

Data Analysis and Machine Learning: Logistic Regression and Gradient Methods

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Addendum to Project 1 about Regularization Parameters

In project 1, when using Ridge (and if you wanted Lasso as well) regression, we end up searching for the optimal parameter λ which minimizes our selected scores (MSE or R^2 values for example). The brute force approach, as discussed in the code here for Ridge regression, consists in evaluating the MSE as function of different λ values. Based on these calculations, one tries then to determine the value of the hyperparameter λ which results in optimal scores (for example the smallest MSE or an $R^2 = 1$).

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn import linear_model

def MSE(y_data,y_model):
    n = np.size(y_model)
    return np.sum((y_data-y_model)**2)/n
# A seed just to ensure that the random numbers are the same for every run.
# Useful for eventual debugging.
np.random.seed(2021)

n = 100
x = np.random.rand(n)
y = np.exp(-x**2) + 1.5 * np.exp(-(x-2)**2)+ np.random.randn(n)

Maxpolydegree = 5
X = np.zeros((n,Maxpolydegree-1))

for degree in range(1,Maxpolydegree): #No intercept column
    X[:,degree-1] = x**(degree)
```

```

# We split the data in test and training data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)

# Decide which values of lambda to use
nlambdas = 500
MSERidgePredict = np.zeros(nlambdas)
lambdas = np.logspace(-4, 2, nlambdas)
for i in range(nlambdas):
    lmb = lambdas[i]
    RegRidge = linear_model.Ridge(lmb)
    RegRidge.fit(X_train, y_train)
    ypredictRidge = RegRidge.predict(X_test)
    MSERidgePredict[i] = MSE(y_test, ypredictRidge)

# Now plot the results
plt.figure()
plt.plot(np.log10(lambdas), MSERidgePredict, 'g--', label = 'MSE SL Ridge Test')
plt.xlabel('log10(lambda)')
plt.ylabel('MSE')
plt.legend()
plt.show()

```

Here we have performed a rather data greedy calculation as function of the regularization parameter λ . There is no resampling here. The latter can easily be added by employing the function **RidgeCV** instead of just calling the **Ridge** function. For **RidgeCV** we need to pass the array of λ values. By inspecting the figure we can in turn determine which is the optimal regularization parameter. This becomes however less functional in the long run.

Grid Search

An alternative is to use the so-called grid search functionality included with the library **Scikit-Learn**, as demonstrated for the same example here.

```

import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.linear_model import Ridge
from sklearn.model_selection import GridSearchCV

def R2(y_data, y_model):
    return 1 - np.sum((y_data - y_model) ** 2) / np.sum((y_data - np.mean(y_data)) ** 2)

def MSE(y_data, y_model):
    n = np.size(y_model)
    return np.sum((y_data - y_model) ** 2) / n

# A seed just to ensure that the random numbers are the same for every run.
# Useful for eventual debugging.
np.random.seed(2021)

n = 100
x = np.random.rand(n)
y = np.exp(-x**2) + 1.5 * np.exp(-(x-2)**2) + np.random.randn(n)

Maxpolydegree = 5
X = np.zeros((n, Maxpolydegree-1))

```

```

for degree in range(1,Maxpolydegree): #No intercept column
    X[:,degree-1] = x**(degree)

# We split the data in test and training data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)

# Decide which values of lambda to use
n_lambdas = 10
lambdas = np.logspace(-4, 2, n_lambdas)
# create and fit a ridge regression model, testing each alpha
model = Ridge()
gridsearch = GridSearchCV(estimator=model, param_grid=dict(alpha=lambdas))
gridsearch.fit(X_train, y_train)
print(gridsearch)
ypredictRidge = gridsearch.predict(X_test)
# summarize the results of the grid search
print(f"Best estimated lambda-value: {gridsearch.best_estimator_.alpha}")
print(f"MSE score: {MSE(y_test,ypredictRidge)}")
print(f"R2 score: {R2(y_test,ypredictRidge)}")

```

By default the grid search function includes cross validation with five folds. The [Scikit-Learn documentation](#) contains more information on how to set the different parameters.

If we take out the random noise, running the above codes results in $\lambda = 0$ yielding the best fit.

Randomized Grid Search

An alternative to the above manual grid set up, is to use a random search where the parameters are tuned from a random distribution (uniform below) for a fixed number of iterations. A model is constructed and evaluated for each combination of chosen parameters. We repeat the previous example but now with a random search. Note that values of λ are now limited to be within $x \in [0, 1]$. This domain may not be the most relevant one for the specific case under study.

```

import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.linear_model import Ridge
from sklearn.model_selection import GridSearchCV
from scipy.stats import uniform as randuniform
from sklearn.model_selection import RandomizedSearchCV

def R2(y_data, y_model):
    return 1 - np.sum((y_data - y_model) ** 2) / np.sum((y_data - np.mean(y_data)) ** 2)

def MSE(y_data, y_model):
    n = np.size(y_model)
    return np.sum((y_data - y_model) ** 2) / n

# A seed just to ensure that the random numbers are the same for every run.
# Useful for eventual debugging.
np.random.seed(2021)

n = 100

```

```

x = np.random.rand(n)
y = np.exp(-x**2) + 1.5 * np.exp(-(x-2)**2) + np.random.randn(n)

Maxpolydegree = 5
X = np.zeros((n,Maxpolydegree-1))

for degree in range(1,Maxpolydegree): #No intercept column
    X[:,degree-1] = x**(degree)

# We split the data in test and training data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)

param_grid = {'alpha': randuniform()}
# create and fit a ridge regression model, testing each alpha
model = Ridge()
gridsearch = RandomizedSearchCV(estimator=model, param_distributions=param_grid, n_iter=100)
gridsearch.fit(X_train, y_train)
print(gridsearch)
ypredictRidge = gridsearch.predict(X_test)
# summarize the results of the grid search
print(f"Best estimated lambda-value: {gridsearch.best_estimator_.alpha}")
print(f"MSE score: {MSE(y_test,ypredictRidge)}")
print(f"R2 score: {R2(y_test,ypredictRidge)}")

```

A more complicated Example: The Ising model

The one-dimensional Ising model with nearest neighbor interaction, no external field and a constant coupling constant J is given by

$$H = -J \sum_k^L s_k s_{k+1}, \quad (1)$$

where $s_i \in \{-1, 1\}$ and $s_{N+1} = s_1$. The number of spins in the system is determined by L . For the one-dimensional system there is no phase transition.

We will look at a system of $L = 40$ spins with a coupling constant of $J = 1$. To get enough training data we will generate 10000 states with their respective energies.

```

import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.axes_grid1 import make_axes_locatable
import seaborn as sns
import scipy.linalg as scl
from sklearn.model_selection import train_test_split
import tqdm
sns.set(color_codes=True)
cmap_args=dict(vmin=-1., vmax=1., cmap='seismic')

L = 40
n = int(1e4)

spins = np.random.choice([-1, 1], size=(n, L))
J = 1.0

energies = np.zeros(n)

```

```

for i in range(n):
    energies[i] = - J * np.dot(spins[i], np.roll(spins[i], 1))

```

Here we use ordinary least squares regression to predict the energy for the nearest neighbor one-dimensional Ising model on a ring, i.e., the endpoints wrap around. We will use linear regression to fit a value for the coupling constant to achieve this.

Reformulating the problem to suit regression

A more general form for the one-dimensional Ising model is

$$H = - \sum_j^L \sum_k^L s_j s_k J_{jk}. \quad (2)$$

Here we allow for interactions beyond the nearest neighbors and a state dependent coupling constant. This latter expression can be formulated as a matrix-product

$$\mathbf{H} = \mathbf{X}\mathbf{J}, \quad (3)$$

where $X_{jk} = s_j s_k$ and \mathbf{J} is a matrix which consists of the elements $-J_{jk}$. This form of writing the energy fits perfectly with the form utilized in linear regression, that is

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}, \quad (4)$$

We split the data in training and test data as discussed in the previous example

```

X = np.zeros((n, L ** 2))
for i in range(n):
    X[i] = np.outer(spins[i], spins[i]).ravel()
y = energies
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)

```

Linear regression

In the ordinary least squares method we choose the cost function

$$C(\mathbf{X}, \boldsymbol{\beta}) = \frac{1}{n} \{ (\mathbf{X}\boldsymbol{\beta} - \mathbf{y})^T (\mathbf{X}\boldsymbol{\beta} - \mathbf{y}) \}. \quad (5)$$

We then find the extremal point of C by taking the derivative with respect to $\boldsymbol{\beta}$ as discussed above. This yields the expression for $\boldsymbol{\beta}$ to be

$$\beta = \frac{\mathbf{X}^T \mathbf{y}}{\mathbf{X}^T \mathbf{X}},$$

which immediately imposes some requirements on \mathbf{X} as there must exist an inverse of $\mathbf{X}^T \mathbf{X}$. If the expression we are modeling contains an intercept, i.e., a constant term, we must make sure that the first column of \mathbf{X} consists of 1. We do this here

```
X_train_own = np.concatenate(
    (np.ones(len(X_train))[:, np.newaxis], X_train),
    axis=1
)
X_test_own = np.concatenate(
    (np.ones(len(X_test))[:, np.newaxis], X_test),
    axis=1
)

def ols_inv(x: np.ndarray, y: np.ndarray) -> np.ndarray:
    return scl.inv(x.T @ x) @ (x.T @ y)
beta = ols_inv(X_train_own, y_train)
```

Singular Value decomposition

Doing the inversion directly turns out to be a bad idea since the matrix $\mathbf{X}^T \mathbf{X}$ is singular. An alternative approach is to use the **singular value decomposition**. Using the definition of the Moore-Penrose pseudoinverse we can write the equation for β as

$$\beta = \mathbf{X}^+ \mathbf{y},$$

where the pseudoinverse of \mathbf{X} is given by

$$\mathbf{X}^+ = \frac{\mathbf{X}^T}{\mathbf{X}^T \mathbf{X}}.$$

Using singular value decomposition we can decompose the matrix $\mathbf{X} = \mathbf{U} \mathbf{\Sigma} \mathbf{V}^T$, where \mathbf{U} and \mathbf{V} are orthogonal(unitary) matrices and $\mathbf{\Sigma}$ contains the singular values (more details below). where $\mathbf{X}^+ = \mathbf{V} \mathbf{\Sigma}^+ \mathbf{U}^T$. This reduces the equation for ω to

$$\beta = \mathbf{V} \mathbf{\Sigma}^+ \mathbf{U}^T \mathbf{y}. \quad (6)$$

Note that solving this equation by actually doing the pseudoinverse (which is what we will do) is not a good idea as this operation scales as $\mathcal{O}(n^3)$, where n is the number of elements in a general matrix. Instead, doing QR -factorization and solving the linear system as an equation would reduce this down to $\mathcal{O}(n^2)$ operations.

