# Assessment 3

# SCHOOL OF ADVANCED TECHNOLOGY

INT10: Advanced Pattern Recognition Mengfan Li

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# 1 Objectives

This assessment aims at evaluating students' ability to exploit the advanced pattern recognition knowledge, which is accumulated during lectures, and after-class study, to analyze, design, implement, develop, test and document the pattern classification methods with Neural Networks (MLP), Discriminant Function (MQDF), and Kernel Methods (Support Vector Machine) typically on the image data.

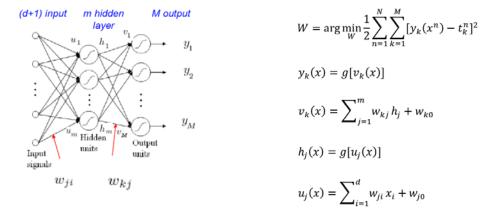
# 2 Materials

Pycharm

# 3 Methods, result and discussion

# 1 Implement Multilayer Perceptron (MLP) on MNIST

An artificial neural network is composed of many artificial neurons that are linked together according to a specific network architecture. The model transforms the inputs into meaningful outputs by iterating a combination of linear and nonlinear functions.



Design an MLP model to achieve the classification task on MNIST. Show the training process and classification results.

Many factors will affect the performance, such as, the number of nodes in hidden layers, the

selection of the activation functions, the normalization method of the samples, the loss function and its regularization term, the learning rate and the stopping policy of training, etc.

## Load data set

train\_set, valid\_set and test\_set are training set, validation set and test set respectively, organized in the form of tuple (x, y), x represents sample, y represents sample label

```
1. def load_data():
2.    f = gzip.open("mnist.pkl.gz", "rb")
3.    train_set, valid_set, test_set = pickle.load(f, encoding="latin1")
4.    f.close()
5.    return [train_set, valid_set, test_set]
```

```
1. datasets = load_data()
```

## Result:

# Define the loss function

For multi-class problems, the negative log-likelihood function is used as the loss function. p\_y\_given\_x is the prediction of the model. It is an m\*10 two-dimensional array. Each row represents a sample, and each column represents the model prediction sample is 0~9 Probability. Np.arange(y.shape[0]) is a one-dimensional array, containing [0,1,...,m-1], y is the true label corresponding to the sample, is a one-dimensional array, p\_y\_given\_x[[0,1,...,m-1][y[0],...y[m-1]] is equivalent to p\_y\_given\_x[0,y[0]], p\_y\_given\_x[1,y[1],...,p\_y\_given\_x[m-1,y[m-1]], that is, read

the predicted value of the model corresponding to the true category of each sample, we want this value bigger.

$$C = -\log y_r$$
$$y_r = \frac{e^{z_r}}{\sum_k e^{z_k}}$$

Derivation:

1. i=r  $\frac{\partial C}{\partial z_r} = \frac{\partial C}{\partial y_r} \frac{\partial y_r}{\partial z_r} = -\frac{1}{y_r} \left( \frac{e^{z_r}}{\sum_k e^{z_k}} - e^{z_r} \frac{e^{z_r}}{(\sum_k e^{z_k})^2} \right) = -\frac{1}{y_r} (y_r - y_r^2) = y_r - 1$ 2. i!=r  $\frac{\partial C}{\partial z_i} = \frac{\partial C}{\partial y_r} \frac{\partial y_r}{\partial z_i} = -\frac{1}{y_r} \left( -e^{z_r} \frac{e^{z_i}}{(\sum_k e^{z_k})^2} \right) = -\frac{1}{y_r} (-y_r^2) = y_r - 0$ 

Unify, have:

$$\frac{\partial C}{\partial z_i} = y_i - \hat{y}_i$$

Code:

```
    # Define loss function
    def loss_function(p_y_given_x, y):
    return -np.mean(np.log(p_y_given_x)[np.arange(y.shape[0]), y])
```

#### Result:

```
mnist_testdata.hdf5
mnist_traindata.hdf5
process_dataset.py
t10k-images-idx3-ubyte.gz
t10k-labels-idx1-ubyte.gz
t10k-labels-idx1-ubyte.gz
test_softmaxRegression_mlp
train-images-idx3-ubyte.qz

images-idx3-ubyte.qz

image
```

# • Count the number of error samples

First, according to the predicted probability of the network, choose the one with the highest probability as the network predicted label

Code:

