importance.

Adagrad Adagrad is an algorithm that adapts the learning rate to the parameters, performing smaller updates (i.e., low learning rates) for parameters associated with frequently occurring features, and larger updates (i.e., high learning rates) for parameters associated with infrequent features. To that end, it is well-suited for dealing with sparse data. Typical gradient descent performs an update for all parameters \mathbf{w} at once, as every parameter w_i uses the same learning rate η . On the other hand, Adagrad uses a different learning rate for every parameter w_i at every time step τ . For brevity, \mathbf{g}_τ denotes the gradient vector at time step τ and $g_{i,\tau}$ denotes the partial derivative of the objective function over the parameter w_i at time step τ ,

$$\mathbf{g}_\tau = \nabla E(\mathbf{w}; \mathbf{X}_{i:i+n}; \mathbf{y}_{i:i+n})$$

and

$$g_{i,\tau} = \frac{\partial E(w_i; \mathbf{X}_{i:i+n}; \mathbf{y}_{i:i+n})}{\partial w_i}$$

Adagrad modifies the general learning rate η at each time step τ for every parameter w_i based on the past gradients that have been computed for w_i as follows,

$$w_{i,\tau} = w_{i,\tau-1} - \frac{\eta}{\sqrt{G_{i,\tau-1} + \epsilon}} g_{i,\tau-1}$$

where $\mathbf{G}_\tau \in \mathbb{R}^{D \times D}$ is a diagonal matrix and each diagonal element is the sum of the squares of the gradients of w_i up to time step τ , while ϵ is a smoothing term that avoids division by zero, typically on the order of 10^{-8} . Interestingly, without the square root operation, the algorithm performs much worse. As \mathbf{G}_τ contains the sum of the squares of the past gradients for all parameters along its diagonal, the implementation can be vectorized by performing a Hadamard product between \mathbf{G}_τ and \mathbf{g}_τ to obtain,

$$\begin{aligned} \mathbf{G}_\tau &= \mathbf{G}_{\tau-1} + \mathbf{I} \odot (\mathbf{g}_\tau^2)^T \\ \mathbf{w}_{\tau+1} &= \mathbf{w}_\tau - \frac{\eta}{\sqrt{\mathbf{G}_\tau + \epsilon}} \odot \mathbf{g}_\tau \end{aligned}$$

One of Adagrad's main benefits is that it eliminates the need to manually tune the learning rate η . On the other hand, Adagrad's main weakness is its accumulation of the squared gradients in the denominator. Since every added term is positive, the accumulated sum keeps growing during training. In turn, the learning rate shrinks and eventually becomes infinitesimally small, at which point the algorithm is no longer able to acquire additional knowledge.

Adadelta Adadelta is an extension of Adagrad that seeks to reduce its aggressive, monotonically decreasing learning rate. Instead of accumulating all past squared gradients, Adadelta restricts the window of accumulated past gradients to some fixed size h . Instead of inefficiently storing h previous squared gradients, the sum of gradients is recursively defined, similar to *Momentum*, as an exponential moving average of all past squared gradients. To avoid confusion I shall use the symbol \mathbf{s} for representing the exponential moving average over the squared gradients. The running average at time step τ then depends only on the previous average and the current gradient as follows,

$$\mathbf{s}_\tau = \beta \mathbf{s}_{\tau-1} + (1 - \beta) \mathbf{g}_\tau^2$$

Similar to the momentum term, β is usually set around 0.9. Then, Adadelta simply replaces the diagonal matrix \mathbf{G}_τ using the decaying average over past squared gradients u_τ ,

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \frac{\eta}{\sqrt{\mathbf{s}_\tau + \epsilon}} \odot \mathbf{g}_\tau$$

Note that the denominator is just the root mean squared (RMS) criterion of the gradient, and thus,

$$RMS(\mathbf{g}_\tau) = \sqrt{\mathbf{s}_\tau + \epsilon}$$

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \frac{\eta}{RMS(\mathbf{g}_\tau)} \mathbf{g}_\tau$$

Note that the units in the update (as well as in SGD, Momentum, or Adagrad) do not match, i.e., the update should have the same hypothetical units as the parameter. To that end, lets define another exponentially decaying average, this time not of squared gradients but of squared parameter updates,

$$\Delta \mathbf{w}_\tau = -\frac{\eta}{RMS(\mathbf{g}_\tau)} \mathbf{g}_\tau$$

$$\mathbf{d}_\tau = \gamma \mathbf{d}_{\tau-1} + (1 - \gamma) \Delta \mathbf{w}_\tau^2$$

Then, the root mean squared error of parameter updates becomes,

$$RMS(\Delta \mathbf{w}_\tau) = \sqrt{\mathbf{d}_\tau + \epsilon}$$

Since $RMS(\Delta \mathbf{w}_\tau)$ is unknown, the RMS of parameter updates until the previous time step is used as an approximation. Replacing the learning rate η in the previous update rule with $RMS(\Delta \mathbf{w}_{\tau-1})$ yields the final Adadelta update rule,

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \frac{RMS(\Delta \mathbf{w}_{\tau-1})}{RMS(\mathbf{g}_\tau)} \mathbf{g}_\tau$$

Note that Adadelta does not even require to set a default learning rate η , as it has been eliminated from the update rule.

RMSprop RMSprop is another adaptive learning rate method developed around the same time with Adadelta, stemming from the need to resolve Adagrad's radically diminishing learning rates. RMSprop in fact is identical to the first update vector of Adadelta derived above,

$$\begin{aligned}\mathbf{s}_\tau &= \beta \mathbf{s}_{\tau-1} + (1 - \beta) \nabla E(\mathbf{w}; \mathbf{X}_{i:i+n}; \mathbf{y}_{i:i+n})^2 \\ \mathbf{w}_{\tau+1} &= \mathbf{w}_\tau - \frac{\eta}{\sqrt{\mathbf{s}_\tau + \epsilon}} \nabla E(\mathbf{w}; \mathbf{X}_{i:i+n}; \mathbf{y}_{i:i+n})\end{aligned}$$

RMSprop also divides the learning rate by an exponentially decaying average of squared gradients. Intuitively, the squares help overstate larger/smaller derivatives, thus overstate steeper areas of the curve, while understate flatten areas, leading to faster learning.

Adam Adaptive Moment Estimation (Adam) is another method that computes adaptive learning rates for each parameter. In addition to storing an exponentially decaying average of past squared gradients \mathbf{s}_τ , like Adadelta and RMSprop, Adam also keeps an exponentially decaying average of past gradients \mathbf{u}_τ , similar to momentum. Whereas momentum can be seen as a ball running down a slope, Adam behaves like a heavy ball with friction, and thus prefers flat minima in the error surface. We compute the decaying averages of past and past squared gradients \mathbf{u}_τ and \mathbf{s}_τ respectively as follows,

$$\begin{aligned}\mathbf{u}_\tau &= \beta_1 \mathbf{u}_{\tau-1} + (1 - \beta_1) \mathbf{g}_\tau \\ \mathbf{s}_\tau &= \beta_2 \mathbf{s}_{\tau-1} + (1 - \beta_2) \mathbf{g}_\tau^2\end{aligned}$$

\mathbf{u}_τ and \mathbf{s}_τ are estimates of the first moment (the mean) and the second moment (the uncentered variance) of the gradients respectively, hence the name of the method. As \mathbf{u}_τ and \mathbf{s}_τ are initialized as vectors of zeros, they are biased towards zero, especially during the initial time steps, and especially when the decay rates are small (i.e. β_1 and β_2 are close to 1). These biases may be counteracted by computing the bias-corrected first and second moment estimates as follows,

$$\begin{aligned}\hat{\mathbf{u}}_\tau &= \frac{\mathbf{u}_\tau}{1 - \beta_1} \\ \hat{\mathbf{s}}_\tau &= \frac{\mathbf{s}_\tau}{1 - \beta_2}\end{aligned}$$

Then use these bias-corrected values to update the parameters just as we have seen in Adadelta and RMSprop, which yields the Adam update rule:

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \frac{\eta}{\sqrt{\hat{\mathbf{s}}_\tau + \epsilon}} \hat{\mathbf{u}}_\tau$$

Sane default values for the hyperparameters are $\beta_1 = 0.9$, $\beta_2 = 0.99$ and $\epsilon = 10^{-8}$.

AdamW Weight decay (quadratic regularizer) is usually implemented by adding a term to the error function (see [Chapter 5](#) for Neural Networks). AdamW modifies the typical implementation of weight decay regularization in Adam, by decoupling the weight decay from the gradient update,

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \eta \left(\frac{1}{\sqrt{\mathbf{s}_\tau + \epsilon}} \hat{\mathbf{u}}_\tau + \lambda \mathbf{w}_\tau \right)$$

It turns out that this detail makes a difference in practice and has been adopted by the machine learning community.

Optimizing Beale's function

There are many [test functions](#) that are useful for evaluating optimization algorithms. In particular, we shall look at Beale's function:

$$f(x, y) = (1.5 - x + xy)^2 + (2.25 - x + xy^2)^2 + (2.625 - x + xy^3)^2$$

$$\nabla f(x, y) = \begin{bmatrix} 2x(y^6 + y^4 - 2y^3 - y^2 - 2y + 3) + 5.25y^3 + 4.5y^2 + 3y - 12.75 \\ 6x(x(y^5 + 0.666667y^3 - y^2 - 0.333333y - 0.333333) + 2.625y^2 + 1.5y + 0.5) \end{bmatrix}$$

```
[3]: f = lambda x, y: (1.5 - x + x * y) ** 2 + (2.25 - x + x * y**2) ** 2

def error_gradient(x: float, y: float) -> np.ndarray:
    return np.array([
        2 * x * (y**6 + y**4 - 2 * y**3 - y**2 - 2 * y + 3) + 5.25 * y**3 + 4.5 * y**2 + 3 * y - 12.75,
        6 * x * (x * (y**5 + 0.666667 * y**3 - y**2 - 0.333333 * y - 0.333333) + 2.625 * y**2 + 1.5 * y + 0.5),
    ])
```

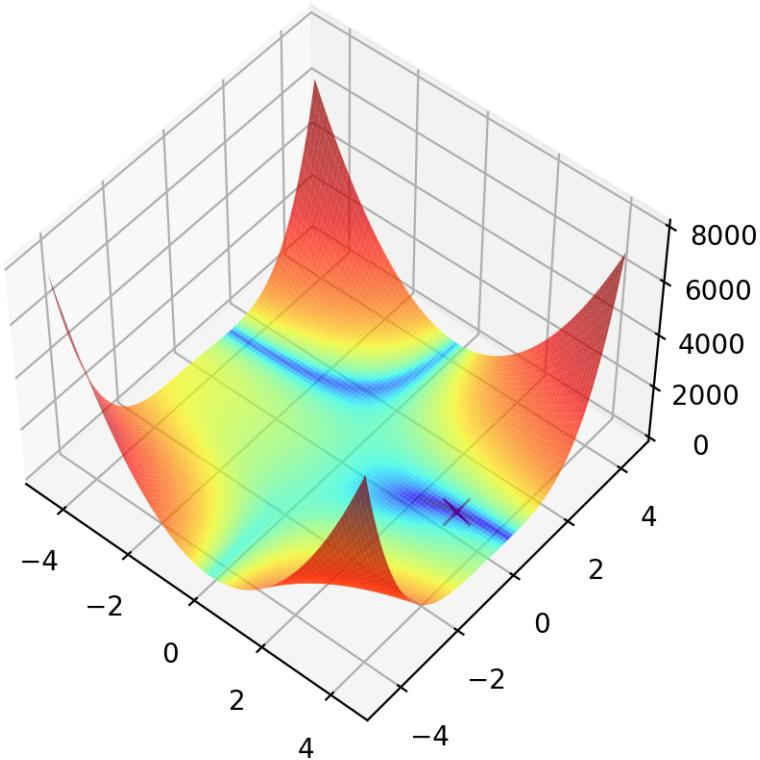
```
[8]: from matplotlib.colors import LogNorm

x, y = np.meshgrid(np.arange(-4.5, 4.5, 0.1), np.arange(-4.5, 4.5, 0.1))
z = f(x, y)

ax = plt.axes(projection="3d", elev=50, azim=-50)
ax.plot_surface(x, y, z, norm=LogNorm(), rstride=1, cstride=1, edgecolor="none", alpha=0.7, cmap=plt.cm.jet)

global_minima = np.array([3.0, 0.5]).reshape(-1, 1)
ax.plot(*global_minima, f(*global_minima), "rx", markersize=10)

plt.show()
```



```
[25]: n_epochs = 1000000
learning_rate = 1e-2
start_point = np.array([1.5, 1.5])

# Simple gradient descent
batch_gd_path = [start_point]
xy_optimal = batch_gd_path[0]
for _ in range(n_epochs):
    xy_optimal = xy_optimal - learning_rate * error_gradient(xy_optimal[0], xy_optimal[1])
    batch_gd_path.append(xy_optimal)

batch_gd_path = np.array(batch_gd_path)

# Momentum gradient descent
u = 0
beta = 0.9
momentum_gd_path = [start_point]
xy_optimal = momentum_gd_path[0]
for _ in range(n_epochs):
    u = beta * u + (1 - beta) * error_gradient(xy_optimal[0], xy_optimal[1])
    xy_optimal = xy_optimal - learning_rate * u
    momentum_gd_path.append(xy_optimal)
```

```

momentum_gd_path.append(xy_optimal)

momentum_gd_path = np.array(momentum_gd_path)

# AdaGrad
adagrad_path = [start_point]

epsilon = 1e-8
g_history = np.zeros((2, 2))
xy_optimal = adagrad_path[0]
for _ in range(n_epochs):
    g = error_gradient(xy_optimal[0], xy_optimal[1])
    g_history = g_history + np.eye(2) * g
    xy_optimal = xy_optimal - (learning_rate / (np.sqrt(np.diag(g_history)) + epsilon)) * g
    adagrad_path.append(xy_optimal)

adagrad_path = np.array(adagrad_path)

# AdaDelta
beta = 0.9
gamma = 0.9
epsilon = 1e-8
adadelta_path = [start_point]
s, d = 0, 0
xy_optimal = adadelta_path[0]
for _ in range(n_epochs):
    g = error_gradient(xy_optimal[0], xy_optimal[1])
    s = beta * s + (1 - beta) * g**2
    rms = np.sqrt(s + epsilon)
    delta = -(learning_rate * g) / rms
    d = gamma * d + (1 - gamma) * delta**2
    rms_delta = np.sqrt(d + epsilon)
    xy_optimal = xy_optimal - (rms_delta / rms) * g
    adadelta_path.append(xy_optimal)

adadelta_path = np.array(adadelta_path)

# Adam
beta_1 = 0.9
beta_2 = 0.99
epsilon = 1e-8
adam_path = [start_point]

u, s = 0, 0
xy_optimal = adam_path[0]
for _ in range(n_epochs):

```

```

g = error_gradient(xy_optimal[0], xy_optimal[1])
u = beta_1 * u + (1 - beta_1) * g
u_hat = u / (1 - beta_1)
s = beta_2 * s + (1 - beta_2) * g**2
s_hat = s / (1 - beta_2)
xy_optimal = xy_optimal - (learning_rate / np.sqrt(s_hat + epsilon)) * u_hat
adam_path.append(xy_optimal)

adam_path = np.array(adam_path)

```

```

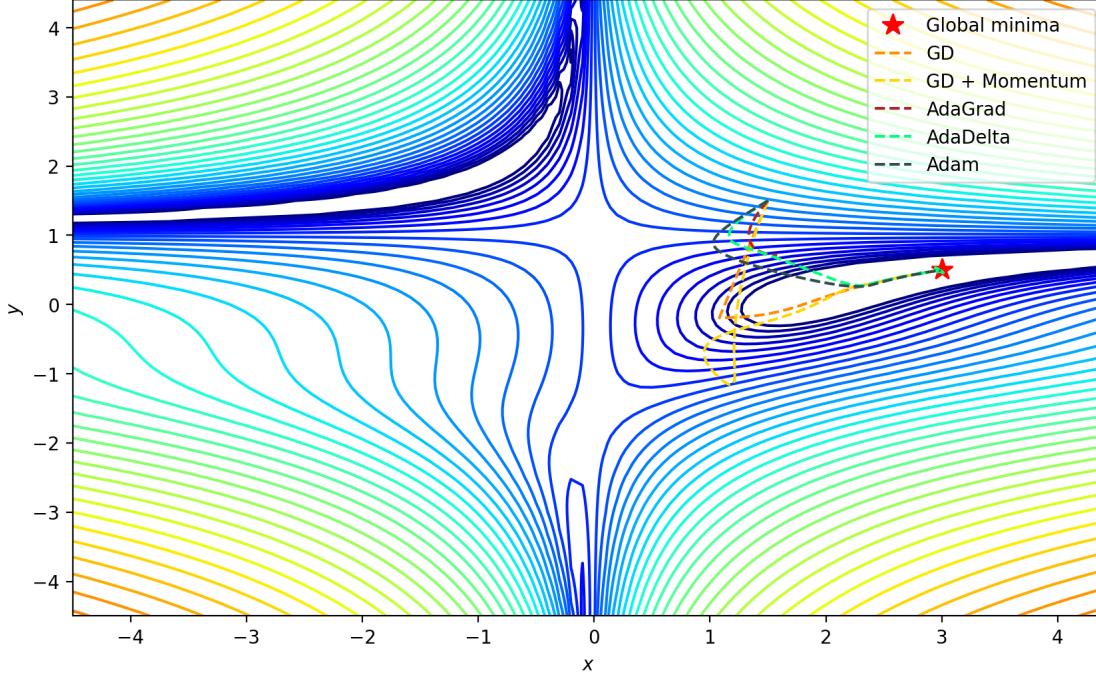
[37]: fig, ax = plt.subplots(figsize=(10, 6))

ax.contour(x, y, z, levels=np.logspace(0, 5, 45), norm=LogNorm(), cmap=plt.cm.
            jet)
ax.plot(*global_minima, "r*", markersize=12)

ax.plot(batch_gd_path[:-1, 0], batch_gd_path[:-1, 1], color="darkorange", □
        linestyle="dashed")
ax.plot(momentum_gd_path[:-1, 0], momentum_gd_path[:-1, 1], color="gold", □
        linestyle="dashed")
ax.plot(adagrad_path[:-1, 0], adagrad_path[:-1, 1], color="firebrick", □
        linestyle="dashed")
ax.plot(adadelta_path[:-1, 0], adadelta_path[:-1, 1], color="springgreen", □
        linestyle="dashed")
ax.plot(adam_path[:-1, 0], adam_path[:-1, 1], color="darkslategray", □
        linestyle="dashed")

plt.xlabel("$x$")
plt.ylabel("$y$")
plt.legend(["Global minima", "GD", "GD + Momentum", "AdaGrad", "AdaDelta", □
            "Adam"])
plt.show()

```



Which optimizer to use? When the input data is sparse, then adaptive learning-rate methods are likely to achieve the best results. In addition, these methods do not require tuning on the learning rate and they often achieve the best results using the default value.

RMSprop avoids the radically diminishing learning rates Adagrad. It is identical to Adadelta, except that Adadelta uses the RMS of parameter updates in the numerator update rule. Adam, adds bias-correction and momentum to RMSprop. Insofar, RMSprop, Adadelta, and Adam are very similar algorithms that perform equally good in similar circumstances. Bias-correction usually helps Adam slightly outperform RMSprop towards the end of optimization as gradients become sparser, and thus, Adam might be the best overall choice.

Vanilla SGD and a simple learning rate annealing schedule finds a minimum but it might take significantly longer than. SGD is much more reliant on robust initialization and annealing schedule, and may get stuck in saddle points rather than local minima. Consequently, if you care about fast convergence, you should choose one of the adaptive learning rate methods.

Adam variants and other improvements

AdaMax The \mathbf{s}_τ factor in the Adam update rule scales the gradient inversely proportionally to the ℓ_2 norm of the past gradients (via the $\mathbf{s}_{\tau-1}$ term) and current gradient \mathbf{g}_τ^2 ,

$$\mathbf{s}_\tau = \beta_2 \mathbf{s}_{\tau-1} + (1 - \beta_2) \mathbf{g}_\tau^2$$

The update rule can be generalized to the ℓ_p norm,

$$\mathbf{s}_\tau = \beta_2^p \mathbf{s}_{\tau-1} + (1 - \beta_2^p) |\mathbf{g}_\tau|^p$$

Norms for large p values generally become numerically unstable, making the ℓ_1 and ℓ_2 norms the most common in practice. However, ℓ_∞ norm generally exhibits stable behavior. To that end, it can be shown using ℓ_∞ converges to the following more stable value,

$$\mathbf{i}_\tau = \beta_2^\infty \mathbf{i}_{\tau-1} + (1 - \beta_2^\infty) |\mathbf{g}_\tau|^\infty = \max(\beta_2 \mathbf{i}_{\tau-1}, |\mathbf{g}_\tau|)$$

Then, by replacing $\sqrt{\mathbf{s}_\tau + \epsilon}$ in the Adam update equation with \mathbf{i}_τ , we obtain AdaMax,

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \frac{\eta}{\mathbf{i}_\tau} \mathbf{u}_\tau$$

Note that, in contrast to the Adam update rule, since AdaMax relies on the max operation, it avoids bias towards zero and does not need to any form of bias correction.

Nesterov accelerated gradient or Nesterov momentum However, a ball that rolls down a hill, blindly following the slope, is highly unsatisfactory. In contrast, a ball that has a notion of where it is going so that it knows to slow down before the hill slopes up again, is preferable. Nesterov accelerated gradient (NAG) is a way to give the momentum term this kind of prescience. Since momentum uses the term $\beta \mathbf{u}_{\tau-1}$ to move the parameters \mathbf{w} , then, computing $\mathbf{w} - \beta \mathbf{u}_{\tau-1}$, gives us an approximation of the next position of the parameters, a rough idea where the parameters are going to be. Thus, we can effectively look ahead by calculating the gradient not w.r.t. to our current parameters but w.r.t. the approximate future position of our parameters:

$$\begin{aligned}\mathbf{u}_\tau &= \beta \mathbf{u}_{\tau-1} + (1 - \beta) \nabla E(\mathbf{w} - \beta \mathbf{u}_{\tau-1}; \mathbf{X}_{i:i+n}; \mathbf{y}_{i:i+n}) \\ \mathbf{w} &= \mathbf{w} - \eta \mathbf{u}_\tau\end{aligned}$$

Simple momentum computes the gradient and then takes a big jump in the direction of the updated accumulated gradient, while NAG makes a big jump in the direction of the previous accumulated gradient, then measures the current gradient and makes a correction. This anticipatory update prevents momentum from going too fast and results in increased responsiveness.

Nadam Adam can be viewed as a combination of RMSprop and momentum. RMSprop contributes the exponentially decaying average of past squared gradients \mathbf{s}_τ , while momentum accounts for the exponentially decaying average of past gradients \mathbf{u}_τ . Moreover, Nesterov accelerated gradient (NAG) is superior to vanilla momentum. Nadam (Nesterov-accelerated Adaptive Moment Estimation) combines Adam and NAG. Expanding the momentum update rule we obtain,

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \eta (\beta \mathbf{u}_{\tau-1} + (1 - \beta) \mathbf{g}_\tau)$$

This demonstrates that momentum involves taking a step in the direction of the previous momentum vector and a step in the direction of the current gradient. NAG allows us to perform a more accurate step in the gradient direction by updating the parameters with the momentum step before computing the gradient. We thus only need to modify the gradient \mathbf{g}_τ to arrive at NAG. Rather

than applying the momentum step twice – one time for updating the gradient \mathbf{g}_τ and a second time for updating the parameters $\mathbf{w}_{\tau+1}$ – we may apply the look-ahead momentum vector directly to update the current parameters,

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \eta(\beta\mathbf{u}_\tau + (1-\beta)\mathbf{g}_\tau)$$

Notice that rather than utilizing the previous momentum vector $\mathbf{u}_{\tau-1}$ as in the equation of the expanded momentum update rule above, we use the current momentum vector \mathbf{u}_τ to look ahead. In order to add Nesterov momentum to Adam, similarly use the current momentum vector in the place of the previous momentum vector. Expanding Adam update rule, using the definitions of \mathbf{u}_τ and $\hat{\mathbf{u}}_\tau$ (note that there is no need to modify $\hat{\mathbf{s}}_\tau$) gives,

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \frac{\eta}{\sqrt{\mathbf{s}_\tau + \epsilon}} \left(\frac{\beta_1 \mathbf{u}_{\tau-1}}{1 - \beta_1^\tau} + \frac{(1 - \beta_1) \mathbf{g}_\tau}{1 - \beta_1^\tau} \right)$$

Note that $\frac{\beta_1 \mathbf{u}_{\tau-1}}{1 - \beta_1^\tau}$ is almost the bias-corrected estimate of the momentum vector of the previous time step, but the denominator is $1 - \beta_1^\tau$ and not $1 - \beta_1^{\tau-1}$. However, since NAG replaces the momentum vector of the previous time step, the term becomes the bias-corrected estimate of the current momentum vector, which gives us the Nadam update rule,

$$\mathbf{w}_{\tau+1} = \mathbf{w}_\tau - \frac{\eta}{\sqrt{\mathbf{s}_\tau + \epsilon}} \left(\beta_1 \hat{\mathbf{u}}_\tau + \frac{(1 - \beta_1) \mathbf{g}_\tau}{1 - \beta_1^\tau} \right)$$

AMSGrad There are some cases where adaptive learning rate methods fail to converge to an optimal solution and are outperformed by simple SGD. In these cases, the short-term memory of the exponential moving average of past squared gradients becomes an obstacle. It has been observed that when some minibatches provide large and informative gradients, but as these minibatches only occur rarely, exponential averaging diminishes their influence, which leads to poor convergence. To that end, AMSGard that uses the maximum of past squared gradients \mathbf{s}_τ (without bias-correction) rather than the exponential average to update the parameters,

$$\hat{\mathbf{s}}_\tau = \max(\hat{\mathbf{s}}_{\tau-1}, \mathbf{s}_\tau)$$

Thus, AMSGard results in a non-increasing step size that avoids the problems suffered by Adam. The full AMSGard update is given by,

$$\begin{aligned} \mathbf{u}_\tau &= \beta_1 \mathbf{u}_{\tau-1} + (1 - \beta_1) \mathbf{g}_\tau \\ \mathbf{s}_\tau &= \beta_2 \mathbf{s}_{\tau-1} + (1 - \beta_2) \mathbf{g}_\tau^2 \\ \hat{\mathbf{s}}_\tau &= \max(\hat{\mathbf{s}}_{\tau-1}, \mathbf{s}_\tau) \\ \mathbf{w}_{\tau+1} &= \mathbf{w}_\tau - \frac{\eta}{\sqrt{\hat{\mathbf{s}}_\tau + \epsilon}} \hat{\mathbf{u}}_\tau \end{aligned}$$

Although AMSGard has shown improved performance compared to Adam on small datasets and on CIFAR-10, other experiments show worse performance and thus it is generally accepted that AMSGard does not perform better than Adam in practice.

