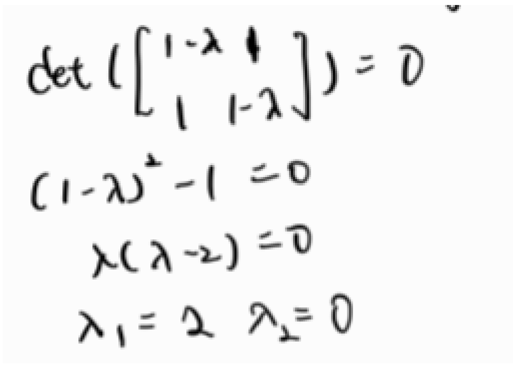
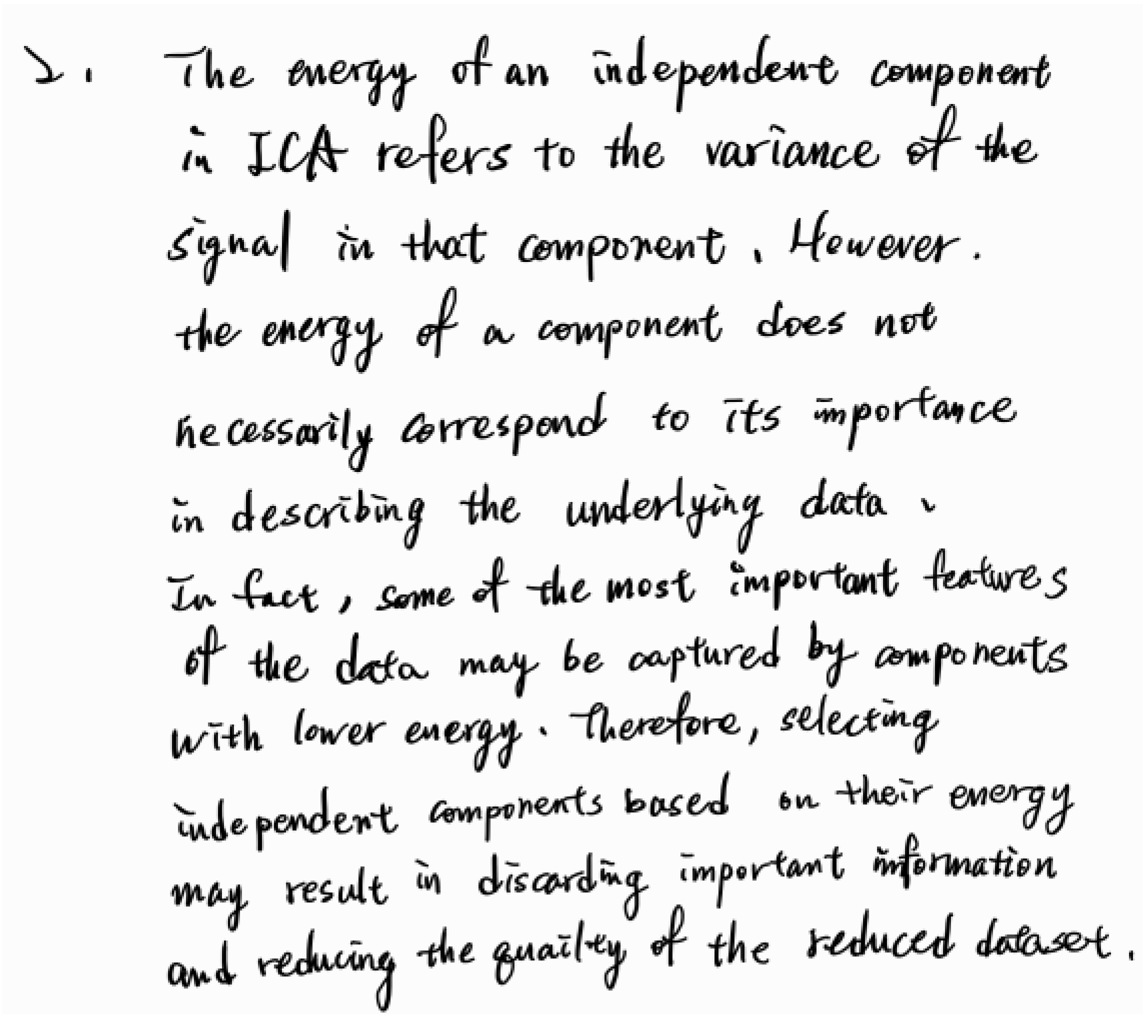
Machine learning : HW 04 王上澤 111598067

1. Since the two attribute are jointly Guassian, we can know that the first principal componentis a linear combination of original attributes, and its length is equal to the square root of the largest eigenvalue of the covariance matrix.
   - compute the largest eigenvalue = 2 from :

     $$\det\left(\begin{bmatrix} 1-\lambda & 1 \\ 1 & 1-\lambda \end{bmatrix}\right) = 0$$
     $$(1-\lambda)^2 - 1 = 0$$
     $$\lambda(\lambda - 2) = 0$$
     $$\lambda_1 = 2 \quad \lambda_2 = 0$$
   - calculate the tatol variance of data : 0+2 = 2
   - PoV(1) = 2/2 = 1, which is bigger than threshold 0.9 .
   - Can we answer the question without computing eigenvalues? Yes! We can use SVD to solve this problem when we encounter the numeric problem in computing the eigenvalue of (X transpose)X.

2. 

