STATS 3DA3

Homework Assignment 6

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Question

1)

Our target variable measure the severity of heart disease which can be defined as binary classification problem. Our goal would then to be able to predict the probability of heart disease. This means we can carry out a logistic regression and a random forest classifier to predict the presence and absence of heart disease.

2)

```
from ucimlrepo import fetch_ucirepo
from sklearn.preprocessing import StandardScaler

heart_disease = fetch_ucirepo(id=45)

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

scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X)
```

3)

We have 13 features and 1 target variable. Starting with our features, we have age (age in years), sex (1 = male; 0 = female), cp (1: typical angina, 2: atypical angina, 3: non-anginal pain, 4: asymptomatic), trestbps (resting blood pressure in mm Hg on admission to the hospital), chol (serum cholestoral in mg/dl), fbs (fasting blood sugar > 120 mg/dl where 1 = true; 0 = false), restecg (resting electrocardiographic results), exang (exercise induced angina), oldpeak (ST depression induced by exercise relative to rest), slope (1 = upsloping, 2 = flat, 3 = downsloping), ca (number of major vessels colored by floursopy), thal (3 = normal; 6 = fixed defect; 7 = reversable defect). Finally our target variable, 'num', is the diagnosis of heart disease.

```
print(f"Observations in X: {len(X)}")
print(f"Summary of X:\n{X.describe()}")
print(f"Summary of y:\n{y.describe()}")
```

```
Observations in X: 303
Summary of X:
              age         sex          cp    trestbps        chol         fbs  \
count  303.000000  303.000000  303.000000  303.000000  303.000000  303.000000
mean    54.438944    0.679868    3.158416  131.689769  246.693069    0.148515
std      9.038662    0.467299    0.960126   17.599748   51.776918    0.356198
min     29.000000    0.000000    1.000000   94.000000  126.000000    0.000000
25%     48.000000    0.000000    3.000000  120.000000  211.000000    0.000000
50%     56.000000    1.000000    3.000000  130.000000  241.000000    0.000000
75%     61.000000    1.000000    4.000000  140.000000  275.000000    0.000000
max     77.000000    1.000000    4.000000  200.000000  564.000000    1.000000

          restecg     thalach       exang     oldpeak       slope          ca  \
count  303.000000  303.000000  303.000000  303.000000  303.000000  299.000000
mean     0.990099  149.607261    0.326733    1.039604    1.600660    0.672241
std      0.994971   22.875003    0.469794    1.161075    0.616226    0.937438
min      0.000000   71.000000    0.000000    0.000000    1.000000    0.000000
25%      0.000000  133.500000    0.000000    0.000000    1.000000    0.000000
50%      1.000000  153.000000    0.000000    0.800000    2.000000    0.000000
75%      2.000000  166.000000    1.000000    1.600000    2.000000    1.000000
max      2.000000  202.000000    1.000000    6.200000    3.000000    3.000000

             thal
count  301.000000
mean     4.734219
std      1.939706
min      3.000000
25%      3.000000
```

```
50%      3.000000
75%      7.000000
max      7.000000
Summary of y:
              num
count  303.000000
mean     0.937294
std      1.228536
min      0.000000
25%      0.000000
50%      0.000000
75%      2.000000
max      4.000000
```

We find that the average age of patients is 54.4 years old, with a standard deviation of 9.1 years.

```
print(f"Data Types of X: \n{X.dtypes}")
print(f"\nData Types of y: \n{y.dtypes}")
```

```
Data Types of X:
age           int64
sex           int64
cp            int64
trestbps      int64
chol          int64
fbs           int64
restecg       int64
thalach       int64
exang         int64
oldpeak     float64
slope         int64
ca          float64
```

```
thal        float64
dtype: object

Data Types of y:
num    int64
dtype: object
```

All of our data types in X are numerical but some representing categorical variables.

