9.2 MNIST classification: pixels versus edge-based features

Repeat the experiment outlined in Example 9.3 and create a pair of cost function/misclassification history plots like the ones shown in Figure 9.11. Your results may vary slightly from those reported in the example depending on the details of your implementation.

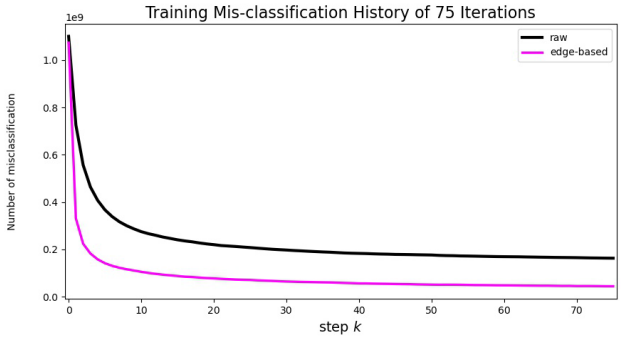
Example 9.3 Handwritten digit recognition

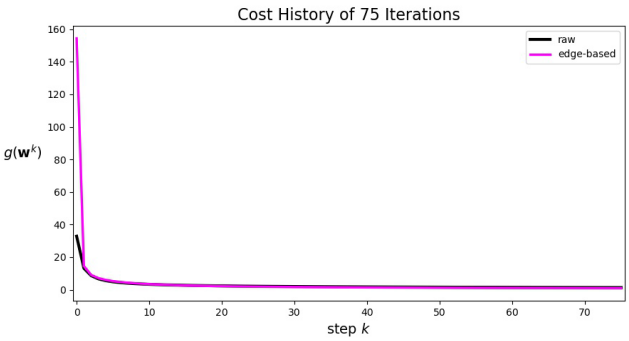
In this example we look at the problem of handwritten digit recognition (introduced in Example 1.10), and compare the training effectiveness of mini-batch gradient descent (20 steps/epochs with a learning rate of $\alpha = 10^{-2}$ and batch size of 200 applied to a multi-class Softmax cost) using $P = 50,000$ raw (pixel-based) data points from the MNIST handwritten digit recognition dataset (introduced in Example 7.10), to the effectiveness of precisely the same setup applied to edge histogram based features extracted from these same data points.

