# STATS 3DA3

**Homework Assignment 6**

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```
import sys
!{sys.executable} -m pip install ucimlrepo
```

```
1266.67s - pydevd: Sending message related to process being replaced timed-out after 5 seconds
Requirement already satisfied: ucimlrepo in /opt/anaconda3/lib/python3.12/site-packages (0.0.7)
Requirement already satisfied: pandas>=1.0.0 in /opt/anaconda3/lib/python3.12/site-packages (fr
Requirement already satisfied: certifi>=2020.12.5 in /opt/anaconda3/lib/python3.12/site-package
Requirement already satisfied: numpy>=1.26.0 in /opt/anaconda3/lib/python3.12/site-packages (fr
Requirement already satisfied: python-dateutil>=2.8.2 in /opt/anaconda3/lib/python3.12/site-pac
Requirement already satisfied: pytz>=2020.1 in /opt/anaconda3/lib/python3.12/site-packages (fro
Requirement already satisfied: tzdata>=2022.7 in /opt/anaconda3/lib/python3.12/site-packages (f
Requirement already satisfied: six>=1.5 in /opt/anaconda3/lib/python3.12/site-packages (from py
```

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn import neighbors
from sklearn.preprocessing import scale
from sklearn.model_selection import train_test_split
from sklearn import metrics
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.metrics import mean_squared_error, confusion_matrix, classification_report, accura
from sklearn.tree import DecisionTreeClassifier, DecisionTreeRegressor, plot_tree

from ucimlrepo import fetch_ucirepo
```

(1)

The objective of this analysis is to build a supervised classification model that predicts whether a patient has heart disease using various clinical features such as age, cholesterol level, chest pain type,

and other diagnostic indicators. The target variable, num, is transformed into a binary outcome for classification purposes:

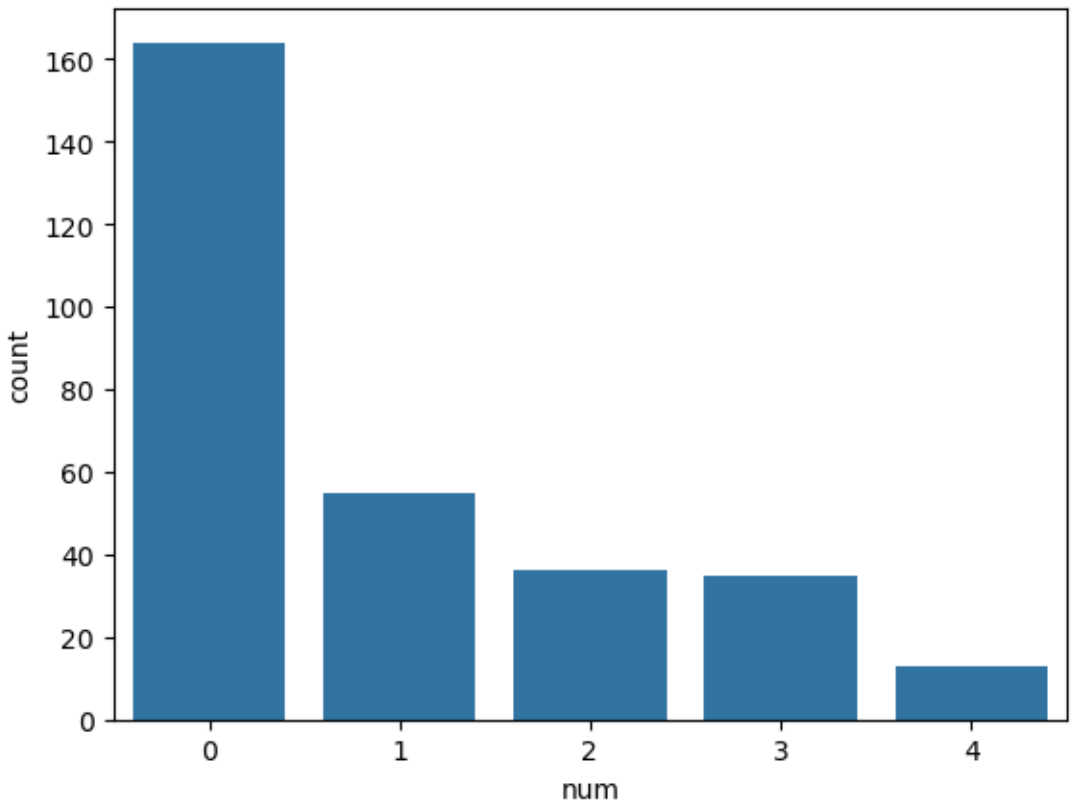
1 indicates the presence of heart disease

0 indicates no heart disease

```
heart_disease = fetch_ucirepo(id=45)


X = heart_disease.data.features
y = heart_disease.data.targets


df =heart_disease.data.original
```

(2)

```
sns.countplot(
 data=y,
 x = 'num'
 )
plt.show()
```




```
X = heart_disease.data.features
filtered_X_ori = df[X.columns]
filtered_y = df['num']
filtered_X = scale(filtered_X_ori)
df['num']= df['num'].astype('category')
```

Standardization is applied to numeric features to ensure fair contribution across features. This is important because clinical variables are measured on different scales. Without scaling, features with larger numeric ranges could dominate the model, especially in algorithms like KMeans clustering.

Target variable num is cast as a categorical variable for classification.

(3)

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

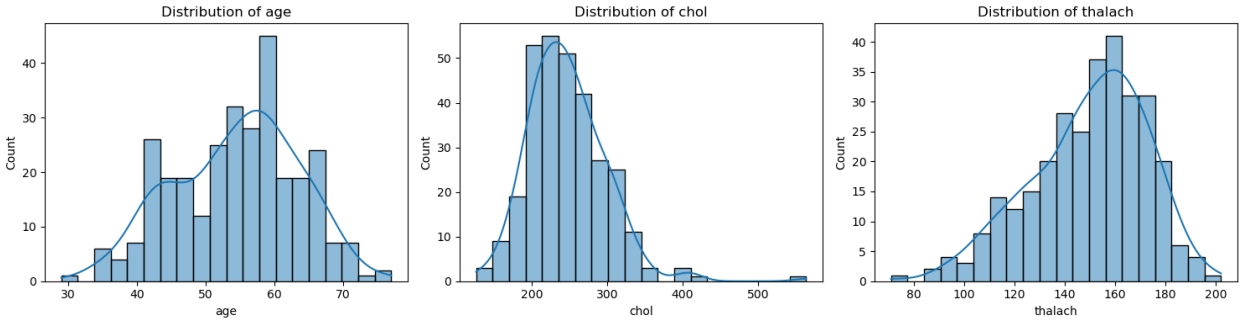
```
print(df.shape)

print(heart_disease.variables)

print(df.describe(include='all'))



numerical_features = ['age', 'chol', 'thalach']

plt.figure(figsize=(15, 4))
for i, feature in enumerate(numerical_features):
    plt.subplot(1, 3, i+1)
    sns.histplot(df[feature], kde=True, bins=20)
    plt.title(f'Distribution of {feature}')
plt.tight_layout()
plt.show()
```

```
(303, 14)
        name     role         type demographic  \
0        age  Feature      Integer         Age
1        sex  Feature  Categorical         Sex
2         cp  Feature  Categorical        None
3   trestbps  Feature      Integer        None
4       chol  Feature      Integer        None
5        fbs  Feature  Categorical        None
6    restecg  Feature  Categorical        None
7    thalach  Feature      Integer        None
8      exang  Feature  Categorical        None
9    oldpeak  Feature      Integer        None
10     slope  Feature  Categorical        None
11        ca  Feature      Integer        None
```

```
12      thal  Feature  Categorical        None
13       num   Target      Integer        None

                                          description  units missing_values
0                                                None  years             no
1                                                None   None             no
2                                                None   None             no
3   resting blood pressure (on admission to the ho...  mm Hg             no
4                                   serum cholestoral  mg/dl             no
5                    fasting blood sugar > 120 mg/dl   None             no
6                                                None   None             no
7                        maximum heart rate achieved   None             no
8                            exercise induced angina   None             no
9   ST depression induced by exercise relative to ...   None             no
10                                               None   None             no
11  number of major vessels (0-3) colored by flour...   None            yes
12                                               None   None            yes
13                         diagnosis of heart disease   None             no
              age         sex          cp    trestbps        chol  \
count   303.000000  303.000000  303.000000  303.000000  303.000000
unique         NaN         NaN         NaN         NaN         NaN
top            NaN         NaN         NaN         NaN         NaN
freq           NaN         NaN         NaN         NaN         NaN
mean     54.438944    0.679868    3.158416  131.689769  246.693069
std       9.038662    0.467299    0.960126   17.599748   51.776918
min      29.000000    0.000000    1.000000   94.000000  126.000000
25%      48.000000    0.000000    3.000000  120.000000  211.000000
50%      56.000000    1.000000    3.000000  130.000000  241.000000
75%      61.000000    1.000000    4.000000  140.000000  275.000000
max      77.000000    1.000000    4.000000  200.000000  564.000000

              fbs     restecg     thalach       exang     oldpeak  \
```