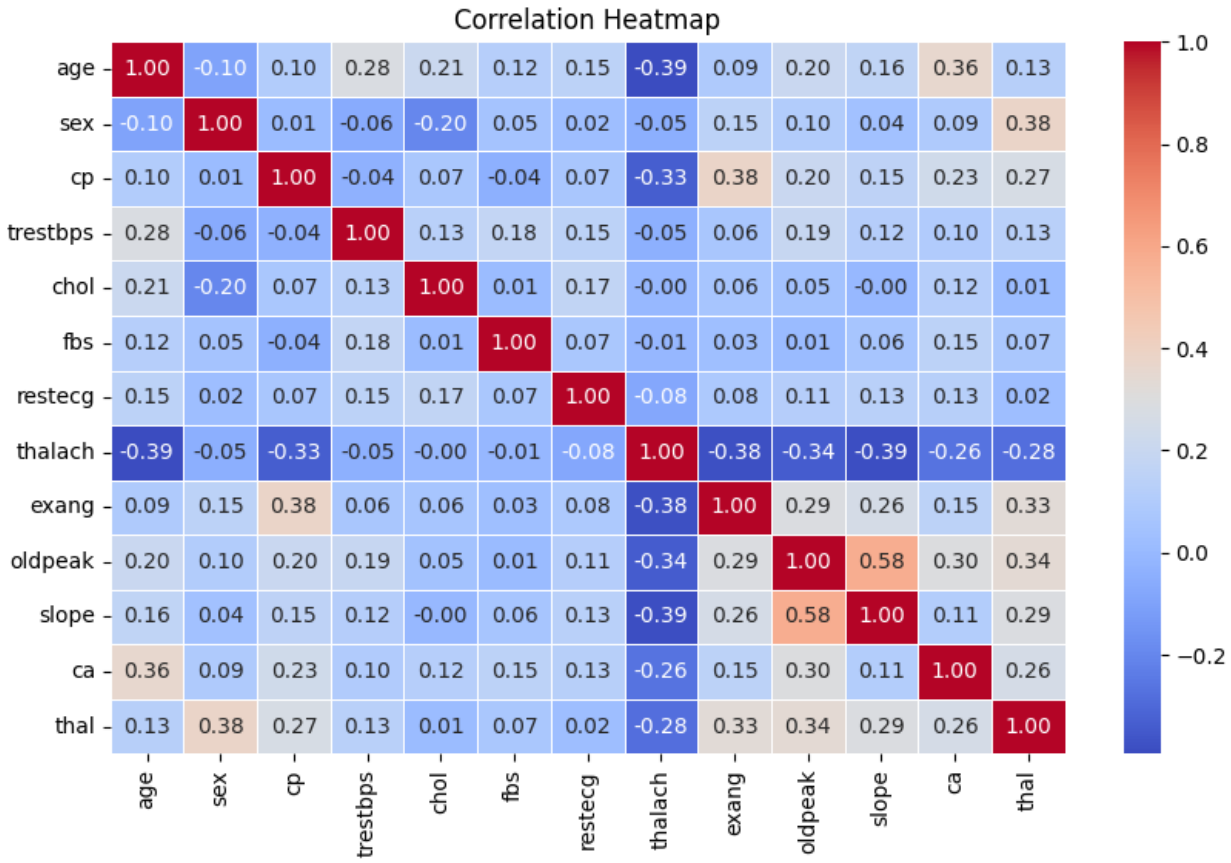
4)

```python
print(f"y before transformation: {y['num'].value_counts()}")
y['num'] = y['num'].apply(lambda x: 1 if x > 0 else 0)
print(f"y before transformation: {y['num'].value_counts()}")
```

```
y before transformation: num
0    164
1     55
2     36
3     35
4     13
Name: count, dtype: int64
y before transformation: num
0    164
1    139
Name: count, dtype: int64

/var/folders/5q/w2pw9gp90mldwv2xvm9ml_jc0000gn/T/ipykernel_9942/2854447611.py:2: SettingWithCo
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/
  y['num'] = y['num'].apply(lambda x: 1 if x > 0 else 0)
```

5)

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

corr_matrix = X.corr()