cost function: multiclass_softmax

study rate: 0.01 train for 75 iterations

batch size: 200 P=50000





● 9-2 MNIST classification

```
import sys
from skimage.feature import hog
from skimage import io
from mlrefined_libraries.math_optimization_library import static_plotter
import autograd.numpy as np
from autograd.misc.flatten import flatten_func
from autograd import grad as gradient
from timeit import default_timer as timer
import edge_extract
import pickle
from sklearn.datasets import fetch_openml

sys.path.append('..')

plotter = static_plotter.Visualizer()




def linear_model(x, w):
    a = w[0] + np.dot(x.T, w[1:])
    return a.T

def multiclass_softmax(w, x, y, iter):
    x_p = x[:, iter]
    y_p = y[:, iter]

    # pre-compute predictions on all points
    all_evals = linear_model(x_p, w)

    # compute softmax across data points
    a = np.log(np.sum(np.exp(all_evals), axis=0))

    # compute cost in compact form using numpy broadcasting
    b = all_evals[y_p.astype(int).flatten(), np.arange(np.size(y_p))]
    cost = np.sum(a - b)

    # return average
    return cost / float(np.size(y_p))

class MNIST_Classification(object):
    def __init__(self, x, y, n_sample):
        self.x = np.array(x.T)
        io.imshow(self.x)
```

```
        self.y = np.array([int(value) for value in y])[np.newaxis, :]
        self.shuffle_data(n_sample)
        self.data_initialization()
        self.x_edge = self.hog_extractor(self.x)
        self.mismatching_his = None

    def decent_initializer(self, x):
        w = np.random.randn(np.shape(x)[0] + 1, len(np.unique(self.y)))
        return w

    @staticmethod
    def hog_extractor(img):
        feature, hog_image = hog(img, orientations=8, pixels_per_cell=(1, 1), cells_per_block=(3, 3),
                                 block_norm='L2-Hys', visualize=True, transform_sqrt=False,
                                 feature_vector=False, multichannel=None)  # 70000, 784
        return hog_image

    def shuffle_data(self, n_sample):
        inds = np.random.permutation(y.shape[0])[:n_sample]
        self.x = self.x[:, inds]
        self.y = self.y[:, inds]

    def data_initialization(self):
        # The whole data processing pipeline
        self.deviation_regulartor(self.x)
        x = self.data_recovery(self.x)
        self.x_mean = np.nanmean(x.T, axis=1)[:, np.newaxis]
        self.data_normalization(x)

    def deviation_regulartor(self, x):
        self.x_std = np.nanstd(x.T, axis=1)[:, np.newaxis]
        regulator = np.zeros(self.x_std.shape)
        for i in range(len(self.x_std)):
            if self.x_std[i] <= 0.01:
                regulator[i] = 1.0
                self.x_std += regulator
            else:
                pass

    def data_normalization(self, x):
        # Generate the normalization function
        normalize = lambda x: (x - self.x_mean) / self.x_std
        self.x = normalize(x.T).T
```

```
    def data_recovery(self, x):
        mean = np.nanmean(self.x, axis=1)
        for i in np.argwhere(np.isnan(x) == True):
            x[i[0], i[1]] = mean[i[0]]
        return x

    def gradient_descent(self, loss_fun, x_train, y_train, alpha, max_its, batch_size, **kwargs):
        w = self.decent_initializer(x_train)
        verbose = True
        if 'verbose' in kwargs:
            verbose = kwargs['verbose']
        g_flat, unflatten, w = flatten_func(loss_fun, w)
        grad = gradient(g_flat)
        num_train = y_train.size
        w_hist = [unflatten(w)]
        train_hist = [g_flat(w, x_train, y_train, np.arange(num_train))]
        num_batches = int(np.ceil(np.divide(num_train, batch_size)))
        for k in range(max_its):
            start = timer()
            train_cost = 0
            for b in range(num_batches):
                # collect indices of current mini-batch
                batch_inds = np.arange(b * batch_size, min((b + 1) * batch_size, num_train))

                # plug in value into func and derivative
                grad_eval = grad(w, x_train, y_train, batch_inds)
                grad_eval.shape = np.shape(w)
                w = w - alpha * grad_eval
            end = timer()

            train_cost = g_flat(w, x_train, y_train, np.arange(num_train))
            w_hist.append(unflatten(w))
            train_hist.append(train_cost)
            if verbose:
                print('step ' + str(k + 1) + ' done in ' + str(np.round(end - start, 1)) + ' secs, train
cost = ' + str(
                    np.round(train_hist[-1][0], 4)))

        if verbose:
            print('finished all ' + str(max_its) + ' steps')
            # time.sleep(1.5)
            # clear_output()
        return w_hist, train_hist
```

```
    # Others
    def one_versus_others_seperator(self, label):
        y = self.y
        y[np.argwhere(self.y == label)[:, 0]] = 1
        y[np.argwhere(self.y != label)[:, 0]] = -1
        return y

    @staticmethod
    def weight_normalizer(w):
        w_norm = sum([v ** 2 for v in w[1:]]) ** 0.5
        return [v / w_norm for v in w]

    def predict(self, x, w_trained):
        class_y = np.argmax(linear_model(x, w_trained), axis=0)
        return class_y

    def counting_mis_classification(self, x, weight_history):
        mismatching_his = []
        for w_p in weight_history:
            count = 0
            class_y = self.predict(x, w_p)
            count = np.sum(np.argwhere(self.y != class_y))
            mismatching_his.append(count)
            print(count)
        self.mismatching_his = mismatching_his
        return mismatching_his

if __name__ == "__main__":
    x, y = fetch_openml('mnist_784', version=1, return_X_y=True)
    mnist = MNIST_Classification(x, y, n_sample=50000)
    weight_his, cost_his = mnist.gradient_descent(multiclass_softmax, mnist.x, mnist.y, alpha=0.01,
                                          max_its=75,
                                          x=mnist.x, batch_size=200, verbose=True)
    weight_edge_his, cost_edge_his = mnist.gradient_descent(multiclass_softmax, mnist.x_edge, mnist.y,
                                                alpha=0.01, max_its=75,
                                                x=mnist.x_edge, batch_size=200, verbose=True)
    mis1 = mnist.counting_mis_classification(mnist.x, weight_his)
    mis2 = mnist.counting_mis_classification(mnist.x_edge, weight_edge_his)
    plotter.plot_mismatching_histories(histories=[mis1, mis2], start=0,
                                labels=['raw', 'edge-based'],
                                title="Training Mis-classification History of 75 Iterations")
    plotter.plot_cost_histories(histories=[cost_his, cost_edge_his], start=0,
                            labels=['raw', 'edge-based'],
                            title="Cost History of 75 Iterations")
```