```
def ols_svd(x: np.ndarray, y: np.ndarray) -> np.ndarray:
    u, s, v = scl.svd(x)
    return v.T @ scl.pinv(scl.diagsvd(s, u.shape[0], v.shape[0])) @ u.T @ y

beta = ols_svd(X_train_own, y_train)
```

When extracting the J -matrix we need to make sure that we remove the intercept, as is done here

```
J = beta[1:].reshape(L, L)
```

A way of looking at the coefficients in J is to plot the matrices as images.

```
fig = plt.figure(figsize=(20, 14))
im = plt.imshow(J, **cmap_args)
plt.title("OLS", fontsize=18)
plt.xticks(fontsize=18)
plt.yticks(fontsize=18)
cb = fig.colorbar(im)
cb.ax.set_yticklabels(cb.ax.get_yticklabels(), fontsize=18)
plt.show()
```

It is interesting to note that OLS considers both $J_{j,j+1} = -0.5$ and $J_{j,j-1} = -0.5$ as valid matrix elements for J . In our discussion below on hyperparameters and Ridge and Lasso regression we will see that this problem can be removed, partly and only with Lasso regression.

In this case our matrix inversion was actually possible. The obvious question now is what is the mathematics behind the SVD?

The one-dimensional Ising model

Let us bring back the Ising model again, but now with an additional focus on Ridge and Lasso regression as well. We repeat some of the basic parts of the Ising model and the setup of the training and test data. The one-dimensional Ising model with nearest neighbor interaction, no external field and a constant coupling constant J is given by

$$H = -J \sum_k^L s_k s_{k+1}, \quad (7)$$

where $s_i \in \{-1, 1\}$ and $s_{N+1} = s_1$. The number of spins in the system is determined by L . For the one-dimensional system there is no phase transition.

We will look at a system of $L = 40$ spins with a coupling constant of $J = 1$. To get enough training data we will generate 10000 states with their respective energies.

```
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.axes_grid1 import make_axes_locatable
import seaborn as sns
import scipy.linalg as scl
from sklearn.model_selection import train_test_split
import sklearn.linear_model as skl
import tqdm
sns.set(color_codes=True)
cmap_args=dict(vmin=-1., vmax=1., cmap='seismic')
```

```

L = 40
n = int(1e4)

spins = np.random.choice([-1, 1], size=(n, L))
J = 1.0

energies = np.zeros(n)

for i in range(n):
    energies[i] = - J * np.dot(spins[i], np.roll(spins[i], 1))

```

A more general form for the one-dimensional Ising model is

$$H = - \sum_j^L \sum_k^L s_j s_k J_{jk}. \quad (8)$$

Here we allow for interactions beyond the nearest neighbors and a more adaptive coupling matrix. This latter expression can be formulated as a matrix-product on the form

$$H = XJ, \quad (9)$$

where $X_{jk} = s_j s_k$ and J is the matrix consisting of the elements $-J_{jk}$. This form of writing the energy fits perfectly with the form utilized in linear regression, viz.

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}. \quad (10)$$

We organize the data as we did above

```

X = np.zeros((n, L ** 2))
for i in range(n):
    X[i] = np.outer(spins[i], spins[i]).ravel()
y = energies
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.96)

X_train_own = np.concatenate(
    (np.ones(len(X_train))[:, np.newaxis], X_train),
    axis=1
)

X_test_own = np.concatenate(
    (np.ones(len(X_test))[:, np.newaxis], X_test),
    axis=1
)

```

We will do all fitting with **Scikit-Learn**,

```
clf = skl.LinearRegression().fit(X_train, y_train)
```

When extracting the J -matrix we make sure to remove the intercept

```
J_sk = clf.coef_.reshape(L, L)
```


And then we plot the results

```
fig = plt.figure(figsize=(20, 14))
im = plt.imshow(J_sk, **cmap_args)
plt.title("LinearRegression from Scikit-learn", fontsize=18)
plt.xticks(fontsize=18)
plt.yticks(fontsize=18)
cb = fig.colorbar(im)
cb.ax.set_yticklabels(cb.ax.get_yticklabels(), fontsize=18)
plt.show()
```

The results perfectly with our previous discussion where we used our own code.

Ridge regression

Having explored the ordinary least squares we move on to ridge regression. In ridge regression we include a **regularizer**. This involves a new cost function which leads to a new estimate for the weights β . This results in a penalized regression problem. The cost function is given by

$$C(\mathbf{X}, \beta; \lambda) = (\mathbf{X}\beta - \mathbf{y})^T (\mathbf{X}\beta - \mathbf{y}) + \lambda \beta^T \beta. \quad (11)$$

```
_lambda = 0.1
clf_ridge = skl.Ridge(alpha=_lambda).fit(X_train, y_train)
J_ridge_sk = clf_ridge.coef_.reshape(L, L)
fig = plt.figure(figsize=(20, 14))
im = plt.imshow(J_ridge_sk, **cmap_args)
plt.title("Ridge from Scikit-learn", fontsize=18)
plt.xticks(fontsize=18)
plt.yticks(fontsize=18)
cb = fig.colorbar(im)
cb.ax.set_yticklabels(cb.ax.get_yticklabels(), fontsize=18)

plt.show()
```

LASSO regression

In the **Least Absolute Shrinkage and Selection Operator** (LASSO)-method we get a third cost function.

$$C(\mathbf{X}, \beta; \lambda) = (\mathbf{X}\beta - \mathbf{y})^T (\mathbf{X}\beta - \mathbf{y}) + \lambda \sqrt{\beta^T \beta}. \quad (12)$$

Finding the extremal point of this cost function is not so straight-forward as in least squares and ridge. We will therefore rely solely on the function “Lasso” from **Scikit-Learn**.

```
clf_lasso = skl.Lasso(alpha=_lambda).fit(X_train, y_train)
J_lasso_sk = clf_lasso.coef_.reshape(L, L)
fig = plt.figure(figsize=(20, 14))
im = plt.imshow(J_lasso_sk, **cmap_args)
plt.title("Lasso from Scikit-learn", fontsize=18)
```

```

plt.xticks(fontsize=18)
plt.yticks(fontsize=18)
cb = fig.colorbar(im)
cb.ax.set_yticklabels(cb.ax.get_yticklabels(), fontsize=18)

plt.show()

```

It is quite striking how LASSO breaks the symmetry of the coupling constant as opposed to ridge and OLS. We get a sparse solution with $J_{j,j+1} = -1$.

Performance as function of the regularization parameter

We see how the different models perform for a different set of values for λ .

```

lambdas = np.logspace(-4, 5, 10)

train_errors = {
    "ols_sk": np.zeros(lambdas.size),
    "ridge_sk": np.zeros(lambdas.size),
    "lasso_sk": np.zeros(lambdas.size)
}

test_errors = {
    "ols_sk": np.zeros(lambdas.size),
    "ridge_sk": np.zeros(lambdas.size),
    "lasso_sk": np.zeros(lambdas.size)
}

plot_counter = 1

fig = plt.figure(figsize=(32, 54))

for i, _lambda in enumerate(tqdm.tqdm(lambdas)):
    for key, method in zip(
        ["ols_sk", "ridge_sk", "lasso_sk"],
        [skl.LinearRegression(), skl.Ridge(alpha=_lambda), skl.Lasso(alpha=_lambda)]
    ):
        method = method.fit(X_train, y_train)

        train_errors[key][i] = method.score(X_train, y_train)
        test_errors[key][i] = method.score(X_test, y_test)

        omega = method.coef_.reshape(L, L)

        plt.subplot(10, 5, plot_counter)
        plt.imshow(omega, **cmap_args)
        plt.title(r"%s, $\lambda = %.4f$" % (key, _lambda))
        plot_counter += 1

plt.show()

```

We see that LASSO reaches a good solution for low values of λ , but will "wither" when we increase λ too much. Ridge is more stable over a larger range of values for λ , but eventually also fades away.

Finding the optimal value of λ

To determine which value of λ is best we plot the accuracy of the models when predicting the training and the testing set. We expect the accuracy of the training set to be quite good, but if the accuracy of the testing set is much lower this tells us that we might be subject to an overfit model. The ideal scenario is an accuracy on the testing set that is close to the accuracy of the training set.

```
fig = plt.figure(figsize=(20, 14))

colors = {
    "ols_sk": "r",
    "ridge_sk": "y",
    "lasso_sk": "c"
}

for key in train_errors:
    plt.semilogx(
        lambdas,
        train_errors[key],
        colors[key],
        label="Train {0}".format(key),
        linewidth=4.0
    )

for key in test_errors:
    plt.semilogx(
        lambdas,
        test_errors[key],
        colors[key] + "--",
        label="Test {0}".format(key),
        linewidth=4.0
    )

