## **Assignment 2, Data Mining**

Put all deliverables into github repository in your profile. Share link to google form 24 hours before defense. Defend by explaining deliverables and answering questions.

Deliverables: .ipynb

 $Google\ form: \underline{https://docs.google.com/forms/d/e/1FAIpQLSe0GyNdOYIvM1tX\_I\_CtlPod5jBf-line form: \underline{https://docs.google.com/forms/d/e/1F$ 

ACLGdHYZq1gVZbUeBzIg/viewform?usp=sf link

### Exercise 1: Feature Selection with SelectKBest

**Objective**: Use SelectKBest from scikit-learn to select the top k features from a dataset.

- 1. Load the Iris dataset from scikit-learn.
- 2. Split the dataset into features and target variable.
- 3. Use SelectKBest with the chi2 score function to select the top 2 features.
- 4. Print the selected feature names.

```
In [1]: import pandas as pd
from sklearn.datasets import load_iris
from sklearn.feature_selection import SelectKBest, chi2

iris = load_iris()
X = iris.data
y = iris.target

df_X = pd.DataFrame(X, columns=iris.feature_names)

s = SelectKBest(score_func=chi2, k=2)
X_new = s.fit_transform(X, y)

mask = s.get_support()

selected_features = df_X.columns[mask]
print("Выбранные признаки:", selected_features)

Выбранные признаки: Index(['petal length (cm)', 'petal width (cm)'], dtype='object')
```

# **Exercise 2: Feature Importance with Random Forest**

**Objective**: Use a Random Forest classifier to determine feature importance.

- 1. Load the Wine dataset from scikit-learn.
- 2. Split the dataset into training and testing sets.
- 3. Train a Random Forest classifier on the training data.
- 4. Extract and visualize feature importances.

```
In [1]: import pandas as pd
            import pandas as pd
from sklearn.datasets import load_wine
from sklearn.feature_selection import SelectKBest, chi2
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
import matplotlib.pyplot as plt
import numby as plt
            import numpy as np
            X = pd.DataFrame(data.data, columns=data.feature_names)
y = data.target
            data = load_wine()
            print(X.head())
            print()
print(X.info())
                 alcohol malic_acid
14.23 1.71
                                                         alcalinity_of_ash
15.6
                                                                                     magnesium
127.0
                                                  ash
                                                                                                      total_phenols \
                                                2.43
                                                                                                                   2.80
2.65
                                               2.14
2.67
2.50
2.87
                    13.20
                                       1.78
                                                                             11.2
                                                                                            100.0
            1
2
3
                    13.16
14.37
                                       2.36
1.95
                                                                             18.6
16.8
                                                                                            101.0
113.0
                                                                                                                   2.80
3.85
            4
                    13.24
                                       2.59
                                                                             21.0
                                                                                            118.0
                                                                                                                    2.80
                                                                                             color_intensity
5.64
4.38
                 flavanoids
                                 nonflavanoid_phenols
                                                                   proanthocyanins
                         3.06
2.76
                                                          0.28
0.26
                                                                                    2.29
1.28
                                                                                                                      1.04
1.05
            0
            1
2
                                                                                                             5.68
7.80
                          3.24
                                                                                    2.81
                                                                                                                      1.03
            3
4
                          3.49
2.69
                                                                                    2.18
1.82
                                                                                                                      0.86
1.04
                                                           0.24
                                                           0.39
                                                                                                              4.32
                 od280/od315_of_diluted_wines
                                                             proline
                                                    3.92
                                                    3.40
3.17
                                                               1050.0
                                                               1185.0
            3
4
                                                    3.45
                                                               1480.0
                                                    2.93
                                                                 735.0
            <class 'pandas.core.frame.DataFrame'>
RangeIndex: 178 entries, 0 to 177
Data columns (total 13 columns):
                                                                 Non-Null Count Dtype
             #
                   Column
             0
                    alcohol
                                                                 178 non-null
                                                                                         float64
                   malic_acid
                                                                 178 non-null
             1
                                                                                         float64
                                                                 178 non-null
                                                                                         float64
                    alcalinity_of_ash
                                                                 178 non-null
178 non-null
                                                                                         float64
float64
                    magnesium 
                    total_phenols
                                                                 178 non-null
                                                                                         float64
                    flavanoids
nonflavanoid_phenols
             6
7
                                                                 178 non-null
                                                                                         float64
                                                                 178 non-null
                                                                                         float64
                    proanthocyanins
                                                                 178 non-null
                                                                                         float64
                    color_intensity
                                                                 178 non-null
                                                                                         float64
                                                                 178 non-null
                                                                                         float64
                    od280/od315_of_diluted_wines
                                                                 178 non-null
178 non-null
             11
                                                                                         float64
```

