Assignment1

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1 Assignment 1

1.1 Author Details

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1.2 Importing Libraries

[1]:
```
# Base libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from tabulate import tabulate
from tqdm import tqdm
from pickle import dump

# Preprocessing
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from imblearn.over_sampling import SMOTE

# Models
from sklearn.pipeline import Pipeline
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier

# Evaluation
from sklearn.model_selection import cross_validate
from sklearn.metrics import classification_report, accuracy_score,␣
 ↪precision_score, recall_score, f1_score, roc_auc_score
```

```
# Initializations
%matplotlib inline
sns.set_style('darkgrid')
pd.set_option('display.max_columns', None)
plt.style.use('ggplot')
```

1.3 Data Preprocessing and Exploratory Data Analysis

1.3.1 Loading dataset

[2]:
```
df = pd.read_csv("./heart_disease_prediction/framingham.csv")
```

1.3.2 Sample data

[3]:
```
df.head()
```

[3]:
```
   male  age  education  currentSmoker  cigsPerDay  BPMeds  prevalentStroke  \
0     1   39        4.0              0         0.0     0.0                0
1     0   46        2.0              0         0.0     0.0                0
2     1   48        1.0              1        20.0     0.0                0
3     0   61        3.0              1        30.0     0.0                0
4     0   46        3.0              1        23.0     0.0                0

   prevalentHyp  diabetes  totChol  sysBP  diaBP    BMI  heartRate  glucose  \
0             0         0    195.0  106.0   70.0  26.97       80.0     77.0
1             0         0    250.0  121.0   81.0  28.73       95.0     76.0
2             0         0    245.0  127.5   80.0  25.34       75.0     70.0
3             1         0    225.0  150.0   95.0  28.58       65.0    103.0
4             0         0    285.0  130.0   84.0  23.10       85.0     85.0

   TenYearCHD
0           0
1           0
2           0
3           1
4           0
```

1.3.3 Information about the dataset

[4]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4240 entries, 0 to 4239
Data columns (total 16 columns):
 #   Column           Non-Null Count  Dtype
```

```
---  ------           --------------  -----
 0   male             4240 non-null   int64
 1   age              4240 non-null   int64
 2   education        4135 non-null   float64
 3   currentSmoker    4240 non-null   int64
 4   cigsPerDay       4211 non-null   float64
 5   BPMeds           4187 non-null   float64
 6   prevalentStroke  4240 non-null   int64
 7   prevalentHyp     4240 non-null   int64
 8   diabetes         4240 non-null   int64
 9   totChol          4190 non-null   float64
 10  sysBP            4240 non-null   float64
 11  diaBP            4240 non-null   float64
 12  BMI              4221 non-null   float64
 13  heartRate        4239 non-null   float64
 14  glucose          3852 non-null   float64
 15  TenYearCHD       4240 non-null   int64
dtypes: float64(9), int64(7)
memory usage: 530.1 KB
```

[5]:
```
df.describe()
```

[5]:
```
              male          age    education  currentSmoker   cigsPerDay  \
count  4240.000000  4240.000000  4135.000000    4240.000000  4211.000000
mean      0.429245    49.580189     1.979444       0.494104     9.005937
std       0.495027     8.572942     1.019791       0.500024    11.922462
min       0.000000    32.000000     1.000000       0.000000     0.000000
25%       0.000000    42.000000     1.000000       0.000000     0.000000
50%       0.000000    49.000000     2.000000       0.000000     0.000000
75%       1.000000    56.000000     3.000000       1.000000    20.000000
max       1.000000    70.000000     4.000000       1.000000    70.000000

            BPMeds  prevalentStroke  prevalentHyp     diabetes      totChol  \
count  4187.000000      4240.000000   4240.000000  4240.000000  4190.000000
mean      0.029615         0.005896      0.310613     0.025708   236.699523
std       0.169544         0.076569      0.462799     0.158280    44.591284
min       0.000000         0.000000      0.000000     0.000000   107.000000
25%       0.000000         0.000000      0.000000     0.000000   206.000000
50%       0.000000         0.000000      0.000000     0.000000   234.000000
75%       0.000000         0.000000      1.000000     0.000000   263.000000
max       1.000000         1.000000      1.000000     1.000000   696.000000

             sysBP        diaBP          BMI    heartRate      glucose  \
count  4240.000000  4240.000000  4221.000000  4239.000000  3852.000000
mean    132.354599    82.897759    25.800801    75.878981    81.963655
std      22.033300    11.910394     4.079840    12.025348    23.954335
min      83.500000    48.000000    15.540000    44.000000    40.000000
```

```
25%     117.000000   75.000000   23.070000   68.000000   71.000000
50%     128.000000   82.000000   25.400000   75.000000   78.000000
75%     144.000000   90.000000   28.040000   83.000000   87.000000
max     295.000000  142.500000   56.800000  143.000000  394.000000