1. # Get the predicted label of each sample

```
# Get the predicted label of each sample

ministpkl.gz

ministpkl.gz

minist testdata.hdf5

minist testdata.hdf5

process dataset.py

totok-images-idx3-ubyte.gz

totok-labels-idx1-ubyte.gz

totok-labels-idx1-ubyte.gz

I:\Anaconda\python.exe C:/Users/123/Desktop/MLP/mlp_mnist_1hidden.py

predicted label of each sample:

[1 4 1 ... 1 1 1]
```

# Construct the sample real label matrix

In the original data set, the label of each sample corresponds to a scalar, which directly indicates which number the sample is. But in calculating the gradient, y needs to be expanded into a vector with the same dimension as the model output.

#### Code:

```
    # Construct the sample real label matrix
    def truth_label_matrix(y):
    matrix = np.zeros((len(y), 10))
    for i in np.arange(len(y)):
    matrix[i, y[i]] = 1
    return matrix
```

## Result:

sigmoid function and its derivative

#### Code:

```
    # Sigmoid
    def sigmoid(x):
    return 1.0 / (1 + np.exp(-x))
    # Sigmoid derivative
    def sigmoid_derivative(x):
    return sigmoid(x) * (1 - sigmoid(x))
```

#### Resule:

```
def sigmoid(x):
nnist traindata.hdf5
                                      print(1.0 / (1 + np.exp(-x)))
10k-images-idx3-ubyte.gz
                                      return 1.0 / (1 + np.exp(-x))
10k-labels-idx1-ubyte.gz
                                  truth label matrix() >> for i in np.arange(len(y))
est softmaxRegression mlp
Sigmoid
[[0.57614162 0.87563348 0.55317976 ... 0.8065404 0.03690942 0.82189086]
 [0.33632718 0.40074588 0.57202115 ... 0.63267408 0.68963405 0.2641659 ]
 [0.7256762 \quad 0.42518456 \quad 0.6282022 \quad \dots \quad 0.72903494 \quad 0.45492821 \quad 0.34955362]
                               # Sigmoid derivative
mnist_testdata.hdf5
                               def sigmoid_derivative(x):
mnist_traindata.hdf5
process dataset.py
                                   print(sigmoid(x) * (1 - sigmoid(x)))
t10k-images-idx3-ubyte.gz
                                   return sigmoid(x) * (1 - sigmoid(x))
t10k-labels-idx1-ubyte.gz
                                sigmoid_derivative()
test_softmaxRegression_mlp
 mlp mnist 1hidden
 Sigmoid derivative
 [[0.24804465 0.22594826 0.23059926 ... 0.043428
                                                       0.22061633 0.05129357]
  [0.2499999 0.14747268 0.10498952 ... 0.23329995 0.15534766 0.04695556]
  [0.13117681 0.21199016 0.18365742 ... 0.24999617 0.17912536 0.17481732]
```

# Initialize weight w

Determine the number of hidden layers, the number of hidden layer neurons, and initialize the connection weight, the neural network model is determined

#### Code:

# Result:

• Calculate the derivative of |w|

Calculate the derivative of |w|, needed when using L1 regularization

### Code:

```
    # Calculate the derivative of |w|, needed when using L1 regularization
    def sign(w):
    w = np.where(w > 0, 1, w)
    w = np.where(w >= 0, w, -1)
    return w
```

# Result:

```
mlp_github.py
mlp_mnist_1hidden.py
mnist_pkl
mnist_pkl.gz
mnist_testdata.hdf5
mnist_traindata.hdf5
process_dataset.py

mlp_mnist_lhidden ×

-0.05808376]]
w derivative
[[ 1. -1. 1. ... 1. 1. -1.]
[-1. -1. 1. ... -1. -1. -1.]
[ 1. -1. 1. ... 1. 1. 1.]
[ -1. -1. 1. ... 1. 1. 1.]
[ -1. -1. 1. ... 1. 1. 1.]
[ -1. -1. 1. ... 1. 1. 1.]
[ -1. -2. 1. 1. 1. 1.]
[ -1. -3. 1. 1. 1. 1.]
[ -1. -4. 1. 1. 1. 1.]
[ -1. -1. 1. ... 1. 1. 1.]
[ -1. -1. 1. ... 1. 1. 1.]
[ -1. -2. 1. 1. 1. 1.]
[ -1. -3. 1. 1. 1.]
[ -1. -4. 1. 1. 1. 1.]
[ -1. -5. 1. 1. 1. 1.]
[ -1. -6. 2.05203995 -0.04863817 0.029334 ... -0.23925191 -0.26270971 -0.00161771]
```

