import numpy as np import pandas as pd import matplotlib.pyplot as plt import sklearn from sklearn import linear model from sklearn import datasets from sklearn.linear model import SGDRegressor from sklearn.linear model import LogisticRegression from sklearn.model selection import train test split from sklearn.neighbors import KNeighborsClassifier from sklearn import svm from sklearn.svm import SVC from sklearn.pipeline import make pipeline from sklearn.preprocessing import StandardScaler from sklearn.datasets import make classification from sklearn.model selection import cross validate from sklearn.model selection import KFold from sklearn.model selection import GridSearchCV Question 1: #Function to implement the (batch) gradient descent algorithm for multiple linear reg. def gradient_descent(X, Y, T, a): # n is the number of features m, n = X.shape# theta is the array of thetas for each parameter theta = np.zeros(n)# f is the loss f = np.zeros(T)for i in range(T): xtdot = X.dot(theta)# loss for current theta f[i] = 0.5 * (np.linalg.norm(xtdot - Y)**2)# steepest ascent at f(theta) g = np.transpose(X).dot(xtdot - Y) # change the thetas to perform a step theta = theta - (a * g)return theta, f **Question 2:** Given: $\theta_{new} = \theta_{old} - \alpha * \frac{d}{d\theta} L(\theta)$ $L = rac{-1}{m} \sum_{i=1}^m [y_i * ln(h_{ heta}(x_i)) + (1-y_i) * ln(1-h_{ heta}(x_i))]$ $ln(rac{h_{ heta}(x_i)}{1-h_{ heta}(x_i)}) = heta_0 + heta_1 * x_{i1} + heta_2 * x_{i2} + \ldots + heta_j * x_{ij}$ $h_{ heta}(x_i) = rac{1}{1 + e^{-(heta_0 + heta_1 * x_{i1} + heta_2 * x_{i2} + \ldots + heta_j * x_{ij})}$ Multiplying the $(1-y_i)$, $L=rac{-1}{m}\sum_{i=1}^m[y_i*ln(h_ heta(x_i))-y_i*ln(1-h_ heta(x_i))+ln(1-h_ heta(x_i))]$ Using: $lg(m)-lg(n)=lg(rac{m}{n})$, $L=rac{-1}{m}\sum_{i=1}^m[y_i*ln(rac{h_{ heta}(x_i)}{1-h_{ heta}(x_i)})+ln(1-h_{ heta}(x_i))]$ Substituting in $ln(rac{h_{ heta}(x_i)}{1-h_{ heta}(x_i)})= heta_0+ heta_1*x_{i1}+ heta_2*x_{i2}+\ldots+ heta_n*x_{in}$, $L = rac{-1}{m} \sum_{i=1}^m [y_i * (heta_0 + heta_1 * x_{i1} + heta_2 * x_{i2} + \ldots + heta_n * x_{in}) + ln(1 - h_ heta(x_i))]$ Setting $z_i = heta_0 + heta_1 * x_{i1} + heta_2 * x_{i2} + \ldots + heta_n * x_{in}$, $h_{ heta}(x_i) = rac{1}{1+e^{-z_i}}$ $1-h_{ heta}(x_i)=1-rac{1}{1+e^{-z_i}}$ $1-h_{ heta}(x_i)=rac{e^{-z_i}}{1+e^{-z_i}}$ Multiplying by $rac{e^{z_i}}{e^{z_i}}$, $1-h_ heta(x_i)=rac{1}{1+e^z}$ Substituting back into L, $L = rac{-1}{m} \sum_{i=1}^m [y_i * (z_i) + ln(rac{1}{1 + e^{z_i}})]$ Taking the derivative of L, $rac{dL}{d heta} = rac{-1}{m} \sum_{i=1}^m [y_i rac{d}{d heta_i} (heta_0 + heta_1 * x_{i1} + heta_2 * x_{i2} + \ldots heta_j * x_{ij} + \ldots + heta_n * x_{in})$ $-rac{d}{d heta_i}(ln(1+e^{(heta_0+ heta_1*x_{i1}+ heta_2*x_{i2}+... heta_j*x_{ij}+...+ heta_n*x_{in})}))]$ $rac{dL}{d heta} = rac{-1}{m} \sum_{i=1}^{m} [y_i * x_{ij} - rac{e^{z_i}}{1 + e^{z_i}} * x_{ij}]$ Substitute in $h_{ heta}(x_i) = rac{e^{z_i}}{1+e^{z_i}}$ $rac{dL}{d heta} = rac{-1}{m} \sum_{i=1}^m [y_i * x_{ij} - h_ heta(x_i) * x_{ij}]$ $rac{dL}{d heta} = rac{-1}{m} \sum_{i=1}^m [(y_i - h_ heta(x_i))x_{ij}]$ $rac{dL}{d heta} = rac{1}{m} \sum_{i=1}^m [(h_ heta(x_i) - y_i) x_{ij}]$ Substituting into $heta_{new} = heta_{old} - lpha * rac{d}{d heta} L(heta)$ gives the final equation of, $heta_{new} = heta_{old} - lpha * rac{1}{m} \sum_{i=1}^m [(h_ heta(x_i) - y_i) x_{ij}]$ Question 3: #Function to implement the batch gradient descent algorithm for multiple linear regre-#but utilizing the logistic regression update equation def gradient descent LR(X, Y, T, a): # n is the number of features m, n = X.shape# theta is the array of thetas for each parameter theta = np.zeros(n)# f is the loss f = np.zeros(T)for i in range(T): # calculate the sigmoid function values h x = 1/(1+np.exp(-np.dot(X, theta)))# calculate the summation part of the loss loss sum = 0for j in range(m): loss sum = loss sum + (Y[j]*np.log(h x[j]) + (1-Y[j])*np.log(1-h x[j]))# loss for current theta f[i] = (-1/m) * loss sum# steepest ascent at f(theta) g = np.transpose(X).dot(h x - Y)# change the thetas to perform a step theta = theta - a * g return theta, f **Problem 4:** In [4]: # Given Code for data simulation: # Simulate data for linear regression gen_data_x, gen_data_y = sklearn.datasets.make_regression(n_samples=100, n_features=20) # Simulate data for logistic regression. This is similar to linear, only now values log_gen_data_x, dump_y = sklearn.datasets.make_regression(n samples=100, n