         TenYearCHD
count  4240.000000
mean      0.151887
std       0.358953
min       0.000000
25%       0.000000
50%       0.000000
75%       0.000000
max       1.000000
```

1.3.4 Null Values inspection

[6]:
```python
df.isnull().sum()
```

[6]:
```
male                 0
age                  0
education          105
currentSmoker        0
cigsPerDay          29
BPMeds              53
prevalentStroke      0
prevalentHyp         0
diabetes             0
totChol             50
sysBP                0
diaBP                0
BMI                 19
heartRate            1
glucose            388
TenYearCHD           0
dtype: int64
```

Simple solution is to drop the rows with missing values. But this is not a good solution as we might lose some important information. So, we will use imputation to fill in the missing values using the mode of the column for nominal values and mean for continuous values.

[7]:
```python
for col in df.columns:
    df[col].fillna(df[col].mode()[0], inplace=True)
```

[8]:
```python
df.isnull().sum()
```

```
[8]: male                0
     age                 0
     education           0
     currentSmoker       0
     cigsPerDay          0
     BPMeds              0
     prevalentStroke     0
     prevalentHyp        0
     diabetes            0
     totChol             0
     sysBP               0
     diaBP               0
     BMI                 0
     heartRate           0
     glucose             0
     TenYearCHD          0
     dtype: int64
```

1.3.5 Changing the data types

```
[9]: df.dtypes
```

```
[9]: male                  int64
     age                   int64
     education           float64
     currentSmoker         int64
     cigsPerDay          float64
     BPMeds              float64
     prevalentStroke       int64
     prevalentHyp          int64
     diabetes              int64
     totChol             float64
     sysBP               float64
     diaBP               float64
     BMI                 float64
     heartRate           float64
     glucose             float64
     TenYearCHD            int64
     dtype: object
```

These are the specifications according to the dataset description:

```
[10]: nominals = ['male', 'currentSmoker', 'BPMeds', 'prevalentStroke',␣
       ↪'prevalentHyp', 'diabetes', 'TenYearCHD']
      continuous = ['age', 'education', 'cigsPerDay', 'totChol', 'sysBP', 'diaBP',␣
       ↪'BMI', 'heartRate', 'glucose']
```