plt.legend(loc="best", fontsize=18)
plt.xlabel(r"$\lambda$", fontsize=18)
plt.ylabel(r"$R^2$", fontsize=18)
plt.tick_params(labelsize=18)
plt.show()
```

From the above figure we can see that LASSO with $\lambda = 10^{-2}$ achieves a very good accuracy on the test set. This by far surpasses the other models for all values of λ .

Logistic Regression

In linear regression our main interest was centered on learning the coefficients of a functional fit (say a polynomial) in order to be able to predict the response of a continuous variable on some unseen data. The fit to the continuous variable y_i is based on some independent variables x_i . Linear regression resulted in analytical expressions for standard ordinary Least Squares or Ridge regression (in terms of matrices to invert) for several quantities, ranging from the variance and thereby the confidence intervals of the parameters β to the mean squared error. If we can invert the product of the design matrices, linear regression gives then a simple recipe for fitting our data.

Classification problems

Classification problems, however, are concerned with outcomes taking the form of discrete variables (i.e. categories). We may for example, on the basis of DNA sequencing for a number of patients, like to find out which mutations are important for a certain disease; or based on scans of various patients' brains, figure out if there is a tumor or not; or given a specific physical system, we'd like to identify its state, say whether it is an ordered or disordered system (typical situation in solid state physics); or classify the status of a patient, whether she/he has a stroke or not and many other similar situations.

The most common situation we encounter when we apply logistic regression is that of two possible outcomes, normally denoted as a binary outcome, true or false, positive or negative, success or failure etc.

Optimization and Deep learning

Logistic regression will also serve as our stepping stone towards neural network algorithms and supervised deep learning. For logistic learning, the minimization of the cost function leads to a non-linear equation in the parameters β . The optimization of the problem calls therefore for minimization algorithms. This forms the bottle neck of all machine learning algorithms, namely how to find reliable minima of a multi-variable function. This leads us to the family of gradient descent methods. The latter are the working horses of basically all modern machine learning algorithms.

We note also that many of the topics discussed here on logistic regression are also commonly used in modern supervised Deep Learning models, as we will see later.

Basics

We consider the case where the dependent variables, also called the responses or the outcomes, y_i are discrete and only take values from $k = 0, \dots, K - 1$ (i.e. K classes).

The goal is to predict the output classes from the design matrix $\mathbf{X} \in \mathbb{R}^{n \times p}$ made of n samples, each of which carries p features or predictors. The primary goal is to identify the classes to which new unseen samples belong.

Let us specialize to the case of two classes only, with outputs $y_i = 0$ and $y_i = 1$. Our outcomes could represent the status of a credit card user that could default or not on her/his credit card debt. That is

$$y_i = \begin{bmatrix} 0 & \text{no} \\ 1 & \text{yes} \end{bmatrix}.$$

Linear classifier

Before moving to the logistic model, let us try to use our linear regression model to classify these two outcomes. We could for example fit a linear model to the default case if $y_i > 0.5$ and the no default case $y_i \leq 0.5$.

We would then have our weighted linear combination, namely

$$\mathbf{y} = \mathbf{X}^T \boldsymbol{\beta} + \boldsymbol{\epsilon}, \quad (13)$$

where \mathbf{y} is a vector representing the possible outcomes, \mathbf{X} is our $n \times p$ design matrix and $\boldsymbol{\beta}$ represents our estimators/predictors.

Some selected properties

The main problem with our function is that it takes values on the entire real axis. In the case of logistic regression, however, the labels y_i are discrete variables. A typical example is the credit card data discussed below here, where we can set the state of defaulting the debt to $y_i = 1$ and not to $y_i = 0$ for one the persons in the data set (see the full example below).

One simple way to get a discrete output is to have sign functions that map the output of a linear regressor to values $\{0, 1\}$, $f(s_i) = \text{sign}(s_i) = 1$ if $s_i \geq 0$ and 0 if otherwise. We will encounter this model in our first demonstration of neural networks. Historically it is called the “perceptron” model in the machine learning literature. This model is extremely simple. However, in many cases it is more favorable to use a “soft” classifier that outputs the probability of a given category. This leads us to the logistic function.

Simple example

The following example on data for coronary heart disease (CHD) as function of age may serve as an illustration. In the code here we read and plot whether a person has had CHD (output = 1) or not (output = 0). This output is plotted the person’s against age. Clearly, the figure shows that attempting to make a standard linear regression fit may not be very meaningful.

```
# Common imports
import os
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.linear_model import LinearRegression, Ridge, Lasso
from sklearn.model_selection import train_test_split
from sklearn.utils import resample
from sklearn.metrics import mean_squared_error
from IPython.display import display
from pylab import plt, mpl
plt.style.use('seaborn')
mpl.rcParams['font.family'] = 'serif'

# Where to save the figures and data files
PROJECT_ROOT_DIR = "Results"
```

```

FIGURE_ID = "Results/FigureFiles"
DATA_ID = "DataFiles/"

if not os.path.exists(PROJECT_ROOT_DIR):
    os.mkdir(PROJECT_ROOT_DIR)

if not os.path.exists(FIGURE_ID):
    os.makedirs(FIGURE_ID)

if not os.path.exists(DATA_ID):
    os.makedirs(DATA_ID)

def image_path(fig_id):
    return os.path.join(FIGURE_ID, fig_id)

def data_path(dat_id):
    return os.path.join(DATA_ID, dat_id)

def save_fig(fig_id):
    plt.savefig(image_path(fig_id) + ".png", format='png')

infile = open(data_path("chddata.csv"), 'r')

# Read the chd data as csv file and organize the data into arrays with age group, age, and chd
chd = pd.read_csv(infile, names=('ID', 'Age', 'Agroup', 'CHD'))
chd.columns = ['ID', 'Age', 'Agroup', 'CHD']
output = chd['CHD']
age = chd['Age']
agegroup = chd['Agroup']
numberID = chd['ID']
display(chd)

plt.scatter(age, output, marker='o')
plt.axis([18, 70.0, -0.1, 1.2])
plt.xlabel(r'Age')
plt.ylabel(r'CHD')
plt.title(r'Age distribution and Coronary heart disease')
plt.show()

```

Plotting the mean value for each group

What we could attempt however is to plot the mean value for each group.

```

agegroupmean = np.array([0.1, 0.133, 0.250, 0.333, 0.462, 0.625, 0.765, 0.800])
group = np.array([1, 2, 3, 4, 5, 6, 7, 8])
plt.plot(group, agegroupmean, "r-")
plt.axis([0, 9, 0, 1.0])
plt.xlabel(r'Age group')
plt.ylabel(r'CHD mean values')
plt.title(r'Mean values for each age group')
plt.show()

```

We are now trying to find a function $f(y|x)$, that is a function which gives us an expected value for the output y with a given input x . In standard linear regression with a linear dependence on x , we would write this in terms of our model

$$f(y_i|x_i) = \beta_0 + \beta_1 x_i.$$

This expression implies however that $f(y_i|x_i)$ could take any value from minus infinity to plus infinity. If we however let $f(y|y)$ be represented by the mean value, the above example shows us that we can constrain the function to take values between zero and one, that is we have $0 \leq f(y_i|x_i) \leq 1$. Looking at our last curve we see also that it has an S-shaped form. This leads us to a very popular model for the function f , namely the so-called Sigmoid function or logistic model. We will consider this function as representing the probability for finding a value of y_i with a given x_i .

The logistic function

Another widely studied model, is the so-called perceptron model, which is an example of a “hard classification” model. We will encounter this model when we discuss neural networks as well. Each datapoint is deterministically assigned to a category (i.e $y_i = 0$ or $y_i = 1$). In many cases, and the coronary heart disease data forms one of many such examples, it is favorable to have a “soft” classifier that outputs the probability of a given category rather than a single value. For example, given x_i , the classifier outputs the probability of being in a category k . Logistic regression is the most common example of a so-called soft classifier. In logistic regression, the probability that a data point x_i belongs to a category $y_i = \{0, 1\}$ is given by the so-called logit function (or Sigmoid) which is meant to represent the likelihood for a given event,

$$p(t) = \frac{1}{1 + \exp -t} = \frac{\exp t}{1 + \exp t}.$$

Note that $1 - p(t) = p(-t)$.

Examples of likelihood functions used in logistic regression and nueral networks

The following code plots the logistic function, the step function and other functions we will encounter from here and on.

```

"""The sigmoid function (or the logistic curve) is a
function that takes any real number, z, and outputs a number (0,1).
It is useful in neural networks for assigning weights on a relative scale.
The value z is the weighted sum of parameters involved in the learning algorithm."""

import numpy
import matplotlib.pyplot as plt
import math as mt

z = numpy.arange(-5, 5, .1)
sigma_fn = numpy.vectorize(lambda z: 1/(1+numpy.exp(-z)))
sigma = sigma_fn(z)

fig = plt.figure()
ax = fig.add_subplot(111)
ax.plot(z, sigma)
ax.set_ylim([-0.1, 1.1])

```

```

ax.set_xlim([-5,5])
ax.grid(True)
ax.set_xlabel('z')
ax.set_title('sigmoid function')

plt.show()

"""Step Function"""
z = numpy.arange(-5, 5, .02)
step_fn = numpy.vectorize(lambda z: 1.0 if z >= 0.0 else 0.0)
step = step_fn(z)

fig = plt.figure()
ax = fig.add_subplot(111)
ax.plot(z, step)
ax.set_ylim([-0.5, 1.5])
ax.set_xlim([-5,5])
ax.grid(True)
ax.set_xlabel('z')
ax.set_title('step function')

plt.show()

"""tanh Function"""
z = numpy.arange(-2*mt.pi, 2*mt.pi, 0.1)
t = numpy.tanh(z)

fig = plt.figure()
ax = fig.add_subplot(111)
ax.plot(z, t)
ax.set_ylim([-1.0, 1.0])
ax.set_xlim([-2*mt.pi, 2*mt.pi])
ax.grid(True)
ax.set_xlabel('z')
ax.set_title('tanh function')