Additional strategies for optimizing SGD

There are some additional strategies that can be used alongside any of the previously mentioned algorithms to further improve the performance of SGD.

Shuffling and Curriculum Learning In general, it's often a good idea to shuffle the training data after every epoch, to avoid providing the training examples in a meaningful order to our model as this may bias the optimization algorithm. On the other hand, in some cases when aiming to solve progressively harder problems, supplying the training examples in a meaningful order (e.g., increasing difficulty) may actually lead to improved performance and better convergence. The method for establishing this meaningful order is called Curriculum Learning.

Learning rate decay Given an initial learning rate η_0 , the learning rate may be adjusted after every pass over the training set as follows,

$$\eta = \frac{1}{1 + r \cdot i} \eta_0$$

where r is the decay rate (hyperparameter) and i is the current training epoch. Another decay formula is the exponential decay,

$$\eta = 0.95^i \cdot \eta_0$$

Gradient noise Another useful strategy is to add noise that follows a Gaussian distribution to each gradient update,

$$g_{i,\tau} = g_{i,\tau} + \mathcal{N}(0, \sigma_\tau^2)$$

and anneal the variance according to the following schedule,

$$\sigma_\tau^2 = \frac{\eta}{(1 + \tau)^\gamma}$$

Adding noise to gradients makes neural networks more robust to poor initialization and helps training particularly deep and complex networks. The intuition is that noise gives the model more chances to escape and find other local minima, which are more frequent for deeper models.

6. Kernel Methods

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- 6.3 Radial Basis Function Networks
- 6.4 Gaussian Processes
 - 6.4.2 Gaussian processes for regression
 - 6.4.3 Learning the hyperparameters

- 6.4.4 Automatic relevance determination
- 6.4.5 Gaussian process for classification
- 6.4.7 Connection to neural networks

```
[65]: import numpy as np
import matplotlib.pyplot as plt
from sklearn.datasets import make_classification

from prml.preprocessing import PolynomialFeature, GaussianFeature, ↴
    SigmoidFeature
from prml.distribution import MultivariateGaussian
from prml.kernel import RBF, GaussianProcessRegression, ↴
    GaussianProcessClassifier
from prml.datasets import generate_toy_data

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'

# Enable autoreload all modules before executing code
%reload_ext autoreload
%autoreload 2
```

In Chapter 3 and 4, we considered linear parametric models governed by a vector \mathbf{w} of adaptive parameters. During the learning phase, a set of training data is used to obtain a point estimate of the parameter vector or determine their posterior distribution. Then, the training set may be discarded and predictions are based only on the learned parameters. The same approach is employed for non-linear models such as neural networks.

However, there is a class of techniques, in which the training data are kept and used also in the prediction phase. For instance, *memory-based* methods, such as Parzen density models and nearest-neighbors, store the entire training set in order to make predictions for future data points. These methods typically require a metric that measures the similarity of any pair of vectors in the input space. They are generally fast to train, because they just store the training data, and slow at making predictions, because they have to pass over the training set, possibly multiple times.

Interestingly, many linear parametric models can be re-cast into an equivalent *dual representation* in which the predictions are also based on linear combinations of a *kernel function* evaluated on the training data points. Assuming models based on a fixed nonlinear *feature space* mapping $\phi(\mathbf{x})$, the kernel function is defined by

$$k(\mathbf{x}, \mathbf{x}') = \phi(\mathbf{x})^T \phi(\mathbf{x}')$$

where the kernel is a symmetric function of its arguments $k(\mathbf{x}, \mathbf{x}') = k(\mathbf{x}', \mathbf{x})$. To that end, the

simplest example of a kernel function is obtained by considering the identity feature mapping, which is $\phi(\mathbf{x}) = \mathbf{x}$, and thus $k(\mathbf{x}, \mathbf{x}') = \mathbf{x}^T \mathbf{x}'$ is referred as the **linear kernel**.

The concept of a kernel formulated as an inner product in a feature space allows us to build interesting extensions of well-known algorithms by making use of the *kernel trick*, also known as *kernel substitution*. The idea is to replace the scalar product of the input vector \mathbf{x} in the formulation of interest with any kernel.

One of the most significant developments has been the extension of kernels to handle symbolic objects.

6.1 Dual Representations

Consider a linear regression model whose parameters are determined by minimizing the regularized sum-of-squares error function given by

$$E(\mathbf{w}) = \frac{1}{2} \sum_{n=1}^N (\mathbf{w}^T \phi(\mathbf{x}_n) - t_n)^2 + \frac{\lambda}{2} \mathbf{w}^T \mathbf{w}$$

If we set the gradient of $E(\mathbf{w})$ with respect to \mathbf{w} equal to zero, then, the solution for \mathbf{w} takes the form of a linear combination of the vectors $\phi(\mathbf{x}_n)$, with coefficients a_n that are functions of \mathbf{w} ,

$$\begin{aligned} \nabla E(\mathbf{w}) = \mathbf{0} &\Leftrightarrow \nabla \frac{1}{2} \sum_{n=1}^N (\mathbf{w}^T \phi(\mathbf{x}_n) - t_n)^2 + \frac{\lambda}{2} \mathbf{w}^T \mathbf{w} = \mathbf{0} \\ &\Leftrightarrow \sum_{n=1}^N (\mathbf{w}^T \phi(\mathbf{x}_n) - t_n) \phi(\mathbf{x}_n) + \lambda \mathbf{w} = \mathbf{0} \\ &\Leftrightarrow \lambda \mathbf{w} = - \sum_{n=1}^N (\mathbf{w}^T \phi(\mathbf{x}_n) - t_n) \phi(\mathbf{x}_n) \\ &\Leftrightarrow \mathbf{w} = -\frac{1}{\lambda} \sum_{n=1}^N (\mathbf{w}^T \phi(\mathbf{x}_n) - t_n) \phi(\mathbf{x}_n) \\ &\Leftrightarrow \mathbf{w} = \sum_{n=1}^N a_n \phi(\mathbf{x}_n) \end{aligned}$$

where $a_n = -\frac{1}{\lambda} (\mathbf{w}^T \phi(\mathbf{x}_n) - t_n)$. Then, using a $(N \times M)$ design matrix Φ , whose n th row is given by $\phi(\mathbf{x}_n)^T$, and $\mathbf{a} = (a_1, \dots, a_N)^T$, we obtain

$$\mathbf{w} = \Phi^T \mathbf{a}$$

The dual representation is obtained if instead of working with the parameter vector \mathbf{w} , we reformulate the least-squares algorithm in terms of the parameter vector \mathbf{a} . If we substitute $\mathbf{w} = \Phi^T \mathbf{a}$ into $E(\mathbf{w})$, we obtain,

$$\begin{aligned}
E(\mathbf{a}) &= \frac{1}{2} \sum_{n=1}^N (\mathbf{a}^T \Phi \phi(\mathbf{x}_n) - t_n)^2 + \frac{\lambda}{2} \mathbf{a}^T \Phi \Phi^T \mathbf{a} \\
&= \frac{1}{2} \left\| \mathbf{a}^T \Phi \Phi^T - \mathbf{t} \right\|_2^2 + \frac{\lambda}{2} \mathbf{a}^T \Phi \Phi^T \mathbf{a} \\
&= \frac{1}{2} \left(\mathbf{a}^T \Phi \Phi^T \Phi \Phi^T \mathbf{a} - 2 \mathbf{a}^T \Phi \Phi^T \mathbf{t} + \mathbf{t}^T \mathbf{t} \right) + \frac{\lambda}{2} \mathbf{a}^T \Phi \Phi^T \mathbf{a} \\
&= \frac{1}{2} \mathbf{a}^T \Phi \Phi^T \Phi \Phi^T \mathbf{a} - \frac{1}{2} \mathbf{a}^T \Phi \Phi^T \mathbf{t} + \frac{1}{2} \mathbf{t}^T \mathbf{t} + \frac{\lambda}{2} \mathbf{a}^T \Phi \Phi^T \mathbf{a}
\end{aligned}$$

By defining the *Gram* matrix $\mathbf{K} = \Phi \Phi^T$, which is a symmetric $N \times N$ matrix with elements, $K_{nm} = k(x_n, x_m) = \phi(x_n)^T \phi(x_m)$, where k is a kernel function, the sum-of-squares error function can be written as,

$$E(\mathbf{a}) = \frac{1}{2} \mathbf{a}^T \mathbf{K} \mathbf{K} \mathbf{a} - \mathbf{a}^T \mathbf{K} \mathbf{t} + \frac{1}{2} \mathbf{t}^T \mathbf{t} + \frac{\lambda}{2} \mathbf{a}^T \mathbf{K} \mathbf{a}$$

If we set the gradient of $E(\mathbf{a})$ equal to zero, then, we obtain the following solution,

$$\begin{aligned}
\nabla E(\mathbf{a}) = \mathbf{0} &\Leftrightarrow \nabla \frac{1}{2} \mathbf{a}^T \mathbf{K} \mathbf{K} \mathbf{a} - \mathbf{a}^T \mathbf{K} \mathbf{t} + \frac{1}{2} \mathbf{t}^T \mathbf{t} + \frac{\lambda}{2} \mathbf{a}^T \mathbf{K} \mathbf{a} = \mathbf{0} \\
&\Leftrightarrow \mathbf{K} \mathbf{K} \mathbf{a} - \mathbf{K} \mathbf{t} + \frac{\lambda}{2} \mathbf{a}^T \mathbf{K} \mathbf{a} = \mathbf{0} \\
&\Leftrightarrow \mathbf{K} \mathbf{K} \mathbf{a} - \mathbf{K} \mathbf{t} = \mathbf{0} \\
&\Leftrightarrow \mathbf{K} \mathbf{a} (\mathbf{K} + \lambda \mathbf{I}) = \mathbf{K} \mathbf{t} \\
&\Leftrightarrow \mathbf{a} (\mathbf{K} + \lambda \mathbf{I}) = \mathbf{t} \\
&\Leftrightarrow \mathbf{a} = (\mathbf{K} + \lambda \mathbf{I})^{-1} \mathbf{t}
\end{aligned}$$

By substituting this back into the linear regression model, we obtain,

$$y(\mathbf{x}) = \mathbf{w}^T \Phi \phi(\mathbf{x}) = \mathbf{a}^T \Phi \phi(\mathbf{x}) = \Phi \phi(\mathbf{x}) (\mathbf{K} + \lambda \mathbf{I})^{-1} \mathbf{t} = \mathbf{k}(\mathbf{x})^T (\mathbf{K} + \lambda \mathbf{I})^{-1} \mathbf{t}$$

where $\mathbf{k}(\mathbf{x})^T = [k(\mathbf{x}_1, \mathbf{x}), \dots, k(\mathbf{x}_N, \mathbf{x})] = [\phi(\mathbf{x}_1)^T \phi(\mathbf{x}), \dots, \phi(\mathbf{x}_N)^T \phi(\mathbf{x})]$

Therefore, the dual formulation allows the solution to the least-squares problem to be expressed entirely in terms of a kernel function.

NOTE: In the dual formulation, we determine the parameter vector \mathbf{a} by inverting an $N \times N$ matrix, whereas in the original parameter space formulation, we had to invert an $M \times M$ matrix in order to determine \mathbf{w} . Because N is typically much larger than M , the dual formulation does not seem to be particularly useful. However, the advantage of the dual formulation is that it is expressed entirely in terms of the kernel function $k(\mathbf{x}, \mathbf{x}')$. Therefore, we work directly in terms of kernels and avoid the explicit introduction of the feature vector $\phi(\mathbf{x})$, which allows us to use feature spaces of high, even infinite, dimensionality.

In fact, the existence of a dual representation based on the Gram matrix is a property of many linear models. For instance, let's develop the same representation for the Perceptron algorithm. The update rule for the Perceptron is as follows,

$$\mathbf{w}^{\tau+1} = \mathbf{w}^\tau + \eta\phi(\mathbf{x}_n)t_n$$

Assuming $\mathbf{w}^0 = \mathbf{0}$, then

$$\begin{aligned}\mathbf{w}^{(1)} &= \eta\phi(\mathbf{x}_n)t_n \\ \mathbf{w}^{(2)} &= 2\eta\phi(\mathbf{x}_n)t_n \\ &\dots \\ \mathbf{w}^{(\tau)} &= \tau\eta\phi(\mathbf{x}_n)t_n \\ \mathbf{w}^{(\tau+1)} &= (\tau+1)\eta\phi(\mathbf{x}_n)t_n\end{aligned}$$

or

$$\mathbf{w} = \sum_{n=1}^N \eta c_n t_n \phi(\mathbf{x}_n) = \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n)$$

By substituting \mathbf{w} back to the original update formula, we obtain,

$$\begin{aligned}\sum_{n=1}^N a_n^{(\tau+1)} t_n \phi(\mathbf{x}_n) &= \sum_{n=1}^N a_n^{(\tau)} t_n \phi(\mathbf{x}_n) + \eta t_n \phi(\mathbf{x}_n) \Leftrightarrow \\ \sum_{n=1}^N a_n^{(\tau+1)} &= \sum_{n=1}^N a_n^{(\tau)} + \eta\end{aligned}$$

In other words, the update process is to add learning rate η to the coefficient a_n , corresponding to input \mathbf{x}_n . Finally, substituting back to the linear model, we obtain,

$$y(\mathbf{x}) = f(\mathbf{w}^T \phi(\mathbf{x})) = f\left(\sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n)^T \phi(\mathbf{x})\right) = f\left(\sum_{n=1}^N a_n t_n k(\mathbf{x}_n, \mathbf{x})\right)$$

6.2 Constructing Kernels

One approach is to choose a feature space mapping $\phi(\mathbf{x})$, e.g., polynomials, gaussian etc, and then use it to find the corresponding kernel.

```
[45]: x_space = np.linspace(-1, 1, 100)

# Create 12 degree polynomial basis functions
polynomial = PolynomialFeature(degree=12)

# Create 12 Gaussian basis functions
gaussian = GaussianFeature(mean=np.linspace(-1, 1, 12), sigma=0.1)

# Create 12 sigmoid basis functions
sigmoid = SigmoidFeature(mean=np.linspace(-1, 1, 12), sigma=0.1)
```

```

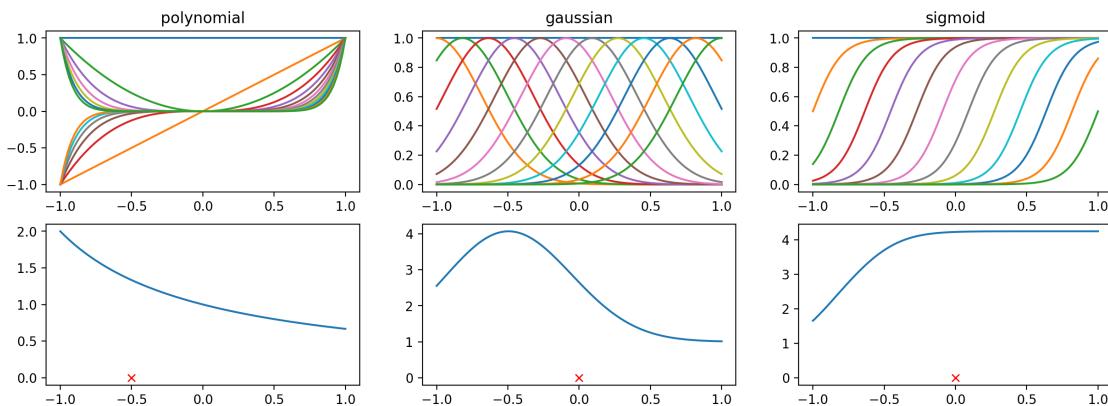
plt.figure(figsize=(15, 5))
for i, phi in enumerate([polynomial, gaussian, sigmoid]):
    x = phi.transform(x_space)

    plt.subplot(2, 3, i + 1)
    for j in range(x.shape[1]):
        plt.plot(x_space, x[:, j])
    plt.title(phi.__class__.__name__.removeprefix("Feature").lower())

    plt.subplot(2, 3, i + 4)
    plt.plot(0, 0, "rx") if i > 0 else plt.plot(-0.5, 0, "rx")
    plt.plot(x_space, x @ phi.transform(-0.5).T)

plt.show()

```



Another approach is to construct kernel functions directly. In order to exploit kernel substitution, we need to be able to construct valid kernel functions, or in other words kernels that correspond to a scalar product in some (perhaps infinite dimensional) feature space. Consider for instance, a kernel function given by $k(\mathbf{x}, \mathbf{z}) = (\mathbf{x}^T \mathbf{z})^2$. Expanding the terms, we can thereby identify the corresponding nonlinear feature mapping,

$$\begin{aligned}
k(\mathbf{x}, \mathbf{z}) &= (\mathbf{x}^T \mathbf{z})^2 = (x_1 z_1 + x_2 z_2 + \dots + x_N z_N)^2 \\
&= \sum_{n=1}^N x_n^2 z_n^2 + 2 \sum_{n=1}^N \sum_{m=1}^{n-1} x_n z_n x_m z_m \\
&= (x_1^2, \sqrt{2}x_1 x_2, \dots, x_N^2)(z_1^2, \sqrt{2}z_1 z_2, \dots, z_N^2)^T \\
&= \phi(\mathbf{x})^T \phi(\mathbf{z})
\end{aligned}$$

One standard technique for constructing kernels is to build them out of simpler kernels as building blocks. This can be done using the properties (6.13) to (6.22) appearing in the book. In general, the kernel should be symmetric and positive semidefinite and express the appropriate form of similarity between \mathbf{x} and \mathbf{x}' .

A commonly used kernel is the Gaussian kernel, which takes the form,

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

In this context, it is not interpreted as a probability density, and hence the normalization coefficient is omitted.

By expanding the square we obtain,

$$\|\mathbf{x} - \mathbf{z}\|^2 = \mathbf{x}^T \mathbf{z} - 2\mathbf{x}^T \mathbf{z} + (\mathbf{z})^T \mathbf{z}$$

thus,

$$\exp(-(\mathbf{x}^T \mathbf{x} - 2\mathbf{x}^T \mathbf{z} + (\mathbf{z})^T \mathbf{z})/2\sigma^2) = \exp(-\mathbf{x}^T \mathbf{x}/2\sigma^2) + \exp(\mathbf{x}^T \mathbf{z}/\sigma^2) + \exp(-\mathbf{z}^T \mathbf{z}/2\sigma^2)$$

which is a valid kernel due to (6.14) and (6.16) and the fact that the linear kernel is valid. Note that the Gaussian kernel is not restricted to Euclidean distance. If we use kernel substitution to replace $\mathbf{x}^T \mathbf{z}$ with a nonlinear kernel $\kappa(\mathbf{x}, \mathbf{z})$, we obtain

$$k(\mathbf{x}, \mathbf{z}) = \exp\left(-\frac{1}{2\sigma^2}(\kappa(\mathbf{x}, \mathbf{x}) - 2\kappa(\mathbf{x}, \mathbf{z}) + \kappa(\mathbf{z}, \mathbf{z}))\right) =$$

Kernel functions may also be defined over generic objects, as diverse as graphs, sets, strings, and text documents. Consider, for instance, a set and define a non-vectorial space consisting of all possible subsets. If A_1 and A_2 are two such subsets, then one simple choice of kernel would be,

$$k(A_1, A_2) = 2^{|A_1 \cap A_2|}$$

6.3 Radial Basis Function Networks

Radial basis functions have the property that each basis function depends only on the radial distance (typically Euclidean) from a centre μ_j , so that $\phi_j(\mathbf{x}) = h(\|\mathbf{x} - \mu_j\|)$. Historically, radial basis functions were introduced for the purpose of exact function interpolation, which is achieved by expressing $f(\mathbf{x})$ as a linear combination of radial basis functions, one centred on every data point. Then, the parameters \mathbf{w} are found by least squares, and because there are the same number of parameters as there are constraints (data points), the resulted function fits every target value exactly. In machine learning applications, however, the target values are generally noisy, and exact interpolation is undesirable (over-fitting). Moreover, because there is one basis function associated with every data point, the corresponding model can be computationally costly to evaluate when making predictions for new data points.

One way of choosing the basis function centres is to randomly chose a subset of the data points. A more systematic approach is to use orthogonal least squares, a sequential selection process, in which, at each step the next data point to be chosen as a basis function centre corresponds to the one that gives the greatest reduction in the sum-of-squares error. Clustering algorithms such as k -means have also been used, which give a set of basis function centres that no longer coincide with training data points.

6.4 Gaussian Processes

In order to motivate the Gaussian process viewpoint, let us return to the linear regression example and re-derive the predictive distribution by working in terms of distributions over functions $y(\mathbf{x}, \mathbf{w})$. Consider the model defined in terms of a linear combination of M fixed basis functions given by the elements of the vector $\phi(\mathbf{x})$ so that,

$$y(\mathbf{x}) = \mathbf{w}^T \phi(\mathbf{x})$$

Then, consider a prior distribution over \mathbf{w} given by an isotropic Gaussian (see also Chapter 3) of the form,

$$p(\mathbf{w}) = \mathcal{N}(\mathbf{w} | \mathbf{0}, \alpha^{-1} \mathbf{I})$$

Since, for any given value of \mathbf{w} , $y(\mathbf{x})$ defines a particular function of \mathbf{x} , the probability distribution over \mathbf{w} induces a probability distribution over functions $y(\mathbf{x})$. For the training data points $\mathbf{x}_1, \dots, \mathbf{x}_N$, we are therefore interested in the joint distribution of the function values $y(\mathbf{x}_1), \dots, y(\mathbf{x}_N)$, or $\mathbf{y} = \Phi\mathbf{w}$, where Φ is the design matrix.

In order to find the probability distribution of \mathbf{y} , note that \mathbf{y} is a linear combination of Gaussian distributed variables given by the elements of \mathbf{w} and hence is itself Gaussian. We therefore need only to find its mean and covariance,

$$E[\mathbf{y}] = E[\Phi\mathbf{w}] = \Phi E[\mathbf{w}] = \Phi\mathbf{0} = \mathbf{0}$$

and

$$\text{cov}[\mathbf{y}] = E[\mathbf{y}\mathbf{y}^T] = E[\Phi\mathbf{w}\mathbf{w}^T\Phi^T] = \Phi E[\mathbf{w}\mathbf{w}^T]\Phi^T = \frac{1}{\alpha}\Phi\Phi^T = \mathbf{K}$$

where \mathbf{K} is the Gram matrix.

This model provides us with a particular example of a Gaussian process, defined by the linear regression model (6.49) with a weight prior (6.50). In cases where the input vector \mathbf{x} is two dimensional, this is also known as a *Gaussian random field*.