10.4 Moore's law

Gordon Moore, co-founder of Intel corporation, predicted in a 1965 paper [47] that the number of transistors on an integrated circuit would double approximately every two years. This conjecture, referred to nowadays as Moore's law, has proven to be sufficiently accurate over the past five decades. Since the processing power of computers is directly related to the number of transistors in their CPUs, Moore's law provides a trend model to predict the computing power of future microprocessors. Figure 10.18 plots the transistor counts of several microprocessors versus the year they were released, starting from Intel 4004 in 1971 with only 2300 transistors, to Intel's Xeon E7 introduced in 2014 with more than 4.3 billion transistors.

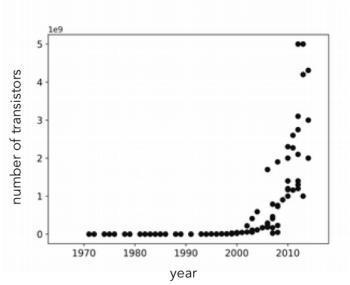
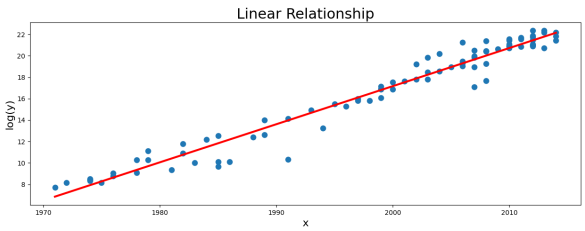


Figure 10.18 Figure associated with Exercise 10.4. See text for details.

(a) Propose a single feature transformation for the Moore's law dataset shown in Figure 10.18 so that the transformed input/output data is related linearly. *Hint: to produce a linear relationship you will end up having to transform the output, not the input.*

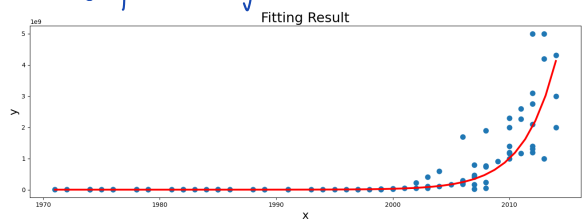
Sol: we can apply a log on y, then, log(y) and x will be linearly related.



(b) Formulate and minimize a Least Squares cost function for appropriate weights, and fit your model to the data in the original data space as shown in Figure 10.18.

Sol: Below is the fitting result:

- Cost function: Least square
- Optimization function: Newtons method.



• 10-4 Moore's Law

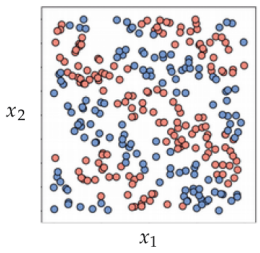
```
import numpy as np
import pandas as pd
import autograd.numpy as np
from autograd import hessian, grad
import matplotlib.pyplot as plt


class Moores_law(object):
    def __init__(self, filename):
        data = np.asarray(pd.read_csv(filename, header=None))
        self.x = data[:, 0]
        self.x.shape = (1, len(self.x))
        self.y = data[:, 1]
        self.y.shape = (1, len(self.y))
        self.y_log = np.log(self.y)

    def data_plotting_linear_transform(self, w):
        fig = plt.figure(figsize=(16, 5))
        ax1 = fig.add_subplot(1, 1, 1)  # panel for original space
        ax1.scatter(self.x, self.y_log, linewidth=3)
        s = np.linspace(np.min(self.x), np.max(self.x))
        t = w[0] + w[1] * s
        ax1.plot(s, t, linewidth=3, color='r')
        ax1.set_xlabel('x', fontsize=16)
        ax1.set_ylabel('log(y)', rotation=90, fontsize=16)
        ax1.set_title('Linear Relationship', fontsize=22)
        plt.show()

    @staticmethod
    def model(x, w):
        a = w[0] + np.dot(x.T, w[1:])
        return a.T

    def least_squares_mean(self, w):
        cost = np.sum((self.model(self.x, w) - self.y_log) ** 2)
        return cost / float(np.size(self.y_log))

    def newtons_method(self, g, max_its, w, **kwargs):
        gradient = grad(g)
        hess = hessian(g)
```

```
        # set numericxal stability parameter / regularization parameter
        epsilon = 10 ** (-10)
        if 'epsilon' in kwargs:
            epsilon = kwargs['epsilon']
        weight_history = [np.array(w)]  # container for weight history
        cost_history = [np.array(g(w))]  # container for corresponding cost function history
        for k in range(max_its):
            grad_eval = gradient(w)
            hess_eval = hess(w)
            hess_eval.shape = (int((np.size(hess_eval)) ** (0.5)), int((np.size(hess_eval)) ** (0.5)))
            A = hess_eval + epsilon * np.eye(w.size)
            b = grad_eval
            w = np.linalg.solve(A, np.dot(A, w) - b)
            weight_history.append(np.array(w))
            cost_history.append(np.array(g(w)))
        self.w = w
        return weight_history, cost_history

    def data_plotting(self, w):
        fig = plt.figure(figsize=(16, 5))
        ax1 = fig.add_subplot(1, 1, 1)  # panel for original space
        ax1.scatter(self.x, self.y, linewidth=3)
        s = np.linspace(np.min(self.x), np.max(self.x))
        t = np.exp(w[0] + w[1] * s)
        ax1.plot(s, t, linewidth=3, color='r')
        ax1.set_xlabel('x', fontsize=18)
        ax1.set_ylabel('y', rotation=90, fontsize=18)
        ax1.set_title('Fitting Result', fontsize=22)
        plt.show()


if __name__ == "__main__":
    filename = '../mlrefined_datasets/nonlinear_superlearn_datasets/transistor_counts.csv'
    w0 = np.random.randn(2, 1)
    Moores = Moores_law(filename)
    Moores.newtons_method(Moores.least_squares_mean, max_its=1000, w=w0)
    Moores.data_plotting_linear_transform(Moores.w)
    Moores.data_plotting(Moores.w)
```