plt.show()

```

Two parameters

We assume now that we have two classes with y_i either 0 or 1. Furthermore we assume also that we have only two parameters β in our fitting of the Sigmoid function, that is we define probabilities

$$p(y_i = 1|x_i, \beta) = \frac{\exp(\beta_0 + \beta_1 x_i)}{1 + \exp(\beta_0 + \beta_1 x_i)},$$

$$p(y_i = 0|x_i, \beta) = 1 - p(y_i = 1|x_i, \beta),$$

where β are the weights we wish to extract from data, in our case β_0 and β_1 .

Note that we used

$$p(y_i = 0|x_i, \beta) = 1 - p(y_i = 1|x_i, \beta).$$

Maximum likelihood

In order to define the total likelihood for all possible outcomes from a dataset $\mathcal{D} = \{(y_i, x_i)\}$, with the binary labels $y_i \in \{0, 1\}$ and where the data points are drawn independently, we use the so-called [Maximum Likelihood Estimation](#) (MLE) principle. We aim thus at maximizing the probability of seeing the observed data. We can then approximate the likelihood in terms of the product of the individual probabilities of a specific outcome y_i , that is

$$P(\mathcal{D}|\beta) = \prod_{i=1}^n [p(y_i = 1|x_i, \beta)]^{y_i} [1 - p(y_i = 1|x_i, \beta)]^{1-y_i}$$

from which we obtain the log-likelihood and our **cost/loss** function

$$\mathcal{C}(\beta) = \sum_{i=1}^n (y_i \log p(y_i = 1|x_i, \beta) + (1 - y_i) \log [1 - p(y_i = 1|x_i, \beta)]).$$

The cost function rewritten

Reordering the logarithms, we can rewrite the **cost/loss** function as

$$\mathcal{C}(\beta) = \sum_{i=1}^n (y_i(\beta_0 + \beta_1 x_i) - \log(1 + \exp(\beta_0 + \beta_1 x_i))).$$

The maximum likelihood estimator is defined as the set of parameters that maximize the log-likelihood where we maximize with respect to β . Since the cost (error) function is just the negative log-likelihood, for logistic regression we have that

$$\mathcal{C}(\beta) = - \sum_{i=1}^n (y_i(\beta_0 + \beta_1 x_i) - \log(1 + \exp(\beta_0 + \beta_1 x_i))).$$

This equation is known in statistics as the **cross entropy**. Finally, we note that just as in linear regression, in practice we often supplement the cross-entropy with additional regularization terms, usually L_1 and L_2 regularization as we did for Ridge and Lasso regression.

Minimizing the cross entropy

The cross entropy is a convex function of the weights β and, therefore, any local minimizer is a global minimizer.

Minimizing this cost function with respect to the two parameters β_0 and β_1 we obtain

$$\frac{\partial \mathcal{C}(\beta)}{\partial \beta_0} = - \sum_{i=1}^n \left(y_i - \frac{\exp(\beta_0 + \beta_1 x_i)}{1 + \exp(\beta_0 + \beta_1 x_i)} \right),$$

and

$$\frac{\partial \mathcal{C}(\boldsymbol{\beta})}{\partial \beta_1} = - \sum_{i=1}^n \left(y_i x_i - x_i \frac{\exp(\beta_0 + \beta_1 x_i)}{1 + \exp(\beta_0 + \beta_1 x_i)} \right).$$

A more compact expression

Let us now define a vector \mathbf{y} with n elements y_i , an $n \times p$ matrix \mathbf{X} which contains the x_i values and a vector \mathbf{p} of fitted probabilities $p(y_i|x_i, \boldsymbol{\beta})$. We can rewrite in a more compact form the first derivative of cost function as

$$\frac{\partial \mathcal{C}(\boldsymbol{\beta})}{\partial \boldsymbol{\beta}} = -\mathbf{X}^T (\mathbf{y} - \mathbf{p}).$$

If we in addition define a diagonal matrix \mathbf{W} with elements $p(y_i|x_i, \boldsymbol{\beta})(1 - p(y_i|x_i, \boldsymbol{\beta}))$, we can obtain a compact expression of the second derivative as

$$\frac{\partial^2 \mathcal{C}(\boldsymbol{\beta})}{\partial \boldsymbol{\beta} \partial \boldsymbol{\beta}^T} = \mathbf{X}^T \mathbf{W} \mathbf{X}.$$

Extending to more predictors

Within a binary classification problem, we can easily expand our model to include multiple predictors. Our ratio between likelihoods is then with p predictors

$$\log \frac{p(\boldsymbol{\beta} \mathbf{x})}{1 - p(\boldsymbol{\beta} \mathbf{x})} = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p.$$

Here we defined $\mathbf{x} = [1, x_1, x_2, \dots, x_p]$ and $\boldsymbol{\beta} = [\beta_0, \beta_1, \dots, \beta_p]$ leading to

$$p(\boldsymbol{\beta} \mathbf{x}) = \frac{\exp(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p)}{1 + \exp(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p)}.$$

Including more classes

Till now we have mainly focused on two classes, the so-called binary system. Suppose we wish to extend to K classes. Let us for the sake of simplicity assume we have only two predictors. We have then following model

$$\log \frac{p(C=1|x)}{p(K|x)} = \beta_{10} + \beta_{11} x_1,$$

and

$$\log \frac{p(C=2|x)}{p(K|x)} = \beta_{20} + \beta_{21} x_1,$$

and so on till the class $C = K - 1$ class

$$\log \frac{p(C=K-1|x)}{p(K|x)} = \beta_{(K-1)0} + \beta_{(K-1)1} x_1,$$

and the model is specified in term of $K - 1$ so-called log-odds or **logit** transformations.

More classes

In our discussion of neural networks we will encounter the above again in terms of a slightly modified function, the so-called **Softmax** function.

The softmax function is used in various multiclass classification methods, such as multinomial logistic regression (also known as softmax regression), multiclass linear discriminant analysis, naive Bayes classifiers, and artificial neural networks. Specifically, in multinomial logistic regression and linear discriminant analysis, the input to the function is the result of K distinct linear functions, and the predicted probability for the k -th class given a sample vector \mathbf{x} and a weighting vector β is (with two predictors):

$$p(C = k|\mathbf{x}) = \frac{\exp(\beta_{k0} + \beta_{k1}x_1)}{1 + \sum_{l=1}^{K-1} \exp(\beta_{l0} + \beta_{l1}x_1)}.$$

It is easy to extend to more predictors. The final class is

$$p(C = K|\mathbf{x}) = \frac{1}{1 + \sum_{l=1}^{K-1} \exp(\beta_{l0} + \beta_{l1}x_1)},$$

and they sum to one. Our earlier discussions were all specialized to the case with two classes only. It is easy to see from the above that what we derived earlier is compatible with these equations.

To find the optimal parameters we would typically use a gradient descent method. Newton's method and gradient descent methods are discussed in the material on [optimization methods](#).

Wisconsin Cancer Data

We show here how we can use a simple regression case on the breast cancer data using Logistic regression as our algorithm for classification.

```
import matplotlib.pyplot as plt
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.datasets import load_breast_cancer
from sklearn.linear_model import LogisticRegression

# Load the data
cancer = load_breast_cancer()

X_train, X_test, y_train, y_test = train_test_split(cancer.data, cancer.target, random_state=0)
print(X_train.shape)
print(X_test.shape)
# Logistic Regression
logreg = LogisticRegression(solver='lbfgs')
logreg.fit(X_train, y_train)
print("Test set accuracy with Logistic Regression: {:.2f}".format(logreg.score(X_test, y_test)))
```

Question: How would you scale the data? Would it make sense?

Using the correlation matrix

In addition to the above scores, we could also study the covariance (and the correlation matrix). We use **Pandas** to compute the correlation matrix.

```
import matplotlib.pyplot as plt
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.datasets import load_breast_cancer
from sklearn.linear_model import LogisticRegression
cancer = load_breast_cancer()
import pandas as pd
# Making a data frame
cancerpd = pd.DataFrame(cancer.data, columns=cancer.feature_names)

fig, axes = plt.subplots(15,2,figsize=(10,20))
malignant = cancer.data[cancer.target == 0]
benign = cancer.data[cancer.target == 1]
ax = axes.ravel()

for i in range(30):
    _, bins = np.histogram(cancer.data[:,i], bins =50)
    ax[i].hist(malignant[:,i], bins = bins, alpha = 0.5)
    ax[i].hist(benign[:,i], bins = bins, alpha = 0.5)
    ax[i].set_title(cancer.feature_names[i])
    ax[i].set_yticks(())
ax[0].set_xlabel("Feature magnitude")
ax[0].set_ylabel("Frequency")
ax[0].legend(["Malignant", "Benign"], loc = "best")
fig.tight_layout()
plt.show()

import seaborn as sns
correlation_matrix = cancerpd.corr().round(1)
# use the heatmap function from seaborn to plot the correlation matrix
# annot = True to print the values inside the square
plt.figure(figsize=(15,8))
sns.heatmap(data=correlation_matrix, annot=True)
plt.show()
```

Discussing the correlation data

In the above example we note two things. In the first plot we display the overlap of benign and malignant tumors as functions of the various features in the Wisconsin breast cancer data set. We see that for some of the features we can distinguish clearly the benign and malignant cases while for other features we cannot. This can point to us which features may be of greater interest when we wish to classify a benign or not benign tumour.

In the second figure we have computed the so-called correlation matrix, which in our case with thirty features becomes a 30×30 matrix.

We constructed this matrix using **pandas** via the statements

```
cancerpd = pd.DataFrame(cancer.data, columns=cancer.feature_names)
```

and then

```
correlation_matrix = cancerpd.corr().round(1)
```

Diagonalizing this matrix we can in turn say something about which features are of relevance and which are not. This leads us to the classical Principal Component Analysis (PCA) theorem with applications. This will be discussed later this semester (week 43).

Other measures in classification studies: Cancer Data again

```
import matplotlib.pyplot as plt
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.datasets import load_breast_cancer
from sklearn.linear_model import LogisticRegression

# Load the data
cancer = load_breast_cancer()

X_train, X_test, y_train, y_test = train_test_split(cancer.data, cancer.target, random_state=0)
print(X_train.shape)
print(X_test.shape)
# Logistic Regression
logreg = LogisticRegression(solver='lbfgs')
logreg.fit(X_train, y_train)
print("Test set accuracy with Logistic Regression: {:.2f}".format(logreg.score(X_test, y_test)))

from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import cross_validate
#Cross validation
accuracy = cross_validate(logreg, X_test, y_test, cv=10)['test_score']
print(accuracy)
print("Test set accuracy with Logistic Regression: {:.2f}".format(logreg.score(X_test, y_test)))