plt.figure(figsize=(10, 6))
sns.heatmap(corr_matrix, annot=True, cmap='coolwarm', fmt=".2f", linewidths=0.5)
plt.title("Correlation Heatmap")
plt.show()
```



From this correlation matrix, we can conclude that thalach (max heart rate) has a strong negative correlation (-0.39) with age and oldpeak. We can assume that younger individuals tend to have a higher heart rate, while those with more severe heart disease (higher oldpeak) have lower thalach.

We also found that ca (number of major vessels) has a strong positive correlation (0.36) with age. We can say that older individuals are more likely to have more blocked vessels.

6)

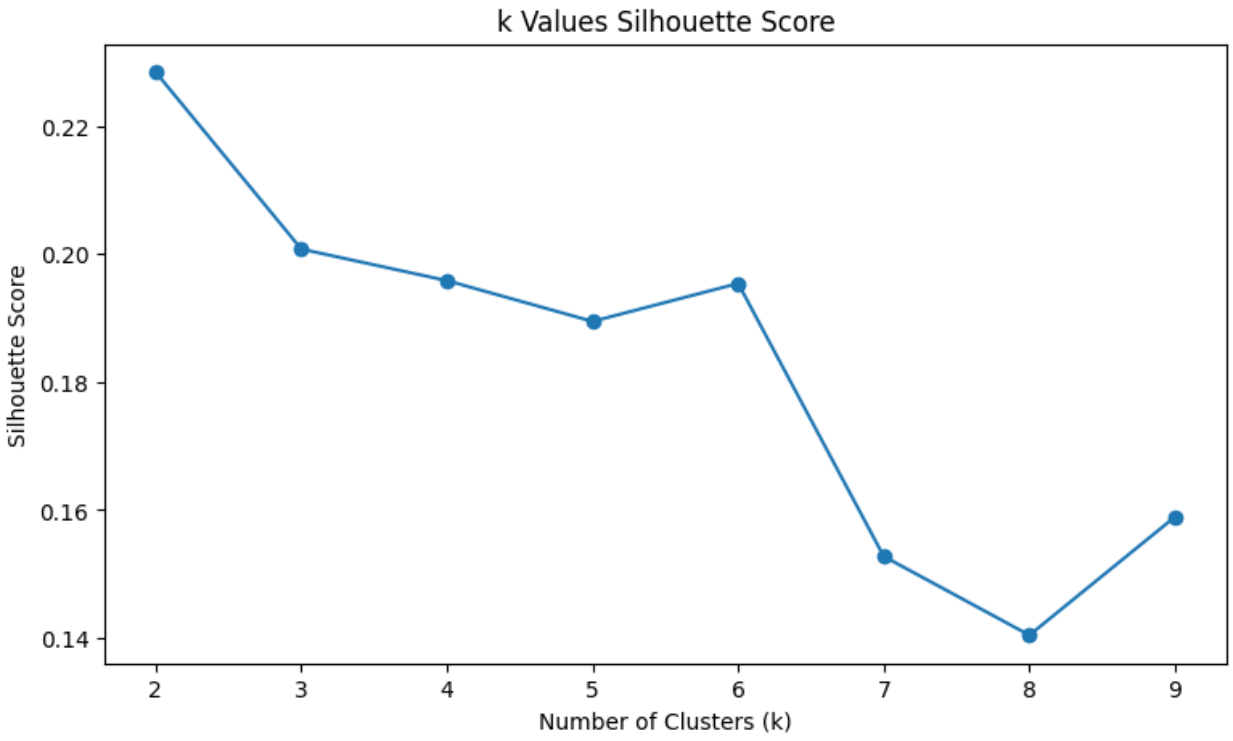
```
X = X.dropna()
y = y.loc[X.index]

print(f"Length of X after transformations: {len(X)}")
print(f"Length of y after transformations: {len(y)}")
```