```
df[nominals] = df[nominals].astype('int64')
df[continuous] = df[continuous].astype('float64')
```

[11]:
```
df.dtypes
```

[11]:
```
male                  int64
age                 float64
education           float64
currentSmoker         int64
cigsPerDay          float64
BPMeds                int64
prevalentStroke       int64
prevalentHyp          int64
diabetes              int64
totChol             float64
sysBP               float64
diaBP               float64
BMI                 float64
heartRate           float64
glucose             float64
TenYearCHD            int64
dtype: object
```

1.3.6 Dividing the dataset into features and target

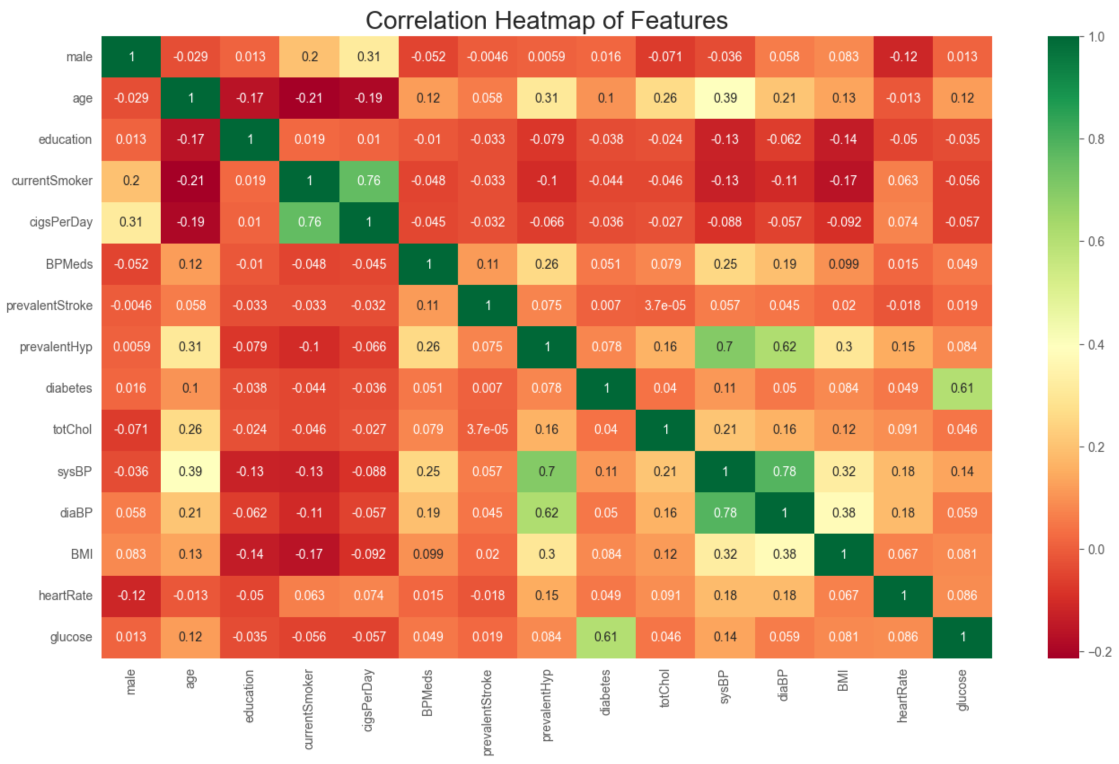
[12]:
```
df_features = df.drop('TenYearCHD', axis=1)
df_target = df['TenYearCHD']
```

1.3.7 Normalizing the data

[13]:
```
scale = StandardScaler()
df_features[continuous] = scale.fit_transform(df_features[continuous])
```

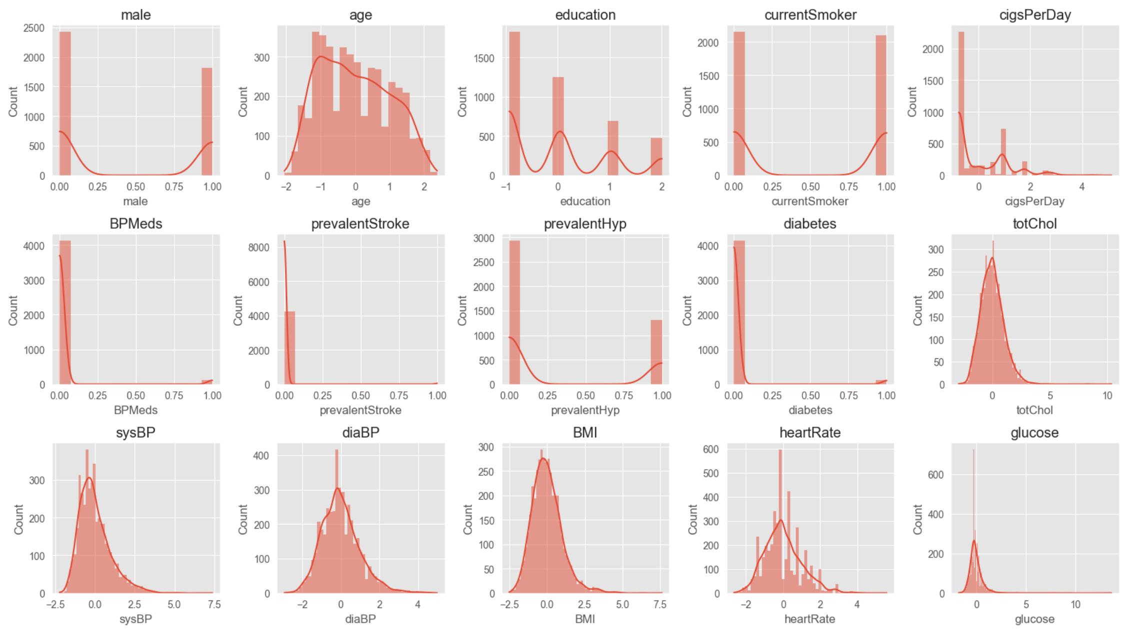
1.3.8 Correlation Heatmap

[14]:
```
plt.figure(figsize=(16, 9))
sns.heatmap(df_features.corr(), annot=True, cmap="RdYlGn")
plt.title("Correlation Heatmap of Features", fontsize=20)
plt.show()
```



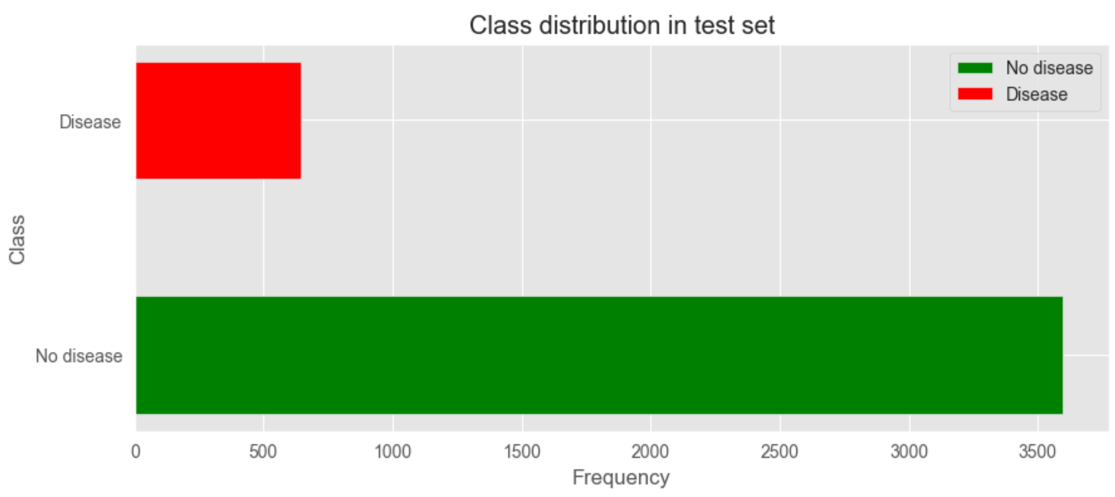
1.3.9 Distribution of individual features

[15]:
```
# Distribution of individual features
plt.figure(figsize=(16, 9))
for i, col in enumerate(df_features.columns):