import scikitplot as skplt
y_pred = logreg.predict(X_test)
skplt.metrics.plot_confusion_matrix(y_test, y_pred, normalize=True)
plt.show()
y_probab = logreg.predict_proba(X_test)
skplt.metrics.plot_roc(y_test, y_probab)
plt.show()
skplt.metrics.plot_cumulative_gain(y_test, y_probab)
plt.show()
```

Optimization, the central part of any Machine Learning algorithm

Almost every problem in machine learning and data science starts with a dataset X , a model $g(\beta)$, which is a function of the parameters β and a cost function $C(X, g(\beta))$ that allows us to judge how well the model $g(\beta)$ explains the observations X . The model is fit by finding the values of β that minimize the cost function. Ideally we would be able to solve for β analytically, however this is not possible in general and we must use some approximative/numerical method to compute the minimum.

Revisiting our Logistic Regression case

In our discussion on Logistic Regression we studied the case of two classes, with y_i either 0 or 1. Furthermore we assumed also that we have only two parameters β in our fitting, that is we defined probabilities

$$\begin{aligned} p(y_i = 1|x_i, \beta) &= \frac{\exp(\beta_0 + \beta_1 x_i)}{1 + \exp(\beta_0 + \beta_1 x_i)}, \\ p(y_i = 0|x_i, \beta) &= 1 - p(y_i = 1|x_i, \beta), \end{aligned}$$

where β are the weights we wish to extract from data, in our case β_0 and β_1 .

The equations to solve

Our compact equations used a definition of a vector \mathbf{y} with n elements y_i , an $n \times p$ matrix \mathbf{X} which contains the x_i values and a vector \mathbf{p} of fitted probabilities $p(y_i|x_i, \beta)$. We rewrote in a more compact form the first derivative of the cost function as

$$\frac{\partial \mathcal{C}(\beta)}{\partial \beta} = -\mathbf{X}^T (\mathbf{y} - \mathbf{p}).$$

If we in addition define a diagonal matrix \mathbf{W} with elements $p(y_i|x_i, \beta)(1 - p(y_i|x_i, \beta))$, we can obtain a compact expression of the second derivative as

$$\frac{\partial^2 \mathcal{C}(\beta)}{\partial \beta \partial \beta^T} = \mathbf{X}^T \mathbf{W} \mathbf{X}.$$

This defines what is called the Hessian matrix.

Solving using Newton-Raphson's method

If we can set up these equations, Newton-Raphson's iterative method is normally the method of choice. It requires however that we can compute in an efficient way the matrices that define the first and second derivatives.

Our iterative scheme is then given by

$$\beta^{\text{new}} = \beta^{\text{old}} - \left(\frac{\partial^2 \mathcal{C}(\beta)}{\partial \beta \partial \beta^T} \right)_{\beta^{\text{old}}}^{-1} \times \left(\frac{\partial \mathcal{C}(\beta)}{\partial \beta} \right)_{\beta^{\text{old}}},$$

or in matrix form as

$$\beta^{\text{new}} = \beta^{\text{old}} - (\mathbf{X}^T \mathbf{W} \mathbf{X})^{-1} \times (-\mathbf{X}^T (\mathbf{y} - \mathbf{p}))_{\beta^{\text{old}}}.$$

The right-hand side is computed with the old values of β .

If we can compute these matrices, in particular the Hessian, the above is often the easiest method to implement.

Brief reminder on Newton-Raphson's method

Let us quickly remind ourselves how we derive the above method.

Perhaps the most celebrated of all one-dimensional root-finding routines is Newton's method, also called the Newton-Raphson method. This method requires the evaluation of both the function f and its derivative f' at arbitrary points. If you can only calculate the derivative numerically and/or your function is not of the smooth type, we normally discourage the use of this method.

The equations

The Newton-Raphson formula consists geometrically of extending the tangent line at a current point until it crosses zero, then setting the next guess to the abscissa of that zero-crossing. The mathematics behind this method is rather simple. Employing a Taylor expansion for x sufficiently close to the solution s , we have

$$f(s) = 0 = f(x) + (s - x)f'(x) + \frac{(s - x)^2}{2}f''(x) + \dots$$

For small enough values of the function and for well-behaved functions, the terms beyond linear are unimportant, hence we obtain

$$f(x) + (s - x)f'(x) \approx 0,$$

yielding

$$s \approx x - \frac{f(x)}{f'(x)}.$$

Having in mind an iterative procedure, it is natural to start iterating with

$$x_{n+1} = x_n - \frac{f(x_n)}{f'(x_n)}.$$

Simple geometric interpretation

The above is Newton-Raphson's method. It has a simple geometric interpretation, namely x_{n+1} is the point where the tangent from $(x_n, f(x_n))$ crosses the x -axis. Close to the solution, Newton-Raphson converges fast to the desired result. However, if we are far from a root, where the higher-order terms in the series are important, the Newton-Raphson formula can give grossly inaccurate results. For instance, the initial guess for the root might be so far from the true root as to let the search interval include a local maximum or minimum of the function. If an iteration places a trial guess near such a local extremum, so that the first derivative nearly vanishes, then Newton-Raphson may fail totally

Extending to more than one variable

Newton's method can be generalized to systems of several non-linear equations and variables. Consider the case with two equations

$$\begin{aligned} f_1(x_1, x_2) &= 0 \\ f_2(x_1, x_2) &= 0, \end{aligned}$$

which we Taylor expand to obtain

$$\begin{aligned} 0 = f_1(x_1 + h_1, x_2 + h_2) &= f_1(x_1, x_2) + h_1 \partial f_1 / \partial x_1 + h_2 \partial f_1 / \partial x_2 + \dots \\ 0 = f_2(x_1 + h_1, x_2 + h_2) &= f_2(x_1, x_2) + h_1 \partial f_2 / \partial x_1 + h_2 \partial f_2 / \partial x_2 + \dots \end{aligned}$$

Defining the Jacobian matrix \mathbf{J} we have

$$\mathbf{J} = \begin{pmatrix} \partial f_1 / \partial x_1 & \partial f_1 / \partial x_2 \\ \partial f_2 / \partial x_1 & \partial f_2 / \partial x_2 \end{pmatrix},$$

we can rephrase Newton's method as

$$\begin{pmatrix} x_1^{n+1} \\ x_2^{n+1} \end{pmatrix} = \begin{pmatrix} x_1^n \\ x_2^n \end{pmatrix} + \begin{pmatrix} h_1^n \\ h_2^n \end{pmatrix},$$

where we have defined

$$\begin{pmatrix} h_1^n \\ h_2^n \end{pmatrix} = -\mathbf{J}^{-1} \begin{pmatrix} f_1(x_1^n, x_2^n) \\ f_2(x_1^n, x_2^n) \end{pmatrix}.$$

We need thus to compute the inverse of the Jacobian matrix and it is to understand that difficulties may arise in case \mathbf{J} is nearly singular.

It is rather straightforward to extend the above scheme to systems of more than two non-linear equations. In our case, the Jacobian matrix is given by the Hessian that represents the second derivative of cost function.

Steepest descent

The basic idea of gradient descent is that a function $F(\mathbf{x})$, $\mathbf{x} \equiv (x_1, \dots, x_n)$, decreases fastest if one goes from \mathbf{x} in the direction of the negative gradient $-\nabla F(\mathbf{x})$.

It can be shown that if

$$\mathbf{x}_{k+1} = \mathbf{x}_k - \gamma_k \nabla F(\mathbf{x}_k),$$

with $\gamma_k > 0$.

For γ_k small enough, then $F(\mathbf{x}_{k+1}) \leq F(\mathbf{x}_k)$. This means that for a sufficiently small γ_k we are always moving towards smaller function values, i.e a minimum.

More on Steepest descent

The previous observation is the basis of the method of steepest descent, which is also referred to as just gradient descent (GD). One starts with an initial guess \mathbf{x}_0 for a minimum of F and computes new approximations according to

$$\mathbf{x}_{k+1} = \mathbf{x}_k - \gamma_k \nabla F(\mathbf{x}_k), \quad k \geq 0.$$

The parameter γ_k is often referred to as the step length or the learning rate within the context of Machine Learning.

The ideal

Ideally the sequence $\{\mathbf{x}_k\}_{k=0}$ converges to a global minimum of the function F . In general we do not know if we are in a global or local minimum. In the special case when F is a convex function, all local minima are also global minima, so in this case gradient descent can converge to the global solution. The advantage of this scheme is that it is conceptually simple and straightforward to implement. However the method in this form has some severe limitations:

In machine learning we are often faced with non-convex high dimensional cost functions with many local minima. Since GD is deterministic we will get stuck in a local minimum, if the method converges, unless we have a very good initial guess. This also implies that the scheme is sensitive to the chosen initial condition.

Note that the gradient is a function of $\mathbf{x} = (x_1, \dots, x_n)$ which makes it expensive to compute numerically.

The sensitiveness of the gradient descent

The gradient descent method is sensitive to the choice of learning rate γ_k . This is due to the fact that we are only guaranteed that $F(\mathbf{x}_{k+1}) \leq F(\mathbf{x}_k)$ for sufficiently small γ_k . The problem is to determine an optimal learning rate. If the learning rate is chosen too small the method will take a long time to converge and if it is too large we can experience erratic behavior.

Many of these shortcomings can be alleviated by introducing randomness. One such method is that of Stochastic Gradient Descent (SGD), see below.

Convex functions

Ideally we want our cost/loss function to be convex(concave).

First we give the definition of a convex set: A set C in \mathbb{R}^n is said to be convex if, for all x and y in C and all $t \in (0, 1)$, the point $(1 - t)x + ty$ also belongs to C . Geometrically this means that every point on the line segment connecting x and y is in C as discussed below.

The convex subsets of \mathbb{R} are the intervals of \mathbb{R} . Examples of convex sets of \mathbb{R}^2 are the regular polygons (triangles, rectangles, pentagons, etc...).

Convex function

Convex function: Let $X \subset \mathbb{R}^n$ be a convex set. Assume that the function $f : X \rightarrow \mathbb{R}$ is continuous, then f is said to be convex if

$$f(tx_1 + (1-t)x_2) \leq tf(x_1) + (1-t)f(x_2)$$

for all $x_1, x_2 \in X$ and for all $t \in [0, 1]$. If \leq is replaced with a strict inequality in the definition, we demand $x_1 \neq x_2$ and $t \in (0, 1)$ then f is said to be strictly convex. For a single variable function, convexity means that if you draw a straight line connecting $f(x_1)$ and $f(x_2)$, the value of the function on the interval $[x_1, x_2]$ is always below the line as illustrated below.

Conditions on convex functions

In the following we state first and second-order conditions which ensures convexity of a function f . We write D_f to denote the domain of f , i.e the subset of \mathbb{R}^n where f is defined. For more details and proofs we refer to: [S. Boyd and L. Vandenberghe. Convex Optimization. Cambridge University Press.](#)

First order condition. Suppose f is differentiable (i.e $\nabla f(x)$ is well defined for all x in the domain of f). Then f is convex if and only if D_f is a convex set and

$$f(y) \geq f(x) + \nabla f(x)^T(y - x)$$

holds for all $x, y \in D_f$. This condition means that for a convex function the first order Taylor expansion (right hand side above) at any point a global under estimator of the function. To convince yourself you can make a drawing of $f(x) = x^2 + 1$ and draw the tangent line to $f(x)$ and note that it is always below the graph.

Second order condition. Assume that f is twice differentiable, i.e the Hessian matrix exists at each point in D_f . Then f is convex if and only if D_f is a convex set and its Hessian is positive semi-definite for all $x \in D_f$. For a single-variable function this reduces to $f''(x) \geq 0$. Geometrically this means that f has nonnegative curvature everywhere.

This condition is particularly useful since it gives us an procedure for determining if the function under consideration is convex, apart from using the definition.

More on convex functions

The next result is of great importance to us and the reason why we are going on about convex functions. In machine learning we frequently have to minimize a loss/cost function in order to find the best parameters for the model we are considering.

Ideally we want the global minimum (for high-dimensional models it is hard to know if we have local or global minimum). However, if the cost/loss function is convex the following result provides invaluable information:

Any minimum is global for convex functions. Consider the problem of finding $x \in \mathbb{R}^n$ such that $f(x)$ is minimal, where f is convex and differentiable. Then, any point x^* that satisfies $\nabla f(x^*) = 0$ is a global minimum.

This result means that if we know that the cost/loss function is convex and we are able to find a minimum, we are guaranteed that it is a global minimum.

Some simple problems

1. Show that $f(x) = x^2$ is convex for $x \in \mathbb{R}$ using the definition of convexity. Hint: If you re-write the definition, f is convex if the following holds for all $x, y \in D_f$ and any $\lambda \in [0, 1]$ $\lambda f(x) + (1 - \lambda)f(y) - f(\lambda x + (1 - \lambda)y) \geq 0$.
2. Using the second order condition show that the following functions are convex on the specified domain.
 - $f(x) = e^x$ is convex for $x \in \mathbb{R}$.
 - $g(x) = -\ln(x)$ is convex for $x \in (0, \infty)$.
3. Let $f(x) = x^2$ and $g(x) = e^x$. Show that $f(g(x))$ and $g(f(x))$ is convex for $x \in \mathbb{R}$. Also show that if $f(x)$ is any convex function then $h(x) = e^{f(x)}$ is convex.
4. A norm is any function that satisfy the following properties
 - $f(\alpha x) = |\alpha|f(x)$ for all $\alpha \in \mathbb{R}$.
 - $f(x + y) \leq f(x) + f(y)$
 - $f(x) \leq 0$ for all $x \in \mathbb{R}^n$ with equality if and only if $x = 0$

Using the definition of convexity, try to show that a function satisfying the properties above is convex (the third condition is not needed to show this).

Standard steepest descent

Before we proceed, we would like to discuss the approach called the **standard Steepest descent** (different from the above steepest descent discussion), which again leads to us having to be able to compute a matrix. It belongs to the class of Conjugate Gradient methods (CG).

The [success of the CG method](#) for finding solutions of non-linear problems is based on the theory of conjugate gradients for linear systems of equations. It belongs to the class of iterative methods for solving problems from linear algebra of the type

$$Ax = b.$$

In the iterative process we end up with a problem like

$$\mathbf{r} = \mathbf{b} - \mathbf{A}\mathbf{x},$$

where \mathbf{r} is the so-called residual or error in the iterative process.

When we have found the exact solution, $\mathbf{r} = 0$.

Gradient method

The residual is zero when we reach the minimum of the quadratic equation

$$P(\mathbf{x}) = \frac{1}{2}\mathbf{x}^T \mathbf{A}\mathbf{x} - \mathbf{x}^T \mathbf{b},$$

with the constraint that the matrix \mathbf{A} is positive definite and symmetric. This defines also the Hessian and we want it to be positive definite.

Steepest descent method

We denote the initial guess for \mathbf{x} as \mathbf{x}_0 . We can assume without loss of generality that

$$\mathbf{x}_0 = 0,$$

or consider the system

$$\mathbf{A}\mathbf{z} = \mathbf{b} - \mathbf{A}\mathbf{x}_0,$$

instead.

Steepest descent method

One can show that the solution \mathbf{x} is also the unique minimizer of the quadratic form

$$f(\mathbf{x}) = \frac{1}{2}\mathbf{x}^T \mathbf{A}\mathbf{x} - \mathbf{x}^T \mathbf{b}, \quad \mathbf{x} \in \mathbf{R}^n.$$

This suggests taking the first basis vector \mathbf{r}_1 (see below for definition) to be the gradient of f at $\mathbf{x} = \mathbf{x}_0$, which equals

$$\mathbf{A}\mathbf{x}_0 - \mathbf{b},$$

and $\mathbf{x}_0 = 0$ it is equal $-\mathbf{b}$.

Final expressions

We can compute the residual iteratively as

$$\mathbf{r}_{k+1} = \mathbf{b} - \mathbf{A}\mathbf{x}_{k+1},$$

which equals

$$\mathbf{b} - \mathbf{A}(\mathbf{x}_k + \alpha_k \mathbf{r}_k),$$

or

$$(\mathbf{b} - \mathbf{A}\mathbf{x}_k) - \alpha_k \mathbf{A}\mathbf{r}_k,$$

which gives

$$\alpha_k = \frac{\mathbf{r}_k^T \mathbf{r}_k}{\mathbf{r}_k^T \mathbf{A} \mathbf{r}_k}$$

leading to the iterative scheme

$$\mathbf{x}_{k+1} = \mathbf{x}_k - \alpha_k \mathbf{r}_k,$$

Steepest descent example