```
Length of X after transformations: 297
Length of y after transformations: 297
```

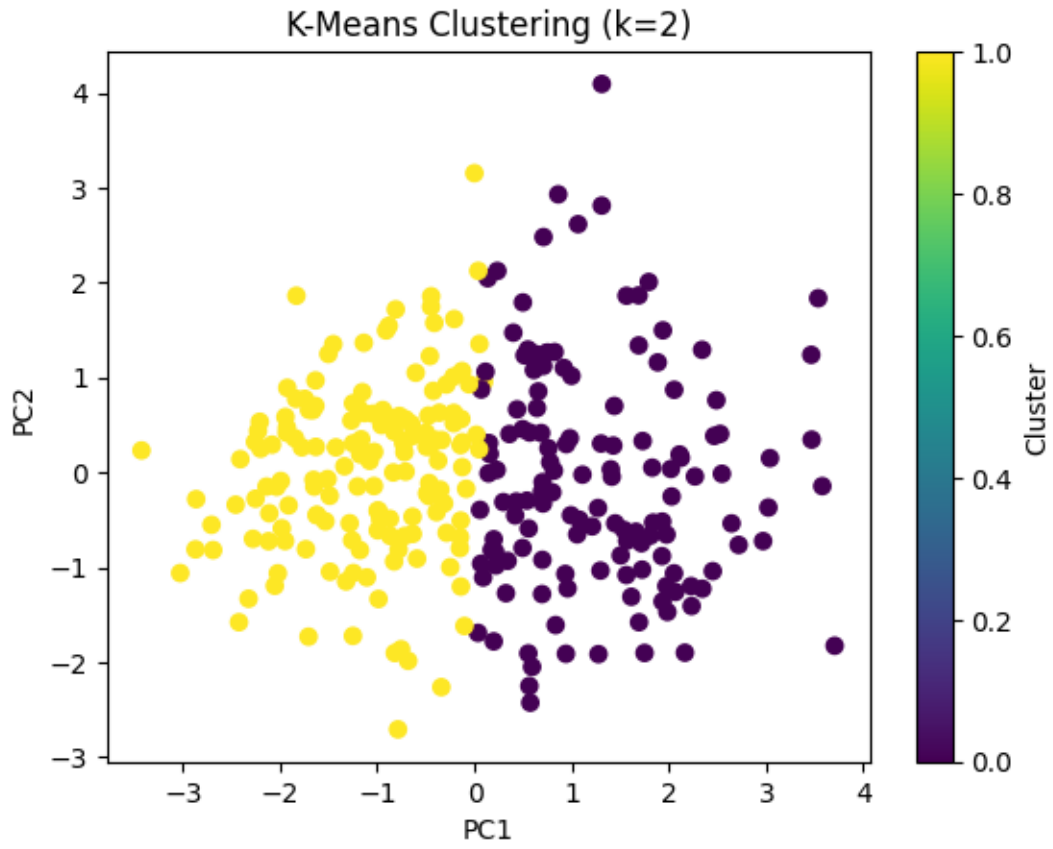
7)

```
import pandas as pd
from sklearn.metrics import silhouette_samples, silhouette_score
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans
import matplotlib.pyplot as plt

categorical_columns = ['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'thal']
X_cleaned = X.drop(columns=categorical_columns)

scaler = StandardScaler()
X_scaled = scaler.fit_transform(X_cleaned)
```

```
k_range = range(2,10)
silhouette_scores = []

for k in k_range:
    kmeans = KMeans(n_clusters = k, n_init = 20, random_state = 0)
    cluster_labels = kmeans.fit_predict(X_scaled)
    silhouette_avg = silhouette_score(X_scaled, cluster_labels)
    silhouette_scores.append(silhouette_avg)

plt.figure(figsize=(9, 5))
plt.plot(k_range, silhouette_scores, marker='o')
plt.ylabel("Silhouette Score")
plt.xlabel("Number of Clusters (k)")
plt.title("k Values Silhouette Score")
plt.show()
```



```
pca = PCA(n_components=2)
X_pca = pca.fit_transform(X_scaled)

kmeans = KMeans(n_clusters=2, random_state=1)
clusters = kmeans.fit_predict(X_scaled)

plt.scatter(X_pca[:, 0], X_pca[:, 1], c=clusters, cmap='viridis')
plt.title("K-Means Clustering (k=2)")
plt.xlabel("PC1")
plt.ylabel("PC2")
plt.colorbar(label="Cluster")
plt.show()

X_scaled_df = pd.DataFrame(X_scaled, columns=X_cleaned.columns)
X_scaled_df['cluster'] = clusters
```



8)

```
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.30, random_state=1)
```

9)

We are going to use logistic regression and random forest. Logistic regression is suitable for this assignment because it predicts a binary outcome, in which case, the target variable is 0 or 1. Random forest is also a good classifier to use because it has high predictive accuracy and does not depend on linear relationships, which is good for this dataset as there are both numerical and categorical variables.

10)

We are going to use accuracy and F1 scores to compare the classifier performance between logistic regression and random forest. We can create the confusion matrix from the predictions to calculate the accuracy and F1 scores. Accuracy scores are calculated by the number of correct predictions over the total number of predictions.

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

Where:

TP = True Positives

TN = True Negatives

FP = False Positives

FN = False Negatives

To obtain the F1 score, we will need to use precision and recall that are derived from the confusion matrix. Once we calculate that, the F1 score can be calculated by:

$$\text{Precision} = \frac{TP}{TP + FP}$$
$$\text{Recall} = \frac{TP}{TP + FN}$$
$$F_1 = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

Using these metrics, we can compare the overall accuracy and balance between the two classifiers to determine which classifier most optimal for predicting heart disease.

11)

Logistic Regression