    plt.subplot(3, 5, i+1)
    sns.histplot(df_features[col], kde=True, linewidth=0)
    plt.title(col)
plt.tight_layout()
plt.show()
```



1.3.10 Class Distribution

[16]:
```python
values = df_target.value_counts()
indices = [k for k in values.index]
plt.figure(figsize=(10,4))
plt.title('Class distribution in test set')
plt.barh(indices, values, color=['green', 'red'], label=['No disease',␣
  ↪'Disease'], height=0.5)
plt.xlabel('Frequency')
plt.ylabel('Class')
plt.yticks(indices, ['No disease', 'Disease'])
plt.legend()
plt.show()
```



1.3.11 Function to load and preprocess the data

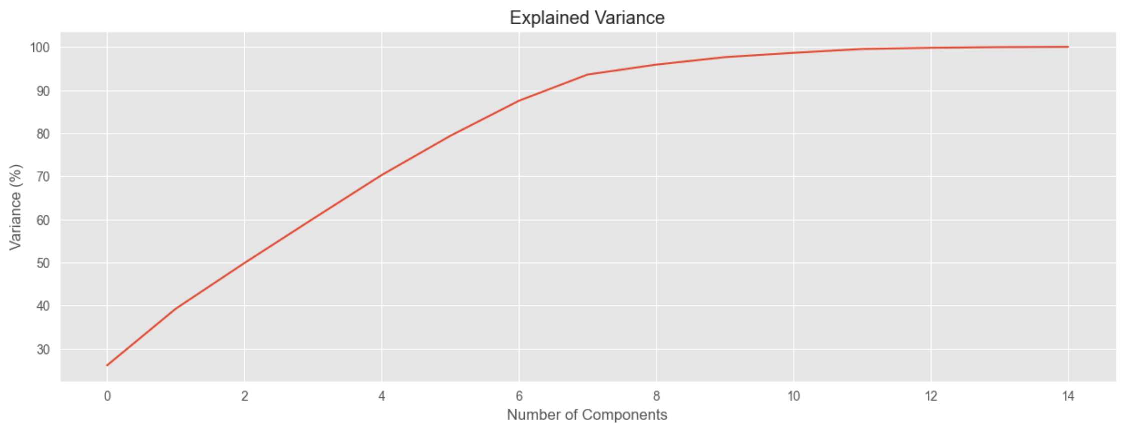
[17]:
```
def load_data():
    df = pd.read_csv("./heart_disease_prediction/framingham.csv")
    nominals = ['male', 'currentSmoker', 'BPMeds', 'prevalentStroke',␣
 ↪'prevalentHyp', 'diabetes', 'TenYearCHD']
    continuous = ['age', 'education', 'cigsPerDay', 'totChol', 'sysBP',␣
 ↪'diaBP', 'BMI', 'heartRate', 'glucose']
    for col in df.columns:
        df[col].fillna(df[col].mode()[0], inplace=True)
    df[nominals] = df[nominals].astype('int64')
    df[continuous] = df[continuous].astype('float64')
    df_features = df.drop('TenYearCHD', axis=1)
    df_target = df['TenYearCHD']
    scale = StandardScaler()
    df_features[continuous] = scale.fit_transform(df_features[continuous])
    return df_features, df_target
```