features=20) log_gen_data_y = [0 if i>0 else 1 for i in dump_y] # Testing on own implementation: tlin, flin = gradient_descent(gen_data_x, gen_data_y, 100, 0.001) tlog, flog = gradient_descent_LR(log_gen_data_x, log_gen_data_y, 100, 0.01) # Testing on sklearn gradient descent: slin = SGDRegressor(max iter=150) slin.fit(gen data x, gen data y) slog = LogisticRegression().fit(log gen data x, log gen data y); Graphing: # Show that the loss decreases in both over the iterations: plt.plot(range(flin.size),flin); plt.title("Linear Regression Loss over Iterations"); plt.xlabel("Iteration Number"); plt.ylabel("Loss"); plt.show(); plt.plot(range(flog.size),flog); plt.title("Logistic Regression Loss over Iterations"); plt.xlabel("Iteration Number"); plt.ylabel("Loss"); Linear Regression Loss over Iterations 2.5 2.0 1.5 1.0 0.5 0.0 20 80 100 Iteration Number Logistic Regression Loss over Iterations 0.7 0.6 0.5 0.4 0.3 0.2 0.1 20 40 80 100 Iteration Number # Compare the weights found with those found by the Scikit implementation plt.show(); plt.plot(tlin, slin.coef); plt.xlabel("Home Made Linear Regression Weights"); plt.ylabel("Scikit-Learn Weights"); plt.show() plt.plot(tlog, slog.coef [0]); plt.xlabel("Home Made Logistic Regression Weights"); plt.ylabel("Scikit-Learn Weights"); 80 Scikit-Learn Weights 60 40 20 0 40 60 100 Home Made Linear Regression Weights 0.25 0.00 Scikit-Learn Weights -0.25-0.50-0.75-1.00-1.25-1.50-2.0 -1.5-1.0-0.50.0 Home Made Logistic Regression Weights Try it Out!\ The goal of this portion will be using Scikit's built in Diabetes dataset, can a model be built to help predict wether an individual will have an above average blood sugar / blood glucose level. This is an important statistic for Diabetics because hyperglycemia and hypoglycemia (high and low blood sugar) can have immediate and long term negative health effects.\ Age, Sex, Body Mass Index, Average Blood Pressure, and five blood serum measurements will all be used to predict wether an individual's Blood Glucose is above or below the average. # Load Scikit's Diabetes Dataset: data = pd.DataFrame(sklearn.datasets.load diabetes()['data'], columns = ['Age', 'Sex'] # Grabs all non-Blood Glucose columns as the X set X = data[['Age', 'Sex', 'BMI', 'BP', 'tc', 'ldl', 'hdl', 'tch', 'ltg']] # Simplifies the Blood Glucose values to 1 for above the average, 0 for below the average bg = data['Blood Glucose'].apply(lambda x : 1 if x >= 0 else 0) # Splits up the data for training (75%) and testing (25%) X_train, X_test, bg_train, bg_test = train_test_split(X, bg, test_size = 0.25) In [8]: # The first algorithm to be utilized will be Linear SVM # The kernel type is determined via a grid search tuned parameters = [{'kernel': ['rbf']}, {'kernel': ['linear']}, {'kernel': ['poly'], 'degree': range(2,6)}, {'kernel': ['sigmoid']}] clf = GridSearchCV(SVC(), tuned parameters, cv=10) # The freshly defined svm is trained on the training data clf.fit(X_train, bg_train); # The second algorithm to be used is K Nearest Neighbors # The number of k neighbors visited is determined via a grid search tuned_parameters = [{'n_neighbors' : range(1,150)}] knnr = GridSearchCV(KNeighborsClassifier(), tuned_parameters, cv=10) knnr.fit(X_train, bg_train); # Next a 10-fold cross-validation is performed on both algorithms tenfold = KFold(n splits=10, shuffle=True) knnr_scores = cross_validate(knnr, X, bg, cv=tenfold) clf scores = cross validate(clf, X, bg, cv=tenfold) # Prints the mean of each algorithm's scores print("Average K Nearest Neighbors Score", (np.mean(knnr_scores['test_score']))) print("Average Linear SVM Score", (np.mean(clf_scores['test_score']))) # Prints the standard deviation of each algorithm's scores print("Standard Deviation of K Nearest Neighbors' Scores", (np.std(knnr_scores['test] print("Standard Deviation of Linear SVM's Scores", (np.std(clf_scores['test_score'])) Average K Nearest Neighbors Score 0.6513636363636364 Average Linear SVM Score 0.68318181818182 Standard Deviation of K Nearest Neighbors' Scores 0.07930066551722209 Standard Deviation of Linear SVM's Scores 0.06769600585901919 In the end, the Linear SVM algorithm proved more effective at predicting based on its higher average cross-validation score. The standard deviations are close, and it varies which is lower each time the model is trained. However, it is worth noting that both metrics were close, indicating both models perform similarly well in predicting wether an individual has high or low blood sugar.