```
import numpy as np
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

import warnings
warnings.filterwarnings('ignore')

scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

log_reg = LogisticRegression(solver='liblinear', max_iter=1000, random_state=42)

param_grid = {
    'penalty': ['l1', 'l2'],
```

```
    'C': [0.001, 0.01, 0.1, 1, 10, 100, 1000] # test this out to see if accuracy improves
}

grid_search = GridSearchCV(estimator=log_reg, param_grid=param_grid, cv=5, scoring='accuracy',
grid_search.fit(X_train_scaled, y_train)

print("Optimal parameters: ", grid_search.best_params_)
print("Cross-validation accuracy: {:.4f}".format(grid_search.best_score_))

best_log_reg = grid_search.best_estimator_
y_pred = best_log_reg.predict(X_test_scaled)
y_pred2 = best_log_reg.predict(X_train_scaled)

accuracy = accuracy_score(y_test, y_pred)
train_accuracy = accuracy_score(y_train, y_pred2)
cm = confusion_matrix(y_test, y_pred)
report = classification_report(y_test, y_pred, target_names=['No Heart Disease', 'Heart Disease

print(f"Test set accuracy: {accuracy:.4f}")
print(f"Train set accuracy: {train_accuracy:.4f}")
print("Confusion Matrix:")
print(cm)
print("Classification Report:")
print(report)
```

```
Fitting 5 folds for each of 14 candidates, totalling 70 fits
Optimal parameters:  {'C': 0.01, 'penalty': 'l2'}
Cross-validation accuracy: 0.8456
Test set accuracy: 0.8556
Train set accuracy: 0.8454
Confusion Matrix:
[[45  6]
```

```
 [ 7 32]]
Classification Report:
                  precision    recall  f1-score   support

No Heart Disease       0.87      0.88      0.87        51
   Heart Disease       0.84      0.82      0.83        39

        accuracy                           0.86        90
       macro avg       0.85      0.85      0.85        90
    weighted avg       0.86      0.86      0.86        90
```

Random Forest

```python
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.preprocessing import StandardScaler
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

import warnings
warnings.filterwarnings('ignore')

rf_clf = RandomForestClassifier(random_state=42)
rf_param_grid = {
    'n_estimators': [100, 200, 300],
    'max_depth': [None, 10, 20, 30],
    'min_samples_split': [2, 5, 10],
    'max_features': ['sqrt', 'log2', None],
    'criterion': ['gini', 'entropy']
}

rf_grid_search = GridSearchCV(estimator=rf_clf, param_grid=rf_param_grid, cv=5, scoring='accura
```

```
rf_grid_search.fit(X_train_scaled, y_train)

print("Optimal Parameters:", rf_grid_search.best_params_)
print("Cross-Validation Accuracy:", rf_grid_search.best_score_)

best_rf_clf = rf_grid_search.best_estimator_
rf_y_pred = best_rf_clf.predict(X_test_scaled)

rf_accuracy = accuracy_score(y_test, rf_y_pred)
rf_cm = confusion_matrix(y_test, rf_y_pred)
rf_report = classification_report(y_test, rf_y_pred, target_names=['No Heart Disease', 'Heart D

print(f"Test Accuracy: {rf_accuracy:.4f}")
print("Confusion Matrix:")
print(rf_cm)
print("Classification Report:")
print(rf_report)
```

```
Fitting 5 folds for each of 216 candidates, totalling 1080 fits
Optimal Parameters: {'criterion': 'gini', 'max_depth': None, 'max_features': 'sqrt', 'min_sampl
Cross-Validation Accuracy: 0.8166085946573751
Test Accuracy: 0.8444
Confusion Matrix:
[[44  7]
 [ 7 32]]
Classification Report:
                  precision    recall  f1-score   support

No Heart Disease       0.86      0.86      0.86        51
   Heart Disease       0.82      0.82      0.82        39

        accuracy                           0.84        90
```

```
       macro avg       0.84      0.84      0.84        90
    weighted avg       0.84      0.84      0.84        90
```

12)

We are going to apply the LASSO for feature selection to our logistic regression classifier.