1.4 Feature Selection and Scaling

[18]:
```
# PCA
pca = PCA()
pca.fit(df_features)
df_pca = pca.transform(df_features)
```

1.4.1 Number of Components vs. Variance Explained

[19]:
```
plt.figure(figsize=(15, 5))
plt.plot(np.cumsum(pca.explained_variance_ratio_)*100)
plt.xlabel('Number of Components')
plt.ylabel('Variance (%)')
plt.title('Explained Variance')
plt.grid(visible=True)
plt.show()
```



1.4.2 Dataset after PCA

As the elbow point is at 7, we will reduce the number of features to 7.

[20]:
```
number_of_components = 7
df_features = pd.DataFrame(df_pca[:, :number_of_components], columns=[f'PC{i}'␣
↪for i in range(1, number_of_components+1)])
df_features.head()
```

[20]:
```
        PC1       PC2       PC3       PC4       PC5       PC6       PC7
0 -1.962665 -0.306698 -1.240161  1.541623  0.783884 -0.377466  0.881480
1  0.125056 -0.014960  0.090382  0.553265  0.502263 -1.724939  0.985375
2 -0.488438  0.799507  0.491221 -1.150302 -0.407634  0.038308  0.087517
3  1.273526  0.929873 -0.106130  0.309940 -0.382192  2.370008 -0.456905
4 -0.397436  1.362755  0.597880  1.248440 -1.026758 -0.033045  0.159698
```

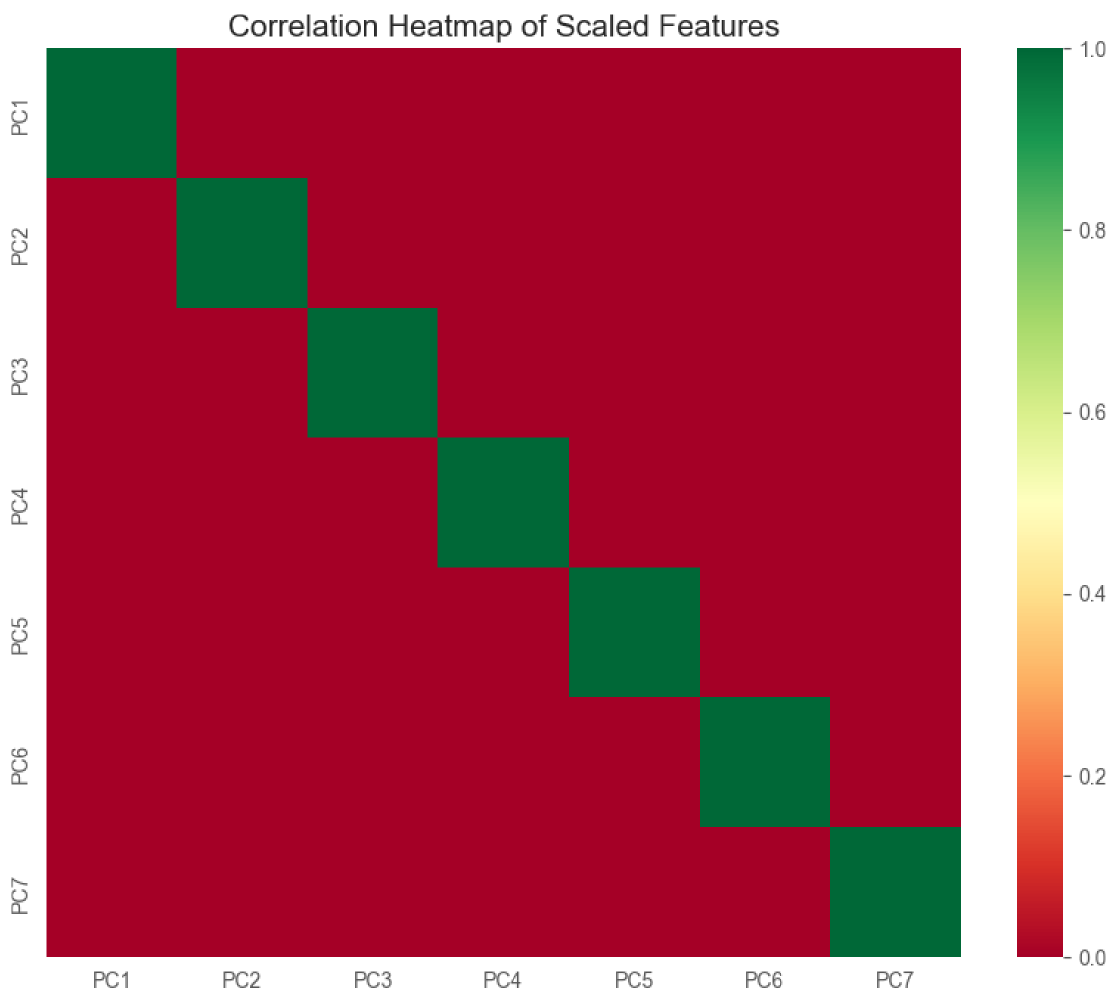
[21]:
```
df_features.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4240 entries, 0 to 4239
Data columns (total 7 columns):
 #   Column  Non-Null Count  Dtype
---  ------  --------------  -----
```