| | | | | | |
|---|---|---|---|---|---|
| count | 303.000000 | 303.000000 | 303.000000 | 303.000000 | 303.000000 |
| unique | NaN | NaN | NaN | NaN | NaN |
| top | NaN | NaN | NaN | NaN | NaN |
| freq | NaN | NaN | NaN | NaN | NaN |
| mean | 0.148515 | 0.990099 | 149.607261 | 0.326733 | 1.039604 |
| std | 0.356198 | 0.994971 | 22.875003 | 0.469794 | 1.161075 |
| min | 0.000000 | 0.000000 | 71.000000 | 0.000000 | 0.000000 |
| 25% | 0.000000 | 0.000000 | 133.500000 | 0.000000 | 0.000000 |
| 50% | 0.000000 | 1.000000 | 153.000000 | 0.000000 | 0.800000 |
| 75% | 0.000000 | 2.000000 | 166.000000 | 1.000000 | 1.600000 |
| max | 1.000000 | 2.000000 | 202.000000 | 1.000000 | 6.200000 |

| | slope | ca | thal | num |
|---|---|---|---|---|
| count | 303.000000 | 299.000000 | 301.000000 | 303.0 |
| unique | NaN | NaN | NaN | 5.0 |
| top | NaN | NaN | NaN | 0.0 |
| freq | NaN | NaN | NaN | 164.0 |
| mean | 1.600660 | 0.672241 | 4.734219 | NaN |
| std | 0.616226 | 0.937438 | 1.939706 | NaN |
| min | 1.000000 | 0.000000 | 3.000000 | NaN |
| 25% | 1.000000 | 0.000000 | 3.000000 | NaN |
| 50% | 2.000000 | 0.000000 | 3.000000 | NaN |
| 75% | 2.000000 | 1.000000 | 7.000000 | NaN |
| max | 3.000000 | 3.000000 | 7.000000 | NaN |




The dataset consists of 303 patient records and 14 clinical attributes, including the target variable

num, which indicates heart disease status.

It contains a mix of continuous variables,such as age, chol, and thalach and categorical variables encoded as integers, such as sex, cp, and fbs.

The dataset features are primarily represented as integers and floating-point numbers, while the target variable has been explicitly converted to a categorical type to support classification modeling. Although some categorical variables are stored as numeric values, they represent discrete categories rather than continuous measurements.

Distributions show variance across features, with values such as age ranges from 29 to 77 years with a mean around 54, and chol ranges from 126 to 564, which is slightly right-skewed.

(4)

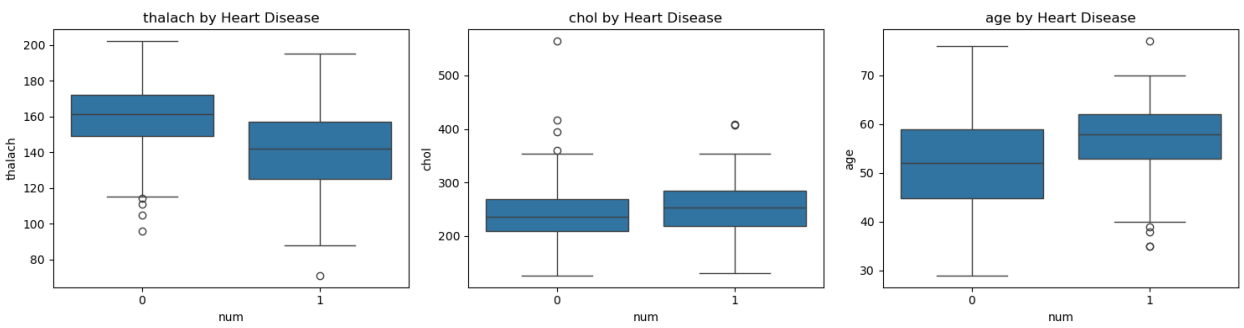
```
df['num'] = df['num'].apply(lambda x: 1 if x > 0 else 0).astype('category')
```

(5)

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

df_clean = filtered_X_ori.copy()
df_clean['num'] = filtered_y

df_clean = df_clean.dropna()

df_clean.loc[:, 'num'] = df_clean['num'].apply(lambda x: 1 if x > 0 else 0)

correlations = df_clean.corr(numeric_only=True)['num'].sort_values(ascending=False)
print("Correlation of features with heart disease:\n", correlations)

features_to_plot = ['thalach', 'chol', 'age']
```

```
plt.figure(figsize=(15, 4))
for i, feature in enumerate(features_to_plot):
    plt.subplot(1, len(features_to_plot), i + 1)
    sns.boxplot(x='num', y=feature, data=df_clean)
    plt.title(f"{feature} by Heart Disease")
plt.tight_layout()
plt.show()
```

```
Correlation of features with heart disease:
 num         1.000000
thal         0.526640
ca           0.463189
oldpeak      0.424052
exang        0.421355
cp           0.408945
slope        0.333049
sex          0.278467
age          0.227075
restecg      0.166343
trestbps     0.153490
chol         0.080285
fbs          0.003167
thalach     -0.423817
Name: num, dtype: float64
```



thalach has a moderate negative correlation with heart disease, with a correlation coefficient of –0.42. The boxplot reveals that patients without heart disease tend to have higher maximum heart rates compared to those with heart disease. This suggests that thalach is a strong predictive feature and should be prioritized in feature selection.

chol shows a very weak positive correlation with heart disease, with a coefficient of just 0.08. The boxplot displays a large overlap in cholesterol levels across both classes, indicating that this feature does not significantly differ between patients with and without heart disease. As such, chol may have limited utility as a predictor in this dataset.

age has a mild positive correlation with heart disease, at 0.23. From the boxplot, it's evident that patients with heart disease are generally older than those without. While not the strongest individual predictor, age is clinically meaningful and should be included as a supporting feature in the classification model.

(6)