```
print(X.shape)
print(y.shape)
print(X_train_scaled.shape)
```

```
(297, 13)
(297,)
(207, 14)
```

Note: When training the LASSO, we realized that X (full feature set) has 13 columns, but LogisticRegression (scaled training data) is expecting 14 features as input. Therefore, we want to make sure the target volumn is not in X.

```
# drop target column
df = pd.concat([X, y], axis=1)
X = df.drop(columns=['num'])
y = df['num']
```

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=1)


from sklearn.preprocessing import StandardScaler


scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test) # scale only X
```

```
print(X_train_scaled.shape)
```

```
(207, 13)
```

Now we can finally train the LASSO.

```
from sklearn.linear_model import LogisticRegressionCV, LogisticRegression
from sklearn.metrics import accuracy_score, roc_curve, roc_auc_score
import pandas as pd
import numpy as np

#lasso with cross-validation
lasso_cv = LogisticRegressionCV(
    penalty='l1',
    solver='saga',
    cv=5,
    max_iter=10000,
    scoring='accuracy',
    random_state=42
)
lasso_cv.fit(X_train_scaled, y_train)
```

```
LogisticRegressionCV(cv=5, max_iter=10000, penalty='l1', random_state=42,
                     scoring='accuracy', solver='saga')
```

```
#find the best c and lambda
best_c = lasso_cv.C_[0]
print("Best C (1/lambda):", best_c)
print("Best lambda (1/C):", 1 / best_c)
```

```
Best C (1/lambda): 2.782559402207126
Best lambda (1/C): 0.3593813663804626
```

```
# train lasso again with the best C
m_lasso = LogisticRegression(
    penalty='l1',
    C=best_c,
    solver='saga',
    max_iter=10000,
    random_state=42
)
m_lasso.fit(X_train_scaled, y_train)
```

```
LogisticRegression(C=2.782559402207126, max_iter=10000, penalty='l1',
                   random_state=42, solver='saga')
```

```
# selected features with coefficients
coeffs = m_lasso.coef_.reshape(-1)
feature_names = X.columns
pd.DataFrame({
    'Feature': feature_names,
    'Coefficient': coeffs
})
```

	Feature	Coefficient
0	age	-0.054183
1	sex	0.893613
2	cp	0.560257
3	trestbps	0.636381
4	chol	0.309335
5	fbs	-0.666898
6	restecg	0.314907
7	thalach	-0.458236
8	exang	0.464750

	Feature	Coefficient
9	oldpeak	0.491677
10	slope	0.289350
11	ca	1.342414
12	thal	0.571055

```
# class 1 probabilities
m_lasso_pre_prob = m_lasso.predict_proba(X_test_scaled)[:, 1]
```

```
df_eval = pd.DataFrame({'prob': m_lasso_pre_prob, 'y_test': y_test})
```

```
# ROC and KS threshold
fpr, tpr, thresholds = roc_curve(df_eval.y_test, df_eval.prob)
ks_statistic = np.max(tpr - fpr)
ks_threshold = thresholds[np.argmax(tpr - fpr)]
print("KS threshold:", ks_threshold)
```

```
KS threshold: 0.42760641677437833
```

```
# sensitivity & specificity
ind = np.where(np.isclose(thresholds, ks_threshold, atol=0.001))
print("Sensitivity:", tpr[ind])
print("Specificity:", 1 - fpr[ind])
```

```
Sensitivity: [0.87179487]
Specificity: [0.76470588]
```

```
# classify based on KS threshold
df_eval['y_test_pred'] = df_eval.prob.map(lambda x: 1 if x > ks_threshold else 0)
```

```
# Accuracy, AUC and Confusion Matrix
print("KS Threshold Accuracy:", accuracy_score(df_eval.y_test, df_eval.y_test_pred))
print("AUC Score:", roc_auc_score(df_eval.y_test, df_eval.prob))
print("Confusion Matrix:", confusion_matrix(df_eval.y_test, df_eval.y_test_pred))
```

```
KS Threshold Accuracy: 0.8
AUC Score: 0.8798391151332328
Confusion Matrix: [[39 12]
 [ 6 33]]
```

```
# Classification Report for LASSO
lasso_report=classification_report(df_eval.y_test, df_eval.y_test_pred, target_names=['No Heart
print("Classification Report:")
print(lasso_report)
```

```
Classification Report:
                  precision    recall  f1-score   support

No Heart Disease       0.87      0.76      0.81        51
   Heart Disease       0.73      0.85      0.79        39

        accuracy                           0.80        90
       macro avg       0.80      0.81      0.80        90
    weighted avg       0.81      0.80      0.80        90
```