# Forward spread

Forward propagation, get model prediction value

```
1.
      # Forward spread
2.
      def forward(x, W):
3.
          layer_input = [x]
                                            # input
4.
          layer_output = [x]
                                    # output
5.
6.
          # hidden layer
7.
          for i in range(len(W) - 1):
              layer_input.append(np.dot(x, W[i]))
8.
              temp_ = sigmoid(np.dot(x, W[i]))
9.
10.
              layer_output.append(temp_)
          # output layer
11.
          layer_input.append(np.dot(temp_, W[-1]))
12.
```

```
13. layer_output.append((np.transpose(np.exp(np.dot(temp_, W[-
1]))) / np.sum(np.exp(np.dot(temp_, W[-1])), axis=1)).T)
14.
15. return (layer_output, layer_input)
```

### Resulr:

# Back propagation

Using the backpropagation algorithm, calculate the gradient of each layer connected W, because:

$$\frac{\partial C}{\partial w_{ij}^l} = \frac{\partial C}{\partial z_i^l} \frac{\partial z_j^l}{\partial w_{ij}^l}$$

The key is to find  $\frac{\partial c}{\partial z_i^l}$  and make it equal to  $\delta_j^l$ 

Output layer

$$\frac{\partial C}{\partial z_i^L} = \frac{\partial C}{\partial y_i^L} \frac{\partial y_j^L}{\partial z_i^L} = \nabla C(y^L) * \delta'(z_j^L)$$

Un-output layer

$$\frac{\partial C}{\partial z_j^L} = \sum_{k} \frac{\partial C}{\partial z_k^{l+1}} \frac{\partial z_k^{l+1}}{\partial a_j^l} \frac{\partial a_j^l}{\partial z_j^l} = \sum_{k} \delta_k^{l+1} \omega_{jk}^{l+1} \, \delta'(z_j^L)$$

```
    # Back propagation
    def back(layer_output, layer_input, w, y, L1_reg, L2_reg):
    grad_w = [np.zeros(weight.shape) for weight in w]
```

```
4.
5.
         # Backpropagation
         delta = layer_output[-1] - y # last layer, m*10
6.
         grad w[-1] = np.dot(np.transpose(layer_output[-2]), delta)
7.
         for l in range(2, len(w) + 1):
8.
9.
             delta = np.dot(delta, w[-
1 + 1].transpose()) * sigmoid derivative(layer input[-1]) # other layer
10.
             grad_w[-1] = np.dot(np.transpose(layer_output[-
1 - 1]), delta) / y.shape[0] + L1_reg * sign(w[-1]) + L2_reg * w[
11.
                 -1]
12.
13.
         return grad_w
```

```
print("Back propagation")

mist pkl.gz

mist testdata.hdf5

mist testdata.hdf5

mip_mrist_Thidden

mip_mrist_Thiden

mip_
```

After calculating the gradient, update w in the opposite direction of the gradient

$$\omega^{n+1} = \omega^n - \alpha \nabla C(\omega^n)$$

```
1.
      # Parameter update
      def gradient_update(y_truth_matrix, w_current, layer_output, layer_input, alpha, L1_
reg, L2_reg):
          if len(w current) > 1:
3.
4.
              # Calculate the gradient using backpropagation
5.
              grad_w = back(layer_output, layer_input, w_current, y_truth_matrix, L1_reg,
L2_reg)
6.
              # Parameter update
7.
              new_w = [w - nw * alpha for w, nw in zip(w_current, grad_w)]
8.
9.
          return new w
```

# • Gradient descent

```
1.
      # Gradient descent
2.
      def gradient_descent(x, y, w_initial, alpha, L1_reg, L2_reg):
3.
          w = w_initial
4.
5.
          y_truth_matrix = truth_label_matrix(y)
6.
          # Forward propagation to get model prediction value
7.
          layer_output, layer_input = forward(x, w)
8.
9.
          probabilities = layer_output[-1]
          if L1_reg != 0.00:
10.
              L1 = sum([abs(w_i).sum() for w_i in w]) # L1 norm
11.
          else:
12.
              L1 = 0
13.
14.
          if L2_reg != 0.00:
              L2\_sqr = sum([(w_i ** 2).sum() for w_i in w]) # L2 norm
15.
          else:
16.
17.
              L2_sqr = 0
18.
          # Total loss = negative log likelihood cost + regularization penalty
19.
20.
          cost = loss_function(probabilities, y) + L1_reg * L1 + 0.5 * L2_reg * L2_sqr #
Error before weight w update
21.
22.
          # Update parameters
23.
          w = gradient_update(y_truth_matrix, w, layer_output, layer_input, alpha, L1_reg,
 L2_reg)
24.
25.
          return (w, cost)
```