10.8 **Engineering features for a two-class classification dataset**

Propose a nonlinear model for the dataset shown in Figure 10.20 and perform nonlinear two-class classification. Your model should be able to achieve perfect classification on this dataset.

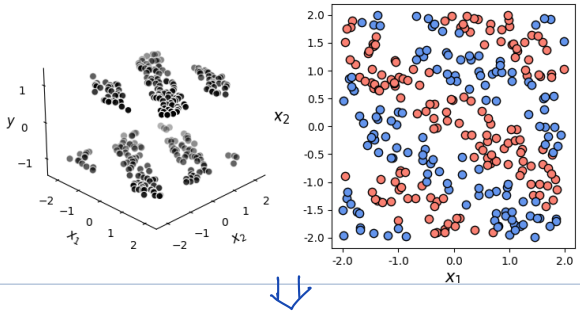
Figure 10.20 Figure associate
Exercise 10.8. See text for det

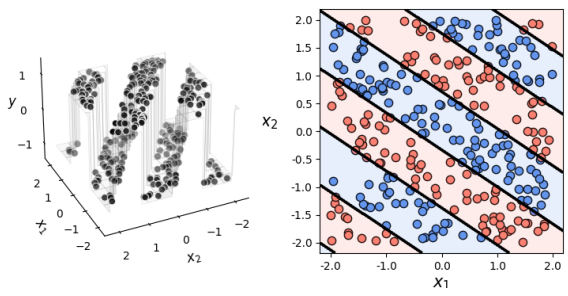


we can use "sin" to transform input data

The model is: $f(x,w) = \sin\left(b + \sum_{p=1}^{P} x_p^T w_p\right)$ here, we only have $f(x,y) = \sin(b + x_1 w_1 + x_2 w_2)$

trained with "Softmax" study_rate = 0.1 for 2000 iteration





As the figure illustrates, our model it can achieve perfect classification over this dataset.

• 10-8 Engineering features transformation

```
from mlrefined_libraries.nonlinear_superlearn_library import nonlinear_classification_visualizer as ncv
from mlrefined_libraries.nonlinear_superlearn_library import basic_runner
import autograd.numpy as np

Visualizer = ncv.Visualizer


class Engineering_Feature_Transformation(Visualizer):
    def __init__(self, file_path):
        super().__init__(file_path)
        self.decent_initializer(2)

    def decent_initializer(self, scale):
        self.w0 = [scale * np.random.randn(3, 1), scale * np.random.randn(2, 1)]

    @staticmethod
    def feature_transforms(x, w):
        f = np.sin(w[0] + np.dot(x.T, w[1:])).T
        return f

    def train(self, loss_fun, study_rate, iters, normalize):
        model = basic_runner.Setup(self.x.T, self.y, self.feature_transforms, loss_fun,
normalize=normalize)
        model.fit(w=self.w0, alpha_choice=study_rate, max_its=iters)
        ind = np.argmin(model.cost_history)
        self.w_best = model.weight_history[ind]
        self.model = model

    def visulizer(self):
        self.static_N2_simple(self.w_best, self.model, view=[30, 160])


if __name__ == "__main__":
    file_path = '../mlrefined_datasets/nonlinear_superlearn_datasets/diagonal_stripes.csv'
    Eng_trans = Engineering_Feature_Transformation(file_path)
    Eng_trans.plot_data()
    Eng_trans.train(loss_fun='softmax', study_rate=0.1, iters=2000)
    Eng_trans.visulizer()
```