   2. The energy of an independent component in ICA refers to the variance of the signal in that component. However. the energy of a component does not necessarily correspond to its importance in describing the underlying data. In fact, some of the most important features of the data may be captured by components with lower energy. Therefore, selecting independent components based on their energy may result in discarding important information and reducing the quailty of the reduced dataset.

3. There are only two classes need to be classified, so we only have to project data to one dimentional space to determined which class is it.

4. Code of the first part :

```python
import pandas as pd

from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.decomposition import PCA
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score

cancer_data = pd.read_csv("../data/breast-cancer-wisconsin.data",
                        names=[i for i in range(11)])
cancer_data = cancer_data.drop(cancer_data.columns[0], axis=1)
cancer_data = cancer_data.replace(to_replace='?', value=pd.NA)

## remove the row that miss the attribute
cancer_data.dropna(inplace = True)
cancer_data = cancer_data.reset_index(drop=True)

# model
model = PCA(
    n_components=9
)

# fit the data
model.fit_transform(cancer_data)

# show the PoV
explain = model.explained_variance_ratio_.cumsum()
for i in range(len(explain)):
    print("{0} component's PoV : {1}".format(i+1, explain[i]))
```

output of the first part :

```
1 component's PoV : 0.6922791476392942 X
2 component's PoV : 0.7634330286918276 X
3 component's PoV : 0.8232826582399932 X
4 component's PoV : 0.8671645576031523 X
5 component's PoV : 0.9056767881037053 O
6 component's PoV : 0.9396796501298136 O
7 component's PoV : 0.9646552635230422 O
8 component's PoV : 0.9868358860997716 O
9 component's PoV : 0.998052210224642 O
```

We can see that after 5 conponents result, the PoV of it start to bigger than the threshold (0.9). Code of Second part :

```
import pandas as pd

from numpy import average
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.ensemble import RandomForestClassifier
from sklearn.decomposition import PCA
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score

cancer_data = pd.read_csv("../data/breast-cancer-wisconsin.data",
                        names=[i for i in range(11)])
cancer_data = cancer_data.drop(cancer_data.columns[0], axis=1)
cancer_data = cancer_data.replace(to_replace='?', value=pd.NA)

## remove the row that miss the attribute
cancer_data.dropna(inplace = True)
cancer_data = cancer_data.reset_index(drop=True)

# split the data
data_train, data_test, target_train, target_test = train_test_split(
    cancer_data[[i for i in range(1, 10)]], cancer_data[10], test_size=0.3
    )


# iterate from 1 to 9 and show the accuracy of it
for n_component in range(1,10):
    accurs = []
    for iter in range(10):
        # split the data
        data_train, data_test, target_train, target_test = train_test_split(
            cancer_data[[i for i in range(1, 10)]], cancer_data[10],
test_size=0.3
        )
        model = PCA(n_components=n_component)
        data_train = model.fit_transform(data_train)
        data_test = model.transform(data_test)

        # random forest classifier
        classifier = RandomForestClassifier()
        classifier.fit(data_train, target_train)

        target_pred = classifier.predict(data_test)
        accurs.append(accuracy_score(target_test, target_pred))
    print("10 times accuracy = {0}  \tin choosing {1} components."
        .format(str(average(accurs)), n_component))
```

Output of Second part :

```
10 times accuracy = 0.9541463414634146          in choosing 1 components.
10 times accuracy = 0.9668292682926829          in choosing 2 components.
10 times accuracy = 0.9717073170731705          in choosing 3 components.
10 times accuracy = 0.9790243902439025          in choosing 4 components.
10 times accuracy = 0.9717073170731707          in choosing 5 components.
10 times accuracy = 0.9712195121951218          in choosing 6 components.
10 times accuracy = 0.9697560975609754          in choosing 7 components.
10 times accuracy = 0.9697560975609754          in choosing 8 components.
10 times accuracy = 0.9746341463414634          in choosing 9 components.
```

5. Code :

```
import numpy as np
import pandas as pd

from sklearn.model_selection import train_test_split
from sklearn.decomposition import FactorAnalysis
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score


url = "https://archive.ics.uci.edu/ml/machine-learning-
databases/iris/iris.data"
names = ['sepal-length', 'sepal-width', 'petal-length', 'petal-width',
'Class']
dataset = pd.read_csv(url, names=names)

# preprocessing
X = dataset.drop('Class', axis = 1)
y = dataset['Class']
# 10 times iteration
for i in range(10):
    # Splitting the dataset into the Training set and Test set
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3)

    fa = FactorAnalysis(n_components=3)
    X_train = fa.fit_transform(X_train)
    X_test = fa.transform(X_test)

    classifier = KNeighborsClassifier(n_neighbors=5)
    classifier.fit(X_train, y_train)

    # Predicting the Test set results
    y_pred = classifier.predict(X_test)
    print('Accuracy ' + str(accuracy_score(y_test, y_pred)), str(i),
"iteration")
```

Output :

```
Accuracy 0.9333333333333333 0 iteration
Accuracy 0.8444444444444444 1 iteration
Accuracy 0.9333333333333333 2 iteration
Accuracy 0.9111111111111111 3 iteration
Accuracy 0.9111111111111111 4 iteration
Accuracy 0.8444444444444444 5 iteration
Accuracy 0.9333333333333333 6 iteration
Accuracy 0.9555555555555556 7 iteration
Accuracy 0.9777777777777777 8 iteration
Accuracy 0.9333333333333333 9 iteration
```