# Validation and testing model

# Code:

```
def model_validation(valid_set_x, valid_set_y, W):
1.
2.
          p_y_given_valid_x = forward(valid_set_x, W)[0][-1]
3.
          valid_y_pred = pred_num_lable(p_y_given_valid_x)
4.
          cost_valid = loss_function(p_y_given_valid_x, valid_set_y)
5.
          error_num_valid = error_num(valid_y_pred, valid_set_y)
          return (cost_valid, error_num_valid)
6.
7.
8.
      def model_test(test_set_x, test_set_y, W):
9.
10.
          p_y_given_test_x = forward(test_set_x, W)[0][-1]
11.
          test_y_pred = pred_num_lable(p_y_given_test_x)
12.
          error_num_test = error_num(test_y_pred, test_set_y)
13.
          test_precision = 1 - error_num_test / test_set_x.shape[0]
14.
          return test_precision
```

# Model construction and optimization

```
# Specify hyperparameters
alpha = 0.005  # learning rate
epochs = 1000  # epoch num
threshold = 0.00001  # Gradient descent early stop threshold
batch_size = 300  # batch size

L1_reg = 0.00  # L1 regularization parameters

L2_reg = 0.001  # L2 regularization parameters

L2_reg = 0.001  # L2 regularization parameters

# 初始化权重w
input_layer_num = 784  # input layer number
output_layer_num = 10  # output layer number
hidden_layer_num = [500]  # hidden layer number
rand = np.random.RandomState(int(time.time()))
W = hidden_layer(input_layer_num, output_layer_num, hidden_layer_num, rand)  # Initialize connection weight

# Model building and tuning
model_build(datasets, W, alpha, epochs, threshold, batch_size, L1_reg, L2_reg)
```

Train model

```
I:\Anaconda\python.exe C:/Users/123/Desktop/MLP/mlp_mnist_1hidden.py
After gradient descent iteration 0 times, Accuracy is: 16.300000%
After gradient descent iteration 100 times, Accuracy is: 65.250000%
After gradient descent iteration 200 times, Accuracy is: 88.310000%
After gradient descent iteration 300 times, Accuracy is: 77.190000%
After gradient descent iteration 400 times, Accuracy is: 89.310000%
After gradient descent iteration 500 times, Accuracy is: 87.650000%
After gradient descent iteration 600 times, Accuracy is: 71.620000%
After gradient descent iteration 700 times, Accuracy is: 90.840000%
After gradient descent iteration 800 times, Accuracy is: 89.680000%
```

# Final result

```
After gradient descent iteration 11500 times, Accuracy is: 94.450000%

After gradient descent iteration 11600 times, Accuracy is: 94.150000%

After gradient descent iteration 11700 times, Accuracy is: 92.440000%

The error on the validation set no longer decreases, and the model training ends

The accuracy of the model on the test set is: 94.030000%
```

# 2 Implement Modified Quadratic Discriminant Function (MQDF) on MNIST

The MQDF model is a classifier based on Bayesian decision theory. Its discriminant function is given as below:

$$\begin{split} g_0(\mathbf{x}, \omega_i) &= -(\mathbf{x} - \mu_i)^T \Sigma_i^{-1} (\mathbf{x} - \mu_i) - \log \left| \Sigma_i \right| \\ &= -[\Phi_i^T (\mathbf{x} - \mu_i)]^T \Lambda_i^{-1} \Phi_i^T (\mathbf{x} - \mu_i) - \log \left| \Sigma_i \right| \\ &= -\sum_{j=1}^d \frac{1}{\lambda_{ij}} [(\mathbf{x} - \mu_i)^T \phi_{ij}]^2 - \sum_{j=1}^d \log \lambda_{ij} \end{split}$$

Design and implement a MQDF model to achieve the classification task on MNIST. Show the training process and classification results. The work in [1] can be used as reference for your work.