```
 0   PC1     4240 non-null   float64
 1   PC2     4240 non-null   float64
 2   PC3     4240 non-null   float64
 3   PC4     4240 non-null   float64
 4   PC5     4240 non-null   float64
 5   PC6     4240 non-null   float64
 6   PC7     4240 non-null   float64
dtypes: float64(7)
memory usage: 232.0 KB
```

1.4.3 Correlation Heatmap after PCA

[22]:
```
plt.figure(figsize=(10, 8))
sns.heatmap(df_features.corr(), annot=False, cmap="RdYlGn")
plt.title("Correlation Heatmap of Scaled Features", fontsize=15)
plt.show()
```



1.4.4 Function to perform feature selection and scaling

[23]:
```
# We selected number of components as 7, because it explains 92% of the␣
↪variance and is an elbow point in the graph.
def feature_selection(df, number_of_components: int = 7):
    # df is df_features in our case
    pca = PCA()
    pca.fit(df)
    df_pca = pca.transform(df)
    df = pd.DataFrame(df_pca[:, :number_of_components], columns=[f'PC{i}' for i␣
↪in range(1, number_of_components+1)])
    return df
```

1.5 Splitting the data into train and test sets

[24]:
```
X_train, X_test, y_train, y_test = train_test_split(df_features, df_target,␣
↪test_size=0.2, random_state=42)
print("X_train shape:", X_train.shape)
print("X_test shape:", X_test.shape)
print("y_train shape:", y_train.shape)
print("y_test shape:", y_test.shape)
```

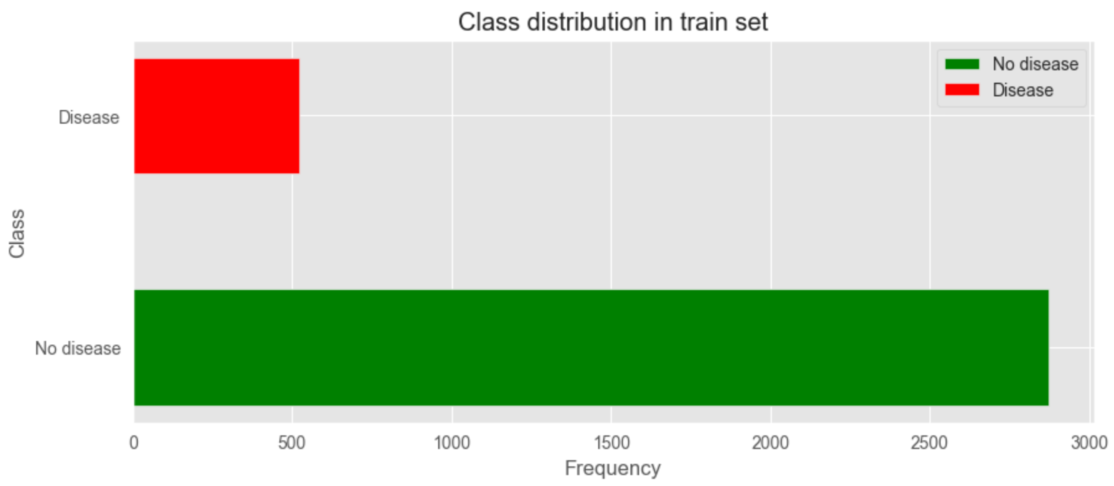
```
X_train shape: (3392, 7)
X_test shape: (848, 7)
y_train shape: (3392,)
y_test shape: (848,)
```

[25]:
```
df_target.value_counts()
```

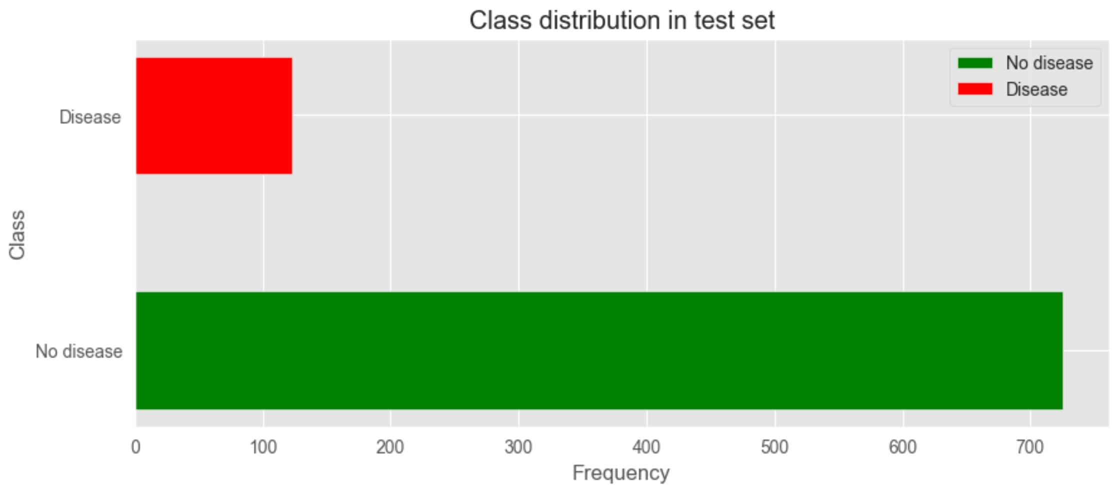
[25]:
```
TenYearCHD
0    3596
1     644
Name: count, dtype: int64
```

1.5.1 Class Distribution

[26]:
```
values = y_train.value_counts()
indices = [k for k in values.index]
plt.figure(figsize=(10,4))
plt.title('Class distribution in train set')
plt.barh(indices, values, color=['green', 'red'], label=['No disease',␣
↪'Disease'], height=0.5)
plt.xlabel('Frequency')
plt.ylabel('Class')
plt.yticks(indices, ['No disease', 'Disease'])
plt.legend()
plt.show()
```



[27]:
```
values = y_test.value_counts()
indices = [k for k in values.index]
plt.figure(figsize=(10,4))
plt.title('Class distribution in test set')
plt.barh(indices, values, color=['green', 'red'], label=['No disease',␣
 ↪'Disease'], height=0.5)
plt.xlabel('Frequency')
plt.ylabel('Class')
plt.yticks(indices, ['No disease', 'Disease'])
plt.legend()
plt.show()
```



1.5.2 Function to split the data into train and test sets

[28]:
```
def split(df_features, df_target, test_size=0.2, random_state=42):
    X_train, X_test, y_train, y_test = train_test_split(df_features, df_target,␣
  ↪test_size=test_size, random_state=random_state)
    return X_train, X_test, y_train, y_test
```

1.6 Resampling

> SMOTE is an oversampling technique where the synthetic samples are generated for the minority class. This algorithm helps to overcome the overfitting problem posed by random oversampling.

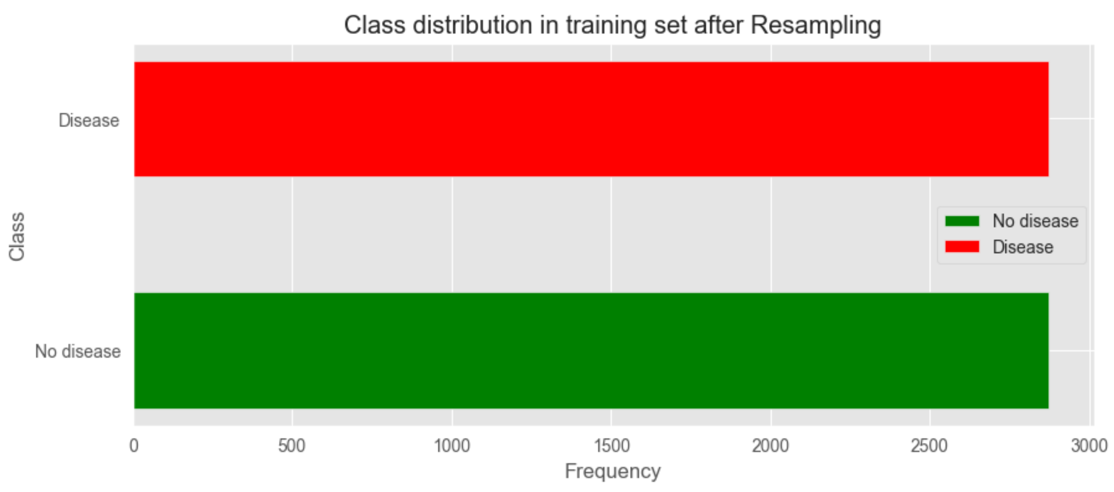
As the dataset is imbalanced, we will use SMOTE to oversample the minority class.

[29]:
```
X_train_smote, y_train_smote = SMOTE().fit_resample(X_train, y_train)
```

[30]:
```
print("X_train_smote shape:", X_train_smote.shape)
print("y_train_smote shape:", y_train_smote.shape)
```