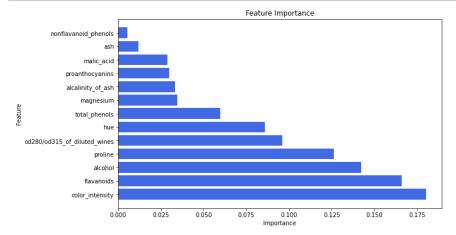
float64

12 proline

None

dtypes: float64(13) memory usage: 18.2 KB

```
In [2]: X1, X2, y1, y2 = train_test_split(X, y, test_size=0.3, random_state=42)
          print(f"Train sets: {X1.shape}")
print(f"Test sets: {X2.shape}")
          Train sets: (124, 13)
          Test sets: (54, 13)
 In [4]: # RandomForest
          rf = RandomForestClassifier(random_state=42)
          rf.fit(X1, y1)
 Out[4]: RandomForestClassifier(random_state=42)
 In [8]: importances = rf.feature_importances_ # Извлечение важности признаков
          fi_df = pd.DataFrame({
               'Feature': X.columns,
               'Importance': importances
          })
          fi_df = fi_df.sort_values(by='Importance', ascending=False)
          print(fi_df)
                                      Feature
                                                Importance
          9
                             color_intensity
                                                  0.180198
          6
                                   flavanoids
                                                  0.165947
          0
                                      alcohol
                                                  0.142041
                                                  0.126080
                                      proline
          12
          11
              od280/od315_of_diluted_wines
                                                  0.096032
          10
                                                  0.085966
                                          hue
          5
                               total_phenols
                                                  0.059758
          4
                                    magnesium
                                                  0.034673
          3
                           alcalinity_of_ash
                                                  0.033211
          8
                                                  0.029778
                             proanthocyanins
          1
                                  malic_acid
                                                  0.028976
          2
                                          ash
                                                  0.011859
                       nonflavanoid_phenols
                                                  0.005480
In [10]: plt.figure(figsize=(10, 6))
    plt.barh(fi_df['Feature'], fi_df['Importance'], color='royalblue')
          plt.xlabel('Importance')
          plt.ylabel('Feature')
plt.title('Feature Importance')
          plt.show()
```



## **Exercise 3: Recursive Feature Elimination (RFE)**

**Objective**: Use Recursive Feature Elimination (RFE) to select features and evaluate model performance.

- 1. Load the Breast Cancer dataset from scikit-learn.
- Split the dataset into training and testing sets.
- 3. Use RFE with a Support Vector Machine (SVM) classifier to select features.
- 4. Train an SVM model with the selected features and evaluate its performance.

```
In [1]: import pandas as pd
from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
                               from sklearn.feature_selection import RFE
from sklearn.metrics import accuracy_score
                                 data = load breast cancer()
                                 Value = Code | Columns = Column
                                 X1, X2, y1, y2 = train_test_split(X, y, test_size=0.2, random_state=42)
                                  svm_classifier = SVC(kernel="linear")
                                 rfe = RFE(estimator=svm_classifier, n_features_to_select=10)
rfe.fit(X1, y1)
                                  selected_features = X.columns[rfe.support_]
                                 print("Выбранные признаки:")
                                 print(selected_features)
                                 print()
                                X1_rfe = rfe.transform(X1)
X2_rfe = rfe.transform(X2)
                                 svm_classifier.fit(X1_rfe, y1)
                                y_pred = svm_classifier.predict(X2_rfe)
accuracy = accuracy_score(y2, y_pred)
                                 print(f"Точность модели: {accuracy:.2f}")
                                  Выбранные признаки:
                                 dtype='object')
                                 Точность модели: 0.97
```