# Load data

```
data_class_list.add(int(row[-1]))
test_x.append(row[:-1])

class_num = len(data_class_list)
feature_num = len(train_x[0])

train_x = np.array(train_x, np.float64)
train_y = np.array(train_y, np.int)
test_x = np.array(test_x, np.float64)
test_y = np.array(test_y, np.int)

if scaled:
train_length = len(train_x)
x_whole = np.vstack((train_x, test_x))
from sklearn.preprocessing import scale
x_whole = scale(x_whole, axis=0, with_std=True)

train_x = x_whole[:train_length, :]
test_x = x_whole[train_length:, :]

print("Load data end!")
return class_num, feature_num, train_x, train_y, test_x, test_y
```

# K-L decomposition

Bayes decision theory is to judge the input sample into the category with the largest posterior probability (Maximum A Posterior, MAP). The quadratic discriminant function (QDF) is the specific manifestation of Bayes decision when the input data meets the Gaussian distribution.

According to Bayes' criterion, the posterior probability of the input sample x belonging to the category is:

$$P(\omega_i|x) = \frac{P(\omega_i)p(x|\omega_i)}{p(x)}$$
1 - 1

The Bayes criterion can become:

$$x \in \omega_k = agr \min g_{qdf}(x, \omega_i)$$
 1 – 2

among them :

$$g_{qdf}(x,\omega_i) = (x - \mu_i)^t \sum_{i=1}^{-1} (x - \mu_i) + \ln|\Sigma_i|$$
 1 - 3

Using K-L decomposition, the covariance matrix  $\Sigma_i$  can be decomposed into the following form:

$$\Sigma_i = P_i \wedge_i P_i^t \qquad 1 - 4$$

Among them  $\Lambda_i = diag(\lambda_{i,1}, \lambda_{i,2}, ..., \lambda_{i,d}), P_i = (p_{i,1}, p_{i,2}, ..., p_{i,d}), \lambda_{i,j}$  are the j-th eigenvalue of  $p_{i,j}$ , and D is the corresponding eigenvector. Bringing 1-4 into equation 1-3, there are:

$$g_{qdf}(x,\omega_i) = \sum_{j=1}^d \frac{\left[ (x - \mu_i)^t p_{i,j} \right]^2}{\lambda_{i,j}} + \sum_{j=1}^d \ln \lambda_{i,j}$$
 1 - 5

```
def MQDF(class_num, train_x, train_y, k):
    feature_num_ = len(train_x[0]) # number of features
    assert(k<feature_num_ and k>0)
        class_index = int(train_y[i])
        data[class_index].append(train_x[i])
    mean = []
    cov_matrix = []
    prior = []
                                                                                                                           A3 A44 ×
       cov_matrix.append(np.matrix(np.cov(data[i].T)))
   eigenvalue_list = []  # store the first largest k eigenvalue_lists of each class
eigenvector_list = []  # the first largest k eigenvector_lists, column-wise of each class
       covariance = cov_matrix[i]
       eig_value, eig_vector = linalg.eigh(covariance)
        eig_value = eig_value[index_]
       eig_vector = eig_vector[:, index_]
       eigenvector_list.append(eig_vector[:, 0:k])
        eigenvalue_list.append(eig_value[:k])
```

```
delta
[matrix([[1753.8439463]]), matrix([[497.17054524]]), matrix([[2260.74667863]]), matrix([[1929.4408
```

# MQDF predict

The parameters required by the QDF classifier can be obtained from the training data according to the maximum likelihood estimation. In comparison, the training is relatively simple and direct, and can obtain high accuracy, so it is widely used in practice. But when the input feature dimensionality is high and the training data is insufficient, there will be a curse of dimensionality phenomenon, which is manifested in the QDF classifier, which is an estimation error. It can be seen from formula (1-5) that for eigenvalues, the same estimation error has a much greater impact on the result when the eigenvalue is smaller than when the eigenvalue is larger.

$$g_2(x,\omega_i) = \frac{1}{h_i^2} \left\{ ||x - \mu_i||^2 - \sum_{j=1}^k \left(1 - \frac{h_i^2}{\lambda_i}\right) \left[ (x - \mu_i)^t p_{ij} \right]^2 + \sum_{j=1}^k \ln \lambda_i + (d - k) \ln h_i^2 \right\}$$