Thus, Gaussian stochastic processes is the joint distribution over N specified completely by the second-order statistics. When, we have no prior knowledge about the mean of $y(\mathbf{x})$ we typically take it to be zero. This is equivalent to choosing the mean of the prior over weight values $p(\mathbf{w})$ to be zero in the basis function viewpoint. The specification of the Gaussian process is then completed by the covariance of $y(\mathbf{x})$ evaluated at any two values of $y(\mathbf{x})$, which is given by the kernel function

$$E[y(\mathbf{x}_n)y(\mathbf{x}_m)] = \mathbf{K}_{nm} = k(\mathbf{x}_n, \mathbf{x}_m)$$

Towards defining kernel functions directly for the covariance, two common choices are the Gaussian kernel and the exponential kernel given by,

$$k(x, z) = \exp(-\theta|x - z|)$$

6.4.2 Gaussian processes for regression

Recall that the noise on the observed target values for linear regression models may be modelled as,

$$t_n = y_n + \epsilon_n$$

where ϵ_n is a random noise variable whose value is chosen independently for each observation. To that end, the noise processes may be modelled as a Gaussian distribution

$$p(t_n|y_n) = \mathcal{N}(t_n|y_n, \beta^{-1})$$

Because the noise is independent for each data point, the joint distribution of the target values is given by an isotropic Gaussian of the form,

$$p(\mathbf{t}|\mathbf{y}) = \mathcal{N}(\mathbf{t}|\mathbf{y}, \beta^{-1}\mathbf{I}_N)$$

From the definition of a Gaussian process, the marginal distribution $p(\mathbf{y})$ is given by a Gaussian whose mean is zero and whose covariance is defined by a Gram matrix so that,

$$p(\mathbf{y}) = \mathcal{N}(\mathbf{y}|\mathbf{0}, \mathbf{K})$$

The kernel function that determines \mathbf{K} is typically chosen to express that, for points \mathbf{x}_n and \mathbf{x}_m that are similar, the corresponding values $y(\mathbf{x}_n)$ and $y(\mathbf{x}_m)$ will be more strongly correlated than for dissimilar points. A widely used kernel function for Gaussian process regression is given by the exponential of a quadratic form, and the addition of constant and linear terms to give,

$$k(\mathbf{x}_n, \mathbf{x}_m) = \theta_0 \exp\left\{-\frac{\theta_1}{2} \|\mathbf{x}_n - \mathbf{x}_m\|^2\right\} + \theta_2 + \theta_3 \mathbf{x}_n^T \mathbf{x}_m$$

```
[147]: x_space = np.linspace(-1, 1, 100)[:, None]

def K(theta, x):
    N = x.shape[0]
    r = np.zeros((N, N))
    for (i, _), xn in np.ndenumerate(x):
        for (j, _), xm in np.ndenumerate(x):
            r[i][j] = theta[0] * np.exp(-(theta[1] / 2) * np.linalg.norm(xn - xm) ** 2) + theta[2] + theta[3] * xn * xm
    return r

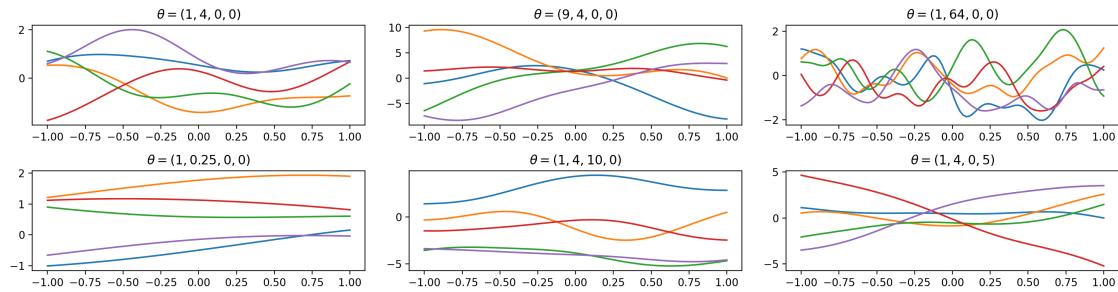
plt.figure(figsize=(15, 4), tight_layout=True)
mu = np.zeros(x_space.shape)
```

```

for i, theta in enumerate([(1, 4, 0, 0), (9, 4, 0, 0), (1, 64, 0, 0), (1, 0.25, 0, 0), (1, 4, 10, 0), (1, 4, 0, 5)]):
    prior_gaussian = MultivariateGaussian(mu, K(theta, x_space))
    plt.subplot(2, 3, i + 1)
    plt.plot(x_space, prior_gaussian.draw(5).T)
    plt.title(f"\$\\theta={theta\$}")

plt.show()

```



In order to find the marginal distribution $p(t)$, conditioned on the input values x_1, \dots, x_N , we need to integrate over y .

$$p(t) = \int p(t|y)p(y)dy = \int \mathcal{N}(t|y, \beta^{-1}\mathbf{I}_N)\mathcal{N}(y|\mathbf{0}, \mathbf{K})dy \stackrel{(2.115)}{=} \mathcal{N}(t|\mathbf{0}, \mathbf{C})$$

where $\mathbf{C} = \beta^{-1}\mathbf{I}_N + \mathbf{K}$ since $\mathbf{A} = \mathbf{I}$ and $\mathbf{b} = \mathbf{0}$ in (2.115). This result reflects the convolution of two independent Gaussian sources of randomness (associated with y and ϵ), and thus their covariances simply sum.

We have used the Gaussian process viewpoint to build a model of the joint distribution over sets of data points. Our goal in regression, however, is to predict the target variables for new inputs, given a set of training data. This requires that we evaluate the predictive distribution $p(t_{N+1}|\mathbf{x}_{N+1}, t_N, \mathbf{X}_N)$. To derive the conditional distribution, we start from the joint distribution $p(t_{N+1})$, thus, from (6.61) we obtain,

$$p(t_{N+1}) = \mathcal{N}(t_{N+1}|\mathbf{0}, \mathbf{C}_{N+1})$$

where, applying the results from Section 2.3.1, we have defined the covariance matrix as follows,

$$\mathbf{C}_{N+1} = \begin{bmatrix} \mathbf{C}_N & \mathbf{k} \\ \mathbf{k}^T & c \end{bmatrix}$$

where vector \mathbf{k} has elements $k(\mathbf{x}_n, \mathbf{x}_{N+1})$ and $c = k(\mathbf{x}_{N+1}, \mathbf{x}_{N+1}) + \beta^{-1}$.

By analogy to Eq. (2.94) - (2.98), we can simply treat t_{N+1} as \mathbf{x}_a , t_N as \mathbf{x}_b , c as Σ_{aa} , \mathbf{k} as Σ_{ba} , \mathbf{k}^T as Σ_{ab} and \mathbf{C}_N as Σ_{bb} . Substituting them into Eq. (2.79) and Eq. (2.80) gives,

$$_{aa} = \begin{pmatrix} & & -1 \\ aa & - ab & bb \\ & & ba \end{pmatrix}^{-1} = (c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k})^{-1}$$

and

$$_{ab} = - \begin{pmatrix} & & -1 \\ aa & - ab & bb \\ & & ba \end{pmatrix}^{-1} \begin{pmatrix} & & -1 \\ ab & - bb & ba \end{pmatrix} = -(c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k})^{-1} \mathbf{k}^T \mathbf{C}_N^{-1}$$

For its mean $\mu_{a|b}$, we have,

$$\mu_{a|b} = \mathbf{0} - \left(c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k} \right) \left(- (c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k})^{-1} \mathbf{k}^T \mathbf{C}_N^{-1} \right) (\mathbf{t}_N - \mathbf{0}) = \left(c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k} \right) \left((c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k})^{-1} \mathbf{k}^T \mathbf{C}_N^{-1} \right) = \left(c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k} \right)$$

Therefore, the predictive distribution is as follows,

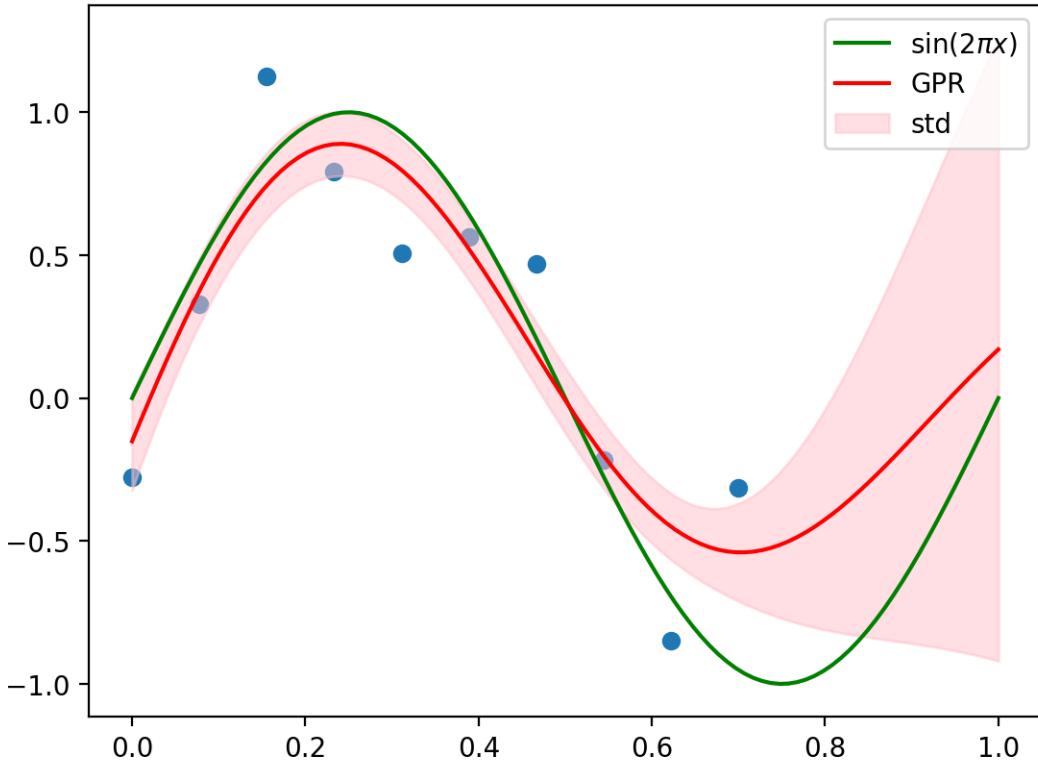
$$p(t_{N+1} | \mathbf{t}_N) = \mathcal{N}(t_{N+1} | \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{t}_N, c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k})$$

Note that for large training data sets, the direct application of Gaussian process methods may become infeasible.

```
[76]: x_space = np.linspace(0, 1, 100)
x, t = generate_toy_data(lambda x: np.sin(2 * np.pi * x), sample_size=10, std=0.5, domain=(0, 0.7))

gpr = GaussianProcessRegression(kernel=RBF(theta=np.ones(x.ndim) * 5), beta=100)
gpr.fit(x, t)
mu, sigma = gpr.predict(x_space)

plt.scatter(x, t)
plt.plot(x_space, np.sin(2 * np.pi * x_space), color="green", label="$\sin(2\pi x)$")
plt.plot(x_space, mu, color="red", label="GPR")
plt.fill_between(x_space, mu - 2 * np.sqrt(sigma), mu + 2 * np.sqrt(sigma), alpha=0.5, color="pink", label="std")
plt.legend()
plt.show()
```



The extension of the Gaussian process formalism to multiple target variables $\mathbf{T} = (\mathbf{t}_1, \dots, \mathbf{t}_N)$, also known as *co-kriging* is as follows,

$$p(\mathbf{t}_{N+1}|\mathbf{T}) = \mathcal{N}(\mathbf{t}_{N+1}|\mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{T}, c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k})$$

which corresponds to a multi-variate Gaussian distribution.

6.4.3 Learning the hyperparameters

In practice, rather than fixing the covariance function, we may use a parametric family of functions and infer the parameters from the data. These parameters may govern the length scale of the correlations and the precision of the noise. Techniques for learning these hyperparameters are based on the evaluation of the likelihood function $p(\mathbf{t}|\theta)$ where θ denotes the hyperparameters of the Gaussian process model. The simplest approach is to make a point estimate of θ by maximizing the log likelihood function. Maximization of the log-likelihood can be done using efficient gradient-based optimization algorithms, such as conjugate gradients.

The log-likelihood function for a Gaussian process regression model is easily evaluated using the standard form for a multivariate Gaussian distribution, giving

$$\begin{aligned}
\ln p(\mathbf{t}|\theta) &= \ln \mathcal{N}(\mathbf{t}|\mathbf{0}, \mathbf{C}) \\
&= \ln \left(\frac{1}{(2\pi)^{N/2} |\mathbf{C}|^{1/2}} \exp \left\{ -\frac{1}{2} \mathbf{t}^T \mathbf{C}^{-1} \mathbf{t} \right\} \right) \\
&= -\ln \left((2\pi)^{N/2} |\mathbf{C}|^{1/2} \right) - \frac{1}{2} \mathbf{t}^T \mathbf{C}^{-1} \mathbf{t} \\
&= -\frac{N}{2} \ln(2\pi) - \frac{1}{2} \ln |\mathbf{C}| - \frac{1}{2} \mathbf{t}^T \mathbf{C}^{-1} \mathbf{t}
\end{aligned}$$

Then, we need the gradient of the log-likelihood function with respect to the parameter vector,

$$\begin{aligned}
\frac{\partial}{\partial \theta_i} \ln p(\mathbf{t}|\theta) &= -\frac{1}{2} \frac{\partial}{\partial \theta_i} \ln |\mathbf{C}| - \frac{1}{2} \frac{\partial}{\partial \theta_i} \mathbf{t}^T \mathbf{C}^{-1} \mathbf{t} \\
&\stackrel{(C.21)}{=} -\frac{1}{2} \frac{\partial}{\partial \theta_i} \ln |\mathbf{C}| + \frac{1}{2} \mathbf{t}^T \mathbf{C}^{-1} \frac{\partial \mathbf{C}}{\partial \theta_i} \mathbf{C}^{-1} \mathbf{t} \\
&\stackrel{(C.22)}{=} -\frac{1}{2} \text{Tr} \left(\mathbf{C}^{-1} \frac{\partial \mathbf{C}}{\partial \theta_i} \right) + \frac{1}{2} \mathbf{t}^T \mathbf{C}^{-1} \frac{\partial \mathbf{C}}{\partial \theta_i} \mathbf{C}^{-1} \mathbf{t}
\end{aligned}$$

where the evaluation of the partial derivatives of \mathbf{C} depends on the covariance functions (kernels).

Note that $\ln p(\mathbf{t}|\theta)$ is a nonconvex function and it can have multiple maxima.

Moreover, we have assumed that the contribution of the predictive variance arising from the additive noise β is a constant. For some problem, known as *heteroscedastic*, the noise variance itself depends on \mathbf{x} . One solution is to introduce a second Gaussian process to represent the dependence of β on the input \mathbf{x} .

6.4.4 Automatic relevance determination

Maximizing the likelihood for learning the length-scale parameter can usefully be extended by incorporating a separate parameter for each input variable. This allows the relative importance of different inputs to be inferred from the data, which represents an example of automatic relevance determination (ARD). Therefore, we may have a kernel function of the form,

$$k(\mathbf{x}, \mathbf{z}) = \exp \left\{ -\frac{1}{2} \|\eta(\mathbf{x} - \mathbf{z})\|^2 \right\}$$

As a particular parameter η_i becomes small, the function becomes relatively insensitive to the corresponding input variable x_i . By adapting these parameters to a data set using maximum likelihood, we can detect input variables that have little effect on the predictive distribution, because the corresponding values of η_i will be small. This is useful in practice because it allows irrelevant inputs to be discarded.

The partial derivative of $k(\mathbf{x}, \mathbf{z})$ with respect to η_i is given by,

$$\begin{aligned}
\frac{\partial}{\partial \eta_i} \exp \left\{ -\frac{1}{2} \|\eta(\mathbf{x} - \mathbf{z})\|^2 \right\} &= \exp \left\{ -\frac{1}{2} \|\eta(\mathbf{x} - \mathbf{z})\|^2 \right\} - \frac{1}{2} \frac{\partial}{\partial \eta_i} \|\eta(\mathbf{x} - \mathbf{z})\|^2 \\
&= \exp \left\{ -\frac{1}{2} \|\eta(\mathbf{x} - \mathbf{z})\|^2 \right\} - \frac{1}{2} \frac{\partial}{\partial \eta_i} \sum_{i=1}^N \eta_i (x_i - z_i)^2 \\
&= \exp \left\{ -\frac{1}{2} \|\eta(\mathbf{x} - \mathbf{z})\|^2 \right\} - \frac{1}{2} (x_i - z_i)^2
\end{aligned}$$

```
[189]: x0 = np.linspace(0, 1, 20)
x1 = x0 + np.random.normal(scale=0.1, size=20)
x2 = np.random.normal(scale=0.1, size=20)
t = np.sin(2 * np.pi * x0) + np.random.normal(scale=0.1, size=20)
x = np.vstack((x0, x1, x2)).T

x0 = np.linspace(0, 1, 100)
x1 = x0 + np.random.normal(scale=0.1, size=100)
x2 = np.random.normal(scale=0.1, size=100)
x_space = np.vstack((x0, x1, x2)).T

model = GaussianProcessRegression(kernel=RBF(np.array([1.0, 1.0, 1.0])), ↴
    ↪beta=100)
model.fit(x, t)
mu, sigma = model.predict(x_space)

plt.figure(figsize=(15, 5))

plt.subplot(1, 2, 1)
plt.scatter(x[:, 0], t)
plt.plot(x_space[:, 0], np.sin(2 * np.pi * x_space[:, 0]), color="green", ↴
    ↪label="$\sin(2\pi x)$")
plt.plot(x_space[:, 0], mu, color="red", label="GPR")
plt.fill_between(x_space[:, 0], mu - 2 * np.sqrt(sigma), mu + 2 * np.
    ↪sqrt(sigma), alpha=0.5, color="pink", label="std")
plt.legend()

model = GaussianProcessRegression(kernel=RBF(np.array([1.0, 1.0, 1.0])), ↴
    ↪beta=100)
model.fit(x, t, 1000, 0.001)
mu_adr, sigma_adr = model.predict(x_space)

plt.subplot(1, 2, 2)
plt.scatter(x[:, 0], t)
plt.plot(x_space[:, 0], np.sin(2 * np.pi * x_space[:, 0]), color="green", ↴
    ↪label="$\sin(2\pi x)$")
plt.plot(
```

```

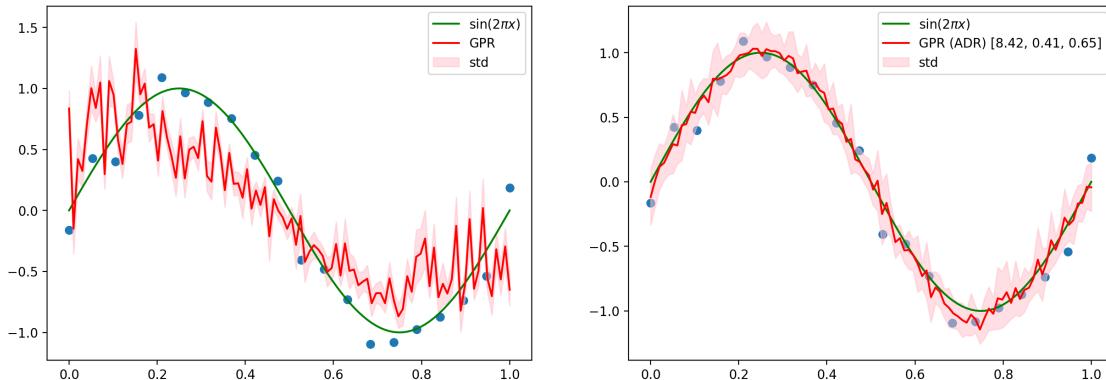
        x_space[:, 0], mu_adr, color="red", label=f"GPR (ADR) {[np.round(p, 2) for
        ↪p in model._kernel.theta.tolist()]}"
    )
    plt.fill_between(
        x_space[:, 0],
        mu_adr - 2 * np.sqrt(sigma_adr),
        mu_adr + 2 * np.sqrt(sigma_adr),
        alpha=0.5,
        color="pink",
        label="std",
    )
plt.legend()
plt.show()

```

```

-- Iterations 0: 106.62105480846333
-- Iterations 100: 16.73499899402815
-- Iterations 200: 10.900800926148609
-- Iterations 300: 8.352834973210353
-- Iterations 400: 6.79206345414369
-- Iterations 500: 5.658719022565627
-- Iterations 600: 4.743421926165226
-- Iterations 700: 3.953116694126315
-- Iterations 800: 3.259548576802345
-- Iterations 900: 2.6734093844879148

```



6.4.5 Gaussian process for classification

Similar to logistic regression, we can adapt Gaussian process to classification problems by transforming the output using an appropriate nonlinear activation function. Consider a binary problem with a target variable $t \in \{0, 1\}$. If we define a Gaussian process over a function $a(\mathbf{x})$ and then transform the function using a logistic sigmoid $y = \sigma(a)$, we obtain a non-Gaussian stochastic process over functions $y(\mathbf{x}) \in (0, 1)$.

As an example, we plot a sample from a Gaussian process prior over functions $a(\mathbf{x})$ and the resulting transformation using the logistic sigmoid function.

```
[63]: x_space = np.linspace(-1, 1, 100)

def logistic(x):
    return 1 / (1 + np.exp(-x))

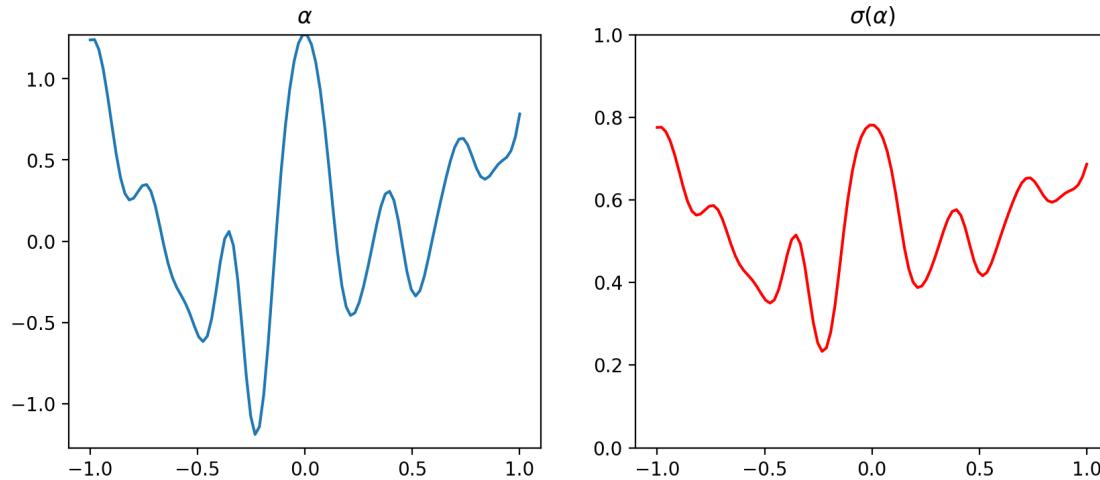
k = RBF(theta=np.ones(x_space.ndim) * 100)
a = np.random.multivariate_normal(np.zeros(x_space.shape), k(x_space, x_space), ↵
    ↵1)[0]

plt.figure(figsize=(10, 4))

plt.subplot(1, 2, 1)
plt.plot(x_space, a)
bound = max(np.abs(a.min()), a.max())
plt.ylim(-bound, bound)
plt.title("$\alpha$")

plt.subplot(1, 2, 2)
plt.plot(x_space, logistic(a), color="red")
plt.ylim(0, 1)
plt.title("$\sigma(\alpha)$")

plt.show()
```



Our goal is to determine the predictive distribution $p(t_{N+1} | \mathbf{t})$. To that end, we introduce a Gaussian process prior over the vector $\mathbf{a}_{N+1} = [a(\mathbf{x}_1), \dots, a(\mathbf{x}_{N+1})]^T$, which in turn, defines a non-Gaussian

process over \mathbf{t}_{N+1} , due to the nonlinear transformation. Then, by conditioning on the training data \mathbf{t}_N we obtain the required predictive distribution. The Gaussian process prior for \mathbf{a}_{N+1} takes the form,

$$p(\mathbf{a}_{N+1}) = \mathcal{N}(\mathbf{a}_{N+1} | \mathbf{0}, \mathbf{C}_{N+1})$$

Unlike the regression case, the covariance matrix no longer includes a noise term because we assume that all training data points are correctly labelled. However, for numerical reasons it is convenient to introduce a noise-like term governed by a parameter β that ensures that the covariance matrix is positive definite. Thus, the covariance matrix has elements given by,

$$C_{nm} = k(\mathbf{x}_n, \mathbf{x}_m) + \beta \delta_{nm}$$

For a binary classification problem, it is sufficient to predict $p(t_{N+1} = 1 | \mathbf{t}_N)$ because $p(t_{N+1} = 0 | \mathbf{t}_N) = 1 - p(t_{N+1} = 1 | \mathbf{t}_N)$. Thus, the required predictive distribution is given by,

$$p(t_{N+1} = 1 | \mathbf{t}_N) = \int p(t_{N+1} = 1 | a_{N+1}) p(a_{N+1} | \mathbf{t}_N) da_{N+1} \stackrel{(6.73)}{=} \int \sigma(a_{N+1}) p(a_{N+1} | \mathbf{t}_N) da_{N+1}$$