# **Exercise 4: L1 Regularization for Feature Selection**

**Objective**: Use L1 regularization (Lasso) for feature selection.

- 1. Load the Diabetes dataset from scikit-learn.
- 2. Split the dataset into training and testing sets.
- 3. Apply Lasso regression for feature selection.
- 4. Train a model using selected features and evaluate its performance.

#### Classification Exercises

## **Exercise 1: Logistic Regression**

**Objective**: Build a logistic regression model to classify data.

- 1. Load the Iris dataset from scikit-learn.
- Split the dataset into training and testing sets.
- 3. Train a logistic regression model on the training set.
- 4. Evaluate the model's performance on the test set using accuracy and a confusion matrix.

```
In [1]:

from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split
from sklearn.model_import LogisticRegression
from sklearn.metrics import accuracy_score, confusion_matrix

iris = load_iris()
X = iris.data
y = iris.target

X1, X2, y1, y2 = train_test_split(X, y, test_size=0.2, random_state=42)

l = LogisticRegression(max_iter=200)
l.fit(X1, y1)

y_pred = l.predict(X2)
result = accuracy_score(y2, y_pred)
print(f"Точность модели: {result:.2f}")

matrix = confusion_matrix(y2, y_pred)
print("Матрица ошибок:")
print(matrix)

Tочность модели: 1.00
Матрица ошибок:
[[10 0 0]
[ 0 9 0]
[ 0 0 11]]
```

## **Exercise 2: Support Vector Machine (SVM)**

Objective: Use an SVM classifier to classify data.

- 1. Load the Breast Cancer dataset from scikit-learn.
- 2. Split the dataset into training and testing sets.
- 3. Train an SVM model on the training data.
- 4. Evaluate the model's performance on the test data using accuracy and a confusion matrix.

```
In [1]: from sklearn.datasets import load_breast_cancer from sklearn.model_selection import train_test_split from sklearn.swm import SVC from sklearn.swm import SVC from sklearn.metrics import accuracy_score, confusion_matrix

data = load_breast_cancer()
    X = data.data
    y = data.target

X1, X2, y1, y2 = train_test_split(X, y, test_size=0.2, random_state=42)
    svm_model = SVC()
    svm_model.fit(X1, y1)

y_pred = svm_model.predict(X2)

accuracy = accuracy_score(y2, y_pred)
    print(f"TOHHOCTD MODENU: {accuracy:.2f}")
print()

conf_matrix = confusion_matrix(y2, y_pred)
    print("Matphula ошибок:")
    print(conf_matrix)

TOHHOCTD MODENU: 0.95

Матрица ошибок:
[[37 6]
    [ 0 71]]
```

#### **Exercise 3: Decision Tree Classifier**

Objective: Build a decision tree classifier and visualize it.

- 1. Load the Wine dataset from scikit-learn.
- 2. Split the dataset into training and testing sets.
- 3. Train a decision tree classifier on the training set.