## Code:

```
# formula
              for i in range(class_num):
4.
                  minus = np.linalg.norm(x.reshape((d,)) - mean[i].reshape((d,))) ** 2
5.
                  matrix_minus = [0] * d
                  for j in range(k):
7.
                      matrix_minus[j] = (((x - mean[i]).T * eigenvector_list[i][:, j])[0,0
])**2
8.
                  g = 0
10.
                  for j in range(k):
                      g += (matrix_minus[j] * 1.0 / eigenvalue_list[i][j])
12.
                  g += ((minus - sum(matrix_minus)) / delta[i])
13.
14.
15.
                  for j in range(k):
                      g += math.log(eigenvalue_list[i][j])
16.
17.
18.
                  g += ((d - k) * math.log(delta[i]))
19.
20.
21.
                  if g < min_posteriori:</pre>
22.
                      min_posteriori = g
23.
                      prediction = i
```

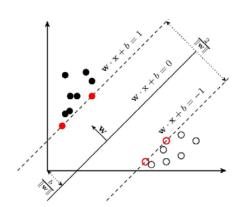
## Result:

# Accuracy

Code running: 0.60min Final correct: 94.38

# 3 Implement Support Vector Machine (SVM) on MNIST

A Support Vector Machine constructs a hyperplane or set of hyperplanes in a high- or infinitedimensional space, which can be used for classification, regression, or other tasks.



$$\begin{aligned} & \max. \ W(\alpha) = \sum_{i=1}^n \alpha_i - \frac{1}{2} \sum_{i=1,j=1}^n \alpha_i \alpha_j y_i y_j K(\mathbf{x}_i, \mathbf{x}_j) \\ & b = 1 - \frac{1}{|i:0 < \alpha_i < C|} \sum_{i:0 < \alpha_i < C} \sum_{j=1}^s \alpha_j y_j k(\mathbf{x}_j, \mathbf{x}_i) \\ & C \ge \alpha_i \ge 0, \sum_{i=1}^n \alpha_i y_i = 0 \end{aligned}$$

Polynomial Kernel:  $k(\mathbf{x}_1, \mathbf{x}_2) = (\mathbf{x}_1^T \mathbf{x}_2 + 1)^d$ 

RBF Kernel:  $k(\mathbf{x}_1, \mathbf{x}_2) = \exp(-||\mathbf{x}_1 - \mathbf{x}_2||^2/2s^2)$ 

Github is a good choice for searching codes (<a href="https://github.com">https://github.com</a>/prashantkh19/MNIST\_SVM. Adjust and modify the codes to implement two SVM models with Polynomial Kernel and RBF Kernel respectively on MNIST. Show the training process and classification results.

## A. Principle

Describe sklearn definition and parameters of SVM.

Here we choose SVC, which means using SVM for classification. The specific use is here. About the introduction of the parameters in the code:

$$\triangleright$$
 C = 1.0

$$L(w, b, \xi, \alpha, \beta) := \frac{1}{2} w^T w + C \sum_{i=1}^{m} \xi_i + \sum_{i=1}^{m} \alpha_i (1 - \xi_i - y_i (w^T \emptyset(x_i) + b)) + \sum_{i=1}^{m} \beta_i (-\xi_i)$$

It can be seen that C is used to balance structural risk and experience risk.

## kernel='rbf'

Specifies the kernel type to be used in the algorithm.

It must be one of 'linear', 'poly', 'rbf', 'sigmoid', 'precomputed' or a callable.

If none is given, 'rbf' will be used. If a callable is given it is used to pre-compute the kernel matrix from data matrices; that matrix should be an array of shape ``(n\_samples, n\_samples)``.

# gamma='scale'

Kernel coefficient for 'rbf', 'poly' and 'sigmoid'.

if ``gamma='scale'`` (default) is passed then it uses:

$$\gamma = \frac{1}{(n\_features * X.var())}$$

if 'auto', uses:

$$\frac{1}{n\_features}$$

## B. Code and Result

## Load data

```
1.
      def load_data():
2.
3.
          Return pattern recognition data containing tuples of training data, verification
 data, and test data
          The training data contains 50,000 pictures, and the test data and verification d
ata only contain 10,000 pictures
5.
          f = gzip.open('mnist.pkl.gz', 'rb')
6.
7.
          training_data, validation_data, test_data = pickle.load(f, encoding='bytes')
8.
          f.close()
9.
          print("load dataset successful")
10.
          return (training_data, validation_data, test_data)
```