11.7 Bagging two-class classification models

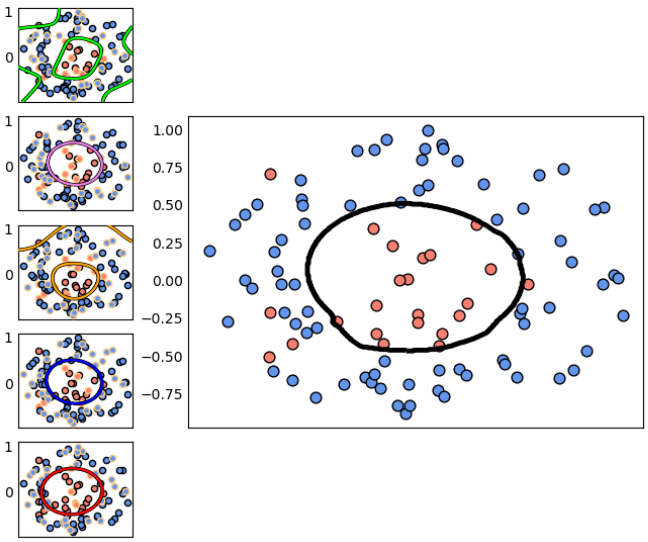
Repeat the first experiment outlined in Example 11.15, producing five naively cross-validated polynomial models to fit different training–validation splits of the two-class classification dataset shown in Figure 11.46. Compare the efficacy – in terms of number of misclassifications over the entire dataset – of each individual model and the final bagged model.

train-set portion: $\frac{2}{3}$ validation portion : $\frac{1}{3}$

5 bags , degree of polynomial : 1-8

model trained for 50 iterations for each degree

Optimized with Newtons method.



Example 11.15 Bagging cross-validated two-class classification models

In the set of small panels in the left column of Figure 11.46 we show five different training–validation splits of the prototypical two-class classification dataset first described in Example 11.7, where $\frac{2}{3}$ of the data in each instance is used for training and $\frac{1}{3}$ is used for validation (the boundaries of these points are colored yellow). Plotted with each split of the original data is the nonlinear decision boundary corresponding to each cross-validated model found via naive cross-validation of the full range of polynomial models of degree 1 to 8. Many of these cross-validated models perform quite well, but some of them (due to the particular training–validation split on which they are based) severely *overfit* the original dataset. By bagging these models using the most popular prediction to assign labels (i.e., the *mode* of these cross-validated model predictions) we produce an appropriate decision boundary for the data shown in the right panel of the figure.

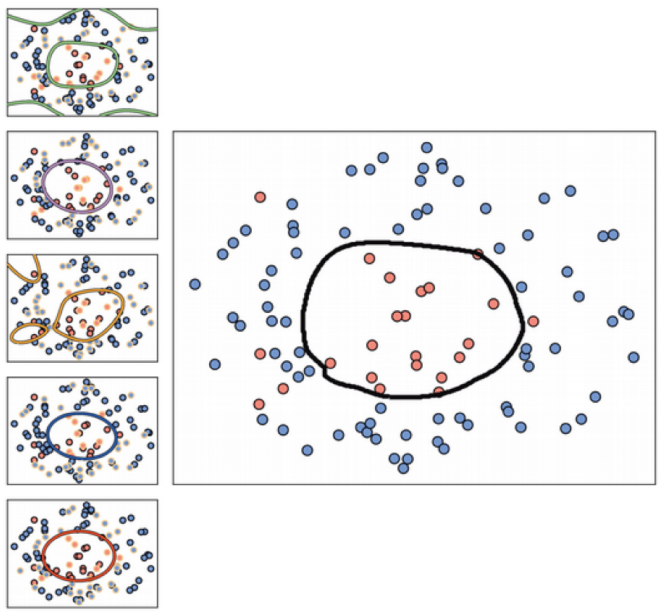


Figure 11.46 Figure associated with Example 11.15. (left column) Five models cross-validated on random training–validation splits of the data, with the validation data in each instance highlighted with a yellow outline. The corresponding nonlinear decision boundary provided by each model is shown in each panel. Some models, due to the split of the data on which they were built, severely overfit. (right column) The original dataset with the decision boundary provided by the bag (i.e., mode) of the five cross-validated models. See text for further details.