#### 4. Visualize the decision tree.

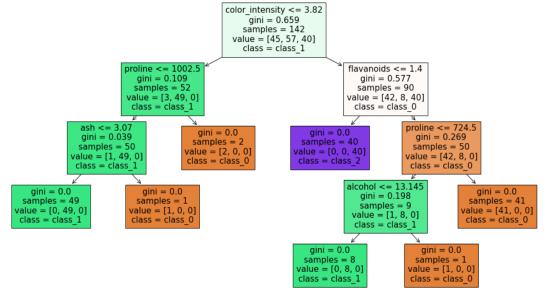
```
In [1]: from sklearn.datasets import load_wine
    from sklearn.model_selection import train_test_split
    from sklearn.tree import DecisionTreeClassifier
    from sklearn import tree
    import matplotlib.pyplot as plt

data = load_wine()
    X = data.data
    y = data.target

X1, X2, y1, y2 = train_test_split(X, y, test_size=0.2, random_state=42)

dtc = DecisionTreeClassifier(random_state=42)
    dtc.fit(X1, y1)

plt.figure(figsize=(20,10))
    tree.plot_tree(dtc, feature_names=data.feature_names, class_names=data.target_names, filled=True)
    plt.show()
```



# Regression Exercises

#### **Exercise 1: Linear Regression**

**Objective**: Build a linear regression model to predict a continuous target variable.

- 1. Load the Boston Housing dataset from scikit-learn.
- Split the dataset into training and testing sets.
- Train a linear regression model on the training set.

4. Evaluate the model's performance using mean squared error (MSE) and R-squared score.

```
In [2]: from sklearn.datasets import fetch_california_housing
    from sklearn.model_selection import train_test_split
    from sklearn.linear_model import LinearRegression
    from sklearn.metrics import mean_squared_error, r2_score

data = fetch_california_housing()
    X = data.data
    y = data.target

X1, X2, y1, y2 = train_test_split(X, y, test_size=0.2, random_state=42)

lr = LinearRegression()
    lr.fit(X1, y1)

y_pred = lr.predict(X2)

mse = mean_squared_error(y2, y_pred)
    print(f"(MSE): {mse:.2f}")

r2 = r2_score(y2, y_pred)
    print(f"(R²): {r2:.2f}")

(MSE): 0.56
    (R²): 0.58
```

### **Exercise 2: Ridge Regression**

**Objective**: Use Ridge regression to perform regularized linear regression.

- 1. Load the Diabetes dataset from scikit-learn.
- 2. Split the dataset into training and testing sets.
- 3. Train a Ridge regression model on the training set.
- 4. Evaluate the model's performance using mean squared error (MSE) and R-squared score.

```
In [1]: from sklearn.datasets import load_diabetes
from sklearn.model_selection import train_test_split
from sklearn.linear_model import Ridge
from sklearn.metrics import mean_squared_error, r2_score

data = load_diabetes()
X = data.data
y = data.target

X1, X2, y1, y2 = train_test_split(X, y, test_size=0.2, random_state=42)

ridge = Ridge(alpha=1.0)
ridge.fit(X1, y1)

y_pred = ridge.predict(X2)

mse = mean_squared_error(y2, y_pred)
r2 = r2_score(y2, y_pred)
print(f"(MSE): {mse:.2f}")
print(f"(R2): {r2:.2f}")

(MSE): 3077.41
(R2): 0.42
```

#### **Exercise 3: Decision Tree Regression**

**Objective**: Build a decision tree regression model and visualize it.

1. Load the Boston Housing dataset from scikit-learn.

- 2. Split the dataset into training and testing sets.
- 3. Train a decision tree regressor on the training set.
- 4. Evaluate the model's performance using mean squared error (MSE).
- 5. Visualize the decision tree.

```
In [1]: from sklearn.datasets import fetch_california_housing
    from sklearn.model_selection import train_test_split
    from sklearn.tree import DecisionTreeRegressor
    from sklearn.tree import plot_tree
    import matplotlib.pyplot as plt

data = fetch_california_housing()
    X = data.data
    y = data.target

X1, X2, y1, y2 = train_test_split(X, y, test_size=0.2, random_state=42)
    tree = DecisionTreeRegressor(random_state=42)
    tree.fit(X1, y1)

y_pred = tree.predict(X2)
    mse = mean_squared_error(y2, y_pred)
    print(f"(MSE): {mse:.2f}")

plt.figure(figsize=(20, 10))
    plot_tree(tree, filled=True, feature_names=data.feature_names, rounded=True, max_depth=3)
    plt.show()
```

(MSE): 0.50