# • SVM

## Code:

```
1. # Pass the parameters of the training model
2. clf = svm.SVC(C=100.0, kernel='rbf', gamma=0.03)
3.
4. # model train
5. clf.fit(training_data[0], training_data[1])
6.
7. # test
8. predictions = [int(a) for a in clf.predict(test_data[0])]
9. num_correct = sum(int(a == y) for a, y in zip(predictions, test_data[1]))
```

#### Result:

```
I:\Anaconda\python.exe C:/Users/123/Desktop/SVM/SVM_RBF.py
start SVM
start load data
load dataset successful
num of correct
9848
SVM end
9848 of 10000 test values correct.
The accuracy rate is 0.9848.
Code running10.17min
```

# Change kernel

Code:

```
    # Pass the parameters of the training model
    clf = svm.SVC(C=100.0, kernel='poly', gamma=0.03)
```

Result:

# 4 Analysis and Comparison

Analyze and compare the advantages and disadvantages of these three models in classification from different aspects, such as effectiveness, efficiency, complexity. Your analysis and conclusion should be well justified theoretically and/or empirically.

	time	accuracy	CPU utilization(i5-1021U)		
MLP	42min	94.86	95%		
MQDF	1.36min	95.53	30%		
SVM RBF	7.96min	98.48	30%		
SVM poly	2.46min	97.78	29%		

The MLP algorithm requires a large number of back propagation and gradient descent processes, so the gradient descent threshold becomes the main parameter that determines the time complexity of the entire algorithm. We can see that the MLP algorithm consumes a lot of time and occupies a lot of CPU because it has a large number of calculation processes and the overall space complexity is very high.

Because MQDF is a Bayesian classification algorithm, it is a kind of lazy algorithm. It does not need train and only uses calculation accuracy. Therefore, MQDF has good time complexity, runs fast, and has accuracy very high.

For SVM, the support vector is the training result of the SVM, and it is the support vector that plays a decisive role in the SVM classification decision. In essence, it avoids the traditional process from induction to deduction, realizes efficient "transduction inference" from training samples to

forecast samples, and greatly simplifies the usual classification and regression problems. The final decision function of SVM is determined by only a few support vectors, and the complexity of the calculation depends on the number of support vectors, not the dimensionality of the sample space, which avoids the "dimension disaster" in a sense. Therefore, the time consumption corresponding to different kernels is also different.

# 4 Comparison and improvement

# A. Processing of data sets

## i. PKL

Because in the program, directly importing the IDX FILE FORMAT format database is more troublesome, so the database should be preprocessed in advance and processed as Numpy format and transferred to B format.

- .pkl data file: In Python, the Pickle module converts any Python object into a system byte, similar to the JSON format, but not readable by humans.
- ➤ One-hot encoding: Use n bits to express n states, the correct state is expressed by 1, and the others are all 0. For example, 2 is represented as [0,0,1,0,0,0,0,0,0]
- """Read into the MNIST data set

#### **Parameters**

-----

normalize: Normalize the pixel value of the image to 0.0~1.0

one\_hot\_label:

When one\_hot\_label is True, the label is returned as a one-hot array

One-hot array refers to an array like [0,0,1,0,0,0,0,0,0,0]

flatten: whether to expand the image into a one-dimensional array

Returns

-----

(Training image, training label), (test image, test label)

\*\* \*\* \*

# Code and Result:

lacktriangle

```
1. # Record data set location
2. url_base = 'http://yann.lecun.com/exdb/mnist/'
3. key_file = {
4. 'train_img': 'train-images-idx3-ubyte.gz',
5. 'train_label': 'train-labels-idx1-ubyte.gz',
6. 'test_img': 't10k-images-idx3-ubyte.gz',
7. 'test_label': 't10k-labels-idx1-ubyte.gz'
8. }
```