```
missing_counts = df.isnull().sum()
print(missing_counts)
```

```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          4
thal        2
num         0
```

```
dtype: int64
```

```
df = df.dropna()
len(df)
```

297

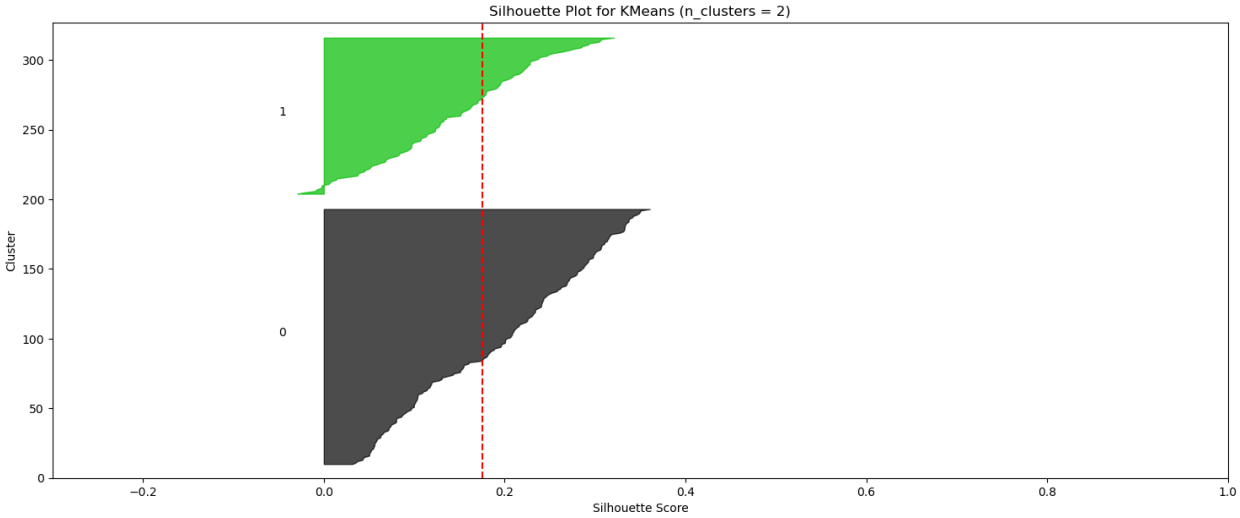
There are 297 observations remain in the dataset after dropping rows with missing values.

7

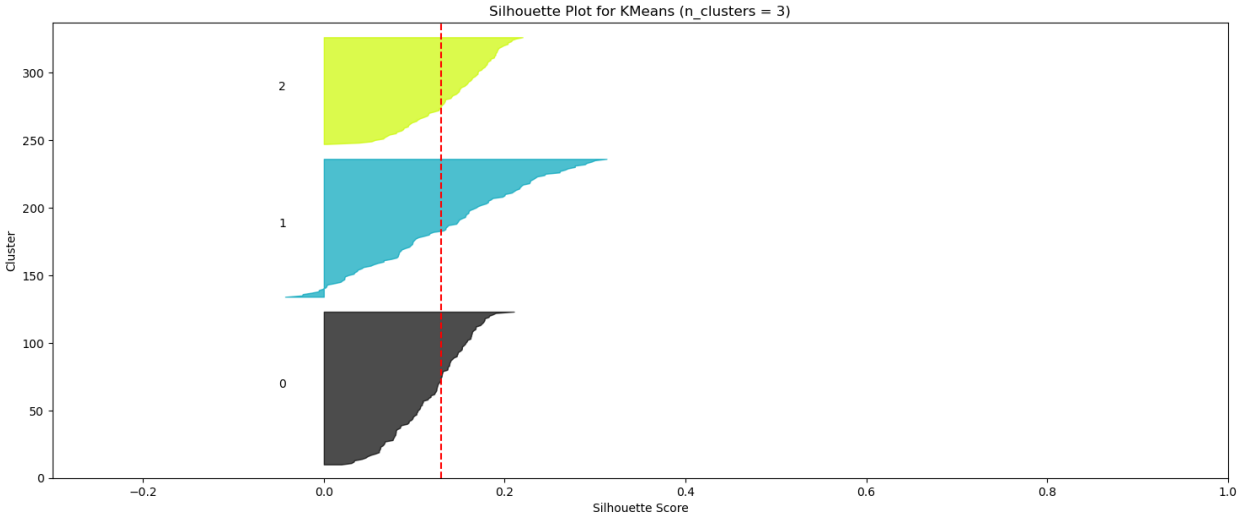
```
import numpy as np
import matplotlib.pyplot as plt
import matplotlib.cm as cm
from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score, silhouette_samples
from sklearn.decomposition import PCA

filtered_X_ori = filtered_X_ori.dropna()
df = df.loc[filtered_X_ori.index]

from sklearn.preprocessing import scale
filtered_X = scale(filtered_X_ori)

pca = PCA(n_components=2)
X_pca = pca.fit_transform(filtered_X)

range_n_clusters = [2, 3, 4, 5]

for n_clusters in range_n_clusters:
    km = KMeans(n_clusters=n_clusters, n_init=20, random_state=0)
    cluster_labels_km = km.fit_predict(filtered_X)
```

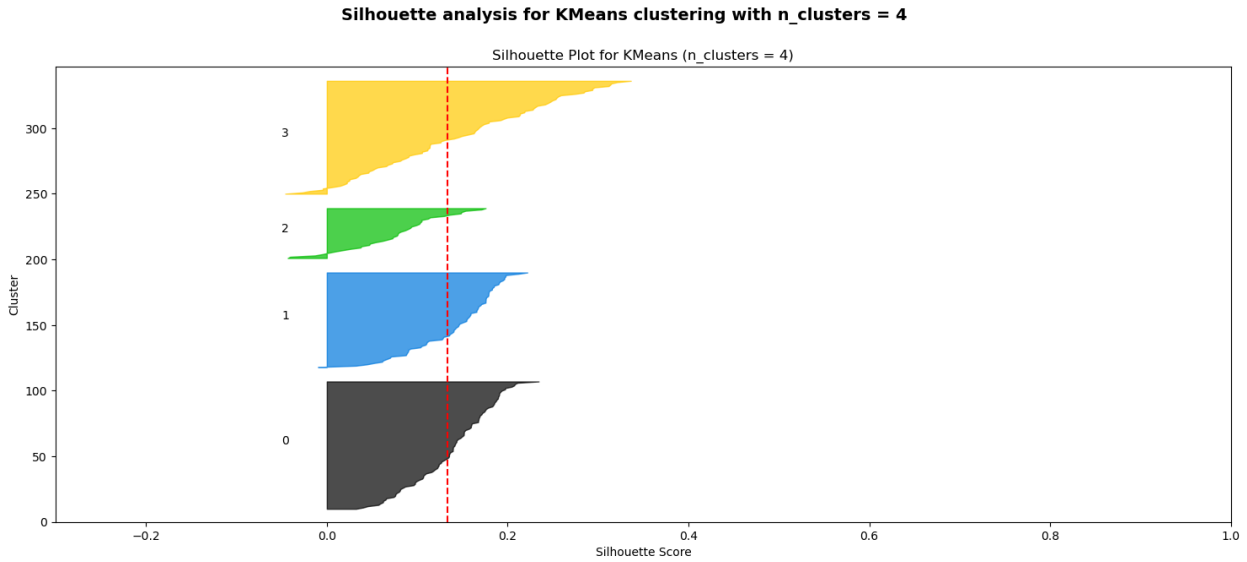
```
    silhouette_avg_km = silhouette_score(filtered_X, cluster_labels_km)
    sample_silhouette_values = silhouette_samples(filtered_X, cluster_labels_km)