This integral is analytically intractable, and so may be approximated. Similar to the previous chapters, we rely on the Laplacian approximation. In particular, we seek a Gaussian approximation to the posterior distribution over a_{N+1} , which using the Bayes theorem, gives

$$\begin{aligned} p(a_{N+1} | \mathbf{t}_N) &= \int p(a_{N+1}, \mathbf{a}_N | \mathbf{t}_N) d\mathbf{a}_N \\ &\stackrel{p(Y|X) \Leftrightarrow \frac{p(X|Y)p(Y)}{p(X)}}{=} \int \frac{p(\mathbf{t}_N | a_{N+1}, \mathbf{a}_N) p(a_{N+1}, \mathbf{a}_N)}{p(\mathbf{t}_N)} d\mathbf{a}_N \\ &\stackrel{p(X,Y) \Leftrightarrow p(Y|X)p(X)}{=} \int \frac{p(\mathbf{t}_N | \mathbf{a}_N) p(a_{N+1} | \mathbf{a}_N) p(\mathbf{a}_N)}{p(\mathbf{t}_N)} d\mathbf{a}_N \\ &\stackrel{p(Y|X) \Leftrightarrow \frac{p(X|Y)p(Y)}{p(X)}}{=} \int p(a_{N+1} | \mathbf{a}_N) p(\mathbf{a}_N | \mathbf{t}_N) d\mathbf{a}_N \end{aligned}$$

The conditional distribution is obtained similar to $p(t_{N+1} | \mathbf{t}_N)$ in Gaussian process regression, invoking (6.66) and (6.67),

$$p(a_{N+1} | \mathbf{a}_N) = \mathcal{N}(a_{N+1} | \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{a}_N, c - \mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{k})$$

Since $p(t_{N+1} = 1 | a_{N+1}) = \sigma(a_{N+1})$, we may generate classification predictions using $\sigma(\mathbf{k}^T \mathbf{C}_N^{-1} \mathbf{a}_N)$.

```
[169]: # number of training points
N = 100
```

```
x, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2,
    n_clusters_per_class=1, n_samples=N, random_state=21)
```

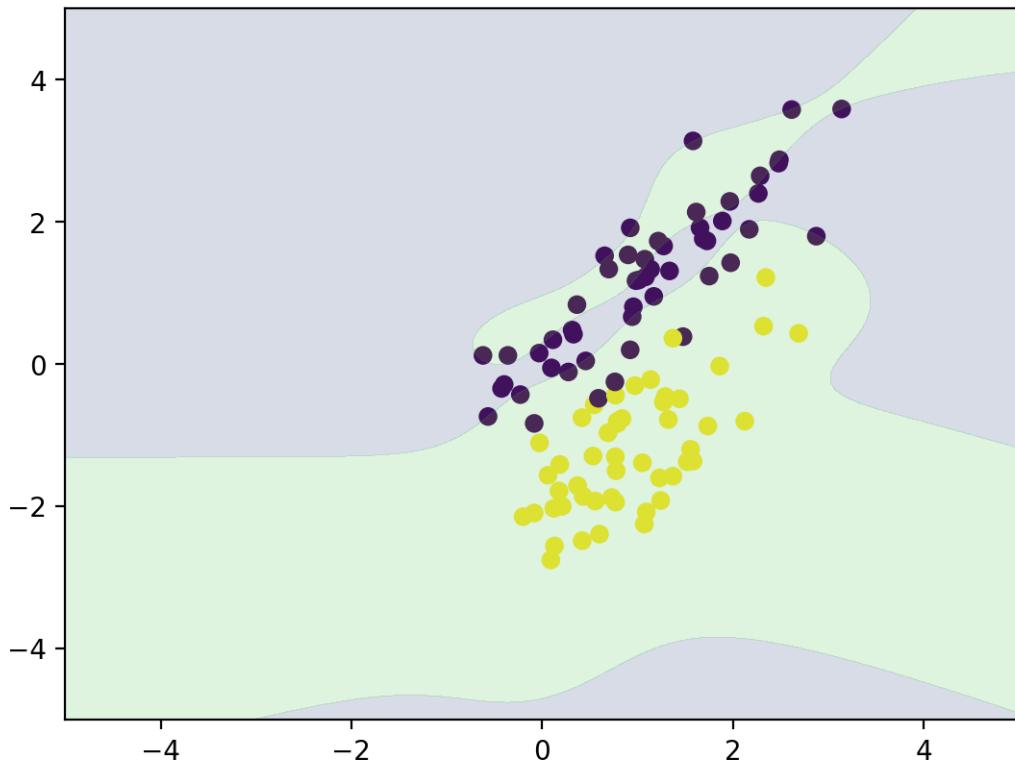
```

)
x1, x2 = np.meshgrid(np.linspace(-5, 5, N), np.linspace(-5, 5, N))
x_test = np.array([x1, x2]).reshape(2, -1).T

model = GaussianProcessClassifier(kernel=RBF(theta=np.array([0.5, 0.5])))
model.fit(x, t)
predicted, _ = model.predict(x_test)

plt.scatter(x[:, 0], x[:, 1], c=t)
plt.contourf(x1, x2, predicted.reshape(N, N), alpha=0.2, levels=np.linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.show()

```



However, in order to derive the full predictive distribution we also need to find a Laplace approximation for the posterior distribution $p(\mathbf{a}_N | \mathbf{t}_N)$ in order to evaluate the integrals (6.77) and (6.76). The posterior is proportional to the product of the likelihood and a prior,

$$p(\mathbf{a}_N | \mathbf{t}_N) \propto p(\mathbf{t}_N | \mathbf{a}_N) p(\mathbf{a}_N)$$

where the prior is given by a zero-mean Gaussian process with covariance matrix \mathbf{C}_N and the likelihood is given by,

$$p(\mathbf{t}_N | \mathbf{a}_N) = \prod_{i=1}^N \sigma(a_i)^{t_i} (1 - \sigma(a_i))^{t_i-1}$$

Then, in order to obtain the Laplace approximation, we derive the logarithm of the posterior,

$$\begin{aligned} \ln p(\mathbf{a}_N | \mathbf{t}_N) &= \ln(p(\mathbf{t}_N | \mathbf{a}_N)p(\mathbf{a}_N)) \\ &= \ln p(\mathbf{t}_N | \mathbf{a}_N) + \ln p(\mathbf{a}_N) \\ &= -\frac{1}{2}\mathbf{a}_N^T \mathbf{C}_N^{-1} \mathbf{a}_N - \frac{N}{2} \ln(2\pi) - \frac{1}{2} \ln |\mathbf{C}_N| + \mathbf{t}_N^T \mathbf{a}_N - \sum_{n=1}^N \ln(1 + e^{a_n}) \end{aligned}$$

6.4.7 Connection to neural networks In a Bayesian neural network, the prior distribution over the parameter vector \mathbf{w} , in conjunction with the network function $f(\mathbf{x}, \mathbf{w})$, produces a prior distribution over functions from y . It has been shown that for a broad class of prior distributions over \mathbf{w} , the distribution of functions generated by the neural network tends to a Gaussian process in the hidden units limit of $M \rightarrow \infty$. Note however, that in this limit, the output variables of the neural network become independent. On the other hand, typical neural network outputs share the hidden units and so the hidden unit weights are influenced by all of the output variables. This property is therefore lost in the Gaussian process limit.

7. Sparse Kernel Machines

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```
[1]: import numpy as np
import matplotlib.pyplot as plt
from sklearn.datasets import make_classification

from prml.kernel import (
    SupportVectorClassifier,
    SupportVectorRegressor,
    RBF,
    RelevanceVectorRegressor,
    RelevanceVectorClassifier,
)
```

```

from prml.datasets import generate_toy_data

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'

# Enable autoreload all modules before executing code
%reload_ext autoreload
%autoreload 2

```

One significant limitation of many kernel-based methods (see [Chapter 6](#)) is that the kernel function $k(\mathbf{x}_n, \mathbf{x}_m)$ must be evaluated for all possible pairs \mathbf{x}_n and \mathbf{x}_m of training data points. This can be computationally infeasible during training (does not scale to large datasets) and also leads to excessive computation overhead when making predictions for new data points.

On the other hand, there are kernel-based algorithms that yield *sparse* solutions (maintain a subset of training data points), so that predictions depend only on the kernel function evaluated at the subset of these training data points. We shall look into *support vector machine* (SVM), which are easy to train using convex optimization, but does not provide posterior probabilities. An alternative sparse kernel technique, known as *relevance vector machine* (RVM), is based on Bayesian formulation and provides posterior probabilistic outputs. Additionally, RVM has much sparser solutions than SVM, but it is slower to optimize.

7.1 Maximum Margin Classifiers

Consider the classification problem using linear models of the form,

$$y(\mathbf{x}) = \mathbf{w}^T \phi(\mathbf{x}) + b$$

The training data set comprises N input vectors $\mathbf{x}_1, \dots, \mathbf{x}_N$ and corresponding target values t_1, \dots, t_N , where $t_n \in \{-1, 1\}$.

We assume for the moment that the training dataset is linearly separable in feature space defined by ϕ , so that there exists at least one choice of parameters such $y(\mathbf{x}_n) > 0$ for points having $t_n = +1$ and $y(\mathbf{x}_n) < 0$ for points having $t_n = -1$. In general, so that $t_n y(\mathbf{x}_n) > 0$ for all training data points.

The support vector machine approaches this problem through the concept of the margin, which is defined to be the smallest distance between the decision boundary and any of the samples. In support vector machine the decision boundary is chosen to be the one for which the margin is maximized. Recall that the perpendicular distance of a point \mathbf{x}_n from the decision boundary, defined by $y(\mathbf{x}) = 0$, is given by $\frac{|y(\mathbf{x})|}{\|\mathbf{w}\|_2}$. Since we are only interested in solutions for which all data points are correctly classified, so that $t_n y(\mathbf{x}_n) > 0$ for all n . Thus, the distance of a point \mathbf{x}_n to the decision surface is given by,

$$d_s(\mathbf{x}_n) = \frac{t_n y(\mathbf{x}_n)}{\|\mathbf{w}\|_2} = \frac{t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b)}{\|\mathbf{w}\|_2}$$

Thus, the margin is defined by the closest point \mathbf{x}_n from the training data points. SVM goal is to optimize the parameters of y in order to maximize the margin or the distance of the closest point. Therefore, the maximum margin solution is found by solving,

$$\begin{aligned} \operatorname{argmax}_{\mathbf{w}, b} \left\{ \min_n d_s(\mathbf{x}_n) \right\} &\stackrel{(7.2)}{=} \operatorname{argmax}_{\mathbf{w}, b} \left\{ \min_n \left[\frac{t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b)}{\|\mathbf{w}\|_2} \right] \right\} \\ &= \operatorname{argmax}_{\mathbf{w}, b} \left\{ \frac{1}{\|\mathbf{w}\|_2} \min_n \left[t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) \right] \right\} \end{aligned}$$

The figure on the left depicts the margin as the distance between the decision boundary and the closest data point. On the right, the margin is maximized leading to a particular choice of the decision boundary (determined by the parameters \mathbf{w} and b). The subset of data points determining the location of the optimized boundary are called *support vectors*.

A direct solution of the above optimization problem is very complex, but there is an equivalent problem that is much easier to solve. Note that the rescaling $\mathbf{w} \mapsto \kappa \mathbf{w}$ and $b \mapsto \kappa b$, does not affect the distance from any point \mathbf{x}_n to the decision surface,

$$\frac{t_n (\kappa \mathbf{w}^T \phi(\mathbf{x}_n) + \kappa b)}{\|\kappa \mathbf{w}\|_2} = \frac{t_n \kappa (\mathbf{w}^T \phi(\mathbf{x}_n) + b)}{\kappa \|\mathbf{w}\|_2} = \frac{t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b)}{\|\mathbf{w}\|_2}$$

Therefore, we can set $t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) = 1$, for the point closest to the surface, which implies that all data points should satisfy the constraints $t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) \geq 1$. Data points for which the equality holds, the constraints are said to be *active*, whereas for the remainder they are said to be *inactive*.

Thus, the reformulated optimization problem simply requires that we maximize $1/\|\mathbf{w}\|$ or equivalently to minimizing $\|\mathbf{w}\|_2^2$,

$$\begin{aligned} \operatorname{argmin}_{\mathbf{w}, b} \frac{1}{2} \|\mathbf{w}\|_2^2 \\ \text{subject to } t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) \geq 1 \end{aligned}$$

This is a *quadratic programming* problem in which we are trying to minimize a quadratic function subject to a set of linear inequality constraints. In order to solve this constrained optimization problem, we introduce Lagrange multipliers $a_n \geq 0$ (one for each constraint), giving the Lagrangian function,

$$L(\mathbf{w}, b, \mathbf{a}) = \frac{1}{2} \|\mathbf{w}\|_2^2 - \sum_{n=1}^N a_n \{t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) - 1\}$$

Setting the derivatives of L with respect to \mathbf{w} and b equal to zero, we obtain,

$$\begin{aligned} dL_{\mathbf{w}} = 0 &\Leftrightarrow \mathbf{w} - \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n) = 0 \\ &\Leftrightarrow \mathbf{w} = \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n) \end{aligned}$$

and

$$dL_b = 0 \Leftrightarrow \sum_{n=1}^N a_n t_n = 0$$

Eliminating \mathbf{w} and b by substituting these conditions back to $L(\mathbf{w}, b, \mathbf{a})$, gives the dual representation of the maximum margin problem,

$$\begin{aligned} \tilde{L}(\mathbf{a}) &= \frac{1}{2} \left\langle \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n), \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n) \right\rangle - \sum_{n=1}^N a_n \left\{ t_n \left(\sum_{m=1}^N a_m t_m \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) + b \right) - 1 \right\} \\ &= \frac{1}{2} \left\langle \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n), \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n) \right\rangle - \sum_{n=1}^N \sum_{m=1}^N a_n t_n a_m t_m \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) - b \sum_{n=1}^N a_n t_n + \sum_{n=1}^N a_n \\ &\stackrel{(7.9)}{=} \frac{1}{2} \left\langle \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n), \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n) \right\rangle - \sum_{n=1}^N \sum_{m=1}^N a_n t_n a_m t_m \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) + \sum_{n=1}^N a_n \\ &= \frac{1}{2} \sum_{n=1}^N a_n t_n \sum_{m=1}^N a_m t_m \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) - \sum_{n=1}^N \sum_{m=1}^N a_n t_n a_m t_m \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) + \sum_{n=1}^N a_n \\ &= \sum_{n=1}^N a_n - \frac{1}{2} \sum_{n=1}^N \sum_{m=1}^N a_n t_n a_m t_m \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) \end{aligned}$$

or

$$\tilde{L}(\mathbf{a}) = \sum_{n=1}^N a_n - \frac{1}{2} \sum_{n=1}^N \sum_{m=1}^N a_n t_n a_m t_m k(\mathbf{x}_n, \mathbf{x}_m)$$

subject to the constraints,

$$\begin{aligned} a_n &\geq 0 \\ \sum_{n=1}^N a_n t_n &= 0 \end{aligned}$$

In order to classify new data points, we evaluate the sign of $y(\mathbf{x})$, which can be expressed in terms of the parameters \mathbf{a} and the kernel function by substituting for \mathbf{w} to give,

$$y(\mathbf{x}) = \mathbf{w}^T \phi(\mathbf{x}) + b = \sum_{n=1}^N a_n t_n \phi(\mathbf{x}_n)^T \phi(\mathbf{x}) + b = \sum_{n=1}^N a_n t_n k(\mathbf{x}_n, \mathbf{x}) + b$$

NOTE: Any data point for which $a_n = 0$ plays no role in making predictions. The remaining data points (where $a_n > 0$) are called support vectors, and because they satisfy $t_n y(\mathbf{x}_n) = 1$, they correspond to points that lie on the maximum margin hyperplanes in feature space. This property is central to the practical applicability of sparse kernel machines. Once the model is trained, a significant proportion of the data points can be discarded, since only the support vectors are required for making predictions.

Having found values for \mathbf{a} , we can then determine the value of the threshold parameter b by noting that support vectors satisfy $t_n y(\mathbf{x}_n) = 1$, thus,

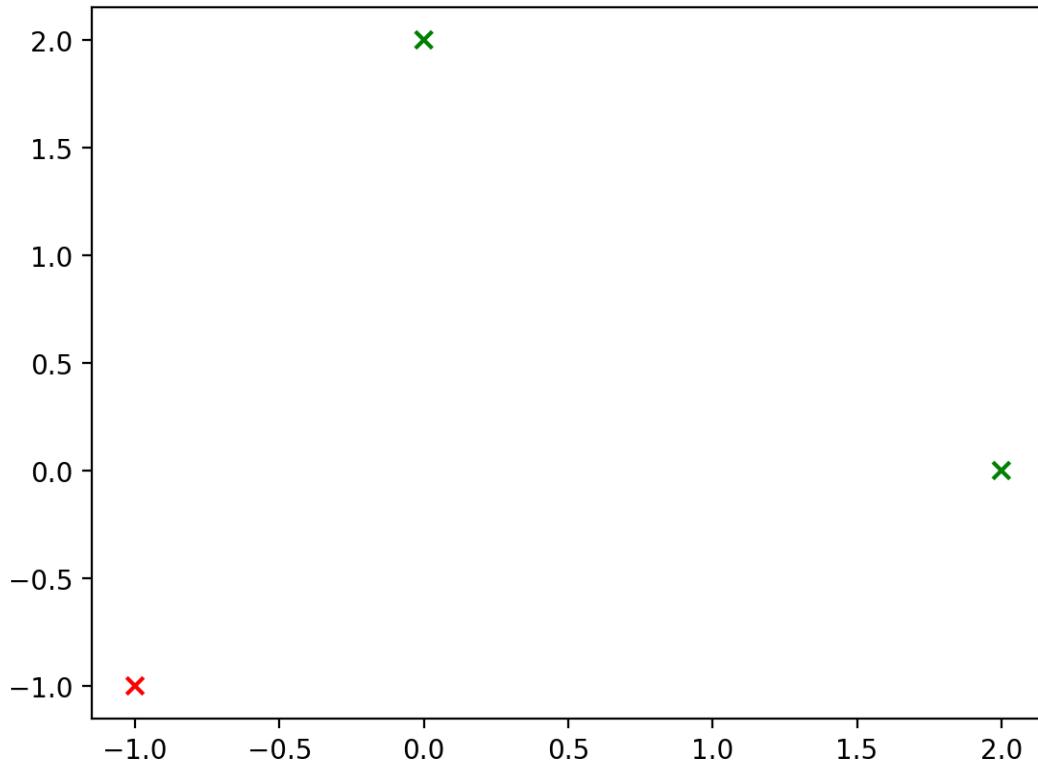
$$\begin{aligned} t_n y(\mathbf{x}_n) = 1 &\Leftrightarrow t_n \left(\sum_{m \in \mathcal{S}} a_m t_m k(\mathbf{x}_m, \mathbf{x}_n) + b \right) = 1 \\ &\stackrel{\times t_n}{\Leftrightarrow} t_n^2 \left(\sum_{m \in \mathcal{S}} a_m t_m k(\mathbf{x}_m, \mathbf{x}_n) + b \right) = t_n \\ &\stackrel{t_n^2=1}{\Leftrightarrow} \sum_{m \in \mathcal{S}} a_m t_m k(\mathbf{x}_m, \mathbf{x}_n) + b = t_n \\ &\Leftrightarrow b = t_n - \sum_{m \in \mathcal{S}} a_m t_m k(\mathbf{x}_m, \mathbf{x}_n) \end{aligned}$$

Although the value of b may be found using any support vector \mathbf{x}_n , a more numerically stable solution is obtained by taking the average over all support vectors,

$$b = \frac{1}{N_S} \sum_{n \in \mathcal{S}} \left(t_n - \sum_{m \in \mathcal{S}} a_m t_m k(\mathbf{x}_m, \mathbf{x}_n) \right)$$

```
[2]: x = np.array([[0.0, 2.0], [2.0, 0.0], [-1.0, -1.0]])
t = np.array([1.0, 1.0, -1.0])

plt.scatter(x[:, 0], x[:, 1], s=40, c=[("g" if label == 1 else "r") for label in t], marker="x")
plt.show()
```



```
[15]: model = SupportVectorClassifier(kernel=None, C=np.inf)
model.fit(x, t)

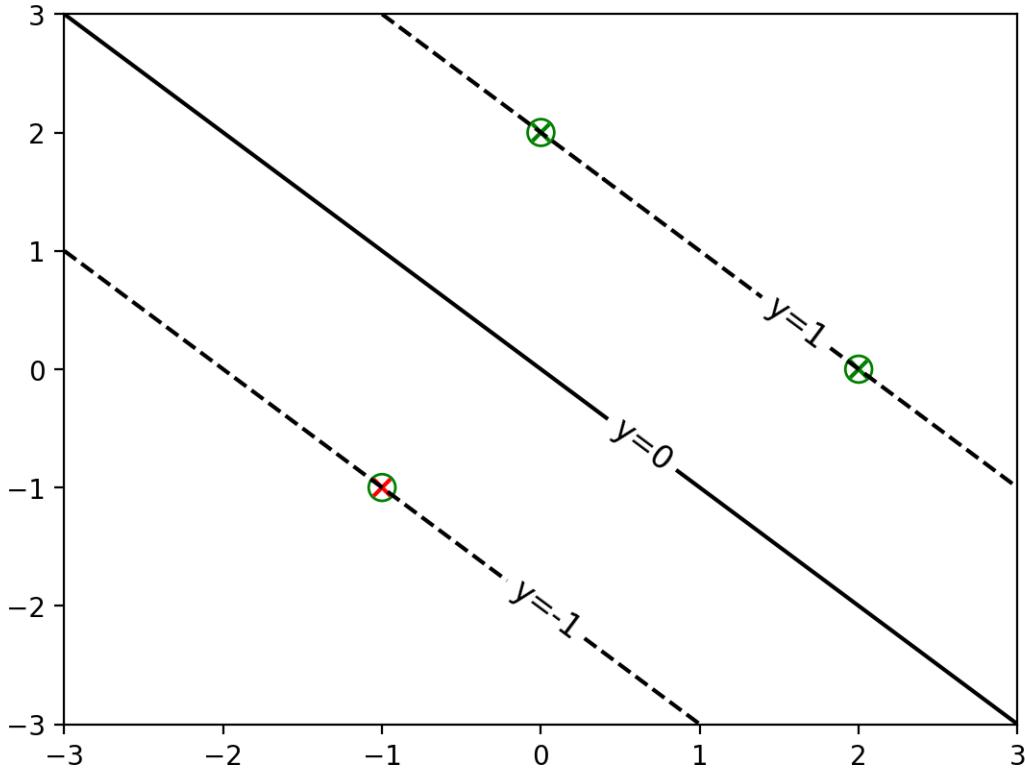
print(f"Found {model.n_support_vectors} support vectors.")
```

Found 3 support vectors.