# Result:

```
[2]: # Record data set location
url_base = 'http://yann.lecun.com/exdb/mnist/'
key_file = {
    'train_img': 'train-images-idx3-ubyte.gz',
    'test_img': 't10k-images-idx3-ubyte.gz',
    'test_label': 't10k-labels-idx1-ubyte.gz',
    'test_label': 't10k-labels-idx1-ubyte.gz'
}

[4]: display(key_file)
{'train_img': 'train-images-idx3-ubyte.gz',
    'train_label': 'train-labels-idx1-ubyte.gz',
    'test_img': 't10k-images-idx3-ubyte.gz',
    'test_label': 't10k-labels-idx1-ubyte.gz'}
```

```
1.     def _change_one_hot_label(X):
2.         T = np.zeros((X.size, 10))
3.         for idx, row in enumerate(T):
4.             row[X[idx]] = 1
5.
6.         return T
```

```
def load mnist(normalize=True, flatten=True, one hot label=False):
1.
2.
          if not os.path.exists(save_file):
3.
4.
              init_mnist()
5.
6.
          with open(save_file, 'rb') as f:
7.
              dataset = pickle.load(f)
8.
9.
          if normalize:
              for key in ('train_img', 'test_img'):
10.
11.
                  dataset[key] = dataset[key].astype(np.float32)
12.
                  dataset[key] /= 255.0
13.
14.
          if one_hot_label:
              dataset['train_label'] = _change_one_hot_label(dataset['train_label'])
15.
              dataset['test_label'] = _change_one_hot_label(dataset['test_label'])
16.
17.
18.
          if not flatten:
19.
              for key in ('train_img', 'test_img'):
20.
                  dataset[key] = dataset[key].reshape(-1, 1, 28, 28)
21.
22.
          return (dataset['train_img'], dataset['train_label']), (dataset['test_img'], dat
aset['test_label'])
```

```
Done
Converting train-labels-idx1-ubyte.gz to NumPy Array ...

Done
Converting t10k-images-idx3-ubyte.gz to NumPy Array ...

Done
Converting t10k-labels-idx1-ubyte.gz to NumPy Array ...

Done
Creating pickle file ...

Done!
```





.py









mnist.pkl

t10k-images-idx 3-ubyte.gz

t10k-labels-idx1 -ubyte.gz

train-images-id x3-ubyte.gz

train-labels-idx1 -ubyte.gz

# ii. CVS

Code:

```
def convert(imgf, labelf, outf, n):
1.
          f = open(imgf, "rb")
2.
          o = open(outf, "w")
3.
          1 = open(labelf, "rb")
4.
5.
6.
          f.read(16)
7.
          1.read(8)
8.
          images = []
9.
          for i in range(n):
10.
              image = [ord(l.read(1))]
11.
              for j in range(28*28):
12.
                  image.append(ord(f.read(1)))
13.
              images.append(image)
14.
15.
16.
          for image in images:
              o.write(",".join(str(pix) for pix in image)+"\n")
17.
18.
          f.close()
19.
          o.close()
20.
          1.close()
21.
22.
      convert("MNIST/train-images.idx3-ubyte", "MNIST/train-labels.idx1-ubyte",
              "mnist_train.csv", 60000)
23.
      convert("MNIST/t10k-images.idx3-ubyte", "MNIST/t10k-labels.idx1-ubyte",
24.
              "mnist_test.csv", 10000)
25.
26.
27.
      print("Convert Finished!")
```

# Result:



# **B.** MLP parameter improvements

We have set certain hyperparameters in the program, we can change them to get the best prediction effect.

```
def mlp(datasets):

# Specify hyperparameters

alpha = 0.005  # learning rate

epochs = 1000  # epoch num

threshold = 0.00001  # Gradient descent early stop threshold

batch_size = 300  # batch size

L1_reg = 0.00  # L1 regularization parameters

L2_reg = 0.001  # L2 regularization parameters
```

alpha	0.001	0.005	0.01	0.015	0.02	0.05	0.1
accuracy	90.91	94.03	94.30	94.86	94.72	92.74	92.37

Activate function	sigmoid	tanh
accuracy	94.86	94.61
Time	42min	29min

# **C.** MQDF parameter improvements

K	2	4	6	8	10	12	14
accuracy	89.11	92.27	93.61	94.38	94.82	95.07	94.88

# **D.** SVM parameter improvements

Ensure that other parameters remain unchanged

gamma	0.01	0.02	0.03	0.04	0.05	0.06
accuracy	0.9823	0.9847	0.9848	0.984	0.9828	0.9804

# 5 Conclusion

We can see that the accuracy of the three strategies is already ideal, but the time consumed by the three strategies and the size of the model are very different, depending on the internal algorithms corresponding to the different strategies. Moreover, under a certain strategy, adjusting the parameters can often achieve a relatively good predictive value.

# **REFERENCES**

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