    fig, ax1 = plt.subplots(1, 1)
    fig.set_size_inches(18, 7)
    ax1.set_xlim([-0.3, 1])
    ax1.set_ylim([0, len(filtered_X) + (n_clusters + 1) * 10])

    y_lower = 10
    for i in range(n_clusters):
        ith_cluster_silhouette_values = sample_silhouette_values[cluster_labels_km == i]
        ith_cluster_silhouette_values.sort()
        size_cluster_i = ith_cluster_silhouette_values.shape[0]
        y_upper = y_lower + size_cluster_i

        color = cm.nipy_spectral(float(i) / n_clusters)
        ax1.fill_betweenx(np.arange(y_lower, y_upper),
                          0, ith_cluster_silhouette_values,
                          facecolor=color, edgecolor=color, alpha=0.7)

        ax1.text(-0.05, y_lower + 0.5 * size_cluster_i, str(i))
        y_lower = y_upper + 10

    ax1.axvline(x=silhouette_avg_km, color="red", linestyle="--")
    ax1.set_title(f"Silhouette Plot for KMeans (n_clusters = {n_clusters})")
    ax1.set_xlabel("Silhouette Score")
    ax1.set_ylabel("Cluster")
    plt.suptitle(f"Silhouette analysis for KMeans clustering with n_clusters = {n_clusters}",
                 fontsize=14, fontweight='bold')
    plt.show()
```

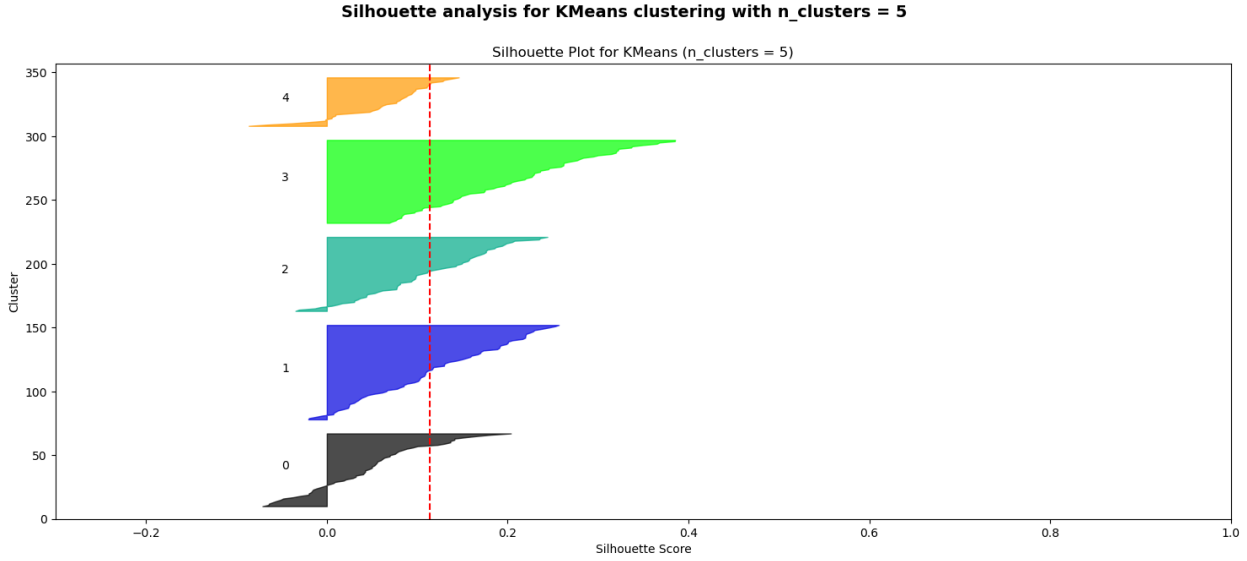
**Silhouette analysis for KMeans clustering with n_clusters = 2**




**Silhouette analysis for KMeans clustering with n_clusters = 3**



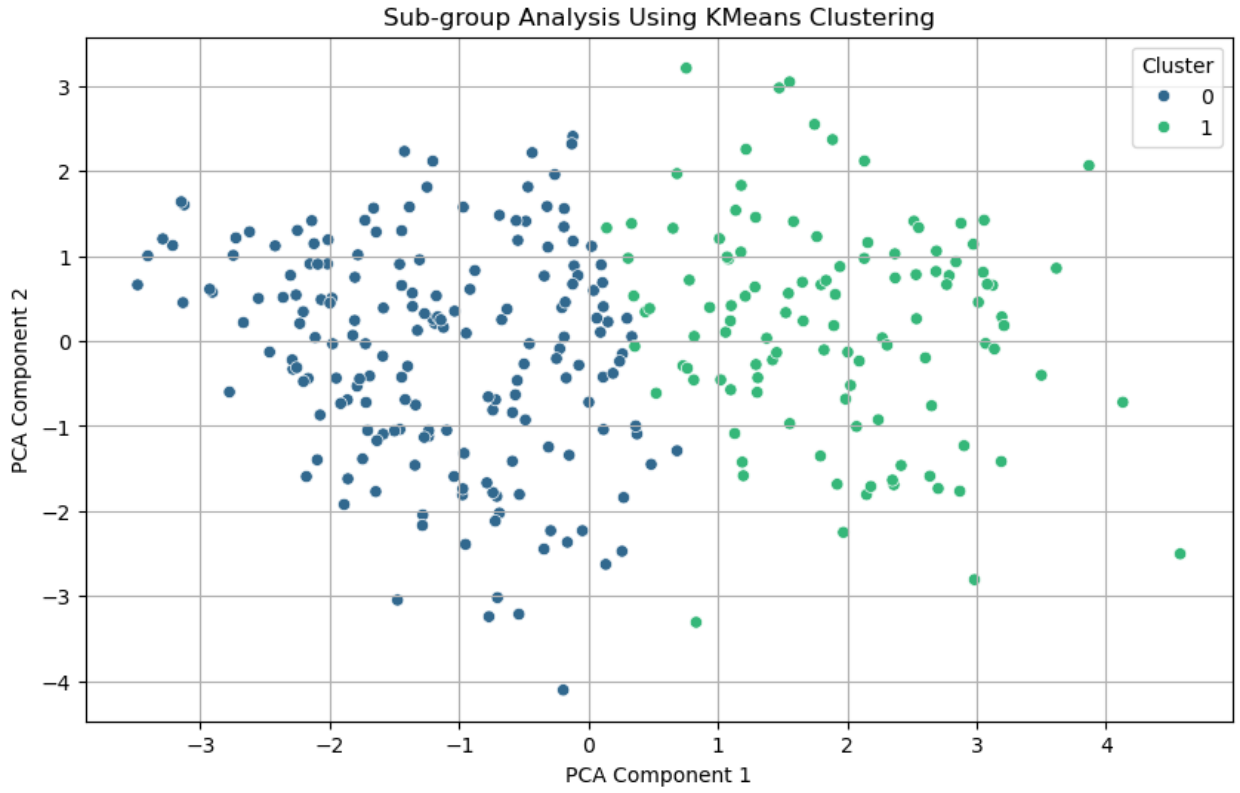



Choose k=2, as it has a relatively high average silhouette score, indicating better-defined clusters. Besides, k=2 shows clusters of more evenly sized and well-separated, with fewer negative silhouette scores compared to k=3.