• 11-7 Bagging two-class classification models

```
import copy
import autograd.numpy as np
from mlrefined_libraries.nonlinear_superlearn_library.classification_bagging_visualizers_v2 import
Visualizer
from mlrefined_libraries.nonlinear_superlearn_library.reg_lib.super_setup import Setup


class Bagging_Two_Class_Classification(Visualizer):
    def __init__(self, file_path):
        data = np.loadtxt(file_path, delimiter=',')
        Visualizer.__init__(self, file_path)
        self.x = data[:-1, :]
        self.y = data[-1:, :]
        self.visulizer = Visualizer(file_path)

    def split_dataset(self, train_portion):
        self.train_portion = train_portion
        r = np.random.permutation(self.x.shape[1])
        train_num = int(np.round(train_portion * len(r)))
        self.train_inds = r[:train_num]
        self.valid_inds = r[train_num:]

        self.x_train = self.x[:, self.train_inds]
        self.x_valid = self.x[:, self.valid_inds]

        self.y_train = self.y[:, self.train_inds]
        self.y_valid = self.y[:, self.valid_inds]

    def train(self, num_bag, train_portion, degree):
        model = []
        for j in range(num_bag):
            model_11_7 = Setup(self.x, self.y)
            model_11_7.preprocessing_steps(name="standard")
            model_11_7.split_dataset(train_portion)
            for d in range(1, degree + 1):
                model_11_7.choose_cost(name='softmax')
                model_11_7.choose_features(name='polys', degree=d)
                model_11_7.fit(algo='newtons_method', max_its=50, verbose=False, lam=10 ** (-8))
            val_costs = [np.min(model_11_7.valid_count_histories[i]) for i in range(degree)]
            min_ind = np.argmin(val_costs)
            min_val = val_costs[min_ind]
```

```
            # get minor of minor
            smallest_ind = np.argmin(model_11_7.valid_count_histories[min_ind])
            model_11_7.train_cost_histories = model_11_7.train_cost_histories[min_ind][smallest_ind]
            model_11_7.valid_cost_histories = model_11_7.valid_cost_histories[min_ind][smallest_ind]
            model_11_7.train_count_histories = model_11_7.train_count_histories[min_ind][smallest_ind]
            model_11_7.valid_count_histories = model_11_7.valid_count_histories[min_ind][smallest_ind]
            model_11_7.weight_histories = model_11_7.weight_histories[min_ind][smallest_ind]
            model_11_7.choose_features(name='polys', degree=min_ind + 1)

            # store
            model.append(copy.deepcopy(model_11_7))
        return model

    def visulization(self, model):
        self.visulizer.show_runs(model)


if __name__ == "__main__":
    file_path = '../mlrefined_datasets/nonlinear_superlearn_datasets/new_circle_data.csv'
    bagging8 = Bagging_Two_Class_Classification(file_path=file_path)
    trained_model = bagging8.train(num_bag=5, train_portion=0.67, degree=8)
    bagging8.show_runs(trained_model)
```

11.10 **Classification of diabetes**

Perform K-fold cross-validation using a linear model and the ℓ_1 regularizer over a popular two-class classification genomics dataset consisting of $P = 72$ data-points, each of which has input dimension $N = 7128$. This will tend to produce a sparse predictive linear model – as detailed in Example 11.18 – which is helpful

L_1 : regularization

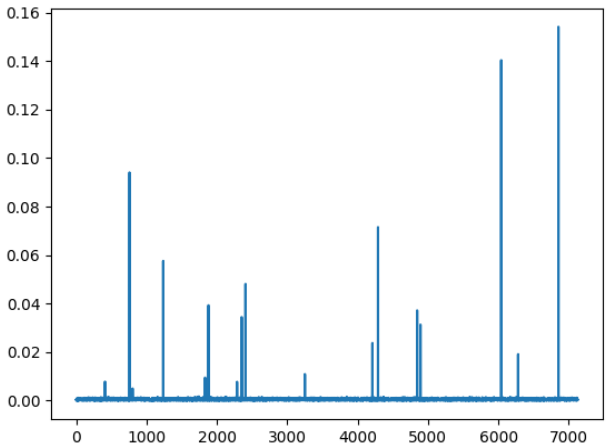
$C = C_0 + \frac{\lambda}{n}\sum_w |w|$

① chose best λ for the regularization

10-folds validation study rate: $\frac{1}{K}$ (K ⇒ iteration)