```
import numpy as np
import numpy.linalg as la

import scipy.optimize as sopt

import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D

def f(x):
    return x[0]**2 + 3.0*x[1]**2

def df(x):
    return np.array([2*x[0], 6*x[1]])

fig = plt.figure()
ax = fig.gca(projection="3d")

xmesh, ymesh = np.mgrid[-3:3:50j, -3:3:50j]
fmesh = f(np.array([xmesh, ymesh]))
ax.plot_surface(xmesh, ymesh, fmesh)
```

And then as contour plot

```
plt.axis("equal")
plt.contour(xmesh, ymesh, fmesh)
guesses = [np.array([2, 2./5])]
```

Find guesses

```
x = guesses[-1]
s = -df(x)
```

Run it!

```
def fid(alpha):
    return f(x + alpha*s)

alpha_opt = sopt.golden(fid)
next_guess = x + alpha_opt * s
guesses.append(next_guess)
print(next_guess)
```

What happened?

```

pt.axis("equal")
pt.contour(xmesh, ymesh, fmesh, 50)
it_array = np.array(guesses)
pt.plot(it_array.T[0], it_array.T[1], "x-")

```

Note that we did only one iteration here. We can easily add more using our previous guesses.

Conjugate gradient method

In the CG method we define so-called conjugate directions and two vectors \mathbf{s} and \mathbf{t} are said to be conjugate if

$$\mathbf{s}^T \mathbf{A} \mathbf{t} = 0.$$

The philosophy of the CG method is to perform searches in various conjugate directions of our vectors \mathbf{x}_i obeying the above criterion, namely

$$\mathbf{x}_i^T \mathbf{A} \mathbf{x}_j = 0.$$

Two vectors are conjugate if they are orthogonal with respect to this inner product. Being conjugate is a symmetric relation: if \mathbf{s} is conjugate to \mathbf{t} , then \mathbf{t} is conjugate to \mathbf{s} .

Conjugate gradient method

An example is given by the eigenvectors of the matrix

$$\mathbf{v}_i^T \mathbf{A} \mathbf{v}_j = \lambda \mathbf{v}_i^T \mathbf{v}_j,$$

which is zero unless $i = j$.

Conjugate gradient method

Assume now that we have a symmetric positive-definite matrix \mathbf{A} of size $n \times n$. At each iteration $i + 1$ we obtain the conjugate direction of a vector

$$\mathbf{x}_{i+1} = \mathbf{x}_i + \alpha_i \mathbf{p}_i.$$

We assume that \mathbf{p}_i is a sequence of n mutually conjugate directions. Then the \mathbf{p}_i form a basis of R^n and we can expand the solution $\mathbf{A} \mathbf{x} = \mathbf{b}$ in this basis, namely

$$\mathbf{x} = \sum_{i=1}^n \alpha_i \mathbf{p}_i.$$

Conjugate gradient method

The coefficients are given by

$$\mathbf{Ax} = \sum_{i=1}^n \alpha_i \mathbf{Ap}_i = \mathbf{b}.$$

Multiplying with \mathbf{p}_k^T from the left gives

$$\mathbf{p}_k^T \mathbf{Ax} = \sum_{i=1}^n \alpha_i \mathbf{p}_k^T \mathbf{Ap}_i = \mathbf{p}_k^T \mathbf{b},$$

and we can define the coefficients α_k as

$$\alpha_k = \frac{\mathbf{p}_k^T \mathbf{b}}{\mathbf{p}_k^T \mathbf{Ap}_k}$$

Conjugate gradient method and iterations

If we choose the conjugate vectors \mathbf{p}_k carefully, then we may not need all of them to obtain a good approximation to the solution \mathbf{x} . We want to regard the conjugate gradient method as an iterative method. This will us to solve systems where n is so large that the direct method would take too much time.

We denote the initial guess for \mathbf{x} as \mathbf{x}_0 . We can assume without loss of generality that

$$\mathbf{x}_0 = 0,$$

or consider the system

$$\mathbf{Az} = \mathbf{b} - \mathbf{Ax}_0,$$

instead.

Conjugate gradient method

One can show that the solution \mathbf{x} is also the unique minimizer of the quadratic form

$$f(\mathbf{x}) = \frac{1}{2} \mathbf{x}^T \mathbf{Ax} - \mathbf{x}^T \mathbf{b}, \quad \mathbf{x} \in \mathbf{R}^n.$$

This suggests taking the first basis vector \mathbf{p}_1 to be the gradient of f at $\mathbf{x} = \mathbf{x}_0$, which equals

$$\mathbf{Ax}_0 - \mathbf{b},$$

and $\mathbf{x}_0 = 0$ it is equal $-\mathbf{b}$. The other vectors in the basis will be conjugate to the gradient, hence the name conjugate gradient method.

Conjugate gradient method

Let \mathbf{r}_k be the residual at the k -th step:

$$\mathbf{r}_k = \mathbf{b} - \mathbf{A}\mathbf{x}_k.$$

Note that \mathbf{r}_k is the negative gradient of f at $\mathbf{x} = \mathbf{x}_k$, so the gradient descent method would be to move in the direction \mathbf{r}_k . Here, we insist that the directions \mathbf{p}_k are conjugate to each other, so we take the direction closest to the gradient \mathbf{r}_k under the conjugacy constraint. This gives the following expression

$$\mathbf{p}_{k+1} = \mathbf{r}_k - \frac{\mathbf{p}_k^T \mathbf{A} \mathbf{r}_k}{\mathbf{p}_k^T \mathbf{A} \mathbf{p}_k} \mathbf{p}_k.$$

Conjugate gradient method

We can also compute the residual iteratively as

$$\mathbf{r}_{k+1} = \mathbf{b} - \mathbf{A}\mathbf{x}_{k+1},$$

which equals

$$\mathbf{b} - \mathbf{A}(\mathbf{x}_k + \alpha_k \mathbf{p}_k),$$

or

$$(\mathbf{b} - \mathbf{A}\mathbf{x}_k) - \alpha_k \mathbf{A}\mathbf{p}_k,$$

which gives

$$\mathbf{r}_{k+1} = \mathbf{r}_k - \mathbf{A}\mathbf{p}_k,$$

Revisiting our first homeworks

We will use linear regression as a case study for the gradient descent methods. Linear regression is a great test case for the gradient descent methods discussed in the lectures since it has several desirable properties such as:

1. An analytical solution (recall homework set 1).
2. The gradient can be computed analytically.
3. The cost function is convex which guarantees that gradient descent converges for small enough learning rates

We revisit an example similar to what we had in the first homework set. We had a function of the type