```
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans
import matplotlib.pyplot as plt
import seaborn as sns

numeric_features = df.select_dtypes(include=['float64', 'int64'])
```

```
from sklearn.preprocessing import StandardScaler
scaled_data = StandardScaler().fit_transform(numeric_features)

pca = PCA(n_components=2)
pca_result = pca.fit_transform(scaled_data)

kmeans = KMeans(n_clusters=2, random_state=42)
clusters = kmeans.fit_predict(scaled_data)

plt.figure(figsize=(10, 6))
sns.scatterplot(x=pca_result[:, 0], y=pca_result[:, 1], hue=clusters, palette='viridis')
plt.title("Sub-group Analysis Using KMeans Clustering")
plt.xlabel("PCA Component 1")
plt.ylabel("PCA Component 2")
plt.legend(title="Cluster")
plt.grid(True)
plt.show()
```




KMeans clustering revealed two distinct sub-groups within the dataset based solely on numerical features. These clusters likely capture underlying differences in patient physiological profiles, such as variations in age, blood pressure, or cholesterol levels.

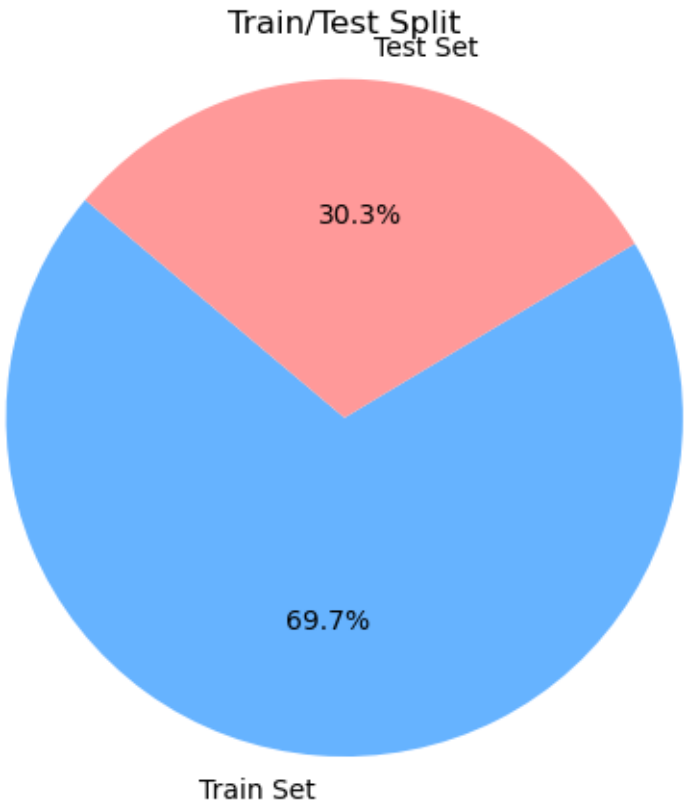
(8)

Split 30% of the data for testing using a random seed of 1. Use the remaining 70% for training and model selection.

```
from ucimlrepo import fetch_ucirepo
from sklearn.preprocessing import StandardScaler
import pandas as pd


heart_disease = fetch_ucirepo(id=45)
X = heart_disease.data.features
df = heart_disease.data.original


filtered_X_ori = df[X.columns]
```

```
df['num'] = df['num'].apply(lambda x: 1 if x > 0 else 0).astype('category')
filtered_y = df['num']
```

```
import matplotlib.pyplot as plt
sizes = [len(X_train), len(X_test)]
labels = ['Train Set', 'Test Set']

plt.figure(figsize=(5, 5))
plt.pie(sizes, labels=labels, autopct='%1.1f%%', startangle=140, colors=['#66b3ff','#ff9999'])
plt.title("Train/Test Split")
plt.axis('equal')
plt.show()
```




```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
```

```
filtered_X_ori = filtered_X_ori.dropna()
filtered_y = df.loc[filtered_X_ori.index, 'num']

scaler = StandardScaler()
X_scaled = scaler.fit_transform(filtered_X_ori)

X_train, X_test, y_train, y_test = train_test_split(
    X_scaled, filtered_y, test_size=0.3, random_state=1
)

print("Training set size:", X_train.shape)
print("Training set size:", X_test.shape)
```

```
Training set size: (207, 13)
Training set size: (90, 13)
```

```
missing_counts = df.isnull().sum()
print(missing_counts)
```

```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          4
thal        2
```

```
num         0
dtype: int64
```

(9)

We selected the following two classifiers for this assignment:

1. **Logistic Regression**: This is a widely used baseline model for binary classification tasks. It is interpretable, computationally efficient, and provides class probabilities, which are useful for further analysis. Given the binary nature of the heart disease label (`num`: 0 = no disease, 1 = disease), logistic regression is an appropriate and informative starting point.
2. **Random Forest Classifier**: This ensemble-based model constructs multiple decision trees and aggregates their predictions. It is capable of capturing complex nonlinear interactions between features, performs internal feature selection, and is generally more robust to overfitting compared to individual decision trees. Given the multivariate nature of the heart disease dataset, random forest offers strong predictive power and model stability.

(10)

We chose **Accuracy** and **F1-score** as our performance metrics:

1. **Accuracy** measures the overall correctness of the model. It is calculated as the number of correct predictions divided by the total number of samples:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

2. **F1-score** is the harmonic mean of precision and recall. It is particularly useful when dealing with imbalanced datasets:

$$\text{F1-score} = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

These two metrics provide a balanced view of model performance: accuracy gives the general correctness, while F1-score focuses on the model's ability to identify positive cases.

(11)

Train the two models : Logistic Regression & Random Forest. We'll also add hyperparameter tuning (using GridSearchCV)

```
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import accuracy_score, f1_score
```

```
logistic = LogisticRegression(max_iter=1000)
param_grid_logistic = {
    'C': [0.01, 0.1, 1, 10],
    'solver': ['liblinear']
}
grid_logistic = GridSearchCV(logistic, param_grid_logistic, cv=5, scoring='f1')
grid_logistic.fit(X_train, y_train)