13)

Recall the three classifiers and their classification reports:

```
print("Logistic Regression Classification Report:")
print(report)
print("Random Forest Classification Report:")
```

```
print(rf_report)
print("LASSO Classification Report:")
print(lasso_report)
```

```
Logistic Regression Classification Report:
                  precision    recall  f1-score   support

No Heart Disease       0.87      0.88      0.87        51
   Heart Disease       0.84      0.82      0.83        39

        accuracy                           0.86        90
       macro avg       0.85      0.85      0.85        90
    weighted avg       0.86      0.86      0.86        90

Random Forest Classification Report:
                  precision    recall  f1-score   support

No Heart Disease       0.86      0.86      0.86        51
   Heart Disease       0.82      0.82      0.82        39

        accuracy                           0.84        90
       macro avg       0.84      0.84      0.84        90
    weighted avg       0.84      0.84      0.84        90

LASSO Classification Report:
                  precision    recall  f1-score   support

No Heart Disease       0.87      0.76      0.81        51
   Heart Disease       0.73      0.85      0.79        39

        accuracy                           0.80        90
       macro avg       0.80      0.81      0.80        90
```

```
weighted avg       0.81      0.80      0.80         90
```

We will only focus on the two metrices we selected: **accuracy and F1 score**. By comparing them among the 3 classifiers, we have the following findings:

1. The **full logistic regression model** from (11) achieved the highest overall accuracy (0.86) and the highest heart disease F1 score (0.83), suggesting that it has excellent general performances.
2. While the **LASSO** has the lowest accuracy, it is still very acceptable (0.80). It aslo holds the highest recall (0.85) for predicting heart disease, meaning that it is the best model at identifying most of the true positive cases. *(recall's definition can be find in (10))*

Impact of Feature Selection:

With the **LASSO**, we successfully reduced the numbers of features used in the model, keeping it interpretable. While the accuracy number went down a bit because of this simplification in the model, it maintained a very strong recall, which helped improve the model's performance on capturing positive heart disease cases. This is very useful and importnant for medical diagnostics dataset like this.

14)

From (13), we mentioned that while full logistic regression model had slightly higher accuracy and F1 score, the LASSO provided a more simplified and interpetable model by selecting only the most important features. For a medical diagnostics dataset like this, we prioritze the ability to catch more true heart disease cases over the higheset possible accuracy - which is why we value a higher recall. We also prefer the simplier model as the reduction in complexity helps prevent overfitting, improves computitional efficiency that are super essential for decision making. That is, we consider the **LASSO** as the best interprertable model.

```
# from (12), we had:
coeffs = m_lasso.coef_.reshape(-1)
feature_names = X.columns
features_coef = pd.DataFrame({
```

```
    'Feature': feature_names,
    'Coefficient': coeffs
})

# we want to make it in descending order to address the largest coef (most iportant feasure)
important_features = features_coef[features_coef['Coefficient'] != 0].sort_values(by='Coefficie

print("Important features by the LASSO:")
print(important_features)
```

```
Important features by the LASSO:
     Feature  Coefficient
11        ca     1.342414
1        sex     0.893613
3   trestbps     0.636381
12      thal     0.571055
2         cp     0.560257
9    oldpeak     0.491677
8      exang     0.464750
6    restecg     0.314907
4       chol     0.309335
10     slope     0.289350
0        age    -0.054183
7    thalach    -0.458236
5        fbs    -0.666898
```

From the output, we have the following findings:

1. The most important predictor variable found by the LASSO was `ca` (number of major vessels colored by fluoroscopy) since it has the largest positive coefficient. Note that we have standalized the train set, so this is in standardized units rather than the original scale of 0–3. This indicates that the more major vessels showing disease or blockage, the more likely an individual is to have heart disease.

2. There is a positive coefficient to `sex` (1 = male, 0 = female). This tells us that in this dataset, biological males are at a higher risk of heart disease. Note that some studies suggest that males do have a higher risk of severe heart attacks compared to women, but some also say this is a myth (Suman et al., 2023).