```
x = 2*np.random.rand(m,1)
y = 4+3*x+np.random.randn(m,1)
```


with $x_i \in [0, 1]$ is chosen randomly using a uniform distribution. Additionally we have a stochastic noise chosen according to a normal distribution $\mathcal{N}(\iota, \infty)$. The linear regression model is given by

$$h_\beta(x) = \mathbf{y} = \beta_0 + \beta_1 x,$$

such that

$$\mathbf{y}_i = \beta_0 + \beta_1 x_i.$$

Gradient descent example

Let $\mathbf{y} = (y_1, \dots, y_n)^T$, $\mathbf{y} = (\mathbf{y}_1, \dots, \mathbf{y}_n)^T$ and $\beta = (\beta_0, \beta_1)^T$

It is convenient to write $\mathbf{y} = X\beta$ where $X \in \mathbb{R}^{100 \times 2}$ is the design matrix given by (we keep the intercept here)

$$X \equiv \begin{bmatrix} 1 & x_1 \\ \vdots & \vdots \\ 1 & x_{100} \end{bmatrix}.$$

The cost/loss/risk function is given by (

$$C(\beta) = \frac{1}{n} \|X\beta - \mathbf{y}\|_2^2 = \frac{1}{n} \sum_{i=1}^{100} [(\beta_0 + \beta_1 x_i)^2 - 2y_i(\beta_0 + \beta_1 x_i) + y_i^2]$$

and we want to find β such that $C(\beta)$ is minimized.

The derivative of the cost/loss function

Computing $\partial C(\beta)/\partial \beta_0$ and $\partial C(\beta)/\partial \beta_1$ we can show that the gradient can be written as

$$\nabla_\beta C(\beta) = \frac{2}{n} \begin{bmatrix} \sum_{i=1}^{100} (\beta_0 + \beta_1 x_i - y_i) \\ \sum_{i=1}^{100} (x_i(\beta_0 + \beta_1 x_i) - y_i x_i) \end{bmatrix} = \frac{2}{n} X^T (X\beta - \mathbf{y}),$$

where X is the design matrix defined above.

The Hessian matrix

The Hessian matrix of $C(\beta)$ is given by

$$\mathbf{H} \equiv \begin{bmatrix} \frac{\partial^2 C(\beta)}{\partial \beta_0^2} & \frac{\partial^2 C(\beta)}{\partial \beta_0 \partial \beta_1} \\ \frac{\partial^2 C(\beta)}{\partial \beta_0 \partial \beta_1} & \frac{\partial^2 C(\beta)}{\partial \beta_1^2} \end{bmatrix} = \frac{2}{n} X^T X.$$

This result implies that $C(\beta)$ is a convex function since the matrix $X^T X$ always is positive semi-definite.

Simple program

We can now write a program that minimizes $C(\beta)$ using the gradient descent method with a constant learning rate γ according to

$$\beta_{k+1} = \beta_k - \gamma \nabla_{\beta} C(\beta_k), \quad k = 0, 1, \dots$$

We can use the expression we computed for the gradient and let use a β_0 be chosen randomly and let $\gamma = 0.001$. Stop iterating when $\|\nabla_{\beta} C(\beta_k)\| \leq \epsilon = 10^{-8}$. **Note that the code below does not include the latter stop criterion.**

And finally we can compare our solution for β with the analytic result given by $\beta = (X^T X)^{-1} X^T y$.

Gradient Descent Example

Here our simple example

```
# Importing various packages
from random import random, seed
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D
from matplotlib import cm
from matplotlib.ticker import LinearLocator, FormatStrFormatter
import sys

# the number of datapoints
n = 100
x = 2*np.random.rand(n,1)
y = 4+3*x+np.random.randn(n,1)

X = np.c_[np.ones((n,1)), x]
# Hessian matrix
H = (2.0/n)* X.T @ X
# Get the eigenvalues
EigValues, EigVectors = np.linalg.eig(H)
print(f"Eigenvalues of Hessian Matrix:{EigValues}")

beta_linreg = np.linalg.inv(X.T @ X) @ X.T @ y
print(beta_linreg)
beta = np.random.randn(2,1)

eta = 1.0/np.max(EigValues)
Niterations = 1000

for iter in range(Niterations):
    gradient = (2.0/n)*X.T @ (X @ beta-y)
    beta -= eta*gradient

print(beta)
xnew = np.array([[0],[2]])
xbnew = np.c_[np.ones((2,1)), xnew]
ypredict = xbnew.dot(beta)
ypredict2 = xbnew.dot(beta_linreg)
plt.plot(xnew, ypredict, "r-")
plt.plot(xnew, ypredict2, "b-")
plt.plot(x, y, 'ro')
```

```
plt.axis([0,2.0,0, 15.0])
plt.xlabel(r'$x$')
plt.ylabel(r'$y$')
plt.title(r'Gradient descent example')
plt.show()
```

And a corresponding example using scikit-learn

```
# Importing various packages
from random import random, seed
import numpy as np
import matplotlib.pyplot as plt
from sklearn.linear_model import SGDRegressor

n = 100
x = 2*np.random.rand(n,1)
y = 4+3*x+np.random.randn(n,1)

X = np.c_[np.ones((n,1)), x]
beta_linreg = np.linalg.inv(X.T @ X) @ (X.T @ y)
print(beta_linreg)
sgdreg = SGDRegressor(max_iter = 50, penalty=None, eta0=0.1)
sgdreg.fit(x,y.ravel())
print(sgdreg.intercept_, sgdreg.coef_)
```

Gradient descent and Ridge

We have also discussed Ridge regression where the loss function contains a regularized term given by the L_2 norm of β ,

$$C_{\text{ridge}}(\beta) = \frac{1}{n} \|X\beta - \mathbf{y}\|^2 + \lambda \|\beta\|^2, \lambda \geq 0.$$

In order to minimize $C_{\text{ridge}}(\beta)$ using GD we adjust the gradient as follows

$$\nabla_{\beta} C_{\text{ridge}}(\beta) = \frac{2}{n} \left[\frac{\sum_{i=1}^{100} (\beta_0 + \beta_1 x_i - y_i)}{\sum_{i=1}^{100} (x_i(\beta_0 + \beta_1 x_i) - y_i x_i)} \right] + 2\lambda \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix} = 2 \left(\frac{1}{n} X^T (X\beta - \mathbf{y}) + \lambda \beta \right).$$

We can easily extend our program to minimize $C_{\text{ridge}}(\beta)$ using gradient descent and compare with the analytical solution given by

$$\beta_{\text{ridge}} = (X^T X + n\lambda I_{2 \times 2})^{-1} X^T \mathbf{y}.$$

The Hessian matrix for Ridge Regression

The Hessian matrix of Ridge Regression for our simple example is given by

$$\mathbf{H} \equiv \begin{bmatrix} \frac{\partial^2 C(\beta)}{\partial \beta_0^2} & \frac{\partial^2 C(\beta)}{\partial \beta_0 \partial \beta_1} \\ \frac{\partial^2 C(\beta)}{\partial \beta_0 \partial \beta_1} & \frac{\partial^2 C(\beta)}{\partial \beta_1^2} \end{bmatrix} = \frac{2}{n} X^T X + 2\lambda \mathbf{I}.$$

This implies that the Hessian matrix is positive definite, hence the stationary point is a minimum. Note that the Ridge cost function is convex being a sum of two convex functions. Therefore, the stationary point is a global minimum of this function.

Program example for gradient descent with Ridge Regression

```
from random import random, seed
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D
from matplotlib import cm
from matplotlib.ticker import LinearLocator, FormatStrFormatter
import sys

# the number of datapoints
n = 100
x = 2*np.random.rand(n,1)
y = 4+3*x+np.random.randn(n,1)

X = np.c_[np.ones((n,1)), x]
XT_X = X.T @ X

#Ridge parameter lambda
lmbda = 0.001
Id = n*lmbda* np.eye(XT_X.shape[0])

# Hessian matrix
H = (2.0/n)* XT_X+2*lmbda* np.eye(XT_X.shape[0])
# Get the eigenvalues
EigValues, EigVectors = np.linalg.eig(H)
print(f"Eigenvalues of Hessian Matrix:{EigValues}")

beta_linreg = np.linalg.inv(XT_X+Id) @ X.T @ y
print(beta_linreg)
# Start plain gradient descent
beta = np.random.randn(2,1)

eta = 1.0/np.max(EigValues)
Niterations = 100

for iter in range(Niterations):
    gradients = 2.0/n*X.T @ (X @ (beta)-y)+2*lmbda*beta
    beta -= eta*gradients