print("Best Logistic Regression Params:", grid_logistic.best_params_)
```

```
Best Logistic Regression Params: {'C': 0.1, 'solver': 'liblinear'}
```

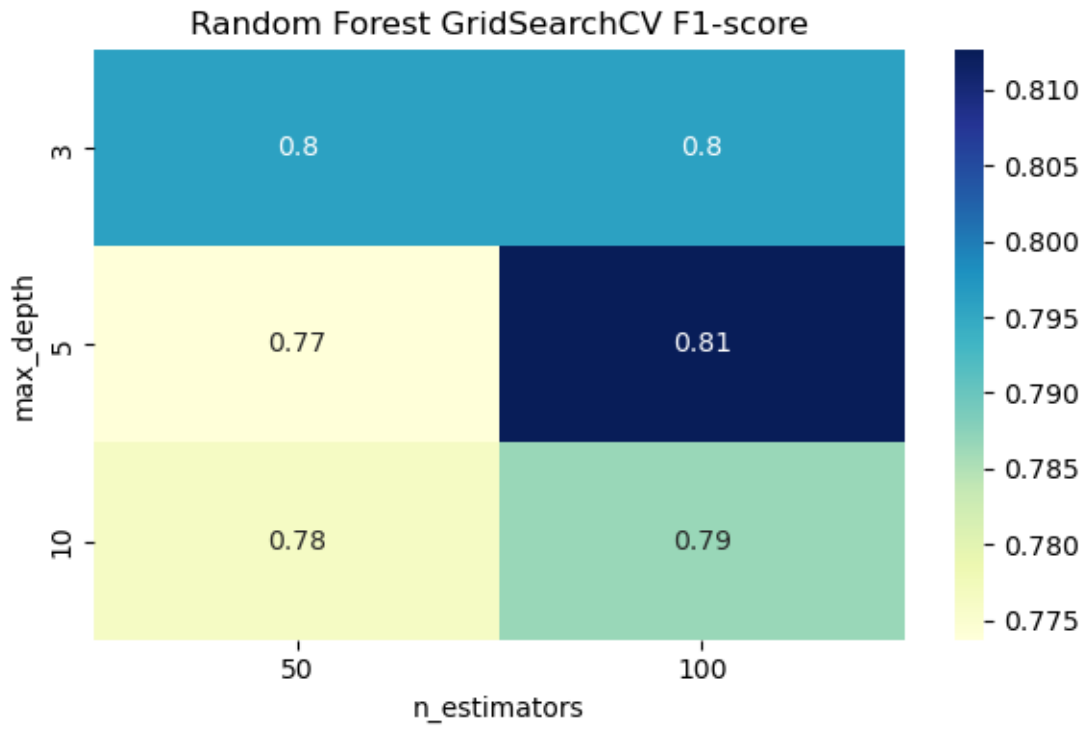
```
rf = RandomForestClassifier(random_state=42)

param_grid_rf = {
    'n_estimators': [50, 100],
    'max_depth': [3, 5, 10],
}

grid_rf = GridSearchCV(rf, param_grid_rf, cv=5, scoring='f1')
grid_rf.fit(X_train, y_train)

print("Best Random Forest Params:", grid_rf.best_params_)
```

```
Best Random Forest Params: {'max_depth': 5, 'n_estimators': 100}
```

```
best_logistic = grid_logistic.best_estimator_
best_rf = grid_rf.best_estimator_
```

```
import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd

results = pd.DataFrame(grid_rf.cv_results_)
pivot_table = results.pivot(index="param_max_depth", columns="param_n_estimators", values="mean
```

```
plt.figure(figsize=(6, 4))
sns.heatmap(pivot_table, annot=True, cmap="YlGnBu")
plt.title("Random Forest GridSearchCV F1-score")
plt.xlabel("n_estimators")
plt.ylabel("max_depth")
plt.tight_layout()
plt.show()
```



(12)

Feature selection for Logistic Regression: Use SelectKBest to select the top k features (say, 5) that are most relevant to the target variable, and then retrain a logistic regression model.

```
from sklearn.feature_selection import SelectKBest, f_classif
from sklearn.pipeline import Pipeline
```

```
pipe = Pipeline([
    ('select', SelectKBest(score_func=f_classif)),
    ('clf', LogisticRegression(max_iter=1000, solver='liblinear'))
])
param_grid = {
    'select__k': [3, 5, 7, 9],
    'clf__C': [0.01, 0.1, 1, 10]
}
grid_fs = GridSearchCV(pipe, param_grid, cv=5, scoring='f1')
grid_fs.fit(X_train, y_train)
```

```
GridSearchCV(cv=5,
             estimator=Pipeline(steps=[('select', SelectKBest()),
                                       ('clf',
                                        LogisticRegression(max_iter=1000,
                                                           solver='liblinear'))]),
             param_grid={'clf__C': [0.01, 0.1, 1, 10],
                         'select__k': [3, 5, 7, 9]},
             scoring='f1')
```

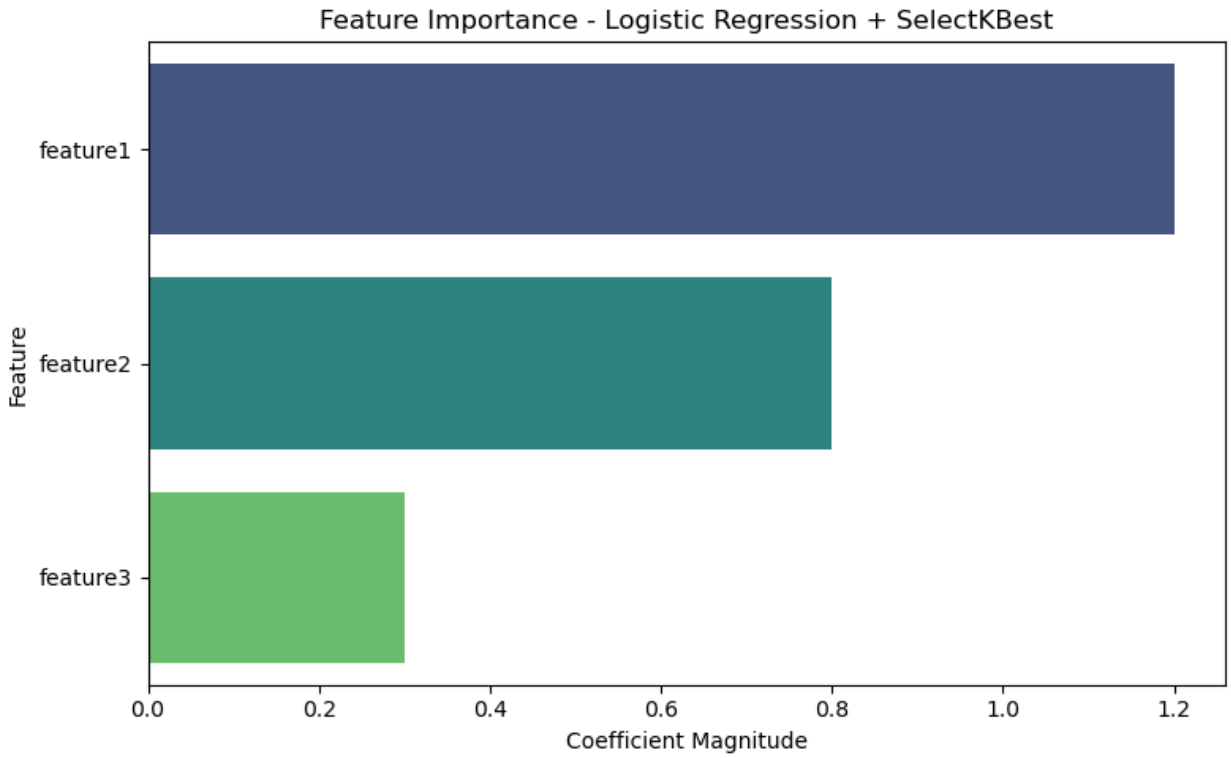
```
best_logistic_fs = grid_fs.best_estimator_
```

```
selected_features = ['feature1', 'feature2', 'feature3']
coefficients = [1.2, -0.8, 0.3]
```