```
[21]: x0, x1 = np.meshgrid(np.linspace(-3, 3, 100), np.linspace(-3, 3, 100))
xx = np.array([x0, x1]).reshape(2, -1).T

plt.scatter(x[:, 0], x[:, 1], s=40, c=[("g" if label == 1 else "r") for label in t], marker="x")
plt.scatter(model.support_vectors[:, 0], model.support_vectors[:, 1], s=100, facecolor="none", edgecolor="g")
cp = plt.contour(
    x0,
    x1,
    model.predict(xx)[1].reshape(100, 100),
    np.array([-1, 0, 1]),
    colors="k",
    linestyles=("dashed", "solid", "dashed"),
)
```

```
plt.clabel(cp, fmt="y=%f", inline=True, fontsize=12)
plt.show()
```



7.1.1 Overlapping class distributions

So far, we have assumed that the training data points are linearly separable in the feature space. Thus, support vector machine gives an exact separation in the original input space, although the corresponding decision boundary is non-linear. In practice, however, the class-conditional distributions may overlap, in which case exact separation of the training data can lead to poor generalization.

We therefore need to modify the support vector machine so as to allow some of the training points to be misclassified. In the case of separable classes, we implicitly used an error function that gave infinite error if a data point was misclassified and zero error if it was classified correctly, and then optimized the model parameters to maximize the margin. We may modify this approach so that data points are allowed to be on the *wrong side* of the margin boundary, but having a penalty that increases proportionally to their distance from that boundary. To that end, we introduce *slack variables*, $\xi_n \geq 0$ (one for each training data point), for which $\xi_n = 0$ when data points that are on or inside the correct margin boundary, and $\xi_n = |t_n - y(\mathbf{x}_n)|$ in any other case. Therefore, a data point that is on the decision boundary $y(\mathbf{x}_n) = 0$ has $\xi_n = 1$, and points having $\xi_n > 1$ are misclassified. The exact classification constraints are then replaced by,

$$t_n y(\mathbf{x}_n) \geq 1 - \xi_n$$

This known as relaxing the hard-margin constraint to give a soft-margin. Note that while slack variables allow for overlapping class distributions, this framework is still sensitive to outliers because the penalty for misclassification increases linearly.

Our goal is thus to maximize the margin while softly penalizing points that lie on the wrong side of the margin boundary,

$$\begin{aligned} & \operatorname{argmin}_{\mathbf{w}, b} \frac{1}{2} \|\mathbf{w}\|_2^2 + C \sum_{n=1}^N \xi_n \\ \text{subject to } & t_n (\mathbf{w}^T \phi(\mathbf{x}_n) + b) \geq 1 - \xi_n \\ & \xi_n \geq 0 \end{aligned}$$

where the parameter $C > 0$ controls the trade-off between the slack variable penalty and the margin. Because any point that is misclassified has $\xi_n > 1$, it follows that $\sum_{n=1}^N \xi_n$ is an upper bound on the number of misclassified points. The parameter C is analogous to (the inverse of) a regularization coefficient because it controls the trade-off between minimizing training errors and controlling model complexity. In the limit $C \rightarrow \infty$, recovers the earlier support vector machine for separable data.

In order to solve the optimization, the corresponding Lagrangian is given by

$$L(\mathbf{w}, b, \mathbf{a}) = \frac{1}{2} \|\mathbf{w}\|_2^2 + C \sum_{n=1}^N \xi_n - \sum_{n=1}^N a_n \{t_n y(\mathbf{x}_n) - 1 + \xi_n\} - \sum_{n=1}^N \mu_n \xi_n$$

and the derivatives for \mathbf{w} and b are identical to the hard-margin case, while the derivatives for ξ_n is as follows,

$$\begin{aligned} \frac{\partial L}{\partial \xi_n} = 0 & \Leftrightarrow \frac{\partial}{\partial \xi_n} \left(\frac{1}{2} \|\mathbf{w}\|_2^2 + C \sum_{n=1}^N \xi_n - \sum_{n=1}^N a_n \{t_n y(\mathbf{x}_n) - 1 + \xi_n\} - \sum_{n=1}^N \mu_n \xi_n \right) = 0 \\ & \Leftrightarrow C - \frac{\partial}{\partial \xi_n} \left(\sum_{n=1}^N a_n \{t_n y(\mathbf{x}_n) - 1 + \xi_n\} \right) - \mu_n = 0 \\ & \Leftrightarrow C - a_n - \mu_n = 0 \\ & \Leftrightarrow C - \mu_n = a_n \end{aligned}$$

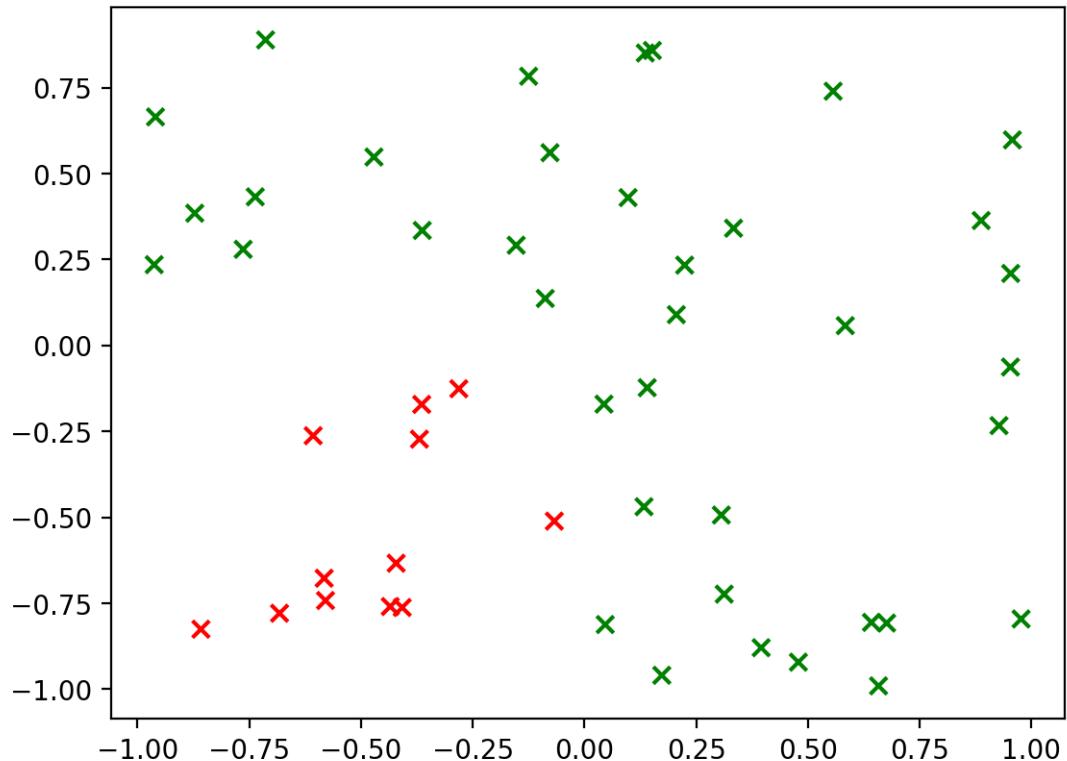
Using these results to eliminate \mathbf{w} , b , ξ_n from the Lagrangian, we obtain the dual representation, which is identical to the separable case, except that we have an additional constraint stating that $a_n \leq C$.

Regarding the solution to the quadratic programming problem tha arise in both cases (separable and non-separable), a global optimum solution can be found since the constraints define a convex region (as a consequence of being linear). Direct solution of a quadratic programming problem may be demanding (in terms of computation and

memory) using traditional techniques. One popular approach to training support vector machines is sequential minimal optimization (SMO). SMO considers two Lagrange multipliers at a time, and in this case, the subproblem can be solved analytically, thereby avoiding numerical quadratic programming altogether. Moreover, heuristics exist to choose the best pair of Lagrange multipliers to be considered at each step. In practice, SMO scales proportionally to the number of data points that is somewhere between linear and quadratic.

```
[3]: x = np.random.uniform(-1, 1, 100).reshape(-1, 2)
t = x < 0
t = (t[:, 0] * t[:, 1]).astype(float)
t = 1 - 2 * t

plt.scatter(x[:, 0], x[:, 1], s=40, c=[("g" if label == 1 else "r") for label in t], marker="x")
plt.show()
```



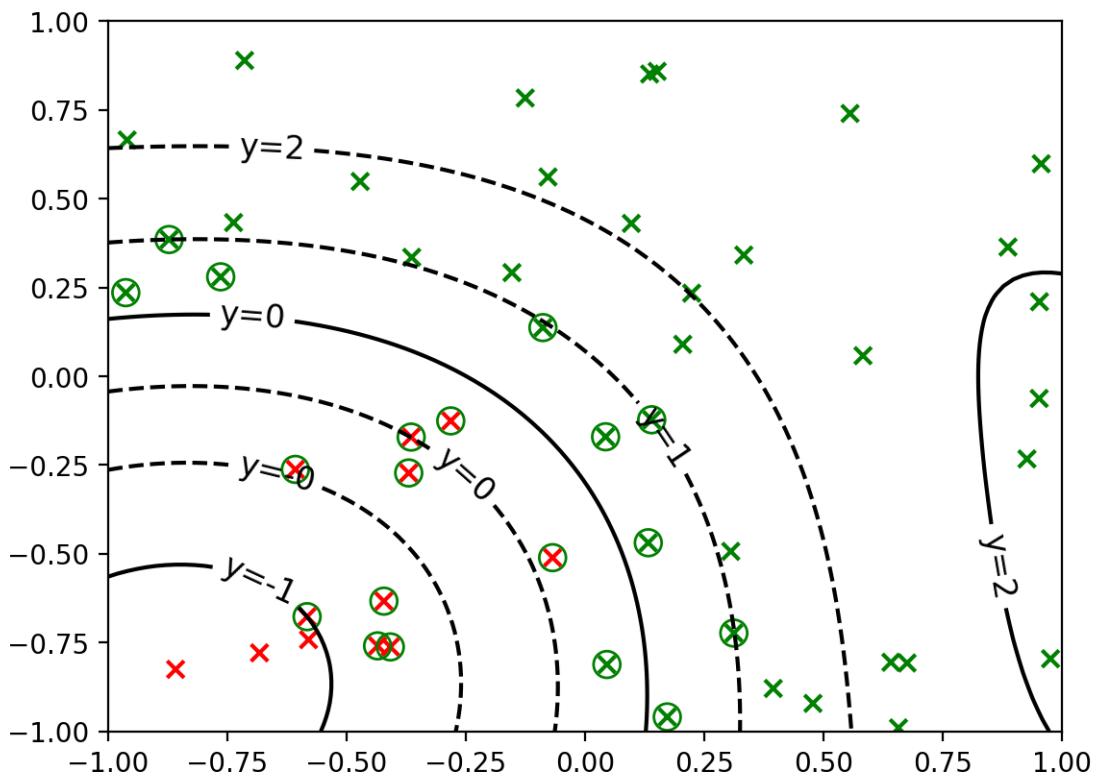
```
[4]: model = SupportVectorClassifier(RBF(theta=np.ones(2)))
model.fit(x, t)
```

```
print(f"Found {model.n_support_vectors} support vectors.")
```

Found 19 support vectors.

```
[5]: x0, x1 = np.meshgrid(np.linspace(-1, 1, 100), np.linspace(-1, 1, 100))
xx = np.array([x0, x1]).reshape(2, -1).T

plt.scatter(x[:, 0], x[:, 1], s=40, c=[("g" if label == 1 else "r") for label in t], marker="x")
plt.scatter(model.support_vectors[:, 0], model.support_vectors[:, 1], s=100, facecolor="none", edgecolor="g")
cp = plt.contour(x0, x1, model.predict(xx)[1].reshape(100, 100), colors="k", linestyles=("dashed", "solid", "dashed"))
plt.clabel(cp, fmt="y=%f", inline=True, fontsize=12)
plt.show()
```



The effect of hyperparameters Let us take a look at how hyperparameters θ of an RBF kernel, and C for trade-off between the slack variable penalty and the margin, affect the resulted SVM model.

```
[6]: theta_grid = [1.0, 5.0, 10.0]
C_grid = [0.5, 1.0, 10.0]

plt.figure(figsize=(15, 10))
```

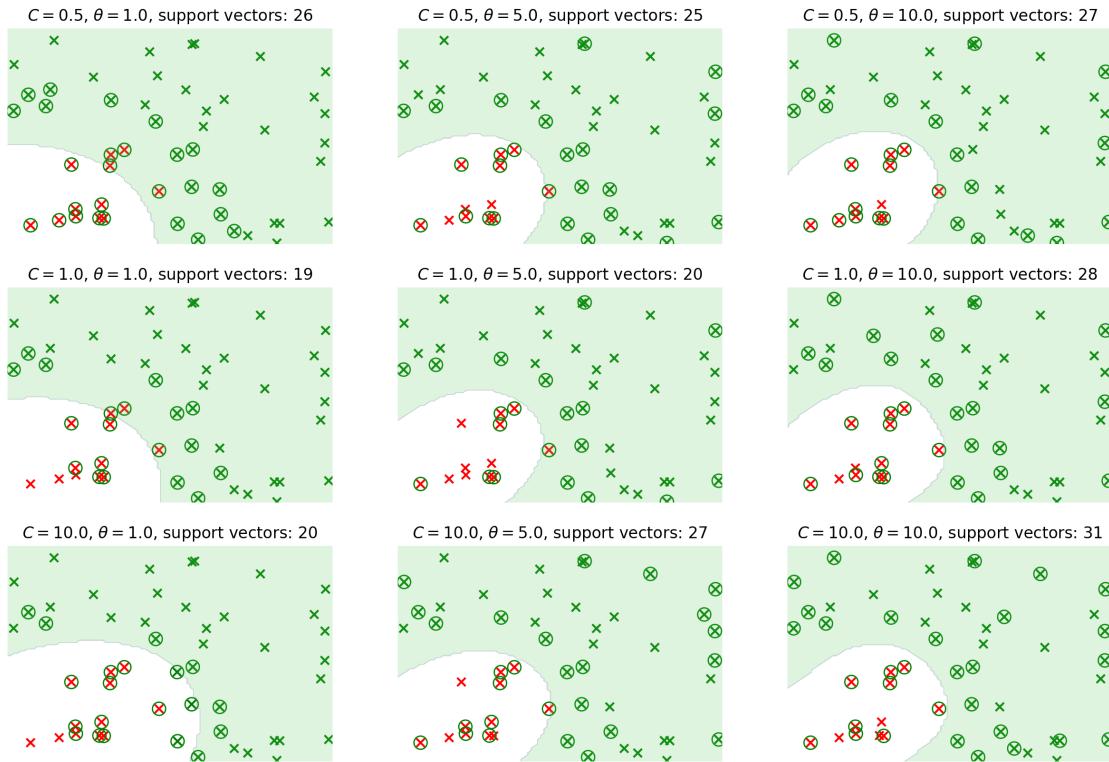
```

for i, c in enumerate(C_grid):
    for j, theta in enumerate(theta_grid):
        model = SupportVectorClassifier(RBF(theta=np.ones(2) * theta), C=c)
        model.fit(x, t)

        plt.subplot(3, 3, (j + 3 * i) + 1)
        plt.scatter(x[:, 0], x[:, 1], s=40, c=[("g" if label == 1 else "r") for
        label in t], marker="x")
        plt.scatter(model.support_vectors[:, 0], model.support_vectors[:, 1], s=100, facecolor="none", edgecolor="g")
        plt.contourf(x0, x1, model.predict(xx)[0].reshape(100, 100), alpha=0.2,
        levels=np.linspace(0, 1, 3))
        plt.title(f"C={c}, \theta={theta}, support vectors: {model.
        n_support_vectors}")
        plt.axis("off")

plt.show()

```



Note that increasing θ makes the decision boundary smoother, and that increasing C results in less misclassification.

7.1.2 Relation to logistic regression

In order to study the relation of SVM to logistic regression, we can cast the SVM for non-separable distributions in terms of the minimization of a regularized error function. Data points that are on the correct side of the margin boundary, satisfy $y_n t_n \geq 1$ and $\xi_n = 0$, while for the remaining points we have $\xi_n = 1 - y_n t_n$. Thus, the objective function in the form,

$$\sum_{n=1}^N E_{SV}(y_n t_n) + \lambda \|\mathbf{w}\|_2^2$$

where $\lambda = (2C) - 1$, and $E_{SV}(\cdot)$ is the *hinge error* function defined by,

$$E_{SV}(y_n t_n) = [1 - y_n t_n]_+$$

In the logistic regression model was convenient to work with target variable $t \in \{0, 1\}$. Thus, for comparison with the support vector machine, we reformulate maximum likelihood logistic regression using the target variable $t \in \{-1, 1\}$. To that end, note that $p(t = 1|y) = \sigma(y)$. Therefore, $p(t = -1|y) = 1 - \sigma(y) = \sigma(-y)$, where we have used the properties of the logistic sigmoid function. Therefore, combining the above cases, we obtain $p(t|y) = \sigma(yt)$.

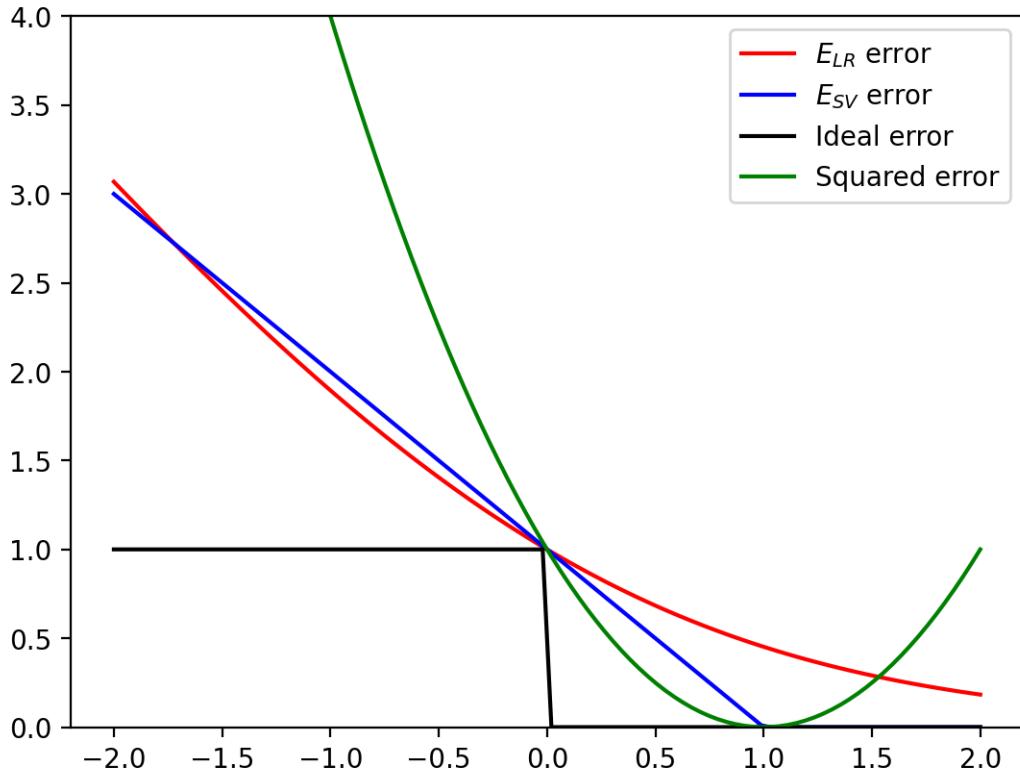
Given this formulation, the negative logarithm of the likelihood function takes the form,

$$\sum_{n=1}^N E_{LR}(y_n t_n) + \lambda \|\mathbf{w}\|_2^2$$

For comparison with other error functions, we divide by $\ln(2)$ so that the error function passes through the point $(0, 1)$. Below we plot the reformulated error function for logistic regression along the hinge loss, the true misclassification error and the squared error.

```
[57]: z = np.linspace(-2, 2, 100)

plt.plot(z, np.log(1 + np.exp(-z)) / np.log(2), label="$E_{LR}$ error", color="red")
plt.plot(z, np.where(1 - z > 0, 1 - z, 0), label="$E_{SV}$ error", color="blue")
plt.plot(z, np.where(z > 0, 0, 1), label="Ideal error", color="black")
plt.plot(z, (1 - z) ** 2, label="Squared error", color="green")
plt.ylim(0, 4)
plt.legend()
plt.show()
```



Note that the logistic regression error E_{LR} has a similar form to the support vector error function. The main difference is that the flat region in E_{SV} leads to sparse solutions. Both the logistic error and the hinge loss can be viewed as continuous approximations to the misclassification error. The squared error, on the other hand, places increasing emphasis on data points that are correctly classified. These points are strongly weighted at the expense of misclassified points, and so if the objective is to minimize the misclassification rate, then a monotonically decreasing error function is a better choice.

7.1.3 Multiclass SVM

The support vector machine is fundamentally a 2-class classifier. To tackle problems involving $K > 2$ classes, usually we combine multiple 2-class SVMs in order to build a multiclass classifier. One commonly used approach is to train K separate SVMs, where the k -th model $y_k(\mathbf{x})$ is trained using the data from class C_k as the positive examples and the data from the remaining $K-1$ classes as the negative. This is known as the *one-versus-the-rest* approach. In order to avoid inconsistent results, that is, assigning input examples to multiple classes simultaneously, the predictions are made as follows,

$$y(\mathbf{x}) = \max_k y_k(\mathbf{x})$$

Issues:

1. Since different each classifier is trained independantly, there is no guarantee that the real-valued quantities $y_k(\mathbf{x})$ for different classifiers will have appropriate scales.
2. Training sets are imbalanced. For ten classes each having equal numbers of training data points, then the individual classifiers are trained on data sets comprising 90% negative and 10% positive examples.

Another approach is to train $K(K - 1)/2$ different 2-class SVM on all possible pairs of classes, and then to classify test points according to which class has the highest number of *votes*, an approach that is sometimes called *one-versus-one*. Note that for large K this approach requires significantly more computation than the *one-versus-the-rest* approach.

7.1.4 SVMs for regression

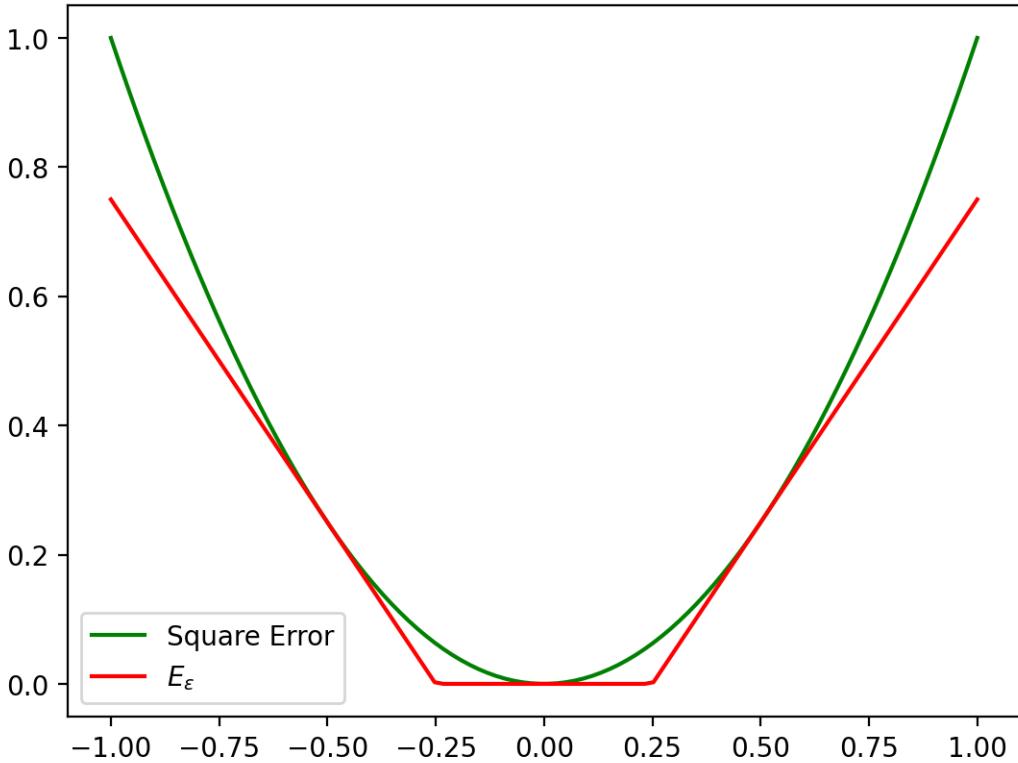
In order to extend support vector machines to regression problems and obtain sparse solutions, the quadratic error function is replaced by an ϵ -insensitive error function, which gives zero error if the absolute difference between the prediction $y(\mathbf{x})$ and the target t is less than ϵ where $\epsilon > 0$. A simple example of an ϵ -insensitive error function, having a linear cost associated with errors outside the insensitive region, is given by

$$E_\epsilon(y(\mathbf{x}) - t) = \begin{cases} 0 & \text{if } |y(\mathbf{x}) - t| < \epsilon \\ |y(\mathbf{x}) - t| - \epsilon & \text{otherwise} \end{cases}$$

```
[74]: epsilon = 0.25

z = np.linspace(-1, 1, 100)

plt.plot(z, z**2, color="green", label="Square Error")
plt.plot(z, np.where(np.abs(z) < epsilon, 0, np.abs(z) - epsilon), color="red", label="$E_\epsilon$")
plt.legend()
plt.show()
```



Thus, we can minimize a regularized error function given by,

$$C \sum_{n=1}^N E_\epsilon(y(\mathbf{x}) - t) + \frac{1}{2} \|\mathbf{w}\|_2^2$$

where C is the (inverse) regularization parameter. For each data point \mathbf{x}_n , we introduce two slack variables $\xi_n, \hat{\xi}_n \geq 0$, where $\xi_n > 0$ corresponds to a point for which $t_n > y(\mathbf{x}_n) + \epsilon$, and $\hat{\xi}_n > 0$ corresponds to a point for which $t_n < y(\mathbf{x}_n) - \epsilon$. These slack variables allows points to lie outside the ϵ -tube provided the slack variables are nonzero, and the corresponding conditions are

$$\begin{aligned} t_n &\leq y(\mathbf{x}_n) + \epsilon + \xi_n \\ t_n &\geq y(\mathbf{x}_n) - \epsilon - \hat{\xi}_n \end{aligned}$$

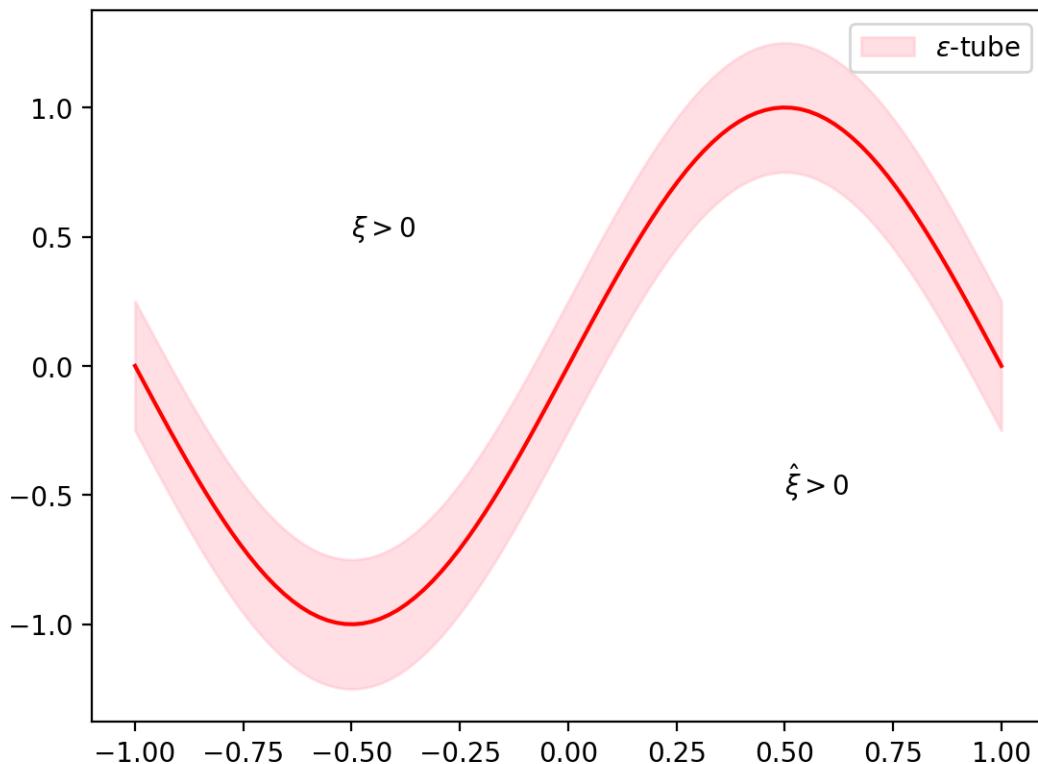
Thus, the error function for support vector regression can then be written as

$$C \sum_{n=1}^N (\xi_n + \hat{\xi}_n) + \frac{1}{2} \|\mathbf{w}\|_2^2$$

where $\xi_n + \hat{\xi}_n$ measures the amount by which data point \mathbf{x}_n lies outside the ϵ -tube.