Best λ for L_1 regularization ≈ 12.245

```
best lambda is:12.244897959183675
```



Example 11.18 **Genome-wide association studies**

Genome-wide association studies (GWAS) aim at understanding the connections between tens of thousands of genetic markers (input features), taken from across the human genome of several subjects, with medical conditions such as high blood pressure, high cholesterol, heart disease, diabetes, various forms of cancer, and many others (see Figure 11.52). These studies typically involve a relatively small number of patients with a given affliction (as compared to the very large dimension of the input). As a result, regularization based cross-validation is a useful tool for learning meaningful (linear) models for such data. Moreover, using a (sparsity-inducing) regularizer like the ℓ_1 norm can help researchers identify the handful of genes critical to the affliction under study, which can both improve our understanding of it and perhaps provoke development of gene-targeted therapies. See Exercise 11.10 for further details.

• 11-10 Classification of diabetes

```
import copy
from autograd import value_and_grad
from autograd.misc.flatten import flatten_func
import autograd.numpy as np
import matplotlib.pyplot as plt
from IPython.display import clear_output
from mlrefined_libraries.nonlinear_superlearn_library.kfolds_reg_lib.superlearn_setup import Setup


class Diabetes_Classification(Setup):
    def __init__(self, file_path, K_fold):
        data = np.loadtxt(file_path, delimiter=',')
        self.x = data[:-1, :]
        self.y = data[-1:, :]
        super().__init__(self.x, self.y)
        self.fold_num = self.fold_assigning(self.y.size, K_fold)
        self.x_mean = np.nanmean(self.x, axis=1)[:, np.newaxis]
        self.x_std = np.nanstd(self.x, axis=1)[:, np.newaxis]
        self.K_fold = K_fold
        self.lam = None

    def decent_ini(self):
        self.w_0 = 0.1 * np.random.randn(self.x.shape[0] + 1, 1)

    @staticmethod
    def fold_assigning(L, K):
        order = np.random.permutation(L)
        c = np.ones((L, 1))
        L = int(np.round((1 / K) * L))
        for s in np.arange(0, K - 2):
            c[order[s * L:(s + 1) * L]] = s + 2
        c[order[(K - 1) * L:]] = K
        return c

    def data_initialization(self):
        self.deviation_regulartor(self.x)
        x = self.data_recovery(self.x)
        self.x_mean = np.nanmean(x, axis=1)[:, np.newaxis]
        self.data_normalization(x)

    def deviation_regulartor(self, x):
```

```
    self.x_std = np.nanstd(x, axis=1)[:, np.newaxis]
    regulator = np.zeros(self.x_std.shape)
    for i in range(len(self.x_std)):
        if self.x_std[i] <= 0.01:
            regulator[i] = 1.0
            self.x_std += regulator
        else:
            pass

def data_normalization(self, x):
    # Generate the normalization function
    normalize = lambda x: (x - self.x_mean) / self.x_std
    self.x = normalize(x)

def data_recovery(self, x):
    mean = np.nanmean(self.x, axis=1)
    for i in np.argwhere(np.isnan(x)):
        x[i[0], i[1]] = mean[i[0]]
    return x

@staticmethod
def linear_model(x, w):
    a = w[0] + np.dot(x.T, w[1:])
    return a.T

def make_train_test_split(self, k):
    train_ind = [v[0] for v in np.argwhere(self.fold_num != k)]
    valid_ind = [v[0] for v in np.argwhere(self.fold_num == k)]
    self.train_x = self.x[:, train_ind]
    self.train_y = self.y[:, train_ind]
    self.valid_x = self.x[:, valid_ind]
    self.valid_y = self.y[:, valid_ind]

def gradient_descent(self, g, x, y, alpha_choice, max_its, batch_size):
    w = self.w_0
    # flatten the input function, create gradient based on flat function
    g_flat, unflatten, w = flatten_func(g, w)
    grad = value_and_grad(g_flat)
    num_train = y.size
    w_hist = [unflatten(w)]
    train_hist = [g_flat(w, x, y, np.arange(num_train))]
    num_batches = int(np.ceil(np.divide(num_train, batch_size)))
    alpha = 0
```

```
    for k in range(max_its):
        if alpha_choice == 'diminishing':
            alpha = 1 / float(k + 1)
        else:
            alpha = alpha_choice
        for b in range(num_batches):