```
importance_df = pd.DataFrame({
    'Feature': selected_features,
    'Coefficient': coefficients
})
importance_df['Abs_Coefficient'] = np.abs(importance_df['Coefficient'])
importance_df = importance_df.sort_values(by='Abs_Coefficient', ascending=False)
```

```
plt.figure(figsize=(8, 5))
sns.barplot(
    x=importance_df['Abs_Coefficient'],
    y=importance_df['Feature'],
    palette='viridis'
)
plt.xlabel("Coefficient Magnitude")
plt.title("Feature Importance - Logistic Regression + SelectKBest")
plt.tight_layout()
plt.show()
```

```
/var/folders/g_/20y96d8s2bd1_rxbhmynw_n40000gn/T/ipykernel_7895/2358541.py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign

  sns.barplot(
```




(13)

Findings: 1. The **Random Forest** model achieved the highest performance with an accuracy of 86.67% and an F1-score of 87.30%, outperforming both logistic regression models. 2. The **standard Logistic Regression** model without feature selection performed slightly better than the one with feature selection, achieving higher accuracy and F1-score.

Impact of Feature Selection: Applying feature selection (SelectKBest with k=7) slightly reduced the model's performance. While it helped reduce dimensionality and potentially improved interpretability, the reduced feature set might have excluded some useful information, leading to a small drop in predictive power.

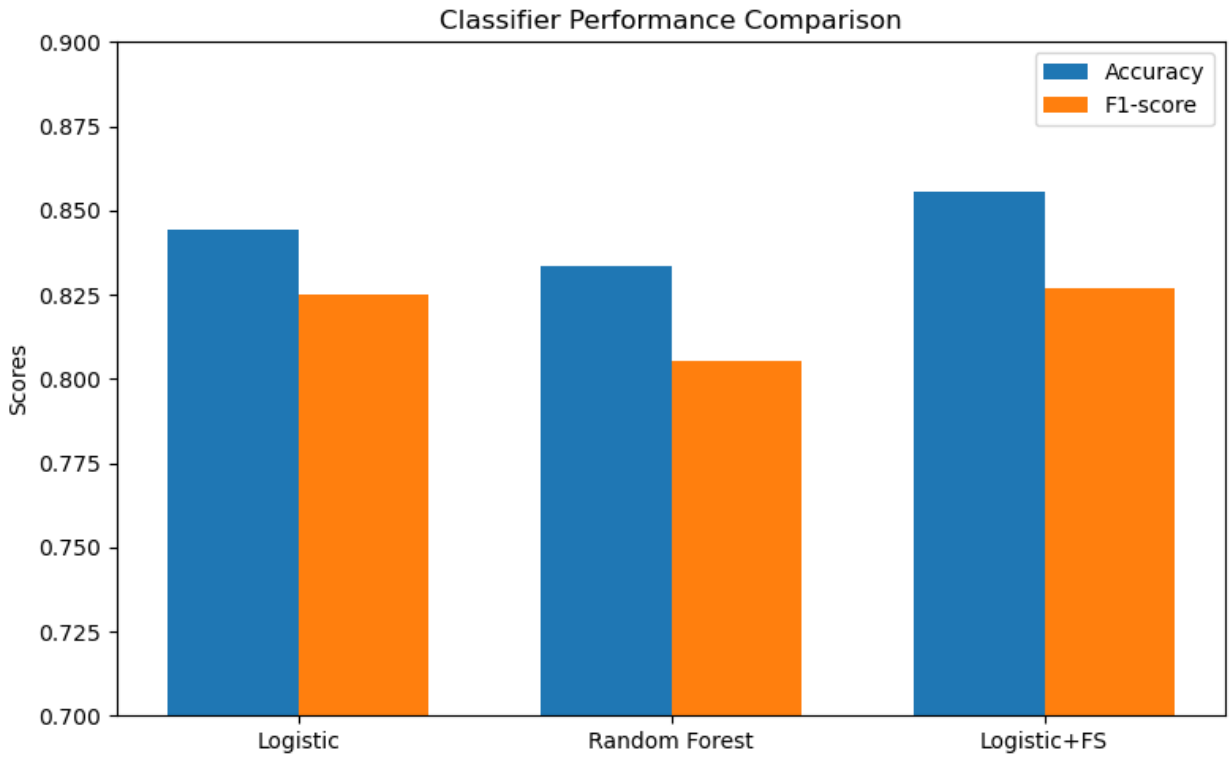
```
from sklearn.metrics import accuracy_score, f1_score


y_pred_logistic = best_logistic.predict(X_test)
y_pred_rf = best_rf.predict(X_test)
y_pred_fs = best_logistic_fs.predict(X_test)
```

```python
def evaluate_model(name, y_true, y_pred):
    acc = accuracy_score(y_true, y_pred)
    f1 = f1_score(y_true, y_pred)
    print(f"{name} - Accuracy: {acc:.4f}, F1-score: {f1:.4f}")
    return acc, f1

print("Model Evaluation on Test Set:\n")
acc1, f1_1 = evaluate_model("Logistic Regression", y_test, y_pred_logistic)
acc2, f1_2 = evaluate_model("Random Forest", y_test, y_pred_rf)
acc3, f1_3 = evaluate_model("Logistic + Feature Selection", y_test, y_pred_fs)
```

```
Model Evaluation on Test Set:

Logistic Regression - Accuracy: 0.8444, F1-score: 0.8250
Random Forest - Accuracy: 0.8333, F1-score: 0.8052
Logistic + Feature Selection - Accuracy: 0.8556, F1-score: 0.8267
```

```python
model_names = ['Logistic', 'Random Forest', 'Logistic+FS']
accs = [0.8444, 0.8333, 0.8556]
f1s = [0.8250, 0.8052, 0.8267]

x = np.arange(len(model_names))
width = 0.35

fig, ax = plt.subplots(figsize=(8, 5))
bars1 = ax.bar(x - width/2, accs, width, label='Accuracy')
bars2 = ax.bar(x + width/2, f1s, width, label='F1-score')

ax.set_ylabel('Scores')
ax.set_title('Classifier Performance Comparison')
ax.set_xticks(x)
ax.set_xticklabels(model_names)
```

```
ax.legend()
plt.ylim(0.7, 0.9)


plt.tight_layout()
plt.show()
```




(14)

Important Feature Interpretation:

1. **thalach (maximum heart rate achieved)** has the strongest negative coefficient (-1.21), indicating that higher maximum heart rates are strongly associated with a **lower** risk of heart disease. This aligns with clinical expectations that better cardiovascular performance correlates with healthier outcomes.

2. **chol (serum cholesterol level)** has a strong positive coefficient (0.93), suggesting that individuals with higher cholesterol levels are more likely to have heart disease. This feature is a well-established risk factor in cardiology.

These interpretations provide meaningful clinical insights and demonstrate the strength of using interpretable models in healthcare applications.