```
[90]: epsilon = 0.25
x = np.linspace(-1, 1, 100)
y = np.sin(np.pi * x)

plt.plot(x, y, color="red")
plt.fill_between(
    x,
    y - epsilon,
    y + epsilon,
    alpha=0.5,
    color="pink",
    label="$\epsilon$-tube",
)
plt.text(-0.5, 0.5, "$\xi > 0$")
plt.text(0.5, -0.5, "$\hat{\xi} > 0$")
plt.legend()
plt.show()
```



The error function can be minimized by introducing Lagrange multipliers $a_n, \hat{a}_n, \mu_n, \hat{\mu}_n$ to obtain,

$$L(\mathbf{w}, b, \mathbf{a}, \hat{\mathbf{a}}) = C \sum_{n=1}^N (\xi_n + \hat{\xi}_n) + \frac{1}{2} \|\mathbf{w}\|_2^2 - \sum_{n=1}^N (\mu_n \xi_n + \hat{\mu}_n \hat{\xi}_n) - \sum_{n=1}^N a_n (\epsilon + \xi_n + y_n - t_n) - \sum_{n=1}^N \hat{a}_n (\epsilon + \hat{\xi}_n - y_n + t_n)$$

By setting the derivatives of the Lagrangian with respect to \mathbf{w} , b , ξ_n , and $\hat{\xi}_n$ to zero, we obtain,

$$\begin{aligned} dL_{\mathbf{w}} = 0 &\Leftrightarrow \mathbf{w} - \frac{d}{d\mathbf{w}} \left(\sum_{n=1}^N a_n (\epsilon + \xi_n + y_n - t_n) + \sum_{n=1}^N \hat{a}_n (\epsilon + \hat{\xi}_n - y_n + t_n) \right) = 0 \\ &\Leftrightarrow \mathbf{w} - \frac{d}{d\mathbf{w}} \left(\sum_{n=1}^N a_n (\epsilon + \xi_n + \mathbf{w}^T \phi(\mathbf{x}_n) + b - t_n) + \sum_{n=1}^N \hat{a}_n (\epsilon + \hat{\xi}_n - \mathbf{w}^T \phi(\mathbf{x}_n) - b + t_n) \right) = 0 \end{aligned}$$

$$\begin{aligned} &\Leftrightarrow \mathbf{w} - \sum_{n=1}^N a_n \phi(\mathbf{x}_n) + \sum_{n=1}^N \hat{a}_n \phi(\mathbf{x}_n) = 0 \\ &\Leftrightarrow \mathbf{w} = \sum_{n=1}^N (a_n - \hat{a}_n) \phi(\mathbf{x}_n) \end{aligned}$$

$$\begin{aligned} dL_b = 0 &\Leftrightarrow -\frac{d}{db} \left(\sum_{n=1}^N a_n (\epsilon + \xi_n + y_n - t_n) + \sum_{n=1}^N \hat{a}_n (\epsilon + \hat{\xi}_n - y_n + t_n) \right) = 0 \\ &\Leftrightarrow -\frac{d}{db} \left(\sum_{n=1}^N a_n (\epsilon + \xi_n + \mathbf{w}^T \phi(\mathbf{x}_n) + b - t_n) + \sum_{n=1}^N \hat{a}_n (\epsilon + \hat{\xi}_n - \mathbf{w}^T \phi(\mathbf{x}_n) - b + t_n) \right) = 0 \\ &\Leftrightarrow -\sum_{n=1}^N a_n + \sum_{n=1}^N \hat{a}_n = 0 \\ &\Leftrightarrow \sum_{n=1}^N (a_n - \hat{a}_n) = 0 \end{aligned}$$

while the derivatives for ξ_n , and $\hat{\xi}_n$ are identical to (7.31). Using these results to eliminate the corresponding variables from the Lagrangian, the dual representation is as follows,

$$\begin{aligned}
\tilde{L}(\mathbf{a}, \hat{\mathbf{a}}) &= C \sum_{n=1}^N (\xi_n + \hat{\xi}_n) + \frac{1}{2} \|\mathbf{w}\|_2^2 - \sum_{n=1}^N (\mu_n \xi_n + \hat{\mu}_n \hat{\xi}_n) - \sum_{n=1}^N a_n (\epsilon + \xi_n + y_n - t_n) - \sum_{n=1}^N \hat{a}_n (\epsilon + \hat{\xi}_n - y_n + t_n) \\
&= \frac{1}{2} \|\mathbf{w}\|_2^2 + \sum_{n=1}^N (C - \mu_n) \xi_n + (C - \hat{\mu}_n) \hat{\xi}_n - \sum_{n=1}^N a_n (\epsilon + \xi_n + y_n - t_n) - \sum_{n=1}^N \hat{a}_n (\epsilon + \hat{\xi}_n - y_n + t_n) \\
&= \frac{1}{2} \|\mathbf{w}\|_2^2 + \sum_{n=1}^N a_n \xi_n + \sum_{n=1}^N \hat{a}_n \hat{\xi}_n - \sum_{n=1}^N a_n (\epsilon + \xi_n + y_n - t_n) - \sum_{n=1}^N \hat{a}_n (\epsilon + \hat{\xi}_n - y_n + t_n) \\
&= \frac{1}{2} \|\mathbf{w}\|_2^2 - \sum_{n=1}^N a_n (\epsilon + y_n - t_n) - \sum_{n=1}^N \hat{a}_n (\epsilon - y_n + t_n) \\
&= \frac{1}{2} \|\mathbf{w}\|_2^2 - \epsilon \sum_{n=1}^N (a_n + \hat{a}_n) - \sum_{n=1}^N (a_n - \hat{a}_n) y_n + \sum_{n=1}^N (a_n - \hat{a}_n) t_n \\
&= \frac{1}{2} \|\mathbf{w}\|_2^2 - \epsilon \sum_{n=1}^N (a_n + \hat{a}_n) - \sum_{n=1}^N (a_n - \hat{a}_n) (\mathbf{w}^T \phi(\mathbf{x}_n) + b) + \sum_{n=1}^N (a_n - \hat{a}_n) t_n \\
&= \frac{1}{2} \|\mathbf{w}\|_2^2 - \epsilon \sum_{n=1}^N (a_n + \hat{a}_n) - \sum_{n=1}^N (a_n - \hat{a}_n) \left(\sum_{m=1}^N (a_m - \hat{a}_m) \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) + b \right) + \sum_{n=1}^N (a_n - \hat{a}_n) t_n \\
&= \frac{1}{2} \|\mathbf{w}\|_2^2 - \epsilon \sum_{n=1}^N (a_n + \hat{a}_n) - \sum_{n=1}^N \sum_{m=1}^N (a_n - \hat{a}_n) (a_m - \hat{a}_m) \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) - b \sum_{n=1}^N (a_n - \hat{a}_n) + \sum_{n=1}^N (a_n - \hat{a}_n) t_n \\
&= \frac{1}{2} \|\mathbf{w}\|_2^2 - \sum_{n=1}^N \sum_{m=1}^N (a_n - \hat{a}_n) (a_m - \hat{a}_m) \phi(\mathbf{x}_m)^T \phi(\mathbf{x}_n) - \epsilon \sum_{n=1}^N (a_n + \hat{a}_n) + \sum_{n=1}^N (a_n - \hat{a}_n) t_n \\
&= -\frac{1}{2} \sum_{n=1}^N \sum_{m=1}^N (a_n - \hat{a}_n) (a_m - \hat{a}_m) k(\mathbf{x}_m, \mathbf{x}_n) - \epsilon \sum_{n=1}^N (a_n + \hat{a}_n) + \sum_{n=1}^N (a_n - \hat{a}_n) t_n
\end{aligned}$$

which we optimize together with the following box constraints,

$$0 \leq a_n \leq C, 0 \leq \hat{a}_n \leq C$$

Substituting (7.57) into (7.1), the predictions for new inputs are made using,

$$y = \sum_{n=1}^N (a_n - \hat{a}_n) k(\mathbf{x}_n, \mathbf{x}) + b$$

The support vectors are those data points that contribute to predictions given by $(a_n - \hat{a}_n)$, or in other words those for which either $a_n = 0$ or $\hat{a}_n = 0$. These are points that lie on the boundary of the ϵ -tube or outside the tube. All points within the tube have $a_n = \hat{a}_n = 0$. The parameter b can be found either by considering a data point for which $0 < a_n < C$ or $0 < \hat{a}_n < C$. For such a point holds $\xi_n = 0$, and thus, from (7.65) must therefore satisfy $\epsilon + y_n - t_n = 0$,

$$\epsilon + y_n - t_n = 0 \Leftrightarrow y_n = t_n - \epsilon \Leftrightarrow \mathbf{w}^T \phi(\mathbf{x}_n) + b = t_n - \epsilon \Leftrightarrow b = t_n - \epsilon - \mathbf{w}^T \phi(\mathbf{x}_n)$$

In practice, its better to average over all such estimates of b .

```
[ ]: x_space = np.linspace(-1, 1, 100)
t_space = np.sin(np.pi * x_space)

x, t = generate_toy_data(lambda x: np.sin(np.pi * x), 20, 0.25, domain=(-1, 1))

epsilon = 0.3
model = SupportVectorRegressor(kernel=RBF(theta=np.array(10)), epsilon=epsilon)
model.fit(x, t)
print(f"Found {model.n_support_vectors} support vectors.")

plt.scatter(x, t)
plt.plot(x_space, t_space, color="green", label="$\sin(2\pi x)$")
plt.fill_between(
    x_space,
    t_space - epsilon,
    t_space + epsilon,
    alpha=0.5,
    color="pink",
    label="$\epsilon$-tube",
)
f = (model._lambda * model._support_labels) @ model.kernel(model.
    _support_vectors, x_space[:, None]) + model.b
plt.plot(x_space, f, color="red", label="SVM")
plt.legend()
plt.show()
```

7.2 Relevance Vector Machines

SVMs suffer from a number of limitations. In particular, the outputs of an SVM represent decisions rather than posterior probabilities. Also, the SVM is formulated for two classes, and the extension to $K > 2$ classes is problematic. Finally, the complexity parameter C , or ν (and ϵ in the case of regression), must be found using a hold-out methods. The *relevance vector machine* (RVM) is a Bayesian sparse kernel technique for regression and classification that is similar to SVM whilst avoiding its principal limitations. Additionally, it leads to much sparser models that yield faster performance on test data, while maintaining comparable generalization error.

7.2.1 RVM for regression

The relevance vector machine for regression is a linear model, similar to the one presented in [Chapter 3](#). The key difference is that we introduce a separate prior hyperparameter α_i for each of the weight parameter w_i instead of a single shared hyperparameter,

$$p(\mathbf{w}|\alpha) = \prod_{i=1}^M \mathcal{N}(w_i|0, \alpha_i^{-1})$$

We shall see that, maximizing the evidence with respect to these hyperparameters, a significant proportion of them go to infinity, and the corresponding weight parameters have posterior distributions that are concentrated at zero, thus resulting in sparse solutions, since the associated basis functions play no role in the predictions and so are effectively pruned out.

Using the result (3.49) for linear regression models, the posterior distribution for the weights is Gaussian and takes the form,

$$p(\mathbf{w}|\mathbf{X}, \mathbf{t}, \alpha, \beta) = \mathcal{N}(\mathbf{w}|\mathbf{m}, \mathbf{S})$$

where the mean and covariance are given by

$$\begin{aligned}\mathbf{m} &= \beta \Phi^T \mathbf{t} \\ &= (\mathbf{A} + \beta \Phi^T \Phi)^{-1}\end{aligned}$$

where $\mathbf{A} = \text{diag}(\alpha_i)$. Note that if $\Phi = \mathbf{K}$, then \mathbf{K} is the symmetric $(N+1) \times (N+1)$ kernel matrix.

The values of α and β are determined using type-2 maximum likelihood, also known as the *evidence approximation*, in which we maximize the marginal likelihood obtained by integrating out the weight parameters,

$$\begin{aligned}p(\mathbf{t}|\mathbf{X}, \alpha, \beta) &= \int p(\mathbf{t}|\mathbf{w}, \mathbf{X}, \alpha, \beta)p(\mathbf{w}|\alpha)d\mathbf{w} \\ &= \int \mathcal{N}(\mathbf{t}|\mathbf{w}^T \Phi, \beta^{-1} \mathbf{I}) \mathcal{N}(\mathbf{w}|\mathbf{0}, \alpha \mathbf{I}) d\mathbf{w} \\ &= \left(\frac{\beta}{2\pi}\right)^{N/2} \int \exp\left\{-\frac{\beta}{2}\|\mathbf{t} - \Phi^T \mathbf{w}\|_2^2\right\} \mathcal{N}(\mathbf{w}|\mathbf{0}, \alpha^{-1} \mathbf{I}) d\mathbf{w} \\ &= \left(\frac{\beta}{2\pi}\right)^{N/2} \frac{1}{(2\pi)^{M/2} |\mathbf{A}|^{1/2}} \int \exp\left\{-\frac{\beta}{2}\|\mathbf{t} - \Phi^T \mathbf{w}\|_2^2\right\} \exp\left\{-\frac{1}{2}\mathbf{w}^T \mathbf{A} \mathbf{w}\right\} d\mathbf{w} \\ &\stackrel{\mathbf{A} \text{ is diagonal}}{=} \left(\frac{\beta}{2\pi}\right)^{N/2} \frac{1}{(2\pi)^{M/2}} \prod_{m=1}^M a_m^{1/2} \int \exp\left\{-\frac{\beta}{2}\|\mathbf{t} - \Phi^T \mathbf{w}\|_2^2\right\} \exp\left\{-\frac{1}{2}\mathbf{w}^T \mathbf{A} \mathbf{w}\right\} d\mathbf{w} \\ &\stackrel{e^a e^b = e^{a+b}}{=} \left(\frac{\beta}{2\pi}\right)^{N/2} \frac{1}{(2\pi)^{M/2}} \prod_{m=1}^M a_m^{1/2} \int \exp\left\{-\frac{1}{2}(\beta\|\mathbf{t} - \Phi^T \mathbf{w}\|_2^2 + \mathbf{w}^T \mathbf{A} \mathbf{w})\right\} d\mathbf{w} \\ &= \left(\frac{\beta}{2\pi}\right)^{N/2} \frac{1}{(2\pi)^{M/2}} \prod_{m=1}^M a_m^{1/2} \int \exp\left\{-\frac{1}{2}E(\mathbf{w})\right\} d\mathbf{w}\end{aligned}$$

where

$$\begin{aligned}
E(\mathbf{w}) &= \beta \|\mathbf{t} - \Phi^T \mathbf{w}\|_2^2 + \mathbf{w}^T \mathbf{A} \mathbf{w} \\
&= \beta \mathbf{t}^T \mathbf{t} - 2\beta \mathbf{t}^T \Phi^T \mathbf{w} + \beta \mathbf{w}^T \Phi^T \Phi \mathbf{w} + \mathbf{w}^T \mathbf{A} \mathbf{w} \\
&= \beta \mathbf{t}^T \mathbf{t} - 2\beta \mathbf{t}^T \Phi^T \mathbf{w} + \mathbf{w}^T (\mathbf{A} + \beta \Phi^T \Phi) \mathbf{w} \\
&= \beta \mathbf{t}^T \mathbf{t} - 2\beta \mathbf{t}^T \Phi^T \mathbf{w} + \mathbf{w}^{T-1} \mathbf{w} \\
&\stackrel{\beta \mathbf{t}^T \Phi^T = \mathbf{m}^{T-1}}{=} \beta \mathbf{t}^T \mathbf{t} - 2\mathbf{m}^{T-1} \mathbf{w} + \mathbf{w}^{T-1} \mathbf{w} \\
&= \beta \mathbf{t}^T \mathbf{t} - \mathbf{m}^{T-1} \mathbf{w} - \mathbf{m}^{T-1} \mathbf{w} + \mathbf{w}^{T-1} \mathbf{w} \\
&= \beta \mathbf{t}^T \mathbf{t} - \mathbf{m}^{T-1} \mathbf{w} + (\mathbf{w} - \mathbf{m})^{T-1} \mathbf{w} \\
&= \beta \mathbf{t}^T \mathbf{t} + (\mathbf{w} - \mathbf{m})^{T-1} (\mathbf{w} - \mathbf{m}) - \mathbf{m}^{T-1} \mathbf{m}
\end{aligned}$$

Therefore, substituting $E(\mathbf{w})$ back into the integral we obtain,

$$\begin{aligned}
p(\mathbf{t} | \mathbf{X}, \alpha, \beta) &= \left(\frac{\beta}{2\pi} \right)^{N/2} \frac{1}{(2\pi)^{M/2}} \prod_{m=1}^M a_m^{1/2} \int \exp \left\{ -\frac{1}{2} E(\mathbf{w}) \right\} d\mathbf{w} \\
&= \left(\frac{\beta}{2\pi} \right)^{N/2} \frac{1}{(2\pi)^{M/2}} \prod_{m=1}^M a_m^{1/2} \int \exp \left\{ -\frac{1}{2} \left(\beta \mathbf{t}^T \mathbf{t} + (\mathbf{w} - \mathbf{m})^{T-1} (\mathbf{w} - \mathbf{m}) - \mathbf{m}^{T-1} \mathbf{m} \right) \right\} d\mathbf{w} \\
&= \left(\frac{\beta}{2\pi} \right)^{N/2} \frac{1}{(2\pi)^{M/2}} \prod_{m=1}^M a_m^{1/2} \exp \left\{ \frac{1}{2} \mathbf{m}^{T-1} \mathbf{m} - \frac{\beta}{2} \mathbf{t}^T \mathbf{t} \right\} \int \exp \left\{ -\frac{1}{2} (\mathbf{w} - \mathbf{m})^{T-1} (\mathbf{w} - \mathbf{m}) \right\} d\mathbf{w} \\
&= \left(\frac{\beta}{2\pi} \right)^{N/2} \frac{1}{(2\pi)^{M/2}} \prod_{m=1}^M a_m^{1/2} (2\pi)^{M/2} |\cdot|^{1/2} \exp \left\{ \frac{1}{2} \mathbf{m}^{T-1} \mathbf{m} - \frac{\beta}{2} \mathbf{t}^T \mathbf{t} \right\} \\
&= \left(\frac{\beta}{2\pi} \right)^{N/2} \prod_{m=1}^M a_m^{1/2} |\cdot|^{1/2} \exp \left\{ \frac{1}{2} \mathbf{m}^{T-1} \mathbf{m} - \frac{\beta}{2} \mathbf{t}^T \mathbf{t} \right\} \\
&= \left(\frac{\beta}{2\pi} \right)^{N/2} \prod_{m=1}^M a_m^{1/2} |\cdot|^{1/2} \exp \left\{ -\frac{1}{2} E(\mathbf{t}) \right\}
\end{aligned}$$

where

$$\begin{aligned}
E(\mathbf{t}) &= \beta \mathbf{t}^T \mathbf{t} - \mathbf{m}^{T-1} \mathbf{m} \\
&= \beta \mathbf{t}^T \mathbf{t} - \beta^2 \mathbf{t}^T \Phi^{-1} \Phi^T \mathbf{t} \\
&= \beta \mathbf{t}^T \mathbf{t} - \beta^2 \mathbf{t}^T \Phi \Phi^T \mathbf{t} \\
&= \mathbf{t}^T (\beta \mathbf{I} - \beta^2 \Phi \Phi^T) \mathbf{t} \\
&= \mathbf{t}^T (\beta \mathbf{I} - \beta \Phi (\mathbf{A} + \beta \Phi^T \Phi)^{-1} \Phi^T \beta) \mathbf{t} \\
&\stackrel{(C.7) \text{ Woodbury identity}}{=} \mathbf{t}^T (\beta^{-1} \mathbf{I} + \Phi \mathbf{A}^{-1} \Phi^T)^{-1} \mathbf{t}
\end{aligned}$$

and for the *Woodbury identity* (C.7) we have used the following mapping,

$$\begin{aligned}\mathbf{A} &= \beta \mathbf{I} \\ \mathbf{B} &= \Phi \\ \mathbf{C} &= \Phi^T \\ \mathbf{D} &= \mathbf{A}\end{aligned}$$

Therefore,

$$\begin{aligned}p(\mathbf{t}|\mathbf{X}, \alpha, \beta) &= \left(\frac{\beta}{2\pi}\right)^{N/2} \prod_{m=1}^M a_m^{1/2} | |^{1/2} \exp \left\{ -\frac{1}{2} \mathbf{t}^T (\beta^{-1} \mathbf{I} + \Phi \mathbf{A}^{-1} \Phi^T)^{-1} \mathbf{t} \right\} \\ &= \left(\frac{\beta}{2\pi}\right)^{N/2} \prod_{m=1}^M a_m^{1/2} | |^{1/2} \exp \left\{ -\frac{1}{2} \mathbf{t}^T \mathbf{C}^{-1} \mathbf{t} \right\} \\ &= \mathcal{N}(\mathbf{t}|\mathbf{0}, \mathbf{C})\end{aligned}$$

where we have defined the $N \times N$ matrix \mathbf{C} given by

$$\mathbf{C} = \beta^{-1} \mathbf{I} + \Phi \mathbf{A}^{-1} \Phi^T$$

Since this represents the convolution of two Gaussians, it can be evaluated to give the log marginal likelihood in the form,

$$\ln p(\mathbf{t}|\mathbf{X}, \alpha, \beta) = \ln \mathcal{N}(\mathbf{t}|\mathbf{0}, \mathbf{C}) = -\frac{1}{2} \{ N \ln(2\pi) + \ln |\mathbf{C}| + \mathbf{t}^T \mathbf{C}^{-1} \mathbf{t} \}$$

In order to maximize the resulting marginal likelihood with respect to the hyperparameters α and β , simply set the derivatives of the marginal likelihood to zero and obtain the following re-estimation equations,

$$\begin{aligned}\alpha_i^{new} &= \frac{1 - \alpha_i \Sigma_{ii}}{m_i^2} \\ (\beta^{new})^{-1} &= \frac{\|\mathbf{t} - \Phi \mathbf{m}\|_2^2}{N - \sum_i (1 - \alpha_i \Sigma_{ii})}\end{aligned}$$

Learning therefore proceeds by choosing initial values for α and β , evaluating the mean and covariance of the posterior, and then alternately re-estimating the hyperparameters, and re-estimating the posterior mean and covariance, until a suitable convergence criterion is satisfied.

As a result of the optimization, a proportion of the hyperparameters α_i are driven to large (in principle infinite) values, and so the corresponding weight parameters w_i have posterior distributions with mean and variance both zero. Thus those parameters, and the corresponding basis functions, are removed from the model and play no role in making predictions. In the case of the dual representation, the inputs \mathbf{x}_n corresponding to the remaining non-zero weights are called relevance vectors, because they are identified through the mechanism of automatic relevance determination, and are analogous to the support vectors of an SVM.

Having found values α^* and β^* for the hyperparameters that maximize the marginal likelihood, we can evaluate the predictive distribution over t for a new input \mathbf{x}^{new} ,

$$p(t|\mathbf{x}^{new}, \mathbf{X}, \mathbf{t}, \alpha^*, \beta^*) = \int p(t|\mathbf{x}^{new}, \mathbf{w}, \beta^*) p(\mathbf{w}|\mathbf{X}, \mathbf{t}, \alpha^*, \beta^*) d\mathbf{w} = \mathcal{N}(t|\mathbf{m}^T \phi(\mathbf{x}), \sigma(\mathbf{x})^2)$$

Similar to [Chapter 3](#), the result of the integral is a Gaussian distribution and the variance of the predictive distribution is given by,

$$\sigma(\mathbf{x})^2 = \frac{1}{\beta^*} + \phi(\mathbf{x})^T \phi(\mathbf{x})$$

The following example presents an RVM applied to the sinusoidal regression data set:

```
[130]: x_space = np.linspace(-1, 1, 100)
t_space = np.sin(np.pi * x_space)

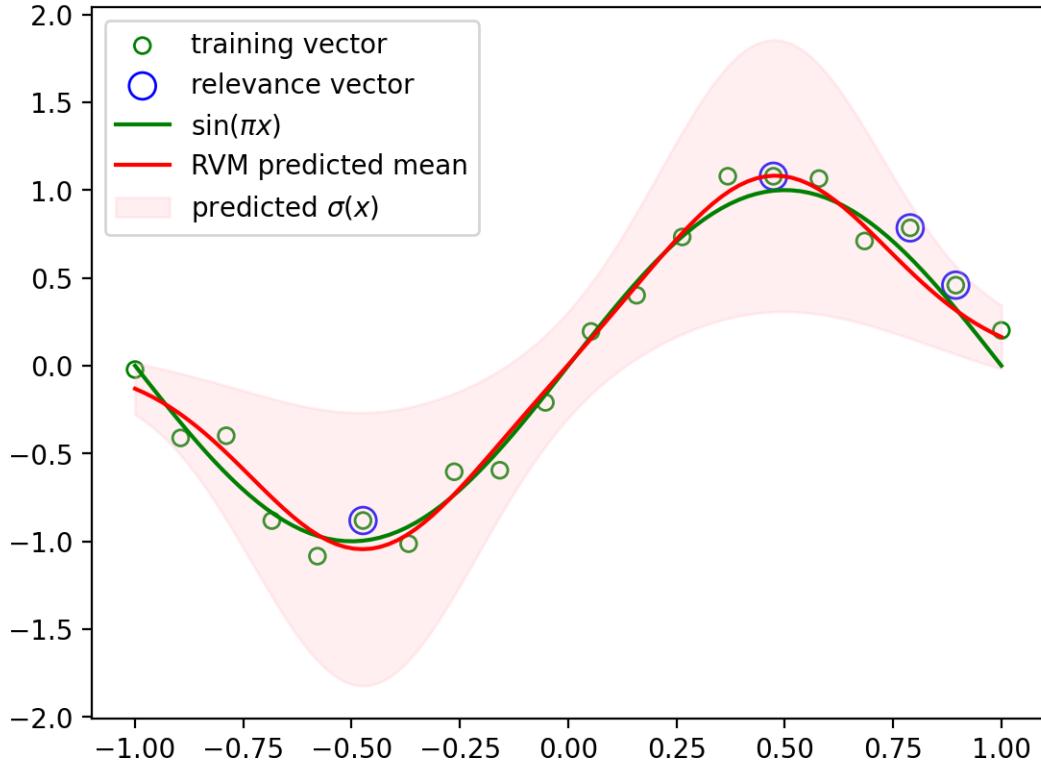
x, t = generate_toy_data(lambda x: np.sin(np.pi * x), 20, 0.2, domain=(-1, 1))

model = RelevanceVectorRegressor(kernel=RBF(theta=np.array([15.0])))
model.fit(x, t)
print(f"Found {model.n_relevance_vectors} relevance vectors.")

mean, variance = model.predict(x_space)

plt.scatter(x, t, facecolor="none", edgecolor="green", label="training vector")
plt.scatter(
    model.relevance_vectors, model.relevance_labels, s=100, facecolor="none", ↴
    edgecolor="blue", label="relevance vector"
)
plt.plot(x_space, t_space, color="green", label="$\sin(\pi x)$")
plt.plot(x_space, mean, color="red", label="RVM predicted mean")
plt.fill_between(x_space, mean - variance, mean + variance, alpha=0.25, ↴
    color="pink", label="predicted $\sigma(x)$")
plt.legend()
plt.show()
```

Found 4 relevance vectors.



For many regression and classification tasks, the RVM is found to give models that are typically an order of magnitude more compact than the corresponding support vector machine, resulting in a significant improvement in the speed of processing on test data. Remarkably, the greater sparsity is achieved with little or no reduction in generalization error. The principal disadvantage of the RVM compared to the SVM is that training involves optimizing a non-convex function, and training times can be longer than for a comparable SVM.

For a model having M basis functions, the RVM requires inversion of a matrix of size $M \times M$, which in general requires $O(M^3)$ computation. In the specific case of the kernel-based SVM model, we have $M = N + 1$. Moreover, there are techniques for training SVMs whose cost is roughly quadratic in N . More significantly, in the relevance vector machine the parameters governing complexity and noise variance are determined automatically from a single training run, whereas in the support vector machine the parameters C and ϵ (or ν) are generally found using cross-validation.

7.2.3 RVM for classification

The relevance vector machine framework can be extended to classification problems by applying the automatic relevance determination (ARD) prior over weights to a probabilistic linear classification model, as the one presented in [Chapter 4](#),

$$y(\mathbf{x}, \mathbf{w}) = \sigma(\mathbf{w}^T \phi(\mathbf{x}))$$

To that end, we introduce a Gaussian prior over the weight vector \mathbf{w} , having separate precision

hyperparameter α_i for each weight parameter. However, similar to logistic regression, we can no longer integrate analytically over the parameter vector, and therefore, similar to Bayesian logistic regression, we employ the Laplace approximation. For a given value of α , we build a Gaussian approximation for the posterior distribution of the parameters and thereby obtain an approximation to the marginal likelihood. Maximization of this approximate marginal likelihood allows us to obtain re-estimated values for α .

The posterior distribution over the parameters is obtained by,

$$p(\mathbf{w}|\mathbf{t}, \mathbf{X}, \alpha) = p(\mathbf{t}|\mathbf{w}, \mathbf{X})p(\mathbf{w}|\mathbf{0}, \alpha^{-1}\mathbf{I})$$

Then, the mode of the posterior distribution is obtained by maximizing,

$$\begin{aligned} \ln p(\mathbf{w}|\mathbf{t}, \mathbf{X}, \alpha) &= \ln p(\mathbf{t}|\mathbf{w}, \mathbf{X}) + \ln p(\mathbf{w}|\mathbf{0}, \alpha^{-1}\mathbf{I}) \\ &= \ln \left(\prod_{n=1}^N y_n^{t_n} (1 - y_n)^{1-t_n} \right) + \ln \left(\frac{1}{(2\pi)^{M/2} |\mathbf{A}^{-1}|^{1/2}} \exp \left\{ -\frac{1}{2} \mathbf{w}^T \mathbf{A} \mathbf{w} \right\} \right) \\ &= \sum_{n=1}^N \left\{ t_n \ln y_n + (1 - t_n) \ln(1 - y_n) \right\} - \frac{1}{2} \mathbf{w}^T \mathbf{A} \mathbf{w} + \ln \left(\frac{1}{(2\pi)^{M/2} |\mathbf{A}^{-1}|^{1/2}} \right) \\ &= \sum_{n=1}^N \left\{ t_n \ln y_n + (1 - t_n) \ln(1 - y_n) \right\} - \frac{1}{2} \mathbf{w}^T \mathbf{A} \mathbf{w} - \frac{M}{2} \ln(2\pi) - \frac{1}{2} \ln |\mathbf{A}^{-1}| \end{aligned}$$

where $\mathbf{A} = \text{diag}(\alpha_i)$. The maximization can be achieved using iterative reweighted least squares (IRLS). Therefore, the gradient vector and Hessian matrix of the log posterior distribution are given by,

$$\begin{aligned} \nabla \ln p(\mathbf{w}|\mathbf{t}, \mathbf{X}, \alpha) &= \nabla_{\mathbf{w}} \left[\sum_{n=1}^N \left\{ t_n \ln y_n + (1 - t_n) \ln(1 - y_n) \right\} - \frac{1}{2} \mathbf{w}^T \mathbf{A} \mathbf{w} \right] \\ &= \sum_{n=1}^N \nabla_{\mathbf{w}} \left\{ t_n \ln y_n + (1 - t_n) \ln(1 - y_n) \right\} - \nabla_{\mathbf{w}} \frac{1}{2} \mathbf{w}^T \mathbf{A} \mathbf{w} \\ &= \sum_{n=1}^N \nabla_{\mathbf{w}} \left\{ t_n \ln y_n + (1 - t_n) \ln(1 - y_n) \right\} - \mathbf{A} \mathbf{w} \\ &\stackrel{(4.88)}{=} \sum_{n=1}^N \left\{ t_n \frac{1}{y_n} y_n (1 - y_n) \phi_n - (1 - t_n) \frac{1}{1 - y_n} y_n (1 - y_n) \phi_n \right\} - \mathbf{A} \mathbf{w} \\ &= \sum_{n=1}^N \left\{ t_n (1 - y_n) \phi_n - (1 - t_n) y_n \phi_n \right\} - \mathbf{A} \mathbf{w} \\ &= \sum_{n=1}^N \left\{ t_n \phi_n - t_n y_n \phi_n - y_n \phi_n + t_n y_n \phi_n \right\} - \mathbf{A} \mathbf{w} \\ &= \sum_{n=1}^N (t_n - y_n) \phi_n - \mathbf{A} \mathbf{w} \end{aligned}$$

and

$$\begin{aligned}
\nabla \nabla \ln p(\mathbf{w}|\mathbf{t}, \mathbf{X}, \alpha) &= \nabla_{\mathbf{w}} \left[\sum_{n=1}^N (t_n - y_n) \phi_n - \mathbf{A} \mathbf{w} \right] \\
&= \sum_{n=1}^N \nabla_{\mathbf{w}} \{(t_n - y_n) \phi_n\} - \nabla_{\mathbf{w}} \mathbf{A} \mathbf{w} \\
&= \sum_{n=1}^N \nabla_{\mathbf{w}} \{(t_n - y_n) \phi_n\} - \mathbf{A} \\
&= - \sum_{n=1}^N \nabla_{\mathbf{w}} y_n \phi_n - \mathbf{A} \\
&\stackrel{(4.88)}{=} - \sum_{n=1}^N y_n (1 - y_n) \phi_n \phi_n^T - \mathbf{A} \\
&= -(\Phi^T \mathbf{B} \Phi + \mathbf{A})
\end{aligned}$$

where \mathbf{B} is a diagonal matrix having elements $b_n = y_n(1 - y_n)$.

The elements of the negative Hessian can be interpreted as the inverse covariance matrix for the Gaussian approximation to the posterior distribution. The mode of the resulting approximation to the posterior distribution is obtained by setting the gradient vector to zero, giving the mean and covariance of the Laplace approximation in the form,

$$\begin{aligned}
\mathbf{w}^* &= \mathbf{A}^{-1} \Phi^T (\mathbf{t} - \mathbf{y}) \\
&= (\Phi^T \mathbf{B} \Phi + \mathbf{A})^{-1}
\end{aligned}$$

Then, we can use the Laplace approximation of the posterior to evaluate the marginal likelihood. Using the general result (4.135) for an integral evaluated using the Laplace approximation, we have

$$\begin{aligned}
p(\mathbf{t}|\mathbf{X}, \alpha) &= \int p(\mathbf{t}|\mathbf{w}, \mathbf{X}) p(\mathbf{w}|\alpha) d\mathbf{w} \\
&\approx p(\mathbf{t}|\mathbf{w}^*, \mathbf{X}) p(\mathbf{w}^*|\alpha) (2\pi)^{M/2} | \mathbf{B} |^{1/2} \\
&= \prod_{n=1}^N p(t_n|\mathbf{w}^*, \mathbf{x}_n) \prod_{n=1}^N \mathcal{N}(w_i^*|0, \alpha_i) (2\pi)^{M/2} | \mathbf{B} |^{1/2} \\
&= \prod_{n=1}^N p(t_n|\mathbf{w}^*, \mathbf{x}_n) \mathcal{N}(\mathbf{w}^*|\mathbf{0}, \mathbf{A}) (2\pi)^{M/2} | \mathbf{B} |^{1/2}
\end{aligned}$$

Taking the logarithm of the marginal likelihood, we obtain,

$$\begin{aligned}
\ln p(\mathbf{t}|\mathbf{X}, \alpha) &= \ln \left(\prod_{n=1}^N y_n^{t_n} (1-y_n)^{1-t_n} \right) + \ln \mathcal{N}(\mathbf{w}^* | \mathbf{0}, \mathbf{A}) + \ln \left((2\pi)^{M/2} |\mathbf{A}|^{1/2} \right) \\
&= \ln \left(\prod_{n=1}^N y_n^{t_n} (1-y_n)^{1-t_n} \right) - \frac{1}{2} (\mathbf{w}^*)^T \mathbf{A} \mathbf{w}^* - \frac{1}{2} \ln |\mathbf{A}| - \frac{M}{2} \ln(2\pi) + \frac{M}{2} \ln(2\pi) + \frac{1}{2} \ln |\mathbf{A}| \\
&= \ln \left(\prod_{n=1}^N y_n^{t_n} (1-y_n)^{1-t_n} \right) - \frac{1}{2} (\mathbf{w}^*)^T \mathbf{A} \mathbf{w}^* - \frac{1}{2} \ln |\mathbf{A}| + \frac{1}{2} \ln |\mathbf{A}| \\
&= \prod_{n=1}^N \left\{ t_n \ln y_n + (1-t_n) \ln(1-y_n) \right\} - \frac{1}{2} (\mathbf{w}^*)^T \mathbf{A} \mathbf{w}^* - \frac{1}{2} \ln |\mathbf{A}| + \frac{1}{2} \ln |\mathbf{A}|
\end{aligned}$$

Then, setting the derivative of the marginal likelihood with respect to α_i equal to zero, we obtain,

$$\begin{aligned}
\frac{\partial \ln p(\mathbf{t}|\mathbf{X}, \alpha)}{\partial \alpha_i} = 0 &\Leftrightarrow \frac{\partial}{\partial \alpha_i} \prod_{n=1}^N \left\{ t_n \ln y_n + (1-t_n) \ln(1-y_n) \right\} - \frac{1}{2} \frac{\partial}{\partial \alpha_i} (\mathbf{w}^*)^T \mathbf{A} \mathbf{w}^* - \frac{1}{2} \frac{\partial}{\partial \alpha_i} \ln |\mathbf{A}| + \frac{1}{2} \frac{\partial}{\partial \alpha_i} \ln |\mathbf{A}| = 0 \\
&\Leftrightarrow -\frac{1}{2} \frac{\partial}{\partial \alpha_i} (\mathbf{w}^*)^T \mathbf{A} \mathbf{w}^* - \frac{1}{2} \frac{\partial}{\partial \alpha_i} \ln |\mathbf{A}| + \frac{1}{2} \frac{\partial}{\partial \alpha_i} \ln |\mathbf{A}| = 0 \\
&\Leftrightarrow -\frac{1}{2} (w_i^*)^2 - \frac{1}{2} \frac{\partial}{\partial \alpha_i} \ln |\mathbf{A}| + \frac{1}{2} \frac{\partial}{\partial \alpha_i} \ln |\mathbf{A}| = 0 \\
&\Leftrightarrow -\frac{1}{2} (w_i^*)^2 + \frac{1}{2\alpha_i} - \frac{1}{2} \Sigma_{ii} = 0 \\
&\Leftrightarrow -(w_i^*)^2 + \frac{1}{\alpha_i} - \Sigma_{ii} = 0 \\
&\Leftrightarrow -\alpha_i (w_i^*)^2 + 1 - \alpha_i \Sigma_{ii} = 0 \\
&\Leftrightarrow 1 - \alpha_i \Sigma_{ii} = \alpha_i (w_i^*)^2 \\
&\Leftrightarrow \alpha_i^{new} = \frac{1 - \alpha_i \Sigma_{ii}}{(w_i^*)^2}
\end{aligned}$$

which is identical to the re-estimation formula obtained for the regression case.

```
[48]: # number of training points
N = 100

x, t = make_classification(
    n_features=2, n_informative=2, n_redundant=0, n_classes=2,
    n_clusters_per_class=1, n_samples=N, random_state=21
)

x1, x2 = np.meshgrid(np.linspace(-5, 5, N), np.linspace(-5, 5, N))
x_test = np.array([x1, x2]).reshape(2, -1).T

model = RelevanceVectorClassifier(kernel=RBF(theta=np.array([1, 1])))
model.fit(x, t, n_iter=100)
```

```

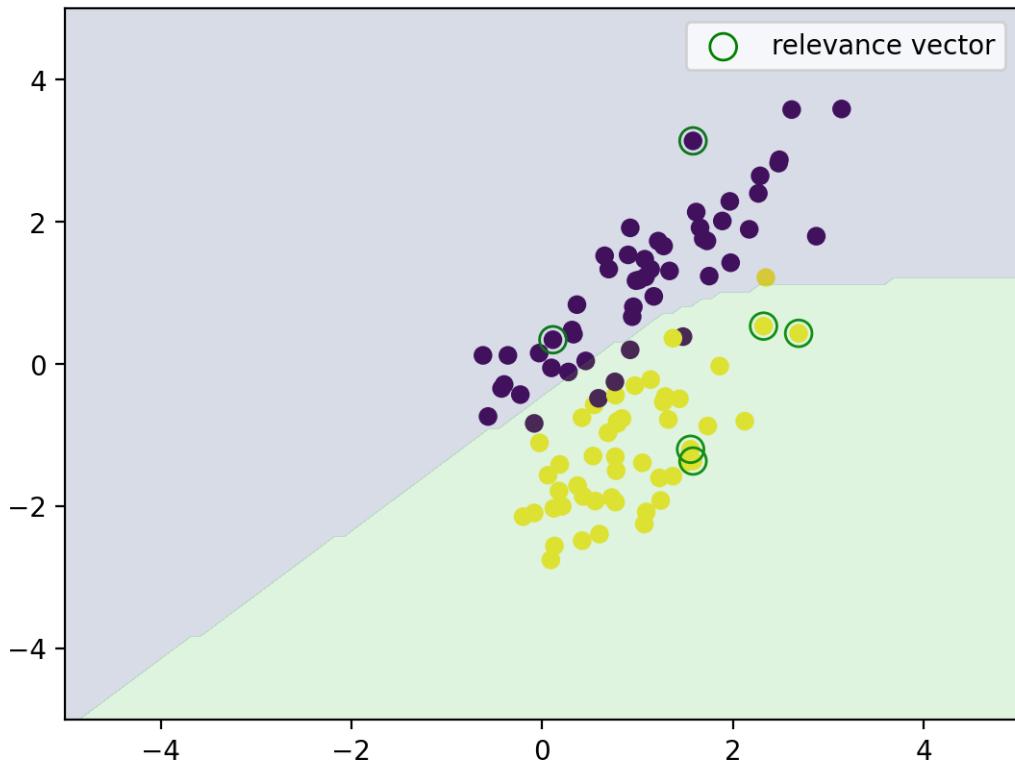
print(f"Found {model.n_relevance_vectors} relevance vectors.")

predicted = model.predict(x_test)

plt.scatter(x[:, 0], x[:, 1], c=t)
plt.scatter(
    model.relevance_vectors[:, 0],
    model.relevance_vectors[:, 1],
    s=100,
    facecolor="none",
    edgecolor="green",
    label="relevance vector",
)
plt.contourf(x1, x2, predicted.reshape(N, N), alpha=0.2, levels=np.linspace(0, 1, 3))
plt.xlim(-5, 5)
plt.ylim(-5, 5)
plt.legend()
plt.show()

```

Found 6 relevance vectors.



Note that the relevance vectors do not lie in the region of the decision boundary, in contrast to the

support vector machine. This is consistent to the sparsity in the RVM, because a basis function $\phi_i(\mathbf{x})$ centered on a data point near the boundary has a vector φ_i that is poorly aligned with the training data vector \mathbf{t} .

9. Mixture Models and EM

Table of Contents

- 9.1 K-means Clustering
 - 9.1.1 Image segmentation and compression
- 9.2 Mixtures of Gaussians

```
[1]: import numpy as np
import matplotlib.pyplot as plt
from prml.clustering import KMeans
from prml.datasets import load_old_faithful

# Set random seed to make deterministic
np.random.seed(0)

# Ignore zero divisions and computation involving NaN values.
np.seterr(divide="ignore", invalid="ignore")

# Enable higher resolution plots
%config InlineBackend.figure_format = 'retina'

# Enable autoreload all modules before executing code
%reload_ext autoreload
%autoreload 2
```

9.1 K-means Clustering

Consider the problem of identifying groups, or clusters, of data points in a multidimensional space. Suppose that we have a data set $\{x_1, \dots, x_N\}$. The goal is to partition the data set into K clusters, for a given value of K . Intuitively, a cluster can be a group of data points whose inter-point distances are small compared to the distances to points outside the cluster.

We can formalize this notion by introducing a set of D -dimensional vectors μ_k . Each such vector is a prototype associated with the k th cluster, essentially representing the centres of the clusters. Then, the goal is then to find an assignment of data points to clusters, and a set of vectors μ_k , such that the sum of the squares of the distances of each data point to its closest vector μ_k is a minimum.

We can then define an objective function, sometimes called a distortion measure, given by

$$J = \sum_{n=1}^N \sum_{k=1}^K r_{nk} \|\mathbf{x}_n - \mu_k\|_2^2$$

where $r_{nk} \in \{0, 1\}$ are binary indicator variables, describing which of the K clusters the data point x_n is assigned. The objective function represents the sum of the squares of the distances of each data point to its assigned cluster center μ_k . Thus, the goal is to find values for the $\{r_{nk}\}$ and the μ_k that minimize J .

K-means algorithm: > This can be achieved using an iterative procedure involving two successive steps. In the first phase we minimize J with respect to the r_{nk} , keeping the μ_k fixed. In the second phase we minimize J with respect to the μ_k , keeping r_{nk} fixed. These two stages are then repeated until convergence. We shall see that these two stages of updating r_{nk} and updating μ_k correspond respectively to the E (expectation) and M (maximization) steps of the EM algorithm.

Consider the determination of the r_{nk} . Because J is a linear function of r_{nk} , the optimization gives a closed form solution. The n terms are independent and so we optimize for each n separately by choosing r_{nk} to be 1 for whichever value of k gives the minimum value of $\|\mathbf{x}_n - \mu_k\|_2^2$. In other words, we simply assign each data point to its closest cluster centre or more formally,

$$r_{nk} = \begin{cases} 1 & \text{if } k = \operatorname{argmin}_j \|\mathbf{x}_n - \mu_j\|_2^2 \\ 0 & \text{otherwise} \end{cases}$$

Then, consider the optimization of μ_k , while keeping r_{nk} fixed. The objective function is a quadratic function of μ_k , and it can be minimized by setting its derivative with respect to μ_k to zero giving,

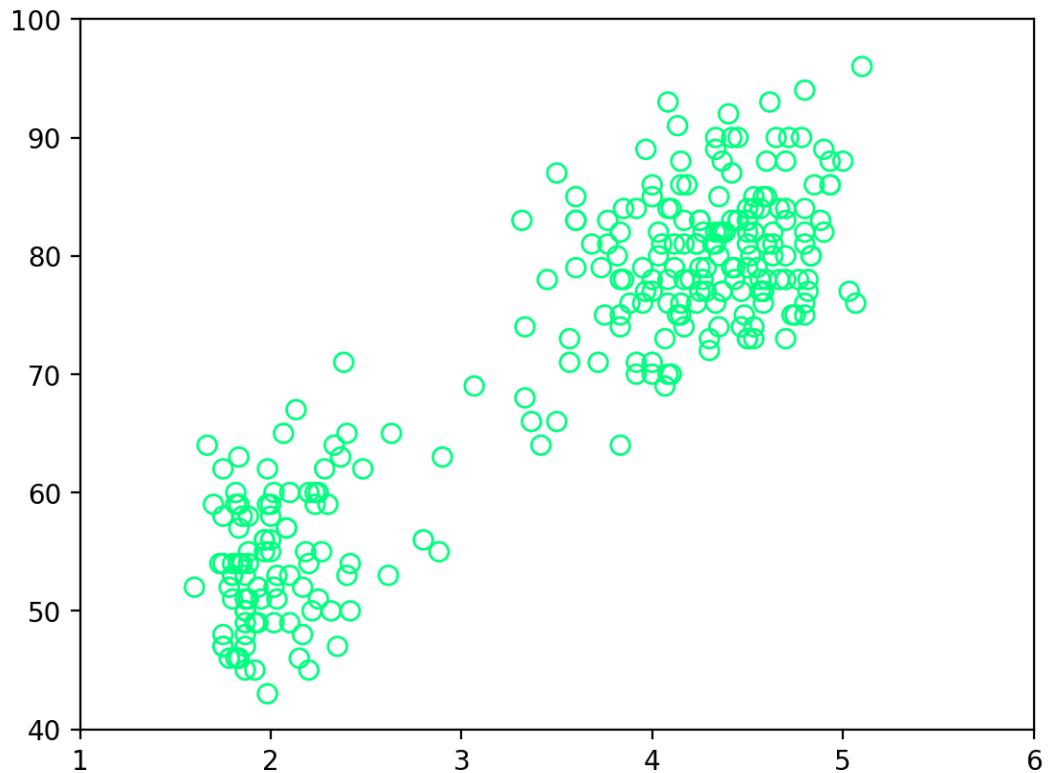
$$\begin{aligned} \frac{\partial J}{\partial \mu_k} = \mathbf{0} &\Leftrightarrow \\ \frac{\partial}{\partial \mu_k} \sum_{n=1}^N \sum_{k=1}^K r_{nk} \|\mathbf{x}_n - \mu_k\|_2^2 &= \mathbf{0} \Leftrightarrow \\ 2 \sum_{n=1}^N r_{nk} (\mathbf{x}_n - \mu_k) &= \mathbf{0} \Leftrightarrow \\ \sum_{n=1}^N r_{nk} \mathbf{x}_n - \sum_{n=1}^N r_{nk} \mu_k &= \mathbf{0} \Leftrightarrow \\ \sum_{n=1}^N r_{nk} \mathbf{x}_n &= \sum_{n=1}^N r_{nk} \mu_k \Leftrightarrow \\ \mu_k &= \frac{\sum_{n=1}^N r_{nk} \mathbf{x}_n}{\sum_{n=1}^N r_{nk}} \end{aligned}$$

The denominator is equal to the number of points assigned to cluster k , and thus, μ_k equal to the mean of all of the data points \mathbf{x}_n assigned to cluster k . For this reason, the procedure is known as the K -means algorithm.

Because each phase reduces the value of the objective function, convergence of the algorithm is assured. However, keep in mind, that it may converge to a local rather than global minimum.

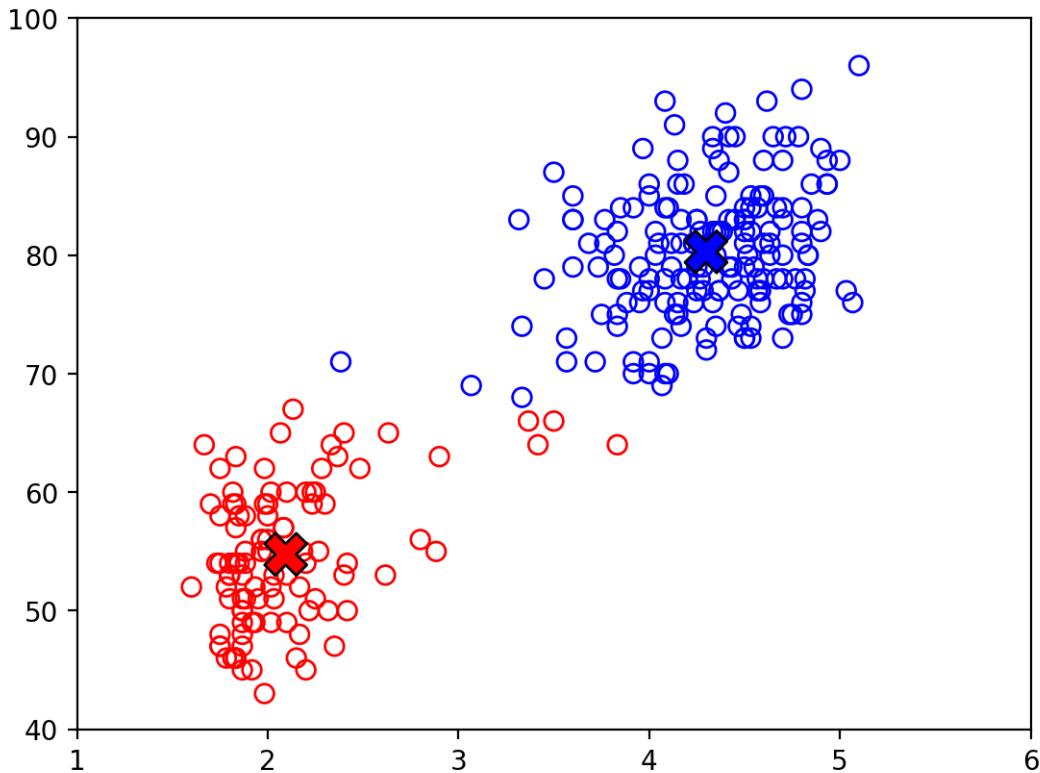
Below the K -means algorithm is applied on the Old Faithful data set:

```
[2]: old_faithful = load_old_faithful()
plt.scatter(old_faithful[:, :1], old_faithful[:, 1:2], color="springgreen", ▾
           facecolors="none", s=50)
plt.xlim(1, 6)
plt.ylim(40, 100)
plt.show()
```



```
[195]: model = KMeans(2)
model.fit(old_faithful, n_iter=10)
classes = model.predict(old_faithful)

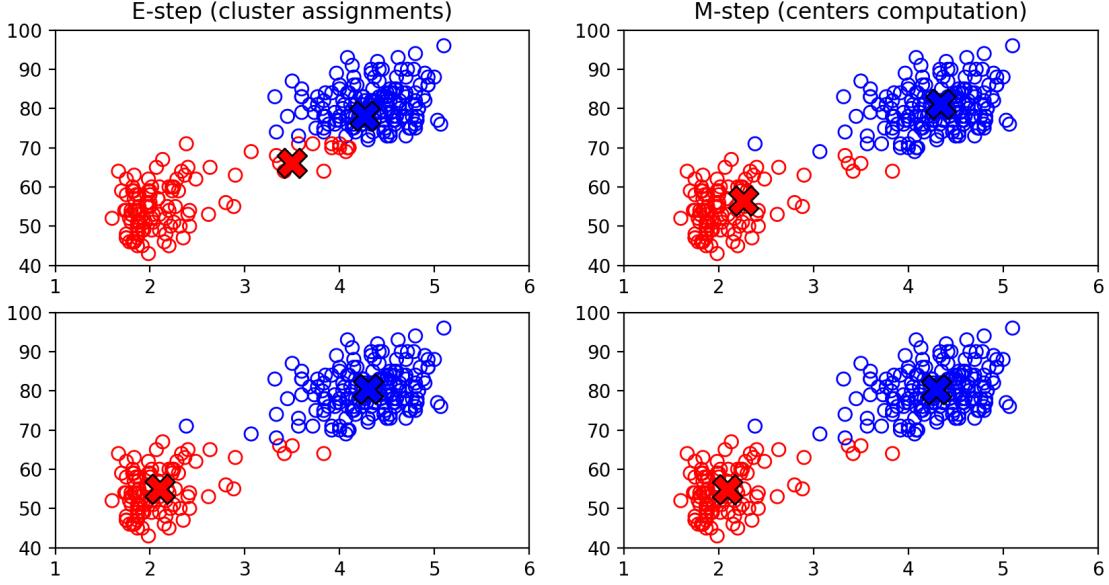
plt.scatter(
    old_faithful[:, :1], old_faithful[:, 1:2], edgecolors=np.where(classes == ▾
        0, "blue", "red"), facecolors="none", s=50
)
plt.scatter(model.centers[:, 0], model.centers[:, 1], color=["blue", "red"], ▾
           marker="X", s=250, edgecolors="black")
plt.xlim(1, 6)
plt.ylim(40, 100)
plt.show()
```



```
[197]: plt.figure(figsize=(10, 5))

# even are E-steps and odd are M-steps
for i, (centers, assignments) in enumerate(model.history):
    plt.subplot(2, 2, i + 1)
    plt.scatter(
        old_faithful[:, :1],
        old_faithful[:, 1:2],
        edgecolors=np.where(assignments == 0, "blue", "red"),
        facecolors="none",
        s=50,
    )
    plt.scatter(centers[:, 0], centers[:, 1], color=["blue", "red"], ▾
    marker="X", s=250, edgecolors="black")
    plt.xlim(1, 6)
    plt.ylim(40, 100)

    if i == 0:
        plt.title("E-step (cluster assignments)")
    elif i == 1:
        plt.title("M-step (centers computation)")
```



The initial values for the cluster centres are chosen to be equal to a random subset of K data points. It is also worth noting that the K -means algorithm itself is often used to initialize the parameters in a Gaussian mixture model before applying the EM algorithm.

The implementation of the K -means algorithm as discussed here can be relatively slow, because for the E-step it is necessary to compute the Euclidean distance between every prototype vector and every data point. Several schemes have been proposed for speeding up K -means, some of which are based on precomputing a data structure (e.g., k-d tree) such that nearby points are in the same subtree. Other approaches make use of the triangle inequality for distances, thereby avoiding unnecessary distance calculations.

Online K-means The batch version of K-means requires for the whole dataset to be used for updating the prototype vectors. We can also derive an on-line stochastic algorithm by applying the Robbins-Monro procedure to the problem of finding the roots of the regression function given by the derivatives of J with respect to μ_k . Decomposing the batch objective function, we obtain,

$$J_N = J_{N-1} + \sum_{k=1}^K r_{Nk} \|\mathbf{x}_N - \mu_k\|_2^2$$

Therefore, in the E-step, the N -th data point is still assigned to the closest center. Suppose that is μ_m . Thus, the expression J_N becomes,

$$J_N = J_{N-1} + \|\mathbf{x}_N - \mu_m\|_2^2$$

For the M-step, setting the derivative of J_N with respect to μ_k equal to $\mathbf{0}$, gives,

$$\begin{aligned}
\frac{\partial J}{\partial \mu_k} = \mathbf{0} &\Leftrightarrow \frac{\partial J_{N-1}}{\partial \mu_k} + \frac{\partial \|\mathbf{x}_N - \mu_m\|_2^2}{\partial \mu_k} = \mathbf{0} \\
&\Leftrightarrow \frac{\partial J_{N-1}}{\partial \mu_m} + \frac{\partial \|\mathbf{x}_N - \mu_m\|_2^2}{\partial \mu_m} = \mathbf{0} \\
&\Leftrightarrow 2 \sum_{n=1}^{N-1} r_{nm}(\mathbf{x}_n - \mu_m) + 2(\mathbf{x}_N - \mu_m) = \mathbf{0} \\
&\Leftrightarrow \sum_{n=1}^{N-1} r_{nm}(\mathbf{x}_n - \mu_m) + \mathbf{x}_N - \mu_m = \mathbf{0} \\
&\Leftrightarrow \sum_{n=1}^{N-1} r_{nm}\mathbf{x}_n - \sum_{n=1}^{N-1} r_{nm}\mu_m + \mathbf{x}_N - \mu_m = \mathbf{0} \\
&\Leftrightarrow \sum_{n=1}^{N-1} r_{nm}\mathbf{x}_n + \mathbf{x}_N = \sum_{n=1}^{N-1} r_{nm}\mu_m + \mu_m \\
&\Leftrightarrow \sum_{n=1}^{N-1} r_{nm}\mathbf{x}_n + \mathbf{x}_N = \mu_m \left(\sum_{n=1}^{N-1} r_{nm} + 1 \right) \\
&\Leftrightarrow \mu_m = \frac{\sum_{n=1}^{N-1} r_{nm}\mathbf{x}_n + \mathbf{x}_N}{\sum_{n=1}^{N-1} r_{nm} + 1}
\end{aligned}$$

Then, we may further decompose the update formula as follows,

$$\begin{aligned}
\mu_m^{(\tau)} &= \frac{\sum_{n=1}^{N-1} r_{nm}\mathbf{x}_n + \mathbf{x}_N}{\sum_{n=1}^{N-1} r_{nm} + 1} \\
&= \frac{\frac{\sum_{n=1}^{N-1} r_{nm}\mathbf{x}_n}{\sum_{n=1}^{N-1} r_{nm}} + \frac{\mathbf{x}_N}{\sum_{n=1}^{N-1} r_{nm}}}{1 + \frac{1}{\sum_{n=1}^{N-1} r_{nm}}} \\
&= \frac{\mu_m^{(\tau-1)} + \frac{\mathbf{x}_N}{\sum_{n=1}^{N-1} r_{nm}}}{1 + \frac{1}{\sum_{n=1}^{N-1} r_{nm}}} \\
&= \mu_m^{(\tau-1)} + \frac{\frac{\mathbf{x}_N}{\sum_{n=1}^{N-1} r_{nm}} - \frac{\mu_m^{(\tau-1)}}{\sum_{n=1}^{N-1} r_{nm}}}{1 + \frac{1}{\sum_{n=1}^{N-1} r_{nm}}} \\
&= \mu_m^{(\tau-1)} + \frac{\mathbf{x}_N - \mu_m^{(\tau-1)}}{1 + \frac{1}{\sum_{n=1}^{N-1} r_{nm}}}
\end{aligned}$$

This leads to a sequential update in which, for each data point \mathbf{x}_n in turn, we update the nearest prototype μ_k using,

$$\mu_k^{(\tau)} = \mu_k^{(\tau-1)} + \eta_n \left(\mathbf{x}_n - \mu_k^{(\tau-1)} \right)$$

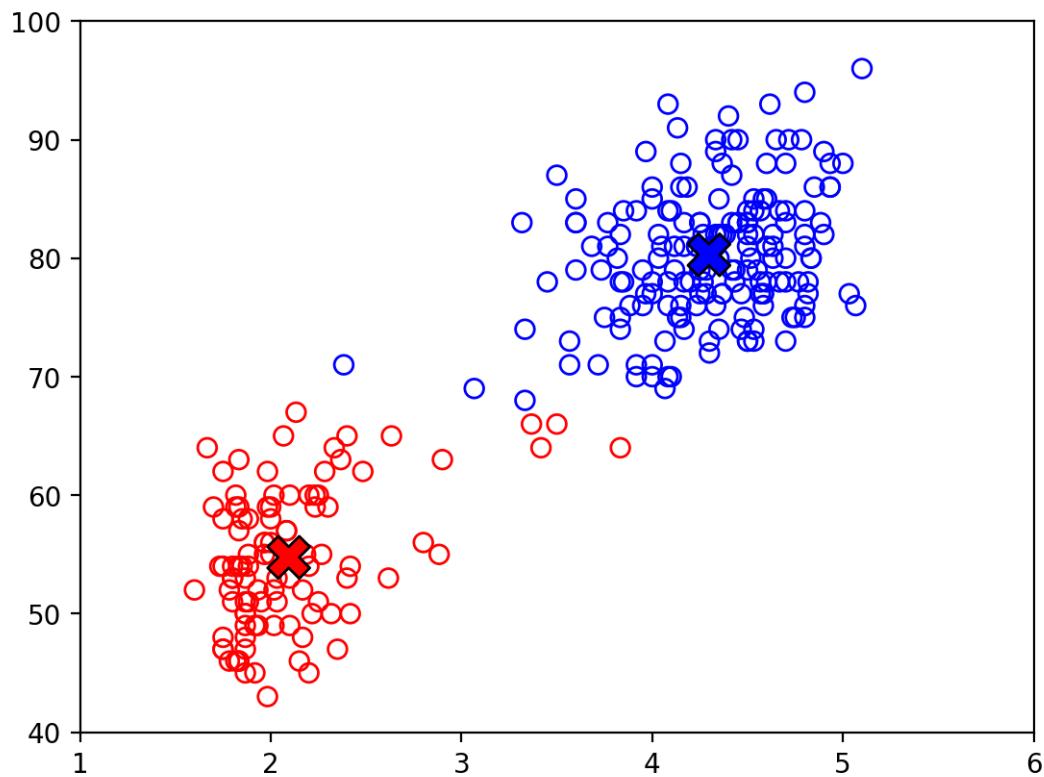
where η_n is a learning rate parameter that decreases monotonically as more data points are accumulated.

```
[198]: model = KMeans(2)

indices = list(range(len(old_faithful)))
np.random.shuffle(indices)
for i in indices:
    model.update(old_faithful[i, :])

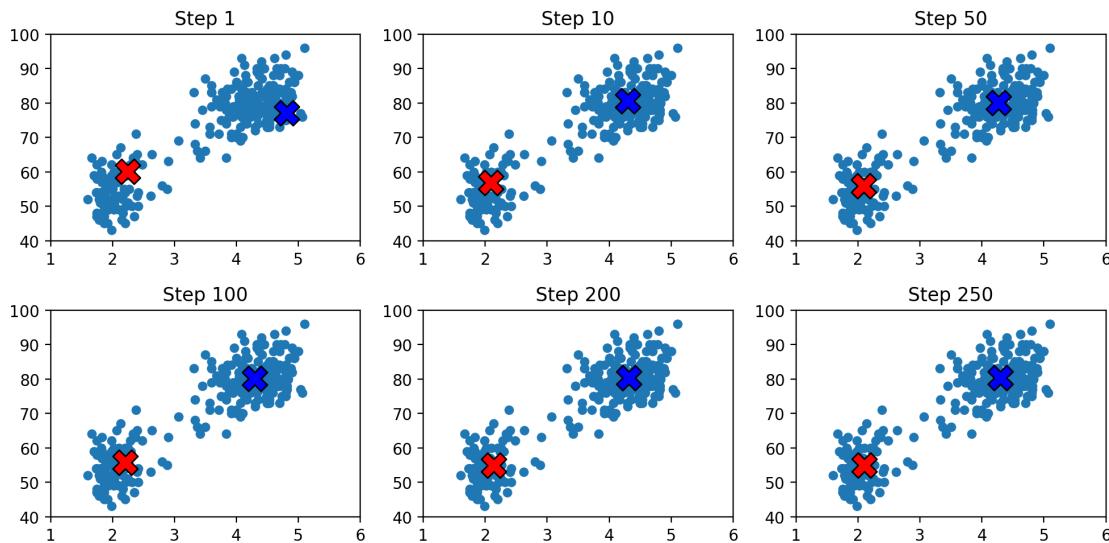
classes = model.predict(old_faithful)

plt.scatter(
    old_faithful[:, :1], old_faithful[:, 1:2], edgecolors=np.where(classes == 0, "blue", "red"), facecolors="none", s=50
)
plt.scatter(model.centers[:, 0], model.centers[:, 1], color=["blue", "red"], marker="X", s=250, edgecolors="black")
plt.xlim(1, 6)
plt.ylim(40, 100)
plt.show()
```



```
[199]: plt.figure(figsize=(10, 5))

plot_idx = 0
for i, (centers, assignments) in enumerate(model.history):
    if i in [1, 10, 50, 100, 200, 250]:
        plot_idx += 1
        plt.subplot(2, 3, plot_idx)
        plt.scatter(
            old_faithful[:, :1],
            old_faithful[:, 1:2],
            s=25,
        )
        plt.scatter(centers[:, 0], centers[:, 1], color=["blue", "red"], marker="X", s=250, edgecolors="black")
        plt.xlim(1, 6)
        plt.ylim(40, 100)
        plt.title(f"Step {i}")
        plt.tight_layout()
```



K-medoids The K-means algorithm is typically based on the squared Euclidean distance for measuring the distance between a data point and a prototype vector. This limits the type of data variables that can be considered (is inappropriate for cases where some or all of the variables represent categorical labels for instance), but it also makes the determination of the cluster means non-robust to outliers. K-means algorithm can be generalized by introducing a more general dissimilarity measure $\mathcal{V}(\mathbf{x}, \mathbf{x}')$ and then minimizing the following distortion measure,

$$\tilde{J} = \sum_{n=1}^N \sum_{m=1}^M r_{nk} \mathcal{V}(\mathbf{x}_n, \mu_k)$$

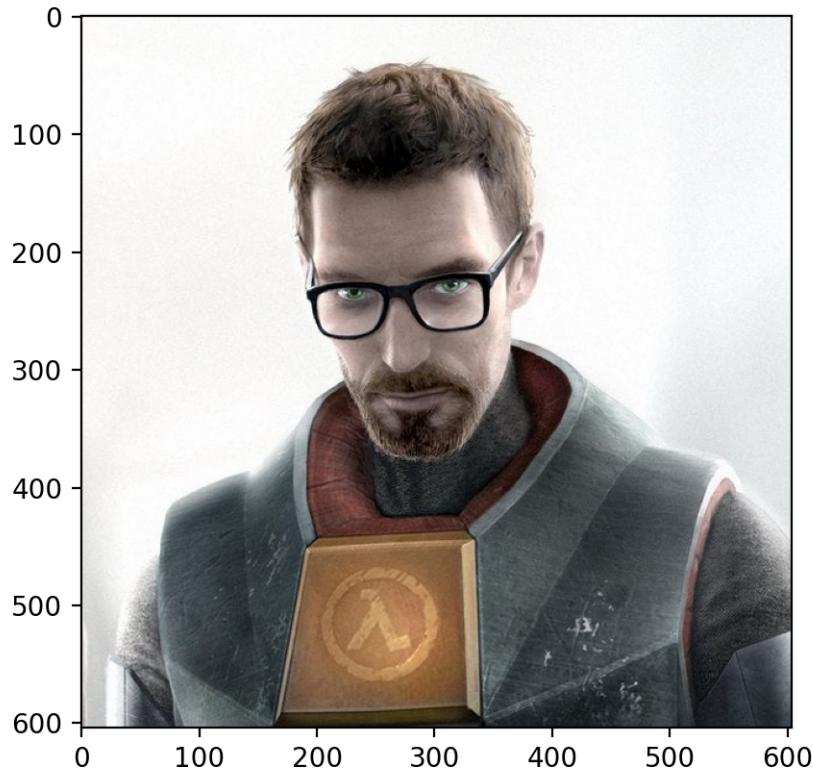
which gives the K -medoids algorithm. For a general choice of dissimilarity measure, the M step is potentially more complex than for K -means, and so it is common to restrict each cluster prototype to be equal to one of the data vectors assigned to that cluster. Thus, the M step involves, for each cluster k , a discrete search over the Nk points assigned to that cluster, which requires $O(N^2k)$ evaluations.

Note that the K -means algorithm assigns every data point uniquely to one, and only one, of the clusters. However, there may be some data points that lie roughly midway between cluster centres. In this case, it is not clear that the hard assignment to the nearest cluster is the most appropriate. By adopting a probabilistic approach, we obtain *soft* assignments of data points to clusters, reflecting the level of uncertainty over the most appropriate assignment. This probabilistic formulation brings numerous benefits.

9.1.1 Image segmentation and compression

As an illustration of the K-means algorithm, consider the problem of image segmentation. The goal is to partition an image into regions each of which has a reasonably homogeneous visual appearance or which corresponds to objects or parts of objects. Each pixel in an image is a point in a 3-dimensional space comprising the intensities of the red, blue, and green channels. The segmentation algorithm treats each pixel as a separate data point. We present the result of running K -means, by re-drawing the image replacing each pixel vector with the RGB intensity triplet given by the centre to which that pixel has been assigned.

```
[266]: from PIL import Image  
  
im = Image.open("../images/gordon_freeman.jpg")  
plt.imshow(im)  
plt.show()
```



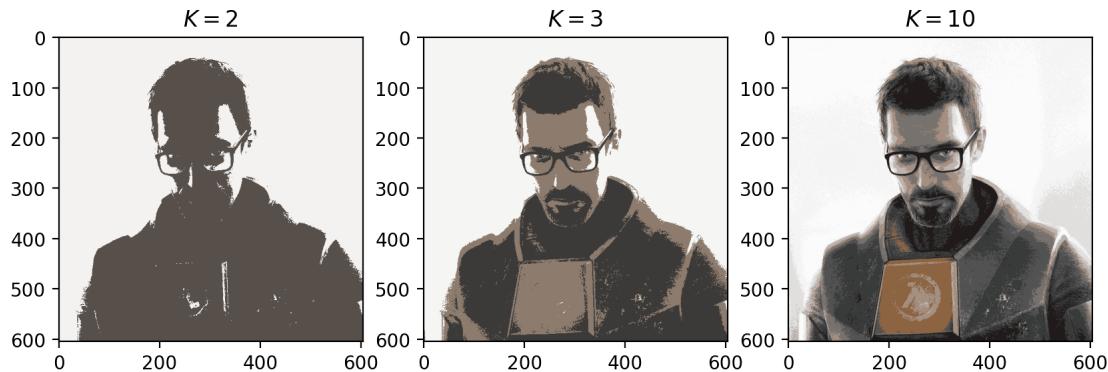
Note that for a given value of K , the algorithm is representing the image using a palette of only K colours. It should be emphasized that the use of K-means is not a particularly sophisticated approach to image segmentation, because it takes no account of the spatial proximity of different pixels.

```
[269]: im_array = np.asarray(im)
pixels = im_array.reshape(-1, 3)
```

```
[279]: plt.figure(figsize=(10, 5))

for i, k in enumerate([2, 3, 10]):
    model = KMeans(k)
    model.fit(pixels)
    segments = model.predict(pixels)
    segmented_im = model.centers[segments].astype(int).reshape(im_array.shape)

    plt.subplot(1, 3, i + 1)
    plt.imshow(segmented_im)
    plt.title(f"$K={k}$")
```



9.2 Mixtures of Gaussians

In Section 2.3.9 we motivated the Gaussian mixture model as a simple linear superposition of Gaussian components, aimed at providing a richer class of density models than the single Gaussian. We now turn to a formulation of Gaussian mixtures in terms of discrete latent variables. This will provide us with a deeper insight into this important distribution, and will also serve to motivate the expectation-maximization algorithm.