print(beta)
ypredict = X @ beta
ypredict2 = X @ beta_linreg
plt.plot(x, ypredict, "r-")
plt.plot(x, ypredict2, "b-")
plt.plot(x, y, 'ro')
plt.axis([0,2.0,0, 15.0])
plt.xlabel(r'$x$')
plt.ylabel(r'$y$')
plt.title(r'Gradient descent example for Ridge')
plt.show()
```

Using gradient descent methods, limitations

- **Gradient descent (GD) finds local minima of our function.** Since the GD algorithm is deterministic, if it converges, it will converge to a

local minimum of our cost/loss/risk function. Because in ML we are often dealing with extremely rugged landscapes with many local minima, this can lead to poor performance.

- **GD is sensitive to initial conditions.** One consequence of the local nature of GD is that initial conditions matter. Depending on where one starts, one will end up at a different local minima. Therefore, it is very important to think about how one initializes the training process. This is true for GD as well as more complicated variants of GD.
- **Gradients are computationally expensive to calculate for large datasets.** In many cases in statistics and ML, the cost/loss/risk function is a sum of terms, with one term for each data point. For example, in linear regression, $E \propto \sum_{i=1}^n (y_i - \mathbf{w}^T \cdot \mathbf{x}_i)^2$; for logistic regression, the square error is replaced by the cross entropy. To calculate the gradient we have to sum over *all* n data points. Doing this at every GD step becomes extremely computationally expensive. An ingenious solution to this, is to calculate the gradients using small subsets of the data called “mini batches”. This has the added benefit of introducing stochasticity into our algorithm.
- **GD is very sensitive to choices of learning rates.** GD is extremely sensitive to the choice of learning rates. If the learning rate is very small, the training process take an extremely long time. For larger learning rates, GD can diverge and give poor results. Furthermore, depending on what the local landscape looks like, we have to modify the learning rates to ensure convergence. Ideally, we would *adaptively* choose the learning rates to match the landscape.
- **GD treats all directions in parameter space uniformly.** Another major drawback of GD is that unlike Newton’s method, the learning rate for GD is the same in all directions in parameter space. For this reason, the maximum learning rate is set by the behavior of the steepest direction and this can significantly slow down training. Ideally, we would like to take large steps in flat directions and small steps in steep directions. Since we are exploring rugged landscapes where curvatures change, this requires us to keep track of not only the gradient but second derivatives. The ideal scenario would be to calculate the Hessian but this proves to be too computationally expensive.
- GD can take exponential time to escape saddle points, even with random initialization. As we mentioned, GD is extremely sensitive to initial condition since it determines the particular local minimum GD would eventually reach. However, even with a good initialization scheme, through the introduction of randomness, GD can still take exponential time to escape saddle points.

Challenge yourself

Write a code which implements gradient descent for a logistic regression example.

Stochastic Gradient Descent

Stochastic gradient descent (SGD) and variants thereof address some of the shortcomings of the Gradient descent method discussed above.

The underlying idea of SGD comes from the observation that the cost function, which we want to minimize, can almost always be written as a sum over n data points $\{\mathbf{x}_i\}_{i=1}^n$,

$$C(\beta) = \sum_{i=1}^n c_i(\mathbf{x}_i, \beta).$$

Overview video on Stochastic Gradient Descent

[What is Stochastic Gradient Descent](#)

Computation of gradients

This in turn means that the gradient can be computed as a sum over i -gradients

$$\nabla_{\beta} C(\beta) = \sum_i^n \nabla_{\beta} c_i(\mathbf{x}_i, \beta).$$

Stochasticity/randomness is introduced by only taking the gradient on a subset of the data called minibatches. If there are n data points and the size of each minibatch is M , there will be n/M minibatches. We denote these minibatches by B_k where $k = 1, \dots, n/M$.

SGD example

As an example, suppose we have 10 data points $(\mathbf{x}_1, \dots, \mathbf{x}_{10})$ and we choose to have $M = 5$ minibatches, then each minibatch contains two data points. In particular we have $B_1 = (\mathbf{x}_1, \mathbf{x}_2), \dots, B_5 = (\mathbf{x}_9, \mathbf{x}_{10})$. Note that if you choose $M = 1$ you have only a single batch with all data points and on the other extreme, you may choose $M = n$ resulting in a minibatch for each datapoint, i.e $B_k = \mathbf{x}_k$.

The idea is now to approximate the gradient by replacing the sum over all data points with a sum over the data points in one the minibatches picked at random in each gradient descent step

$$\nabla_{\beta} C(\beta) = \sum_{i=1}^n \nabla_{\beta} c_i(\mathbf{x}_i, \beta) \rightarrow \sum_{i \in B_k}^n \nabla_{\beta} c_i(\mathbf{x}_i, \beta).$$

The gradient step

Thus a gradient descent step now looks like

$$\beta_{j+1} = \beta_j - \gamma_j \sum_{i \in B_k}^n \nabla_{\beta} c_i(\mathbf{x}_i, \beta)$$

where k is picked at random with equal probability from $[1, n/M]$. An iteration over the number of minibatches (n/M) is commonly referred to as an epoch. Thus it is typical to choose a number of epochs and for each epoch iterate over the number of minibatches, as exemplified in the code below.

Simple example code

```
import numpy as np

n = 100 #100 datapoints
M = 5   #size of each minibatch
m = int(n/M) #number of minibatches
n_epochs = 10 #number of epochs

j = 0
for epoch in range(1, n_epochs+1):
    for i in range(m):
        k = np.random.randint(m) #Pick the k-th minibatch at random
        #Compute the gradient using the data in minibatch Bk
        #Compute new suggestion for
        j += 1
```

Taking the gradient only on a subset of the data has two important benefits. First, it introduces randomness which decreases the chance that our optimization scheme gets stuck in a local minima. Second, if the size of the minibatches are small relative to the number of datapoints ($M < n$), the computation of the gradient is much cheaper since we sum over the datapoints in the k -th minibatch and not all n datapoints.

When do we stop?

A natural question is when do we stop the search for a new minimum? One possibility is to compute the full gradient after a given number of epochs and check if the norm of the gradient is smaller than some threshold and stop if true. However, the condition that the gradient is zero is valid also for local minima, so this would only tell us that we are close to a local/global minimum. However, we could also evaluate the cost function at this point, store the result and continue the search. If the test kicks in at a later stage we can compare the values of the cost function and keep the β that gave the lowest value.

Slightly different approach

Another approach is to let the step length γ_j depend on the number of epochs in such a way that it becomes very small after a reasonable time such that we do not move at all.

As an example, let $e = 0, 1, 2, 3, \dots$ denote the current epoch and let $t_0, t_1 > 0$ be two fixed numbers. Furthermore, let $t = e \cdot m + i$ where m is the number of minibatches and $i = 0, \dots, m - 1$. Then the function

$$\gamma_j(t; t_0, t_1) = \frac{t_0}{t + t_1}$$

goes to zero as the number of epochs gets large. I.e. we start with a step length $\gamma_j(0; t_0, t_1) = t_0/t_1$ which decays in time t .

In this way we can fix the number of epochs, compute β and evaluate the cost function at the end. Repeating the computation will give a different result since the scheme is random by design. Then we pick the final β that gives the lowest value of the cost function.

```
import numpy as np

def step_length(t,t0,t1):
    return t0/(t+t1)

n = 100 #100 datapoints
M = 5   #size of each minibatch
m = int(n/M) #number of minibatches
n_epochs = 500 #number of epochs
t0 = 1.0
t1 = 10

gamma_j = t0/t1
j = 0
for epoch in range(1,n_epochs+1):
    for i in range(m):
        k = np.random.randint(m) #Pick the k-th minibatch at random
        #Compute the gradient using the data in minibatch Bk
        #Compute new suggestion for beta
        t = epoch*m+i
        gamma_j = step_length(t,t0,t1)
        j += 1

print("gamma_j after %d epochs: %g" % (n_epochs,gamma_j))
```

Program for stochastic gradient

```
# Importing various packages
from math import exp, sqrt
from random import random, seed
import numpy as np
import matplotlib.pyplot as plt
from sklearn.linear_model import SGDRegressor

m = 100
x = 2*np.random.rand(m,1)
y = 4+3*x+np.random.randn(m,1)
```



```

X = np.c_[np.ones((m,1)), x]
theta_linreg = np.linalg.inv(X.T @ X) @ (X.T @ y)
print("Own inversion")
print(theta_linreg)
sgdreg = SGDRegressor(max_iter = 50, penalty=None, eta0=0.1)
sgdreg.fit(x,y.ravel())
print("sgdreg from scikit")
print(sgdreg.intercept_, sgdreg.coef_)

theta = np.random.randn(2,1)
eta = 0.1
Niterations = 1000

for iter in range(Niterations):
    gradients = 2.0/m*X.T @ ((X @ theta)-y)
    theta -= eta*gradients
print("theta from own gd")
print(theta)

xnew = np.array([[0],[2]])
Xnew = np.c_[np.ones((2,1)), xnew]
ypredict = Xnew.dot(theta)
ypredict2 = Xnew.dot(theta_linreg)

n_epochs = 50
t0, t1 = 5, 50
def learning_schedule(t):
    return t0/(t+t1)

theta = np.random.randn(2,1)

# note: here the number of minibatches is equal to the number of points!!
for epoch in range(n_epochs):
    for i in range(m):
        random_index = np.random.randint(m)
        xi = X[random_index:random_index+1]
        yi = y[random_index:random_index+1]
        gradients = 2 * xi.T @ ((xi @ theta)-yi)
        eta = learning_schedule(epoch*m+i)
        theta = theta - eta*gradients
print("theta from own sdg")
print(theta)

plt.plot(xnew, ypredict, "r-")
plt.plot(xnew, ypredict2, "b-")
plt.plot(x, y, 'ro')
plt.axis([0,2.0,0, 15.0])
plt.xlabel(r'$x$')
plt.ylabel(r'$y$')
plt.title(r'Random numbers ')
plt.show()

```

Challenge: try to write a similar code for a Logistic Regression case.

Code with a Number of Minibatches which varies

In the code here we vary the number of mini-batches.

```
# Importing various packages
from math import exp, sqrt
from random import random, seed
import numpy as np
import matplotlib.pyplot as plt

n = 100
x = 2*np.random.rand(n,1)
y = 4+3*x+np.random.randn(n,1)

X = np.c_[np.ones((n,1)), x]
XT_X = X.T @ X
theta_linreg = np.linalg.inv(X.T @ X) @ (X.T @ y)
print("Own inversion")
print(theta_linreg)
# Hessian matrix
H = (2.0/n)* XT_X
EigValues, EigVectors = np.linalg.eig(H)
print(f"Eigenvalues of Hessian Matrix:{EigValues}")

theta = np.random.randn(2,1)
eta = 1.0/np.max(EigValues)
Niterations = 1000

for iter in range(Niterations):
    gradients = 2.0/n*X.T @ ((X @ theta)-y)
    theta -= eta*gradients
    print("theta from own gd")
    print(theta)

xnew = np.array([[0],[2]])
Xnew = np.c_[np.ones((2,1)), xnew]
ypredict = Xnew.dot(theta)
ypredict2 = Xnew.dot(theta_linreg)

n_epochs = 50
M = 5 #size of each minibatch
m = int(n/M) #number of minibatches
t0, t1 = 5, 50
def learning_schedule(t):
    return t0/(t+t1)

theta = np.random.randn(2,1)

for epoch in range(n_epochs):
    # Can you figure out a better way of setting up the contributions to each batch?
    for i in range(m):
        random_index = M*np.random.randint(m)
        xi = X[random_index:random_index+M]
        yi = y[random_index:random_index+M]
        gradients = (2.0/M)* xi.T @ ((xi @ theta)-yi)
        eta = learning_schedule(epoch*m+i)
        theta = theta - eta*gradients
    print("theta from own sdg")
    print(theta)

plt.plot(xnew, ypredict, "r-")
plt.plot(xnew, ypredict2, "b-")
plt.plot(x, y, 'ro')
```

```
plt.axis([0,2.0,0, 15.0])
plt.xlabel(r'$x$')
plt.ylabel(r'$y$')
plt.title(r'Random numbers ')
plt.show()
```