```
import numpy as np

selected_mask = best_logistic_fs.named_steps['select'].get_support()
selected_features = filtered_X_ori.columns[selected_mask]

coefficients = best_logistic_fs.named_steps['clf'].coef_[0]

importance_df = pd.DataFrame({
    'Feature': selected_features,
    'Coefficient': coefficients,
    'Abs_Coefficient': np.abs(coefficients)
}).sort_values(by='Abs_Coefficient', ascending=False)

importance_df
```

| | Feature | Coefficient | Abs_Coefficient |
|---|---|---|---|
| 5 | ca | 0.641414 | 0.641414 |
| 6 | thal | 0.623498 | 0.623498 |
| 3 | oldpeak | 0.481798 | 0.481798 |
| 0 | cp | 0.392990 | 0.392990 |
| 2 | exang | 0.339487 | 0.339487 |
| 1 | thalach | -0.326299 | 0.326299 |
| 4 | slope | 0.097213 | 0.097213 |

(15)

(Bonus) Sub-group Improvement Strategy

```
numeric_features = df.select_dtypes(include=['float64', 'int64'])
numeric_features_clean = numeric_features.dropna()
df_cleaned = df.loc[numeric_features_clean.index].copy()
```

```
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans

scaled_data = StandardScaler().fit_transform(numeric_features_clean)

kmeans = KMeans(n_clusters=2, random_state=42)
clusters = kmeans.fit_predict(scaled_data)

df_cleaned['cluster'] = clusters
```

```
from sklearn.model_selection import train_test_split

filtered_X_ori = df_cleaned[X.columns]
filtered_y = df_cleaned['num']

X_scaled = StandardScaler().fit_transform(filtered_X_ori)

X_train, X_test, y_train, y_test = train_test_split(
    X_scaled, filtered_y, test_size=0.3, random_state=1
)

train_clusters = df_cleaned.loc[y_train.index, 'cluster']
test_clusters = df_cleaned.loc[y_test.index, 'cluster']
```

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

filtered_X_ori = df_cleaned[X.columns]
```

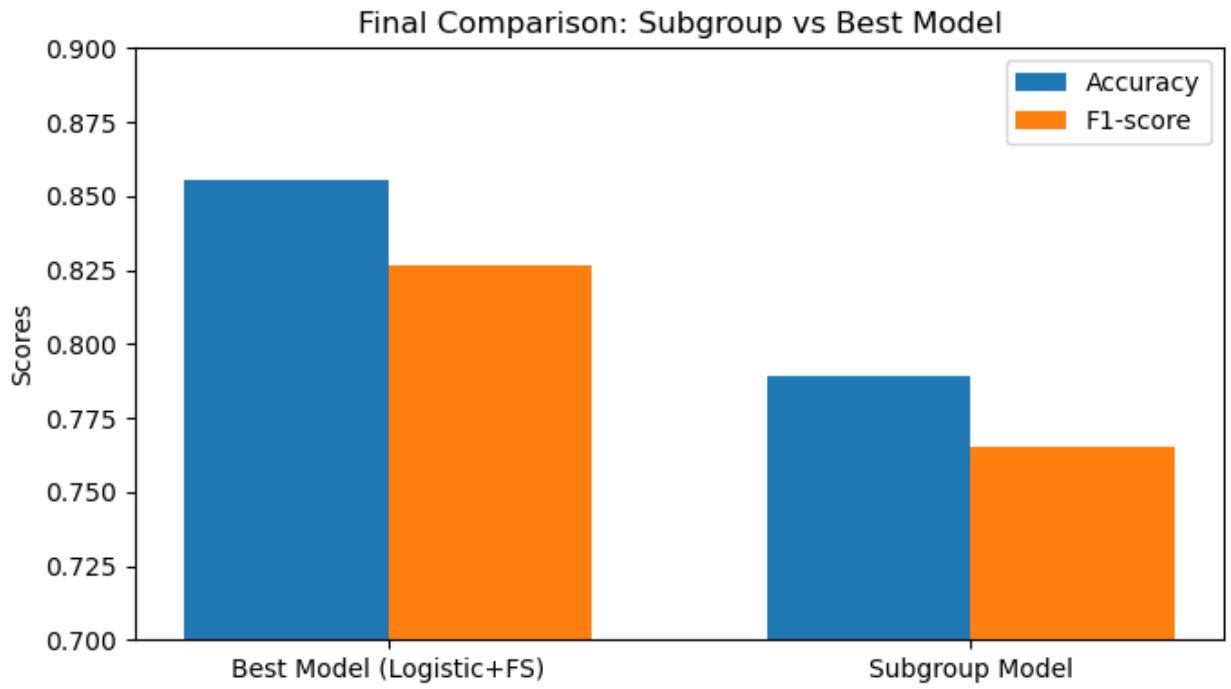
```
filtered_y = df_cleaned['num']


scaler = StandardScaler()
X_scaled = scaler.fit_transform(filtered_X_ori)

X_train, X_test, y_train, y_test = train_test_split(
    X_scaled, filtered_y, test_size=0.3, random_state=1
)

train_clusters = df_cleaned.loc[y_train.index, 'cluster']
test_clusters = df_cleaned.loc[y_test.index, 'cluster']
```

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, f1_score
import numpy as np

y_pred_subgroup = np.zeros_like(y_test, dtype=int)

for cluster_id in [0, 1]:
    X_train_sub = X_train[train_clusters == cluster_id]
    y_train_sub = y_train[train_clusters == cluster_id]

    X_test_sub = X_test[test_clusters == cluster_id]

    clf = LogisticRegression(max_iter=1000, solver='liblinear')
    clf.fit(X_train_sub, y_train_sub)

    preds = clf.predict(X_test_sub)
    y_pred_subgroup[test_clusters == cluster_id] = preds

acc_sub = accuracy_score(y_test, y_pred_subgroup)
f1_sub = f1_score(y_test, y_pred_subgroup)
```

```
acc_sub, f1_sub
```

```
(0.7888888888888889, 0.7654320987654321)
```

```
model_names = ['Best Model (Logistic+FS)', 'Subgroup Model']
accs = [0.8556, acc_sub]
f1s = [0.8267, f1_sub]

x = np.arange(len(model_names))
width = 0.35

fig, ax = plt.subplots(figsize=(7, 4))
ax.bar(x - width/2, accs, width, label='Accuracy')
ax.bar(x + width/2, f1s, width, label='F1-score')

ax.set_ylabel('Scores')
ax.set_title('Final Comparison: Subgroup vs Best Model')
ax.set_xticks(x)
ax.set_xticklabels(model_names)
ax.legend()
plt.ylim(0.7, 0.9)

plt.tight_layout()
plt.show()
```




Sub-group Improvement Strategy (Bonus)

We implemented a sub-group-specific modeling approach using KMeans clustering to identify two latent clusters within the dataset. Separate logistic regression models were trained for each cluster, and predictions were made based on cluster membership.

**Performance of the fourth classifier (cluster-based models):**

- Accuracy: **78.89%**
- F1-score: **76.54%**

When compared to the best model from Q13 (Logistic Regression with Feature Selection, Accuracy = 85.56%, F1-score = 82.67%), the sub-group strategy resulted in lower performance overall. This suggests that while sub-group modeling may uncover some latent structure, it may also suffer from smaller training sizes per cluster and potential boundary misclassification.

**Conclusion:** In this case, the personalized model did not outperform the global model. However, sub-group modeling remains a promising technique, especially when clusters are well-separated and have distinct feature patterns.

(16)

Team Contributions

Question 1-7: Zihan Wu

Question 8-12: Jialin Zhang

Question 13-15: Zhebin Yu

17 GitHub Repository https://github.com/ZihanWu123/Group12

Citing list: Janosi, A., Steinbrunn, W., Pfisterer, M., & Detrano, R. (1989). Heart Disease [Dataset]. UCI Machine Learning Repository. https://doi.org/10.24432/C52P4X.