3. Another feature with high positive coefficient is `trestbps`, indicating that higher resting blood pressure is associated with a higher risk of heart disease.

4. `thalach` has a strong negative coefficient, meaning that individuals who achieves lower peak heart rates are more likely to have heart disease. This aligns with the clinical research result (Saxena et al., 2013).

5. `age` has a very small negative coefficient, which is surprising since there exist a lot of studies on the how heart disease risk increases with age, regardless of gender. However, this result only reflects that age is not the most dominant factor in this particular dataset.

15) [Bonus]

We are using the sub-groups from KMeans as a feature to improve the logistic regression model. After adding this feature and retraining the model, the classifier showed improved performance compared to the original model. We see that the test set accuracy improved from 0.8556 to 0.9000 and the F1-score also increased for both classes.

```
import warnings
warnings.filterwarnings('ignore')


categorical_columns = ['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'thal']
numerical_columns = [col for col in X.columns if col not in categorical_columns]
X_num = X[numerical_columns]


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


kmeans = KMeans(n_clusters=2, random_state=42)
```

```
clusters = kmeans.fit_predict(X_pca)

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)

X_train_num = X_train[numerical_columns]
X_test_num = X_test[numerical_columns]

X_train_pca = pca.transform(X_train_num)
X_test_pca = pca.transform(X_test_num)

train_clusters = kmeans.predict(X_train_pca).reshape(-1, 1)
test_clusters = kmeans.predict(X_test_pca).reshape(-1, 1)

X_train_num = np.hstack((X_train.values, train_clusters))
X_test_num = np.hstack((X_test.values, test_clusters))

scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train_num)
X_test_scaled = scaler.transform(X_test_num)

log_reg = LogisticRegression(solver='liblinear', max_iter=1000, random_state=42)

param_grid = {
    'penalty': ['l1', 'l2'],
    'C': [0.001, 0.01, 0.1, 1, 10, 100, 1000]
}

grid_search = GridSearchCV(
    estimator=log_reg,
    param_grid=param_grid,
    cv=5,
```

```
    scoring='accuracy',
    n_jobs=-1,
    verbose=1
)
grid_search.fit(X_train_scaled, y_train)

print("Optimal parameters: ", grid_search.best_params_)
print("Cross-validation accuracy: {:.4f}".format(grid_search.best_score_))

best_log_reg = grid_search.best_estimator_
y_pred = best_log_reg.predict(X_test_scaled)
y_pred2 = best_log_reg.predict(X_train_scaled)

accuracy = accuracy_score(y_test, y_pred)
train_accuracy = accuracy_score(y_train, y_pred2)
cm = confusion_matrix(y_test, y_pred)
report = classification_report(y_test, y_pred, target_names=['No Heart Disease', 'Heart Disease

print(f"\nTest set accuracy: {accuracy:.4f}")
print(f"Train set accuracy: {train_accuracy:.4f}")
print("Confusion Matrix:")
print(cm)
print("Classification Report:")
print(report)
```

```
Fitting 5 folds for each of 14 candidates, totalling 70 fits
Optimal parameters:  {'C': 0.01, 'penalty': 'l2'}
Cross-validation accuracy: 0.8211

Test set accuracy: 0.9000
Train set accuracy: 0.8309
Confusion Matrix:
```

```
[[47  2]
 [ 7 34]]
Classification Report:
                  precision    recall  f1-score   support

No Heart Disease       0.87      0.96      0.91        49
   Heart Disease       0.94      0.83      0.88        41

        accuracy                           0.90        90
       macro avg       0.91      0.89      0.90        90
    weighted avg       0.90      0.90      0.90        90
```

Compared to our results in (13), the new logistic regression model achieved the highest overall accuracy (0.90) and F1 score (0.88) among all classifiers. It also showed improvement in precision and maintained a relatively similar recall for heart disease prediction, even though those were not part of our initail metrics. This suggests that the added cluster feature was very helpful in capturing subgroup patterns. Overall, this model has the most well-rounded performance and it is a very smart approach.

16)

Team Contributions:

- JC: Questions 1-6
- Jasmine: Questions 7-11 and 15
- Zhiyan: Questions 12-14 and 15

17)

https://github.com/j-asmineho/STATS_3DA3_A6

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