            batch_inds = np.arange(b * batch_size, min((b + 1) * batch_size, num_train))
            cost_eval, grad_eval = grad(w, x, y, batch_inds)
            grad_eval.shape = np.shape(w)
            w = w - alpha * grad_eval

        train_cost = g_flat(w, x, y, np.arange(num_train))
        w_hist.append(unflatten(w))
        train_hist.append(train_cost)
    return w_hist, train_hist

def softmax(self, w, x, y, iter):
    x_p = x[:, iter]
    y_p = y[:, iter]
    cost = np.sum(np.log(1 + np.exp(-y_p * (self.linear_model(x_p, w)))))
    cost += (self.lam * np.sum(np.abs(w[1:])))
    return cost / float(np.size(y_p))

def counting_mis_classification(self, w, x, y):
    y_predict = np.sign(self.linear_model(x, w))
    num_misclass = len(np.argwhere(y != y_predict))
    return num_misclass

def train(self, lams, max_its, study_rate):
    all_train_counts = []
    all_valid_counts = []
    for k in range(self.K_fold):
        print("---------fold" + str(k + 1) + "------")
        print("---------*****---------")
        # self.data_normalization(self.x)
        self.choose_normalizer(name='standard')
        self.make_train_test_split(k)
        self.find_best_reg(lams, max_its, study_rate)
        all_train_counts.append(copy.deepcopy(self.train_count_misclass))
        all_valid_counts.append(copy.deepcopy(self.valid_count_misclass))
    print("finish")
    best_lam = self.count_mis_class_total(all_train_counts, all_valid_counts)
    return best_lam
```

```
    def single_trail(self, lams, max_its, study_rate):
        self.data_normalization(self.x)
        train_inds = np.argwhere(self.fold_num != -1)
        train_inds = [v[0] for v in train_inds]
        valid_inds = np.argwhere(self.fold_num == -1)
        valid_inds = [v[0] for v in valid_inds]
        self.valid_x = self.x[:, valid_inds]
        self.valid_y = self.y[:, valid_inds]
        self.train_x = self.x[:, train_inds]
        self.train_y = self.y[:, train_inds]
        self.find_best_reg(lams, max_its, study_rate)

    def find_best_reg(self, lams, max_its, study_rate):
        self.train_count_misclass = []
        self.valid_count_misclass = []
        self.weights = []
        batch_size = np.size(self.train_y)
        self.decent_ini()
        for i in range(len(lams)):
            print('running ' + str(i + 1) + ' of ' + str(len(lams)) + ' rounds')
            self.lam = lams[i]
            weight_history, cost_history = self.gradient_descent(self.softmax, self.train_x,
                                                    self.train_y, alpha_choice=study_rate,
                                                    max_its=max_its, batch_size=batch_size)
            w_p = weight_history[np.argmin(cost_history)]
            self.weights.append(w_p)
            self.train_count_misclass.append(self.counting_mis_classification(w_p, self.train_x,
self.train_y))
            self.valid_count_misclass.append(self.counting_mis_classification(w_p, self.valid_x,
self.valid_y))
        bset_ind = np.argmin(self.valid_count_misclass)
        self.best_lam = lams[bset_ind]
        self.best_weights = self.weights[bset_ind]

    @staticmethod
    def count_mis_class_total(all_train_counts, all_valid_counts):
        all_train_counts = np.array(all_train_counts)
        train_totals = np.sum(all_train_counts, 0)
        all_valid_counts = np.array(all_valid_counts)
        valid_totals = np.sum(all_valid_counts, 0)
        best_valid_ind = np.where(valid_totals == valid_totals.min())[0][-1]
        best_lam = lamda[best_valid_ind]
        return best_lam
```

```
if __name__ == "__main__":
    k_fold = 10
    lamda = np.linspace(0, 20, 50)
    file_path = '../mlrefined_datasets/nonlinear_superlearn_datasets/new_gene_data.csv'
    diabetes = Diabetes_Classification(file_path=file_path, K_fold=k_fold)
    lamda_chose = diabetes.train(lamda, max_its=100, study_rate='diminishing')
    print("best lambda is:" + str(lamda_chose))
    clear_output()
    diabetes2 = Diabetes_Classification(file_path=file_path, K_fold=k_fold)
    diabetes2.single_trail(lams=np.array([lamda_chose]), max_its=200, study_rate='diminishing')
    plt.plot(np.abs(diabetes2.best_weights[1:]))
    plt.show()
```