```
X_train_smote shape: (5742, 7)
y_train_smote shape: (5742,)
```

[31]:
```
values = y_train_smote.value_counts()
indices = [k for k in values.index]
plt.figure(figsize=(10, 4))
plt.title('Class distribution in training set after Resampling')
plt.barh(indices, values, color=['green', 'red'], label=['No disease',␣
  ↪'Disease'], height=0.5)
plt.xlabel('Frequency')
plt.ylabel('Class')
plt.yticks(indices, ['No disease', 'Disease'])
plt.legend()
plt.show()
```



1.6.1 Function to perform resampling

[32]:
```python
def resample(X_train, y_train):
    X_train_smote, y_train_smote = SMOTE().fit_resample(X_train, y_train)
    return X_train_smote, y_train_smote
```

1.7 Model Pipelines

[33]:
```python
# Logistic Regression Model Pipeline
logistic_pipeline = Pipeline([
    ('Logistic Regression', LogisticRegression(solver='saga', max_iter=10000))
])

# SVM Model Pipeline
linear_svc_pipeline = Pipeline([
    ('Support Vector Machine', SVC())
])

# Decision Tree Model Pipeline
decision_tree_pipeline = Pipeline([
    ('Decision Tree', DecisionTreeClassifier())
])

# KNN Model Pipeline
knn_pipeline = Pipeline([
    ('K Nearest Neighbors', KNeighborsClassifier())
])
```

```
pipelines = [logistic_pipeline, linear_svc_pipeline, decision_tree_pipeline,␣
 ↪knn_pipeline]
```

1.8 Modelling & Evaluation

[34]:
```
# Train the models with cross validation
def train_model_cv(model_pipeline: Pipeline, X_train, y_train):
    cross_validate_results = cross_validate(model_pipeline, X_train, y_train,␣
 ↪cv=5, scoring=['accuracy', 'precision', 'recall', 'f1', 'roc_auc'],␣
 ↪return_train_score=True)
    return cross_validate_results
```

[35]:
```
results = []
for pipeline in tqdm(pipelines):
    results.append(train_model_cv(pipeline, X_train_smote, y_train_smote))
```

```
100%|      | 4/4 [00:08<00:00,  2.22s/it]
```

1.8.1 Results comparison of different models

[36]:
```
table = []
for i in range(len(pipelines)):
    table.append([
        list(pipelines[i].named_steps.keys())[0],
        results[i]['test_accuracy'].mean(), results[i]['test_precision'].mean(),
        results[i]['test_recall'].mean(), results[i]['test_f1'].mean()
    ])
print(tabulate(table, headers=['Model', 'Accuracy', 'Precision', 'Recall',␣
 ↪'f1-score'], tablefmt='grid'))
```

```
+------------------------+------------+-------------+----------+------------+
| Model                  |   Accuracy |   Precision |   Recall |   f1-score |
+========================+============+=============+==========+============+
| Logistic Regression    |   0.664406 |    0.665482 | 0.660752 |   0.663071 |
+------------------------+------------+-------------+----------+------------+
| Support Vector Machine |   0.706549 |    0.68874  | 0.753751 |   0.719744 |
+------------------------+------------+-------------+----------+------------+
| Decision Tree          |   0.762977 |    0.739813 | 0.812616 |   0.774393 |
+------------------------+------------+-------------+----------+------------+
| K Nearest Neighbors    |   0.811564 |    0.736243 | 0.971438 |   0.837575 |
+------------------------+------------+-------------+----------+------------+
```

1.9 Inferencing

1.9.1 Problem Statement and Dataset Description

Heart disease is a major cause of death worldwide. The main objective of this project is to predict whether a person has heart disease or not based on the given features. The dataset contains 15 features and 1 target variable.

1.9.2 Preprocessing

The dataset is imbalanced. So, we have used SMOTE to oversample the minority class. PCA is used to reduce the number of features to 7. The dataset is then split into train and test sets.

1.9.3 Training

I have used 4 models: Logistic Regression, Support Vector Machine, Decision Tree and K-Nearest Neighbors. The models are trained using 5-fold cross validation with the following results of mean accuracy, precision, recall, f1 score and roc auc score:

Model	Accuracy	Precision	Recall	F1 Score	ROC AUC
Logistic Regression	0.673065	0.672859	0.673684	0.673227	0.728765
Support Vector Machine	0.70418	0.689422	0.743344	0.715261	0.771742
Decision Tree	0.763003	0.74574	0.799071	0.771323	0.763003
K Nearest Neighbors	0.811765	0.735244	0.974923	0.838154	0.917557

1.9.4 Strengths and weaknesses of the models

Logistic Regression:

- **Strengths:**
  - **Balanced Performance:** Logistic regression shows a relatively balanced performance across accuracy, precision, recall, and F1 score.
  - **Interpretability:** Coefficients of logistic regression provide insights into the importance of features.
- **Weaknesses:**
  - **Limited Predictive Power:** The model may not capture complex non-linear relationships effectively, reflected in slightly lower performance compared to other models.

Support Vector Machine (SVM):

- **Strengths:**
  - **High Recall:** SVM shows high recall, indicating its effectiveness in identifying true positives (patients with heart disease) accurately.
  - **Non-Linear Decision Boundary:** SVM effectively models non-linear relationships.
- **Weaknesses:**
  - **Complexity and Computation:** SVM tends to be computationally intensive, especially as the dataset size grows.
  - **Sensitivity to Hyperparameters:** Performance is sensitive to kernel choice and hyperparameter tuning.

Decision Tree:

- **Strengths:**
  - **High Recall:** Decision trees demonstrate a high recall, indicating effective identification of individuals with heart disease.
  - **Interpretability:** Easy to interpret and explain due to its hierarchical structure.
- **Weaknesses:**
  - **Overfitting:** Prone to overfitting, as reflected in the difference in performance between training and testing data.

K Nearest Neighbors (KNN):

- **Strengths:**
  - **High Recall:** KNN shows very high recall, suggesting it effectively identifies individuals with heart disease, minimizing false negatives.
  - **Non-Parametric and Lazy Learning:** KNN is non-parametric and adapts to any new data without retraining.
- **Weaknesses:**
  - **Computationally Intensive:** The model is computationally intensive, especially as the dataset size increases.
  - **Sensitivity to Distance Metric:** Performance can vary based on the choice of distance metric.

Overall Comparison:

- Decision Tree performs well, striking a balance between recall and precision. It is also interpretable, aiding understanding.
- Logistic Regression offers a good balance across metrics but may lack the predictive power compared to more complex models.
- SVM performs well, particularly in recall, but requires careful parameter tuning due to sensitivity.
- In this context, KNN stands out with very high recall, crucial for identifying individuals at risk of heart disease. However, it sacrifices precision, leading to a lower F1 score.

1.9.5 Best Model

The best model is K-Nearest Neighbors with an accuracy of 81.12% and roc auc score (efficiency) of 91.76%. For the purpose of detecting heart disease, we would want to minimize the false negatives, i.e., the number of people who have heart disease but are predicted to not have heart disease as it is more dangerous. So, we will choose the model with the highest recall, which is, again, K-Nearest Neighbors.

1.10 Apply Model

1.10.1 Loading and preprocessing the data

[37]:
```
df_features, df_target = load_data()
df_features = feature_selection(df_features)
X_train, X_test, y_train, y_test = split(df_features, df_target)
X_train, y_train = resample(X_train, y_train)
```

1.10.2 Training K-Nearest Neighbors model

[38]:
```
model = KNeighborsClassifier()
```

[39]:
```
history = model.fit(X_train, y_train)
```

1.10.3 Predicting and Evaluating the model on the test set

[40]:
```
y_pred = model.predict(X_test)
```

[41]:
```
print(classification_report(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       0.89      0.68      0.77       725
           1       0.21      0.49      0.29       123

    accuracy                           0.65       848
   macro avg       0.55      0.58      0.53       848
weighted avg       0.79      0.65      0.70       848
```

[42]:
```
print(f"Accuracy: {accuracy_score(y_test, y_pred)*100:.2f}%")
print(f"Precision: {precision_score(y_test, y_pred)*100:.2f}%")
print(f"Recall: {recall_score(y_test, y_pred)*100:.2f}%")
print(f"F1 Score: {f1_score(y_test, y_pred):.6f}")
print(f"ROC AUC Score: {roc_auc_score(y_test, y_pred):.6f}")
```

```
Accuracy: 65.21%
Precision: 20.55%
Recall: 48.78%
F1 Score: 0.289157
ROC AUC Score: 0.583902
```

1.11 Saving the model

[43]:
```
dump(model, open('model.pkl', 'wb'))
```